meap Documentation

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MEAP Tutorial

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Part I: Preprocessing Your Data

2.1 Step 1: Creating your Input File

Note: MEAP also allows the user to input individual files one-by-one. However, when batch processing data we recommend creating an input file as specified below. For more on importing files individually, see Step 2: Importing & Mapping the Channels below.

The first step is to create an input file that tells MEAP where the data you want to analyze is stored. MEAP can accomodate both AcqKnowledge (`.acq`) and matlab (`.mat`) files. Each file should contain the cardiovascular reactivity data collected from one participant including electrocardiogram (ECG), impedance (IKG), blood pressure (BP) waveforms , and respiration (optional). Data must be collected continuously and sampled at at least 1,000 HZ.

Warning: DON'T USE COMMAS IN YOUR FILE NAMES

In addition to the data file(s) you are scoring, you will need to create a comma separated text file (.csv) or excel file (.xlsx) that contains the path to each data file to be scored. This file will be used to import the data for initial preprocessing. Later you will create a design file that contains information specific to your experimental design and analysis method. This initial input file MUST contain the columns containing the following information labeled as such:

1. **File** - specify the full path to each file to be scored
2. Inter-electrode distances-
    (a) When using a mylar band configuration label columns:

    electrode_distance_front - the distance between impedance electrodes on the front of the torso.

    electrode_distance_back - the distance between impedance electrodes on the back of the torso.

(a) When using a spot electrode configuration label columns:

electrode_distance_left

electrode_distance_right and enter the corresponding measurements.

Note: All measurements must be in centimeters.

For a complete list of input file options see participant-parameters.

Here is an example input file:

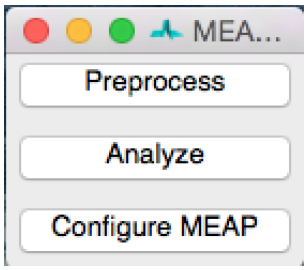
	A	B	C	D	E
1	subject	electrode_distance_front	electrode_distance_back	condition	file
2	301	28	29	band	/Users/Will/Documents/Coldpress Scoring/301_bands.acq
3	302	28	29	band	/Users/Will/Documents/Coldpress Scoring/302_bands.acq
4	302	28	29	spot	/Users/Will/Documents/Coldpress Scoring/302_spots.acq
5	303	28	29	band	/Users/Will/Documents/Coldpress Scoring/303_bands.acq
6	303	28	29	spot	/Users/Will/Documents/Coldpress Scoring/303_spots.acq
7	304	28	29	band	/Users/Will/Documents/Coldpress Scoring/304_bands.acq
8	304	28	29	spot	/Users/Will/Documents/Coldpress Scoring/304_spots.acq
9	305	28	29	band	/Users/Will/Documents/Coldpress Scoring/305_bands.acq
10	305	28	29	spot	/Users/Will/Documents/Coldpress Scoring/305_spots.acq
11	306	28	29	band	/Users/Will/Documents/Coldpress Scoring/306_bands.acq
12	306	28	29	spot	/Users/Will/Documents/Coldpress Scoring/306_spots.acq
13	307	28	29	band	/Users/Will/Documents/Coldpress Scoring/307_bands.acq
14	307	28	29	spot	/Users/Will/Documents/Coldpress Scoring/307_spots.acq
15	308	28	29	band	/Users/Will/Documents/Coldpress Scoring/308_bands.acq
16	308	28	29	spot	/Users/Will/Documents/Coldpress Scoring/308_spots.acq
17	309	28	29	band	/Users/Will/Documents/Coldpress Scoring/309_bands.acq
18	309	28	29	spot	/Users/Will/Documents/Coldpress Scoring/309_spots.acq
19	311	25	35	band	/Users/Will/Documents/Coldpress Scoring/311_bands.acq
20	311	25	35	spot	/Users/Will/Documents/Coldpress Scoring/311_spots.acq
21	312	25	35	band	/Users/Will/Documents/Coldpress Scoring/312_bands.acq
22	312	25	35	spot	/Users/Will/Documents/Coldpress Scoring/312_spots.acq
23	313	25	35	band	/Users/Will/Documents/Coldpress Scoring/313_bands.acq
24	313	25	35	spot	/Users/Will/Documents/Coldpress Scoring/313_spots.acq
25	315	25	35	band	/Users/Will/Documents/Coldpress Scoring/315_bands.acq
26	315	25	35	spot	/Users/Will/Documents/Coldpress Scoring/315_spots.acq
27	316	25	35	band	/Users/Will/Documents/Coldpress Scoring/316_bands.acq
28	316	25	35	spot	/Users/Will/Documents/Coldpress Scoring/316_spots.acq
29	318	25	35	band	/Users/Will/Documents/Coldpress Scoring/318_bands.acq
30	318	25	35	spot	/Users/Will/Documents/Coldpress Scoring/318_spots.acq
31	319	25	35	band	/Users/Will/Documents/Coldpress Scoring/319_bands.acq
32	319	25	35	spot	/Users/Will/Documents/Coldpress Scoring/319_spots.acq
33	323	25	31	band	/Users/Will/Documents/Coldpress Scoring/323_bands.acq
34	323	25	31	spot	/Users/Will/Documents/Coldpress Scoring/323_spots.acq
35	324	25	31	band	/Users/Will/Documents/Coldpress Scoring/324_bands.acq
36	324	25	31	spot	/Users/Will/Documents/Coldpress Scoring/324_spots.acq
37	326	25	31	spot	/Users/Will/Documents/Coldpress Scoring/326_spots.acq
38	327	25	29	band	/Users/Will/Documents/Coldpress Scoring/327_bands.acq
39	327	25	29	spot	/Users/Will/Documents/Coldpress Scoring/327_spots.acq

To add the file paths more quickly create columns for study condition, task, and any other variables relavant to your design. Name your Acknowlege files based on these values and use excel's **CONCATENATE** function to populate the file path. For example, here the path for the first row of data is CONCATENATE = ("/Users/Will/Documents/Coldpress Scoring/", A2, "_", D2, "s.acq"). Simply drag this equation down the column to populate the rest of the file paths.

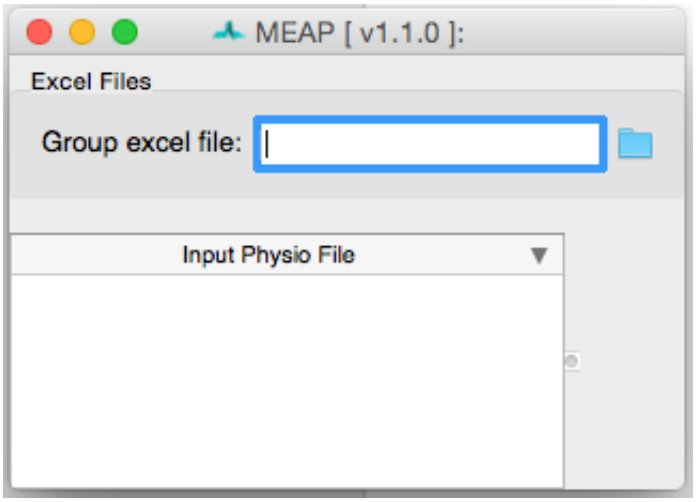
Warning: If you have a lot of data, it may be best to create several smaller input files with only a subset of your participants or cases. This will reduce the amount of data that MEAP has to load at one time and can prevent the program or your computer from crashing or running slowly.

2.2 Step 2: Importing Data & Mapping the Channels

When you launch MEAP, you will see a window that looks like this:



Select **Preprocess**. This will open a window that looks like this:



Click on the folder in the upper right corner to navigate to your input file. Information from this spreadsheet will be called and a window will appear that contains all of your files to be scored and also serves as the primary user interface.

Files to be processed appear in white. Once you finish the preprocessing pipeline and save as `.mea.mat` file, the row will turn light blue. The file currently being processed appears in dark blue. To import files individually, right click within the "Input Physio file" portion of the window and select **Add New Item**. Then click within the blank line that appears and then navigate to the file you wish to score using the blue folder icon to the right of the *File* field.

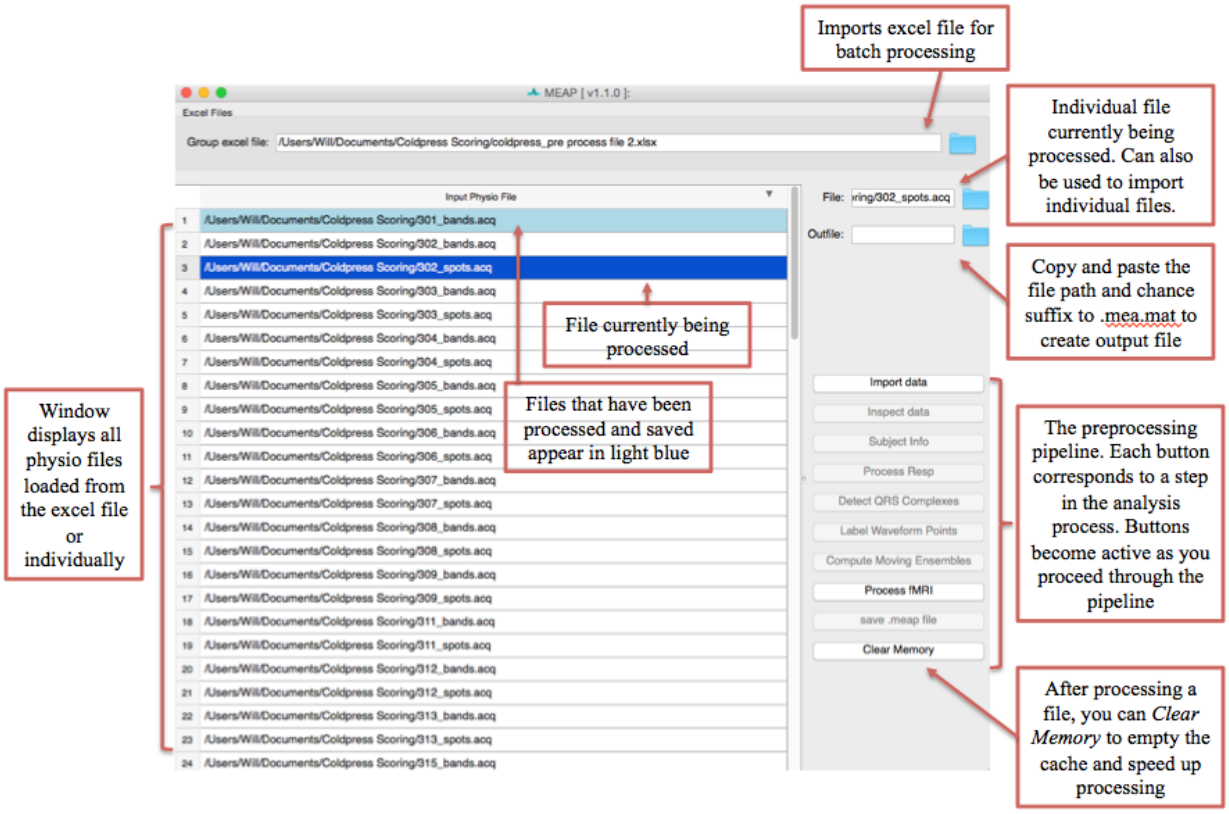
Now select the first file you would like to process. Then click on the **Import data** button at the right of the screen to begin preprocessing.

Once your Aqcknowledge file is imported you'll need to let MEAP know which channel contains each data source. If loading from a mea.mat file, the channels have already been stored. For Acqknowledge files, specify the data contained within each channel using this GUI:

The channel names from your data file appear on the left. Match these with the data types specified in the dropdown menus on the right. If blood pressure data was collected using a wireless blood pressure system or other system that generates separate channels for diastolic and systolic blood pressure, map each of these accordingly; systolic and diastolic are both options in the drop down menu. Any remaining channels that you do not wish to import data from should be set to *None*.

Regardless, of the number of channels that appear in the `.acq` file and their names, you should have the following channels mapped:

1. **ECG** - Electrocardiogram data


Imports excel file for batch processing
MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
1 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
2 /Users/Will/Documents/Coldpress Scoring/302_bands.acq
3 /Users/Will/Documents/Coldpress Scoring/302_spots.acq
4 /Users/Will/Documents/Coldpress Scoring/303_bands.acq
5 /Users/Will/Documents/Coldpress Scoring/303_spots.acq
6 /Users/Will/Documents/Coldpress Scoring/304_bands.acq
7 /Users/Will/Documents/Coldpress Scoring/304_spots.acq
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9 /Users/Will/Documents/Coldpress Scoring/305_spots.acq
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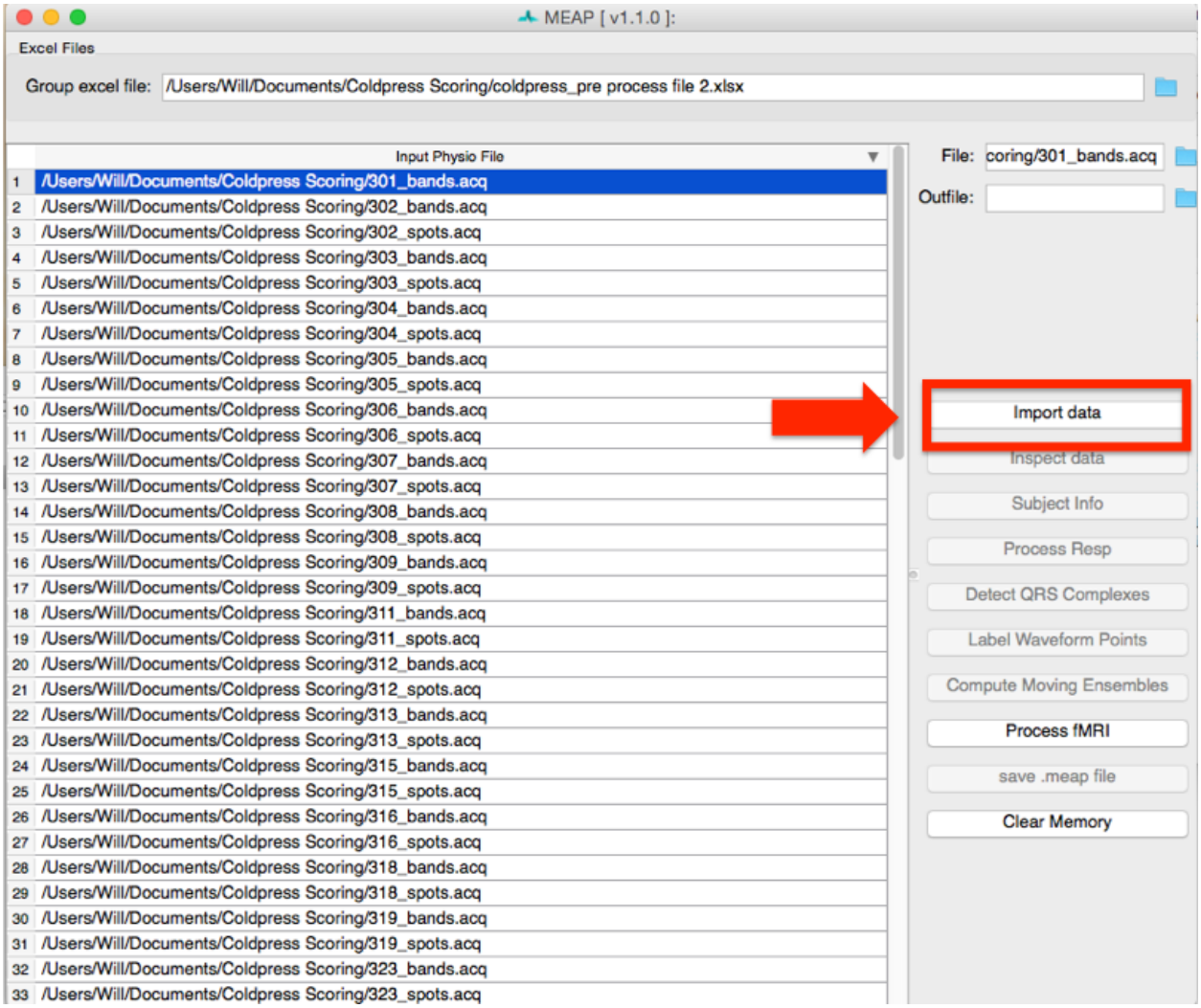
22 /Users/Will/Documents/Coldpress Scoring/313_bands.acq
23 /Users/Will/Documents/Coldpress Scoring/313_spots.acq
24 /Users/Will/Documents/Coldpress Scoring/315_bands.acq
File: ring/302_spots.acq
Outfile:
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory
Individual file currently being processed. Can also be used to import individual files.
Copy and paste the file path and chance suffix to .mea.mat to create output file
File currently being processed
Files that have been processed and saved appear in light blue
Window displays all physio files loaded from the excel file or individually
The preprocessing pipeline. Each button corresponds to a step in the analysis process. Buttons become active as you proceed through the pipeline
After processing a file, you can Clear Memory to empty the cache and speed up processing


MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
1 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
2 /Users/Will/Documents/Coldpress Scoring/302_bands.acq
3 /Users/Will/Documents/Coldpress Scoring/302_spots.acq
4 /Users/Will/Documents/Coldpress Scoring/303_bands.acq
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6 /Users/Will/Documents/Coldpress Scoring/304_bands.acq
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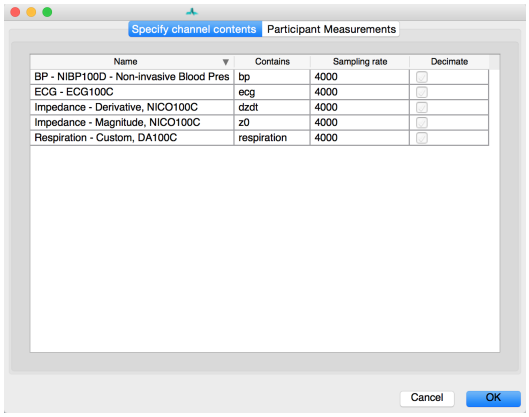
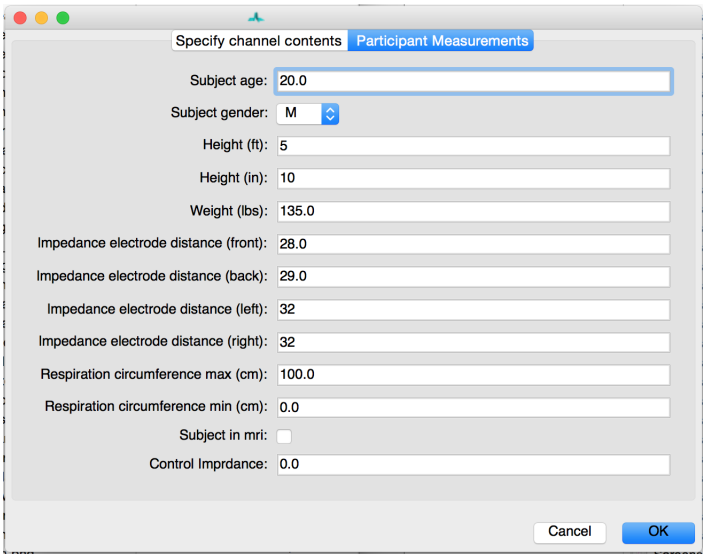
30 /Users/Will/Documents/Coldpress Scoring/319_bands.acq
31 /Users/Will/Documents/Coldpress Scoring/319_spots.acq
32 /Users/Will/Documents/Coldpress Scoring/323_bands.acq
33 /Users/Will/Documents/Coldpress Scoring/323_spots.acq
File: coring/301_bands.acq
Outfile:
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory


Specify channel contents
Participant Measurements
Name
Contains
Sampling rate
Decimate
BP - NIBP100D - Non-invasive Blood Pres
bp
4000
ECG - ECG100C
ecg
4000
Impedance - Derivative, NICO100C
dzdt
4000
Impedance - Magnitude, NICO100C
z0
4000
Respiration - Custom, DA100C
respiration
4000
Cancel
OK

2. **z0** - Magnitude of impedance
3. **bp** - Blood pressure (or systolic and diastolic; optional)
4. **dzdt** - First derivative of impedance magnitude.
5. **respiration**- breath data (optional)
6. **doppler** - Cardiac doppler radar signal (optional)

This window also contains a tab in which you can specify or correct the participant's measurements. The inter-electrode distances are imported directly from your input file as is any other information you specified including height, weight, respiration circumference, and whether data was collected during Magnetic Resonance Imaging (MRI). This latter specification in critical as MEAP utilizes a customized point-marking algorithm for data collected within the scanner.



When importing files individually you MUST manually enter the participant measurements here. These values can also be edited after the fact by clicking on the **Subject Info** button.

For more information on these parameters and how to specify them in your input file see participant-parameters.

2.3 Step 3: Check the Quality of Your Waveforms

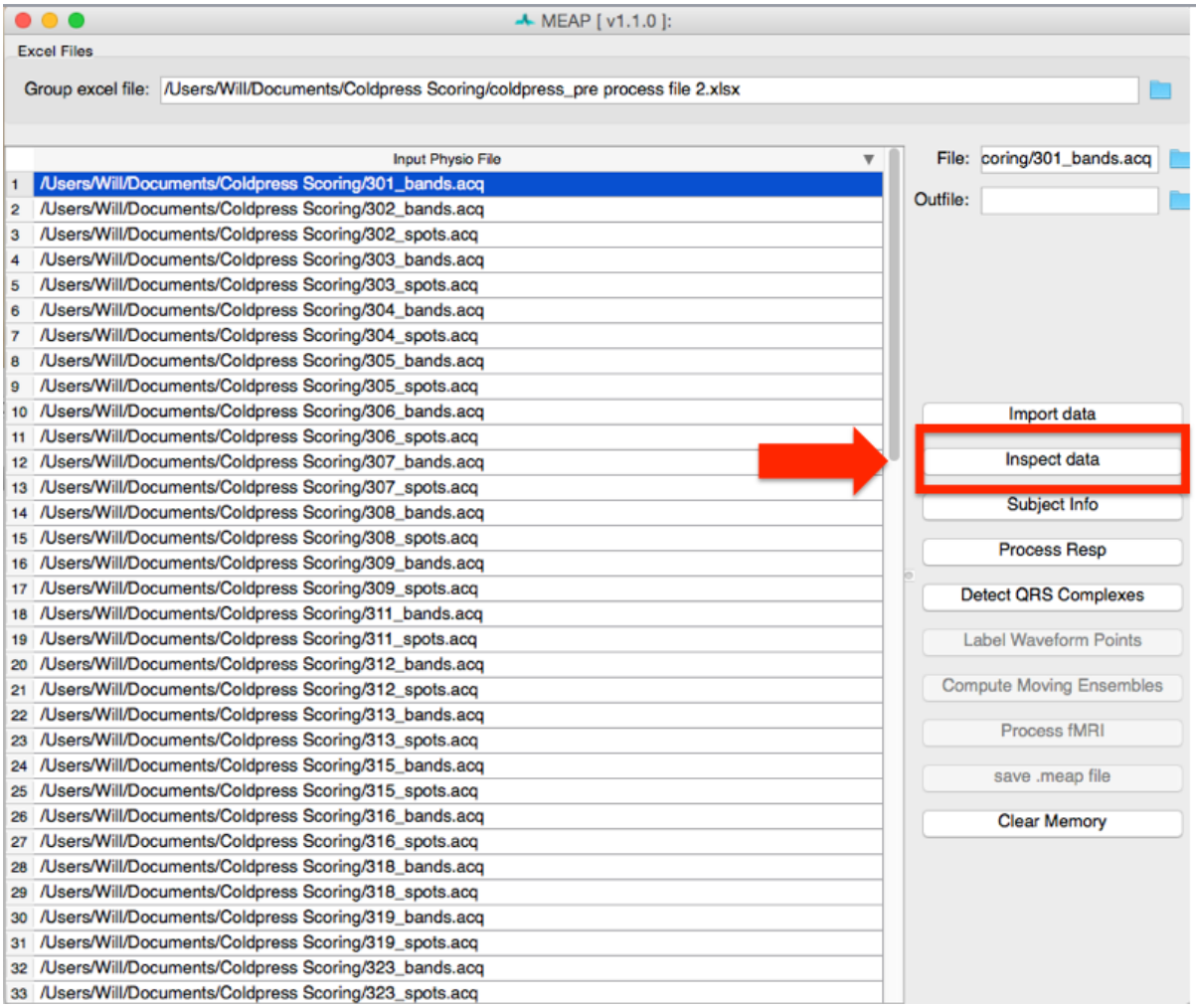
Now that you have specified the type of data contained within each channel and updated participant measurements as desired, click on the **Inspect data** button at the bottom of the GUI.

