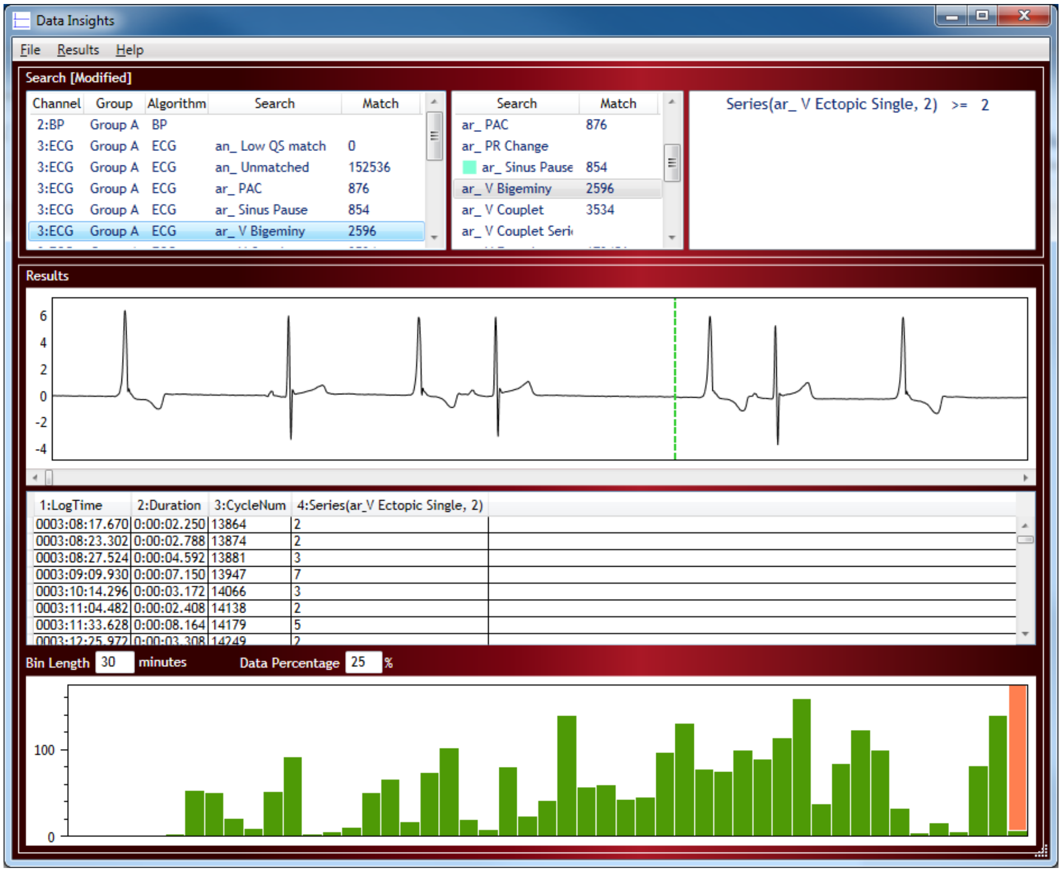
DSI

Data Insights

Model: PNM-110-INSIGHTS
Manual: 007703-001
Revision: 1



Channel	Group	Algorithm	Search	Match
2:BP	Group A	BP		
3:ECG	Group A	ECG	an_ Low QS match	0
3:ECG	Group A	ECG	an_ Unmatched	152536
3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ Sinus Pause	854
3:ECG	Group A	ECG	ar_ V Bigeminy	2596

Search	Match
ar_ PAC	876
ar_ PR Change	
🟩 ar_ Sinus Pause	854
ar_ V Bigeminy	2596
ar_ V Couplet	3534
ar_ V Couplet Seri	

Series(ar_ V Ectopic Single, 2) >= 2

1:LogTime	2:Duration	3:CycleNum	4:Series(ar_V Ectopic Single, 2)
0003:08:17.670	0:00:02.250	13864	2
0003:08:23.302	0:00:02.788	13874	2
0003:08:27.524	0:00:04.592	13881	3
0003:09:09.930	0:00:07.150	13947	7
0003:10:14.296	0:00:03.172	14066	3
0003:11:04.482	0:00:02.408	14138	2
0003:11:33.628	0:00:08.164	14179	5
0003:12:25.972	0:00:03.308	14249	2

Bin Length 30 minutes

Data Percentage 25 %

DSI™

Data Sciences International
119 14th Street NW, Suite 100
St. Paul, MN 55112
Phone: +1 (651) 481-7400
US: +1 (800) 262-9687
Email: support@datasci.com
www.datasci.com

Data Sciences International
119 14th Street NW, suite Suite 100

St. Paul, MN 55112
P:
Phone: +1 (651) 481.-7400 • F:
US: +1 (651) 481.7404800) 262-9687
Email:

Contents

Overview

Introduction

Data Insights is a tool that can be used to locate, classify, and report on normal or abnormal cycles to provide greater insight into data. Data Insights can be used for:

- Data analysis and validation.
- Arrhythmia, data pattern, anomaly detection, classification, and reporting.

Installation

To install **Data Insights**, please install the following:

- Ponemah v5.20
- Service Pack 7 or greater

In order to access **Data Insights**, this option must be enabled in the license file.

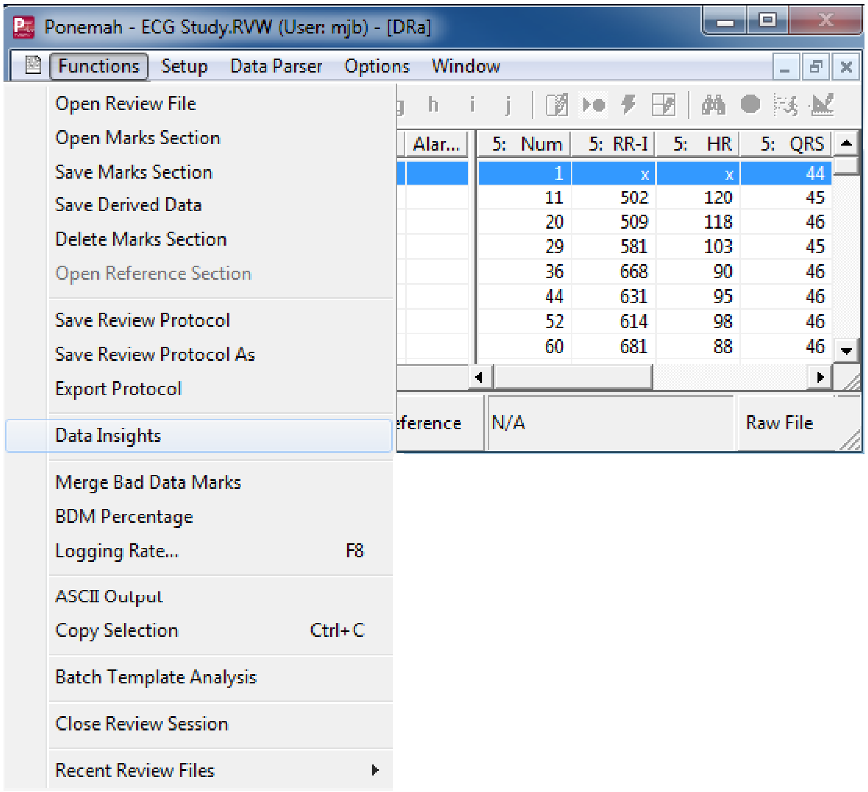
NOTE: **Data Insights** is a **Review** only feature and is only compatible with Ponemah v5.20-SP7 or greater. **Data Insights** in not compatible with the Ponemah v6 software platform.

Feature Overview

Launching Data Insights

Functions Menu

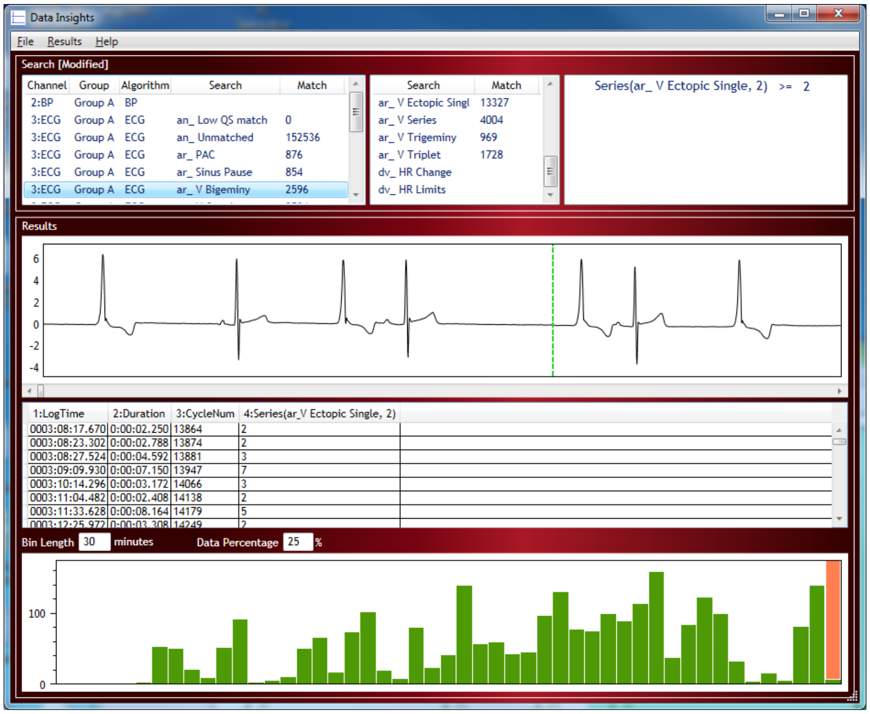
Data Insights is accessed from the **Functions** pull-down menu when in Review. All active channels loaded into Review will be available for use within **Data Insights**.



Alar...	5: Num	5: RR-I	5: HR	5: QRS
	1	x	x	44
	11	502	120	45
	20	509	118	46
	29	581	103	45
	36	668	90	46
	44	631	95	46
	52	614	98	46
	60	681	88	46

Data Insights Dialog

After selecting **Data Insights** from the **Functions** menu, the dialog below is displayed allowing configuration of the search criteria. After associating a search with a channel, information matching the search criteria is automatically displayed in graphical and table format.



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3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ Sinus Pause	854
3:ECG	Group A	ECG	ar_ V Bigeminy	2596

Search	Match
ar_ V Ectopic Singl	13327
ar_ V Series	4004
ar_ V Trigeminy	969
ar_ V Triplet	1728
dv_ HR Change	
dv_ HR Limits	

Series(ar_ V Ectopic Single, 2) >= 2

1:LogTime	2:Duration	3:CycleNum	4:Series(ar_V Ectopic Single, 2)
0003:08:17.670	0:00:02.250	13864	2
0003:08:23.302	0:00:02.788	13874	2
0003:08:27.524	0:00:04.592	13881	3
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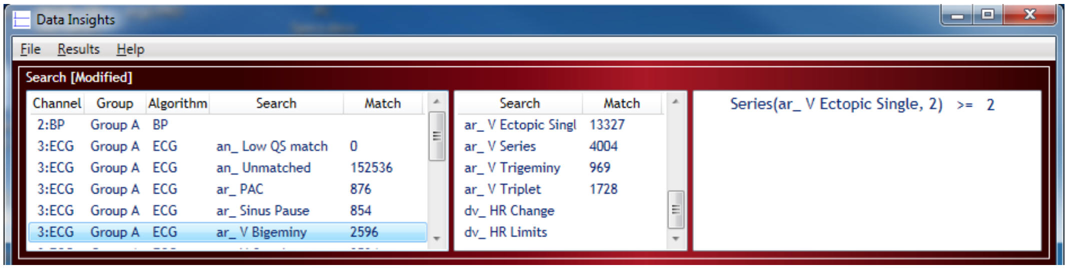
0003:10:14.296	0:00:03.172	14066	3
0003:11:04.482	0:00:02.408	14138	2
0003:11:33.628	0:00:08.164	14179	5
0003:12:25.972	0:00:03.308	14249	2

Bin Length 30 minutes Data Percentage 25 %

Search Window

The window is divided into two sections, **Search** and **Results**. The **Search** portion of the dialog contains channel/search association information (left grid), search and match results (middle grid), and the rule search definition of the currently selected search (right grid). This window provides a means to define search criteria and associated searches to channels in order to obtain a desired match or set of matches.



Channel	Group	Algorithm	Search	Match
2:BP	Group A	BP		
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ar_ V Triplet	1728
dv_ HR Change	
dv_ HR Limits	

Series(ar_ V Ectopic Single, 2) >= 2

Channel/Search Association Grid

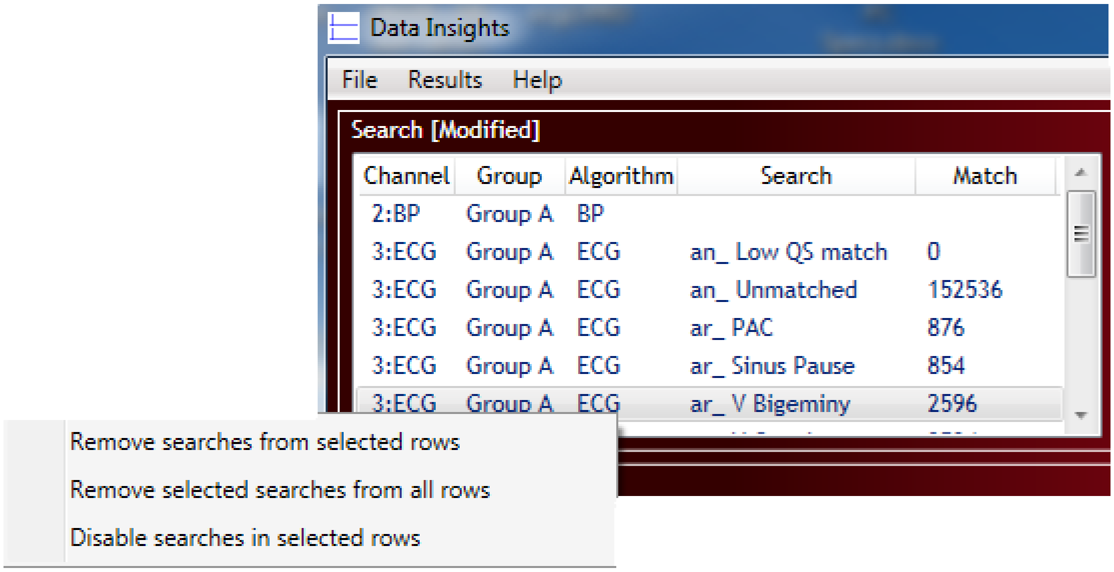
The Channel/Search Association grid includes the physical channel from the **PPP3 Setup** menu, the **Group** name, analysis module assigned to that channel and all searches that have been applied to that channel. In the above example, the **V Bigeminy** search has been applied to channel 3.

Searches are applied to a channel by click-and-dragging one of the searches from the middle Search and Match Results grid to the channel of interest. Selection of multiple searches is also supported to apply two or more at the same time by multi-selecting the searches of interest. Dragging-and-dropping the search to a single channel will apply that search only to that channel, while dropping it on the grid header will apply that search to all channels loaded into Review to which that search is applicable.

NOTE: Searches are specific to a channel and specie type. For example, searches constructed using ECG parameter information cannot be applied to pressure channels. Searches should be created specific to both specie and signal type. Searches that do not match the signal type will not be allowed to be dragged and dropped on that channel.

Once associated with a channel, the search name will appear under the **Search** column next to the channel information. Analysis will automatically be performed and the number of occurrences matching the search criteria will be listed under **Match**.

Once a **Search** has been associated with a channel, right clicking the mouse on any of the **Searches** will display a pop-up menu that allows the **Search** to be removed or disabled across one or multiple channels.



Channel	Group	Algorithm	Search	Match
2:BP	Group A	BP		
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3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ Sinus Pause	854
3:ECG	Group A	ECG	ar_ V Bigeminy	2596

Clicking on the column headers will sort the columns in alphabetical or numerical order depending on the content of the column that is sorted. Click the column header once to sort from descending to ascending values. Click the header a second time to sort in ascending to descending order.

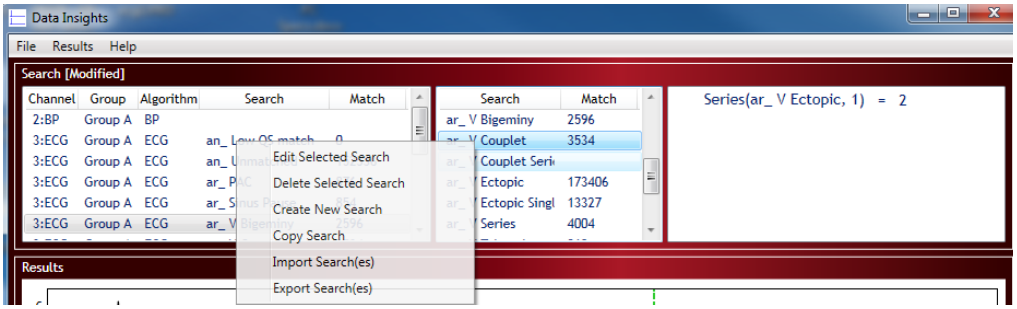
Search and Match Grid

This section of the dialog displays the names associated with the defined **Searches** and the total number of occurrences matching that rule or search criteria. If the same rule is applied across multiple channels, the **Match** field will list the total number of matches across all of those channels.

A list of predefined Searches is present by default and available for use. To learn more about the default Searches, please see the **Default Searches** section of this manual.

Edit Selected Search

Double left click the mouse (or right click for more options) to access the criteria used for each Search or use the right click option to select **Edit Selected Search**.

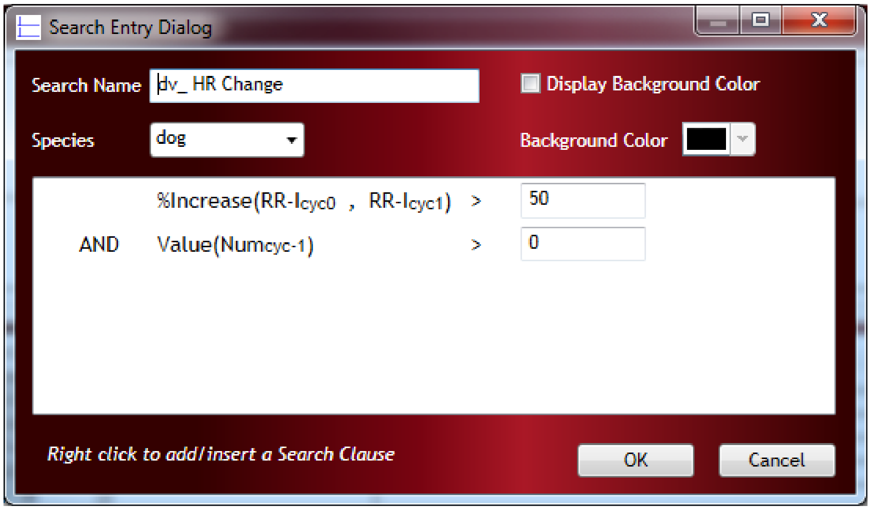


Channel	Group	Algorithm	Search	Match
2:BP	Group A	BP		
3:ECG	Group A	ECG	an_ Low QS match	0
3:ECG	Group A	ECG	an_ Unmatched	
3:ECG	Group A	ECG	ar_ PAC	
3:ECG	Group A	ECG	ar_ Sinus Pause	854
3:ECG	Group A	ECG	ar_ V Bigeminy	2596

Search	Match
ar_ V Bigeminy	2596
ar_ V Couplet	3534
ar_ V Couplet Seri	
ar_ V Ectopic	173406
ar_ V Ectopic Singl	13327
ar_ V Series	4004

Series(ar_ V Ectopic, 1) = 2

The **Search Entry Dialog** displayed below shows the criteria used to define the **dv_HR Change** search. A set of conditions is defined to locate changes in the RR Interval from one cycle to the next in this search. To be a valid match in this example, a change of greater than 50% in the RR Interval from the current cycle (RR-Icyc0) to the following cycle (RR-Icyc1), as well as the Cycle Number from the previous cycle greater than a value of 0 must be met. Left-click on any of the desired fields to begin editing the criteria.



Search Entry Dialog

Search Name: dv_ HR Change

☐ Display Background Color

Species: dog

Background Color: ■

%Increase(RR-I$_{cyc0}$, RR-I$_{cyc1}$) > 50

AND Value(Num$_{cyc-1}$) > 0

Right click to add/insert a Search Clause

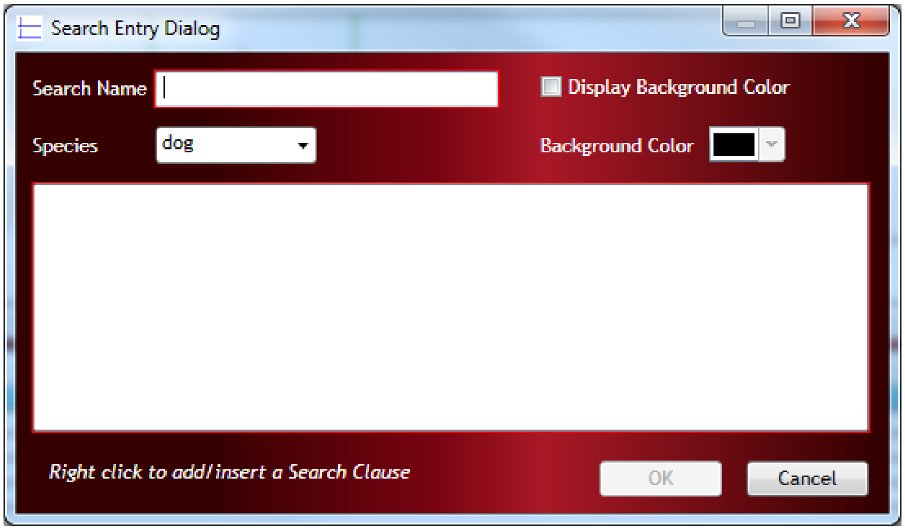
Delete Selected Search

The Delete Selected Search allows you to remove the selected search from the list. Once removed, the search will no longer appear in the list and be available for use. In addition, if the Search was associated to any channel or group of channels, that search will be removed from analysis and all data associated with that search will be removed.

Create new Search

Custom Searches can also be created based on user defined criteria and added to this list. Select **Create New Search** from the right-click menu.

NOTE: Any edit field that expects input to be provided will be outlined in red. Below, the **Search Name** and field to enter search criteria are both highlighted along the border of the edit field in red.



Search Entry Dialog

Search Name:

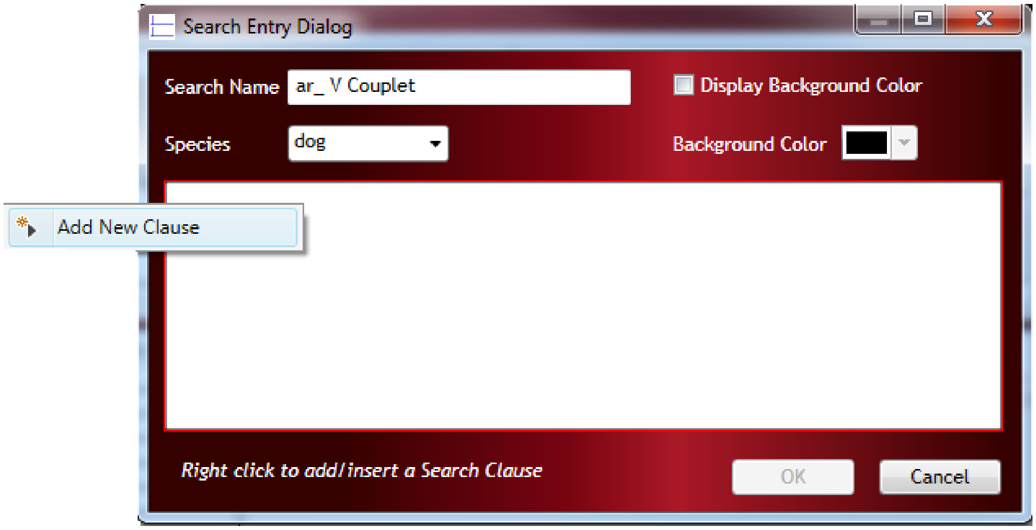
☐ Display Background Color

Species: dog

Background Color: ■

Right click to add/insert a Search Clause

To begin creating a custom search, enter a name that will be used to identify the search in the list. Next, right click within the the main edit field and choose **Add New Clause** to begin constructing search clauses. A complete search clause is needed in order to save the search. The OK button will not be available until all edit boxes expecting information have been updated completely.



