

DSI Ponemah™

Implantable Telemetry System Manual



OVERVIEW

This manual highlights Ponemah's Data Insights feature. This document will provide an overview of Data Insights, as well as detailed procedures on how to use it to assess the quality of your data, as well as locate, classify, and report on normal or abnormal cycles.

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WELCOME

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

This manual will help you start using Data Insights to assess the quality of your data, as well as locate, classify, and report on normal or abnormal cycles. The structure of the manual was designed to sequentially guide you through using your Data Insights.

WHAT YOU WILL BE LEARNING

1. Understand Data Insights' interactive dialog.
2. Executing Searches.
3. Navigating Results.
4. Processing Results.
5. Reporting Results.
6. Building Custom Search Definitions.

DATA INSIGHTS

Data Insights allows researchers to assess the quality of their data analysis and target problem areas for additional cleaning and analysis without having to manually over read the dataset. Data Insights reveals these problem areas by applying user-defined search rules to the dataset and displaying cycles that match the search criteria. Match results are displayed in graphical and tabular formats to provide researchers a multi-faceted view of each search result and how the results are distributed throughout their dataset. This provides researchers the necessary information to better understand their data and make an informed decision on whether or not to exclude certain sections of data due to signal artifact or data dropout without investing a significant amount of time.

In addition to searches for data validation and analysis, researchers may create Data Insights searches to locate, present, and report on any data pattern or anomaly within the dataset, e.g., cardiac arrhythmias. The use of Data Insights permits the user to move beyond snapshots of data for efficient coverage of large volumes of data.

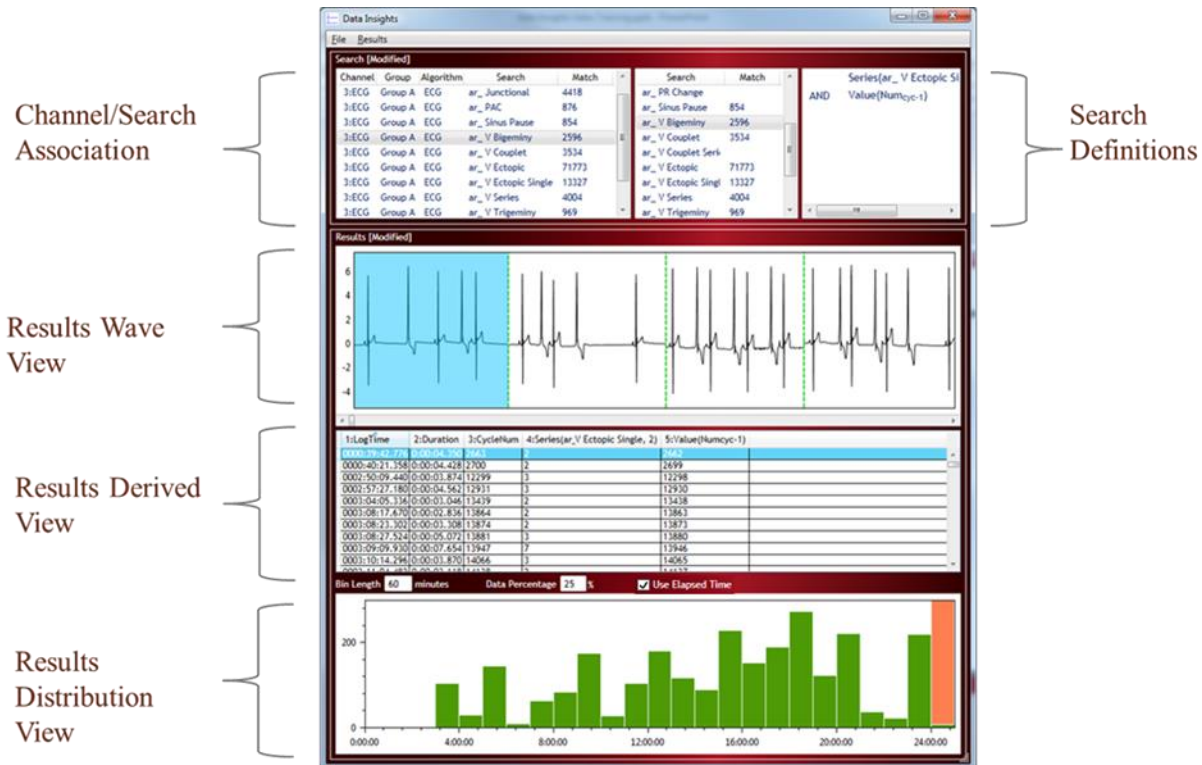
Using Data Insights searches, researchers can optimize their data review and analysis process to achieve consistent, reproducible results for reporting purposes.

Note: Data Insights is a Review only feature.

DATA INSIGHTS DIALOG OVERVIEW

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

The Data Insights' dialog is displayed below:



SEARCH SECTION

The **Search** section of the dialog provides a means to define search criteria and associated desired searches to channels to populate the **Results** section. The Search section is split into three grids:

- **Channel/Search Association and Match Results** (left grid)

The Channel/Search Association grid includes the physical channel, Subject name, analysis module assigned to that channel and all searches that have been applied to that channel. In the above example, the ar_V Bigeminy search has been applied to channel 3.

- **Search and Match grid** (middle 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 associated channels. A list of predefined Searches is present by default and available for use.

The list of default Searches follow the following naming convention:

- an_ Searches used to aid in data analysis. Currently used to help construct high value ECG PRO Template Libraries.
- ar_ Searches used to aid in arrhythmia detection.
- dv_ Searches used to aid in data validation by quickly exposing outliers and potentially mismarked data that may require focused attention.

To learn more about the default Searches, please see the **Data Insights** section of the **Software Appendix**.

- **Search Definition**
(right grid)

This section displays the Search Definition for a given Search. Click on any Search under the **Search** header and the search criteria used to define the search will be displayed within this grid. Searches are composed of one or more Search Clauses that may be combined using Boolean operators (AND, OR). One or more Search Definitions may be associated with each acquired signal.

See **Customizing Search Definitions** to learn more about Search Definitions.

RESULTS SECTION

The **Results** section of the dialog contains graphical and numerical information based on the results from the searches that have been performed. This section is also divided into three sections:

- **Results Wave View**
(top)

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.

- **Results Derived View**
(middle)

Displays numeric data for each clause within the search, as well as the Log Time associated with the match. The example below illustrates how each clause of the Search Definition Clauses is associated with its own column in the Derived View.

1:LogTime	2:CycleNum	3:%Decrease(RR-Icyc-1, RR-Icyc0)	4:%Change(RR-Icyc-1, RR-Icyc1)	5:Value(Numcyc-2)
0005:48:43.812	30438	51.1236	2.247191	30436
0002:16:03.926	12228	49.54128	9.174312	12226
0003:58:33.942	20862	41.29213	11.51685	20860
0021:52:47.866	10166	18.69159	18.2243	10164
0021:52:48.784	10168	18.57708	16.20553	10166
0020:54:25.344	4766	17.63441	8.387096	4764
0006:55:11.506	36036	17.50663	16.97613	36034

%Decrease(RR-Icyc-1, RR-Icyc0) > 10
AND %Change(RR-Icyc-1, RR-Icyc1) < 20
AND Value(Numcyc-2) > 0

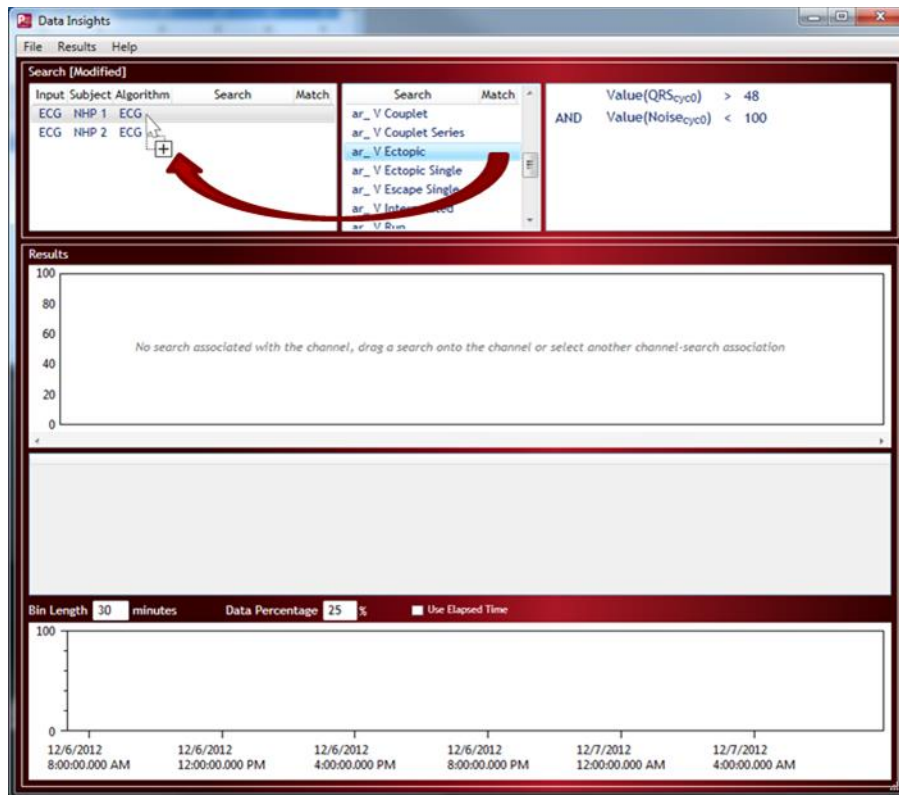
- **Results Distribution View**
(bottom)

Displays a histogram graph of the match results binned into user defined time segments to visualize the result distribution across the period of data loaded into Ponemah Review.

EXECUTING SEARCHES

To apply a **Search** to a channel, click-and-drag a Search from the **Search and Match** 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. Drag-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.

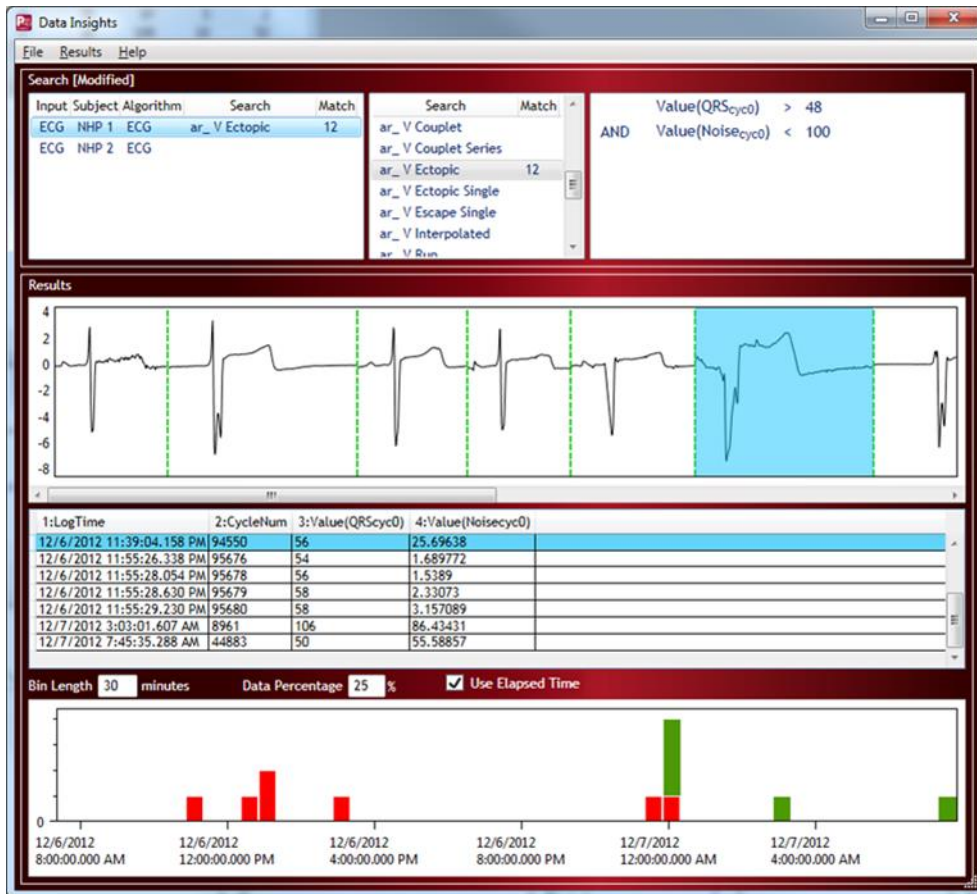
Note: Searches are specific to a channel and specie type. For example, Searches constructed using ECG parameter information cannot be applied to pressure channels. Searches should be created specific to both specie and signal type. Searches that do not match the signal type will not be allowed to be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



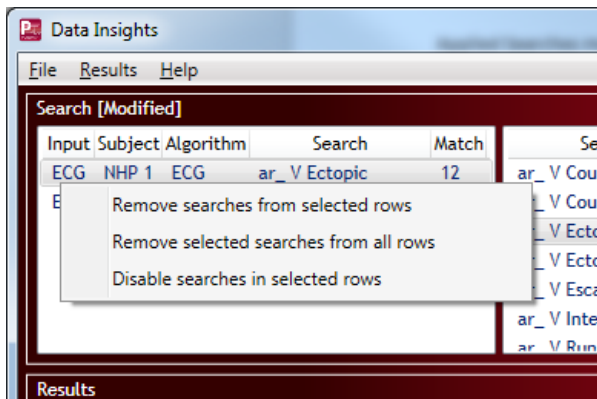
Once associated with a channel, the Search name will appear under the **Search** column next to the channel information. Analysis will automatically be performed, populating the number of occurrences matching the search criteria under the **Match** column and the **Results** section.



Warning: The Data Insights match results reflects the current state of the cycle marks and, therefore, dynamically updates if the cycle marks are changed; e.g. reanalyzing data with the analysis module or manually moving marks may change the match results.



Applied Searches may be disassociated from a channel by right-clicking the mouse on any of the Channel/Searches pairs. This will display a pop-up menu to permit the Search to be removed or disabled across one or multiple channels.



NAVIGATING RESULTS

Data is displayed in the **Results** section by clicking on a specific Channel/Search. Only one signal may be viewed at a time. Data is scaled in user units.

NAVIGATING THE WAVE VIEW

The following may be used to move forward (toward the end of the data) and backward (toward the beginning of the data) through the results in the Wave View

- **Scroll Bar** The scroll bar below the Wave View is used to move through the data by using the mouse to drag the scroll bar left and right.
- **Mouse Wheel** The mouse wheel may also be used to scroll through the match results. With the cursor hovering within the Wave View, scrolling the mouse wheel up will move forward in the data, while scrolling down will move backwards in the data.
- **Arrow Keys** The Right Arrow key moves forward in the data, while the Left Arrow key moves backwards. Progression will be one result at a time.
- **Page Up/Page Down** The Page Up key moves forward in the data, while the Page Down key moves backwards in the data. Progression will be one result page at a time.