MEAP will load and display the data in a GUI like this:

This feature is designed to allow the user to check the quality of the data, remove outliers, and flag any segments of data that contain noise or artifacts or that the researcher would like to exclude from analyses for whatever reason. Flagged sections will then be removed from all future analysis steps including point marking and ensemble or moving ensemble averaging.

> **Warning:** It is critical that all data included in calculations be as clean as possible. Attempting to analyze data with significant artifacts will not yield interpretable values.

Windsorizing: Removing Extreme Outliers


MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
1 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
2 /Users/Will/Documents/Coldpress Scoring/302_bands.acq
3 /Users/Will/Documents/Coldpress Scoring/302_spots.acq
4 /Users/Will/Documents/Coldpress Scoring/303_bands.acq
5 /Users/Will/Documents/Coldpress Scoring/303_spots.acq
6 /Users/Will/Documents/Coldpress Scoring/304_bands.acq
7 /Users/Will/Documents/Coldpress Scoring/304_spots.acq
8 /Users/Will/Documents/Coldpress Scoring/305_bands.acq
9 /Users/Will/Documents/Coldpress Scoring/305_spots.acq
10 /Users/Will/Documents/Coldpress Scoring/306_bands.acq
11 /Users/Will/Documents/Coldpress Scoring/306_spots.acq
12 /Users/Will/Documents/Coldpress Scoring/307_bands.acq
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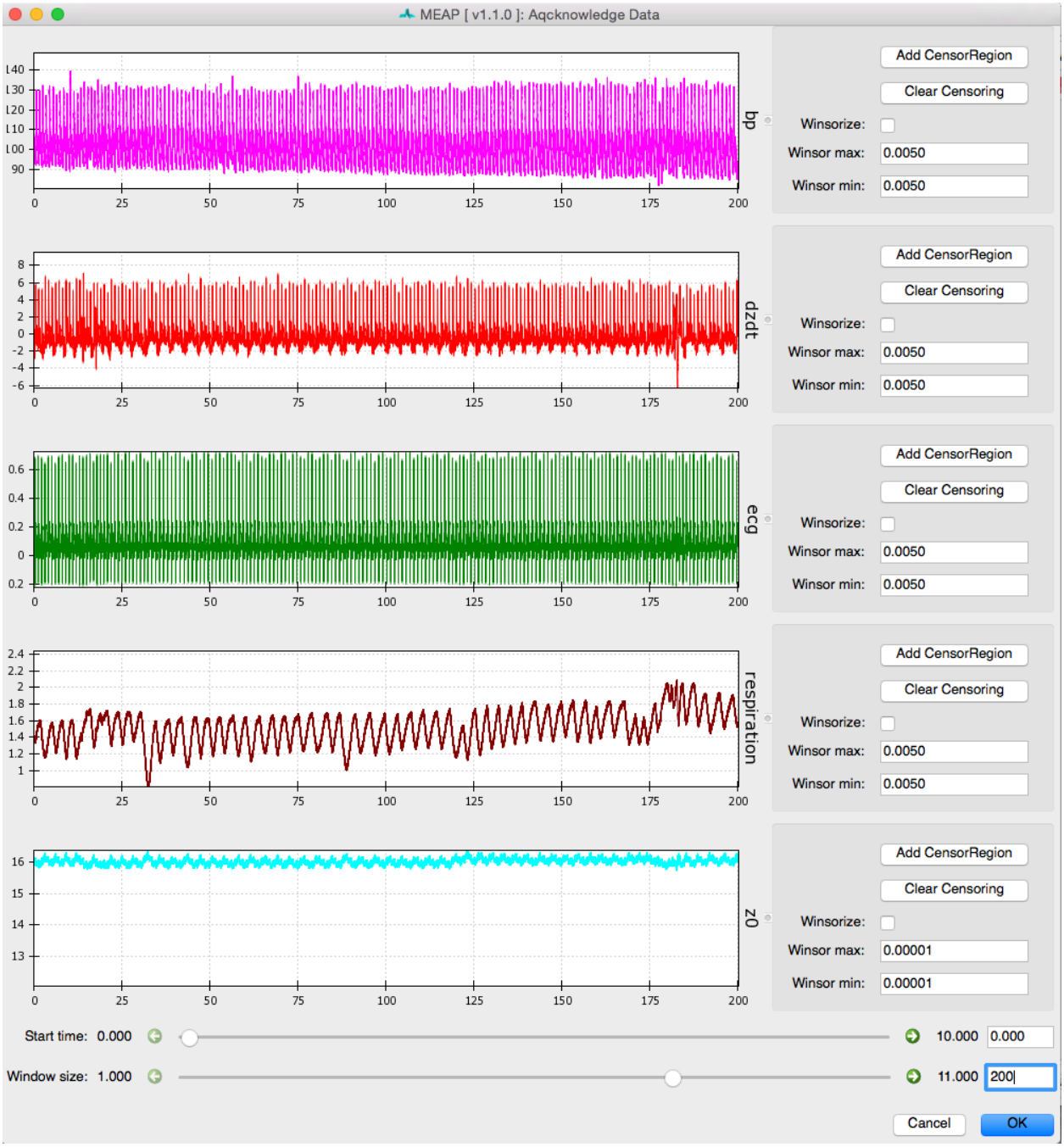
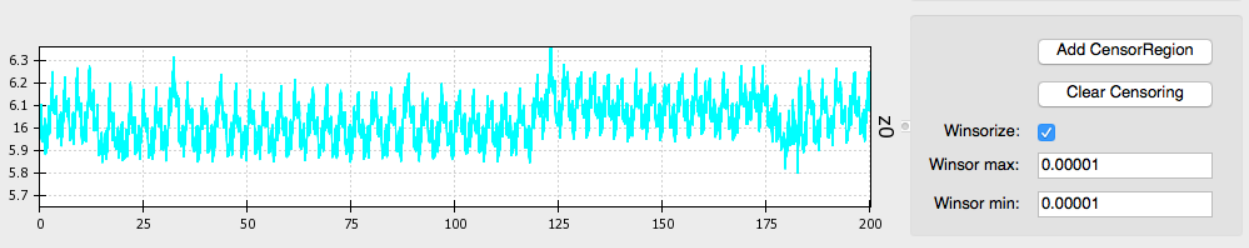
27 /Users/Will/Documents/Coldpress Scoring/316_spots.acq
28 /Users/Will/Documents/Coldpress Scoring/318_bands.acq
29 /Users/Will/Documents/Coldpress Scoring/318_spots.acq
30 /Users/Will/Documents/Coldpress Scoring/319_bands.acq
31 /Users/Will/Documents/Coldpress Scoring/319_spots.acq
32 /Users/Will/Documents/Coldpress Scoring/323_bands.acq
33 /Users/Will/Documents/Coldpress Scoring/323_spots.acq
File: coring/301_bands.acq
Outfile:
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory


MEAP [v1.1.0]: Aqcknowledge Data
bp
dzdt
ecg
respiration
z0
Add CensorRegion
Clear Censoring
Winsorize:
Winsor max:
0.0050
Winsor min:
0.0050
0.00001
Start time: 0.000
10.000
0.000
Window size: 1.000
11.000
200
Cancel
OK

The first thing to do when inspecting your data is to Windsorize outliers, if necessary. For example, the Z0 signal may drop to zero at the beginning or end of a file leading the wave form to appear small and uncentered in the window, as shown in image above. Such extreme outliers can be removed by selecting the **Windsorize** button next to the waveform that contains outliers and setting the maximum and minimum cutoffs for outliers. For example, setting both the max and min values to .005 means that you are pulling in the top and bottom 0.5% of the data to just inside that cutoff. You may need to adjust one or both of these parameters depending on the outliers contained within your data. Ideally, you want to set these cutoffs so that you are removing only extreme outliers and not any meaningful data. If Windsorizing leads to your waveforms appearing truncated, set lower cutoff values. If you don't see your window update, check and uncheck the **Windsorize** button for that waveform.

Post-windsorizing your Z0 data should look like this:



Censor Regions: Removing Noise & Aritfacts

Next, use the *Window size* slider at the bottom of the screen to select a widow size that optimizes viewing your data. We recommend a window size of between 20 and 60 seconds to allow the user to clearly visualize each waveform and inspect it for anomalies.

Like so:

Using the *Start time* slider you can scroll through the length of your data file. You'll notice that if you start at time 0 and move the slider to the far right, you do NOT reach the end of the file (unless it is very short). To do this you must use the green arrows to increase the sensitivity of the slider by a factor of 10 each time. Alternatively, you can jump to a specific time point by entering it into the box to the right.

As you scroll through, look for any sections where the waveform deviates significantly from it's canonical shape.

Artifacts can look like this, where the signal drops off or shoots up beyond expected values:

Artifacts can also look like this, where the signal deviates from its canonical shape, although values do not appear out of bounds:

Artifacts are most likely to occur in the dz/dt signal, but may occur in any of the data streams.

Note: For more info on what wave forms should look like, see physiological data

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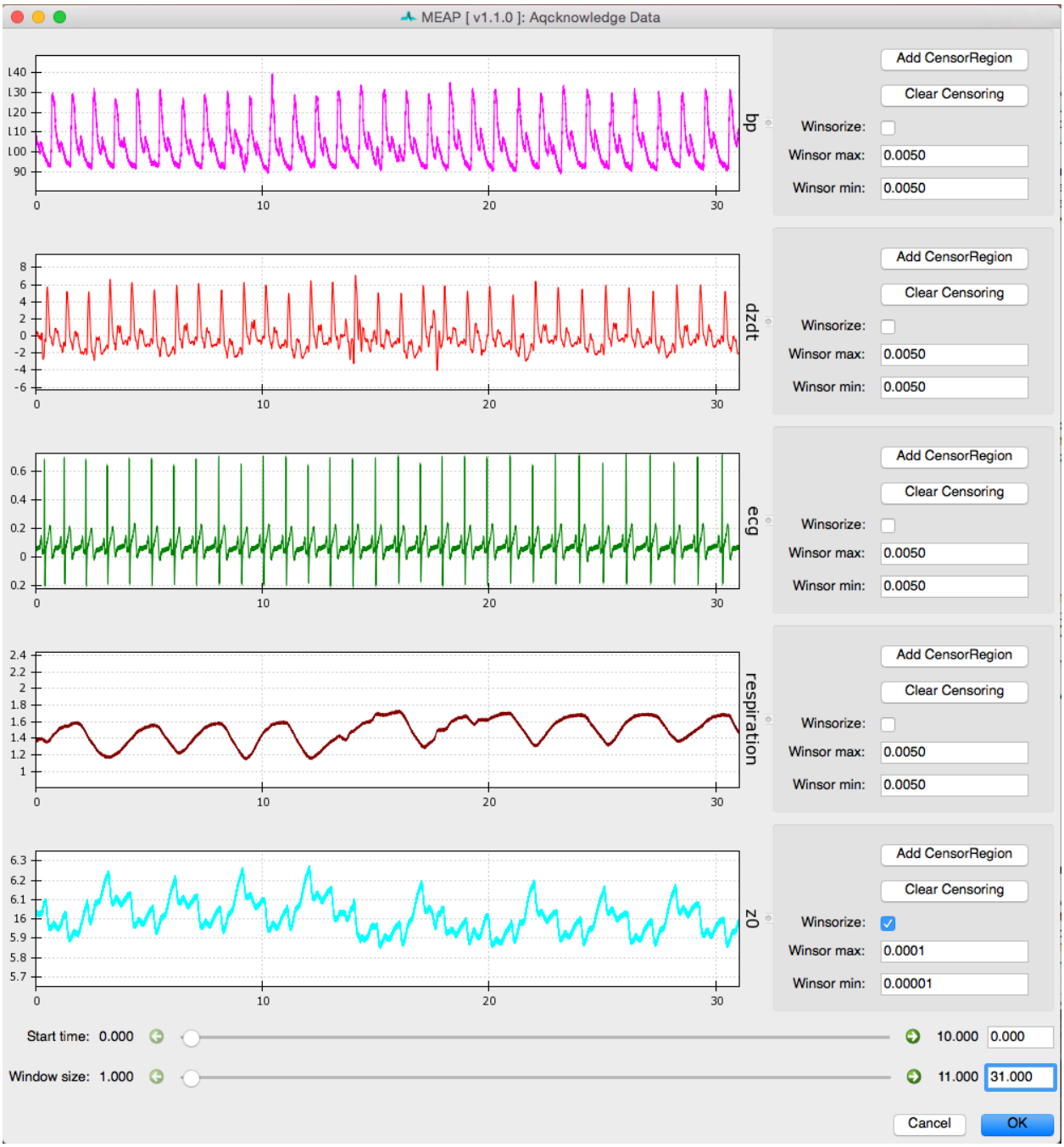
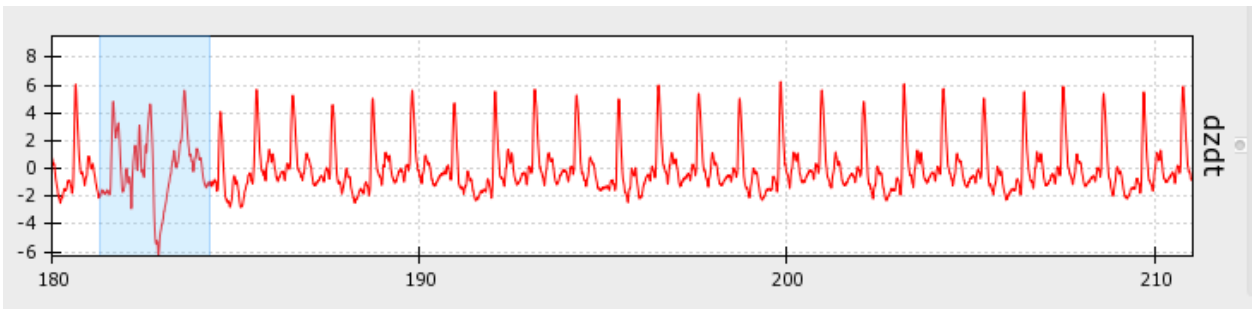
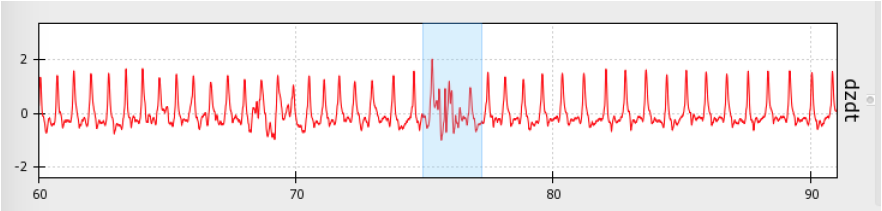
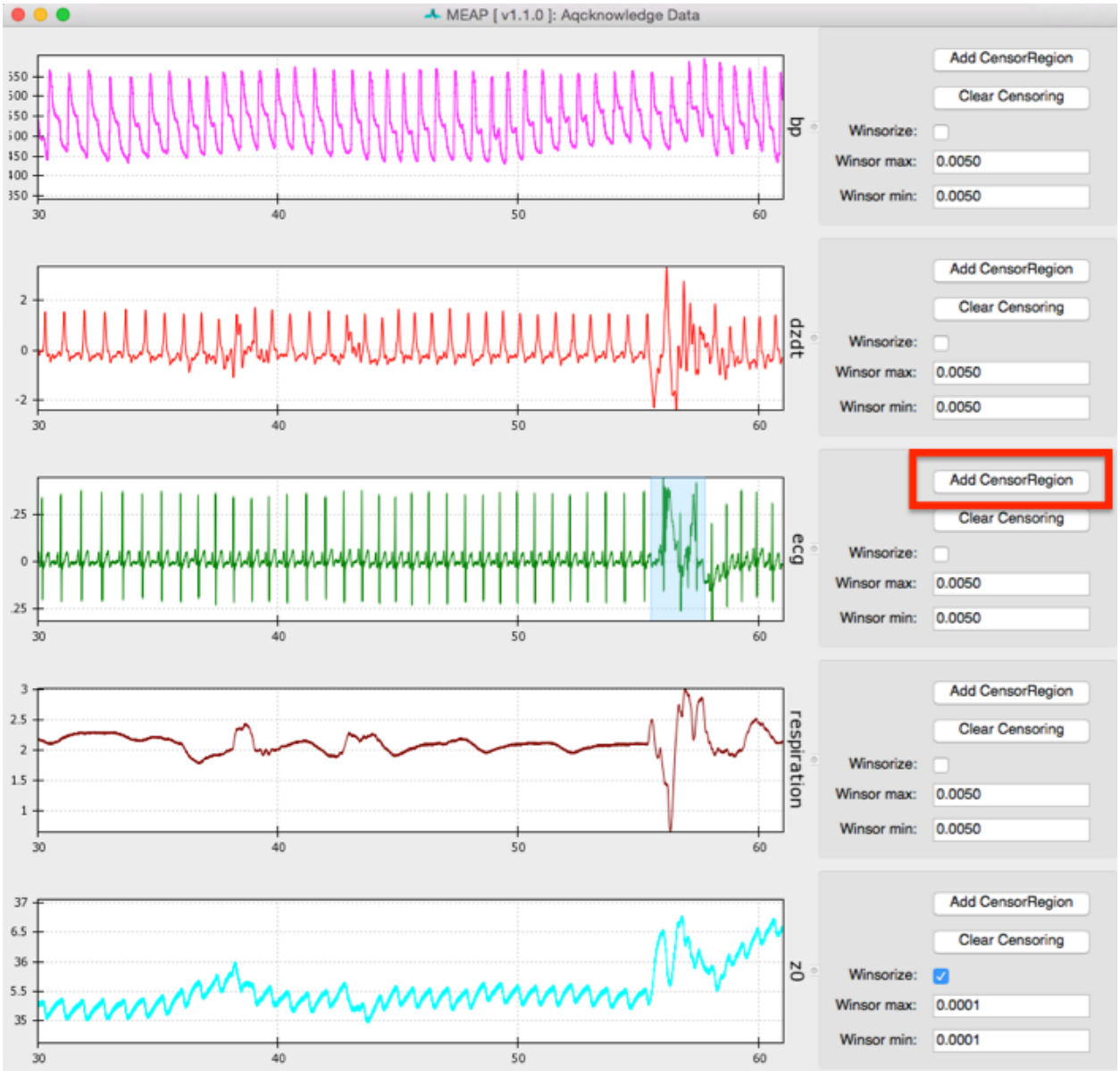
Whenever you come across an area of noise like this, you will want to remove it from analyses by censoring it out. This is accomplished using the *Censor* buttons to the right of each signal. Select the button that matches the waveform you wish to edit and use your curser to highlight the region you would like to exclude. If you would like to remove multiple regions, simply click on the *Censor dz/dt* again and select another region. To censor regions on additional waveforms, simply select the relevant *Censor* button and highlight the region.

Do this as necessary for each waveform. If a region is censored out on one waveform (the *dz/dt* wave, for example) this same time interval is censored out of all other waves as well. Therefore, if artifacts occur in multiple waveforms


MEAP [v1.1.0]: Aqcknowledge Data
bp
dzdt
ecg
respiration
z0
Add CensorRegion
Clear Censoring
Winsorize:
Winsor max:
0.0050
Winsor min:
0.0050
0.0001
0.00001
Start time: 0.000
Window size: 1.000
10.000
11.000
0.000
31.000
Cancel
OK


dzdt


2
0
-2
60
70
80
90
dzdt


MEAP [v1.1.0]: Aqcknowledge Data
bp
dzdt
ecg
respiration
z0
Add CensorRegion
Clear Censoring
Winsorize:
Winsor max:
0.0050
Winsor min:
0.0050
0.0001

simultaneously, it is not necessary to censor them separately on each waveform (as in the image above). This means that if one signal is bad throughout it is best not to edit this out, but to leave it and remove calculated values later in the analysis pipeline. For example, if BP data is bad throughout this approach will allow you to still analyze the impedance and ECG data. Without good ECG data, however, MEAP cannot calculate and align cardiac cycles and analysis will not be possible.

Note: This editing feature can also be employed to remove epochs of data that the researcher does not wish to include in analyses.

Once you are satisfied with the regions to be removed, select *OK*.

This is a good time to save your work. To do so, copy the *File* path and paste it into the *Outfile* field and change the file type from `.acq` to `.mea.mat`, then click **Save .meap file**. You could also provide any file name as long as it ends with .mea.mat.

2.4 Step 4: Processing Respiration Data

If you collected respiration data as part of your study MEAP can calculate the number of breaths. MEAP can also calculate breath rate from the ICG data. Additionally, by processing respiration in this way the user can remove the low frequency fluctuation in ICG signals due to respiration rather than changes in blood flow. Because the torso expands with each inhalation, the respiration cycle impacts impedance data in ways that may or may not be of interest to the researcher.

Select **Process Resp**:

This will load a window like the one below which shows dz/dt, Z0, and respiration waveforms.

Click the **Process Respiration** button at the bottom of the screen and MEAP will use either the measured respiration signal or low frequency components of the ICG wave to determine respiration rate and remove its influence on the dz/dt and Z0 waveforms. The blue lines represent raw data and green represents data with variation due to respiration removed. Black dots mark inhalation and exhalation.

Sliders can be used to change the size and start point of the viewing window just like at the *Inspect Data* step.