Search Name: ar_ V Couplet

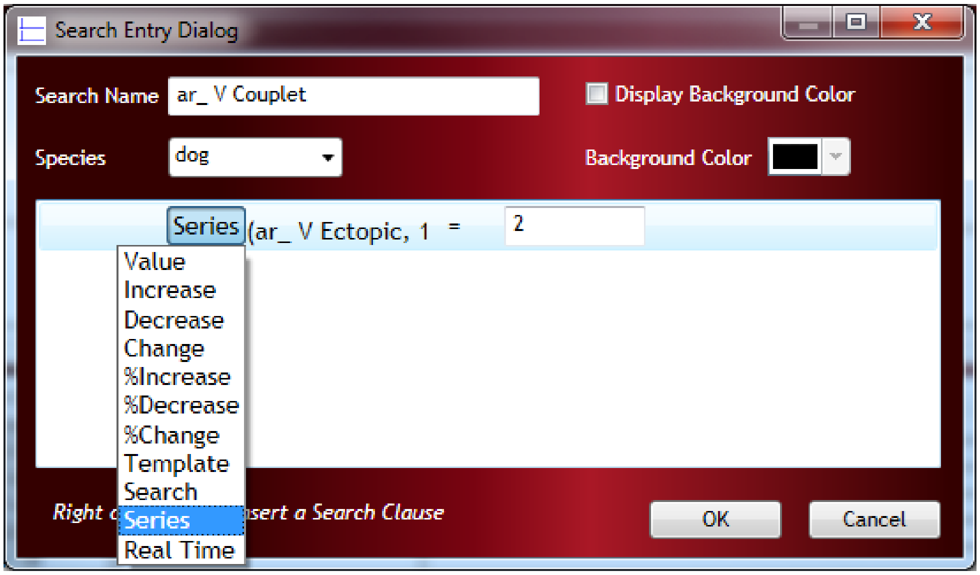
Species: dog

☐ Display Background Color

Right click to add/insert a Search Clause

In the image below, a function must be selected. Click on each function to edit the specific clause. Depending on the function selected, the right portion of the menu will change. If only looking for a **Value**, the Algorithm, Parameter and Range only need to be defined. If comparing changes from cycle to cycle (or logged data), you must define the current cycle of interest and the position of the comparison cycle. For exmple, comparing the current cycle to the previous cycle would be an offset of 1 (cycle -1) from the current cycle (cycle 0). This will allow you to create specific criteria for a given cycle(s) or range of data and compare that criteria to previous and/or following data to recognize specific abnormalities or complexes of interest. To learn more about creating custom searches, please see the Creating a New Search section of this manual.

NOTE: It is important to note that Searches are specific to a channel and specie type. For example, searches constructed using ECG parameter information cannot be applied to pressure channels. Searches should be created specific to both specie and signal type. Searches that do not match the signal type will not be allowed to be dragged and dropped on that channel.


Search Entry Dialog

Search Name: ar_ V Couplet

☐ Display Background Color

Species: dog

Background Color

Series (ar_ V Ectopic, 1 = 2

Functions

The basic functions are defined below. Note that these are not discrete functions and can be grouped together with other predefined searches or with custom searches.

Search Types

- **Value:** Represents a given value for a parameter. For example, a Search can be constructed to find all cycles with Systolic pressures greater than 180mmHg.
- **Increase:** Represents an increase in value from parameter 1(**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Decrease:** Represents an decrease in value from parameter 1 (**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Change:** Represents a change in value from parameter 1 (**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Percent Increase:** Represents a percent increase in value from parameter 1 (**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Percent Decrease:** Represents a percent decrease in value from parameter 1 (**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Percent Change:** Represents a percent change in value from parameter 1 (**From:**) to parameter 2 (**To:**). For example, this is used to compare the current RR Interval value to the previous RR Interval value or RR-Icyc0, RR-Icyc-1.
- **Template:** Used in conjunction with ECG PRO, Template searches can be performed to pull specific complexes that have been identified and labeled with “Tags” using ECG PRO
- **Search:** Utilized existing Searches, such as **HR Check** or **Atrial Beat**, as part of the search criteria. Current Searches may be pulled in and used just like creating any other rule and can be used in conjunction with other defined criteria.

- **Series:** Used to define sequences or patterns within the data. For example, this can be used for finding couplets or triplets within the dataset.
- **Real Time:** Used to find cycles within a specific time range such as during light or dark cycles. Can be used to define other periods as well, such as baseline or a defined period of time after a dose event.

Search Criteria

- **Algorithm:** Analysis module used to analyze the channel (ECG, BP, LVP, etc.).
- **Parameter:** Derived parameter calculated by the software (Heart Rate, Systolic, or R Height).
- **Range:** Specifies whether cycle information, averaged data, or standard deviation will be used for purposes of determining the type of change desired. The clause will look at changes from the reference cycle to a surrounding cycle, or logged based data from the derivations table.

Data Value Criteria

- **Cycle:** Uses cycle information to determine offset for comparison. For example, "**cyc0**" refers to the current cycle under investigation. "cyc-1" will compare the current cycle (**cyc0**) to the previous cycle (cyc-1).
- **Average:** Utilizes the logged, or averaged, data found in the DRx spreadsheet. This is dependent on the **Logging Rate** defined by the system. This function is similar to **Cycle** by determining your current value versus an offset value but utilizes averaged data values.
- **Standard Deviation:** Utilizes Standard Deviation values when comparing data.
- **Offset:** Used to specify the location of the cycle relative to the cycle of interest. An Offset of 0 denotes the current cycle of interest. An offset of -1 denotes the cycle just prior to the current cycle

Copy Search

The **Copy Search** function copies the currently highlighted Search in the list. Once copied, the duplicate Search will be visible below the copied Search and be denoted by "_Copy" added to the end of the Search name. This allows you to utilize previously constructed Searches without needing to start from the beginning.

Import Search(es)

The **Import Search(es)** function allows users to import searches. Searches can be created locally and saved to an .xml file in the Ponemah directory or the directory where the program is installed, by default. Saved Searches can then be copied to additional systems or network locations and imported on other Ponemah systems.

NOTE: When importing searches, referenced searches must also be present in the.xml file that is being imported. If the referenced search is not contained in the xml file, the search or searches using the missing reference will not be loaded. Additionally, none of the searches in the .xml file being imported should be present in the current **Search** list. Remove any duplicates before importing. In some cases it may be advisable to remove all searches prior to importing a new list.

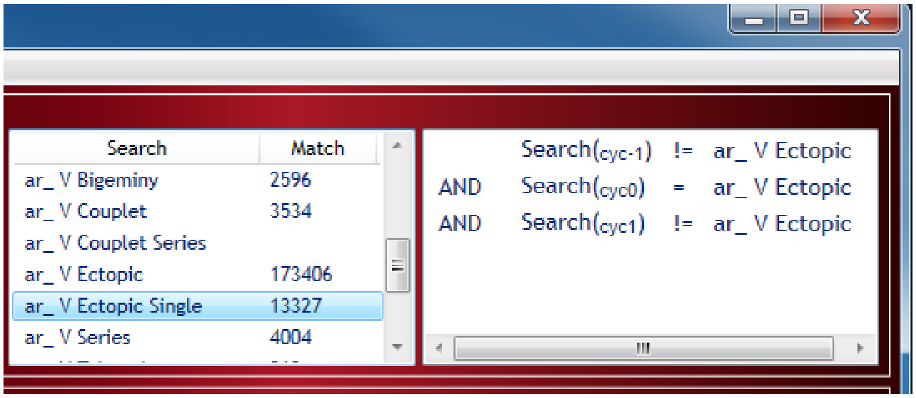
Export Search(es)

The **Export Search(es)** function allows users to export searches. Searches can be created locally and saved to an .xml file in the Ponemah directory or the directory where the program is installed, by default. Searches can also be saved to other locations, including network locations. Exported Searches can then be imported to other systems.

NOTE: When importing searches, referenced searches must also be present in the.xml file that is being imported. If the referenced search is not contained in the xml file, the search or searches using the missing reference will not be loaded. Additionally, none of the searches in the .xml file being imported should be present in the current **Search** list. Remove any duplicates before importing.

Search Definition

Displays the Search Definition created for a given search without the need to access the search itself. Click on any predefined search under the **Search** header and the rule information will be displayed to the right.

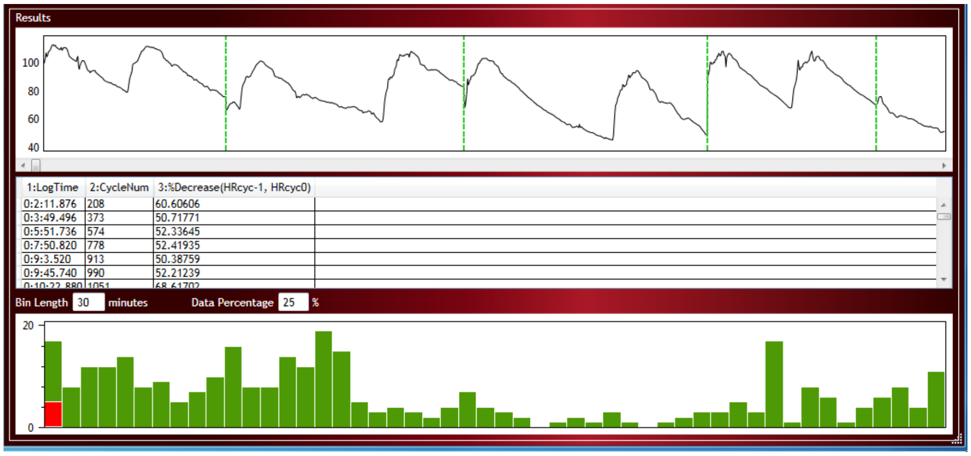


Search	Match
ar_ V Bigeminy	2596
ar_ V Couplet	3534
ar_ V Couplet Series	
ar_ V Ectopic	173406
ar_ V Ectopic Single	13327
ar_ V Series	4004

Search($_{cyc-1}$) != ar_ V Ectopic
AND Search($_{cyc0}$) = ar_ V Ectopic
AND Search($_{cyc1}$) != ar_ V Ectopic

Results Window

The Results portion of the dialog contains graphical and numerical information based on the results from the searches that have been performed.



1:LogTime	2:CycleNum	3:%Decrease(HRcyc-1, HRcyc0)
0:2:11.876	208	60.60606
0:3:49.496	373	50.71771
0:5:51.736	574	52.33645
0:7:50.820	778	52.41935
0:9:3.520	913	50.38759
0:9:45.740	990	52.21239
0:10:22.880	1051	68.61702

Bin Length 30 minutes Data Percentage 25 %

Waveform Data

Displays the waveform data that matches the search criteria assigned to that channel. Dashed green lines indicate the cycles that match the search criteria for a contiguous time segment. The number of segments displayed in the graphical view corresponds to the number of matches found and listed under the **Match** heading in the Channel/Search Association section of the dialog.

Data is displayed in this window by clicking on a specific channel from the channel list above the graphical window. Only one signal is viewed at a time. Data is scaled in user units.

Scrolling Functions

A scroll bar below the window is used to move through the data by using the mouse and dragging the scroll bar left or right. A single mouse click on the waveform data will highlight the waveform data as well as highlight and synchronized the numerical data listed below. Double left clicking the mouse on either the waveform data or the numerical data in this view will also synchronize with the DRx and Data Reduction files as well as with all other graph pages configured in Ponemah.

Additionally, depress the Control key and left click the mouse on any portion of the waveform to get x and y axis information at that point.

Mouse Wheel

Scrolling up with the mouse wheel will move forward in the dataset. Scrolling down using your mouse wheel will move backward, or towards the beginning of the data.

Page Up and Page Down

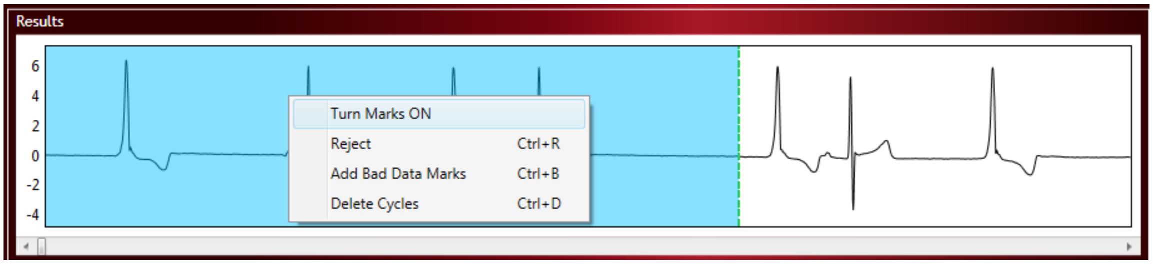
The **Page Up** and **Page Down** keys can also be used to move through the waveform data. Use the **Page Up** key to move forward in the data. Use the **Page Down** key to move backwards in the data, or towards the beginning of the dataset.

Arrow Keys Left and Right

The **Left Arrow** and **Right Arrow** keys can also be used to move through the waveform data. Use the **Right Arrow** key to move forward in the data. Use the **Left Arrow** key to move backwards in the data, or towards the beginning of the dataset.

Right Click Functions

Right click the mouse to access additional functionality for viewing and manipulating the cycle or cycles of interest.



Turn Marks ON

Toggles validation marks on and off of the waveform data.

NOTE: Validation Marks cannot be manipulated within the Data Insight dialog. To augment cycle marks, sync the match to the Primary graph by double-clicking the match and update the marks within the Primary graph page.

Reject

Removes the cycle or cycles from the **Match** information. Cycles will be removed from not only the graphical presentation but also from the table and **Match** information as well. You will note the number under the **Match** column decrease when a match is rejected. Rejecting a Match does not affect the derived data outside of the Data Insights dialog.

Add Bad Data Marks

Add Bad Data Marks will remove cycles from the search. Using this feature will also add Bad Data Marks in the graph pages outside of the Data Insights dialog, as well as the derived data tables (DRx and Data Reduction tables). This feature functions the same as using Bad Data Marks in Review (outside of using Data Insights).

Delete Cycles

The **Delete Cycles** function allows validation marks to be removed from cycles without adding Bad Data Marks. Affected data will also be removed from the DRx and Data Reduction tables, in addition to the **Match** information.

Graphical Scaling Functions

In addition to the Right and Left Mouse clicks mentioned above, the mouse and keyboard can be used to zoom in and out on the waveform data.

Ctrl + Mouse Wheel

Using the Control key and the mouse wheel will allow you to zoom in and out on the data. With the **Ctrl** key depressed, use the mouse wheel up to zoom out. With the **Ctrl** key depressed, use the mouse wheel down to zoom in on the data.

Left Click-and-Drag

You may also **Left Click**-and-drag your mouse to zoom in on the waveform. This functions in the same manner as zooming in on the waveforms when working with the graph pages in Review. While holding the Left mouse button, drag either left or right in the waveform data. The area will change color as you drag your mouse. When the desired amount of data is selected, let go of the mouse button to zoom in on the area highlighted.

NOTE: You cannot zoom out using this functionality. Use the Ctrl key with the mouse wheel to zoom out as described above.

Numerical Data

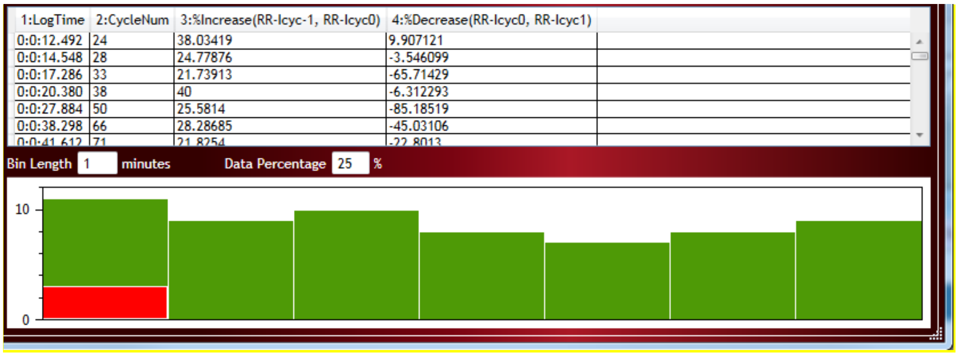
The numerical or table information provides results of the searches that have been applied to the channels. The data presented changes based on the criteria described in the search and is identified by the header listed at the tip of each column.

A scroll bar is available at the far right side of the table and can be used to scroll up or down in the data. Clicking on the column headers will sort the data from descending to ascending order and a second click will sort the data from ascending to descending order. Clicking on the **LogTime** column header will sort the data by time from beginning to the end of the dataset. A second click will sort the data from the end of the dataset to the beginning of the dataset.

NOTE: Sorting the numerical data will also sort the graphical results, providing a method to view the graphic results in a sorted order based on the numerical header. For example, in the Results Distribution Histogram Screenshot, sorting on the %Increase of RR Interval header will sort the graphical data in order based on the %Increase.

Results Distribution Histogram

The **Results Distribution Histogram** graph provides a visual of the entire data collection period binned in user defined time segments. Users can specify the interval, in minutes, to review the results of the searches, provide information as to the current location in the dataset when the search results are found, and also determine if an adequate amount of data is present in the binned intervals.



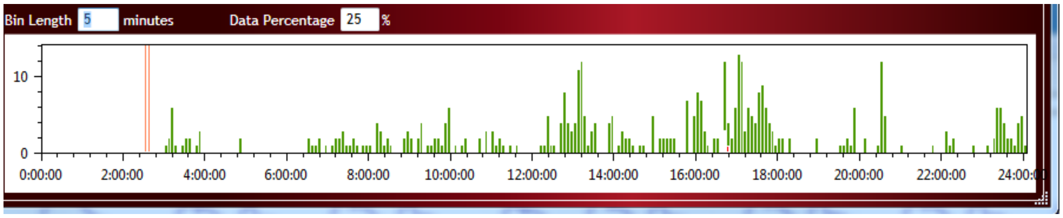
1:LogTime	2:CycleNum	3:%Increase(RR-Icyc-1, RR-Icyc0)	4:%Decrease(RR-Icyc0, RR-Icyc1)
0:0:12.492	24	38.03419	9.907121
0:0:14.548	28	24.77876	-3.546099
0:0:17.286	33	21.73913	-65.71429
0:0:20.380	38	40	-6.312293
0:0:27.884	50	25.5814	-85.18519
0:0:38.298	66	28.28685	-45.03106
0:0:41.612	71	21.8254	-22.8013

Bin Length 1 minutes Data Percentage 25 %

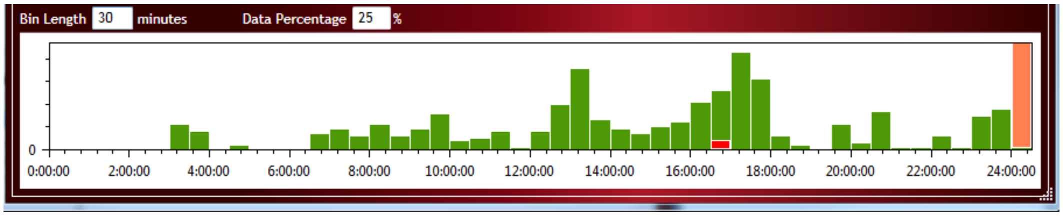
Bin Length

The **Bin Length** specifies the amount of time, in minutes, for viewing the results of the searches that have been executed. This graph provides information on the number of results found per bin, as well as a representation of how much data is present in each bin.

With longer duration datasets, longer **Bin Lengths** may be needed to more easily view and work with the data. In the examples below, the **Bin Lengths** have been set to 5 minute and 30 minute intervals for comparison.



Bin Length 5 minutes Data Percentage 25 %



Bin Length 30 minutes Data Percentage 25 %

To modify the **Bin Length**, simply type in the desired length, in minutes, and the graphical component will update automatically.

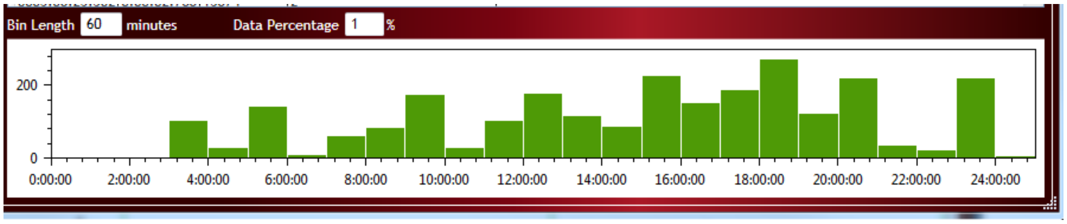
Data Percentage

Data Percentage is specified in terms of the percentage of viable data within a specific bin. A setting of 25% states that at least 25% of the data contained within that binned time frame contains viable data. Deletion of data due to Bad Data Marks or using the Noise feature reduces the amount of viable data. Additional information on the features of the **Distribution Histogram** graph is outlined below.

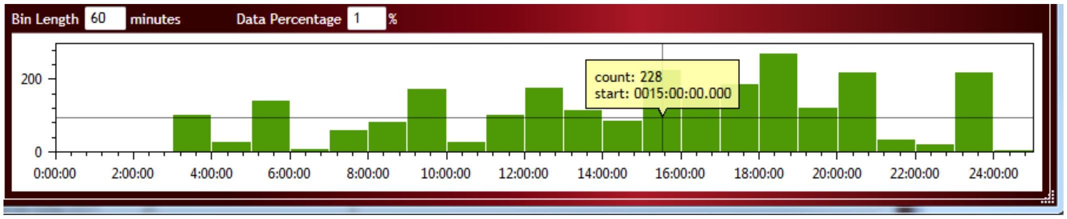
Distribution Histogram

The **Distribution Histogram** contains information on the search results as mentioned previously. To view the results, select a specific search that has been executed under the **Search** portion of the dialog. Selecting a specific search will update the waveform graph, numerical data, and bin graph with the appropriate information.

The green bins correspond to the number of matches found in any given bin. In the example below, the Y axis displays the scale for the number of matches found over the entire dataset. The X axis always displays the entire duration of the data collection. Scheduled acquisitions will not be displayed in their compressed form but will display the entire time span for that collection.


Bin Length 60 minutes Data Percentage 1 %

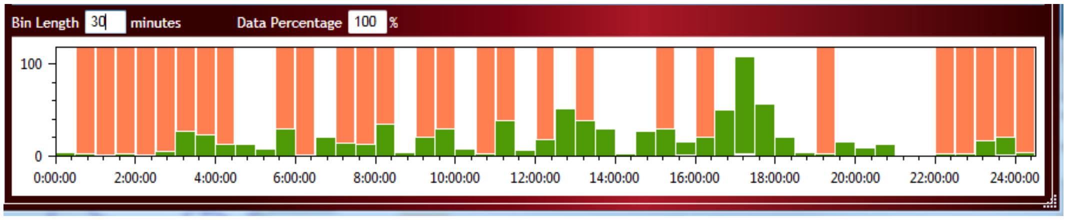
Left-click the mouse and hold for information on the search results for a given bin. In the example below, 228 matches were found for the search. The start time for each bin is also provided.


Bin Length 60 minutes Data Percentage 1 %

count: 228
start: 0015:00:00.000

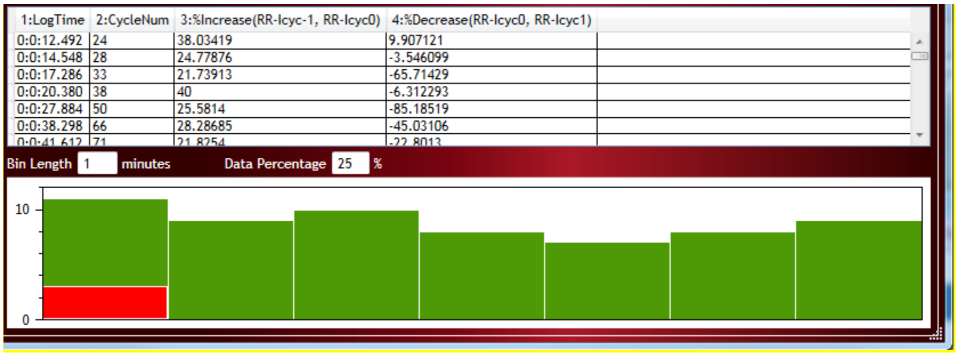
Coral colored segments provide information on bins that do not contain the amount of data specified in the **Data Percentage** field. For example, setting the Data Percentage to 25% would display coral colored bins if less than 25% of the data is available within the binned time frame.

