



dopOSCCI_m2 Manual

A Guide to using the dopOSCCI Functional
Transcranial Doppler Summary Suite

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Introduction

We have developed a functional Transcranial Doppler summary software package based on the methods developed by Deppe, Knecht, Henningsen, and Ringelstein (1997). 'dopOSCCI' is an amalgamation of 'doppler' and 'OSCCI', the name of our research group, the Oxford Study of Children's Communication Impairments. The software has been developed in order to overcome some difficulties we had with establishing trial event markers as well as the repetitive process of single file data processing.

dopOSCCI processes multiple raw .TX and .TW files from the Multi-dop system and now supports .EXP files from the Doppler Box system. It searches for these within a specified folder, performs raw data processing (down-sampling, heart rate correction, and normalisation), calculates a series of summary statistics for sets of epochs which are saved into a tab-delimited file (easily accessed with SPSS or Excel), and also creates a selectable set of figures which can also be saved for later inspection. A series of additional features also allows for manual epoch screening, group summaries, behavioural epoch selection (summaries by experimental conditions or behavioural performance), and session combination (combining independent raw Doppler files). We have found that dopOSCCI is a useful tool for quickly and easily exploring and summarising Doppler data.

This manual provides an overview of the graphical user interface (gui) in Matlab as well as the data summaries which are created.

If you do find the software helpful and include it in your publications, please cite the dopOSCCI article in the Journal of Neuroscience Methods (Badcock, Holt, Holden, & Bishop, 2012)

Acknowledgments

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Installation

Copy the dopOSCCI folder onto the C drive or in any alternative desired location. This manual will however assume that you have placed it at C:\dopOSCCI\.

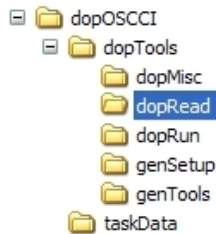


Figure 1: Directory Paths

Set Matlab path

To do this open Matlab, and then select:

- File
- Set path
- Add with Subfolders

Browse the C drive for the dopOSCCI folder (C:\dopOSCCI) and click OK and save. You should only have to do this the first time that you use dopOSCCI if you have sufficient user privileges (see [Administrator rights, p.64](#)).

It is critical that all the dopOSCCI functions are available on the Matlab path – a very common source of errors is simply that Matlab is unaware of the specific function that is being accessed. The error may be in the form:

??? Undefined function or variable 'XXXX'

??? Undefined function or method 'XXXX' for input arguments of type 'double'

Running dopOSCCI in Matlab

In the Matlab command window type:

```
>> dopOSCCI
```

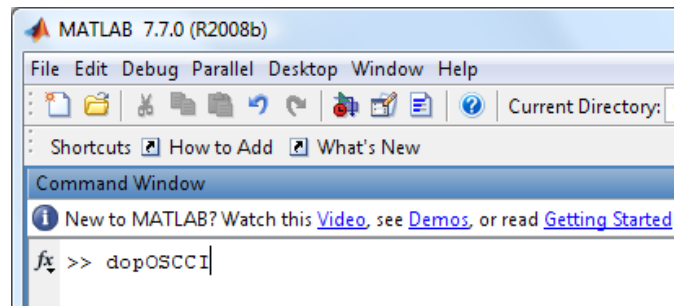


Figure 2: Command Window in Matlab

This will open the dopOSCCI graphical user interface (gui). It is useful to arrange the gui so as you can see the Matlab command window.

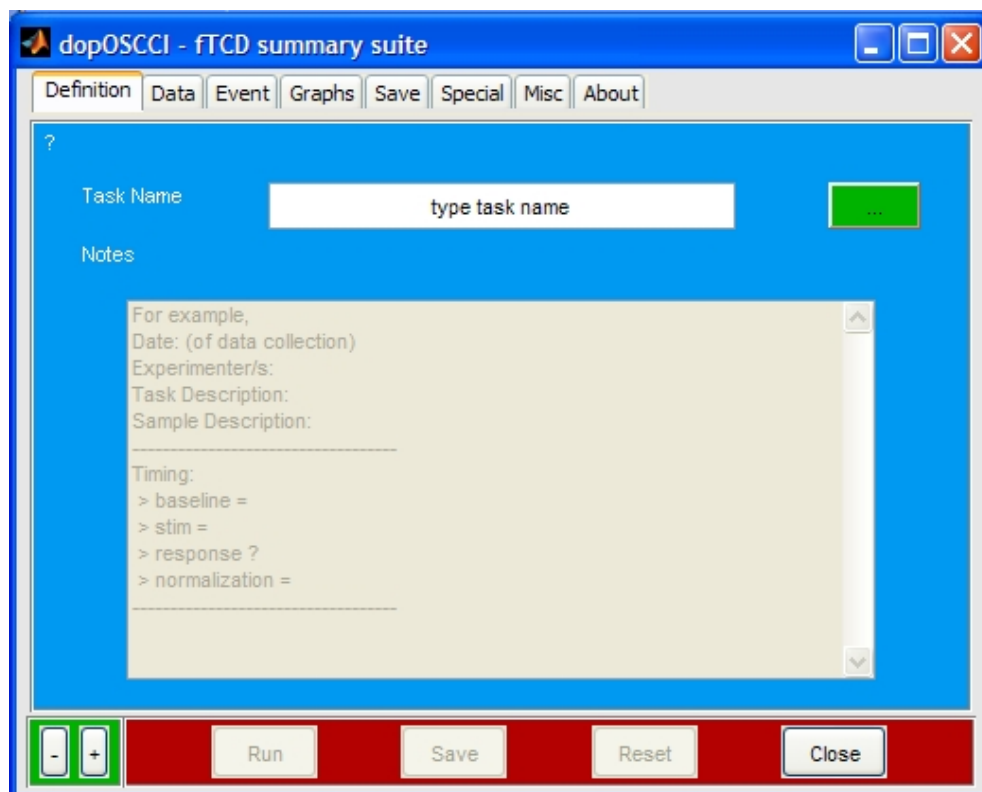


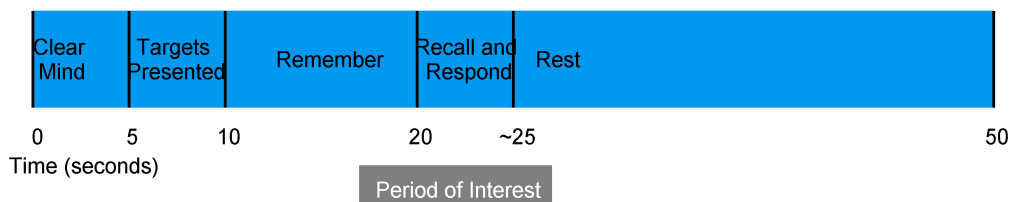
Figure 3: The gui; Definition Tab waiting for definition name

dopOSCCI Demo

In order to demonstrate the various functions of dopOSCCI, this manual will refer to some sample data, collected from a task entitled dopOSCCIdemo. For speed and ease of demonstration this is a very short task consisting of only 12 trials and we have only included 8 raw data files. The raw data and associated files for dopOSCCIdemo can be downloaded with dopOSCCI and could be saved in your C drive. This would allow you to work through the examples in the manual for yourself and should give you a good idea of how dopOSCCI works.

dopOSCCI Demo 1: Introducing the task

For this visual short term memory task participants were shown a blank screen and were asked to 'Clear Mind' for 5 seconds. A visual display with spatially variable targets was then presented for a further 5 seconds before being replaced by a blank screen. Participants were instructed to remember the location of the target. They were then shown a blank screen for 10 seconds, during which they were free to non-verbally retain the location of the targets. The visual display then reappeared (without targets) and participants were asked to indicate on a touch screen the original location of the targets. The time it took different participants to respond varied between about 3 and 10 seconds. A 25 second rest period followed before the next trial.



Introducing the gui

The gui consists of 8 function tabs ([Tab 1: Definition, p.10](#); [Tab 2: Data, p.11](#); [Tab 3: Event, p.16](#); [Tab 4: Graphs, p.23](#); [Tab 5: Save, p. 25](#); [Tab 6: Special, p.39](#); [Tab 7: Misc, p.48](#); [Tab 8: About, p.50](#)). This manual will explain how to use these tabs to define the parameters for your Doppler summary. Initially these parameters will all be set to default values. Once these parameters are changed to fit the specific requirements of your task, they will be saved under a given [Task Name](#) and be available to use each time you open dopOSCCI.

Each tab has a white question mark in the top-left corner. Holding the mouse over this should provide an overview of the tab's functions. A number of the interaction features also provide tips about what a particular variable is, so hovering around with the mouse can be helpful.

The standard set of buttons includes [Font Adjustment](#), [Run](#), [Save](#), [Reset](#) and [Close](#). These appear at the bottom of each tab of the gui.

Font Adjustment

The dopOSCCI gui can be resized as a regular window by clicking and dragging the edge or corner of the window. In doing so, it may be desirable to adjust the font size. This can be achieved by clicking the '+' and '-' buttons located in the bottom left of the gui.

Run

The **Run** button initiates the dopOSCCI summary based on the parameters set in the gui.

Save

Changes made to the dopOSCCI parameters will be saved as variables during your dopOSCCI session and then will be automatically saved to the definition file when the program is run. However, if you want to save changes without running dopOSCCI, this can be done by clicking the **Save** button.

Reset

The **Reset** button clears gui settings, returning it to its initial state, waiting for [Task Name](#) input.

Close

The **Close** button closes the dopOSCCI gui.

Tab 1: Definition

Task Name

In the **Task Name** field enter the name of the experimental task from which you want to process data. Use the **Notes** box below to enter any details of the task that you may find helpful when returning to look at the data at a later stage. For example, you may want to make a note of when the data was collected, by whom, and from what sample. It is also beneficial to record the timings of the specific experimental task, for example the length of the baseline, the timing of the trial onset and response period, as well as the duration of the recovery period. Avoid leaving a blank line within the notes section, as anything after this will not be saved and re-presented when reloaded. You only need to complete the **Task Name** and **Notes** fields the first time you begin to process data from a particular task. In subsequent dopOSCCI sessions the chosen task name, together with the notes and all other associated changes to the default settings will be stored under your chosen task name within the **taskData** folder in dopOSCCI (C:\dopOSCCI\taskData\). This, and all other saved tasks, can then be accessed in future by clicking on the **Browse** button ('...') to the right of the **Task Name** field. This will open the **taskData** folder and allow you to select your task name. Click **Open** and dopOSCCI will automatically update the default settings across all domains to those you previously specified for that task. Alternatively you can manually type in the task name and press enter.

dopOSCCI Demo 2: Loading the demo

To explore the dopOSCCIdemo data for yourself type dopOSCCIdemo into the Task Name field. The gui will update with the saved settings for this task. As you can see, the Notes field contains details of the experiment, outlining the timings of the task as explained above. You only need to type the task name in the first time. After that simply click on the Browse ('...') button to the right of the Task Name field in the gui. This will open the taskData folder in which you will find the dopOSCCIdemo file. Open this folder and the saved settings for this task will again be updated on the gui.

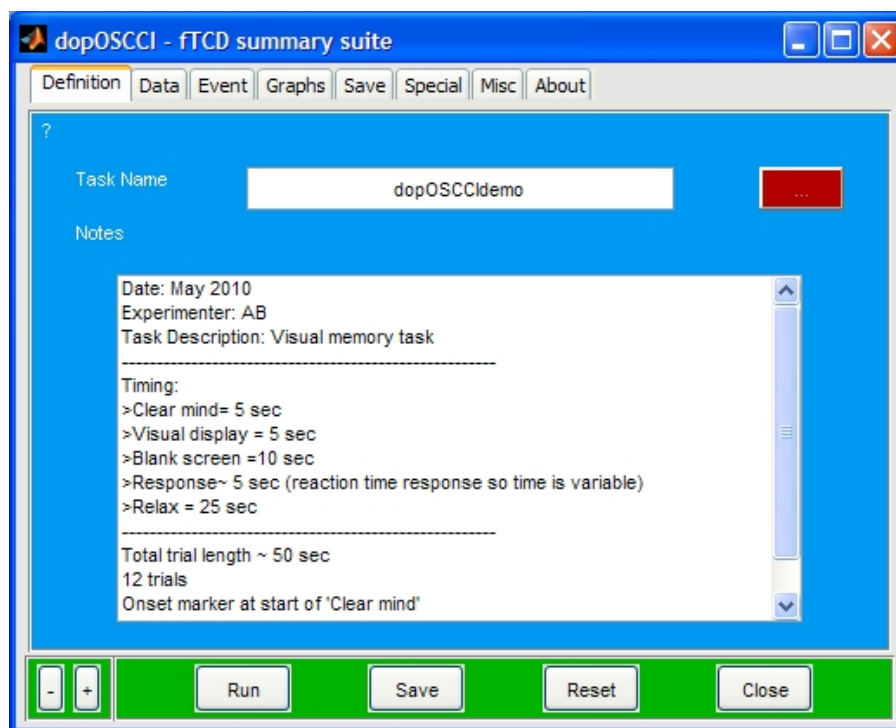


Figure 4: The Definition Tab of the gui

Tab 2: Data

Data Directory

Before specifying a **Data Directory** it is important that all your raw data files are in a suitable folder together. The analogue Doppler recording produces four different raw data files (.TF, .TS, .TW, .TX) and digital recordings produce .EXP files. dopOSCCI searches for the .TX files (general text information in ASCII format) with matching .TW files (binary data of the Doppler signal which is saved in the standard 16 bit integer format) or .EXP files.

For analogue files, the number at the end of the file extension indicates the recording session for a particular NLA number. For example, NLA999.TX0 is the first recording, then NLA999.TX1, NLA999.TX2, and so on. It is important to ensure that all of the raw Doppler files from your experiment are together within the same folder, not divided into separate subfolders for each participant, before you begin the data processing¹.

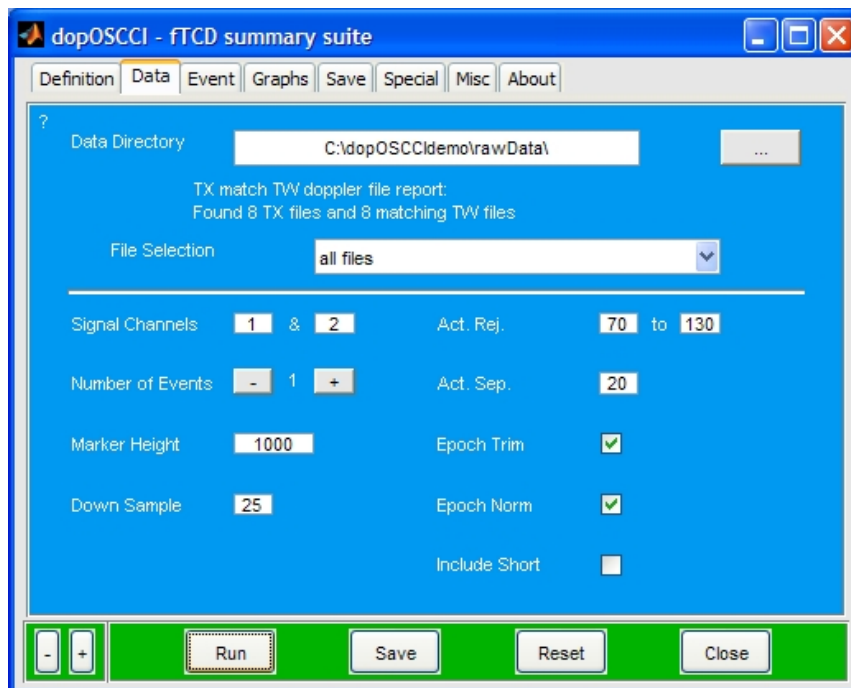


Figure 5: The Data Tab of the gui

To set your **Data Directory**, use the **Browse** button ('...') to locate the folder containing all of your raw data. Click **OK** and dopOSCCI will automatically complete the **Data Directory** field with the location of your raw data file. The **Data Directory** can also be typed but we recommend using the **Browse** button (to avoid frustration that can easily arise from typos!). Once a data directory has been selected, the number of .TX or .EXP files that have been found in that folder will be displayed below.

¹ It is possible to summarise an individual participant if the data are housed in separate folders but this can also be done using the Specific File selection (see p. 12), even when all the data are in the same folder.

dopOSCCI Demo 3: Locating the raw data

Browse ('...') in the C drive for a folder called dopOSCCIdemo and click on the folder called RawData. This will complete the Data Directory field with 'C:\dopOSCCIdemo\rawData\'. There are 8 .TX files and 8 matching .TW files contained in this folder.

File Selection

This function allows you to specify a particular raw data file for processing. This is particularly useful for looking at problematic individual data. If the **Data Directory** is left empty, 'no list' is displayed. However, as soon as you specify a data directory, a drop-down menu containing a list of all the raw data files contained within your specified data directory will be available for file selection. The first option on the list (and the default setting) is 'all files'. This means no specific file has been selected and therefore all the raw data files within the specified data directory will be processed. If instead you wish to process a specific file, simply click on the file name from the drop down list. Please note that if you wish to process a selection (i.e. more than one, but not all) of your raw data files at once, the **Group File** function can be used ([p.42](#)). Please note that the Group File and **Session File** functions do not operate for individual file selection.

