Ponemah Analysis Modules

USER MANUAL

Publication MU00231 Rev #60

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Welcome

Congratulations on joining the community of users worldwide who rely on DSI products to perform preclinical physiologic research. Thank you for your interest in DSI products. We are committed to providing you with quality products and services.

This manual will help you get to know the analysis modules for the Ponemah Software. It covers the common functionality between all analysis modules. The functionality that is similar between analysis modules will not be discussed in detail in the individual analysis sections unless there is a change from the normal operation of the setup dialog.

Application Overview

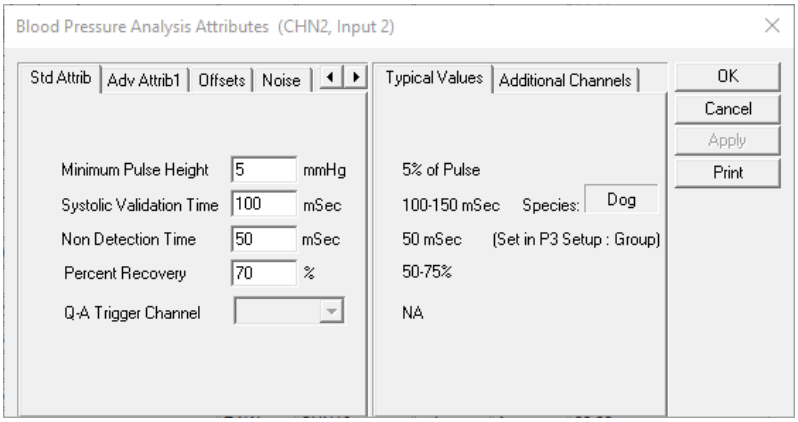
Analysis Attribute Dialogs

All analysis modules have a common setup dialog with specific attributes for the type of analysis being set up.

The attributes dialog can be accessed during setup without the waveform window being displayed. The attributes dialog can also be accessed during acquisition or replay, and the waveform window will be displayed with the most current waveform data. To view the attributes dialog in Idle mode, select the Attributes for that Input.

Please refer to the Review manual for details on the effects of each attribute type.

Displayed below is a typical Blood Pressure Attributes dialog.



Blood Pressure Standard Attributes Tab

The attributes dialog is organized as a tabbed dialog and will always have the following selections:

- **Std Attrib** are the standard attributes that are the most common attributes that would need to be changed during acquisition or replay for the specific analysis module.
- **Adv Attrib1** are advanced attributes that normally do not need to be changed during the acquisition or replay mode. The attributes in this tab require greater knowledge and understanding of how these attributes affect the analysis module.
- **Adv Attrib2 or other named Tabs not listed below** are attributes that are on a few specific analysis modules. This tab requires a great understanding of how the attributes affect the analysis module.

- **Marks** allow the turning on and off of individual validation marks and the cycle count. This helps un-clutter the validation marks on the signal if certain validation marks are not needed. The marks are turned on and off by the on-line menu **Functions** - **Validate F10**.
- **Notes** allow a user to select a predefined note or enter a free form text note for the attribute change.
- **Precision** allows the user to specify how the derived parameters are going to be reported.
- **Typical Values** displays recommended values for a particular set of criteria. This tab will be updated according to which tab on the left has been selected. The values are for reference only, and the values in this tab have no effect on the analysis.
- **Additional Channels** will display all Inputs that have the same type of analysis that the attributes can be applied to. Select all channels that would need the attributes assigned to them and select **Apply** or **OK** to apply the attributes.

NOTE: Changes are not applied to attributes that require the selection of a dependent channel for calculating data when using the Additional Channels feature. This is done to ensure that the sample rates don't vary between both channels to ensure proper calculation of parameter data. Examples would be Blood Pressure's Q-A Trigger Channel or Upstream Channel.

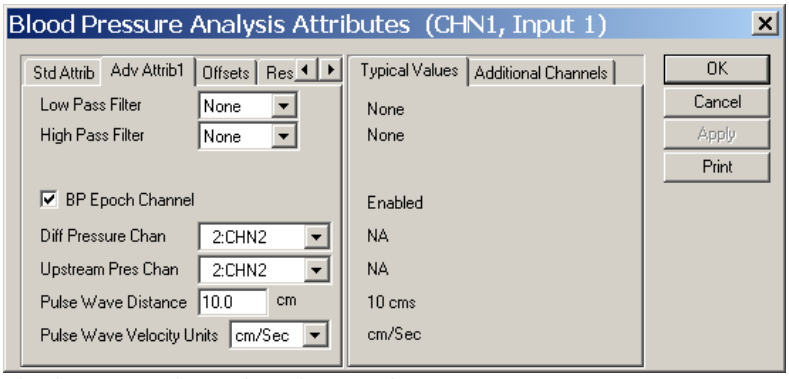
Standard Attributes

This tab in the Attributes dialog allows the user to set the most common attributes for the signal analysis. This tab will have the attributes that are specific to the type of analysis being done. ***For most users, this will be the only area in which changes to the analysis attributes will be needed.***

Advanced Attributes

This tab in the dialog has analysis attributes that are not normally changed. Common to all analysis modules will be Low Pass Filter selection and High Pass Filter selection. All other attributes in this dialog box are specific to the analysis module and normally do not need adjustment.

Displayed below is a typical **Blood Pressure Advanced Attribute 1** dialog:



Blood Pressure Advanced Attribute 1 Tab

Common to all analysis attributes will be:

- **Low Pass Filter** allows the selection of the filter in hertz that attenuates any frequencies higher than the frequency selected. This list box will display the available frequencies for the specific sample rate for the channel. Any filtering applied to the input only affects the data going through the system, and only the unfiltered data will be saved in the raw data file. None will disable the filter.
- **High Pass Filter** allows the selection of the filter in hertz that attenuates any frequency lower than the frequency selected (for example, 3Hz simulates A/C coupling). This list box will display the available frequencies for the specific sample rate for the channel. Any filtering applied to the input only affects the

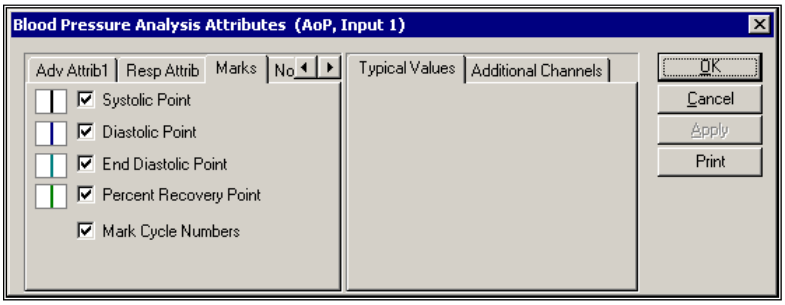
data going through the system, and only the unfiltered data will be saved in the raw data file. None will disable the filter.

Marks

This tab in the dialog allows enabling or disabling validation marks for the analysis. This is useful if there are many marks close together and only a few validation marks are of importance.

To enable or disable the validation marks during acquisition or replay, the user would toggle the **Functions - Validate F10** menu selection.

Displayed below is a typical **Blood Pressure Marks** tab.



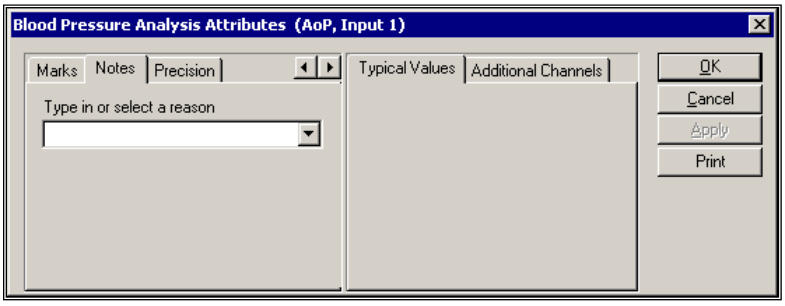
Blood Pressure Marks Tab

Each validation mark that is available for the analysis has the validation mark color displayed next to a check box with a description. When the check box is checked, the mark is enabled.

For the **Mark Cycle Numbers**, this will display a cycle count of the waveform on the graph screen. This number is the same as the derived parameter **Num**. This will assist in locating cycles from the raw data set to the derived data set.

Notes

This tab allows the user to enter a note for the change that has occurred. This is used in conjunction with the Audit Reason Codes (21 CFR Part 11 compliance).

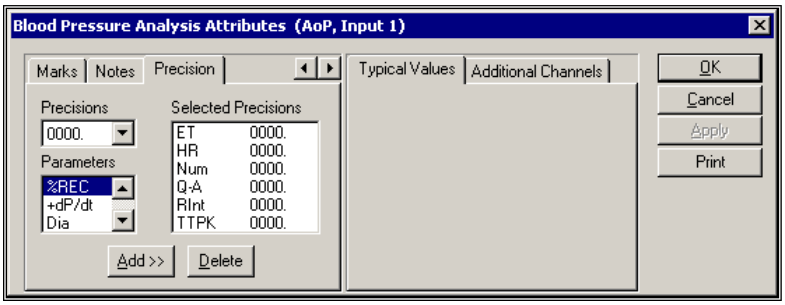


Blood Pressure Notes Tab

The user can either select one of the predefined reasons or enter a text message. This entry is then inserted into the experimental log file along with the user who made the change and the time that the note was entered.

Precision

This tab allows the user to define the precision at which all derived parameters will be reported.



Blood Pressure Precision Tab

This tab will display the associated derived parameter along with its precision.

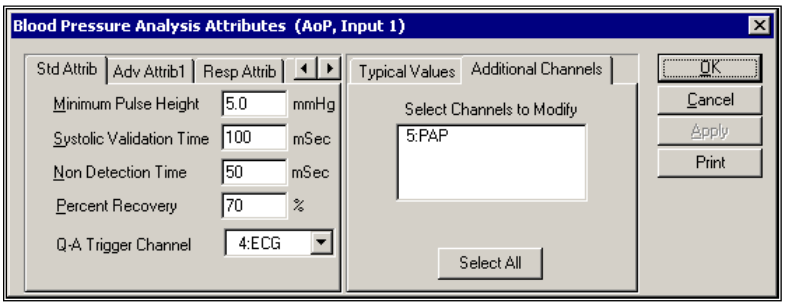
Typical Values

The Typical Values tab of the attributes window is only a reference tool. Anything selected here will not affect or change anything. Likewise, anything done elsewhere in the window will not affect the typical values section.

Additional Channels

This displays all channels that are using the same type of analysis.

Select all channels that will use the same attribute settings as this channel. Then select the OK or Apply button. This automatically sets the attributes in the selected channels.



Typical Additional Channels Tab

In the above dialog, channel 5 also has the Blood Pressure Analysis Module assigned to it. By highlighting 5:PAP in Select Channels to Modify, the attributes used for the current channel will also be applied to that channel.

NOTE: Changes are not applied to attributes that require the selection of a dependent channel for calculating data when using the Additional Channels feature. This is done to ensure that the sample rates don't vary between both channels to ensure proper calculation of parameter data. Examples would be Blood Pressure's Q-A Trigger Channel or Upstream Channel.

Channel Attributes

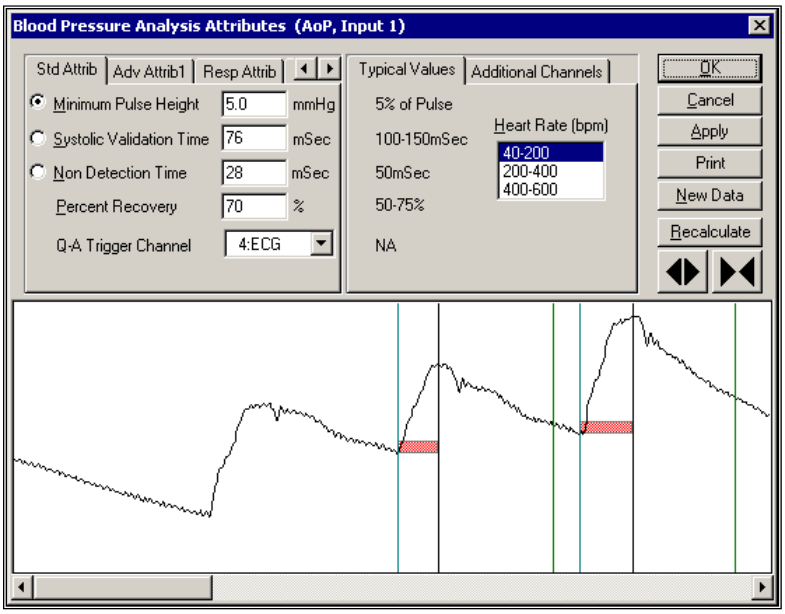
The analysis setup dialog can be selected during acquisition or replay from the Status window. When the attributes dialog is selected in this mode, a waveform window will appear and allow the attributes to be changed graphically.

The dialog will display all attributes that can be changed during acquisition or replay. The attributes that have a radio button next to them are the attributes that can be changed graphically. When a radio button is pressed, a red attribute box will be displayed on the area of the signal that is affected by the attribute change. Placing the cursor in the red attribute box area causes the pointer to change. Pressing and holding the left mouse button

while moving the cursor will change the attribute. When the mouse button is released, the selected attribute value will be updated in the dialog.

The new attribute value is not applied until the Apply or OK button has been pressed. At the time that the button has been pressed, the .LOG file is updated with the old attribute value, the new attribute value, the channel that the change occurred on, and a time stamp of the change.

Displayed below is a typical Blood Pressure dialog with the waveform window:



Attribute Dialog with Waveform Window

Waveform Window

The waveform window contains a segment of the signal data with validation marks if the analysis is triggering correctly. No waveform window will be displayed if there are not enough points to display the signal.
There are two ways to change the attributes in this dialog:

1. Edit the value in the attribute window.
2. Resize the red attribute box in the waveform window. For example, to change Minimum Pulse Height on the graphics window, follow the steps outlined below.
    a. Select the Minimum Pulse Height radio button in the attributes window if not already selected.
    b. Resize the red attribute box using one of the following methods:
    c. Move the cursor into the red attributes box and press the left mouse button. The cursor will jump to the top edge of the attribute box and it will change to a double arrow. Keep holding the left mouse button while moving the cursor to the desired location. Release the mouse button and the Minimum Pulse Height value will update.
    d. Move the cursor to the top of the red attributes box and the cursor will change to a double arrow. Press the left mouse button and hold down while moving the cursor to the desired location. Release the mouse button and the Minimum Pulse Height value will update.

If an attribute is not within the visible waveform window, or the attribute is set so that the analysis is not triggering, the red attributes box associated with that attribute will be set to the far left, far right, or at the zero line of the signal in the waveform window depending on which type of attribute is selected. The first and last waveform in the window may not be completely analyzed because the analysis may require the previous or next waveform to calculate marks.

The waveform window buttons on the right have the following functions:

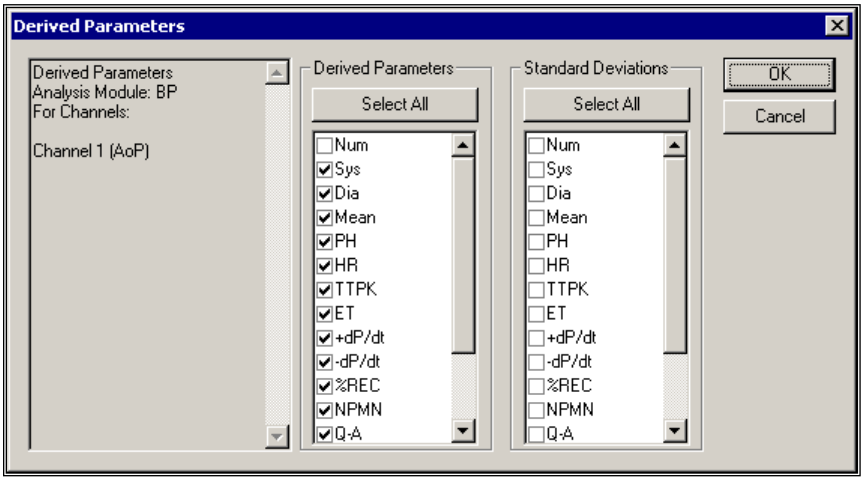
Button	Description
OK	Causes changes to be applied immediately to the analysis, and closes the attributes window. Also updates the .LOG file with the change and the time the change was made.
Apply	Causes changes to be applied immediately to the analysis. The attributes window stays open. Also updates the .LOG file with the change and the time the change was made.
Print	This prints the dialog to the default printer.
New Data	This will get the latest data and display the data in the waveform window. This is useful for verifying attribute changes on the data currently going through the system.
Recalculate	Causes changes to be made **only** to the waveforms displayed in the attributes window, **not** to the analysis. This is after a change to an attribute.
	Increases or decreases the number of logging points the graphics screen contains.

Derived Parameters

Most analysis modules have derived parameters that can be enabled or disabled through the P3 Setup menu selection under the Setup menu. Once the P3 Setup dialog is opened, right click on the analysis module and select Derived Parameters.

The Derived Parameters dialog has a check box for each derived parameter that has an Input with an analysis assigned to it.

Displayed below is a typical Derived Parameters dialog:



Derived Parameters Dialog

The user can enable or disable all derived parameters for a specific **Input** by clicking on the **Select All** button. This will toggle all check marks each time the mouse is double-clicked. The standard deviation derived parameters are calculated as being the entire population.

NOTE: Due to file structures, the derived parameters can only be turned on or off during the setup mode and not Please refer to the Review manual for details on each averaging method.

Analysis Modules

RAW, BARO, TEMP and ACT

The RAW Electrical Mean analysis is designed to record and measure any signal that does not have a specific signal analysis. This includes signals that are generated from any instrumentation supplying an analog output. Such instruments include temperature probes, blood gas analyzers, and scales. Three additional modules are available and are identical in function to the RAW analysis. These modules include Barometric (BARO), Temperature (TEMP) and Activity (ACT). The primary reason for distinct names is to ease setup. This allows the user to easily identify a specific RAW channel based on function. Otherwise, the modules are identical except where noted.

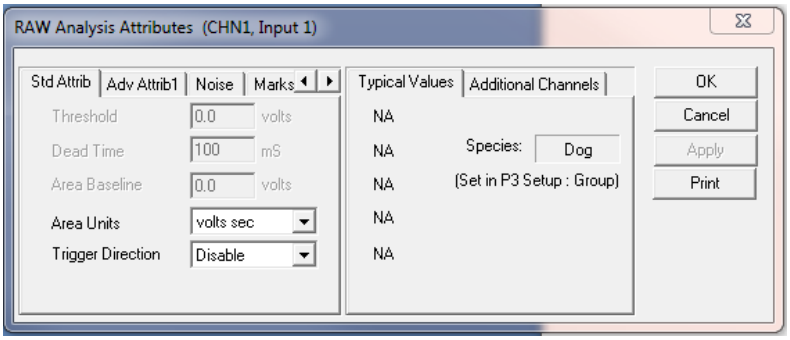
Every P3 Plus system has this analysis available.

The Attributes and Derived Parameters dialogs are accessed through the **Channel Input Setup** configuration of the **PPP3 Setup** dialog, and are described below:

Attribute Window

The RAW Electrical Mean Attributes menu allows the User to modify the signal analysis for different types of signals and different signal conditions.

Standard Attributes



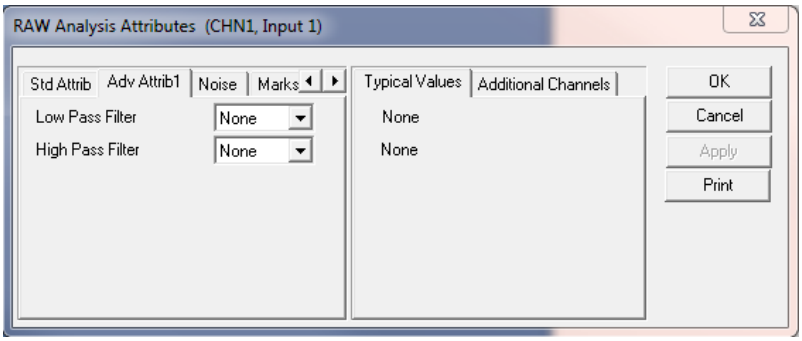
RAW Electrical Mean Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Threshold	Signal Interpretation	Specifies the threshold that the incoming signal must cross before the analysis will trigger and track the maximum and minimum value from the previous threshold level. The signal must go above and below this level before the derived parameters **Rmax**, **Rmin**, **Period**, **BPM**, and **Area** are updated. The **Threshold Level** does not function if the **Trigger Direction** is disabled.
Dead Time	Signal Interpretation	This is the amount of time that the analysis does not look for a threshold once the analysis module has been triggered. The **Dead Time** does not function if the **Trigger Direction** is disabled.
Area Baseline	Calculation	This is the reference line in which area is calculated to. The **Area Baseline** does not function if the **Trigger Direction** is disabled.
Area Units	Calculation	This selects the units that the **area** is reported in. The choices are: • **msec** - for units * milliseconds • **sec** - for units * seconds • **min** - for units * minutes • **hr** – for units * hours
Trigger Direction	Signal Interpretation	Specifies the direction of the slope for which the analysis will track **Rmax**, **Rmin**, **Period**, and **BPM**. If **Trigger Direction** is disabled, these derived parameters will contain 0, which is invalid data. The **Mean** derived parameter will produce a mean for the entire Logging Period. Valid choices are: • **Disable** disables the **Trigger Direction.** A RAW cycle will be generated every second, permitting all derived parameters to be reported. • **Rising** specifies that the slope must be going in the positive direction when the **Threshold Level** is met. • **Falling** specifies that the slope must be going in the negative direction when the **Threshold Level** is met.

Advanced Attributes

This tab contains functions that normally do not need to be changed during the acquisition or replay process.



Advanced Attributes 1 Tab

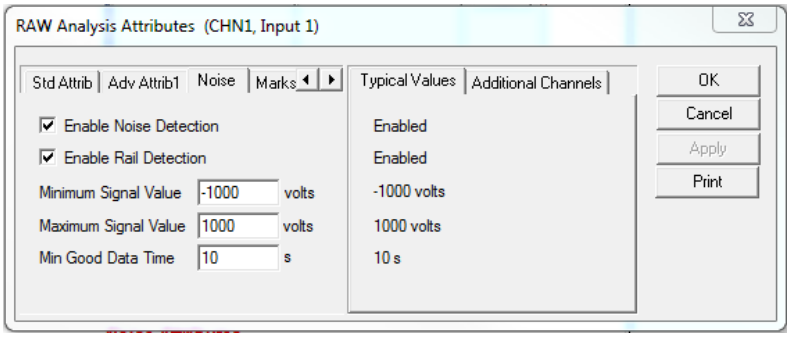
Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	This selects a Low Pass Filter frequency in Hertz. This filter attenuates frequencies higher than the selected value.
High Pass Filter	Signal Conditioning, Calculation, Redraw	This selects a High Pass Filter frequency in Hertz. This type of filter removes a DC component from the input signal.

Typical Values

The typical values cannot be specified here. They are specific to the application.

Noise Attributes

Enable Noise Detection attribute enables/disables all controls in the Noise Tab.



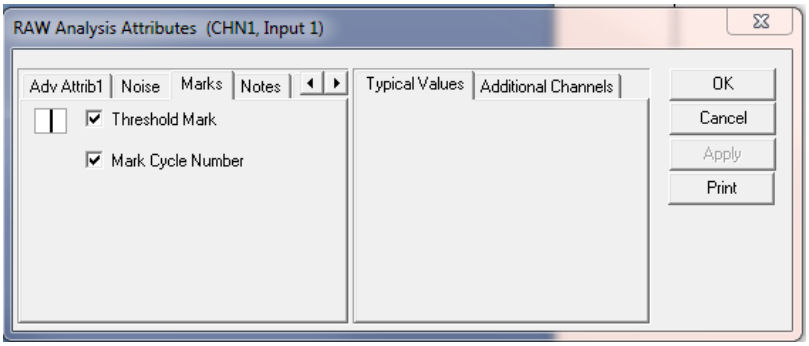
Attribute	Description
Enable Noise Detection	Determines if noise detection will be used to determine bad data marks
Enable Rail Detection	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.

Attribute	Description
Minimum Signal Value/ Maximum Signal Value	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.
Minimum Good Data Time	When Noise detection is enabled and a range of data is analyzed, any bad data marks that have less than or equal to the Min Good Data Time of good data between them shall be combined into a single bad data region.

Marks (Validation)

The Marks dialog allows turning on and off the validation marks for threshold and the cycle numbers that are placed on the signal during processing. This also allows the turning off and on of the cycle number that is placed on a graph page.

Displayed below is the Raw Electrical Mean **Marks** tab:



Marks Tab

Selecting **Validate** from the Functions menu causes the validation marks to display on primary graphs.

The validation mark and its meaning is listed below:

Color	Meaning
Black	Threshold Mark

Derived Parameters

The derived parameters selected in this dialog will be calculated and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Displayed below is the **Derived Parameters** section for the Raw Electrical Mean analysis module.

The output is identical for all modules with the exception of the names for the derived parameters. Derived parameters will be preceded by the first letter of the module. For example, the Mean derived parameter for a BARO channel will be B_Mean. The only exception will be Period which will be abbreviated to Per due to a character limit (example, B_Per).

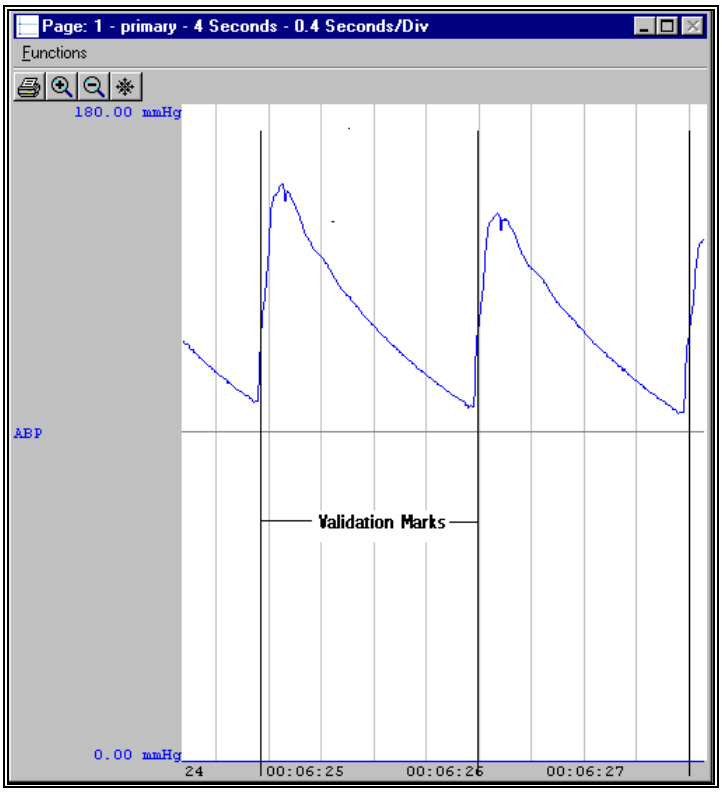
Name	Averaging In Review	Definition
Num	Recent	NUM is the number assigned to the cycle when using a Threshold. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Mean	Mean	MEAN is the sum of all the A/D samples that occurred for a cycle divided by the number of those samples.
Rmax	Mean	The maximum value that occurred within a cycle.
Rmin	Mean	The minimum value that occurred within a cycle.
Per (Period)	Mean	The Period is the amount of time (in milliseconds) between validation marks
BPM	Harmonic Mean	Beats per minute is computed in cycles per minute and is the reciprocal of the time interval for the cycle multiplied by 60. BPM = (1/period)* 60
Area	Mean	Area is calculated over a cycle between the signal and the Area Baseline. The Area is reported in the selected Area Units.
TA	The portion of the signal that lies within the logging interval is averaged	Total Activity parameter integrates the input over the entire logging period.
NPMN		NPMN averages the input over the entire logging period.

Calibration

A typical calibration cannot be given here. The calibration is application specific and depends on the instrumentation being used.

On-line Screens and Functions

The following is an example of a Primary graph displaying the raw analog format of the input signal.



RAW Electrical Mean Validation Marks

In the above figure, the input signal is displayed with the validation tick marks and their meanings. The validation marks identify where the threshold criteria is met.

Presentation Signals

Below is a list of presentation signals that are available for the RAW Analysis Module:

Signal	Description
Input	This is the input signal (after applying any software filters).
Derivative	This will display the derivative of the signal.
Activity	This is the instantaneous value of the TA parameter.

Data Review

The Data Review related features of the Raw Electrical Mean Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.20 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

The Threshold mark is the only mark supported by RAW,BARO, TEMP, and ACT and defines a RAW cycle.

Inserting Marks

A Threshold mark may be inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert a RAW cycle.

Insert RAW Cycle

Inserts a RAW cycle. When a RAW cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu.

Moving Marks

Moving the Threshold mark follows the standard rules used in Data Review.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

Logging Mark

The logging mark for a RAW cycle is the Threshold Mark. The time at the logging mark is the time used to report a cycle's derived data. If a RAW cycle's logging mark falls within a logging interval, the RAW cycle's data will be included in the logging interval.

End of Cycle

The start of a RAW cycle is at the point after the previous Threshold mark. The end of a RAW cycle occurs one nano second after the Threshold mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Rmax, Rmin, Period, BPM, and/or Area not responding (all zeroes or incorrect values).	The **Threshold Level** is not properly set. The input signal must go above and below the **Threshold Level** in order to report the **Rmax**, **Rmin**, **Period**, and **BPM** values. If the input signal is a DC level, the User must disable **the Trigger Direction**, and disable the **Rmax**, **Rmin**, **Period**, and **BPM** derived parameters.
"x" in .DER or .DRx list view instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed. **NOTE: The "x" will be replaced with 9.9999e+15 in the ODBC connection. This value represents invalid data.**

Blood Pressure/Pulmonary Artery Pressure (BP/PAP)

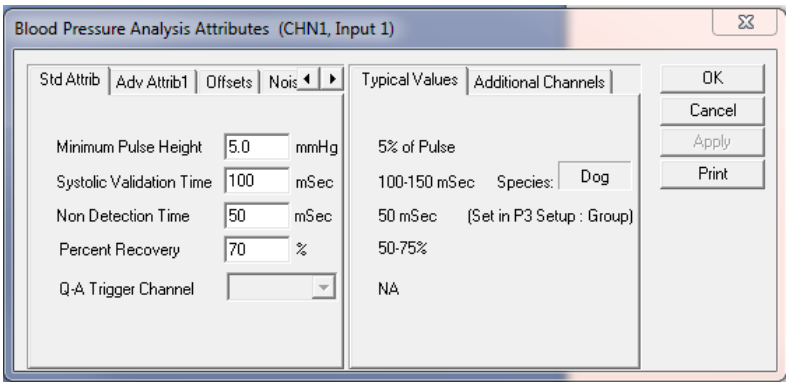
The Blood Pressure analysis can analyze any pressure from the circulatory system and can derive, on a beat-to-beat basis, values for the cardiac cycle.

NOTE: Even though the Blood Pressure Analysis Module can be used on a Left Ventricular Pressure, it is highly recommended that the Left Ventricular Pressure Analysis Module be used when analyzing left ventricular pressure from the heart. This will assure that the pressure is analyzed correctly due to the different waveform morphology.

Attribute Window

The Blood Pressure attributes window allows you to modify the signal analysis for different types of blood pressure signals and signal conditions. If an analysis change in the **Attributes** dialog is performed mid-cycle, then the attribute change will not take effect until the following cycle.

Standard Attributes



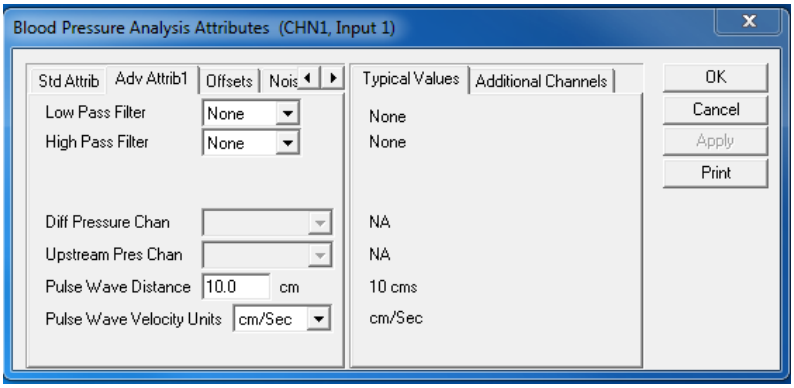
Blood Pressure Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect on Review	Description
Minimum Pulse Height	Signal Interpretation	Sets the minimum developed pressure that must be achieved before the analysis will detect and validate a cardiac cycle. The **Minimum Pulse Height** is useful for preventing the analysis from triggering on artifacts.
Systolic Validation Time	Signal Interpretation	Specifies the period, in milliseconds, a valid peak must be held before the cardiac cycle is terminated. This value helps the system determine the correct systolic pressure.
Non Detection Time	Signal Interpretation	Specifies the period, in milliseconds, of ***dead time*** that the analysis does not look for a pulse pressure. This is used to move the peak analysis past the dicrotic notch.
Percent Recovery	Calculation, Redraw	Defines a **Percent Recovery Point** from the developed pulse pressure. The **%REC** derived parameter reports the amount of time it takes to reach this pressure.

Attribute	Effect on Review	Description
Q-A Trigger Channel	Calculation	Permits the selection of an ECG channel for the calculation of the Q-A Interval. If no ECG channels are set up, this control is disabled. ECG channels must be set up prior to using this attribute.

Advanced Attributes



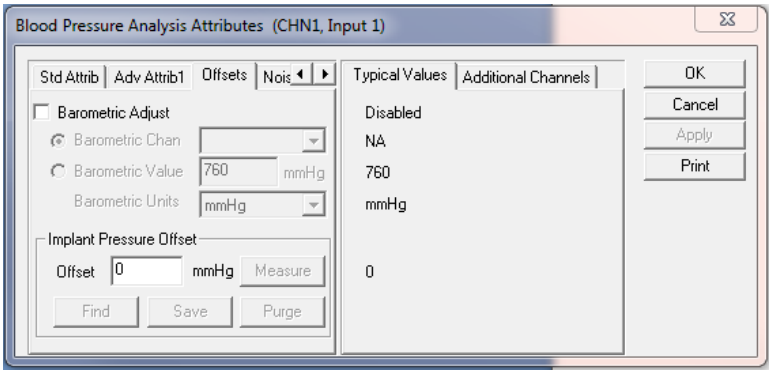
Blood Pressure Advanced Attribute Tab

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
BP Epoch Channel	None	When the **Respiration from Blood Pressure** option has been installed, the Blood Pressure channel can update the logging buffer when in beat mode either by the cardiac cycle (check box enabled) or by respiratory cycle (check box disabled).
Diff Pressure Chan	Signal Conditioning, Calculation, Redraw	This list box allows the selection of a channel that can be used to subtract another channel from the input. The only effect that this has is for display. To display the difference, the **Presentation** field in a **Primary** graph must be set to **Diff**.
Upstream Pres Chan	Calculation	Sets the upstream pressure channel for calculating Pulse Wave Velocity. This drop down list will display all BP channels within a single group that are sampled at the same sampling rate.

Attribute	Effect On Review	Description
Pulse Wave Distance	Calculation	User defined distance (in cm) used in the calculation of Pulse Wave Velocity. The default setting is 10cm.
Pulse Wave Velocity Units	Calculation	The units for the Pulse Wave Velocity (PWV) derived parameter are user selectable and can be specified as cm/Sec or m/Sec.

Offsets



Offsets Tab

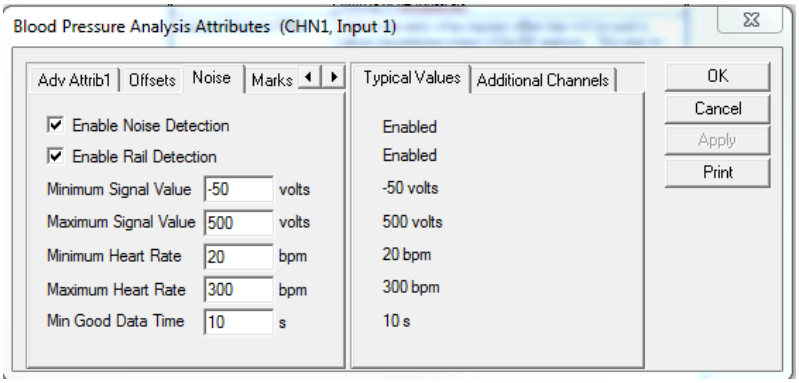
The Offsets tab allows the designation of barometric channels, barometric values and implant offset values to be used for compensating pressures from the BP analysis.

Attribute	Effect On Review	Description
Barometric Adjust	Signal Conditioning, Calculation, Redraw	This check box enables the correction for barometric pressure. This is used for certain telemetry systems that do not compensate for barometric pressure internally. The correction factor is applied by using a RAW channel as the input. The pressure offset is in kilopascals. ***NOTE: If the system is being used with the OpenART or Digital acquisition engines, do not check this box. If the system is being used with the JET acquisition engine, check the box and choose the channel associated with the eAPR-1 as the Barometric Channel. Refer to the JET manual (MU00257) for additional information regarding Barometric channel setup and pressure offsets when using the Jacketed External Telemetry system (JET).***
Barometric Chan	Signal Conditioning, Calculation	This list box will display the available RAW inputs that could be used for the offset adjustment and is only used when the **Barometric Adjust** check box is enabled.
Barometric Value	Signal Conditioning, Calculation	User defined value that can be used to account for pressure offset when not continuously monitoring barometric pressure using the eAPR-1.

Attribute	Effect On Review	Description
Barometric Units	Signal Conditioning, Calculation	User selectable units for barometric pressure. Can define mmHg or hectopascals.
Implant Pressure Offset	Signal Conditioning, Calculation	Allows the entry of an implant offset that will be used to adjust the pressure output of the BP analysis. This may be manually typed in by the user or physically measured by selecting the Measure button. Performing an acquisition will allow the user to Measure the pressure offset from the implant. Find, Save and Purge are used in conjunction with the JET interface and will be disabled if any other acquisition interface is selected. The pressure offset may be saved in the protocol file upon selecting the Save button. This pressure value is stored in the PressureCalibration.ini file. The Find button allows the user to recall the value stored for a specific transmitter and Purge allows the user to remove this offset form the ini file. This feature is also disabled in review mode.

*Refer to the JET manual (MU00257) for additional information regarding Barometric channel setup and pressure offsets when using the Jacketed External Telemetry system (JET).

Noise



Noise Tab

This tab is used to exclude data from analysis which is determined to be noise by the end user.

Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Enables the Noise Detection attributes

Attribute	Effect On Review	Description
Enable Rail Detection	Signal Interpretation	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value	Signal Interpretation	User defined threshold for determining the minimum value for acceptable data. Data that falls below this threshold will be considered noise and bracketed by Bad Data Marks.
Maximum Signal Value	Signal Interpretation	User defined threshold for determining the maximum value for acceptable data. Data that exceeds this threshold will be considered noise and bracketed by Bad Data Marks.
Minimum Heart Rate	Signal Interpretation	User defined threshold for determining the minimum HR for acceptable data. Data that falls below this threshold will be considered noise and bracketed by Bad Data Marks.
Maximum Heart Rate	Signal Interpretation	User defined threshold for determining the maximum HR for acceptable data. Data that exceeds this threshold will be considered noise and bracketed by Bad Data Marks.
Minimum Good Data Time	Signal Interpretation	Provides the user the ability to mark data as bad between two Bad Data Mark regions if the time between the regions is less than the value specified. If the time is less than what is specified the, the Bad Data Mark region will appear as one contiguous segment.

Typical Values

The table contains typical values for different heart rates. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Heart Rate	Attribute	Setting	Units
40-600 (All)	Minimum Pulse Height	5% of Pulse	mmHg
	Percent Recovery	50-75	%
	Q-A Trigger Channel	NA	NA
40-200 (Dog and Monkey)	Systolic Validation Time	100-150	mSec
	Non-Detection Time	50	mSec
200-400 (Rat)	Systolic Validation Time	50-100	mSec
	Non-Detection Time	25	mSec
400-600 (Mouse)	Systolic Validation Time	20-50	mSec

Heart Rate	Attribute	Setting	Units
	Non-Detection Time	20	mSec

Marks (Validation)

The **Blood Pressure** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the blood pressure signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Systolic Point
Blue	Diastolic Point
Cyan	End Diastolic Point
Green	Percent Recovery Point
Yellow	Max Slope Point

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging in Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Sys	Mean	The systolic pressure is the maximum pressure that occurs during the cardiac cycle.
Dia	Mean	The diastolic pressure is the minimum pressure that occurs during the cardiac cycle.
Mean	Mean	The mean blood pressure is the average of samples in a cardiac cycle. The average is calculated between diastolic marks.

Name	Averaging in Review	Definition
PH	Mean	The pulse height is the difference between the systolic pressure and the diastolic pressure for a cardiac cycle.
HR	Harmonic Mean	The heart rate is computed in beats-per-minute. It is calculated by taking the reciprocal of the time interval for the cardiac cycle multiplied by 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
TTPK	Mean	Time to peak is the time from the rise of the systolic pressure to the peak pressure. The value is reported in milliseconds.
ET	Mean	Ejection time is the time from the rise of the systolic pressure to the point of -dP/dt. The time value is reported in milliseconds.
+dP/dt	Mean	+dP/dt is the maximum positive value of the first derivative of the pressure that occurs during the cardiac cycle.
-dP/dt	Mean	-dP/dt is the maximum negative value of the first derivative of the pressure that occurs during a cardiac cycle.
%REC	Mean	The %REC is the amount of time it takes the pressure to recover from the rise of the systolic pressure to the **Percent Recovery** point. The time is in milliseconds.
NPMN*	Analysis	The NPMN is the non-pulsatile mean pressure reported for a logging period. This parameter is reported even if no pulse pressure exists.
Q-A	Mean	The Q-A Interval is the time in milliseconds from the start of the Q-wave, in the ECG trigger channel, to the start of the systolic pressure rise.
RNum*	Not available. Must be configured as a separate BPR channel in order to utilize Review.	Now available only in the BPR module. The analysis will report 0's if selected during acquisition and replay and X's when in Review.
RInt*		Now available only in the BPR module. The analysis will report 0's if selected during acquisition and replay and X's when in Review.
RBpm*		Now available only in the BPR module. The analysis will report 0's if selected during acquisition and replay and X's when in Review.
Mean2	Mean	An alternate representation for Mean calculated as (Systolic + 2 * Diastolic)/3.
PTT	Mean	Pulse Transit Time (PTT) is the time between the prior systolic time of the upstream channel and the systolic time of the selected channel. This time is reported in ms.
PWV	Mean	Pulse Wave Velocity (PWV) is the velocity calculated by using the Pulse Wave Distance (PWD) and Pulse Transit Time (PTT). PWV is calculated as: Pulse Wave Velocity = Pulse Wave Distance / Pulse Transit Time.

Name	Averaging in Review	Definition
IBIs	Mean	Inter-beat-interval systolic is the time in ms between the systolic marks of the current cycle and previous cycle
IBIms	Mean	Inter-Beat Interval maximum slope is the time (ms) between the current average maximum slope and the previous average maximum slope.
IBIed	Mean	Inter-Beat Interval end diastolic is the time (ms) between the current end diastolic mark and the previous end diastolic mark.
Count	Sum	The number of cycles within a logging interval or a data reduction interval. In Beat (epoch) mode, Count = 1
*These parameters are available when enabled in the PNM-BPR100W option. To configure these parameters, a dedicated channel must be configured and the analysis set to BPR. Please see PNM-BPR100W for additional information.		

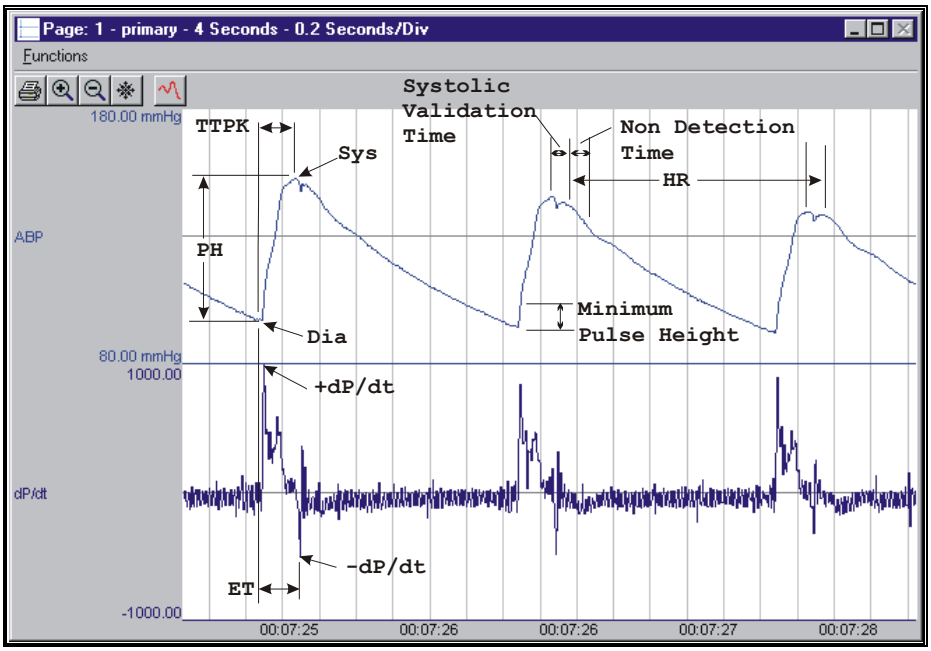
Calibration

The recommended calibration of the system for a Blood Pressure signal depends on the area where the Blood Pressure signal is measured. The following chart displays typical calibration values for a ±5.00Volt A/D range.

Area	High Calibration Value	Actual mV
Arterial pressure	100 mmHg	≈800-1200 mV
Pulmonary pressure	20.0 mmHg	≈1500-2500 mV
Central venous pressure	30.0 mmHg	≈2500-3500 mV
Left ventricular pressure	100 mmHg	≈800-1200 mV

On-Line Screens and Functions

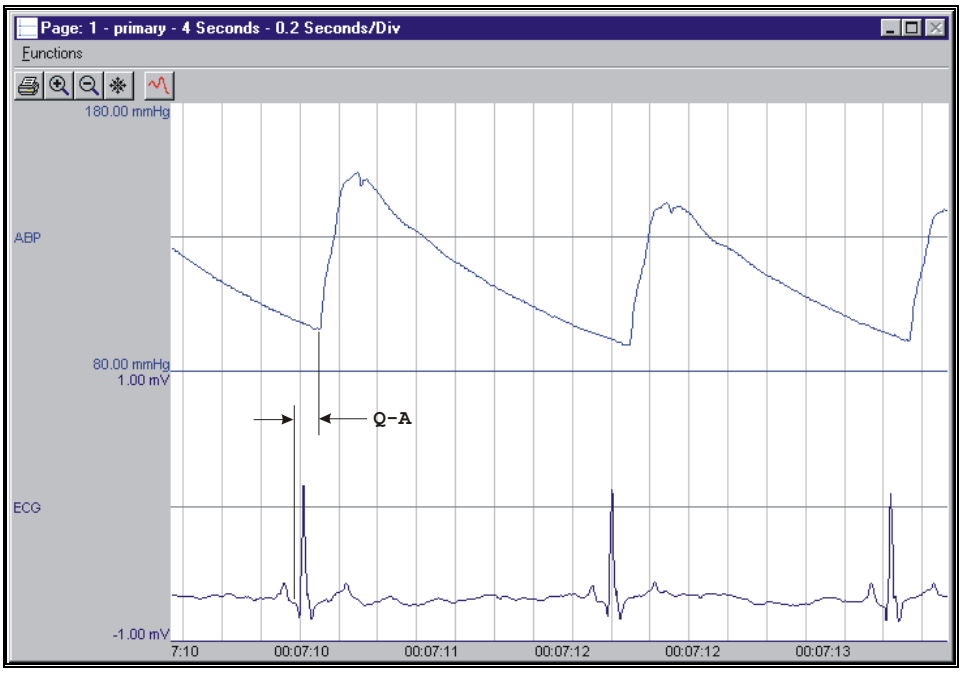
The following is an example of a Primary graph displaying the raw analog format of an aorta blood pressure signal along with its differential.



Blood Pressure Key Marks

In the above figure, the **Blood Pressure** is displayed with validation tick marks and their meanings. The validation marks identify the ***Systolic Pressure***, ***Diastolic Pressure***, and the ***%Recovery*** point.

The image below defines the measurement of Q-A Interval.



Blood Pressure Q-A Interval Mark

Presentation Signals

Below is a list of presentation signals that are available for the BP Analysis Module:

Signal	Description
Pressure	This is the original pressure signal after applying any software filters.
Derivative	This will display the derivative of the pressure signal.
Mean	This will display the mean pressure updated at every cardiac cycle.
Heart Rate	This will display the heart rate updated at every cardiac cycle.
Difference	This will display the difference between this input signal, and an input signal selected in the Advanced Attributes tab (other available pressure signals). The analysis module will subtract the current blood pressure signal from the signal selected from the list box and make the resulting signal available to be graphed.

Data Review

The Data Review related features of the Blood Pressure Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.10 or greater and if the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

Blood Pressure marks are divided into two types, marks that always exist when a valid cycle is found (Diastolic, End Diastolic, and Systolic) and marks that may or may not exist, depending on the signal morphology (Percent Recovery).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert BP Cycle

Inserts an entire Blood Pressure cycle, Diastolic, End Diastolic, Systolic, and Percent Recovery, if applicable. This set of marks may be inserted between a Percent Recovery Mark and a Diastolic Mark. If a Percent Recovery Mark is not present, the cycle may be inserted between a Systolic Mark and a Diastolic Mark. When a Blood Pressure cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Blood Pressure cycle's marks cannot be deleted individually. They are linked to the Systolic Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Systolic Mark and the right mouse

button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving of the Diastolic and End Diastolic and Systolic Marks follow the standard rules used in Data Review. There are special considerations when dealing with the Percent Recovery Mark. The Percent Recovery Mark is a calculated mark; its position is dependent on the systolic and diastolic levels and cannot be adjusted by the user. If the user changes the position of either the Diastolic or Systolic Marks, the Percent Recovery Mark will be recalculated.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of +dP/dt and -dP/dt. For non-pulsatile parameters, the start point is the point after the previous log time. The end point is the point at which the line is logged.

The -dP/dt parameter is obtained from the data between the peak and the end of the peak detection time. In Replay, it is obtained from the data between the point that clears Minimum Pulse Height to the end of peak detection time (Parameters affected are -dP/dt and ET).

In Review, +dP/dt is obtained from the data between the end diastolic point and the systolic point. In Replay, it is obtained from the data between two successive end of peak detection times (Parameters affected -dP/dt).

Logging Mark

The logging mark for a Blood Pressure cycle is the Systolic Mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a Blood Pressure cycle occurs one sample prior to the next cycles diastolic mark. When BP and ECG data are brought into Review, the ECG channel should be used as the epoch channel to ensure that related cycles are kept together.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Heart Rate is doubled	The analysis is triggering on the dicrotic notch. This can be rectified by lengthening the **Systolic Validation Time** and **Non-Detection Time** values. Refer to the chart of **Typical Values** for a specific heart rate range.
Heart Rate is halved	The analysis is pausing too long for the specified heart rate. The problem can be rectified by shortening the **Systolic Validation Time** and **Non-Detection Time** values. Refer to the chart of **Typical Values** for a specific heart rate.
All Derived Parameters are reporting zero	The **Minimum Pulse Height** may be set too high for the specified signal. Lower the **Minimum Pulse Height**.

Problem	Solution
Heart Rate is out of range (very high)	The analysis may be triggering on noise. The two solutions for this are: 1) Increase the **Minimum Pulse Height** to a value of 10% of pulse pressure. 2) Increase the **Low Pass Filter** (in the **Adv Attrib** tab) to remove the noise or artifact. Select a lower value in the list box.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the **Product Information** option of the **Help** menu.
Analysis does not trigger (No marks)	Reduce the sample rate to 250-1000Hz (A/D Sample Rate under Acquisition menu).
0 or "x" reported for PWV	No upstream pressure channel available for the selected channel. Cycles that have 0 Pulse Transit Time (PTT) reported.
Pulse Transit Time (PTT) and Pulse Wave Velocity (PWV) report 0 in replay	No cycles exist between the downstream cycle's systolic mark and a segment start time. Applicable when "Analysis Reset across Time Breaks (Replay only)" option is selected in Application Configuration.
Pulse Transit Time (PTT) and Pulse Wave Velocity (PWV) report "x" in review	No cycles exist between the downstream cycle's systolic mark and a segment start or a bad data mark end.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Blood Pressure]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Pulse Height(low)	This sets the minimum allowable value for **Minimum Pulse Height**. The default value is 0.
Minimum Pulse Height(high)	This sets the maximum allowable value for **Minimum Pulse Height**. The default value is 100.

Entry Name	Description
Systolic Validation Time(low)	This sets the minimum allowable value for **Systolic Validation Time** in milliseconds. The default value is 0.
Systolic Validation Time(high)	This sets the maximum allowable value for **Systolic Validation Time** in milliseconds. The default value is 5000.
Non Detection Time(low)	This sets the minimum allowable value for **Non Detection Time** in milliseconds. The default value is 0.
Non Detection Time(high)	This sets the maximum allowable value for **Non Detection Time** in milliseconds. The default value is 1000.
Percent Recovery(low)	This sets the minimum allowable value for **Percent Recovery** in percent. The default value is 0.
Percent Recovery(high)	This sets the maximum allowable value for **Percent Recovery** in percent. The default value is 100.
Pulse Wave Distance(low)	This sets the lowest value that the Pulse Wave Distance can be set to. The default value is 0.
Pulse Wave Distance(high)	This sets the highest value that the Pulse Wave Distance can be set to. The default value is 1000.
Minimum Signal Value(low)	This sets the lowest value that the Minimum Signal Value can be set to. The default value is -500.
Minimum Signal Value(high)	This sets the highest value that the Minimum Signal Value can be set to. The default value is 500.
Maximum Signal Value(low)	This sets the lowest value that the Maximum Signal Value can be set to. The default value is 0.
Maximum Signal Value(high)	This sets the highest value that the Maximum Signal Value can be set to. The default value is 2000.
Minimum Heart Rate(low)	This sets the lowest value that the Minimum Heart Rate can be set to. The default value is 0.
Minimum Heart Rate(high)	This sets the highest value that the Minimum Heart Rate can be set to. The default value is 1000.
Maximum Heart Rate(low)	This sets the lowest value that the Maximum Heart Rate can be set to. The default value is 0.
Maximum Heart Rate(high)	This sets the highest value that the Maximum Heart Rate can be set to. The default value is 2000.
Minimum Good Data Time(low)	This sets the lowest value that the Minimum Good Data Time can be set to. The default value is 0.

Entry Name	Description
Minimum Good Data Time(high)	This sets the highest value that the Minimum Good Data Time can be set to. The default value is 1000.

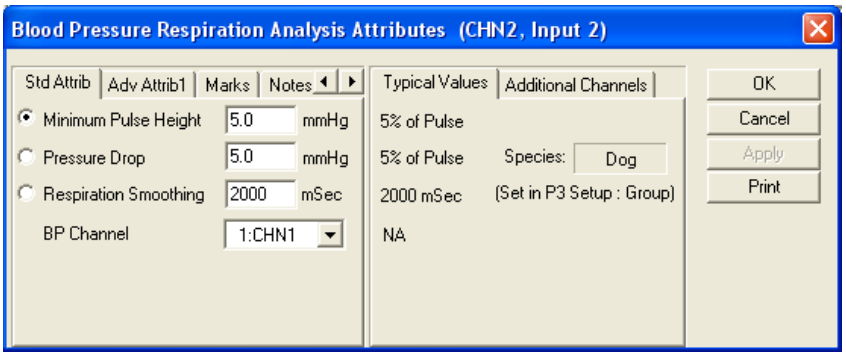
Blood Pressure Respiration (BPR)

The Blood Pressure Respiration analysis can analyze any pressure from the circulatory system and can derive, on a beat-to-beat basis, respiration values from the cardiac cycle. In order for the BPR analysis to function properly, a BP channel needs to be configured and the BPR channel must be associated with the acquired BP channel.

Attribute Window

The Blood Pressure Respiration attributes window allows you to modify the signal analysis for different types of blood pressure signals and signal conditions. If an analysis change in the **Attributes** dialog is performed mid-cycle, then the attribute change will not take effect until the following cycle. If only examining one cycle, and a change in the **Attributes** dialog is made, then the user must stop replay and restart replay in order to see the attribute change take effect on the analysis of the cycle (not necessary when post processing data in Review).

Standard Attributes



Blood Pressure Respiration Attributes Tab

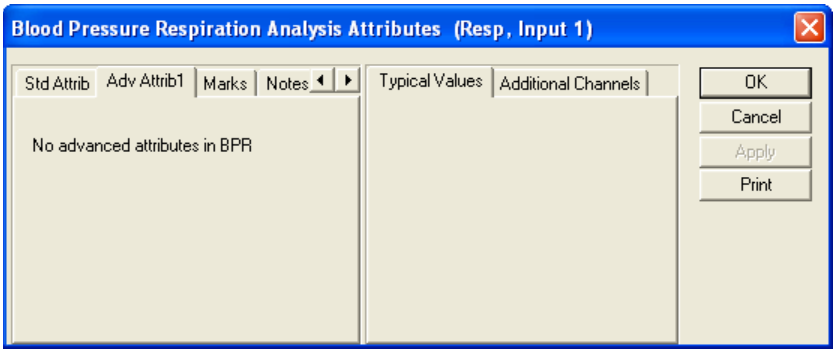
The Respiration Attributes tab is used to calculate respiration from the blood pressure signal. It can only be used if BPR is set in the license file.