Processed respiration using measured respiration signal:

Processed respiration using dz/dt waveform:

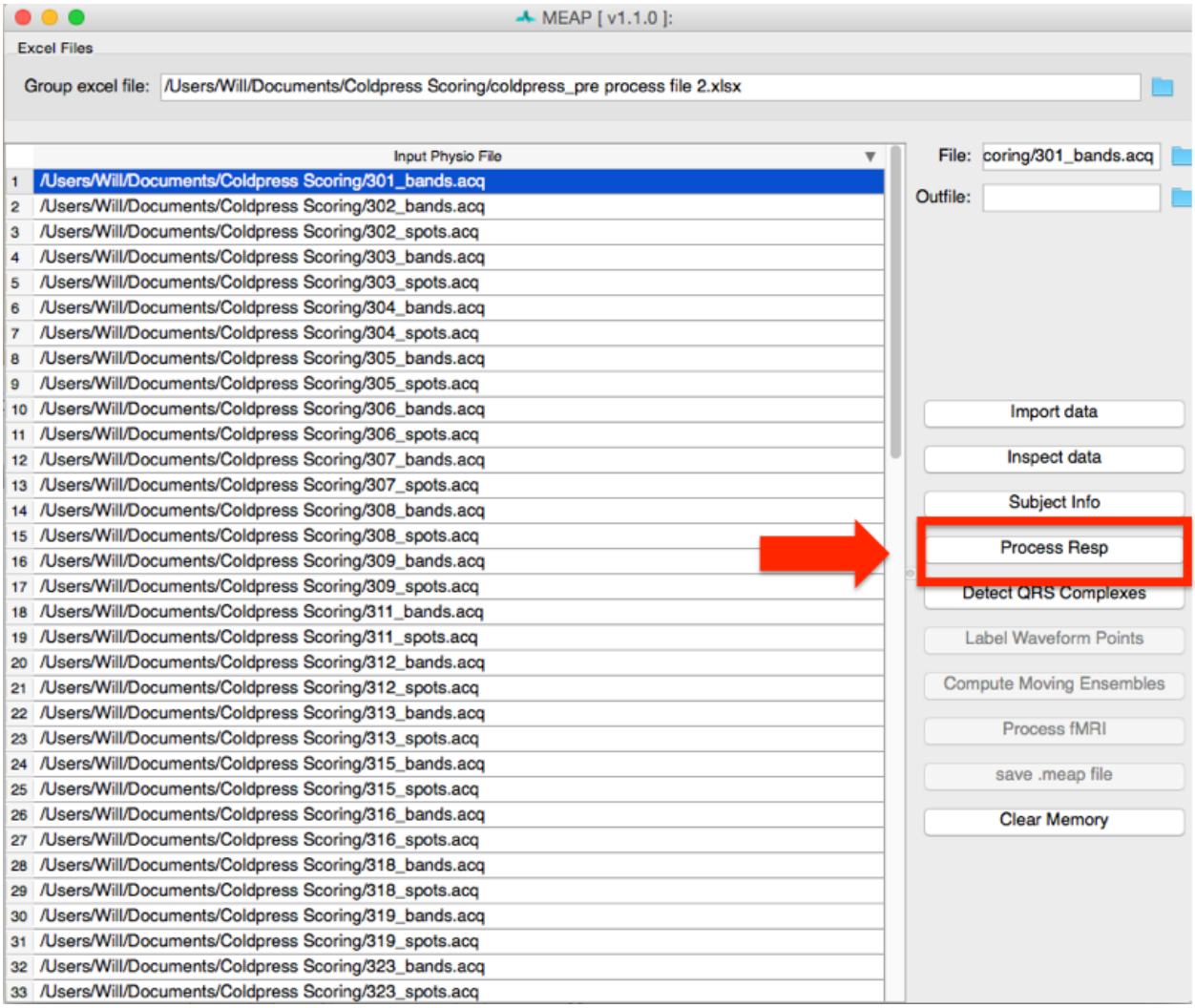
After respiration has been processed, simply close the window and proceed to the next step.

Respiration correction is a very useful preprocessing step. Consider the Kubicek equation for calculating stroke volume. The Z0 term is directly included, which means that respiration-related signals will be incorporated in stroke volume and impact all measurements that use stroke volume. These include cardiac output and TPR. One remedy to respiration artifact is ensemble averaging. However, unless the same portions of the respiratory cycle are included in each time window, respiration-driven changes will only add to your model's noise term.

2.5 Step 5: Detecting R-Peaks

Now that you have loaded your data, checked its quality, and removed areas of artifact, the next step is to detect each heartbeat. Click on the **Detect QRS Complexes** button.

MEAP automatically detects each R-peak using a modified Pan-Tomkins algorithm (for more information on the Pan-Tompkins method see beat-detector). There are other options for QRS detection that work better for data collected in an MRI scanner. However, all methods share the same basic editing tools.


MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
1 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
2 /Users/Will/Documents/Coldpress Scoring/302_bands.acq
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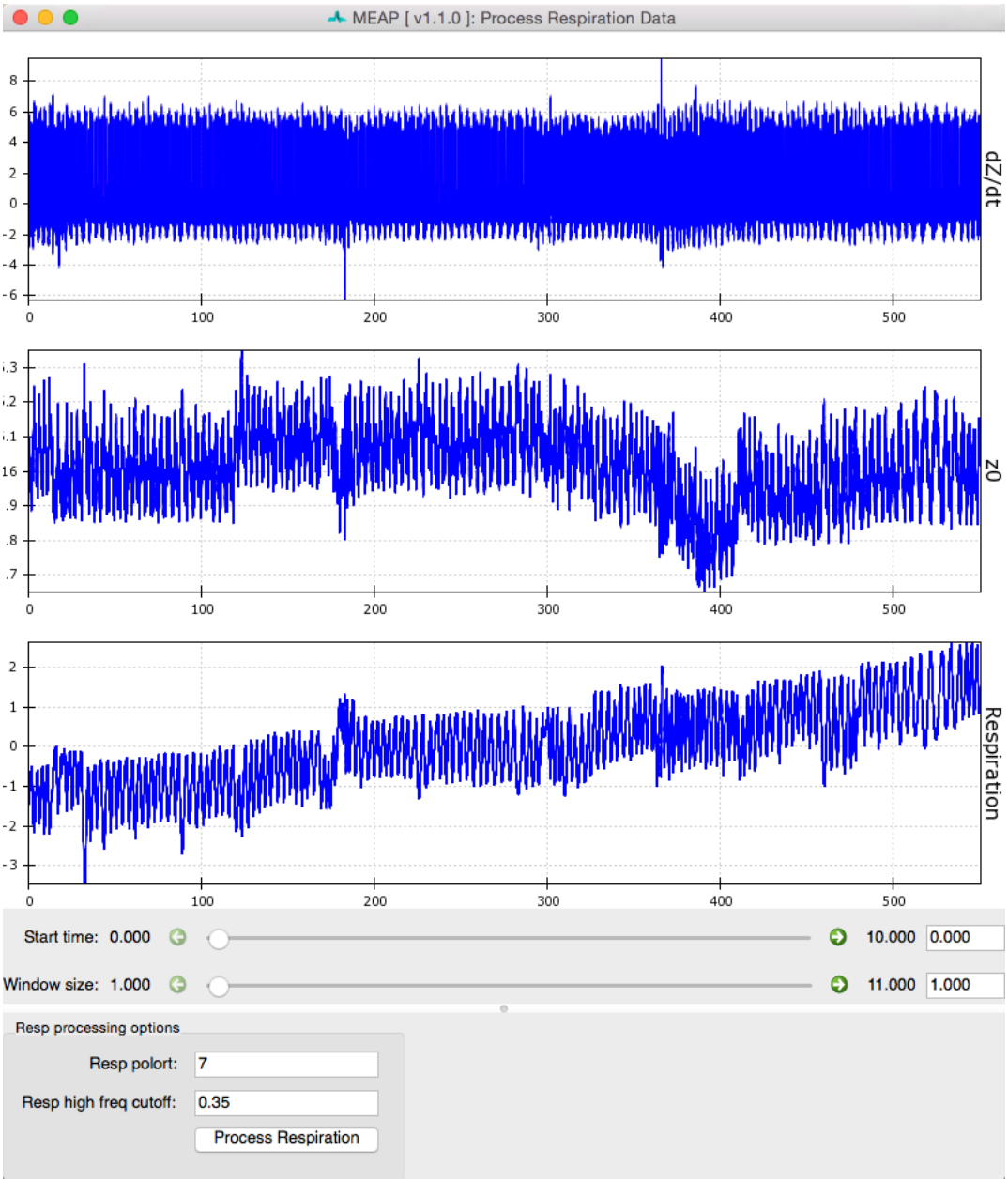
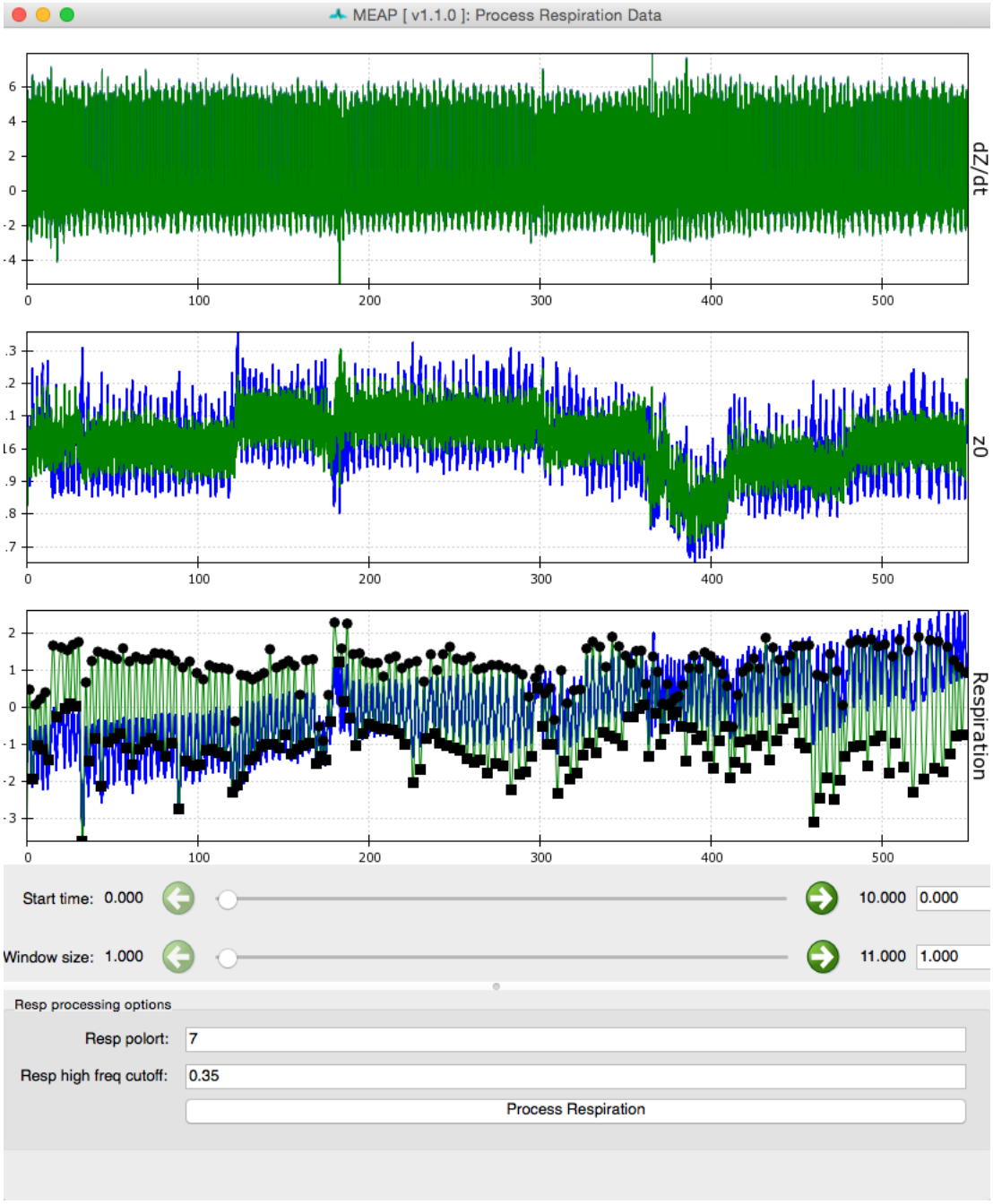
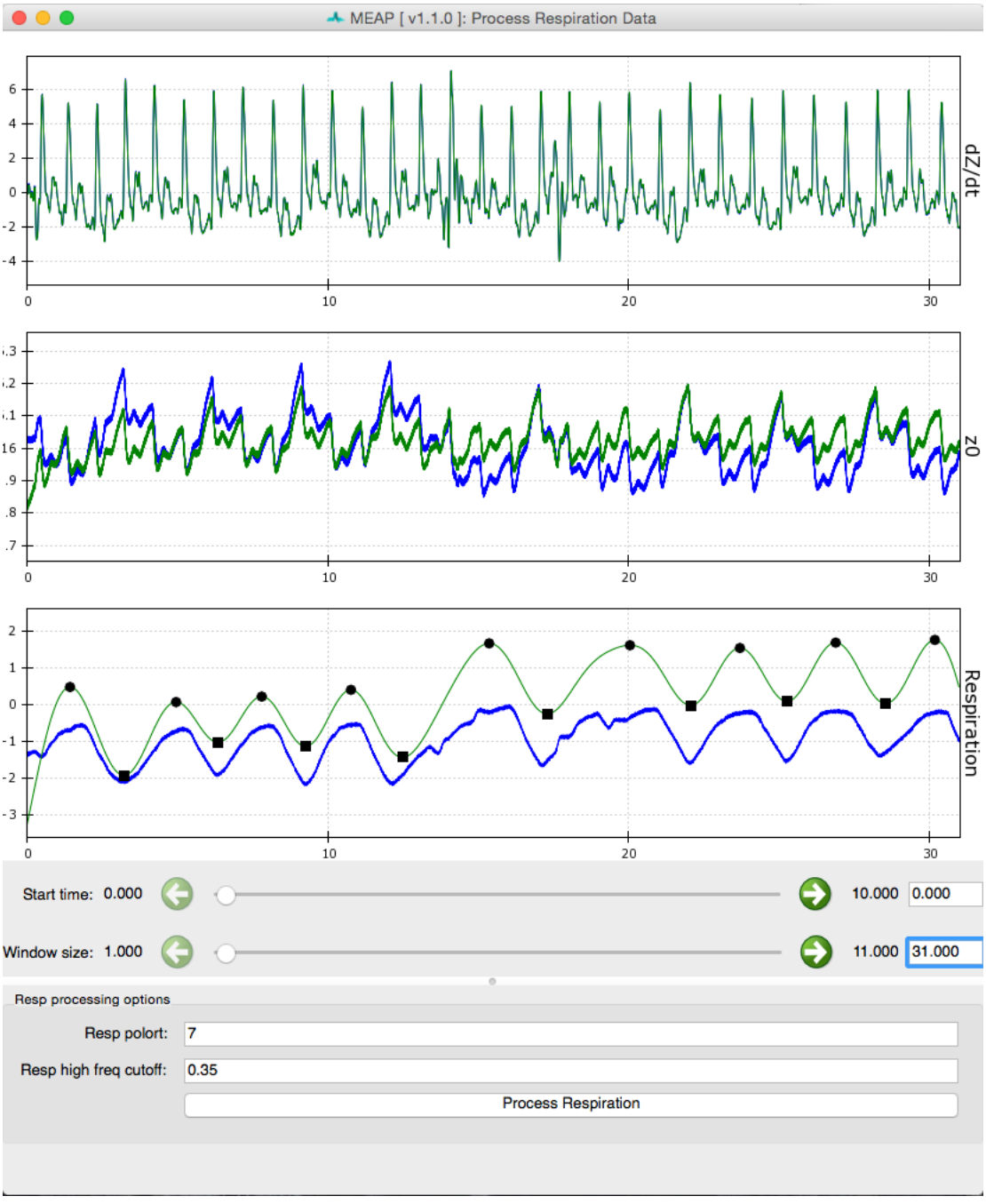
33 /Users/Will/Documents/Coldpress Scoring/323_spots.acq
File: coring/301_bands.acq
Outfile:
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory


MEAP [v1.1.0]: Process Respiration Data
dZ/dt
z0
Respiration
Start time: 0.000
10.000
0.000
Window size: 1.000
11.000
1.000
Resp processing options
Resp polort: 7
Resp high freq cutoff: 0.35
Process Respiration


MEAP [v1.1.0]: Process Respiration Data
dZ/dt
z0
Respiration
Start time: 0.000
10.000
0.000
Window size: 1.000
11.000
1.000
Resp processing options
Resp polort: 7
Resp high freq cutoff: 0.35
Process Respiration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dZ/dt
z0
Respiration
Start time: 0.000
10.000
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Window size: 1.000
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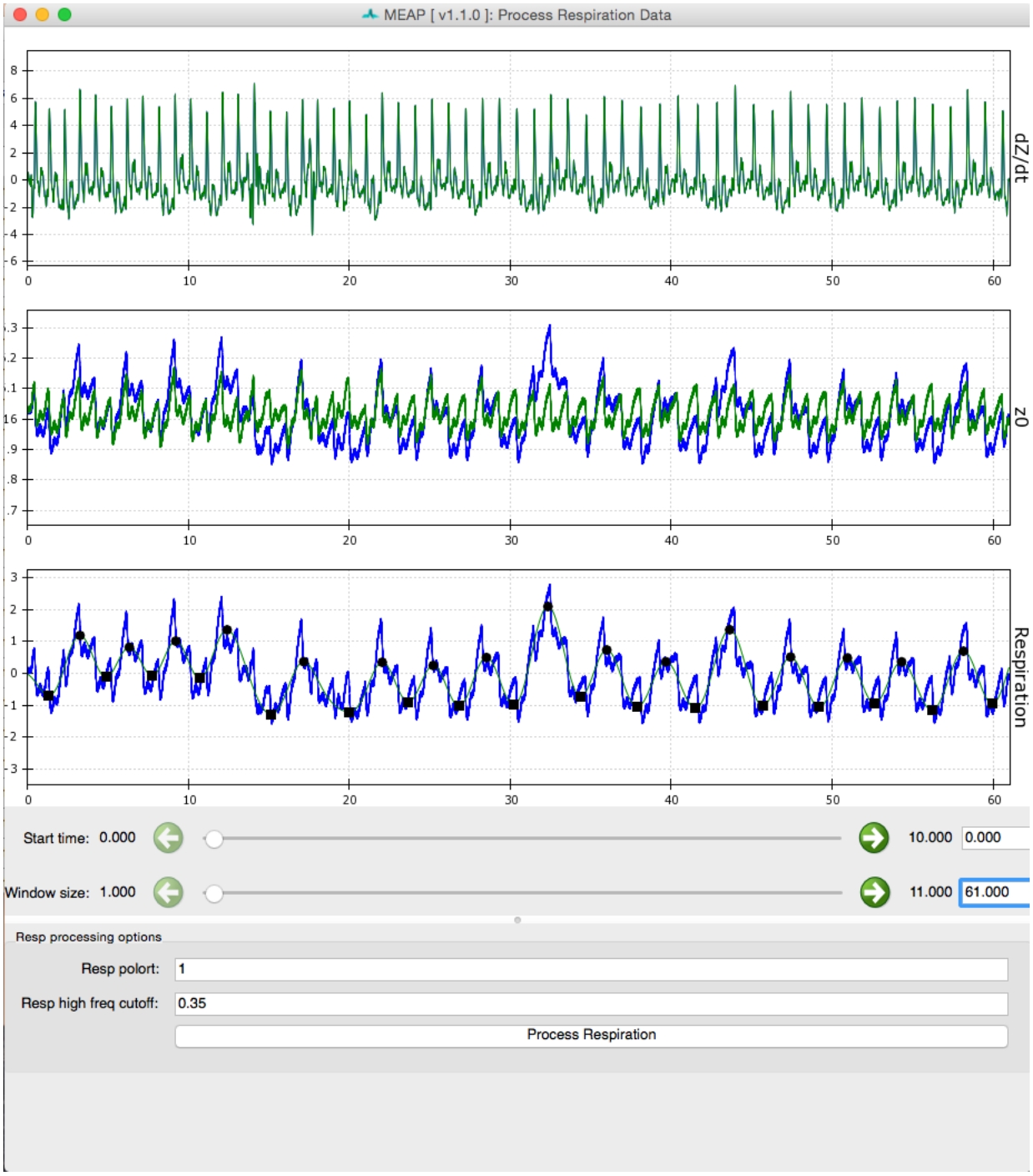
31.000
Resp processing options
Resp polort: 7
Resp high freq cutoff: 0.35
Process Respiration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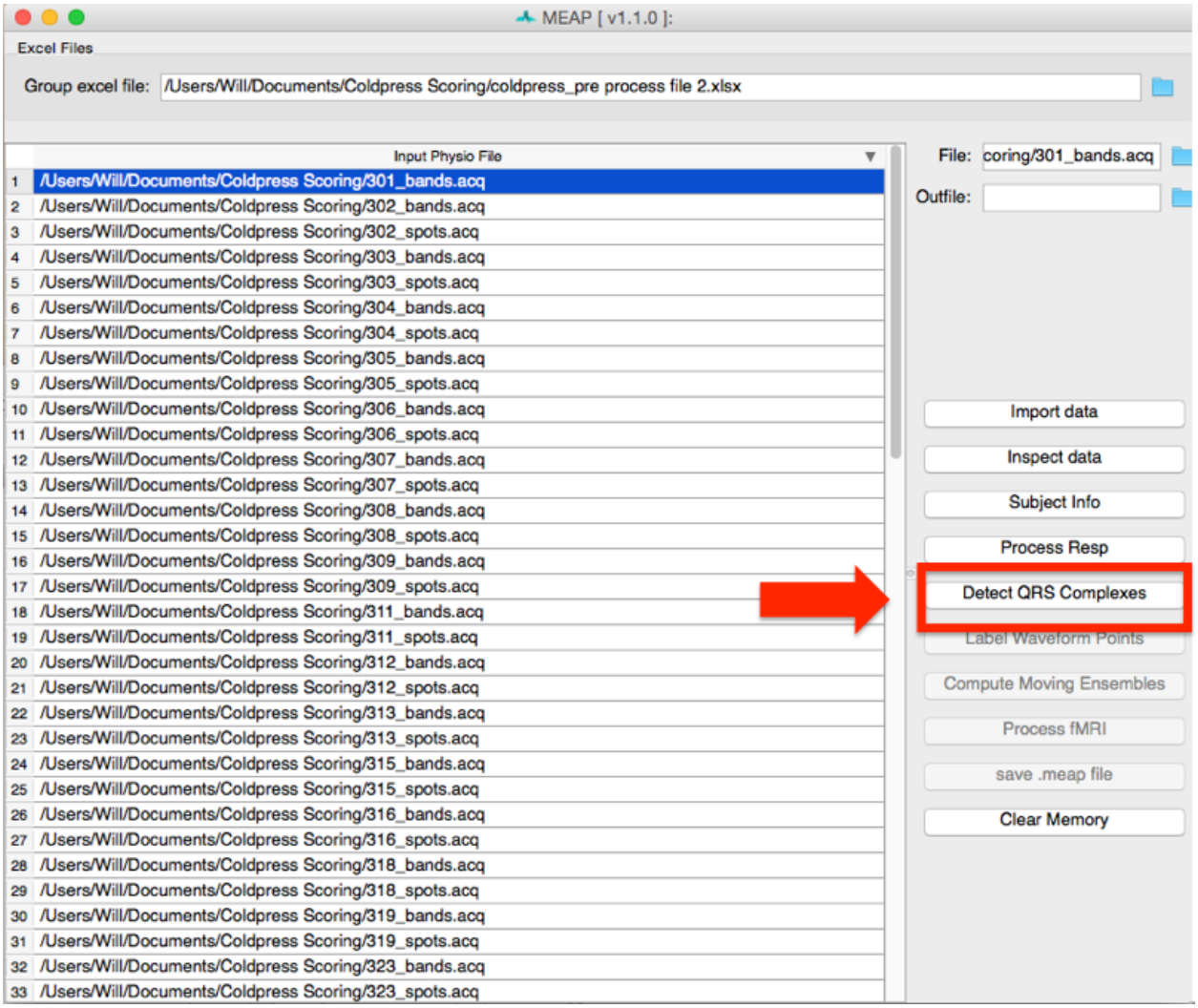
dZ/dt
z0
Respiration
Start time: 0.000
10.000
0.000
Window size: 1.000
11.000
61.000
Resp processing options
Resp polort:
1
Resp high freq cutoff:
0.35
Process Respiration


MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
1 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
2 /Users/Will/Documents/Coldpress Scoring/302_bands.acq
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File: coring/301_bands.acq
Outfile:
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory

Each R peak on the ECG wave is marked with a black square.