General Data handling

The **Data tab** also allows for adjustment of general parameters.

Signal Channels

Enter the channel numbers of the left and right inputs. This is set in the Multi-dop software and is likely to be 1 and 2 for .TX files and 3 and 4 for .EXP files.

Marker Height

Event markers are detected by searching for event channel values above the event marker height value. Generally this variable should be above zero and the exact number will vary dependent upon Doppler hardware settings.

Number of Events

This is the number of event markers to be used for the Doppler summary. One is standard but additional markers can be considered for more complex summaries (see **Event Type & Event Match**). The number of events is simply increased or decreased using the '+' and '-' buttons with 1 event being the minimum possible. As the number of events is increased, additional **Event tabs** will be created along the top of the gui, after the standard tabs, labelled, for example, Event2. This function is also available on [Tab 3: Event](#).

Down sample

This is the sampling rate in Hertz (the number of data points per second) you wish to use in the data processing. The raw Doppler data collection is set at 100Hz; i.e. 100 data points per second. This temporal resolution is excessive when examining the metabolic flow of blood which occurs over the course of 5 to 7 seconds. From a data handling point of view, the temporal resolution can be reduced. Entering 25 will result in samples of 0.04 seconds in length.

Activation Rejection

Use this function to define the acceptable blood flow velocity limits. In instances where the data may be noisy, with large variations in blood flow velocity, it may be beneficial to exclude epochs with

unusual levels of activation, in either of the extremes. Such anomalies may reflect data recording artefacts caused by problematic probe contact. The default values are 70 and 130, whereby any epochs with activation less than 70% or greater than 130% of the average blood flow velocity will be excluded from the analysis. The **Normed** graphs ([p.56](#)), which are created during analysis, can be examined to determine whether appropriate limits for your data have been set.

dopOSCCI Demo 4: Activation rejection and the normed graph

Select file NLA820 from the drop down file selection menu and on the Graphs Tab select to display the Normed graph. Click the run button at the bottom of the gui. A Normed graph will be created which depicts the left (blue) and right (red) Doppler velocity after normalisation. The 12 epochs in the task are outlined in yellow. The light blue lines indicate the activation rejection limits set to 70 and 130%. The data in this file is quite noisy. Note how the right activation crosses the lower limit in the 1st epoch, and both left and right activation cross the lower limit in the 4th epoch, and the right activation crosses both limits in the 7th epoch.

After viewing the graph, make a right arrow button press for the summary to continue. Follow the link to the output folder and open file BNLA820 in the Notes folder. This is a record of the Matlab command window during processing. Scroll down to the section where dopOSCCI was running 'dopEpochScreen'. The epochs excluded due to activation (act) are also recorded here.

The dopOSCCI gui will have closed itself at this point (reopen by running it from Matlab again). To avoid automatic closure, go to the Misc tab and uncheck the 'Close Gui' box under Admin Extras.

Activation Separation

Use this function to define the acceptable left-right blood flow velocity difference. In some instances, a single channel may drop out but may not drop enough to be outside the **Activation Rejection** limits. In this case, the left-right channel difference can be used to exclude the epoch from summary. This value reflects the percentage acceptable difference relative to normalized channels recording of 100% blood flow velocity. If this variable is set high > 50, it will not affect epoch selection.

dopOSCCI Demo 5: Activation Separation and the normed graph

The activation separation is set by default to 20%. This time select file NLA829 and run the summary to display a normed graph. Note that no activation crosses the activation rejection limits and whilst the left activation suddenly drops a few times relative to the right, the difference is not sufficient to cause that epoch to be rejected (the BNLA829 notes file under 'Running dopEpochScreen – act' shows all 12 epochs are accepted).

Run the summary again with 15% activation separation. Look in the notes file to see that with activation separation set lower at 15%, epochs 1, 3 and 7 are now rejected.

Epoch Trim

It is common to have additional noise (e.g., from participant movement) in the data recording prior to task onset, as well as after the task, before the recording is stopped. This noise, albeit small, will necessarily affect the raw data normalisation. We therefore recommend that the **Epoch Trim** checkbox is selected. dopOSCCI will then remove the raw data prior to the first event marker, and will similarly remove the raw data after the last event marker, relative to your specified lower and upper Epoch values respectively ([Tab 3: Event, p. 16](#)). For example, for epoch values of -12 and 40

seconds, data recorded prior to 12 seconds before the first event marker and 40 seconds after the final event marker will be excluded.

Epoch Trim will always cut away the excess pre and post raw data but will only affect the summary calculations when the **Epoch Norm** checkbox is not selected.

Epoch Norm

Select **Epoch Norm** checkbox to normalise data using an epoch by epoch method based upon the lower Epoch value. Unselected, the mean Doppler velocity will be set to 100 using a standard formula:

$$normalised = \frac{raw * 100}{mean(raw)}$$

In some of our recordings we have noticed that independent channel 'drift' occurs. That is, the average velocity in the left channel will remain relatively constant across the experiment whereas the right channel will reduce over time, e.g. start out higher than the left and end up lower. Under these circumstances normalising across the entire time period creates biases in the early versus late trials. Normalising data within epoch intervals reduces the impact of such drift.

With **Epoch Norm** selected, normalisation is conducted from the lower to the upper Epoch values for each trial. Any gaps between the n and $n+1$ epochs are normalised independently – these are not used in the analysis but are normalised in order to display in the **Normed graphs (p.56)**. In the event that the trial n upper Epoch value is greater than the $n+1$ lower Epoch value, normalisation is performed between the lower Epoch values for these trials.

Include Short

A short epoch occurs when an inadequate amount of recording is made before the first or after the last event marker. A short baseline could occur, for example, if the **Lower Baseline** is set to -10 seconds but data is only available from -8 seconds, e.g. because the recording was started late. Alternatively, a short epoch could occur, for example, if the **Upper Epoch** is set to 30 seconds but only 25 seconds are available because the recording was stopped early. In this situation the existing data will be extrapolated to fill in the blank time interval for all and individual trial summaries. By default, such trials will be excluded from the screened epoch summaries but included in the all epoch summaries. Select the **Include Short** checkbox to include reduced length epochs in the 'combined' screening summaries (see **Epoch Selection**). However, it is recommended that these are not included in the screened epoch summaries as they will not contain 'real' recorded data.

dopOSCCI Demo 6: Demonstrating Epoch Trim, Epoch Norm and Include short

Return the activation separation back to 20%. Repeat the summary for file NLA829, selecting to save both normed and epoch graphs. Note that on the normed graph the first epoch is short. The recording was started late so there is not a full 12 seconds before the first clearMind marker. As long as the 'include short' checkbox is not selected, this epoch would normally be rejected on the basis of length. The notes file for BNLA829 under 'Running dopEpochScreen – length' confirms that epoch 1 would be excluded from the summary.

The epoch graph is created regardless and shows how data is extrapolated to 'fill in' the missing data. (A separate window will open for each epoch; to view a particular graph, rearrange using the window bar. Clicking elsewhere will close all epoch graphs.) Look at the first epoch graph and note that the epoch is now complete – running from -12 to 40 seconds. Data that was missing in the normed graph has now been filled in with a mirror image of the data that comes after. If the 'include short' checkbox is ticked this extrapolated data will be taken into account in the summary.

Repeat the summary but this time with the epoch trim turned off. See how on the normed graph, the data now continues after the end of the 12th epoch. We recommend that this noisy data, collected after the end of the experiment, not be included in the normalisation procedure. This can be achieved by using the Epoch Trim or better still using the Epoch Norm function. Ensure both functions are selected again.

Tab 3: Event

The **Event** tab allows you to specify the timings of your task and the period you are interested in using to determine the laterality index.



Figure 6: The Event Tab of the gui

Event Name

This is the name of the **event marker** and is used for variable labeling within the dopOSCCI summary as well as when the data are saved and graphed. Leave no spaces between words when entering a name (although any spaces will be automatically removed).

Channel

Enter the channel number of the **event marker**. As with the signal channels, this is set in the Multi-dop software and is likely to be 3 (possibly 9 for .EXP files).

Epochs

Enter the number of epochs in your task in the Epochs field. dopOSCCI assumes that the final event marker correctly specifies the final epoch. From here, it locates the other event markers, working backwards until it has found the number specified in the epochs field. The reason for this is that we have sometimes found additional event markers at the start of some of our data files.

Separation

This is the minimum time between one event marker and the next and is used to correctly identify the event markers. As explained above, dopOSCCI finds the final event marker first and then looks for the previous event marker, ignoring any additional markers which appear before the specified

separation time. It continues in this way until it has found the number specified in the *Epochs* field or has exhausted all available markers. If the **separation** is too large, dopOSCCI will ignore some markers and not correctly locate all the trials (see *Normed*, p.56). If it is too small it is possible that some spurious markers will be incorrectly identified as 'true' event markers².

dopOSCCI Demo 7: Choosing a separation value

For the dopOSCCIdemo, the epochs varied in length as the participants took different amounts of time to respond. Not including this variable response time, one trial takes 45 seconds. The separation is therefore set to 48 seconds as it is unlikely anyone would complete their response in less than 3 seconds (participants were required to report the location of multiple targets). The separation time is effectively the minimum length of time a trial could possibly take. dopOSCCI counts back from the final event marker, ignoring any markers which occur less than 48 seconds before the previous one. It continues in this way until all 12 event markers are located.

To see how this works try selecting a specific file. Ensure the 'save normed graph' checkbox is selected on Tab 4 and run the summary using the default separation value of 48. Follow the link at the end of the summary to the graphs folder and open the normed graph. You should see how the pink and green markers are perfectly matched. Compare this graph with one produced using a separation of 60 seconds. When the separation is too great, dopOSCCI will miss out some of the correct event markers and not find all of the epochs.

Activation Window

The **activation window** is a duration in seconds that is used in calculating the laterality index. The window is centred on the sample with the maximum difference between left and right activation, within a specified time period in the epoch, known as the *Period of Interest* (POI, p. 18). An activation window of 2 seconds means that the activation difference will be averaged over a 2 second window, centred on the point with the maximum activation difference in the POI; i.e. one second either side of the sample with the maximum difference³.

Epoch

This dictates the time range that will appear on your graph as well as the amount of raw data output included. This information is also used in the raw data processing for *Epoch Trim* and *Epoch Norm* (see p.14). Note that the upper **epoch** value must be less than or equal to the *Separation* value.

Baseline

The **baseline** refers to the lower and upper time points between which the average blood flow velocity is calculated. This is then used as a reference velocity, against which activation is compared. That is to say the mean baseline activation is subtracted from all left and right activation outside of the baseline time period. The time points specified for the baseline are relative to the trial event marker (time 0 in *Figure 7: Epoch Schematic*). For example, -10 and 0 refers to a 10 second period prior to trial onset.

² Spurious markers can only be identified if they were erroneously inserted by the display program software – dopOSCCI will NOT spuriously insert markers!

³ This period will therefore be 2 seconds plus 1 sample; i.e., 2.04 seconds if the down-sample is set to 25 Hertz.

dopOSCCI Demo 8: Choosing epoch and baseline periods

For dopOSCCIdemo the Epoch is set from -12 seconds to 40 seconds. This allows us to explore activation differences throughout each stage of the experimental task, from baseline resting levels prior to the ClearMind event marker (at 0 seconds), through to seeing the visual display (at 5 seconds), rehearsing/memorising the location of the targets (from 10 to 20 seconds), and recalling them/making a response (from 20 to around 25). For the remaining 15 seconds of the epoch we should be able to see the activation levels gradually return to baseline as the participant is once again asked to rest. It is important to allow for a 5-7 second delay in blood flow change when deciding which time periods are of interest (see Kuschinsky, 1991). For example when choosing a suitable baseline for dopOSCCIdemo we do not want to include the part of the epoch where activation levels are still recovering from the response. The response finishes 25 seconds before the event marker (i.e. at -25 seconds). To allow time for recovery and for the subsequent delay in blood flow change, the baseline has been taken from -10 seconds, by which point activation should have returned to baseline levels.

Period of Interest

The **Period of Interest** (POI) refers to the lower and upper time points, between which the point of the maximum left-right activation difference will be taken as the latency for the Laterality Index calculation. In order to allow for the delay in the subsequent blood flow change, the POI would typically begin several seconds (approximately 5 -7) after the event that you are interested in. The POI values must be set within the limits defined in the epoch field.

dopOSCCI Demo 9: Laterality Index and the Overall graph

In dopOSCCIdemo we are interested in the laterality during the recall and response part of the task which occurred from 20 seconds onwards. To allow for the delay in blood flow we set the POI to between 25 and 35 seconds.

Select all files and choose to display the overall graph (ensure the separation is set back to 48 seconds). Run the summary to find the average laterality index for these 8 participants. The green box on the overall graph represents the POI with the peak difference in activation shown in pale blue. This maximum difference between left and right activation occurred 32 seconds after the ClearMind marker. The activation window is shown in yellow. The average difference in activation within this window is the Laterality Index (LI). The LI is shown in the grey box at the top right of the Difference graph below.

Make a button press for the summary to continue and follow the hyperlink to the save directory. Look in the dopOverallSummaryData file to see the saved statistics.

Epoch Schematic

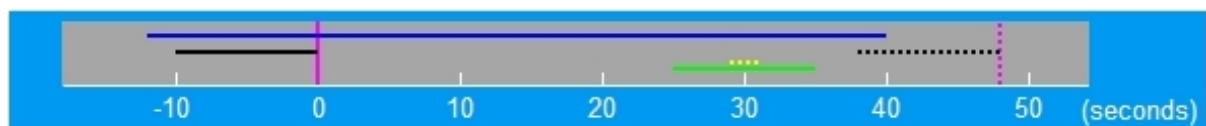


Figure 7: Epoch Schematic

Any changes made to the parameters outlined above will be automatically updated and represented on the **Figure 7: Epoch Schematic** at the bottom of the tab. This figure displays a hypothetical

timeline (in seconds) of a specified section of your experiment, for example one epoch. Pink lines represent **Event Markers**, the blue line shows the **Epoch** and is the period that will be displayed on a single graph, the black lines are the **Baseline** periods, and the green line indicates the **Period of Interest** (POI) for laterality. The **Activation Window** is displayed in yellow and is shown in the schematic as centred within the POI; however, its true location will depend upon where the point of maximum activation difference is in your data. The hypothetical nature of the figure should be emphasised, as the **Separation** variable sets the minimum separation between event markers. On some trials the separation between event markers may therefore be greater than the period indicated. On the **Epoch Schematic** the placement of the next trial **Baseline** and **Event Markers** is not therefore absolute and will vary with trial length, which may fluctuate if the timing of the experimental trials varies. For this reason they are represented by a dashed line on the schematic.

Event Type & Event Match

One event marker is the standard used for the Doppler summary and is used to specify variable details and timing for each epoch. However, additional markers can be used for more complex summaries. It can be useful to incorporate more than one event marker in a single summary, if, for example, independent markers were recorded for the baseline and participant response, especially if the participants start to respond at different times or take a variable amount of time to make their response.

If only one event is selected on **Tab 2: Data**, or at the top right of **Tab 3: Event**, the **Event Type** and **Event Match** fields are not active. However, as soon as the **Number of Events** field in either location is increased to two or more, additional Event tabs will appear along the top of the gui and the **Event Type** and **Event Match** fields become active. Changes to all the parameters described above in Tab 3: Event can then be made independently for the two events, allowing you to assign the events different names using the **Event Name** field, as well as assign **Channel** numbers and timings for the periods you are interested in. In addition the **Event Type** field becomes active and can now be specified.

Event Types can take one of three forms: **Base & POI**, **Base Only**, or **POI Only**. The standard setting is **Base & POI** where the **Baseline** and **Period of Interest** values are set relative to a single event marker. The **Base Only** or **POI Only** options allow for the Baseline and Period of Interest values to be set to independent markers. In these cases, the events must be matched. That is, a **POI Only** event type requires a corresponding **Base Only** match. Although possible to have multiple **POI Only** events set to a single **Base Only** event, this must be done carefully. If using the Epoch Norm ([p. 14](#)) setting, then normalization is completed for an extended epoch using the lower and upper epoch values of the **Base Only** and **POI Only** settings. Therefore, unless the multiple **POI Only** epochs are exactly the same, the normalization of the **Base Only** event will be normalized to the first **POI Only** event.

This matching also assumes that the **Base Only** event occurs before the **POI Only** event as this is conventionally the case.

An alternative use for the Event type and Event Match function would be to have more than one Base & POI channel for coding different conditions. Having said this, it is possible to separate conditions coded with the same event marker using the special **Behavioural File** function ([p. 44](#)).

dopOSCCI Demo 10: Additional events

In dopOSCCIdemo, participants began to respond 20 seconds after the ClearMind event marker. With just one event marker we would therefore be interested in a POI beginning around 25 seconds (allowing approximately 5 seconds for the delay in the subsequent blood flow change). However, participants' response times varied from 3 to 10 seconds so in reality some participants may not have shown any change in blood flow until 30 seconds. It would therefore be useful to use a second event marker to record the actual time of each participant's response. This would mean the timings for the POI for each participant would be specified relative to their own response and not simply a standard time after the beginning of the epoch.