Below are the respiration attributes that are derived from the blood pressure signal:

Attribute	Effect On Review	Description
Minimum Pulse Height	Signal Conditioning, Calculation, Signal Interpretation, and Redraw	Sets the minimum developed pressure that must be achieved before the analysis will detect and validate a cycle. The Minimum Pulse Height is useful for preventing the analysis from triggering on small variations in the signal.
Pressure Drop	Signal Conditioning, Calculation, Signal Interpretation, and Redraw	This setting is used to set the minimum level by which the signal must fall, relative to its recent maximum, for the analysis to identify a cycle. This setting is useful in eliminating false triggering on small variations in the signal.

Attribute	Effect On Review	Description
Respiration Smoothing	Signal Conditioning, Calculation, and Redraw	This sets the duration over which data derived from the blood pressure signal is smoothed to yield the respiration signal. This should be set to approximately ¼ of a respiration cycle. If this parameter is set too small, the respiration signal will appear jagged. If it is set too large, the respiration signal will appear washed out, and the pulse height of individual cycles will become smaller.
BP Channel	Signal Conditioning, Calculation, Signal Interpretation, and Redraw	This associates the proper BP channel with the BPR channel. These two channels must be configured in the same group. If no BP channel is associated with the BPR channel, the analysis will not trigger. NOTE: The BP channel must be sampled at, or faster than the BPR sample rate. NOTE: If using BP version 4.50 or earlier, the BP Channel drop down box will not list any BP channels.

Advanced Attributes



Blood Pressure Respiration Advanced Attribute Tab

There are no Advanced Attributes for the BPR analysis module.

NOTE: The BPR channel is not automatically reanalyzed when a reanalysis is performed on the BP channel.

Typical Values

The table contains typical values for different heart rates. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Species	Attribute	Setting	Units
(All) Dog, Monkey, Rat, and Mouse	Minimum Pulse Height	5% of Pulse	mmHg
	Pressure Drop	5% of Pulse	mmHg
	Respiration Smoothing	2000	mSec
	BP Channel	NA	NA

Marks (Validation)

The **Blood Pressure Respiration** analysis displays validation tick marks for each respiration cycle. Each cycle should have only one set of validation marks. These marks verify that the system is analyzing the blood pressure respiration signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Max Volume Mark

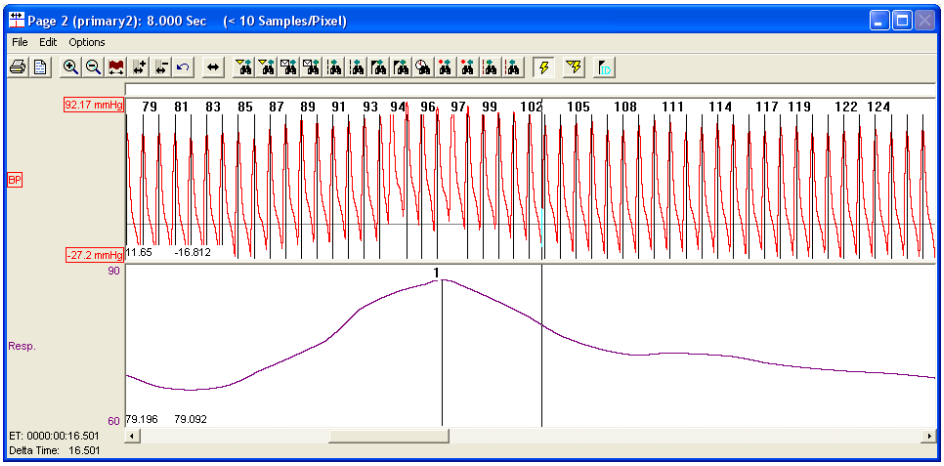
Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog (Channel Input Setup). The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
RNum	Recent	The RNum is the cycle number of each complete respiration waveform.
RInt	Mean	The RInt is the time, in milliseconds, over which a full respiration waveform is detected.
RBpm	Harmonic Mean	Respiration rate in breaths-per-minute.

On-Line Screens and Functions

The following is an example of a Primary graph displaying the raw analog format of a blood pressure signal along with the respiration presentation signal.



Blood Pressure Respiration Key Marks

In the above figure, the **Blood Pressure Respiration signal** is displayed with validation tick marks and their meanings. The validation mark identifies the ***Max Volume Mark*** point.

Presentation Signals

Below is a list of presentation signals that are available for the BPR Analysis Module:

Signal	Description
Respiration	This will display the calculated respiration signal.

Data Review

The Data Review related features of the Blood Pressure Respiration Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.10 or greater and if the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

Marks are divided into two types, marks that always exist when a valid cycle is found (Diastolic, End Diastolic, and Systolic) and marks that may or may not exist, depending on the signal morphology (Percent Recovery). BPR has only a single mark (Max Volume Mark) that exists when a valid cycle is found.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate.

Insert BPR Cycle

Inserts an entire Blood Pressure Respiration cycle, with the associated Max Volume Mark. This mark may be inserted at any point along the waveform. When a Blood Pressure Respiration cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. When deleting these marks, the entire cycle will be deleted; the cursor is positioned on the Max Volume Mark and the right mouse button is clicked to delete the mark.

Moving Marks

Moving the Max Volume Marks follow the standard rules used in Data Review. A Max Volume Mark cannot be dragged past another Max Volume Mark.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of RBpm (see Averaging in Review). For non-pulsatile parameters, the start point is the point after the previous log time. The end point is the point at which the line is logged.

Logging Mark

The logging mark for a Blood Pressure Respiration cycle is the Max Volume Mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a Blood Pressure Respiration cycle occurs one sample prior to the next cycles Max Volume Mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis. This includes issues that may exist in the BP analysis module which may affect the BPR module:

Problem	Solution
Heart Rate is doubled	The analysis is triggering on the dicrotic notch. This can be rectified by lengthening the **Systolic Validation Time** and **Non-Detection Time** values. Refer to the chart of **Typical Values** for a specific heart rate range.
Heart Rate is halved	The analysis is pausing too long for the specified heart rate. The problem can be rectified by shortening the **Systolic Validation Time** and **Non-Detection Time** values. Refer to the chart of **Typical Values** for a specific heart rate.
All Derived Parameters are reporting zero	The **Minimum Pulse Height** may be set too high for the specified signal. Lower the **Minimum Pulse Height**.
Heart Rate is out of range (very high)	The analysis may be triggering on noise. The two solutions for this are: 1) Increase the **Minimum Pulse Height** to a value of 10% of pulse pressure. 2) Increase the **Low Pass Filter** (in the **Adv Attrib** tab) to remove the noise or artifact. Select a lower value in the list box.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the **Product Information** option of the **Help** menu.
Analysis does not trigger (No marks)	Reduce the sample rate to 250-1000Hz (A/D Sample Rate under Acquisition menu).

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Blood Pressure Respiration]** section of the file. The user may change these settings if the ranges of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Resp Minimum Pulse Height(low)	This sets the minimum allowable value for respiration **Minimum Pulse Height**. The default is 0.
Resp Minimum Pulse Height(high)	This sets the maximum allowable value for respiration **Minimum Pulse Height**. The default value is 100.
Resp Pressure Drop(low)	This sets the minimum allowable value for **Respiratory Pressure Drop**. The default value is 0.
Resp Pressure Drop(high)	This sets the maximum allowable value for **Respiratory Pressure Drop**. The default value is 100.
Resp Smoothing(low)	This sets the minimum allowable value for **Respiratory Smoothing** in milliseconds. The default value is 6.
Resp Smoothing(high)	This sets the maximum allowable value for **Respiratory Smoothing** in milliseconds. The default value is 10000.

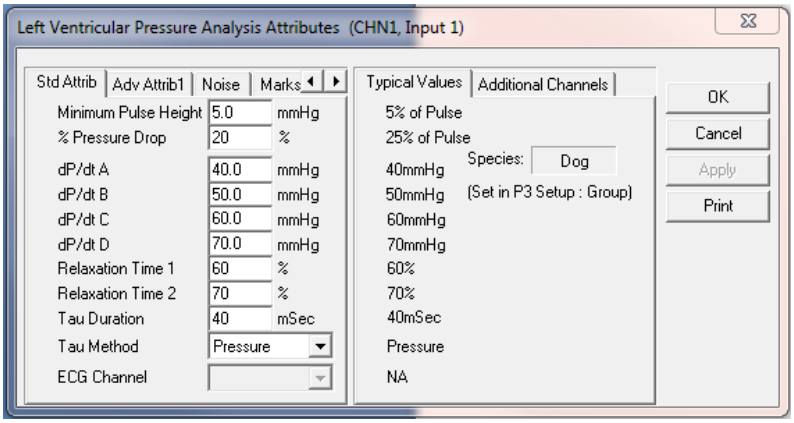
Left Ventricular Pressure (LVP)

The Left Ventricular Pressure Analysis Module analyzes the left ventricular pressure from the heart. The analysis calculates the common parameters that are associated with left ventricular pressure on a beat-to-beat basis.

Attribute Window

The Left Ventricular Pressure dialog allows you to modify the signal analysis for different types of left ventricular pressure signals and different signal conditions.

Standard Attributes



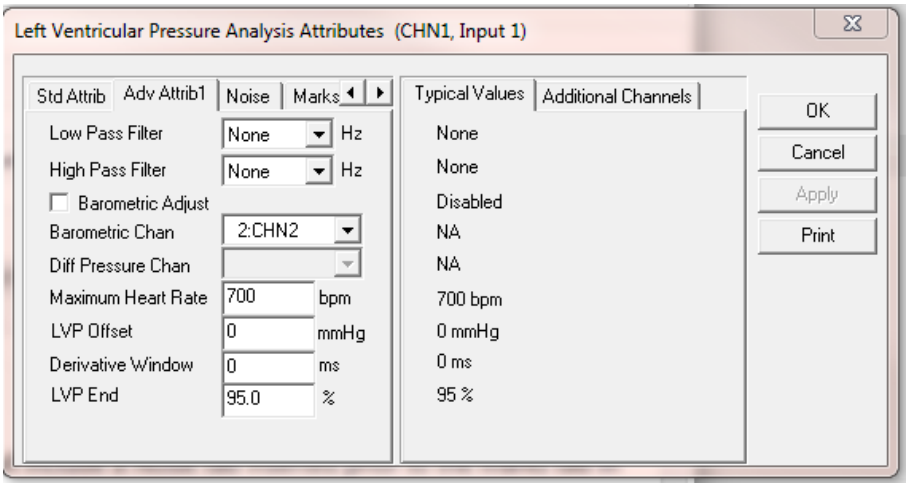
Left Ventricular Pressure Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Pulse Height	Signal Interpretation	Sets the minimum developed pressure that the signal must achieve before the analysis will detect and validate a cardiac cycle. The **Minimum Pulse Height** prevents the analysis from triggering on artifacts.
% Pressure Drop	Signal Interpretation	Defines how far the ***Systolic*** pressure must drop before the cardiac cycle will terminate. The pressure used in determining the percentage is the difference from the ***Systolic*** pressure to the ***Minimum*** pressure.
dP/dt (A, B, C, and D)	Calculation	Defines four pressure levels that the dP/dt will be sampled at during the systolic period.
Relaxation Time 1, 2	Calculation, Redraw	Defines levels in the derivative signal at which relaxation times will be reported. A relaxation period begins when $-dP/dt_{MAX}$ occurs, and ends when the derivative signal reads zero. For example, if **Relaxation Time** is set to 60%, then the system will report how long it took (in milliseconds) for the derivative to rise by 60% of $-dP/dt_{MAX}$.
Tau Duration	Calculation	Defines the duration over which **Tau** is to be calculated, starting at $-dP/dt_{MAX}$. **Tau Duration** is measured in milliseconds. Three methods are used for calculating Tau: **Pressure**, **dP/dt**, and **DevPressure**. **Pressure:** Tau is calculated as the negative inverse of the slope of the regression line of the natural logarithm of Left Ventricular Pressure versus time. **dP/dt:** Tau is calculated as the negative inverse of the slope of the regression line of the natural logarithm of -dP/dt versus time. **DevPressure:** Tau is calculated as the negative inverse of the slope of the regression line of the natural log of left ventricular pressure - the previous end diastolic level versus time.
Tau Method	Calculation	Defines which two values are used in the calculation of **Tau**. Use different methods for different conditions. Each method passes the data into the formula that calculates the linear line equation using the least square method. The three available methods are: Pressure, dP/dt, and DevPressure.
ECG Channel	Calculation	Permits the selection of an ECG channel for the calculation of the Q-A Interval. If no ECG channels are set up, this control is inactivated. ECG channels must be set up prior to using this attribute.

Advanced Attributes

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.



Left Ventricular Pressure Advanced Attributes Tab

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Barometric Adjust	Signal Conditioning, Calculation, Redraw	This check box enables the correction for barometric pressure. This is used for certain telemetry systems that do not compensate for barometric pressure internally. The correction factor is applied by using a raw electrical mean channel as the input. The pressure offset is in kilopascals. NOTE: If the system is being used with the OpenART or Digital acquisition engines, do not check this box. If the system is being used with the JET acquisition engine, check the box and choose the channel associated with the eAPR-1 as the Barometric Channel.
Barometric Chan	Signal Conditioning, Calculation, Redraw	This list box will display the available RAW inputs that could be used for the offset adjustment and is only used when the Barometric Adjust check box is enabled.
Diff Pressure Chan	Signal Conditioning, Calculation, Redraw	This list box allows the selection of a channel that can be used to subtract another channel from the input. The only effect that this has is for display. To display the difference, the Presentation field in a Primary graph must be set to Diff.

Attribute	Effect On Review	Description
Maximum Heart Rate	Signal Interpretation	This attribute is used to assist the analysis in the rejection of noise, to ensure that large rapid signal fluctuations due to noise are not marked as cardiac cycles. Maximum Heart Rate should be set higher than the highest expected heart rate.
LVP Offset	Signal Conditioning, Calculation, Redraw	This attribute is used when negative LVP values are present during the experiment. When an LVP offset value is entered, it will be applied to the entire channel and will calculate the derived parameters accordingly. The default LVP offset is zero. NOTE: this offset is applied to the entire dataset and cannot be applied to sections of the data. If only specific sections require an offset, it is recommended to use the Parser functionality (see Data Parser in the Review manual, MU00196).
Derivative Window	Signal Conditioning, Calculation, Redraw	The Derivative Window defines the range of samples over which the LVP's derivative signal is calculated. This window acts as a smoothing function for the derivative by calculating across a larger range. Using a value of 0ms will provide the derivative between two consecutive points, whereas entering a larger value may provide the derivative across non-consecutive points. Ex: If sampling at 1000 Hz, the time between consecutive points is 1ms. By choosing a Derivative Window of 2ms, the derivative will be calculated across every other point. NOTE: The default value of 0ms will provide the derivative functionality seen in previous versions.
LVP End	Redraw	The LVP End attribute controls the placement of the LVP End Mark. The mark is placed at the point where the derivative signal rises by "LVP End" % of –dP/dtMAX

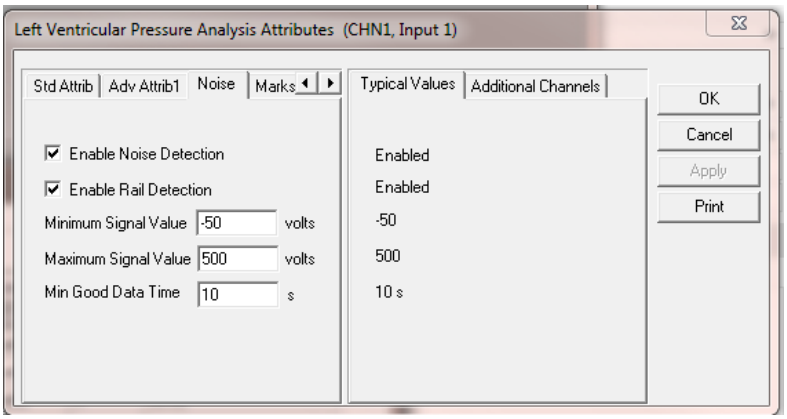
Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Minimum Pulse Height	5% of Pulse	mmHg
% Pressure Drop	25% of Pulse	%
dP/dt A	40	mmHg
dP/dt B	50	mmHg
dP/dt C	60	mmHg
dP/dt D	70	mmHg
Relaxation Time 1	60	%
Relaxation Time 2	70	%
Tau Duration	40	mSec
Tau Method	Pressure	NA

Noise Attributes

Enable Noise Detection attribute enables/disables all controls in the Noise Tab.

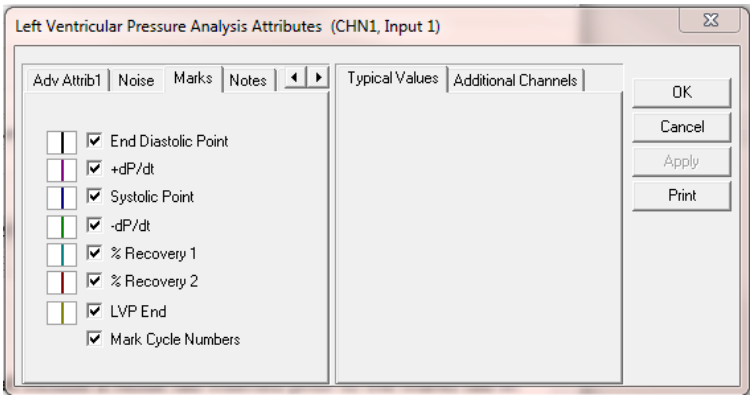


Noise Attributes Tab

Attribute	Description
Enable Noise Detection	Determines if noise detection will be used to determine bad data marks
Enable Rail Detection	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value/ Maximum Signal Value	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.
Minimum Good Data Time	When Noise detection is enabled and a range of data is analyzed, any bad data marks that have less than or equal to the Min Good Data Time of good data between them shall be combined into a single bad data region.

Marks (Validation)

The **Left Ventricular Pressure** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the left ventricular pressure signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.



The validation marks and their meanings are listed below:

Color	Meaning
Black	Left Ventricular End Diastolic Point
Blue	Systolic Point
Green	-dP/dt
Cyan	% Recovery 1
Red	% Recovery 2
Magenta	+dP/dt
Yellow	Left Ventricular Pressure End Point

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Sys	Mean	The systolic pressure is the maximum pressure that occurs during the cardiac cycle.
LVEDP	Mean	The left ventricular end diastolic pressure is the pressure at 1/15th of the max slope during the rise of the systolic period of the next cycle.
Min	Mean	The minimum pressure during the cardiac cycle. Not defined over a specific cycle. Min is calculated over the period of time that the logging period takes place.
TTI	Mean	Tension-Time Index is the area under the left ventricular pressure during the ejection phase of the contraction. This is the integration between the LVEDP point and -dP/dtMAX.
DP	Mean	Developed pressure is the difference between the systolic pressure and the left ventricular end diastolic pressure (SYS-LVEDP).

Name	Averaging In Review	Definition
HR	Harmonic Mean	The heart rate is computed in beats-per-minute. It is calculated by taking the reciprocal of the time interval for the cardiac cycle multiplied by 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
+dP/dt	Mean	+dP/dt is the maximum positive value of the first derivative of the pressure that occurs during the cardiac cycle.
-dP/dt	Mean	-dP/dt is the maximum negative value of the first derivative of the pressure that occurs during the cardiac cycle.
CI	Mean	Contractility index is +dP/dt divided by the pressure at that point.
RT1, RT2	Mean	The Relaxation Time is the time period from -dP/dt to the time specified by the Relaxation Time attribute. The time is reported in milliseconds.
dP (A, B, C, and D)	Mean	These parameters report the value of dP/dt at the pressure levels specified in dP/dt A, dP/dt B, dP/dt C, and dP/dt D (in the attributes window). These values will not be reported accurately if these pressure values are set too close to the Pressure Threshold Value (Minimum Pulse Height). The dP/dt (A, B, C, and D) pressure settings in the attribute dialog under the Std Attributes tab should at least be set to a value 20 units above that of the Minimum Pulse Height value.
NPMN	Analysis	The non-pulsatile mean pressure reported for a logging period. This parameter is still reported even if no pulse pressure exists.
Q-A	Mean	The Q-A Interval is the time in milliseconds from the start of the Q-wave, in the ECG trigger channel, to the start of the systolic pressure rise (LVEDP)
IVT	Mean	The time in milliseconds from the start of the systolic pressure rise (LVEDP) to the maximum slope of the systolic pressure rise (+dP/dt)
TTI-T	Mean	LVEDP to -dP/dt. The time is in milliseconds.
Tau	Mean	Tau is the time constant isovolumic left ventricular pressure decay. It is reported in milliseconds, and can be defined as described in the Attributes window section.
Period	Mean	The duration of the current cycle time, in milliseconds.
EMw	Mean	Electro-mechanical window (EMw) reports the time, in ms, between the LVP's end mark (where the LVP signal returns to its resting level) and the ECG's end of T-wave. EMw = (LVP End mark) – (ECG Tend mark) The associated ECG cycle shall be identified by the ECG Channel attribute. The associated ECG cycle shall be identified as the ECG cycle within which the current LVP cycle's logging mark falls.
Count	Count	The number of cycles within a logging interval or a data reduction interval In Beat mode, Count = 1
SysD	Mean	Systolic Duration. The time, in milliseconds, between the End Diastolic and the following LVP End validation marks.
DiaD	Mean	Diastolic Duration. The time, in milliseconds, between the LVP End validation mark and the following End Diastolic validation marks.

Calibration

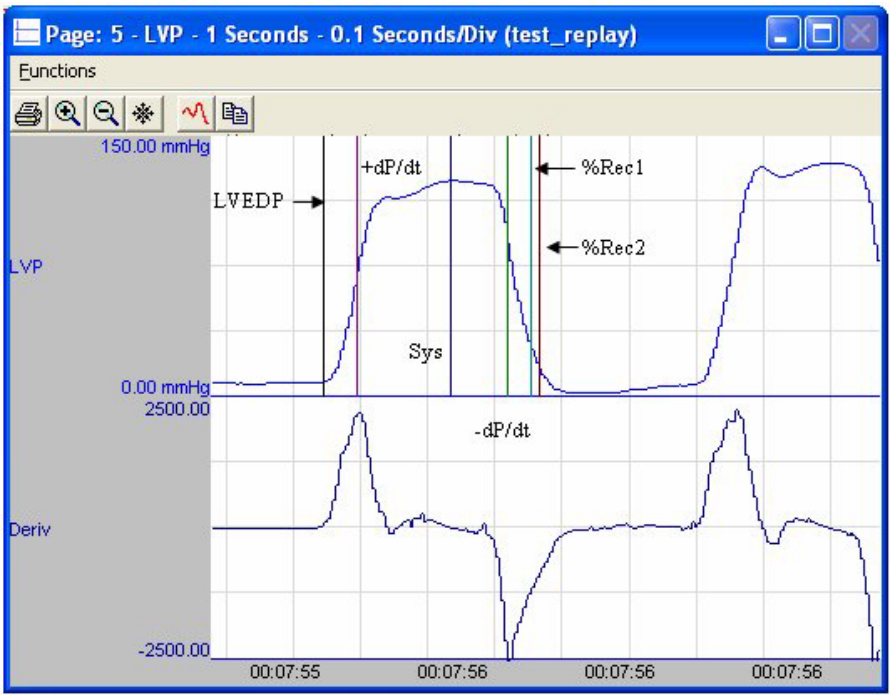
The recommended calibration for the system for a Left Ventricular Pressure signal depends on the accuracy level that the derived parameters will be reported in. In most cases, the Left Ventricular Pressure values can be

reported to a whole number (for example, 100mmHg). In other cases, the Left Ventricular Pressure may need to be accurate to 1/10 of a mmHg (100.0mmHg). The following chart shows typical calibration values:

Accuracy	High Calibration Value	Actual mV
0000	100mmHg	≈800-1200 mV
000.0	100.0mmHg	≈1500-2500 mV

On-Line Screens and Functions

Below is a Primary graph displaying the raw analog format of a typical left ventricular pressure signal with its digitally generated differential. The validation tick marks also are displayed on the waveform.



Left Ventricular Pressure Key Marks

In the above figure, the **Left Ventricular Pressure** is displayed with the validation tick marks. These marks identify the ***Left Ventricular End Diastolic Pressure, Systolic Pressure, Recoveries*** and ***-dP/dt***.

Presentation Signals

Below is a list of presentation signals that are available for the LVP Analysis Module:

Signal	Description
Pressure	This is the original pressure signal after applying any software filters.
Derivative	This will display the derivative of the pressure signal.
Heart Rate	This will display the heart rate updated at every cardiac cycle.

Signal	Description
Difference	This will display the difference between this input signal, and an input signal selected in the Advanced Attributes tab (other available pressure signals). The analysis module will subtract the current blood pressure signal from the signal selected from the list box and make the resulting signal available to be graphed.

Data Review

The Data Review related features of the Left Ventricular Pressure Analysis Module are accessible when the analysis module is used with P3 Plus Version 4.10 or greater. The analysis specific portion of Data Review centers on the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review window channel are controlled through the Marks Tab in the attribute dialog accessed via the Analyze selection in the Right click menu.

Mark Operations

Left Ventricular Pressure marks are divided into two types, marks that always exist when a valid cycle is found (End Diastolic, Systolic, Min Slope) and marks that may or may not exist, depending on the signal morphology (Recovery 1, Recovery 2).

NOTE: +dP/dt was added in LVP Version 4.30 for use with P3 Plus 4.40. If the LVP analysis module is used with an earlier version of P3 Plus, this mark will not function and its check box in the marks tab will be disabled. If a marks section that was created with an earlier version of the LVP module is loaded, the marks information will be converted to support +dP/dt. When converting a large file, a redraw may be necessary to see the +dP/dt mark. The mark is updated as the derived parameters are calculated.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert LVP Cycle

Inserts an entire Left Ventricular Pressure cycle: End Diastolic, Systolic, Min Slope, and Recoveries, if applicable. This set of marks may be inserted between the second Recovery Mark and an End Diastolic Mark. If a Recovery Mark is not present, the cycle may be inserted between a Min Slope Mark and an End Diastolic Mark. When a Left Ventricular Pressure cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Left Ventricular Pressure cycle's marks cannot be deleted individually. They are linked to the Systolic Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Systolic Mark and the right mouse button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving of the End Diastolic, Systolic, and Min Slope marks follow the standard rules used in Data Review. The Recovery marks are calculated marks; their positions are dependent on the Min Slope value and cannot be adjusted by the user. If the user changes the position of the Min Slope Mark, the Recovery marks will be recalculated.

The Min Slope Mark may be moved past the Recovery marks.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of Min. For non-pulsatile parameters, the start point is the point after the previous log time. The end point is the point at which the line is logged.

In Review the Min parameter is calculated between the Min Slope mark and the following cycle's LVEDP mark. In Replay, it is obtained from the data between the previous cycles Min Slope and the current cycles LVEDP point.

Logging Mark

The logging mark for a Left Ventricular Pressure cycle is the Systolic Mark. The time at the logging mark is the time used to report a cycle's derived data. If an LVP cycle's logging mark falls within a logging interval, the LVP cycle's data will be included in the logging interval.

End of Cycle

The end of an LVP cycle occurs one nanosecond prior to the next cycles LVEDP mark. For the last cycle in a data segment, the logging time +1 nanosecond is used.

When LVP and ECG data are brought into Review, the ECG channel should be used as the epoch channel to ensure that related cycles are kept together.

Averaging in Review

The following table lists the averaging method used for each derived parameter. Please refer to the Review manual for details on each averaging method. For derived parameters that use Analysis as their averaging method, refer to the Derived Parameter section for details.

Derived Parameter	Averaging
Num	Recent
Sys	Mean
LVEDP	Mean
Min	Mean
TTI	Mean
DP	Mean

Derived Parameter	Averaging
HR	Harmonic Mean
+dP/dt	Mean
-dP/dt	Mean
CI	Mean
RT1	Mean
RT2	Mean
dP-A	Mean
dP-B	Mean
dP-C	Mean
dP-D	Mean
NPMN	Analysis
Q-A	Mean
IVT	Mean
TTI-T	Mean
Tau	Mean
Period	Mean

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Heart Rate is doubled	The analysis is triggering on an artifact. Increase the Minimum Pulse Height and/or the % Pressure Drop. Refer to the chart of Typical Analysis Attribute Settings for typical values.
All Derived Parameters are reporting zero	The Minimum Pulse Height may be set too high for the specified signal. Lower the Minimum Pulse Height.

Problem	Solution
Heart Rate is out of range (very high)	The analysis may be triggering on noise. The two solutions for this are: Increase the Minimum Pulse Height to a value of 10% of pulse pressure. Increase the Low Pass Filter (in the Adv Attrib1 tab) to eliminate noise on the signal. Select a lower value in the list box.
Tau is negative or very large	The method being used to calculate Tau influences the values that are reported. When the Pressure vs. Time method is used, this field may report values that do not exist. This occurs when the pressure goes to zero, because the natural log of zero is undefined and the system will return an infinite value for this reading. If this occurs, use another method for Tau.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.
Algorithm does not trigger (No marks)	Reduce the sample rate to 250Hz, or increase the Low Pass Filter in the Adv Attrib1 tab. Select a lower value in the list box.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Left Ventricular Pressure]** section of the file. The user may change these settings if the range of the values for a specific attributes needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Pulse Height(low)	This sets the minimum allowable value for **Minimum Pulse Height**. The default value is 5.

Entry Name	Description
Minimum Pulse Height(high)	This sets the maximum allowable value for **Minimum Pulse Height**. The default value is 100.
dP/dt A(low)	This sets the minimum allowable value for **dP/dt A** in mmHg. The default value is 20.
dP/dt A(high)	This sets the maximum allowable value for **dP/dt A** in mmHg. The default value is 100.
dP/dt B(low)	This sets the minimum allowable value for **dP/dt B** in mmHg. The default value is 20.
dP/dt B(high)	This sets the maximum allowable value for **dP/dt B** in mmHg. The default value is 100.
dP/dt C(low)	This sets the minimum allowable value for **dP/dt C** in mmHg. The default value is 20.
dP/dt C(high)	This sets the maximum allowable value for **dP/dt C** in mmHg. The default value is 100.
dP/dt D(low)	This sets the minimum allowable value for **dP/dt D** in mmHg. The default value is 20.
dP/dt D(high)	This sets the maximum allowable value for **dP/dt D** in mmHg. The default value is 100.
Percentage Pressure Drop(low)	This sets the minimum allowable value for **% Pressure Drop**. The default value is 10.
Percentage Pressure Drop(high)	This sets the maximum allowable value for **% Pressure Drop**. The default value is 80.
Relaxation Time 1(low)	This sets the minimum allowable value for **Relaxation Time 1** in percent. The default value is 30.
Relaxation Time 1(high)	This sets the maximum allowable value for **Relaxation Time 1** in percent. The default value is 90.
Relaxation Time 2(low)	This sets the minimum allowable value for **Relaxation Time 2** in percent. The default value is 30.
Relaxation Time 2(high)	This sets the maximum allowable value for **Relaxation Time 2** in percent. The default value is 90.
Tau Duration(low)	This sets the minimum allowable value for **Tau duration** in milliseconds. The default value is 5.
Tau Duration(high)	This sets the maximum allowable value for **Tau duration** in milliseconds. The default value is 99.

Entry Name	Description
Maximum Heart Rate(low)	This sets the minimum allowable value for **Maximum Heart Rate**. The default value is 2000.
Maximum Heart Rate(high)	This sets the maximum allowable value for **Maximum Heart Rate**. The default value is 2000.
LVP Offset(low)	This sets the minimum allowable value for **LVP Offset**. The default value is -500.
LVP Offset(high)	This sets the maximum allowable value for **LVP Offset**. The default value is 500.
Derivation Window(low)	This sets the minimum allowable value for **Derivative Window** in milliseconds. The default value is 0.
Derivation Window(high)	This sets the maximum allowable value for **Derivative Window** in milliseconds. The default value is 40.
Reset Time	This sets the amount of time, in milliseconds, where the analysis will reset if a noise spike causes the analysis to stop triggering.
Tau Duration(low)	This sets the minimum allowable value for **Tau Duration** in milliseconds. The default value is 5.
Tau Duration(high)	This sets the maximum allowable value for **Tau Duration** in milliseconds. The default value is 99.

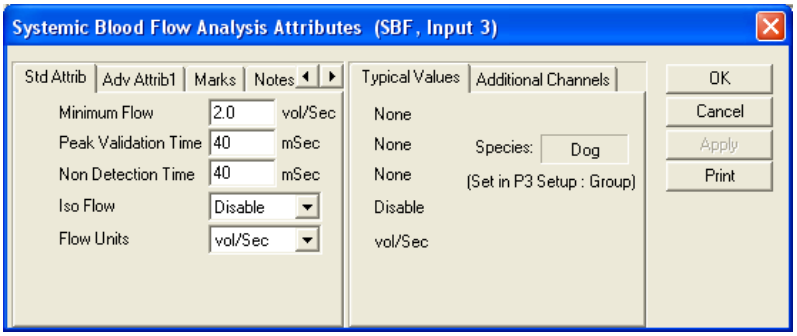
Systemic Blood Flow (SBF)

The Systemic Blood Flow Analysis Module analyzes systemic blood flow from the circulatory system. The analysis calculates the common parameters that are associated with a blood flow on a beat-to-beat basis.

Attribute Window

The Systemic Blood Flow dialog allows you to modify the signal analysis for different types of blood flow signals and different signal conditions.

Standard Attributes



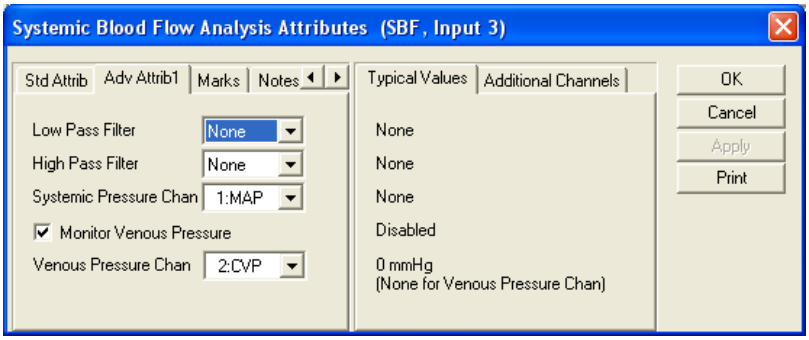
Systemic Blood Flow Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Flow	Signal Interpretation	Sets the level that the flow must achieve before the analysis validates the flow for the cardiac cycle.
Peak Validation Time	Signal Interpretation	The period, in milliseconds, over which a peak is validated. The peak is validated if the signal level at the peak is not exceeded over the validation period. Once a peak is validated, the cardiac cycle terminates.
Non Detection Time	Signal Interpretation	Sets the length of *dead time* in milliseconds that the signal is not analyzed for maximum and minimum flow values. This is used to eliminate double triggering on noise.
Iso Flow	Calculation	Eliminates drift common to certain types of electromagnetic flow meters. When this field is enabled, the analysis will sample a new Iso-flow point on the upstroke of the flow, use this value as a new zero point, and subtract this value from the derived parameters MEAN, FMAX, and FMIN. This value is reported as the ISO derived parameter.
Flow Units	Calculation	Specifies the units of flow being measured so that the system calculates the volume correctly. The choices are: vol/Sec: volume per second vol/Min: volume per minute

Advanced Attributes

The Advanced Attributes for Systemic Blood Flow are the Low and High Pass Filter selections as well as channel selections for determining which signals will be used in calculating Total Peripheral Resistance.



Systemic Blood Flow Advanced Attributes 1 Tab

The Advanced Attributes 1 tab allows the selection of attributes that would less likely need to be changed during acquisition, replay or review.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of high pass filter in hertz.
Systemic Pressure Chan	Calculation	Allows the selection of a BP channel to be used in the calculation of Total Peripheral Resistance. The BP channel must be in the same Group as the SBF channel and the BP and SBF channels must be sampled at the same rate.
Monitor Venous Pressure (check box)	Calculation	Determines whether the software will monitor venous pressure continuously or allow the user to type in a fixed value to represent venous pressure. If the box is checked, a drop down listbox will allow the selection of a BP channel for continuous monitoring. If the box is unchecked, the user will be allowed to manually type in a fixed value to represent venous pressure.
Venous Pressure Chan	Calculation	Allows the selection of a BP channel for continuous monitoring of venous pressure which is used to calculate Total Peripheral Resistance. The BP channel must be in the same Group as the SBF channel and the BP and SBF channels must be sampled at the same rate (shown above in Advanced Attributes 1 Tab).
Venous Pressure	Calculation	Allows a fixed value to be typed in which represent venous pressure. This value would be used in the calculation of Total Peripheral Resistance.

Typical Values

The table contains typical values based on species. Use these values as guidelines for a first time setup. Since various species are used, no typical values exist for this analysis module.

Marks (Validation)

The **Systemic Blood Flow** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the systemic blood flow signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation mark and its meaning is listed below:

Color	Meaning
Black	Iso Level Mark

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

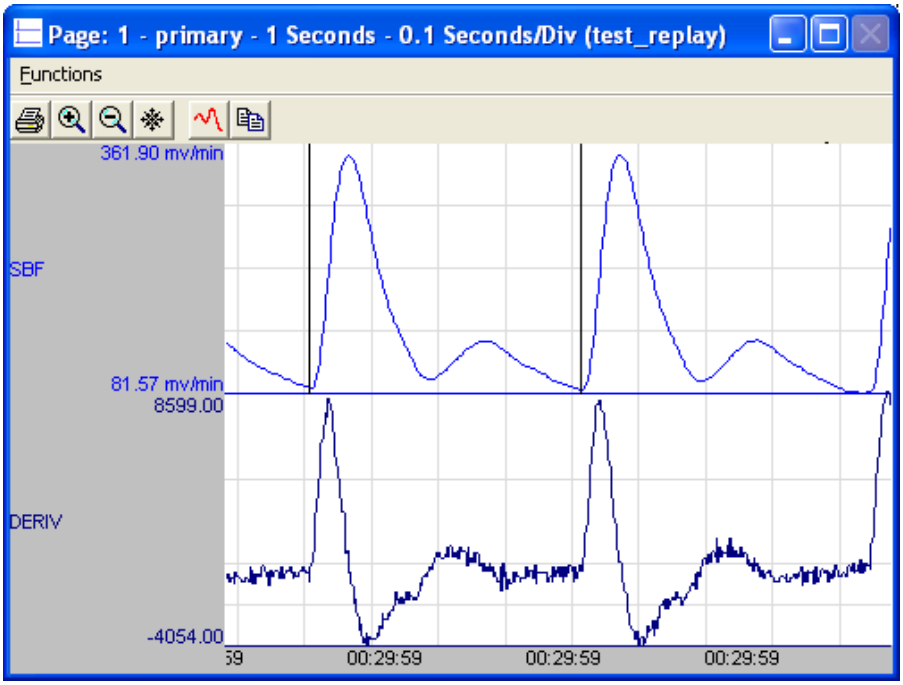
Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Mean	Mean	The integrated level of the flow for the cardiac cycle.
FMax	Mean	Maximum Flow, relative to isoelectric, that occurred for a cardiac cycle.
Fmin	Mean	Minimum Flow, relative to isoelectric, that occurred for a cardiac cycle.
CO	Analysis Define	Cardiac Output is the mean flow normalized to mL/Min. Note: When running in a logging mode other than 1 epoch, the CO value will be calculated from the averaged mean flow value.
SV	Mean	Stroke Volume is the mean flow normalized to mL/Sec times the Period. Note: When running in a logging mode other than 1 epoch, the SV value will be calculated from the averaged mean flow and averaged cycle duration.
+dQ	Mean	+dQ is the maximum positive value of the first derivative of the flow that occurs during the cardiac cycle.
Iso	Mean	The value of flow during the rapid up rise of the flow signal.
TPR	Analysis Define	Total Peripheral Resistance is calculated as: TPR = (P1 - P2)/CO. P1 is the Non Pulsatile Mean (NPMN) from the Systemic Pressure Channel and P2 is the value from the Venous Pressure attribute (either fixed or NPMN if continuously monitored). CO is the cardiac output parameter from the SBF channel.
NPMN	Analysis Define	The non-pulsatile mean calculated over the complete logging interval.

Calibration

The recommended calibration for the system for a Systemic Blood Flow signal depends on the type of instrumentation and the species that the signal is coming from. Doppler systems report flow in units of cm/sec, while electromagnetic flow meters can report flow in mL/sec, mL/min, l/sec, or l/min.

On-Line Screens and Functions

Below is an example of a Primary graph displaying the raw analog format of an aortic blood flow and derivative signal.



Systemic Blood Flow Key Marks

In the above figure, the aortic blood flow and derivative signal are displayed along with a validation tick mark. The validation mark identifies a single cardiac cycle that has been detected.

Presentation Signals

Below is a list of presentation signals that are available for the SBF Analysis Module:

Signal	Description
Flow	This is the original flow signal after applying any software filters.
Derivative	This will display the derivative of the flow signal.

Data Review

The Data Review related features of the Systemic Blood Flow Analysis Module listed here are accessible when the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

Systemic Blood Flow supports one Mark, This mark is the Iso Level Mark.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. With the Systemic Blood Flow module, only the insertion of a cycle is permitted. Upon insertion, the Iso Level Mark will be displayed.

Insert SBF Cycle

Insert SBF Cycle, will insert an entire Systemic Blood Flow cycle, including the Iso Level Mark. When a Systemic Blood Flow cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Systemic Blood Flow cycle's mark is linked to the Iso Level Mark. Deleting this mark will delete the entire cycle. Positioning the cursor over the Iso Level Mark will provide the option to delete the entire cycle from the right click menu.

Moving Marks

Moving of the Iso Level Mark follows the standard rules used in Data Review. The user shall be able to move the Iso Level Mark between two Iso Level Marks.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of how a cycle is determined. In acquisition and replay, a SBF cycle is the point from the termination of the Peak Validation Time of the previous cycle to the termination of the Peak Validation Time of current cycle. In Review mode, a cycle is from the current cycles' Iso Level mark to the next cycles' Iso Level mark.

Logging Mark

The logging mark for a Coronary Blood Flow cycle is the Iso Level Mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a Systemic Blood Flow cycle occurs one sample prior to the next cycles Iso Level Mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
All Derived Parameters are reporting zero	The Minimum Flow may be set too high for the specified signal.
FMax reads low	The analysis may be triggering on an artifact. Verify that the Minimum Flow value is correct.

Problem	Solution
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Systemic Blood Flow]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Flow(low)	This sets the minimum allowable value for **Minimum Flow**. The default value is .1.
Minimum Flow(high)	This sets the maximum allowable value for **Minimum Flow**. The default value is 100.
Peak Validation Time(low)	This sets the minimum allowable value for **Peak Validation Time** in milliseconds. The default value is 0.
Peak Validation Time(high)	This sets the maximum allowable value for **Peak Validation Time** in milliseconds. The default value is 500.
Non Detection Time(low)	This sets the minimum allowable value for **Non Detection Time** in milliseconds. The default value is 0.
Non Detection Time(high)	This sets the maximum allowable value for **Non Detection Time** in milliseconds. The default value is 500.
Mean Venous Pressure(low)	This sets the minimum allowable value for Mean Venous Pressure. The default value is 0.
Mean Venous Pressure(high)	This sets the maximum allowable value for Mean Venous Pressure. The default value is 5000.

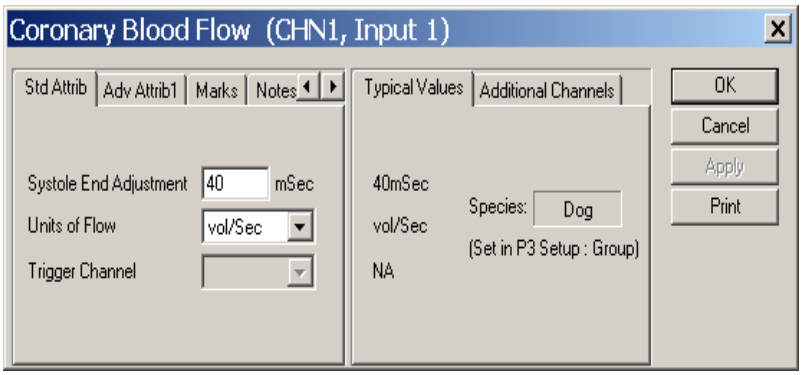
Coronary Blood Flow (CBF)

The Coronary Blood Flow Analysis Module analyzes coronary blood flow from the circulatory system. The analysis calculates the common parameters that are associated with a blood flow on a beat-to-beat basis. The Coronary Blood Flow Analysis Module can be used in conjunction with the Left Ventricular Pressure analysis for timing information. The timing information allows flow and volume to be calculated during the systolic and diastolic periods of the cardiac cycle.

Attribute Window

The Coronary Blood Flow dialog allows you to modify the signal analysis for different types of signal conditions.

Standard Attributes



Coronary Blood Flow Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Systole End Adjustment	Signal Interpretation	Defines the location of the end of systolic relative to LVP -dp/dt.
Units of Flow	Calculation	Specifies the units of flow being measured so that the system calculates the volume correctly. The choices are: • vol/Sec: volume per second vol/Min: volume per minute
Trigger Channel	Signal Interpretation	Specifies which input channel (performing Left Ventricular Pressure analysis) will be used as a trigger source. When using a trigger signal, the analysis relies on the logic of the Left Ventricular Pressure analysis to process the timing information. **WARNING: No analysis will be performed if a trigger channel is not selected.**

Advanced Attributes

The only Advanced Attributes for Coronary Blood Flow are the Low and High Pass Filter selections. Refer to **Error! Reference source not found.** in the **Error! Reference source not found.** section for more information.

Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Systole End Adjustment	40	mSec
Units of Flow	vol/Sec	vol/Sec
Trigger Channel	NA	Must be an LVP defined channel

Marks (Validation)

The **Coronary Blood Flow** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the coronary blood flow signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Blue	End Systolic Point
Black	End Diastolic Point

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported. The SD parameter will always report 0.
Mean	Mean	The integrated level of the flow for the cardiac cycle.
FMax	Mean	Maximum Flow that occurred for a cardiac cycle
FMin	Mean	Minimum Flow that occurred for a cardiac cycle.
CO	Analysis Define	Cardiac Output is the mean flow normalized to mL/Min. Note: When running in a logging mode other than 1 epoch, the CO value will be calculated from the averaged mean flow value. The SD parameter will always report 0.

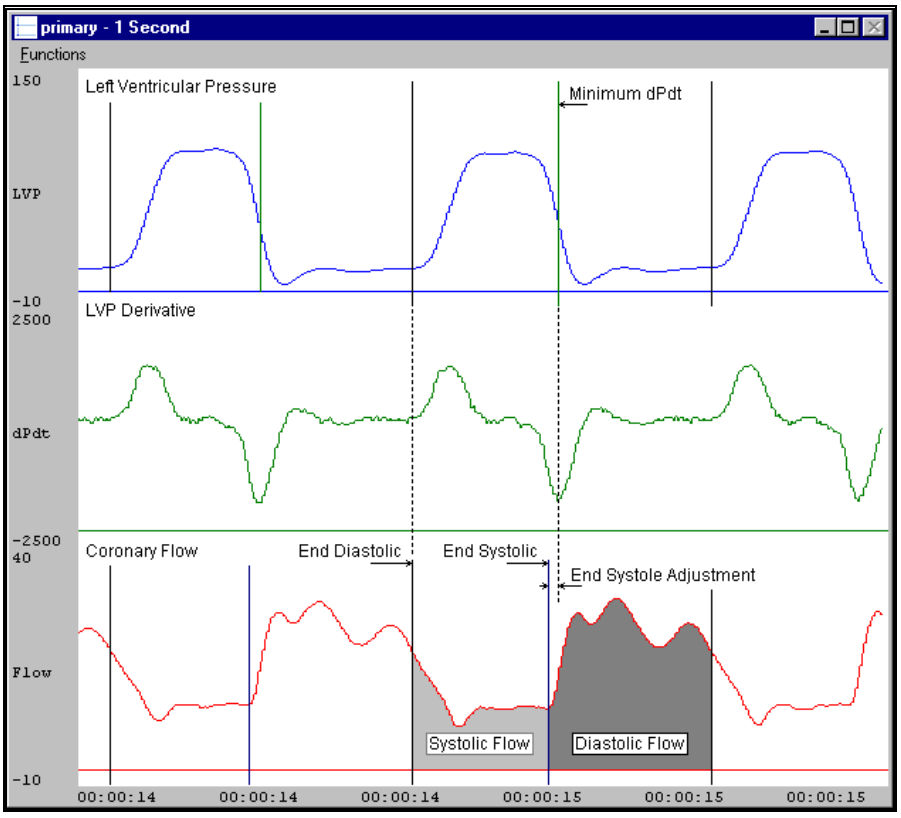
Name	Averaging In Review	Definition
SV	Mean	Stroke Volume is the mean flow normalized to mL/Sec times the period. Note: When running in a logging mode other than 1 epoch, the SV value will be calculated from the averaged mean flow and averaged cycle duration.
+dQ	Mean	+dQ is the maximum positive value of the first derivative of the flow that occurs during the cardiac cycle.
SFlw	Mean	Flow during systolic part of cardiac cycle.
DFlw	Mean	Flow during diastolic part of cardiac cycle.
SVol	Mean	Volume during the systolic part of the cardiac cycle.
DVol	Mean	Volume during the diastolic part of the cardiac cycle.
-Flow	Mean	Any negative flow that occurred during the cardiac cycle.
TVol	Mean	Total Volume is the sum of Systolic Volume and Diastolic Volume: SVol + DVol.
NPMN	Analysis Define	The non-pulsatile mean calculated over the complete logging interval. The SD parameter will always report 0.

Calibration

The recommended calibration for the system for a Coronary Blood Flow signal depends on the type of instrumentation, and the species that the signal is coming from. Doppler systems report flow in units of cm/sec, while electromagnetic flow meters can report flow in mL/sec, mL/min, l/sec, or l/min.

On-Line Screens and Functions

The following is an example of a Primary graph displaying the raw analog format of a coronary blood flow with the left ventricular pressure signal.



In the above figure, the Coronary Blood Flow is displayed along with validation tick marks used from the Left Ventricular Pressure analysis. The two validation marks identify the End Diastolic point and the End Systolic point.

Presentation Signals

Below is a list of presentation signals that are available for the CBF Analysis Module:

Signal	Description
Flow	This is the original flow signal after applying any software filters.
Derivative	This will display the derivative of the flow signal.

Data Review

The Data Review related features of the Coronary Blood Flow Analysis Module listed here are accessible when the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

Coronary Blood Flow supports two Marks, End Systolic Point and End Diastolic Point.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. With the Coronary Blood Flow module, only the insertion of a cycle is permitted. Both the End Systolic Point and End Diastolic Point marks will be inserted using this function.

Insert CBF Cycle

Insert CBF Cycle, will insert an entire Coronary Blood Flow cycle, including the End Systolic Point and End Diastolic Point marks. This set of marks may be inserted between the End Systolic Point of a cycle and the End Diastolic Point of the next cycle. When a Coronary Blood Flow cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Coronary Blood Flow cycle's marks are linked to the End Systolic Point mark. Deleting this mark will delete the entire cycle. Positioning the cursor over the End Systolic Point will provide the option to delete the entire cycle from the right click menu. Deletion of the End Diastolic Point mark is not permitted.

Moving Marks

Moving of the End Systolic Point and End Diastolic Point marks follow the standard rules used in Data Review. The user shall be able to move the End Systolic Point Mark between End Diastolic Point of previous cycle and End Diastolic Point of current cycle. Likewise, the user shall be able to move the End Diastolic Point Mark between End Systolic Point of current cycle and End Systolic Point of next cycle.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of how a cycle is determined. In acquisition and replay, a CBF cycle is the point where the LVP Min Pulse Height is reached for the current cycle to the point where LVP Min Pulse Height is reached for the next cycle. In review mode, a cycle is from the End Diastolic Point of current cycle to the End Diastolic Point of next cycle.

Logging Mark

The logging mark for a Coronary Blood Flow cycle is the End Systolic Point mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a Coronary Blood Flow cycle occurs one sample prior to the next cycles End Diastolic Point mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
All Derived Parameters are reporting zero	The Trigger Channel does not have a valid Left Ventricular Pressure channel or the Left Ventricular Pressure channel is not being analyzed correctly.
FMax reads low	The analysis may be triggering on artifact. Verify that the Trigger Channel has a Left Ventricular Pressure channel set.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Coronary Blood Flow]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Systole End Adjustment(low)	This sets the minimum allowable value for **Systole End Adjustment**. The default value is 0.
Systole End Adjustment(high)	This sets the maximum allowable value for **Systole End Adjustment**. The default value is 1000.

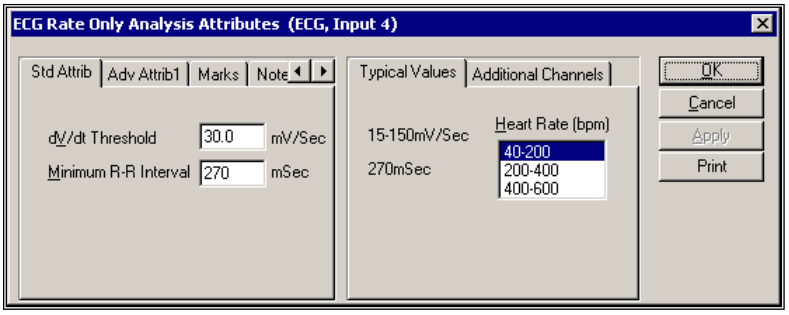
Electrocardiogram Rate Only (ECG)

The ECG Rate Only Analysis Module derives the heart rate and the R-R Interval from valid Lead II ECG complexes. The analysis module can be used with other ECG leads, as long as distinct R waves can be detected.

Attribute Window

The Electrocardiogram Rate Only attributes dialog allows you to modify the signal analysis for different electrocardiogram signal conditions.

Standard Attributes



ECG Rate Only Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
dV/dt Threshold	Signal Interpretation	Sets the ***triggering level*** of the **R** wave. The derivative must pass the dV/dt threshold value before the system will validate that cardiac cycle. The units are in millivolts/second.
Minimum R-R Interval	Signal Interpretation	Sets the minimum time value between cardiac cycles. This helps to prevent the analysis from triggering on elevated S waves or large P waves. The units are in milliseconds.

Advanced Attributes

The only Advanced Attributes for ECG Rate Only are the Low and High Pass Filter selections. Refer to **Error! Reference source not found.** in the **Error! Reference source not found.** section for more information.

Typical Values

The table contains typical values for different heart rates. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Heart Rate	Attribute	Setting	Units
40-600 (All)	dVdt Threshold	15-150	mV/Sec
40-200	Minimum R-R Interval	270	mSec
200-400	Minimum R-R Interval	135	mSec
400-600	Minimum R-R Interval	90	mSec

Marks (Validation)

The **ECG Rate Only** analysis displays a validation tick mark for each cardiac cycle. Each cardiac cycle should have only one validation mark. This mark verifies that the system is analyzing the electrocardiogram signal correctly. If there is more than one validation mark per cardiac cycle, correct the problem by changing the analysis attributes. This tab also gives you the option of enabling the mark cycle number function via a check box.

The validation mark and its meaning is listed below:

Color	Meaning
Black	QRS Mark

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
RR-I	Mean	The time interval in milliseconds from one R wave to the next R wave.

Name	Averaging In Review	Definition
HR	Harmonic Mean	The heart rate is computed in beats-per-minute and is the reciprocal of the RR-I for the cardiac cycle multiplied by 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.

Calibration

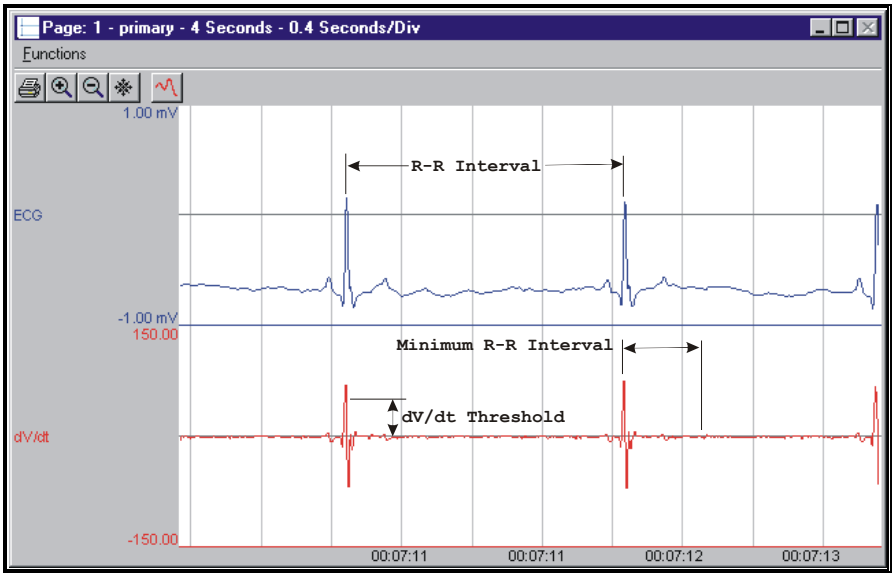
The recommended calibration for the system for an ECG signal depends on the amplifier instrumentation that the system is connected to.

The ECG Rate Only algorithm must be calibrated with two digits of precision. For example, if the amplifier has a 1mV calibration signal, the **High Cal** in the calibration menu must be set to 1.00mV.

There are two methods for calibrating the ECG channel. The first is a constant DC level applied to the channel. The second method is an ECG pulsed calibration. The pulse cannot be less than 100millisecond. The system automatically determines if this is a DC or pulsed signal.

On-Line Screens and Functions

The following is an example of a Primary graph displaying an ECG signal and its derivative.



ECG Key Marks

In the above figure, the ECG is displayed with validation tick marks labeling the R-R Interval, Minimum R-R Interval, and the dV/dt Threshold.

Presentation Signals

Below is a list of presentation signals that are available for the ECGRO Analysis Module:

Signal	Description
ECG*	This is the original ECG waveform after applying any software filters

Signal	Description
Derivative*	This will display the derivative of the ECG signal.
Heart Rate*	This will display the heart rate updated at every cardiac cycle.
***ECGRO is not currently supported in Review.**	

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Heart Rate is doubled, tripled, or very high	The **dV/dt Threshold** level may be set too low. Adjust the height of the **dV/dt Threshold** value such that the derivative exceeds the threshold only at the QRS complex.
Heart Rate is erratic or drops to zero	The dV/dt Threshold may be set too high. Adjust the height of the **dV/dt Threshold** value such that the derivative exceeds the threshold only at the QRS complex.
All derived values are zero	Adjust the height of the dV/dt Threshold value such that the derivative exceeds the threshold only at the QRS complex.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the **Product Information** option of the **Help** menu.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[ECG Rate Only]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
dVdt Threshold(low)	This sets the minimum allowable value for **dV/dt Threshold**. The default value is -1000.

