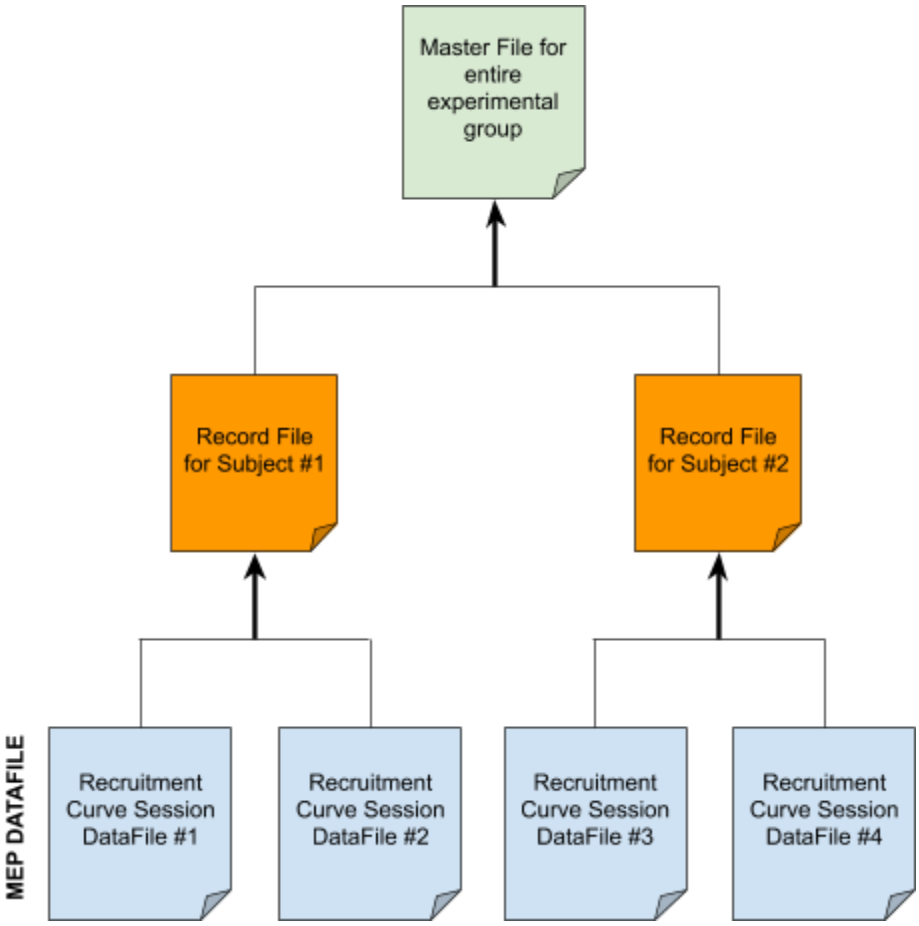
Motometrics User manual

Understanding data organization under Motometrics

Motometrics assumes various levels of data organization for quantifying MEPs, and fitting and analyzing recruitment curves. The three levels of data organization is illustrated below:



At the lowest level is the MEP data recorded and saved by the electrophysiology system. This data must be conditioned to be compatible with Motometrics as Recruitment Curve Session files. These files contain enough information to generate a single recruitment curve. In the immediate section below we detail how the data must be conditioned to be compatible with Motometrics.

At the next level, we have the record files. Here, we annotate the experiment by providing information on the session ID, stimulation intensities used, and the number of recorded trials performed for each stimulation intensity. These record files, allows us to also group multiple recruitment curve sessions for a single subject/animal.

Finally, let us assume we have multiple record files corresponding to different subjects or animals. Here, the same type of experimental conditions have been applied across the subjects/animals for recording each recruitment curve sessions MEP data. Now if we wish to compare how different experimental conditions affect computed recruitment curves across multiple subjects/animals, we can do so by grouping related record files into a single master file. Using master files for analysis allows us to take a more statistical approach to analyzing recruitment curves since it includes recruitment data for multiple subjects/animals.