In the **Number of Events** field use the + button to create an additional event marker. On the original Event Tab 3, name the first marker ClearMind, and assign it to Channel 3. On the newly created **Event2 Tab** name the new marker Response and assign it to Channel 4. We still want to use the original ClearMind onset marker to define the **Baseline** period but will no longer define the **Period of Interest** in relation to this marker so on the first **Event Tab** change the **Event Type** to **Base Only**.

We now wish to use the **Response Marker** to define the **Period of Interest**, so on the **Event2 Tab** change the Event Type and Event Match to **POI only**. Note that when **Base only** or **POI only** is selected, only the timings for these fields can be altered on each tab, i.e. the **POI** field is no longer active on the ClearMind Event tab and the **Baseline** field is not active on the Response Event tab.

On the **Event2 Tab** change the timings in the **POI field** to allow for the fact that they are now relative to the new Response marker, e.g. to - 5 to 5 seconds⁴. We still need to use the baseline measurements taken relative to the ClearMind marker to correct for the level of activity in the new response-dependent POI. We therefore need to use the **Event Match** field to match the **baseline** from **Event1** with the **POI** from **Event2** and vice versa. Use the drop down menu to select Response on the first Event tab and ClearMind on the second Event tab.

It is also worth changing the epoch time range for each event independently. The ClearMind event is being used to get our baseline. The baseline is set from -10 to 0 i.e. the 10 seconds before the ClearMind marker onset. We only really need epoch information from the few seconds surrounding this so change the epoch range to -12 and 2.

Similarly the Response event is only being used to get the POI, currently set between -5 and 5 seconds after the marker. We only need epoch information from the few seconds either side so change the epoch range to -10 and 10. See [Figure 8](#) for gui setup.

⁴ As dopOSCCIdemo involved multiple responses, there will be six response markers in every epoch (see multiple pink raw events on normed graph). dopOSCCI searches from the end of the file backwards so will mark the participant's final response in each epoch. Participants will have begun their response several seconds prior to this final marker so the POI begins before the final response marker to allow for this.

On Tab 2 select all files and on Tab 4 elect to save the normed and overall graphs. Run the summary and follow the link to the saved data and open the graphs folder. The pink raw markers on the lower normed graphs show there is indeed some variability within and between participants in the time they took to respond. The response markers are correctly matched to the final responses made by each participant in each epoch. View the overall graph. The left graph shows the baseline and the right graph the chosen POI and peak difference in activation. In contrast to the overall graph in demo 9, there is a gap between the graphs representing the variable time between the ClearMind marker and the response.



Figure 8: dopOSCCIdemo gui setup for two events

Tab 4: Graphs

Choose the types of graph you wish to be created by selecting the appropriate checkboxes. A brief description of each type of graph can be found alongside the checkboxes but for a more detailed explanation please refer to the [Graphs Folder](#) sections starting on [p.56](#).

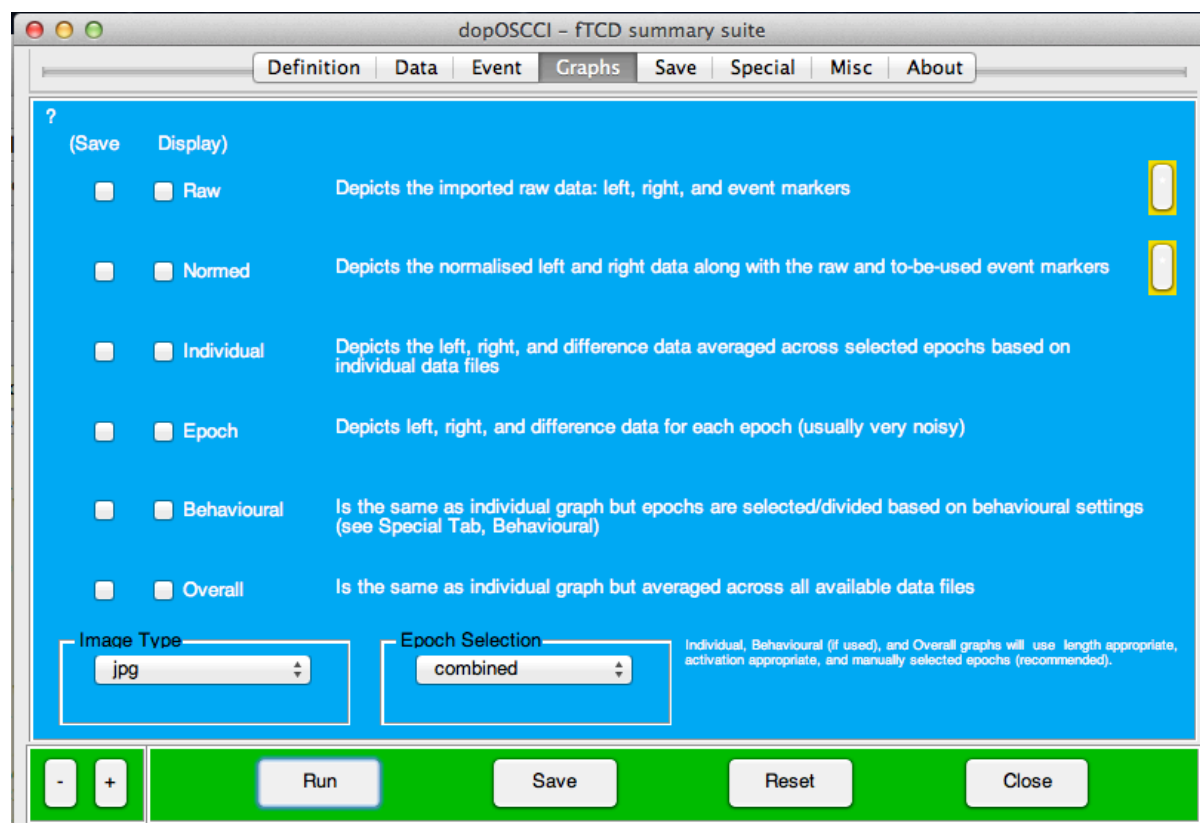


Figure 9: The Graphs Tab of the gui

Save and Display

Selecting the **Save** setting will result in graph images being saved to the location specified on [Tab 5: Save](#). Selecting the **Display** setting checkbox will result in the graphs being displayed throughout the data processing. This is, however, not the case for the **Overall** graphs, which are created after the summary is complete. It is recommended that you do not display the graphs during the data processing as each will be viewed in turn, and dopOSCCI will only move onto the next type by pressing any key on the keyboard. This can be very time consuming and, provided you have the **Save** setting checkbox selected, the graphs will be saved for later inspection anyway. Being able to display the graphs without saving can however be useful, particularly when only one data file is selected for processing, e.g. for viewing problematic data. If you select to display **Epoch** graphs they will be shown in quick succession and then placed one on top of the other for viewing.

The two pushbuttons on the right-hand-side in the Raw and Normed rows allow you to create the corresponding graph with the push of a button. This is done for the first file in the file list, or the selected file. Inspecting the Raw graph useful way of checking the number of event markers (see [Epochs](#), p 16) in a file, whereas the Normed graph may help to determine whether the event Separation (p 16) is adequate.

Image Type

The Image Type drop-down menu can be used to adjust the type of image file the graph will be saved as.

Epoch Selection

The Epoch Selection drop down menu can be used to select the level of epoch screening you wish to use for the Individual, Behavioural and Overall⁵ graphs. Selecting **all** means that data from all recorded epochs will be used. Epochs will be included, regardless of whether they were cut short, contained activation outside the rejection or separation limits, or were manually excluded using the [Manual Screen file](#) function. Selecting **length** means only length-appropriate epochs will be included. Short epochs will be excluded i.e. when recording was started late or stopped early (see [Include Short](#)). Selecting **activation** means only activation-appropriate epochs will be included. This refers to epochs in which activation fell within the limits defined by both [Activation Rejection](#) and [Activation Separation](#). Selecting **manual** means only data from epochs manually selected using the Manual Screen File function will be used (provided the Manual Screen file function is set up). Selecting **combined** provides a combination of **length**, **activation** and **manual** epoch selection. This is the recommended setting and means that the graphs will only include length-appropriate, activation-appropriate and manually-selected epochs.

⁵ The overall graph is created based on a saved data file (see [Graph Data File](#)). Therefore the epoch selection determines what is saved in this file.

Tab 5: Save

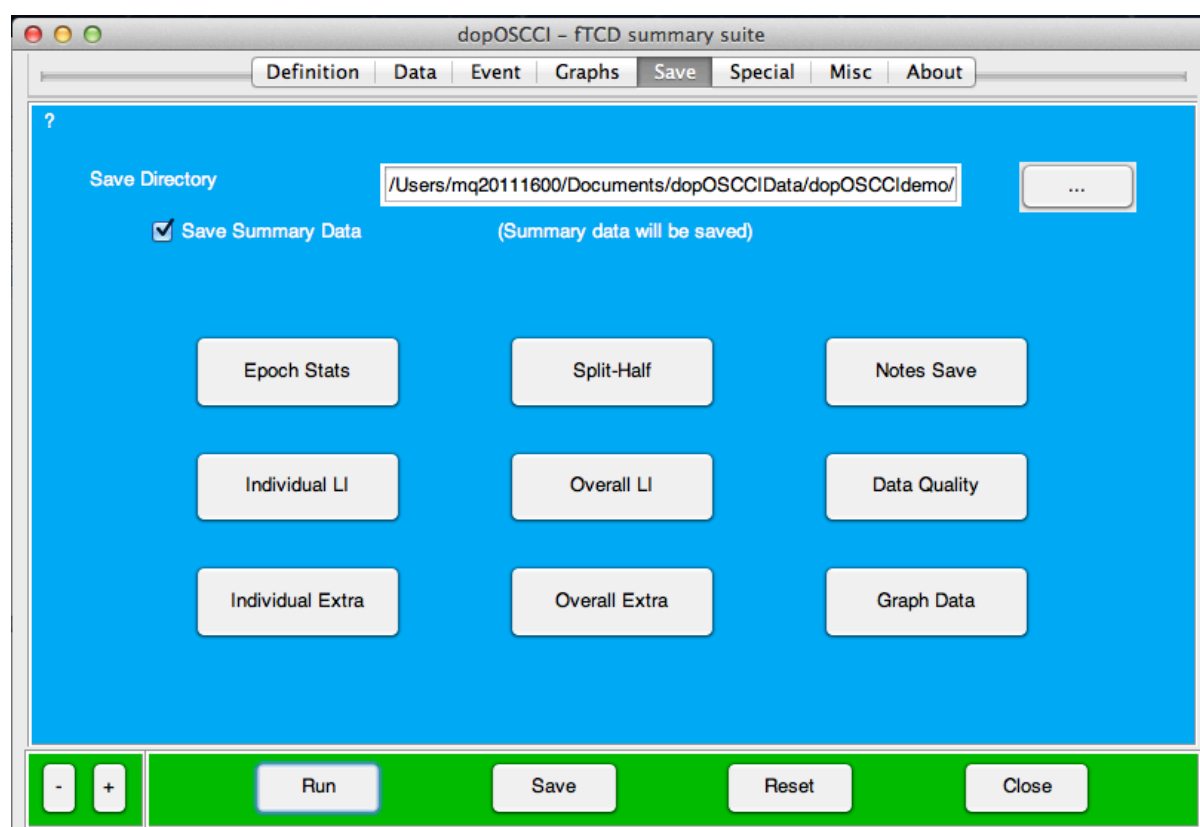


Figure 10: The Save Tab of the gui

Save Directory

dopOSCCI will automatically create a folder called **dopOSCCIdata** in your C drive (C:\dopOSCCIdata\). This folder will be created at the same directory level as the dopOSCCI folder (C:\dopOSCCI\). Within this, another folder will be created, based on your chosen task name (C:\dopOSCCIdata\taskName\). If however, you wish the output data to be saved elsewhere, you can use the **Browse** button ('...') to select the desired location. Each time you run a summary, an additional folder will be created based upon the epoch, baseline, and period of interest settings (C:\dopOSCCIdata\taskName\epoch-12to40_base-10to0_poi25to35\). If this specific folder already exists, '+' characters will be appended to the end until an original is created (...epoch-12to40_base-10to0_poi25to35+).

Save Summary Data

Selecting the **Save Summary Data** checkbox will save the results of the calculations performed during processing in the aforementioned Save Directory folder. These will be saved into a summary file which can be imported into SPSS or EXCEL. Exactly what data will be saved can be modified using the Supplementary Save Buttons outlined below. If you do not elect to save summary data, these buttons will become inactive.

Supplementary save buttons

The default settings on the Save tab are set up to save the most important data in the output summary. The supplementary buttons provide options to modify exactly which aspects of the data

summaries are saved in the *Individual Summary File*, *Overall Summary File* or *Notes Folder*. They enable you to simplify the output to just the information you need, or to look into your data in more complex ways. You can opt to save **general** and **laterality descriptive** and **statistical** summaries on an **epoch** by epoch, **individual**, or **overall** basis. There is also an option to save information on *Split-Half* reliability and to decide how detailed you want the accompanying *Notes Folder* to be. By clicking on a supplementary button, a new window containing all the saving options will open beneath the gui.

Epoch Statistics

Here you can modify which general and laterality descriptive statistics you want to be saved in the *Individual Summary File*. Statistics are available for each independent epoch of each individual file.

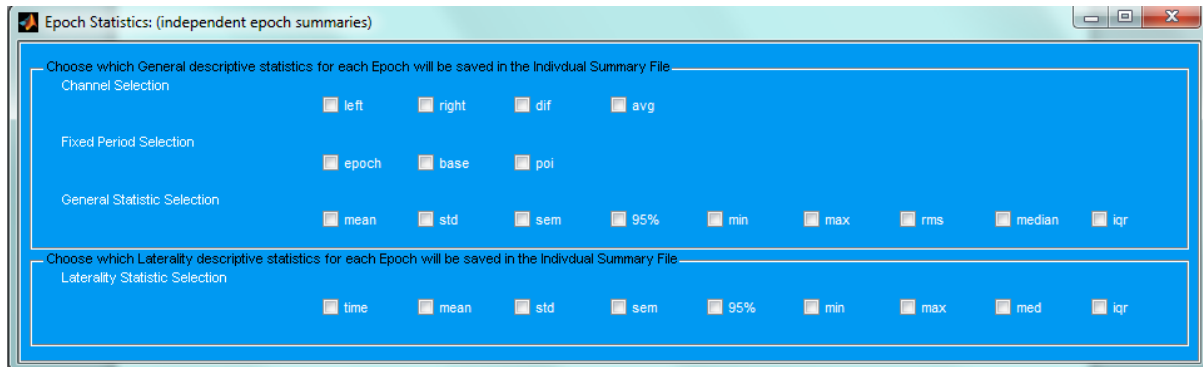


Figure 11: Epoch Statistics Saving Options

Epoch General Statistics Selection

Channel Selection

Select which **channel(s)** you would like indices to be saved from, i.e. **left**, **right**, left minus right **difference** or left/right average (**avg**). At least one of these must be selected in order for the statistical selections to save.

Fixed Period Selection

Select the **fixed period** in the epoch within which the statistical calculation will be made. This can be the whole **epoch**, or just the **baseline** or period of interest (**POI**). Fixed periods are referred to as 'fixed' because they are independent of data channels. At least one selection must be made in order for the statistical selections made below to save.

General Statistic Selection

Choose which general descriptive statistics (based on the channel and fixed period selections above) will be saved for each independent epoch e.g. mean of left channel activation during the baseline period. Statistic options include the **mean**, standard deviation (**std**), standard error of the mean (**sem**), 95% confidence interval (**95%**), the minimum value (**min**), the maximum value (**max**), the root mean squared (**rms**), **median** and interquartile range (**iqr**).

Epoch Laterality Statistic Selection

Choose which laterality descriptive statistics will be saved for each independent epoch. By definition these will always be based on the left minus right difference within the *Activation Window* surrounding the peak difference within the *Period of Interest*. Options include the **time** of peak left minus right difference in seconds, the laterality index i.e. mean left minus right difference over peak time interval (**mean**), the standard deviation (**std**), standard error of the mean (**sem**) and 95% confidence interval (**95%**), and the minimum (**min**), maximum (**max**), median (**med**) and interquartile range (**iqr**) of the left-right difference over the peak time interval.

Individual Laterality Index

Here you can modify which laterality descriptive and inferential statistics you want to be saved in the *Individual Summary File*. Statistics are available for each individual file, averaged over all selected epochs. Use the *Epoch Selection* tool described below to select which ‘collection’ of epochs you would like to use for calculations.