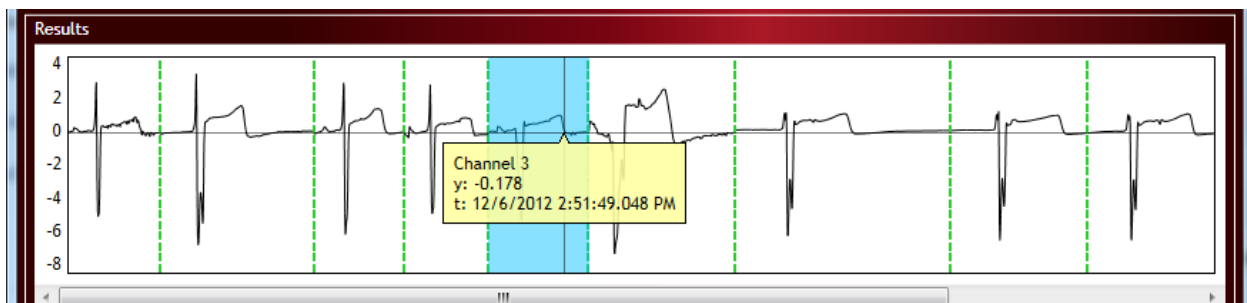
SCALING/ZOOM

The Wave View autoscales the y-axis range based on the match results being displayed.

Use **<Ctrl> + Mouse Wheel** to change the x-axis range. Scrolling down will zoom out, compressing the data and effectively displaying more results within the Wave View. Scrolling up will zoom in, expanding the data to display fewer results. Alternatively, **left-click-and-drag** may also be used to zoom in on results, providing more control of exactly which Results will be displayed by the zoom.

Note: Zooming out may not be performed via a click-and-drag function. Use the **<Ctrl> + Mouse Wheel** to zoom out as described above.

Additionally, pressing **<Ctrl> + Left-click** on a point in the Wave View will display its corresponding x- and y-axis values at that point.



PROCESSING RESULTS

The following features assist in the processing of large sets of results and the identification of appropriate thresholds for use in search definitions.

SORTING RESULTS BY SEARCH INPUT

By default, the search results are ordered chronologically. However, the search results may be sorted by any of the columns in the Results Derived View by clicking on the column header. Sorting updates the order of results in both the Results Derived View and the Results Wave View. Clicking the **LogTime** column header will bring the results back to their sort default by time.

RESULT ACTIONS

The following are a list of actions that can be taken on each result and their associated hot keys and definitions:

- **Reject**
<Ctrl> + <R>
Removes the match result(s) from the Wave View, Derived View, and Distribution View and reduces the number of matches listed in the **Match** columns of the associated searches. Rejecting a match result does not affect the derived data outside of the Data Insights dialog, it simply removes it as a match.
- **Add Bad Data Marks**
<Ctrl> +
Adds Bad Data Marks around the currently selected match result(s) within the Ponemah Review graph pages. This feature functions the same as using Bad Data Marks in Review (outside of using Data Insights). This will result in the match result being removed from the Search Results, as well as the cycle being removed from the data reported to the Derived Parameter and Data Reduction List Views.
- **Delete Cycles**
<Ctrl> + <D>
Removes the validation marks from match result cycle without adding Bad Data Marks. This will result in the match result being removed from the Search Results, as well as the cycle being removed from the data reported to the Derived Parameter and Data Reduction List Views.

Multiple results may be selected and either rejected as not belonging to the set of results or marked as bad data to prevent further analysis on the data samples. The number of results that may be selected at once is limited to less than 5000 results. A notification will popup if this limit is exceeded.

Note: These Result Actions may be executed from the Results Wave and Results Derived Views.

SYNCHRONIZING RESULTS

A single mouse left-click on a result in the Wave View will highlight the result and synchronize it with its associated numerical Result in the Derived View. Similarly, if a numeric result is selected from the Derived View, Data Insights will select and synchronize to the result in the Wave View.

A double left-click on the result from either the Wave View or the Derived View will also synchronize with the Parameter and Data Reduction List Views within the main Ponemah dialog, as well as with all other configured graph pages.

To aid in locating the exact match being synchronized to within the Ponemah Primary Graph page for additional observation, a background color may be applied to the match results. This is also helpful when over-reading data to determine if regions have already been identified by an applied Search within Data Insights.

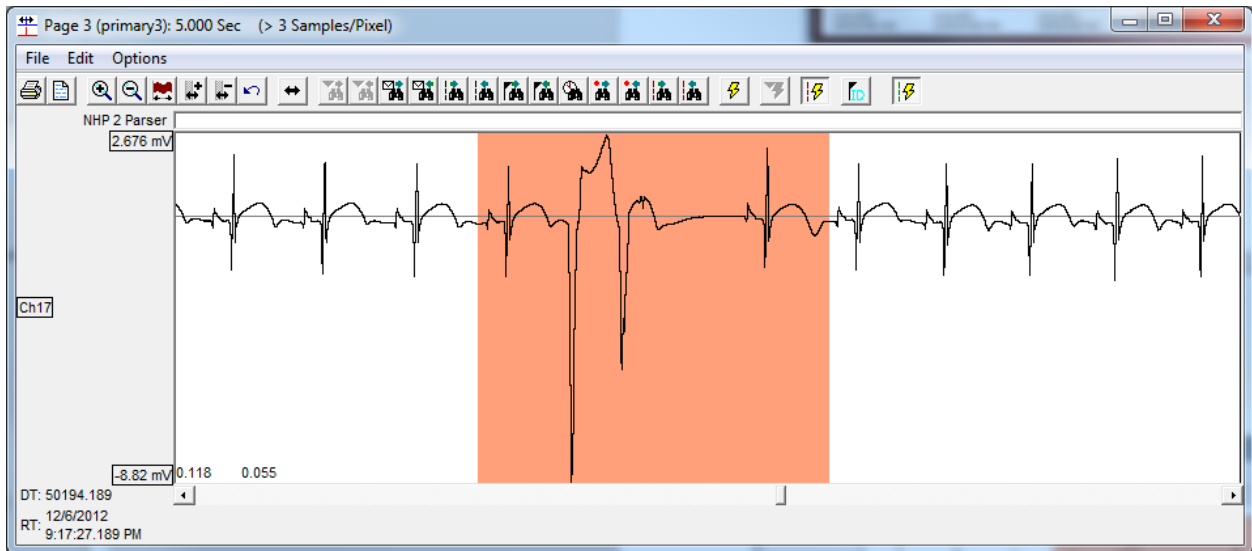
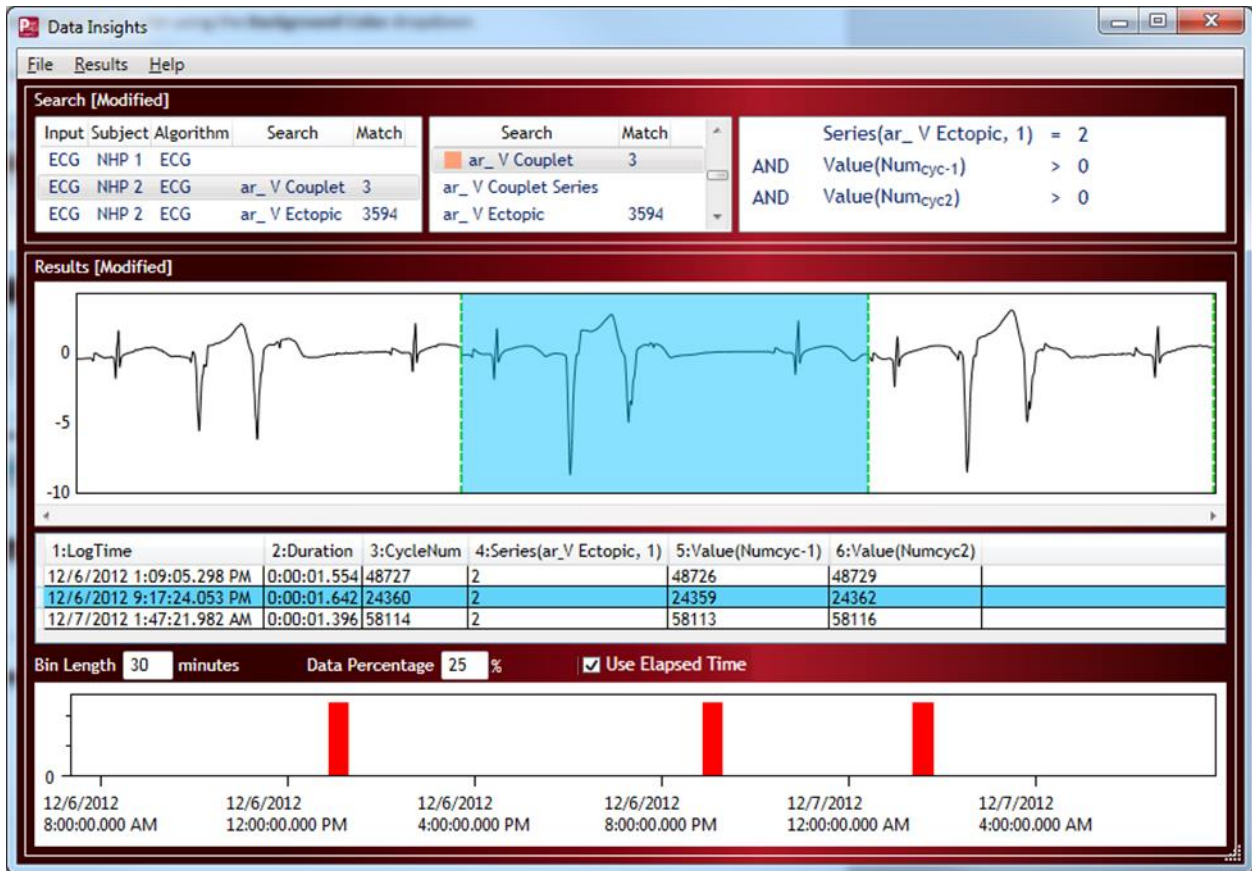
To add a background color for a particular Search:

1. Locate the Search of interest within the **Search and Match Grid** (center grid in the top section).
2. Double-click the Search name.
3. Check the checkbox for **Display Background Color**.
4. Select the desired background color using the **Background Color** dropdown.
5. Click **OK**.
6. Double-click a match result to synchronize with the **Primary Graph**.

If the user decides the result within a colored region should not be included as a match, it may be rejected by right-clicking the mouse on the colored waveform segment in the Primary Graph and select **Reject Selected Search Result**. Match Results will be removed from Search Results and added to the Reject Results. Rejecting a result does not affect the derived data outside of the Data Insights dialog. In addition, **Add Bad Data Marks** and **Delete Cycles** can be used from the Primary Graph page to remove mismarked data from the Derived Parameter and Data Reduction List Views and subsequently the Data Insights Search Results. 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**.

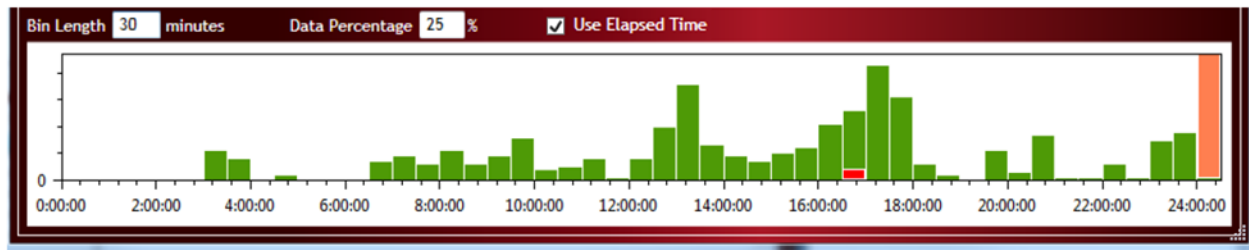
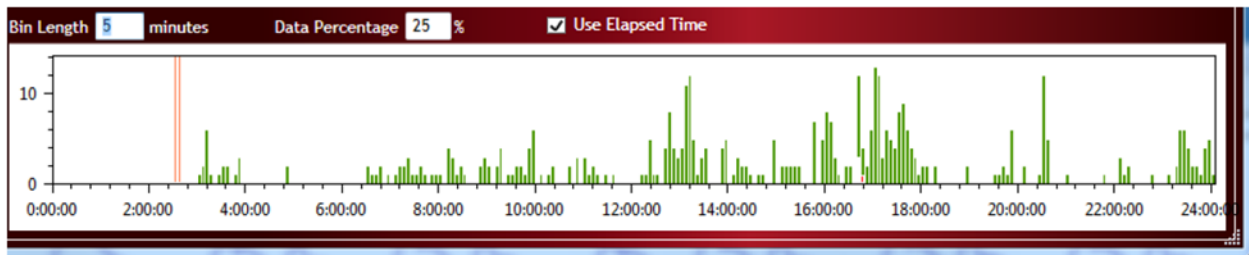
Note:

- The Search column within the **Search and Match Grid** will display the selected color associated with the search.
- 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.

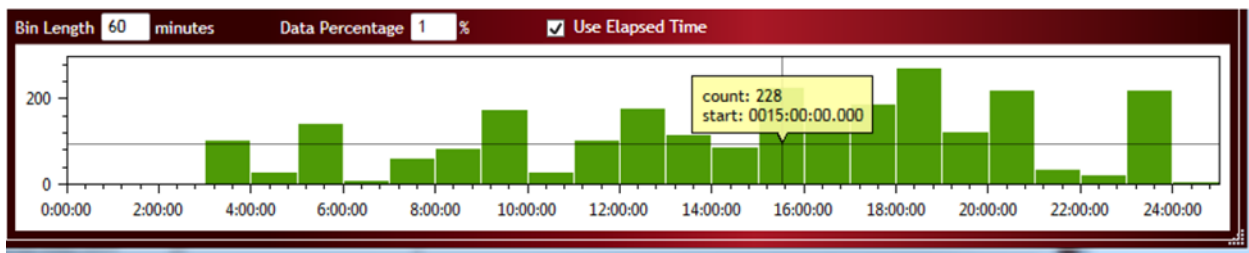


RESULTS DISTRIBUTION VIEW

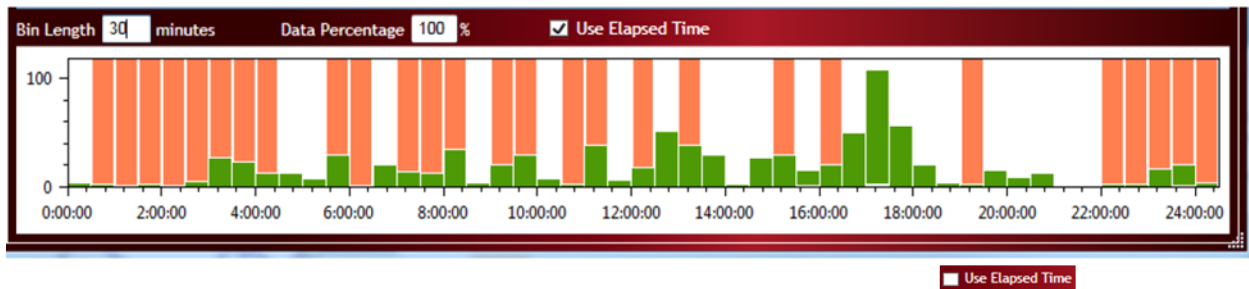
Match results are also displayed in a histogram. The width of each histogram bar corresponds to a user defined **Bin Length** (time in minutes), which only impacts the visualization of the data. To modify the Bin Length, simply type in the desired length, in minutes, and the graphical component will update automatically. In the examples below, the **Bin Lengths** have been set to 5-minute and 30-minute intervals for comparison.