Conditioning MEP data for use in Motometrics

In order to use motometrics, the MEP data must first be organized in a certain way. Essentially, the data must be stored in a structure with 2 fields:

The first field is 'values'.This is an 3-dimensional matrix that holds all the MEP data pertaining to the generation of a single recruitment curve. The first dimension is the number of time points of each MEP signal. The second dimension is the channel of recording (ranging from 1-16) depending on how many EMG electrodes are used in an experiment. The final dimension is the total number of recorded MEP signals. The total number of MEP signals is computed as the product of number of different stim intensities, and the number of trial recordings per stim intensity.

The second field is 'interval'. This is the inverse of the sampling rate of the MEP recordings.

Below is an example for how the data would look for 1 sec MEP recorded segments @ 5Khz, for 2 channels, with a range of 5 stimulation intensities, and 5 trials per stimulation intensity:

Struct1
|_____ interval
|_____ values

Here, Struct1.interval = 0.0002 corresponding to 1/5000 Hz.
Struct1.values is a 3D matrix of size: 5000 (number of time points per signal) X 2 (number of channels) X 25 (product of 5 stim intensities with 5 trials per stim).

The format described above is directly achievable with matlab datafiles exported by Cambridge Electronic Design LTD. electrophysiology systems through their signal software. For other systems such as TDT, or ADInstruments, a simple custom script can convert exported matlab datafiles to the required Motometrics format.

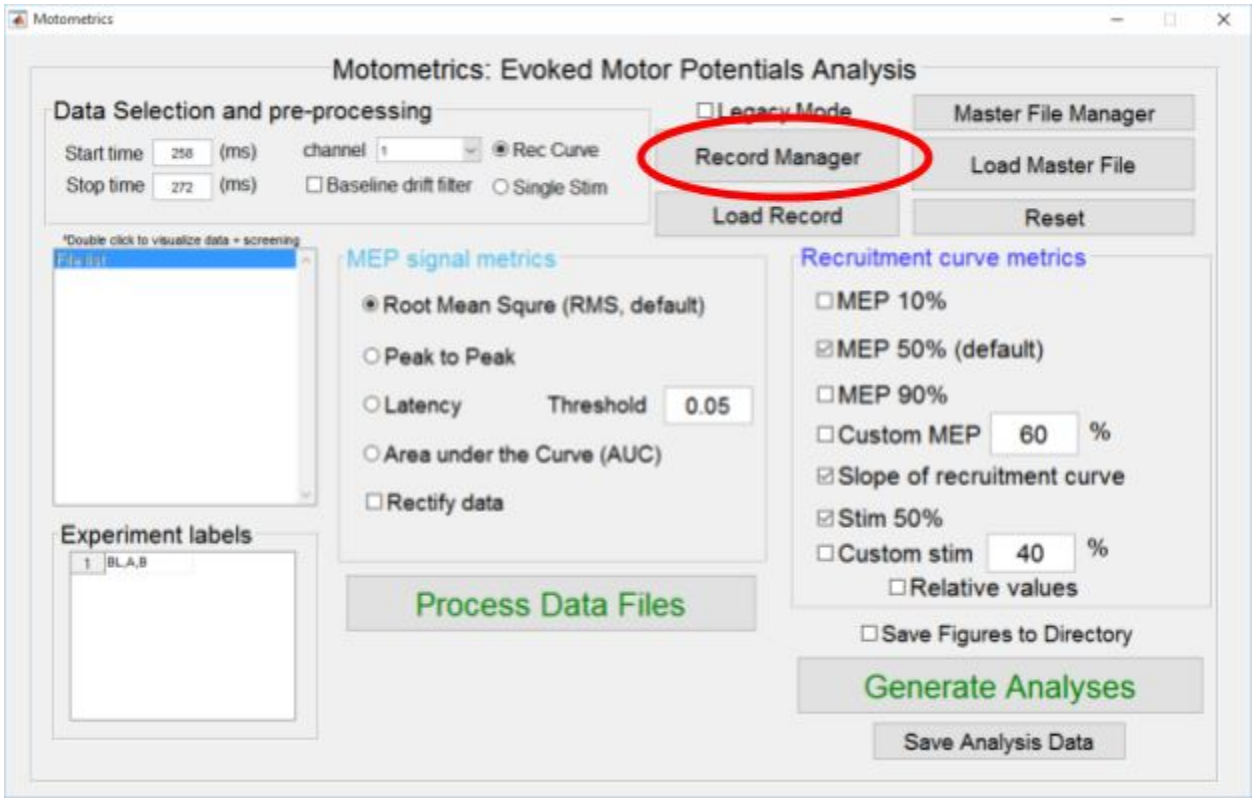
Continuous MEP recordings

In the event that all MEPs pertaining to a recruitment curve have been recorded continuously as a single long time series signal, it is possible to write a basic script to reorganize and cut the single signal into the required format described above.