_static/qrs_all.png

Again, the sliders below the displayed data allow the user to scroll through the file and change the window size.

If you censored any ECG data in the previous step, the R-peaks that fall within this region will be ignored. R-peaks in regions censored due to noise in other signals will still be detected.

The bottom right corner of this window displays a topographical image of all detected R-peaks. This image displays all R-peaks aligned with one another and viewed from above. The peak of each waveform appears in red while troughs appear in blue. This image allows the user to easily visualize the data and whether R-peaks have been correctly detected. When R-peaks are incorrectly marked, this image will apear jumbled rather than stripes of color corresponding to the topography of the canonical ECG waveform.

In most cases the default settings will allow for accurate detection of each R-peak. Depending on the noisiness of the data and/or idiosyncratic differences in waveform shape, however, the user may need to adjust the default settings. Adjustments are usually required only where a participant has a very high t-wave or where there is significant respiration or other artifact.

The beat detector GUI allows the user to edit the parameters of a modified Pan Tomkins QRS detector in order to more accurately mark the R-peaks in cases such as those just described. The most likely change you will need to make is to change the **Pt adjust** setting to be slightly higher or lower. If it is falsely detecting t-waves as peaks, adjust it up, if true R-peaks are being missed, adjust it down. Usually a change of .05 to .1 does the trick. Don't forget if you sensored regions previously, R-peaks that fall within these regions will not be marked.

If there is an R-peak that is incorrectly marked due to noise that you missed in the previous step, you can remove this point now. Hold down the right-click button and mouse over the R-peaks you wish to delete, then right click again within that region to remove those point markings.

Simply click within the portion of the window displaying each R-peak. The squares marking these will change from black to yellow. Use the mouse to highlight the are surrounding any points you want to remove (just like in the *edit data* step above.

You can also mark individual R-peaks as needed by highlighting the peak you wish using the left-click button on your mouse.

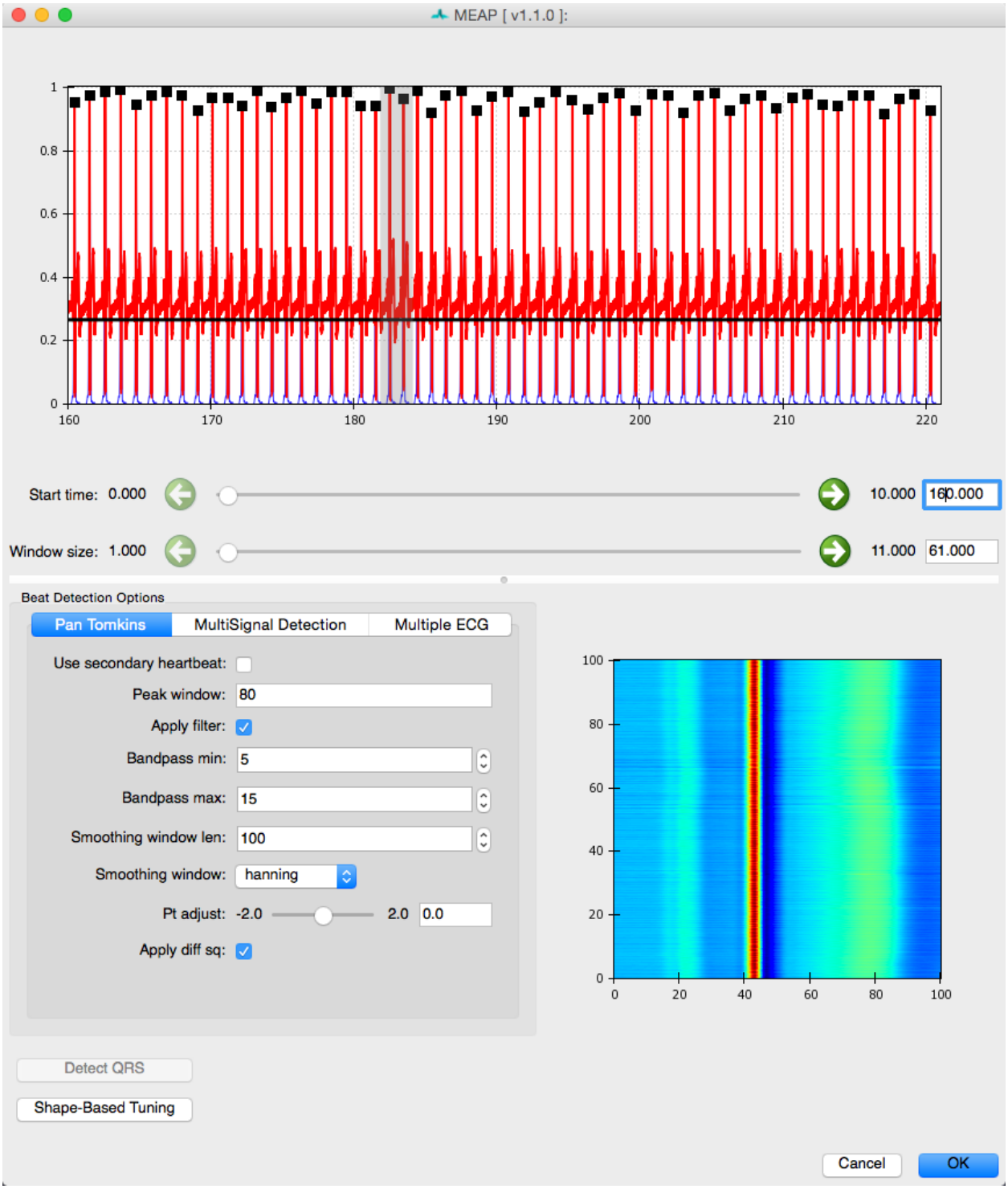
Note: For more information on the Pan-Tompkins method and parameter options, see the beat-detector section of this documentation.

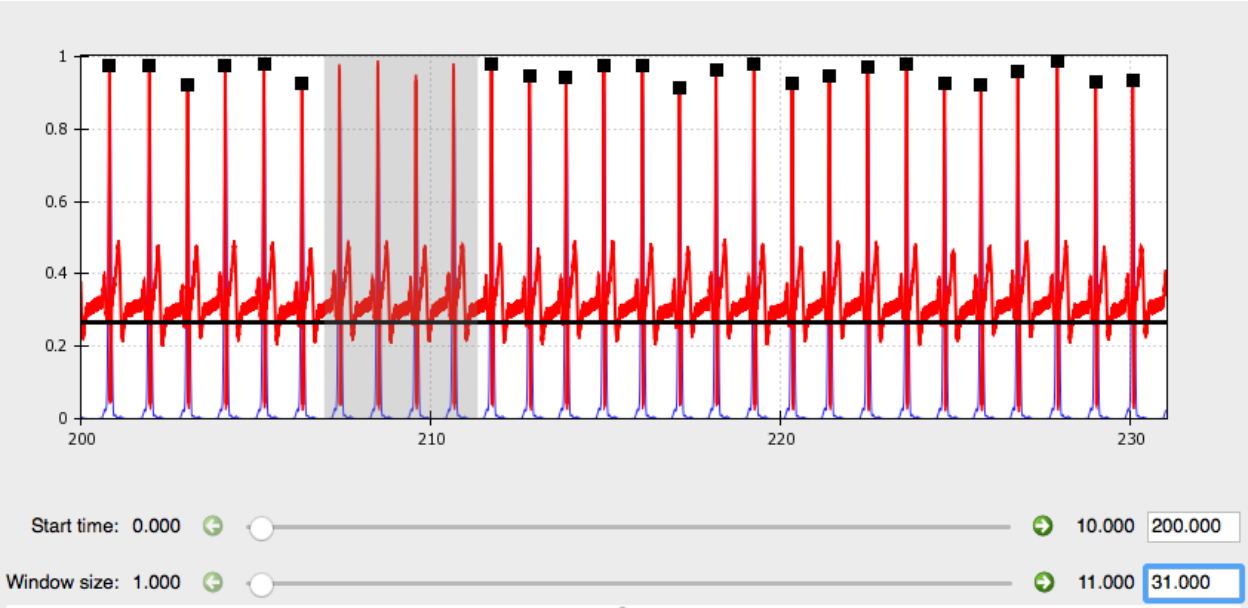
2.6 Step 5a: Finding QRS complexes in the MRI

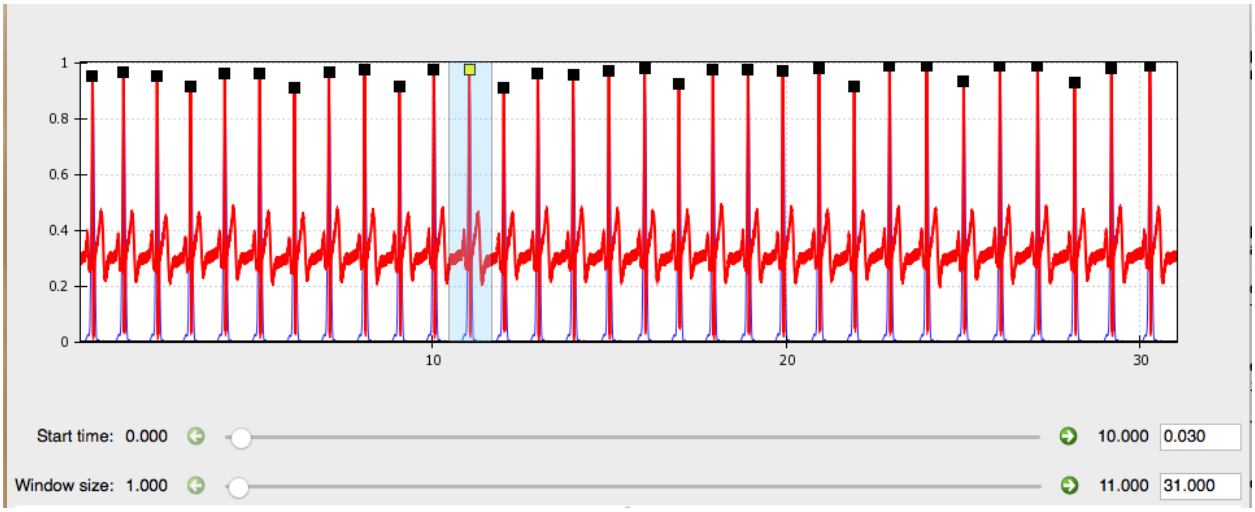
The ECG signal is much noisier in the MRI scanning environment. This is due to a number of factors, including magnetohydrodynamics (the effect of the magnetic field on blood) and RF noise from the scanner. One option is to use a second signal that captures some aspect of the cardiac cycle that is less impacted by scanner noise, such as dZ/dt or a pulse oximiter. We call this Multi Signal Detection. To enable Multi Signal Detection, check this box:

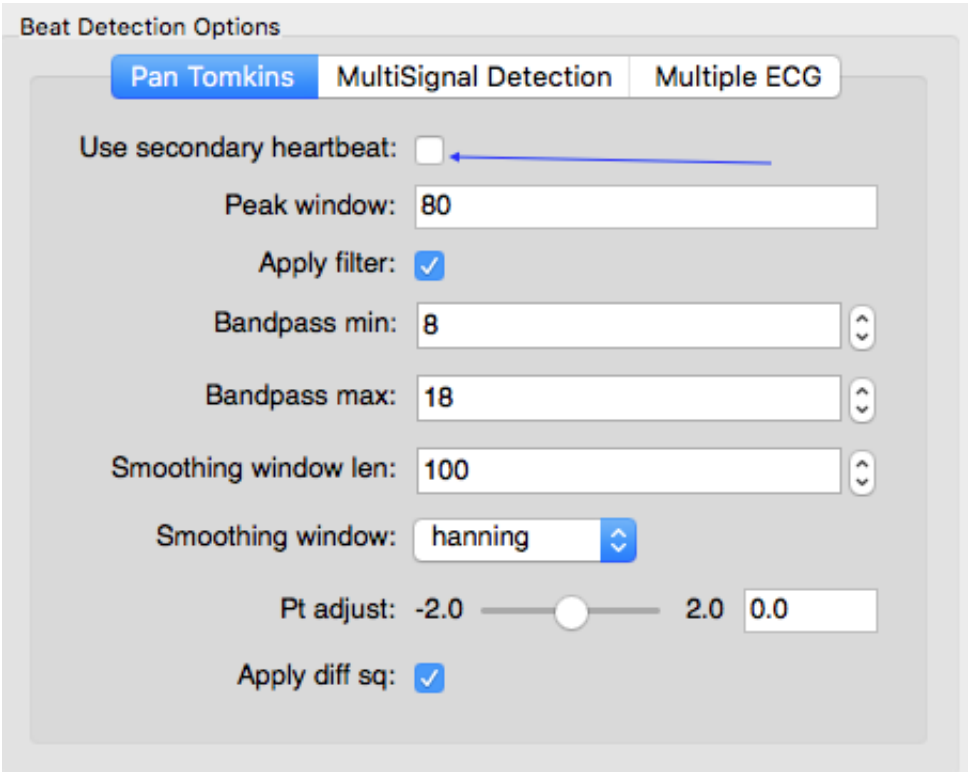
Select which signal you want to use as the secondary cardiac cycle indicator

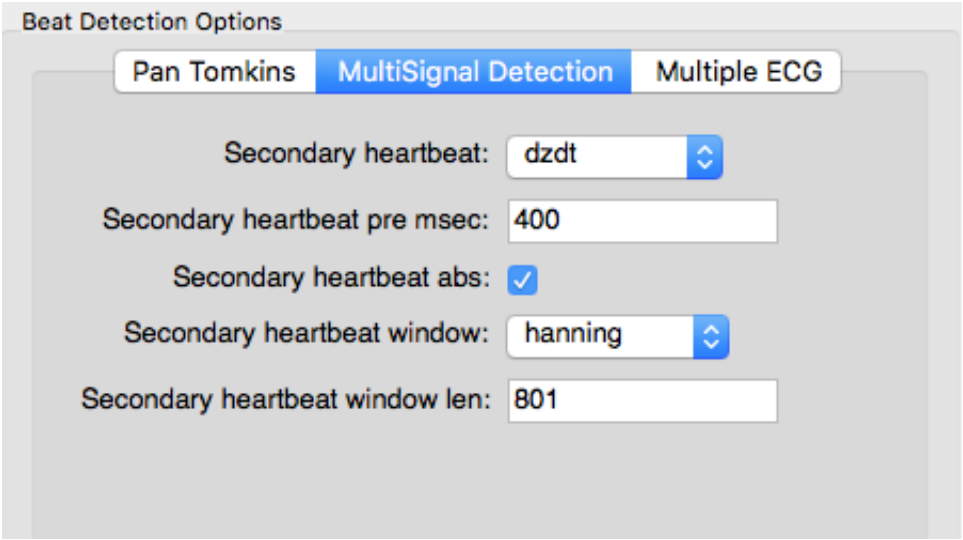
and indicate how to filter this signal. Ideally there should be a single local maximum corresponding to each heart beat. The secondary signal gets low-pass filtered according to these options and peaks are identified. Then a search window is built around each peak and an attempt is made to identify a QRS complex within each search window:

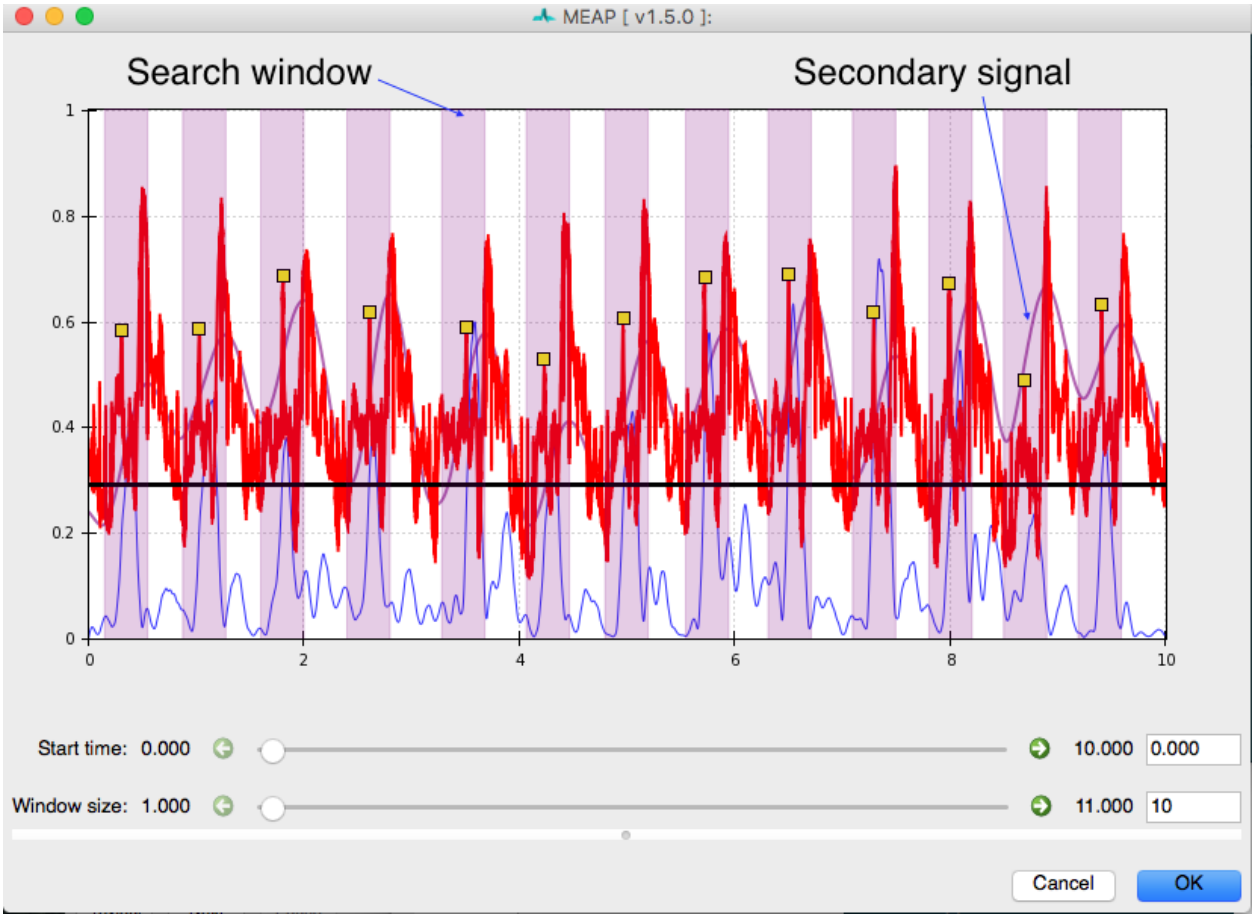

MEAP [v1.1.0]:
Start time: 0.000
10.000
160.000
Window size: 1.000
11.000
61.000
Beat Detection Options
Pan Tomkins
MultiSignal Detection
Multiple ECG
Use secondary heartbeat:
Peak window: 80
Apply filter:
Bandpass min: 5
Bandpass max: 15
Smoothing window len: 100
Smoothing window: hanning
Pt adjust: -2.0 2.0 0.0
Apply diff sq:
Detect QRS
Shape-Based Tuning
Cancel
OK


1
0.8
0.6
0.4
0.2
0
200
210
220
230
Start time: 0.000
10.000
200.000
Window size: 1.000
11.000
31.000


1
0.8
0.6
0.4
0.2
0
10
20
30
Start time: 0.000
10.000
0.030
Window size: 1.000
11.000
31.000


Beat Detection Options
Pan Tomkins
MultiSignal Detection
Multiple ECG
Use secondary heartbeat:
Peak window:
80
Apply filter:
Bandpass min:
8
Bandpass max:
18
Smoothing window len:
100
Smoothing window:
hanning
Pt adjust:
-2.0
2.0
0.0
Apply diff sq:


Beat Detection Options
Pan Tomkins
MultiSignal Detection
Multiple ECG
Secondary heartbeat:
dzdt
Secondary heartbeat pre msec:
400
Secondary heartbeat abs:
Secondary heartbeat window:
hanning
Secondary heartbeat window len:
801


MEAP [v1.5.0]:
Search window
Secondary signal
1
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
Start time: 0.000
10.000
0.000
Window size: 1.000
11.000
10
Cancel
OK

The search windows are light purple and highlight the area around peaks in the secondary signal. In this instance dZdt is the secondary signal, so the window is placed in front of its peaks (because the QRS precedes the peak of dZ/dt). QRS complexes identified in this way can still be edited using the same clicking tools described above.

2.7 Step 6: Marking Custom Points

The next step is to provide MEAP with information about where to look for inflection points of interest in this subject's file.

Clicking the **Label Waveform Points** button brings up a window displaying an ensemble averaged waveform for the entire data file. The **ICG Editor** tab shows the dz/dt wave produced by ensemble averaging the entire file (excluding any censored regions). The full dz/dt signal as well as it's first and second derivatives are displayed along side a zoomed-in view of the R to C portion of the dz/dt wave. These features are designed to assist the user in selecting the B-point on the ensemble averaged waveform. By hovering over any of these images, the dashed line indicating the b-point crossing can be adjusted to the desired position.

The **All Signals** tab displays the ensemble averaged waveforms for all physiological signals (except respiration) across the entire `.acq` file. Using a classifier derived from previous data, MEAP has attempted to mark each of the relevant inflection points on this waveform. It is the job of the user to examine these points, determine whether each is marked in the correct location, and to adjust their placement where necessary. Point markings can be adjusted by simply clicking on each and dragging it to the correct location. Moving the B-point in either of the two tabs adjusts its placement in the other. Correct point markings should look like this:

> **Warning:** If you cannot find where one of the points is marked, it may be hidden beneath one of the other points. Occasionally with messy data one point will be placed on top of one another such that one is not visible.

