Turbo-Satori 1.4

Getting Started Guide

Overview

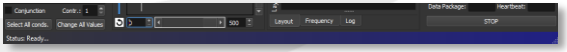
About Turbo-Satori

Turbo-Satori (TSI) is a real-time analysis program for functional near-infrared spectroscopy (fNIRS) data. While the also available Satori program is aimed at offline analysis, Turbo-Satori is optimized for real-time applications, such as neurofeedback and brain computer interface (BCI) implementations. The software supports online oxy/deoxy concentration value calculations from raw wavelength data, comprehensive real-time statistical data analysis, machine learning routines, quality assurance tools, and it provides advanced built-in BCI and neurofeedback options. Furthermore, it allows online analysis of already acquired fNIRS data, reading directly from NIRStar header information or Satori project files. An extensive plugin and network interface allows to access the processed information from Turbo-Satori in real-time.

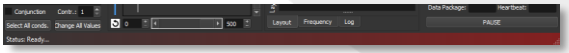
Let's get started

1. If you have not already installed the latest Turbo-Satori version, you can do so by running the TSI installation routine. Follow the instructions on the screen and install TSI to a location, where you have read and write access.
2. After installation, you can start TSI. The links have been placed in the start menu. There are two different TSI applications: Turbo-Satori and Turbo-Satori_SimulMode. If you want to perform a real-time experiment, please use the Turbo-Satori executable. If you want to rerun an already performed experiment, run the Turbo-Satori_SimulMode, which simulates real-time processing. The two modes can be easily differentiated by the blue (real-time) or red (SimulMode) icon and status bar.

Turbo-Satori



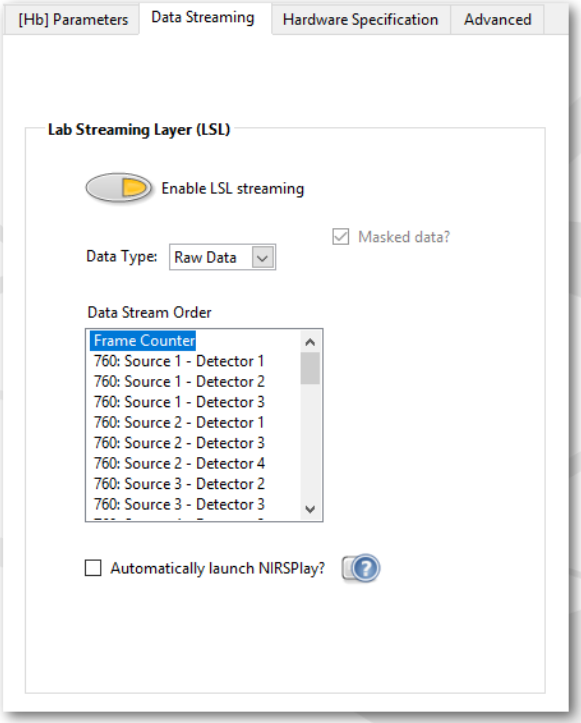
Turbo-Satori SimulMode



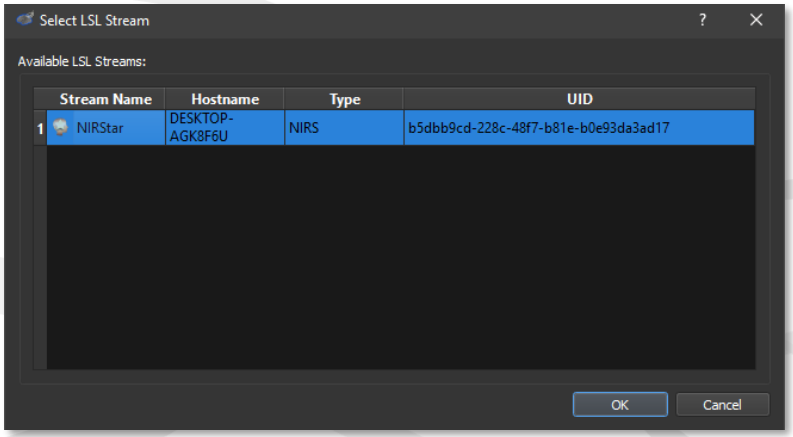
NOTE: Turbo-Satori SimulMode is automatically activated after you have been successfully connected and disconnected to NIRStar or Aurora using the Turbo-Satori real-time mode. The activation lasts for one month and is automatically renewed for another month after each successful connection.