Entry Name	Description
dVdt Threshold(high)	This sets the maximum allowable value for **dV/dt Threshold**. The default value is 1000.
Min RR Interval(low)	This sets the minimum allowable value for **Minimum R-R Interval** in milliseconds. The default value is 1.
Min RR Interval(high)	This sets the maximum allowable value for **Minimum R-R Interval** in milliseconds. The default value is 5000.

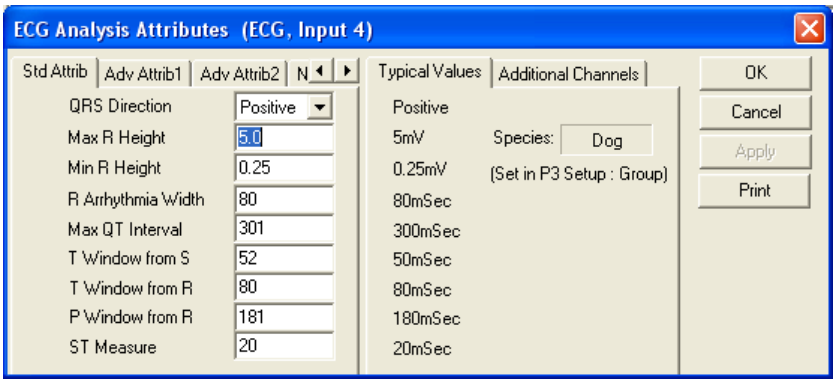
Electrocardiogram with Multilead Analysis (ECG)

The Electrocardiogram Analysis Module analyzes ECG complexes. The analysis calculates derived parameters from the input signal on a beat-to-beat basis. The detection of complexes is controlled by attributes that are set by the user.

Attribute Window

The Electrocardiogram attributes dialog allows you to modify the signal analysis for different types of electrocardiograms and the optional multilead analysis for different signal conditions.

Standard Attributes



ECG Standard Attributes Tab

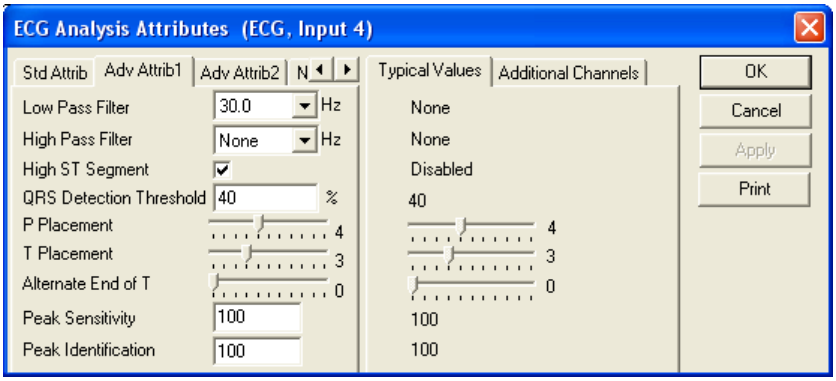
The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
QRS Direction	Signal Interpretation	Determines the direction that the analysis will search for the R wave. The selections are Positive or Negative.
Max R Height	Signal Interpretation	If the peak of the R wave, measured from the Iso-electric level, exceeds this value, this beat will be marked invalid.
Min R Height	Signal Interpretation	Specifies a minimum threshold that the R wave must exceed, relative to iso-electric, in order to be considered a valid R wave. This attributes ensures that the analysis does not falsely trigger on low level noise artifact.

Attribute	Effect On Review	Description
R Arrhythmia Width	Signal Interpretation	If the width of the signal from the beginning of the Q wave to the beginning of the S wave exceeds the R Arrhythmia Width, the associated beat will be marked invalid.
Max QT Interval	Signal Interpretation	After the analysis has determined the location of the end of the T wave, it will accept it as a valid end of T provided the QT interval (measured from the beginning of the Q wave to the end of the T wave) does not exceed the Max QT Interval.
T Window from S **T Window from R**	Signal Interpretation	These two parameters define the region in which the analysis will look for an end of T. The analysis will scan the portion of the signal *to the right of the T Window from S* and *to the left of the T window from R.* T Window from S uses S end.
P Window From R	Signal Interpretation	Defines the region where the analysis will look for the beginning of the P wave.
ST Measure	Calculation	The number of milliseconds after the end of the S wave, at which the ST elevation is measured.

WARNING: If the Intra Cardiac setting is enabled, it is important to correctly set the P Window from R setting. If the P Window from R is set too large or too small, the analysis may mis-trigger. For example, if the P Window from R is too small, the analysis may mark some of the P waves as R waves. If the P Window from R is too large, the P wave may be marked where the T wave of the previous cycle is located.

Advanced Attributes 1



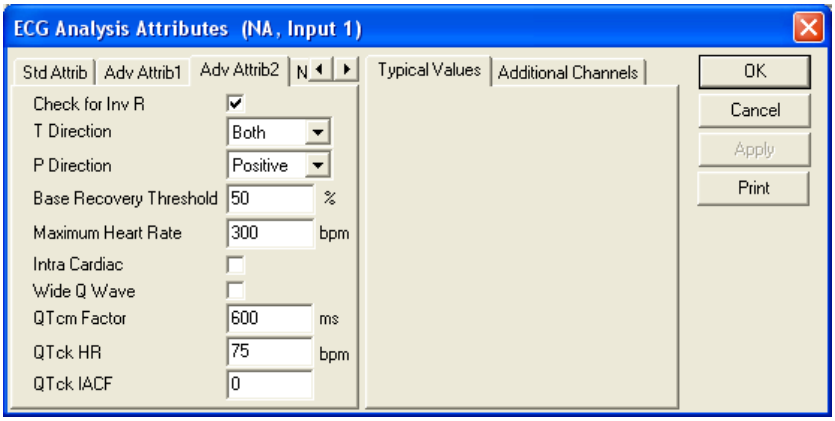
ECG Advanced Attributes 1 Tab

The Advanced Attributes 1 tab allows the selection of attributes that would less likely need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of high pass filter in hertz.
High ST Segment	None	This attribute may be used in the case of a signal in which the T wave runs into the QRS complex resulting in a high ST segment. This attribute should be enabled only if the analysis is incorrectly marking the T wave.

Attribute	Effect On Review	Description
QRS Detection Threshold	Signal Interpretation	Derivative values from previous cycles are used to calculate and aids in the identifying R waves
P Placement	Signal Interpretation	This attribute permits the user to shift the P mark towards the peak or away from the peak of the P wave. A lower value (slider towards the left) moves the P mark away from the peak. The effect of this attribute is more pronounced on P waves that exhibit a gradual rise from the baseline.
T Placement	Signal Interpretation	This attribute permits the user to shift the T mark towards the peak or away from the peak of the T wave. A lower value (slider towards the left) moves the T mark away from the peak. The effect of this attribute is more pronounced on T waves that exhibit a gradual return to the baseline.
Alternate End of T	Signal Interpretation	The alternate end of T attribute permits the algorithm to search beyond the first potential end of T for another end of T further in the complex. A lower value (slider towards the left) causes the analysis to select the first end of T that it finds. A higher value (slider towards the right), utilizes a more aggressive search for an alternate end of T. This attribute is useful when dealing with complexes in which the T wave, after the peak, does not return to the baseline smoothly, but shows a second peak.
Peak Sensitivity	Signal Interpretation	When dealing with extremely small P or T waves, the analysis may not identify the end of T or beginning of P, in such cases, the Peak Sensitivity attribute may help in correctly validating the signal. The default sensitivity level is 100, reducing this attribute permits greater sensitivity with 0 being maximum sensitivity. Adjust this parameter in steps of 25. This parameter should be used in conjunction with Peak Identification. Peak Sensitivity controls the elimination of small peaks when identifying T and P peaks. Peak Identification controls the thresholds used to identify potential T and P peaks. If small peaks are not identified, Peak Sensitivity should be lowered. If the problem persists after Peak Sensitivity is lowered to 0, Peak Identification should be lowered as well.
Peak Identification	Signal Interpretation	This attribute appears in the dialog box only if the following entry is found in the [ECG] section in the PPP3.INI file: Peak Sensitivity=1 See Peak Sensitivity for details. Default value = 100(matches performance in ECG 4.40) Minimum value = 0 (most sensitive) Maximum value = 100 (least sensitive)

Advanced Attributes 2



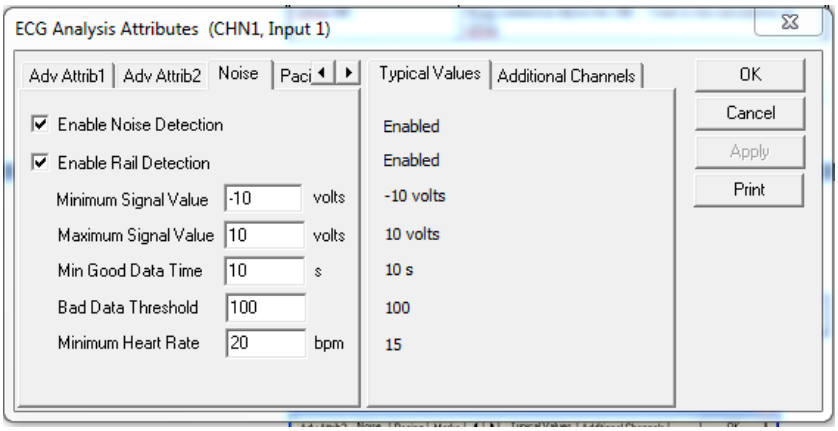
ECG Advanced Attributes 2 Tab

The Advanced Attributes 2 tab allows the selection of attributes that would less likely need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Check for Inv R	Signal Interpretation	Check for inverted R waves. When this check box is enabled, the analysis will flag any beats that have inverted R waves as invalid. R waves are expected to peak in the same direction as the dVdt Threshold polarity. i.e. If dVdt Threshold is positive we expect positive R waves and negative R waves would be considered to be inverted. If a signal has a very pronounced Q wave the analysis may mistake the Q wave for an inverted R, this can be prevented by disabling Check for Inv R.
T Direction	Signal Interpretation	This attribute directs the analysis to look for a T wave that is either exclusively Positive, exclusively Negative, or Both (either positive, negative, or bi-directional). In most cases a setting of Both should work, and the analysis will determine the nature of the T wave. Positive and Negative settings may be used to help the analysis along when dealing with troublesome data.
P Direction	Signal Interpretation	This attribute directs the analysis to look for a P wave that is either exclusively Positive, exclusively Negative, or Both (either positive, negative, or bi-directional). In most cases a setting of Both should work, and the analysis will determine the nature of the P wave. Positive and Negative settings may be used to help the analysis along when dealing with troublesome data

Attribute	Effect On Review	Description
Base Recovery Threshold	Signal Interpretation	When a disturbance is seen on the leading or lagging edge of the R wave, the analysis may mark the Q or S wave at the point of the disturbance. This attribute may be used to prevent the analysis from looking for the Q or S wave until after the disturbance. The number in the edit field represents the percentage of the leading edge of the R wave by which the signal must return (from the R peak) before the analysis will look for the Q or S wave. If this value is set to 0 (default), the analysis will start looking for the Q or S wave from the level of the R peak. If it is set to 70, the signal will have to recover by 70% of the R height before the analysis starts looking for the Q or S wave.
Maximum Heart Rate	Signal Interpretation	This attribute is used to assist the analysis in the rejection of noise, to ensure that large rapid signal fluctuations due to noise are not marked as cardiac cycles. Maximum Heart Rate should be set higher than the highest expected heart rate.
Intra Cardiac	Signal Interpretation	This checkbox is used to enable processing of ECG signals which exhibit rapid changes in the P wave such that the derivative of the P wave exceeds the dVdt threshold. Enabling this check box prevents the analysis from marking the P wave as the R wave. When this check box is disabled, ECG cycles are reported on reaching the beginning of S of the following cycle. When this check box is enabled, ECG cycles that are followed by a high derivative P wave are reported on reaching the beginning of S of the following cycle. Cycles that do not have a high P wave derivative are reported P window from R milliseconds after crossing the dVdt Threshold. When multilead analysis is being performed, the data for the previous cycle will be reported when the first S in the group is found. The default value when opening older protocol files is disabled.
Wide Q Wave	Signal Interpretation	This sets how the Q wave will be detected. The Q wave detection has been improved and the user can use the new way, or the original way of detecting Q waves. When enabled, the new detection is used. When disabled, the original detection is used. The default is disabled.
QT cm Factor	Calculation	Matsunaga correction factor. This sets the RR value in ms used in the correction factor. This default value is based on a HR of 100 beats per minute.
QTck HR	Calculation	King correction factor for HR. Used in the calculation of QTck.
QTck IACF	Calculation	Individual animal correction factor (King) used in calculating QTck.

Noise Attributes

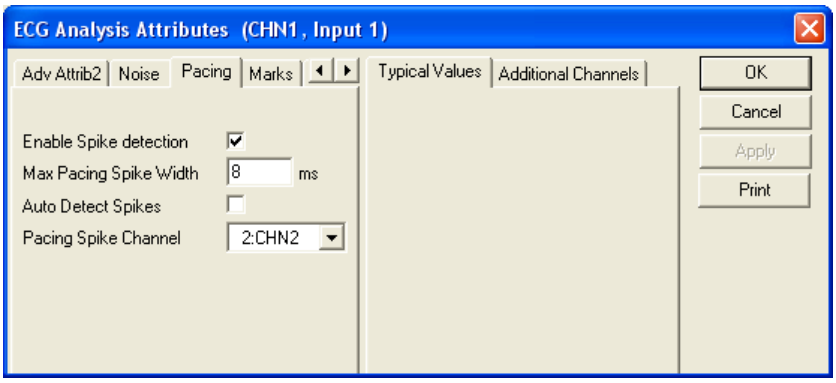


ECG Noise Tab

The Noise Tab contains attributes that are used to identify noisy data. On identifying noisy data, Bad Data Marks will be placed to span the noisy sections.

Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Allows the attributes to be edited and used by the software.
Enable Rail Detection	Signal Interpretation	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value/ Maximum Signal Value	Signal Interpretation	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.
Minimum Good Data Time	Signal Interpretation	When Noise detection is enabled and a range of data is analyzed, any bad data marks that have less than or equal to the Min Good Data Time of good data between them shall be combined into a single bad data region.
Bad Data Threshold	Signal Interpretation	This edit box specifies a noise level. When the level set in this box is exceeded, the data will be interpreted as noise and Bad Data Marks will be inserted to remove the section of data from analysis.
Minimum Heart Rate	Signal Interpretation	Heart rates detected by the analysis that fall below the level specified will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis.

Pacing



ECG Pacing Tab

The Pacing tab allows the software to identify pacing spikes in the ECG signal and remove them from analysis based on spike width or by specifying an external pacing spike channel.

Attribute	Description
Enable Spike Detection	Allows the attributes to be edited and used by the software.
Max Pacing Spike Width	Used to remove the pacing spike from the analysis and eliminate the possibility of the spike being marked as an R wave. This attribute should be set to a value, in milliseconds, wider than the pacing spike but shorter than the QRS complex. If the value is shorter than the duration of the spike, the spike will be marked as an R wave. If the value is set too wide, QRS complexes will not be analyzed. This feature is used when Enable Spike Detection is enabled.
Auto Detect Spikes	Determines whether an external pacing spike channel is used or whether the analysis monitors the ECG channel for pacing spikes.
Pacing Spike Channel	This box lists all channels set to RAW analysis. When using an external channel to monitor the pacing spike, set the analysis of the spike channel to RAW in the P3 Input Setup menu. Additionally, the attributes for this channel must be set to properly identify the spike by using the Trigger Direction attribute. The software will use this channel to identify the spike and remove it from the associated ECG channel. This feature is used when Auto Detect Spikes is disabled.

Typical Values

The table contains typical values for different heart rates based on species selection in the P3 Setup Group Tab. Selection of a species will automatically update these values in the attributes dialog. When using a species other than those listed, choose a species designation based on similar HR. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Standard Attribute	Dog HR=40-200	Monkey HR=120-180	Rat HR=300-480	Mouse HR=400-600
R Direction	Positive	Positive	Positive	Positive

Standard Attribute	Dog HR=40-200	Monkey HR=120-180	Rat HR=300-480	Mouse HR=400-600
Max R Height	5mV	5mV	5mV	5mV
Min R Height	0.25mV	0.25mV	0.25mV	0.25mV
R Arrhythmia Width	80mSec	80mSec	80mSec	80mSec
Max QT Interval	300mSec	300mSec	150mSec	100mSec
T Window from S	50mSec	50mSec	25mSec	10mSec
T Window from R	80mSec	80mSec	40mSec	20mSec
P Window from R	180mSec	180mSec	100mSec	70mSec
ST Measure	20mSec	20mSec	20mSec	20mSec

Marks (Validation)

The **ECG** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the ECG signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Q Wave
Blue	R Wave
Green	End of S Wave
Red	End of T Wave
Cyan	Beginning of P Wave
Magenta	End of P Wave
Yellow	Beginning of S Wave
Gray	T Peak

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be

calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

In order for the ECG analysis to accurately calculate and report the multi-lead parameters, all channels which are enabled with the ECG analysis should be validating the signal correctly. Otherwise, this might lead to errors in the reported parameter values.

Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
RR-I	Mean	Time interval in milliseconds from one R wave to the next R wave.
HR	Harmonic Mean	The heart rate is computed in beats-per-minute and is the reciprocal of the RR-I for the cardiac cycle multiplied by 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
R-H	Mean	Height of the R wave from the Iso-electric level, in millivolts.
P-H	Mean	Height of the P wave from the Iso-electric level, in millivolts.
T-H	Mean	Highest point between the end of the S wave and the end of the T wave relative to the Iso-electric point.
T-HN	Mean	Lowest point between the end of the S wave and the end of the T wave relative to the Iso-electric point.
ST-I	Mean	Time interval in milliseconds from the S wave to end of the following T wave.
ST-E	Mean	The ST elevation, measured “ST Measure” milliseconds after the S wave, from the Iso-electric level.
QRS	Mean	Time interval of the QRS complex, from the Q wave to the S wave, measured in milliseconds.
PR-I	Mean	PR interval measured from the start of the P wave to the beginning of the Q wave, in milliseconds.
QT-I	Mean	QT interval measured from the Q wave to the end of the following T wave, in milliseconds.
QAT	Mean	Q Alpha T is the time interval from the Q wave to the peak of the following T wave in milliseconds.
QTcb	Analysis	The corrected QT interval, using Bazett’s method. Computed as the QT interval divided by the square root of the RR-I in seconds. The corrected QT is reported in milliseconds. When running in a multiple epoch logging rate, or second logging rate, the averaged value will be calculated off of the averaged RR-I value.
QTcf	Analysis	The corrected QT interval, using Fridericia’s method. Computed as the QT interval divided by the cube root of the RR-I in seconds. The corrected QT is reported in milliseconds. When running in a multiple epoch logging rate, or second logging rate, the averaged value will be calculated off of the averaged RR-I value.

Name	Averaging In Review	Definition
QTcv	Analysis	The corrected QT interval, using Van de Water's method. Computed as: QT Interval – 0.087 * (RR Interval – 1) Where the RR Interval and the QT Interval are in seconds. The resultant corrected QT is reported in milliseconds. When running in a multiple epoch logging rate, or second logging rate, the averaged value will be calculated off of the averaged RR-I value.
EQTS*	Mean	Extended QT in a single lead. The longest QT interval in any of the recorded leads in a single group.
EQTSc*	Max Times	The channel from which the longest QT Interval was obtained, in the current group. This is the channel from which the EQTS parameter was reported. Note: When running in a logging mode other than 1 epoch, the averaged value will be reported as the channel that was reported most in the logging period. A 'tie' of two or more channels will report the lowest numbered channel.
EQTM*	Mean	Extended QT for multileads. The QT Interval measured from the first occurrence of the Q wave to the last occurrence of the T wave across all recorded leads in a single group.
EQTMcs*	Max Times	The channel from which the first Q was found, in the current group. This is the Q used to report the EQTM parameter. Note: When running in a logging mode other than 1 epoch, the averaged value will be reported as the channel that was reported most in the logging period. A 'tie' of two or more channels will report the lowest numbered channel.
EQTMce*	Max Times	The channel from which the last T was found, in the current group. This is the T used to report the EQTM parameter. Note: When running in a logging mode other than 1 epoch, the averaged value will be reported as the channel that was reported most in the logging period. A 'tie' of two or more channels will report the lowest numbered channel.
QTD*	Mean	QT Dispersion, which is the longest QT interval measured in any recorded lead minus the shortest QT measure in any recorded lead in a single group.
QTMc*	Max Times	The channel from which the shortest QT interval was found, in the current group. Note: When running in a logging mode other than 1 epoch, the averaged value will be reported as the channel that was reported most in the logging period. A 'tie' of two or more channels will report the lowest numbered channel.
QR-I	Mean	QR interval measured from the Q wave to the following R wave, in milliseconds.
QRSA	Mean	QR amplitude in the lowest point on the Q wave to the peak of the R wave. This is calculated as R wave value minus the lowest point between the Q and R marks.
MxdV	Mean	Maximum derivative of the R wave.
T-A	Mean	Area of the T wave from the Iso-electric level calculated from the S end mark to the point prior to the T end mark.
PCt	Sum	The number of valid P waves encountered in the logging period. Note: When running in a logging mode other than 1 epoch, the averaged value will be the number of counts over the logging period.
TCt	Sum	The number of valid T waves encountered in the logging period. Note: When running in a logging mode other than 1 epoch, the averaged value will be the number of counts over the logging period.

Name	Averaging In Review	Definition
QTCt*	Min	QT count, the number of channels in a group from which the EQTS, EQTM, and QTD parameters are calculated. Note: When running in a logging mode other than 1 epoch, the averaged value will be the smallest number obtained from the lines of data that are used.
BAD	Sum	The number of arrhythmic beats detected during a specified logging period. This counter does not count missing T waves as BAD. Note: When running in a logging mode other than 1 epoch, the averaged value will be the number of counts over the logging period.
GW	Sum	The Good Wave counter counts the total number of complete complexes detected during the logging period. A complex is considered to be complete when the Q, P, and T waves are detected. Note: When running in a logging mode other than 1 epoch, the averaged value will be the number of counts over the logging period.
TW	Sum	The total number of good and bad complexes that were detected during a logging period. The sum of the BAD and GW does not necessarily equal the TW, since the system can analyze a complex even if there are no end of T waves detected. Note: When running in a logging mode other than 1 epoch, the averaged value will be the number of counts over the logging period.
QATN	Mean	Reports the time, in milliseconds, between the Q wave and the lowest point between the end of S and the end of T wave.
PWdth (Pwidth)	Mean	Reports the time, in milliseconds, between the start and end of the P wave.
Tpe-I	Mean	This parameter reports the time in milliseconds between the peak of the T wave and the end of the T wave. The peak of the T is identified as the greatest deflection from the Iso-electric level between the end of S and the End of T and is marked with the T peak mark.
T-P	Mean	This parameter reports the signal value at the peak of the T wave relative to the Iso-electric level. The peak of the T is identified as the greatest deflection from the Iso-electric level between the end of S and the End of T and is marked with the T peak mark.
Match	Mean	Used specifically with Template Analysis. Reports the percentage of cycles that match a template in a given logging period.
Pmatch	Mean	Used specifically with Template Analysis. Reports the average degree of match for the P Region for cycles within the logging interval.
Qmatch	Mean	Used specifically with Template Analysis. Reports the average degree of match for the Q Region for cycles within the logging interval.
Smatch	Mean	Used specifically with Template Analysis. Reports the average degree of match for the S Region for cycles within the logging interval.
Tmatch	Mean	Used specifically with Template Analysis. Reports the average degree of match for the T Region for cycles within the logging interval.

Name	Averaging In Review	Definition
Noise	Mean	This parameter reports an approximation of the noise level in the ECG cycle. The value reported is the RMS value of the derivative between the 2 R marks after excluding the following regions: 10% of the signal following the start R mark 10% of the signal prior to the end R mark 10% of the signal around the 2 largest derivative peaks If a derivative greater than 3 times the largest QRS derivative is encountered, T and P regions will not be removed.
QT cm	Analysis	The corrected QT interval, using Matsunaga's method. Computed as QTcm = log(QTcm Factor) * QT/ log(RR) (where RR is expressed in mSec).
QTck	Analysis	The corrected QT interval using King's method. Computed as QT + Beta * (HR – "QTck HR").
Count	Count	The number of cycles within a logging interval or a data reduction interval In Beat mode, Count = 1
PP-I	Mean	Reports the time, in milliseconds, between 2 continuous cardiac cycles' P start marks. If the preceding cycle has been removed due to bad data marks, a value "x" is reported.
TP-I	Mean	Reports the time, in milliseconds, from a preceding T end mark to the current P start mark. The 2 cycles need to be continuous cardiac cycles and have the T mark on the preceding T wave and a P start mark on the current cycle. If the required validation marks are not placed or the data is not continuous, a value "x" is reported.
TQ-I	Mean	Reports the time, in milliseconds, from a preceding T end mark to the current Q mark. The 2 cycles need to be continuous cardiac cycles and have the T mark on the preceding T wave and a Q mark on the current cycle. If the required validation marks are not placed or the data is not continuous, a value "x" is reported.
JTp-I	Analysis	Reports the time, in milliseconds, between the S end and the T peak of a cycle.
***Available only when performing multilead analysis.**		

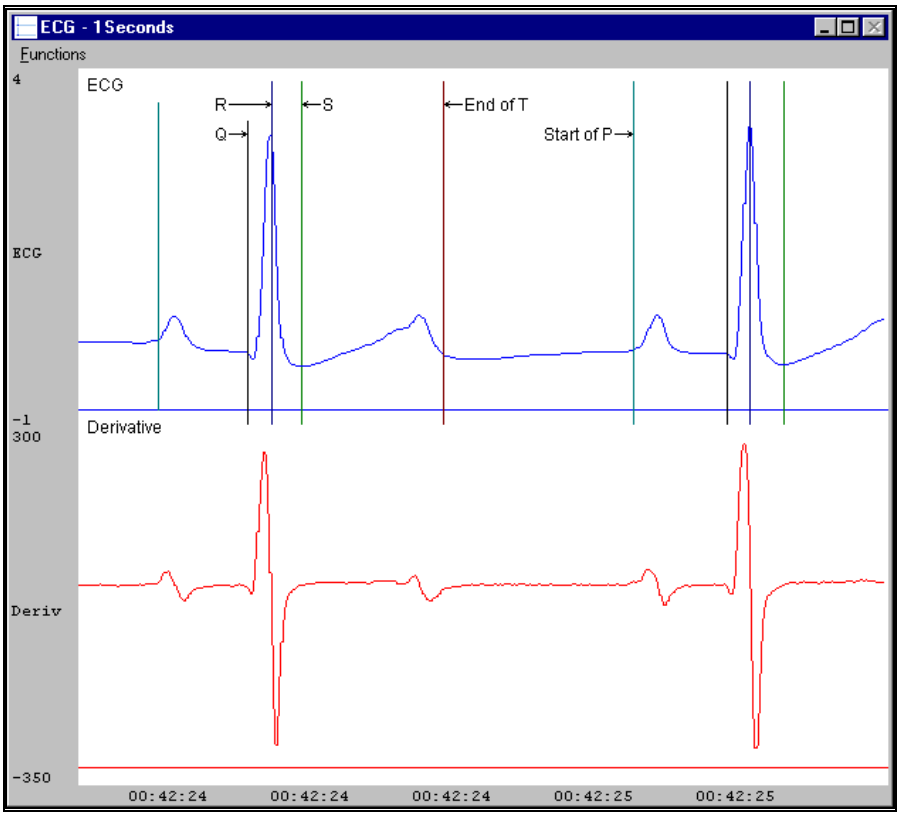
Calibration

The recommended calibration for the system for an ECG signal depends on the amplifier instrumentation that is connected to the system.

There are two methods for calibrating the ECG channel. The first is a constant DC level applied to the channel. The second method is an ECG pulsed calibration. The pulse cannot be less than 100millseconds. The system automatically recognizes if this is a DC or pulsed signal.

On-Line Screens and Functions

The following is an example of a Primary graph displaying an ECG signal and its derivative.



ECG Key Marks

In the above figure, the Electrocardiogram signal is displayed along with its validation tick marks. The validation marks identify Q, R, End of S, End of T, and Beginning of P.

Presentation Signals

Below is a list of presentation signals that are available for the ECG Analysis Module:

Signal	Description
ECG	This is the original ECG waveform after applying any software filters and spike removal algorithms (if spike detection is enabled)
Derivative	This will display the derivative of the ECG signal.
Heart Rate*	This will display the heart rate updated at every cardiac cycle.
Spike*	This is the original ECG waveform after applying any software filters. If spike detection is enabled, this presentation signal will include the spikes.
***Presentation signals not available in Review.**	

Data Review

The Data Review related features of the ECG analysis module listed here are accessible when the analysis module is used with P3 Plus Version 4.10 or greater and if the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu – Analyze.

Mark Operations

ECG marks are divided into two types, marks that always exist when a valid cycle is found (Q, R, Sstart, Send) and marks that may or may not exist, depending on the signal quality and morphology (Pstart, Pend, Tend, and Tpeak). The R mark may exist by itself (Arrhythmic R mark) to indicate a bad cycle.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The popup menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion, signal morphology is not considered.

Insert QRS

Inserts QRSsSe. This set of marks may be inserted at any location except between a Ps, Pe, and anywhere within a set of QRSsSe marks. When a QRS is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Insert Arrhythmic R

An Arrhythmic R may be inserted between two ECG cycles, but not within a cycle. An ECG cycle is composed of PsPeQRSsSeTe. The PsPe and Te marks may not be present. The first and last marks present in a cycle represent the limits prior to and after which the Arrhythmic R may be inserted.

Insert P Start (P3 Plus 4.30 and earlier)

This selection will be available if an insert is attempted at the start of a cycle and P Start is not present for the cycle.

Insert P End (P3 Plus 4.30 and earlier)

This selection will be available if an insert is attempted to the left of a Q mark and a P End is not present in the current cycle.

Insert T End

This selection will be available if an insert is attempted to the right of an S End mark and a T End is not present for the current cycle. In P3 Plus 4.40 and later Tp is added along with Te.

Insert S End

This selection will be available if an insert is attempted to the right of an S Start mark and an S End mark is not present for the current cycle. The only location where an S Start is present without an S End, may be at the end of the review file depending on how much of the next cycle is available.

Insert Pse

This selection will be available if an insert is attempted at the start of a cycle and P marks are not present for the cycle.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. Ps, Pe, Tp and Te may be deleted in this fashion. Q, Ss, and Se marks cannot be deleted individually. They are linked to an R wave. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the R wave and the right mouse button is clicked to delete the marks. One of the selections in the popup menu will permit deletion of all the marks in the cycle, including any Ps, Pe, Tp, Te marks associated with the R wave.

In P3 Plus 4.40 or greater, deleting either of the P wave marks will delete both P wave marks. Deleting Tend will delete the T peak mark as well.

Moving Marks

Moving Ps, Pe, Q, R, Ss, Se, Tp and Te marks follow the standard rules used in Data Review. One exception in P3 Plus versions 4.40 and greater is the interaction between the T marks and the subsequent cycles P marks. The T marks can be moved past the P and vice versa.

Calculations

The calculations of all derived parameters are identical to those performed during acquisition and replay modes with one exception, P height. During acquisition and replay mode, the P direction is determined by the shape of the P wave relative to the T-P segment. During Data Review, the P direction is based on the shape of the P wave relative to the points at which the P start and P end are marked. In both cases, the P height is calculated as the distance of the highest/lowest point from the Iso-electric line, depending on whether the P direction is positive or negative. If the P start and P end marks are not placed correctly, the P direction determined by Data Review may be different from the P direction determined during acquisition and replay modes.

Logging Mark

The logging mark for an ECG cycle is the R wave mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of an ECG cycle follows the R wave by 66.7% of the interval between the current cycles R wave and the following R wave. When BP and ECG data are brought into Review, the ECG channel should be used as the epoch channel to ensure that related cycles are kept together.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
A complex is incorrectly marked as an arrhythmia	Verify R Arrhythmia Width is wide enough to accommodate the QRS complex. Ensure that Max R Height setting is large enough to accommodate the R wave.
Start of P wave not marked	Ensure that P Window from R extends beyond the P wave.
End of T wave not marked correctly	Ensure that the T Window from S and the T Window from R correctly define the region in which the end of T is expected. Ensure that Max QT Interval extends beyond the T wave.

Problem	Solution
Algorithm does not trigger (No marks)	Reduce the sample rate to 250-1000Hz (Calibration - A/D Setup).
The R waves are marked with a single mark, and nothing else is marked	Is Max R Height too low? Is R Arrhythmia Width too small? Is Check for Inv R enabled and does the data exhibit a large Q wave?
T mark is not displayed	Ensure that the Max QT Interval extends beyond the end of the T wave. The T window from R should encompass the P wave. The T window from S should end prior to the start of the T wave and be close to the Iso electric level.
T mark is not displayed even though the T windows are set correctly	Check T Direction.
P mark is not displayed	Verify that the P window from R extends beyond the beginning of the P wave. If the P mark does not appear, check the P Direction attribute.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[ECG]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Maximum R Height(low)	This sets the minimum allowable value for Max R Height. The default value is 1.
Maximum R Height(high)	This sets the maximum allowable value for Max R Height. The default value is 25.
Minimum R Height(low)	This entry sets the minimum allowable value that the Min R Height attribute may be set to, in user units. The default value is 0.
Minimum R Height(high)	This entry sets the maximum allowable value that the Min R Height attribute may be set to, in user units. The default value is 25.
Maximum QRS Width(low)	This sets the minimum allowable value for R Arrhythmia Width in milliseconds. The default value is 20.

Entry Name	Description
Maximum QRS Width(high)	This sets the maximum allowable value for R Arrhythmia Width in milliseconds. The default value is 150.
Maximum QT Interval(low)	This sets the minimum allowable value for Max QT Interval in milliseconds. The default value is 50.
Maximum QT Interval(high)	This sets the maximum allowable value for Max QT Interval in milliseconds. The default value is 5000.
T Window from S(low)	This sets the minimum allowable value for T Window from S in milliseconds. The default value is 0.
T Window from S(high)	This sets the maximum allowable value for T Window from S in milliseconds. The default value is 5000.
T Window from R(low)	This sets the minimum allowable value for T Window from R in milliseconds. The default value is 0.
T Window from R(high)	This sets the maximum allowable value for T Window from R in milliseconds. The default value is 5000.
P Window from R(low)	This sets the minimum allowable value for P Window from R in milliseconds. The default value is 50.
P Window from R(high)	This sets the maximum allowable value for P Window from R in milliseconds. The default value is 5000.
ST Measure Interval(low)	This sets the minimum allowable value for ST Measure in milliseconds. The default value is 10.
ST Measure Interval(high)	This sets the maximum allowable value for ST Measure in milliseconds. The default value is 100.
Peak Sensitivity(low)	This sets the minimum allowable value for the Peak Sensitivity value, which is used to detect small P or T waves. The default value is 0.
Peak Sensitivity(high)	This sets the minimum allowable value for the Peak Sensitivity value, which is used to detect small P or T waves. The default value is 150.
S Recovery Threshold(low)	This sets the minimum allowable value for Base Recovery Threshold in percent. The default value is 0.
S Recovery Threshold(high)	This sets the maximum allowable value for Base Recovery Threshold in percent. The default value is 100.
Maximum Heart Rate(low)	This sets the minimum allowable value for Maximum Heart Rate. The default value is 1.
Maximum Heart Rate(high)	This sets the maximum allowable value for Maximum Heart Rate. The default value is 10000.
Pacing Spike Width(low) Unsupported feature	This sets the minimum allowable value for Max Pacing Spike Width. The default value is 0.
Pacing Spike Width(high) Unsupported feature	This sets the maximum allowable value for Max Pacing Spike Width. The default value is 100.
Peak Identification(low)	This entry sets the minimum allowable value for Peak Identification, in milliseconds. The default value is 0.
Peak Identification(high)	This entry sets the maximum allowable value for Peak Identification, in milliseconds. The default value is 100.
QRS Threshold(low)	This entry sets the minimum allowable value that the QRS Detection Threshold attribute may be set to, in %. The default value is 0.
QRS Threshold(high)	This entry sets the maximum allowable value that the QRS Detection Threshold attribute may be set to, in %. The default value is 100.

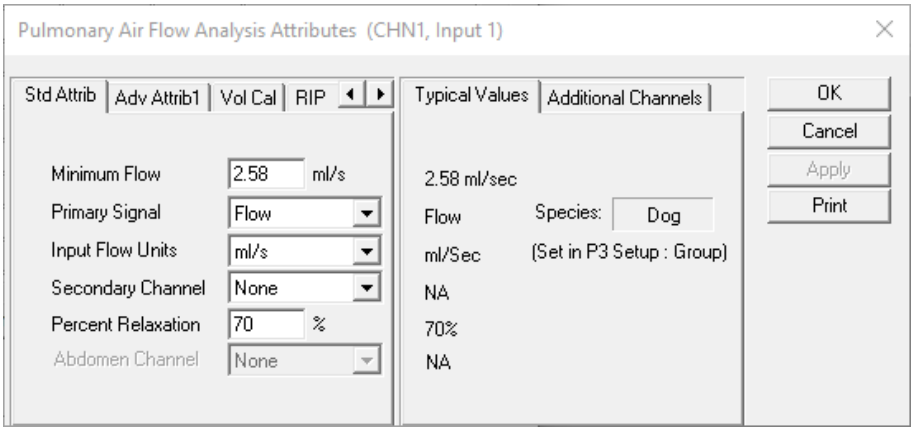
Pulmonary Air Flow & Airway Resistance (PAF)

The Pulmonary Air Flow Analysis Module analyzes pulmonary airflow signals obtained from a plethysmograph box, a pneumotachograph or via respiratory inductive plethysmography (RIP). It also calculates, on a breath-to-breath basis, values for the respiratory cycle.

If the optional airway resistance module has been installed, the system will also calculate the phase difference between a dual chamber plethysmograph to calculate specific airway resistance, phase shift, and the delta time between the two chambers.

Attribute Window

The Pulmonary Air Flow Analysis attributes window allows you to modify the signal analysis for different types of air flow signals and different signal conditions.



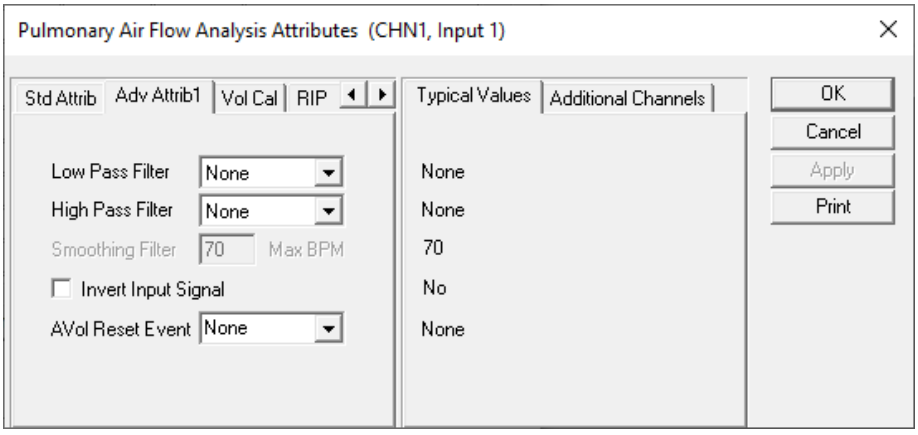
Pulmonary Air Flow Standard Attribute Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Flow	Signal Interpretation	Sets the minimum flow that the analysis must achieve before the analysis will detect and validate a pulmonary cycle. The Minimum Flow stops the analysis from triggering on artifacts such as cardiac noise.
Primary Signal	Signal Conditioning, Calculation, Redraw	Sets the system for either a Flow input signal or a Volume input signal or RIP input signals. If Volume is selected as the primary signal, you can display the digitally derived flow signal on a primary graphic page by selecting Flow as the Presentation in the Primary Graph Page Setup window. If Flow is selected as the primary signal, you can display the digitally derived volume signal on the primary graph page by selecting Volume as the Presentation in the Primary Graph Page Setup window.

Attribute	Effect On Review	Description
Input Flow Units / Calculated Flow Units	Signal Conditioning, Calculation, Redraw	Input Flow Units is active when Flow is selected as the Primary Signal. Input Flow Units specifies the units of flow being measured so that the system calculates the volume correctly. Calculated Flow Units is active when Volume or Vol-RIP-Chest is selected as the Primary Signal. Calculated Flow Units specifies the volume units used so that the system calculates the flow values correctly. mL/Sec (milliliters per second) mL/Min (milliliters per minute) L/Sec (liters per second) L/Min (liters per minute)
Secondary Channel	Calculation	This field is only available if the PNM-AWR100W option has been installed. The channel used as the second chamber must be specified in this list box, and the channel must be defined as Pulmonary Air Flow.
Percent Relaxation	Calculation, Redraw	Used to draw the percent relaxation mark and to calculate Penh and RT. The Percent Relaxation Mark is drawn when the volume signal drops from its maximum value by the specified percentage.
Abdomen Channel	Calculation	This attribute is used to define the Abdomen channel in a RIP setup. This attribute is selected from the chest channel and is enabled when Vol-RIP-Chest is selected as the Primary signal. When enabled, the Abdomen channel displays all PAF channels that are sampled at the same sample rate as the current channel.

Advanced Attributes

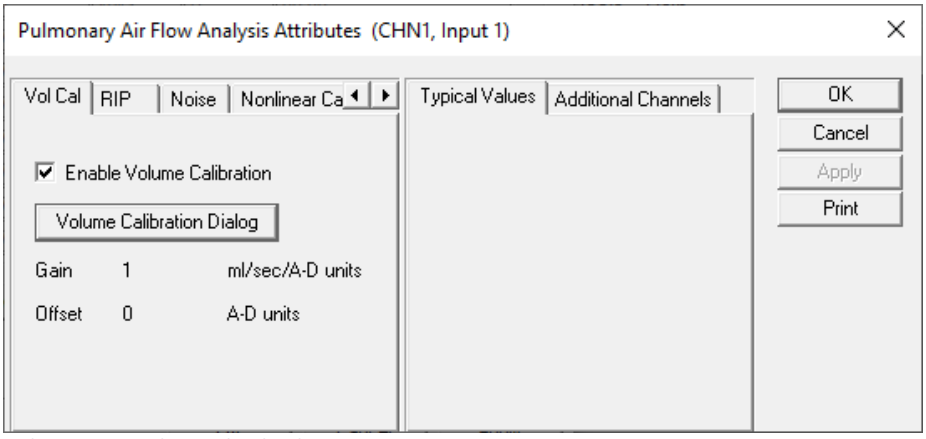


Pulmonary Air Flow Advanced Attributes Tab

The Advanced Attributes 1 tab allows selection of attributes that would less likely need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Smoothing Filter	Signal Conditioning, Calculation, Redraw	Defines a smoothing function by specifying the maximum breaths per minute that will not experience signal loss due to the filter. This filter is only applied when the Primary Signal is a volume signal, either Volume or Vol-RIP-chest. If Flow is selected as the Primary Signal, this attribute will be disabled and a smoothing filter will not be applied. Setting the Smoothing Filter to a high value (e.g. 999) will effectively disable this filter.
Invert Input Signal	Signal Conditioning, Calculation, Redraw	This check box should be enabled if the respiration signal is acquired such that inspiration is negative. The PAF Analysis Module requires that inspiration is positive. Selecting the check box will reverse the polarity of the acquired signal.
AVol Reset Event	Calculation	Used to determine the start point for the Accumulated Volume derived parameter (AVol). The selection of an event, "a" through "J", will determine the start point for the calculation of AVol. If "None" is selected, the AVol derived parameter will report zero (acquisition and replay) or "x" (Review). The start of an acquisition, a break in the data, or subsequent entries of the event to trigger the start point for the AVol calculation will result in the derived parameter being reset.

Vol Cal

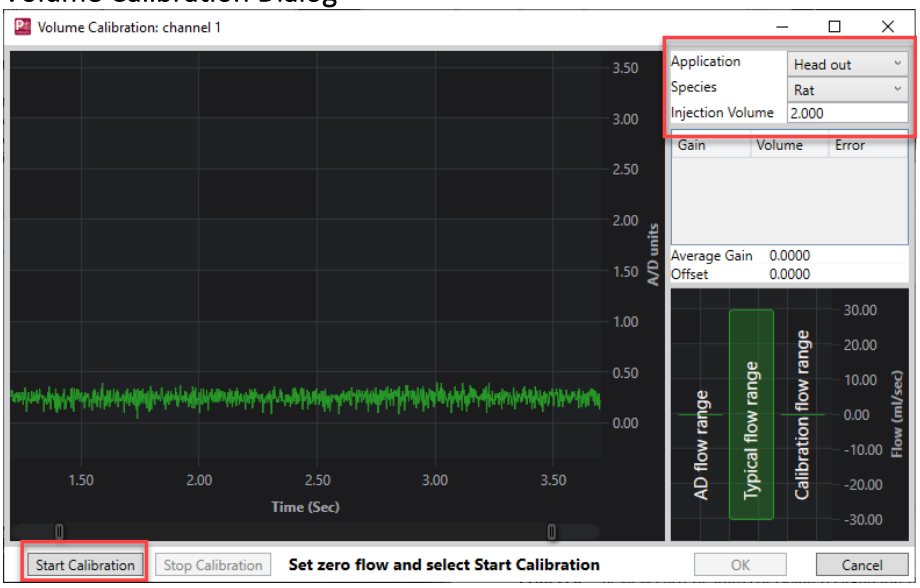


Pulmonary Air Flow Vol Cal Tab

The Vol Cal tab stands for volume calibration and is used for calibrating an air flow signal using an injection of a known volume of air.

Attribute	Description
Enable Volume Calibration	Enables the volume calibration feature and applies the gain and offset to the signal. This option is only available when the Primary Signal is set to 'Flow' in Std Attrib.
Volume Calibration Dialog	Launches the Volume Calibration in a separate window.
Gain	The gain that has been calculated from previous calibration session.
Offset	The offset that has been calculated from previous calibration session.

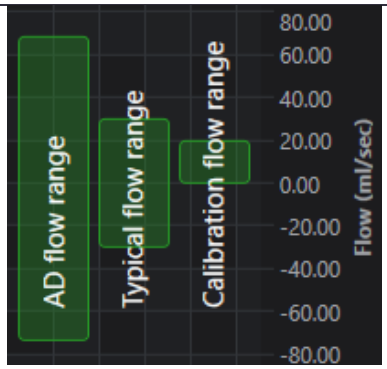
Volume Calibration Dialog



Pulmonary Air Flow Volume Calibration Dialog

Selecting the 'Volume Calibration Dialog' button will bring up the volume calibration window. This is comprised of a graph as well as some user input fields and a button to start and stop calibration. Immediately when the window is opened the graph will begin displaying currently sampled data from the selected channel.

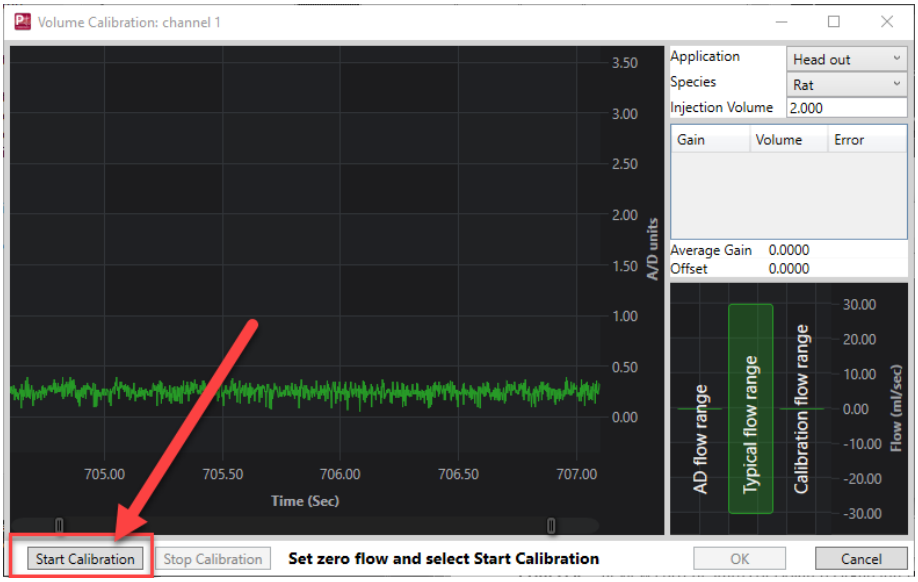
Attribute	Description
Application	Allows selection of a specific application which is loaded from an XML file. Each application has preset species and injection volume settings.
Species	Will list the available species that are available for the selected application.

Attribute	Description
Injection Volume	A preset volume that is typical for the application and species selected. This can be modified. The Injection Volume should be close to the TV of the species. The injection volume must match the actual volume being injected via syringe or pipette for an accurate calibration.
Gain/Volume/Error box	Will list the Gain, Volume and Error for each injection that was detected. An injection can be selected from the table to view in the graph, where the boundaries can be adjusted (blue and red lines) or it can be deleted.
Average Gain/Offset	Calculates the average gain and offset for the injections saved in the table.
Mini flow range Graph	
• **AD flow range**	Reflects the range of flow values that can be acquired based on the Span of the signal that is currently set in the ACQ7700 setup and the volume calibration gain and offset values. The AD flow range should exceed the typical flow range by 20-50%. If AD flow range is too small the signal will rail and appear clipped at the max and min, and if it is too large the signal will have poor resolution. To adjust AD flow range, go back to the ACQ7700 setup and adjust span setting.
• **Typical flow range**	Reflects the calculated typical flow range for the application/species selected and the injection volume that is set.
• **Calibration flow range**	Reflects the flow range used during the injections
Start Calibration	Clicking start will begin a calibration session. A calibration session will run for 120 seconds in which time all injections need to be performed. If the time runs out a new calibration session can be started.
Stop Calibration	Stops the calibration after all injections are performed within the 120 second window. If calibration is not stopped it will end automatically when the 120 second timer runs down.
Message Notification area	To the right of the Stop Calibration button, this area notifies the user of calibration session status.

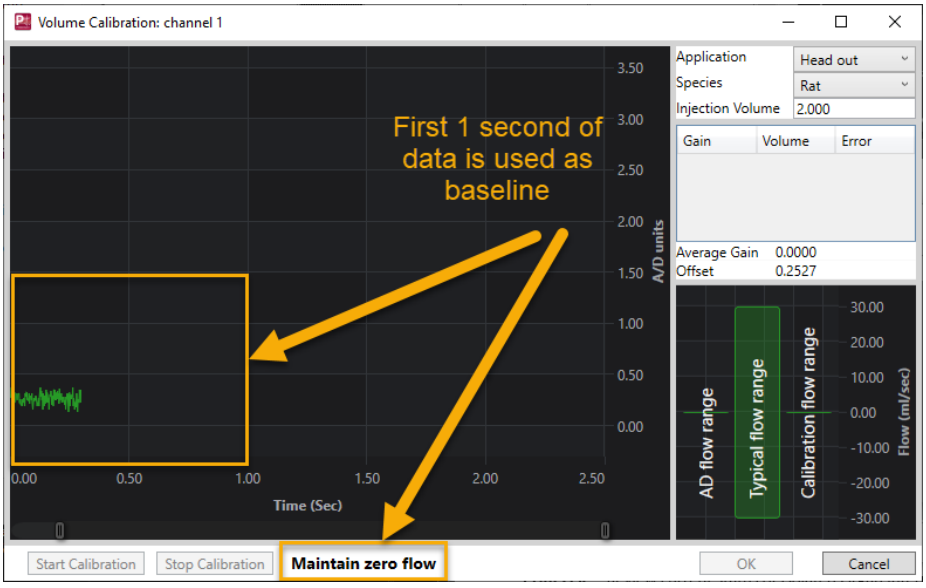
Performing a Calibration:

Make sure the flow rate is at zero or at a desired baseline value and is steady.

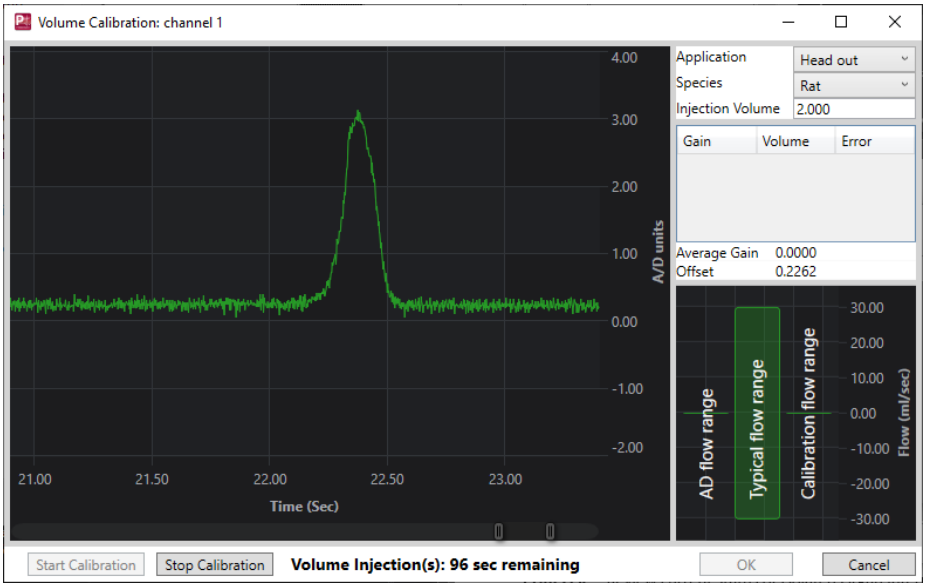
Click **Start Calibration** button at the bottom of the window.



When the Start Calibration button is pressed the first second of data that is sampled will be used as baseline. Very briefly the Message area will display the message **Maintain zero flow** as it measures baseline. After one second it will switch to **Volume Injection(s): xx sec remaining.**



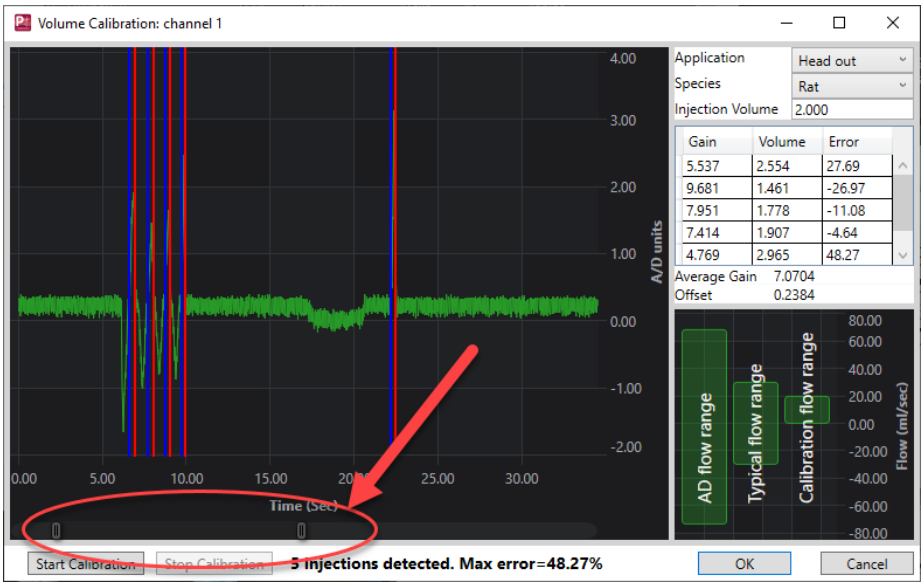
A period of 120 seconds is given to perform a calibration and a timer displays the time in seconds as it counts down to 0. The user has 120 seconds to perform as many volume injections as desired. A volume injection is an injection of a known volume of air with a syringe, pipette or other controlled method. The injection must be value of the **Injection Volume** that is set to have an accurate calibration.



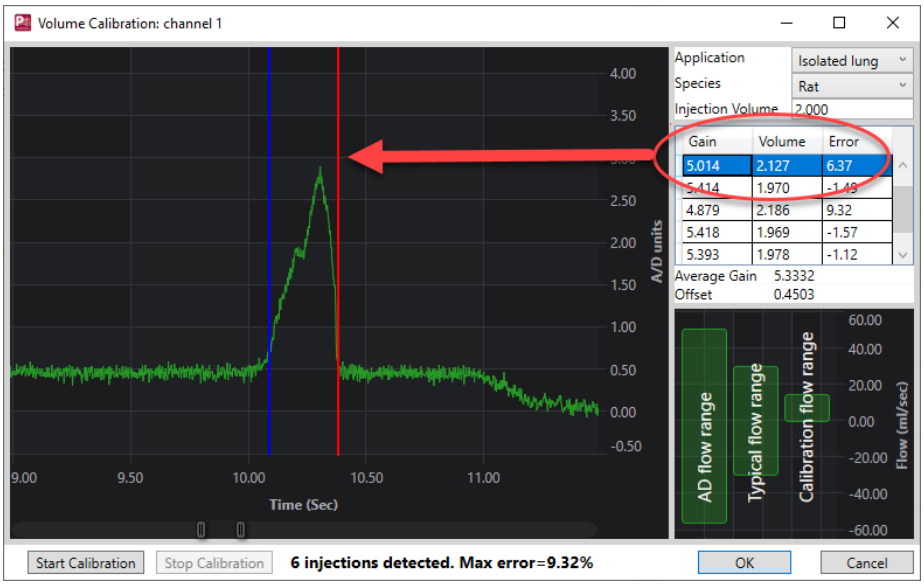
If a satisfactory number of calibrations have been entered the user can end the calibration session at any time by selecting the **Stop Calibration** button. Alternatively, when the timer runs down to 0 the calibration session automatically ends.