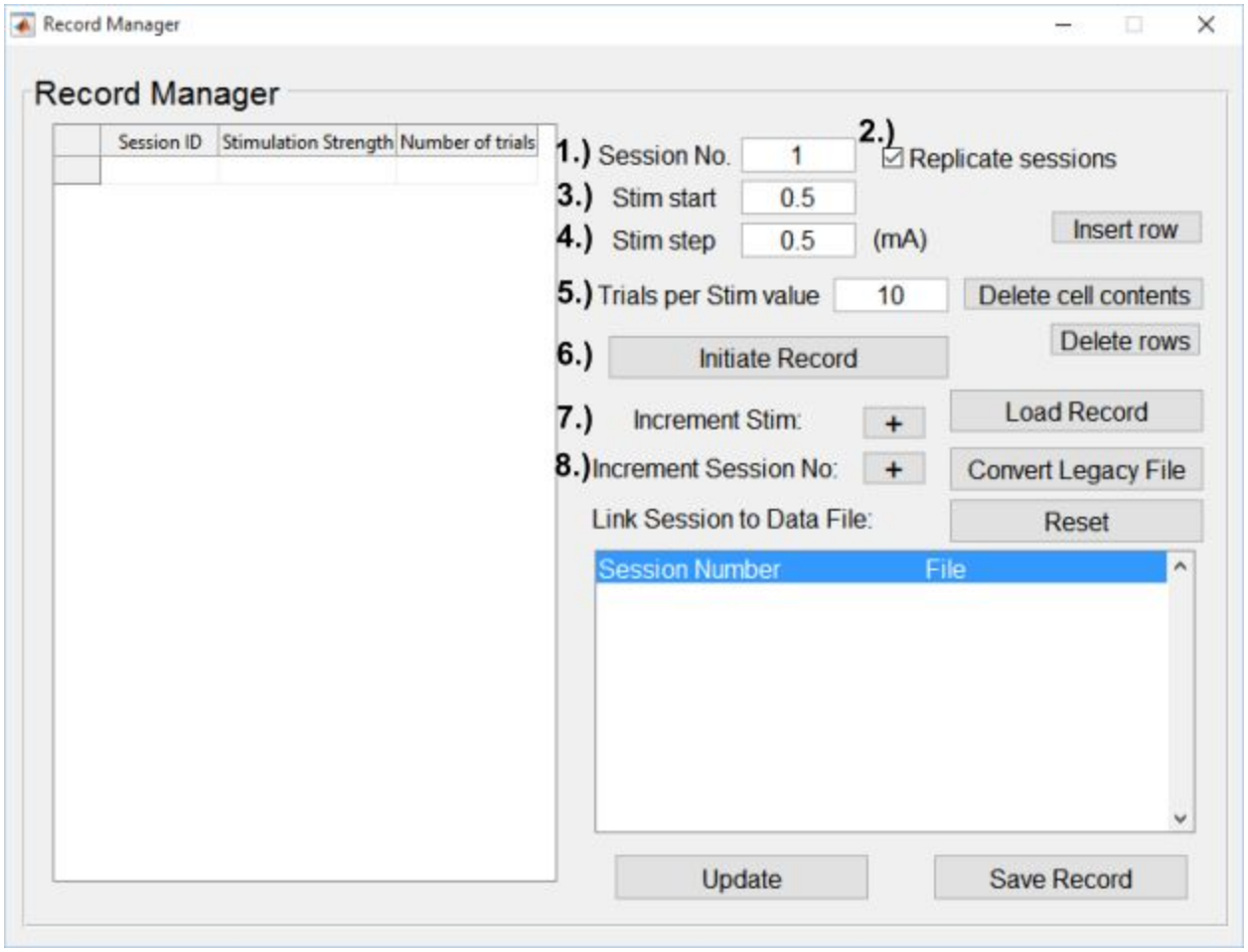
Scripts for converting data from multiple electrophysiology systems to a Motormetrics compatible format have been tested. Scripts for reorganizing a single long recording of all MEPs into a 3D matrix format have also been tested.
If you encounter issues while trying to write your own scripts for conditioning the data, please email shr3006@med.cornell.edu with your issue, as well as a small sample of your original matlab datafile.
NOTE: Please use the subject heading "Motometrics: <issue description>" while emailing. You may not receive a response otherwise.