3. Let us start with the real-time version and connect to NIRStar. First, you need to ensure that NIRStar (version 15.2 or higher) is installed and running, either on the same system, or on a computer that is in the same network or directly connected to the computer running TSI.
4. To be able to connect to NIRStar, we first need to enable the data streaming. Open the “Configure Hardware” menu item and navigate to the “Data Streaming” tab.
5. Enable the “Lab Streaming Layer” (LSL) by checking the button next to the “Enable LSL streaming”, as shown on the right.
6. The transferred data type can be set to “Raw Data” if TSI should take care of the HbO/Hb transform of the wavelengths. Otherwise, select the “Hb States” option, so that NIRStar performs the transformation.
7. After checking all necessary settings in NIRStar (including the montage), you can go back to TSI and connect to NIRStar. TSI automatically uses the LSL as a default connection type. Press the 

button to start the connection. The LSL will now automatically try to find available streams.



8. A window with available LSL streams will appear (see below). Select the preferred stream and confirm by clicking “OK”.

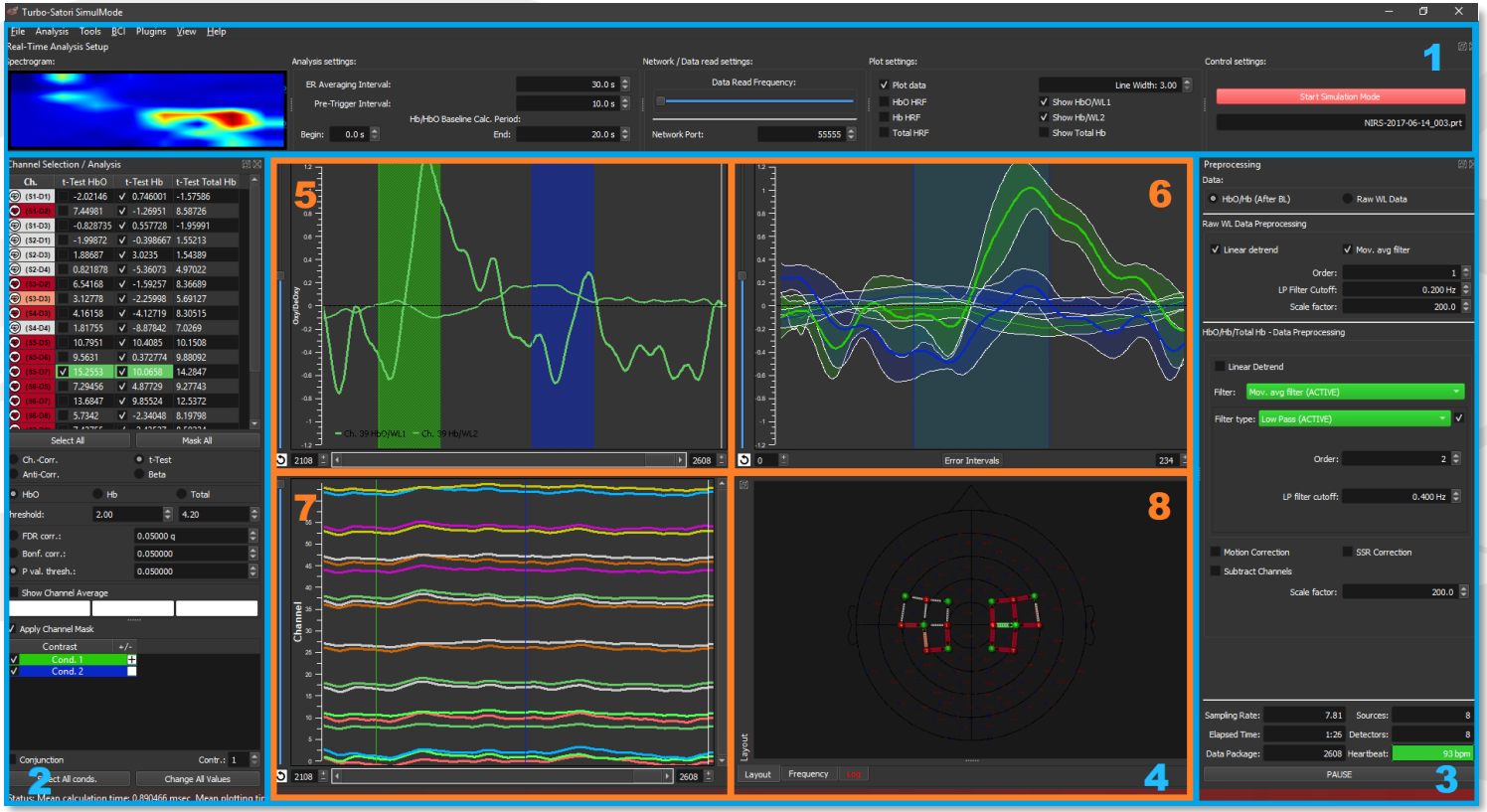


9. The connection should now be established and the connect button should have changed from red to green. The text on the button should now say “Disconnect From NIRStar”: 