The height of each green histogram bar corresponds to the number of matches in the bin. 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.



If the usable data in a bin drops below the value specified in the **Data Percentage** field, the background of the bin will change to a coral color. This alerts the user to regions that have a break in acquired data or have lost a significant amount of data to noise. In the example below, the Data Percentage was changed to 100% to illustrate the color change.

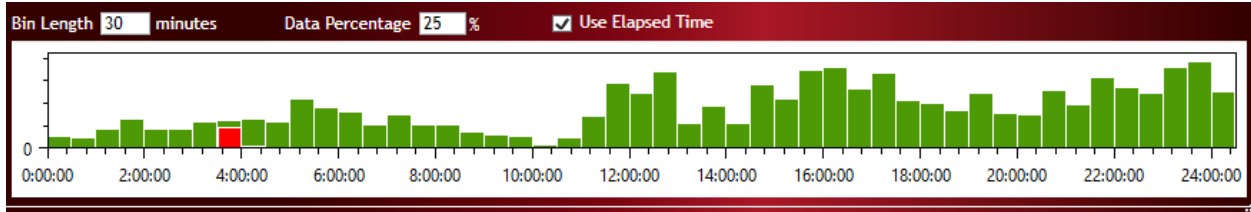


Note: The last column in the histogram will likely always contain a coral color bin, as the end of the data set typically does not align with the Bin Length. This is based on when the acquisition was stopped.

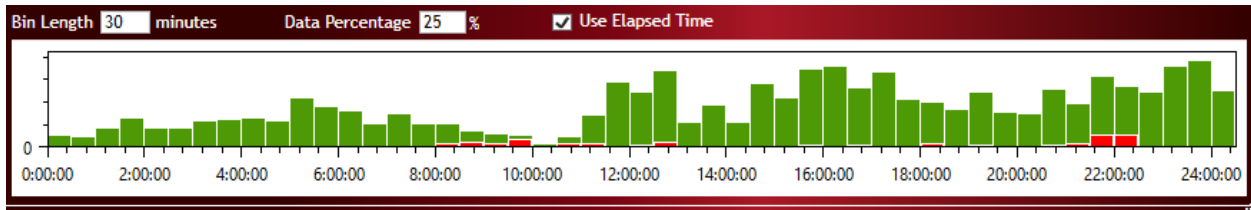
The red regions within the green bins indicate the location and number of matches currently displayed in the *Results Wave View*. If red segments are not visible, it is likely that too few match results are visible within the *Results Wave View* as compared to the total number of matches present within each bin, making the red match

indicator very thin and difficult to see. To see the match indicator, reduce the size of your bins or zoom out within the *Results Wave View* to bring more matches into the viewing area.

The red segment updates automatically based on your location in the *Results Wave View*. Using one of the scrolling functions to move forward or backward through the match results also move the location of the red segment to the green bin location where the match was found.



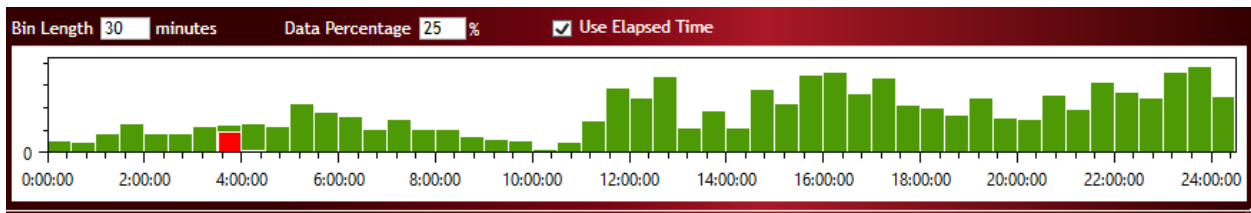
If sorting is performed within the Results Derived View, the red segments may appear across multiple bins since data is no longer sorted chronologically. This provides an easy way to see if the results with the highest or lowest match values are spread throughout the dataset or are localized to a particular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



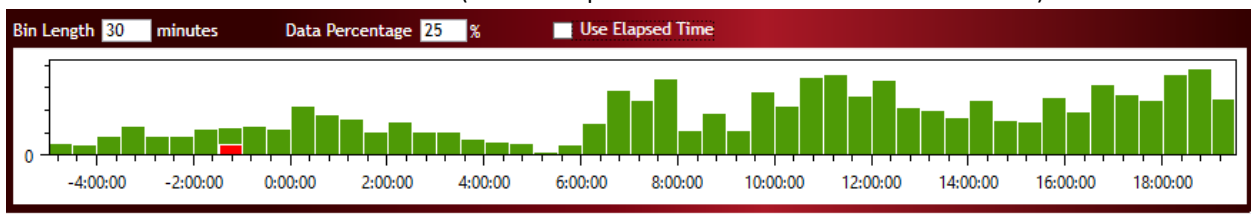
Note: Right-click the Results Distribution View to enable or disable the **Time Axis**.

Time may also be expressed using either Elapsed Time (checked) – i.e. time 0 is the start of the acquisition – or unchecked, where time 0 is equal to T0 define from the Data Reduction T0 event or user defined time. The example below shows the difference when the Data Reduction T0 is defined to Event A, which was marked in the data.

USE ELAPSED TIME CHECK BOX ENABLED (time 0 is the start of the acquisition):



ELAPSED TIME CHECK BOX DISABLED (time 0 is equal to T0 define from the Data Reduction):

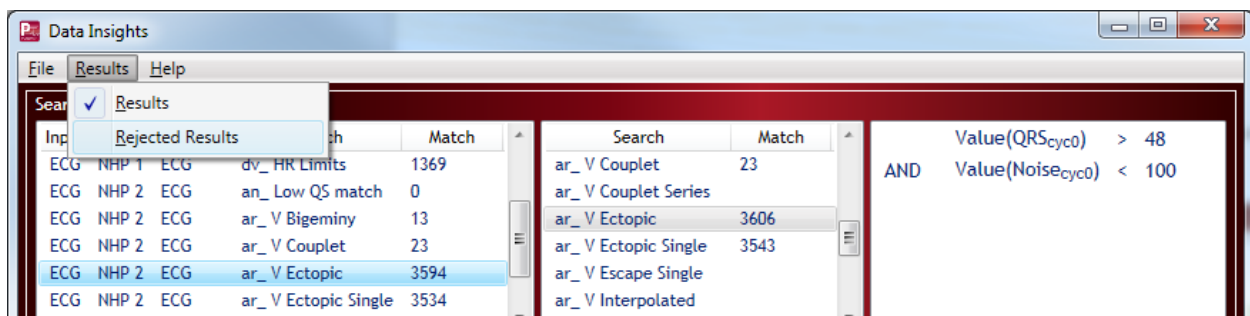


Notice, when Use Elapsed Time is disabled, any match results prior to the T0 event will be associated with a negative time.

RECOVERING REJECT RESULTS

Each Search will track the match results, as well as any match results that has been **Rejected**. The *Results* dropdown menu allows the use to toggle between displaying **Results** and **Reject Results**. When Reject Results is selected, each Channel/Search pair Match Count will update with the number of rejected match results. The Results Wave View, Derived View, and Distribution View will also update to display the rejected results for the active (selected) Channel/Search pair.

Rejecting a Rejected Match Result, ultimately moves the match result back to the Results view and effectively recovers that match result from being rejected.

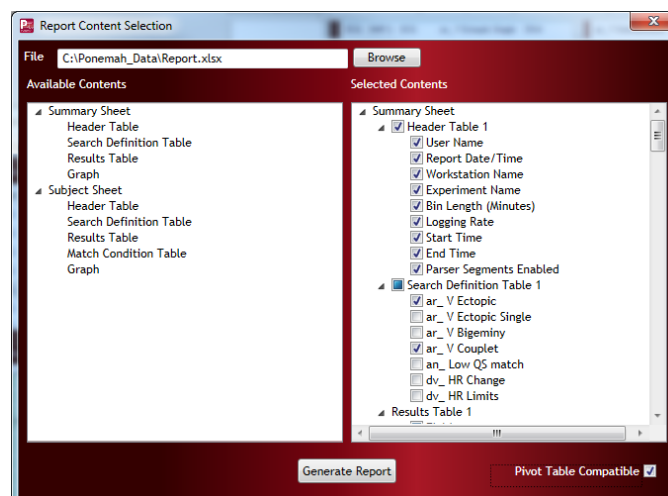


To aid in locating reject results, the **Time/Date Rejected** field in the Results Derived View may be used.

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.

REPORTING RESULTS

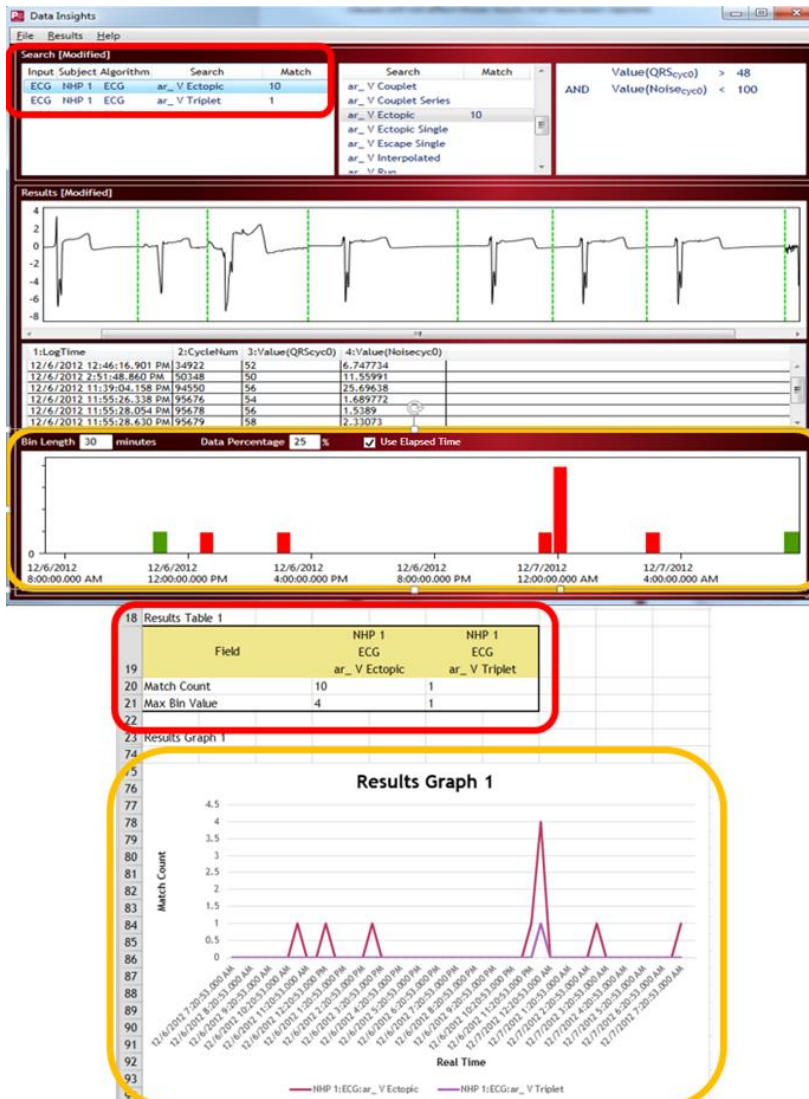
The **File** menu provides access to the Data Insights report functionality. Selecting **Report** will open the **Report Content Selection** dialog. This dialog allows customization of the report output including file information, search criteria, graphical information, and table information.



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. All information displayed within the Data Insights dialog is available as a selection within the Report. Reports are generated in the form of a Microsoft Excel Workbook and consists of one Summary sheet and a Subject sheet for each subject included in the report.

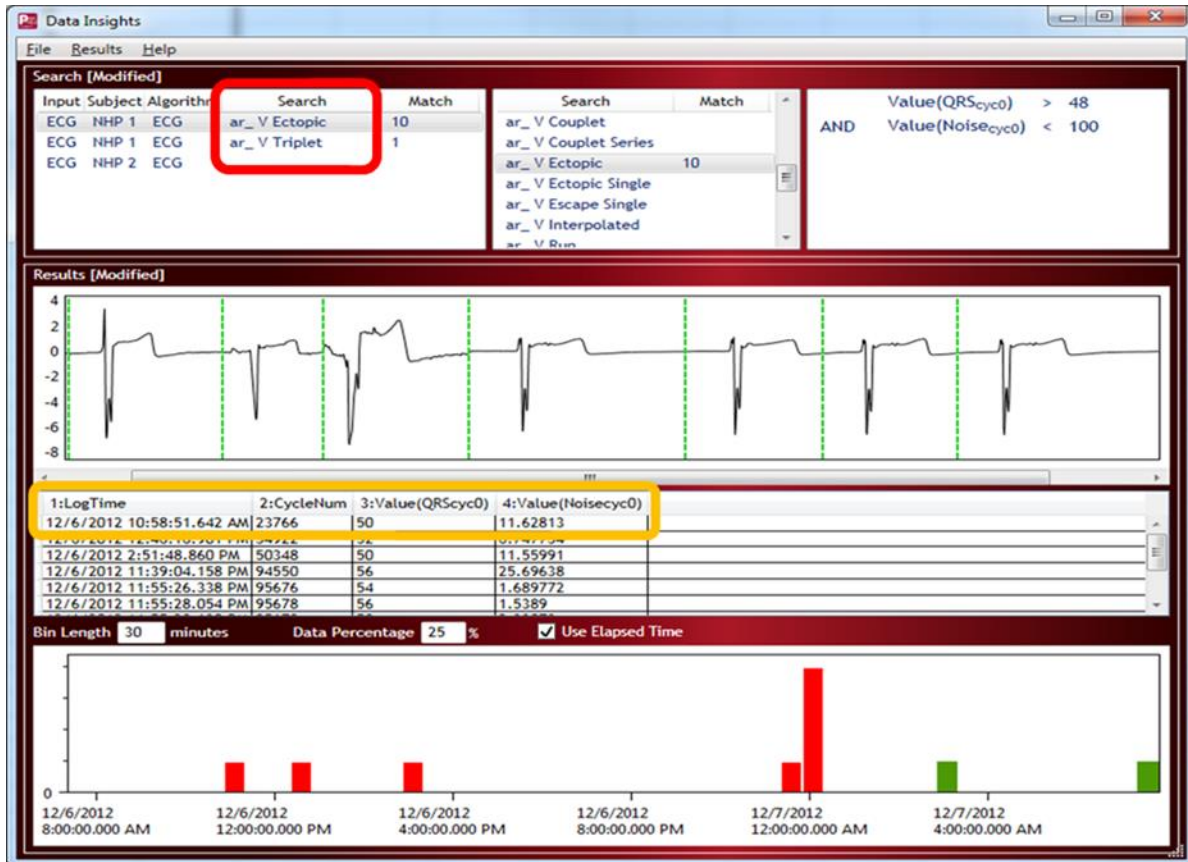
SUMMARY SHEET

The Summary Sheet Results Table contains the high-level match information as displayed in the Data Insights Channel/Search Pairs area for all subject that have searches associated. In the example below, only 1 subject group is being used, resulting in only the search results from this 1 subject being displayed. The Summary Sheet may also contain a Results Graph, which represents the Results Distribution View