To illustrate this, the Data Percentage was changed to 100% in the image below. Therefore, all data within each bin must be present and not removed from analysis. Viewing the graph below, the majority of the segments do not have access to all data within that binned time frame. This does not affect the search results. This provides information where areas of noise or bad data occurs to determine if excluding information from these noisy areas is desired.


Bin Length 30 minutes Data Percentage 100 %

Red colored segments are displayed within the green bins and represent the location of the currently displayed match(es) currently being viewed in the graphical results section. If red segments are not visible, it is likely that too few matches are visible within the graphical results window as compared to the total number of matches present within each bin, making the red match indicator more difficult to view. To see the match indicator, reduce the size of your bins or zoom out within the graphical results section to bring more matches into the viewing area.

The red segment updates automatically based on your location in the graphical results. Using one of the scrolling functions to move forward or backward in the dataset in the waveform graph will also move the location of the red segment to the green bin location where the match was found.



1:LogTime	2:CycleNum	3:%Increase(RR-Icyc-1, RR-Icyc0)	4:%Decrease(RR-Icyc0, RR-Icyc1)
0:0:12.492	24	38.03419	9.907121
0:0:14.548	28	24.77876	-3.546099
0:0:17.286	33	21.73913	-65.71429
0:0:20.380	38	40	-6.312293
0:0:27.884	50	25.5814	-85.18519
0:0:38.298	66	28.28685	-45.03106
0:0:41.612	71	21.8254	-22.8013

Bin Length 1 minutes

Data Percentage 25 %

If sorting is performed on the numerical results section, red segments may appear in multiple bins since data is no longer sorted in chronological order. This provides an easy way to see if the results with the highest or lowest match values are spread throughout the dataset or are localized to a particular area. To restore chronological order, simply click on the **LogTime** column header.

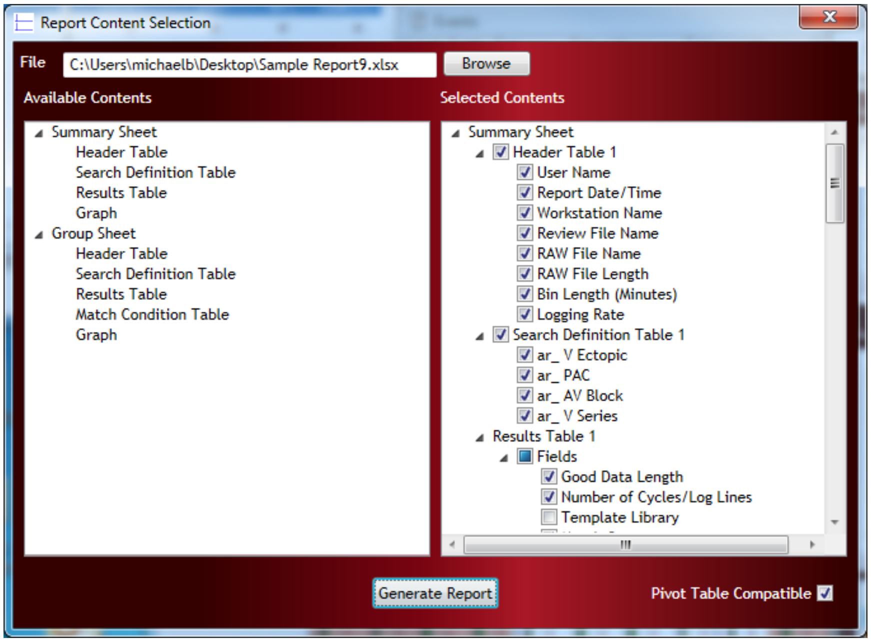
File Pull-down Menu

The **File** menu provides access to the report functionality. Selecting **Report** will open the **Report Content Selection** dialog. This dialog allows customization of the report output including file information, search criteria, graphical information, and table information.

A report name and file location can be inputted and a report generated in Microsoft® Excel format. To enable specific output, ensure that the feature is checked. Uncheck to remove the information from the report output.

Additional content can be added by right-clicking a content section from the Available Contents column and choosing **Add**. This provides a method to generate specific tables and graphs based on your needs. For instance, instead of graphing all arrhythmia types on a signle summary graph, you may wish to have a summary graph to display only Ventricular Ectopics from all groups (subjects) and another graph to display the occurences of AV Blocks across all groups (subjects). This can be done by adding addition Graph contents and making the appropriate selections.

The output can be configured ready to create Pivot Tables for additioanl analysis or for importing into other programs. If this is desired, check the Pivot Table Compatible checkbox.



File C:\Users\michaelb\Desktop\Sample Report9.xlsx

Available Contents

- Summary Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Graph
- Group Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Match Condition Table
  - Graph

Selected Contents

- Summary Sheet
  - ☑ Header Table 1
    - ☑ User Name
    - ☑ Report Date/Time
    - ☑ Workstation Name
    - ☑ Review File Name
    - ☑ RAW File Name
    - ☑ RAW File Length
    - ☑ Bin Length (Minutes)
    - ☑ Logging Rate
  - ☑ Search Definition Table 1
    - ☑ ar_ V Ectopic
    - ☑ ar_ PAC
    - ☑ ar_ AV Block
    - ☑ ar_ V Series
  - Results Table 1
    - ■ Fields
      - ☑ Good Data Length
      - ☑ Number of Cycles/Log Lines
      - ☐ Template Library

Pivot Table Compatible ☑

Summary Sheet

Header Table 1

The **Summary Sheet** provides general information that is populated in the Summary tab that includes the user of the system, date and time, workstation information and file information.

- **User Name:** User logged in when report is generated.
- **Report Date/Time:** Date and time in regional settings.
- **Workstation Name:** Computer name.
- **Review File Name:** Name and data path.
- **Raw File Name:** Name and data path.
- **RAW File Length (Minutes):** Time reported in hh:mm:ss (24 hour time clock).

Search Definition Table

The **Search Definition Table** provides a listing of the Searches and their definitions that are currently selected and applied to a channel or group of channels. Only those searches that are applied to a channel will be available for inclusion in the report.

- Provides the name and definition of the Searches used in analysis

Results Table

- **Good Data Length:** Sum of the data times data outside of Bad Data Marks.
- **Number of Cycles/Log Lines:** Sum of the cycles or logged lines of data.
- **Template Library:** Template information only when executing Template based searches. Note that a valid template must be applied and bound to a channel.
- **Match Count:** Number of matches for the Search and Channel combination.

- **Match Percentage:** Percentage of the number of cycles matched (total number of cycles or logged lines).
- **Max Bin Value:** Max value listed for the Bin Value.
- **Max Bin Percentage:** Max Bin Value as a percentage of cycles in the bin.

Graph

This function provides graphical output from the results of the search data. By default, one graph is enabled. Multiple graphs can be enabled to better represent the information being graphed.

Group Sheet

Header Table 1

The **Summary Sheet** provides general information that is populated in the Summary tab that includes the user of the system, date and time, workstation information and file information.

- **User Name:** User logged in when report is generated.
- **Report Date/Time:** Date and time in regional settings.
- **Workstation Name:** Computer name.
- **Review File Name:** Name and data path.
- **Raw File Name:** Name and data path.
- **RAW File Length (Minutes):** Time reported in hh:mm:ss (24 hour time clock).

Search Definition Table

The **Search Definition Table** provides a listing of the Searches and their definitions that are currently selected and applied to a channel or group of channels. Only those searches that are applied to a channel will be available for inclusion in the report.

- Provides the name and definition of the Searches used in analysis.

Results Table

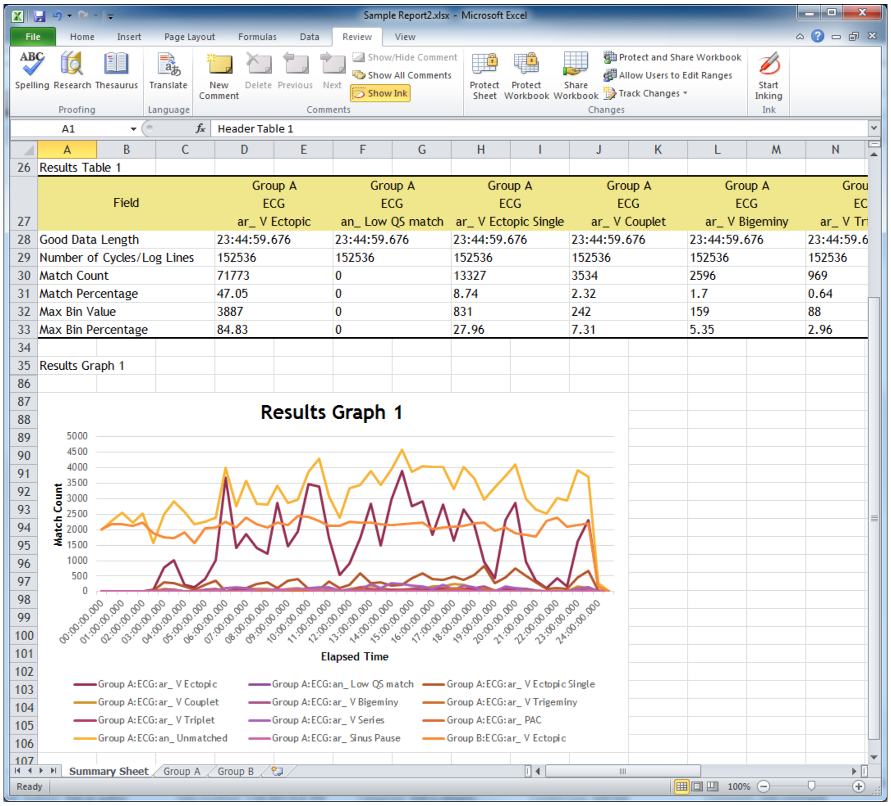
- **Good Data Length:** Sum of the data times data outside of Bad Data Marks.
- **Number of Cycles/Log Lines:** Sum of the cycles or logged lines of data.
- **Template Library:** Template information only when executing Template based searches. Note that a valid template must be applied and bound to a channel.
- **Match Count:** Number of matches for the Search and Channel combination.
- **Match Percentage:** Percentage of the number of cycles matched (total number of cycles or logged lines).
- **Max Bin Value:** Max value listed for the Bin Value (Length).
- **Max Bin Percentage:** Max Bin Value as a percentage of cycles in the bin.
- **Bin x Value:** Provides the value reported for each bin
- **Bin x Data Length:** Provides the time for each bin based on the **Bin Length**
- **Bin x Data Percentage:** Provides percentage of data in each bin

Match Condition table

This table displays the specific searches used and the conditions for the searches. In addition this table logs the time the match was found, the duration, and the value for each match.

Graph

The graph function provides graphical output from the results of the search. The Summary worksheet provides a comprehensive graph based on the selections checked. Individual graphs are also created and can be configured to include one or more results of the searches. If additional graph pages are desired, right click on **Graph** under the **Available Contents** menu and select **Graph**.



Results Table 1

Field	Group A ECG ar_ V Ectopic	Group A ECG an_ Low QS match	Group A ECG ar_ V Ectopic Single	Group A ECG ar_ V Couplet	Group A ECG ar_ V Bigeminy	Grou EC ar_ V Tr
Good Data Length	23:44:59.676	23:44:59.676	23:44:59.676	23:44:59.676	23:44:59.676	23:44:59.6
Number of Cycles/Log Lines	152536	152536	152536	152536	152536	152536
Match Count	71773	0	13327	3534	2596	969
Match Percentage	47.05	0	8.74	2.32	1.7	0.64
Max Bin Value	3887	0	831	242	159	88
Max Bin Percentage	84.83	0	27.96	7.31	5.35	2.96

Results Pull-down Menu

The **Results** pull-down menu provides access to **Results** and **Rejected Results**. The default setting is set to **Results**. This displays the graphical and table information that matches the criteria from active searches. The ability to reject data from your search is also available. Once rejected, this data is removed from your search and graphical and table information is updated accordingly. Selecting **Rejected Results** allows you to view data that has been manually rejected for a given search.

NOTE: Adding or removing search clauses will result in all rejected data to be removed. Changing values in the clauses will not affect those results that have been rejected.

Operation

Search Creation and Modification

Predefined searches are installed with the installation and activation of Data Insights. Searches can be created or existing searches can be modified and saved as part of the configuration. These searches may also be exported and imported on additional workstations (see **Import Search(es)**. Several examples will be discussed showing some of the available options. Searches can be constructed using any or all combinations of the available criteria. The types of searches constructed will depend on the results of the data desired.

Predefined searches are listed under the **Search** column in the top portion of the Data Insights menu. These predefined searches contain a prefix to help group their anticipated function. These prefixes are defined as follows:

- dv_: Represents searches used for the purpose of data validation
- ar_: Represents searches used to locate arrhythmias
- an_: Represents searches to aid in analyzing problematic data when used in conjunction with ECG PRO (see manual MU00279 for complete information on using ECG PRO).

Searches

Predefined Searches are provided with the installation of Data Insights. The searches can be used immediately for purposes of data validation, arrhythmia detection and other purposes. The following searches are defined below:

Default Searches

Analysis Searches

- **an_Low P match** (Low P Match - requires ECG PRO): Searches for high value P templates. While building a Template Library it is good to use the default Minimum Match % of 85%, this helps keep matched results well marked. Using the Low P Match Search to look for new templates to add ensures the use of low noise cycles that are significantly different from existing templates, i.e. cycles with a match of 84.9% will not be used
- To view the distribution of low P matches
- Select a match result from a region with many match results for inclusion as a new template

Species	Definition		
Dog		Value($PMatch_{cyc0}$)	< 70
Monkey	AND	Value($Noise_{cyc0}$)	< 30
Rat	AND	Value(Num_{cyc-1})	> 0
Mouse			

- **an_Low QS match** (Low QS Match - requires ECG PRO): searches for high value QS templates. While building a Template Library it is good to use the default Minimum Match % of 85%, this helps keep matched results well marked. Using the Low QS Match Search to look for new templates to add ensures the use of low noise cycles that are significantly different from existing templates, i.e. cycles with a match of 84.9% will not be used.

  - Used to view the distribution of low QS matches
  - Select a match result from a region with many match results for inclusion as a new template

Species	Definition			
Dog	(	Value(QMatch$_{cyc0}$)	< 70	
Monkey	OR	Value(SMatch$_{cyc0}$)	< 70	)
Rat	AND	Value(Noise$_{cyc0}$)	< 100	
Mouse				

  - **an_Unmatched** (Unmatched Cycles - requires ECG PRO): Searches for unmatched cycles
  - For viewing the distribution of unmatched cycles
  - Aids in selecting templates

Species	Definition		
Dog		Value(Match$_{cyc0}$)	< 100
Monkey			
Rat			
Mouse			

- **an_Unmatched Clean** (Clean Unmatched Cycles - requires ECG PRO): Searches for unmatched cycles with low noise
  - To view the distribution of clean unmatched cycles
  - Select a match result from a region with many match results for inclusion as a new template

Species	Definition		
Dog		Value(Match$_{cyc0}$)	< 100
Monkey	AND	Value(Noise$_{cyc0}$)	< 20
Rat			
Mouse			

- **an_Low T Match** (Low T Match - requires ECG PRO): Searches for high value T templates. While building a Template Library it is good to use the default Minimum Match % of 85%, this helps keep matched results well marked. Using the Low T Match Search to look for new templates to add ensures the use of low noise cycles that are significantly different from existing templates, i.e. cycles with a match of 84.9% will not be used.
  - To view the distribution of low matches
  - Select a match result from a region with many match results for inclusion as a new template

Species	Definition		
Dog Monkey Rat Mouse		$\text{Value}(\text{TMatch}_{\text{cyc0}})$	< 70
	AND	$\text{Value}(\text{Noise}_{\text{cyc0}})$	< 30
	AND	$\text{Value}(\text{Num}_{\text{cyc1}})$	> 0

Arrhythmia Searches

- **ar_AV Block 1st** (First Degree AV Block): The First Degree AV Block search looks for a long PR interval that is not an isolated P wave.
    - Requires well place Q and P marks

Species	Definition		
Dog		$\text{Value}(\text{PR-I}_{\text{cyc0}})$	> 130
	AND	$\text{Value}(\text{PR-I}_{\text{cyc0}})$	< 250
	AND	$\text{Value}(\text{Num}_{\text{cyc-1}})$	> 0
	AND	$\text{Value}(\text{Noise}_{\text{cyc0}})$	< 30
Monkey		$\text{Value}(\text{PR-I}_{\text{cyc0}})$	> 100
	AND	$\text{Value}(\text{PR-I}_{\text{cyc0}})$	< 200
	AND	$\text{Value}(\text{Num}_{\text{cyc-1}})$	> 0
	AND	$\text{Value}(\text{Noise}_{\text{cyc0}})$	< 30
Rat	Not supported		
Mouse	Not supported		

- **ar_AV Block 2nd**(Second Degree AV Block): The second degree AV Block search looks for a long PR interval and depends on the use of Template Specific Attributes to mark an isolated P wave.
    - Requires well place Q and P marks
    - Requires P marks placed on isolated waves

Species	Definition		
Dog		$\text{Value}(\text{PR-I}_{\text{cyc0}})$	> 250
	AND	$\text{Value}(\text{Num}_{\text{cyc-1}})$	> 0
	AND	$\text{Value}(\text{Noise}_{\text{cyc0}})$	< 30

Monkey		Value(PR-I_{cyc0})	> 200
	AND	Value(Num_{cyc-1})	> 0
	AND	Value(Noise_{cyc0})	< 30
Rat		Value(PR-I_{cyc0})	> 100
	AND	Value(Num_{cyc-1})	> 0
	AND	Value(Noise_{cyc0})	< 30
Mouse		Value(PR-I_{cyc0})	> 100
	AND	Value(Num_{cyc-1})	> 0
	AND	Value(Noise_{cyc0})	< 30

- **ar_Junctional** (Junctional Beat): The Junctional beat search looks for a sinus beat (non-ventricular) that either does not have a P or has a P with a markedly shortened PR interval relative to the local average. The value used in the noise clause can be used to exclude cycles that have poorly marked P waves due to noisy data.
    - Sort results by %Decrease in PR interval, largest to smallest (requires well place Q and P marks and ar_V Ectopic Search). Note that all cycles with no P wave will be listed as Nan (not a number) after cycles with P waves
    - Reject cycles with insufficient shortening or mismarked P waves
    - When dealing with noisy data, it helps to sort by Noise and to work through clean data until either the signal or marking becomes unreliable

Species	Definition			
Dog	(	Value(PCt_{cyc0})	= 0	
Monkey	OR	%Decrease(PR-I_{avg0}, PR-I_{cyc0})	> 35	)
Rat	AND	Search($_{cyc0}$)	!= ar_ V Ectopic	
Mouse	AND	Value(Noise_{cyc0})	< 30	
	AND	Value(Num_{cyc-1})	> 0	

- **ar_PAC** (Premature Atrial Contraction): The Premature Atrial Contraction search looks for a marked shortening in RR sandwiched between 2 beats that do not show much change in RR. The expectation is that the premature atrial beat was preceded by a sinus beat and that it reset the sinus node and as a result was followed by a sinus beat as well.

  This search works well when dealing with a subject that has a steady heart rate. In the presence of Respiratory Sinus Arrhythmia, this search may yield false positives, however the ability to sort on the % decrease in RR makes it possible to quickly scan through the large decreases in RR. Note that focusing on only the large changes and rejecting the rest may result in the loss of some PACs.

  - Sorts results by %Decrease in RR-I, from largest to smallest (Requires R wave marks)
  - Identify the cutoff between normal sinus variation and premature beats
  - Reject matches below the threshold

Species	Definition		
Dog		%Decrease(RR-I$_{\text{cyc-1}}$, RR-I$_{\text{cyc0}}$)	> 30
Monkey	AND	%Change(RR-I$_{\text{cyc-1}}$, RR-I$_{\text{cyc1}}$)	< 25
Rat	AND	Value(Num$_{\text{cyc-2}}$)	> 0
Mouse	AND	Value(Noise$_{\text{cyc0}}$)	< 100

- **ar_V Interpolated** (Ventricular Interpolated): Identifies Ventricular beat that is inserted within normal sinus beats (non-ventricular) beats. The search assumes that adjacent RR intervals are from sinus.
  - Requires ar_V Ectopic and ar_V Ectopic Single

Species	Definition		
	%Decrease(RR-I$_{\text{cyc-1}}$, RR-I$_{\text{cyc0}}$)		> 40
	AND	%Change(RR-I$_{\text{cyc0}}$, RR-I$_{\text{cyc1}}$)	< 35
	AND	%Decrease(RR-I$_{\text{cyc2}}$, RR-I$_{\text{cyc1}}$)	> 40
	AND	Search($_{\text{cyc0}}$)	= ar_ V Ectopic Single
	AND	Value(Num$_{\text{cyc-2}}$)	> 0

- **ar_Sinus Pause** (Sinus Pause): The Pause search looks for a long RR or a 200% increase relative to the previous beat. The criteria may be made more stringent by changing the OR to an AND. Note that If Dog is used as the Species setting for Minipig, use RR-I > 2000
  - Requires well place R wave marks

Species	Definition			
Dog	(	Value(RR-I$_{\text{cyc0}}$)	> 3000	
	OR	%Increase(RR-I$_{\text{cyc-1}}$, RR-I$_{\text{cyc0}}$)	> 200	)
	AND	Value(Num$_{\text{cyc-2}}$)	> 0	
Monkey	(	Value(RR-I$_{\text{cyc0}}$)	> 2000	
	OR	%Increase(RR-I$_{\text{cyc-1}}$, RR-I$_{\text{cyc0}}$)	> 200	)

	AND	Value(Num_{cyc-2})	> 0	
Rat	(	Value(RR-I_{cyc0})	> 500	
	OR	%Increase(RR-I_{cyc-1}, RR-I_{cyc0})	> 200	)
	AND	Value(Num_{cyc-2})	> 0	
Mouse	(	Value(RR-I_{cyc0})	> 400	
	OR	%Increase(RR-I_{cyc-1}, RR-I_{cyc0})	> 200	)
	AND	Value(Num_{cyc-2})	> 0	

- **ar_V Bigeminy** (Ventricular Bigeminy): Identifies a repeating pattern of 2 or more Ventricular beats that are separated by a single sinus (non-ventricular) beat. If a larger number of repetitions are desired to establish the pattern >=2 may be increased to the desired number of repetitions.
    - Requires ar_V Ectopic and ar_V Ectopic Single

Species	Definition	
	Series(ar_ V Ectopic Single, 2)	>= 2

- **ar_V Couplet** (Ventricular Couplet): Identifies two contiguous Ventricular Ectopic beats that are sandwiched between 2 sinus (non-ventricular) beats.
    - Requires ar_V Ectopic

Species	Definition	
	Series(ar_ V Ectopic, 1)	= 2

- **ar_V Couplet Series** (Ventricular Couplet Series): Identifies multiple Ventricular Couplets that are separated by a single sinus (non-ventricular) beat.
    - Requires ar_V Ectopic and ar_V Couplet

Species	Definition	
	Series(ar_ V Couplet, 3)	>= 2

- **ar_V Ectopic** (Ventricular Ectopic): This search looks for any ventricular ectopic without attempting to differentiate between premature or escape beats. Once a ventricular beat has been identified, a distinction can be made between premature and escape beats.

  The search for Ventricular Ectopics does not depend on P identification, this is intentional since a Ventricular Ectopics depolarization generally provides Data Insights sufficient differentiation from normal beats. Requiring P identification adds greater marking effort and also requires higher data quality.

  Search results will include all cycles with QRS widening, this will result in conditions such as Bundle Branch Block being identified as Ventricular Ectopics. Bundle Branch Blocks with a unique morphology can be isolated and removed from the search results by using a Template based search clause.