When calibration is ended, all valid calibration points will be displayed in the table on the right of the window.

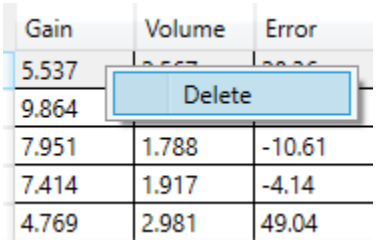
The user can move around in the graph to view the injections using the slider bars at the bottom of the graph.



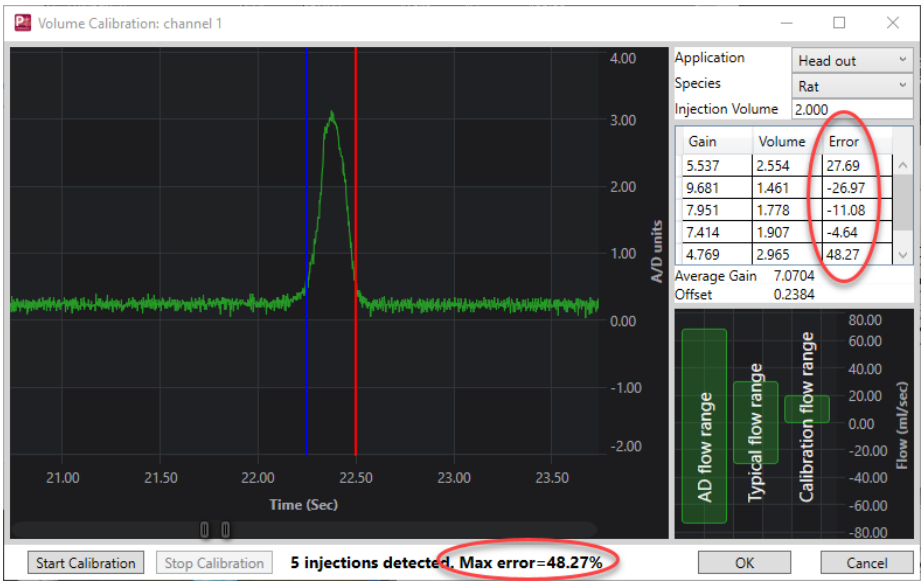
The Blue line indicates start of injection and the Red line indicates end of injection. Either line can be moved by the user if desired. Moving either line will trigger recalculation of the Gain, Volume and Error for that injection. An injection can also be selected from the table on the right side of the window and the graph will move to the location of that injection.



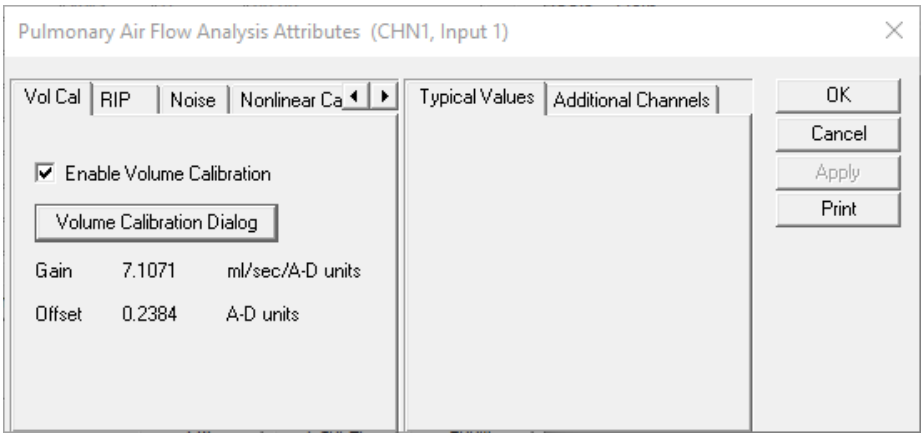
If an injection was detected that the user does not desire to keep in the calibration, right clicking the table will allow deleting of that injection.



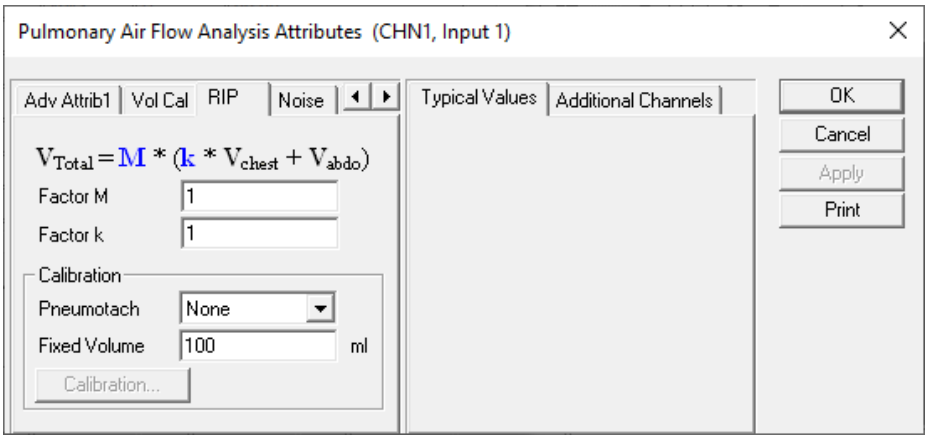
The calculated error is listed for each injection in the table, and the maximum error is highlighted at the bottom of the window. The offset is the same for all injections. The individual gain is calculated for each injection to yield a volume equal to the injection volume. The individual gains are averaged, this averaged gain is used to calculate the volume in the volume column and this volume compared with the injection volume provides the error value. There is no requirement for the max. error allowed, however a lower error means the injections are more consistent.



The user can begin a new calibration if a desired calibration was not determined or accept the calibrations and select **OK**. Clicking OK will return to the PAF Analysis Attributes window where the Average Gain and Offset from the calibration will be entered. These values will be saved with the protocol and used to scale the signal during acquisition.

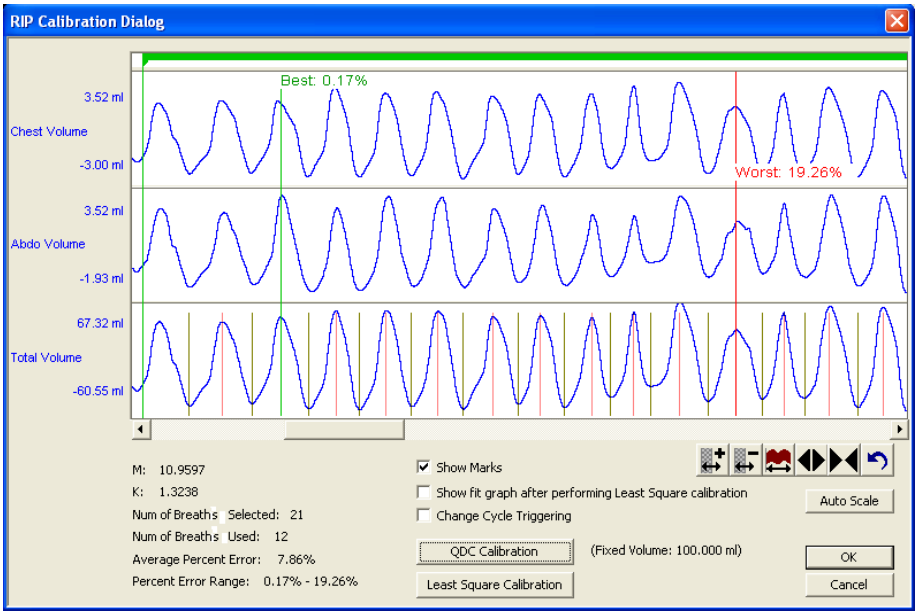


Respiratory Inductive Plethysmography (RIP)



Attribute	Description
Factor M	Represents the fixed volume scaling factor between the total RIP volume and a reference source (such as a calibrated pneumotachograph or user specified tidal volume value).
Factor k	Represents the relationship of the volumes from the chest and abdomen.
Calibration	There are two methods of RIP Volume Calibration available: Qualitative Diagnostic Calibration (QDC) and Least Squares. The calibration coefficients (Factor M and Factor k) are computed regardless of the calibration method. It is possible to edit these coefficients by highlighting the value and typing in the desired value. Fixed Volume - a user entered reference for tidal volume value for use with QDC calibration. When the Fixed Volume value is entered prior to acquisition, this sets the calibration coefficients and applies it to the acquired parameter values. In Review, breaths to be used in the calibration process can be selected from a graph screen. Pneumotach - designates the channel associated with the use of a pneumotachograph. The control box will list all channels that have PAF selected as their analysis.

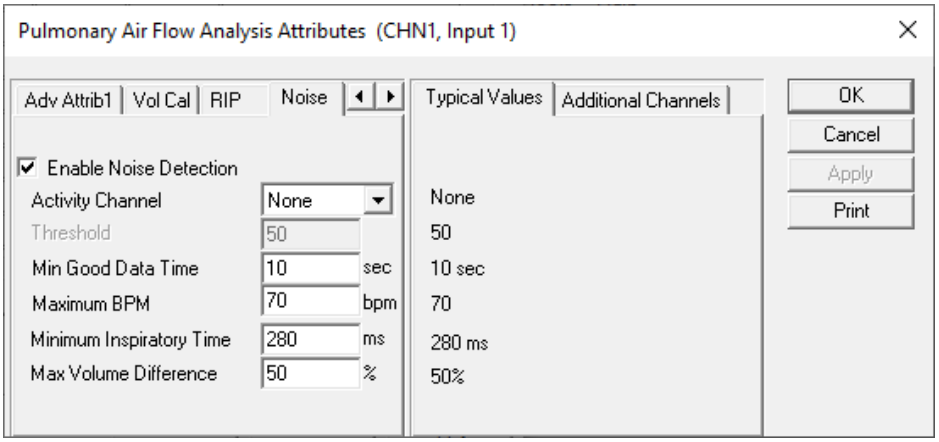
RIP Calibrations



Attribute	Description
Show Marks	Check box enables and disables validation marks for the reference waveforms. If a pneumotach channel has been specified, it serves as the "reference". If no pneumotach channel has been specified then the total volume serves as the "reference".
Show fit graph after performing Least Square calibration	Check box enables and disables a pop up graph screen that displays the line fit used in assessing Least Square calibration.
Change Cycle Triggering	Check box enables and disables the display of a slider control that allows for the adjustment of the cycle (breath) trigger level.
Calibration Segment(s)	The green bar (Calibration Segment) at the top of the Rip Calibration screen denotes the breaths selected to be used for calibration. Additional segments can be added with a right click of the mouse in the top of the graph screen. Segments can be shortened or expanded by dragging the end the segment bar. Segments may also be moved by dragging and dropping with the mouse. A segment can be deleted by right clicking on the bar.
Num of Breaths Selected	The number of breaths found within the Calibration Segment.
Num of Breaths Used	The number of breaths used for calibration within the Calibration Segment.
Average Percent Error	The average percent error of the breaths used in the calibration. $[(V_{total} - V_{Pneumo})/V_{Pneumo}]$

Attribute	Description
Percent Error Range	The lowest and highest percent error of the breaths used in the calibration.

Noise



The Noise Tab contains attributes that are used to identify noisy data. On identifying noisy data, Bad Data Marks will be placed to span the noisy sections.

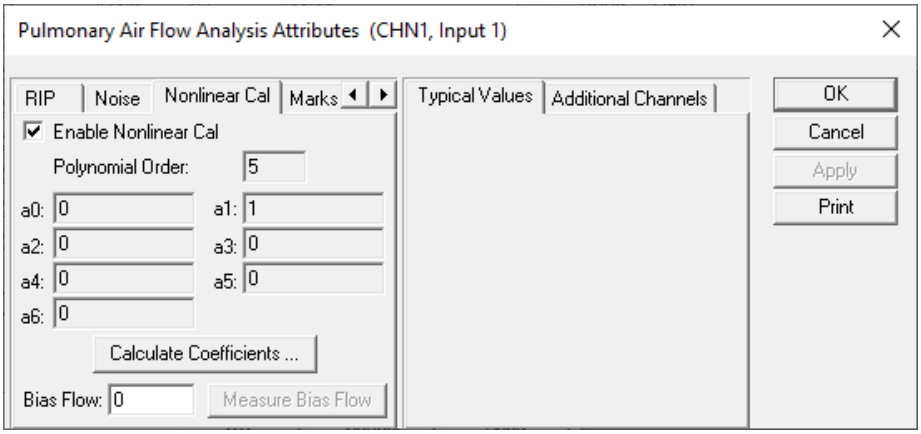
Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Allows the attributes to be edited and used by the software.
Activity Channel	Calculations	Allows user to identify which channel is to be used as the Activity channel for this Primary Chest channel. Typically this will be the accelerometer channel of the JET device used with this RIP channel.
Threshold	Signal Interpretation	This edit box specifies a noise level. When an activity channel level set in this box is exceeded, the data will be interpreted as noise and Bad Data Marks will be inserted to remove the section of data from analysis.
Min Good Data Time	Signal Interpretation	This is a Review only feature. If multiple Bad Data Marks exist in the file and are separated by less than the time specified in the window, the analysis will combine the sections to create one contiguous Bad Data Mark section.
Maximum BPM	Signal Interpretation	Respiratory rates (breaths per minute) detected by the analysis that exceed the level specified will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis.
Minimum Inspiratory Time	Signal Interpretation	This sets the minimum allowable value for Minimum Inspiratory Time.
Max Volume Difference	Signal Interpretation	Differences between volumes of inspiration and expiration greater than this percentage will be regarded as bad data.

Nonlinear Calibration

Nonlinear Calibration allows the collection and measure of multiple values for purposes of calibrating a nonlinear signal. This data can then be processed using a polynomial equation with the Order of that polynomial defined by the user.

The **Enable Nonlinear Cal** checkbox enables the use of the Nonlinear Calibration menu. Information about the Order and Coefficients are listed in this menu once the calibration has been performed. To perform a calibration, the user must select the **Calculate Coefficients** button.

The **Bias Flow** allows the user to measure an offset flow. This will be subtracted from the flow signal. Clicking on **Measure Bias Flow**, the software will sample the active flow for five seconds and record the value.



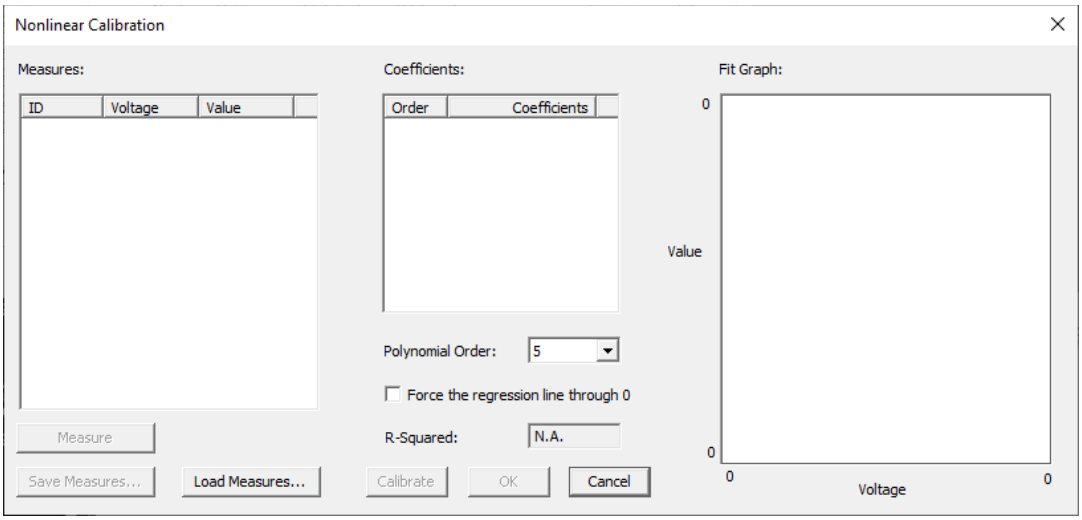
After clicking on the **Calculate Coefficients** button, the Nonlinear Calibration dialog will appear. To use this feature, the User should be in an acquisition and actively sampling the desired flows. However, once the values have been collected, they may be recalled or manually modified without the need to actively sample data.

Under the **Measures** box, information for the **Voltage**, **Value** and **ID** are listed. When sampling a given flow, click the **Measure** button to record this value. The **ID**, **Value** and **Voltage** will be recorded. The **Voltage** and **Value** may be manually modified after measured. Repeat this for each desired calibration point. Once complete, the user has the option to **Save Measures**. This allows the data sampled to be saved and recalled at any point. This allows the user to characterize a number of configurations and recall the configuration specific to a given experiment. To recall a Measures configuration, click on the **Load Measures** button. A dialog will be presented allowing the User to select the appropriate configuration.

The Coefficients box displays the Order and Coefficients used. The **Polynomial Order** is user defined from 2-6. Users may choose to force the regression through 0 by selecting the check box. The R-Squared value provides an indication as to the fit.

Once the order has been defined, clicking on **Calibrate** will update the Coefficients box and provide the desired calibration curve.

The **Fit Graph** will display the output of the calibration.



Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Minimum Flow	Dog 2.58	mL/Sec
	Monkey 0.65	
	Rat 0.18	
	Mouse 0.02	
Primary Signal	Flow	NA
Input Flow Units	User Defined	
Percent Relaxation	70	%

Marks (Validation)

The **Pulmonary Air Flow** analysis displays validation tick marks for each respiratory cycle. Each respiratory cycle should have only one set of validation marks. These marks verify that the system is analyzing the PAF signal correctly. If there is more than one set of validation marks per respiratory cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Start of Inspiration

Color	Meaning
Blue	Start of Expiration
Green	Start of Apnea
Cyan	Percent Relaxation

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the respiratory cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
PIF	Mean	Peak Inspiratory Flow is the maximum inspiratory flow that occurs during a valid breath.
PEF	Mean	Peak Expiratory Flow is the maximum expiratory flow that occurs during a valid breath.
TV	Mean	The Tidal Volume is the total volume of air that was inspired during a breath and is always reported in milliliters.
MV	Mean	The Minute Volume is the product of the tidal volume and the number of breaths-per-minute. The equation is: MV = TV * BPM. Note: When running in a logging mode other than 1 epoch, the averaged value will be calculated off of the averaged TV and averaged BPM values.
BPM	Harmonic Mean	The number of breaths-per-minute is calculated on a breath-to-breath basis. It is computed as the reciprocal of the total time for a respiratory cycle times 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
IT	Mean	The Inspiratory Time is calculated from the first zero crossing of the flow in the inspiratory direction to the zero crossing of the flow in the expiratory direction. The time is in milliseconds.
ET	Mean	The Expiratory Time is calculated from the zero crossing of the flow in the expiratory direction until flow reaches zero again. The time is in milliseconds.
TT	Mean	The Total Time is the time period, in milliseconds, from one valid breath to the next valid breath.
AT	Mean	The Apnea Time is computed as follows: $AT = TT - (IT + ET)$

Name	Averaging In Review	Definition
CaRaw*	Mean	Specific Airway Resistance This parameter is the product of Alveolar Compliance and Airway Resistance CaRaw = tan θ/ω where: Ca Alveolar Compliance Raw Airway Resistance θ phase shift between mouth and chest volume ω Angular frequency
Phase	Mean	Phase shift between mouth and chest volume, in degrees. For RIP, phase difference between the chest and abdomen. ***If PNM-AWR100W has not been purchased or RIP is not enabled, this parameter will not be available.***
dT*	Mean	The delay, in milliseconds, between the mouth and chest volumes.
PEnh	Mean	Enhanced Pause. Calculated as: ((ET+AT)/RT-1) * (PEF/PIF) Formula from Noninvasive Measurement of Airway Responsiveness in Allergic Mice Using Barometric Plethysmography Hamelmann et al.
RT	Mean	Relaxation Time. This is the time from the start of expiration to the point where the volume signal drops by the Percent Relaxation value from its maximum value for the cycle.
TVe	Mean	This is the difference between the volume at the start expiration mark and the volume at the point prior to the next cycles start inspiration mark. It is always reported in milliliters.
IF50	Mean	IF50 reports the inspiratory flow value at the point where the volume signal rises to 50% of the tidal volume.
EF50	Mean	EF50 reports the expiratory flow value at the point where the volume signal drops to 50% of the tidal volume.
AVol	Recent	Accumulated Volume is the summed total of the Tidal Volume (TV) from a reset point forward and is reported in milliliters. Reset points include the start of data collection, break in the data or the selection of the event associated with the AVol Reset Event attribute.
***Available only if the PNM-AWR100W option has been purchased.**		

Calibration

The recommended calibration of a system with a Pulmonary Air Flow signal depends on the species being measured and the type of calibration. Calibrate the system with a constant flow or by volume injection. Both methods require that you know the typical flow or volume that will be measured in the system.

Pulmonary Air Flow Calibration - Constant Flow

Use a constant air flow or vacuum attached to a pneumotachograph or a plethysmograph with a flow meter. Use the flow meter reading as the **High Calibration** value.

Typical calibration values are listed in the table below:

Species	High Calibration Value	Actual mV
Small Rodent	200 mL/Sec	≈ 400-800 mV
Dog	5.00 L/Sec	≈ 500-1000 mV

Pulmonary Air Flow Calibration - Volume Injection

Volume injection is a common method used to calibrate air flow. With this type of calibration, inject a known volume into the pneumotachograph or the plethysmograph. The system will calculate the correct flow calibration from this injection. This is applicable for use with EPP (enhanced parallel port) version of the ACQ16 and not the USB version.

Typical calibration values are listed in the table below:

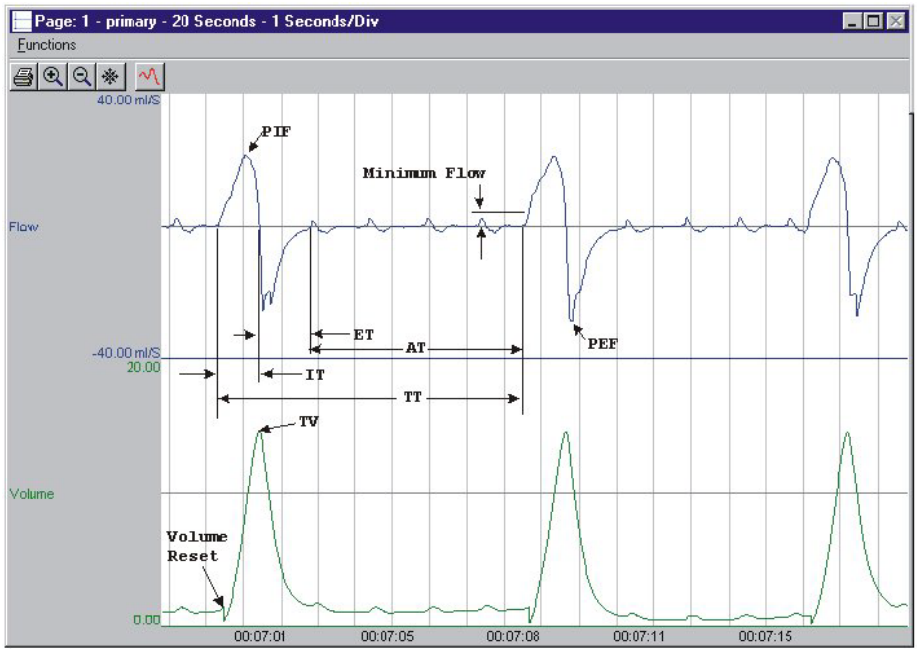
Species	High Calibration Value	Actual mV
Small Rodent	2.00 mL Flow in Units of mL/Sec	≈400-1000 mV
Dog	100 mL (100 cc Injection) Flow in Units of L/Sec	≈200-500 mV

JET RIP (Respiratory Inductive Plethysmography) Calibration

See JET Option Manual (MU000257)

On-Line Screens and Functions

Below is an example of a Primary graph displaying a typical pulmonary air flow signal with the digitally integrated volume signal.



Pulmonary Air Flow Key Marks

In the above figure, the Pulmonary Air Flow is displayed with validation tick marks and their meanings. The validation marks label the **Start of Inspiration**, **Start of Expiration**, and **Start of Apnea** marks.

Presentation Signals

Below is a list of presentation signals that are available for the PAF Analysis Module:

Signal	Description
Flow	For Primary Signal=Flow, this will be the original flow signal. For Primary Signal=Volume, this will display the differential of the signal, and it is generated as a two-point differential
Volume	For Primary Signal=Flow, this will display the integration of the flow signal over the entire breath and reset at the start of the next valid breath. For Primary Signal=Volume, this will display the original volume signal.
CaRaw*	Displays the corresponding derived output on a cycle by cycle basis
Phase*	Displays the corresponding derived output on a cycle by cycle basis
***Presentation signals not available in Review.**	

Data Review

The Data Review related features of the PAF Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.10 or greater and if the customer's license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

PAF marks are divided into two types, marks that always exist when a valid cycle is found (Start Inspiration and Start Expiration) and marks that may or may not exist, depending on the signal morphology (Percent Relaxation and Start Apnea).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion, signal morphology is not considered.

Insert PAF Cycle

Inserts an entire PAF cycle, Start Inspiration, Start Expiration, and Percent Relaxation if applicable. Start Apnea is not inserted; if Apnea exists this must be inserted manually. This set of marks may be inserted between a Start Inspiration mark and the last mark of the preceding cycle. Cycles may also be inserted prior to the first cycle and after the last cycle. When a PAF cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Insert Start Apnea

Inserts a Start Apnea mark. This mark may be inserted prior to a Start Inspiration mark or after the last cycle, as long as the preceding mark is not a Start Apnea mark.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. Only the Start Apnea mark may be deleted in this fashion. The rest of the marks cannot be deleted individually. An entire cycle may be deleted. A cycle is deleted by positioning the cursor on the Start Inspiration mark, bringing up the right mouse menu, and selecting Delete Cycle.

Moving Marks

Moving of the Start Inspiration, Start Expiration and Start Apnea marks follow the standard rules used in Data Review. There are special considerations when dealing with the Percent Relaxation mark. The Percent Relaxation mark is a calculated mark; its position is dependent on the Tidal Volume and cannot be adjusted by the user. If the user changes the position of the Start Inspiration, Start Expiration, or Start Apnea marks, the Percent Relaxation mark will be recalculated. When the Percent Relaxation mark is moved the derived parameter RT may change and will not be marked as a grayed cell unless a reanalyze is performed. This is also the case when the Secondary Channel is changed for the derived parameters CaRaw, Phase, and dT.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay. Review reports the volume at the start of expiration as the Tidal Volume. Replay reports the maximum volume over the entire cycle. In most cases the values reported from Review and Replay are identical.

When a Review file is opened, the trace data may not be identical to the acquired data. The difference arises because of the scaling involved in the storage and reconstitution of the data. The difference for a point, on average, is less than 0.05%.

One of the consequences of this difference is seen with Calculated Marks. If, after opening a Review file, Review is prompted to recalculate a Calculated Mark, the mark may move with no change to the marks on which it depends. This is because the original placement of the Calculated Mark was based on the Replay data values whereas, recalculation uses the data values present in Review.

Logging Mark

The logging mark for a PAF cycle is the Start Inspiration mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a PAF cycle occurs at the point prior to the next cycle's Start Inspiration mark. When a PAF channel is the epoch channel, all review channels that display their cycle's logging mark prior to the end of the epoch channel's cycle will be included in the derived output.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Breaths-per-Minute is doubled, halved, etc.	This usually occurs when the analysis triggers on noise or artifacts. It can be corrected by changing the Minimum Flow to a higher or lower value to eliminate rates higher or lower than normal. If the signal has a lot of baseline noise, change the Low Pass Filter (in the Adv Attrib1 tab) to a higher value to remove the noise. Select a lower value in the list box.
All derived parameters are reporting zero	The Minimum Flow may be set too high for the specified signal. Lower the Minimum Flow value.
Tidal Volume incorrect	1. This can be caused by the flow signal drifting above or below the zero line. Enable a High Pass Filter at 3Hz (in the Adv Attrib1 tab) if the flow signal is drifting. 2. The wrong Input Flow Units are being used. Since the volume is derived mathematically, the system must know the real units of flow being measured. 3. If the Tidal Volume is low, there could be a problem with the experimental setup. If the animal is in a plethysmograph, verify that there are no air leaks. This also pertains to any other setup. There can be no air leaks.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Pulmonary Air Flow]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Use Averaged dT	If TRUE, dT is averaged from the start and end of inspiration. The default value is 1 (TRUE).

Entry Name	Description
Use Start Expiration for dT	Used only if Use Averaged dT is FALSE. If TRUE, dT is calculated from the start of exp. The default value is 1 (TRUE).
Minimum Flow (low)	This sets the minimum allowable value for **Minimum Flow**. The default value is .1.
Minimum Flow (high)	This sets the maximum allowable value for **Minimum Flow**. The default value is 100.
Percent Relaxation (low)	This sets the minimum allowable value for **Percent Relaxation**. The default value is 10.
Percent Relaxation (high)	This sets the maximum allowable value for **Percent Relaxation**. The default value is 90.
Smoothing Filter (low)	This sets the minimum allowable value for Smoothing filter. The default value is 5.
Smoothing Filter (high)	This sets the maximum allowable value for Smoothing filter. The default value is 999.
M (low)	Calibration constant. The default value is 0.
M (high)	Calibration constant. The default value is 100000.
k (low)	Calibration constant. The default value is 0.
k (low)	Calibration constant. The default value is 100000.
Minimum Good Data Time (low)	This sets the minimum allowable value for Minimum Good Data Time. The default value is 0.
Minimum Good Data Time (high)	This sets the maximum allowable value for Minimum Good Data Time. The default value is 1000.
Noise Threshold (low)	This sets the minimum allowable value for Noise Threshold. The default value is 0.
Noise Threshold (high)	This sets the maximum allowable value for Noise Threshold. The default value is 1000.
Maximum Breaths per Minute (low)	This sets the minimum allowable value for **Maximum BPM**. The default value is 0.
Maximum Breaths per Minute (high)	This sets the maximum allowable value for **Maximum BPM**. The default value is 1000.
Minimum Inspiratory Time (low)	This sets the minimum allowable value for **Minimum Inspiratory Time**. The default value is 0.
Minimum Inspiratory Time (high)	This sets the maximum allowable value for **Minimum Inspiratory Time**. The default value is 10000.
Maximum Volume Difference Percentage (low)	Sets the maximum volume difference allowed. The default value is 0.
Maximum Volume Difference Percentage (high)	Sets the maximum volume difference allowed. The default value is 10000.
Polynomial Order (low)	2
Polynomial Order (high)	6
Coefficient A0(low)	-10000
Coefficient A0(high)	10000
Coefficient A1(low)	-10000
Coefficient A1(high)	10000
Coefficient A2(low)	-10000
Coefficient A2(high)	10000
Coefficient A3(low)	-10000
Coefficient A3(high)	10000
Coefficient A4(low)	-10000
Coefficient A4(high)	10000
Coefficient A5(low)	-10000
Coefficient A5(high)	10000

Entry Name	Description
Coefficient A6(low)	-10000
Coefficient A6(high)	10000
Bias Flow (low)	-10000
Bias Flow (high)	10000

Pulmonary Compliance Resistance and Pulmonary Compliance Resistance Pressure (PCR/PCRP)

The Pulmonary Compliance Resistance(PCR) and Pulmonary Compliance Resistance Pressure (PCRP) Analysis Modules analyze pulmonary air flow and pulmonary pressure signals obtained from a plethysmograph box or from a pneumotach. They also calculate, on a breath-to-breath basis, derived values for the respiratory cycle.

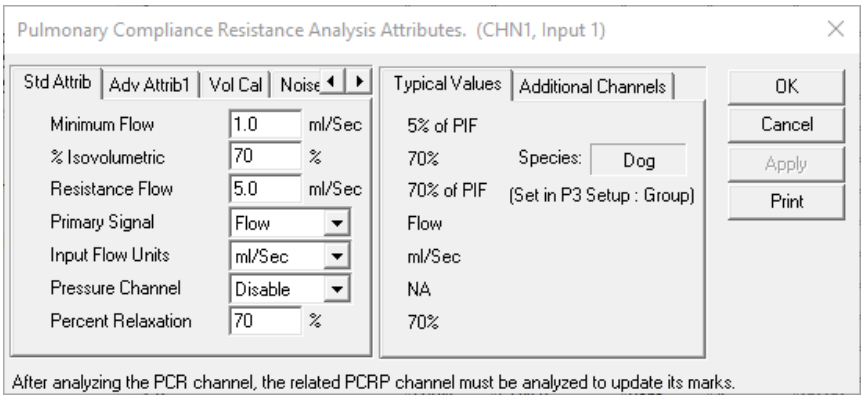
If the Pressure Channel (PCRP) is not selected in the attributes window, the analysis will not be able to calculate some derived parameters (Cdyn, RES, Cond, etc.). See the Attribute Window and Derived Parameters sections below.

Attribute Window

The Pulmonary Compliance Resistance (PCR) Analysis attributes window allows you to modify the signal analysis for different types of air flow signals and different signal conditions.

The Pulmonary Compliance Resistance Pressure (PCRP) Analysis Module does not have any available standard attributes.

Standard Attributes (PCR)



Pulmonary Compliance Resistance (PCR) Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Flow	Signal Interpretation	Sets the minimum flow that the analysis must achieve before the analysis will detect and validate a pulmonary cycle. The Minimum Flow stops the analysis from triggering on artifacts such as cardiac noise.
%Isovolumetric	Calculation, Redraw	Sets the percent of tidal volume used to determine the flow and pressure points in the calculation of resistance. The value is normally set between 60% and 70% and relates to peak inspiratory and expiratory flow.

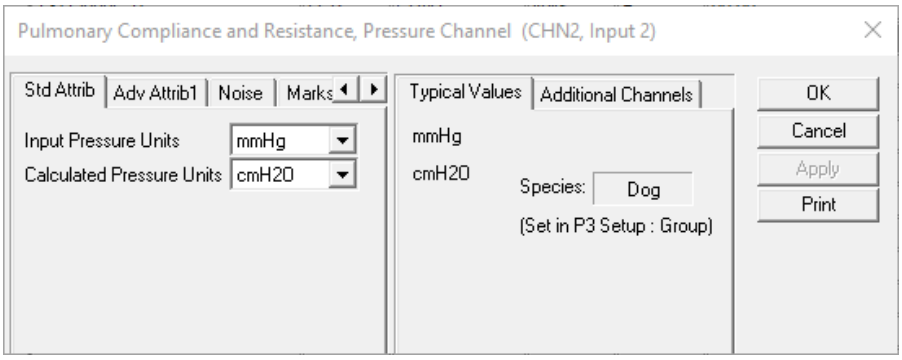
Attribute	Effect On Review	Description
Resistance Flow	Calculation	This is the flow level at which the resistance values ResI1, ResI2, ResE1, and ResE2 are reported. Resistance Flow must be greater than Minimum Flow. If the positive or negative flows do not reach the level of Resistance Flow, ResI1, ResI2, ResE1, and ResE2 will not be reported or averaged in to the logged value.
Primary Signal	Signal Conditioning, Calculation, Redraw	Sets the system for either a Flow input signal or a Volume input signal. If Volume is selected as the primary signal, you can display the digitally derived flow signal on a primary graphic page by selecting Flow as the Presentation in the Primary Graph Page Setup window. If Flow is selected as the primary signal, you can display the digitally derived volume signal on the primary graph page by selecting Volume as the Presentation in the Primary Graph Page Setup window.
Input Flow Units / Calculated Flow Units	Signal Conditioning, Calculation, Redraw	Input Flow Units is active when Flow is selected as the Primary Signal. Input Flow Units specifies the units of flow being measured so that the system calculates the volume correctly. Calculated Flow Units is active when Volume is selected as the Primary Signal. Calculated Flow Units specifies the volume units used so that the system calculates the flow values correctly. mL/Sec (milliliters per second) mL/Min (milliliters per minute) l/Sec (liters per second) l/Min (liters per minute)
Pressure Channel	Calculation	The pressure channel must be specified in this list box, and the channel must be defined as a PCRP channel.
Percent Relaxation	Calculation, Redraw	Used to draw the percent relaxation mark and to calculate PEnh and RT. The Percent Relaxation Mark is drawn when the volume signal drops from its maximum value by the specified percentage.

Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Minimum Flow	5% of PIF	mL/Sec
%Isovolumetric	70%	percent
Resistance Flow	70% of PIF	mL/Sec
Primary Signal	Flow	NA
Input Flow Units	User defined	
Pressure Channel	Disable	NA
Percent Relaxation	70%	percent

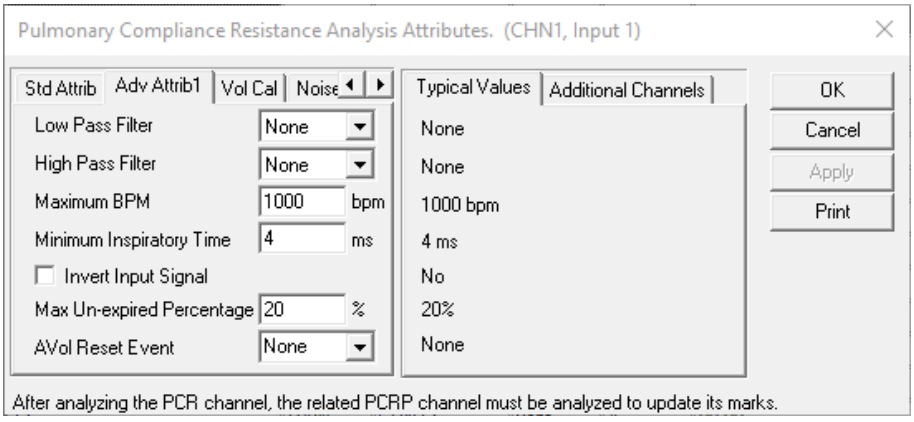
Standard Attributes (PCRP)



Pulmonary Compliance Resistance Pressure (PCRP) Channel Standard Attributes Tab

The pressure channel has Input Pressure Units and Calculated Pressure Units attributes associated with it. The user may select which unit of measurement is desired. For older versions of the software that did not have this conversion feature, the Input Pressure Units were in mmHg if collected from the DSI transmitter. This data may be reanalyzed with the output converted to cmH2O, if desired.

Advanced Attributes (PCR)



Pulmonary Compliance Resistance (PCR) Advanced Attributes 1 Tab

The Advanced Attributes 1 tab allows selection of attributes that would less likely need to be changed during acquisition or replay.

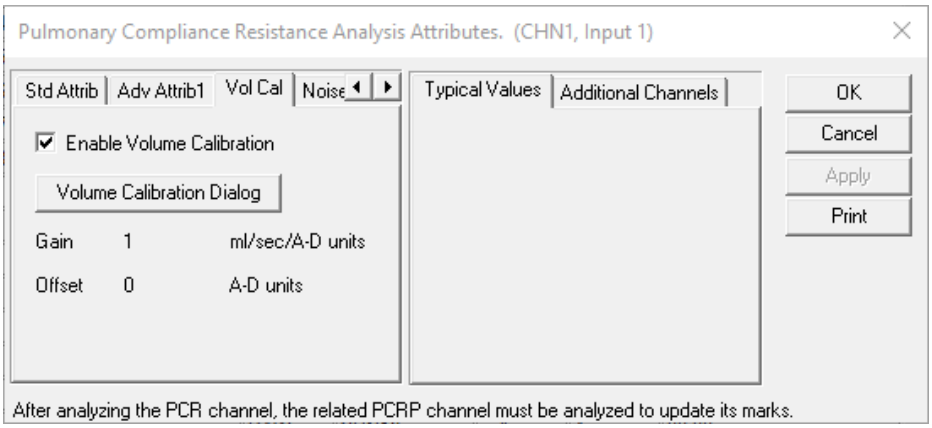
Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.

Attribute	Effect On Review	Description
Maximum BPM	Signal Interpretation	Maximum Breaths Per Minute. Once the analysis identifies a potential respiration cycle, it will accept the cycle if its BPM value is less than or equal to the Maximum BPM value, else the cycle will be rejected. This attribute should be used to reject noise and unwanted sniffing.
Minimum Inspiratory Time	Signal Interpretation	Once the analysis identifies a potential respiration cycle, it will accept the cycle if its Inspiratory Time value is greater than or equal to the Minimum Inspiratory Time value, else the cycle will be rejected. This attribute should be used to reject noise and unwanted sniffing.
Invert Input Signal	Signal Conditioning, Calculation, Redraw	This check box should be enabled if the respiration signal is acquired such that inspiration is negative. The PCR Analysis Module requires that inspiration is positive. Selecting the check box will reverse the polarity of the acquired signal.
Max Un-expired Percentage	Signal Interpretation	Maximum Un-expired Percentage. This attribute is used to exercise some control over the switchover from expiration to apnea. Prior to switching from expiration to apnea, the analysis will verify that the un-expired volume, expressed as a percentage of Tidal Volume, is not greater than Max Un-expired Percentage. Setting this percentage to 100% would not restrict switching over to apnea. Setting it to 0% would require that the entire tidal volume be expired prior to switching to apnea. ***NOTE: This parameter does not affect switching to inspiration.***
AVol Reset Event	Calculation	Used to determine the start point for the Accumulated Volume derived parameter (AVol). The selection of an event, “a” through “J”, will determine the start point for the calculation of AVol. If “None” is selected, the AVol derived parameter will report zero (acquisition and replay) or “x” (Review). The start of an acquisition, a break in the data, or subsequent entries of the event to trigger the start point for the AVol calculation will result in the derived parameter being reset.

Advanced Attributes (PCRP)

The only Advanced Attributes for the Pulmonary Compliance Resistance Pressure Channel is the Low and High Pass Filter selections. Refer to **Error! Reference source not found.** in the **Error! Reference source not found.** section for more information.

Vol Cal

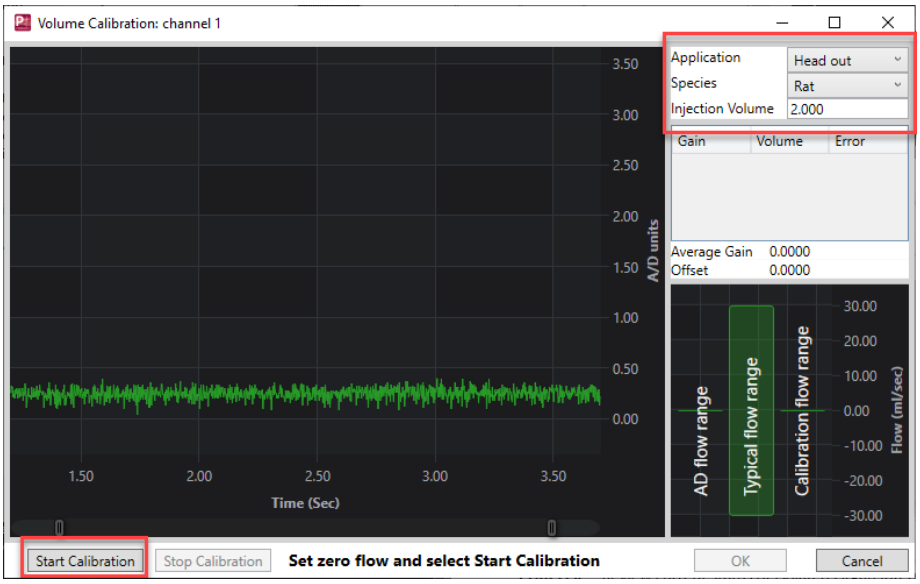


Pulmonary Compliance Resistance Vol Cal Tab

The Vol Cal tab stands for volume calibration and is used for calibrating an air flow signal using an injection of a known volume of air.

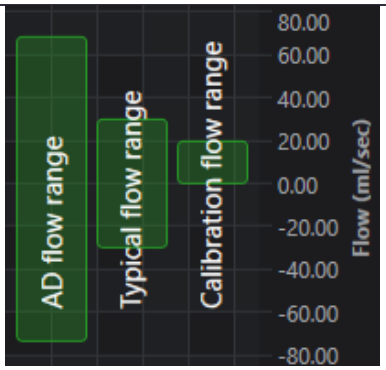
Attribute	Description
Enable Volume Calibration	Enables the volume calibration feature and applies the gain and offset to the signal. This option is only available when the Primary Signal is set to 'Flow' in Std Attrib.
Volume Calibration Dialog	Launches the Volume Calibration in a separate window.
Gain	The gain that has been calculated from previous calibration session.
Offset	The offset that has been calculated from previous calibration session.

Volume Calibration Dialog



Pulmonary Compliance Resistance Volume Calibration Dialog

Selecting the 'Volume Calibration Dialog' button will bring up the volume calibration window. This is comprised of a graph as well as some user input fields and a button to start and stop calibration. Immediately when the window is opened the graph will begin displaying currently sampled data from the selected channel.

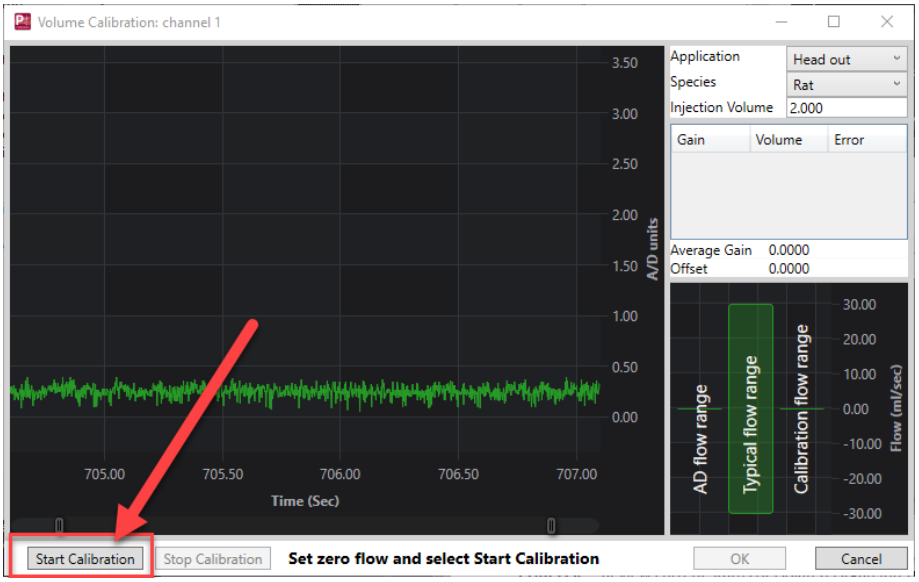
Attribute	Description
Application	Allows selection of a specific application which is loaded from an XML file. Each application has preset species and injection volume settings.
Species	Will list the available species that are available for the selected application.
Injection Volume	A preset volume that is typical for the application and species selected. This can be modified. The Injection Volume should be close to the TV of the species. The injection volume must match the actual volume being injected via syringe or pipette for an accurate calibration.
Gain/Volume/Error box	Will list the Gain, Volume and Error for each injection that was detected. An injection can be selected from the table to view in the graph, where the boundaries can be adjusted (blue and red lines) or it can be deleted.
Average Gain/Offset	Calculates the average gain and offset for the injections saved in the table.
Mini flow range Graph	
AD flow range	Reflects the range of flow values that can be acquired based on the Span of the signal that is currently set in the ACQ7700 setup and the volume calibration gain and offset values. The AD flow range should exceed the typical flow range by 20-50%. If AD flow range is too small the signal will rail and appear clipped at the max and min, and if it is too large the signal will have poor resolution. To adjust AD flow range, go back to the ACQ7700 setup and adjust span setting.
Typical flow range	Reflects the calculated typical flow range for the application/species selected and the injection volume that is set.
Calibration flow range	Reflects the flow range used during the injections
Start Calibration	Clicking start will begin a calibration session. A calibration session will run for 120 seconds in which time all injections need to be performed. If the time runs out a new calibration session can be started.

Attribute	Description
Stop Calibration	Stops the calibration after all injections are performed within the 120 second window. If calibration is not stopped it will end automatically when the 120 second timer runs down.
Message Notification area	To the right of the Stop Calibration button, this area notifies the user of calibration session status.

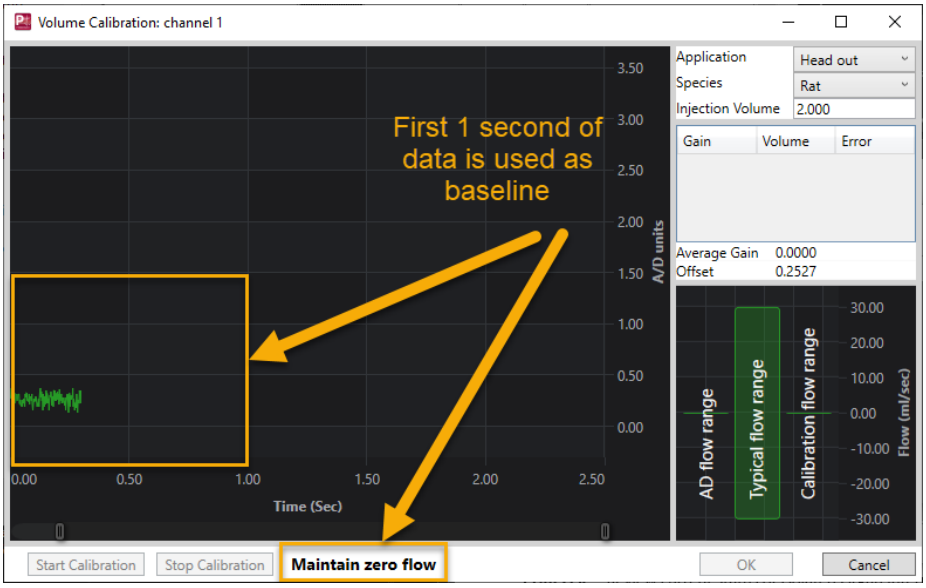
Performing a Calibration:

Make sure the flow rate is at zero or at a desired baseline value and is steady.

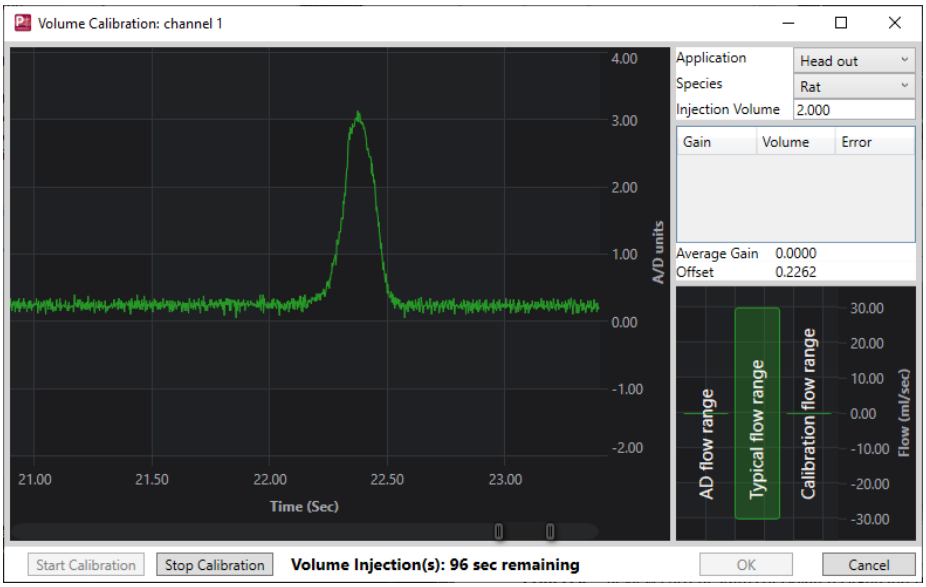
Click **Start Calibration** button at the bottom of the window.



When the Start Calibration button is pressed the first second of data that is sampled will be used as baseline. Very briefly the Message area will display the message **Maintain zero flow** as it measures baseline. After one second it will switch to **Volume Injection(s): xx sec remaining.**



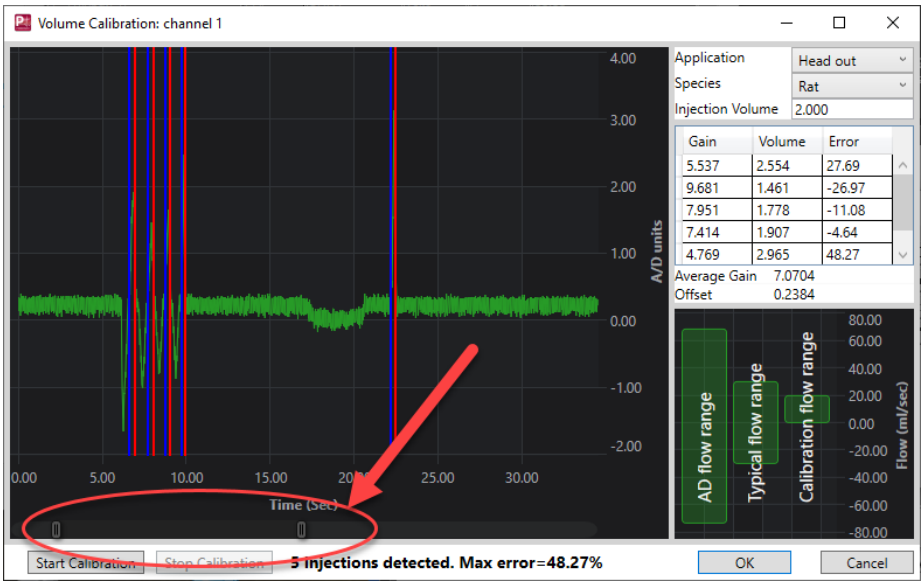
A period of 120 seconds is given to perform a calibration and a timer displays the time in seconds as it counts down to 0. The user has 120 seconds to perform as many volume injections as desired. A volume injection is an injection of a known volume of air with a syringe, pipette or other controlled method. The injection must be value of the **Injection Volume** that is set to have an accurate calibration.



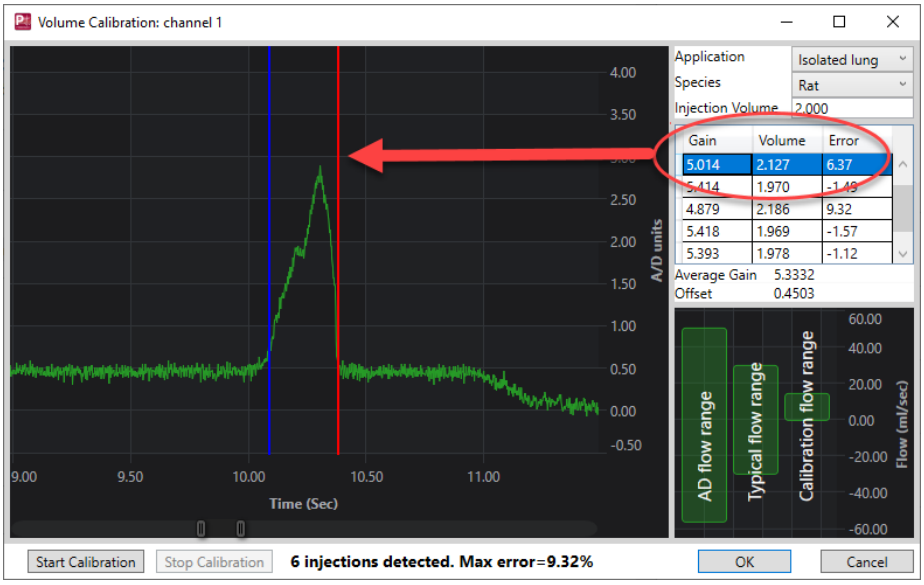
If a satisfactory number of calibrations have been entered the user can end the calibration session at any time by selecting the **Stop Calibration** button. Alternatively, when the timer runs down to 0 the calibration session automatically ends.

When calibration is ended, all valid calibration points will be displayed in the table on the right of the window.

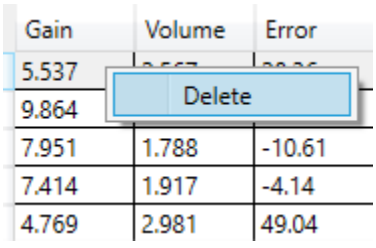
The user can move around in the graph to view the injections using the slider bars at the bottom of the graph.



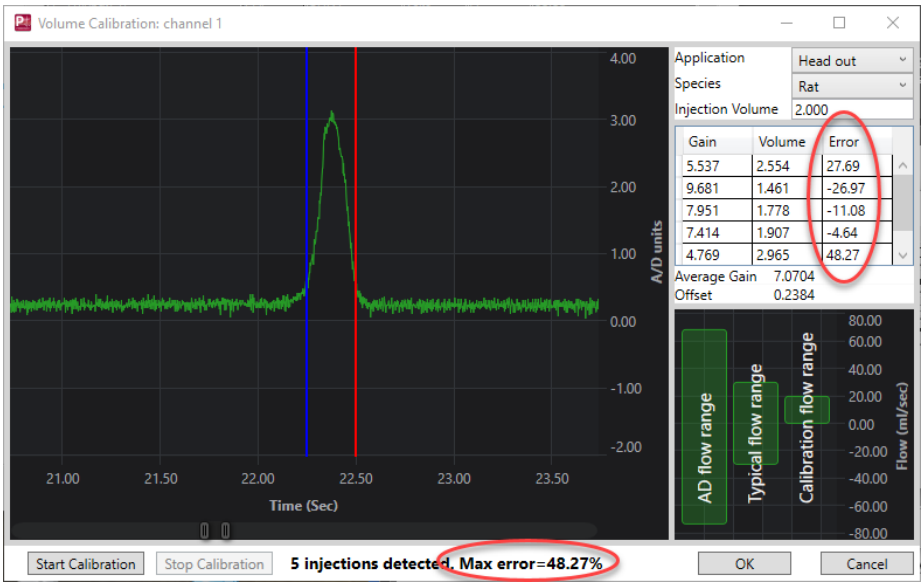
The Blue line indicates start of injection and the Red line indicates end of injection. Either line can be moved by the user if desired. Moving either line will trigger recalculation of the Gain, Volume and Error for that injection. An injection can also be selected from the table on the right side of the window and the graph will move to the location of that injection.