10. Turbo-Satori is now connected and will show the incoming fNIRS data from NIRStar as soon as you start previewing or recording. It is advised to connect to NIRStar before you start the recording. This ensures a synchronized data processing for the generated protocols in TSI.

    Please refer to the TSI User’s Guide for more information about different connection types, network troubleshooting and settings.

User interface



The user interface of Turbo-Satori mainly consists of four parts with specific settings and options.

1. The **real-time analysis setup window**, which includes configurations to set up the real-time analysis as well as connection, plotting, and control settings.

2. The **channel selection and analysis window** contains the basic parameters and table to perform real-time analysis of the available channels.

3. The **preprocessing window** allows to change the preprocessing parameters for raw wavelength data as well as for the HbO/Hb converted data. Additionally, the status information is shown in the bottom of the window.

4. The **main application window** provides three different plots and a layout view, frequency spectrogram and log window area (numbers 5-8), showing useful information or the layout of the sources, detectors and channels.

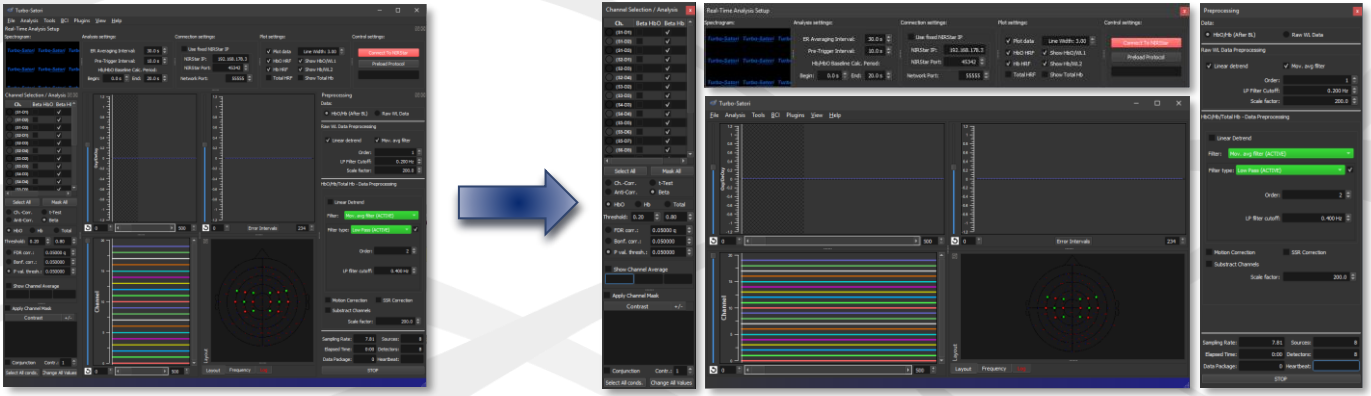
    5. The time course of the **selected channels** (or average) for Raw wavelength 1 and/or 2, HbO and/or Hb signal.