SUBJECT SHEET

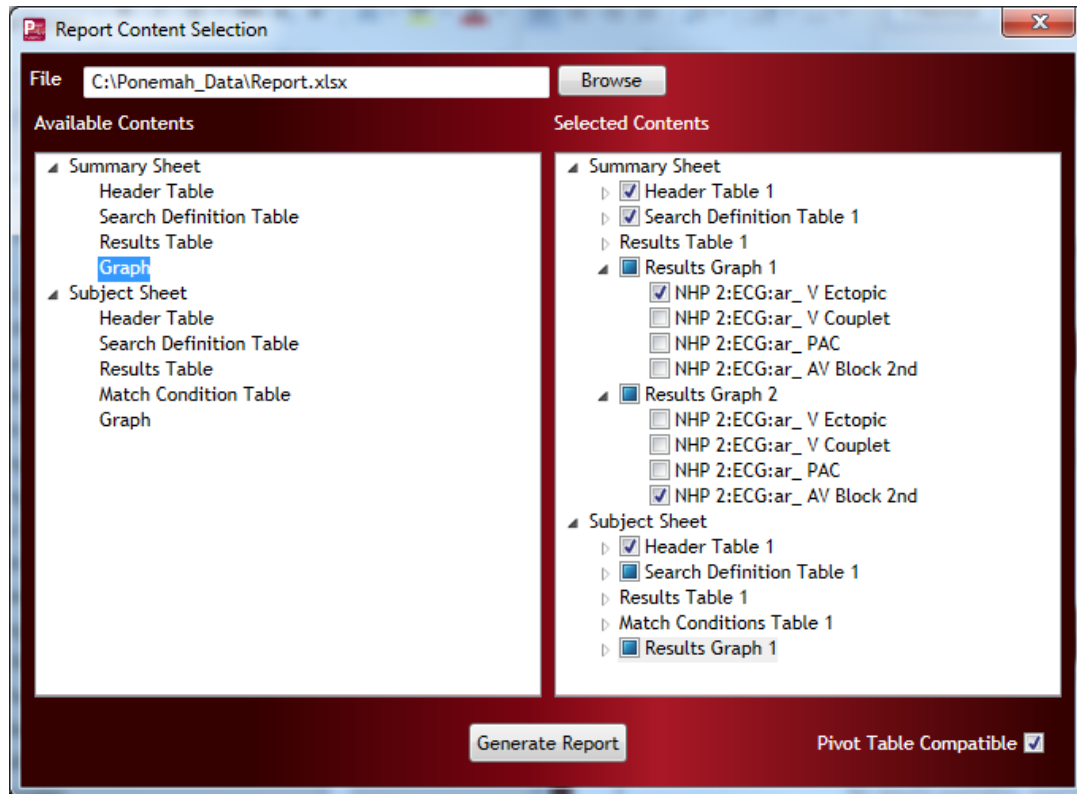
The Subject sheet contain the same information as the Summary sheet broken out by subject. The Subject sheet also contains a **Match Conditions Table**. The Match Conditions table contains all Channel/Searches pairs. In the example below, the V Ectopic and V Triplet searchers are listed, along with their associated Results Derived View values.



Match ID	Channel	Search	Condition	LogTime	Log Duration	Value
74						
75	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 10:58:51.642 AM	406	50
76	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 10:58:51.642 AM	406	11.628
77	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 12:46:16.901 PM	673	52
78	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 12:46:16.901 PM	673	6.748
79	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 2:51:48.860 PM	439	50
80	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 2:51:48.860 PM	439	11.56
81	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 11:39:04.158 PM	635	56
82	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 11:39:04.158 PM	635	25.696
83	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 11:55:26.338 PM	940	54
84	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 11:55:26.338 PM	940	1.69
85	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 11:55:28.054 PM	597	56
86	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 11:55:28.054 PM	597	1.539
87	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 11:55:28.630 PM	590	58
88	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 11:55:28.630 PM	590	2.331
89	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/6/2012 11:55:29.230 PM	872	58
90	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/6/2012 11:55:29.230 PM	872	3.157
91	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/7/2012 3:03:01.607 AM	257	106
92	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/7/2012 3:03:01.607 AM	257	86.434
93	ECG	ar_V Ectopic	Value(ECG:QRScyc0)	12/7/2012 7:45:35.288 AM	239	50
94	ECG	ar_V Ectopic	Value(ECG:NoiseCyc0)	12/7/2012 7:45:35.288 AM	239	55.589
95	ECG	ar_V Triplet	Series(ar_V Ectopic, 1)	12/6/2012 11:55:28.054 PM	2064	3

CUSTOMIZING REPORTS

Additional content may 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 the desired reporting needs. For instance, instead of graphing all arrhythmia types on a single summary graph, the user may configure a specific graph to display only Ventricular Ectopics from all subjects and another graph to display the occurrences of AV Blocks across all subjects. This is done by adding a second Summary Graph content section and making the appropriate selections, as illustrated below as selected in the Summary Sheet's Result Graph 1 and Results Graph 2.



Checking the **Pivot Table Compatible** checkbox will output the data with minimal formatting to permit Excel Pivot Tables to be created from the Results Tables. This is useful when additional analysis is desired or if importing into third-party programs is desired.

Please see the **Software Appendix | Data Insights** section for a description of each of the Content sections.

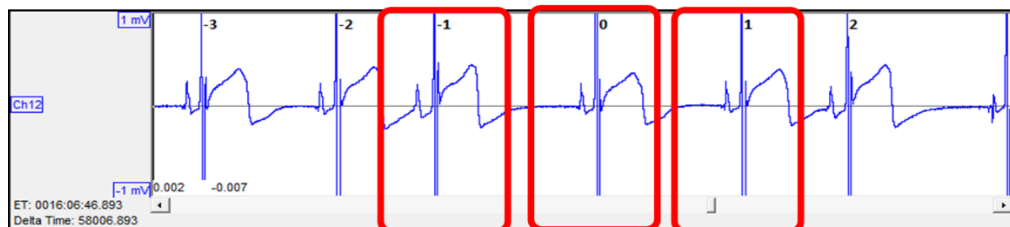
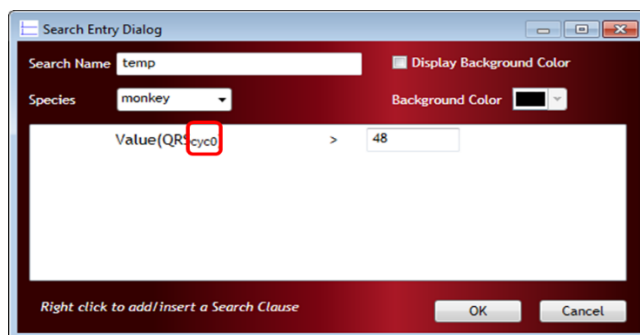
CUSTOMIZING SEARCH DEFINITIONS

A list of predefined Searches is present and available for use by default in *the Search and Match Grid*. Existing Search Definitions may be modified, or new Search Definitions may be created by the user. Before modifying or creating new Search Definitions, it is important to understand how Searches are composed.

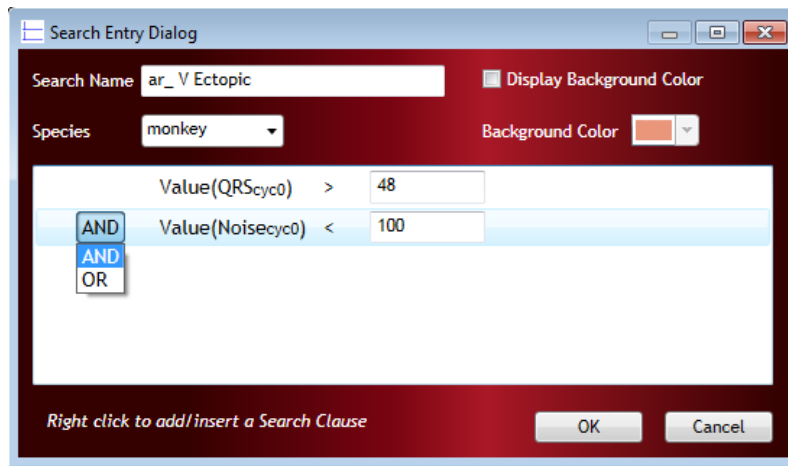
Understanding Search Definitions

Searches are composed of one or more Search Clauses that may be combined using Boolean operators (AND, OR). Each Search Clause is a Boolean expression composed of the following:

- **Function** The functions (Value, %Increase, % Change, etc.) determine how inputs are used when evaluating the Boolean expression that forms a Search Clause.
- **Input** The inputs include amplitude and timing data calculated by Ponemah (RR interval, Heart Rate, LVEDP, etc.), pattern matching results, and time of day information. When selecting an input, the Analysis Algorithm (ECG, BP, LVP, etc.) must be selected first, then choose the desired input.
- **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. If averaged data or standard deviation is used, the data from the Derived Parameter List Views will be used at the active logging rate defined.
- **Offset** The Offset is 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. The permitted range is +/- 10.

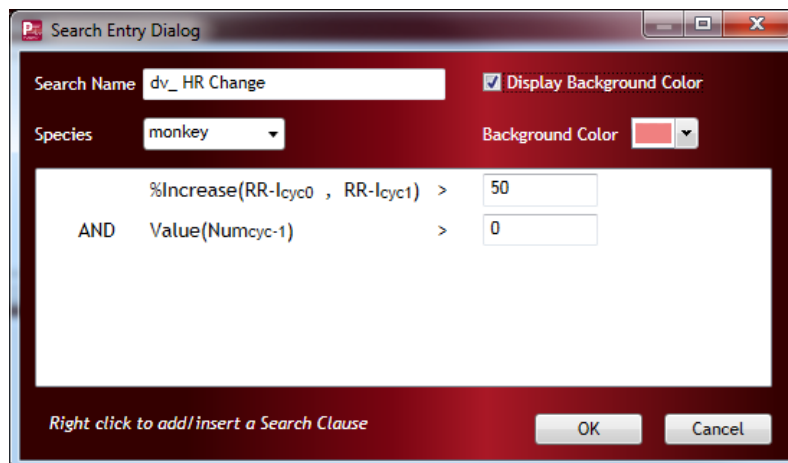


- **Operator** Operators include greater than (>), less than (<), greater than and equal to (>=), less than and equal to (<=), equal to (=), not equal to (!=). However, those offered change with the Function being used.
- **Value** The value is also dependent on the Function and is used as a threshold for the Function to determine a match. Values are in user units; i.e. if the signal is calibrated in mmHg, then amplitude values will also be in mmHg.
- **Boolean Operators** Boolean AND or OR operators are used to combine clauses. When AND is used to combine clauses, each condition must be satisfied to be considered a match. When OR is used, either condition may be satisfied to be considered a match.



Note: Clauses may be grouped to create more elaborate searches.

In the example below, a set of conditions is defined to locate Heart Rate changes using the RR Interval. To be a valid match in this example, a percent increase of greater than 50% in the RR Interval from the current cycle (RR-_{I_{cy0}}) to the following cycle (RR-_{I_{cy1}}) must occur, as well as the Cycle Number from the previous cycle (RR-_{I_{cy-1}}) must be greater than a value of 0.



In this example the components of the search are as follows:

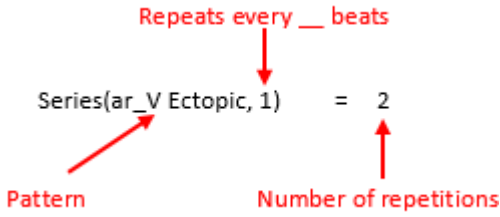
- Function: Percent Increase
- Input: RR-1 (from ECG)
- Range and Offset: Cycle-based from the previous cycle to the current cycle
- Operator: Greater than (>)
- Value: 50%

Note: Data Insights will only display the cycles directly called out within the search in the Results Wave View. In the example below, it was desired to also see the previous ECG cycle. Therefore, a condition that is always true was added to ensure the inclusion of that particular cycle; i.e. Ponemah numbers waveform cycles starting at cycle 1, consequently all cycle numbers are greater than 0.

FUNCTIONS

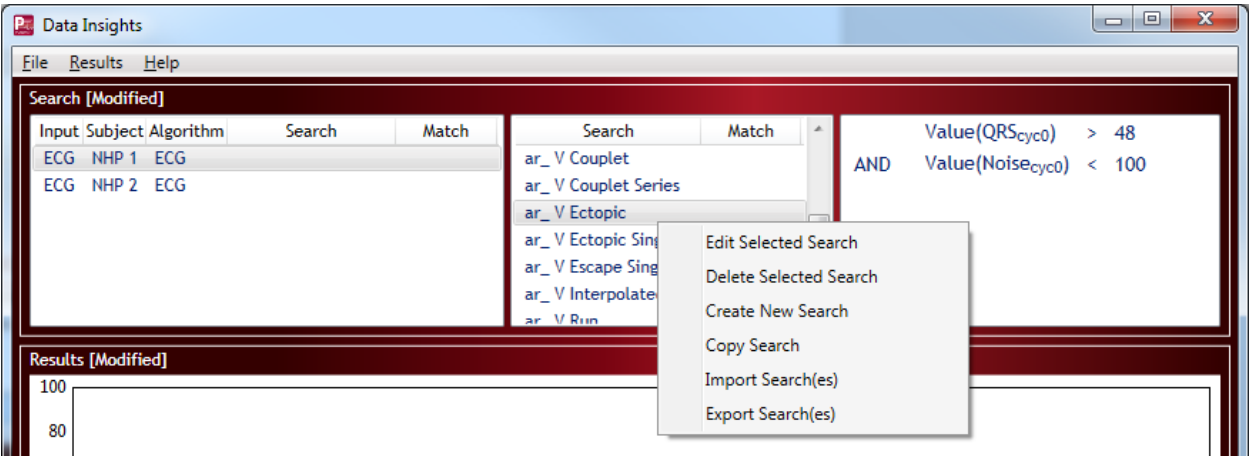
The basic functions and their definitions are listed below.