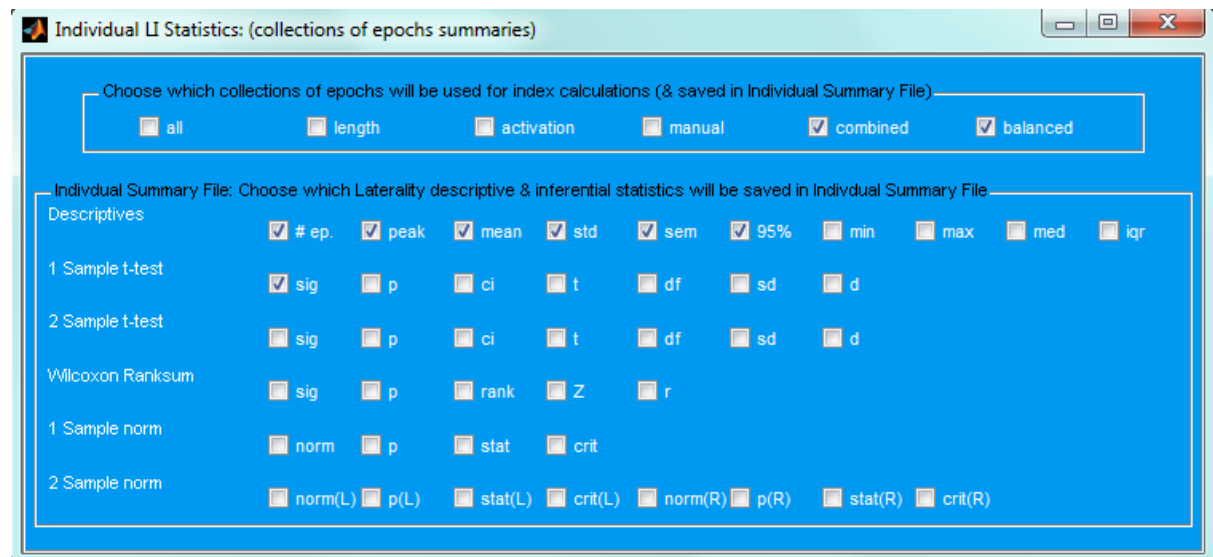


Figure 12: Individual LI Statistics Saving Options

Epoch Selection

First choose which collections of epochs will be used for index calculations and saved in the *Individual Summary File*. Selecting the **all** checkbox means that data from all available epochs will be saved. Epochs will be included, regardless of whether they were cut short, contained activation outside the rejection limits, or were excluded using the *Manual Screen file* function. Selecting the **length** checkbox means only length-appropriate epochs, i.e. not short epochs, will be included. Selecting the **activation** checkbox will save data only from those epochs in which activation fell within the limits defined by *Activation Rejection* and *Activation Separation*. Selecting the **manual** checkbox means only the data from epochs manually selected using the *Manual Screen file* function will be saved. Selecting the **combined** checkbox provides a combination of **length**, **activation** and **manual** epoch selection. This means that the summary will include length-appropriate epochs, activation-appropriate epochs and manually-selected epochs. In addition the **balanced** checkbox can be used to save an equal number of screened epochs for each session (see *Session File*).

Please note that the screening options available here only affect which information is saved and available to view in the summary data files. They do not affect which epochs are used in the summary in the first place. The actual screening of epochs occurs on *Tab 2: Data* using the *Include Short*, *Activation Rejection* and *Activation Separation* fields as well as on *Tab 6: Special*.

Individual Laterality descriptive and inferential statistics

Descriptives

A series of checkboxes to indicate which descriptive statistics you want to be saved in the *Individual Summary File*. These include the number of included epochs (**# ep.**); the time of peak left minus right difference in seconds (**peak**); the laterality index i.e. mean left minus right difference over peak time interval (see *Activation Window*) (**mean**); the standard deviation (**std**), standard error of the mean (**sem**) and 95% confidence interval (**95%**); and the minimum (**min**), maximum (**max**), median (**med**) and inter-quartile range (**iqr**) of the mean of left-right difference over the peak time interval.

1 and 2 Sample t-tests

Saving options include the significance of test (**sig**) where 1 indicates a significant difference and 0 does not, the **p** value of the test, a 95% confidence interval of the mean difference (**ci**), the **t** value of the test, the degrees of freedom (**df**), the standard deviation (**sd**) and Cohen's D value (effect size) (**d**).

Wilcoxon Ranksum

Saving options include the significance of test (**sig**) where 1 indicates a significant difference and 0 does not, the **p** value of the test, the ranksum value (**rank**), the **Z** value of ranksum and the Z conversion to **r** (effect size).

1 and 2 Sample Norm

Saving options include the normality of the data (**norm**) where 0 is normal and 1 is different, the **p** value of the test, the Jarque-Bera value (**stat**) and the critical value for the test (**crit**).

Individual Extra Statistics

Here you can modify which collections of epochs (averaged over epochs for each individual) will be used for statistical calculations and saved in the *Individual Summary File*. Here you can also choose to save statistics based on a specified **Fixed Period** (a period of time, e.g. whole epoch, baseline, or POI, which is independent of data channels) or based on a specified **Calculated Period** (a period of time which is dependent upon channels, e.g. point of maximum left activation).

Figure 13: Individual Extra Statistics Saving Options

Epoch Selection

See *Epoch Selection p.28*. This provides a further opportunity to choose which collections of epochs will be used for index calculations and saved in the *Individual Summary File*. The Epoch Selection choices made on the *Individual Extra Statistics* supplementary button are the same as those made on the *Individual Laterality Index* supplementary button. Any changes made to checkboxes under one supplementary button will automatically update selections on the other (provided both windows are not open simultaneously).

Fixed Period Descriptive Statistics

Channel Selection

Select which channel(s) you would like indices to be saved from, i.e. **left**, **right**, left minus right **difference** or **average**. At least one of these must be selected in order for the statistical selections to save.

Fixed Period Selection

Select the **fixed period** in the epoch within which the statistical calculation will be made. This could be the whole **epoch**, or just the **baseline** or period of interest (**POI**). At least one selection must be made in order for the statistical selections made below to save.

General Statistic Selection

Choose which averaged descriptive statistics (based on the channel and fixed period selections above) will be saved for each individual in the *Individual Summary File*. Options include the **mean**, standard deviation (**std**), standard error of the mean (**sem**), 95% confidence interval (**95%**), the

minimum value (**min**), the maximum value (**max**), the root mean squared (**rms**), **median** and interquartile range (**iqr**).

Calculated Period Descriptive Statistics

Channel Selection

Select which channel(s) you would like indices to be saved from, i.e. **left**, **right**, left minus right **difference** or **average**. At least one of these must be selected in order for the statistical selections to save.

Calculated Period Channel

Select which channel (**left**, **right**, left minus right **difference** or **average**) you want to use to calculate the period selected in the *Calculated Period Selection* below. For example selecting 'left' here means that whatever calculated period is selected below, e.g. 'minimum', will refer to the left channel only, i.e. the statistic will be based on the period around the minimum left activation in the epoch. At least one of these must be selected in order for the statistical selections to save.

Calculated Period Selection

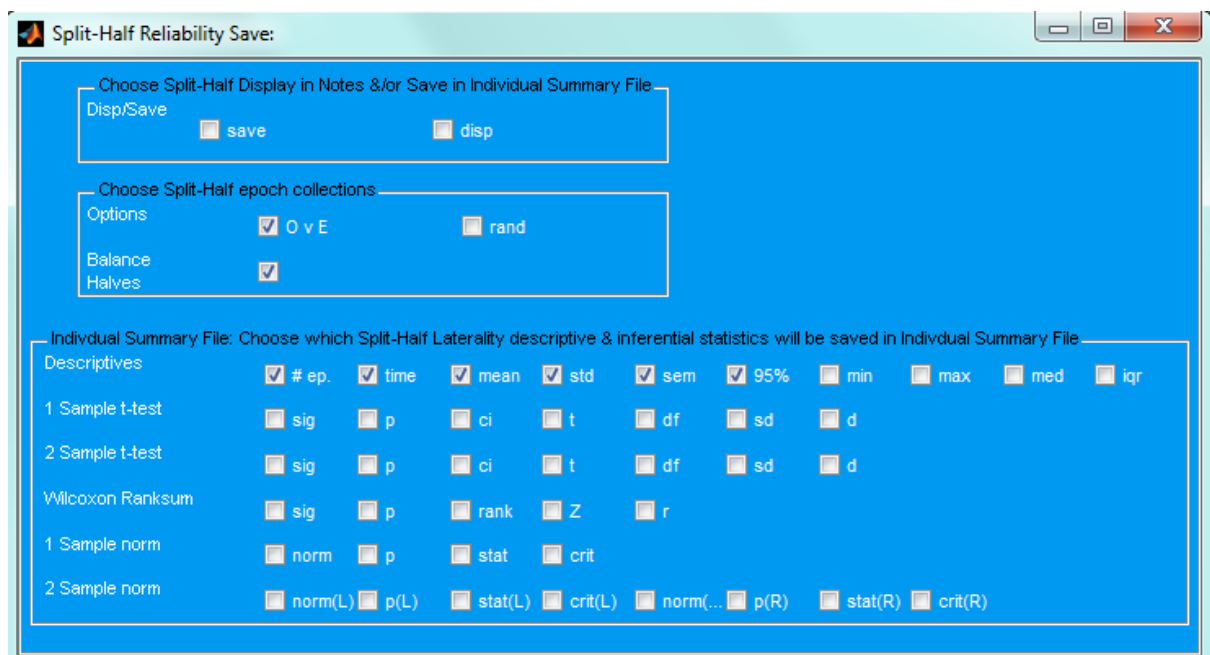
Select the calculated period within which the statistical calculation is to be made. This point is chosen in reference to the selection made for *Calculated Period Channel*, e.g. the maximum right activation in the epoch. The statistic is then calculated based on the *Activation Window* period surrounding this value. There are options to select the **maximum** value (positive only) or the **absolute maximum** (in a positive or negative direction) in the **POI** or the whole **epoch** as well as their **minimum** counterparts. At least one of these must be selected in order for the statistical selections to save.

General Statistic Selection

Choose which averaged descriptive statistics (based on the *Channel Selection*, *Calculated Period Channel* and *Calculated Period Selection* above) will be saved for each individual in the *Individual Summary File*. Options include the peak **time** point in seconds, **mean**, standard deviation (**std**), standard error of the mean (**sem**), 95% confidence interval (**95%**), the minimum value (**min**), the maximum value (**max**), the root mean squared (**rms**), **median** and interquartile range (**iqr**). The statistic will be calculated in reference to all the selections made above e.g. the mean (general statistic selection) of the difference data (channel selection) at the minimum (calculated period selection) of left activation (calculated period channel).

Split-Half

Split-half summaries are available for individual data files which can be used to estimate the internal reliability of a task. Choose whether to **save** split-half values in the *Individual Summary File* or to **display** them at the command line. Like all information reported to the Matlab command window during processing, the split-half values would still be available to view later in the *File Notes ('B' files)*. You would need to specify which collection of epochs you want to use for the split-half calculations; choose either halves based on odd and even (**O v E**) epochs or halves based on a random (**rand**) selection of epochs. Selecting the **Balance Halves** checkbox will ensure an even number of epochs in each half and will result in an additional epochs being dropped from the calculation if there are more in one half than the other. Finally choose which Split-Half Laterality descriptive and inferential statistics you would like to be saved. For details of abbreviations of these options please refer to the section in *Individual Laterality descriptive and inferential statistics* or use the cursor to hover over each checkbox.



Split-Half Reliability Save:

Choose Split-Half Display in Notes &/or Save in Individual Summary File

Disp/Save ☐ save ☐ disp

Choose Split-Half epoch collections

Options ☒ O v E ☐ rand

Balance Halves ☒

Individual Summary File: Choose which Split-Half Laterality descriptive & inferential statistics will be saved in Individual Summary File

Descriptives ☒ # ep. ☒ time ☒ mean ☒ std ☒ sem ☒ 95% ☐ min ☐ max ☐ med ☐ iqr

1 Sample t-test ☐ sig ☐ p ☐ ci ☐ t ☐ df ☐ sd ☐ d

2 Sample t-test ☐ sig ☐ p ☐ ci ☐ t ☐ df ☐ sd ☐ d

Wilcoxon Ranksum ☐ sig ☐ p ☐ rank ☐ Z ☐ r

1 Sample norm ☐ norm ☐ p ☐ stat ☐ crit

2 Sample norm ☐ norm(L) ☐ p(L) ☐ stat(L) ☐ crit(L) ☐ norm(...) ☐ p(R) ☐ stat(R) ☐ crit(R)

Figure 14: Split-Half Reliability Saving Options

Overall Laterality Index

Here you can modify which laterality descriptive and inferential statistics you want to be saved in the **Overall Summary File**. Statistics are averaged across all individual summaries.

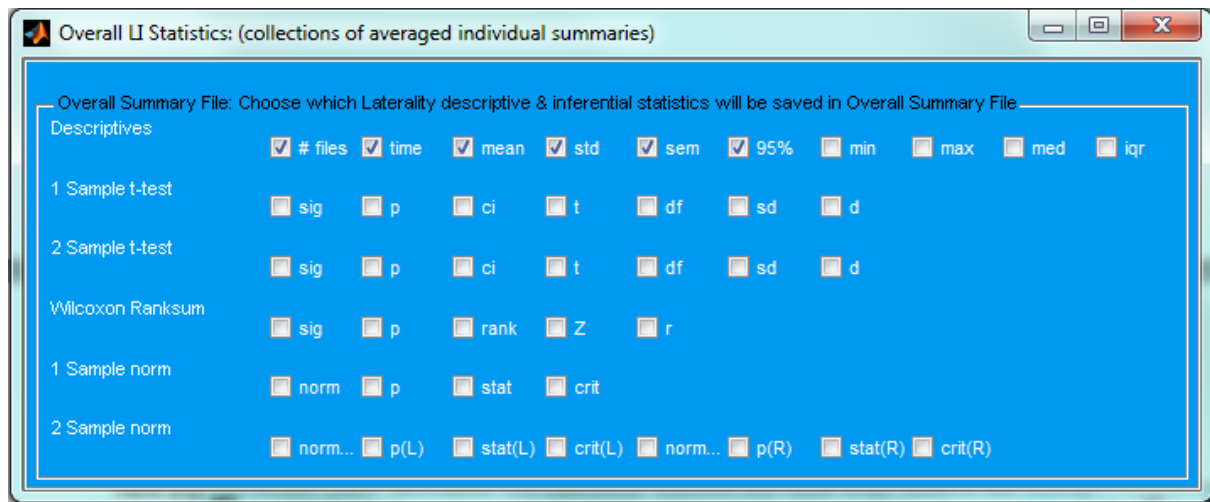


Figure 15: Overall LI Statistics Saving Options

Overall Laterality descriptive and inferential statistics

Descriptives

A series of checkboxes to indicate which descriptive statistics you want to be saved in the **Overall Summary File**. These include the number of included files (**# files**); the **time** of peak left minus right difference in seconds; the laterality index i.e. mean left minus right difference over peak time interval (see **Activation Window**) (**mean**); the standard deviation (**std**), standard error of the mean (**sem**) and 95% confidence interval (**95%**); and the minimum (**min**), maximum (**max**), median (**med**) and inter-quartile range (**iqr**) of the mean of left-right difference over the peak time interval.

1 and 2 Sample t-tests

Saving options include the significance of test (**sig**) where 1 indicates a significant difference and 0 does not, the **p** value of the test, a 95% confidence interval of the mean difference (**ci**), the **t** value of the test, the degrees of freedom (**df**), the standard deviation (**sd**) and Cohen's D value (effect size) (**d**).

Wilcoxon Ranksum

Saving options include the significance of test (**sig**) where 1 indicates a significant difference and 0 does not, the **p** value of the test, the ranksum value (**rank**), the Z value of ranksum and the **Z** conversion to **r** (effect size).

1 and 2 Sample Norm

Saving options include the normality of the data (**norm**) where 0 is normal and 1 is different, the **p** value of the test, the Jarque-Bera value (**stat**) and the critical value for the test (**crit**).

Overall Extra Statistics

Here you can modify which descriptive statistics you want to be saved in the *Overall Summary File*. Statistics are averaged across all individual summaries.

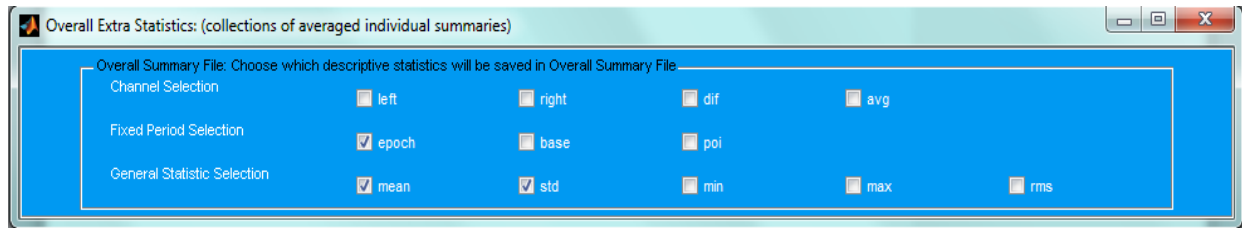


Figure 16: Overall Extra Saving Options

Channel Selection

Select which channel(s) you would like indices to be saved from, i.e. **left**, **right**, left minus right **difference** or **average**. At least one of these must be selected in order for the statistical selections to save.

Filter Period Selection

Select the **fixed period** in the epoch within which the statistical calculation will be made. This could be the whole **epoch**, or just the **baseline** or period of interest (**POI**). At least one selection must be made in order for the statistical selections made below to save.