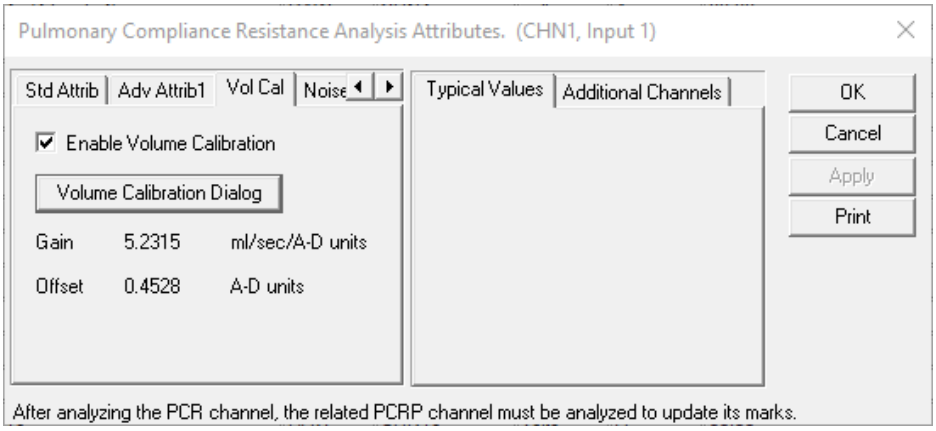
If an injection was detected that the user does not desire to keep in the calibration, right clicking the table will allow deleting of that injection.



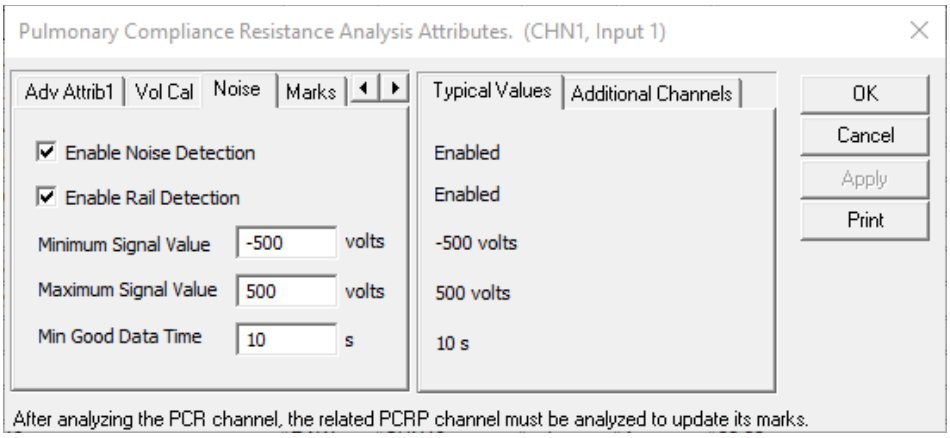
The calculated error is listed for each injection in the table, and the maximum error is highlighted at the bottom of the window. The offset is the same for all injections. The individual gain is calculated for each injection to yield a volume equal to the injection volume. The individual gains are averaged, this averaged gain is used to calculate the volume in the volume column and this volume compared with the injection volume provides the error value. There is no requirement for the max. error allowed, however a lower error means the injections are more consistent.



The user can begin a new calibration if a desired calibration was not determined or accept the calibrations and select **OK**. Clicking OK will return to the PAF Analysis Attributes window where the Average Gain and Offset from the calibration will be entered. These values will be saved with the protocol and used to scale the signal during acquisition.



Noise Attributes Tab (same for PCR and PCRP)



Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Determines if noise detection will be used to determine bad data marks
Enable Rail Detection	Signal Interpretation	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value/ Maximum Signal Value	Signal Interpretation	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.
Minimum Good Data Time	Signal Interpretation	When Rail detection is enabled and a range of data is analyzed, any bad data marks that have less than or equal to the Min Good Data Time of good data between them shall be combined into a single bad data region.

Marks (Validation)

The **Pulmonary Compliance Resistance (PCR)** and **Pulmonary Compliance Resistance Pressure** (PCRP) analyses display validation tick marks for each respiratory cycle. Each respiratory cycle should have only one set of validation marks. These marks verify that the system is analyzing the pulmonary air flow signal correctly. If there is more than one set of validation marks per respiratory cycle, correct the problem by changing the analysis attributes. The Pulmonary Compliance Resistance Pressure channel does not display the marks on the signal in the waveform window, although the marks are correctly placed and can be toggled on and off of the signal on the Primary graph page.

The validation marks for the **Pulmonary Compliance Resistance** (PCR) channel and their meanings are listed below:

Color	Meaning
Black	Start of inspiration
Blue	Start of expiration
Green	Start of apnea time

Color	Meaning
Cyan	Iso vol rise mark
Red	Iso vol fall mark
Violet	Percent Relaxation Mark

The validation marks for the **Pulmonary Compliance Resistance Pressure** (PCRP) channel and their meanings are listed below:

Color	Meaning
Cyan	Iso vol rise mark
Red	Iso vol fall mark

Derived Parameters

This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

The table below is the derived parameters for the Pulmonary Compliance Resistance channel. The NPMN parameter is not reported as an average of beat data instead the portion of the signal that lies within the logging interval is averaged.

Name	Averaging In Review	Definition
Num	Recent	The number of the respiratory cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
PIF	Mean	Peak Inspiratory Flow is the maximum inspiratory flow that occurs during a valid breath.
PEF	Mean	Peak Expiratory Flow is the maximum expiratory flow that occurs during a valid breath.
TV	Mean	The Tidal Volume is the total volume of air that was inspired during a breath and is always reported in milliliters.
MV	Mean	The Minute Volume is the product of the tidal volume and the number of breaths-per-minute. The equation is: MV = TV * BPM. Note: When running in a logging mode other than 1 epoch, the averaged value will be calculated off of the averaged TV and averaged BPM values.
BPM	Harmonic Mean	The number of breaths-per-minute is calculated on a breath-to-breath basis. It is computed as the reciprocal of the total time for a respiratory cycle times 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.

Name	Averaging In Review	Definition
IT	Mean	The Inspiratory Time is calculated from the first zero crossing of the flow in the inspiratory direction to the zero crossing of the flow in the expiratory direction. The time is in milliseconds.
ET	Mean	The Expiratory Time is calculated from the zero crossing of the flow in the expiratory direction until flow reaches zero again. The time is in milliseconds.
TT	Mean	The Total Time is the time period, in milliseconds, from one valid breath to the next valid breath.
AT	Mean	The apnea time is computed as follows: $AT = TT - (IT + ET)$
Cdyn	Mean	Compliance is computed as follows: $Cdyn = \frac{TidalVolume}{\Delta Pressure}$ at zero flow crossing points. Where Tidal Volume is the peak volume that occurs for a breath and $\Delta Pressure$ is the pressure measured at the flow zero crossing points. $\Delta Pressure$ is P2-P1 in the graphic under On-Line Screens and Functions. NOTE: If a Pressure Channel was not selected in the attributes window, the system will not be able to calculate this derived parameter, and a 0 will be given as the value of this derived parameter.
Res	Mean	Resistance is computed as follows: $RES = \frac{\Delta Pressure}{\Delta Flow}$ at the %Isovolumetric points. Where $\Delta Pressure$ is the pressure measured at the %Isovolumetric points on the volume signal, and $\Delta Flow$ is the corresponding flow measured at the %Isovolumetric points on the volume signal. $\Delta Pressure$ is P3-P4 and $\Delta Flow$ is F1-F2 in the graphic under On-Line Screens and Functions. NOTE: If a Pressure Channel was not selected in the attributes window, the system will not be able to calculate this derived parameter, and a 0 will be given as the value of this derived parameter.
Cond	Mean	Conductance is the reciprocal of Resistance. NOTE: If a Pressure Channel was not selected in the attributes window, the system will not be able to calculate this derived parameter, and a 0 will be given as the value of this derived parameter.
ResI1	Mean	ResI1 - Resistance during inspiration at the point where the flow signal rises above the level specified in the Resistance Flow attribute.
ResI2	Mean	ResI2 - Resistance during inspiration at the point where the flow signal falls below the level specified in the Resistance Flow attribute.
ResE1	Mean	ResE1 - Resistance during expiration at the point where the flow signal falls below the negative of the level specified in the Resistance Flow attribute.
ResE2	Mean	ResE2 - Resistance during expiration at the point where the flow signal rises above the negative of the level specified in the Resistance Flow attribute.
CAvg	Mean	Compliance value averaged over the portion of the cycle between isovolumetric points.
RAvg	Mean	Resistance value averaged over the portion of the cycle between isovolumetric points.
PInspS (P1)	Mean	Pressure at start of Inspiration. This is the pressure value that occurs at the point in time when the flow signal starts inspiration. PInspS is one of the pressure values used in the calculation of compliance.

Name	Averaging In Review	Definition
PExpS (P2)	Mean	Pressure at start of Expiration. This is the pressure value that occurs at the point in time when the flow signal starts expiration. PExpS is one of the pressure values used in the calculation of compliance.
Piso1 (P3)	Mean	Pressure on clearing the Isovolumetric level, during inspiration. This is the pressure value that occurs when the volume signal rises above the user-specified Isovolumetric Level. Piso1 is used in the calculation of resistance.
Piso2 (P4)	Mean	Pressure on clearing the Isovolumetric level, during expiration. This is the pressure value that occurs when the volume signal falls below the user-specified Isovolumetric Level. Piso2 is used in the calculation of resistance.
Fiso1 (F1)	Mean	This is the Flow on clearing the Isovolumetric level, during inspiration. This is the flow value that occurs when the volume signal rises above the user-specified Isovolumetric Level. Fiso1 is used in the calculation of resistance.
Fiso2 (F2)	Mean	This is the Flow on clearing the Isovolumetric level, during expiration. This is the flow value that occurs when the volume signal falls below the user-specified Isovolumetric Level. Fiso2 is used in the calculation of resistance.
PEnh	Mean	Enhanced Pause. Calculated as: ((ET+AT)/RT-1) * (PEF/PIF) Formula from Noninvasive Measurement of Airway Responsiveness in Allergic Mice Using Barometric Plethysmography Hamelmann et al.
RT	Mean	Relaxation Time. This is the time from the start of expiration to the point where the volume signal drops by the Percent Relaxation value from its maximum value for the cycle.
WOBi	Mean	Work of Breathing (Inspiration). This is calculated as the area within the inspiration portion of the Volume vs. Pressure loop. The partially formed loop is closed by connecting the start of expiration point with the start of inspiration. The area is reported in mL - Pressure units. If the pressure signal is calibrated in cmH_20, the resultant units are gm-cm.
WOBe	Mean	Work of Breathing (Expiration). This is calculated as the area within the expiration portion of the Volume vs. Pressure loop. The partially formed loop is closed by connecting the end of expiration point with the start of expiration. The area is reported in mL - Pressure units. If the pressure signal is calibrated in cmH_20, the resultant units are gm-cm.
WOB	Mean	Work of Breathing. This is the sum of WOBi and WOBe. The area is reported in mL - Pressure units. If the pressure signal is calibrated in cmH_20, the resultant units are gm-cm.
POBi	Mean	Power of Breathing (Inspiration). This is the rate at which the inspiration work was performed and equals WOBi/(inspiration time in seconds). The units are Work units/seconds.
POBe	Mean	Power of Breathing (Expiration). This is the rate at which the expiration work was performed and equals WOBe/(expiration time in seconds). The units are Work units/seconds.
POB	Mean	Power of Breathing. This is the rate at which work was performed over the inspiration and expiration portion of the respiratory cycle and equals WOB/(inspiration time + expiration time in seconds). The units are Work units/seconds.
TVe	Mean	This is the difference between the volume at the start expiration mark and the volume at the point prior to the next cycles start inspiration mark. It is always reported in milliliters.

Name	Averaging In Review	Definition
AVol	Recent	Accumulated Volume is the summed total of the Tidal Volume (TV) from a reset point forward and is reported in milliliters. Reset points include the start of data collection, break in the data or the selection of the event associated with the AVol Reset Event attribute.
IF50	Mean	IF50 reports the inspiratory flow value at the point where the volume signal rises to 50% of the tidal volume.
EF50	Mean	EF50 reports the expiratory flow value at the point where the volume signal drops to 50% of the tidal volume.

The table below is the derived parameters for the Pulmonary Compliance Resistance pressure channel:

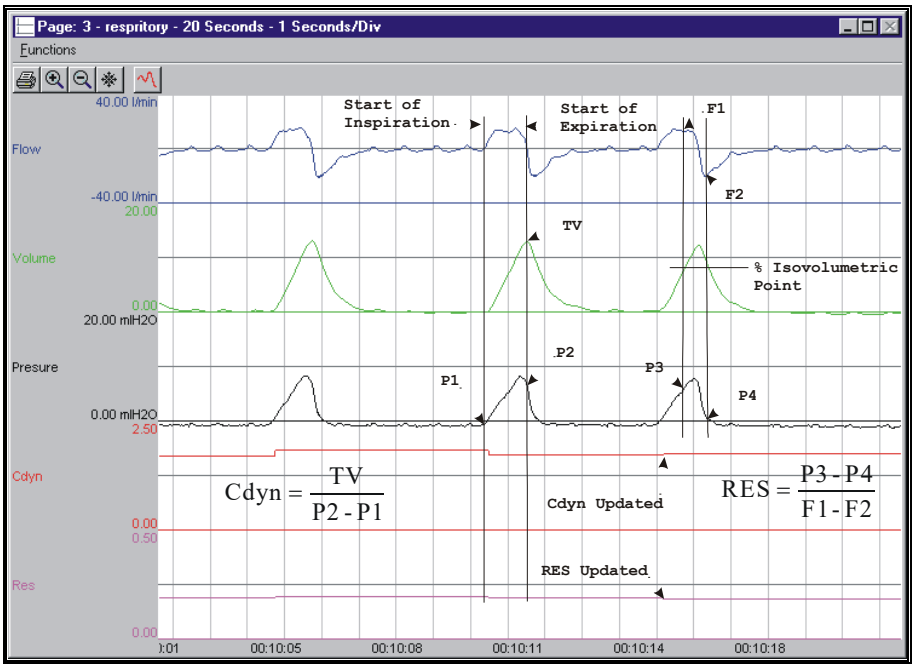
Name	Averaging In Review	Definition
Num	Recent	The number of the respiratory cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled.
Mean	Mean	The average pressure for breath.
Max	Maximum	The maximum pressure during a breath.
Min	Minimum	The minimum pressure during a breath.

Calibration

For the Pulmonary Compliance Resistance and Pulmonary Compliance Resistance Pressure signals, refer to the calibration section for the **Pulmonary Air Flow** Analysis Module.

On-Line Screens and Functions

Below is an example of a Primary graph displaying the raw analog format of a typical pulmonary air flow signal and pulmonary pressure with the digitally integrated volume, compliance, and resistance signals.



Pulmonary Compliance Resistance Key Marks

In the above figure, the Pulmonary Air Flow is displayed with validation tick marks and their meanings. The validation marks label the Start of Inspiration and the Start of Expiration.

Presentation Signals

Below is a list of presentation signals that are available for the PCR Analysis Module:

Signal	Description
Flow	For Primary Signal=Flow, this will be the original flow signal. For Primary Signal=Volume, this will display the differential of the signal, and it is generated as a two-point differential.
Volume	For Primary Signal=Flow, this will display the integration of the flow signal over the entire breath and reset at the start of the next valid breath. For Primary Signal=Volume, this will display the original volume signal.
Resistance*	Resistance will display the Res calculated value on a breath-to-breath basis.
Compliance*	Compliance will display the Cdyn calculated value on a breath-to-breath basis.
Conductance*	Conductance will display the Cond calculated value on a breath-to-breath basis.
ResCont*	The continuous resistance signal is calculated using the previous value of Cdyn and the current A/D sample points from flow, pressure and volum, as displayed in the formula below. The continuous resistance value is not calculated when the flow signal drops below the Minimum Flow attribute. $$\text{ResCont} = \frac{\left(\text{Pressure} - \frac{\text{Volume}}{\text{Cdyn}}\right)}{\text{Flow}}$$
***Presentation signals not available in Review.**	

Data Review

The Data Review related features of the PCR/PCRP Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.40 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

PCR marks are divided into two types, marks that always exist when a valid cycle is found (Start Inspiration, Start Expiration, Iso Vol Rise, and Iso Vol Fall) and marks that may or may not exist, depending on the signal morphology (Percent Relaxation and Start Apnea).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion, signal morphology is not considered.

Insert PCR Cycle

Inserts an entire PCR cycle which includes Start Inspiration, Start Expiration, and Percent Relaxation. Iso Vol Rise and Iso Vol Fall will be inserted if applicable. Start Apnea is not inserted; if Apnea exists this must be inserted manually. This set of marks may be inserted between a Start Inspiration mark and the last mark of the preceding cycle. Cycles may also be inserted prior to the first cycle and after the last cycle. When a PCR cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Insert Start Apnea

Inserts a Start Apnea mark. This mark may be inserted prior to a Start Inspiration mark or after the last cycle, as long as the preceding mark is not a Start Apnea mark.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. Only the Start Apnea mark may be deleted in this fashion. The rest of the marks cannot be deleted individually. An entire cycle may be deleted. A cycle is deleted by positioning the cursor on the Start Inspiration mark, bringing up the right mouse menu, and selecting Delete Cycle.

Moving Marks

Moving of the Start Inspiration, Start Expiration, and Start Apnea marks follow the standard rules used in Data Review. The Percent Relaxation, Iso Vol Rise and Iso Vol Fall marks are calculated marks; their position is dependent on the Tidal Volume and cannot be adjusted by the user. If the user changes the position of either the Start Inspiration, Start Expiration, or Start Apnea marks, the calculated marks will be recalculated.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay. Review reports the volume at the start of expiration as the Tidal Volume. Replay reports the maximum volume over the entire cycle. In most cases the values reported from Review and Replay are identical.

When a Review file is opened, the trace data may not be identical to the acquired data. The difference arises because of the scaling involved in the storage and reconstitution of the data. The difference for a point, on average, is less than 0.05%.

One of the consequences of this difference is seen with Calculated Marks. If, after opening a Review file, Review is prompted to recalculate a Calculated Mark, the mark may move with no change to the marks on which it depends. This is because the original placement of the Calculated Mark was based on the Replay data values whereas, recalculation uses the data values present in Review.

Logging Mark

The logging mark for a PCR cycle is the Start Inspiration mark. The time at the logging mark is the time used to report a cycle's derived data. If a cycle's logging mark falls within a logging interval, the cycle's data will be included in the logging interval.

End of Cycle

The end of a PCR cycle occurs at the point prior to the next cycle's Start Inspiration mark. When a PCR channel is the epoch channel, all review channels that display their cycle's logging mark prior to the end of the epoch channel's cycle will be included in the derived output.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Breaths-per-Minute is doubled, halved, etc.	This usually occurs when the analysis triggers on noise or artifacts. It can be corrected by changing the Minimum Flow to a higher or lower value to eliminate rates higher or lower than normal. If the signal has a lot of baseline noise, change the Low Pass Filter (in the Adv Attrib1 tab) to remove the noise or artifact. Select a lower value in the list box.
All Derived Parameters are reporting zero	The Minimum Flow may be set too high for the specified signal. Lower the Minimum Flow value.
Tidal Volume incorrect	1. This can be caused by the flow signal drifting above or below the zero line. Enable a High Pass Filter at 3Hz (in the Adv Attrib1 tab) if the flow signal is drifting. 2. The wrong Input Flow Units are being used. Since the volume is derived mathematically, the system must know the real units of flow being measured. 3. If the Tidal Volume is low, there could be a problem with the experimental setup. If the animal is in a plethysmograph, verify that there are no air leaks. This also pertains to any other setup. There can be no air leaks.
Compliance and Resistance are zero, or very high	Verify that the Pressure Channel has a valid Pulmonary Compliance Resistance Pressure Analysis Module assigned to it.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Pulmonary Compliance Resistance]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Flow(low)	This sets the minimum allowable value for Minimum Flow. The default value is .1.
Minimum Flow(high)	This sets the maximum allowable value for Minimum Flow. The default value is 100.
Resistance Flow Level(low)	This sets the minimum allowable value for Resistance Flow. The default value is .1.
Resistance Flow Level(high)	This sets the maximum allowable value for Resistance Flow. The default value is 100.
Iso Volume Percentage(low)	This sets the minimum allowable value for %Isovolumetric. The default value is 0.
Iso Volume Percentage(high)	This sets the maximum allowable value for %Isovolumetric. The default value is 99.
Percent Relaxation(low)	This sets the minimum allowable value for Percent Relaxation. The default value is 10.
Percent Relaxation(high)	This sets the maximum allowable value for Percent Relaxation. The default value is 90.
Maximum Breaths per Minute(low)	This sets the minimum allowable value for Maximum BPM. The default value is 0.
Maximum Breaths per Minute(high)	This sets the maximum allowable value for Maximum BPM. The default value is 1000.
Minimum Inspiratory Time(low)	This sets the minimum allowable value for Minimum Inspiratory Time. The default value is 0.
Minimum Inspiratory Time(high)	This sets the maximum allowable value for Minimum Inspiratory Time. The default value is 10000.
Maximum Un-expired Percentage(low)	This sets the minimum allowable value for Max Un-expired Percentage. The default value is 0.
Maximum Un-expired Percentage(high)	This sets the maximum allowable value for Max Un-expired Percentage. The default value is 100.

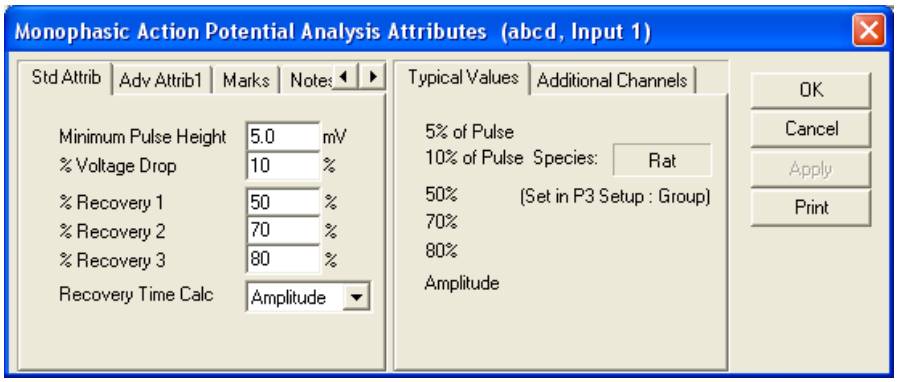
Monophasic Action Potential (MAP)

The Monophasic Action Potential Analysis Module analyzes monophasic action potential signals. The analysis calculates derived parameters from the input signal on a beat-to-beat basis. The detection of complexes is controlled by attributes that are set by the user.

Attribute Window

The Monophasic Action Potential attributes window allows you to modify the signal analysis for different types of signals and signal conditions.

Standard Attributes



Monophasic Action Potential Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Standard Attributes

Attribute	Effect On Review	Description
Minimum Pulse Height	Signal Interpretation	The minimum voltage pulse that the signal must achieve before a new cycle is detected. The pulse is measured as the difference between the current point and the lowest point in the cycle so far. This attribute is used to prevent false triggering.
% Voltage Drop	Signal Interpretation	Determines the drop in voltage from the peak that indicates the end of a cycle. The voltage drop is calculated as a percentage of the pulse height.
% Recovery 1, 2, and 3	Calculation, Redraw	The analysis will report the time from just before the upstroke of the action potential to the point where the signal drops below the voltage levels indicated by each of the % Recoveries. The user determines whether the recovery level is calculated as a percentage drop from the maximum voltage or as a percentage drop from the plateau voltage, when selecting the Recovery Time Calc attribute.

Attribute	Effect On Review	Description
Recovery Time Calc	Calculation, Redraw	This attribute determines the voltage range used in the calculation of the recovery levels, for the % Recovery attributes. The two options are: Amplitude (default setting): This uses the peak voltage minus EDV. Plateau: This is the Plateau voltage minus EDV. EDV is the voltage just prior to the upstroke of the action potential.

Advanced Attributes

The only Advanced Attributes for Monophasic Action Potential are the Low and High Pass Filter selections.

Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Minimum Pulse Height	5% of Pulse	mV
%Voltage Drop	10% of Pulse	%
% Recovery 1	50	%
% Recovery 2	70	%
% Recovery 3	80	%
Recovery Time Calc	Amplitude	NA

Marks (Validation)

The **Monophasic Action Potential** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the MAP signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	End Diastolic Voltage Mark
Blue	Maximum Slope Mark
Green	Peak Value Mark
Cyan	Plateau Voltage
Brown	Recovery 1 Mark
Yellow	Recovery 2 Mark
Gray	Recovery 3 Mark
Magenta	Maximum Recovery Mark

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be

calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

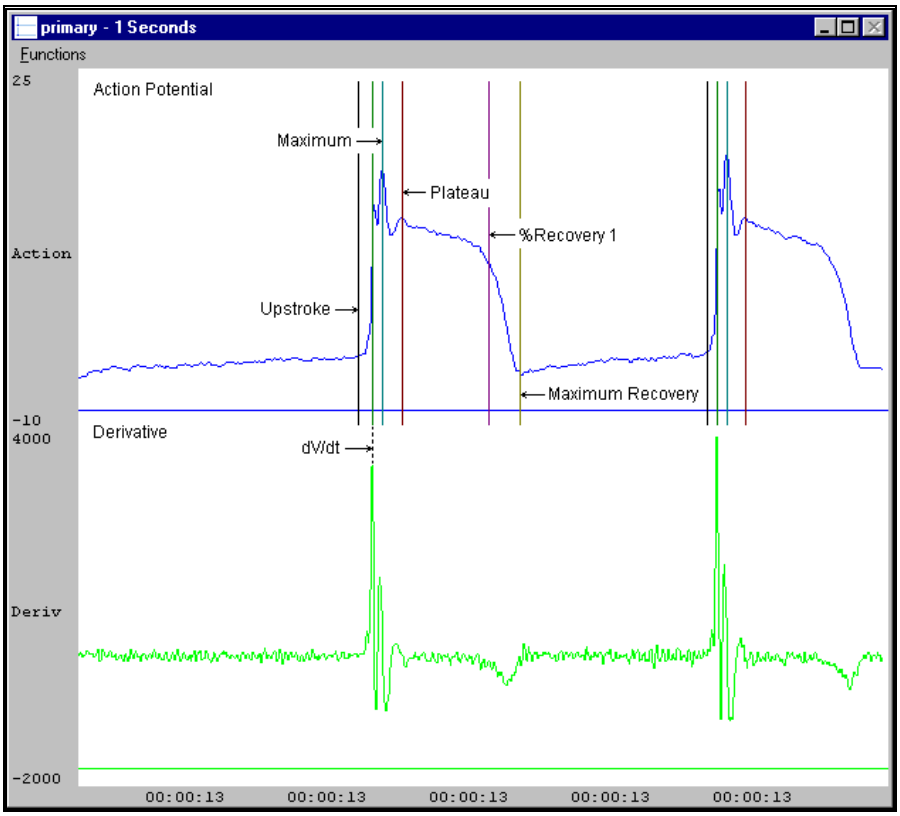
Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Max	Mean	The Maximum Voltage that occurred during a cardiac cycle.
EDV	Mean	The voltage prior to the upstroke of the action potential.
Min	Mean	The minimum voltage that occurred during a cardiac cycle.
Plto	Mean	The plateau voltage.
Amp	Mean	PLTO minus EDV.
Rate	Harmonic Mean	The beats-per-minute. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
+dV	Mean	The maximum positive rate of change that occurred.
-dV	Mean	The maximum negative rate of change that occurred between the Plateau and the Maximum Recovery Mark.
REC1	Mean	The time, in milliseconds, from the beginning of the upstroke of the action potential, to the point where the signal drops below the level corresponding to the % Recovery 1 level.
xR1	Sum	The number of cycles that did not reach the % Recovery 1 level, within the logging period.
REC2	Mean	The time, in milliseconds, from the beginning of the upstroke of the action potential, to the point where the signal drops below the level corresponding to the % Recovery 2 level.
xR2	Sum	The number of cycles that did not reach the % Recovery 2 level, within the logging period.
REC3	Mean	The time, in milliseconds, from the beginning of the upstroke of the action potential, to the point where the signal drops below the level corresponding to the % Recovery 3 level.
xR3	Sum	The number of cycles that did not reach the % Recovery 3 level, within the logging period.
%Max	Mean	The time, in milliseconds, from the beginning of the upstroke of the action potential, to the point where the signal recovers to 100% or as close to 100% as possible.
Time	Mean	The time interval between action potentials. For Acquisition it shall be the time interval in milliseconds between the previous cycle's EDV Mark and the current cycle's EDV Mark. For Review it shall be the time interval in milliseconds between the current cycle's EDV Mark and the following cycle's EDV Mark
Cnt	Sum	The number of cycles in the logging period.
RiseT	Mean	The time, in milliseconds, between the EDV and Max points.

Calibration

The recommended calibration for a system with a Monophasic Action Potential signal depends on the amplifier instrumentation that the system is connected to. Typical values for the high calibration value are in the range of 5.0 to 100.0mV.

On-Line Screens and Functions

The following is an example of a Primary graph displaying the raw analog format of an aorta blood pressure signal.



Monophasic Action Potential Key Marks

In the above figure, the **Monophasic Action Potential** is displayed with validation tick marks and their meanings.

Presentation Signals

Below is a list of presentation signals that are available for the MAP Analysis Module:

Signal	Description
Input	The original input signal after applying any software filters.
Derivative	Derivative of the input signal.

Data Review

The Data Review related features of the MAP Analysis Module listed here are accessible when the analysis module is used with Ponemah Version 4.80 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

MAP marks are divided into two types, marks that always exist when a valid cycle is found (End Diastolic Voltage, Maximum Slope, Peak Value, and Plateau) and marks that may or may not exist, depending on the signal morphology (Recovery Mark 1, Recovery Mark 2, Recovery Mark 3, and Maximum Recovery Mark).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion, signal morphology is not considered.

Insert MAP Cycle

This function inserts an entire MAP cycle which includes End Diastolic Voltage, Maximum Slope, Peak Value, and Plateau Marks. Recovery Mark 1, Recovery Mark 2, Recovery Mark 3, and Maximum Recovery Mark all will be inserted if applicable, based on signal morphology. Cycles may be inserted between the Maximum recovery of a cycle and the EDV of the next cycle. When a MAP cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Individual marks are not able to be deleted from a MAP cycle. Only the Peak Value Mark may be deleted which will remove the entire MAP cycle. The rest of the marks cannot be deleted individually. A cycle is deleted by positioning the cursor on the Peak Value Mark, bringing up the right mouse menu, and selecting Delete Cycle.

Moving Marks

Moving of the End Diastolic Voltage, Maximum Slope, Peak Value, and Plateau Marks follow the standard rules used in Data Review. The Recovery Mark 1, Recovery Mark 2, Recovery Mark 3, and Maximum Recovery Mark are calculated marks; their position is based on the time in milliseconds from the beginning of the upstroke of the action potential, or from the +dV point, to the point where the signal drops below the level corresponding to the % Recovery level and cannot be adjusted by the user. In Review, the Recovery Marks are calculated independent of the Plateau Mark.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

When a Review file is opened, the trace data may not be identical to the acquired data. The difference arises because of the scaling involved in the storage and reconstitution of the data. The difference for a point, on average, is less than 0.05%.

One of the consequences of this difference is seen with Calculated Marks. If, after opening a Review file, Review is prompted to recalculate a Calculated Mark, the mark may move with no change to the marks on which it depends. This is because the original placement of the Calculated Mark was based on the Replay data values, whereas recalculation uses the data values present in Review.

Logging Mark

The logging mark for a MAP cycle is the Peak Value Mark. The time at the logging mark is the time used to report a cycle's derived data. If a cycle's logging mark falls within a logging interval, the cycle's data will be included in the logging interval.

End of Cycle

The end of a MAP cycle occurs one nanosecond prior to the End Diastolic Voltage of the following cycle. When a MAP channel is the epoch channel, all review channels that display their cycle's logging mark prior to the end of the epoch channel's cycle will be included in the derived output.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Rate is doubled	Minimum Pulse Height and/or %Voltage Drop is set too low.
Rate is halved	Minimum Pulse Height and/or %Voltage Drop is set too high.
All derived parameters are reporting zero	Minimum Pulse Height and/or %Voltage Drop is set too high.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.
Algorithm does not trigger (No marks)	Reduce the sample rate to 250-1000Hz (Calibration - A/D Setup).

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Monophasic Action Potential]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Pulse Height(low)	This sets the minimum allowable value for Minimum Pulse Height. The default value is 1.
Minimum Pulse Height(high)	This sets the maximum allowable value for Minimum Pulse Height. The default value is 100.

Entry Name	Description
Percentage Voltage Drop(low)	This sets the minimum allowable value for %Voltage Drop. The default value is 0.
Percentage Voltage Drop(high)	This sets the maximum allowable value for %Voltage Drop. The default value is 80.
% Recovery 1(low)	This sets the minimum allowable value for % Recovery 1. The default value is 30.
% Recovery 1(high)	This sets the maximum allowable value for % Recovery 1. The default value is 100.
% Recovery 2(low)	This sets the minimum allowable value for % Recovery 2. The default value is 30.
% Recovery 2(high)	This sets the maximum allowable value for % Recovery 2. The default value is 100.
% Recovery 3(low)	This sets the minimum allowable value for % Recovery 3. The default value is 30.
% Recovery 3(high)	This sets the maximum allowable value for % Recovery 3. The default value is 100.
MPH Deriv Time	This is an entry in the .INI file that may be used to correct the condition where the EDV point is marked high on the upstroke of the MAP signal instead of being marked prior to the rise. This setting should be changed only after confirming that the full range of the A/D is being used and that the sample rate is not unreasonably high. MPH Deriv Time is the number of milliseconds over which the analysis will look for the EDV point. The default setting for MPH Deriv Time and its most appropriate setting is 1 millisecond. Increasing this number will result in the averaging out of any stair stepping caused by low span. Increase this parameter by one millisecond at a time until the EDV point is correctly marked.
Reset Time	This is an entry in the .INI file that is used to prevent the analysis from getting hung up on a spike in the data. The Reset Time is specified in milliseconds. If no cycle is encountered over the duration of the Reset Time the Analysis is reinitialized. The default value is 2000.
EDV Adjust	This entry is used to shift the End Diastolic Voltage Mark, calculated by the analysis, to the left by the specified number of milliseconds. The default value is 0.
Action Potential Start At EDV	This entry allows the user to control the start point of the action potential. Setting the value to 1 will use the EDV as the start of the action potential. Setting the value to 0 will use the +dV as the start of the action potential. The default value is 1.

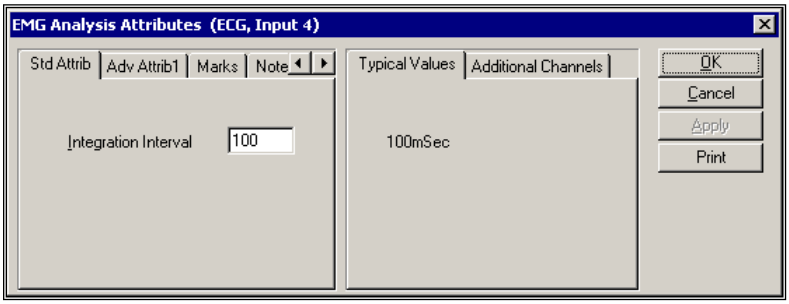
Electromyogram/Electroencephalogram (EMG)

The Electromyogram/ Electroencephalogram Analysis Module analyzes electromyogram or electroencephalogram signals. The analysis calculates derived parameters from the input signal over a user specified logging period.

Attribute Window

The Electromyogram attributes window allows you to modify the signal analysis for different types of signal conditions.

Standard Attributes



EMG Standard Attribute Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Integration Interval	Calculations	The period over which the EMG signal is integrated before resetting. The result of the previous integration is displayed over this period.

Advanced Attributes

The only Advanced Attributes for Electromyogram are the Low and High Pass Filter selections. Refer to **Error! Reference source not found.** in the **Error! Reference source not found.** section for more information.

Typical Values

Use this value as a guideline for a first time setup. Under different situations, a value above or below the typical value will have to be used.

Attribute	Setting	Units
Integration Interval	100	mSec

Noise Attributes Tab

Attribute	Description
Enable Noise Detection	Determines if noise detection will be used to determine bad data marks
Enable Rail Detection	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value/ Maximum Signal Value	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.

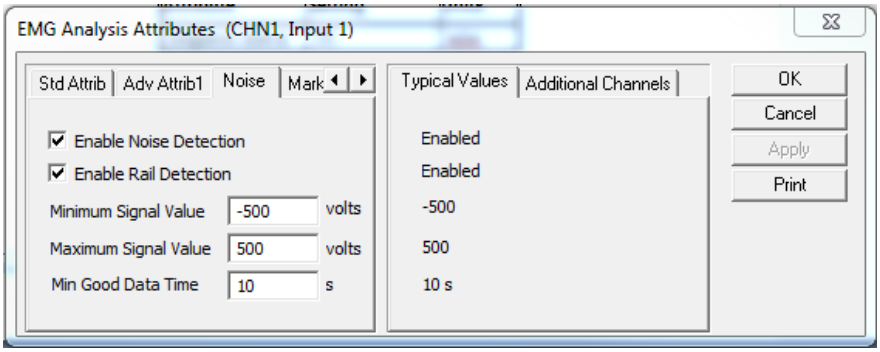
Attribute	Description
Minimum Good Data Time	When Noise detection is enabled and a range of data is analyzed, any bad data marks that have less than or equal to the Min Good Data Time of good data between them shall be combined into a single bad data region.

Marks (Validation)

The **EMG** analysis displays a validation tick mark at the end of each Integration Interval. This mark is used to denote the logging mark of the cycle (interval) as well as used to determine the cycle number.

The following chart defines the validation marks:

Color	Type	Meaning
Black	Integration Interval	The system will display a black validation mark at the end of the Integration Interval. The Integration Interval is set in the Standard Attributes tab.



Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

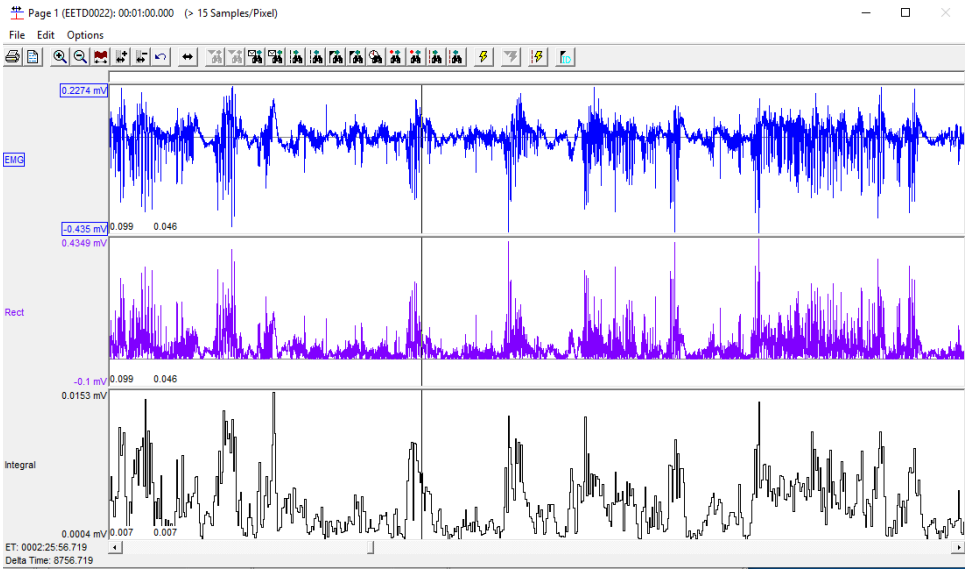
Name	Averaging In Review	Definition
NUM	Recent	The number of the Integration Interval (cycle). This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
INT	Mean	The integral of the rectified signal over the integration interval.
PEAK	Maximum	This is the maximum INT value over the logging period.

Calibration

The calibration for the system for an EMG signal depends on the amplifier instrumentation that is connected to the system.

On-Line Screens and Functions

The following is an example of a Primary graph displaying an EMG signal.



EMG, Rectified EMG and EMG Integration

In the above figure, the Electromyogram signal is displayed along with the rectified signal and its integral over the **Integration interval**.

Presentation Signals

Below is a list of presentation signals that are available for the EMG Analysis Module:

Signal	Description
Input	The original input signal after applying any software filters.
Derivative	Derivative of the input signal.

Data Review

The Data Review related features of the Electromyogram Analysis Module listed here are accessible when the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

EMG supports only the Integration Interval Mark.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. With the Electromyogram module, inserting marks is not permitted.

Insert EMG Cycle

Insert EMG cycle is not permitted..

Deleting Marks

Deleting marks in EMG is not permitted.

Moving Marks

Moving marks in EMG is not permitted.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

Logging Mark

The logging mark for an EMG cycle is the Integration Interval mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of an EMG cycle occurs at the Integration Interval mark.

Troubleshooting

There is no troubleshooting for this analysis module.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[EMG]** section of the file. The user may change these settings if the range of values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Integration Interval(low)	This sets the minimum allowable value for **Integration Interval** in milliseconds. The default value is 100.
Integration Interval(high)	This sets the maximum allowable value for **Integration Interval** in milliseconds. The default value is 10000.

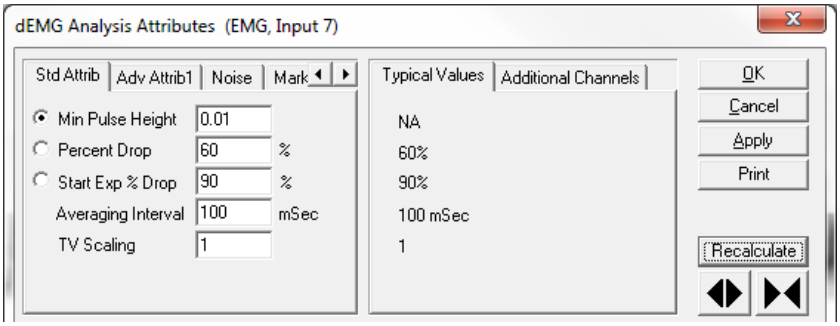
Diaphragmatic Electromyogram (dEMG)

The Diaphragmatic Electromyogram (dEMG) Analysis Module analyzes electromyogram signals obtained the diaphragm. The analysis calculates derived parameters from the input signal over a user specified logging period.

Attribute Window

The dEMG attributes window allows you to modify the signal analysis for different types of signal conditions.

Standard Attributes



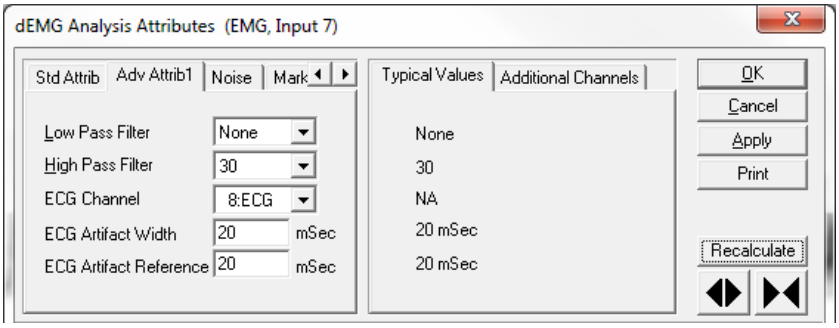
dEMG Standard Attribute Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Min Pulse Height	Signal Interpretation	Used in the identification of a respiratory cycle. The Averaged EMG signal must rise from its lowest point by Min Pulse Height in order to be recognized as a cycle.
Percent Drop	Signal Interpretation	Used in the identification of a respiratory cycle. The Averaged EMG signal must fall by Percent Drop percentage of the rise from its lowest point in order to be recognized as a cycle.
Start Exp % Drop	Signal Interpretation	Used in the estimation of the start expiration point. The point at which the Averaged EMG signal drops by Start Exp % Drop is marked as the start of expiration. NOTE: This is a rough estimate which will not be accurate in the case of cycles that exhibit marked variation in the averaged EMG signal.

Attribute	Effect On Review	Description
Averaging Interval	Signal Conditioning, Calculation, Redraw	Used in the creation of the Averaged EMG signal. The averaged EMG signal is created by taking a rolling average of the rectified EMG signal. The range of data included in the rolling average is determined by the averaging interval. This is the signal that is used for cycle identification and for placement of cycle marks. NOTE: The longer the averaging interval, the greater the smoothing and the longer the processing time when analyzing a signal NOTE: The actual increase in EMG activity occurs half an averaging interval after the mark appears
TV Scaling	Calculation	Used to scale the TV and TV2 derived parameters based on an externally calculated scaling factor. TV and TV2 values calculated from the Rectified EMG signal will be multiplied by the TV Scaling attribute.

Advanced Attributes



Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz. NOTE: It is not recommend to use the low pass filter since this will dampen the signal, use the Averaging Interval instead
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz. NOTE: Set a High Pass Filter with a cut off at 30Hz to remove the low frequency components and to bring the signal back to baseline.

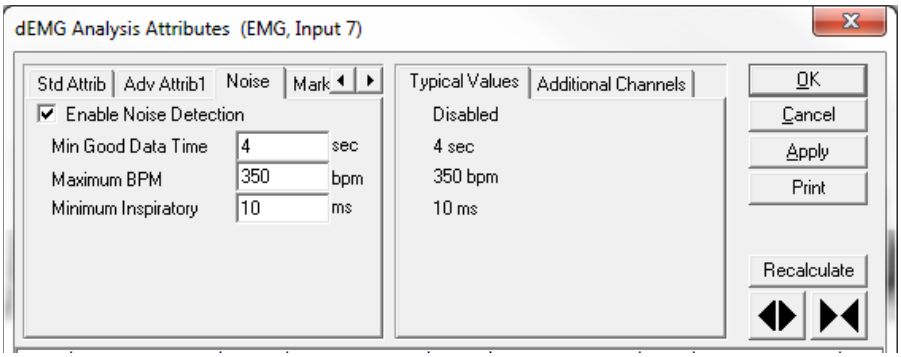
Attribute	Effect On Review	Description
ECG Channel	Signal Conditioning, Calculation, Redraw	Defines the ECG channel that should be used to remove ECG artifact from the EMG signal. This may be set to None if no ECG channel is available. The ECG Channel attribute is used in conjunction with ECG Artifact Width and ECG Artifact Reference.
ECG Artifact Width	Signal Conditioning, Calculation, Redraw	Defines the time span that will be modified to remove ECG artifact from the rectified EMG signal. In Acquisition, the region affected starts at each Q mark in the channel defined by the ECG Channel attribute. In Review, the region affected is centered on R mark in the channel defined by the ECG Channel attribute. NOTE: If the ECG Channel attribute is set to None, the ECG Artifact Width attribute is disabled.
ECG Artifact Reference	Signal Conditioning, Calculation, Redraw	Defines the time span over which data will be averaged to generate a replacement value for data affected by the ECG artifact. The time span is split on either side of the ECG Artifact Width. NOTE: If the ECG Channel attribute is set to None, the ECG Artifact Reference attribute is disabled.

Typical Values

Use this value as a guideline for a first time setup. Under different situations, a value above or below the typical value will have to be used.

Attribute	Setting	Units
Min Pulse Height	NA	NA
Percent Drop	60	%
Start Exp % Drop	90	%
Averaging Interval	100	mSec
TV Scaling	1	NA
Low Pass Filter	None	NA
High Pass Filter	30	Hz
ECG Artifact Width	20	mSec
ECG Artifact Reference	20	mSec

Noise Tab



Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	When this checkbox is selected, the dEMG analysis will place Bad Data Marks in the data based on the attributes listed below.
Min Good Data Time	Signal Interpretation	This defines the minimum time that must exist between Bad Data Marks. If less than Min Good Data Time exists between two sets of Bad Data Marks, the two sets will be combined into a single set of Bad Data Marks encompassing both regions.
Maximum BPM	Signal Interpretation	If a cycle's respiratory rate exceeds the Maximum BPM attribute, it will be replaced with Bad Data Marks.
Minimum Inspiratory Time	Signal Interpretation	If a cycle's Inspiratory Time drops below the Minimum Inspiratory attribute, it will be replaced with Bad Data Marks.

Marks (Validation)

The **EMG** analysis displays a validation tick mark at the end of each Integration Interval. This mark is used to denote the logging mark of the cycle (interval) as well as used to determine the cycle number.

The following chart defines the validation marks:

Color	Type	Meaning
Black	Start Inspiration	The Start Inspiration mark is placed at the start of the rise in the Averaged Presentation signal.
Blue	Start Expiration	The Start Expiration mark is placed at the point where the Averaged Presentation signal drops by Start Exp % Drop percent of the amplitude change in the decreasing portion of the respiratory cycle. A Start Expiration mark may not be placed if the following cycle is a partial cycle.

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be

calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
NUM	Recent	The number of the Respiratory Cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
TV	Mean	Tidal Volume is calculated by multiplying the unscaled TV by the TV Scaling attribute. The unscaled TV value is obtained by integrating the Rectified EMG signal between the following points: Start Inspiration of the current cycle and Start Inspiration of the following cycle. ***NOTE: Start Inspiration on the Rectified signal is located to the right of the Start Inspiration mark by ½ of the Averaging Interva***l. Tidal volume is reported in arbitrary units since it an estimation of true tidal volume.
MV	Mean	Minute Ventilation is the product of the TV and BPM.
BPM	Harmonic Mean	Breaths Per Minute is calculated from the time interval between Start Inspiration marks. The calculation is 1000/TT * 60 where TT (total time) is the time between Start Inspiration marks in mSec.
IT	Mean	The Inspiration Time is the time between Start Inspiration and Start Expiration, expressed in mSec. ***NOTE: Start Inspiration is located to the right of the Start Inspiration mark by ½ of the Averaging Interval. Start Expiration is located to the left of the Start Expiration mark by ½ of the Averaging Interval.***
TT	Mean	Total Time is the time between Start Inspiration of the current cycle and Start Expiration of the following cycle, expressed in mSec. ***NOTE: Start Inspiration is located to the right of the Start Inspiration mark by ½ of the Averaging Interval. Start Expiration is located to the left of the Start Expiration mark by ½ of the Averaging Interval.***
ET	Mean	Expiration Time is the time between Start Expiration and the following Start Inspiration, expressed in mSec. ***NOTE: Start Inspiration is located to the right of the Start Inspiration mark by ½ of the Averaging Interval. Start Expiration is located to the left of the Start Expiration mark by ½ of the Averaging Interval.***

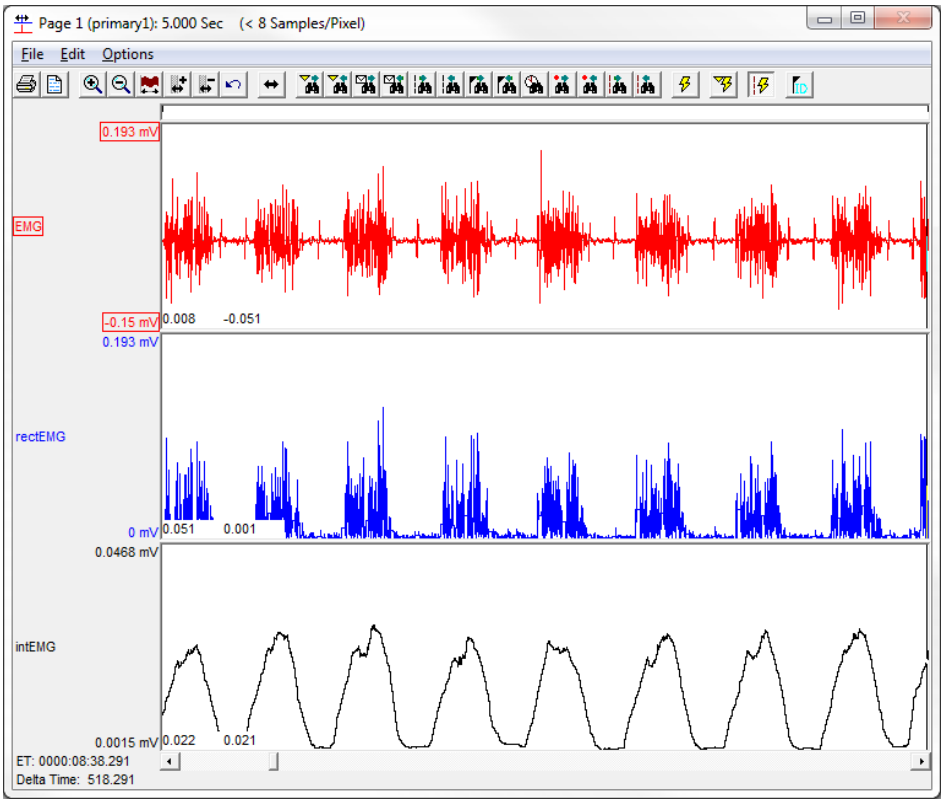
Name	Averaging In Review	Definition
TV2	Mean	Tidal Volume 2 is calculated by multiplying the unscaled TV 2 by the TV Scaling attribute. The unscaled TV 2 value is obtained by integrating the Rectified EMG signal between the following points: Start Inspiration and Start Expiration. ***NOTE: Start Inspiration is located to the right of the Start Inspiration mark by ½ of the Averaging Interval. Start Expiration is located to the left of the Start Expiration mark by ½ of the Averaging Interval.*** Tidal volume is reported in arbitrary units since it an estimation of true tidal volume.
MV2	Mean	Minute Ventilation 2 is the product of TV2 and BPM.

Calibration

The calibration for the system for a dEMG signal depends on the amplifier instrumentation that is connected to the system.

On-Line Screens and Functions

The following is an example of a Primary graph displaying an EMG signal.



dEMG, Rectified dEMG and dEMG Integration

In the above figure, the Diaphragmatic Electromyogram signal is displayed along with the rectified signal and its integral over the **Integration interval**.

Presentation Signals

Below is a list of presentation signals that are available for the EMG Analysis Module:

Signal	Description
Input	The original input signal after applying any software filters.
dEMG	A High Pass Filter is applied to the input signal to form the dEMG Presentation Signal.
Rectified	The dEMG signal is rectified and ECG artifact is removed to form the Rectified Presentation Signal.
Averaged	The Rectified presentation signal is smoothed by using an averaging filter to form the Averaged Presentation Signal. The Averaged Presentation Signal is the signal that is used for cycle identification.

Data Review

The Data Review related features of the Diaphragmatic Electromyogram Analysis Module listed here are accessible when the customer's current license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

In order to analyze a diaphragmatic EMG signal, the signal is filtered to remove low frequency components, rectified and ECG artifact is removed. The resultant signal is smoothed using an averaging filter. The smoothed signal is used to identify the location of respiratory cycles

Start Inspiration and Start Expiration marks are marks placed on the smoothed signal. Due to the use of an averaging filter, the location of the Start Inspiration and Start Expiration mark will not coincide with the rise in EMG activity seen in the Rectified Presentation signal. In order to translate the mark positions from the smoothed signal to the Rectified signal, the Start Inspiration mark should be visualized ½ the Averaging Interval to the right and the Start Expiration mark should be visualized ½ the Averaging Interval to the left.

Inserting Marks

Inserting individual Start Inspiration or Start Expiration marks is not permitted. These are controlled based on inserting an entire dEMG cycle.

Insert dEMG Cycle

Inserts an entire dEMG cycle: Start Inspiration and Start Expiration. This set of marks may be inserted between Start Expiration and Start Inspiration marks. When a dEMG cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Deleting individual Start Inspiration or Start Expiration marks is not permitted. These are controlled based on inserting an entire dEMG cycle. To delete a dEMG cycle, right-click on the Start Inspiration mark and select Delete Cycle.

Moving Marks

Moving Start Inspiration and Start Expiration marks follow the standard rules used in Data Review.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay, with the exception of ECG Artifact Width. During Acquisition and Replay, the region affected starts at each Q mark in the channel defined by the ECG Channel attribute. In Review, the region affected is centered on R mark in the channel defined by the ECG Channel attribute.

Logging Mark

The logging mark for a dEMG cycle is the Start Inspiration mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of the dEMG cycle occurs one sample prior to the next cycle's Start Inspiration mark.

Troubleshooting

There is no troubleshooting for this analysis module.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[dEMG]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Averaging Interval(low)	This sets the minimum allowable value for Averaging Interval in milliseconds. The default value is 1.

Entry Name	Description
Averaging Interval(high)	This sets the maximum allowable value for Averaging Interval in milliseconds. The default value is 10000.
Smoothing Filter(low)	This sets the minimum allowable value for Smoothing Filter in milliseconds. The default value is 0.
Smoothing Filter(high)	This sets the maximum allowable value for Smoothing Filter in milliseconds. The default value is 10000.
Min Pulse Height(low)	This sets the minimum allowable value for Min Pulse Height in millivolts. The default value is 0.0001.
Min Pulse Height(high)	This sets the maximum allowable value for Min Pulse Height in millivolts. The default value is 1000.
% Pressure Drop(low)	This sets the minimum allowable value for % Pressure Drop in percent. The default value is 0.
% Pressure Drop(high)	This sets the maximum allowable value for % Pressure Drop in percent. The default value is 10000.
TV Scaling(low)	This sets the minimum allowable value for TV Scaling. The default value is 0.
TV Scaling(high)	This sets the maximum allowable value for TV Scaling. The default value is 1000.
Start Expiration % Drop(low)	This sets the minimum allowable value for Start Expiration % Drop in percent. The default value is 0.
Start Expiration % Drop(high)	This sets the maximum allowable value for Start Expiration % Drop in percent. The default value is 10000.
ECG QRS Width(low)	This sets the minimum allowable value for ECG QRS Width in milliseconds. The default value is 0.
ECG QRS Width(high)	This sets the maximum allowable value for ECG QRS Width in milliseconds. The default value is 10000.
ECG QRS Reference(low)	This sets the minimum allowable value for ECG QRS Reference in milliseconds. The default value is 0.
ECG QRS Reference(high)	This sets the maximum allowable value for ECG QRS Reference in milliseconds. The default value is 10000.
Minimum Good Data Time(low)	This sets the minimum allowable value for Minimum Good Data Time in seconds. The default value is 0.
Minimum Good Data Time(high)	This sets the maximum allowable value for Minimum Good Data Time in seconds. The default value is 1000.
Max BPM(low)	This sets the minimum allowable value for Max BPM in bpm. The default value is 0.