Annotating data

Once MEP datafiles have been conditioned to work with Motometrics, the data must next be annotated before we can fit and analyze recruitment curves. In order to do this, the Motometrics.m file is opened and run in Matlab. The following Motometrics UI then appears.



To begin annotation, click the “Record Manager” button circled above. The Record Manager UI shown below will now open to allow annotation of experiments.

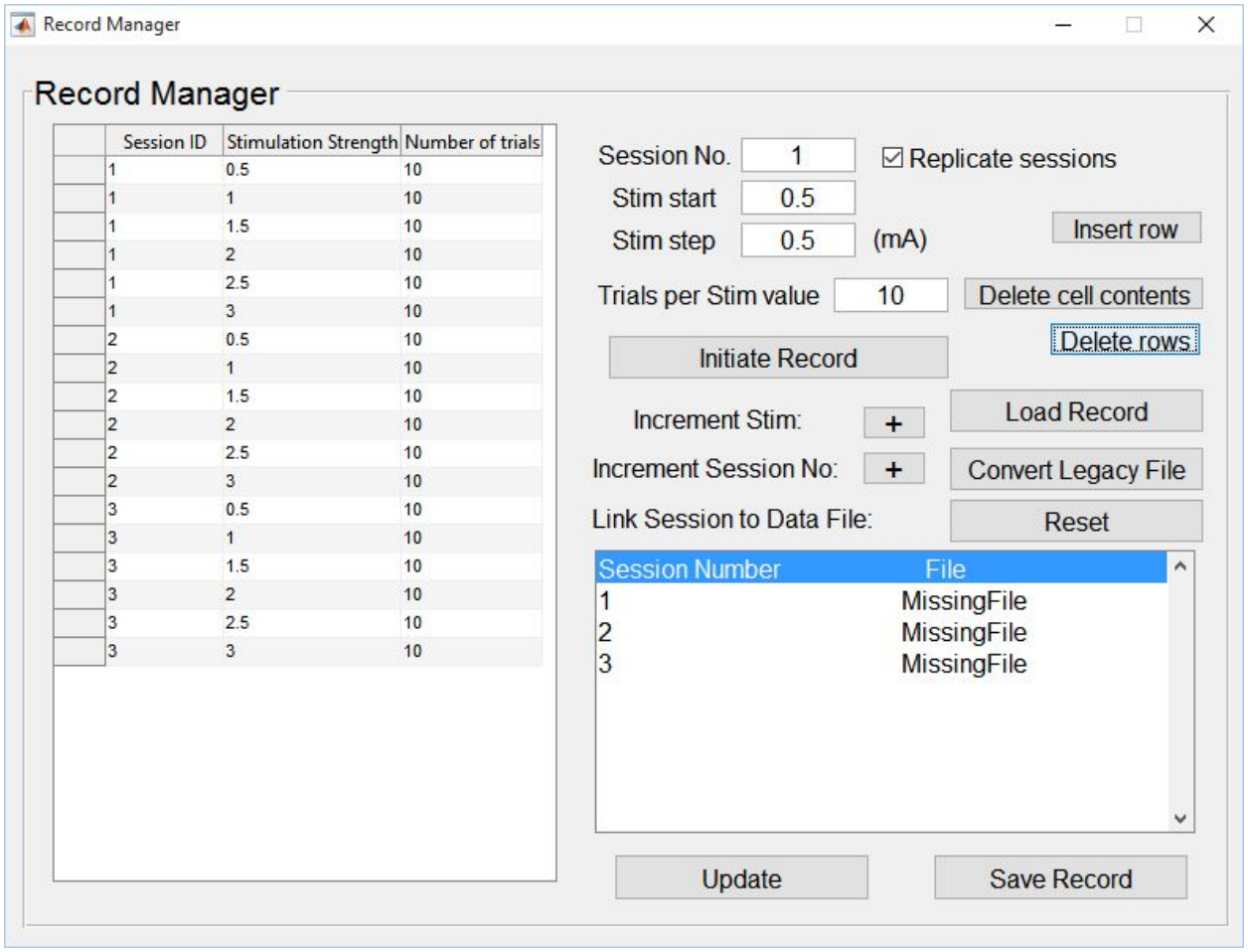


Initial Steps for using Record Manager:

1.) Enter suitable session no./ID in the first field, to differentiate between different recruitment curves sessions.
2.) Tick the checkbox “Replicate sessions” if each recruitment curve session is identical.
3.) Select the lowest stimulation intensity used during the recruitment curve session.
4.) Enter the incremental steps of stimulation intensity to automatically be applied.
5.) Enter number of trials taken per step.
6.) Click “Initiate Record” to begin.