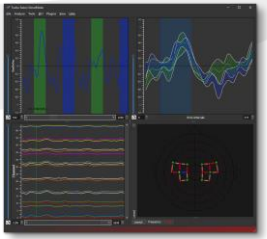
    6. The **event related average** of the selected channels time course.

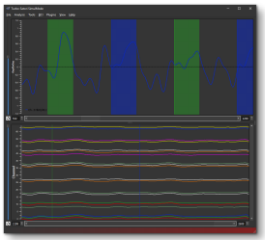
    7. The combined plot for **all marked channels**.

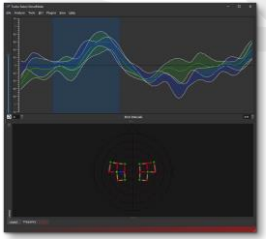
    8. The **layout view**, **frequency spectrogram** and **log window** area.

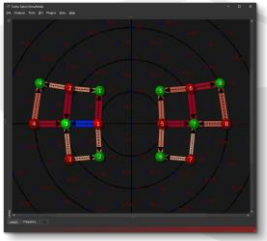
The user interface is also freely adjustable, meaning windows can be set into a floating state or completely hidden, in case they are not needed. The main window can also be arranged to visualize only the data of interest.







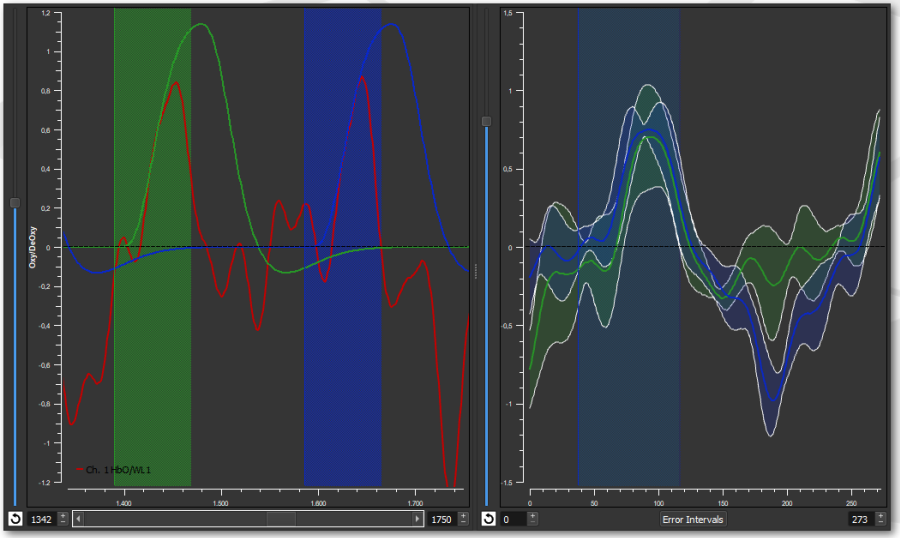


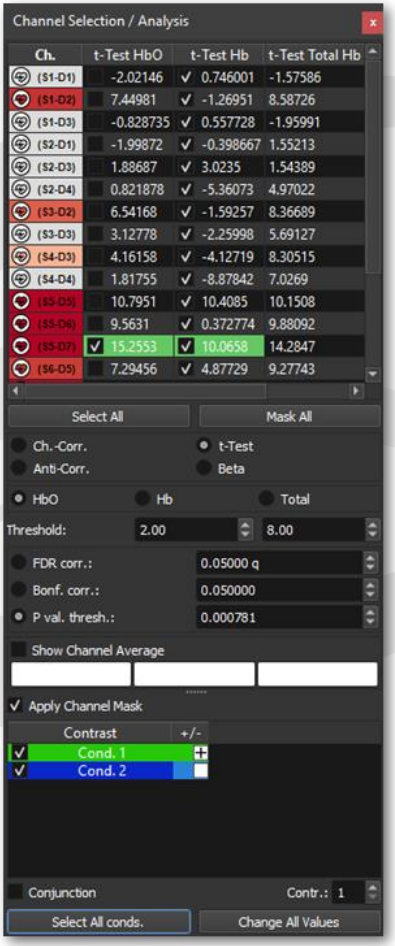


Getting more advanced

Turbo-Satori allows real-time analysis of fNIRS data. To be able to define conditions for your experiment, Turbo-Satori will either directly read the trigger information from NIRStar or use a protocol file (“prt”), if provided. The coding of the triggers follows a very straightforward scheme: The first trigger (value 1) is always the rest or baseline condition and is used to declare the end of an active task condition. The values for the task conditions range from 2 to 10. Take care that you use the right trigger values in your stimulus presentation software, so that Turbo-Satori can read the trigger properly. A task can be started by sending the specific task trigger to NIRStar and is finished by sending the baseline (1) trigger.

Triggers are marked using different colors and visualized as zones in the background of the plots. The convolution of the hemodynamic response function (HRF) with the condition is created in real-time as soon as a trigger is received. The HRF is the basis for the general linear model (GLM) statistics, which are also calculated and updated in real-time. The HRF parameters can be changed in the GLM Dialog of the analysis menu. The event related average plot on the right of the figure allows to inspect differences between conditions in one view.





The statistical analysis consists of four major options:

- Channel Correlation
- Anti-Correlation of HbO and Hb per channel
- T-Test statistic of the GLM
- Beta output of the GLM

These results are calculated for HbO, Hb and Total Hb separately. The corresponding values are shown in the specific rows and columns of the table.