General Statistic Selection

Choose which averaged descriptive statistics (based on the channel and fixed period selections above) will be saved in the *Overall Summary File*. Options include the **mean**, standard deviation (**std**), the minimum value (**min**), the maximum value (**max**) and the root mean squared (**rms**).

Notes Save

dopOSCCI can save a series of notes files which hold information about the summary.

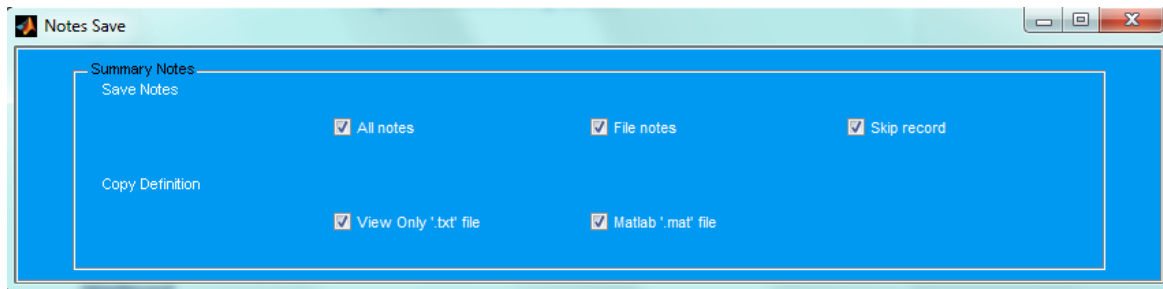


Figure 17: Notes saving options

Save Notes

All notes

These include an Overall file with a copy of all notes contained within the Notes Save directory (by default, ~dopOSCCIData\taskName\notes\). The notes include all Matlab command window output in a text (.txt extension) file (see [A1allNotes](#)).

File Notes

Independent notes files can be saved for each file, which is useful for seeing what happened with a particular file (See [File Notes \('B' files\)](#)).

SkipRecord

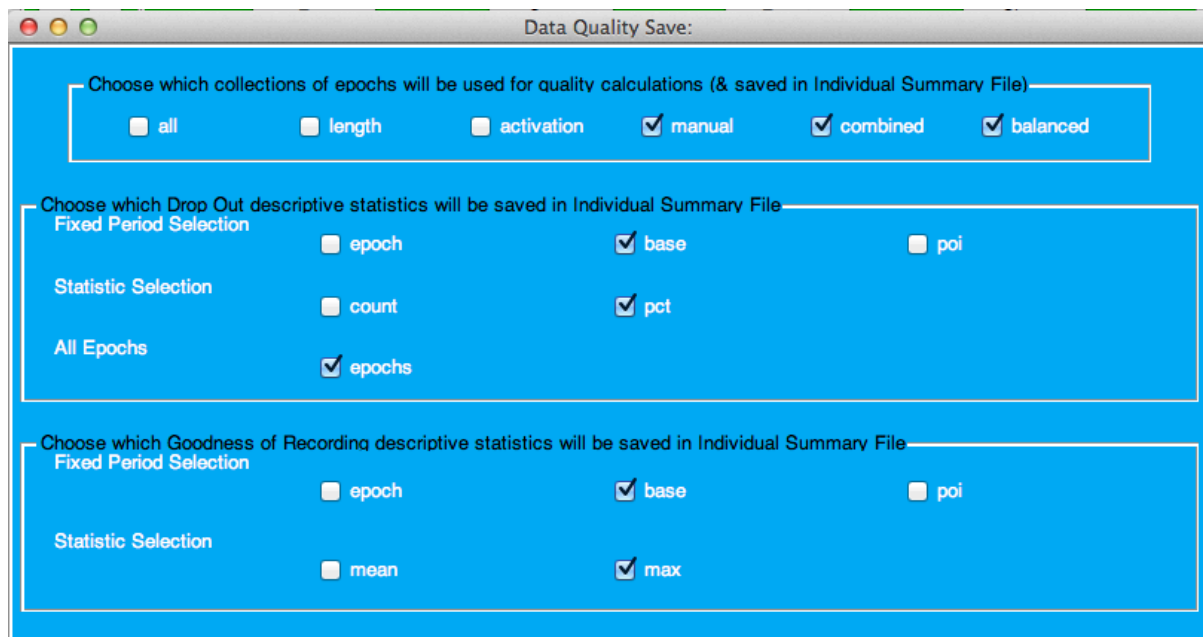
Sometimes there is an error processing an individual file which results in that file being skipped in the summary. In this instance, it's useful to know why this is the case. Selecting the SkipRecord checkbox creates a [A4skipRecord](#) in the notes folder which records any files which have not been included in the processing and the reason that they were skipped. A file could be skipped if it was not selected on [Tab 2: Data](#), if no markers were found, if all trials were excluded after using the [Manual Screen file](#) function, if no group was specified when the [Group File](#) function was selected or if the file was not matched to another when the [Session File](#) function was selected.

Copy definition

On running a summary, a Task Definition Matlab.mat File (and readable .txt. version) is automatically created in the **TaskData** folder. The .mat file holds details of all the dopOSCCI settings selected on the gui for that particular task. This means that on returning to dopOSCCI and completing the [Task Name](#) field, all previously chosen settings for that task will automatically be updated on the gui. Select the **view only .txt file** or **Matlab.mat file** checkboxes to copy this definition file in both .mat and .txt formats to the [Notes Folder](#). This can then be easily referred to at a later date when returning to your summary output to check exactly which dopOSCCI settings were used for the summary (see [Task Definition Notes: A2viewOnly.txt. File and Matlab .mat File](#)).

Data Quality

dopOSCCI can save a series of Data Quality indices which provide an indication of the quality of the data recording for each individual file.



Data Quality Save:

Choose which collections of epochs will be used for quality calculations (& saved in Individual Summary File)

☐ all ☐ length ☐ activation ☒ manual ☒ combined ☒ balanced

Choose which Drop Out descriptive statistics will be saved in Individual Summary File

Fixed Period Selection ☐ epoch ☒ base ☐ poi

Statistic Selection ☐ count ☒ pct

All Epochs ☒ epochs

Choose which Goodness of Recording descriptive statistics will be saved in Individual Summary File

Fixed Period Selection ☐ epoch ☒ base ☐ poi

Statistic Selection ☐ mean ☒ max

Figure 18: Data Quality Save options

Epoch Selection

See [Epoch Selection p.28](#). This provides an opportunity to choose which collections of epochs will be used for Data Quality calculations and saved in the *Individual Summary File*.

Drop Out

If the contact between the head and Doppler probe is poor or if the participant moves a lot, the signal may dropout. Although this will influence the normalization of the signal (this value will be recorded as a 0) and it is likely that the epoch will be rejected, it can be useful to have a record of Drop Out, which could be used to screen participants if necessary.

Filter Period Selection

Select the **fixed period** in the epoch within which the calculation will be made. This could be the whole **epoch**, or just the **baseline** or period of interest (**POI**). At least one selection must be made in order for the statistical selections made below to save.

Statistic Selection

Count and **pct** (percentage) statistics are available which represent to total number of dropouts and the percentage of dropouts within the selected period respectively.

All Epochs

By default these statistics are saved for the overall left and right channels and by selecting the **epochs** checkbox, these values will be saved for each independent epoch.

Goodness of Recording

Stefan Knecht et al. (2001) introduced a 'Goodness of Recording' index which they used to excluded individual data sets from their analyses. This index is the mean root mean square of the baseline period and they used a rejection criterion of values greater than 2 or 2%.

Filter Period Selection

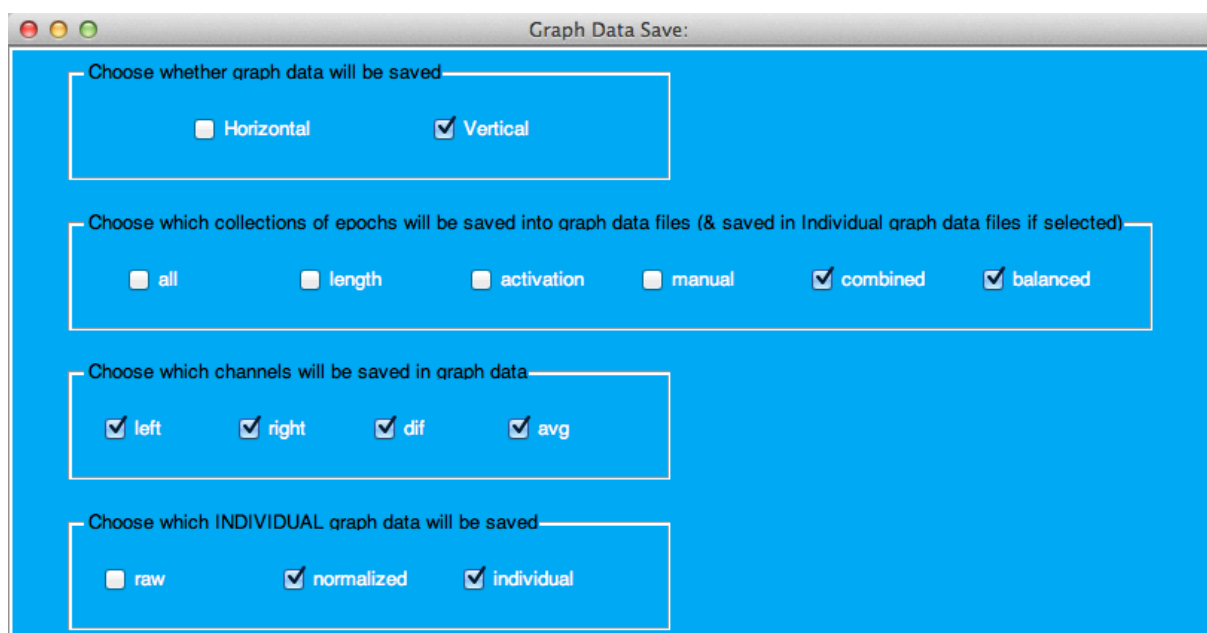
Select the **fixed period** in the epoch within which the calculation will be made. This could be the whole **epoch**, or just the **baseline** or period of interest (**POI**). At least one selection must be made in order for the statistical selections made below to save. Knecht et al. (2001) used the baseline period for their exclusion procedure.

Statistic Selection

The **mean** and **maximum** goodness of recording values can be saved. In personal communications with Michael Deppe, he indicated that both of these indices were experimented with as methods of exclusion in the Knecht et al. (2001) paper but it was the **mean** that they used in the end

Graph Data

dopOSCCI can save a series of options for saving summarised and individual data for later inspection or graphing in other programs.



Graph Data Save:

Choose whether graph data will be saved

☐ Horizontal ☒ Vertical

Choose which collections of epochs will be saved into graph data files (& saved in Individual graph data files if selected)

☐ all ☐ length ☐ activation ☐ manual ☒ combined ☒ balanced

Choose which channels will be saved in graph data

☒ left ☒ right ☒ dif ☒ avg

Choose which INDIVIDUAL graph data will be saved

☐ raw ☒ normalized ☒ individual

Which graph data?

Horizontally and vertically aligned **Graph Data Files** data files can be saved in the **Graph Data Folder**. A horizontally aligned file is arranged in rows with the time sample for the left, right, difference and average shown in blocks through the first row, with the corresponding activation levels for each participant at each time sample in the rows below. The vertically aligned file has the same information as the horizontal file, but arranged in vertical columns instead. The time sample is shown in the first column, followed by columns for left, right, difference and average activation for each participant. This can be useful for copying the data directly into graphing packages like Prism.

Epoch Selection

See **Epoch Selection p.28**. This provides an opportunity to choose which collections of epochs will be used for and saved in the data files.

Channel Selection

Select which channel(s) you would like saved in the graph data files, i.e. **left**, **right**, left minus right difference or **average**.

Individual Graph Data Files

The individual options allow you to save the Raw, Normed and Individual graph data to individual data files. For a more detailed explanation of these graphs see the ***Graphs Folder*** sections starting on ***p.56***. If you are working with .EXP files, the Raw data will be redundant as this information is readily available in the original data file. This option was created for the older .TX and .TW files which are not so easily accessible. For the Individual graph, left, right, difference, and left-right averaged data will be saved for the all the utilised epochs (based upon the epoch selection).

Tab 6: Special

The Special tab allows you to summarise the Doppler data in more complex ways. It is possible to manually screen certain epochs for specific individuals, separate the data output for group comparison, summarise epochs based upon behaviourally relevant groupings such as experimental conditions or performance characteristics, and combine individual but matched raw data files to produce a single output. All these special functions can be used at the same time to produce a sophisticated summary of your data.

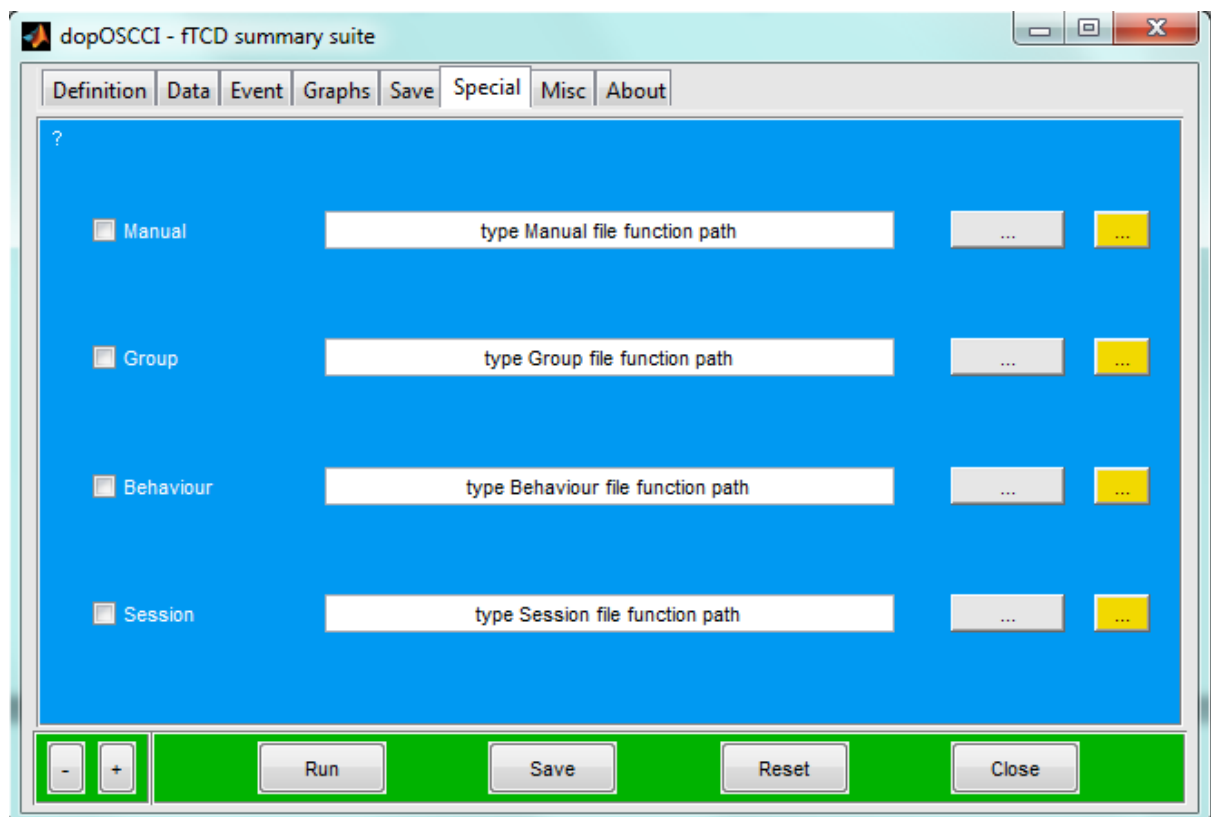


Figure 19: The Special tab of the gui

Manual Screen file

When the summary is run, dopOSCCI will screen out epochs based on the settings selected on **Tab 2: Data** e.g. because they are too short (**length**), or because the **Activation Rejection** or **Activation Separation** limits are exceeded (**activation**). In addition, the **Manual Screen file** function allows you to manually exclude any epochs for specific individuals (**manual**) if, for example, a participant was not on task during a particular trial.

First you need to prepare a Manual Screen file outlining which epochs need to be excluded. To ensure all raw data files are included in the Manual Screen file, first check that '**All files**' has been made in the **File Selection** field on **Tab 2: Data**. To create the Manual Screen file click on the yellow button to the right of the Manual Screen file field. Go to the Matlab command window and follow the link which says '**Open Windows Explorer to save directory**' (note: this is not yet functional for non-Windows operating systems). This opens the **taskData** folder (C:\dopOSCCIdata\taskData\) in which dopOSCCI will have automatically created a Manual Screen file, named after the current task name, i.e. TaskNameMan. This Manual Screen file can be opened in Microsoft Excel and lists all the raw data files found in the specified **Data Directory** under the heading **fileName**. The trials to be excluded need to be entered in the second column under the heading **epochScreen**. This should be in the format '3~' where trial three is to be excluded from the summary. As many trials as required can be excluded, e.g. 3~9~14~. If no trials need to be excluded for that participant, leave it as the default setting 'none'. Once you have specified which trials need to be excluded for all data files, save the Manual Screen file as a tab-delimited *.txt file in the **taskData** folder.

| | A | B |
|---|------------|-------------|
| 1 | fileName | epochScreen |
| 2 | NLA820.TX0 | none |
| 3 | NLA822.TX0 | none |
| 4 | NLA826.TX0 | 1~2~3~ |
| 5 | NLA828.TX0 | none |
| 6 | NLA829.TX0 | none |
| 7 | NLA831.TX0 | none |
| 8 | NLA838.TX0 | 1~7~ |
| 9 | NLA840.TX0 | none |

Figure 20: Defining epochs for exclusion

To use this Manual Screen file in the summary, select the **Manual Screen file** checkbox and click on the browse ('...') button. This opens the **TaskData** folder where the manual screening files can be found for each task. Open the required file and the Manual Screen file field will be completed with the location of that file. The number of raw data files that are listed in the Manual Screen file is displayed below.