    - Sort results by QRS width, largest to smallest
    - Identify the transition between ectopic and normal beats
    - Reject normal beats

Species	Definition		
Dog		Value(QRS_{cyc0})	> 54
	AND	Value($Noise_{cyc0}$)	< 100
Monkey		Value(QRS_{cyc0})	> 48
	AND	Value($Noise_{cyc0}$)	< 100
Rat		Value(QRS_{cyc0})	> 30
	AND	Value($Noise_{cyc0}$)	< 100
Mouse		Value(QRS_{cyc0})	> 20
	AND	Value($Noise_{cyc0}$)	< 100

- **Ar_V Ectopic Single** (Isolated Ventricular Ectopic): Identifies a Ventricular Ectopic that is sandwiched between 2 sinus (non-ventricular) beats.
    - Requires ar_V Ectopic Search

Species	Definition		
		Search($_{cyc-1}$)	!= ar_ V Ectopic
	AND	Search($_{cyc0}$)	= ar_ V Ectopic
	AND	Search($_{cyc1}$)	!= ar_ V Ectopic

- **ar_V run** (Ventricular Run): Identifies more than three contiguous Ventricular Ectopic beats that are sandwiched between 2 sinus (non-ventricular) beats.

  - Requires ar_V Ectopic

Species	Definition
	Series(ar_ V Ectopic, 1) > 3

- **ar_PVC Single** (Premature Ventricular Complex): Identifies premature Single Ventricular Ectopics that have sinus beats adjacent to it.
  - Requires ar_V Ectopic and ar_V Ectopic Single

Species	Definition
	%Decrease(RR-I_{cyc-1}, RR-I_{cyc0}) > 0 AND Search($_{cyc0}$) = ar_ V Ectopic Single AND Value(Num_{cyc-2}) > 0

- **ar_V Escape** (Ventricular Escape Complex): Identifies escape Single Ventricular Ectopics that have sinus beats adjacent to it.
  - Requires ar_V Ectopic and ar_V Single

Species	Definition
	%Increase(RR-I_{avg0}, RR-I_{cyc0}) > 40 AND Search($_{cyc0}$) = ar_ V Ectopic Single AND Value(Num_{cyc-2}) > 0

- **ar_V Trigeminy** (Ventricular Trigeminy): Identifies a repeating pattern of 2 or more Ventricular beats that are separated by a two sinus (non-ventricular) beat. If a larger number of repetitions are desired to establish the pattern >=2 may be increased to the desired number of repetitions.
  - Requires ar_V Ectopic and ar_V Ectopic Single

Species	Definition
	Series(ar_ V Ectopic Single, 3) >= 2

- **ar_V Triplet** (Ventricular Triplet): Identifies three contiguous Ventricular Ectopic beats that are sandwiched between 2 sinus (non-ventricular) beats.
  - Requires ar_V Ectopic

Species	Definition
	Series(ar_ V Ectopic, 1) = 3

Data Validation Searches

- **dv_HR Limits** (Heart Rate Limits): Searches for cycles that are at HR extremes. The matches may be valid beats, missed beats or incorrectly marked beats, however there is a greater likelihood of mismarked beats.
    - Used to complete attribute based analysis (requires R waves marked)
    - Sort the HR column and step through extremes until normal results are reached
    - Place **BDM** or reanalyze as needed

Species	Definition			
Dog	(	Value(HR$_{cyc0}$)	> 200	
	OR	Value(HR$_{cyc0}$)	< 35	)
	AND	Value(Num$_{cyc-1}$)	> 0	
Monkey	(	Value(HR$_{cyc0}$)	> 200	
	OR	Value(HR$_{cyc0}$)	< 50	)
	AND	Value(Num$_{cyc-1}$)	> 0	
Rat	(	Value(HR$_{cyc0}$)	> 500	
	OR	Value(HR$_{cyc0}$)	< 250	)
	AND	Value(Num$_{cyc-1}$)	> 0	
Mouse	(	Value(HR$_{cyc0}$)	> 550	
	OR	Value(HR$_{cyc0}$)	< 300	)
	AND	Value(Num$_{cyc-1}$)	> 0	

- **dv_HR Change** (Heart Rate Change): Searches for a marked increase in RR-I between the current and the following cycle. The matches may be valid beats, missed beats or incorrectly marked beats, however there is a greater likelihood of mismarked beats.
    - To complete attribute based analysis (requires R waves marked)
    - Sort the RR increase column largest to smallest and step through the results until normal results are reached
    - Place **BDM** or reanalyze as needed

Species	Definition		
Dog		%Increase(RR-I$_{cyc0}$, RR-I$_{cyc1}$)	> 50
Monkey	AND	Value(Num$_{cyc-1}$)	> 0
Rat			

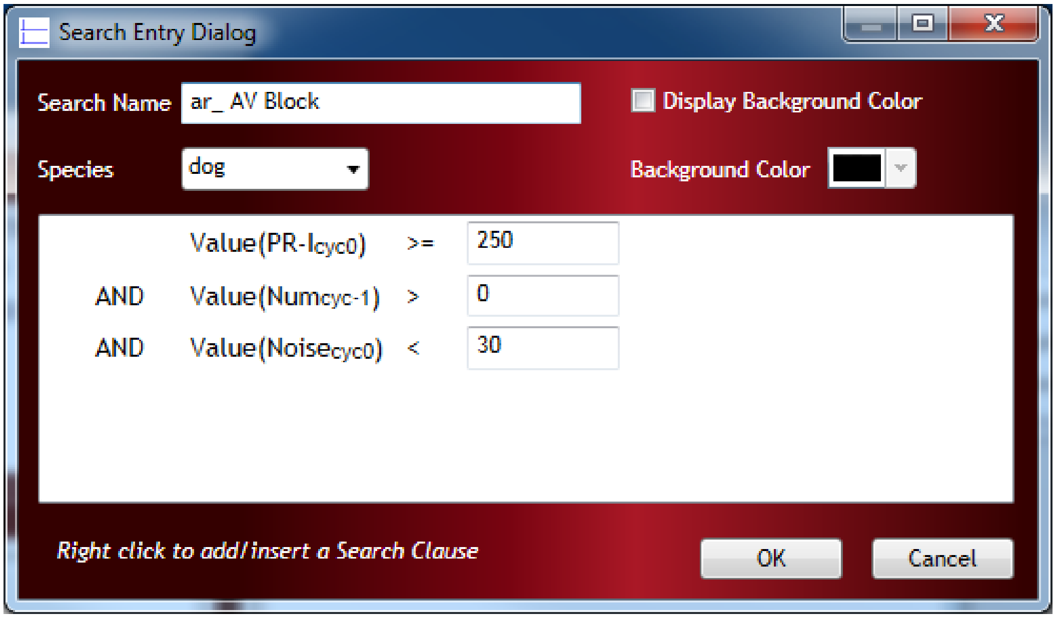
Mouse	

- **dv_Missed Beats** (Missed Beats): Searches for skipped beats
    - To complete attribute based analysis (requires R waves marked)
    - Place **BDM** or reanalyze as needed

Species	**Definition**		
Dog		%Increase(RR-I_{cyc0}, RR-I_{cyc1})	> 90
	AND	%Change(RR-I_{cyc-1}, RR-I_{cyc0})	< 10
	AND	Value(HR_{cyc0})	> 140
	AND	Value($Noise_{cyc0}$)	< 100
Monkey		%Increase(RR-I_{cyc0}, RR-I_{cyc1})	> 90
	AND	%Change(RR-I_{cyc-1}, RR-I_{cyc0})	< 10
	AND	Value(HR_{cyc0})	> 150
	AND	Value($Noise_{cyc0}$)	< 100
Rat		%Increase(RR-I_{cyc0}, RR-I_{cyc1})	> 90
	AND	%Change(RR-I_{cyc-1}, RR-I_{cyc0})	< 10
	AND	Value(HR_{cyc0})	> 400
	AND	Value($Noise_{cyc0}$)	< 100
Mouse		%Increase(RR-I_{cyc0}, RR-I_{cyc1})	> 90
	AND	%Change(RR-I_{cyc-1}, RR-I_{cyc0})	< 10
	AND	Value(HR_{cyc0})	> 475
	AND	Value($Noise_{cyc0}$)	< 100

Modifying an Existing Search

To edit an existing Search, double click on the Search to open or right click the mouse and select **Edit Selected Search**. In the example below, **ar_AV Block** has been selected.



Search Name: ar_ AV Block

☐ Display Background Color

Species: dog

Background Color: ■

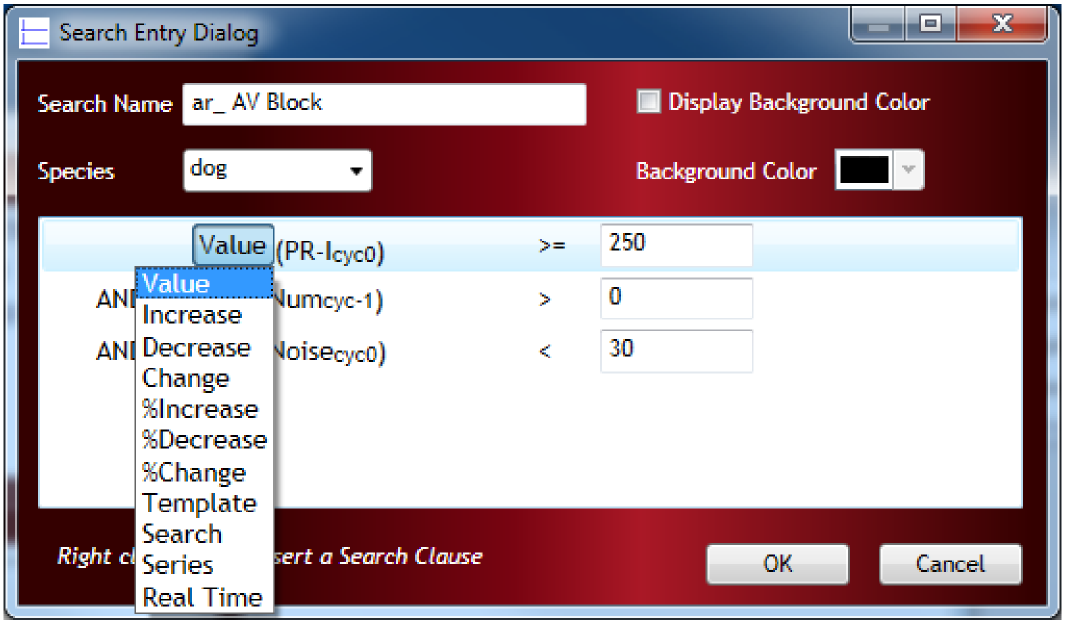
Value(PR-I$_{cyc0}$) >= 250

AND Value(Num$_{cyc-1}$) > 0

AND Value(Noise$_{cyc0}$) < 30

Right click to add/insert a Search Clause

Each search clause contains multiple values or operations that can be selected and edited. The first clause contains multiple valuess that can be modifed. To edit any of these values, simply click the mouse on the desired value to open a selection dialog. For example, click on **Value**. The following is a list of values or actions that can be selected based on what information is desired (see Create New Search for definitions of each operation).



Search Name: ar_ AV Block

☐ Display Background Color

Species: dog

Background Color: ■

Value(PR-I$_{cyc0}$) >= 250

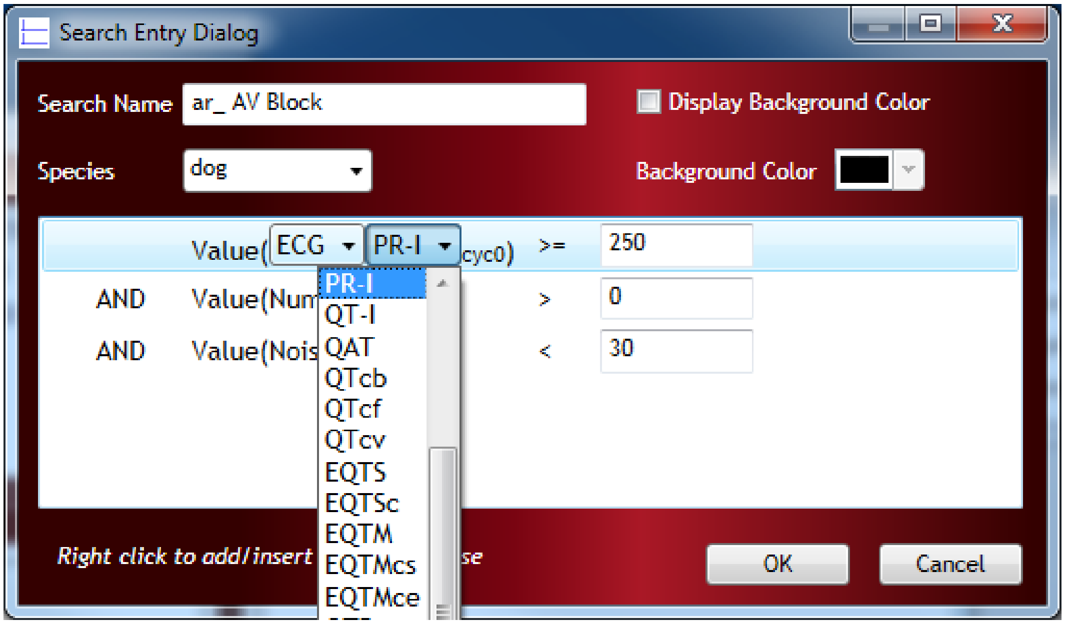
AND Value(Num$_{cyc-1}$) > 0

AND Value(Noise$_{cyc0}$) < 30

Right click to add/insert a Search Clause

In this Search, the desire is to find PR Intervals greater than 250ms. **Value** represents the actual value for this parameter as defined by analysis and listed in the Derivations table for the subject. Next, clicking on the PR-1 value will access a pull-down menu to select the desired analysis alogrithm. In this case ECG will be displayed but all available analysis modules can be selected. The analysis modules that are available will be based on the data that was loaded in Review.

Once the analysis module has been defined, the software will automatically display all derived parameters that are available based on the analysis algorithm selected (see below).



Search Name: ar_ AV Block

☐ Display Background Color

Species: dog

Background Color

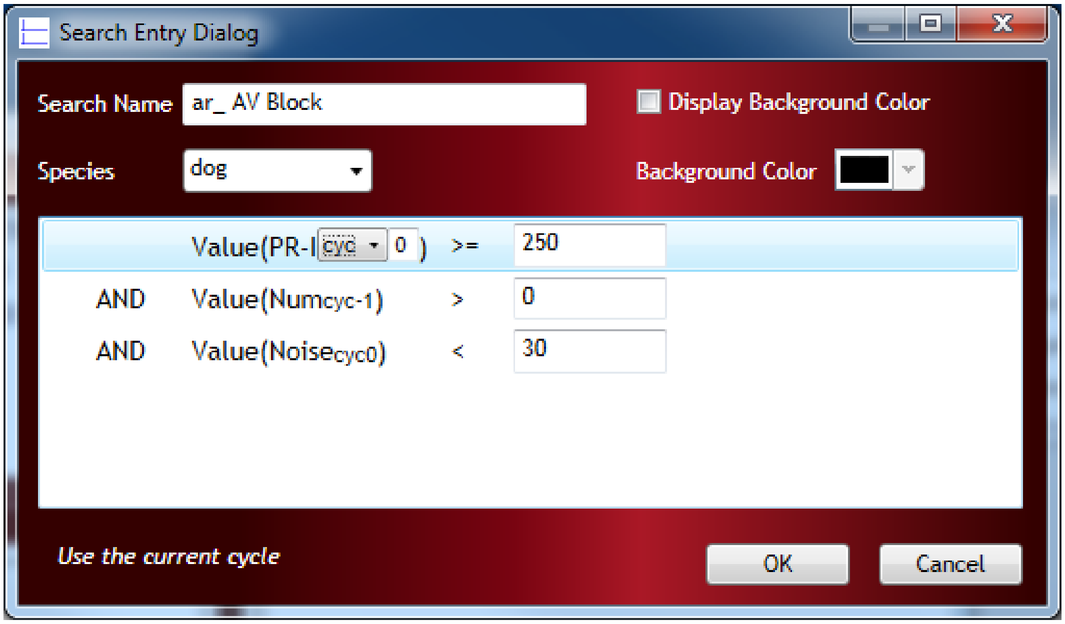
Value(ECG PR-I cyc0) >= 250

AND Value(Num > 0

AND Value(Nois < 30

Right click to add/insert *se*

The next value in the first search clause is **cyc0**. This defines which cycle we are interested in identifying or if we are interested in using an offset from preceeding or following cycles to help define a specific condition. Since we are only interested in a specific value, PR Interval, "0" has been defined as our cycle of interest, or our "reference" cycle.



Search Name: ar_ AV Block

☐ Display Background Color

Species: dog

Background Color

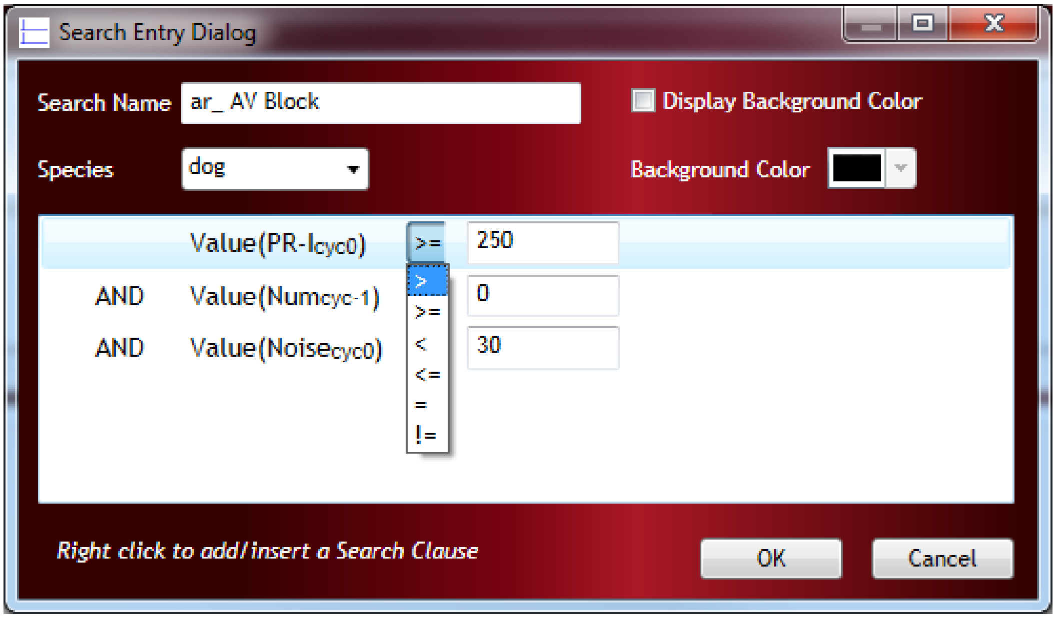
Value(PR-I cyc 0) >= 250

AND Value(Numcyc-1) > 0

AND Value(Noisecyc0) < 30

Use the current cycle

Next, the operation of greater than or equal to (>=) has been defined. Additional operations are availabe that include greater than (>), less than (<), then than or equal to (<=), equal to (=), and not equal to (!=). This can be changed to greater than to define values about a specific interval.



Search Name: ar_ AV Block

☐ Display Background Color

Species: dog

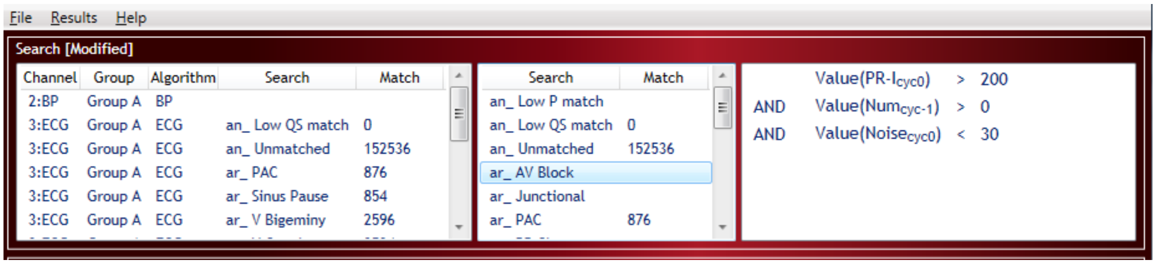
Background Color

	Value(PR-I_{cyc0})	>=	250
AND	Value(Num_{cyc-1})	>	0
AND	Value($Noise_{cyc0}$)	<	30

Right click to add/insert a Search Clause

To edit this existing clause, we can change the final value in the clause from 250 to 200. This now updates that first clause to search for PR Intervals (from our ECG channel) that are greater than 200ms in duration. The following clauses help to define the boundaries of the search. The second clause utilizes the NUM parameter (cycle number) to define that the previous cycle, -1, must have a cycle number greater than zero and provides information on the previous cycle. This may be important when looking at certain conditions. The final clause is used to exlcude noisy regions in the data by defining a Noise value of less than 30. See the **Derived Parameters** section for the specific analysis modules in the Ponemah Analysis Modules manual, MU00231, for additonal information on derived and calculated values.

Upon completing modifications to the rule, select OK to apply the changes. If a rule is incomplete, the **OK** button will not be available. Check to make sure that all search criteria and information in the editable fields have been completed. When editing has been completed, click on the search clause under **Search** to view any changes that have been made to that Search. Below, shows the first search clause was upated to find all PR Intervals that are greater than 200ms in duration. To apply and use this newly edited Search, see **Applying Rules**.



Channel	Group	Algorithm	Search	Match
2:BP	Group A	BP		
3:ECG	Group A	ECG	an_ Low QS match	0
3:ECG	Group A	ECG	an_ Unmatched	152536
3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ Sinus Pause	854
3:ECG	Group A	ECG	ar_ V Bigeminy	2596

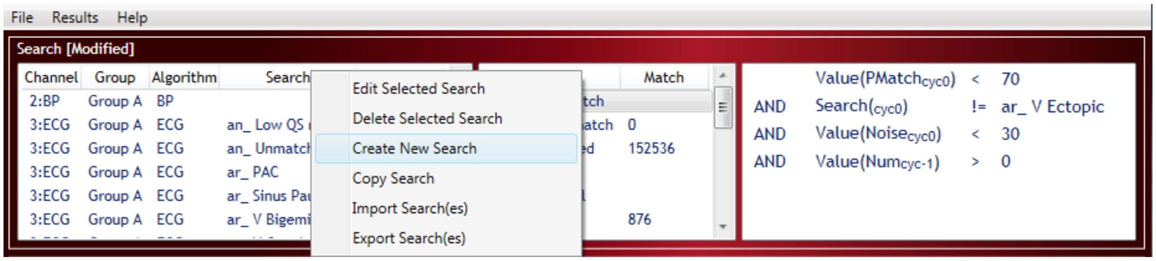
Search	Match
an_ Low P match	
an_ Low QS match	0
an_ Unmatched	152536
ar_ AV Block	
ar_ Junctional	
ar_ PAC	876

	Value(PR-I_{cyc0})	>	200
AND	Value(Num_{cyc-1})	>	0
AND	Value($Noise_{cyc0}$)	<	30

Creating a New Search

Using Value Operation

To create a new Search, right click the mouse anywhere within the **Search/Match** dialog or on the **Search/Match** column headers. The right click menu with the various options will be displayed. Select **Create New Search**.

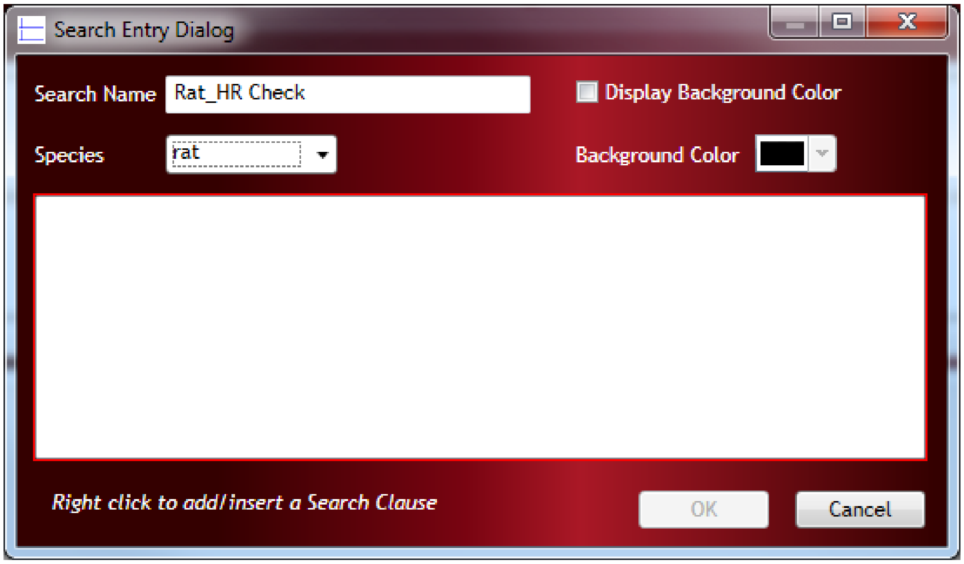


Value($PMatch_{cyc0}$) < 70
AND Search($_{cyc0}$) != ar_ V Ectopic
AND Value($Noise_{cyc0}$) < 30
AND Value(Num_{cyc-1}) > 0

A dialog with no **Search Name** or identified search clauses will be displayed. Required fields will be outlined in red. These fields must be filled in otherwise the **OK** button will not be available. To create a new search, provide a unique name. In this example, a Search for finding Heart Rate values that may be suspect will be created for the rat species.