Function	Definition	Example
Value	Represents a given value for a parameter.	Identifies all cycles where the Systolic value is greater than 170 mmHg. Value(Sys _{cyc0}) > 170
Increase, Decrease, Change	Represents an increase, decrease, or change in value from parameter 1 to parameter 2.	Identifies all cycles that show an increase in the RR interval of more than 300 milliseconds from the previous cycle (cyc -1) to the current (cyc0). Functions that are similar to Increase() are Decrease() and Change(). Increase(RR-I _{cyc-1} , RR-I _{cyc0}) > 300
%Increase, %Decrease, %Change	Represents a percent increase, decrease, or change in value from parameter 1 to parameter 2.	Identifies all cycles that show a decrease in the RR interval of more than 30% from the previous cycle (cyc -1) to the current (cyc0). Functions that are similar to %Decrease() are %Increase() and %Change(). %Decrease(RR-I _{cyc-1} , RR-I _{cyc0}) > 30
Template	Used in conjunction with ECG PRO, Template searches can be performed to pull specific ECG complexes/morphologies that match a tagged Template Cycle into the Data Insights dialog for review. See the Tutorials Data Insights Finding Morphology Changes using Template Tags for an example.	Identifies all cycles that match templates tagged with a Ventricular Ectopic tag. Template(ECG _{cyc0}) = Ventricular Ectopic
Search	Permits users to utilize existing Searches as part of the criteria used within the Search Definition. <i>Note:</i> The search used within the Search-based search must also be applied to the channel. If not, the Search-based search will not be able to be applied to the channel.	Identifies all cycles that do not match a PAC search. A Search() function would typically be used in conjunction with other clauses. Search(_{cyc0}) != ar_PAC

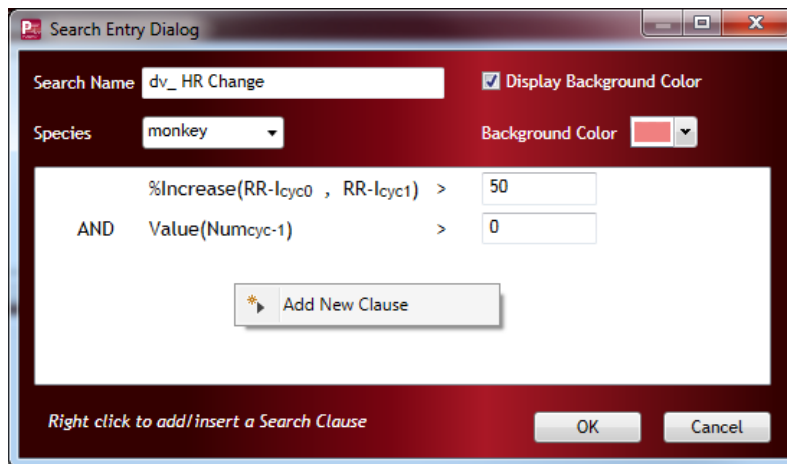
<p>Series</p>	<p>Used to define sequences or patterns within the data utilizing an existing search.</p> <p><i>Note:</i> The search used within the Series search must also be applied to the channel. If not, the Series search will not be able to be applied to the channel.</p>	<p>Identifies multiple occurrences of a pattern. In this example, all instances where exactly two consecutive cycles match an <i>ar_V Ectopic</i> search are identified.</p> 
<p>Real Time</p>	<p>Used to find cycles within a specific time range; such as before and after dosing, during light and dark cycles, or during any other period of interest.</p>	<p>Identifies all cycles that fall between 8:00 AM and 8:00 PM within each 24 hour cycle, such a search would typically be used in conjunction with other clauses.</p> <pre> RealTime() > 08:00:00 AND RealTime() < 20:00:00 </pre>

EDITING SEARCHES

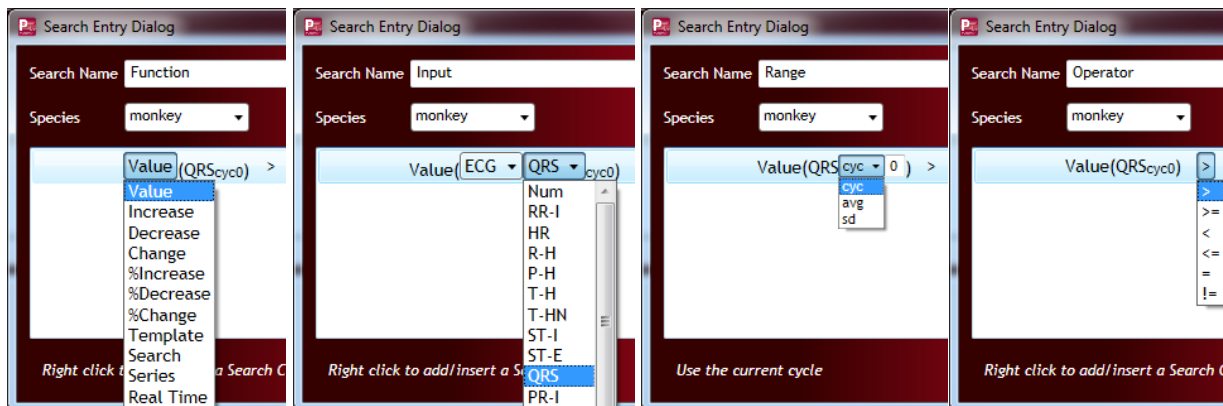
Existing Search Definitions may be modified or new Search Definitions may be created by the user. Right-click the *Search and Match Grid* to access the Search modification menu.



Select **Edit Selected Search** or **Create New Search** to launch the *Search Entry* dialog. This dialog is also accessible by double-clicking a Search. The *Search Entry* dialog displays the criteria used to define the Search. Additional **Search Clauses** may be added by right-clicking within the white box and selecting **Add New Clause**.

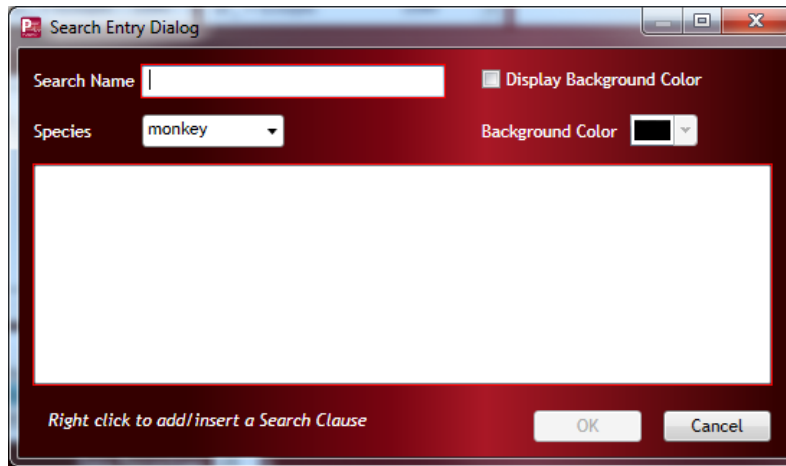


Selecting the **Function**, **Input**, **Range** or **Operator** will display a dropdown menu to permit selection of the desired method, while **Offset** and **Value** are text fields for direct user entry.



CREATING/DELETING/COPYING SEARCHES

Right-click the **Search and Match Grid** and select **Create New Search**. The user will be presented with an empty *Search Entry* dialog. Any edit field that expects an input to be provided will be outlined in red. Below, the **Search Name** and field to enter search clauses are both highlighted along the border of the edit field in red. A **Search Name** and a complete search clause is needed to save the search. The **OK** button will not be available until all edit boxes expecting information have been updated completely.



The **Delete Selected Search** allows you to remove the selected search from the list. Once removed, the search will no longer appear in the **Search and Match Grid** 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.

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” appended to the end of the Search name. This permits the utilization of previously constructed Searches without needing to start from an empty Search.

EXPORTING/IMPORTING SEARCHES

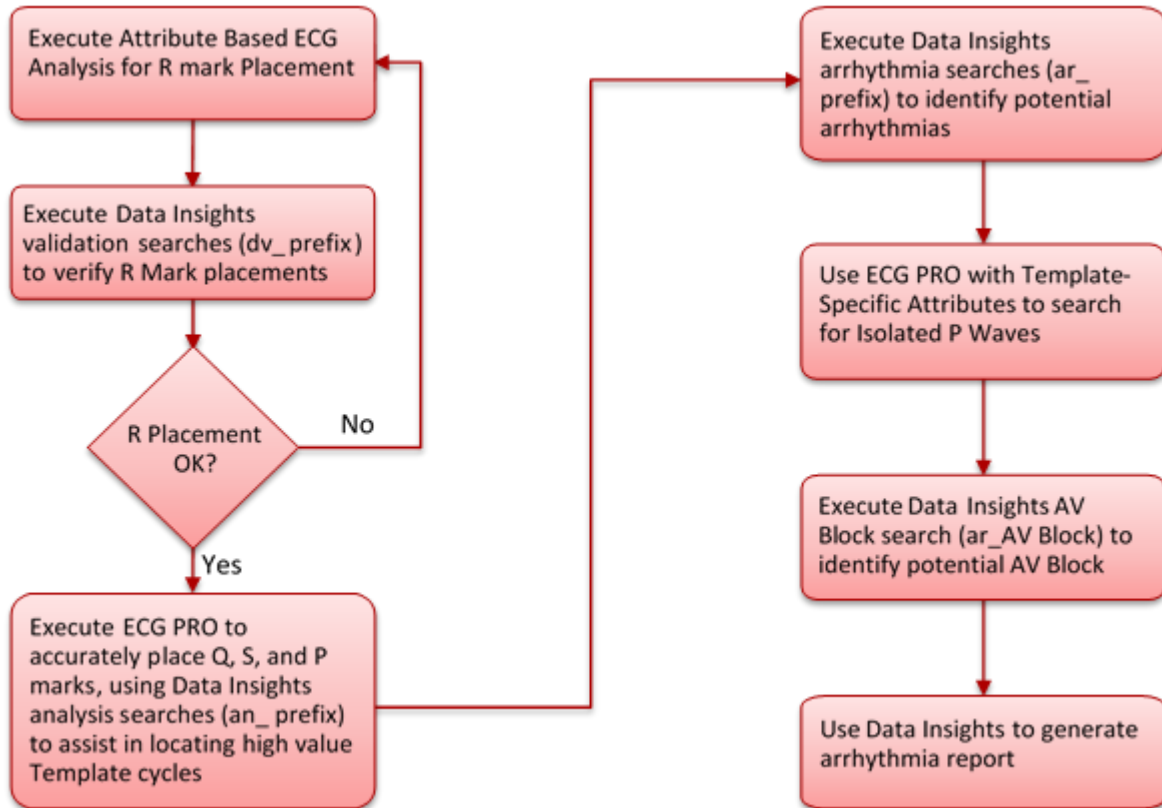
The **Export Search(es)** function allows users to export customized searches for deployment across all workstations. This is intended to help improve consistency in data analysis and cleanup to ensure results are consistent and repeatable. Exported custom Searches are saved to an .xml file in the Ponemah directory or the directory where the program is installed, by default. Alternatively, Searches may be saved to a location of the users’ choice, such as external USB drives or network locations. Exported Searches can then be imported to other systems using the **Import Search(es)** function.

Both the Export and Import functions are available from the **Search and Match Grid** right-click menu.

Note: When importing searches that reference other searches, the 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.

PROCESS FLOW DIAGRAM

The following outlines the recommend process for users performing ECG analysis and arrhythmia detection with Data Insights.



DEFAULT SEARCH DEFINITION BY SPECIES

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:

ANALYSIS SEARCHES

Analysis Searches are used to aid in data analysis process. Currently these are used to help construct high value ECG PRO Template Libraries.

- **an_Low P match** (Low P Match - requires ECG PRO):
Searches for high value P templates by displaying the distribution of P waves with low match percentages. 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.

Select a match result from a region of the waveform with many match results for inclusion as a new template cycle.

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 by displaying the distribution of Q and S waves with low match percentages. 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.

Select a match result from a region of the waveform with many match results for inclusion as a new template cycle.

Species	Definition
Dog	(Value(QMatch _{cyc0}) < 70
Monkey	OR Value(SMatch _{cyc0}) < 70)
Rat	AND Value(Noise _{cyc0}) < 30
Mouse	

- **an_Unmatched** (Unmatched Cycles - requires ECG PRO):
Searches for unmatched cycles with low noise to display the distribution of unmatched cycles.

Select a match result from a region of the waveform with many match results for inclusion as a new template cycle.

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

- **an_Unmatched Clean** (Clean Unmatched Cycles - requires ECG PRO):
Searches for unmatched cycles with low noise to display the distribution of clean unmatched cycles.

Select a match result from a region of the waveform with many match results for inclusion as a new template cycle.

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

- **an_Low T Match** (Low T Match - requires ECG PRO):
Searches for high value T templates by displaying the distribution of T waves with low match percentages. 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.

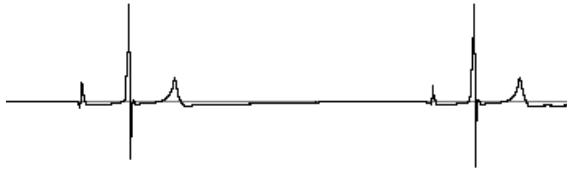

Select a match result from a region of the waveform with many match results for inclusion as a new template cycle.

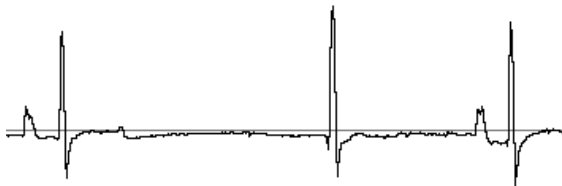
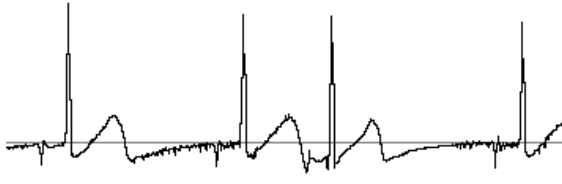

Species	Definition
Dog Monkey Rat Mouse	Value(TMatch _{cyc0}) < 70 AND Value(Noise _{cyc0}) < 30 AND Value(NUM _{cyc-1}) > 0


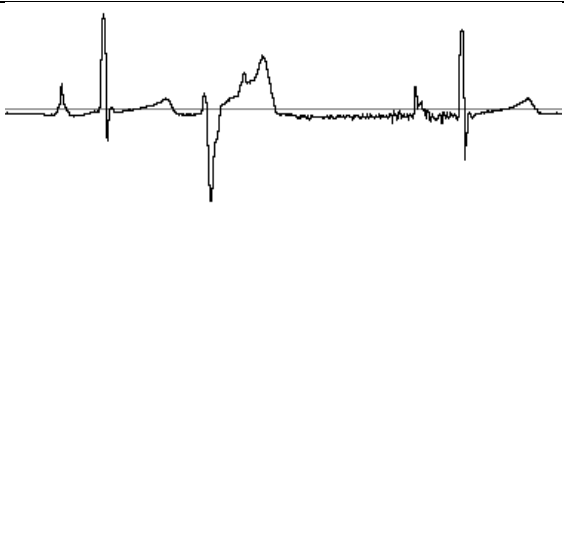
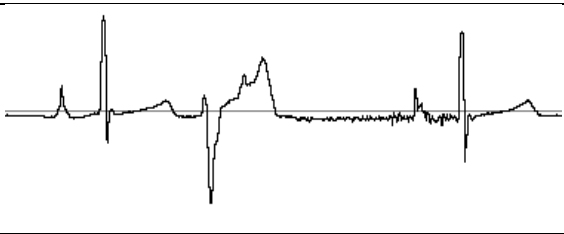
ARRHYTHMIA SEARCHES

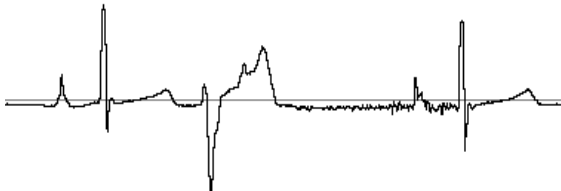
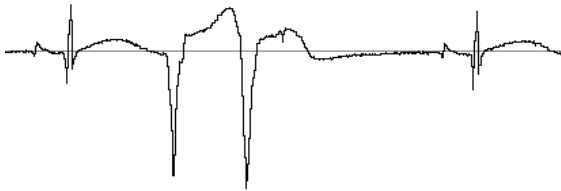
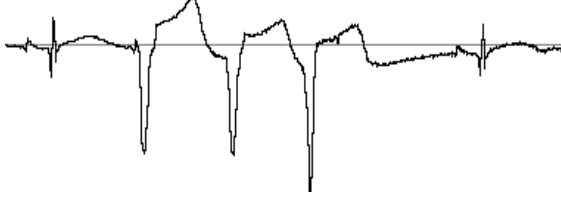
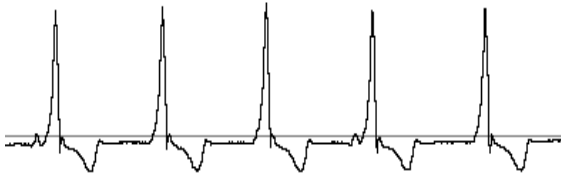
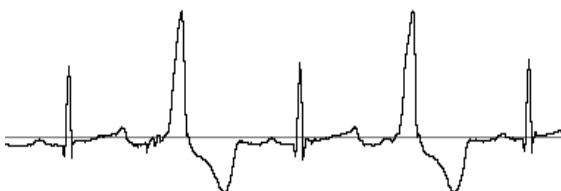

Arrhythmia Searches are used to aid in arrhythmia detection.

