**Chapter\_3\_Scripts\Step1\_TimeToPeak folder README**

This document describes the contents of the folder named Step1\_TimeToPeak, and the steps involved in completing the time-to-peak analysis.

**Dependencies**

* CED Spike 2 v8.10
* Microsoft Excel

**Contents**

* \_README.docx. This document.
* aa\_cmep6\_032713.s2rx. Spike 2 resource file for the example data file aa\_cmep6\_032713.smrx.
* aa\_cmep6\_032713.smrx. Example Spike 2 data file for testing the steps described below.
* S1\_ClearAll.s2s. Spike 2 script for clearing all channel processing and resetting time views which contain EMG data.
* S1\_Overdraw.s2s. Spike 2 script to overdraw waveforms aligned at the stimulus artefact, which must be marked into the channel “32 Memory”.
* S1\_Rect.s2s. Spike 2 script which adds rectification channel process to waveform channels 2 and 3.
* S1\_StimMeas.s2s. Spike 2 script for marking stimulus artefacts and taking measurements of response parameters.
* S2\_Macros\_TimeToPeak.xlsm. Microsoft Excel macro-enabled workbook which contains Macros for sorting data, displaying results, and doing preliminary individual and group time-to-peak analysis.
* S2\_Results\_Template.xlsx. Microsoft Excel workbook which is a template for how results must be laid out for the macros in S2\_Macros\_TimeToPeak.xlsm to work properly.
* S3\_Curlat.s2s. Spike 2 script for placing cursors on results views generated from averages.
* S3\_WavfmAvg.s2s. Spike 2 script for generating average traces for one individual when stimulus artefacts are marked in the channel “32 Memory”.
* S4\_Grandavwav.s2s. Spike 2 script for generating a grand average of traces from multiple individuals once they have been saved as .srf files.

***Step 1*** **- Mark stimulus artefacts and take latency measurements in Spike 2**

In the data files provided, the stimulus artefacts are marked in the marker channel named "32 Memory". However, you may wish to add the stimulus artefacts yourself. This section will therefore take you through the process as though the stimulus artefact has not yet been marked.

1. Open the example datafile (this file is "aa\_cmep6\_032713.smrx") into Spike 2. You can use S1\_ClearAll.s2s to clear all channel processing and reset the view.
2. Run S1\_Overdraw.s2s if you want waveforms to be overdrawn whilst conducting the analysis, and S1\_Rect.s2s if you want data to be rectified.
3. Run S1\_StimMeas.s2s and set the parameters. Input the required parameters (select “32 Memory if you have already marked stimulus artefacts into the marker channel). Unless you change it, data will be rectified so you will use "peak" rather than "trough". The default values are set to values which have been found to be useful for identifying stimulus artefacts. Click "OK".
4. Use the "Search Left" and "Search Right" buttons or the keyboard shortcut Ctrl+Shift+← or Ctrl+Shift+→ to cursor search for the artefact. "Add Marker" inserts a marker into memory channel.
5. Use "Params" to change the Cursor(0) search parameters if required. You may need to adjust the parameters or place the "Stim" cursor manually if you cannot identify artefacts automatically.

Note: you may wish to mark all of the stimulus artefacts first, click “Print Results”, which will save the markers in “32 Memory”, THEN go back and “Take measurements” of the response features because once the marker channel exists, the traces will be overdrawn when “Channel for Stimulus” in the parameters is set to a marker channel. There should be 10 stimulus artefacts in each data file (5 for Mwave data).

1. Once the stimuli are marked into “32 Memory”, You can run the script again or change the “Channel for Stimulus” in “Params” to “32 Memory”, then use the “Search Left” and “Search Right” buttons or the keyboard shortcut Alt+Shift+← or Alt+Shift+→ to iterate between stimuli.
2. If you need, adjust the cursors which mark response features. When satisfied, click "Take measurements" to add these to the output file.
3. Once you have taken all the measurements you require, click "Print results" to print the results to your output .txt file. IMPORTANT: check the .txt file for duplicate measurements and remove if they exist.
4. With the results window .txt file selected, press Ctrl+A to select all of the text and then paste it into the cells indicated in a copy of the excel template named “S2\_Results\_Template.xlsx”. Name the copy after the condition. You can include less than, but not more than 10 results for each subject and muscle.
5. The scripts called S1\_ClearAll.s2s, S1\_Overdraw.s2s, and S1\_Rect.s2s may be useful for exploring the data during this stage.