A heartbeat detection algorithm is continuously analyzing the data. If a heartbeat is detected in a specific channel, a small heartbeat symbol will appear. This is a very important quality measure, since it is expected to record visible heartbeat in every channel.

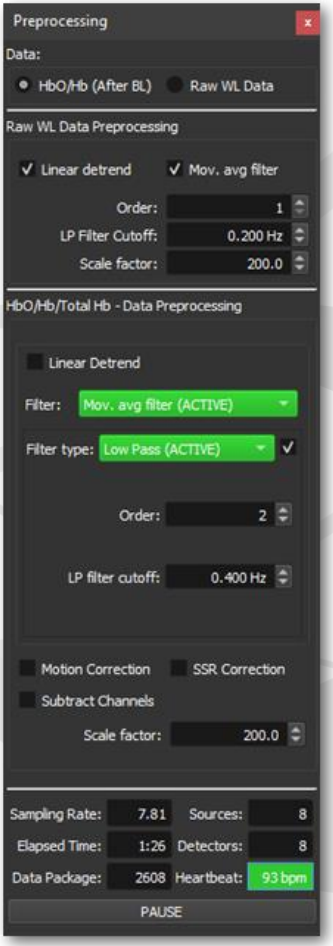
The Contrasts Window shows a list of all defined contrasts. They are typically defined automatically, based on either triggers or a protocol file (.prt). The Contrast column lists the names of available contrasts. These can be enabled by clicking in the “+/-” column of the respective contrast. A square with a plus in these columns indicates that the positive contrast (+1) is enabled, while a square with a minus indicates that the negative (-1) contrast is enabled. An empty square indicates that the contrast is disabled. Contrasts are always enabled in a two-sided fashion. This means that a “+” will highlight all channels exceeding the selected minimal t-threshold in both directions, positive (red color coding) and negative (blue color coding). The resulting statistical map of each enabled contrast is superimposed on channel names and in the layout view.

There are multiple preprocessing options available. In the HbO/Hb data processing section, one can select the **linear detrending** and **moving average** option as in the raw WL preprocessing, but the section also allows to apply different additional IIR filters:

- **Exponential moving average (EMA)**
- **Butterworth**
- **RBJ Biquad**
- **Chebyshev I**
- **Chebyshev II**
- **Elliptic**
- **Bessel**
- **Legendre**

To enable a specific filter, choose a filter from the *Filter:* drop-down menu and check the *Filter type:* underneath. The drop-down menu of the filter types can contain different filter types for the selected filter above. To activate the filter, check mark the type using the little check box right to the filter type drop-down menu. The settings of the filter type are defined below the drop-down menu. Multiple filter types can be applied at the same time and are marked in green. It is also possible to mix filter types from different filters. Note that the filters are marked in green if one of the filter types of the individual filter is activated.