Once each point is marked on the ensemble averages, MEAP will use these values to update it's classifier and determine where to look for and mark the corresponding points at each individual ensemble average or beat (depending on type of analysis).

When you are satisfied with the placement of each point on the heuristic ensemble average, simply close the window and proceed to the next step.

2.8 Step 7: Compute Moving Ensembles

The next step is to compute moving ensemble averages.

It takes some processing power for MEAP to use its classifier to compute the moving ensembles and mark relevant points on each ensembled beat. While it's processing you will see a window like this:

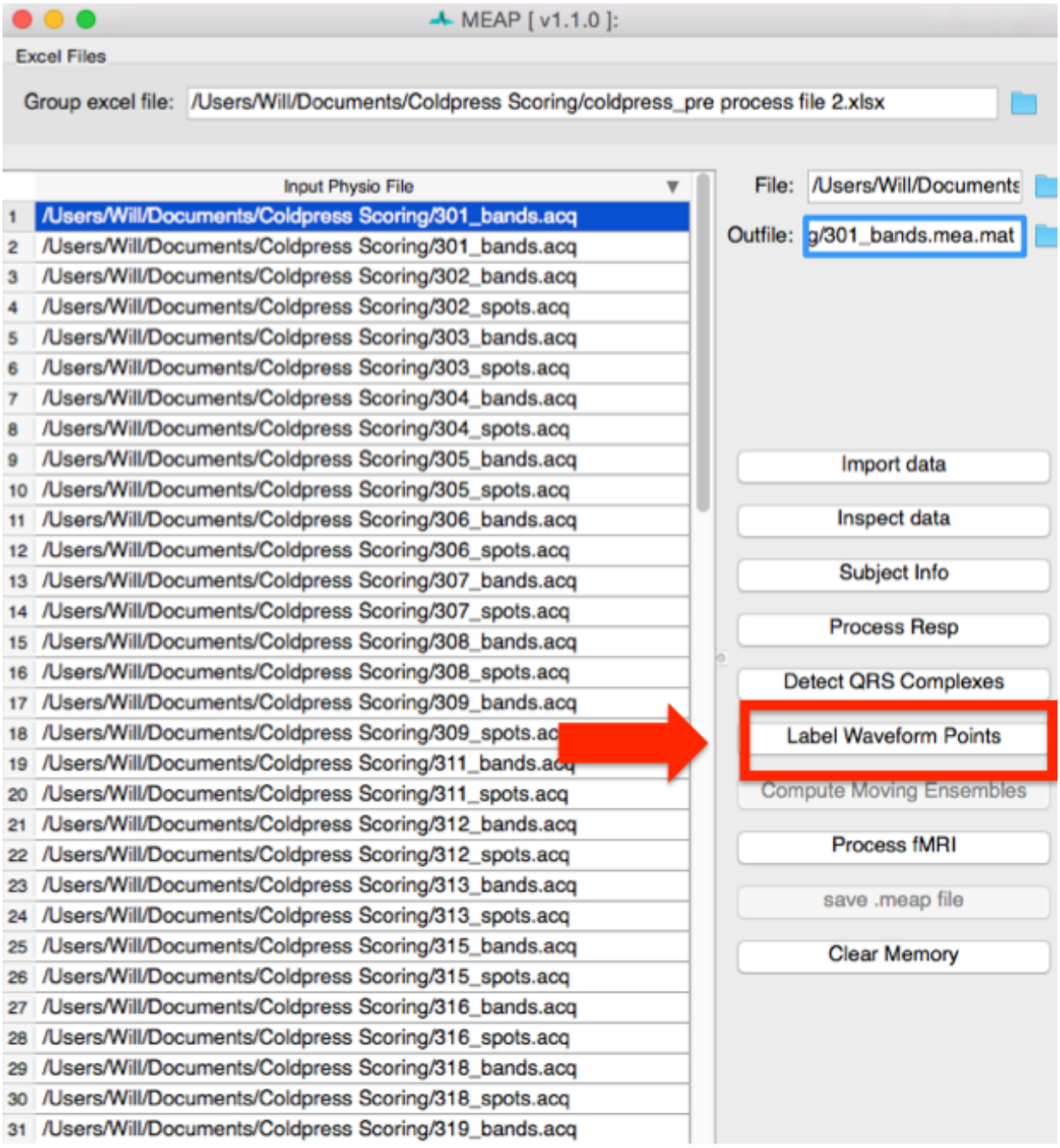
When it's done you will see a window like this:

Along the left panel are displayed each of the main physiological indices MEAP computes plotted as a time series. In green are the values as calculated using the moving ensemble average. The purple trace indicates what these values would be using just the raw data.

The right panel displays a topographical map of the raw dz/dt data corrected for respiration. Changing the setting for **Signal** allows the user to view each of the different data streams in this manner. The **Visualize** option allows the user to select to view the raw or *Original* data, the data after the moving ensemble average is applied, or the residuals of this moving ensemble analysis.

Moving Ensembled:

Note, how much cleaner the moving ensemble is than the raw data.


MEAP [v1.1.0]:
Excel Files
Group excel file: /Users/Will/Documents/Coldpress Scoring/coldpress_pre process file 2.xlsx
Input Physio File
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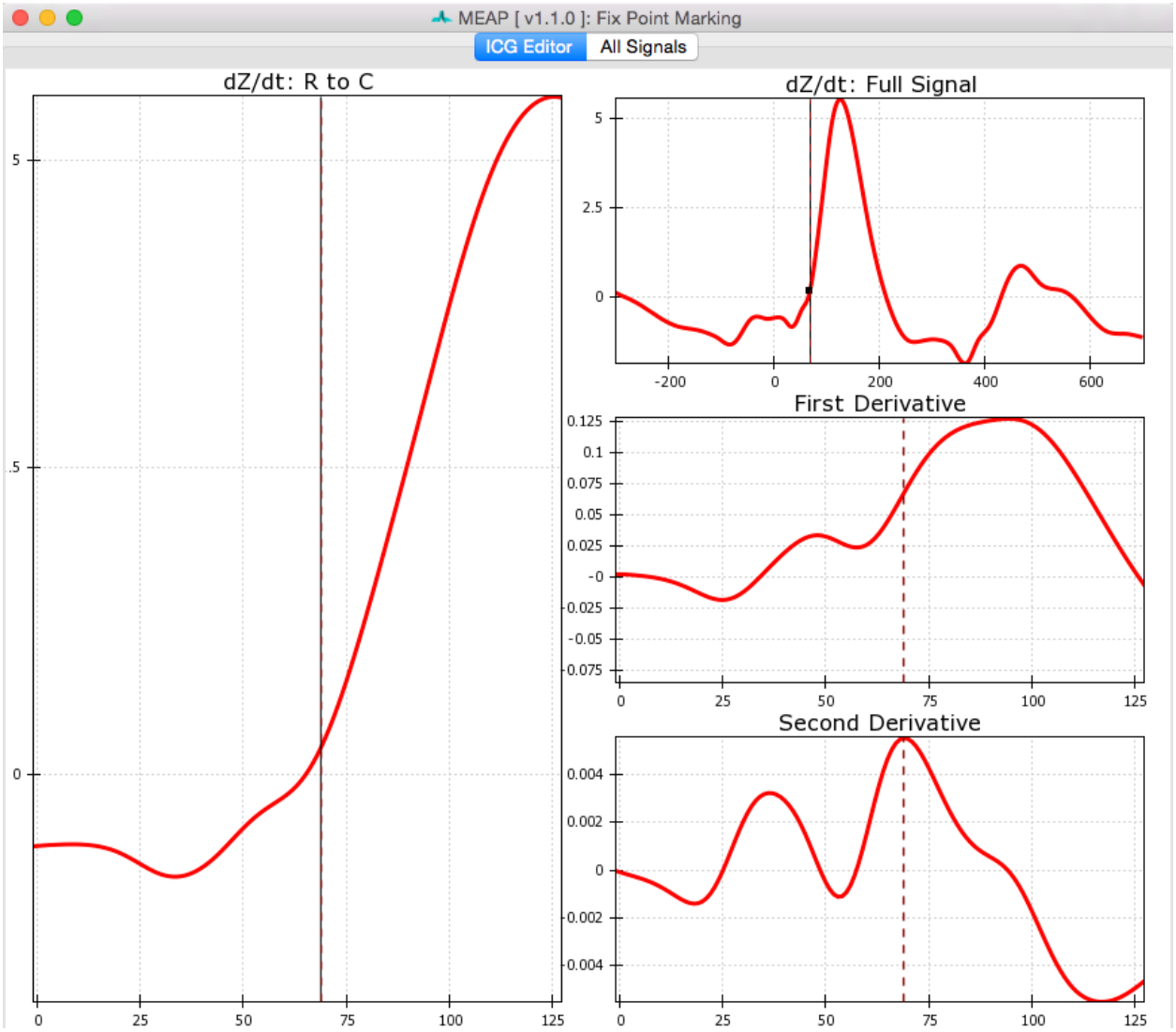
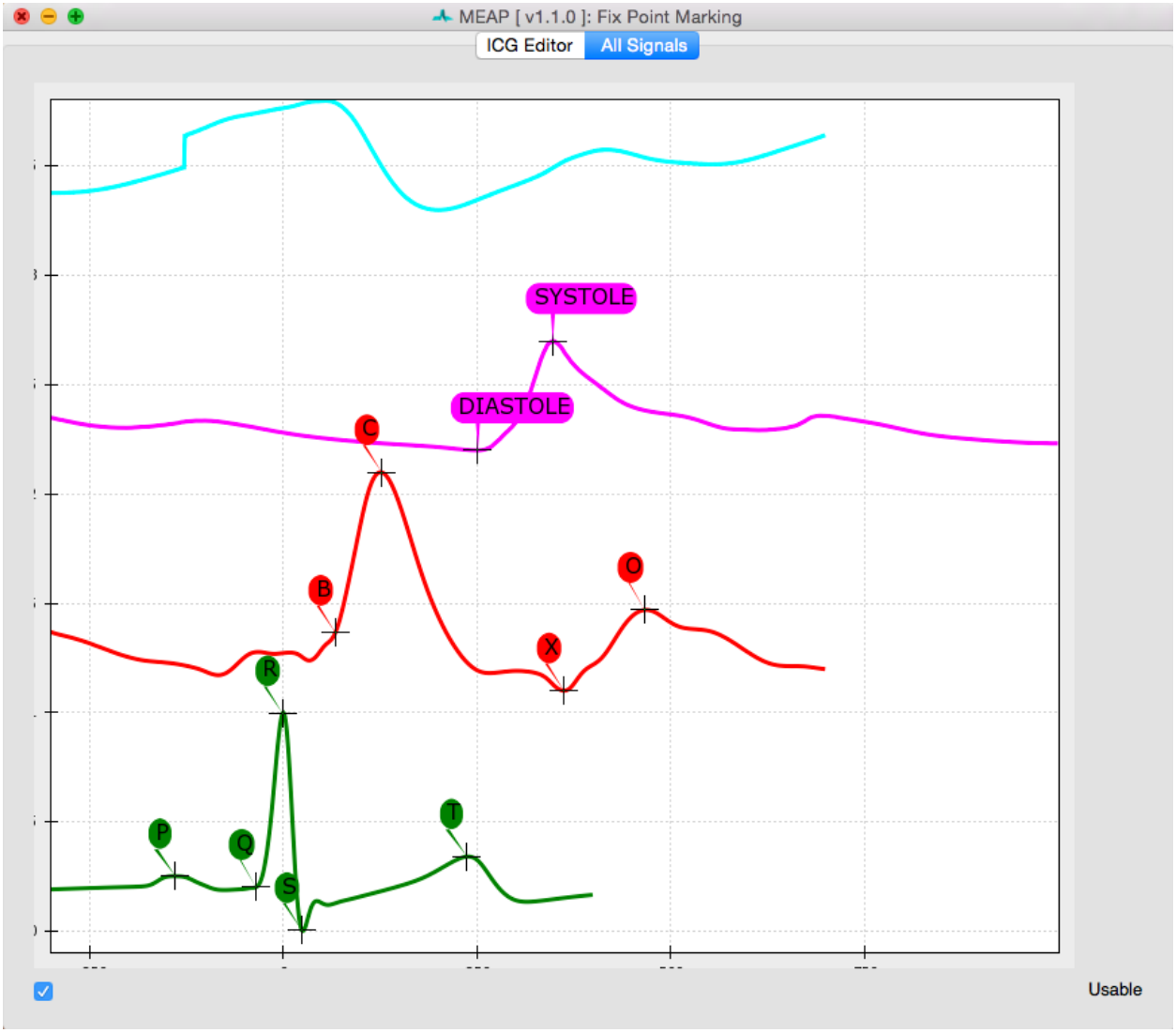
31 /Users/Will/Documents/Coldpress Scoring/319_bands.acq
File: /Users/Will/Documents
Outfile: g/301_bands.mea.mat
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory


MEAP [v1.1.0]: Fix Point Marking
ICG Editor
All Signals
dZ/dt: R to C
dZ/dt: Full Signal
First Derivative
Second Derivative


MEAP [v1.1.0]: Fix Point Marking
ICG Editor
All Signals
SYSTOLE
DIASTOLE
C
B
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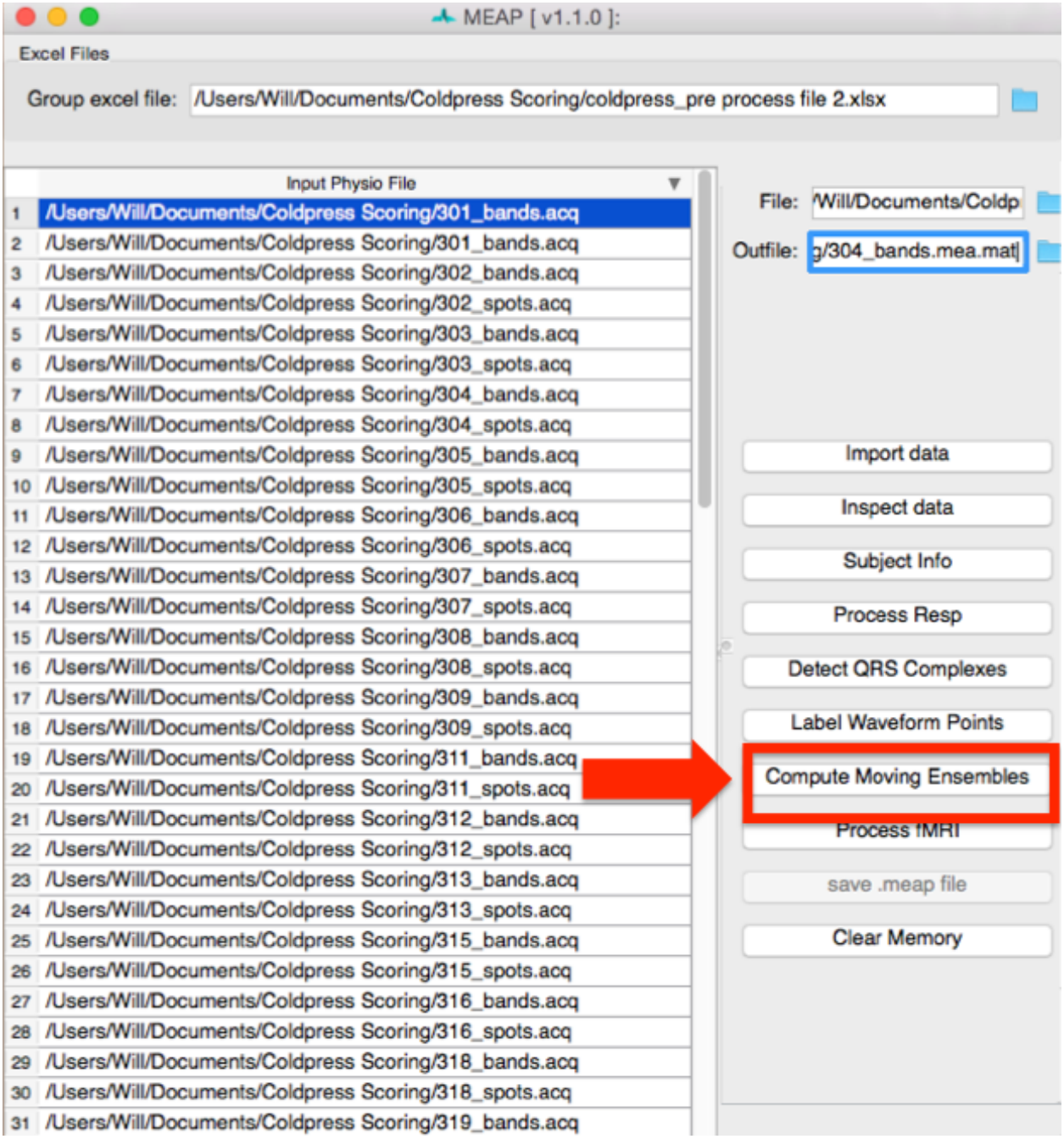
X
R
P
Q
S
T
Usable