***Step 2 – Preliminary individual and group analysis***

1. Once the time-to-peak data from Spike 2 has been copied into Excel workbooks for each condition as shown in S2\_Results\_Template.xlsx (see Step 1, points 9 and 10), you can run Macros to organise the data for exporting to Matlab and R for the time-frequency and statistical analyses. Start by opening the file S2\_Macros\_TimeToPeak.xlsm, and an .xslx file into which you have copied the time-to-peak data into based on the template file.
2. Ensure that macros are enabled and both S2\_Macros\_TimeToPeak.xlsm and the Excel book containing your results are open.
3. S2\_Marcros.xlsm contains a module called TimeToPeak which contains 4 macros. If you have copied your data in the required format, Macros 1-3 will sort the results, and generate plots of individual and group data, and perform some statistics. You should be able to run each one in sequence by pressing Ctrl+Q, then Ctrl+W, and then Ctrl+E.

NOTE: if you are also sorting the data to input these times for the Matlab frequency analysis or want to format data for exporting all the data to a single .txt file, you can also use Macro 4. This can be run after Macro 3 by pressing Ctrl+R.

Information about the macros in the TimeToPeak module can be found below or in comments in the macro scripts.

M1\_SortResults()

Keyboard Shortcut: Ctrl+Q

Macro 1, for copying time-to-peak results for individual subjects into single new worksheet. Copies all data from first 10 workbooks and transposes it into sheet 11, and names this sheet All\_results.

M2\_P1Only()

Keyboard Shortcut: Ctrl+W

Macro 2, for deleting all data except the time-to-peak (the parameter called P1) so that preliminary bar charts and stats can be generated.

M3\_BarCharts()

Keyboard Shortcut: Ctrl+E

Macro 3 for generating bar charts for time-to-peak analysis for preliminary individual and group analysis.

M4\_SortForExport()

Keyboard Shortcut: Ctrl+R

Macro 4, for sorting time-to-peak results for export to Matlab/R. M1\_SortResults must be run first. Adds a worksheet named ForExport containing data from all subjects in one table formatted for Matlab.

***Step 3 – Generate average waveform traces for individuals***

1. Open Spike 2 and add S3\_WavfmAvg.s2s to the script bar.
2. In windows explorer, sort the folder containing the the .smrx/.smr datafiles for the condition you are interested in (e.g., \Data\EMG\_Data\_smrx\CMEP\_CYCLE\_6) by type.
3. In windows explorer, select the .smrx/.smr files and then drag and drop into Spike 2.
4. Click Window > Cascade. They will now be in order with the last file you clicked to select them on the top.
5. Making sure the directory containing the data files contains a subdirectory called “Average”, click on the title bar of the first file, and then click S3\_WavfmAvg.s2s script bar.
6. If you press Ctrl+Tab you can now cycle through each one and run S3\_WavfmAvg.s2s on each one. If you want to automatically save the files, you must create a folder called “Average” in the same directory as the .smrx file. The generated results files can be found in corresponding folders, e.g. \Data\Results\_Data\_Average\_srf\ CMEP\_CYCLE\_6\.

***Step 4 – Generate Grand Average waveform traces***

1. Open Spike 2 and add S4\_Grandavwav.s2s to the script bar.
2. In windows explorer, sort the folder containing the the .srf datafiles for the condition you are interested in (e.g., Data\Results\_Data\_Average\_srf\CMEP\_CYCLE\_6) by type.
3. In windows explorer, select the .srf files and then drag and drop into Spike 2.
4. Click Window > Cascade. They will now be in order with the last file you clicked to select them on the top.
5. Click on the title bar of the first file, and then click S4\_Grandavwav.s2s in the script bar.
6. You can now cycle through adding them to the grand average one at a time by pressing Ctrl+Tab and clicking “Add”. When you have added each one (be careful to only add each one once), you can save it using the condition as the filename. Be careful not to include the grand averages themselves as they are also provided in the corresponding folder corresponding folders, e.g. \Data\Results\_Data\_Average\_srf\ CMEP\_CYCLE\_6\.