Entry Name	Description
Max BPM(high)	This sets the maximum allowable value for Max BPM in bpm. The default value is 1000.
Min Inspiration Time(low)	This sets the minimum allowable value for Min Inspiration Time in milliseconds. The default value is 0.
Min Inspiration Time(high)	This sets the maximum allowable value for Min Inspiration Time in milliseconds. The default value is 10000.

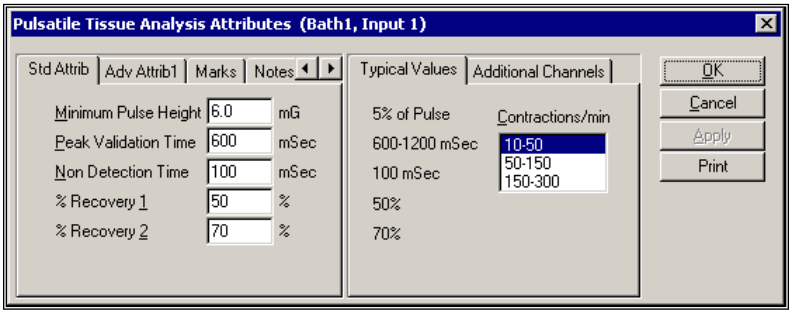
Pulsatile Tissue and Gut Motility

The Pulsatile Tissue and Gut Motility Analysis Module analyzes any pulsatile tissue signal, and calculates, on a contraction-to-contraction basis, derived values for the cycle.

Attribute Window

The Pulsatile Tissue attributes window allows you to modify the signal analysis for different types of tissue signals and different signal conditions.

Standard Attributes



Pulsatile Tissue Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Pulse Height	Signal Interpretation	Sets the minimum developed contraction that the signal must achieve before the analysis will detect and validate a contraction. The Minimum Pulse Height is useful for stopping the analysis from triggering on artifacts.
Peak Validation Time	Signal Interpretation	The period, in milliseconds, over which a peak is validated. The peak is validated if the signal level at the peak is not exceeded over the validation period. Once a peak is validated, the cycle terminates.

Attribute	Effect On Review	Description
Non Detection Time	Signal Interpretation	Sets the length of *dead time* in milliseconds that the analysis does not look for a contraction. This is used to move the peak analysis past artifacts that occur after the maximum contraction.
% Recovery 1 and 2	Calculation, Redraw	Defines a level at which the % recovery times are reported. The level is calculated as a reduction in the signal from the new contraction in terms of a percentage of the delta value.

Advanced Attributes

The only Advanced Attributes for Pulsatile Tissue and Gut Motility are the Low and High Pass Filter selections. Refer to **Error! Reference source not found.** in the **Error! Reference source not found.** section for more information.

Typical Values

The table contains typical values for different contraction rates. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Contraction Rate	Attribute	Setting	Units
10-300 (All)	Minimum Pulse Height	5% of Pulse	mG
	% Recovery 1	50	%
	% Recovery 2	70	%
10-50 (Dog, Monkey)	Peak Validation	600-1200	mSec
	Non Detection Time	100	mSec
50-150 (Rat)	Peak Validation	200-800	mSec
	Non Detection Time	75	mSec
150-300 (Mouse)	Peak Validation	50-250	mSec
	Non Detection Time	50	mSec

Marks (Validation)

The **Pulsatile Tissue** and Gut Motility analysis displays validation tick marks for each contraction cycle. Each contraction should have only one set of marks. These marks verify that the system is analyzing the tissue signal correctly. If there is more than one set of validation marks per contraction, change the analysis attributes to correct the problem.

The following chart defines the validation marks:

Color	Type	Meaning
Black	Maximum Mark	The system will display a black validation mark at the Maximum Mark. The Maximum Mark is placed at the maximum value that occurs after clearing the Min Pulse Height till the point Peak Validation Time is satisfied.
Blue	Minimum Mark	The system will display a blue validation mark at the Minimum Mark. The Minimum Mark is placed at the minimum value that occurs after clearing the Non detection time for the previous cycle to the point where the Min Pulse Height attribute for the current cycle is satisfied.
Green	Recovery 1 Mark	The system will display a green validation mark at the Recovery 1 Mark.
Cyan	Recovery 2 Mark	The system will display a cyan validation mark at the Recovery 2 Mark.
Red	Start of Contraction	The system will display a red validation mark at the Start Contraction Mark. The Start Contraction Mark is placed at the last point that has a derivative less than or equal to 0 between the end of the Non Detection Time and satisfying the Min Pulse Height requirement.

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the tissue contraction cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Max	Mean	The Maximum value that occurs during the contraction cycle.
Min	Mean	The Minimum value that occurs during the contraction cycle.
Avg	Mean	Avg is the area under the curve for a valid cycle divided by the number of logging points under the curve. In Acquisition and Replay this is calculated between the point after clearing Peak Validation time for the previous cycle to the point at which peak validation time is cleared for the current cycle. In Review, the Average is calculated from the current cycle's Minimum mark to the point prior to the following cycles Minimum mark.
Delta	Mean	The Delta is the difference between the maximum and minimum values of a cycle.

Name	Averaging In Review	Definition
Rate	Harmonic Mean	Rate is the reciprocal of the time interval for the cycle multiplied by 60. During Replay and Acquisition, the rate is calculated based on the interval between the completion of the previous cycles peak validation time and the current cycles peak validation time. In Review it is calculated off the duration between the previous cycle's Maximum mark and the current cycles Maximum Mark. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
TTPK	Mean	Time To Peak is the time from the start of the rise of the contraction to the maximum contraction value. The value is reported in milliseconds.
+d_/dt	Mean	The maximum positive value of the first derivative of the contraction that occurs between the Start Contraction Mark and the completion of Peak Validation Time. In Review +d_/dt is calculated between the Minimum Mark and the Maximum Mark.
-d_/dt	Mean	The maximum negative value of the first derivative of the contraction that occurs between the Maximum Mark and the point that clears the minimum pulse height. In Review -d_/dt is calculated between the Maximum Mark and the next cycle's Minimum Mark.
%Rec1	Mean	Percent Recovery 1 is the period of time after the maximum contraction has occurred until a pre-defined percentage of the delta has occurred. The time is in milliseconds.
%Rec2	Mean	Percent Recovery 2 is the period of time after the maximum contraction has occurred until a pre-defined percentage of the delta has occurred. The time is in milliseconds.
+dd/dt	Mean	The maximum positive value of the second derivative of the contraction that occurs between the Start Contraction point and the peak validation time. In Review +d'/dt is calculated between the Minimum Mark and the Maximum Mark.
-dd/dt	Mean	The maximum negative value of the second derivative of the contraction that occurs between the maximum point and the point that clears the minimum pulse height. In Review –d'/dt is calculated between the Maximum Mark and the next cycle's Minimum Mark.
MI	Mean	The Motility Index is the product of DELTA multiplied by RATE for a given logging period. Note: When running in a logging mode other than 1 epoch, MI is calculated from the averaged Delta and averaged Rate values.

Name	Averaging In Review	Definition
Area	Mean	Area is the area under the curve for a valid cycle. In Acquisition and Replay this is calculated between the point after clearing Peak Validation time for the previous cycle to the point at which peak validation time is cleared for the current cycle. In Review, the Average is calculated from the current cycle's Minimum mark to the point prior to the following cycles Minimum mark.

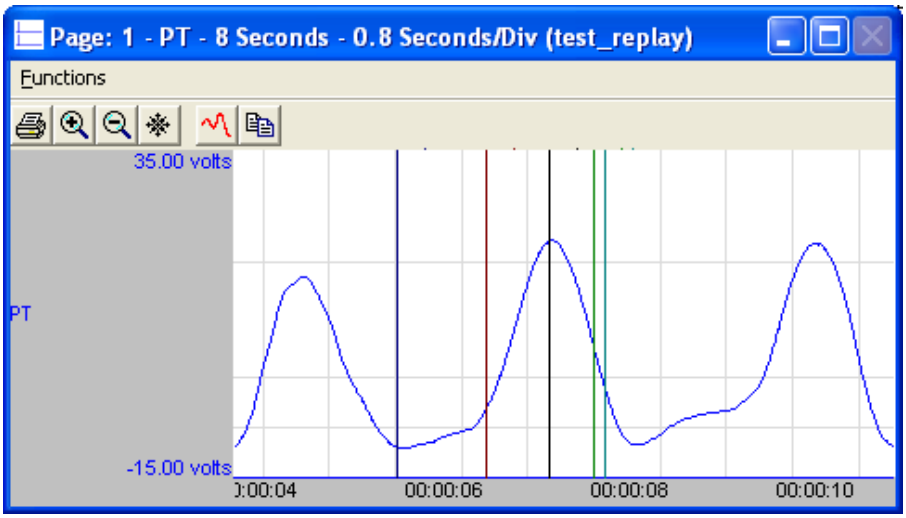
Calibration

The recommended calibration for the system for a Pulsatile Tissue and Gut Motility signal depends on the units that the signal is measured in and the required precision that the derived parameters need to be reported in. Typical calibration values are listed in the following table:

Precision	High Calibration Value	Actual mV
1/100 of a gram	1.00 grams	≈800-1200 mV
milligrams	1000 mg	≈1000-2000 mV

On-Line Screens and Functions

Below is an example of a Primary graph displaying the raw analog format of a typical pulsatile tissue signal with its differential displayed.



Pulsatile Tissue Key Marks

In the above figure, the **Pulsatile Tissue** signal is displayed with validation tick marks and their meanings. The validation marks identify the ***Maximum Contraction***, ***Minimum Contraction***, ***Recovery 1***, and ***Recovery 2*** marks.

Presentation Signals

Below is a list of presentation signals that are available for the PT Analysis Module:

Signal	Description
Input	The original input signal after applying any software filters.
Derivative	Derivative of the input signal.

Data Review

The Data Review related features of the Pulsatile Tissue Analysis Module are accessible when the analysis module is used with P3 Plus Version 4.40 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review window channel are controlled through the Marks Tab in the attribute dialog accessed via the Analyze selection in the Right click menu.

Mark Operations

Pulsatile Tissue marks are divided into two types; marks that always exist when a valid cycle is found (Minimum, Start Contraction, and Maximum) and marks that may or may not exist, depending on the signal morphology (Percent Recovery).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert PT Cycle

Inserts an entire Pulsatile Tissue cycle, Minimum, Start Contraction, Maximum, and Percent Recovery if applicable. This set of marks may be inserted between a Percent Recovery Mark and a Minimum Mark. If a Percent Recovery Mark is not present, the cycle may be inserted between a Maximum Mark and a Minimum Mark. When a Pulsatile Tissue Pressure cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Pulsatile Tissue cycle's marks cannot be deleted individually. They are linked to the Maximum Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Maximum Mark and the right mouse button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving of the Minimum, Start Contraction, and Maximum Marks follow the standard rules used in Data Review. The Percent Recovery Mark is a calculated mark; its position is dependent on the Maximum and Minimum levels and cannot be adjusted by the user. If the user changes the position of either the Maximum or Minimum Marks, the Percent Recovery Mark will be recalculated.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay for most parameters, exceptions are noted for specific derived parameters in the derived parameters section.

When a Review file is opened, the trace data may not be identical to the acquired data. The difference arises because of the scaling involved in the storage and reconstitution of the data. The difference for a point, on average, is less than 0.05%.

One of the consequences of this difference is seen with Calculated Marks. If, after opening a Review file, Review is prompted to recalculate a Calculated Mark, the mark may move with no change to the marks on which it depends. This is because the original placement of the Calculated Mark was based on the Replay data values whereas, recalculation uses the data values present in Review.

Logging Mark

The logging mark for a cycle is the Maximum Mark. The time at the logging mark is the time used to report a cycle's derived data. If a cycle's logging mark falls within a logging interval, the cycle's data will be included in the logging interval.

End of Cycle

The end of a cycle occurs one nanosecond prior to the next cycles Minimum mark. For the last cycle in a data segment, the logging time + 1 nanosecond is used.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Rate is doubled	The analysis is triggering on artifact. This can be rectified by lengthening the Peak Validation Time and Non Detection Time values. Refer to the chart of Typical Values for typical values.
Rate is halved	The analysis is pausing too long for the specified contraction. The problem can be rectified by shortening the Peak Validation Time and Non Detection Time values. Refer to the chart of Typical Values for typical values.
All derived parameters are reporting zero	The Minimum Pulse Height may be set too high for the specified signal. Lower the Minimum Pulse Height.
Rate is out of range (very high)	The analysis may be triggering on noise. The two solutions are: Increase the Minimum Pulse Height to a value of 10% of pulse pressure. Increase the Low Pass Filter (in Adv Attrib1 tab) to remove noise on the signal. Select a lower value in the list box.

Problem	Solution
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Pulsatile Tissue]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Pulse Height(low)	This sets the minimum allowable value for Minimum Pulse Height. The default value is .1.
Minimum Pulse Height(high)	This sets the maximum allowable value for Minimum Pulse Height. The default value is 100.
Peak Validation Time(low)	This sets the minimum allowable value for Peak Validation Time in milliseconds. The default value is 0.
Peak Validation Time(high)	This sets the maximum allowable value for Peak Validation Time in milliseconds. The default value is 2000.
Non Detection Time(low)	This sets the minimum allowable value for Non Detection Time in milliseconds. The default value is 0.
Non Detection Time(high)	This sets the maximum allowable value for Non Detection Time in milliseconds. The default value is 200.
% Recovery 1(low)	This sets the minimum allowable value for % Recovery 1 in percent. The default value is 1.
% Recovery 1(high)	This sets the maximum allowable value for % Recovery 1 in percent. The default value is 99.

Entry Name	Description
% Recovery 2(low)	This sets the minimum allowable value for % Recovery 2 in percent. The default value is 1.
% Recovery 2(high)	This sets the maximum allowable value for % Recovery 2 in percent. The default value is 99.

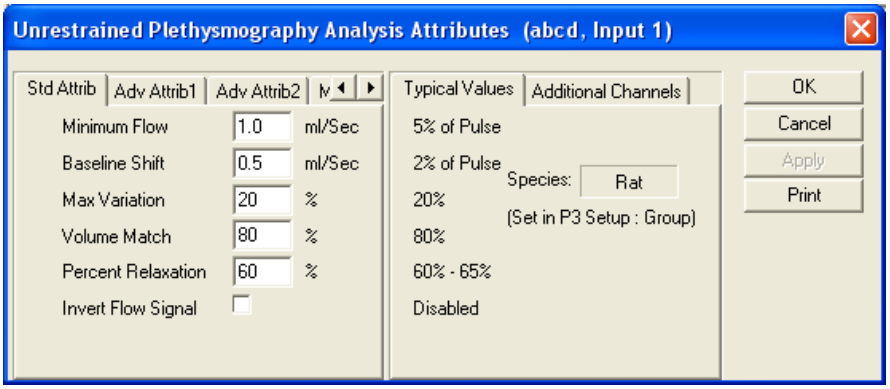
Unrestrained Plethysmography (URP)

The Unrestrained Plethysmography Analysis Module analyzes unrestrained plethysmography signals. The analysis calculates the common parameters that are associated with unrestrained plethysmography.

Attribute Window

The Unrestrained Plethysmography dialog allows you to modify the signal analysis for different types of respiratory signals and different signal conditions.

Standard Attributes



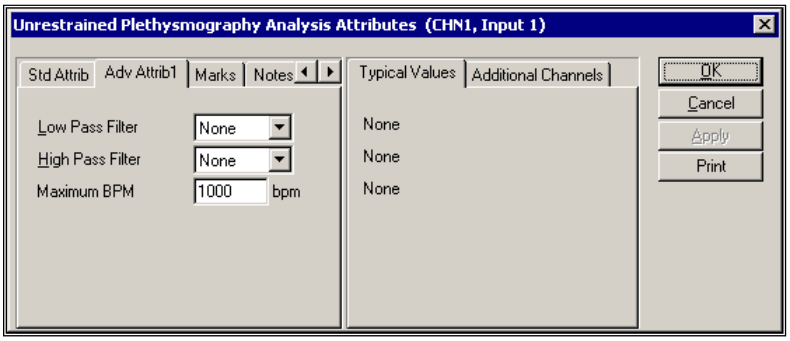
Unrestrained Plethysmography Standard Attributes Tab

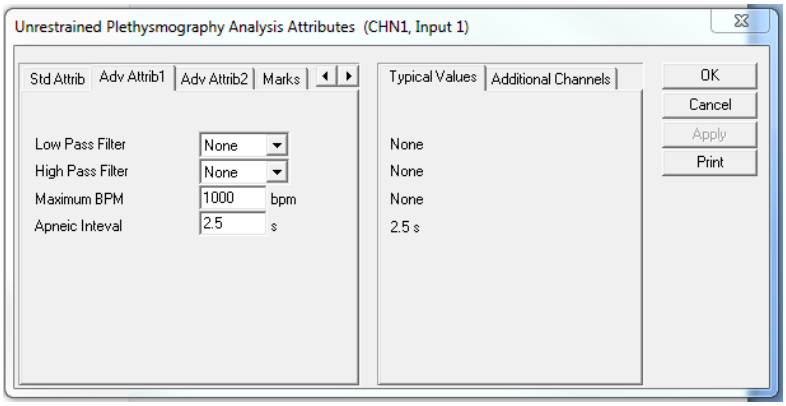
The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Minimum Flow	Signal Interpretation	Sets the minimum flow that the signal must achieve before the analysis will detect and validate a cycle. The Minimum Flow prevents the analysis from triggering on artifacts.
Baseline Shift	Signal Interpretation	Sets how sensitive the algorithm is to changes in the baseline from one cycle to the next.
Max Variation	Signal Interpretation	Sets the level that is used to eliminate breaths that exhibit fluctuations during inspiration or expiration. This attribute is specified in terms of a percentage of the peak inspiration and peak expiration.

Attribute	Effect On Review	Description
Volume Match	Signal Interpretation	Sets the percentage difference in volume that is permitted between inspiration and expiration.
Percent Relaxation	Calculation, Redraw	Sets the point in time used to obtain timing information for Pause and PEnh.
Invert Flow Signal	Signal Conditioning, Calculation, Redraw	Inverts the URP signal.

Advanced Attributes 1





Unrestrained Plethysmography Advanced Attributes 1 Tab

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.

Attribute	Effect On Review	Description
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Maximum BPM	Signal Interpretation	Sets the approximate upper limit that the respiratory cycle can reach.
Apneic Interval	Signal Interpretation	The Apneic Interval attribute is used to specify the inter breath duration that signifies an apneic event.

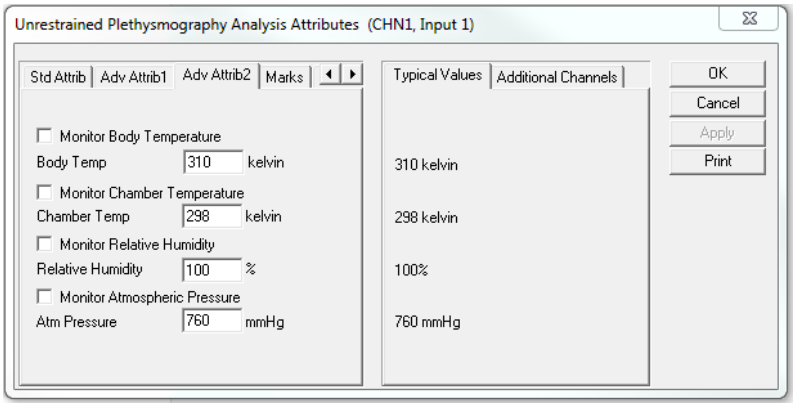
Advanced Attributes 2

The Advanced Attributes 2 tab contains attributes that are used to calculate a corrected Tidal Volume and Minute Volume based on the formula by Fenn and Drorbaugh. The adjustment factor is calculated as

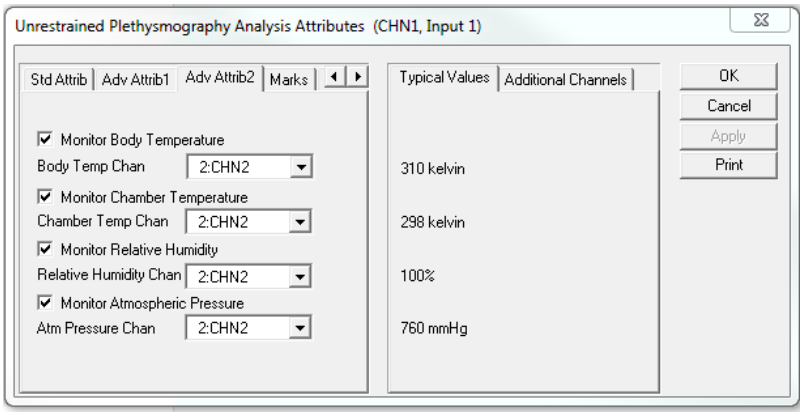
$$Adj = \frac{T_A(P_B - P_C)}{T_A(P_B - P_C) - T_C(P_B - P_A)}$$

T_A the animal temperature in Kelvin
P_A the saturation vapor pressure of water at T_A in mmHg
T_C the chamber temperature in Kelvin
P_C the vapor pressure of water at T_C taking the relative humidity into account in mmHg
P_B the atmospheric pressure in mmHg

During replay and Acquisition, if continuous monitoring of chamber temperature, relative humidity or atmospheric pressure is used, the point at which the monitoring channels are sampled is approximately 1¼ cycles beyond the end of the cycle being reported on. In Review, the monitoring channels are sampled at the start Inspiration point of the cycle being reported on.



Unrestrained Plethysmography Advanced Attributes 2 Tab – edit fields



Unrestrained Plethysmography Advanced Attributes 2 Tab –Monitoring channels

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

NOTE when reanalyzing URP data in Review, cycles that precede bad cycle marks will show an inserted Percent Relaxation mark, this mark is not saved when saving a marks section and is not used to calculated derived output.

Attribute	Effect On Review	Description
Monitor Body Temperature	Calculation	The Monitor Body Temperature checkbox controls the visibility of the Body Temp/Body Temp Chan attribute. This checkbox should be selected if the user plans to acquire the subject's body temperature during an acquisition session
Body Temp	Signal Conditioning, Calculation, Redraw	The Body Temp edit box is available when the Monitor Body Temp checkbox is unchecked and provides a means of entering the subject's body temperature in kelvin (K). This edit field is used to enter the animal's body temperature in Kelvin The Body Temperature Chan dropdown list box is available when the Monitor Body Temp checkbox is checked and provides a means of selecting the channel used to monitor subjects Body Temp. The dropdown list box is populated with RAW and TEMP channels. The channel used to monitor Body Temp should be calibrated to provide the temperature in kelvin.
Monitor Chamber Temperature	Calculation	This checkbox controls the source for Chamber Temperature values. When the checkbox is unselected, the value from the Chamber Temperature edit field is used. If the checkbox is selected, the values from the Chamber Temperature channel are used. This checkbox is disabled if no suitable Chamber Temperature channels exist
Chamber Temperature	Calculation	This edit field is used to enter the chamber temperature in kelvin. This field is not used and not visible if the Monitor Chamber Temperature check box is selected.

Attribute	Effect On Review	Description
Chamber Temperature Channel	Calculation	This dropdown list box is displayed only when the Monitor Chamber Temperature checkbox is selected. The dropdown list box is populated with RAW channels. The selected channel should represent the chamber temperature in kelvin.
Monitor Relative Humidity	Calculation	This checkbox controls the source for Relative Humidity values. When the checkbox is unselected, the value from the Relative Humidity edit field is used. If the checkbox is selected, the values from the Relative Humidity channel are used. This checkbox is disabled if no suitable Relative Humidity channels exist.
Relative Humidity	Calculation	This edit field is used to enter the chamber relative humidity. This field is not used and not visible if the Monitor Relative Humidity check box is selected.
Relative Humidity Channel	Calculation	This dropdown list box is displayed only when the Monitor Relative Humidity checkbox is selected. The dropdown list box is populated with RAW channels. The selected channel should represent the chamber relative humidity.
Monitor Atmospheric Pressure	Calculation	This checkbox controls the source for Atmospheric Pressure values. When the checkbox is unselected, the value from the Atmospheric Pressure edit field is used. If the checkbox is selected, the values from the Atmospheric Pressure channel are used. This checkbox is disabled if no suitable Atmospheric Pressure channels exist.
Atm Pressure	Calculation	This edit field is used to enter the atmospheric pressure in mmHg. This field is not used and not visible if the Monitor Atmospheric Pressure check box is selected.
Atm Pressure Channel	Calculation	This dropdown list box is displayed only when the Monitor Atmospheric Pressure checkbox is selected. The dropdown list box is populated with RAW channels. The selected channel should represent the atmospheric pressure in mmHg.

Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Minimum Flow	5% of Pulse	mL/Sec
Baseline Shift	2% of Pulse	mL/Sec
Max Variation	20	%
Volume Match	80	%
Percent Relaxation	60-65	%
Invert Flow Signal	Disabled	NA

Marks (Validation)

The **Unrestrained Plethysmography** analysis displays validation tick marks for each cycle. Each cycle should have only one set of validation marks. These marks verify that the system is analyzing the unrestrained plethysmography signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Start Inspiration Mark
Blue	Start Expiration Mark
Green	Percent Relaxation Mark

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

The URP signal has a shifting baseline. The signals baseline is established by connecting successive start inspiration/start expiration marks.

Derived parameters are not reported for bad cycles and bad cycles are not averaged into logged lines that span multiple cycles

Name	Averaging In Review	Definition
Num	Recent	The number of the cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
PIF	Mean	The Peak Inspiratory Flow is the highest value measured from the baseline. The baseline is formed by connecting the start inspiration mark and the start expiration mark
PEF	Mean	The Peak Expiratory Flow is the lowest value measured from the baseline. The baseline is formed by connecting the start expiration mark and the next cycles start inspiration mark This derived parameter is not available if a following cycle is not present
TV	Mean	Tidal Volume is the integral of the difference between the inspiration signal and the baseline expressed in flow units-seconds. The baseline is formed by connecting the start inspiration mark and the start expiration mark.

Name	Averaging In Review	Definition
MV	Mean	Minute Volume is the product of TV and BPM. When running in a multiple epoch logging rate or second logging rate, the averaged value will be calculated off of the averaged TV and averaged BPM values. In Review the MV values generated in epoch mode are averaged as opposed to multiplying the averaged TV and BPM values. This derived parameter is not available if a following cycle is not present.
BPM	Harmonic Mean	Breaths Per Minute is the reciprocal of the period, in seconds, associated with a breath, multiplied by 60. This derived parameter is not available if a following cycle is not present. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
IT	Mean	Inspiration Time is the time, in milliseconds, from the start of inspiration to the end of inspiration. The start of inspiration is marked at the point where the respiration signal crosses the baseline with a positive slope. The end of inspiration signal is marked at the point where the respiration signal crosses the baseline with a negative slope.
ET	Mean	Expiration Time is the time, in milliseconds, from the end of inspiration to the end of expiration. This derived parameter is not available if a following cycle is not present.
TT	Mean	Total Time is the sum of inspiration and expiration times: IT + ET. This derived parameter is not available if a following cycle is not present.
AT	Mean	Apnea Time in not currently used.
Pause	Mean	Pause provides a timing comparison of early and late expiration. It is calculated as the following: (time interval between the Percent Relaxation Mark and the end of expiration) / (time interval between the start of expiration and the Percent Relaxation Mark) This derived parameter is not available if a following cycle is not present.
PEnh	Mean	Enhanced Pause is the product of the ration of PEF to PIF and Pause. It is calculated as the following: Pause * PEF/PIF This derived parameter is not available if a following cycle is not present.
TVadj	Mean	The adjusted Tidal Volume is calculated by multiplying the reported TV by an adjustment factor as specified in Adv Attrib2.

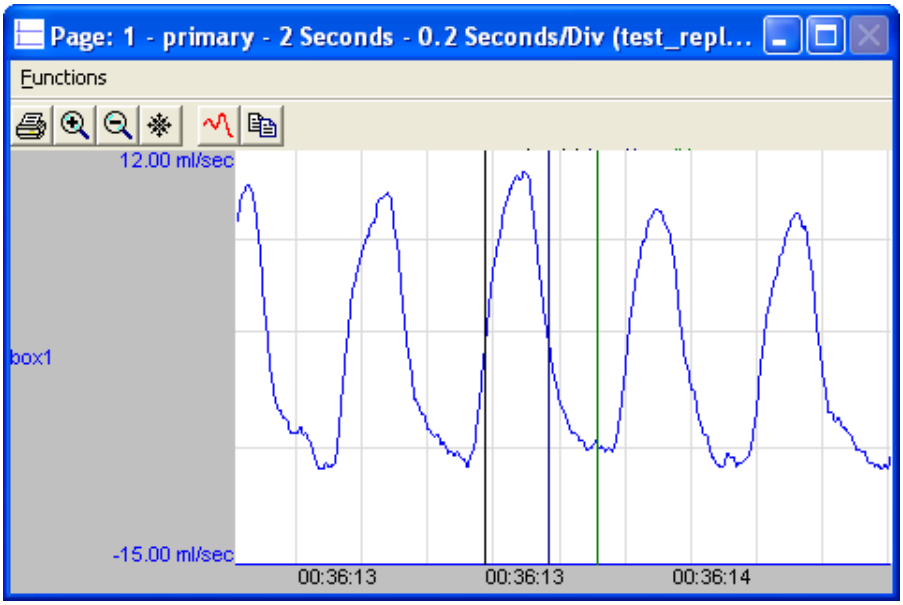
Name	Averaging In Review	Definition
MVadj	Mean	The Minute Volume adj is the product of TVadj and BPM During Replay and Acquisition, when running in a multiple epoch logging rate or second logging rate, the averaged value will be calculated off of the averaged TVadj and averaged BPM values. In Review the MVadj values generated in epoch mode are averaged as opposed to multiplying the averaged TVadj and BPM values.
IF50	Mean	The inspiratory flow value at 50% tidal volume.
EF50	Mean	The expiratory flow value at 50% tidal volume
E/IF50	Mean	The ratio of EF50 and IF50
ApCt	Count	The Apnea Count indicates whether a cycle duration exceeds the Apneic Interval Attribute. When multiple cycles are averaged, the Apnea Count reported is the sum of the Apnea Count values from individual cycles.

Calibration

The recommended calibration for the system for an Unrestrained Plethysmography signal depends on the type of instrumentation and the species that the signal is coming from.

On-Line Screens and Functions

Below is a Primary graph displaying the raw analog format of a typical unrestrained plethysmography signal with its digitally generated differential. The validation tick marks also are displayed on the waveform.



Unrestrained Plethysmography Key Marks

In the above figure, the **Unrestrained Plethysmography** is displayed with the validation tick marks. These marks identify the ***Start Inspiration Mark***, ***Start Expiration Mark***, and ***Percent Relaxation Mark***.

Presentation Signals

Below is a list of presentation signals that are available for the URP Analysis Module:

Signal	Description
Flow	This will display the original flow signal after applying any software filters.
Volume	This will display the tidal volume of the previous cycle.

Data Review

The Data Review related features of the URP Analysis Module are accessible when the analysis module is used with P3 Plus Version 4.20 or greater and if the license file supports Data Review. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review window channel are controlled through the Marks Tab in the attribute dialog accessed via the Analyze selection in the Right click menu.

Mark Operations

URP marks are divided into two types, marks that always exist when a valid cycle is found (Start Inspiration, Start Expiration) and marks that may or may not exist, depending on the signal morphology (Percent Relaxation).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert URP Cycle

Inserts an entire URP cycle, Start Inspiration, Start Expiration and Percent Relaxation if applicable. This set of marks may be inserted prior to a Start Inspiration Mark. When a URP cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Insert Bad Cycle

Inserts a single Start Inspiration Mark, signifying a bad URP cycle. This mark may be inserted prior to a Start Inspiration Mark. When a URP cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A URP cycle's marks cannot be deleted individually. They are linked to the Start Inspiration Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Start Inspiration Mark and the right mouse button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving of the Start Inspiration and Start Expiration marks follow the standard rules used in Data Review. The Percent Relaxation mark is a calculated mark; their positions are dependent on the expiration volume and cannot be adjusted by the user. If the user changes the position of the Start Expiration Mark or the next cycle's Start Inspiration Mark, the Percent Relaxation mark will be recalculated.

Calculations

The calculations of epoch derived parameters are identical to those performed during acquisition and replay. When averaging multiple cycles, the averaging method for MV and MVadj are different between Review and Replay, as listed in the derived parameter section.

Logging Mark

The logging mark for a URP cycle is the Start Inspiration Mark. The time at the logging mark is the time used to report a cycle's derived data. If a URP cycle's logging mark falls within a logging interval, the URP cycle's data will be included in the logging interval.

End of Cycle

The start of a URP cycle is at the Start Inspiration Mark. The end of a URP cycle occurs one nano second prior to the next cycles Start Inspiration Mark. For the last cycle, the cycle end is one nanosecond after the start.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Analysis is not triggering	Minimum Flow setting is set too high or the rejection criteria (Baseline Shift, Max Variation, and Volume Match) are too restrictive.
Analysis is triggering too often	Minimum Flow is set too low or the rejection criteria (Baseline Shift, Max Variation, and Volume Match) are not restrictive enough.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Unrestrained Plethysmography]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Flow(low)	This sets the minimum allowable value for Minimum Flow in mL/Sec. The default value is .1.
Minimum Flow(high)	This sets the maximum allowable value for Minimum Flow in mL/Sec. The default value is 100.
Baseline Shift(low)	This sets the minimum allowable value for Baseline Shift in mL/Sec. The default value is .1.
Baseline Shift(high)	This sets the maximum allowable value for Baseline Shift in mL/Sec. The default value is 100.
Percent Relaxation(low)	This sets the minimum allowable value for Percent Relaxation. The default value is 0.
Percent Relaxation(high)	This sets the maximum allowable value for Percent Relaxation. The default value is 99.
Volume Match(low)	This sets the minimum allowable value for Volume Match. The default value is 50.
Volume Match(high)	This sets the maximum allowable value for Volume Match. The default value is 99.
Maximum Variation(low)	This sets the minimum allowable value for Max Variation. The default value is 0.
Maximum Variation(high)	This sets the maximum allowable value for Max Variation. The default value is 99.
Maximum breaths per minute(low)	This sets the minimum allowable value for Maximum BPM. The default value is 0.
Maximum breaths per minute(high)	This sets the maximum allowable value for Maximum BPM. The default value is 1000.

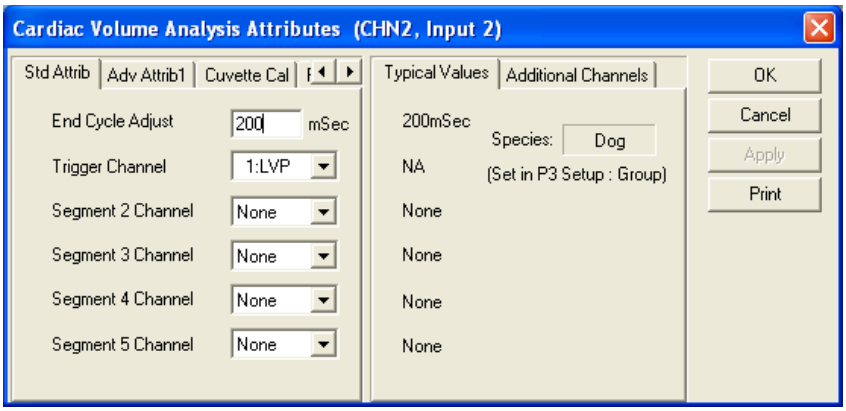
Cardiac Volume (CVO)

The Cardiac Volume analysis can analyze any volume from the circulatory system and can derive, on a beat-to-beat basis, values for the cardiac cycle.

Attribute Window

The Cardiac Volume attributes window allows you to modify the signal analysis for different types of cardiac volume signals and signal conditions. If an analysis change in the **Attributes** dialog is performed mid-cycle, then the attribute change will not take effect until the following cycle. If only examining one cycle, and a change in the **Attributes** dialog is made, then the user must stop replay and restart replay in order to see the attribute change take effect on the analysis of the cycle.

Standard Attributes

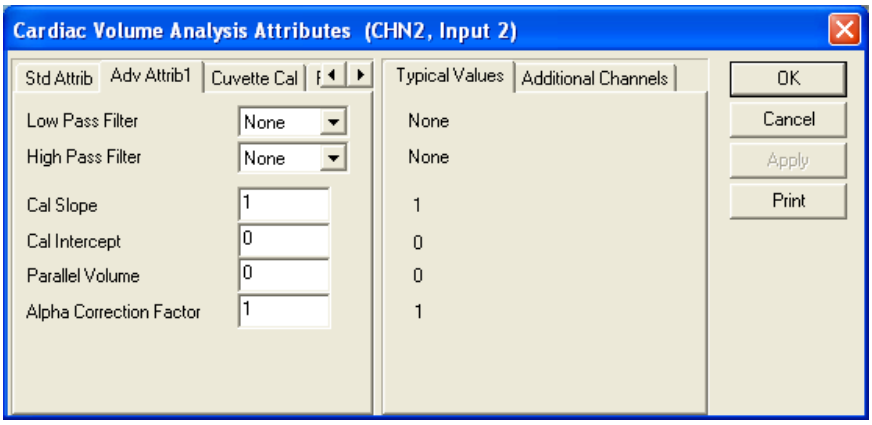


Cardiac Volume Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
End Cycle Adjust	Signal Interpretation	This edit field specifies the number of milliseconds after the minimum dPdt point in the corresponding LVP signal after which the Cardiac Volume cycle ends. The default value is 200milliseconds.
Trigger Channel	Calculation	This drop down list box lists LVP channels that are available as trigger channels for the Cardiac Volume channel. Only LVP channels that are sampled at the same sample rate and are present in the same group as the Cardiac Volume channel are available. A valid trigger channel must be specified in order for the Cardiac Volume analysis to function.
Segment 2 Channel	Calculation	This drop down list box lists segment channels that are available for a multi-segment catheter. Segment 2 typically represents the second pair of conductance rings on a multi-segment catheter to measure volume.
Segment 3 Channel	Calculation	This drop down list box lists segment channels that are available for a multi-segment catheter. Segment 3 typically represents the third pair of conductance rings on a multi-segment catheter to measure volume.
Segment 4 Channel	Calculation	This drop down list box lists segment channels that are available for a multi-segment catheter. Segment 4 typically represents the fourth pair of conductance rings on a multi-segment catheter to measure volume.
Segment 5 Channel	Calculation	This drop down list box lists segment channels that are available for a multi-segment catheter. Segment 5 typically represents the fifth pair of conductance rings on a multi-segment catheter to measure volume.

Advanced Attributes



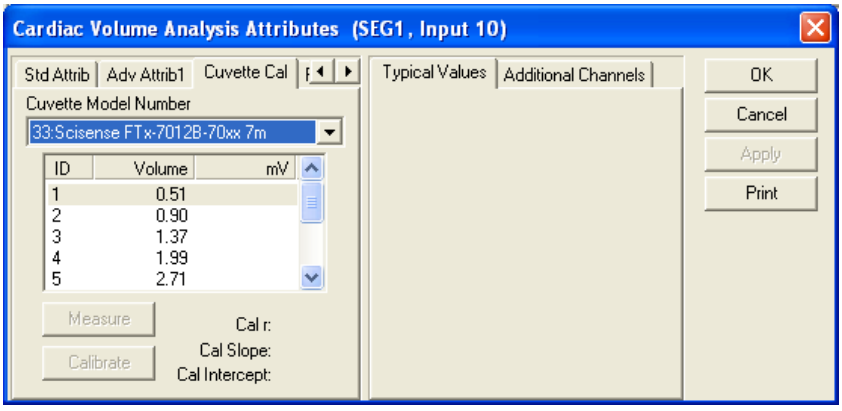
Cardiac Volume Advanced Attribute Tab

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Cal Slope	Signal Conditioning, Calculation, Redraw	The change in segment volume per change in input volume. I.e. the slope of a line that defines the relationship between segment volume and the volume signal acquired by P3 Plus. Along with Cal Intercept the Cal Slope defines the conversion that is applied to input volume data to convert it to segment volume units. Values may be typed in to define the conversion or a Cuvette call may be performed to calculate the conversion factors. The default value is 1. Segment Vol = Cal Slope * Input Volume + Cal Intercept True Vol = (Σ(All Segment Vols) – Parallel Volume) / Alpha

Attribute	Effect On Review	Description
Cal Intercept	Signal Conditioning, Calculation, Redraw	The segment volume represented by an input volume of 0. I.e. the y axis intercept of a line that defines the relationship between segment volume and the volume signal acquired by P3 Plus. Along with Cal Slope the Cal Intercept defines the conversion that is applied to input volume data to convert it to segment volume units. Values may be typed in to define the conversion or a Cuvette Cal may be performed to calculate the conversion factors. The default value is 0. Segment Vol = Cal Slope * Input Volume + Cal Intercept True Vol = (Σ(All Segment Vols) – Parallel Volume) / Alpha
Parallel Volume	Signal Conditioning, Calculation, Redraw	This edit field lists the volume component due to parallel conductance, in true volume * Alpha units. The parallel volume is subtracted from the summed segment volume signal. A value may be typed in or calculated using the Parallel Vol tab. The default value is 0. Segment Vol = Cal Slope * Input Volume + Cal Intercept True Vol = (Σ(All Segment Vols) – Parallel Volume) / Alpha
Alpha Correction Factor	Signal Conditioning, Calculation, Redraw	This edit field lists the correction factor that is used to reconcile the Volume obtained through a conductance measurement with the volume obtained by other means. Traditional conductance catheters do not span the entire ventricle, nor do they create a non-uniform electrical field inside the ventricle. If the alpha factor is not applied, the calculated volumes will be underestimated. The Stroke Volume result obtained from the conductance measurement is divided by Alpha. The default value is 0. Segment Vol = Cal Slope * Input Volume + Cal Intercept True Vol = (Σ(All Segment Vols) – Parallel Volume) / Alpha

Cuvette Calibration Tab



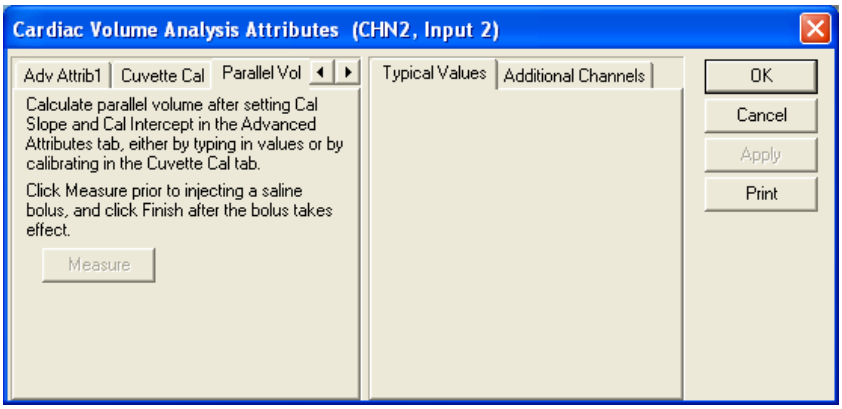
This tab is used to calibrate the volume signal using a Cuvette. The tab displays a list of Cuvettes that are listed in the PPP3.INI file, under [Cuvettes]. 100 cuvettes with 20 measurements per Cuvette are supported. Cuvette information is entered as Cuvette Name=ID1, Vol1, ID2, Vol2 …

This tab is supported in acquisition and replay. To record a measurement, highlight a cuvette volume, dip the catheter into the cuvette and press the **Measure** button. The current input mV value (unscaled) will be recorded, and the next cuvette volume will be highlighted. Once measurements have been taken, selecting the **Calibrate** button will perform a curvilinear fit to the data, report the **Cal Slope**, **Cal Intercept**, and goodness of fit values (r) on the tab, and enter the **Cal Slope** and **Cal Intercept** on the **Adv Attrib1** tab.

A minimum of 2 points must be measured in order to perform a cuvette calibration.

NOTE: If Cal Slope, Cal Intercept, or parallel volume are not 1, 0, and 0, the recorded value may not be the same as the current presentation signal.

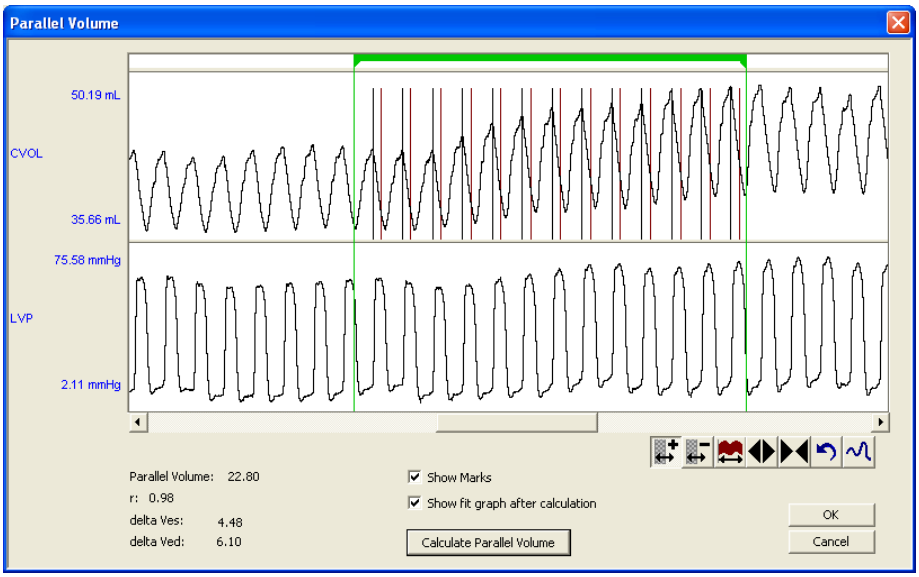
Parallel Volume Tab



The **Parallel Volume** tab is used calculate the component of the volume signal that is due to the parallel conductance of the heart wall and adjoining tissues. This operation must be performed after the **Cal Slope** and **Cal Intercept** have been initialized in the Advanced Attributes tab. This can be done either by typing in values or by calibrating in the Cuvette Cal tab. The procedure is to inject a saline bolus that will cause a change in resistivity of the blood but not alter the pressure/volume characteristics. The accompanying perceived change in volume is used to calculate the **Parallel Volume**.

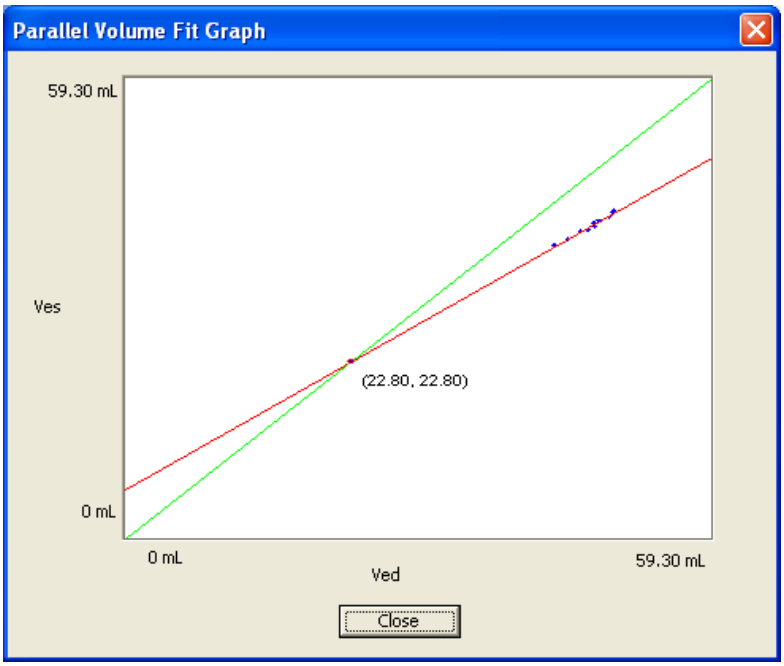
Set up the cardiac volume (CVOL) attributes to ensure cycle detection. Select the **Parallel Vol** tab and click on the **Measure** button prior to injecting a saline bolus. Click on the **Finish** button after the bolus has taken full effect. Once the **Finish** button is selected, a **Parallel Volume** dialog box will pop up.

NOTE: If the Finish button is not pressed within 2 minutes of clicking Measure to initiate the bolus injection, the Parallel Volume dialog box will automatically pop up,



The parallel volume is calculated by using the Ves and Ved data from the rising portion of the bolus effect. This is obtained by sizing and adjusting the green parser bar to identify the area of interest. Up to 10 parser segments can be added to identify the bolus injection period. The use of multiple parser bars helps eliminate a bad cardiac cycle so it is not included in the analysis calculation The area of interest searches the bolus period for a max Ved and uses it and cycles that precede it until the Ved values drop below a threshold based on the Delta Ved value. Once the area of interest has been defined, click on the **Calculate Parallel Volume** button. If two or more beats are available, a straight line fit is calculated and if a valid slope is obtained, values are displayed. If no beats are available, **Invalid** is displayed. The Ves values are plotted against Ved and a straight line fit is performed. The intersection of the fit with the line representing Ves=Ved represents the parallel volume. This can be presented graphically by placing a check mark in the **Show fit graph after calculation** box.

Term	Note
Parallel Volume	in true volume units
r	goodness of fit
delta Ves	change in Ves as a result of the bolus
delta Ved	change in Ved as a result of the bolus



Typical Values

The table contains typical values. Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
End Cycle Adjust	200	milliseconds
Trigger Channel	NA	NA
Segment 2 Channel	NA	NA
Segment 3 Channel	NA	NA
Segment 4 Channel	NA	NA
Segment 5 Channel	NA	NA

Marks (Validation)

The **Cardiac Volume** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	LVEDP Mark
Blue	LVP Min Slope Mark
Green	Minimum Volume Mark
Cyan	Maximum Volume Mark
Red	End Systole Mark
Magenta	End Cycle Mark

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

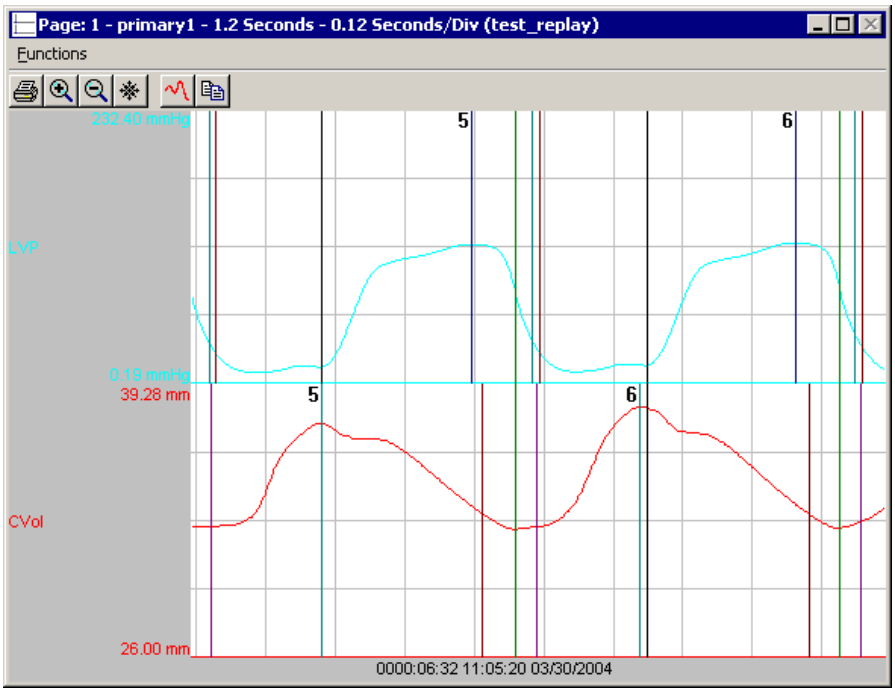
Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Vmin	Mean	The minimum volume value in a cycle.
Vmax	Mean	The maximum volume value in a cycle.
SV	Mean	The stroke volume, which equals Vmax - Vmin.
-dPV	Mean	The volume at the LVP Min Slope mark.
Ped	Mean	The pressure at the LVEDP mark.
Ved	Mean	The volume at the LVEDP mark.
%EF	Mean	Ejection fraction, calculated as Stroke Volume/Vmax * 100.
PFR	Mean	Peak filling rate. The maximum rate of increase of the volume signal between the end of the previous cycle and the Vmax point.
-dV	Mean	Peak emptying rate. The maximum rate of decrease of the volume signal, between Vmax and the end of the cycle.
TPFR	Mean	Time to peak filling rate. The time in milliseconds between the previous cycles LVP Min Slope and the current cycles PFR point.
DFT	Mean	Diastolic Filling Time. The time in milliseconds between the previous cycles LVP Min Slope and the current cycles LVEDP point.
%FT	Mean	Time to peak filling as a percentage of Diastolic fill time, equals TPFR/DFT * 100.
Pes	Mean	Pressure at max elastance. The LVP value at the point in the cycle where the ratio of Pressure to volume reaches a maximum. This point is expected to lie between the LVEDP mark and the Min Volume mark.
Ves	Mean	Volume at max elastance. The volume value at the point in the cycle where the ratio of Pressure to volume reaches a maximum. This point is expected to lie between the LVEDP mark and the Min Volume mark.
SW	Mean	Stroke Work. This is the area of the pressure volume loop; the loop is closed by connecting the current cycles end cycle point with the previous cycle's end cycle point.
Ea	Mean	Arterial elastance. Calculated as Pes/SV.
HR	Harmonic Mean	Heart rate. Computed in beats-per-minute. It is calculated by taking the reciprocal of the time interval for the cardiac cycle multiplied by 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
CO	Analysis Define	Cardiac output. The volume of blood being pumped out of the heart in a minute. This is calculated by multiplying stroke volume (SV) by the heart rate (HR).

Calibration

The recommended calibration for the system for Cardiac Volume signals depends on the type of instrumentation, and the species that the signal is coming from.

On-Line Screens and Functions

The following is an example of a Primary graph displaying the raw analog format of a cardiac volume signal along with its differential.



Cardiac Volume With LVP Signal

Presentation Signals

Below is a list of presentation signals that are available for the CVOL Analysis Module:

Signal	Description
Volume	This will display the original volume signal after applying any software filters.
Derivative	This will display the derivative of the input signal.
Segment Volume (SegVol)	This will display the individual segment volume after applying any software filters.

Data Review

The Data Review related features of the Cardiac Volume Analysis Module are accessible when the analysis module is used with P3 Plus Version 4.20 or greater and if the customer's current license file supports Data Review. The analysis specific portion of Data Review centers on the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review window channel are controlled through the Marks Tab in the attribute dialog accessed via the Analyze selection in the Right click menu.

Mark Operations

All Cardiac Volume marks exist in each cardiac volume cycle.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert CVOL Cycle

Inserts an entire Cardiac Volume cycle. This set of marks may be inserted between an End Cycle Mark and the first mark of the following cycle. When a Cardiac Volume cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A Cardiac Volume cycle's marks cannot be deleted individually. They are linked to the Maximum Volume Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Maximum Volume Mark and the right mouse button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving of the Cardiac Volumes marks follow the standard rules used in Data Review.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

Logging Mark

The logging mark for a Cardiac Volume cycle is the Maximum Volume Mark. The time at the logging mark is the time used to report a cycle's derived data. If a Cardiac Volume cycle's logging mark falls within a logging interval, the Cardiac Volume cycle's data will be included in the logging interval.

End of Cycle

The end of a Cardiac Volume cycle occurs at and includes the end cycle mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
All Derived Parameters are reporting zero	The associated LVP signal is not triggering. View the troubleshooting guide in the LVP section of this manual.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.
Analysis does not trigger (No marks)	The associated LVP signal is not triggering. View the troubleshooting guide in the LVP section of this manual.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Cardiac Volume]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
End Cycle Adjust(low)	This sets the minimum allowable value for End Cycle Adjust. The default value is 10.
End Cycle Adjust(high)	This sets the maximum allowable value for End Cycle Adjust. The default value is 1000.

Cystometry (CYS)

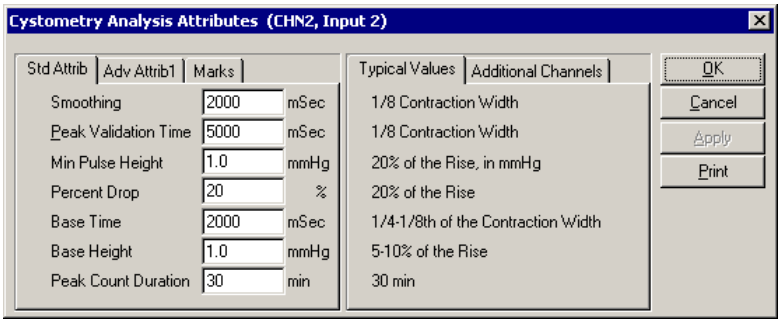
Cystometry Analysis has been designed to record and analyze pressures resulting from phasic, non-voiding bladder contraction cycles, or longer time-scale pressure changes resulting from bladder filling / voiding cycles. The analysis was developed primarily to assist researchers studying Overactive Bladder (OAB) and related incontinence investigations.

In a typical application, blood pressure will be recorded in addition to bladder pressure to allow correlation between these signals. In some applications an additional pressure channel may be defined as an abdominal pressure. The analysis can then be configured to automatically subtract this pressure value from the recorded bladder pressure. This isolates the effect of abdominal muscular activity from the resultant intravesical pressure data. Biopotential data, (EMG) obtained from the bladder wall, may also be recorded to assist in isolation of true bladder contraction, as opposed to abdominal contraction.

Attribute Window

The Cystometry Analysis Attributes window allows the user to modify the signal analysis for different types of bladder pressure signals and signal conditions. If an analysis change in the Attributes Dialog is performed mid-cycle, then the attribute change will not take effect until the following cycle. If only examining one cycle, and a change in the Attributes Dialog is made, then the user must stop replay and restart replay in order to see the attribute change take effect on the analysis of the cycle.