Once the summary has run, details of all types of screening, including manual screening, appear in the notes file for each individual e.g. length 11 (rejected = 1), act 11 (rejected = 1), man 9 (rejected = 2 3), combined 9 (rejected = 1 2 3). 'Combined' in this situation refers to a combination of length, activation and manual screening. It is possible to save data in the individual and overall summary files from each type of epoch selection independently using the **Epoch Selection** tool on the

supplementary buttons on [Tab 5: Save](#). This can be useful to see what effect each type of screening has on the laterality index.

dopOSCCI Demo 11: Using the Manual Screen function

To create a Manual Screen file for dopOSCCI demo, click on the yellow button to the right of the Manual Screen file field. Follow the link on the Matlab command window to the TaskData folder where dopOSCCI will have created a file called dopOSCCIdemoMan. Open this file (or the preset version) in Microsoft Excel. The eight file names contained in the dopOSCCIdemo data directory are listed under the heading fileName. Alter the epochScreen column to exclude trials 1-3 from file NLA826.TXO and trials 1 and 7 from NLA838.TXO as shown in Figure 20. Save this file as a text file (tab delimited).

Select the Manual Screen file checkbox and search for the updated dopOSCCIdemoMan file (or dopOSCCIdemoMan_preset file) using the browse ('...') button. The screen field should be completed with the location of this file and '8 individual series' should be displayed below. To demonstrate the screen function, change the number of events back to 1 and adjust the epoch range back to -12 to 40 seconds. Select file NLA826 on the Data tab and select the checkbox to display an individual graph using the Graphs Tab. This creates a graph of the average left, right, and difference activation after manual screening. Note that of the 12 epochs in the file, only 9 were included in the summary (n= 9 in grey box on difference graph). The BNLA826 notes file also shows that manual screening took place to reject the first 3 epochs (man 9 (rejected = 1 2 3)).

To see the effect of manual screening on the laterality index, run the summary again, but use the epoch selection tool on the Individual LI button of Tab 5 to select the 'all' and 'manual' checkboxes. Look in the individual summary file to see the different LI values for all 12 epochs versus the 9 manually selected epochs.

Group File

This function separates the output of the data processing based upon different groups within your data set (e.g., left handers and right handers, or males and females).

Again, you first need to prepare a **Group File** in which the raw data files are assigned to groups. To ensure all raw data files are included in the Group file, first check that '**All files**' has been made in the **File Selection** field on **Tab 2: Data**. To create the group file click on the yellow button to the right of the Group file field. Go to the Matlab command window and follow the link which says '**Open Windows Explorer to save directory**'. This opens the **taskData** folder (C:\dopOSCCIdata\taskData\)) in which dopOSCCI will have automatically created a group file, named after the current task name, i.e. TaskNameGroups. This group file can be opened in Microsoft Excel and lists all the raw data files found in the specified **Data Directory** under the heading **fileName**. You need to enter your group names, e.g. Males and Females, across the top of subsequent columns. It is possible to split your raw data files into as many groups as you wish. Indicate using 1 and 0 whether a raw data file belongs to a group (e.g. if the participant is a male then a 1 will be placed in the Male column and a 0 in the Female column). Several group files can exist for each task to allow different comparisons to be made⁶. Once you have specified your groups, save the group file as a tab-delimited *.txt file in the **taskData** folder.

| | A | B | C | D |
|---|------------|--------|--------|--------|
| 1 | fileName | groupA | groupB | groupC |
| 2 | NLA820.TX0 | 1 | 0 | 0 |
| 3 | NLA822.TX0 | 1 | 0 | 0 |
| 4 | NLA826.TX0 | 0 | 1 | 0 |
| 5 | NLA828.TX0 | 0 | 1 | 0 |
| 6 | NLA829.TX0 | 1 | 0 | 0 |
| 7 | NLA831.TX0 | 1 | 0 | 0 |
| 8 | NLA838.TX0 | 0 | 0 | 1 |
| 9 | NLA840.TX0 | 0 | 0 | 1 |

Figure 21: Defining groups

To use this group file in the summary, select the **Group File** checkbox and click on the browse ('...') button. This opens the **taskData** folder where the group files can be found for each task. Open the required file and the Group File field will be completed with the location of that file. The number of groups that have been found is displayed below.

⁶ If more than one group is specified for an individual file, the first (left-most) grouping will be used.

dopOSCCI Demo 12: Using the group function

In the dopOSCCI demo task, participants belonged to one of three groups; A, B, or C. To create a Group file for dopOSCCI demo, click on the yellow button to the right of the Group File field. Follow the link on the Matlab command window to the taskData folder where dopOSCCI will have created a file called dopOSCCIdemoGroups. Open this file (or the preset version) in Microsoft Excel. The eight file names contained in the dopOSCCIdemo data directory are listed under the heading fileName. Alter the GroupName column headings to Group A and Group B and add another heading, Group C. Enter a '1' to indicate that a particular participant belongs to a group as shown in Figure 21. Save this file as a text file (tab delimited).

Select the Group File checkbox and search for the updated dopOSCCIdemoGroups file (or dopOSCCIdemoGroups_preset file) using the browse ('...') button. The Group File field should be completed with the location of this group file and '3 groups found: groupAgroupBgroupC' should be displayed below. To demonstrate the group function, ensure that all files have been selected on the Data Tab. On the Graphs Tab select to save the overall graphs. Run the summary. When the summary is complete, click on the 'Open Windows Explorer to save directory' link. Open the graphs folder and view the Overall graph for each group. Descriptive and inferential statistics for each group are also saved in the Overall Summary Data File.

Behavioural File

The Behavioural facility allows for Doppler trials to be summarised based upon behaviourally relevant groupings such as experimental conditions or performance characteristics.

Again, you first need to prepare a **Behavioural File**. To ensure all raw data files are included in the Behavioural file, first check that '**All files**' has been selected in the **File Selection** field on **Tab 2: Data**. To create the behavioural file click on the yellow button to the right of the Behavioural file field. Go to the Matlab command window and follow the link which says 'Open Windows Explorer to save directory'. This opens the **taskData** folder (C:\dopOSCCIdata\taskData\)) in which dopOSCCI will have automatically created a behavioural file, named after the current task name, i.e. TaskNameBeh. This behavioural file can be opened in Microsoft Excel and lists all the raw data files found in the specified **Data Directory** under the heading **fileName**.

The column headers are critical for specifying the particular variable. dopOSCCI is programmed to search for 'varEpoch#', where 'var' is the variable label which will be used in the output. There needs to be one of these for epoch 1 to epoch n and this can be repeated for different variables. For example, conditionEpoch1 to conditionEpochn, then RTEpoch1 to RTEpochn (where RT stands for reaction time).

For each individual, for each epoch, the level of the behavioural variable should be specified. These should be indicated by integer or whole number values, e.g. 1, 2, 3.⁷ Be sure to make provision in your experimental procedure for an adequate number of epochs for each behavioural variable: at least 10 is recommended. (See dopOSCCIdemoBeh_preset file for an example of how to create a behavioural file)

To use the Behavioural function in a summary, select the **Behavioural File** checkbox on the gui and click on the browse ('...') button. This opens the **taskData** folder where the behavioural file will have been created. Open the required file and the Behavioural File field will be completed with the location of that file. The variable names will be listed below, as specified in the column headings of the behavioural file.

⁷ One exception to this is the reserved words 'Correct', 'correct', 'Cor', and 'cor'. These have been reserved to indicate response accuracy and expect to have the values 0 for incorrect and 1 for correct.

dopOSCCI Demo 13: Using the behavioural function

To view the behavioural file for dopOSCCI demo, click on the yellow button to the right of the behaviour field. Follow the link on the Matlab command window to the taskData folder where there is a file called dopOSCCIdemoBeh_preset. Open this file in Microsoft Excel.

The dopOSCCI demo task had 12 trials for each participant, evenly split between condition 1 and condition 2, with 6 trials in each condition⁸. Performance data was also collected for every trial whereby correct responses were indicated by a 1 and incorrect responses by a 0. Close this file and return to the gui to select the Behavioural checkbox. Browse for the file named dopOSCCIdemoBeh_preset and open this file to fill in the Behavioural File field with its location. Below the field '2 variables found: condition (1 2) cor (0 1)' is displayed.

To demonstrate the behavioural function, ensure that all files has been selected on the Data Tab and select the Behavioural save checkbox on the Graphs tab. Run the summary and follow the link to the saved data. In the graphs folder you will be able to view individual graphs for each participant by performance (cor) and condition.

⁸ These categorisations were artificially created and not behaviourally relevant – purely created for the sake of demonstration. Therefore, you should not expect to see any meaningful difference between condition results.

Session File

The session facility combines the data from two or more separate, individually matched, raw data files to be joined together to provide a combined output. This can be useful if, for example, participants completed the task over two or more separate experimental sessions.

Again, you first need to prepare a **Session File**. To ensure all raw data files are included in the Session file, first check that '**All files**' has been chosen in the **File Selection** field on **Tab 2: Data**. To create the session file click on the yellow button to the right of the Session file field. Go to the Matlab command window and follow the link which says '**Open Windows Explorer to save directory**'. This opens the **taskData** folder (C:\dopOSCCIData\taskData\) in which dopOSCCI will have automatically created a group file, named after the current task name, i.e. TaskNameSes. This file can be opened in Microsoft Excel and edited to specify which raw data files should be combined together. The first row of each column is used for labelling purposes, e.g. session1 and session2 with the horizontally matched raw data files listed below (see **Figure 22: Creating a Session File**). The first column will later be referred to as Session 1 and the second column Session 2. Session 3 refers to the combined outputs. This file should be then be saved as a tab-delimited *.txt file in the **taskData** folder (C:\dopOSCCIData\taskData\).

| | A | B |
|---|------------|------------|
| 1 | mon | tues |
| 2 | NLA820.TX0 | NLA822.TX0 |
| 3 | NLA826.TX0 | NLA828.TX0 |
| 4 | NLA829.TX0 | NLA831.TX0 |
| 5 | NLA838.TX0 | NLA840.TX0 |

Figure 22: Creating a Session File

To use the Session function in a summary, select the **Session** checkbox on the gui and click on the browse ('...') button. This opens the **taskData** folder where the saved Session files can be found for each task. Open the required file and the Session field will be completed with the location of that file. The headings of the two sessions are displayed below.

If you wish to summarise data based on an equal number of screened epochs for each session, an option is available to balance/equate the number of epochs per session. This option is referred to as **balanced** and can be selected on the **Individual Laterality Index button** on **Tab 5: Save** (see **Epoch Selection**).

There is also an option **on Tab 7: Misc** to save an individual graph containing an equal number of epochs from each session (**Save Balanced Graph**).

dopOSCCI Demo 14: Using the session function

In the dopOSCCI demo task, each participant performed the task twice, once on Monday and once on Tuesday. These two matched files, each 12 trials long, can be sessioned together to provide a combined output based on 24 trials.

To view the session file for dopOSCCIdemo, click on the yellow button to the right of the session field. Follow the link on the Matlab command window to the taskData folder where there is a file called dopOSCCIdemoSes_preset. Open this file in Microsoft Excel. The raw data files for the Monday response sessions are matched to the raw data files for the Tuesday response sessions under the headings Mon and Tues.

Select the Session File checkbox and browse for the dopOSCCIdemoSes_preset file to fill in the Session File field with its location. Below the field '2 sessions found: montues' is displayed. To demonstrate the Session function, select the individual checkbox on the Graphs Tab and ensure that 'all files' has been selected on the Data Tab. Run the summary. Individual graphs will be produced for session 1 (e.g. file NLA820 containing data from up to 12 epochs), for session 2 (e.g. NLA822 containing data from up to 12 epochs) and for session 3 (e.g. NLA820_NLA822 – which is produced using the data from all 24 epochs). Altering the epoch selection on the graphs tab will affect the actual number of epochs used to create the graphs.

Tab 7: Misc

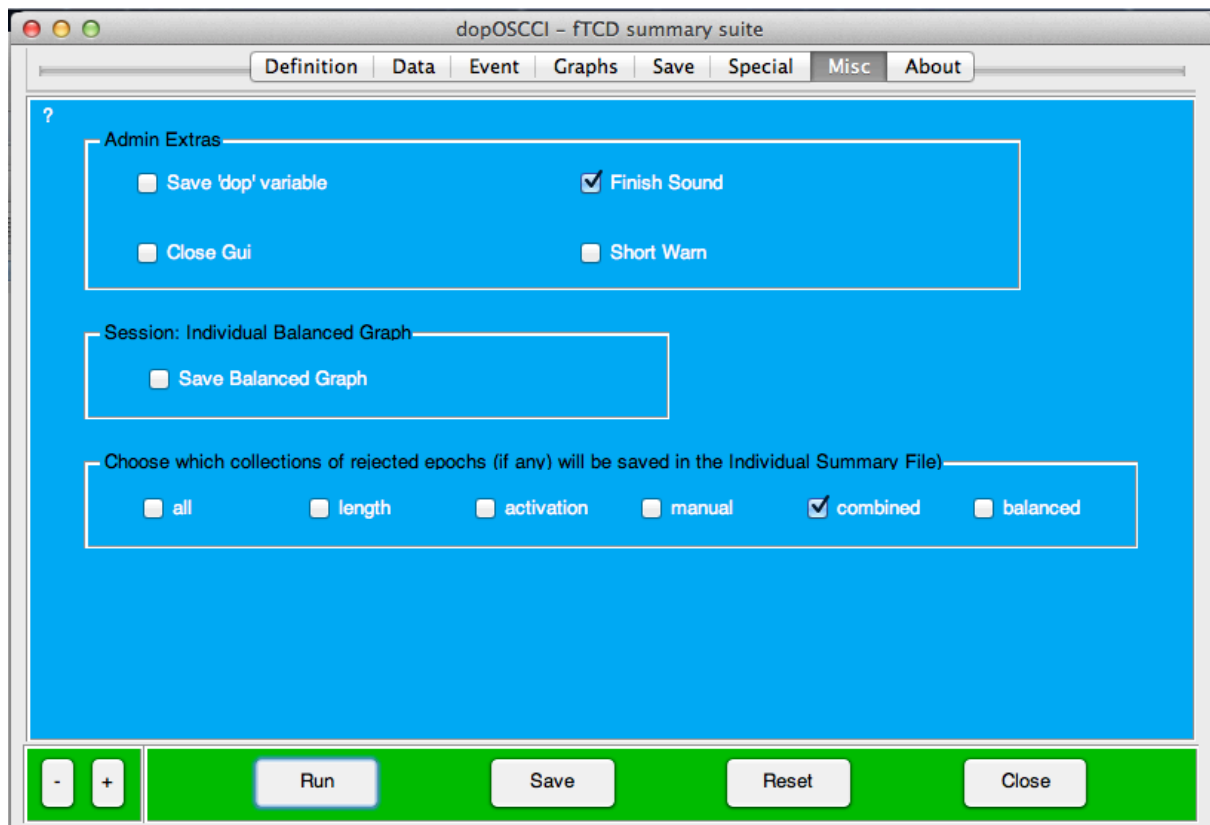


Figure 23: The Misc Tab of the gui

Save 'dop' variable

This allows you to adjust whether the 'dop' Matlab structure is saved at the end of the summary. This is setup for the development of dopOSCCI.

Finish sound

dopOSCCI plays a short .wav file at the end of the summary. This can be turned off or replaced with your own sound (~dopOSCCIm2\dopTools\genTools\finishSound.wav).

Close gui

Select this checkbox if you want the dopOSCCI gui to close when the summary is started.

Short Warn

Select this checkbox if you wish to receive pop up dialog warning boxes when the available data is short.

Save Balanced Graph

If you are using the [Session File](#) function you may choose to save an individual graph with an equal or balanced number of epochs per session. Note that the individual graph checkbox must be selected on the graphs tab for this to function.

Save Rejected Epochs

Select these checkboxes to save a record of which epochs were rejected for particular sets of screened epochs. This is saved as a string or text variable with epoch numbers separated by a tilde; for example, if epochs number 4, 6, were rejected, the output variable would be saved as 4~6~7.

Tab 8: About

The about tab contains version and date information which is useful to determine whether you have the most up-to-date copy of dopOSCCI.