Additional preprocessing procedures include **motion correction**, **short separation regression (SSR)** and **subtraction of specific channels**. All preprocessing steps are performed on HbO, Hb and Total Hb data separately.



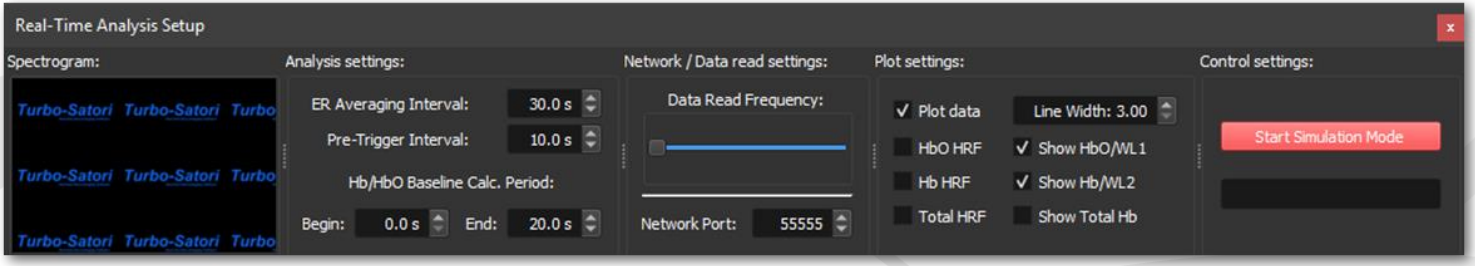
Review your data

Turbo-Satori SimulMode

Turbo-Satori operates in two modes: real-time and SimulMode. As stated in the beginning, we provide a separate executable for each mode. This enables one to review data during an ongoing recording using the real-time mode.

The Simulation Mode allows reading ".sri" (Satori project files) and ".hdr" (NIRStar header files) file types. To start, click the "Start Simulation Mode" button and a file selection dialog will pop up. Select the ".hdr" or ".sri" file you want to simulate.
In the Simulation Mode you have the same preprocessing and analysis options as in the real-time mode. The output is stored in the folder of the loaded ".sri" or ".hdr" file.

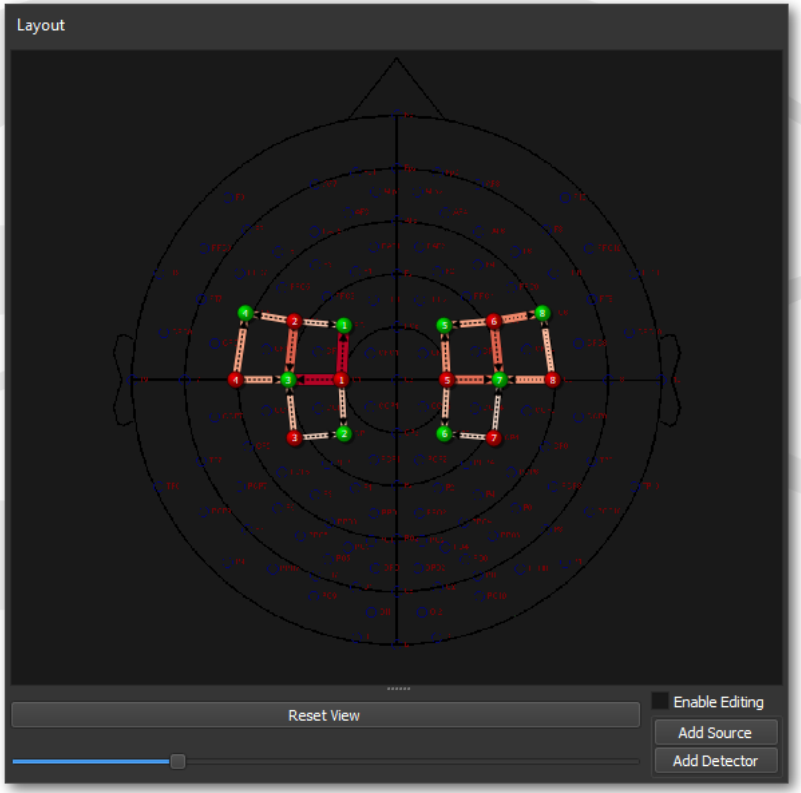
If a layout was used during recording with NIRStar, this layout will be automatically loaded in the Simulation Mode. You can also provide a "hdrname_ProbeInfo.mat" file afterwards, by placing it in the folder of the ".hdr" file.