Standard Attributes



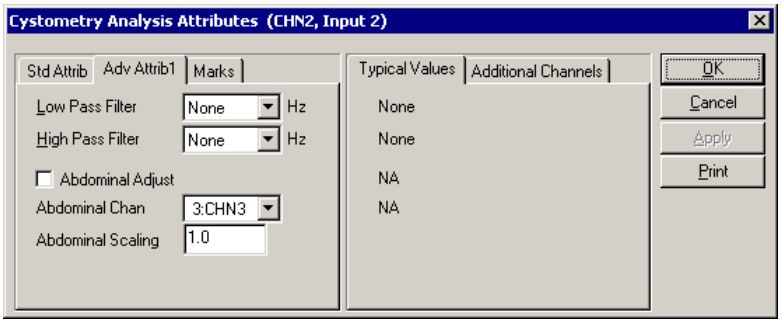
Cystometry Setup Standard Attributes Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Smoothing	Signal Conditioning, Calculation, Redraw	The number associated with this attribute represents the period over which the waveform is smoothed. The larger this value, the greater the reduction in signal variation. This removes unwanted noise from the pressure signal.
Peak Validation Time	Signal Interpretation	This attribute is used to ensure that a peak is found. This attribute is useful when dealing with a wide or doubled peak instead of a clean peak. In such cases the Peak Validation Time should extend such that it ends on the down slope of the peak. Usually 1/8th of the peak width is appropriate. This parameter is used in conjunction with Percent Drop to establish the end of a cycle.
Min Pulse Height	Signal Interpretation	This sets the minimum level that a peak must rise before it is considered to be a peak.

Attribute	Effect On Review	Description
Percent Drop	Signal Interpretation	This attribute is used to prevent false triggering on signal disturbance in the upper region of a peak. The analysis will not accept a peak until the signal has dropped by the Percent Drop value. If this parameter is set to 20%, the analysis, after passing the peak value, will wait until the signal has dropped by 20% of the rise before continuing with the analysis.
Base Time	Signal Interpretation	The Base Time attribute along with the Base Height attribute are used to determine the location of the baseline. The size of the light red and orange boxes are determined by these attribute values. The orange boxes are positioned as close to the peak as possible keeping the signal rise less than Base Height over the time period defined by Base Time. The location of the orange boxes provides the algorithm with an approximate location of the start and end of the peak. The analysis looks for a true start and end, which are marked. The settings of these two attributes depend on the nature of the baseline between the peaks. If the signal has a relatively flat baseline, a long and low light red box will work well, which is the preferred case. Greater variation in the baseline will necessitate shortening the light red box and increasing its height, this will result in the orange boxes being placed higher up on the pressure pulse.
Base Height	Signal Interpretation	See the above Base Time description.
Peak Count Duration	Calculation	This defines the time period over which peaks are counted - if this were set to 30 min the analysis will report the number of peaks encountered over the last 30 minutes. Until the Peak Count Duration minutes of data has passed, the PkCntT derived parameter indicates the number of minutes over which the peaks are summed and reported in the PkCnt derived parameter.

Advanced Attributes



Cystometry Advanced Attributes Tab

The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz. Use of the High Pass Filter is NOT RECOMMENDED for this analysis type, and should remain set to NONE. Filters do not affect the RAW data file being saved. The RAW waveform data is always saved un-filtered.
Abdominal Adjust	Signal Conditioning, Calculation, Redraw	The Abdominal Adjust attribute along with the Abdominal Chan and Abdominal Scaling attributes are used to reduce the effects of abdominal contractions from the CYS signal. The abdominal pressure channel must be configured as a RAW channel. The Abdominal Adjust check box, the Abdominal Chan list box, and Abdominal Scaling edit box will be enabled if a RAW channel exists. If this check box is selected, the signal on the channel listed in the Abdominal Chan attribute will be multiplied by the Abdominal Scaling value and then subtracted from the CYS channel prior to analyzing the signal. The Abdominal Channel must be calibrated in the same units as the CYS channel. The value to be used in the Abdominal Scaling edit box is determined by comparing a pressure change in the abdominal signal with the resultant change in the un-subtracted, unfiltered bladder pressure signal. The ratio of the change in the bladder signal to the change abdominal signal should be used as the Abdominal Scaling value. This value should be checked over a number of abdominal pressure changes.
Abdominal Chan	Signal Conditioning, Calculation, Redraw	See the above Abdominal Adjust description.
Abdominal Scaling	Signal Conditioning, Calculation, Redraw	See the above Abdominal Adjust description.

Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Smoothing	1/8 Contraction Width	mSec
Peak Validation Time	1/8 Contraction Width	mSec
Min Pulse Height	20% of the Rise	mmHg
Percent Drop	20% of the Rise	%

Attribute	Setting	Units
Base Time	1/4-1/8th of the Contraction Width	mSec
Base Height	5-10% of the Rise	mmHg
Peak Count Duration	30	min

Marks (Validation)

The **Cystometry** analysis displays validation tick marks for each cardiac cycle. Each cardiac cycle should have only one set of validation marks. These marks verify that the system is analyzing the cystometry signal correctly. If there is more than one set of validation marks per cardiac cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Start Contraction Point
Blue	Peak Point
Green	End Contraction Point

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is a selection in the **Input Setup** dialog (From the main menu - **Setup** - **Input Setup** - **Derived Parameters**). The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the cardiac cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
PeakP	Mean	Peak Pressure. Pressure at the highest point in a contraction.
BaseP	Mean	Base Pressure. Pressure at the start of a contraction.
Rise	Mean	Difference between PeakP and BaseP.
Period	Mean	Time between the beginning of one contraction to the beginning of the following contraction.
PeakD	Mean	Peak Duration. Time from the start of a contraction to the end of a contraction.
ICI	Mean	Inter-Contraction Interval. Time between the end of one peak and the beginning of the next.
DutyC	Mean	Duty Cycle. Ratio of PeakD to Period. Calculated as PeakD / Period.
TTPK	Mean	Time To Peak. Time from the start of a contraction to the PeakP.
PkCnt	Analysis	Peak Count. Number of peaks encountered in the last Peak Count Duration minutes.
PkCntT	Analysis	Peak Count Time. Duration corresponding to PkCnt - counts up to Peak Count Duration. When mm:ss is the selected precision, it will be reported as hh:mm.
Area	Mean	The area of the signal bounded by the peak and a line connecting the start of a contraction and the end of a contraction. Expressed in units-seconds.
StartT	Recent	Start Time. Time at the start of a contraction - the last peak in a logging period will be listed.

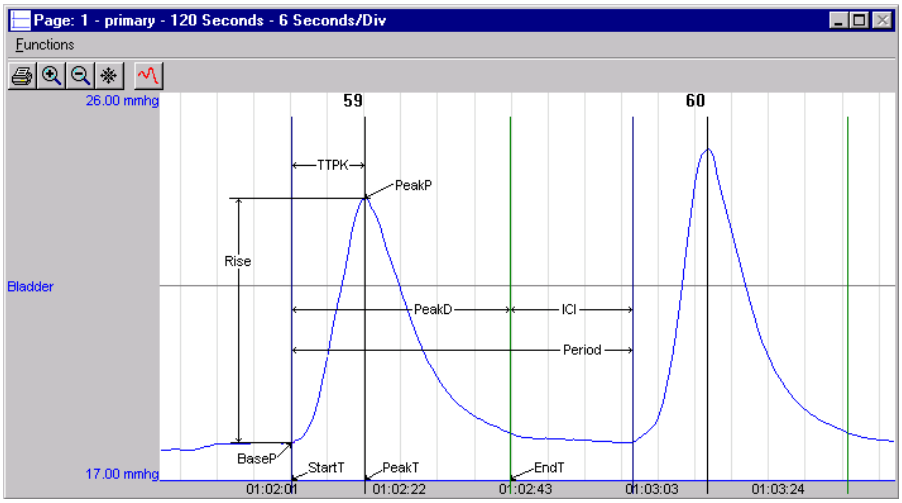
Name	Averaging In Review	Definition
PeakT	Recent	Peak Time. Time at the peak value in a contraction - the last peak in a logging period will be listed.
EndT	Recent	End Time. Time at the end of a contraction - the last peak in a logging period will be listed.
MaxDer	Mean	The Maximum Derivative that occurred during the cycle.
MinDer	Mean	The Minimum Derivative that occurred during the cycle.

Calibration

The recommended calibration for the system for Cystometry signals depends on the type of instrumentation, and the species that the signal is coming from.

On-Line Screens and Functions

Below is a Primary graph displaying the raw analog format of a typical cystometry signal with its digitally generated differential. The validation tick marks also are displayed on the waveform.



Cystometry Key Marks

In the above figure, the **Cystometry** is displayed with the validation tick marks. These marks identify the **Start T**, **PeakT**, and **EndT**.

Presentation Signals

Below is a list of presentation signals that are available for the Cystometry Analysis Module:

Signal	Description
Pressure	This displays the smoothed bladder pressure signal, after the subtraction of the Abdominal Channel, if enabled.
Derivative	This will display the derivative of the pressure signal.
UnSub	This will display the un-smoothed bladder pressure signal, before the subtraction of the Abdominal Channel.
Sub	This will display the un-smoothed bladder pressure signal, after the subtraction of the Abdominal Channel, if enabled.

Data Review

The Data Review related features of the CYS Analysis Module are accessible when the analysis module is used with P3 Plus Version 4.40 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review window channel are controlled through the Marks Tab in the attribute dialog accessed via the Analyze selection in the Right click menu.

Mark Operations

CYS supports 3 marks, Start Contraction, Peak Contraction and End Contraction.

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion; signal morphology is not considered.

Insert CYS Cycle

Inserts a CYS cycle. When a CYS cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. A CYS cycle's marks cannot be deleted individually. They are linked to the Peak Contraction Mark. To delete these marks, the entire cycle must be deleted; the cursor is positioned on the Peak Contraction Mark and the right mouse button is clicked to delete the marks. One of the selections in the pop-up menu will permit deletion of all the marks in the cycle.

Moving Marks

Moving the CYS marks follows the standard rules used in Data Review.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

Logging Mark

The logging mark for a CYS cycle is the Peak Contraction Mark. The time at the logging mark is the time used to report a cycle's derived data. If a CYS cycle's logging mark falls within a logging interval, the CYS cycle's data will be included in the logging interval.

End of Cycle

The start of a CYS cycle is at the Start Contraction mark. The end of a CYS cycle occurs one nano second prior to the next cycle's Start Contraction mark. The last cycle ends at its End Contraction mark.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Analysis is not triggering	Several issues could be causing this problem. 1. Peak Validation Time is set to high; reduce the Peak Validation Time. 2. Min Pulse Height is set to high; reduce the Min Pulse Height. 3. Percent Drop is set to high; reduce the Percent Drop.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Cystometry]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Minimum Pulse Height(low)	This sets the minimum allowable value for Min Pulse Height. The default value is .01.
Minimum Pulse Height(high)	This sets the maximum allowable value for Min Pulse Height. The default value is 100.
Base Height(low)	This sets the minimum allowable value for Base Height. The default value is .01.
Base Height(high)	This sets the maximum allowable value for Base Height. The default value is 100.
Abdominal Scaling(low)	This sets the minimum allowable value for Abdominal Scaling. The default value is -100.
Abdominal Scaling(high)	This sets the maximum allowable value for Abdominal Scaling. The default value is 100.
Peak Validation Time(low)	This sets the minimum allowable value for Peak Validation Time. The default value is 100.

Entry Name	Description
Peak Validation Time(high)	This sets the maximum allowable value for Peak Validation Time. The default value is 30000.
Smoothing(low)	This sets the minimum allowable value for Smoothing. The default value is 6.
Smoothing(high)	This sets the maximum allowable value for Smoothing. The default value is 20000.
Base Time(low)	This sets the minimum allowable value for Base Time. The default value is 1.
Base Time(high)	This sets the maximum allowable value for Base Time. The default value is 50000.
Peak Count Duration(low)	This sets the minimum allowable value for Peak Count Duration. The default value is 1.
Peak Count Duration(high)	This sets the maximum allowable value for Peak Count Duration. The default value is 200.
Percent Drop(low)	This sets the minimum allowable value for Percent Drop. The default value is 0.
Percent Drop(high)	This sets the maximum allowable value for Percent Drop. The default value is 100.
Reset Time	If the analysis does not detect a cycle for a given length of time, it will reset itself. The time period that triggers this reset is specified in the PPP3.INI file under the section [Cystometry]. The time is listed in milliseconds. When the analysis triggers consistently on successive cycles, this parameter does not come into play. The default value is 400000.

Pulmonary Volume (PVO)

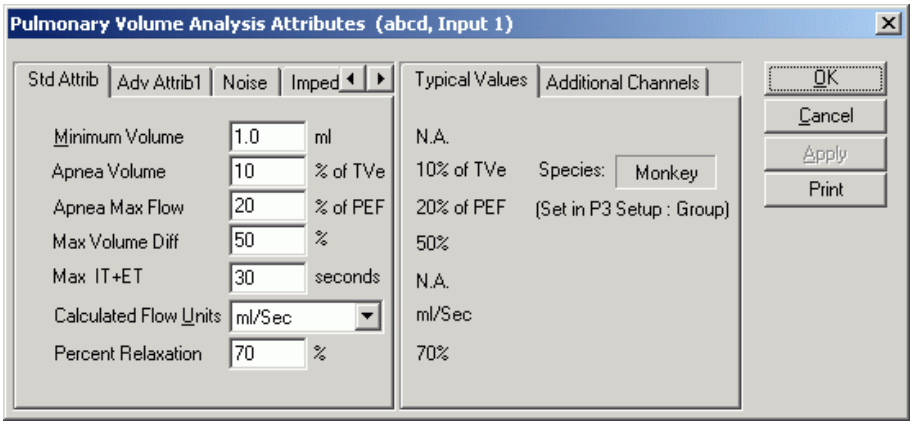
The Pulmonary Volume Analysis Module analyzes pulmonary volume signals obtained from the respiratory impendence transmitter. It also calculates, on a breath-to-breath basis, values for the respiratory cycle using volume based attributes.

Note: For optimal analysis it is recommended that impedance data from the D70-PCTR be collected at a sample rate of 50 Hz. Higher rates may lead to both degradation in performance and analysis capability.

Attribute Window

The Pulmonary Volume Analysis attributes window allows you to modify the signal analysis for different types of volume signals and different signal conditions.

Standard Attributes



Pulmonary Volume Standard Attribute Tab

The standard attributes allow setting the most common attributes that would need to be changed during acquisition or subsequent post processing.

Attribute	Effect On Review	Description
Minimum Volume	Signal Interpretation	Sets the minimum volume that the analysis must achieve before the analysis will detect and validate a pulmonary cycle. The Minimum Volume stops the analysis from triggering on artifacts such as cardiac noise.
Apnea Volume	Signal Interpretation	Sets the maximum volume as a percent of Tidal Volume Expired that could be included within the Apnea Time. If the volume exceeds this value the time prior to this will not be marked as an apnea. This feature is used in combination with Apnea Max Flow to determine periods of apnea.

Attribute	Effect On Review	Description
Apnea Max Flow	Signal Interpretation	Sets the maximum flow as a percent of Peak Expiratory Flow that could be included within the Apnea Time. If the flow exceeds this value the time prior to this may not be marked as an apnea. This feature is used in combination with Apnea Volume to determine periods of apnea.
Max Volume Diff	Signal Interpretation	The comparison is between inspiration and expiration within a breath. If the difference is greater than this setting, a breath will not be marked.
Max IT + ET	Signal Interpretation	Sets the maximum inspiratory time plus expiratory time for a breath to be considered valid. For PNM-PVO100W Rev 1.0 the total breath time (IT+ET+AT) is used.
Calculated Flow Units	Signal Conditioning, Calculation, Redraw	Flow Units specifies the volume units used so that the system calculates the flow values correctly. • mL/Sec (milliliters per second) • mL/Min (milliliters per minute) • L/Sec (liters per second) • L/Min (liters per minute)
Percent Relaxation	Calculation, Redraw	Used to draw the percent relaxation mark and to calculate Penh and RT. The Percent Relaxation Mark is drawn when the volume signal drops from its maximum value by the specified percentage.

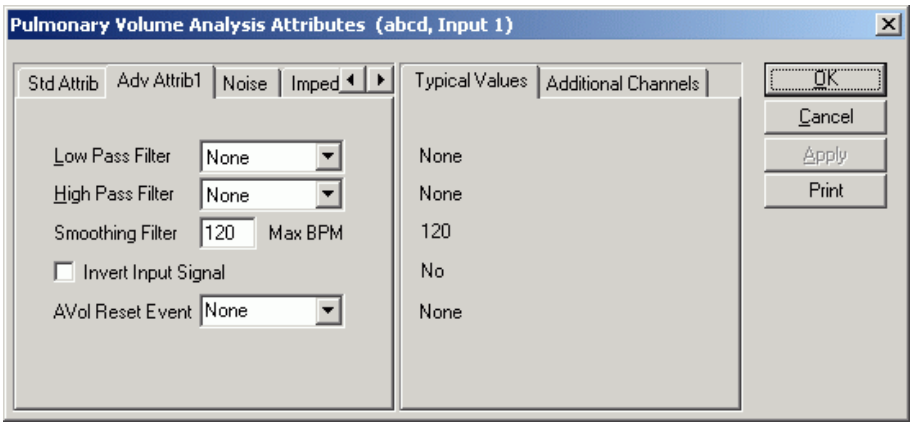
Typical Values

Use these values as guidelines for a first time setup. Under different situations, values above or below the typical values will have to be used.

Species	Attribute	Setting	Units
Dog	Minimum Volume	20	mL
	Minimum Volume	2	ohms
	Apnea Volume	10	%
	Apnea Max Flow	20	%
	Max Volume Diff	50	%
	Max IT+ET	60	Sec
	Calculated Flow Units	n/a	mL/Sec
	Percent Relaxation	70	%
	Smoothing Filter*	30-50	Max BPM
Monkey	Minimum Volume	5	mL
	Minimum Volume	1	ohms
	Apnea Volume	10	%
	Apnea Max Flow	20	%
	Max Volume Diff	50	%
	Max IT+ET	30	Sec

Species	Attribute	Setting	Units
	Calculated Flow Units	n/a	mL/Sec
	Percent Relaxation	70	%
	Smoothing Filter*	40-60	Max BPM
*** A value below the actual breaths per minute is not recommended. Additionally, the user should take caution to set a value which does not significantly alter the amplitude or width of the volume waveform.**			

Advanced Attributes



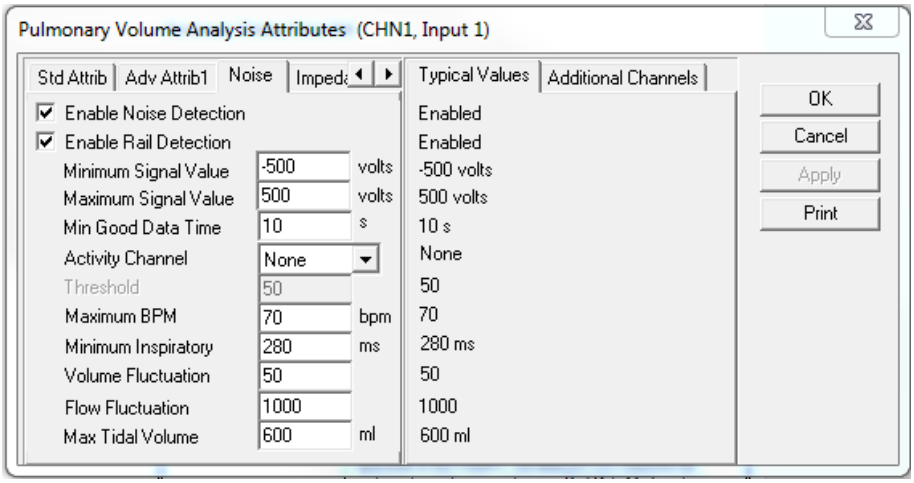
Pulmonary Volume Advanced Attribute1 Tab

The Advanced Attributes 1 tab allows selection of additional attributes that may need to be changed during acquisition or replay.

Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Smoothing Filter	Signal Conditioning, Calculation, Redraw	Defines a smoothing function by specifying the maximum breaths per minute that will not experience signal loss due to the filter. Setting the Smoothing Filter to a high value (e.g. 999) will effectively disable this filter.
Invert Input Signal	Signal Conditioning, Calculation, Redraw	This check box should be enabled if the respiration signal is acquired such that inspiration is negative. The PVO Analysis Module requires that inspiration is positive. Selecting the check box will reverse the polarity of the acquired signal.

Attribute	Effect On Review	Description
AVol Reset Event	Calculation	Used to determine the start point for the Accumulated Volume derived parameter (AVol). The selection of an event, “a” through “J”, will determine the start point for the calculation of AVol. If “None” is selected, the AVol derived parameter will report zero (acquisition and replay) or “x” (Review). The start of an acquisition, a break in the data, or subsequent entries of the event to trigger the start point for the AVol calculation will result in the derived parameter being reset.

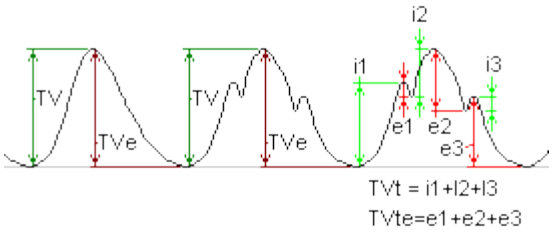
Noise Attributes Tab



Pulmonary Volume Noise Tab

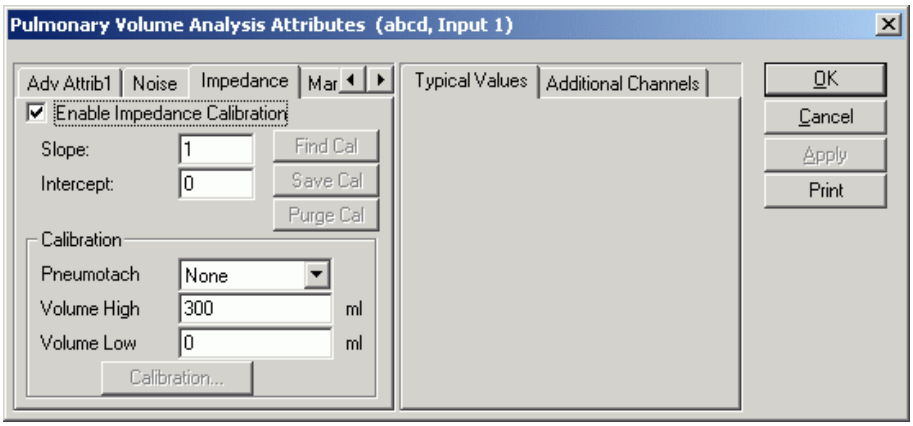
The Noise Tab contains attributes that are used to identify noisy data. On identifying noisy data, Bad Data Marks will be placed to span the noisy sections.

Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Allows the attributes to be edited and used by the software.
Enable Rail Detection	Signal Interpretation	If Rail detection is enabled, any railed data, positive or negative, encountered when analyzing data, shall be bracketed by Bad Data Marks such that the railed data falls within the Bad Data start and end marks. The Rail check shall be performed on unfiltered samples.
Minimum Signal Value/ Maximum Signal Value	Signal Interpretation	If any filtered samples fall below the Min Signal Value or rise above the Max Signal Value they shall be bracketed by Bad Data Marks.

Attribute	Effect On Review	Description
Minimum Good Data Time	Signal Interpretation	If multiple Bad Data Marks exist in the file and are separated by less than the time specified in the window, the analysis will combine the sections to create one contiguous Bad Data Mark section.
Activity Channel	Signal Interpretation	Allows user to identify which channel is to be used as the Activity channel.
Threshold	Signal Interpretation	This edit box specifies a noise level. When an activity channel level set in this box is exceeded, the data will be interpreted as noise and Bad Data Marks will be inserted to remove the section of data from analysis.
Maximum BPM	Signal Interpretation	Respiratory rates (breaths per minute) detected by the analysis that exceed the level specified will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis.
Minimum Inspiratory Time	Signal Interpretation	This sets the minimum allowable value for Minimum Inspiratory Time.
Volume Fluctuation	Signal Interpretation	Volume fluctuation compares all of the inspiratory and expiratory volumes within a breath (TVt and TVte) to the Tidal volume inspired and expired (TV and TVe). If the volume fluctuation exceeds this setting it will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis. The volume fluctuation is calculated as $$= 100\left(\frac{TVt + TVte}{TV + TVe} - 1\right)$$ The below graphic shows a cycle with no volume fluctuation and then two cycles with volume fluctuation. For clarity the marks have been placed on different cycles; however this fluctuation is calculated within a single breath cycle. 

Attribute	Effect On Review	Description
Flow Fluctuation	Signal Interpretation	Flow fluctuation compares all of the inspiratory and expiratory flows in a manner similar to volume fluctuation. If the flow fluctuation exceeds this setting it will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis. The flow fluctuation is calculated as $$=100\left(\frac{CumulativeFlow}{2PIF+2PEF}-1\right)$$ where CumulativeFlow is the sum of the range of flows covered by all continuously increasing or decreasing flows in cycle
Max Tidal Volume	Signal Interpretation	Sets the maximum allowed tidal volume. Cycles with volumes greater than this will be treated as noise and Bad Data Marks will be inserted to remove the data from analysis.

Impedance



Pulmonary Volume Impedance Tab

Attribute	Effect On Review	Description
Enable Impedance Calibration	N/A	Allows the impedance calibration attributes to be edited and used by the software.
Slope	Signal Conditioning, Calculation	The Slope value for Impedance Calibration.
Intercept	Signal Conditioning, Calculation	The Intercept value for Impedance Calibration.

Attribute	Effect On Review	Description
Pneumotach	N/A	Select a pneumotach channel for Impedance Calibration.
Volume High	N/A - used to determine Slope and Intercept	The high volume used for Impedance Calibration when pneumotach channel is not available.
Volume Low	N/A - used to determine Slope and Intercept	The low volume used for Impedance Calibration when pneumotach channel is not available.
Find Cal	N/A	Find previously saved calibration results from the ImpedanceCalibration.ini file. The location of the file is specified by Directories.CalValueDatabase in advanced settings. This feature is only enabled in Ponemah 5.00 or newer.
Save Cal		Save calibration results to the ImpedanceCalibration.ini file. This feature is only enabled in Ponemah 5.00 or newer.
Purge Cal		Clear all saved calibration results from the ImpedanceCalibration.ini file. This feature is only enabled in Ponemah 5.00 or newer.
Calibration		Bring up the calibration dialog.

Marks (Validation)

The **Pulmonary Volume** analysis displays validation tick marks for each respiratory cycle. Each respiratory cycle should have only one set of validation marks. These marks verify that the system is analyzing the PVO signal correctly. If there is more than one set of validation marks per respiratory cycle, correct the problem by changing the analysis attributes.

The validation marks and their meanings are listed below:

Color	Meaning
Black	Start of Inspiration
Blue	Start of Expiration
Green	Start of Apnea
Cyan	Percent Relaxation

Derived Parameters

Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the derivation files and the on-line text screens during acquisition or replay.

Name	Averaging In Review	Definition
Num	Recent	The number of the respiratory cycle. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
PIF	Mean	Peak Inspiratory Flow is the maximum inspiratory flow that occurs during a valid breath.
PEF	Mean	Peak Expiratory Flow is the maximum expiratory flow that occurs during a valid breath.
TV	Mean	This is the volume at start of expiration for this breath minus the volume at the start of inspiration for this breath.
MV	Mean	The Minute Volume is the product of the tidal volume and the number of breaths-per-minute. The equation is: MV = TV * BPM. Note: When running in a logging mode other than 1 epoch, the averaged value will be calculated off of the averaged TV and averaged BPM values.
BPM	Harmonic Mean	The number of breaths-per-minute is calculated on a breath-to-breath basis. It is computed as the reciprocal of the total time for a respiratory cycle times 60. Note: When running in a logging rate other than 1 epoch, sum the cycles in seconds in the logging period, divide by the number of cycles, take the reciprocal, and multiply the value by 60.
IT	Mean	The Inspiratory Time is calculated from the start of inspiration mark to the start of expiration mark. The time is in milliseconds.
ET	Mean	The Expiratory Time is calculated from the start of expiration mark to the start of apnea mark if present or next breaths start of inspiration marl if no apnea mark is present. The time is in milliseconds.
TT	Mean	The Total Time is the time period, in milliseconds, from one valid breath to the next valid breath.
AT	Mean	The Apnea Time is computed as follows: $AT = TT - (IT + ET)$

Name	Averaging In Review	Definition
PEnh	Mean	Enhanced Pause. Calculated as: ((ET+AT)/RT-1) * (PEF/PIF) Formula from Noninvasive Measurement of Airway Responsiveness in Allergic Mice Using Barometric Plethysmography Hamelmann et al.
RT	Mean	Relaxation Time. This is the time from the start of expiration to the point where the volume signal drops by the Percent Relaxation value from its maximum value for the cycle.
TVe	Mean	This is the volume at start of expiration for this breath minus the volume at the point prior to the start of inspiration of the next breath.
IF50	Mean	IF50 reports the inspiratory flow value at the point where the volume signal rises to 50% of the tidal volume.
EF50	Mean	EF50 reports the expiratory flow value at the point where the volume signal drops to 50% of the tidal volume.
AVol	Recent	Accumulated Volume is the summed total of the Tidal Volume (TV) from a reset point forward and is reported in milliliters. Reset points include the start of data collection, break in the data or the selection of the event associated with the AVol Reset Event attribute.
VolBa	Mean	The Volume Baseline is the volume at start of inspiration. It is reported in the same units as the volume waveform.
VFluc	Mean	Volume fluctuation compares all of the inspiratory and expiratory volumes within a breath (TVt and TVte) to the Tidal volume inspired and expired (TV and TVe). The difference is reported as a percent change.
FFluc	Mean	Flow fluctuation compares all of the inspiratory and expiratory flows in a manner similar to volume fluctuation.
TVm	Median	The median tidal volume (TV) – available for trending (in Ponemah 5.00 and later systems)
MVm	Median	The median tidal volume expired (TVe) – available for trending (in Ponemah 5.00 and later systems)
TVt	Mean	The Tidal Volume Throughout is the total volume of air that was inspired at any time during a breath and is always reported in milliliters. This is the sum of all positive changes in volume from start of inspiration to start of expiration.
TVte	Mean	The Tidal Volume Expired Throughout is the total volume of air that was expired at any time during a breath and is always reported in milliliters. This is the sum of all negative changes in volume from start of inspiration to start of expiration.
PZr	Mean	If a pneumotach is available and defined within the calibration dialog this derived data point will output the ratio of pneumotach volume divided by volume signal (calibrated if enabled) for the logging period.

Calibration

The respiratory impedance signal when uncalibrated reports volumetric changes as impedance (in ohms). In order to transform from impedance into units of volume a calibration is required. The respiratory impedance volume signal may be calibrated versus a pneumotach or versus manually input values.

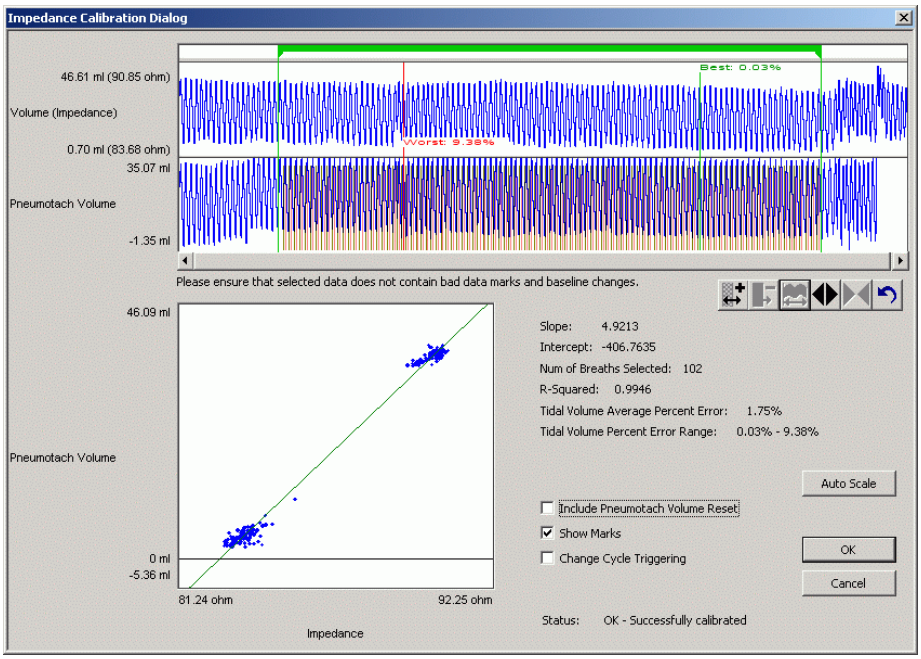
Pulmonary Volume Calibration with a Pneumotach

In order to calibrate versus a pneumotach the user is required to have previously set up and calibrated the pneumotach within the software in such a way that it may be used in a synchronized manner with the D70-PCTR implant (using a pneumotach interface to either a C11V or C12V if used with OpenART or interfaced to an ACQ16USB or ACQ7700USB if used with ACQ16USB-OpenART or ACQ7700USB-OpenART).

Once the user has the hardware configured correctly and attached to the animal the user must collect data from the pneumotach and the D70-PCTR. The data will preferably be very clean and with the animal in a posture representative of the posture which the animal will be in during a normal data collection. Data may be collected for as long or short as desired; however, during the calibration process only 5 consecutive minutes may be used. It is also strongly recommended to only calibrate during periods when the impedance signal baseline is consistent and bad data marks are not present.

Following data collection the user will need to find the start of that "calibration period" and have it within a graph window during review. Then the user will right click on the impedance waveform and select analyze. Then the user will select the impedance tab, enable the impedance calibration, define the pneumotach, and select the calibration button.

Note: The Fixed Volume entry is disabled when using the Pneumotach option.



The Impedance Calibration Dialog will then display up to a five-minute segment of data from the user selected area of normal waveforms. The green bar located near the top of the dialog is the Calibration Segment Bar. The Calibration Segment Bar allows the user to select which breaths to calibrate versus the pneumotach signal. The bar can be shorted or elongated using the computer mouse. Multiple segments can be added so as to maximize the number of typical breaths used in the calibration. Additional segments are added by right clicking in the Calibration Segment Bar portion of the dialog.

After placing the Calibration Segment Bar(s) the slope and intercept will automatically be calculated. Also displayed are the Number of Breaths Selected (determined by the placement of the Calibration Segment Bar(s)); Number of Breaths Used in the calibration; the Average Percent Error [(Vtotal - VPneumo)/VPneumo] of the breaths used in the calibration and the Percent Error Range.

The ability to include or not include volume resets on the pneumotach channel is also available via a checkbox.

If the user deems the calibration to be unacceptable the user should modify the segments as needed or Cancel the calibration.

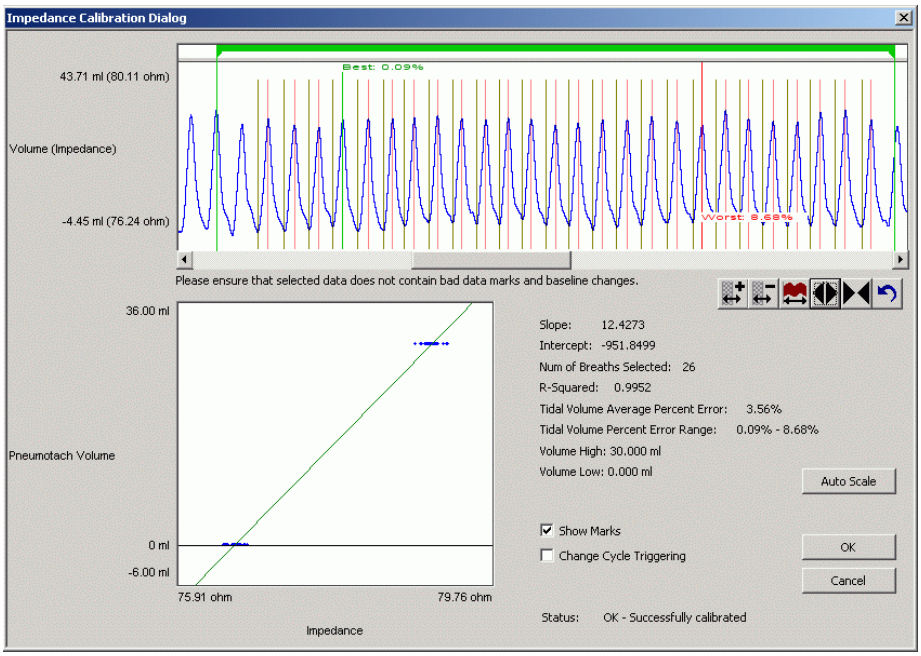
Once the user deems the calibrations to be acceptable the user should select the OK button. After this the slope and intercept values will be automatically entered into the Impedance Calibration dialog. The user may then

reanalyze the data set. Scaling of graphs, minimum flows, etc will need to be adjusted to obtain an appropriate analysis.

Pulmonary Volume Calibration without a Pneumotach

In order to calibrate without a pneumotach the user must collect data from the animal during which they measure the volume via an external method, or assume it based upon a reference or experience. The data will preferably be very clean and with the animal in a posture representative of the posture which the animal will be in during a normal data collection. Data may be collected for as long or short as desired; however, during the calibration process only 5 consecutive minutes may be used. It is also strongly recommended to only calibrate during periods when the impedance signal baseline is consistent and bad data marks are not present.

Following data collection the user will need to find the start of that "calibration period" and have it within a graph window during review. Then the user will right click on the impedance waveform and select analyze. Then the user will select the impedance tab, enable the impedance calibration, define the volume high (as the expected average tidal volume), define the volume low (zero), and select the calibration button.



The Impedance Calibration Dialog will display up to a five minute segment of data from the user selected area of normal waveforms. The green bar located near the top of the dialog is the Calibration Segment Bar. The Calibration Segment Bar allows the user to select typical breaths that fit the Fixed Volume value. The bar can be shorted or elongated using the computer mouse. Multiple segments can be added so as to maximize the number of typical breaths used in the calibration. Additional segments are added by right clicking in the Calibration Segment Bar portion of the dialog.

After placing the Calibration Segment Bar(s) the slope and intercept will automatically be calculated. Also displayed are the Number of Breaths Selected (determined by the placement of the Calibration Segment Bar(s)); Number of Breaths Used in the calibration; the Average Percent Error [(Vtotal - VPneumo)/VPneumo] of the breaths used in the calibration and the Percent Error Range.

If the user deems the calibration to be unacceptable the user should modify the segments as needed or Cancel the calibration.

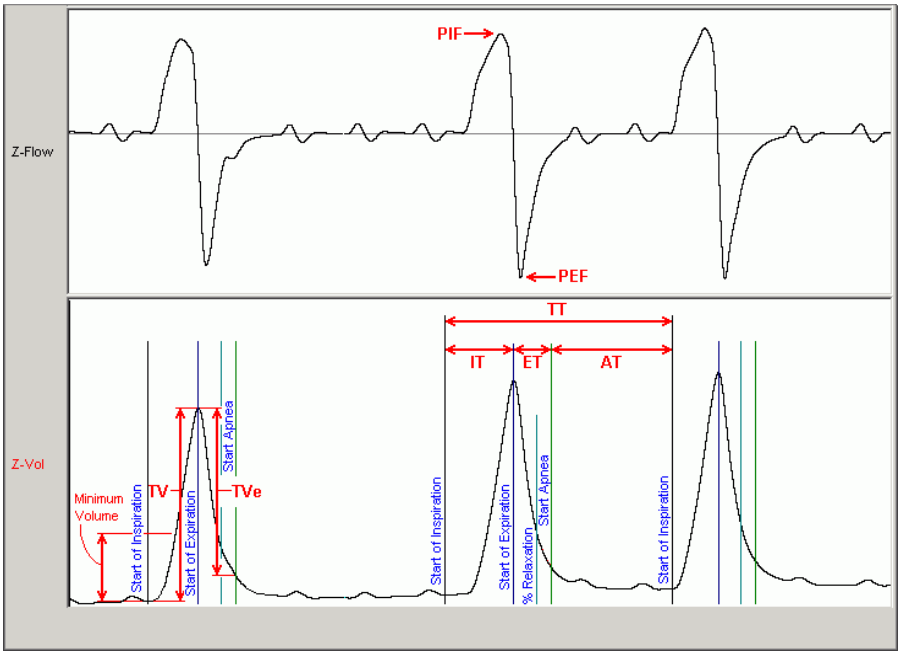
Once the user deems the calibrations to be acceptable the user should select the OK button. After this the slope and intercept values will be automatically entered into the Impedance Calibration dialog. The user may then reanalyze the data set. Scaling of graphs, minimum flows, etc will need to be adjusted to obtain an appropriate analysis.

Typical calibration values are listed in the table below:

Species	High Volume	Impedance	Slope
Dog	~150-300 ml	~8-10 ohms	~15-45
Primate	~10-30 ml	~3-5 ohms	~4-15

On-Line Screens and Functions

Below is an example of a Primary graph displaying a typical pulmonary flow and volume signal.



Pulmonary Volume Key Marks

In the above figure, the Pulmonary Volume is displayed with validation tick marks. The validation marks label the **Start of Inspiration**, **Start of Expiration, Percent Relaxation, and Start of Apnea marks.**

Presentation Signals

Below is a list of presentation signals that are available for the PVO Analysis Module:

Signal	Description
Flow	This will display the differential of the signal, and it is generated as a two-point differential
Volume	This will display the original volume signal (in ohms if uncalibrated, in ml if calibrated).
Input*	This will display the original volume signal (in ohms) regardless of calibration

Data Review

The Data Review related features of the PVO Analysis Module listed here are accessible when the analysis module is used with P3 Plus Version 4.60 or greater. The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Graph Page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu - Analyze.

Mark Operations

PVO marks are divided into two types, marks that always exist when a valid cycle is found (Start Inspiration and Start Expiration) and marks that may or may not exist, depending on the signal morphology (Percent Relaxation and Start Apnea).

Inserting Marks

Marks are inserted by right clicking at the point of insertion in the Review window. The pop-up menu that is displayed will provide the option to insert marks as appropriate. The list of marks available for insertion will depend on the marks adjacent to the point of insertion, signal morphology is not considered.

Insert PVO Cycle

Inserts an entire PVO cycle, Start Inspiration, Start Expiration, and Percent Relaxation if applicable. Start Apnea is not inserted; if Apnea exists this must be inserted manually. This set of marks may be inserted between a Start Inspiration mark and the last mark of the preceding cycle. In many cases the last mark of the preceding cycle and that start inspiration mark of the current cycle will overlap. When this occurs, movement of these marks is required before a new cycle may be inserted. Cycles may also be inserted prior to the first cycle and after the last cycle. When a PVO cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Insert Start Apnea

Inserts a Start Apnea mark. This mark may be inserted prior to a Start Inspiration mark or after the last cycle, as long as the preceding mark is not a Start Apnea mark. In many cases, a start apnea mark will already exist and be overlapped by the subsequent cycle's start of inspiration mark. Movement of these marks may be necessary to differentiate and place them as needed.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu. Only the Start Apnea mark may be deleted in this fashion. The rest of the marks cannot be deleted individually. An entire cycle may be deleted. A cycle is deleted by positioning the cursor on the Start Inspiration mark, bringing up the right mouse menu, and selecting Delete Cycle.

Moving Marks

Moving of the Start Inspiration, Start Expiration and Start Apnea marks follow the standard rules used in Data Review. There are special considerations when dealing with the Percent Relaxation mark. The Percent Relaxation mark is a calculated mark; its position is dependent on the Tidal Volume and cannot be adjusted by the user. If the user changes the position of the Start Inspiration, Start Expiration, or Start Apnea marks, the Percent Relaxation mark will be recalculated. When the Percent Relaxation mark is moved the derived parameter RT may change and will not be marked as a grayed cell unless a reanalyze is performed.

Calculations

The calculations of derived parameters are identical to those performed during acquisition and replay.

When a Review file is opened, the trace data may not be identical to the acquired data. The difference arises because of the scaling involved in the storage and reconstitution of the data. The difference for a point, on average, is less than 0.05%.

One of the consequences of this difference is seen with Calculated Marks. If, after opening a Review file, Review is prompted to recalculate a Calculated Mark, the mark may move with no change to the marks on which it depends. This is because the original placement of the Calculated Mark was based on the Replay data values whereas, recalculation uses the data values present in Review.

Logging Mark

The logging mark for a PVO cycle is the Start Inspiration mark. The time at the logging mark is the time used to report a cycle's derived data.

End of Cycle

The end of a PVO cycle occurs at the point prior to the next cycle's Start Inspiration mark. When a PVO channel is the epoch channel, all review channels that display their cycle's logging mark prior to the end of the epoch channel's cycle will be included in the derived output.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Breaths-per-Minute is doubled, halved, etc.	This usually occurs when the analysis triggers on noise or artifacts. It can be corrected by changing the Minimum Volume to a higher or lower value to eliminate rates higher or lower than normal. If the signal has significant noise, change the Smoothing Filter (in the Adv Attrib1 tab) to a lower value to smooth the signal. A value below the actual breaths per minute is not recommended and the user should take caution to set a value which does not significantly alter the amplitude or width of a breath waveform.
All derived parameters are reporting zero	The Minimum Volume may be set too high for the specified signal. Lower the Minimum Volume value.
Tidal Volume incorrect	Verify the impedance calibration is correct. Adjust noise settings.

Problem	Solution
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed. Additionally, the derived parameters TVm and MVm are only available when using Ponemah version 5.00 or newer.
Cannot find the analysis module in the Input Setup dialog	The analysis software may have been installed in the wrong directory. Re-install the software for this analysis. The destination directory must be the same directory as the P3 Plus software. To verify that the analysis has been installed correctly, select the Product Information option of the Help menu.
Waveform validation marks only appear on the volume presentation	The appearance of waveform validation marks on the volume and/or flow waveforms is only possible with Ponemah version 5.00 or newer.
Species specific default attributes are not available	These values are only available when using Ponemah version 5.00 or newer.
Cannot interact with Biaera software application	The ability to communicate with the Biaera software application requires Ponemah version 5.00 or newer as well as additional configuration. Please see the P3Plus Manual (MU00060-001) for the additional configuration information.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Pulmonary Volume]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Use Averaged dT	This setting informs the analysis module to use a 0.020 sec interval for deriving the Flow from Volume. The default value is 1 which represents that this is turned on. A value of 0 will turn off this feature.
Use Start Expiration for dT	This setting informs the analysis module to use the start of expiration as the initial interval period to use when Use Averaged dT is enabled. The default value is 1 which represents that this is turned on. A value of 0 will turn off this feature.
Maximum Volume Difference Percentage(low)	This sets the minimum allowable value for Maximum Volume Difference. The default value is 0.
Maximum Volume Difference Percentage(high)	This sets the maximum allowable value for Maximum Volume Difference. The default value is 10000.

Entry Name	Description
Max Breath Time(low)	This sets the minimum allowable value for Max Breath Time. The default value is 0
Max Breath Time(high)	This sets the maximum allowable value for Max Breath Time. The default value is 1000
Apnea Max Flow(low)	This sets the minimum allowable value for Apnea Max Flow. The default value is 0
Apnea Max Flow(high)	This sets the maximum allowable value for Apnea Max Flow. The default value is 1000100
Apnea Volume(low)	This sets the minimum allowable value for Apnea Volume. The default value is 0
Apnea Volume(high)	This sets the maximum allowable value for Apnea Volume. The default value is 1000100
Smoothing filter (low)	This sets the minimum allowable value for Smoothing filter. The default value is 5.
Smoothing filter (high)	This sets the maximum allowable value for Smoothing filter. The default value is 999.
Minimum Good Data Time (low)	This sets the minimum allowable value for Minimum Good Data Time. The default value is 0.
Minimum Good Data Time (high)	This sets the maximum allowable value for Minimum Good Data Time. The default value is 1000.
Noise Threshold (low)	This sets the minimum allowable value for Noise Threshold. The default value is 0.
Noise Threshold (high)	This sets the maximum allowable value for Noise Threshold. The default value is 1000.
Maximum Breaths per Minute (low)	This sets the minimum allowable value for Maximum Breaths per Minute. The default value is 0.
Maximum Breaths per Minute (high)	This sets the maximum allowable value for Maximum Breaths per Minute. The default value is 1000.
Minimum Inspiratory Time (low)	This sets the minimum allowable value for Minimum Inspiratory Time. The default value is 0.
Minimum Inspiratory Time (high)	This sets the maximum allowable value for Minimum Inspiratory Time. The default value is 10000.
Volume Fluctuation(low)	This sets the minimum allowable value for Volume Fluctuation. The default value is 0
Volume Fluctuation(high)	This sets the maximum allowable value for Volume Fluctuation. The default value is 100000
Flow Fluctuation(low)	This sets the minimum allowable value for Flow Fluctuation. The default value is 0
Flow Fluctuation(high)	This sets the maximum allowable value for Flow Fluctuation. The default value is 100000
Max Tidal Volume(low)	This sets the minimum allowable value for Max Tidal Volume. The default value is 0
Max Tidal Volume(high)	This sets the maximum allowable value for Max Tidal Volume. The default value is 100000
Impedance Calibration Slope (low)	This sets the minimum allowable value for Impedance Calibration Slope. The default value is -10000.
Impedance Calibration Slope (high)	This sets the maximum allowable value for Impedance Calibration Slope. The default value is 10000.
Impedance Calibration Intercept (low)	This sets the minimum allowable value for Impedance Calibration Intercept. The default value is -10000.
Impedance Calibration Intercept (high)	This sets the maximum allowable value for Impedance Calibration Intercept. The default value is 10000.
Impedance Calibration Volume High (low)	This sets the minimum allowable value for Impedance Calibration Volume High. The default value is -10000.
Impedance Calibration Volume High (high)	This sets the maximum allowable value for Impedance Calibration Volume High. The default value is 10000.
Impedance Calibration Volume Low (low)	This sets the minimum allowable value for Impedance Calibration Volume Low. The default value is -10000.

Entry Name	Description
Impedance Calibration Volume Low (high)	This sets the maximum allowable value for Impedance Calibration Volume Low. The default value is 10000.

Glucose (GLU)

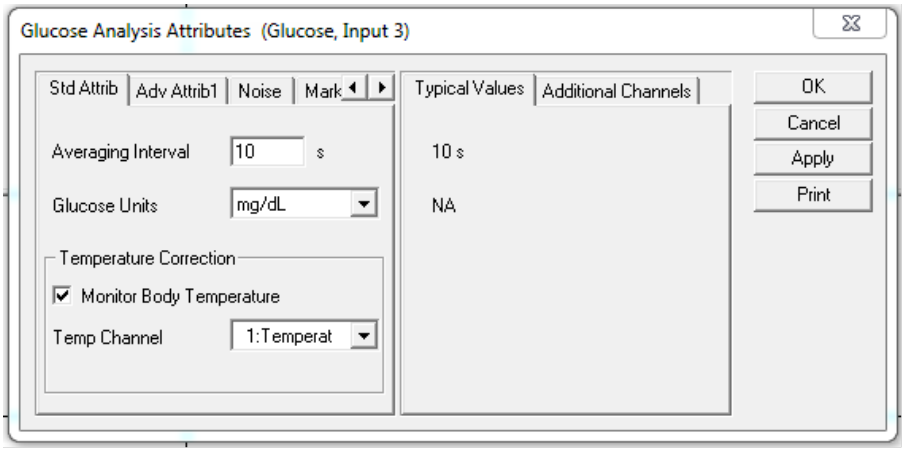
The **Glucose** analysis module analyzes the blood glucose signal obtained from the HD-XG implant. The analysis calculates the common parameters that are associated with glucose after the signal has been calibrated.

Attributes Window

The **Glucose Analysis Attributes** dialog allows you to modify the signal analysis for different types of glucose signals and signal conditions. If an analysis change in the **Attributes** dialog is performed **Averaging Interval**, then the attribute change will not take effect until the following cycle.

Standard Attributes

The **Standard** attributes allow setting the most common attributes that would need to be changed during Acquisition or Review.

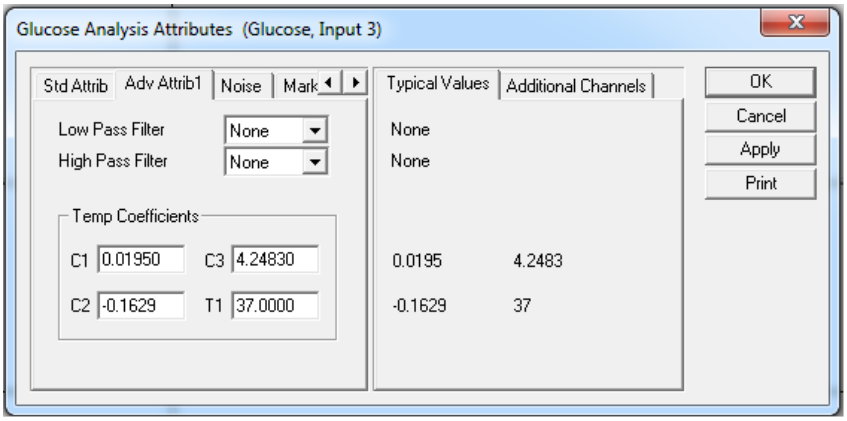


Attribute	Effect On Review	Description
Averaging Interval	Calculation	Interval at which glucose "cycles" will be reported by the analysis module. This represents the finest granularity at which data are reported. Data may be further averaged depending on the Logging Rate or Data Reduction settings. A Mark will be placed every Averaging Interval, referenced from the start of the acquisition i.e. elapsed time 0.
Glucose Units	Calculation	Allows the user to select either mg/dL or mmol/L. This selection is used to set the Units for other attributes and to update the "Min Calibration Range" value and units within the Glucose Calibrations | Calibration Settings dialog.

Attribute	Effect On Review	Description
Monitor Body Temperature	Calculation	Checking this box will enable the selection of the Temp Channel.
Temperature Channel	Calculation	The channel from which temperature values are retrieved for calculating corrected nA. This will default to the temperature channel from the HD-XG device associated with the Subject.

Advanced Attributes

The **Advanced** attributes allow selection of attributes which are not commonly changed during Acquisition or Review.



Attribute	Effect On Review	Description
Low Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of Low Pass filter in hertz.
High Pass Filter	Signal Conditioning, Calculation, Redraw	Selection of High Pass filter in hertz.
Temp Coefficients	Signal Conditioning, Calculation, Redraw	Coefficients used to apply temperature correction to the input nA signal. Four coefficients are required. DSI recommends not changing these values.

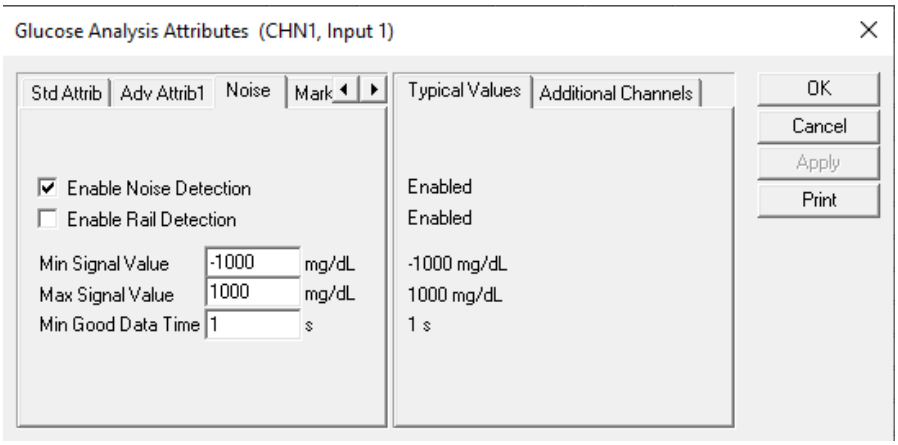
Typical Values

Use these values as guidelines for a first-time setup. Under different situations, values above or below the typical values will have to be used.

Attribute	Setting	Units
Averaging Interval	10	S
Glucose Units	Mg/dL or mmol/L	N/A
Monitor Body Temperature	Enabled	N/A
Low Pass Filter	None	Hz
High Pass Filter	None	Hz
Temp Coefficients	C1=0.0195 C2=-0.169 C3=4/2483 T1=37	N/A

Noise Attributes Tab

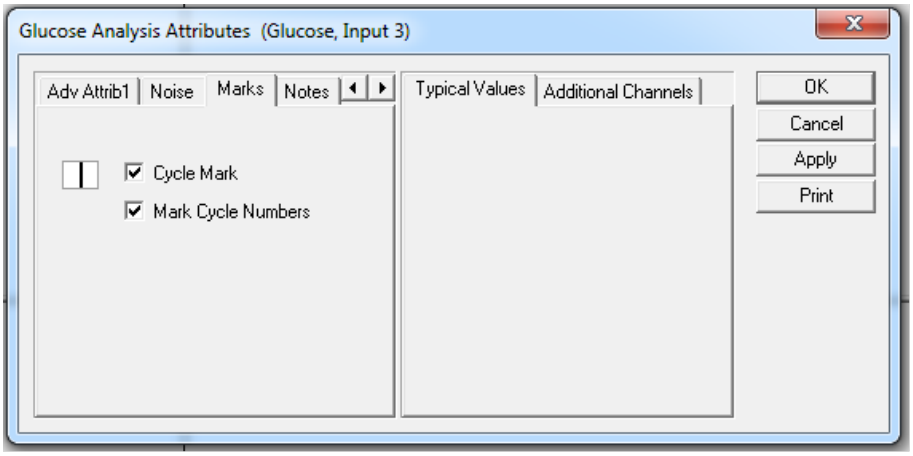
The **Noise Tab** contains attributes that are used to identify noisy data. On identifying "noisy" data, as defined by the user, **Bad Data Marks** will be placed to span the noisy sections.