7.) Click “Increment stim” to automatically increment stim by the value entered in step 4 within a session.
8.) Click “Increment Session No.” to begin annotating the next recruitment curve session. If the “Replicate Session” checkbox in Step 2 is checked, then the previous sessions annotation will be completely copied over to the new session as well.

NOTE: The steps listed above helps speed up annotation by automatically entering/duplicating data, but each cell in the table on the left of the Fig, is also directly editable. One can select multiple elements (eg. session ID) and edit them simultaneously. One can also edit the table of annotation by clicking on “Insert Row”, “Delete Cell Contents” and, “Delete Rows”.

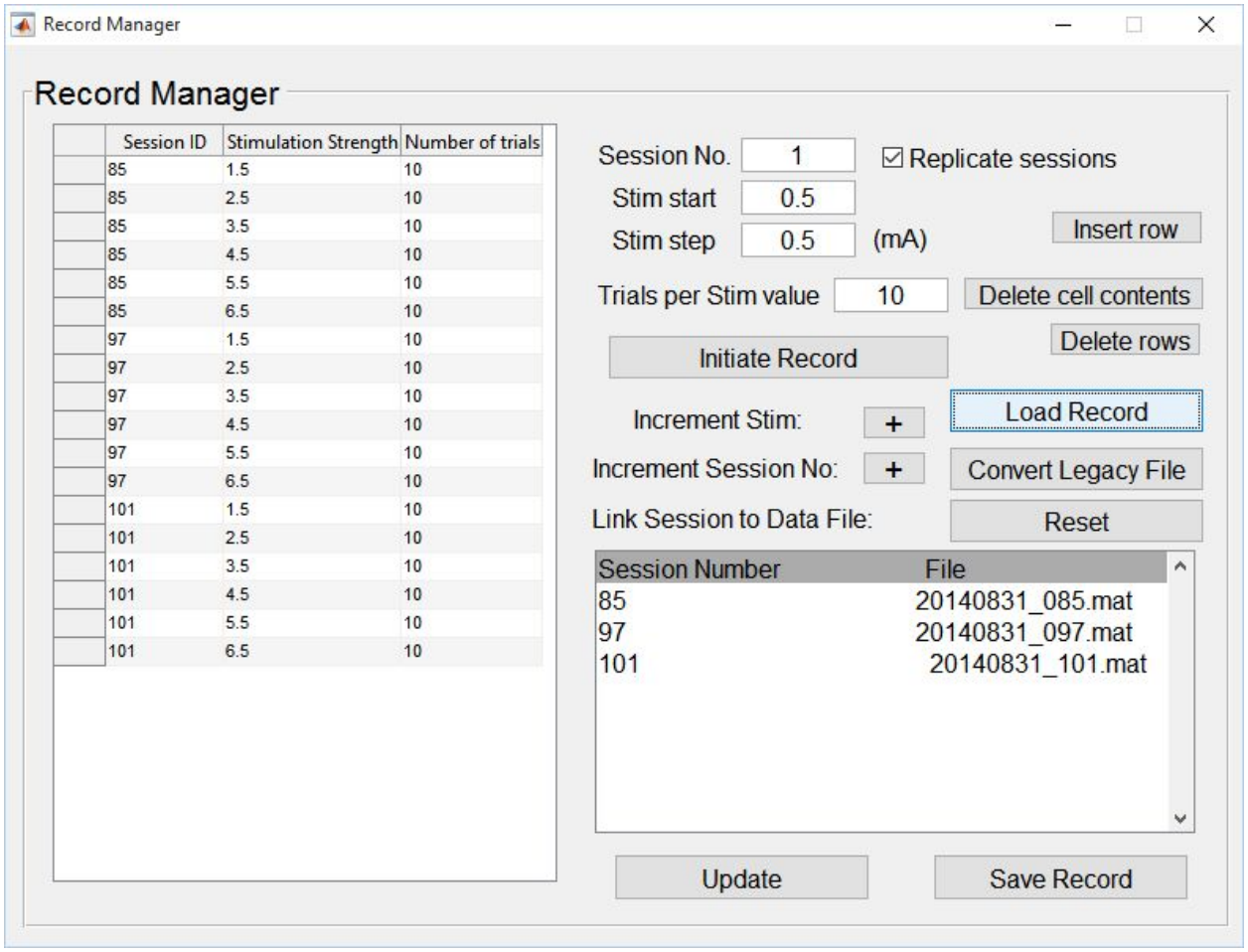
After entering the annotation information, the Record Manager UI should look something like below depending on how many sessions are included. In the figure below we have annotated 3 sessions, with stimulation intensities ranging from 0.5 to 3, with 10 trials each.



