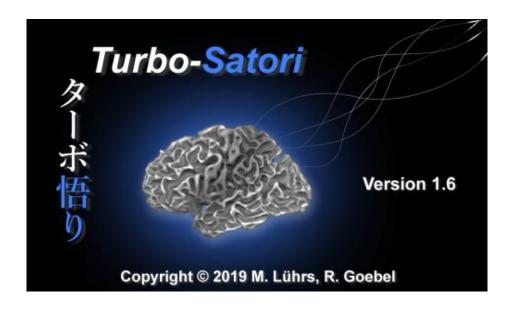


# Turbo-Satori



# **Practical Guide**

Version 1.2.2 for TSI 1.6

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#### ABOUT THIS DOCUMENT

#### **PREFACE**

Welcome to the Turbo-Satori (TSI) Practical Guide! This guide offers an overview of the essential features of the software and should be used as a self-study tool. Note that you do not have to proceed sequentially through the steps of the Practical Guide, but that files saved at an earlier step are needed at later stages of data analysis. Turbo-Satori will soon be available for several computer platforms but is currently only supporting the 32-bit and 64-bit versions of Windows 7 to 10. Take your time going through the steps. If the steps you are performing do not make sense to you, consider repeating some of the previous steps. If you still have problems or concerns, please don't hesitate to contact our support team (for details please refer to our website). In the beginning, all actions will be explicitly written out, in later steps, acquired knowledge is needed to complete the steps.

#### **CONTACT**

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#### DATA

You can find the raw data for the "fNIRS\_tapping" example on our web server:

http://download.brainvoyager.com/Satori/TSI-SampleData.zip

Please download "TSI-SampleData.zip" and extract all files in the following folder (replace <USER> with your login name):

Windows: "C:\Users\<USER>\Documents\TSIData\TSI-SampleData"

#### **ICONS**

The following icons highlight certain aspects of using Turbo-Satori throughout this Practical Guide:



This icon indicates that you should enter some information (e.g. a file name or a number).



This icon indicates that you should use the mouse to perform an action (e.g. click a button).

### Load / Save

This icon indicates that you should load or save a file.

#### **Attention!**

This icon indicates an important step.

#### (i) Extra Information

This icon indicates the following information is optional and only included to provide some background knowledge. No actions have to be performed.

#### **Bold**

Bold body text indicates that you should perform an action.

A black arrow indicates you should enter some information.

A green arrow indicates you should check some information, no further action is required.

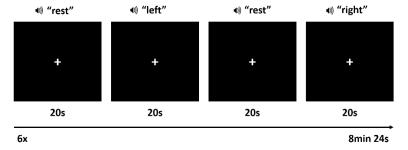
#### THE "HAND SQUEEZING" TUTORIAL

This tutorial gives an introduction into essential data processing steps with Turbo-Satori. The aim is to enable you to start using the program quickly and easily. The tutorial uses raw data from a simple block experiment described below.

#### The hand squeezing experiment

Participants were asked to close their eyes and follow the instructions presented through standard computer speakers. When they heard the word "right", they were instructed to start squeezing their right fist with a constant speed and reasonable force. Similarly, they started squeezing their left fist, when they heard the word "left". They stopped and relaxed when they heard "rest". The experiment can be found on the <a href="NIRX support website">NIRX support</a> website.

Initial baseline was 24 seconds long. The following 12 blocks of alternating left- and right-hand squeezing and intermediate rest periods were all 20 seconds long.



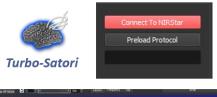
Session information		
Experiment:	Hand squeezing	
Conditions:	Rest	
	Right hand squeezing	
	Left hand squeezing	
Device	NIRSport (NIRx)	
Recording software	NIRStar (NIRx)	
Number of Sources	8	
Number of detectors	8	
Number of channels	20	
Sampling rate	7.81/s	
Sample information		
Participant	4	
Handedness	Right	
Number of trials	12	
Run number	3	

### PART I PREPARATION

#### 1. THE USER INTERFACE

Before starting, note that Turbo-Satori is used for real-time recording and data analysis. Offline inspection and analysis can be done with Turbo-Satori SimulMode, a separate executable in the same folder. As seen below, the two versions can be visually separated by the background color of the icon (blue for Turbo-Satori and red for Turbo-Satori SimulMode), the initial loading window and, once opened, the band color on the bottom of the window (blue in Turbo-Satori and red in Turbo-Satori SimulMode) and the main button in the control settings ("Connect to NIRStar" in Turbo-Satori and "Start Stimulation Mode" in Turbo-Satori SimulMode.