NOTE: Selection of **Species** within the **Search Entry Dialog** is dependent upon the data loaded into Review. If data is loaded that has been specified as dog, selection of a different species cannot be performed. Data with the desired species must be loaded into Review in order to create the species specific search. Additionally, **Searches** identified as one species cannot be applied to data from a different species.

Enter a unique Search Name, for example **Rat_HR Check**, and the corresponding **Species** should be loaded automatically based upon the data loaded.

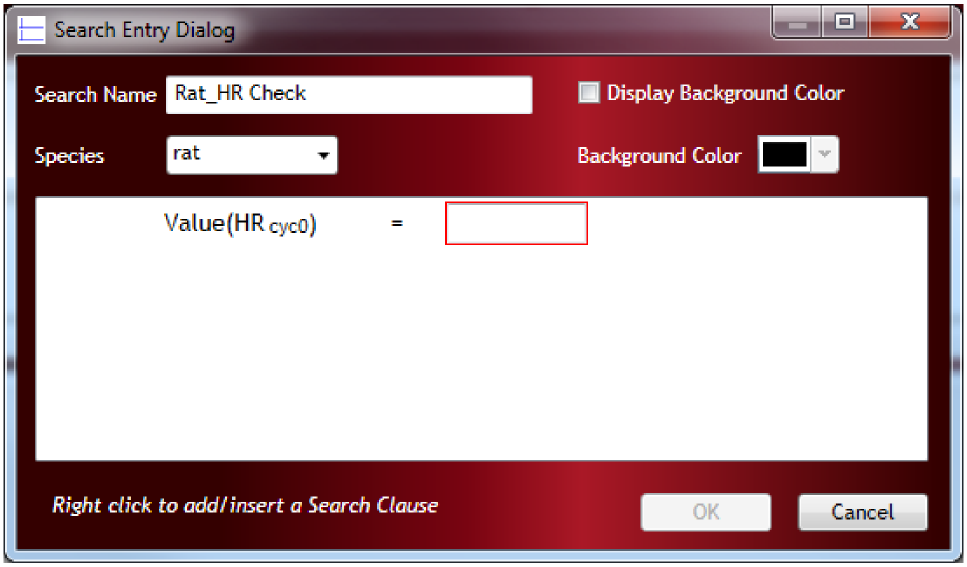


Search Name: Rat_HR Check

Species: rat

☐ Display Background Color

Next, right click within the Search Clause edit field and select **Add New Clause** to begin constructing the search criteria. Since information on Heart Rate is desired, use **Value** (default selection) as the start of the clause. **Value** represents the actual value for this parameter as defined by analysis and listed in the Derivations table for the subject (see Create New Search for definitions of each operation). Next, click on the **NUM** value to access a pull-down menu to select the desired analysis alogrithm. In this case **ECG** will be used but all available analysis modules can be selected. The analysis modules that are available will be based on the data that was loaded in Review. Once the analysis module has been defined, the software will automatically display all derived parameters that are available based on the analysis algorithm selected. Select **HR** as the parameter. The next value in the first search clause is **cyc0**. This defines which cycle we are interested in identifying or if we are interested in using an offset from preceeding or following cycles to help define a specific condition. A value of zero is desired as we are interested in the reference cycle or current cycle.



Search Name: Rat_HR Check

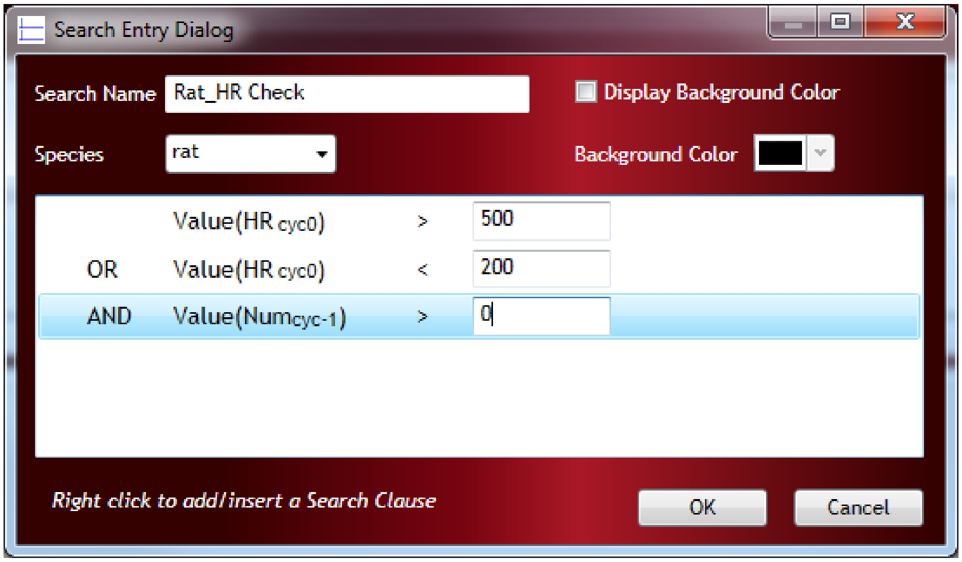
☐ Display Background Color

Species: rat

Background Color: ■

Value(HR $_{cyc0}$) =

Since this Search is intended to locate areas where HR values may be suspect, construct the first clause to define HR values above the expected values. The "=" operation is the default value listed. Additional operations are availabe that include greater than (>), less than (<), less than or equal to (<=), greater than or equal to (>=), equal to (=), and not equal to (!=). Select > and enter a value of 500, for example. Right click and add another clause to define the lower end of acceptable data. Utilize the structure for the first clause (**Value**, **ECG**, **HR** and **cyc0**). You will notice that additional clauses display **AND** prior to the search clause. You can use this discriminator or click on this to select **OR**. A selection of **OR** prior to this clause will allow the Search to look for values above or below the ranges entered. To finish this clause, select the < operation and enter a value of 200. This effectively brackets our good or expected data to be within the range of 200-500 beats per minute and will locate all cycles whose Heart Rate falls outside of this range. Finally, enter a finish clause to also include the previous cycle. It is useful to see additional data (preceding or following the reference cycle) when interpreting the results of the search. To do this, create a third search clause using the **AND** function. Utilize **Value** and **ECG** as above. However, select **NUM** as the derived parameter. The **NUM** parameter (cycle number) can be used to specify an offset to the current cycle. In this case, -1 will also include the previous cycle in the search results. Finally, enter greater than zero (>0) to return information with valid cycle numbers.



Search Name: Rat_HR Check

☐ Display Background Color

Species: rat

Background Color: ■

Value(HR $_{cyc0}$) > 500

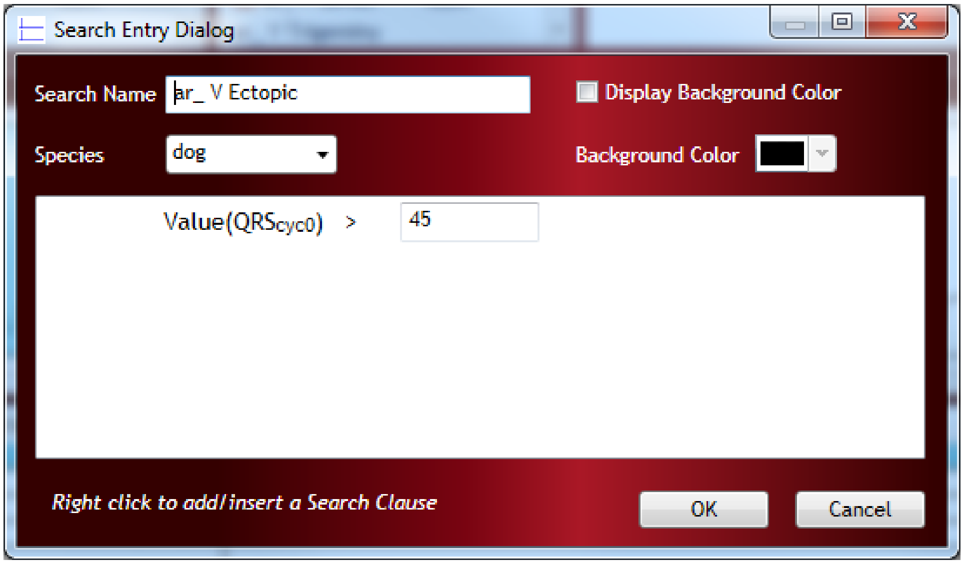
OR Value(HR $_{cyc0}$) < 200

AND Value(Num$_{cyc-1}$) > 0

Using Series Operation

Using the **Series** operation is similar to the above examples. However, **Series** utilizes an existing search within the search clause. Additionally, the embedded search within the **Series** clause needs to be applied to a channel. If the embedded search is not applied to a channel, you will not be able to drag and apply your **Series** search.

If interested in finding ectopic beats as well as a series of ectopic beats, two searches can be constructed. The first search criteria must define the single ectopic beat. This is done by using the existing Search (predefined **ar_V Ectopic**) or creating a new rule to define this beat. Create or modify the search clause to utilize **Value** to define the duration of a QRS complex that is out of the expected range. Utilize **cyc0** to define the current cycle and duration greater than 45ms.



Search Entry Dialog

Search Name: ar_ V Ectopic

☐ Display Background Color

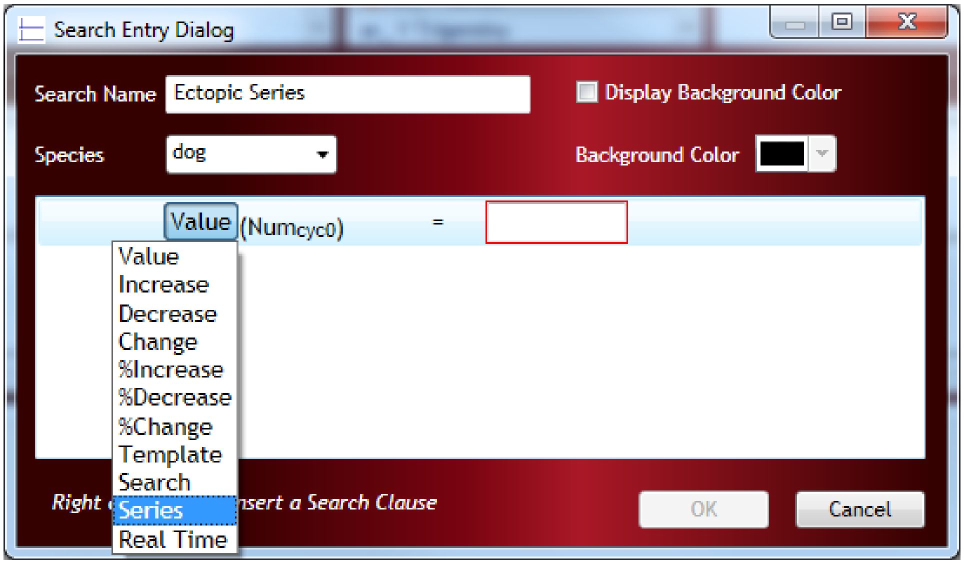
Species: dog

Background Color

Value(QRS_{cyc0}) > 45

Right click to add/insert a Search Clause

Next, create a search for a run of ectopic beats using the **Series** function.



Search Entry Dialog

Search Name: Ectopic Series

☐ Display Background Color

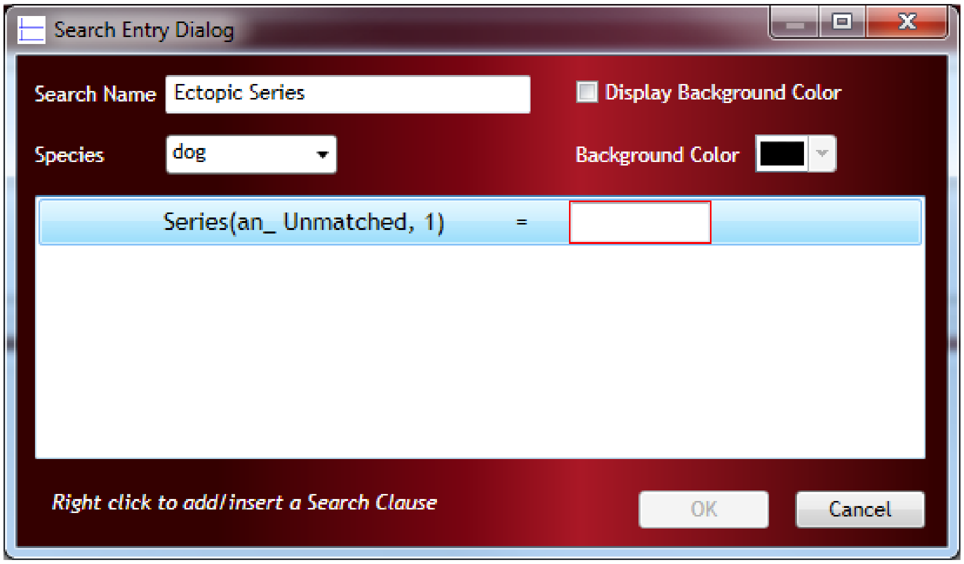
Species: dog

Background Color

Value(Num_{cyc0}) =

Right click to add/insert a Search Clause

Once **Series** has been selected, the folowing function will update to include on of the previously defined searches from the **Search** list. In the example shown below, an_Unmatched, 1, is automatically loaded.



Search Name: Ectopic Series

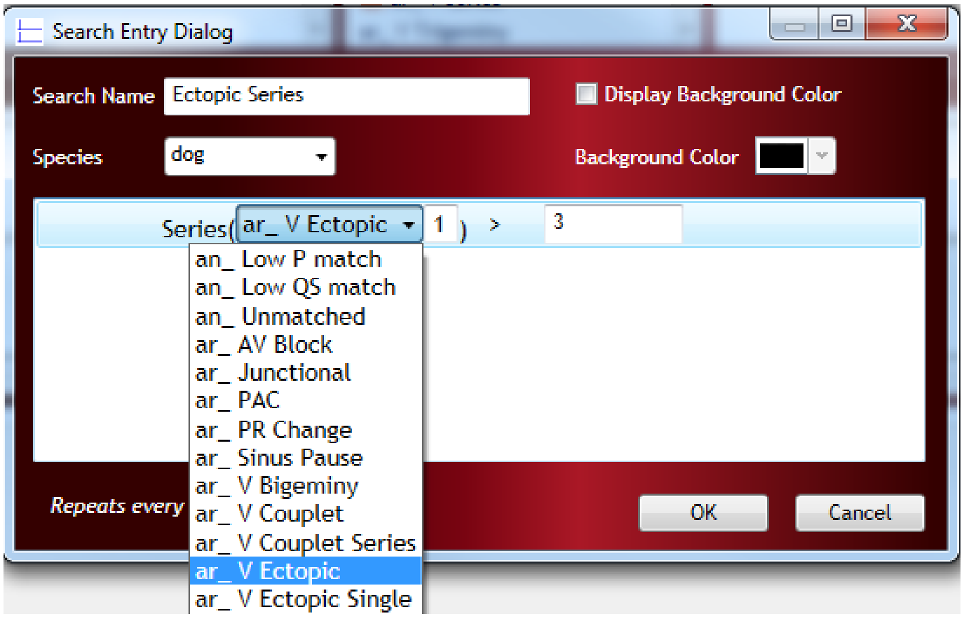
☐ Display Background Color

Species: dog

Background Color: ■

Series(an_ Unmatched, 1) =

Clicking on the **an_Unmatched, 1** rule provides a pull-down menu that will display all available searches in the list. Select the previous rule used to define the ectopic beat ,**ar_V Ectopic**, and specify the number of contigous complexes desired for the series. This has been set to greater than 3 (> **3**) from the current cycle defined.



Search Name: Ectopic Series

☐ Display Background Color

Species: dog

Background Color: ■

Series(ar_ V Ectopic 1) > 3

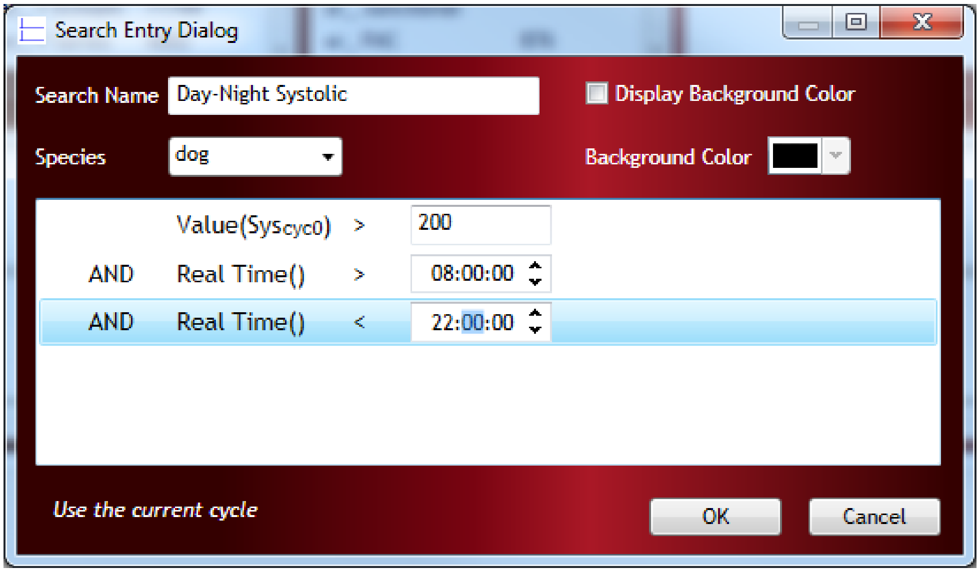
To apply this **Series** search, you must first apply the Search that is embedded in the **Series** search. If this is not applied to a channel, or channels, you will not be able to drag and apply your **Series** search to a channel.

NOTE: A **Series** search depends on an embedded search with one or more of it clauses. If the embedded clauses are not applied to a channel, or channels, the **Series** search will not be able to be dragged and applied to a channel.

Using Real Time Operation and Grouping Clauses

The **Real Time** function can be used to define periods of interest such as before and after dosing, during light and dark cycles, or during any other period of interest. In addition, **Grouping** or bracketing can be used to combine clauses to ensure that all clauses are satisfied as a combined group.

To illustrate this, a **Real Time** search grouping clauses will be used to find outliers in Systolic values between day and night. First, create a clause to define the systolic value of interest. Then define the time period over which this search is to be applied. Below, a Systolic value exceeding 200mmHg between the hours of 8:00AM to 10:00PM is defined.



Search Name: Day-Night Systolic

☐ Display Background Color

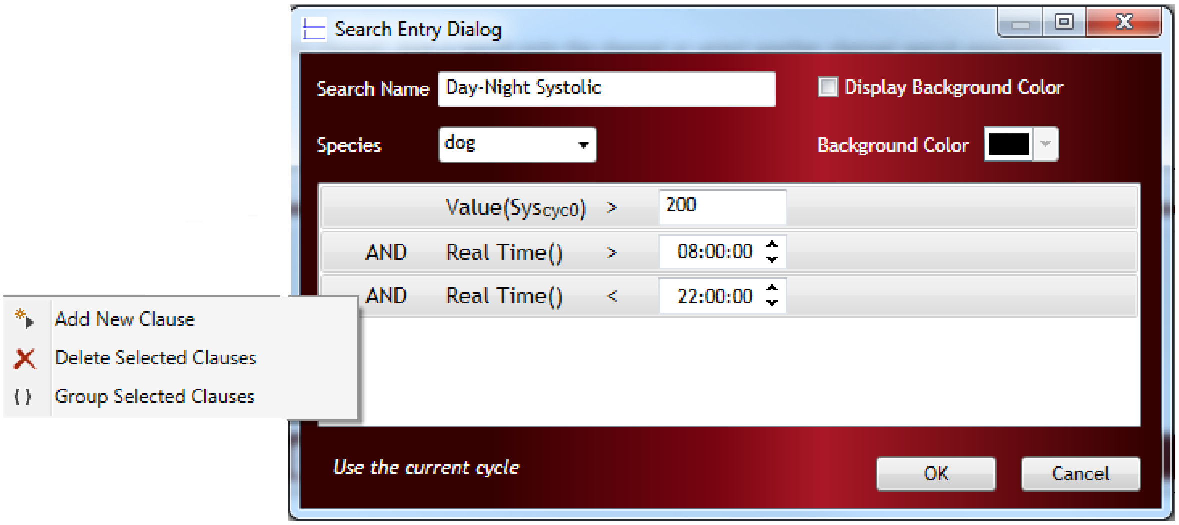
Species: dog

Background Color: ■

	Value(Syscyc0)	>	200
AND	Real Time()	>	08:00:00
AND	Real Time()	<	22:00:00

Use the current cycle

In order to group these functions, highlight all three lines using the Control key and the mouse or using the Shift key and selecting the first and last lines. To aid in selecting the lines, it is recommended to click on the lines between the left side of the dialog and the **AND** function. This will prevent the selection of one of the functions by clicking to close to one of the values. Once all search clauses are highlighted, left click the mouse and select **Group Selected Clauses**.



Search Name: Day-Night Systolic

☐ Display Background Color

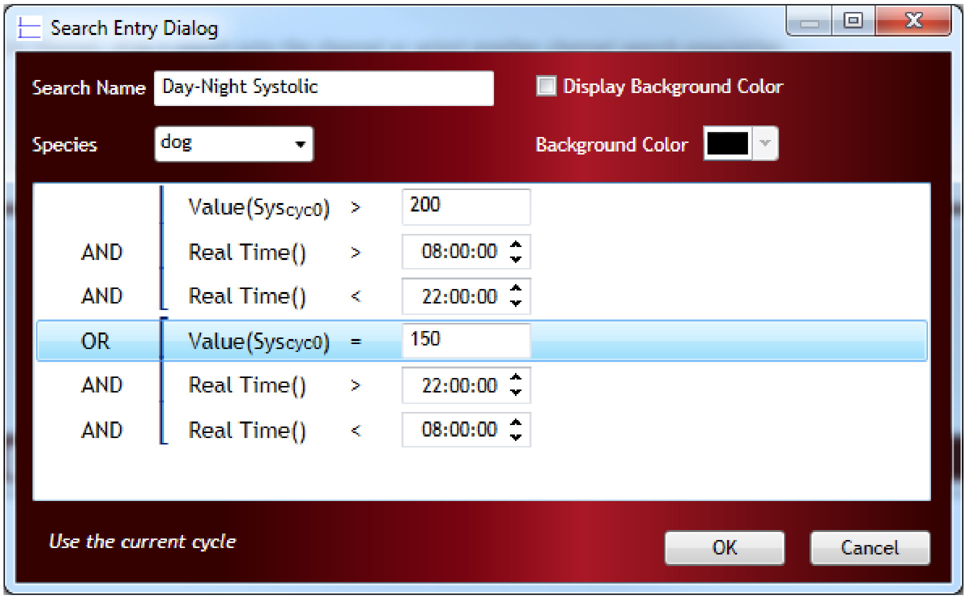
Species: dog

Background Color: ■

	Value(Syscyc0)	>	200
AND	Real Time()	>	08:00:00
AND	Real Time()	<	22:00:00

Use the current cycle

Repeat these steps to define the Systolic value desired during the night and group those clauses. Use the **OR** function between clauses to return values for either grouped clause. Once grouped, you will notice the bracket placed around the grouped functions which appears just to the right of the **AND/OR** statements.