MEAP [v1.1.0]:
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Input Physio File
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2 /Users/Will/Documents/Coldpress Scoring/301_bands.acq
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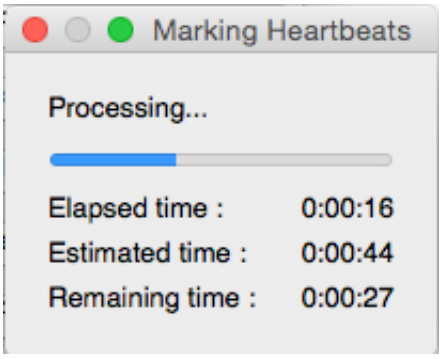
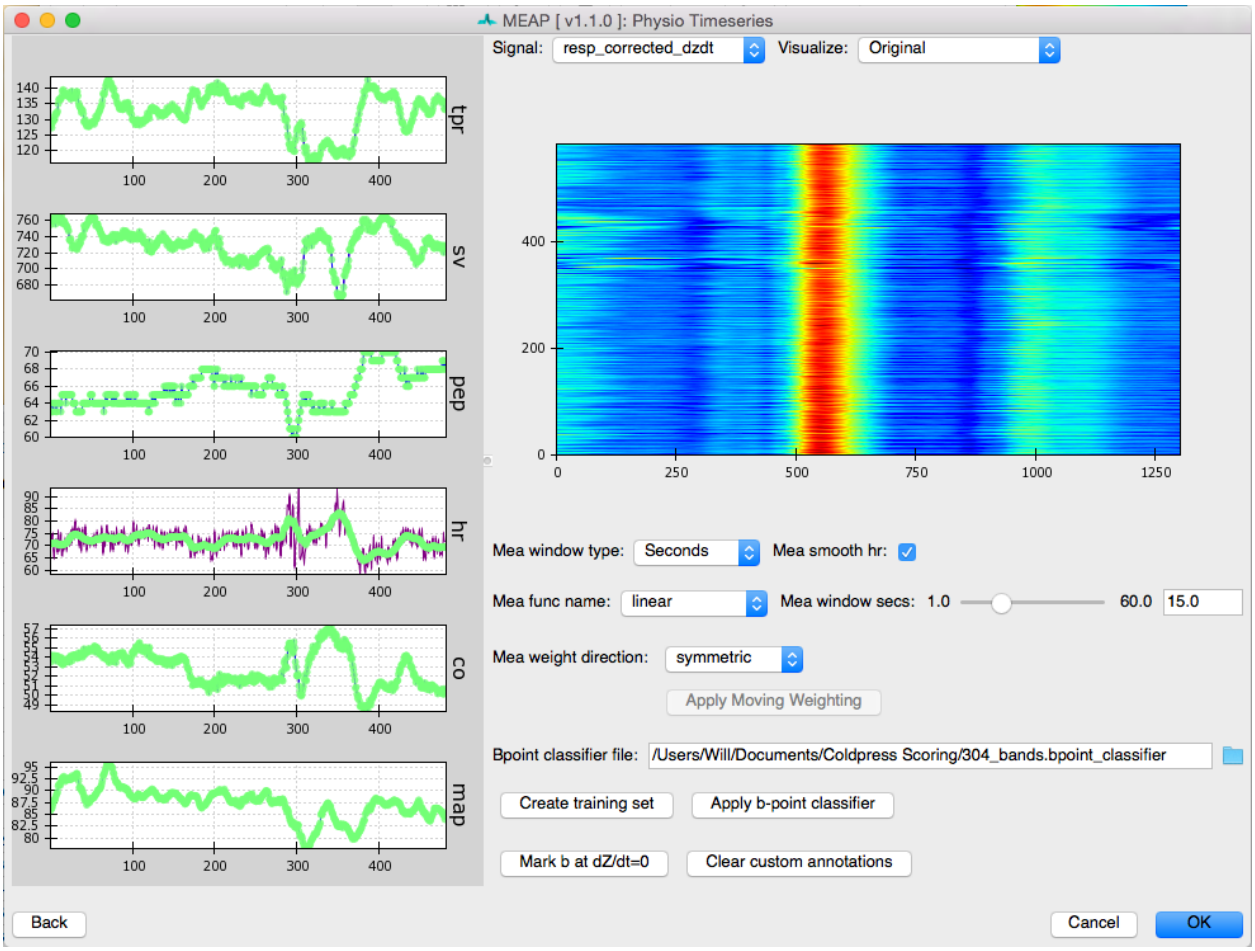
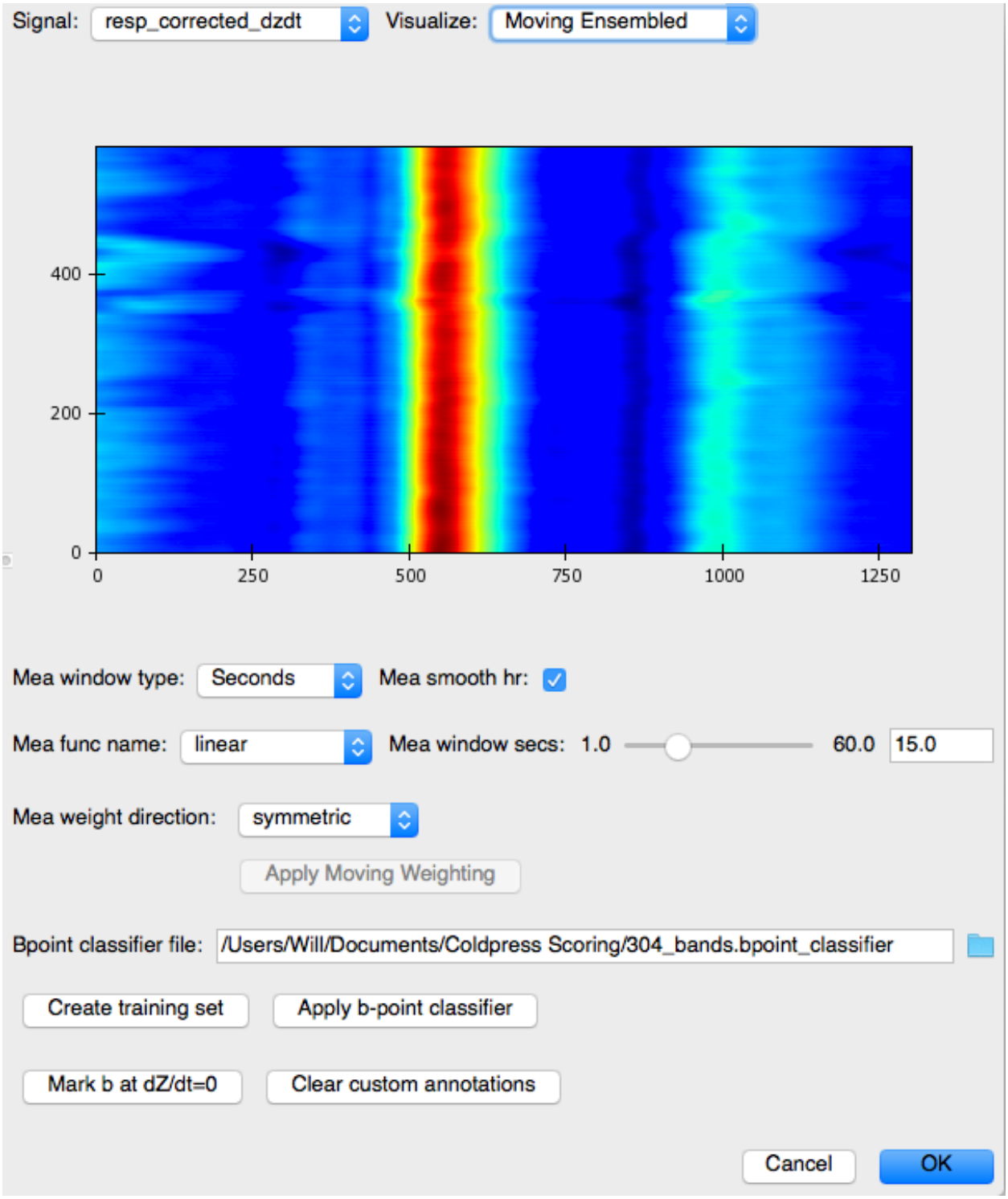
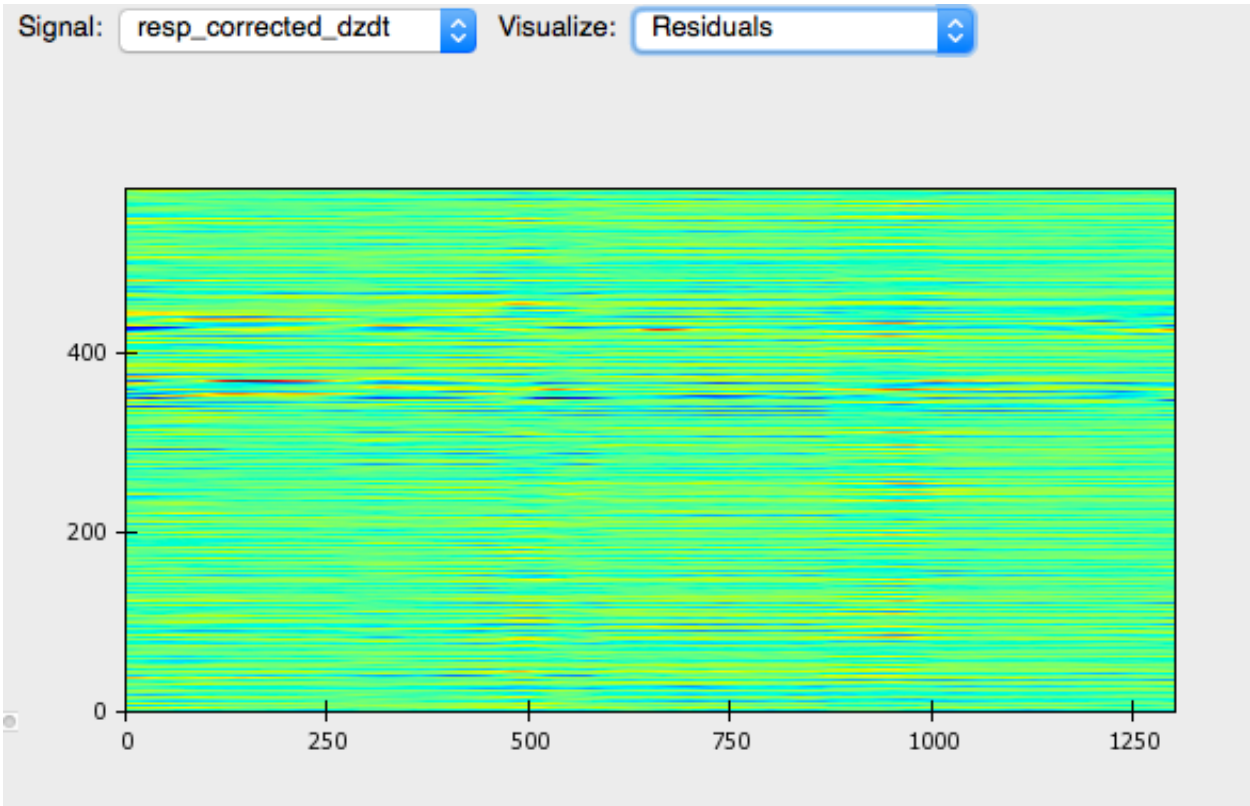
6 /Users/Will/Documents/Coldpress Scoring/303_spots.acq
7 /Users/Will/Documents/Coldpress Scoring/304_bands.acq
8 /Users/Will/Documents/Coldpress Scoring/304_spots.acq
9 /Users/Will/Documents/Coldpress Scoring/305_bands.acq
10 /Users/Will/Documents/Coldpress Scoring/305_spots.acq
11 /Users/Will/Documents/Coldpress Scoring/306_bands.acq
12 /Users/Will/Documents/Coldpress Scoring/306_spots.acq
13 /Users/Will/Documents/Coldpress Scoring/307_bands.acq
14 /Users/Will/Documents/Coldpress Scoring/307_spots.acq
15 /Users/Will/Documents/Coldpress Scoring/308_bands.acq
16 /Users/Will/Documents/Coldpress Scoring/308_spots.acq
17 /Users/Will/Documents/Coldpress Scoring/309_bands.acq
18 /Users/Will/Documents/Coldpress Scoring/309_spots.acq
19 /Users/Will/Documents/Coldpress Scoring/311_bands.acq
20 /Users/Will/Documents/Coldpress Scoring/311_spots.acq
21 /Users/Will/Documents/Coldpress Scoring/312_bands.acq
22 /Users/Will/Documents/Coldpress Scoring/312_spots.acq
23 /Users/Will/Documents/Coldpress Scoring/313_bands.acq
24 /Users/Will/Documents/Coldpress Scoring/313_spots.acq
25 /Users/Will/Documents/Coldpress Scoring/315_bands.acq
26 /Users/Will/Documents/Coldpress Scoring/315_spots.acq
27 /Users/Will/Documents/Coldpress Scoring/316_bands.acq
28 /Users/Will/Documents/Coldpress Scoring/316_spots.acq
29 /Users/Will/Documents/Coldpress Scoring/318_bands.acq
30 /Users/Will/Documents/Coldpress Scoring/318_spots.acq
31 /Users/Will/Documents/Coldpress Scoring/319_bands.acq
File: /Will/Documents/Coldp
Outfile: g/304_bands.mea.mat
Import data
Inspect data
Subject Info
Process Resp
Detect QRS Complexes
Label Waveform Points
Compute Moving Ensembles
Process fMRI
save .meap file
Clear Memory


Marking Heartbeats
Processing...
Elapsed time : 0:00:16
Estimated time : 0:00:44
Remaining time : 0:00:27


MEAP [v1.1.0]: Physio Timeseries
Signal: resp_corrected_dzdt
Visualize: Original
tpr
sv
pep
hr
co
map
Mea window type: Seconds
Mea smooth hr:
Mea func name: linear
Mea window secs: 1.0 60.0 15.0
Mea weight direction: symmetric
Apply Moving Weighting
Bpoint classifier file: /Users/Will/Documents/Coldpress Scoring/304_bands.bpoint_classifier
Create training set
Apply b-point classifier
Mark b at dZ/dt=0
Clear custom annotations
Back
Cancel
OK


Signal:
resp_corrected_dzdt
Visualize:
Moving Ensembled
400
200
0
0
250
500
750
1000
1250
Mea window type:
Seconds
Mea smooth hr:
Mea func name:
linear
Mea window secs:
1.0
60.0
15.0
Mea weight direction:
symmetric
Apply Moving Weighting
Bpoint classifier file:
/Users/Will/Documents/Coldpress Scoring/304_bands.bpoint_classifier
Create training set
Apply b-point classifier
Mark b at dZ/dt=0
Clear custom annotations
Cancel
OK

Residuals:



Ideally, residuals will be random, producing no clear pattern in the image.

2.9 Identifying B-Points

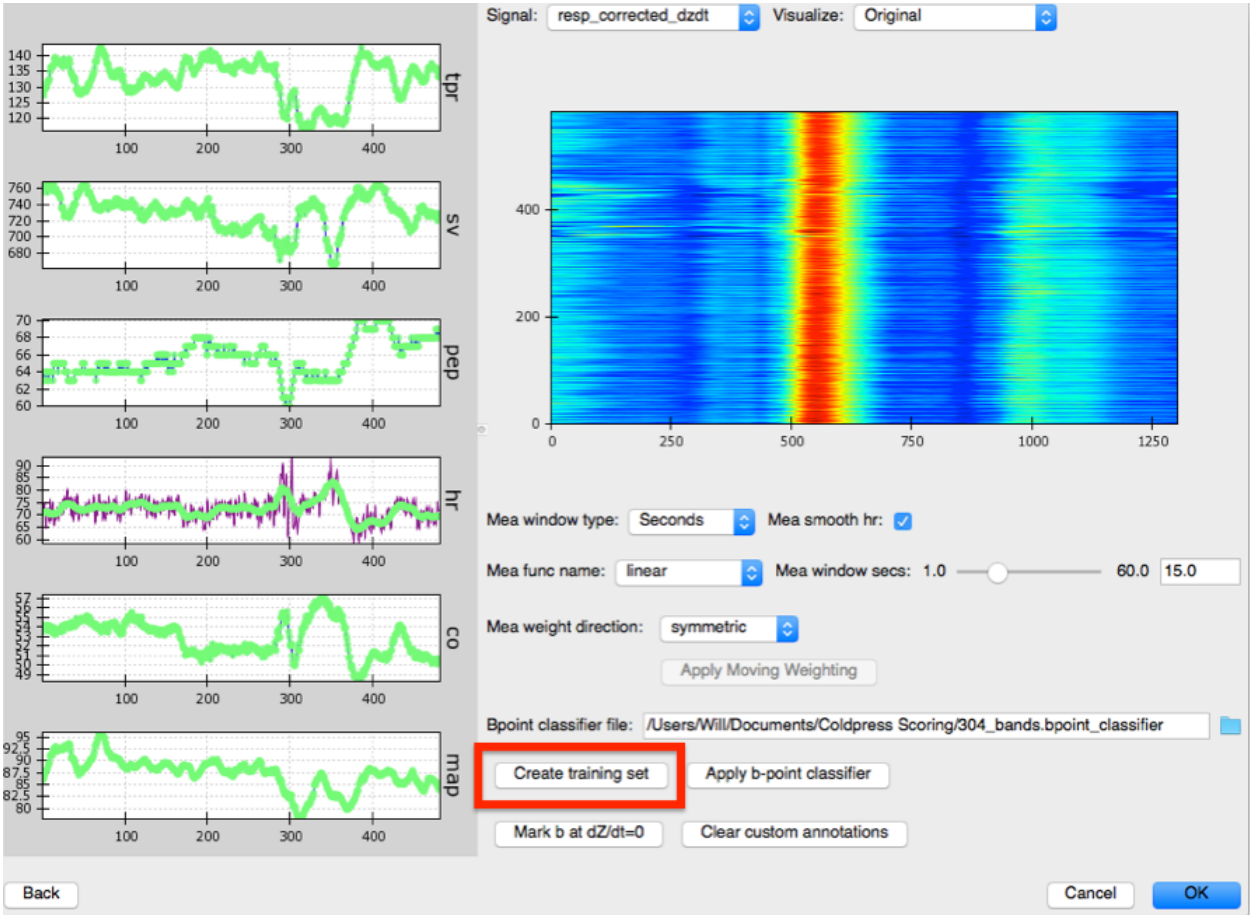
The most time-consuming and error-prone part of ICG analysis is identifying B-Points. This is a critical time for determining systolic intervals and therefore great care should be taken when marking this point.

MEAP provides two methods for automating this process. The first, an AdaBoost-based B-Point classifier was described in our 2018 Psychophysiology paper. This approach works very well, but requires manually labeling hundreds of points per recording to train the classifier. The second is unpublished, but relies on time series registration to "warp" B-points from a set of ICG shape templates. This method is much faster and has nice theoretical properties.

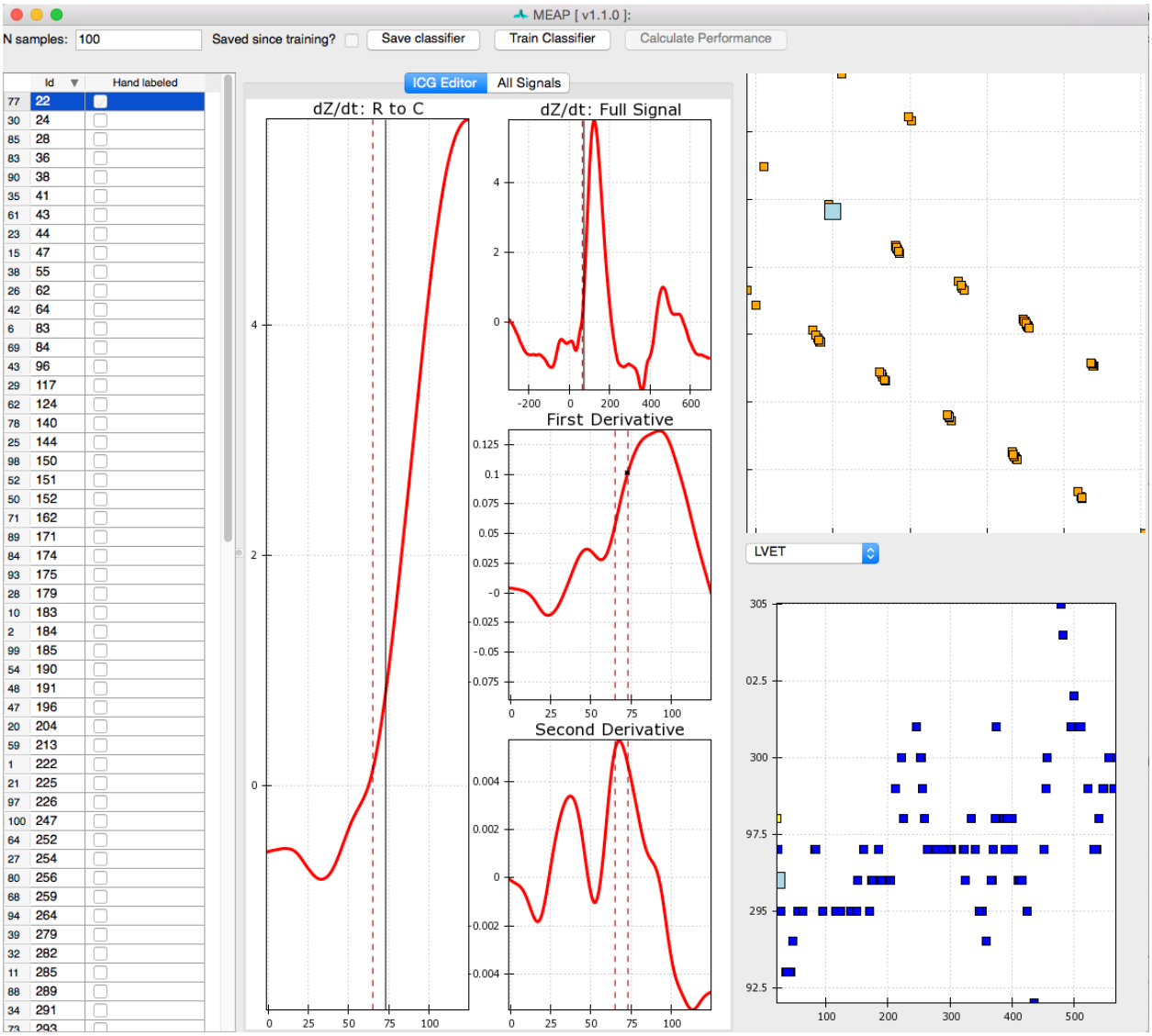
Training the B-Point Classifier

B-points are notoriously difficult to mark as they are neither a maximum or a minimum. Thus, although we have provided a prior to MEAP to tell it where to look for the b-point, we want to provide MEAP with more data with which to train its b-point classifier. To do this click on: **Create Training Set**. With this button press, MEAP will randomly select a number of beats from the file (the default is 100 beats) for the user to hand mark.

This window looks almost exactly like the one we used to mark the ensembled average points except that this time a series of randomly selected moving ensembled heart beats is listed in the left most panel. Clicking on each brings up that heart beat. Once you've hand labeled it, the box in that column will be checked. The top image in the top right panel displays the results of a principle components analysis of all marked inflection points. This plot allows the user to easily visualize the spread of the data and identify potential outliers. The bottom right panel plots the values for *LVET*, *PEP*, or *SV*, depending on which the user selects. The *N samples* field in the top left corner of the window allows the user to specify the number of randomly selected beats to be hand marked and employed by the classifier. If


Signal:
resp_corrected_dzdt
Visualize:
Original
tpr
sv
pep
hr
co
map
Mea window type:
Seconds
Mea smooth hr:
Mea func name:
linear
Mea window secs:
1.0
60.0
15.0
Mea weight direction:
symmetric
Apply Moving Weighting
Bpoint classifier file:
/Users/Will/Documents/Coldpress Scoring/304_bands.bpoint_classifier
Create training set
Apply b-point classifier
Mark b at dZ/dt=0
Clear custom annotations
Back
Cancel
OK

there are any beats that you wish not to include in analyses, due to noise or whatever reason, unselect the *Usable* box at the bottom of the window. This will remove data from this beat from all further analyses.



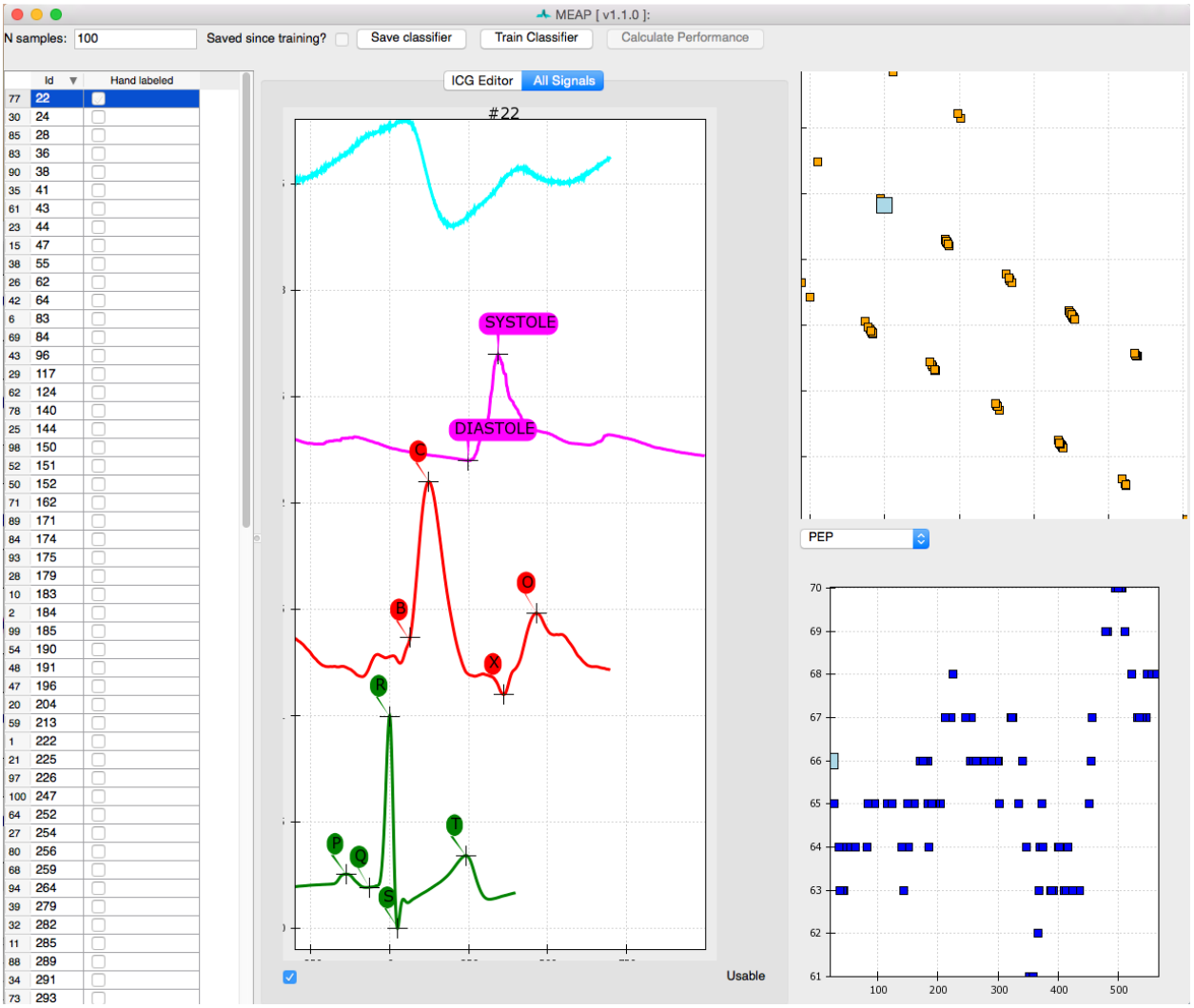
As in the *Marking Custom Points* stage, the user can toggle between the **ICG Editor** and **All Signals** tabs to view just the ICG signal, or all data streams together. The other aspects of this window remain the same.

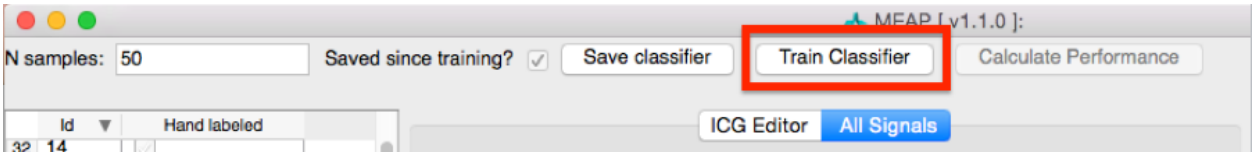
Once you are satisfied with all marked points, select **Train Classifier**. This may take a moment or two to process. Once complete, select **Save Classifier**. You can then close out of this window.