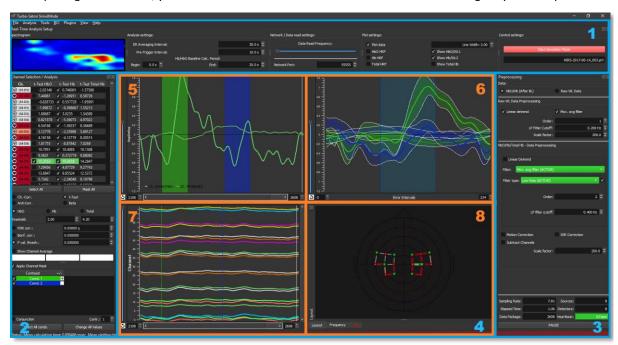








- 1. Launch Turbo-Satori by **clicking** the "Turbo-Satori" icon. Once open, you can see the main window with the main menu. Please, refer to point 2A to start a real-time recording in Turbo-Satori or 2B to begin with a simulation in Turbo-Satori SimulMode. Steps from point 3 on are the same for both, real-time and offline analysis.
  - 2. After opening Turbo-Satori, you see the main window which is divided into different logically distinct parts:



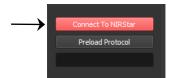
- 1. The **real-time analysis setup window**, which includes configurations to set up the real-time analysis as well as connection, plotting, and control settings.
- 2. The **channel selection and analysis window** contains the basic parameters and table to perform real-time analysis of the available 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.
- The layout view, frequency spectrogram and log window area.

#### 2A. TURBO-SATORI: CONNECTING TO NIRSTAR

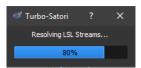
1. To start measuring, first **enter** the correct connection details in connection settings. The IP of the device running NIRStar can be checked in the NIRStar settings.

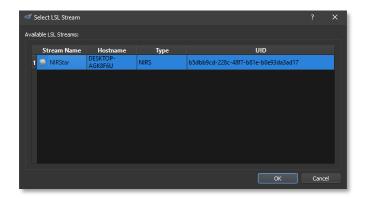


2. Then, connect Turbo-Satori to NIRStar by **clicking** on "Connect to NIRStar".



A progress window will appear showing progress of searching for LSL streams (see on the right). Then, a list of all available LSL streams will appear (see below). This enables you to select the acquisition computer in case you have more available.

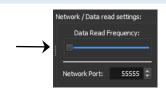


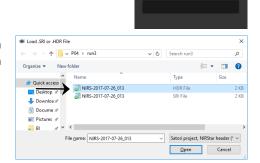


4. When the LSL is selected, and the connection is established, the "Connect to NIRStar" button will turn green. Please, refer to the log tab in the Layout window for more information about the current TSI connection status.

#### 2B. TURBO-SATORI SIMULMODE: STARTING A SIMULATION

- Adjust the data reading frequency to a low value (move slider towards the left), if you want to perform any contrasting or change filtering (described below). If the frequency is high (slider positioned at the right end), the data will load at maximum speed; this option is mostly used for reloading the already preprocessed data. Use the slider to speed up or slow down the loading.
- To perform offline analysis: Clicking on "Start Simulation Mode" will enable you to select a single run.
- Select a header file (\*.hdr) to load. In case you have already run the simulation before or prepared a Satori project file (\*.sri) in advance then the latter can also be selected.





For this demonstration, a run called "NIRS-2017-07-26\_013" will be used in a simple neurofeedback paradigm. Standard filtering options will be used as set during the first start of TSI. If you would like to use different filtering settings, it is possible to change them in the *preprocessing* window.

#### 3. CREATION OF THE STIMULATION PROTOCOL

In this step, you will learn how to create a stimulation protocol.

Note: if your stimulation includes triggers, you do not need to create and load a protocol file in advance.

There are two ways to create a stimulation protocol. If the header contains trigger information, it is also possible to automatically create a .prt file by loading the header file in the Turbo-Satori SimulMode. The name of the output file corresponds to the name of the header file and has "-autosave" added to it.

The other option is manual. The values (see below) are entered into a .txt editor and saved as a .prt file. For an example of a .prt file look at the figure below or in the User's Guide under Help in the *main menu*.



1. Temporal resolution can be **defined** in volumes (time \* sampling rate) or seconds. This will determine how the time points in each of the conditions will be interpreted.



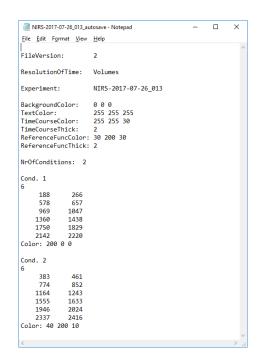
 The Experiment Name should be **defined** as something meaningful. If the conditions or timings in different runs are not the same (perhaps due to randomization of trials), we suggest including session, run or participant information, which will help to distinguish different files.

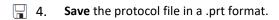


 Make sure to define the correct number of conditions (excluding baseline) under NrOfConditions. In this study we have two conditions, one for left hand squeezing and one for right.

In order to **define** the first condition, enter the name of it. In the next line define the number of trials. Then define the starting and ending time point of each trial (separated by a tab) in separate rows.

Do the same for the second condition.







You can load the prepared protocol file by clicking "Preload Protocol" in the *control settings* window. If your stimulation does not have triggers, it is essential that you start the measurement and stimulation at the same time! Make sure that TSI is connected to NIRStar in advance.