Note: If the Species is not specifically called out within the Search Definition, the set of search clauses and the values within are the same for Dog, Monkey, Rat, and Mouse.

Search Definition	Example Waveform Morphology
<p>First-degree AV block (ar_AV Block 1st): Identifies cycles that have a long PR interval that is shorter than the PR interval for a potential isolated P wave</p> <p>Dog Value(PR-I_{cyc0}) > 130 AND Value(PR-I_{cyc0}) < 250 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p> <p>Monkey Value(PR-I_{cyc0}) > 100 AND Value(PR-I_{cyc0}) < 200 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p> <p>Rat Not Supported</p> <p>Mouse Not Supported</p>	
<p>Second-degree AV block (ar_AV Block 2nd): Identifies cycles that have a significantly elongated PR intervals. This search is used after marking isolated P waves using ECG PRO's Template Specific Attributes – See the <i>Data Insights Finding Second Degree AV Block using Template Specific Attributes</i> section of the <i>Tutorials</i>.</p> <p>Dog Value(PR-I_{cyc0}) > 250 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p> <p>Monkey Value(PR-I_{cyc0}) > 200 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p> <p>Rat Value(PR-I_{cyc0}) > 100 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p> <p>Mouse Value(PR-I_{cyc0}) > 250 AND Value(NUM_{cyc-1}) > 0 AND Value(Noise_{cyc0}) < 30</p>	

<p>Junctional Complex (ar_Junctional): Identifies cycles that do not have a P or have a P with a short PR interval and are not Ventricular Ectopics</p> <p>(Value(PCT_{cyc0}) = 0 OR %Decrease(PR-I_{avg0}, PR-I_{cyc0}) > 35) AND Search(_{cyc0}) != ar_V Ectopic</p>	
<p>Premature Atrial Complexes (ar_PAC): Identifies cycles that show a decrease in RR interval relative to the previous cycle, while showing little change in RR interval between the previous and following cycles.</p> <p>%Decrease(RR-I_{cyc-1}, RR-I_{cyc0}) > 30 AND %Change(RR-I_{cyc-1}, RR-I_{cyc1}) < 25 AND Value(Num_{cyc-2}) > 0 AND Value(Noise_{cyc0}) < 100</p>	
<p>Sinus Pause (ar_Sinus Pause): Identifies cycles with a long RR interval or a marked increase in RR relative to the previous cycle.</p> <p>Dog (Value(RR-I_{cyc0}) > 3000 OR %Increase(RR-I_{cyc-1}, RR-I_{cyc0}) > 200) AND Value(Num_{cyc-2}) > 0</p> <p>Monkey (Value(RR-I_{cyc0}) > 2000 OR %Increase(RR-I_{cyc-1}, RR-I_{cyc0}) > 200) AND Value(Num_{cyc-2}) > 0</p> <p>Rat (Value(RR-I_{cyc0}) > 500 OR %Increase(RR-I_{cyc-1}, RR-I_{cyc0}) > 200) AND Value(Num_{cyc-2}) > 0</p> <p>Mouse (Value(RR-I_{cyc0}) > 400 OR %Increase(RR-I_{cyc-1}, RR-I_{cyc0}) > 200) AND Value(Num_{cyc-2}) > 0</p>	

<p>Ventricular Interpolated (ar_Interpolated): Identifies when a ventricular beat is inserted within normal sinus beats.</p> <pre> %Decrease(RR-I_{cyc-1}, RR-I_{cyc0}) > 40 AND %Change(RR-I_{cyc0}, RR-I_{cyc1}) < 35 AND %Decrease(RR-I_{cyc2}, RR-I_{cyc1}) > 40 AND Search(_{cyc0}) = ar_V Ectopic Single AND Value(Num_{cyc-2}) > 0 </pre>	
<p>Ventricular Ectopic (ar_V Ectopic): Identifies cycles with a widened QRS.</p> <pre> 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 </pre>	
<p>Ventricular Ectopic Single (ar_V Ectopic Single): Identifies isolated Ventricular Ectopics bracketed by two sinus (non-ventricular) beats.</p> <pre> Search(_{cyc-1}) != ar_V Ectopic AND Search(_{cyc0}) = ar_V Ectopic AND Search(_{cyc1}) != ar_V Ectopic </pre>	
<p>Ventricular Escape Complex (ar_V Escape Single): Identifies single Escape beats bracketed by two sinus (non-ventricular) beats.</p> <pre> %Increase(RR-I_{cyc-1}, RR-I_{cyc0}) > 40 AND Search(_{cyc0}) = ar_V Ectopic Single AND Value(Num_{cyc-2}) > 0 </pre>	<p>Example not currently available.</p>

<p>Premature Ventricular Complex (ar_PVC Single): Identifies single Premature Ventricular Ectopics bracketed by two sinus (non-ventricular) beats.</p> <p>$\%Decrease(RR-I_{cyc-1}, RR-I_{cyc0}) > 0$</p> <p>AND $Search(cyc0) = ar_V\ Ectopic\ Single$</p> <p>AND $Value(Num_{cyc-2}) > 0$</p>	
<p>Couplet (ar_Couplet): Identifies two contiguous Ventricular Ectopic beats that are bracketed by two sinus (non-ventricular) beats.</p> <p>$Series(ar_V\ Ectopic, 1) = 2$</p>	
<p>Triplet (ar_V Triplet): Identifies three contiguous Ventricular Ectopic beats that are bracketed by two sinus (non-ventricular) beats.</p> <p>$Series(ar_V\ Ectopic, 1) = 3$</p>	
<p>Run (ar_V Run): Identifies greater than three contiguous Ventricular Ectopic beats that are bracketed by two sinus (non-ventricular) beats.</p> <p>$Series(ar_V\ Ectopic, 1) > 3$</p>	
<p>Bigeminy (ar_V Bigeminy): Identifies a repeating pattern of two or more Ventricular beats that are separated by one sinus (non-ventricular) beat.</p> <p>$Series(ar_V\ Ectopic\ Single, 2) >= 2$</p>	
<p>Trigeminy (ar_V Trigeminy): Identifies a repeating pattern of two or more Ventricular beats that are separated by two sinus (non-ventricular) beats.</p> <p>$Series(ar_V\ Ectopic\ Single, 3) >= 2$</p>	

DATA VALIDATION SEARCHES

Data Validation Searches are used to aid in the data validation process by quickly exposing outliers and potentially mismarked data that may require focused attention.

- dv_HR Limits (Heart Rate Limits):**
 Searches for cycles that are at HR extremes to help complete the attribute based analysis process to improve the accuracy of R mark placement. The matches may be valid beats, missed beats or incorrectly marked beats, however there is a greater likelihood of mismarked beats.

Sort the HR column within the **Results Derived View** and step through the extremes until the remaining matches are well mark cycles. Displaying the validation marks in the **Results Wave View** may be helpful. Place Bad Data Marks, Delete Cycles, or reanalyze particular data sections as needed to correct the mismarked data.

Species	Search 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 to help complete the attribute based analysis process to improve the accuracy of R mark placement. The matches may be valid beats, missed beats or incorrectly marked beats, however there is a greater likelihood of mismarked beats.

Sort the RR-I column within the **Results Derived View** and step through the extremes until the remaining matches are well mark cycles. Displaying the validation marks in the **Results Wave View** may be helpful. Place Bad Data Marks, Delete Cycles, or reanalyze particular data sections as needed to correct the mismarked data.

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

- dv_Missed Beats (Missed Beats):**
 Searches for skipped beats to help complete the attribute based analysis process to improve the accuracy of R mark placement.

Sort the RR-I column within the **Results Derived View** and step through the extremes until the remaining matches are well mark cycles. Displaying the validation marks in the **Results Wave View** may be helpful. Place Bad Data Marks, Delete Cycles, or reanalyze particular data sections as needed to correct the mismarked data.

Species	Search Definition
Dog	%Increase(RR-I _{cyc-1} , RR-I _{cyc0}) > 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 _{cyc-1} , RR-I _{cyc0}) > 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 _{cyc-1} , RR-I _{cyc0}) > 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 _{cyc-1} , RR-I _{cyc0}) > 90
	AND %Change(RR-I _{cyc-1} , RR-I _{cyc0}) < 10
	AND Value(HR _{cyc0}) > 475
	AND Value(Noise _{cyc0}) < 100

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 its 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 useful to include a Noise Clause in searches. This permits the exclusion of noisy data from match results. By default, the Noise threshold in the Noise clause should be set high to prevent exclusion and lowered as necessary.

TUTORIALS

The following sections provides examples of how to use certain Ponemah features to achieve an example goal.

FINDING SECOND DEGREE AV BLOCK

BACKGROUND

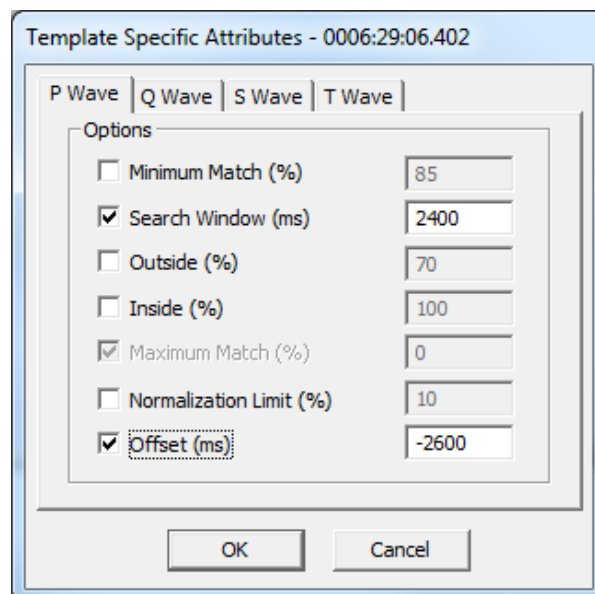
To locate and mark instances of Second Degree AV Block (isolated P waves), a new concept has been introduced in ECG PRO called Template Specific Attributes. Ponemah uses these attributes to mark an isolated P wave by shifting the marks from valid P wave to the isolated P wave. Data Insights can then be used to search for instances of abnormally large PR intervals to find isolated P waves.

This approach is needed as Ponemah will currently only mark one P wave per ECG cycle. When an isolated P is present in the signal, Ponemah is required to choose which P to mark. When using the attribute-based ECG analysis or ECG PRO analysis with standard settings, Ponemah will mark the P wave associated with QRS complex. Isolated P wave will be passed over since they are not directly associated with a valid ECG cycle.

UNDERSTANDING TEMPLATE SPECIFIC ATTRIBUTES

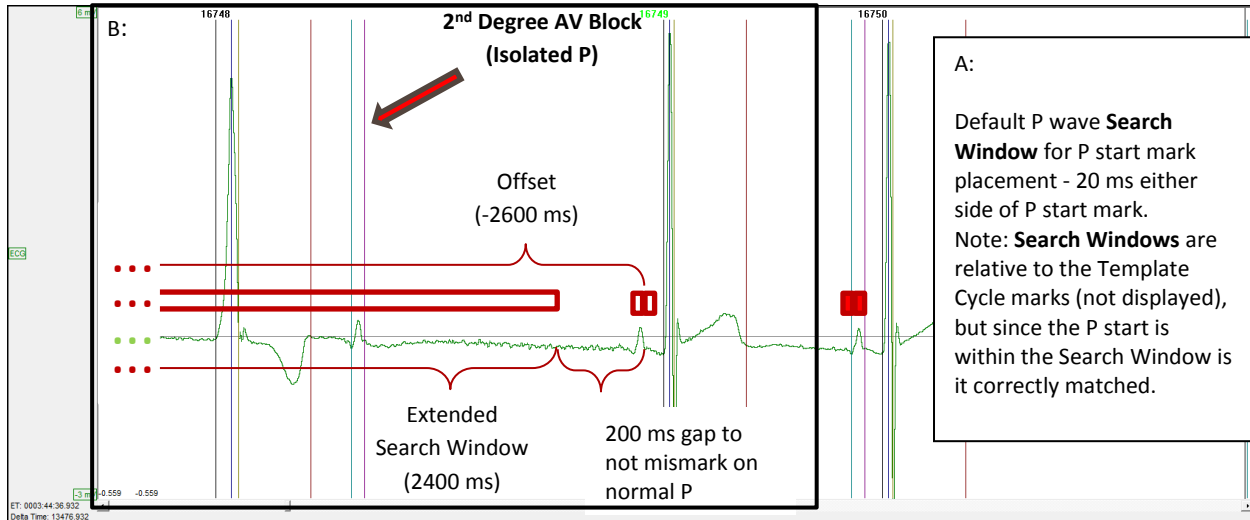
When locating instances of Second Degree AV Block (isolated P waves), normal P waves will need to be temporarily ignored. The P marks are instead placed on one of the isolated P waves without affecting the mark placement of surrounding cycles' Q, R, S, and T waves. This is achieved using Template Specific Attributes to shift and extend the P match Search Region past the normal P wave to an area where the isolated P wave is expected to exist.

To do this, the P wave **Search Window** and **Offset** attributes within the **Template Specific Attributes dialog** need to be enabled. These are defaulted to appropriate durations for an initial search for isolated Ps, but may be augmented based on your data, if necessary.



Note: The **Search Window** and **Offset** attributes are species specific. Values displayed in the example screenshot (right) are for **Dog** and **Monkey**.

To better understand how Template Specific Attributes work, it is important to understand how the **Search Window** and **Offset** Template attributes work under normal conditions. The **Search Window** is the time range over which Template Analysis searches for the best match and is centered on the mark trying to be matched; e.g. P Start mark. The **Offset** attribute then shifts the **Search Window** center point by the time in milliseconds (ms) entered in the associated text field. The images below illustrates the typical ECG PRO Search Window case (A) and how these attributes are applied when updated for isolated P wave searches (B) visually.