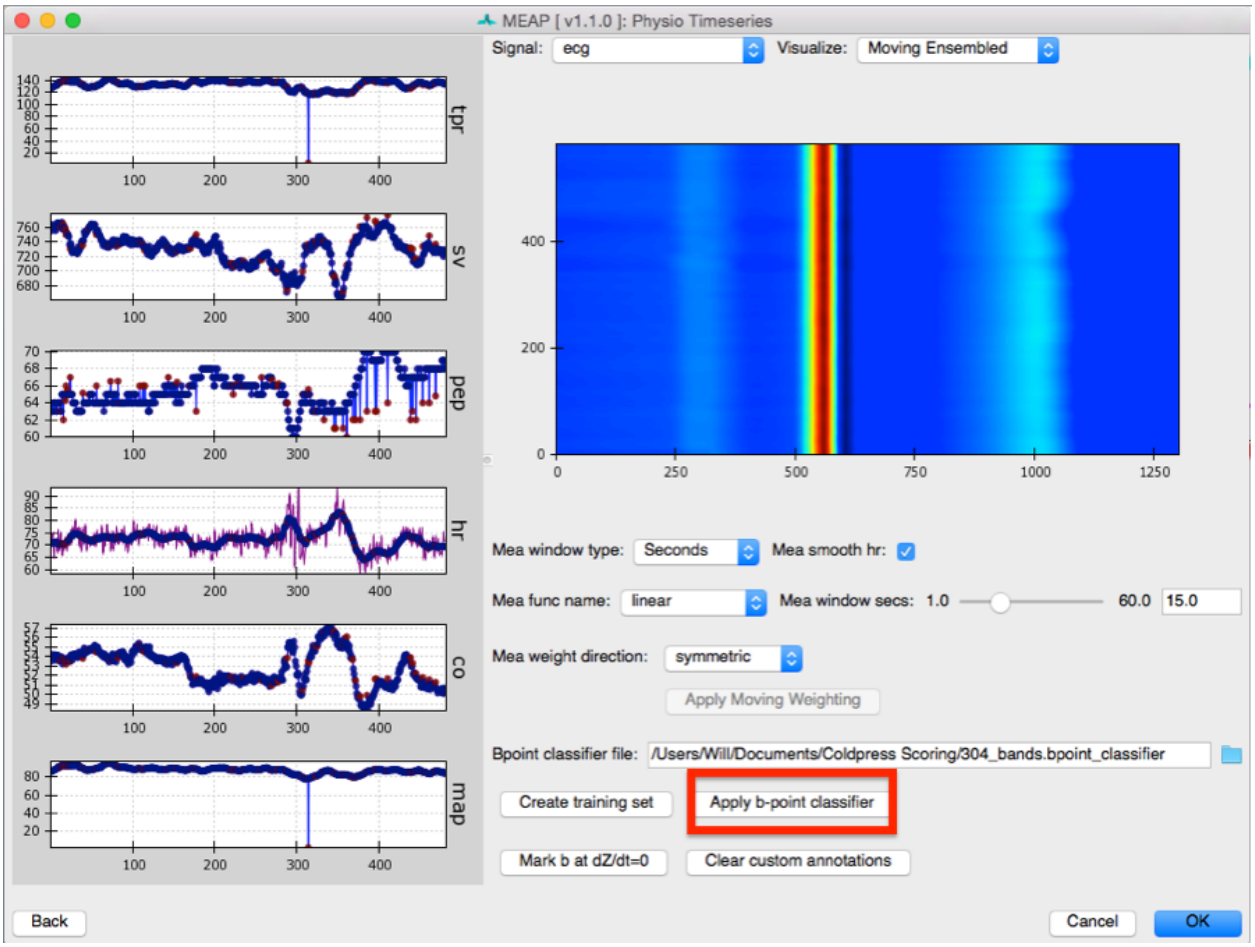
Then return to the *Physio Timeseries* Window. Note that the points that we hand-marked now appear in purple. The reason for MAP and TPR values dropping to zero is that blood pressure data was censored at that point. Select **Apply b-point classifier**.

Using SRVF-based dZ/dt registration

Starting at MEAP version 1.5 you can use SRVF-based timeseries registration. You can think of this method as similar to diffeomorphic spatial normalization used in neuroimaging group studies. Instead of manually identifying a specific region in each brain, you can warp all the brains to a template, draw the region on the template, then inverse warp the region into each individual brain. Here we're doing the same thing with dZ/dt waveforms.

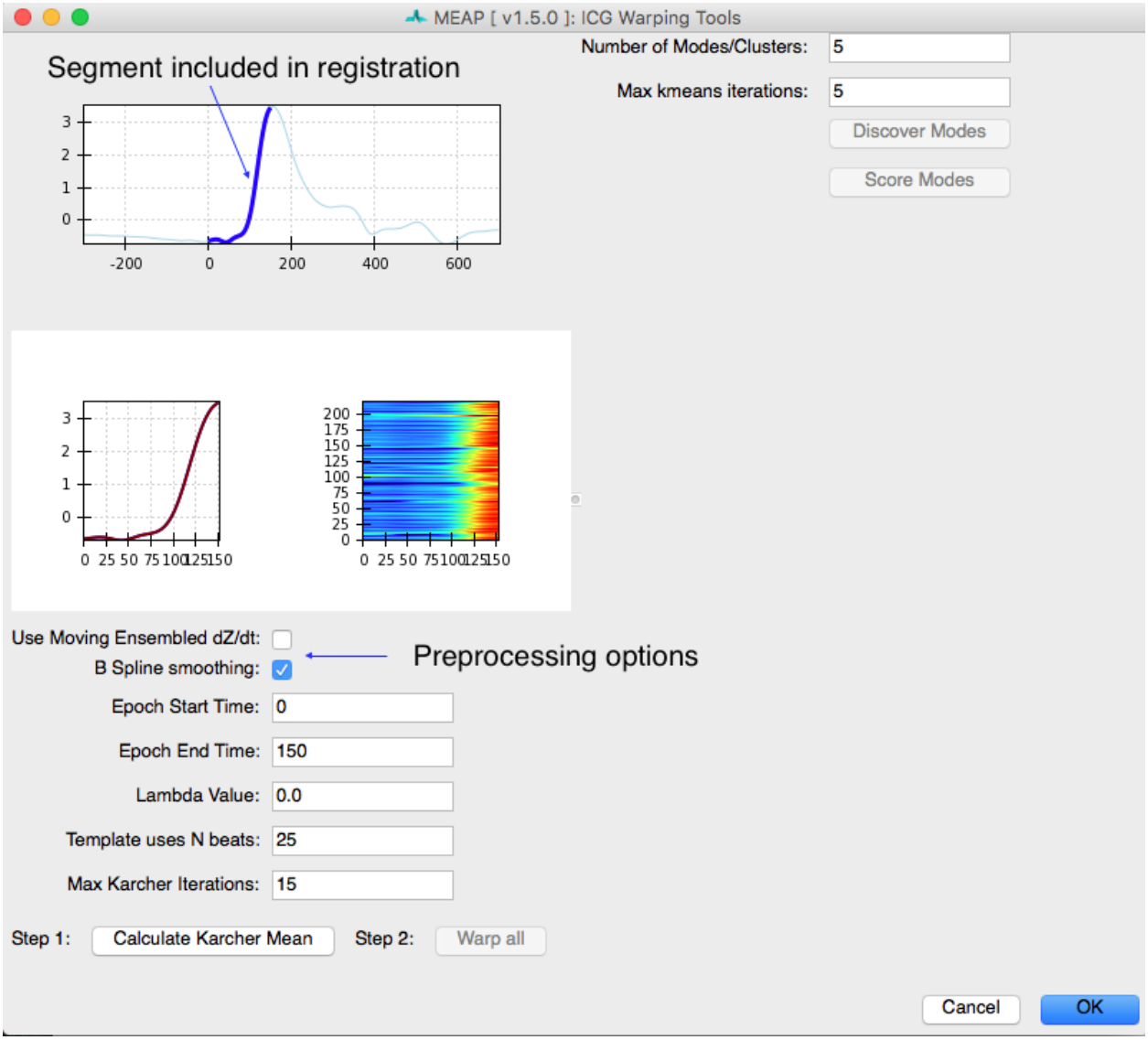

MEAP [v1.1.0]:
N samples: 100
Saved since training?
Save classifier
Train Classifier
Calculate Performance
Id
Hand labeled
ICG Editor
All Signals
#22
SYSTOLE
DIASTOLE
C
B
O
X
R
P
Q
S
T
Usable
PEP


MEAP [v1.1.0]:
N samples: 50
Saved since training?
Save classifier
Train Classifier
Calculate Performance
Id
Hand labeled
ICG Editor
All Signals


MEAP [v1.1.0]: Physio Timeseries
Signal: ecg
Visualize: Moving Ensembled
tpr
sv
pep
hr
co
map
Mea window type: Seconds
Mea smooth hr:
Mea func name: linear
Mea window secs: 1.0
60.0
15.0
Mea weight direction: symmetric
Apply Moving Weighting
Bpoint classifier file: /Users/Will/Documents/Coldpress Scoring/304_bands.bpoint_classifier
Create training set
Apply b-point classifier
Mark b at dZ/dt=0
Clear custom annotations
Back
Cancel
OK

You can access this tool by clicking **Register dZ/dt** from the pipeline window. This process involves 4 steps. First, a single template is created from a randomly-selected subset of all heartbeats. Next, all heartbeats are registered to this initial template. Third, the warps to the initial template are used to cluster individual heartbeats into similarly-shaped subsets. A template for each of these shape "modes" is created. Finally, the user hand-marks B-Points on each mode template and these are inverse-warped to each heartbeat.

To create an initial shape template, or Karcher Mean, of your dZ/dt signals you will use the widgets in the left half of this screen:

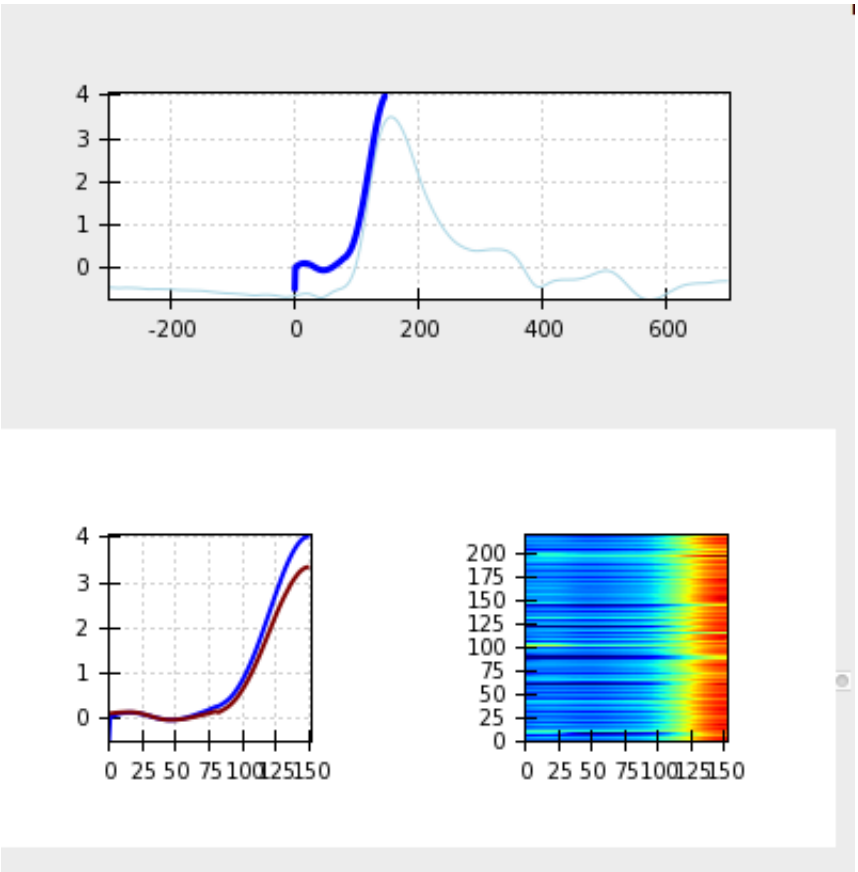


It is important to decide whether you want to use moving ensembled dZ/dt signals or the original raw signals. Original signals will vary in shape depending on the part of the respiratory cycle in which they occurred and will also have pronounced pre-load and after-load effects on the locations of the B-Points. Also, data with abrupt spikes can fail to produce a meaningful Karcher Mean. If your data has spikes, we recommend filtering it in AcqKnowledge and/or using the B-Spline smoothing option here.

Only a portion of the dZ/dt waveform is used for this procedure. Using the entire waveform causes the template-building process to be incredibly time-consuming and also produces poor results during clustering. You select the portion of the dZ/dt signal that will be included in this analysis in the Epoch Start Time and Epoch End Time fields. Lambda controls how much the time series are allowed to deform. The number of beats used and the maximum

number of template-building iterations can be specified here. Once you are satisfied, click “Calculate Karcher Mean”.

After a few minutes the plots will update and the “Warp All” button will be enabled.



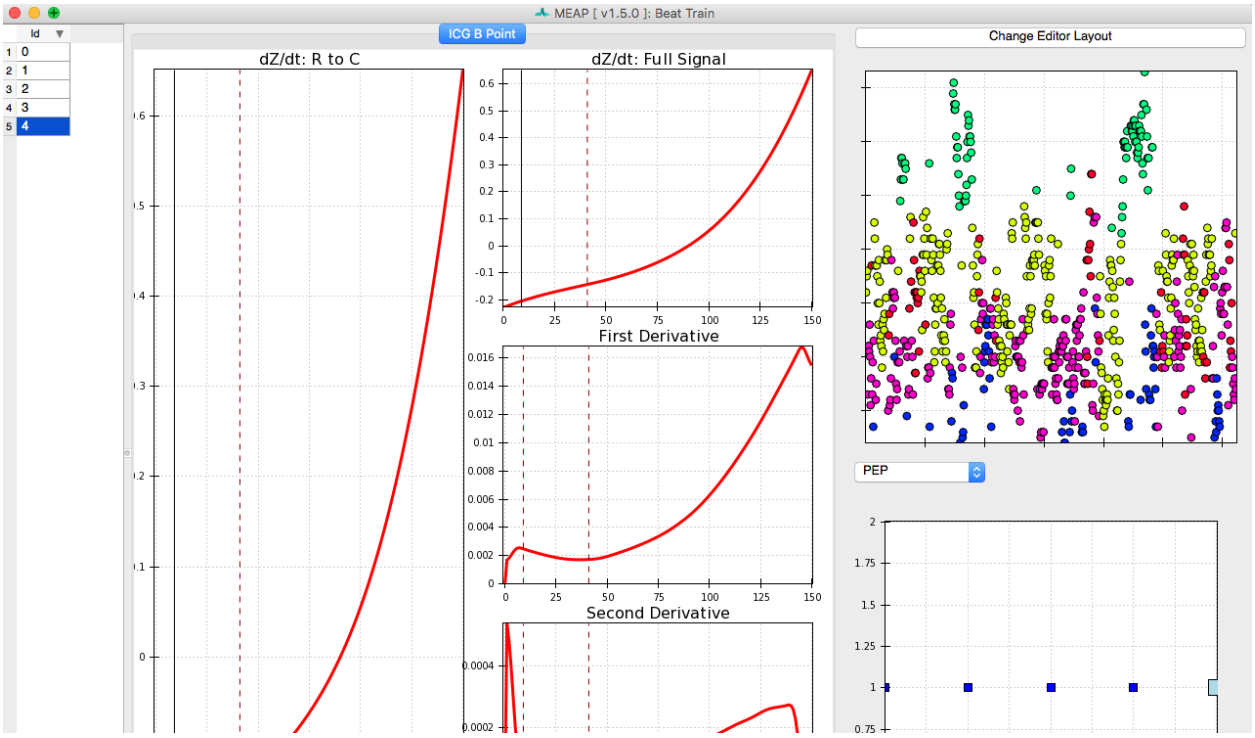
The updated plots will look something like the above. You will notice that the Karcher Mean (dark blue line) has higher amplitude than the global ensemble average (light blue line) and contains sharper features. These are all benefits of using an elastic time series approach. Click “Warp All” and all of your heartbeats will be registered to this initial Karcher Mean. The bottom two plots will show the individual dZ/dt signal in red after it is aligned to the Karcher Mean in blue. The image plot on the right is a heat map of the aligned dZ/dt signals.

Once all beats have been aligned to the initial Karcher Mean, you can cluster heart beats based on the similarity of their warps using the widgets in the right panel. We use the distance metrics and general procedure described in Kurtek 2017 to cluster heart beats. Choose the number of clusters and the maximum number of K-means iterations. Once satisfied with your choices, click “Detect Modes”. This will take a long time to run. If you are using MacOS, it will take much longer than any other operating system. Once completed, the “Score Modes” button will be enabled.

Clicking the “Score Modes” button will open an editor like the one below:

There will be one beat listed in the left panel for each mode you requested. Clicking on that beat will show what that cluster’s template dZ/dt looks like. The B-Point times are plotted in the upper-right panel. By editing the B-Points, the corresponding time in each original beat will be updated. Manually identify te B-Point on each Mode and the inverse warp to the original beats will be used to identify the corresponding point on the original waveform.

Once you’re satisfied, you can visit the “Compute Moving Ensembles” window again to edit individual B-Point placements.



2.10 Step 8: Process fMRI

This feature not yet functional, but coming soon.

2.11 Step 9: Save Your Preprocessed File (Again!)

Save your Work! If you have not done so already, copy the *File* path and paste it into the *Outfile* field and change the file type from `.acq` to `.mea.mat`, then click **Save .meap file**.

The file you just preprocessed should now be highlighted in blue. Proceed to the next file and repeat these steps until you have scored the data for all of your subjects.

To improve processing speed click the **Clear Memory** button to clear the memory cache before proceeding to the next file.

CHAPTER 3

PART II: Calculating Ensemble and Moving Ensemble Averages

3.1 Step 1: Create a Design Spread Sheet

This should specify your subjects, your experimental design, and the path to the `mea.mat` files that you preprocessed:

	A	B	C	D	E	F	G	H
1	subject	session	condition	event	onset	duration	file	
2	302	1	band	BL1	0	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
3	302	1	band	BL2	30	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
4	302	1	band	BL3	60	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
5	302	1	band	BL4	90	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
6	302	1	band	BL5	120	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
7	302	1	band	BL6	150	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
8	302	1	band	BL7	180	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
9	302	1	band	BL8	210	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
10	302	1	band	BL9	240	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
11	302	1	band	BL10	270	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
12	302	1	band	D1	300	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
13	302	1	band	D2	330	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
14	302	1	band	R1	360	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
15	302	1	band	R2	390	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
16	302	1	band	R3	420	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
17	302	1	band	R4	450	30	\Users\Research Assistant\Documents\Doc Scoring\302_bands.mea.mat	
18	302	2	spot	BL1	0	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
19	302	2	spot	BL2	30	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
20	302	2	spot	BL3	60	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
21	302	2	spot	BL4	90	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
22	302	2	spot	BL5	120	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
23	302	2	spot	BL6	150	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
24	302	2	spot	BL7	180	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
25	302	2	spot	BL8	210	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
26	302	2	spot	BL9	240	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
27	302	2	spot	BL10	270	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
28	302	2	spot	D1	300	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
29	302	2	spot	D2	330	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
30	302	2	spot	R1	360	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
31	302	2	spot	R2	390	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
32	302	2	spot	R3	420	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
33	302	2	spot	R4	450	30	\Users\Research Assistant\Documents\Doc Scoring\302_spots.mea.mat	
34	303	1	band	BL1	0	30	\Users\Research Assistant\Documents\Doc Scoring\303_bands.mea.mat	
35	303	1	band	BL2	30	30	\Users\Research Assistant\Documents\Doc Scoring\303_bands.mea.mat	
36	303	1	band	BL3	60	30	\Users\Research Assistant\Documents\Doc Scoring\303_bands.mea.mat	
37	303	1	band	BL4	90	30	\Users\Research Assistant\Documents\Doc Scoring\303_bands.mea.mat	
38	303	1	band	BL5	120	30	\Users\Research Assistant\Documents\Doc Scoring\303_bands.mea.mat	

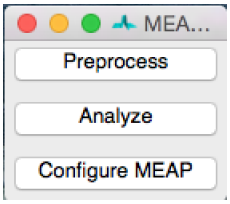
Exactly how this file should be set up will depend on the length of the ensemble average window you are using and on

other specifics of your study design.

This same file is also where your data will ultimately be printed. Thus it serves as both the input and output file for this stage of the scoring process.

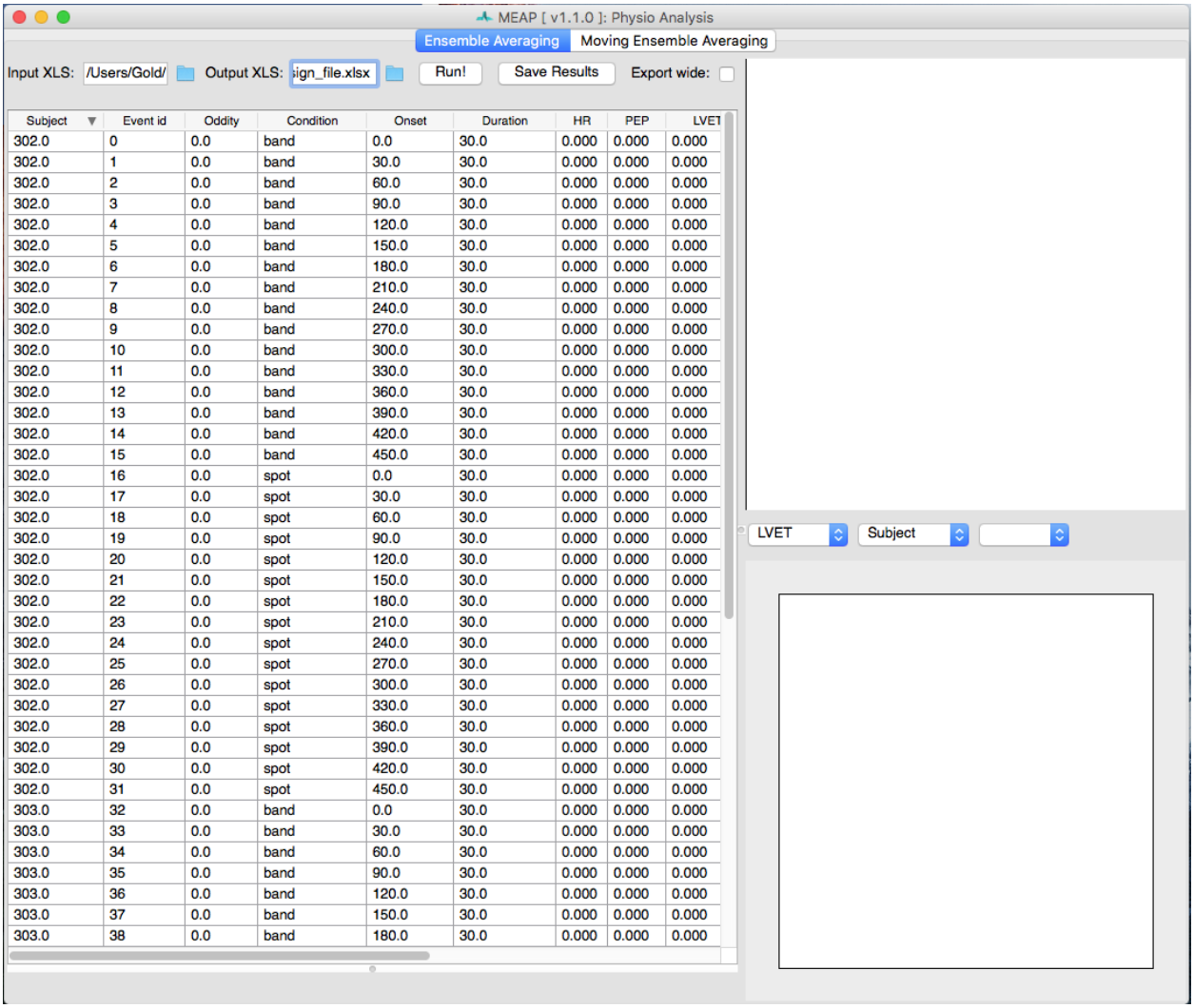
3.2 Step 2: Analysis

For step 2, select **Analyze** on the MEAP launch window.



