

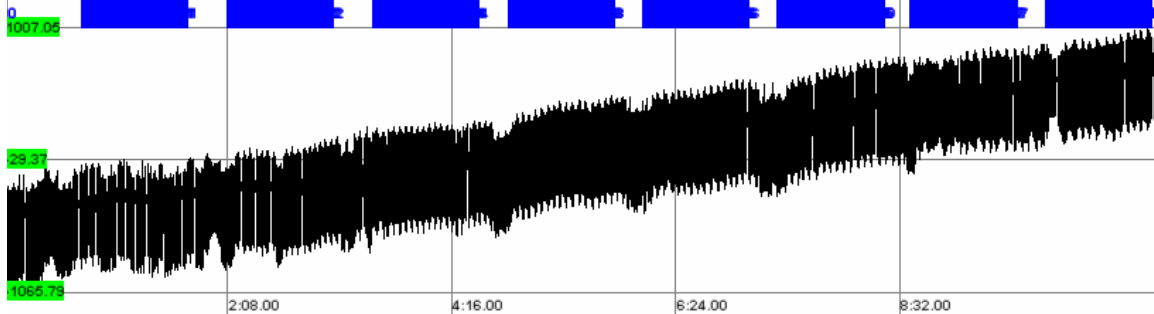
A Pragmatic Manual for Getting Started with QRSTool: Reducing ECG Data and Obtaining Many Metrics with CMetX


This overview will provide basic steps for importing EKG data to QRSTool, identify interbeat intervals (IBI), correct for instances where QRSTool misidentified beats, and finally export the IBI series and calculate the metrics of cardiac variability using CMetX. Full documentation for QRSTool is available in the Help files within QRSTool.

Step 1: If you have more than a single channel of EKG, although it is not necessary to strip out the other channels using something like Neuroscan's Linear Derivation function, it may speed up the import process if you have very many channels. But QRSTool will work properly without doing so.

Step 2: Getting Started with QRSTool

1. Open QRSTool
2. File→Import→.CNT File (or Text File)
 - a. File: Click on the ... to select the new file that only has the EKG data
 - b. If you have a CNT file, select 16 bit (older) or 32 bit (more recent versions)
 - c. Select Import Events
 - d. If you have more than one channel, highlight the EKG channel
 - e. Select OK
3. QRSTool will load the EKG series into the bottom frame.
4. If you imported a Neuroscan file, you'll notice there are blue numbers along the top of each window. These are the codes that in the Neuroscan file if you used such to code which task was occurring during the recording:
5. Often Neuroscan data has undocumented data of large magnitude at the end of the file. If so, the EKG series may appear as a flat line because the auto scaling will be biased by the large amplitude "crud" at the end. If this is the case, will wish to place the cursor very close to the end of the file, right click, crop, to end. You'll now see the EKG series. If it was recorded in DC mode, you may note the baseline drift over time, illustrated in the figure as the series rises from left to right:

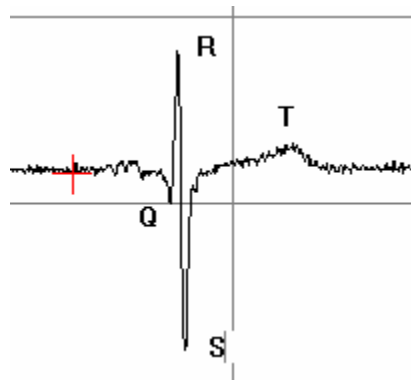



6. We will wish to zoom in on a small section that will have relatively little drift. On the toolbar, select the magnifying glass .
 - a. Use this tool to select a small region near the beginning of the EKG series by holding down on the left button and pulling it across a portion of the screen.
 - b. Continue to zoom in by selecting a portion until you can see the ecg series clearly. (If you're using a mouse with a wheel, you can use the wheel to zoom in and out when you have the magnifying glass selected)

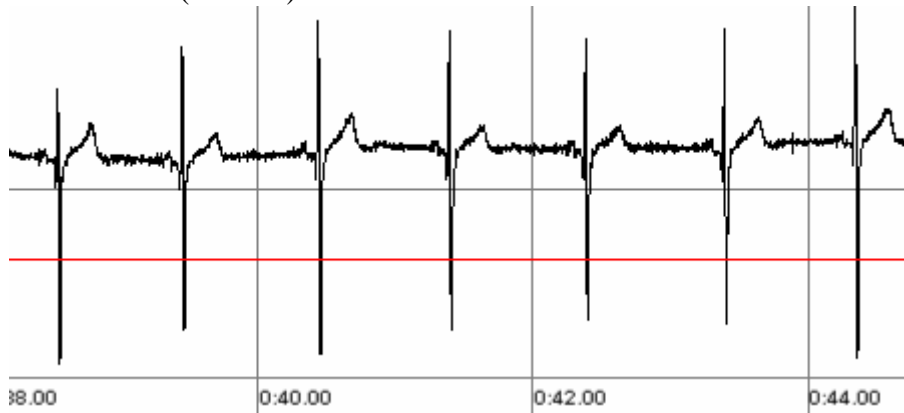
Step 3: Train the program how to find R-Waves