Now to complete the annotation and save this record file, we must link the conditioned MEP data (Recruitment curve session files) to this record. Notice the text box on the bottom right, with two columns: Session Number and File. Currently under the ‘File’ column, the text “MissingFile” indicates that no MEP data files have been linked to this record.

By double clicking each row, corresponding to a session number/ID, we get a file browser window that lets us select the corresponding conditioned MEP datafile. Once all sessions have been linked to their corresponding datafiles, click the “Update” button and then “Save Record”. Now you have created a record file ready for analysis. A real world case is shown in Fig below.

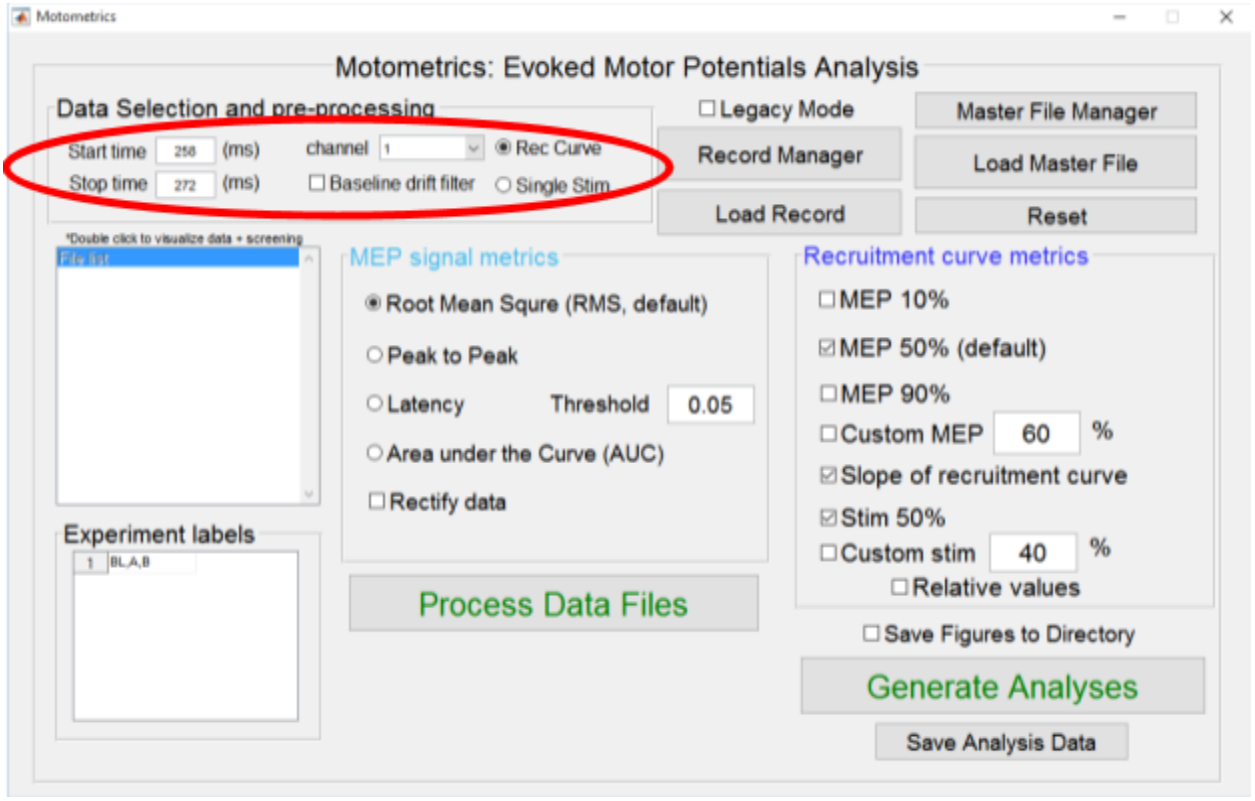
VERY IMPORTANT NOTE!!!! For generating and comparing recruitment curve sessions, we ALWAYS assume the first session number/session ID is the baseline condition (eg. MEPs recorded without therapy OR without injury etc.). All fitted curves are normalized by baseline.