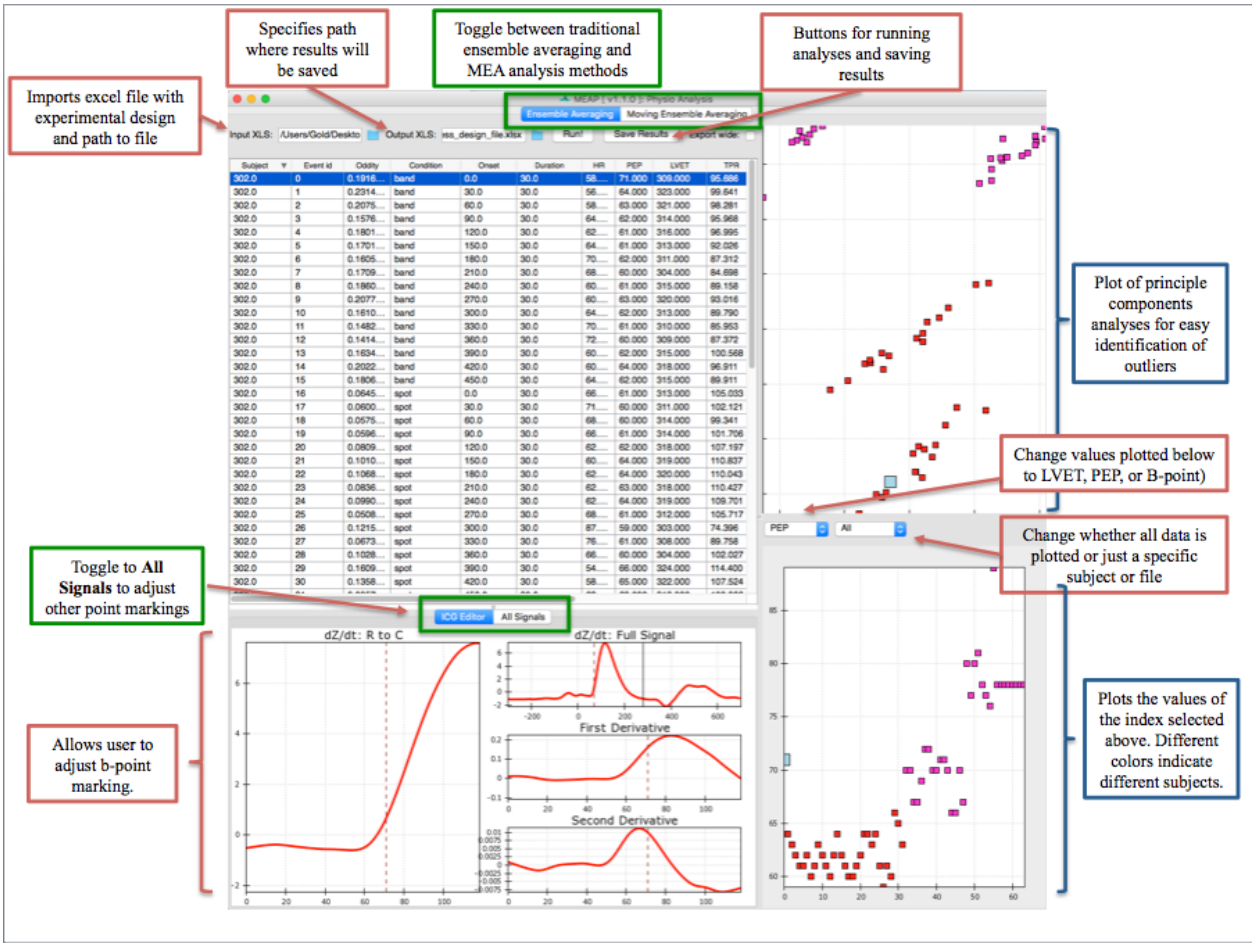
Ensemble Averaging

The first step is to load your prepared design file. The analyze interface will then look like this:



Subject	Event id	Oddity	Condition	Onset	Duration	HR	PEP	LVET
302.0	0	0.0	band	0.0	30.0	0.000	0.000	0.000
302.0	1	0.0	band	30.0	30.0	0.000	0.000	0.000
302.0	2	0.0	band	60.0	30.0	0.000	0.000	0.000
302.0	3	0.0	band	90.0	30.0	0.000	0.000	0.000
302.0	4	0.0	band	120.0	30.0	0.000	0.000	0.000
302.0	5	0.0	band	150.0	30.0	0.000	0.000	0.000
302.0	6	0.0	band	180.0	30.0	0.000	0.000	0.000
302.0	7	0.0	band	210.0	30.0	0.000	0.000	0.000
302.0	8	0.0	band	240.0	30.0	0.000	0.000	0.000
302.0	9	0.0	band	270.0	30.0	0.000	0.000	0.000
302.0	10	0.0	band	300.0	30.0	0.000	0.000	0.000
302.0	11	0.0	band	330.0	30.0	0.000	0.000	0.000
302.0	12	0.0	band	360.0	30.0	0.000	0.000	0.000
302.0	13	0.0	band	390.0	30.0	0.000	0.000	0.000
302.0	14	0.0	band	420.0	30.0	0.000	0.000	0.000
302.0	15	0.0	band	450.0	30.0	0.000	0.000	0.000
302.0	16	0.0	spot	0.0	30.0	0.000	0.000	0.000
302.0	17	0.0	spot	30.0	30.0	0.000	0.000	0.000
302.0	18	0.0	spot	60.0	30.0	0.000	0.000	0.000
302.0	19	0.0	spot	90.0	30.0	0.000	0.000	0.000
302.0	20	0.0	spot	120.0	30.0	0.000	0.000	0.000
302.0	21	0.0	spot	150.0	30.0	0.000	0.000	0.000
302.0	22	0.0	spot	180.0	30.0	0.000	0.000	0.000
302.0	23	0.0	spot	210.0	30.0	0.000	0.000	0.000
302.0	24	0.0	spot	240.0	30.0	0.000	0.000	0.000
302.0	25	0.0	spot	270.0	30.0	0.000	0.000	0.000
302.0	26	0.0	spot	300.0	30.0	0.000	0.000	0.000
302.0	27	0.0	spot	330.0	30.0	0.000	0.000	0.000
302.0	28	0.0	spot	360.0	30.0	0.000	0.000	0.000
302.0	29	0.0	spot	390.0	30.0	0.000	0.000	0.000
302.0	30	0.0	spot	420.0	30.0	0.000	0.000	0.000
302.0	31	0.0	spot	450.0	30.0	0.000	0.000	0.000
303.0	32	0.0	band	0.0	30.0	0.000	0.000	0.000
303.0	33	0.0	band	30.0	30.0	0.000	0.000	0.000
303.0	34	0.0	band	60.0	30.0	0.000	0.000	0.000
303.0	35	0.0	band	90.0	30.0	0.000	0.000	0.000
303.0	36	0.0	band	120.0	30.0	0.000	0.000	0.000
303.0	37	0.0	band	150.0	30.0	0.000	0.000	0.000
303.0	38	0.0	band	180.0	30.0	0.000	0.000	0.000

Until you click **Run** all values for indices will be zero and nothing will be plotted in the windows on the right. After selecting run, the interface will look something like this:



The Ensemble Average window allows the user to visualize each ensemble average (duration specified in your excel file) as well as the values for key indices (B-point, PEP, LVET) for all subjects, for a specific subject only, or for a specific data file only. In the top right corner is an ICA plot which takes all of the features of the ensemble averages into account and then plots them in two dimensions based on their covariance.

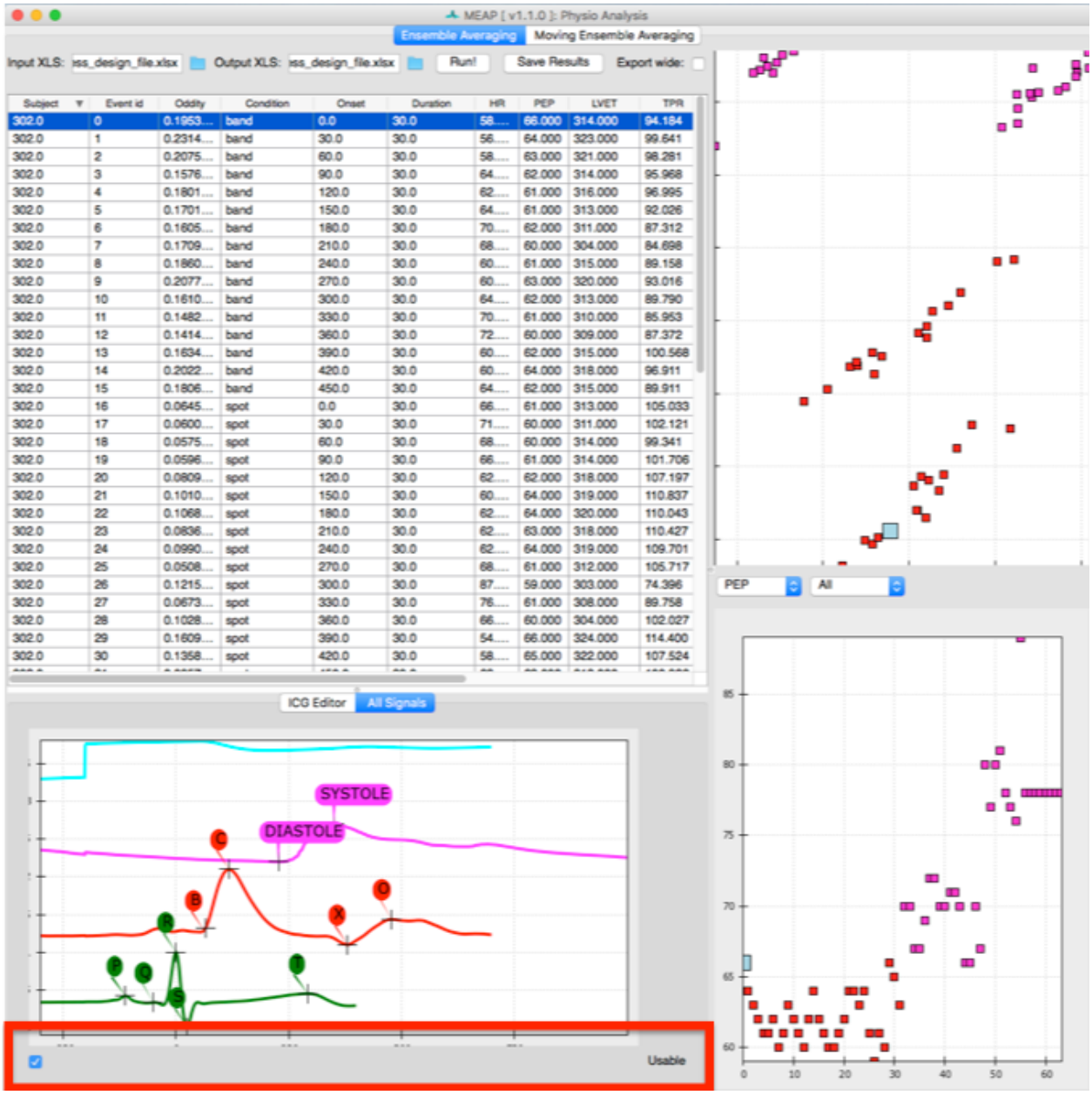
Using the column headers you can sort by subject, event, or by "oddity index" which reflects that EAs distance from the center of the ICA plot. This allows you to quickly identify problematic EAs and adjust point markings as necessary.

_static/sort_by_oddity.png

To view all point markings (not just the B-points) toggle the bottom window to **All Signals**. There you can adjust the placement of any of the inflection points. If the data for a specific EA is too noisy or you decide you don't want to include it in analyses for whatever reason simply uncheck the *Usable* button at the bottom of this window and that EA will be removed from the dataset.

Using these point markings MEAP calculates the following cardiovascular indices:

1. **Total Peripheral Resistance** (TPR)
2. **Cardiac Output** (CO)


MEAP [v1.1.0]: Physio Analysis
Ensemble Averaging
Moving Ensemble Averaging
Input XLS:
Output XLS:
Run!
Save Results
Export wide:
Subject
Event id
Oddity
Condition
Onset
Duration
HR
PEP
LVET
TPR
PEP
All
ICG Editor
All Signals
SYSTOLE
DIASTOLE
Usable

3. **Stroke Volume** (SV)
4. **Pre-Ejection Period** (PEP)
5. **Mean Arterial Pressure** (MAP)
6. **Heart Rate** (HR)
7. **Heart Rate Variability** (HRV)

All of these values for each EA will be exported to your excel output file:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
1		subject	de_distanc	de_distanc	session	condition	event	onset	duration	file	hr	tpr	sv	svk	svsb	pep	co	map	hrv	lvet	sbp	dbp
2	0	302.0	28	29	1	band	BL1	0	30	/Users/Gol	58	94.18367	1422.643	1422.643	1221.317	66	82.51327	97.14253	0.062206	314	133.1541	79.13675
3	1	302.0	28	29	1	band	BL2	30	30	/Users/Gol	56	99.64092	1454.808	1454.808	1247.235	64	81.46923	101.4709	0.074445	323	139.2019	82.60535
4	2	302.0	28	29	1	band	BL3	60	30	/Users/Gol	58	98.28064	1419.9	1419.9	1218.198	63	82.35417	101.1728	0.087074	321	139.1101	82.20411
5	3	302.0	28	29	1	band	BL4	90	30	/Users/Gol	64	95.96757	1331.072	1331.072	1143.001	62	85.18864	102.1918	0.094906	314	141.2394	82.66807
6	4	302.0	28	29	1	band	BL5	120	30	/Users/Gol	62	96.99464	1402.886	1402.886	1202.01	61	86.97894	105.4561	0.053591	316	147.045	84.66171
7	5	302.0	28	29	1	band	BL6	150	30	/Users/Gol	64	92.02582	1380.352	1380.352	1182.199	61	88.34252	101.6224	0.070473	313	142.4513	81.20796
8	6	302.0	28	29	1	band	BL7	180	30	/Users/Gol	70.53597	87.31199	1348.353	1348.353	1154.629	62	95.10736	103.8002	0.081034	311	144.6199	83.39028
9	7	302.0	28	29	1	band	BL8	210	30	/Users/Gol	68	84.69843	1310.899	1310.899	1127.46	60	89.14117	94.37646	0.093008	304	131.3706	75.87938
10	8	302.0	28	29	1	band	BL9	240	30	/Users/Gol	60	89.15838	1427.966	1427.966	1224.672	61	85.67798	95.48637	0.076059	315	133.7928	76.33317
11	9	302.0	28	29	1	band	BL10	270	30	/Users/Gol	60	93.01592	1435.248	1435.248	1230.729	63	86.11488	100.1257	0.111059	320	140.1469	80.11507
12	10	302.0	28	29	1	band	D1	300	30	/Users/Gol	64	89.79007	1346.747	1346.747	1156.342	62	86.19182	96.73963	0.059868	313	135.8884	77.16526
13	11	302.0	28	29	1	band	D2	330	30	/Users/Gol	70	85.95252	1302.544	1302.544	1113.307	61	91.17808	97.96233	0.070959	310	136.7651	78.56096
14	12	302.0	28	29	1	band	R1	360	30	/Users/Gol	72	87.37213	1264.545	1264.545	1078.361	60	91.04726	99.43741	0.08236	309	136.6106	80.85079
15	13	302.0	28	29	1	band	R2	390	30	/Users/Gol	60	100.5678	1344.526	1344.526	1129.228	62	80.67154	101.412	0.126877	315	141.4109	81.41249
16	14	302.0	28	29	1	band	R3	420	30	/Users/Gol	60	96.91107	1426.838	1426.838	1196.858	64	85.61028	103.7073	0.084598	318	147.4272	81.84733
17	15	302.0	28	29	1	band	R4	450	30	/Users/Gol	64	89.91098	1403.548	1403.548	1179.229	62	89.82707	100.9555	0.066306	315	143.2027	79.83189
18	16	302.0	28	29	2	spot	BL1	0	30	/Users/Gol	66.93412	105.0327	1022.325	1022.325	979.8165	61	68.42843	89.84029	0.036956	313	124.756	72.38244
19	17	302.0	28	29	2	spot	BL2	30	30	/Users/Gol	71.60543	102.1209	972.4744	972.4744	922.7824	60	69.63445	88.88914	0.064688	311	122.6552	72.00613
20	18	302.0	28	29	2	spot	BL3	60	30	/Users/Gol	68	99.34093	997.7865	997.7865	946.0981	60	67.84948	84.25288	0.041608	314	114.9765	68.89106
21	19	302.0	28	29	2	spot	BL4	90	30	/Users/Gol	66	101.7061	1005.743	1005.743	952.8418	61	66.37902	84.3894	0.072902	314	113.6993	69.73447
22	20	302.0	28	29	2	spot	BL5	120	30	/Users/Gol	62	107.197	1020.457	1020.457	965.8695	62	63.26831	84.77717	0.049205	318	114.7818	69.77488
23	21	302.0	28	29	2	spot	BL6	150	30	/Users/Gol	60	110.8369	1018.048	1018.048	963.8124	64	61.08286	84.62794	0.078081	319	114.4438	69.71999
24	22	302.0	28	29	2	spot	BL7	180	30	/Users/Gol	62	110.043	1011.98	1011.98	960.3513	64	62.74273	86.30497	0.071162	320	117.6635	70.62568
25	23	302.0	28	29	2	spot	BL8	210	30	/Users/Gol	62	110.427	1003.362	1003.362	950.635	63	62.20847	85.86868	0.082547	318	117.5153	70.04536
26	24	302.0	28	29	2	spot	BL9	240	30	/Users/Gol	62	109.7009	1008.41	1008.41	957.7643	64	62.52141	85.73319	0.090627	319	117.922	69.63879
27	25	302.0	28	29	2	spot	BL10	270	30	/Users/Gol	68	105.7168	968.9008	968.9008	920.5485	61	65.88525	87.06473	0.106445	312	119.6632	70.76549
28	26	302.0	28	29	2	spot	D1	300	30	/Users/Gol	87.66418	74.39591	934.3196	934.3196	885.3258	59	81.90637	76.16874	0.085595	303	98.8687	64.81876
29	27	302.0	28	29	2	spot	D2	330	30	/Users/Gol	76	89.75807	955.5709	955.5709	907.5936	61	72.62339	81.48169	0.063224	308	100.9135	71.7658
30	28	302.0	28	29	2	spot	R1	360	30	/Users/Gol	66	102.0268	922.2123	922.2123	872.7398	60	60.86601	77.62452	0.145759	304	99.14991	66.86183
31	29	302.0	28	29	2	spot	R2	390	30	/Users/Gol	54	114.3999	1046.153	1046.153	984.7744	66	56.49227	80.78387	0.103909	324	110.11	66.1208
32	30	302.0	28	29	2	spot	R3	420	30	/Users/Gol	58	107.5236	1042.153	1042.153	982.8966	65	60.44488	81.24065	0.10737	322	112.9613	65.38034
33	31	302.0	28	29	2	spot	R4	450	30	/Users/Gol	62	100.9256	1054.249	1054.249	993.0321	63	65.36343	82.46055	0.056925	318	116.5571	65.41226
34	32	303.0	31	31	1	band	BL1	0	30	/Users/Gol	82	134.1516	573.0485	573.0485	688.9224	70	46.98998	78.79725	0.041637	282	94.65644	70.86766
35	33	303.0	31	31	1	band	BL2	30	30	/Users/Gol	88.69101	124.5367	563.9078	563.9078	679.8818	70	50.01355	77.85655	0.044238	289	91.6136	70.97803
36	34	303.0	31	31	1	band	BL3	60	30	/Users/Gol	80	143.1254	520.4718	520.4718	626.2438	67	41.63774	74.49274	0.038644	290	88.18457	67.64683
37	35	303.0	31	31	1	band	BL4	90	30	/Users/Gol	80	129.537	595.6076	595.6076	713.0996	67	47.64861	77.15323	0.051329	287	92.86912	69.29529
38	36	303.0	31	31	1	band	BL5	120	30	/Users/Gol	86	131.1941	557.7982	557.7982	669.4194	69	47.97064	78.66834	0.023211	282	97.25879	69.37311
39	37	303.0	31	31	1	band	BL6	150	30	/Users/Gol	82	135.358	576.1282	576.1282	694.0485	72	47.24251	79.93313	0.032965	278	100.272	69.76368
40	38	303.0	31	31	1	band	BL7	180	30	/Users/Gol	86	138.2042	539.1765	539.1765	647.963	72	46.36918	80.10516	0.045594	278	100.7775	69.76897
41	39	303.0	31	31	1	band	BL8	210	30	/Users/Gol	78	137.2501	596.9617	596.9617	719.0513	70	46.56302	79.88473	0.036414	289	100.6268	69.51368

3.3 Step 3: Save Your Work!!

Click the "Save Results" button at the top of the GUI to save your work. Do this frequently as you are working. All of your custom point markings will be saved and you can reload and return to them by using the newly created output spreadsheet as input.

CHAPTER 4

PART III: Analyzing your Scored Data

At this point you have completed the data scoring process. You now have a `.csv` file with values for each cardiovascular index for each ensemble average. MEAP calculates a slope and an intercept for each EA.

If you want to use the time series data from the moving ensemble averages computed during preprocessing, those can be pulled from the .mea.mat file using R or another statistical package of your choice.

You are now ready to move this data into whatever statistical software you prefer for analyses. Depending on what type of analyses you wish to conduct you may need to reformat the data. As it is, the data appears in *long format* with multiple rows of data for each subject. Some analyses require *wide format* where each subject has only one row of data but multiple variables for each cardiovascular index reflecting the values for each ensemble average.

Again, depending on your study design and the analyses you wish to conduct you may want to create reactivity values that reflect values for each index minus baseline values (E.g. CO_min1 - CO_BL). All analyses and data transformations are done outside of MEAP in your statistical software of choice. You should also use this software to check for outliers or any other issues with your data.

CHAPTER 5

Indices and Tables

- genindex
- modindex
- search