1. Method 1 – amplitude threshold

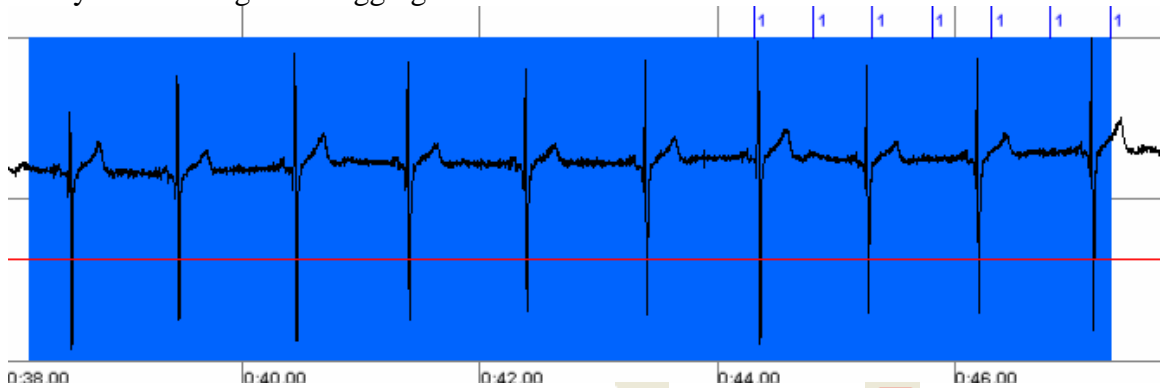
- a. Decide whether the positive or negative voltage spike is better differentiated from the rest of the waveform. In the sample waveform below, positive (up) or negative (down) would be fine, but the negative spike (S wave) is better than the positive spike (R wave) in that it is unlikely to overlap with the later positive slower wave (T wave).





- b. Now “draw” the threshold by using the  tool to mark the threshold that must be exceeded to count as a beat. In this example, it is drawn in the negative direction (red line)

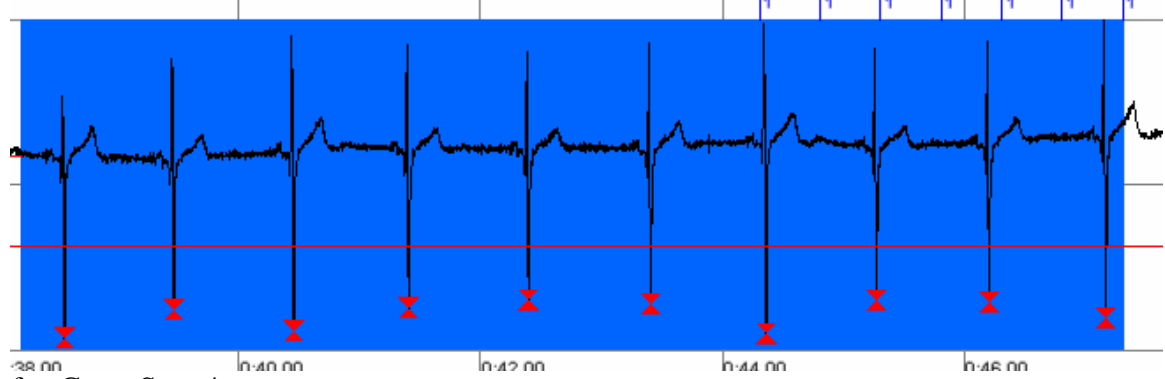


- c. Now choose the pointer  and highlight a short region of the EKG time series by left clicking and dragging. It will turn blue:






- d. Now select the direction of beat detection:  for positive or  for negative (as in this example).