Search Name: Day-Night Systolic

☐ Display Background Color

Species: dog

Background Color: ■

	Value(Syscyc0)	>	200
AND	Real Time()	>	08:00:00
AND	Real Time()	<	22:00:00
OR	Value(Syscyc0)	=	150
AND	Real Time()	>	22:00:00
AND	Real Time()	<	08:00:00

Use the current cycle

Using Searches with ECG PRO

In conjunction with ECG PRO, Data Insights can be used to isolate cycles that have poor Match results (refer to the Template Analysis manual for additional information on ECG PRO).

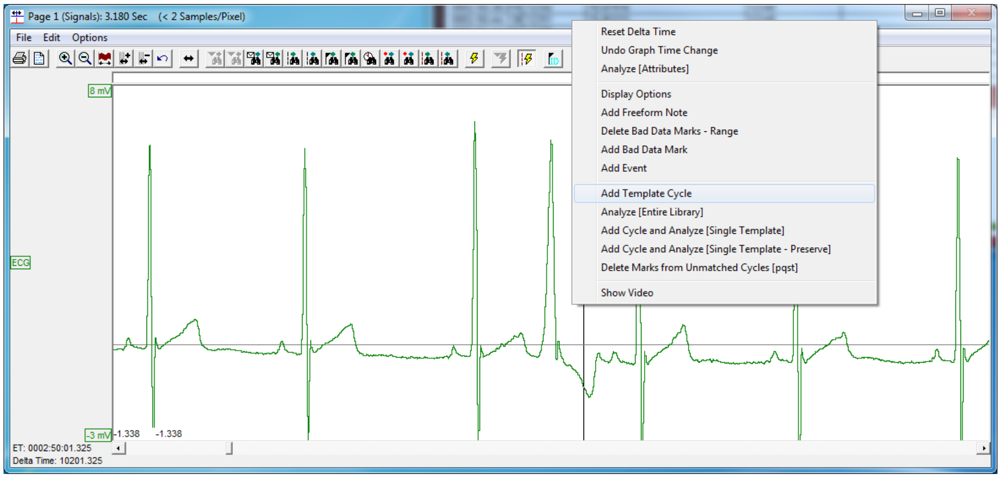
For example, ECG PRO can be used to locate and analyze P, Q, S, and T regions that match the representative Template cycle(s) to a user specified degree of match. The predefined **"an_"** searches, such as **an_Low P Match**, can be use to quickly find cycles or areas where P waves are poorly marked. Once these cycles are found, they can be added to the Template Library to complete analysis. In addition Data Insights can also be used to exclude cycles, locate false positives, and find unmatched cycles. Refer to the **Default Searches** section for a complete listing of predefined Searches to assist in analysis.

See the **Data Insights Process Flow** chart outlined in Appendix 2 for potential process flows for analyzing data. The predefined Searches can be used to accomplish a number of analysis tasks described but construction of additional searches may be required.

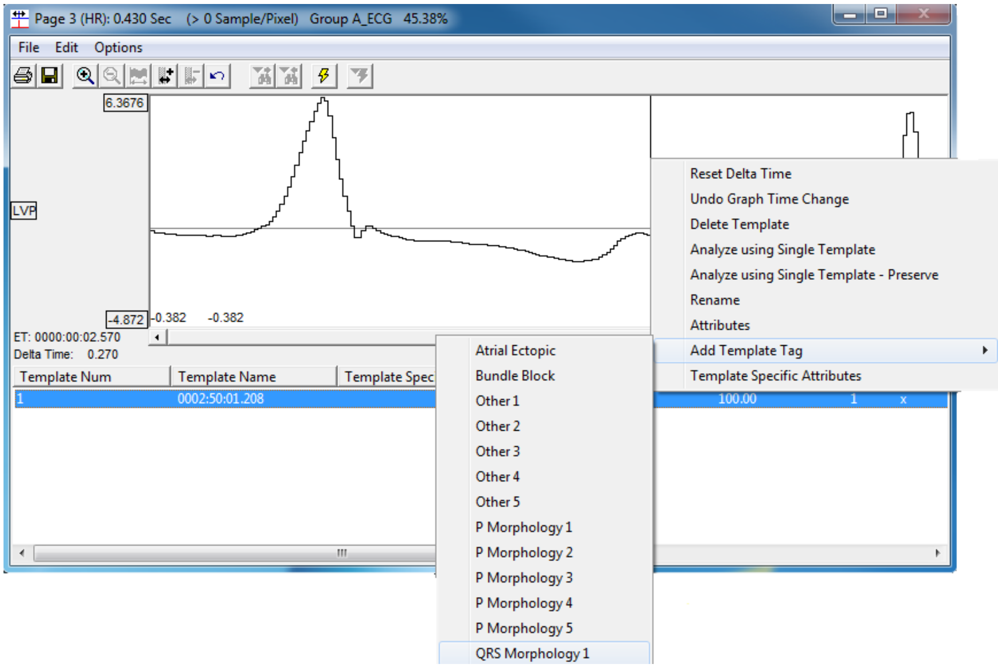
Using Template Tags

ECG PRO allows **Tags** to be applied to Template cycles when saved to the Template library. **Tags** allow identification of specific cycle morphologies. By providing **Tags**, Data Insights can be used to quantify the cycles associated with those **Tags**. This is useful in instances where count or other derived parameters are desired that are not included in the analysis module's derived parameter list. **Tags** can also be used to exclude certain morphologies from analysis. By tagging unwanted morphologies, Searches can be constructed to eliminate these cycles from analysis. Once the desired results have been obtained, use the **Report** feature to provide an output file.

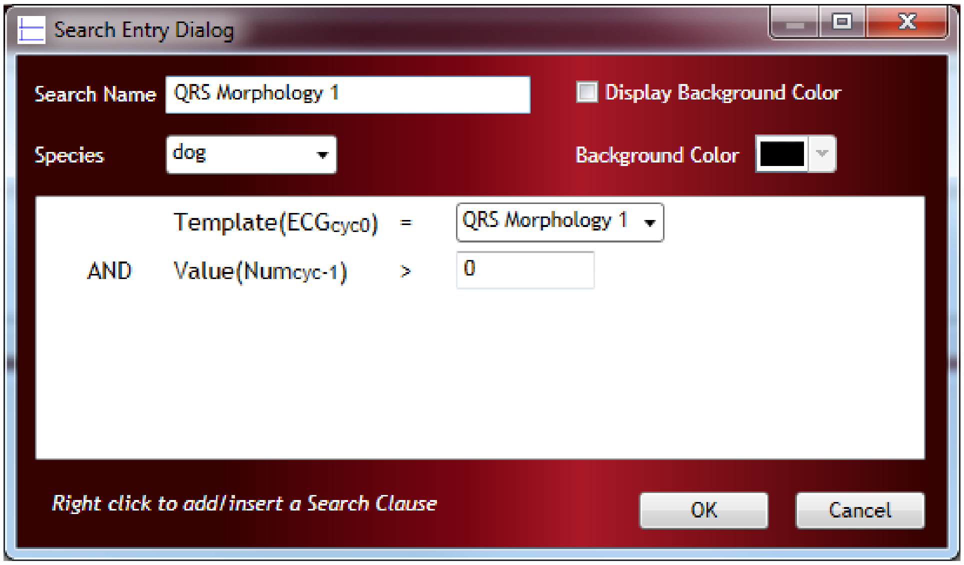
From the primary graph page, select a cycle of interest and add this to the Template graph page.



Within the Template graph page, right click the mouse and select **Add Template Tag**. Select one of the predefined **Tags** to mark the cycle and associated Matches, for example **QRS Morphology 1**. Run Template analysis to find like cycles in the dataset. Continue this process for all cycle types of interest.



To pull information specific to this **Tag**, construct a Search to find all related matches to **QRS Morphology 1.** **Template** was selected as the search type and the analysis set to ECG. The current cycle is of interest but viewing the previous cycle is often helpful for purposes of analysis. The second clause was constructed to provide **Value** as the search type, **NUM** (cycle number) was selected as the paramater of interest, and -1 was added to pull in the preceeding cycle.



Search Name: QRS Morphology 1

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Species: dog

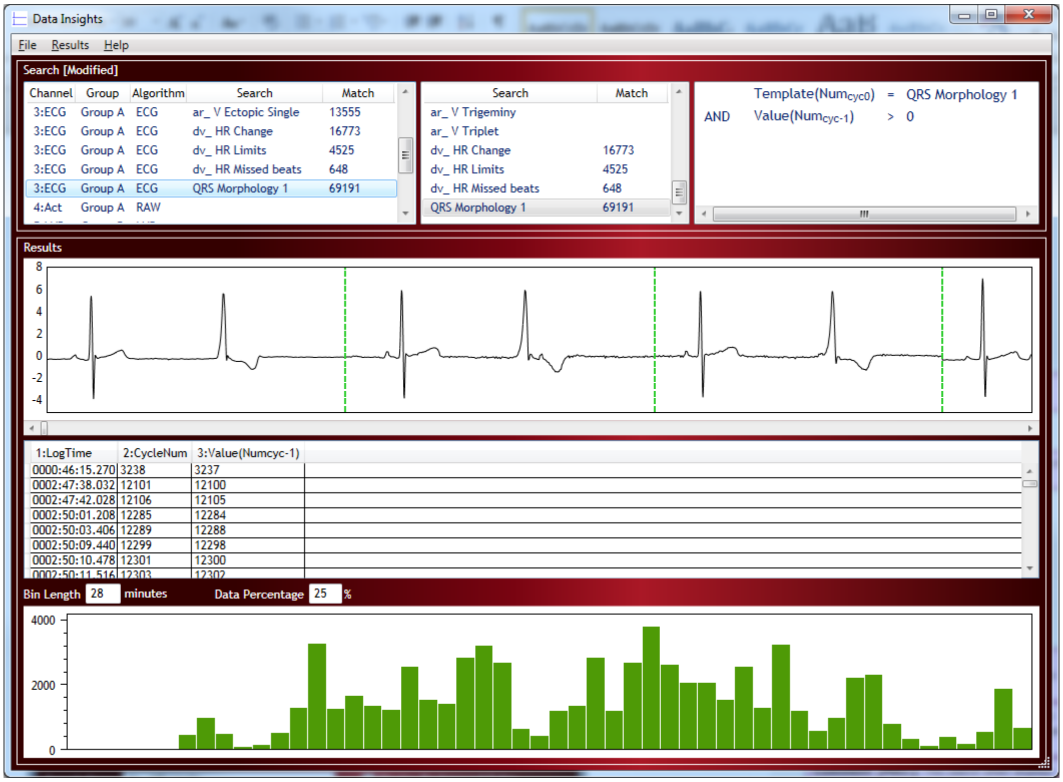
Background Color

Template(ECG_{cyc0}) = QRS Morphology 1

AND Value(Num_{cyc-1}) > 0

Right click to add/insert a Search Clause

Match information is displayed in the **Search** dialog for the newly created **QRS Morphology 1**Search. Additional Searches can be added to capture other morphologies or can be added to exclude these morphologies from analysis. Once analysis is complete, use the **Report** function to output the data for purposes of reporting or further analysis.



Channel	Group	Algorithm	Search	Match
3:ECG	Group A	ECG	ar_ V Ectopic Single	13555
3:ECG	Group A	ECG	dv_ HR Change	16773
3:ECG	Group A	ECG	dv_ HR Limits	4525
3:ECG	Group A	ECG	dv_ HR Missed beats	648
3:ECG	Group A	ECG	QRS Morphology 1	69191
4:Act	Group A	RAW		

Search	Match
ar_ V Trigeminy	
ar_ V Triplet	
dv_ HR Change	16773
dv_ HR Limits	4525
dv_ HR Missed beats	648
QRS Morphology 1	69191

Template(Num_{cyc0}) = QRS Morphology 1

AND Value(Num_{cyc-1}) > 0

1:LogTime	2:CycleNum	3:Value(Numcyc-1)
0000:46:15.270	3238	3237
0002:47:38.032	12101	12100
0002:47:42.028	12106	12105
0002:50:01.208	12285	12284
0002:50:03.406	12289	12288
0002:50:09.440	12299	12298
0002:50:10.478	12301	12300
0002:50:11.516	12303	12302

Bin Length 28 minutes

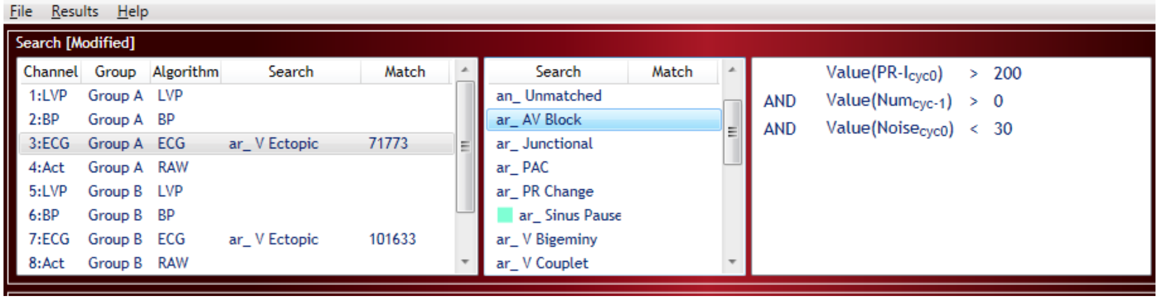
Data Percentage 25 %

Applying Searches

Searches aid in proper cycle detection. For example, the predefined "**dv_**" searches can be used to verify proper cycle marking when performing your initial analysis. One example of this is using the Heart Rate searches (**dv_)** to verify proper R wave marking after the initial attribute analysis has been performed. These searches can be used to find areas where R detection is poor or locate cycles that are out of expected range.

After creating, modifying, or selecting one of the predefined searches for data validation or other purpose, drag the **Search** to a channel. You must apply a **Search** created for a specific analysis module (ECG, BP, LVP, etc.) to a channel in the list that has the same module designation. If the analysis module in the Search criteria does not match the module in the channel, you will not be able to apply that search to the channel.

Drag the Search **ar_V Ectopic** and drop this on one or all of the ECG channels in the list. You must drop the Search on the text for the **Channel**, **Group** or **Algorithm** in order to apply the Search. The software will process the Search that has been applied and update the **Search** column with the Search name as well as provide the number of results found under **Match** for that channel. Results for two ECG channels are shown below.

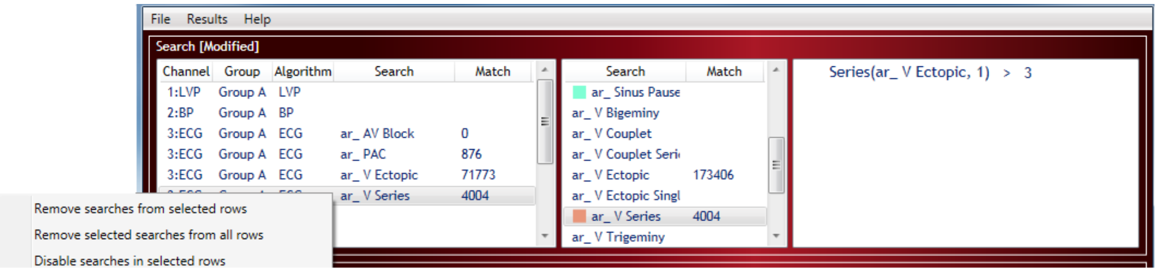


Channel	Group	Algorithm	Search	Match
1:LVP	Group A	LVP		
2:BP	Group A	BP		
3:ECG	Group A	ECG	ar_ V Ectopic	71773
4:Act	Group A	RAW		
5:LVP	Group B	LVP		
6:BP	Group B	BP		
7:ECG	Group B	ECG	ar_ V Ectopic	101633
8:Act	Group B	RAW		

Search	Match
an_ Unmatched	
ar_ AV Block	
ar_ Junctional	
ar_ PAC	
ar_ PR Change	
🟩 ar_ Sinus Pause	
ar_ V Bigeminy	
ar_ V Couplet	

Value(PR-I$_{cyc0}$) > 200
AND Value(Num$_{cyc-1}$) > 0
AND Value(Noise$_{cyc0}$) < 30

Continue to apply all desired searches to the appropriate channels. If a **Series** Search is applied, you must ensure that the embedded Search is also applied or you will not be able to apply your **Series** Search. Even though there may be only one ECG channel in the list, you may drag and drop as many ECG related Searches to that channel as desired. If needed, use the right click option to remove or disable searches applied to a channel. Using the Shift key on the keyboard, select multiple channels to be removed at one time.

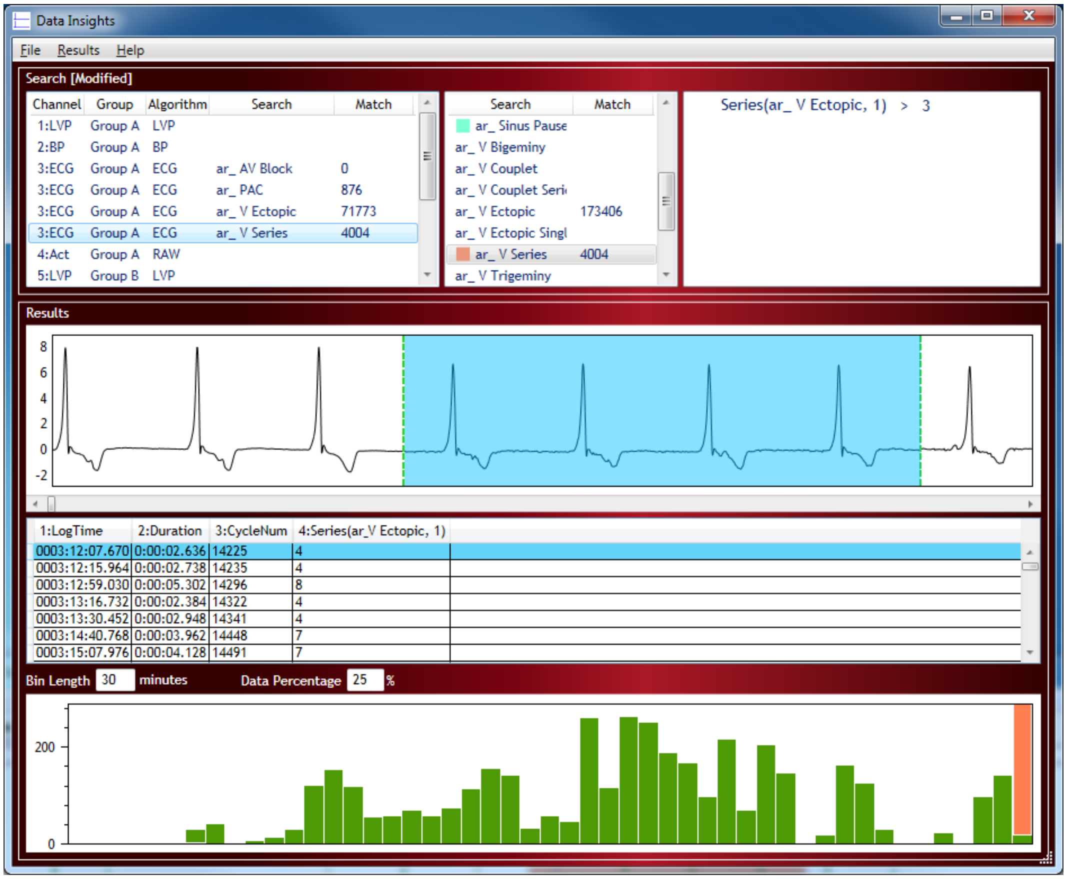


Channel	Group	Algorithm	Search	Match
1:LVP	Group A	LVP		
2:BP	Group A	BP		
3:ECG	Group A	ECG	ar_ AV Block	0
3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ V Ectopic	71773
			ar_ V Series	4004

Search	Match
🟩 ar_ Sinus Pause	
ar_ V Bigeminy	
ar_ V Couplet	
ar_ V Couplet Seri	
ar_ V Ectopic	173406
ar_ V Ectopic Singl	
🟧 ar_ V Series	4004
ar_ V Trigeminy	

Series(ar_ V Ectopic, 1) > 3

Once Searches have been applied, click on any of the applied Searches to view the graphical and numerical results of the Search. **Ar_V Series** has been selected. The graphical information has been updated along with the derived parameter values which are specific to a given search. The derived parameters will update based on the specific search that is being viewed. Finally, a distribution of the Matches is displayed at the bottom of the dialog and binned according to the desired length in time.



Channel	Group	Algorithm	Search	Match
1:LVP	Group A	LVP		
2:BP	Group A	BP		
3:ECG	Group A	ECG	ar_ AV Block	0
3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ V Ectopic	71773
3:ECG	Group A	ECG	ar_ V Series	4004
4:Act	Group A	RAW		
5:LVP	Group B	LVP		

Search	Match
🟩 ar_ Sinus Pause	
ar_ V Bigeminy	
ar_ V Couplet	
ar_ V Couplet Seri	
ar_ V Ectopic	173406
ar_ V Ectopic Singl	
🟧 ar_ V Series	4004
ar_ V Trigeminy	

1:LogTime	2:Duration	3:CycleNum	4:Series(ar_V Ectopic, 1)
0003:12:07.670	0:00:02.636	14225	4
0003:12:15.964	0:00:02.738	14235	4
0003:12:59.030	0:00:05.302	14296	8
0003:13:16.732	0:00:02.384	14322	4
0003:13:30.452	0:00:02.948	14341	4
0003:14:40.768	0:00:03.962	14448	7
0003:15:07.976	0:00:04.128	14491	7

Bin Length 30 minutes

Data Percentage 25 %

Working with Waveform Segments

A scroll bar below the graph window is used to move through the data by using the mouse and dragging the scroll bar left or right. A single mouse click on the waveform data will highlight the waveform data as well as highlight and synchronize the numerical data. Double left clicking the mouse on either the waveform data or the numerical data in this view will also synchronize with the Derived Data (DRx) and Data Reduction files as well as with all other graph pages configured in Ponemah. Additionally, depress the Control key and left click the mouse on any portion of the waveform to get x and y axis information at that point.

Use of the mouse and keyboard can be used to zoom in and out on the waveform data. Using the Control key and the mouse wheel will allow you to zoom in and out on the data. Depress the **Ctrl** key on the keyboard and hold down. With the **Ctrl** key depressed, use the mouse wheel up to zoom out. With the **Ctrl** key depressed, use the mouse wheel down to zoom in on the data. You may also **Left Click** and hold your mouse to zoom in on the waveform. This functions in the same manner as zooming in on the waveforms when working with the graph pages in Review. While holding the Left mouse button, drag either left or right in the waveform data. The area will change color as you drag your mouse. When the desired amount of data is selected, let go of the mouse button to zoom in on the area highlighted.

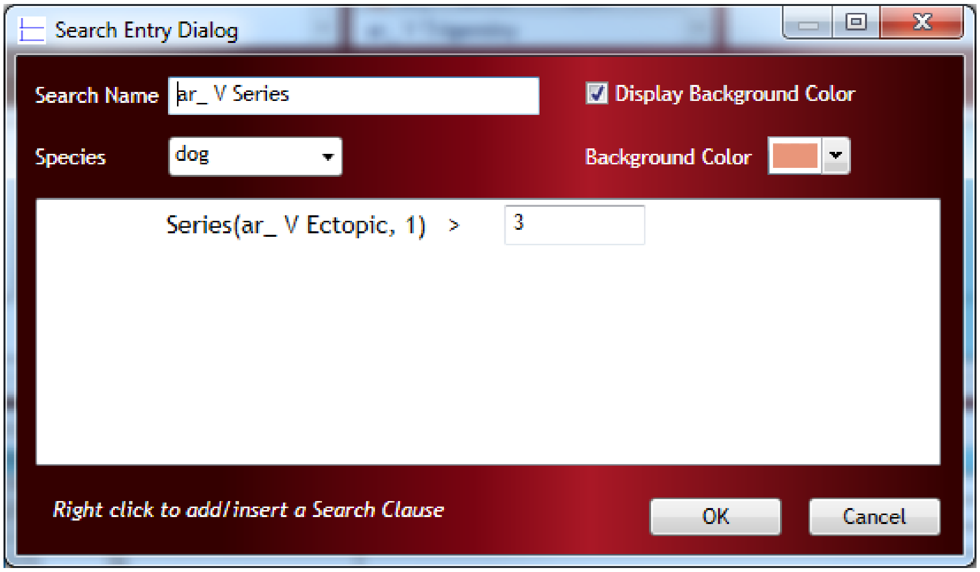
NOTE: You cannot zoom out using this function. Use the Ctrl key with the mouse wheel to zoom out as described above.