#### PART II RUNNING THE REAL-TIME DATA ANALYSIS

Once the data acquisition (or simulation) starts, data will appear in the *combined plot* and predicted HRF response will be shown in the *time course window*.

As soon as the first trial starts, an area of the *event related* average time course will become dimmed in the color of the condition. The size of the area corresponds to the length of the trial. Each trial of each condition will be plotted on top of the previous one, combining and averaging trials of the same condition (e.g., event related average). This enables an easy comparison between event related averages of different conditions.

By selecting two or more channels, it is also possible to visually inspect the differences in event related averages of the same condition between different channels.

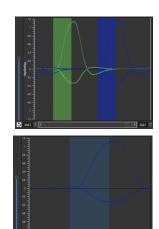
First, the contrast should be **defined** in the bottom of the *channel selection and analysis* window. To find the best channel for both left- and right-hand squeezing, the white box next to both condition 1 and 2 should be **clicked** so that a plus "+" appears. This way, both conditions will be contrasted with baseline and the resulting statistical calculations of your choice (t-test on the figure) will be presented on the right side of each channel's name. Channel names will also become color-coded based on the statistical values. The darker the red, the higher the (positive) t-value for this channel; the darker the blue, the lower the (negative) t-value. It is possible to sort the values from the lowest to highest and vice versa by **double clicking** on the name of the column ("t-test HbO" on figure). A small triangle will appear next to it (as in the figure) indicating the sorting.

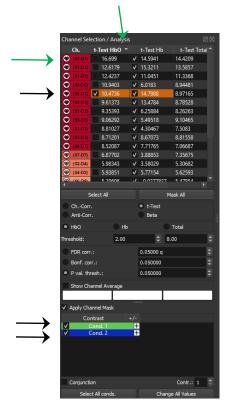
**(i)** 

**(i)** 

On the far left, a heart can appear, which indicates that the heartbeat has been detected (note that an average detected heartbeat can be found in the bottom of the preprocessing window). It is recommended that only channels with a detected heartbeat are used, although no detected heartbeat does not necessary mean that the channel does not provide actual task-related information.

By **checking** a channel (S6-D7 on figure), a channel is selected. Its signal is then represented in the *time course* and *event related average time course* windows. The selected channel is also highlighted in the *layout view*.

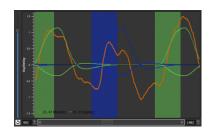




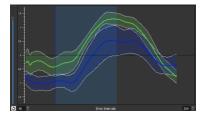




The t-value in the *channel list*, *time course*, and marked channel in the *layout* are all color-coded with the same color (orange in this case). Selecting a different channel will result in a different color, which makes it easy to distinguish what information and which signal belongs to which channel. The selection can also be done using the layout view as shown on the right. Just **click** on the channel of interest (S6-D7 on figure) to select it.



In the current study, the *event related average time course* will show four different curves with standard errors for each selected channel. The red thick curve represents Oxy average and the thin one Deoxy average for condition 1. The green thick line similarly shows Oxy average for condition 2, while the thin one represents its Deoxy average.



Note that during simulation, GLM results are saved automatically in a .txt file, but any contrasting and/or filtering needs to be set before the run is completely loaded, otherwise this change will not be captured in the resulting GLM file. In case you would like to compare different filtering and/or contrasts, make sure to rename the resulting file, because it will otherwise be overwritten by the following file with new settings!

#### NEUROFEEDBACK RUN

This step describes how to set up Turbo-Satori to run a real-time data acquisition and analysis.

Besides establishing the connection between NIRStar and Turbo-Satori, a stimulation program, such as NIRStim, should be used. Before recording, make sure that the trigger cable is plugged in and that NIRStar is "receiving" triggers or is connected using shared variables in NIRStim.

1. For this experiment, another software will be used; TSIBCIDemo is a neurofeedback software that offers multiple different neurofeedback displays. **Click** on the TSIBCIDemo icon to run the software.

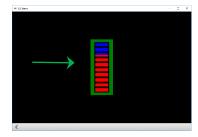


2. Select a neurofeedback display.

In the next steps, Thermometer Neurofeedback display will be used.



BCI demo is connected to Turbo-Satori, when the band around the thermometer is green. If the band is yellow, no channel has been selected. If there is no connection between TSI and the BCI demo, then the band is displayed in red. In this case try to restart TSI. With increased signal in the selected channel, the red color will start filling in the blue thermometer. The higher the red color reaches, the higher the measured brain activity.



## PART III APPENDIX

### APPENDIX A: OVERVIEW OF IMPORTANT FILES

File	Information
.hdr	<ul> <li>Header file</li> <li>Includes the information about the measurement: information about the system, gain values from the calibration, event (trial) time points, masking details, dark noise values and channel distances.</li> </ul>
.sri	<ul> <li>Satori project</li> <li>Includes connections to all the files used for analysis, information about preprocessing, and masking.</li> </ul>
.prt	<ul> <li>Protocol file</li> <li>Includes information about different conditions and timing of trials.</li> </ul>



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