- e. Beats identified by the program appear as a red “hourglass”




- f. Go to Step 4

2. Method 2 – Manually



- a. Select the pointer on the toolbar
- b. Make sure the following buttons are selected on the toolbar:
 - i. A crossed out heart  (overwrite existing beats)
 - ii. The button to the right of the crossed out heart: it is a blue box with a light blue arrow pointing upwards.  (find positive peaks); to find negative peaks, choose the blue box with a light blue arrow pointing down 
- c. While holding down the shift button, hold the left click button on the mouse, and highlight an r-spike. The program will automatically find the apex of the R-wave and will place a red hour glass on the top of the R-spike. Repeat this process on 10 R-spikes. If you selected the down arrow, it will find the nadir of the S wave.
- d. If you make a mistake, then you can “erase” a beat by holding Ctl-Shift-Left-click and drag to highlight a small region around the beat. Any beats in the highlighted region will disappear.
- e. You’ll notice as you add more hour glasses, a waveform appears in the upper window. The distance between two R-spikes is called the Interbeat Interval (IBI). QRSTool plots consecutive IBIs in the upper frame. We’ll focus on this window in step #5.

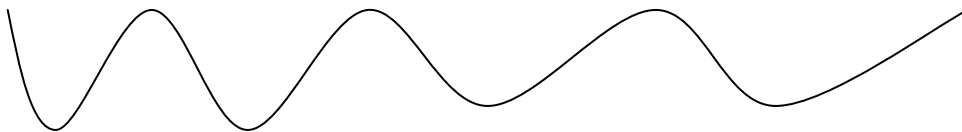
Step 4: Automate the process of finding the R-waves

1. The peri-beat average correction helps to identify beats by using a prototypical EKG waveform (based on the beats you identified in step 3) to filter the EKG series and identify r-spikes. This corrects for drift, and also tends to be rather robust to other artifacts in the series.
2. *Optional:* Check that the average waveform to be used by the peri-beat filter tool looks appropriate, and to see what a prototypic waveform looks like. Select Tools→Statistics→IBI series. You’ll see a graph of the average EKG waveform with shaded areas representing the standard error. You may wish to examine the length of the prototypic EKG waveform to use as parameters in the next step.
3. Use the peri-beat filter tool: . A window will appear allowing you to enter different parameters for the peri-beat average algorithm. These values are initialized to those set in the Tools→Preferences→Export window. The first two parameters (pre- and post-beat window length) are likely to be the only ones that need to be changed; in general, these should range from 80 to 250ms. Longer times use more data points (centered on existing

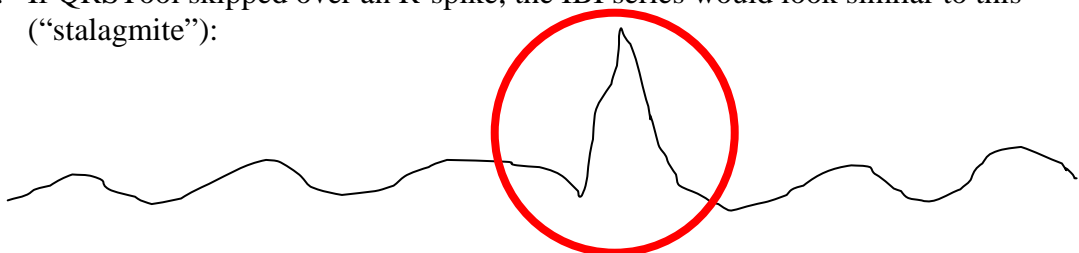
- beats) to form the “prototype” beat, however, long windows are also likely to capture variability due to changing IBI.
4. Select this button and QRSTool will filter through the series to correct for the drift and then it will find the R-spikes based on an algorithm that takes into account the R-spikes you manually selected.
 - a. QRSTool has now created a new series, called pb_filter.
 - b. Return to the original series by going to the tool bar, find Series: and use the up or down arrow to find the original series. Then click anywhere in the lower EKG waveform window.
 5. *Optional:* Check that the average waveform used by the peri-beat filter tool looks appropriate; if it does not, then there may be problems with the IBI series. Then select Tools→Statistics→IBI series. You’ll see a graph of the average EKG waveform. If this looks peculiar, it may mean that the peri-beat function identified things other than the R-Spikes as beats (e.g. high t-wave amplitudes).