Analyzing annotated data with Motometrics

Set pre-processing parameters and settings

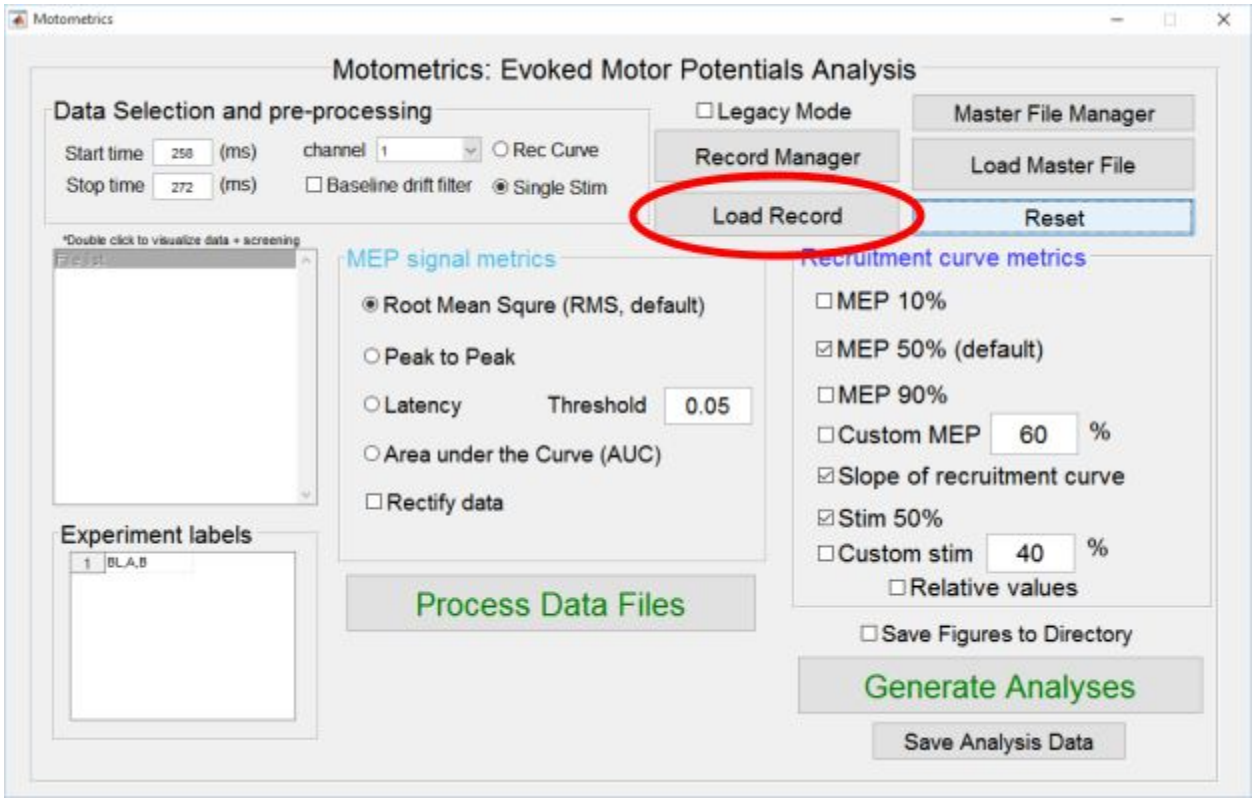
Currently, it is required for the user to specify the signal window during which the MEP occurs. This is entered as the start and stop time as shown in the figure below. The start time is usually specified just after stimulus ends, and the stop time is usually a few milliseconds later (10-15ms).