The Data Read Frequency slider allows to change the frequency of reading in the data during the simulation. If the slider position is at leftmost, the reading frequency is set to the sampling rate as defined in the header or project. The more the slider is moved to the right, the higher the reading frequency. If you move the slider all the way to the right, then the data will be processed as fast as possible (fast forward). At the begin of the experiment, these settings will be changed automatically to the sampling rate of the current experiment. If you load another experiment while the slider is at the rightmost position, the new experiment will also be loaded as fast as possible. You can check the loading status using the frame counter at the bottom right of the main window.

The control settings are used to start and stop the simulation of an experiment. In Simulation Mode, a protocol is automatically loaded from the project information.

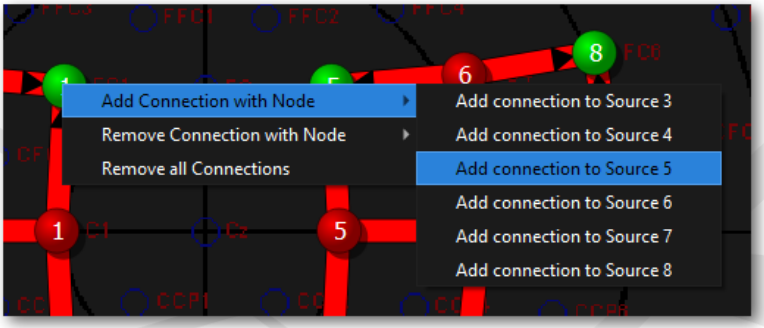
Layout Manager

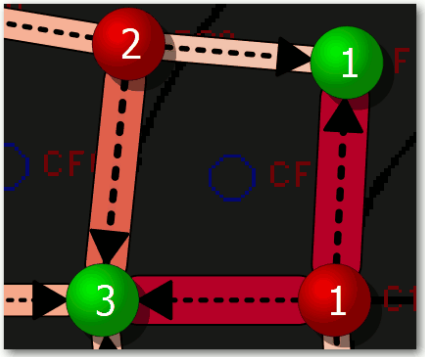


The layout manager shows the montage of an fNIRS experiment and visualizes the statistical parameters as a connection strength and color coding between sources and detectors. In the bottom of the layout window, an editor is provided to manually create layouts for Turbo-Satori. Clicking and holding the little dotted bar at the bottom of the layout window and moving it upwards will show the editor area. To hide it, follow the same procedure, but move it downwards.

A montage is automatically loaded if it was defined during recording in NIRStar. An additional *_probeInfo.mat* is then stored in the fNIRS data folder of the specific experiment. Turbo-Satori tries to load this file when loading a *".hdr"* or *".sri"* file or at the beginning of a connection to NIRStar using the LSL interface (NIRx SDK Interface does not provide layout information). If no montage was found, the last loaded layout file will be kept in the layout view.

The layout editor can be used to create Turbo-Satori layout files manually. To do so, enable the *Enable Editing* check box and click on *Add Source* or *Add Detector* to add a source or detector to the layout view. These sources and detectors can now freely be moved around by clicking and holding the cursor on the specific source or detector and move it to the target position. To connect sources and detectors, right click on a source or detector and navigate to the context menu Add Connection with Node. Here you will find a list of possible sources or detectors to which you can create a connection. The same mechanism can be used to remove a connection. There is also a convenient function to remove all connections from a source or detector to all other sources or detectors.





Additionally, the detected heartbeat is shown as moving pattern on top of the specific channel, as shown on the left. This allows to easily inspect channels, which do not provide enough signal quality to separate a heartbeat related frequency from the fNIRS frequency spectrogram. The heartbeat detection algorithm is performed on either oxy, deoxy or total data and runs as an incremental moving window, keeping the calculation time constant. The frequency spectrogram of the individual channels can be inspected using the frequency spectrogram plot in bottom right (frequency tab).

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