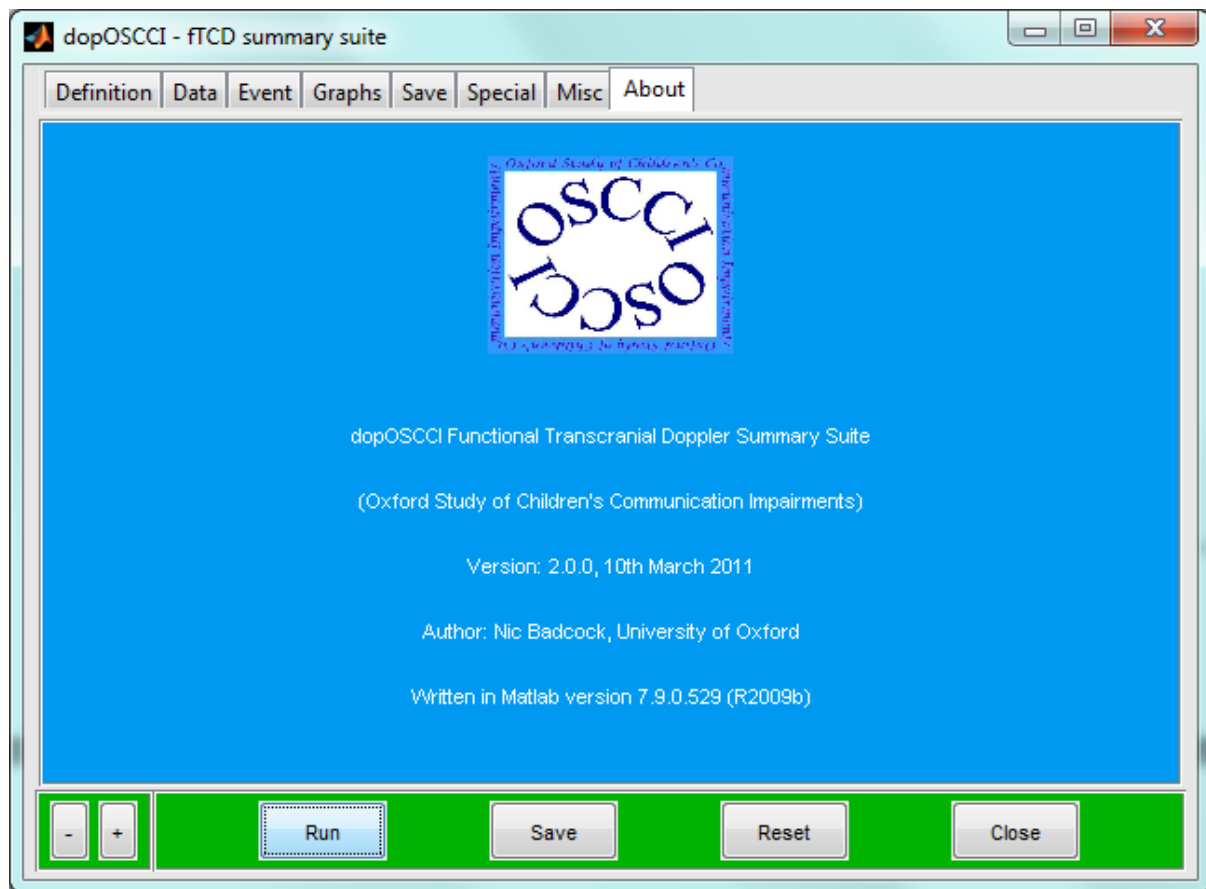


Figure 24: The About Tab of the gui

Running Data Processing

To initiate the dopOSCCI data summary press the **Run** button, which is found at the bottom of the gui display. With any luck, things will run smoothly. In some circumstances it is worth looking out for warning messages and sounds. These may indicate that there is something that needs to be amended before the summary will complete successfully. After the first file has been successfully processed it will show an approximate time left until completion. Make a keyboard press through the graphs if you have selected for graphs to be displayed ([see p.23](#)). Once the data analysis is complete click on the hyperlink, '[Open Windows Explorer to save directory](#)', to where data is stored⁹.

dopOSCCI carries out the following processes on the raw data (see [General Data handling p.12](#)).

Down-sampling

Raw Doppler data is collected is at 100Hz, i.e. 100 data points are recorded every second. This input is down-sampled by dopOSCCI to a more manageable rate, e.g. values being calculated every 0.04 seconds instead of every 0.01.

Heartbeat corrections

dopOSCCI corrects for fluctuations due to heart beat by determining local peaks in the left Doppler channel. Activation from one peak to the next is then averaged to remove distortions due to heartbeat (see Deppe et al., 1997). As a standard, the mean value between peaks is used, however if drop-out is detected (signal values of zero), a median value is taken in order to reduce the influence of this artefact.

Normalisation

In order to control for global differences in recorded velocities, unrelated to the task, between channels, raw data is normalised to a mean of 100 using a standard formula:

$$normalised = \frac{raw * 100}{mean(raw)}$$

See [Epoch Trim p. 13](#) and [Epoch Norm p. 14](#) for specific modifications to normalisation.

Difference activation

Relative to baseline blood flow velocity, activation in the right channel is subtracted from the left in order to calculate the difference activation.

⁹ Please note this hyperlink will only be operational provided the Matlab current directory remains unchanged.

Data Processing Output

When Matlab finishes processing the data there will be a hyperlink to the location of the saved data called '[Open Windows Explorer to save directory](#)'. This will take you to the output folder containing your data, labelled according to the epoch, baseline, and period of interest settings, e.g. epoch-12to40_base-10to0_poi25to35. This output folder is found within the folder that you specified as your **Save Directory** under **Tab 5: Save** of the gui. Any subsequent analysis carried out under the same task will automatically be saved here. If identical baseline and POI parameters are used, a separate folder will be created, differentiated from previous analyses using the + symbol, e.g. epoch-12to40_base-10to0_poi25to35+.

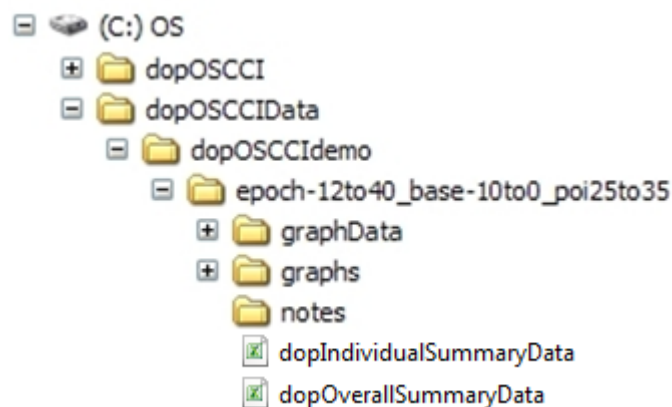


Figure 25: Location of Data Output

Individual Summary File

This contains the descriptive and inferential statistics for each data file, e.g. number of epochs used, Laterality index, time of maximum peak difference, SEM, standard deviation, 95% confidence interval. The amount of detail saved here depends on the checkboxes selected on the **Epoch Statistics**, **Individual Laterality Index** and **Individual Extra Statistics** supplementary buttons on **Tab 5: Save**.

Overall Summary File

This contains the average descriptive and inferential statistics for the overall summary, e.g. number of epochs used, Laterality index, time of maximum peak difference, SEM, 95% confidence interval. The amount of detail saved here depends on the checkboxes selected on the **Overall Laterality Index** and **Overall Extra Statistics** on **Tab 5: Save**.

Output Variable Titles

The Individual and Overall summary files include a custom series of summary variables. Due to the large number and variety of options available, the variable titles incorporate detailed descriptive information for identification. The basic format of the titles includes reference to:

- the channel summarised (left, right, difference, or average);

- the period used to calculate statistics. These could be fixed or calculated periods. Fixed periods are referred to as 'fixed' because they are independent of data channels (epoch, baseline and period of interest). Calculated periods are dependent upon channels: for example the maximum of the difference channel, either within the POI or across the whole epoch;
- the variable type or statistic (e.g. mean, standard deviation, 95% confidence interval);
- the epochs selection (e.g. all, activation, length, manual, combined); and
- the name of the event marker.

These are abbreviated in order to deliver more manageable title lengths.

General Variable Titles

A list of these abbreviations appears in [Table 1](#). The variable titles include capital letters and underscores to disambiguate information. Some examples follow:

- Depoch_Mcomb_eventName
 - o difference data, epoch filter, mean, combined epochs
- Dbase_SDep3_eventName
 - o difference data, base filter, standard deviation, epoch 3
- Lpoi_MEp11_eventName
 - o left data, mean, epoch 11
- DAbsMaxPOldif_Mcomb_eventName
 - o difference data, filter based on absolute maximum within period of interest of difference data, mean, combined epochs

Table 1. General list of variable title abbreviations (Abb.) and explanations (Exp.)

| Data | | Filter (based on) | | Type (statistic) | | Epochs | |
|-------|-----------------|-------------------|----------------------------------|------------------|----------------------------|--------|--------------------------------|
| Abb. | Exp. | Abb. | Exp. | Abb. | Exp. | Abb. | Exp. |
| L | left | epoch | data from whole epoch | T | time | all | all available |
| R | right | base | data from baseline period | M | mean | length | length appropriate |
| D | difference | poi | data from period of interest | SD | standard deviation | act | activation appropriate |
| A | average | left | left data | SEM | Standard error of the mean | man | manually selected |
| drop | dropout | right | right data | 95CI | 95% confidence interval | comb | combined: includes above |
| epRej | Epoch rejection | dif | left minus right difference data | MIN | minimum value | bal | balanced: see Session function |
| | | avg | left:right average data | MAX | maximum value | ep# | Individual epoch |
| | | AbsMaxPOI | absolute max in poi * | RMS | root mean squared | | |
| | | AbsMax | absolute max in epoch* | MED | median | | |
| | | MaxPOI | max in poi* | IQR | inter-quartile range | | |
| | | Max | max in epoch* | count | total number | | |
| | | AbsMinPOI | absolute min in poi* | pct | percentage | | |
| | | AbsMin | absolute min in epoch* | gor | goodness of recording | | |
| | | Min | min in poi* | | | | |
| | | MinPOI | min in epoch* | | | | |

* these points are calculated and statistics are based upon activation window sized data around this point

Laterality Index Variable Titles

The titles for the laterality index (LI) calculations are provided with the abbreviations displayed in **Table 2**. The variable titles include capital letters and underscores to disambiguate information. Two examples are:

- Llepochs_comb_eventName
 - o laterality index, number of epochs, combined epochs
- LI95pctCI_comb_eventName
 - o laterality index, 95% confidence interval, combined epochs

Table 2. Laterality Index variable title abbreviations and explanations.

| Abbreviation | Explanation | Note |
|--------------|--|---|
| Llepochs | number of epochs used for calculation | |
| LlpeakSec | peak time of left minus right difference within POI in seconds | |
| Llmean | mean of LI values for included epochs | |
| Llstd | standard deviation of LI values | |
| Llsem | standard error of the mean of LI values | |
| LI95pctCI | 95% confidence interval of LI values | |
| Llmin | minimum LI value | |
| Llmax | maximum LI value | |
| Llmedian | median LI value | |
| Lliqr | Inter-quartile range of LI values | |
| Llt#sig | logical significance of t-test (different = 1, not = 0) | # = 1 or 2, referring to t-test values: 1-sample (LI different to zero) or 2-sample (left versus right) |
| Llt#p | p-value of t-test | |
| t#ci | confidence interval of t-test | |
| t#t | t-value | |
| t#df | degrees of freedom of t-test | |
| t#sd | standard deviation of t-test | |
| Llt#cohen | effect size estimate of difference: Cohen's <i>d</i> | |
| Llrsg | logical significance of rank (different = 1, not = 0) | |
| Llrp | p-value of rank test | |
| Llrsum | rank sum value | |
| Llrzval | rank sum z-value | |
| LlrZr | effect size estimate of rank sum based on z-value | |
| jb1_norm | normality test (different = 1, not = 0) | Jarque-Bera test of normality: based upon LI values |
| jb1_p | p-value | |
| jb1_stat | statistic (see Matlab help jbtest) | |
| jb1_crit | critical value | |
| jb2?_norm | normality test (different = 1, not = 0) | Jarque-Bera test of normality: ? = L or R, referring to left or right values |
| jb2?_p | p-value | |
| jb2?_stat | statistic (see Matlab help jbtest) | |
| Jb2?_crit | critical value | |

Graphs Folder

dopOSCCI offers several different options in which you can visually display your data output. Each of these will now be addressed in turn.

Raw

When **Raw** is selected on [Tab 4: Graphs](#), a graph is created for each data file showing the Multi-dop imported data. Raw Doppler velocity (cm/sec) for the left (blue) and right (red) Doppler channels are shown across time in samples during a single experimental session. Event markers are displayed in green (see [Figure 26](#)).

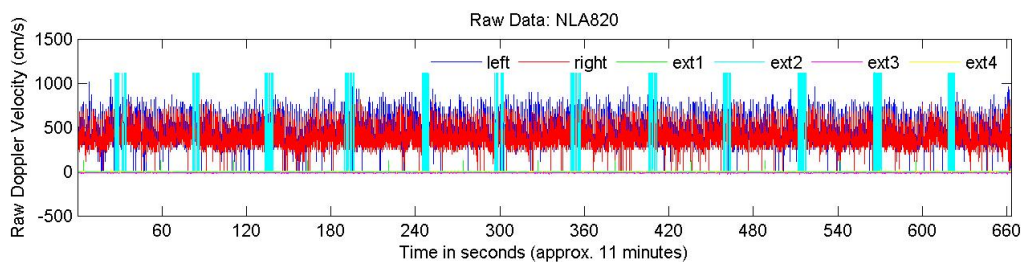


Figure 26: Raw graph

Normed

A Normed Graph (selected on [Tab 4: Graphs](#)) depicts the left (blue) and right (red) Doppler velocity after [Normalisation](#). It also shows the chosen [Epochs](#) period (yellow) and [Baseline](#) (black), as well as the number of raw (pink) and matched (green) event markers. The light blue lines indicate the limits set on the [Activation Rejection](#) boxes on [Tab 3: Event](#). Epochs in which left or right activation crosses either of these lines will be excluded from the analysis.¹⁰ In [Figure 27](#) the activation rejection is set to 70 to 130% of baseline blood flow velocity. Under these parameters, epochs 1, 4, and 7 would be excluded from the summary as activation in the left or right channel exceeds the upper or lower limits.

¹⁰ Ensure either the activation or combined checkboxes are selected on the Individual LI or Extra Statistics button on Tab 5: Save for activation rejection to take effect.

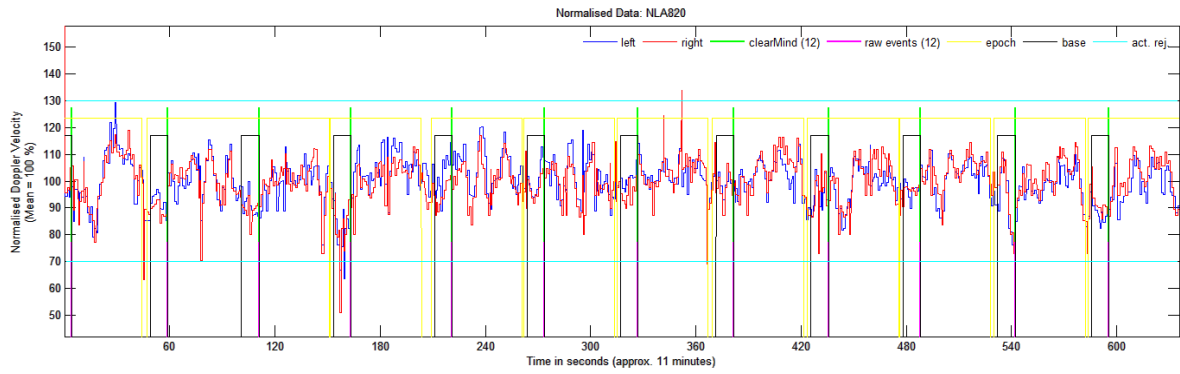


Figure 27: Correctly Matched Normed Graph

The Normed graph is also useful for checking which markers dopOSCCI will use for the summary (see [Separation p. 16](#) for more information). [Figure 28](#) demonstrates how dopOSCCI will first search for the final event marker and then locate the previous markers by searching backwards by the amount specified in the [Separation](#) field until all requested epochs have been found (in this case 9 epochs). In this way, dopOSCCI will ignore any additional spurious markers found at the beginning of some of our raw data files.