The **Page Up** and **Page Down** keys can also be used to move through the waveform data. Use the **Page Up** key to move forward in the data. Use the **Page Down** key to move backwards in the data, or towards the beginning of the dataset. The **Left Arrow** and **Right Arrow** keys can also be used to move through the waveform data. Use the **Right Arrow** key to move forward in the data. Use the **Left Arrow** key to move backwards in the data, or towards the beginning of the dataset.

Use one of the functions above to move through the waveform data. When a specific waveform (or waveforms) requires additional Review, double left click on the waveform segment. This will synchronize all data as previously mentioned.

Synchronize with Primary Graph

To aid in finding the exact cycles in the Primary graph page for additional observation, open the Search from the **Search** column as if editing the search clauses. From the **Search Entry Dialog**, select the **Display Background Color** checkbox. This will allow you to choose a specific color to identify the waves in the Primary graph pages and will be associated with that specific Search.



Search Name: ar_ V Series

☑ Display Background Color

Species: dog

Background Color

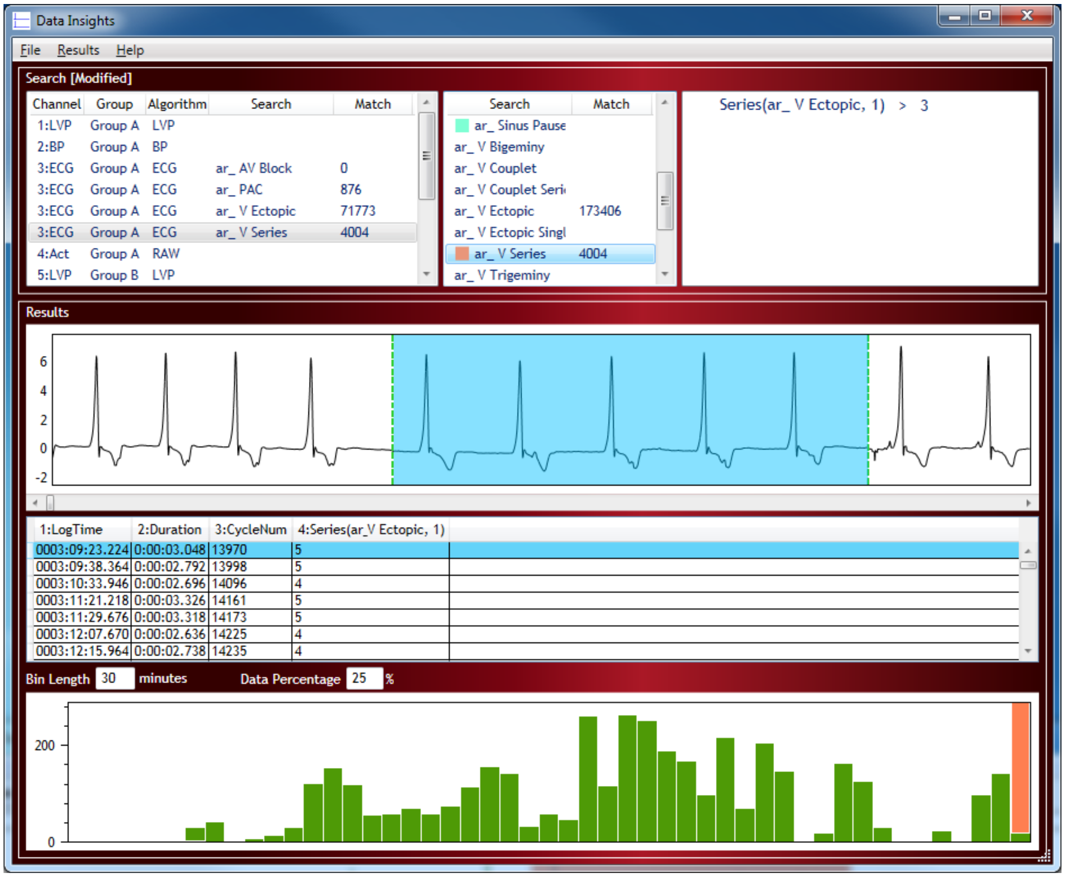
Series(ar_ V Ectopic, 1) > 3

Right click to add/insert a Search Clause

Under the Search column, you will notice that all defined colors are associated with their search. Double left click on the waveform segments to synchronize with the Primary graph page. You will note that the color specified for the Search is applied to the waves in the Primary graph page. This is helpful when overreading data to determine if regions have already been identified by an applied Search within Data Insights.

NOTE:

- Background colors will also be displayed in Page View Graphs.
- Should a region be matched by multiple applied Searches with associated background colors, these colors will stack within the graph pages to allow the user to see both background colors.



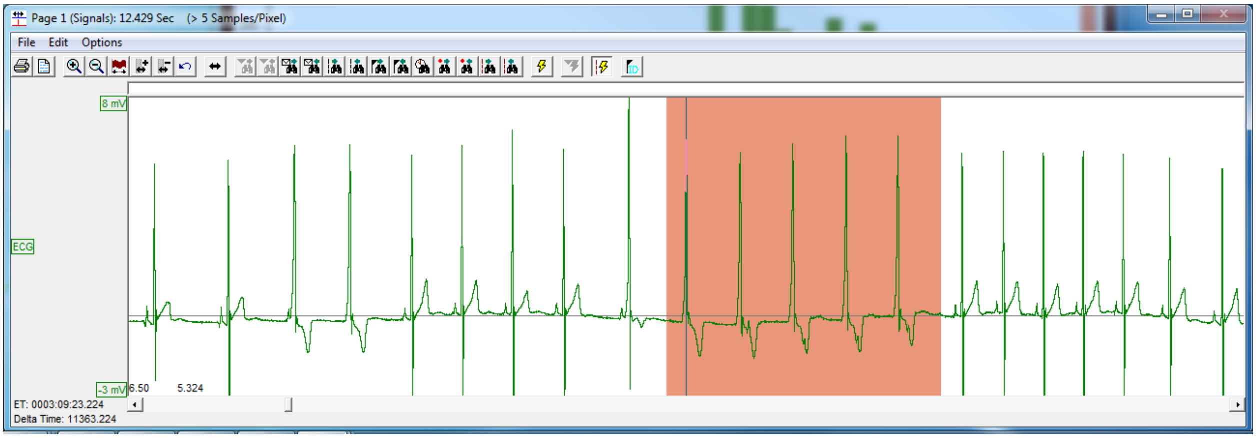
Channel	Group	Algorithm	Search	Match
1:LVP	Group A	LVP		
2:BP	Group A	BP		
3:ECG	Group A	ECG	ar_ AV Block	0
3:ECG	Group A	ECG	ar_ PAC	876
3:ECG	Group A	ECG	ar_ V Ectopic	71773
3:ECG	Group A	ECG	ar_ V Series	4004
4:Act	Group A	RAW		
5:LVP	Group B	LVP		

Search	Match
🟩 ar_ Sinus Pause	
ar_ V Bigeminy	
ar_ V Couplet	
ar_ V Couplet Seri	
ar_ V Ectopic	173406
ar_ V Ectopic Singl	
🟥 ar_ V Series	4004
ar_ V Trigeminy	

Series(ar_ V Ectopic, 1) > 3

1:LogTime	2:Duration	3:CycleNum	4:Series(ar_V Ectopic, 1)
0003:09:23.224	0:00:03.048	13970	5
0003:09:38.364	0:00:02.792	13998	5
0003:10:33.946	0:00:02.696	14096	4
0003:11:21.218	0:00:03.326	14161	5
0003:11:29.676	0:00:03.318	14173	5
0003:12:07.670	0:00:02.636	14225	4
0003:12:15.964	0:00:02.738	14235	4

Bin Length 30 minutes Data Percentage 25 %



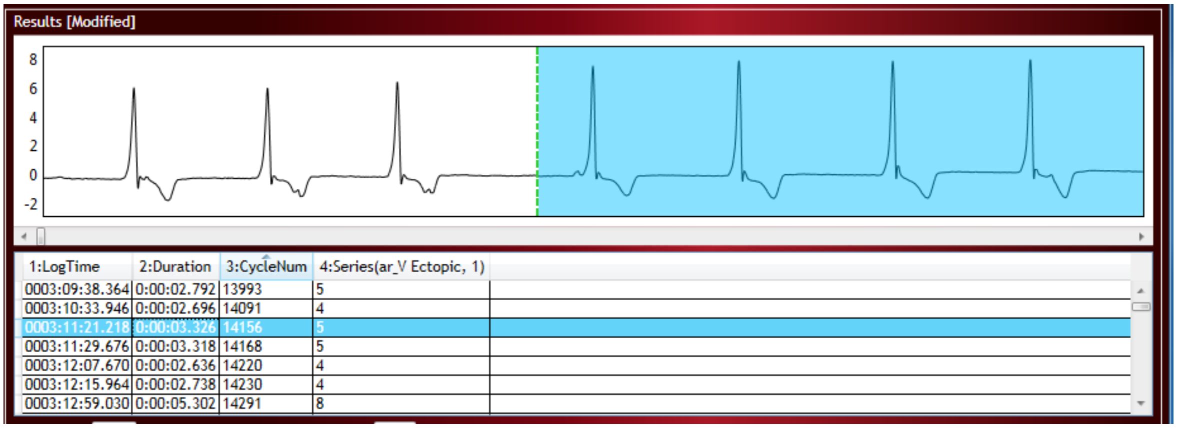
ET: 0003:09:23.224
Delta Time: 11363.224

If returned results of the search should not be included, right click your mouse on the highlighted waveform segment in the Data Insights dialog and Select **Reject.** Cycles will be removed from not only the graphical presentation but also from the table and **Match** information as well. You will note the number under the **Match** column decrease when a match is rejected. Rejecting a Match does not affect the derived data outside of the Data Insights dialog. In addition, A**dd Bad Data Marks** and **Delete Cycles** can be used to remove the data not only from the **Match** information, but also from Derived data (DRx and Data Reduction) files. To view data that has been removed using the **Reject** function, select **Results** from the pull-down menu from the top of the Data Insights dialog and select **Rejected Results**.

Working with Numerical Data

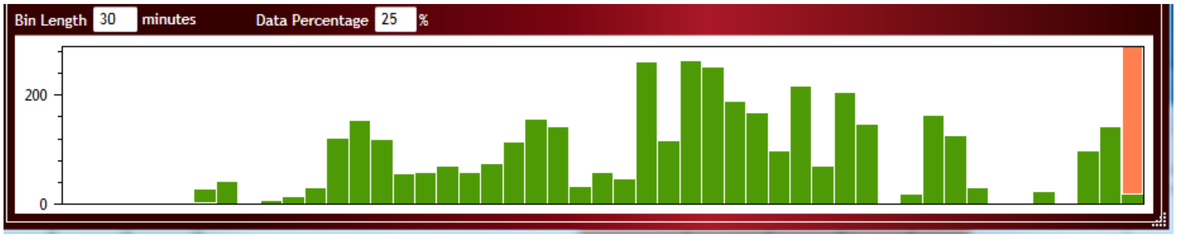
A scroll bar is available at the far right side of the table and can be used to scroll up or down in the data. Clicking on the column headers will sort the data from descending to ascending order and a second click will sort the data from ascending to descending order. Clicking on the **LogTime** column header will sort the data by time from beginning to the end of the dataset. A second click will sort the data from the end of the dataset to the beginning of the dataset.

This can be used in conjunction with scrolling through the waveform segments. This allows you to quickly sort **Match** values to find outliers. Left-clicking the mouse on a particular row then synchronizes that graphical results to display the graphical result that corresponds to that particular data row. You can then decide to remove any unwanted data using the **Reject**, **Bad Data Marks** or **Delete Cycle** functions.



1:LogTime	2:Duration	3:CycleNum	4:Series(ar_V Ectopic, 1)
0003:09:38.364	0:00:02.792	13993	5
0003:10:33.946	0:00:02.696	14091	4
0003:11:21.218	0:00:03.326	14156	5
0003:11:29.676	0:00:03.318	14168	5
0003:12:07.670	0:00:02.636	14220	4
0003:12:15.964	0:00:02.738	14230	4
0003:12:59.030	0:00:05.302	14291	8

As you scroll through that data, a red mark will be displayed at the bottom of the binned data to show the current segment location. This provides the approximate location of the **Match** within the dataset. This is helpful in providing an overall picture of the amount of data present within the binned data as well as the distribution of the **Match** results. See **Distribution Histogram** for additional information. If red segments are not visible (see below), it is likely that too few matches are visible within the graphical results window as compared to the total number of matches present within each bin, making the red match indicator more difficult to view. To see the match indicator, reduce the size of your bins or zoom out within the graphical results section to bring more matches into the viewing area.



Bin Length 30 minutes

Data Percentage 25 %

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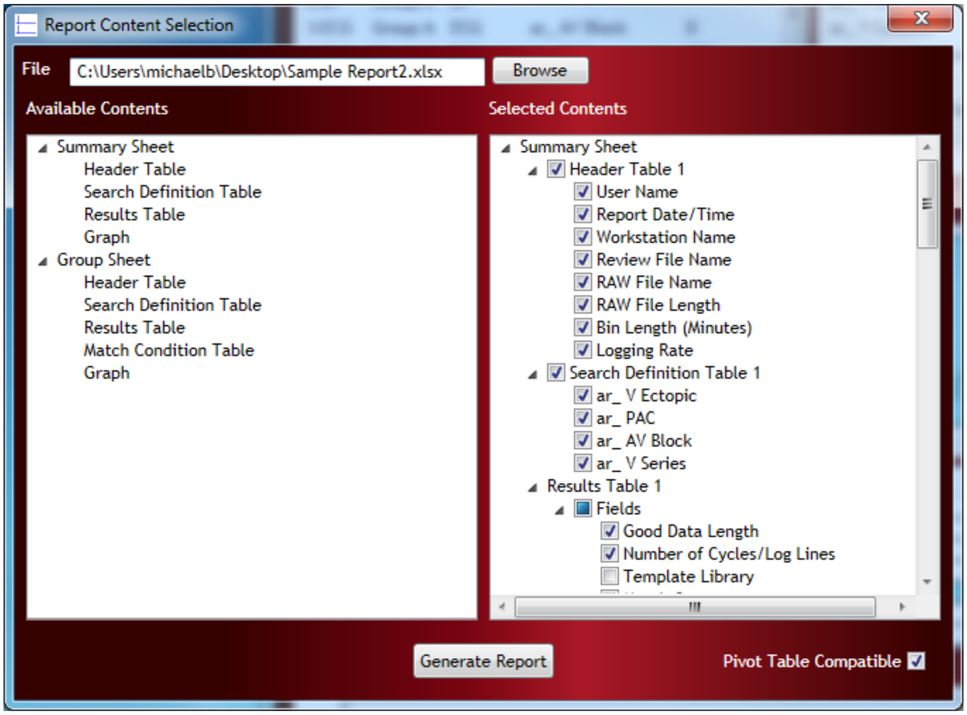
Reporting

Working through the Waveform and Derived data as described above, use the results of the Searches to identify and remove outliers by using the **Reject** feature, **Bad Data Marks** feature, or **Delete Cycles** feature. In addition, Data Insights can be used to validate existing analysis. Once the data has been properly analyzed and reviewed, the reporting tool can be used to generate individual and summary information.

Report Configuration

From the **File** menu, select **Report.** The **Report Content Selection** dialog will appear. The **Available Contents** section provides a listing of available tables for both the Summary and Group worksheet output. The corresponding information that can be included in each table is listed under the **Selected Contents** section.



File: C:\Users\michaelb\Desktop\Sample Report2.xlsx

Available Contents:

- Summary Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Graph
- Group Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Match Condition Table
  - Graph

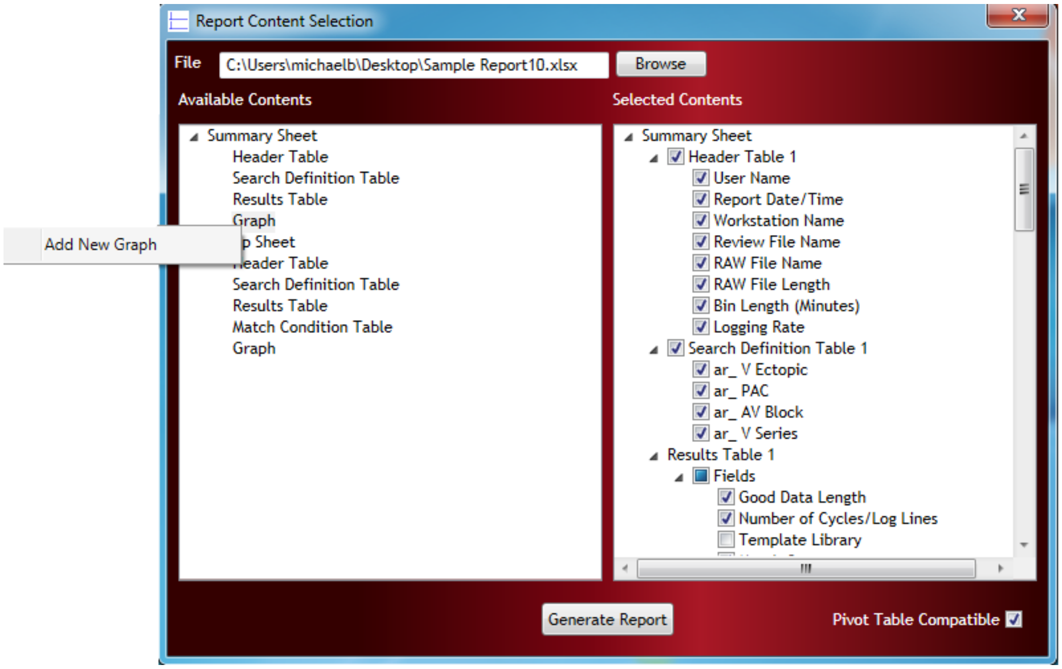
Selected Contents:

- Summary Sheet
  - ☑ Header Table 1
    - ☑ User Name
    - ☑ Report Date/Time
    - ☑ Workstation Name
    - ☑ Review File Name
    - ☑ RAW File Name
    - ☑ RAW File Length
    - ☑ Bin Length (Minutes)
    - ☑ Logging Rate
  - ☑ Search Definition Table 1
    - ☑ ar_ V Ectopic
    - ☑ ar_ PAC
    - ☑ ar_ AV Block
    - ☑ ar_ V Series
  - Results Table 1
    - ■ Fields
      - ☑ Good Data Length
      - ☑ Number of Cycles/Log Lines
      - ☐ Template Library

Pivot Table Compatible ☑

Select the checkbox next to each parameter that is to be included in the report (see **File Pull-Down Menu** for details of each item). Information that is not desired can be unckecked. Repeat this step for both the Summary Sheet and the Group Sheet. You will notice that identical information can be included any or all sheets. Once the report is generated, multiple worksheets will be created within one Microsoft® Excel workbook.

If a large number of Searches has been used, the need to create additional tables or graphs may be necessary. This will help to better manage and format the data as well as provide a more clear representation of the graphical information. It may be necessary to graph waveform informaton on multiple graph pages to provide more resolution of the waveform data as well as scaling information. To enable additional tables or graphs, right click on the desired line (table or graph) under the **Available Contents** section. A menu will be displayed allowign you to add the appropriate function. Below shows the addition of an additonal graph page for the **Summary Sheet**.



File: C:\Users\michaelb\Desktop\Sample Report10.xlsx

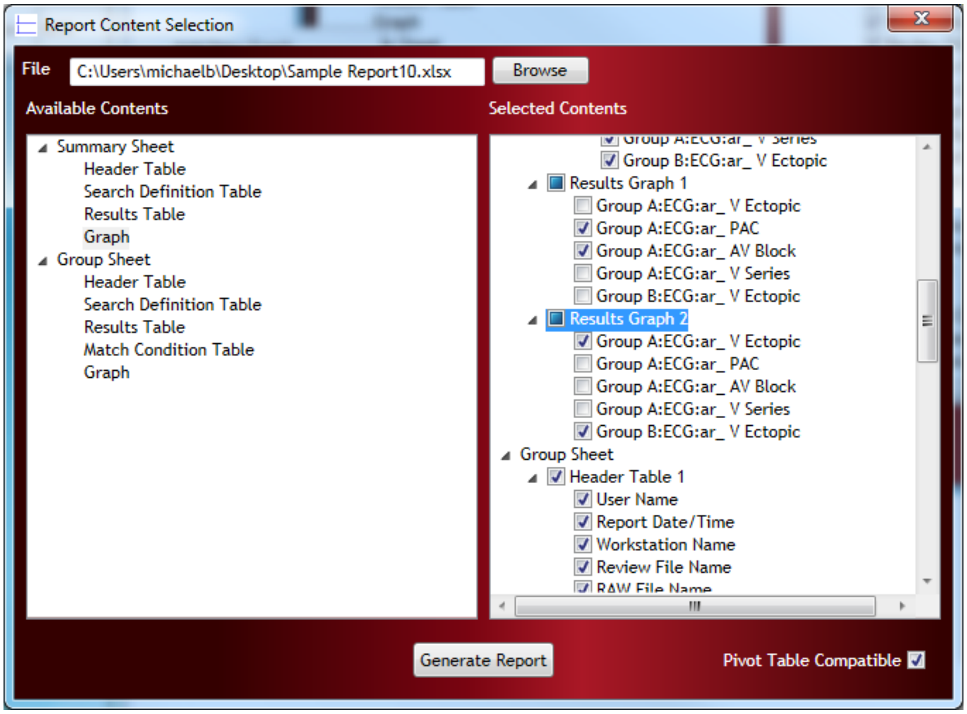
Available Contents:

- Summary Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Graph
- p Sheet
  - eader Table
  - Search Definition Table
  - Results Table
  - Match Condition Table
  - Graph

Selected Contents:

- Summary Sheet
  - ☑ Header Table 1
    - ☑ User Name
    - ☑ Report Date/Time
    - ☑ Workstation Name
    - ☑ Review File Name
    - ☑ RAW File Name
    - ☑ RAW File Length
    - ☑ Bin Length (Minutes)
    - ☑ Logging Rate
  - ☑ Search Definition Table 1
    - ☑ ar_ V Ectopic
    - ☑ ar_ PAC
    - ☑ ar_ AV Block
    - ☑ ar_ V Series
  - Results Table 1
    - ▣ Fields
      - ☑ Good Data Length
      - ☑ Number of Cycles/Log Lines
      - ☐ Template Library

After adding an additional graph or table, **Selected Contents** will update according. You will notice that two graphs are now included on the **Summary Sheet**, labeled Results **Graph 1** and Results **Graph 2**. In this example, results of the Ectopic search for Subjects one and two were grouped together on Graph 2 while additional search information was applied to **Graph 1**. Repeat as needed based on the number of search information is being used and the desired format.