Attribute	Effect On Review	Description
Enable Noise Detection	Signal Interpretation	Enables the Noise Detection attributes for the automatic placement of Bad Data Marks. Enabling this function will also places Bad Data Marks around data that is defined as Dropout.
Minimum Signal Value	Signal Interpretation	User defined threshold for determining the minimum value for acceptable data. Data that falls below this threshold will be considered noise and bracketed by Bad Data Marks.
Maximum Signal Value	Signal Interpretation	User defined threshold for determining the maximum value for acceptable data. Data that exceeds this threshold will be considered noise and bracketed by Bad Data Marks.
Minimum Good Data Time	Signal Interpretation	If multiple Bad Data Marks exist in the file and are separated by less than the time specified in the window, the analysis will combine the sections to create one contiguous Bad Data Mark section.

Marks (Validation)

The **Glucose** analysis does NOT display validation tick marks for each cycle. See the Online Screens and Functions section for more details.



The validation marks and their meanings are listed below:

Color	Meaning
Black	NOT USED

Derived Parameters

Derived Parameters are selected within the **Channel Details** of the **Subject Setup** dialog. The derived parameters selected in this dialog box will be calculated, and the results will be placed in the **Derived Parameter List View(s)**. The following details the available **Derived Parameters** from the ECG module and the averaging method used within Review.

Name	Averaging In Review	Definition
Num	Recent	The number of the cycles. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
nAavg	Mean	Average of nA samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks
nAmax	Mean	Maximum of nA samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks

Name	Averaging In Review	Definition
nAmin	Mean	Minimum of nA samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks
Gavg	Mean	Average of calibrated Glucose signal samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks
Gmax	Mean	Maximum of calibrated Glucose signal samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks
Gmin	Mean	Minimum of calibrated Glucose signal samples within the averaging interval. All samples within a cycle are included in the calculation, with the following exceptions: • Railed samples • Samples within bad data marks
Samp	Minimum	The number of samples used in reporting nAxxx and Gxxx derived parameters.
Ref-Ds	Mean	The averaged Reference values of all disabled calibration points during the logging interval.
Ref-En	Mean	The averaged Reference values of all enabled calibration points during the logging interval.
Slope	Mean	The averaged interpolated Slope during the logging period.
Offset	Mean	The averaged interpolated Offset during the logging period.

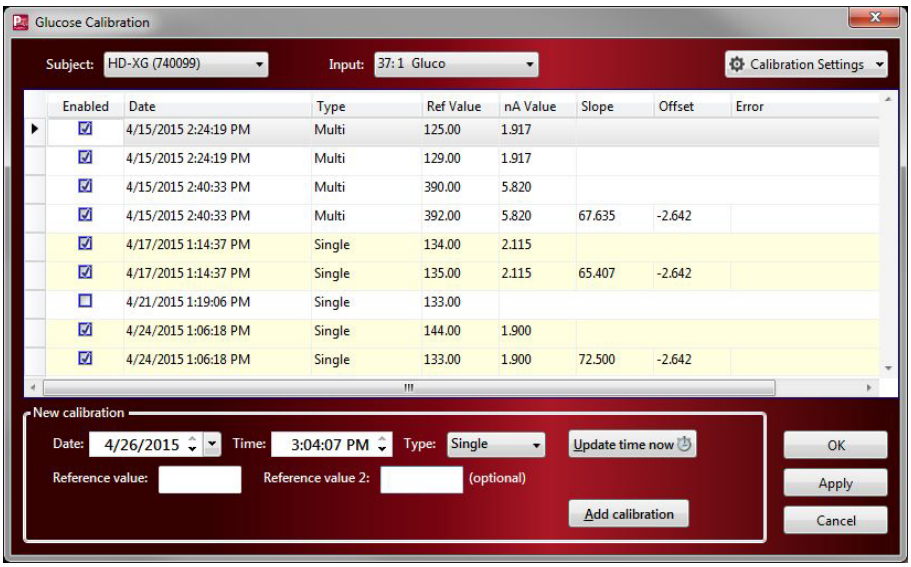
Calibration – In Vivo

It is necessary to perform an initial multi-point calibration and to collect periodic calibration points at least twice per week throughout the duration of a glucose study. Calibration data is collected using blood samples from the tail or other appropriate sampling point with analysis performed by the StatStrip Xpress glucose meter or an

equivalent analytical method. Calibration reference points should always be collected while the Ponemah Acquisition program is actively collecting data, and ideally, while the Subject is on or within range of the telemetry receiver (typically within about 25 cm of the receiver).

Ponemah Acquisition provides a dialog to facilitate entry of the calibration values that will later be used during Review. This can be accessed from the **Toolbar** menu by clicking on the **Glucose Calibration** icon. This provides several important features to facilitate the process:

- Automated or manual entry of date/time stamps associated with each sample point
- Entry of individual or duplicate samples for each time point
- Designation of calibration as single-point or multi-point calibration (this can be changed later)
- Ability to add multiple calibration values without dismissing the dialog
- Ability to switch between available subjects without dismissing the dialog



Each subject will have its own list of Glucose calibration reference values. If the dialog provided in Ponemah doesn't meet your particular needs, it is also possible to add these calibration reference values to an Excel file and import them during a Review session.

Calibration Frequency Recommendation

The glucose sensor is affected over the implant duration by the presence of fibrin, tissue, and glucose levels. For optimal performance, the HD-XG must be calibrated using reference measurements over the course of a study:

- Initial multi-point calibration
- Twice weekly single-point calibration
- End-of-study multi-point calibration

Raw telemetry data is recorded in nanoamperes (nA) and calibration reference values are recorded in milligrams per deciliter (mg/dL) or millimoles per liter (mmol/L). The calibration algorithm converts the telemetry (nA) data to values that are equivalent to the appropriate mg/dL or mmol/L values.

Selecting A Calibration Reference

Several calibration reference options exist, including glucose analyzers, reagents and diagnostics equipment, and glucometers with test strips. DSI recommends the Nova StatStrip Xpress meter and test strips, as it provides

comparable results to other laboratory analytics with the advantage and convenience of requiring smaller blood samples (1.2 µL) and providing immediate results. The StatStrip Xpress provides measurement and correction for hematocrit and other common interferents, as well as a higher level of accuracy than most alternative hand-held glucometers. See the DSI website www.datasci.com/glucose for more information on the StatStrip Xpress.

Multi-Point Calibration

A multi-point calibration establishes a linear relationship between the sensor output and blood glucose levels. DSI typically recommend using two points (baseline and slightly post-peak) for calibration purposes, but can support multiple points over the course of the challenge, such as an Oral Glucose Tolerance Test (OGTT). The blood glucose levels should differ by at least 200 mg/dL (11 mmol/L) to minimize calibration error caused by inaccuracies of the glucose reference. DSI recommends using an OGTT for multi-point calibration; however, an Intraperitoneal Glucose Tolerance Test (IPGTT) may also be used.

DSI recommends that at least two people are involved in the calibration process. One person is responsible for recording the calibration values on the Ponemah system and providing direction on the appropriate sample times. The second person handles the subjects, collects the samples, and reports the measurements. Additional personnel can be leveraged to streamline the process and increase throughput.

In a normal rat, the baseline blood glucose level might be approximately 100 mg/dL (5.5 mmol/L); while the peak value after an OGTT might be at least 300 mg/dL (16.7 mmol/L). Peak glucose values will typically occur 12-16 minutes post-dose during an OGTT in a healthy animal. DSI recommends taking a reading 5 to 10 minutes after this peak for an OGTT or 3 to 5 minutes after this peak for an IPGTT. If telemetry data cannot be viewed in real-time, such as when the computer is not physically located in the procedure room, please characterize the animal prior to collecting calibration values to estimate an appropriate post-dose time for the appropriate post peak blood glucose sample.

To learn how to perform a multi-point calibration, please see the DSI Support Center for more information.

Single Point Calibration

Single-point calibrations help account for non-physiologic changes in the baseline glucose value over time. Examples of non-physiologic changes include sensor drift due to enzyme instability or fibrin and tissue growth on the sensor. Single-point calibrations should be performed at least twice per week at the same time of day, and during a time period when the animal's blood glucose is relatively stable.

To learn how to perform a single-point calibration, please see the DSI Support Center for more information.

Best Practices

LEAVE TELEMETRY DEVICE ON DURING THE ENTIRE STUDY

Leave the HD-XG implant in **ON** mode throughout the entire study to improve glucose sensor stability. Turning the device **ON** after extended time in **OFF** mode will result in a positive spike and it will take 1-5 hours for the glucose values to return to normal. If an implant is turned **OFF** mid-study, a single-point calibration should be performed at least 5 hours after turning **ON**. If there is a notable change in the baseline from the previous on time, it is advisable to perform a new multi-point calibration.

TAKE DUPLICATE SAMPLES FOR EACH REFERENCE VALUE

Duplicate samples should be used to minimize error and establish the most reliable calibration of the implantable glucose sensor. If duplicate samples vary by >10%, one or more additional samples are recommended to establish a more accurate reference value.

Take duplicate glucose samples from a single point in time by drawing blood from the animal and testing the blood glucose level twice (e.g. using two different test strips). Enter the two reference values in the Glucose Calibration dialog in the Reference value and Reference value 2 text fields, the software will average them.

MINIMIZE STRESS, ANESTHESIA ARTIFACTS

Taking blood samples too frequently from animals that are stressed (due to restraint) can cause significant bias and variability in reference samples.

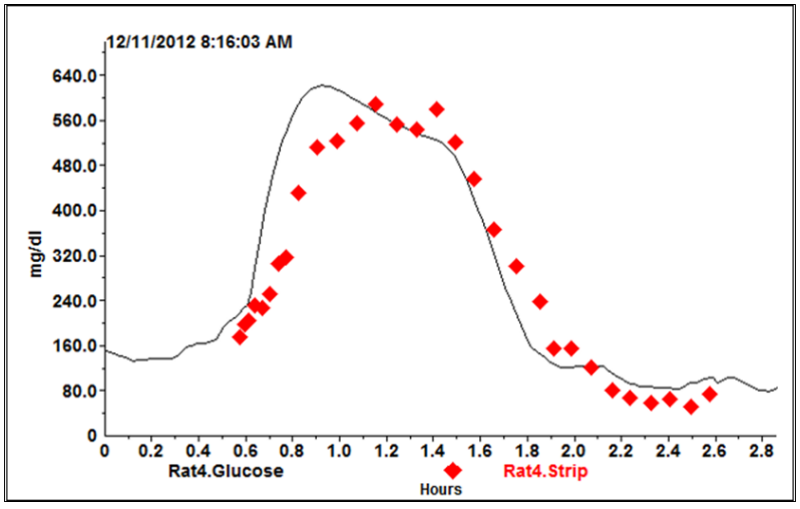
Taking samples from anesthetized animals is discouraged as isoflurane has been demonstrated to impact the glucose sensor reading in some cases, particularly at later points in the study period.

Considerations and Alternatives

In order to optimize implant calibration, there are several factors to consider.

Potential lag time between the glucose values

Potential lag time between the glucose values taken by the implanted sensor and the calibration reference. In a normal, healthy rat the peak glucose value is typically observed 4-7 minutes post dose for an intraperitoneal glucose tolerance test (IPGTT) and 12-16 minutes post dose for an OGTT. These durations will vary based on the glucose dose, whether or not the animal was fasted, and the animal strain. A blood sample taken from the tip of a rat's tail may have a 2-5 minute (or more) delayed response to the glucose dose due to stress artifact and the hemodynamics of the tail. Figure 23 below demonstrates the glucose measurement lag between the descending abdominal aorta and tail. The tail sample has a peak glucose value that occurs later than the peak value detected by the sensor in the descending aorta, which could result in errors during the calibration process. By sampling a few minutes after the peak is observed in the telemetry signal, the stable periods for the implant and reference signal can be more closely aligned and the theoretical calibration error can be reduced. This has a similar effect to shifting the tail samples backwards in time to better align with the telemetry signal. Data illustrated below is an example of the blood glucose measurement lag in the tail (Rat4.Strip) vs. descending aorta (Rat4.Glucose). This lag is variable and can last as little as a few seconds or greater than 10 minutes depending on animal stress, tail blood hemodynamics.



The method used to increase glucose levels to record baseline and peak values

Several methods can be used to increase blood glucose levels if an increase of at least 200 mg/dL (11 mmol/L) needs to be achieved. Oral or IP glucose tolerance tests can be used and the method chosen depends on your

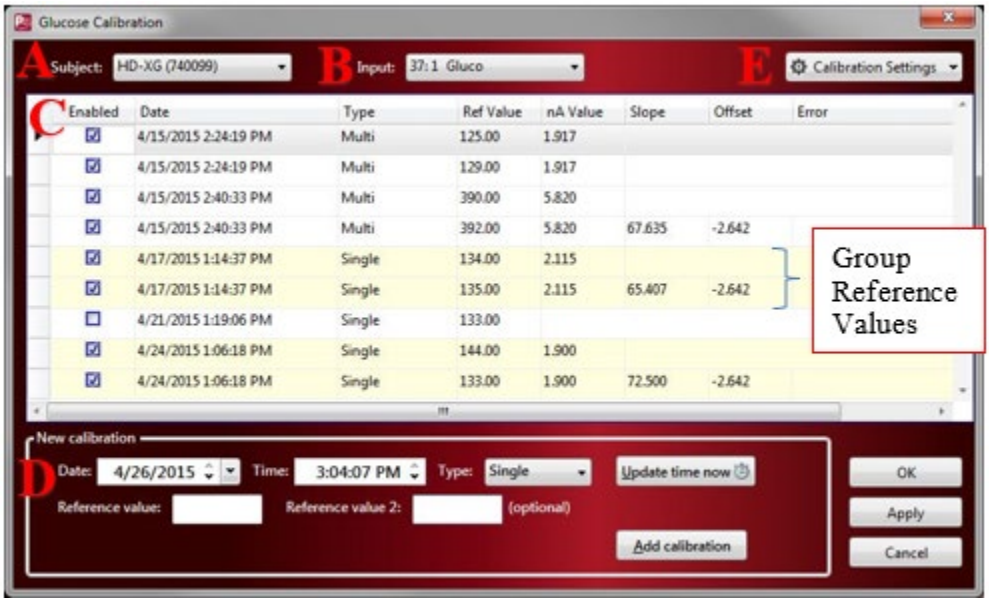
study needs. IPGTTs typically result in faster and higher glucose peaks, which can expedite the calibration process and aid in achieving the desired glucose difference of 200 mg/dL (11 mmol/L), however, glucose is metabolized more quickly and the peak glucose value lasts for a shorter period of time. OGTTs require a large bolus of glucose to achieve the target 200 mg/dL (11 mmol/L) difference. However, peak glucose levels typically remain stable for a longer period of time, resulting in an easier and more accurate calibration process.

When using Type 1 or Type 2 diabetic animals, an IP insulin tolerance test can be substituted for the glucose tolerance test.

Glucose Calibration Dialog

The **Glucose Calibration** dialog is used during Acquisition and Review to enter **Glucose Calibration Reference** values obtained by your Glucose Reference during Multi- and Single-point calibrations. The following describes dialog in detail. For instructions on how to use while performing a Multi- or Single-point calibration, please see the **Glucose Calibration Process Tutorial** located in the **DSI Support Center (support.datasci.com).**

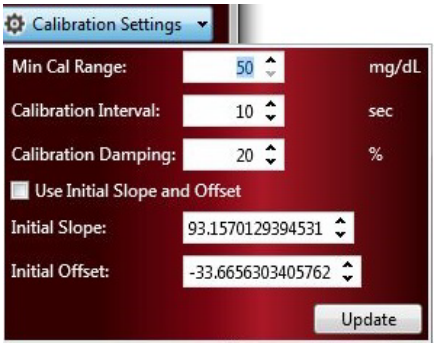
Note: It is not recommended to leave the Glucose Calibration dialog up while acquiring over a .RAW file incrementation period as it could disable values prior to the time of incrementation.



The following describes the components of the dialog:

Component	Description
Subject	Dropdown box used to select the **Subject** whose calibrations information is desired to be displayed. Ensure the correct Subject is chosen before entering calibration values.
Input	Dropdown box used to designate which implant **Input** channel is displayed within the dialog. Since the HD-XG only has one glucose input channel, it will automatically be displayed and cannot be changed.

Component	Description
Calibration List View	This is an interactive **List View**, displaying information on all calibration values recorded for the selected **Subject** and **Input**. *Note*: Visual cues (row highlights) are provided to indicate when **Calibration Reference** values are used together to calculate the calibration **Slope** and **Offset**. Information on when these are grouped together is provided in the **Slope/Offset** section below. Each column is explained below:
Enabled	Allows the user to enable (checked) or disabled (unchecked) calibration values without losing the record. This permits the researcher to view the Glucose signal with certain calibration values disabled in order to improve the quality of the resultant signal.
Date	Displays the Date and Time the Glucose Reference value was taken, as recorded when entering the calibration value. If necessary, this may be updated directly in the List View by left-clicking the associated Date/Time text.
Type	Displays the Type of calibration to which the associated Glucose Reference value was defined; e.g. Mult- or Single-point.
Ref Value	Displays the recorded Reference Value measured by the Glucose Reference during the Multi- or Single-point calibration process. This can be augmented directly in the List View by left-clicking the Ref Value text.
nA Value	Displays the corresponding averaged nano Ampere (nA) value recorded by the implant at the time the Ref Value was recorded.
Slope/Offset	The Slope and Offset values are calculated by Ponemah based on the recorded calibration information and are used to generate the Glucose signal from the nA signal. These cannot be modified directly, as they are calculations. Only the last entry in a set of Multi-point calibrations will report a Slope and Offset. Each set of Single-points will report a Slope and Offset. A set of Single-points meaning those recorded with the same date/time point; e.g. Reference value and Reference value 2. In the case of a set of Multi-point, the Slope and Offset are obtained calculating a regression line through the Reference (y axis) and nA (x axis) values. All consecutive Multi-points within one hour of the last Multi-point will be grouped as part of the same challenge, yielding a single Slope and Offset value. The resultant Slope and Offset values will be applied from the start of the Multi-point sequence. In the case of each Single-point calibration, the Offset remains unchanged from the previous time point and the Slope is adjusted by Calibration Damping % of the difference between the previous Slope and the Slope that would yield a 100% correction.
Error	This will list any validation errors associated with the record. These must be corrected prior to closing the Glucose Calibration dialog.

Component	Description
New Calibration	Permits the user to add additional Glucose Calibration Reference values to the selected Subject. The user can enter the Date and Time at the time of the blood draw or simply select Update Time now to automatically update these fields with the current computer time. The user would also choose the calibration Type from the dropdown box and then enter the blood glucose Reference values measured by the Glucose Reference. Once all information is entered, select the Add Calibration button to add the reference information to the Calibration List View.
Calibration Settings	Provides access to advanced calibration settings. These settings are Subject specific; i.e. changes made are only applied to the currently selected Subject.  The following describes the settings listed within this dialog
Min Cal Range	Used to ensure the Reference values entered for a Multi-point calibration span at least the specified range to be valid. In this example, the Multi-point calibration Reference values must span at least 50 mg/dL to be a valid Multi-point calibration.
Calibration Interval	Used to define the range of data averaged when retrieving the nA value that corresponds to the recorded glucose Reference value reading.

Component	Description
Calibration Damping	Used to adjust the aggressiveness of the linear scaling during the calibration process. • Can be set to a value of 0-50%, defaults to 20%. • Is only applied to the Single-point calibration values and does not affect Multi-point calibration. • If the Damping Factor is set to 0% the interpolation will be undamped and scale factor will be adjusted to compensate completely for each enabled single-point calibration value. The resulting calibrated telemetry data will pass directly through the single-point calibration value (or the average value of duplicate calibration samples). • If the Damping Factor is set to 20% the applied scale factor will compensate for all but 20% of the difference between the previously used scale factor and the scale factor calculated for this point if 0% damping were used. The resulting calibrated telemetry data will not pass directly through the single-point calibration value unless 0% damping is used. • If the Damping Factor is set to 50% the applied scale factor will compensate for all but 50% of the difference between the previously used scale factor and the scale factor calculated for this point if 0% damping were used. The resulting calibrated telemetry data will not pass directly through the single-point calibration value unless 0% damping is used. • Use of a damping factor greater than zero will minimize the amount that the glucose signal “bounces” between Single-point calibrations based on potential error in the Calibration Reference values. It may also under correct for a signal which is drifting due to loss of sensitivity.

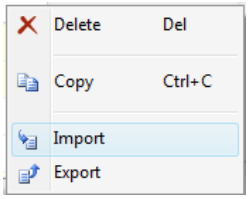
Component	Description
Use Initial Slope and Offset	Used during the calibration process to define a slope and offset to use until such time as reference values are available. The use of the initial slope and offset are not typically required, as the Ponemah calibration algorithms apply the first multipoint calibration both forward and backward in time. Below are some examples of when using this feature may prove beneficial: • User desires to have estimates of blood glucose levels reported during acquisition and prior to a multipoint calibration. • User suspects the validity of a multipoint calibration and deems not to use it in the calibration process. (reference values lost, reference values suspect, timing of reference measurements concerning, …) • A valid multipoint calibration is not available (was not performed) • Animal applied to another experiment and data directory changed. • In this case even if a valid multipoint calibration were previously performed, the data from that portion of the study is in a different directory and would not be available for calibration purposes. As such, one would obtain the slope and offset by performing a calibration in the other experiment and then could apply that slope and offset in this new experiment using the initial slope and offset feature. ***Note that in the examples above it is up to the user to define the slope and offset based upon their expert opinion and/or available data.***

Import/Export Calibration Data

IMPORT

Calibration data can be recorded using Excel during the blood draw and glucose reference measurement periods and imported into the Glucose Calibration dialog at a later time. To import Glucose Calibration Reference values:

1. Start a Review session by selecting **Actions | Start Review**
2. Select the **Glucose Calibration** toolbar icon for a **Primary** graph page.
3. Select the **Subject** to which the calibration values will be imported.
4. Right-click the **List View** within the **Glucose Calibration** dialog.
5. Select **Import**.



6. Select the file to import.
    a. **.csv files**: allows the user to import calibration values from Excel, when saved as a CSV.
    b. **.glu files**: allows the user to import calibration data previously entered using Dataquest A.R.T.

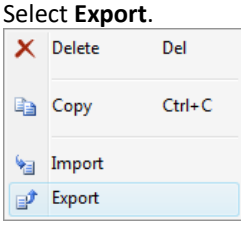
Note: .csv files should be in the following format to properly import Glucose Calibration Reference values.

	A	B	C	D
1	#DateTime	RefValue	CalType	Enabled
2	2/17/2014 9:42	101	1	1
3	2/17/2014 9:42	95	1	1
4	2/17/2014 9:52	180	1	1
5	2/17/2014 9:52	222	1	1
6	2/24/2014 8:21	95	0	1

Export

Calibration data can be exported from the Calibration dialog to a .csv file, permitting the user to view these in Excel. To export Glucose Calibration Reference values:

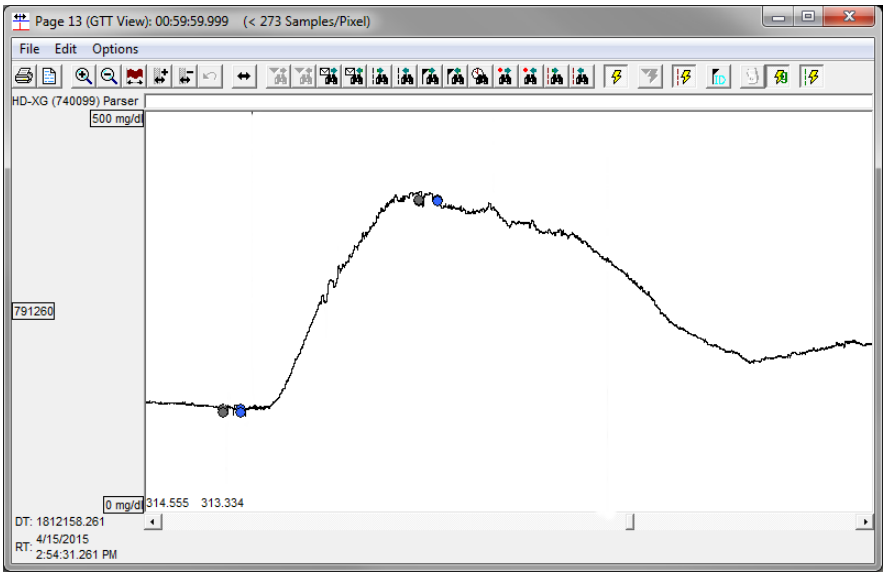
1. Within a Review session, select the **Glucose Calibration** toolbar icon for a **Primary** graph page.
2. Right-click the **List View** within the **Glucose Calibration** dialog.
3. Select **Export**.



4. Enter a **File name** and browse to the folder location desired to save the file.
5. Select **Save.**

Online Screens and Functions

The following is an example of a **Primary** graph displaying a Glucose signal during a **Glucose Tolerance Test (GTT).**

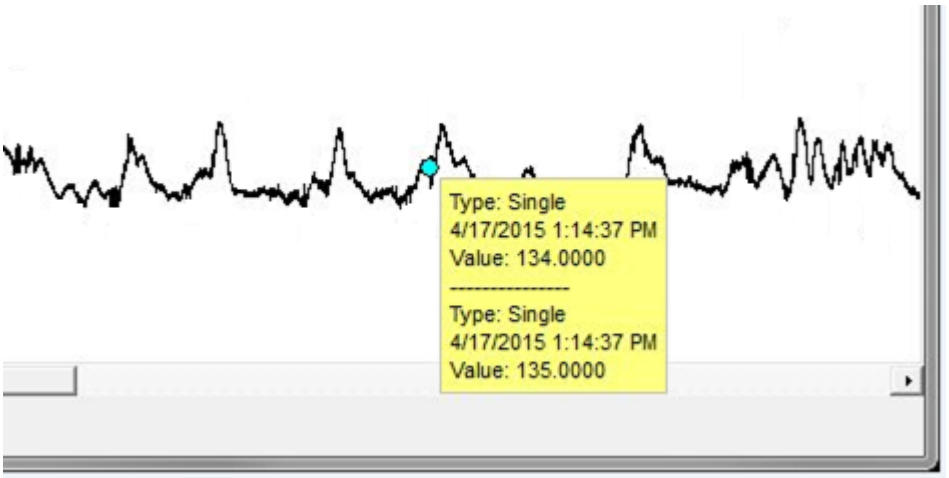


The **Validation Mark** for Glucose is the **Cycle** mark. It is not displayed to provide a full view of the signal. The circular, colored marks displayed on the waveform are **Calibration Reference Points**. These points were entered in the **Glucose Calibration** dialog and correspond to glucose measurements taken manually using a **Glucose Reference**; e.g. glucometer.

The mark color indicators are described below:

Signal	Color	Description
Blue		Enabled Single-point Reference Value
Cyan		Enabled Multi-point Reference Value
Gray		Disabled Reference Value
Red		Error with recorded Reference Value

Hovering over these marks will provide information on the reference value, as shown below:



Note: **Calibration Reference Value** marks can be toggled **ON/OFF** using the **Glucose Reference Value Toggle** toolbar icon. 

Presentation Signals

Below is a list of presentation signals that are available for the Glucose Analysis Module.

Signal	Description
nA_uc	This will display the nA input signal without the temperature correction applied.
nA	This will display the nA input signal with temperature correction applied.
Glucose	This will display the nA input signal converted to glucose readings using slope(s) and offset(s) from the Glucose Calibration dialog. The resultant units will depend on the units of the reference values entered during calibration.

Data Review

The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Primary graph page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu – Analyze [Attributes].

Mark Operations

The Cycle mark is the only mark supported by Glucose and defines a glucose cycle.

Inserting Marks

A **Cycle** mark may be inserted by right clicking at the point of insertion in the **Primary** graph's **Display Pane** of the Channel of interest. The pop-up menu that is displayed will provide the option to insert a **Cycle** mark.

Insert Glucose Cycle

Inserts a **Glucose** "cycle". When a **Glucose** cycle is inserted, it is assigned a sequential cycle number and subsequent cycle numbers are incremented.

Deleting Marks

Marks are deleted by positioning the mouse cursor on the mark to be deleted and bringing up the right click menu.

Moving Marks

Moving the **Cycle** mark is permitted between the previous **Cycle** mark/**Data Break**/**Bad Data Mark** and the following **Cycle** mark/**Data Break**/**Bad Data Mark**

Calculations

The calculations of **Derived Parameters** are identical to those performed during Acquisition.

Logging Mark

The **Logging Mark** for a **Glucose** "cycle" is the **Cycle Mark**. The time at the logging mark is the time used to report a "cycle's" derived data. If a **Glucose** "cycle's" logging mark falls within a logging interval, the **Glucose** "cycle's" data will be included in the Logging interval.

End of Cycle

The start of a **Glucose** "cycle" is at the **Cycle** mark. The end of a "cycle" depends on what follows its **Logging Mark**:

- If the **Logging Mark** is not followed by a data break or another **Logging Mark** within 600s, the "cycle" will end at the last sample within 600s of the **Logging Mark**.
- If the logging mark is followed by a **Data Break** with no intervening logging marks, the "cycle" will end on the sample that coincides with the **Data Break**.

If the **Logging Mark** is followed by a **Logging Mark** with no intervening **Data Breaks**, the "cycle" will end on the sample that precedes the **Logging Mark**.

Troubleshooting

See the Best Practices and Considerations and Alternatives for answers to common questions or the DSI Support Center.

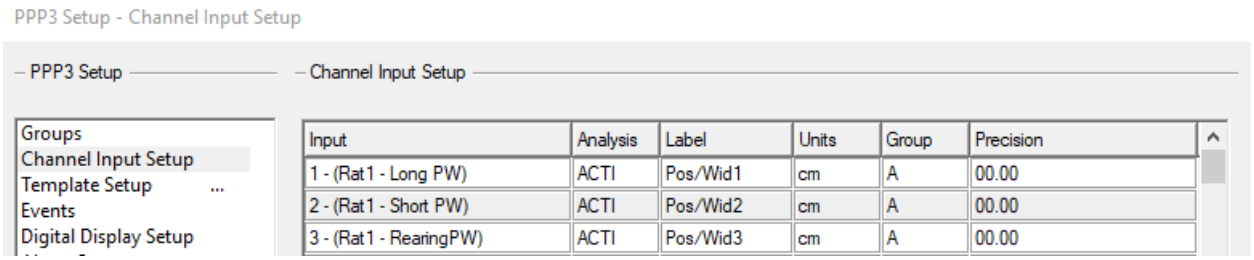
.INI File Settings

There are no settings to adjust in the .INI file for the glucose analysis module.

Actimetry (ACTI)

The **Actimetry** analysis module analyzes the locomotor activity signals that are collected from the Viva Mobile Activity Rack System (VivaMARS). A VivaMARS sensor box contains infrared sensor beams on the x and y axis at a low height (referred to as the activity level) and infrared sensor beams on the z axis at a high height (referred to as the rearing level). There are 3 channels associated with each sensor box: Long PW, Short PW and RearingPW. Channels are auto-configured every time the Actimetry Configuration window is exited by selecting OK. The auto-configure sets the Analysis, Label, Units and Group columns in the Channel Input Setup.

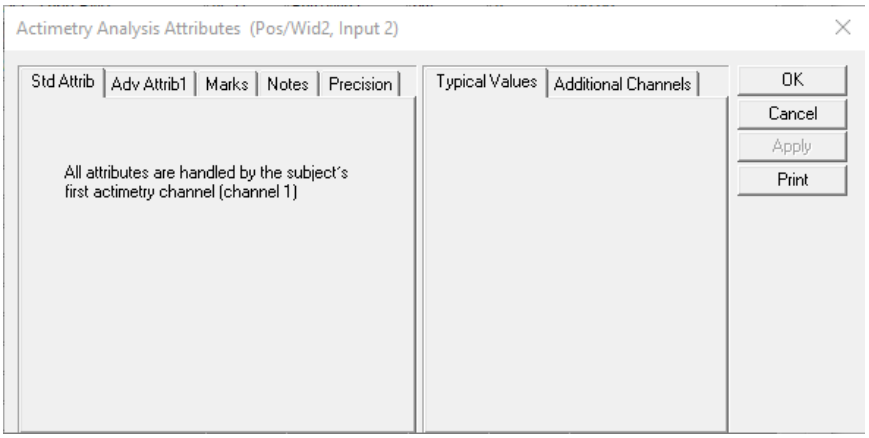
Although there are 3 channels per sensor box, the parameter calculations are reported for the first channel for each sensor box. Auto-Configure will disable all parameters for the second and third channels and will enable parameters for the first channel for each sensor box.



Attributes Dialog

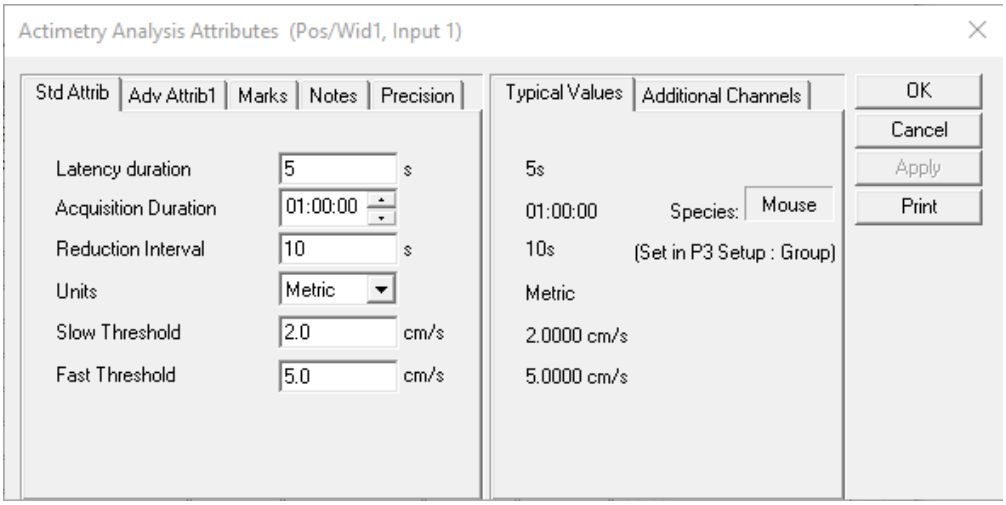
The **Actimetry Analysis Attributes** dialog allows you to modify the signal analysis for locomotor activity signals. Select the first channel for a sensor box to display Analysis attributes settings.

NOTE: The second and third channels for each sensor box are not used independently and will display the following if selected.



Analysis Attributes not used for second/third channels

Standard Attributes



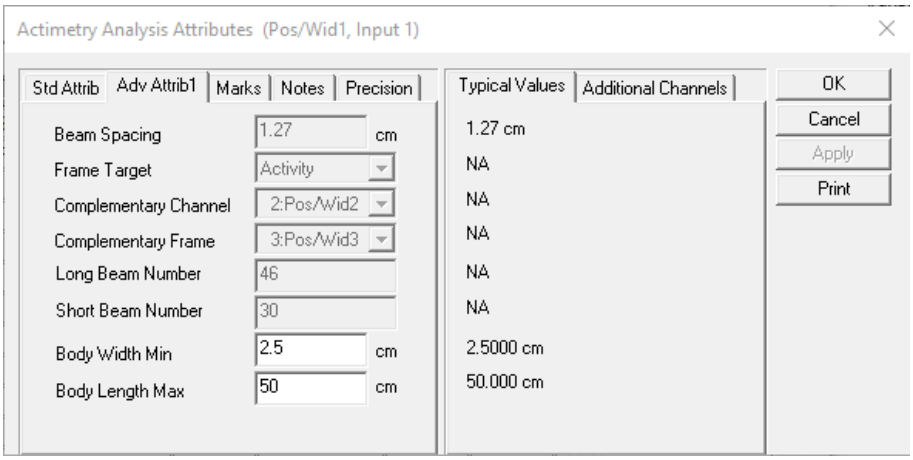
Actimetry Standard Attributes Tab

The Standard attributes allow setting the most common attributes that would need to be changed during Acquisition or Review.

Attribute	Effect On Review	Description
Latency duration	Calculations	The time interval, in seconds, between detecting a subject and marking T0 for the subject. The maximum is 999 Seconds.
Acquisition Duration	Calculations	The minimum duration the acquisition will run after the latency duration has expired. This value is used if Auto Complete Acquisition is enabled
Reduction Interval	Calculations	The smallest interval, in seconds, over which derived parameters will be reported. The reported values will be aggregated into logging intervals and data reduction intervals based on each derived parameters averaging requirements.
Units	Calculations	Units can be set as Metric or Imperial for all derived parameters; for metrics: distance is centimeter (cm) and seconds; and imperial would be in inches (in) and seconds
Slow Threshold	Calculations	The speed of the subject that will determine whether the animal speed is characterized as rest time or slow time. Units cm/s or in/s. See table below for relationship between rest time, slow time, and fast time.
Fast Threshold	Calculations	The speed of the subject that will determine whether the animal speed is characterized as fast time or slow time. Units cm/s or in/s. See table below for relationship between rest time, slow time, and fast time.

Comparison of Resting, Slow, and Fast Time definition		
Resting Time	**Slow Time**	**Fast Time**
Subject speed is less than the value defined as the **Slow threshold** set in Std Attrib	Subject speed is greater than or equal to the value defined as the **Slow threshold** but less than or equal to the value set as the **Fast Threshold** set in Std Attrib	Subject speed is greater than the value defined as the **Fast threshold** set in Std Attrib
Subject's Speed < Slow Threshold	Slow Threshold ≤ Subject's Speed ≤ Fast Threshold	Subject's Speed > Fast Threshold

Advanced Attributes



Actimetry Advanced Attributes 1 Tab

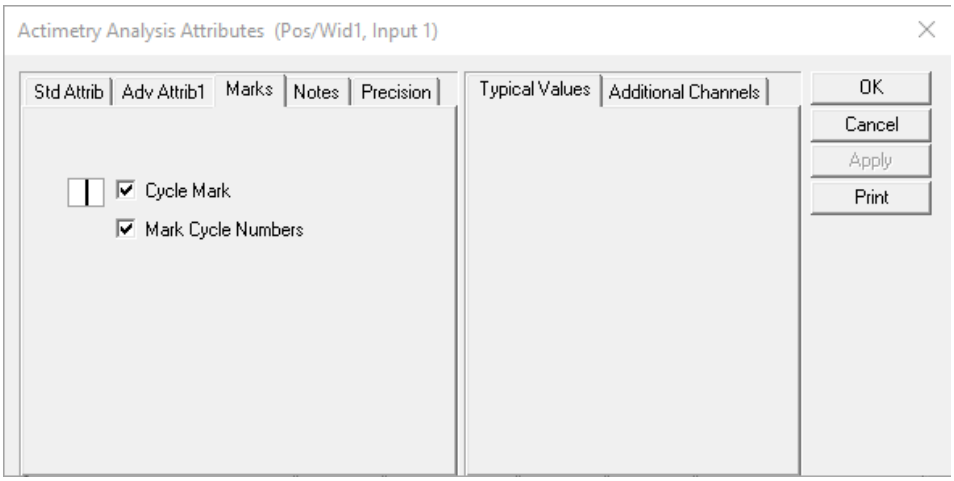
The Advanced attributes allow selection of attributes which are not commonly changed during acquisition or replay.

Attribute	Description
Beam Spacing	The distance between 2 beams; This is set from the product definition file (ProductDefinitionActimetry.xml).
Frame Target	The analysis algorithm that is chosen. This is set from the product definition file (ProductDefinitionActimetry.xml).
Complementary Channel	Select the additional channels used for calculation of the activity derived parameters. This is set from the product definition file (ProductDefinitionActimetry.xml).

Attribute	Description
Complementary Frame	Select the additional channels used for calculation of the activity derived parameters. This is set from the product definition file (ProductDefinitionActimetry.xml).
Long Beam Number	This is set from the product definition file (ProductDefinitionActimetry.xml) regarding the long axis beam count.
Short Beam Number	This is set from the product definition file (ProductDefinitionActimetry.xml) regarding the long axis beam count.
Body Width Min	This is the body width of the animal set for each specie that is coming from the product definition file (ProductDefinitionActimetry.xml).
Body Length Max	This is the length width of the animal set for each specie that is coming from the product definition file (ProductDefinitionActimetry.xml).

Marks (Validation)

The **Actimetry** analysis displays validation tick marks for each cycle. Each cycle should have only one validation mark.



Color	Meaning
Black	Cycle Mark

Derived Parameters

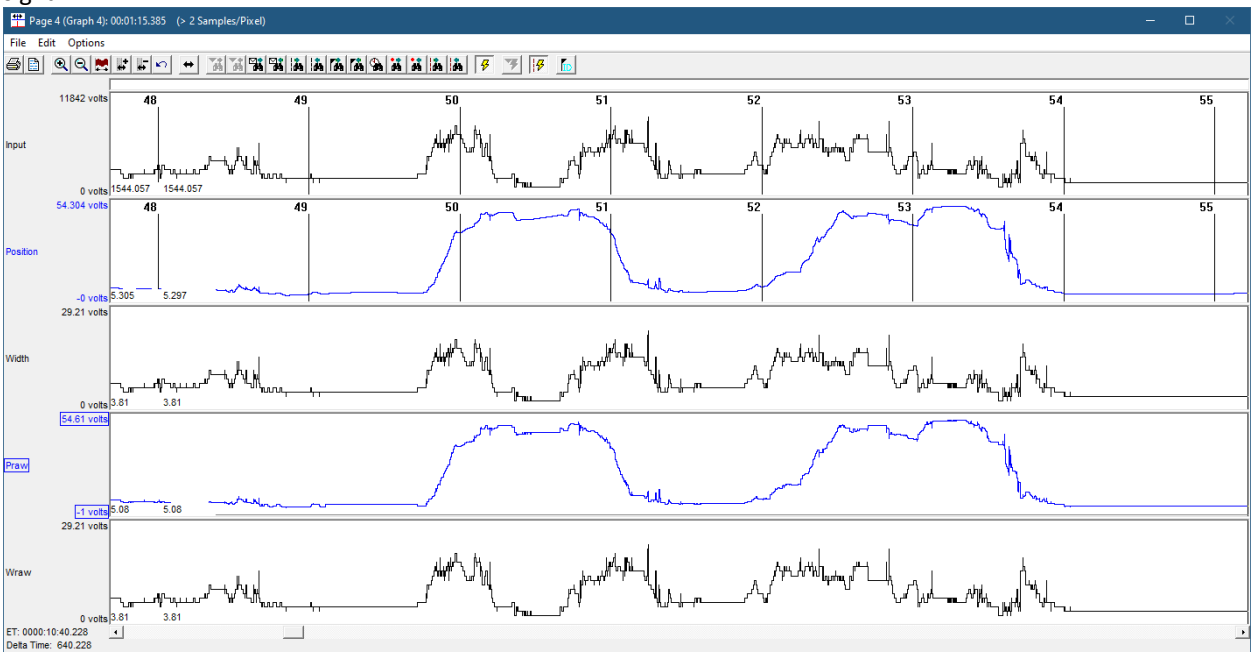
Derived parameters are selected by bringing up the **Derived Parameters** dialog box. This is done by right clicking on the analysis module or selecting the "Derived Parameters" button in the **P3 Setup** dialog. The derived parameters selected in this dialog box will be calculated.

Name	Averaging In Review	Definition
Num	Recent	The number of the cycles. This number will appear on a primary graph page when validation marks are turned on and the cycle numbers are enabled. When running in a logging mode other than 1 epoch, the last cycle number will be reported.
Activ	Sum	Sum of ActiND and ActiD
ActiND	Sum	Reports a count of activity without displacement events in an averaging interval. The count is reset at the start of an averaging interval and increments over a 200ms interval if an ActiD event does not occur within that interval and if the subject position within the interval was not static
ActiD	Sum	Reports a count of activity with displacement (locomotion) events in an averaging interval. The count is reset at the start of an averaging interval and increments when the position of the subject relative to its reference position exceeds the Displacement Threshold of 1.5cm over the preceding 200ms, resulting in an ActiD event. If an ActiD event is recorded, the reference position is set to the position at the end of the 200ms evaluation interval
Smax	Max	Maximum speed (Dist/reduction interval) observed over the reduction interval. Default is cm/s;
SMin	Min	Minimum speed (Dist/reduction interval) observed over the reduction interval. Default is cm/s;
SMean	Mean	Average speed (Dist/reduction interval) observed over the reduction interval. Default is cm/s;
Dist	Sum	Distance travelled during the averaging interval
R Time	Sum	Resting Time: Cumulative duration within the averaging interval when the subject's speed is less than or equal to the Slow threshold
R Time %	Mean	Resting Time%: Resting Time expressed as a percentage of the averaging interval
S Time	Sum	Slow Time: Cumulative duration within the averaging interval when the subject's speed is greater the Slow threshold and less than the fast threshold
S Time %	Mean	Slow Time%: Slow Time expressed as a percentage of the averaging interval
F Time	Sum	Fast Time: Cumulative time within the averaging interval when the subject's speed is greater than or equal to the fast threshold
F Time %	Mean	Fast Time%: Fast Time expressed as a percentage of the averaging interval
ReaCt	Sum	Rearing Count: Number of rearing episodes that end in the averaging interval. A rearing episode starts from the moment a subject goes from a non-rearing to a rearing position and then back to a non-rearing position.

Name	Averaging In Review	Definition
ReaAvD	Mean	Rearing Averaged Duration: Average duration of rearing episodes that end within the averaging interval. The duration of all rearing events that end within the reduction interval are averaged by the number of rearing events.
ReaT	Sum	Rearing Time: Cumulative duration of rearing samples within the averaging interval. This parameter is not related to the completion of a rearing event and will be reported exclusively based on the rearing samples within a reduction interval.
JmpCt	Sum	Jump Count: Number of jumping episodes that end within the averaging interval.
JAvgD	Mean	Jump Average Duration: Average time spent jumping during the averaging interval.
JTime	Sum	Jump Time: Cumulative time spent jumping during the averaging interval.
TRem	Recent	Time Remaining: The time required to finish acquiring data for the subject in an hh:mm:ss format. The start value equals the value entered as Acquisition Duration for the Body frame. The time, if other than 99:99:99, will decrement once T0 has been defined.;

On-Line Screens and Functions

Below example display the **Actimetry** Primary graph page type and the 5 types of presentation of the actimetry signal.



Presentation Signals

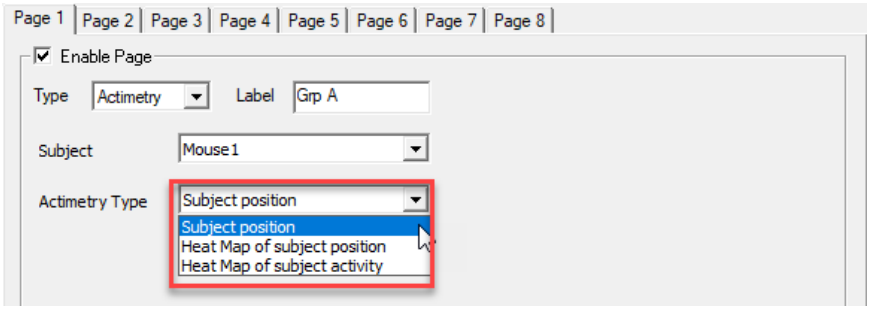
Below is a list of presentation signals that are available, but not typically used (see Default Presentation of Actimetry Graphs) for the ACTI Analysis Module:

Signal	Description
Input	The input signal of the position of the animal in real time (units in cm)
Position	Position of the animal derived from the Praw signal that has a smoothing filter applied.
Width	Position of the animal derived from the Wraw signal that has a smoothing filter applied.
Praw	Position of the animal derived from the Input signal.
Wraw	Width of the animal derived from the Input signal.

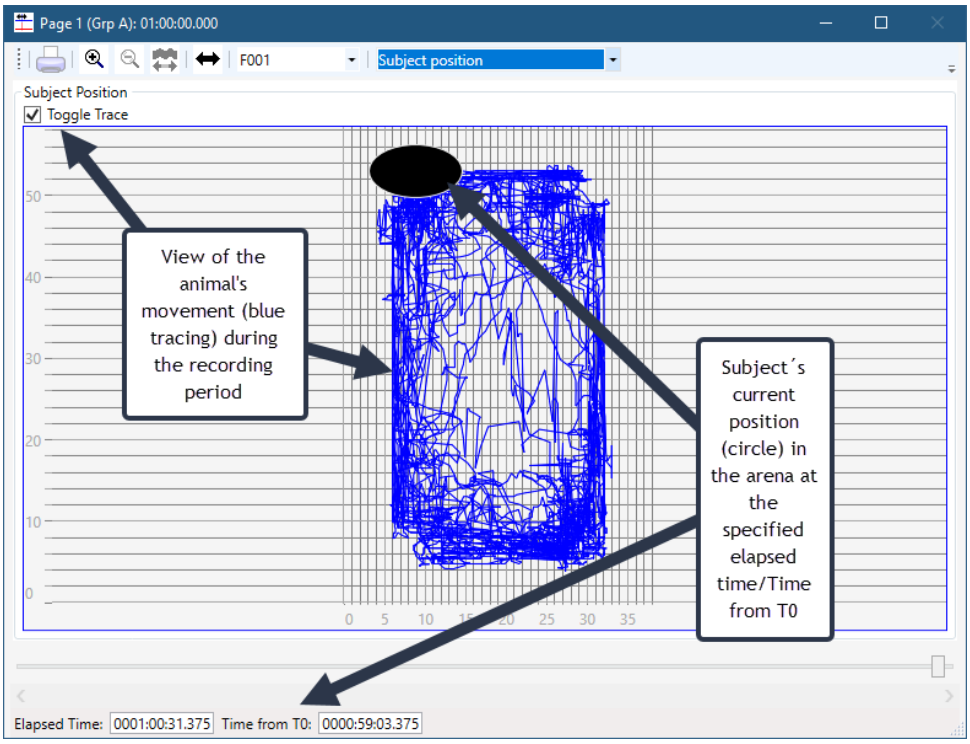
Default Presentation of Actimetry Graphs

The actimetry graph type allows for additional presentation of the actimetry data. The following tables covers the additional types of displays that are available for the ACTI Analysis Module. When selecting OK from the VivaMARS Hardware Configuration the auto-configure will set up an Actimetry graph page type with defualt display of Subject Position. This can be easily changed during acquisition and in Review.

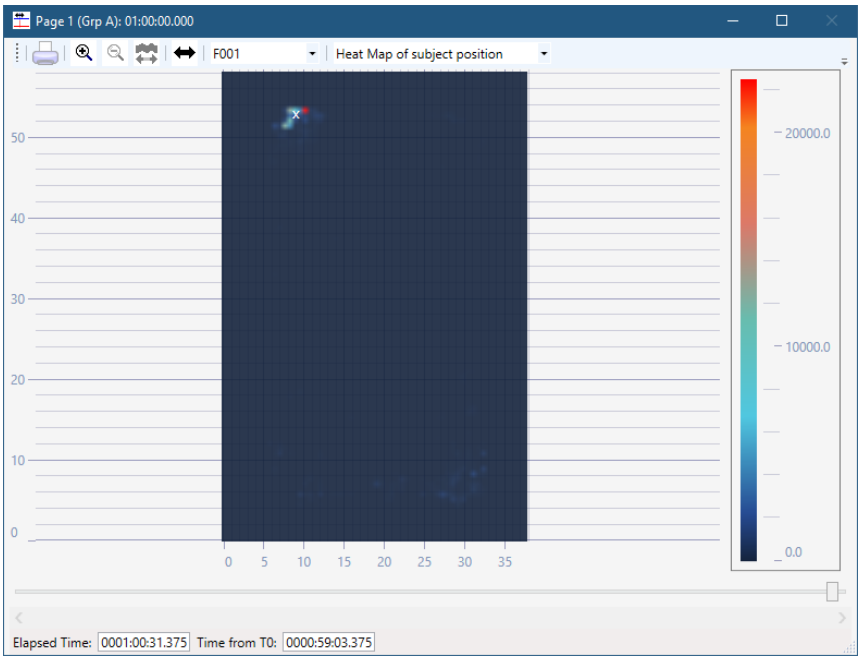
Actimetry Type	Description
Subject Position	This will display the subject indicated by a black oval shape as well as a trace of the subject movement indicated by a blue line.
Heat Map of Subject Position	This will display a heat map of the subject location over time. Areas where subject has spent more time will be on red end of heat spectrum and areas the subject has not spent much time will be on blue end of spectrum.
Heat Map of Subject Activity	This will display a heat map of the subject activity over time. Areas with high levels of activity will be on red end of heat spectrum and areas with low levels of activity will be on blue end of spectrum.



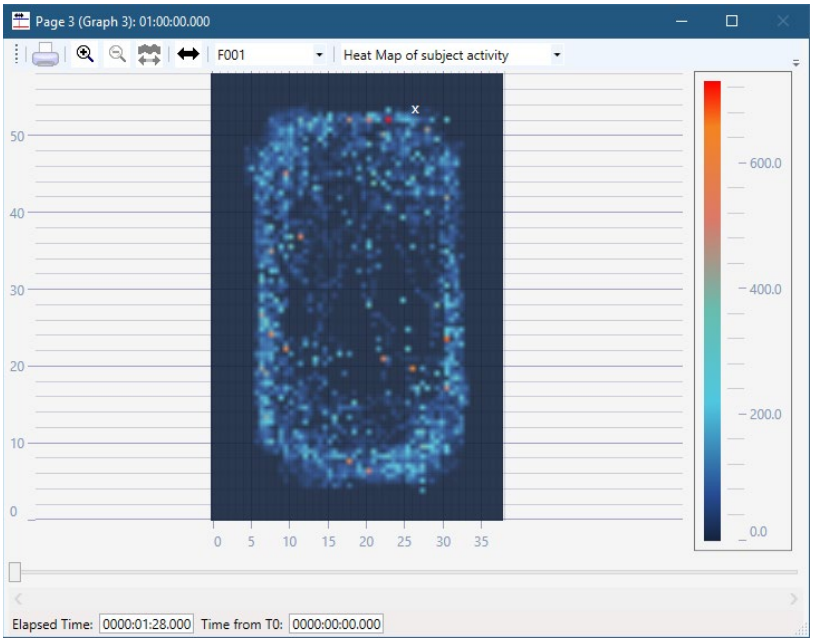
Subject Position Graph



Heat Map of Subject Position Graph



Heat Map of Subject Activity Graph



Data Review

The analysis specific portion of Data Review centers around the marks that the User is permitted to display, insert, and delete and how the User is permitted to move them.

NOTE: To calculate derived output for a timepoint, past and future samples are used. In acquisition, derived output is delayed by 2.275 seconds to accommodate the collection of future samples. In Review, since all samples are available, the delay is eliminated, this may result in a slight difference between the derived output in Acquisition and Review.

Displaying Marks and Cycle Numbers

The marks and cycle numbers displayed in a Review Primary graph page Display Pane are controlled through the Marks Tab in the Analysis Attributes dialog. The Analysis Attributes dialog is accessed through the right click menu – Analyze [Attributes].

Cycle marks cannot be moved due to its placement from the J event based on the reduction interval.

Mark Operations

The Cycle mark is the only mark supported by Actimetry.

Calculations

The calculations of **Derived Parameters** are identical to those performed during Acquisition.

Troubleshooting

Use the following table to assist in troubleshooting the analysis:

Problem	Solution
Analysis is not triggering	A **J event** must be placed for analysis to begin. J events should trigger automatically after 5 seconds of movement when subject is placed in the cage, if not a J event can be added manually.
"x" in .DER or .DRx window instead of a number	The derived number is too large for the field. An "x" was placed here, so that a truncated number would not be displayed.

.INI File Settings

When the analysis module is loaded in the application the first time, the analysis module updates the PPP3.INI file with default settings in the **[Actimetry]** section of the file. The user may change these settings if the range of the values for a specific attribute needs to be changed.

The ranges listed here only affect the values that the dialog will accept. The ranges also validate the attribute values before they are used. If the attribute values are out of range, a default value will replace the out of range value.

The table below lists the default settings and section of the .INI file:

Entry Name	Description
Slow Threshold(low)	This sets the minimum allowable value for Slow Threshold in cm/sec. The default value is 0
Slow Threshold(high)	This sets the maximum allowable value for Slow Threshold in cm/sec. The default value is 10
Fast Threshold(low)	This sets the minimum allowable value for Fast Threshold in cm/sec. The default value is 0
Fast Threshold(high)	This sets the maximum allowable value for Fast Threshold in cm/sec. The default value is 10
Latency Duration(low)	This sets the minimum allowable value for Latency Duration. The default value is 0
Latency Duration(high)	This sets the maximum allowable value for Latency Duration. The default value is 999
Acquisition Duration(low)	This sets the minimum allowable value for Acquisition Duration. The default value is 0
Acquisition Duration(high)	This sets the maximum allowable value for Acquisition Duration. The default value is 90000
Reduction Interval(low)	This sets the minimum allowable value for Reduction Interval. The default value is 0
Reduction Interval(high)	This sets the maximum allowable value for Reduction Interval. The default value is 9999
Beam Separation(low)	This sets the minimum allowable value for Beam Spacing. The default value is 1
Beam Separation(high)	This sets the maximum allowable value for Beam Spacing. The default value is 2
Minimum Body Width(low)	This sets the minimum allowable value for Body Width Min. The default value is 0.0
Minimum Body Width(high)	This sets the maximum allowable value for Body Width Min. The default value is 60.0
Maximum Body Length(low)	This sets the minimum allowable value for Body Length Max. The default value is 0.0

Entry Name	Description
Maximum Body Length(high)	This sets the maximum allowable value for Body Length Max. The default value is 60.0
Long Beam Number(Low)	This sets the minimum allowable value for Long Beam Number. The default value is 0
Long Beam Number(high)	This sets the maximum allowable value for Long Beam Number. The default value is 10000
Short Beam Number(low)	This sets the minimum allowable value for Short Beam Number. The default value is 0
Short Beam Number(high)	This sets the maximum allowable value for Short Beam Number. The default value is 10000

Contact Information

We are available to help you with your questions and concerns. Should you hit a roadblock or need some additional training, please feel free to visit the DSI Support Center at https://support.datasci.com to find articles and helpful information in our knowledge base, chat with an agent, or setup time to receive one-on-one consultation. We are happy to help!

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