Step 5: Correct any errors the peri-beat filter created

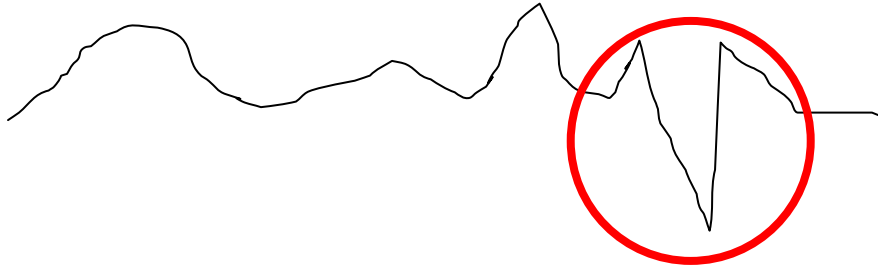
1. First, ensure that the peri-beat filter placed markers on the actual peak (or trough). Looking at the original series in the lower window (not the pbfilter series), examine to markers to determine if they are at the actual peak or trough (depending on the direction your r-spike). Sometimes the peribeat filter will place the marker a few samples to either side of the peak. To ensure that QRSTool places the markers at the peak, use the lock beats tool to lock the beats to the nearest peak  or the nearest trough . Now scan for artifacts as indicated below.
2. On the top window you will notice the IBI waveform is similar to the respiration waveform. Indeed, the IBI series reflects the relationship of respiration to heart rate: when one inhales, heart rate increases (and the distance between sequential R-spikes are shorter) and when one exhales, heart rate decreases (and the distance between sequential R-spikes are longer)
3. The purpose of this task is to make sure the QRSTool did not mark another portion of the waveform as an R-spike, or skip over an R-spike. You’ll need to zoom in again to be able to see the waveform in more detail. Select the magnifying glass and zoom in to the beginning of the wave.
 - a. A file that requires no editing on your part would have an IBI series (top window) that should look similar to respiration throughout the entire file (this will likely occur only rarely):



- b. If QRSTool skipped over an R-spike, the IBI series would look similar to this (“stalagmite”):



- c. If QRSTool marked another part of the ecg series as an R-spike, the IBI series would look like this (“stalactite”):




- d. Stalagmites and stalactites may typically appear between tasks (indicated by different number codes) if you paused your recording. Don't worry about these stalagmites and stalactites because when we export the data, we will be exporting data within each task and not the data between tasks.
- e. To fix a missed or extra beat, zoom in (scroll wheel) on that portion of the waveform, and then you can use Ctl-Shift-Click and drag to remove beats from a highlighted region, and use Shift-Click and drag to insert a beat at the maximum in point in a highlighted region.
- f. Repeat as needed until all artifacts are removed.

Step 6: Make sure all of the event markers appear

1. If you have event markers to delimit the beginning and end of a segment (or task) you don't need to do more at this time – skip to step 7. Also, if your EKG file begins with the start of the task or segment, and ends with the end of the task or segment (i.e. not non-task data), you will not need event codes and can skip to step 7.

If you have a file with some non-task data, or a file with multiple tasks, you need event codes. If you did not have such event codes, you'll need to insert them as detailed in the next step. If your file is a single task, but begins after the beginning of the file or ends before the end of the file, then all you need to have is a marker at the beginning and another at the end of the task. If you have multiple tasks in the file, then you need to have pairs of markers, each pair delineating the start and end of a segment. The marker at the beginning and end of the segment should be the same number. These markers will delineate what portions CMetX will provide summary statistics for (see step 7).

2. Select the Keymap Editor  button on the toolbar
 - a. Place the cursor in the Key field
 - i. Select the function key F2 on the top of the keyboard
 - b. Place the cursor in the Value field
 - i. Select a code for a given task/segment (e.g resting baseline might be 1, stress task might be 2, etc.);
 - c. Click Add/Change, OK
 - d. Go to the part of the EKG series where a code is needed.
 - i. Select the cursor button
 - ii. Left click right on top of the event codes that are already there and press F2.
 1. You should see the event number appear in blue
 - e. Go to the part of the EKG series that the other set of markers should be


- i. Select the cursor button
- ii. Left click on the series and press F2.
 1. You should see the event number appear in blue
- f. Repeat as needed to insert all necessary events.

Step 7: Running CMetX (this program calculates common heart rate metrics, including RSA)


1. Make sure QRSTool knows where CMET lives

- a. Go to Tools→Preferences→Export
- b. CMET Path will typically be
C:\Program Files\QRSTool\CMet\CMetX.exe
- c. OK


2. If your file does not need event codes, because the entire file is task data, then run CMetX on the entire file. But if you have event codes, then skip to one of the next two options. To export then entire file and run CMetX:

- a. Select File, Export CMetX ( button on the toolbar).
 - i. The options “Run CMET on exported IBI series:” and the option “Export All” should be enabled
 - ii. Under Export file, press the “...”
 - iii. Find the folder where you’d like to save this output and type in a file name for the output (e.g. “FILENAME_ibi”)
- b. Several new files will appear in this folder.