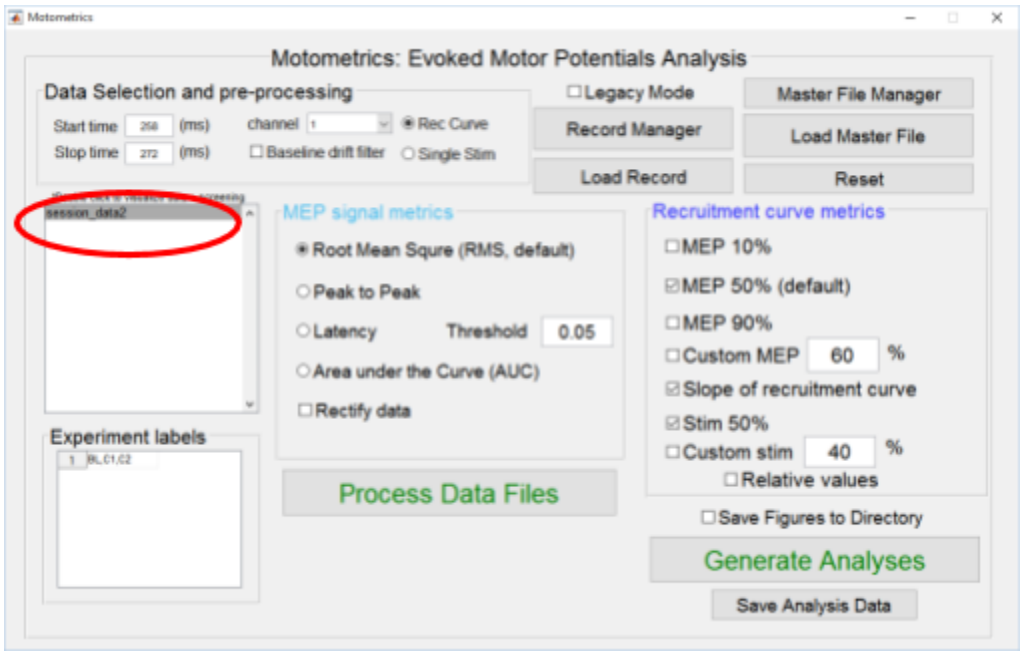
One can also specify which channel to process for MEPs, where each channel generally specifies a different EMG electrode or muscle. Optionally, a Baseline drift filter may also be used to correct signal drifts and also remove low frequency artifacts. There is also an option for switching between recruitment curve type data and just MEP comparison type data. For MEP level comparisons, the data is assumed to have just a single stimulation intensity (and multiple trials) for each session ID.

Analyzing a record file

To compare recruitment curve sessions, one can load a recruitment curve session file by clicking the “Load Record” button as illustrated below.



Clicking on the “Load Record” button will bring up a file browser window for selecting the desired record file (which was created during the annotation process as described previously). Once the desired record file is selected, one can either process the data and generate analyses, OR one can inspect the data. It is always recommended to inspect data before proceeding with analyses. To adjust/inspect data, double click on the loaded record as indicated below.



This will bring up the following pop-up window from which adjustments to data can be made.