In B, the **Search Window** extends past the data being displayed on the graph. The R wave of the previous cycle acts as a hard cutoff for the **Search Window**. This algorithm has additional logic built in to prevent ECG PRO from marking the T wave of the previous cycle as the isolated P wave.

Note: **Template Specific Attributes** are available for all Search Regions, however the current use case is for isolated P waves.

PROCESS

ECG PRO's Template Specific Attributes provide the user a mechanism to override the global/general ECG PRO Match attributes (Match % and Advanced Setup) for one or more of the Templates within the Template Library, while keeping the global/general Match attributes for the remaining Templates.

The process to find instances of Second Degree AV Block (isolated P waves) is:

1. Run ECG Attribute based analysis with ECG analysis module
2. Use ECG PRO to accurately mark the ECG cycles' Q and S waves (Optional: Required to identify Ventricular and Junctional beats)
3. Use ECG PRO to accurately mark the ECG cycles' P wave
4. Save Marks Section (Saving at this time will save the derived data and mark placement prior to shifting the P marks to the

isolated P waves for a more accurate representation of the interval-base analysis. See Derived Output Impact section below for more details.)

5. Choose one or more of the Template Cycles used for P wave mark placement for use with Template Specific Attributes.
 - a. Template Cycles with the largest match percentage should be used.
 - b. Enable the **Search Window** and **Offset** attributes. DSI recommends starting with the default values.
6. Execute ECG PRO, enabling only the P wave Match Region.
7. Use Data Insights to find and report on instances of AV Block.

DATA OUTPUT IMPACT

Using ECG PRO Template Specific Attributes may impact your Derived Output. This is due to the shifting of the P wave marks from the ECG cycles associated P wave to the isolated P wave, as this will result in an abnormally large PR interval being calculated for that cycle. This will be averaged into the Log Line averages reported to the Derived Parameter and Data Reduction List Views (spreadsheets).

If only a few isolated P waves exist, then the large PR intervals will not have much of an effect on the derived parameters (based on species and logging rate). However, if a large number of these exist in the data set or are clustered together, the reported PR interval in the Derived Data and Data Reduction List Views will be misrepresented. It is recommended to Save a Mark Section prior to using ECG PRO to search and report on Second Degree AV Block. Once your Second Degree AV Block search is complete, the Template Specific Attributes can be disabled and P wave Match Template analysis can be re-run to return to a state where the normal P waves are marked and reported appropriately.

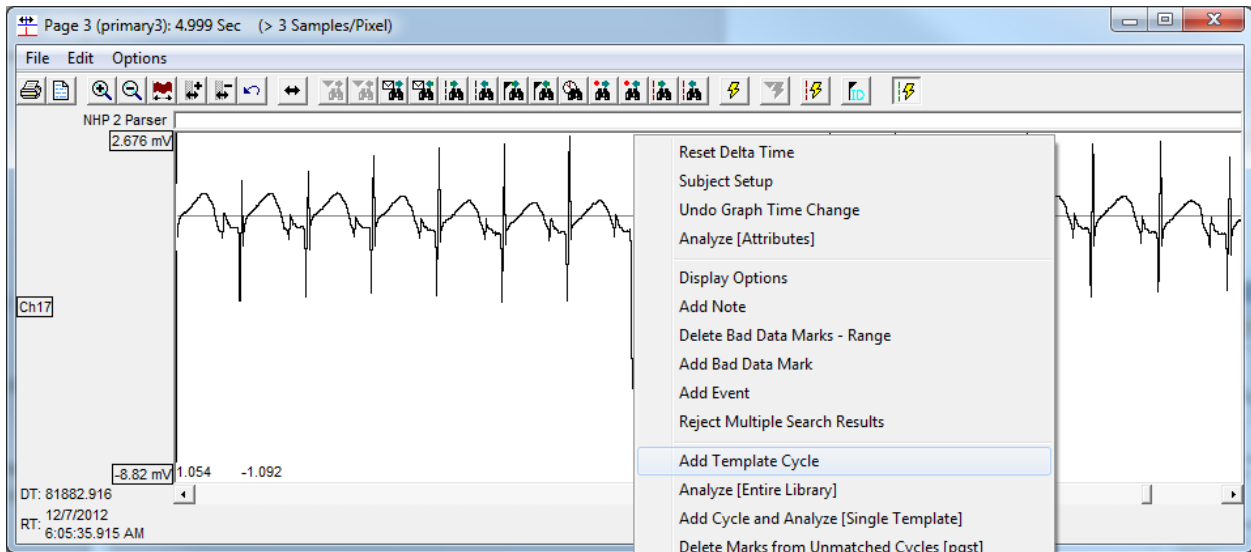
If you should have any questions, please contact DSI Technical Support.

FINDING UNIQUE CYCLE MORPHOLOGIES USING TEMPLATE TAGS

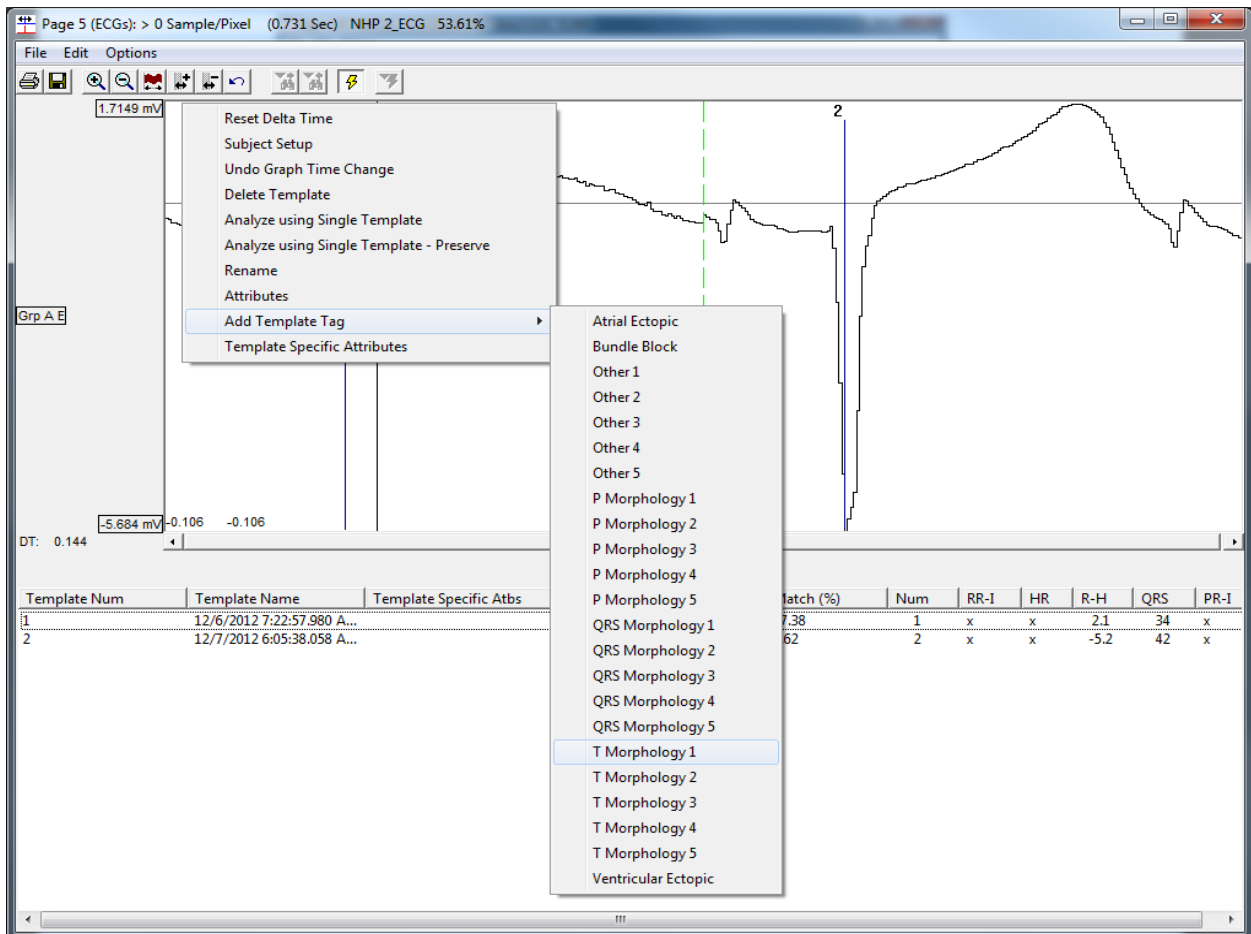
ECG PRO allows **Tags** to be applied to Template cycles when saved to the Template library. Tags allow identification of specific cycle morphologies. By associating Tags to specific cycles, Data Insights can be used to quantify these Tagged cycles. This is useful in instances where count or other derived 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 obtain an output file.

To add Template Tags and create a Data Insights Search to locate Tagged cycles:

1. Select a cycle of interest from the **Primary Graph** page and add this to the **Template Graph** page by right-clicking the cycle and selecting **Add Template Cycle**.

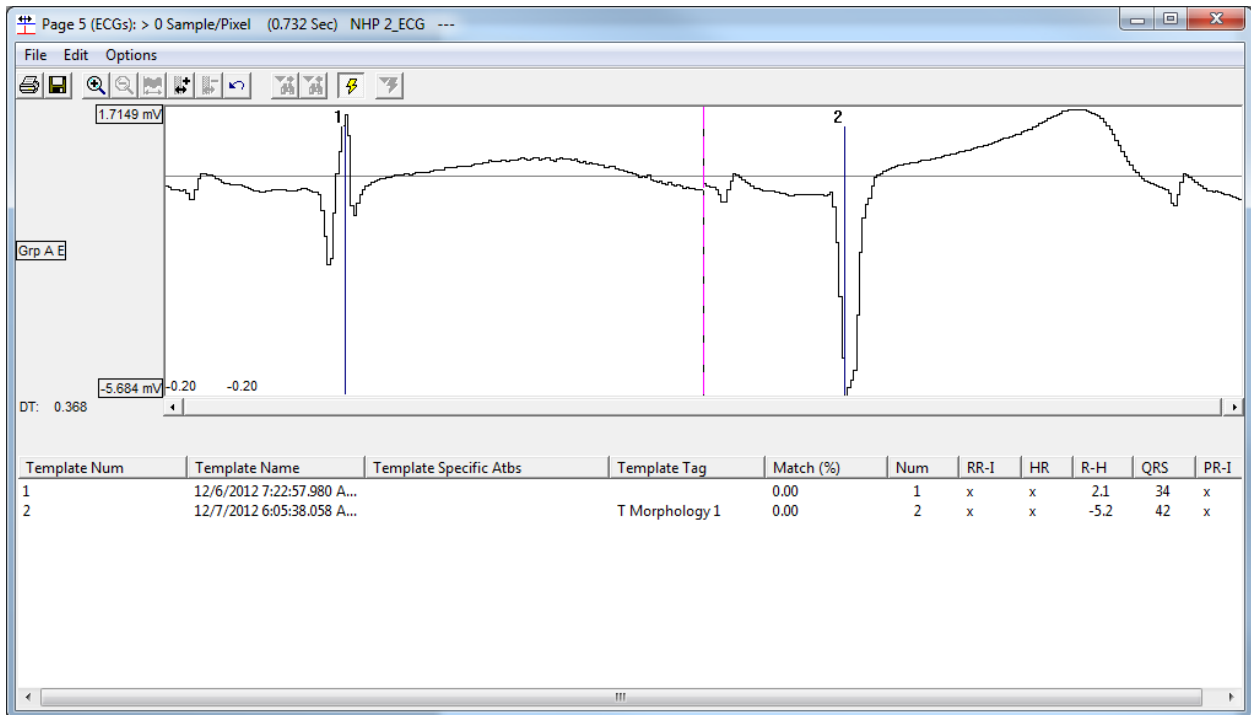


2. Within the **Template Graph** page, right-click and select **Add Template Tag**. Select one of the predefined Tags to mark the cycle and associated Matches, for example T Morphology 1.

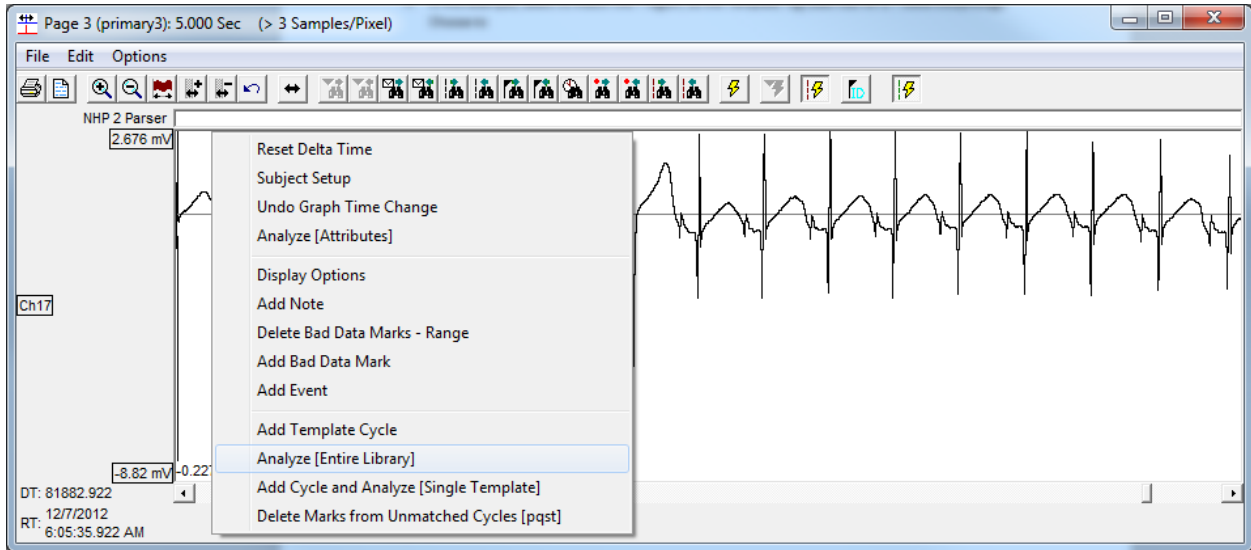


The Tag will be listed under the Template Tag column with its associated Template cycle row within the Template Graph List View.