3. Event Codes Option 1 – Running CMetX Manually from Menus

- a. **Select a range of events for CMetX to analyze:**
 - i. Events→Edit Events 
 - ii. Check “Select using events”
 - iii. Change “variables” to StimType
 - iv. If you have a section that has the same code that identifies the beginning and end of a section (e.g. “1” at the start of the resting baseline and “1” again at the end), or a section that has the same code repeating throughout it (e.g. “1” repeats every second during the resting baseline), then choose “First to Last” and select the code of interest.
 - v. If you have different codes for beginning and end, then use the “between events” option to select the starting code and ending code.
 - vi. Determine whether you wish to compensate for the loss of data in CMetX due to the filter. When CMetX filters the data to pass the respiratory frequency range, the first 12 seconds and the last 12 seconds of data are lost to the filter. QRSTool offers an option to avoid this problem if you have EKG data collected before and after your segment of interest. If you wish to fully compensate for the CMetX filter-related data loss, then change the values under “Time Window” to indicate 12 seconds before and 12 seconds after.
 - vii. Click OK

b. Now export the IBI series and run CMetX

- i. File→Export CMetX ( button on the toolbar).
- ii. Other options should be correctly set (“Selection” and “Unlock after write”)

- iii. Check the filename and change if you wish. This is the name of the file that will contain the IBI series for this segment of data (e.g. the IBI series for resting baseline). It will have your filename followed by the number of the code(s) used to identify this segment.
- iv. Click Export – three files are created (or appended): your IBI file, HRVMETRC.DAT (file with CMetX output) and HRVMETRC.LOG (CMetX logging of unusual IBI sequences to check for possible error in IBI identification).

4. Event Codes Option 2 – Using Scripting Macros

- a. Full information is available from the Help Files in QRSTool, but below is a script that will work for files with Neuroscan codes. Comments about this script:
 - i. Scripts commands should be saved as an ASCII text files with a TXT extension
 - ii. This script expects to find Neuroscan Stimulus codes
 - iii. This data file has eight segments, each of which has a code repeating during a segment. You'd need at the very least, a code to demark the start and another to demark the end of a segment for analysis.
 - iv. The event select selects neuroscan codes, and also “pads” the file with 12 seconds before and after the codes, as CMetX will not analyze the first and last 12 seconds of data due to the filter.
 - v. For the first 7 segments, the data segment will include 12 seconds before and after the codes, and if the file would not permit this (e.g. not enough data precedes or follows the segment), the data segment would not be clipped – and it would not be analyzed. For the 8th segment, however, 12 seconds before and after the codes are to be included, unless there is insufficient data, in which case the data are clipped to the available data length, padding with what is available.

Sample Script File

```
START_LOG <C:\Program Files\QRSTool\logs\log_cmet.txt>
CMET_PATH <C:\Program Files\QRSTool\cmet\CMETX.EXE>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 1 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 2 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 3 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 4 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 5 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 6 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 7 12.0 12.0 NO_CLIP NO_STOP
EXPORT_CMET SELECT <> <>
EVENT_SELECT FIRST_TO_LAST <cnt2> <StimType> 8 12.0 12.0 CLIP NO_STOP
EXPORT_CMET SELECT <> <>
RESET_SKIP
END_LOG
```

- b. .If you had to add event markers, you'll need to edit this script to look for internal codes, like the following line – to look for a segment you demarcated with a keyboard code “1”:

```
EVENT_SELECT FIRST_TO_LAST <internal> <internal> 1 12.0 12.0 NO_CLIP NO_STOP
```

- c. Now – run the script! On toolbar find “Script”, and click on the button with “...”.
Select: your script (note that scripts are ASCII files with a TXT extension)
- d. Select “Run”
- e. QRSTool will export IBI series and run CMET
- f. Several new files will appear in your directory or the CMetX directory

Other suggestions:

1. Be sure to check the help file of QRSTool and also examine the included sample scripts usually installed under C:\Program Files\QRSTool\scripts.
2. In a CMD window (Start, run, CMD), type CMetX with no parameters to receive more information about CMetX and it’s metrics
3. Consider running QRSTool to the point of obtaining artifact free IBI series and then save the results as a native QRS file. The later use scripting to open the file and export the relevant sections to CMetX.
4. Check out the following paper for more details about the metrics and recording considerations:
Allen, J.J.B., Chambers, A.S., & Towers, D.N. (2007). The many metrics of cardiac chronotropy: A pragmatic primer and a brief comparison of metrics. *Biological Psychology*, 74, 243–262.