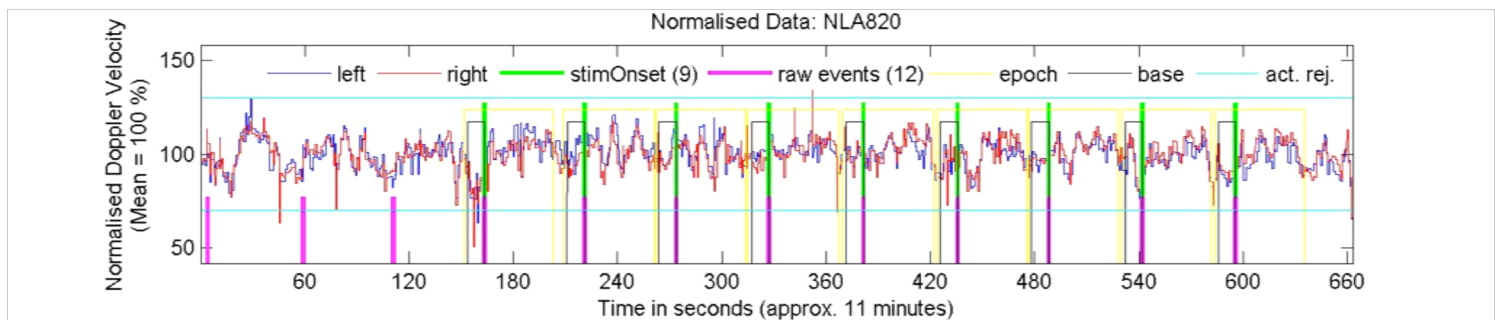


Figure 28: Matched graph - looking for markers

If the separation value is too high, dopOSCCI will not be able to correctly identify all the event markers. [Figure 29](#) shows the same raw data file as in [Figure 28](#). However in [Figure 29](#) the [Separation](#) value was incorrectly set at 55 seconds rather than 48 seconds. This results in dopOSCCI ignoring trial markers and therefore only finding half of the trials¹¹.

¹¹ This is a very serious problem if you are attempting to use the special behavioural function – it is crucially important that all trial makers exist and are correctly related to behavioural characteristics.

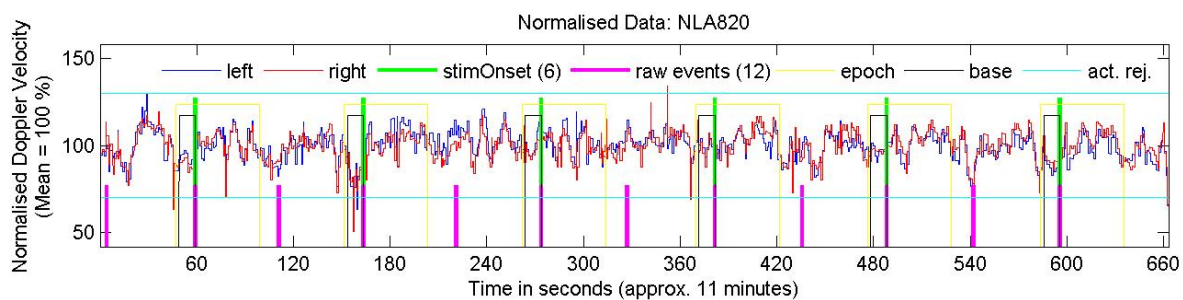


Figure 29: Normed Graph - Incorrect Separation

Epoch, Individual and Overall Graphs

When the **Epoch**, **Individual** and **Overall** options are selected on [Tab 4: Graphs](#), two graphs will be produced, one above the other. The top one plots the left (blue) and right (red) Doppler Velocity (cm/sec), after the **baseline** has been subtracted, and the lower one plots the difference in Doppler Velocity between the left and right channels (black). The grey field represents the specified **Baseline**, and the green field the specified **Period of Interest** (POI). The **Activation Window**, depicted by the yellow box, is centred on the **Peak Difference in Activation** (light blue), within the **POI**. The average difference in activation within this window is the **Laterality Index**. This is recorded on the right hand side of the **Difference Graph** (lower panel). As the difference activation is the left minus right channels, positive lateralisation indices reflect left lateralisation and negative reflect right. The significance, standard error of the mean (SEM) and number of epochs (on individual graphs) or files (on overall graphs) used for the calculation is also recorded.

The LI estimate is depicted on the difference graph by a red cross. The horizontal line simply reflects the time period of the **Activation Window** (e.g. 2 sec) whereas the vertical line reflects the 95% confidence interval surrounding the LI. Some researchers 'test' the significance of their LI by determining whether the 95% confidence interval overlaps with zero.

Epoch

Epoch by epoch graphs show left, right and difference activation for every epoch for each individual file. Epoch graphs will be produced even for screened or excluded epochs.

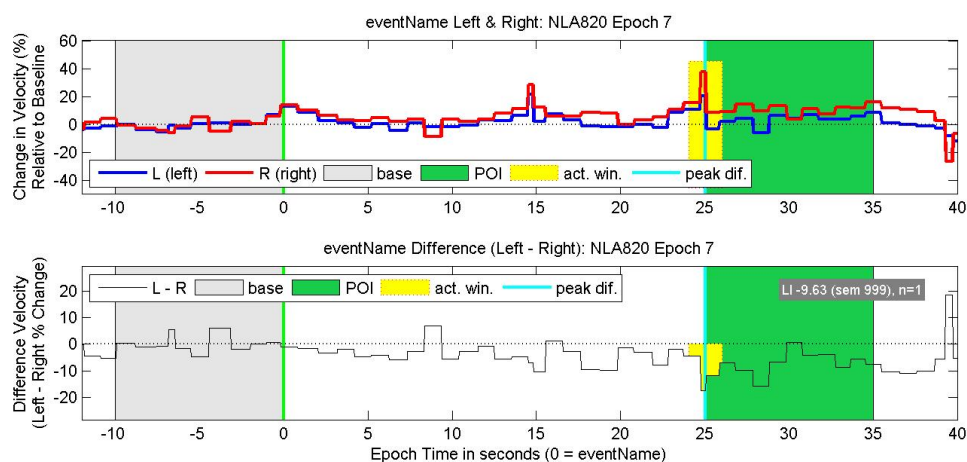


Figure 30: Epoch Graph

Individual

The Averaged Individual graphs show the left, right, and difference activation for each participant, averaged across all accepted epochs (after screening). The number of epochs used is shown at the top right of the graph with that individual's Laterality Index and SEM.

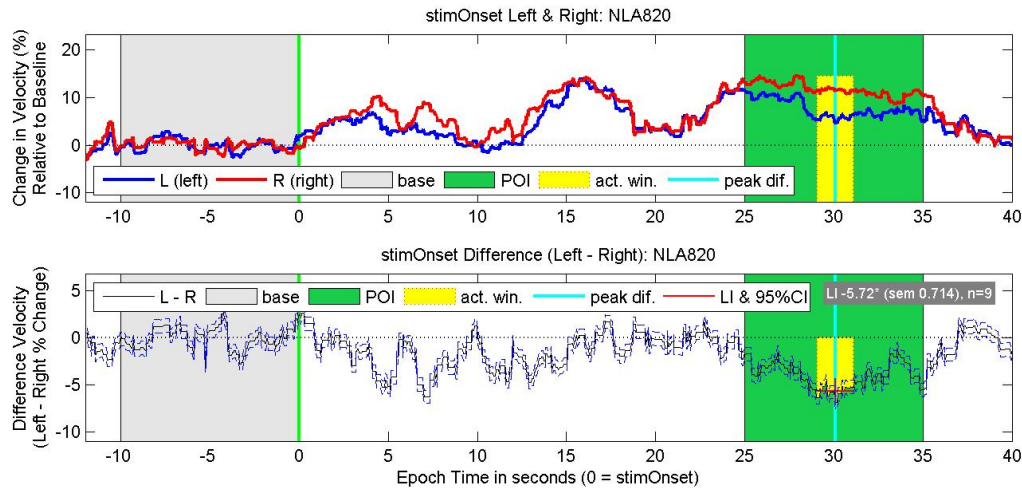


Figure 31: Individual Graph

Overall

The Overall graph shows the left, right, and difference activation, averaged across all summarised individual files. The number of files included in the analysis is displayed in the grey laterality index box, e.g. n=8.

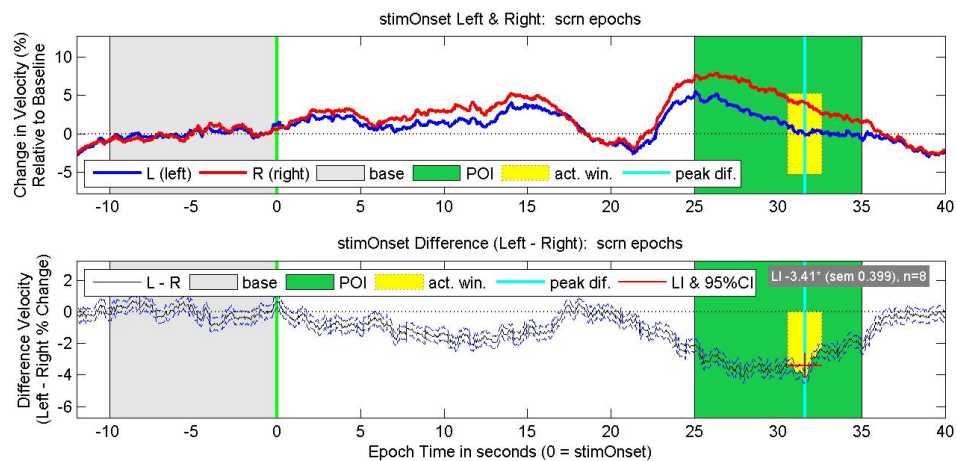


Figure 32: Overall Graph

Graph Data Folder

The graphs produced by dopOSCCI are unlikely to be suitable for publication and are merely aimed at providing a quick and easy visualisation of the data. Therefore, the normalised data that these figures are based upon is saved in tab-delimited files so that graphs suitable for publication can be easily created (for Graph Data save options see [p.37](#)). These files can be found in the '**graphData**' folder (see [Figure 33](#)).

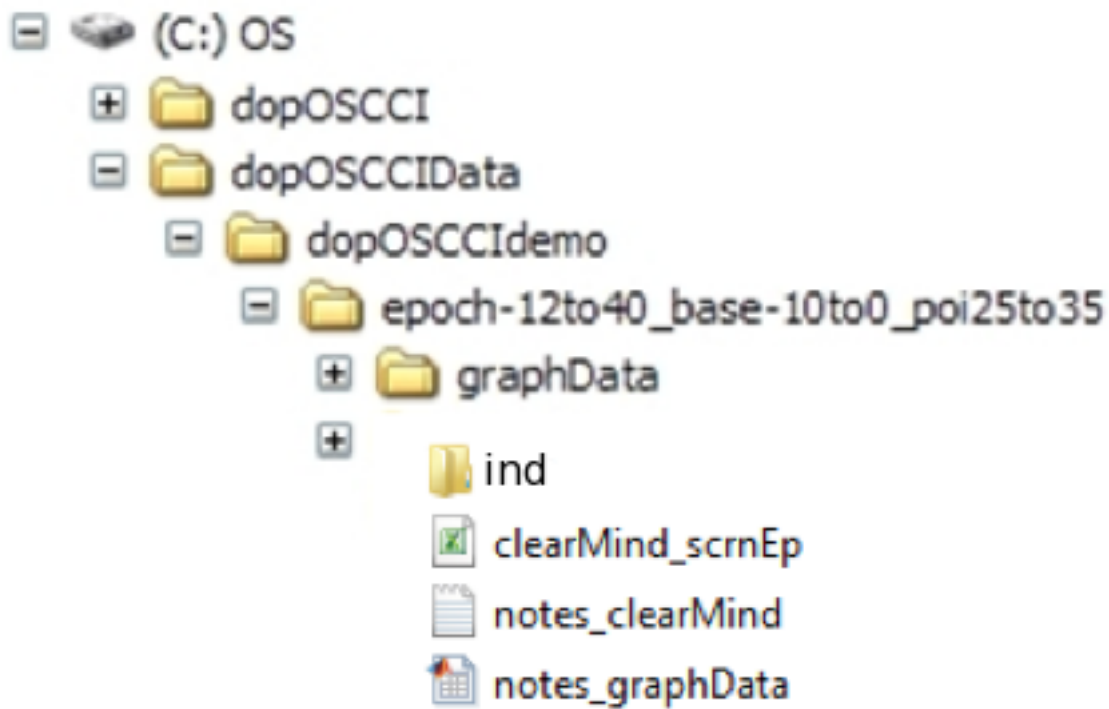


Figure 33: Location of Graph Data Files

Graph Data File

Horizontally or vertically aligned data files (for Graph Data save options see [p.37](#)). arranged in rows with the time sample for the left, right, difference and average shown in blocks through the first row, with the corresponding activation levels for each participant at each time sample in the rows below.

Notes_EventName

This is a record of the timing and matching details of the event as specified on [Tab 3: Event](#). It also records which channels (left, right, difference, average) were saved under channel selection.

Notes_graphData

This is a Matlab '.mat' file which holds information used in the processing of the Overall graph data and summary statistics.

Ind folder

The data for individual data sets can be saved (see Graph Data save options see [p.37](#)) and will be saved into a separate folder. If there are multiple data sets for each individual, then individual folders will be created, labelled by the Doppler data file name.

Notes Folder

The following note files will be created in the notes folder within the main data output folder. They contain information about the summary setup, processing and output and can be a useful record to check exactly what was done at a later date. The default setting creates six types of note file every time the summary runs.¹² If you do not want all these files to be produced uncheck the boxes on the **Notes Save** button on **Tab 5: Save**.¹³

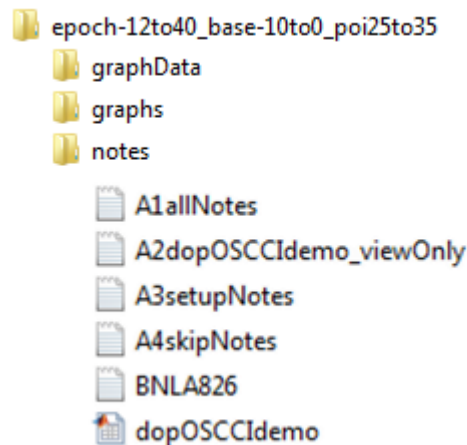


Figure 34: Notes Folder

File Notes ('B' files)

Each **B file** is named using the NLA file and includes a summary of the parameters selected for the analysis, along with the details of the processing as it appeared in the Matlab command window. This includes such information as the file name, location and time the file was made, number of epochs found, which epochs were rejected and why, split-half calculations and the laterality index (this is not an exhaustive list). It is useful to note the warning messages which point out, for example, if there is not enough data for a baseline for a particular epoch and other reasons why an epoch might be excluded. These files contain the same information that can be found in the **A1allNotes** file, only separated into individual files for each participant.

A1allNotes

A text file which records everything that appeared in the Matlab command window during the data processing. It combines the information from all the **File Notes ('B' files)** into one file.

Task Definition Notes: A2viewOnly.txt. File and Matlab .mat File

On running a summary, a **Matlab.mat task definition file** (and readable .txt version) is automatically created in the **TaskData** folder. The .mat file holds details of all the dopOSCCI settings selected on

¹² SkipNotes will only be created if necessary i.e. if files were skipped during processing.

¹³ There is no option in Notes Save to stop the SetupNotes being created. However they will not be made if the All Notes and File Note checkboxes are not selected.

the gui for that particular task. This means that on returning to dopOSCCI and completing the *Task Name* field, all previously chosen settings for that task will automatically be updated on the gui.

The default setting is to make a copy of this definition file in both .mat and .txt formats to the **Notes Folder** (this option can be turned off on the Save Notes button on *Tab 5: Save*). These files outline all the dopOSCCI settings selected for your summary. The **A2viewOnly.txt** file is a readable version of the **Matlab.mat** file.

A3setupNotes

This is a record of the initial setup before the summary began. It shows which raw data files were selected for the summary and records which special functions were used.

A4skipRecord

Here dopOSCCI will record which files, if any, have not been included in the processing and the reason for skipping them. Skipping a file can occur for five reasons: firstly, if the file was not selected on *Tab 2: Data*; secondly, if no markers were found; thirdly, if all trials were excluded using the *Manual Screen file* function; fourthly, if the Group File function was selected but no group was specified in the *Group File* and lastly, if the Session function was selected but the file was not matched up with another file in the *Session File*.

Miscellaneous

Administrator rights

Windows restricts user privileges based upon the type of access that is given to an individual's login. Without sufficient rights, a user won't be able to write to certain directories on the computer's hard drive. Windows Vista is particularly rigid in this sense. Therefore, in order to modify Matlab's path definition file you are required to have a high level of user access. See your network administrator if this is a problem for you.

Operating systems

dopOSCCI was developed on a Windows XP and has also been used with Vista and 7. More recently it has been adapted for Mac use (Mac OS X version 1.7.2 to be precise). Some of the hyperlinks from the Matlab command window are not yet operational outside of Windows.

Matlab versions

dopOSCCI was written in Matlab 2009 but has been used in 2010, 2011, and even 2008 versions without any functional complications.

Matlab Toolboxes

If available, dopOSCCI makes use of the Signal Processing and Statistical Toolboxes. In the absence of the Signal Processing Toolbox, a supplementary function 'dopDownsample' is utilised. In the absence of the Statistical Toolboxes, some of the advanced statistical tests are not available and will appear as 999 if set to be saved in the output files.

References

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- Kuschinsky, W. (1991). Coupling of function, metabolism, and blood flow in the brain. *Neurosurgical Review*, 14(3), 163-168.
- Knecht, S., Dräger, B., Flöel, A., Lohmann, H., Breitenstein, C., Deppe, M., Henningsen, H., & Ringelstein, E. B. (2001). Behavioural relevance of atypical language lateralization in healthy subjects, *Brain* 124(8) , 1657-1665.