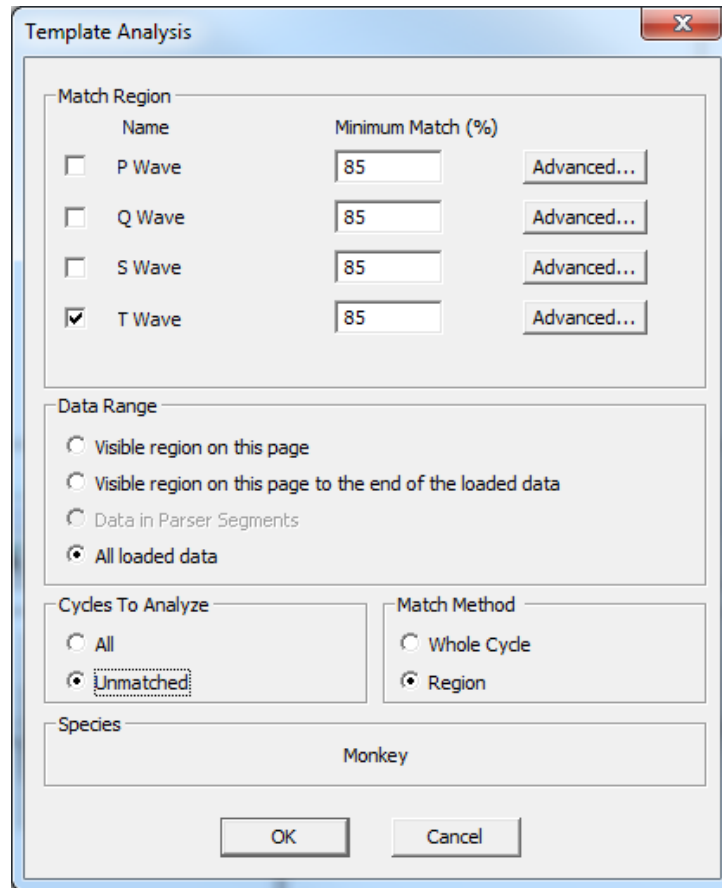
Note: Multiple Tags may be associated with a single Template cycle.



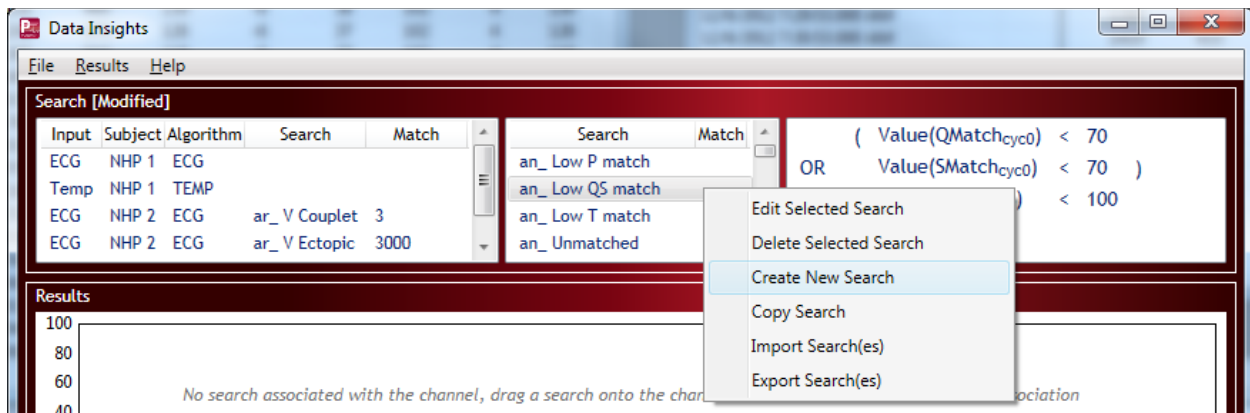
- Execute the **Template Analysis** from the **Primary Graph** page by right-clicking the ECG signal and selecting **Analyze [Entire Library]**.



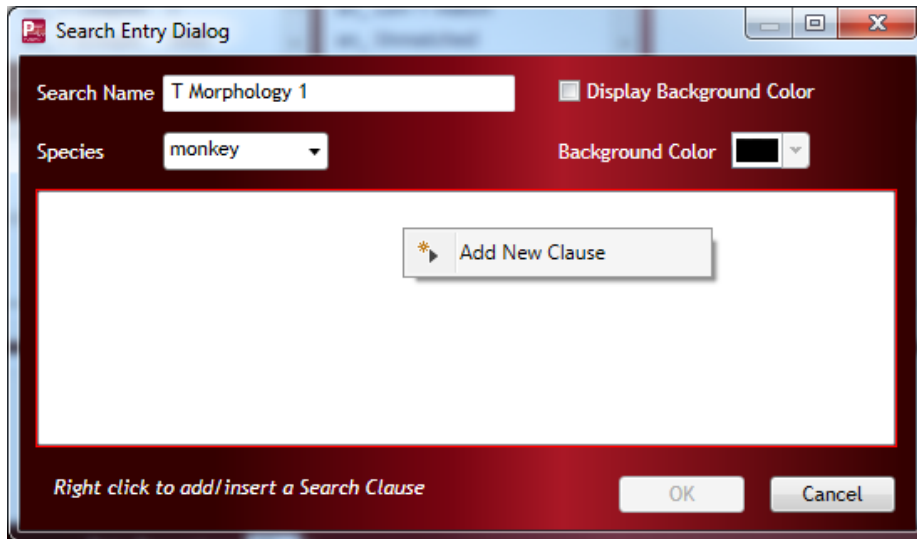
- In this example, select **T Wave** as the *Match Region*, as the Template Tag used was for a T wave Morphology. Use the default 85% *Minimum Match (%)*. Choose **All loaded data** as the *Data Range*, select **Unmatched** for *Cycles to Analyze*, and **Region** for *Match Method*. Then, click **OK**.



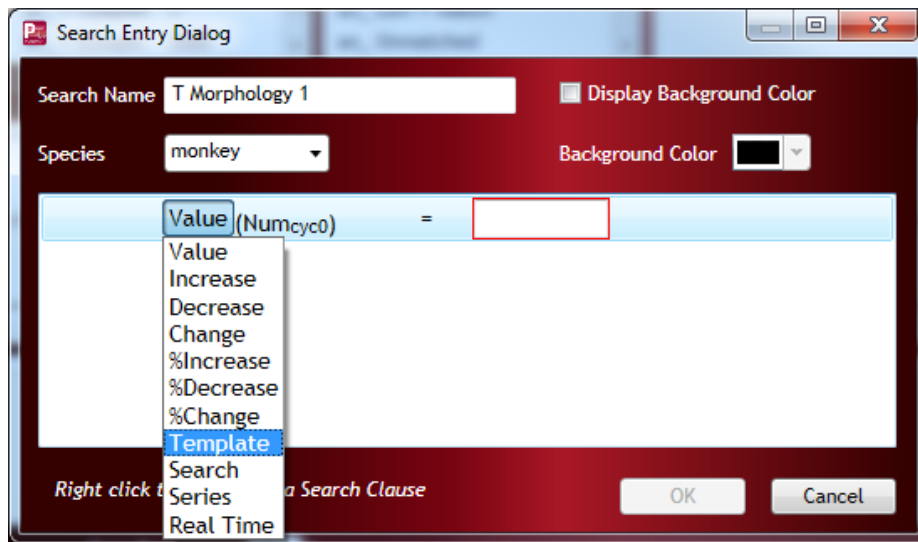
5. Repeat Steps 1-4 for all cycle types of interest.
6. Launch **Data Insights** from the **Experiment** menu.
7. Right-click the **Search and Match Grid** and choose **Create New Search**.



8. Within the *Search Entry* dialog, enter a unique **Search Name**.
9. Right-click within the large white area and select **Add New Clause**.

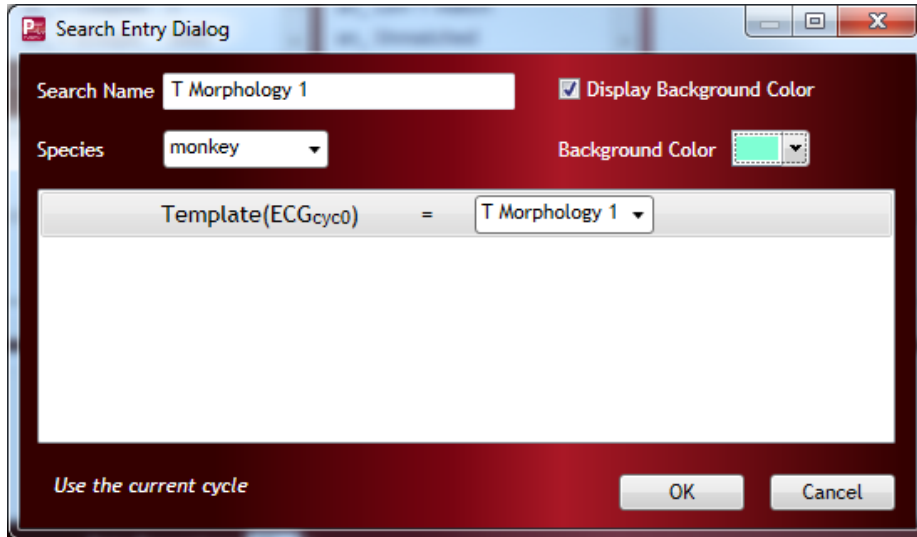


10. Left-click the Value function and select Template.

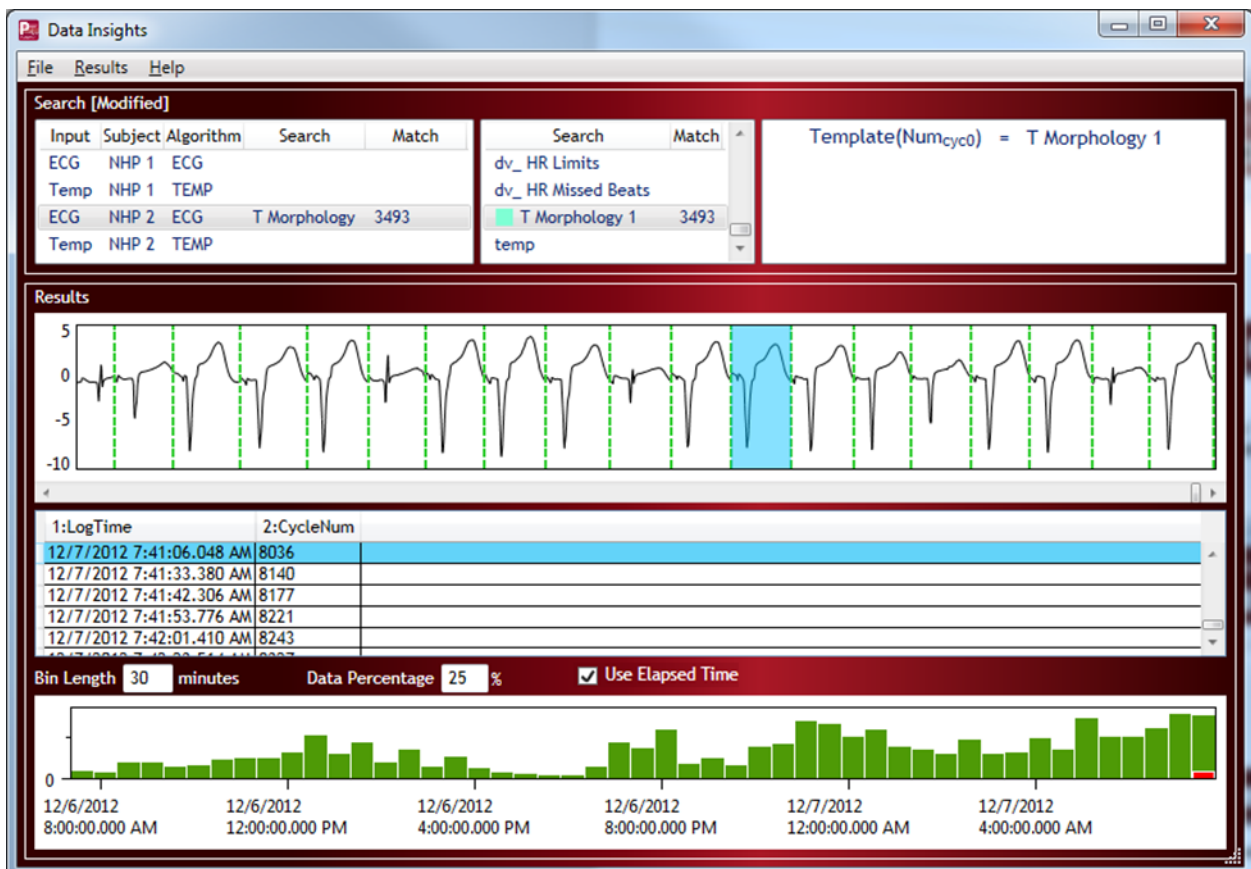


11. Select the Input dropdown and choose the appropriate Template Tag used; e.g. T Morphology 1.
Optional: Check the **Display Background Color** and choose a light shaded **Background Color** to more easily identify match results from the **Primary Graph** page.

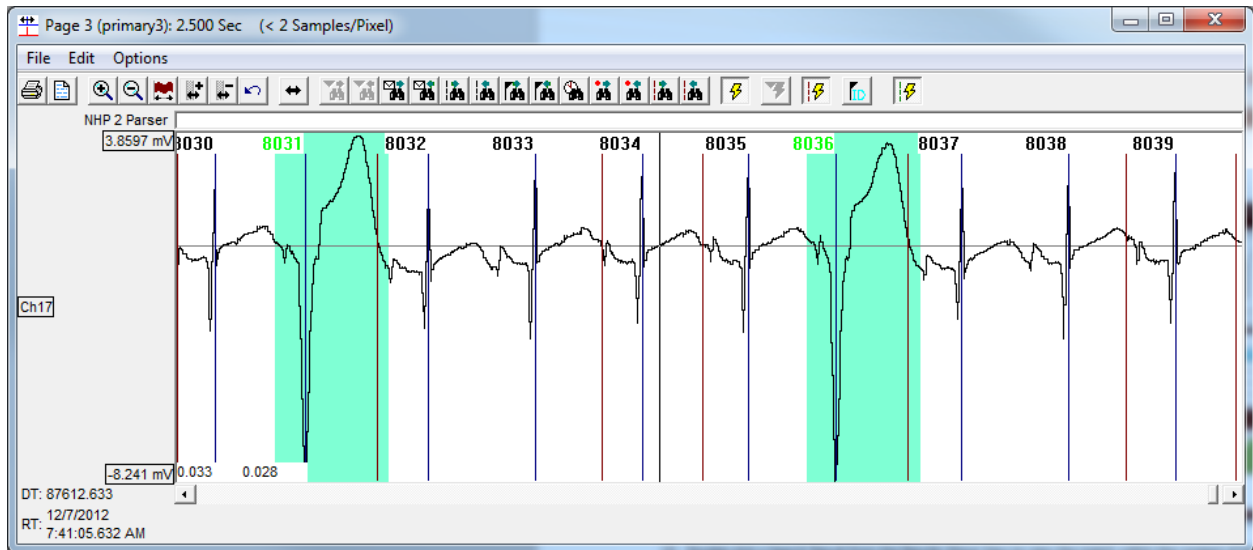
12. Click **OK**.



13. Drag-and-drop the new Search onto the appropriate channel within the **Channel/Search Pair Grid** to execute the Search.



14. Double-click a Search Result from the Results Wave View to view the match within the context of the waveform amongst adjacent beats.



15. Use the Data Insight dialog to review match results. Reject matches if necessary; e.g. the morphology of the cycle is not a close enough match based on desire.
16. Once match results have been reviewed, generate a **Report** via the **File** menu.

CONTACTING TECHNICAL SUPPORT

DSI™ is available to help you with your questions and concerns. Should you hit a road block or need some additional training, please feel free to contact us. We are happy to help!

DSI SUPPORT CENTER

DSI provides easy access to the following self-help tools when they are need most:

Please visit support.datasci.com to access the following resources:

- Quick start guides and videos
- User Manuals
- Technical Notes
- Troubleshooting guides
- The latest software and firmware downloads



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