File: C:\Users\michaelb\Desktop\Sample Report10.xlsx

Available Contents:

- Summary Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Graph
- Group Sheet
  - Header Table
  - Search Definition Table
  - Results Table
  - Match Condition Table
  - Graph

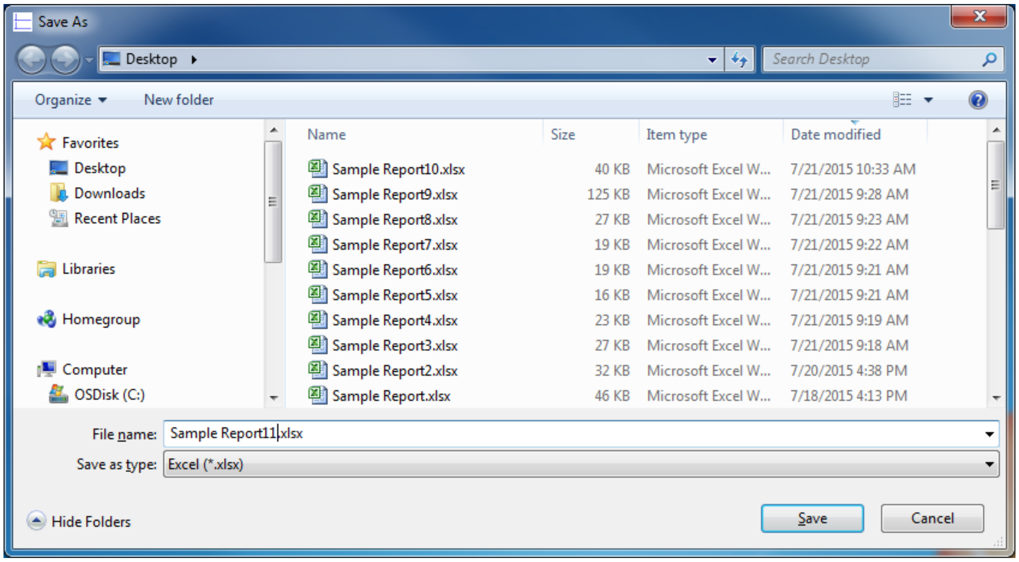
Selected Contents:

- ☑ Group B:ECG:ar_ V Ectopic
- ▣ Results Graph 1
  - ☐ Group A:ECG:ar_ V Ectopic
  - ☑ Group A:ECG:ar_ PAC
  - ☑ Group A:ECG:ar_ AV Block
  - ☐ Group A:ECG:ar_ V Series
  - ☐ Group B:ECG:ar_ V Ectopic
- ▣ Results Graph 2
  - ☑ Group A:ECG:ar_ V Ectopic
  - ☐ Group A:ECG:ar_ PAC
  - ☐ Group A:ECG:ar_ AV Block
  - ☐ Group A:ECG:ar_ V Series
  - ☑ Group B:ECG:ar_ V Ectopic
- Group Sheet
  - ☑ Header Table 1
    - ☑ User Name
    - ☑ Report Date/Time
    - ☑ Workstation Name
    - ☑ Review File Name
    - ☑ RAW File Name

The format of the output can also be changed to accommodate the use of Pivot Tables. Pivot Tables can be used for additional analysis or grouping of information or for importing into other programs. If a Pivot Table ready output is desired, check the **Pivot Table Compatible** checkbox.

Creating Report

After selecting the appropriate information for the report, use the **Browse** button to define a location and name for the report. After defining the location and name, you will be returned to the **Report Content Selection** dialog.

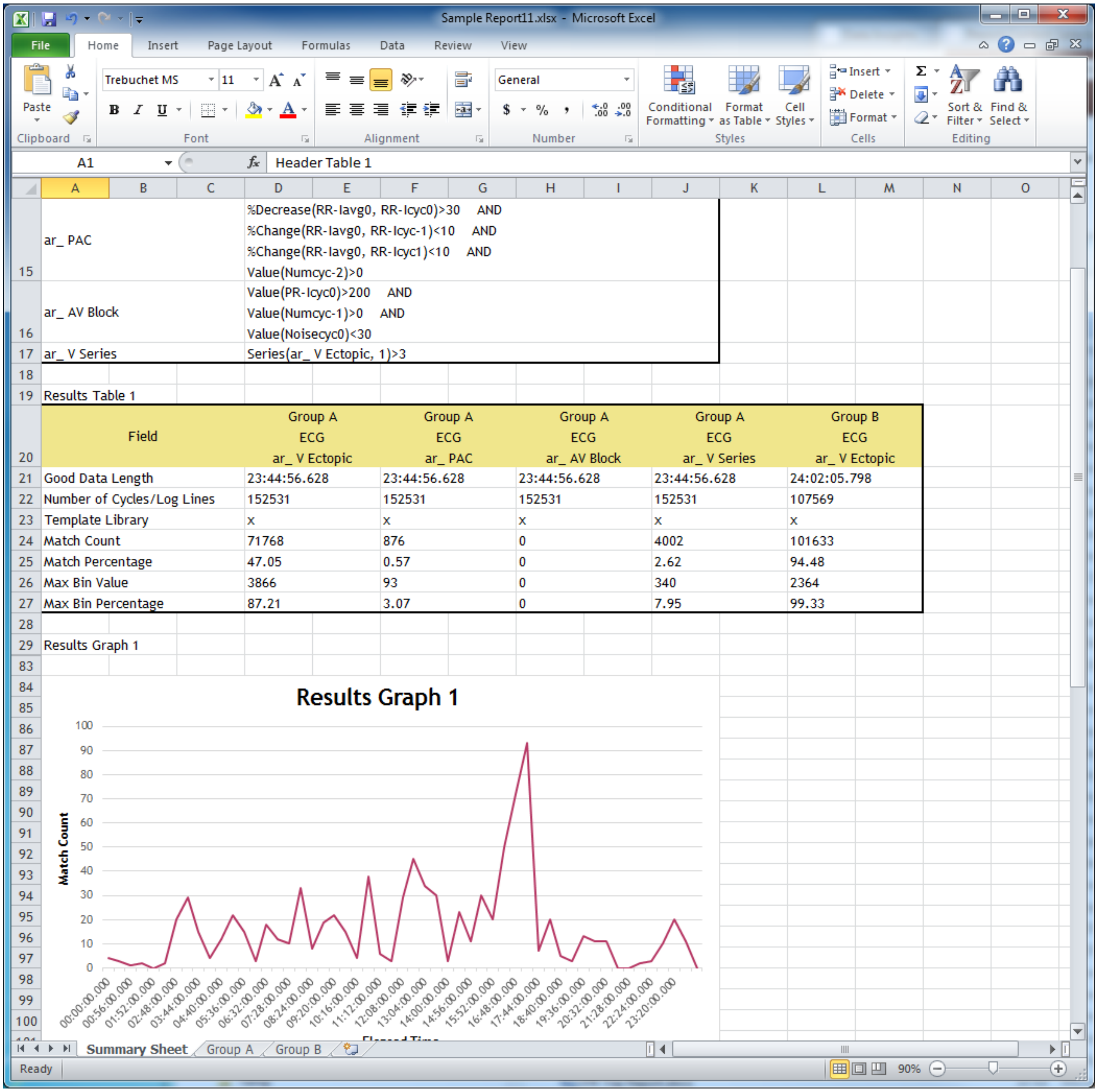


Name	Size	Item type	Date modified
Sample Report10.xlsx	40 KB	Microsoft Excel W...	7/21/2015 10:33 AM
Sample Report9.xlsx	125 KB	Microsoft Excel W...	7/21/2015 9:28 AM
Sample Report8.xlsx	27 KB	Microsoft Excel W...	7/21/2015 9:23 AM
Sample Report7.xlsx	19 KB	Microsoft Excel W...	7/21/2015 9:22 AM
Sample Report6.xlsx	19 KB	Microsoft Excel W...	7/21/2015 9:21 AM
Sample Report5.xlsx	16 KB	Microsoft Excel W...	7/21/2015 9:21 AM
Sample Report4.xlsx	23 KB	Microsoft Excel W...	7/21/2015 9:19 AM
Sample Report3.xlsx	27 KB	Microsoft Excel W...	7/21/2015 9:18 AM
Sample Report2.xlsx	32 KB	Microsoft Excel W...	7/20/2015 4:38 PM
Sample Report.xlsx	46 KB	Microsoft Excel W...	7/18/2015 4:13 PM

File name: Sample Report11.xlsx

Save as type: Excel (*.xlsx)

Click on the **Generate Report** button to create the report. Navigate to the location of the file and open the file to view the contents. Below, the output for the Summary page is shown. This provides information for all subjects based on the selections made in the reporting dialog.



Header Table 1

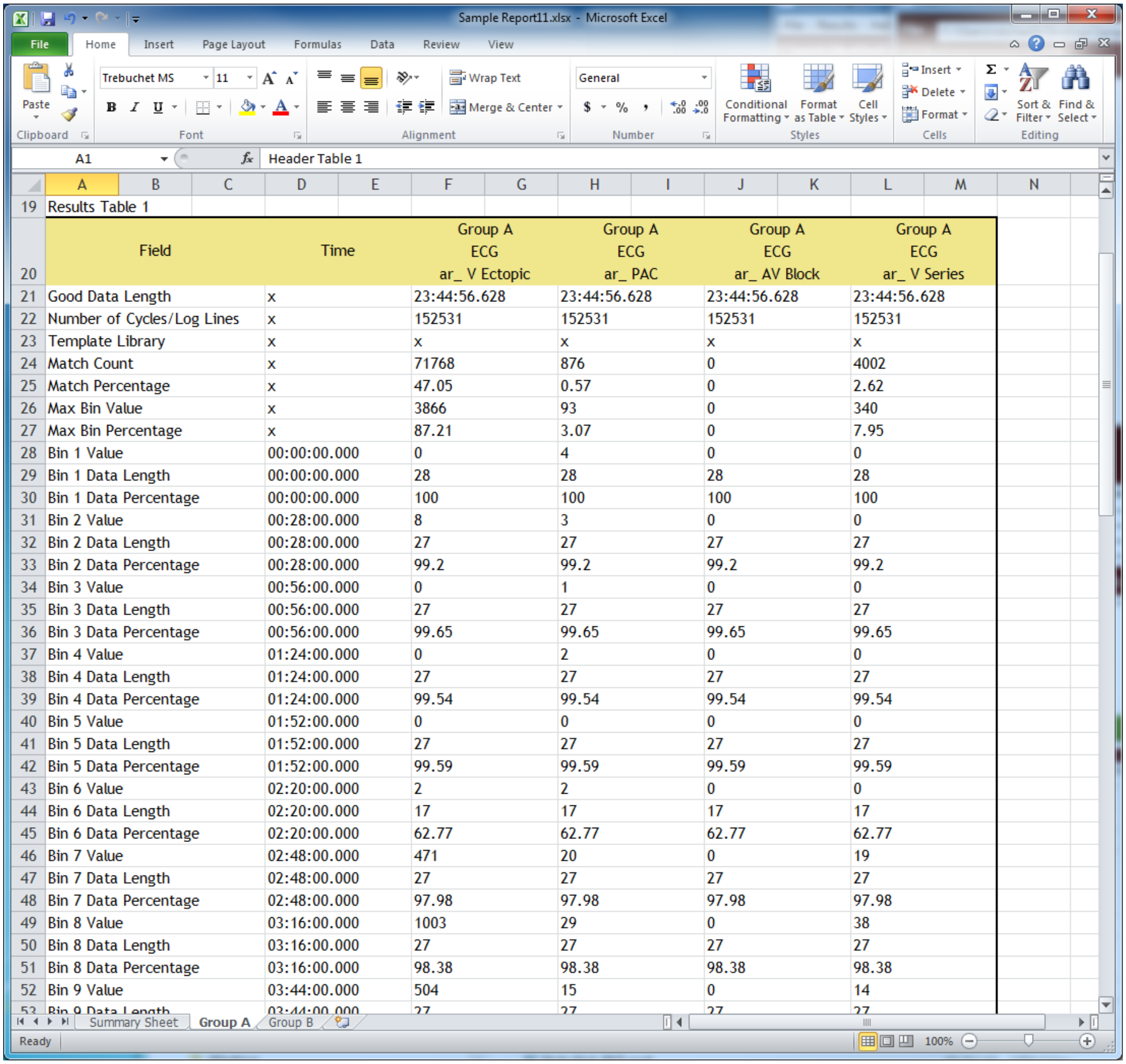
ar_ PAC	%Decrease(RR-Iavg0, RR-Icyc0)>30 AND %Change(RR-Iavg0, RR-Icyc-1)<10 AND %Change(RR-Iavg0, RR-Icyc1)<10 AND Value(Numcyc-2)>0
ar_ AV Block	Value(PR-Icyc0)>200 AND Value(Numcyc-1)>0 AND Value(Noisecyc0)<30
ar_ V Series	Series(ar_ V Ectopic, 1)>3

Results Table 1

Field	Group A ECG ar_ V Ectopic	Group A ECG ar_ PAC	Group A ECG ar_ AV Block	Group A ECG ar_ V Series	Group B ECG ar_ V Ectopic
Good Data Length	23:44:56.628	23:44:56.628	23:44:56.628	23:44:56.628	24:02:05.798
Number of Cycles/Log Lines	152531	152531	152531	152531	107569
Template Library	x	x	x	x	x
Match Count	71768	876	0	4002	101633
Match Percentage	47.05	0.57	0	2.62	94.48
Max Bin Value	3866	93	0	340	2364
Max Bin Percentage	87.21	3.07	0	7.95	99.33

Results Graph 1

At the bottom of the workbook, you will see three worksheets. The first is the **Summary Sheet** that was displayed when the file was opened. The **Group** sheets provide information for each subject used in the study. More detailed information can be included in this sheet that includes specific bin information such as time, data length and results of the searches for a given bin. Additionally, graphical elements are located at the bottom of the page for the subject.



A1 — Header Table 1

19 Results Table 1

	Field	Time	Group A ECG ar_ V Ectopic	Group A ECG ar_ PAC	Group A ECG ar_ AV Block	Group A ECG ar_ V Series
21	Good Data Length	x	23:44:56.628	23:44:56.628	23:44:56.628	23:44:56.628
22	Number of Cycles/Log Lines	x	152531	152531	152531	152531
23	Template Library	x	x	x	x	x
24	Match Count	x	71768	876	0	4002
25	Match Percentage	x	47.05	0.57	0	2.62
26	Max Bin Value	x	3866	93	0	340
27	Max Bin Percentage	x	87.21	3.07	0	7.95
28	Bin 1 Value	00:00:00.000	0	4	0	0
29	Bin 1 Data Length	00:00:00.000	28	28	28	28
30	Bin 1 Data Percentage	00:00:00.000	100	100	100	100
31	Bin 2 Value	00:28:00.000	8	3	0	0
32	Bin 2 Data Length	00:28:00.000	27	27	27	27
33	Bin 2 Data Percentage	00:28:00.000	99.2	99.2	99.2	99.2
34	Bin 3 Value	00:56:00.000	0	1	0	0
35	Bin 3 Data Length	00:56:00.000	27	27	27	27
36	Bin 3 Data Percentage	00:56:00.000	99.65	99.65	99.65	99.65
37	Bin 4 Value	01:24:00.000	0	2	0	0
38	Bin 4 Data Length	01:24:00.000	27	27	27	27
39	Bin 4 Data Percentage	01:24:00.000	99.54	99.54	99.54	99.54
40	Bin 5 Value	01:52:00.000	0	0	0	0
41	Bin 5 Data Length	01:52:00.000	27	27	27	27
42	Bin 5 Data Percentage	01:52:00.000	99.59	99.59	99.59	99.59
43	Bin 6 Value	02:20:00.000	2	2	0	0
44	Bin 6 Data Length	02:20:00.000	17	17	17	17
45	Bin 6 Data Percentage	02:20:00.000	62.77	62.77	62.77	62.77
46	Bin 7 Value	02:48:00.000	471	20	0	19
47	Bin 7 Data Length	02:48:00.000	27	27	27	27
48	Bin 7 Data Percentage	02:48:00.000	97.98	97.98	97.98	97.98
49	Bin 8 Value	03:16:00.000	1003	29	0	38
50	Bin 8 Data Length	03:16:00.000	27	27	27	27
51	Bin 8 Data Percentage	03:16:00.000	98.38	98.38	98.38	98.38
52	Bin 9 Value	03:44:00.000	504	15	0	14
53	Bin 9 Data Length	03:44:00.000	27	27	27	27

Appendix 1

Hints and Troubleshooting

General Configuration

- OK button is not available for selection after making changes to edit fields. Ensure that all information within boxes outlined in red have been filled in. If information is absent for any field outlined in red, the OK button will not be available.
- Use of the Average function (**avg**) is based on the current averaging interval defined in the Logging Rate field. This is the same logging rate applied to the derived output (DRx) files.
- Derived data is displayed under the **Results** section within the Data Insights dialog. The number of columns and the information provided in each column will differ based on the search criteria (Search, Series, Template, Real Time, etc.) used. Some examples are below.
    - Search: Utilizes existing searches within its search clause and provides Cycle Number as the output.
    - Series: Utilizes existing searches within its search clause and provides Cycle Number and the number of cycles found for that data segment or **Series** query**.**
- **Match Condition Table** displays the specific searches used and the conditions for the searches. In addition this table logs the time the match was found, the duration, and the value for each match. If a number of searches are utilized, this could result in a very large number of entries into the report. An informational message may be posted informing the user that information will be truncated. You can remove the number of items selected for the report to address this. This information is typically reported when doing **Series** based searches because it provides content of the runs as opposed to only the number of runs encountered.

Search Configuration

- It is important to note that Searches are specific to a channel and specie type. For example, searches constructed using ECG parameter information cannot be applied to pressure channels. Searches should be created specific to both specie and signal type. Searches that do not match the signal type will not be allowed to be dragged and dropped on that channel.
- When importing searches, referenced searches must also be present in the.xml file that is being imported. If the referenced search is not contained in the xml file, the search or searches using the missing reference will not be loaded. Additionally, none of the searches in the .xml file being imported should be present in the current **Search** list. Remove any duplicates before importing. In some cases it may be advisable to remove all searches prior to importing a new list.

  To delete searches, select all that apply. This can be done one at a time or can be done using the Control or Shift keys and selecting multiple Searches at once. Right click the mouse and select **Delete Selected Searches**.
- Selection of **Species** within the **Search Entry Dialog** is dependent upon the data loaded into Review. If data is loaded that has been specified as dog, selection of a different species cannot be performed. Data with the desired species must be loaded into Review in order to create the species specific search. Additionally, **Searches** identified as a one species cannot be applied to data from a different species.

- A **Series** search depends on an embedded search with one or more of it clauses. If the embedded clauses are not applied to a channel, or channels, the **Series** search will not be able to be dragged and applied to a channel.

Analysis

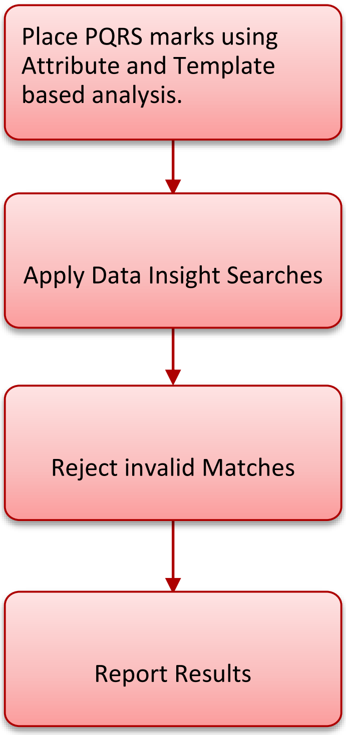
- Templates created in previous versions are not backwards compatible. Contact Technical Support if specific version information is needed. Error messages will be posted stating the adding the Template Library has failed.
- Performing searches looking for increases and decreases greater than a specified value can yield negative results. If only positive results are desired, construct a search clause designating the specific range desired, for example, greater than 0.
- Performing a Search using NUM (cycle number) ensure that the correct channel (algorithm) has been selected. If the incorrect algorithm has not been selected, the Search cannot be applied to the channel. Also, if using NUM as a comparison within a clause, ensure that all clauses using NUM are from the same algorithm. It is possible to apply a Search where NUM has been constructed from different algorithms. However, **Match** results will equal zero.
- Adding **Bad Data Marks** (**BDM**) may appear to slow down analysis. Adding **BDM** at the beginning of the file will update quickly and allow continued analysis or changes within Data Insights. However, adding **BDM** at the end of the file while parameters are updating will result in the system appearing to slow down. This is due to the fact that **BDM** placed at the end of the file will wait for the parameters to update before applying the **BDM**. Removing data in chronological order typically does not show this behavior.

  This may often be seen when sorting on the derived parameters and removing data using **BDM**. Since the data is no longer in chronological order, removal of data is dependent upon completion of all calculations. Two segments next to each other may be from the opposite ends of the file. Removal of one segment may be performed quickly if it is at the beginning of the dataset. However, removal of the next segment may need to wait for calculations to be completed before applying the BDM updates.
- Adding or removing search clauses will result in all rejected data to be removed. Changing values in the clauses will not affect those results that have been rejected.
- It is helpful to use Noise clauses in Searches. This permits the exclusion of noisy data from the **Match** results.

Appendix 2

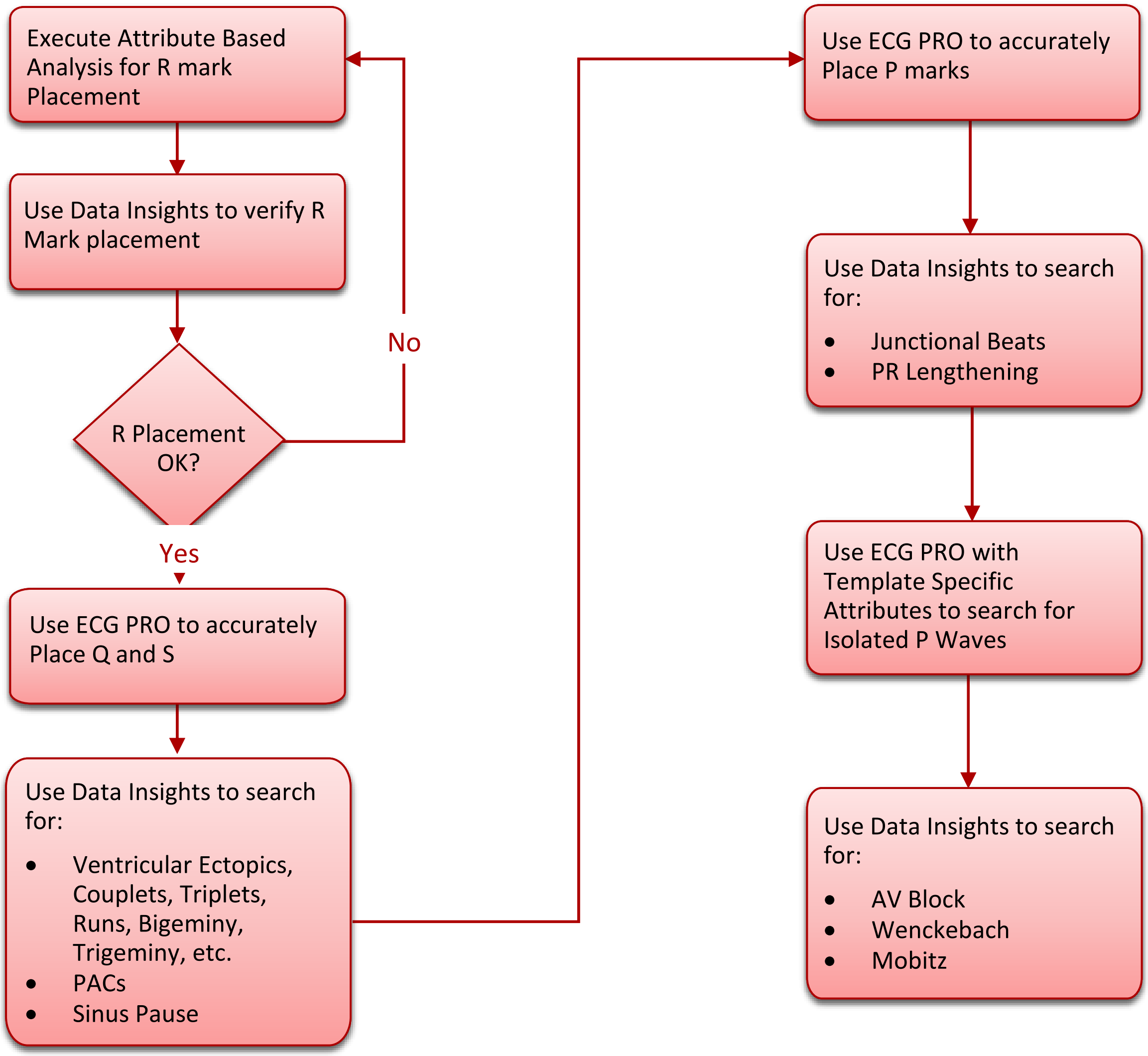
Data Insights Process Flow

High Level Overview



Detailed Overview

The chart below outlines potential process flows for analyzing data. The predefined Searches can be used to accomplish a number of analysis tasks described but construction of additional searches may be required.


Execute Attribute Based Analysis for R mark Placement
Use Data Insights to verify R Mark placement
R Placement OK?
No
Yes
Use ECG PRO to accurately Place Q and S
Use Data Insights to search for:
• Ventricular Ectopics, Couplets, Triplets, Runs, Bigeminy, Trigeminy, etc.
• PACs
• Sinus Pause
Use ECG PRO to accurately Place P marks
Use Data Insights to search for:
• Junctional Beats
• PR Lengthening
Use ECG PRO with Template Specific Attributes to search for Isolated P Waves
Use Data Insights to search for:
• AV Block
• Wenckebach
• Mobitz