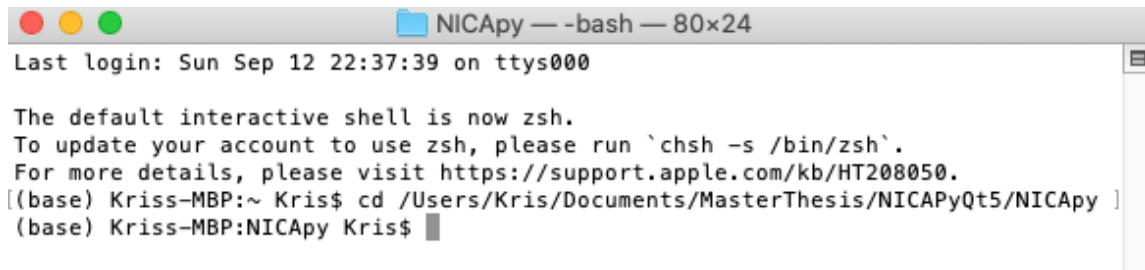


## A short introduction on how to install, run and use NICAPy from the terminal

By starting the terminal, the directory has to be changed to the path (cd command) where NICAPy.py and all its subfolders and files are stored. All the subdirectories should be left as provided, because NICAPy takes care internally about the import of modules from the subfolders. As NICAPy is developed in Python 3.7, make sure to have that Python version available. Below a screenshot of the terminal is shown with the already selected directory.



```
NICAPy — -bash — 80x24
Last login: Sun Sep 12 22:37:39 on ttys000

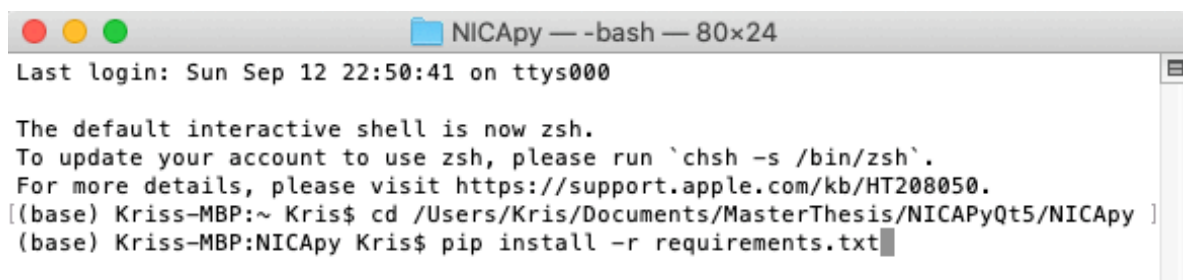
The default interactive shell is now zsh.
To update your account to use zsh, please run `chsh -s /bin/zsh`.
For more details, please visit https://support.apple.com/kb/HT208050.
[(base) Kriss-MBP:~ Kris$ cd /Users/Kris/Documents/MasterThesis/NICAPyQt5/NICAPy ]
(base) Kriss-MBP:NICAPy Kris$
```

Figure 1: Switch to directory where the folder including NICAPy is located

NICAPy comes with a requirements.txt file which includes all the necessary third-party Python packages. These are necessary in order to obtain all functionalities of NICAPy. The requirements file should be kept in the original NICAPy directory. These packages can be installed by running the requirements.txt file with the following command:

*pip install -r requirements.txt*

A screenshot of how to run the requirements.txt file is shown below.



```
NICAPy — -bash — 80x24
Last login: Sun Sep 12 22:50:41 on ttys000

The default interactive shell is now zsh.
To update your account to use zsh, please run `chsh -s /bin/zsh`.
For more details, please visit https://support.apple.com/kb/HT208050.
[(base) Kriss-MBP:~ Kris$ cd /Users/Kris/Documents/MasterThesis/NICAPyQt5/NICAPy ]
(base) Kriss-MBP:NICAPy Kris$ pip install -r requirements.txt
```

Figure 2: How to install the necessary third-party packages with the requirements.txt file

After successful installation of the necessary packages NICAPy can be started by simply typing:

*python3 NICAPy.py*

Figure 3 shows how to start NICAPy from the terminal.

```

NICApY — python3 NICApY.py — 80x24
b/python3.7/site-packages (from matplotlib==3.2.2->-r requirements.txt (line 5))
(2.8.2)
Requirement already satisfied: PyQt5-sip<13,>=12.8 in /Users/Kris/miniconda3/lib
/python3.7/site-packages (from PyQt5==5.15.4->-r requirements.txt (line 7)) (12.
8.1)
Requirement already satisfied: PyQt5-Qt5==5.15 in /Users/Kris/miniconda3/lib/pyt
hon3.7/site-packages (from PyQt5==5.15.4->-r requirements.txt (line 7)) (5.15.2)
Requirement already satisfied: six in /Users/Kris/miniconda3/lib/python3.7/site-
packages (from cyclo==0.10->matplotlib==3.2.2->-r requirements.txt (line 5)) (1
.12.0)
WARNING: Value for scheme.headers does not match. Please report this to <https:/
/github.com/pypa/pip/issues/9617>
distutils: /Users/Kris/miniconda3/include/python3.7m/UNKNOWN
sysconfig: /Users/Kris/miniconda3/include/python3.7m
WARNING: Additional context:
user = False
home = None
root = None
prefix = None
WARNING: You are using pip version 21.1; however, version 21.2.4 is available.
You should consider upgrading via the '/Users/Kris/miniconda3/bin/python -m pip
install --upgrade pip' command.
[(base) Kriss-MBP:NICApY Kris$ python3 NICApY.py

```

Figure 3: How to start NICApY

Then the GUI opens, and a standard single analysis, a Grand Average analysis or a modified t-test can be performed. The GUI is shown below. Since the GUI was developed on a Mac the layout will differ on Windows and Linux but can be easily changed by applying a different css-stylesheet in the file stylesheet.py.

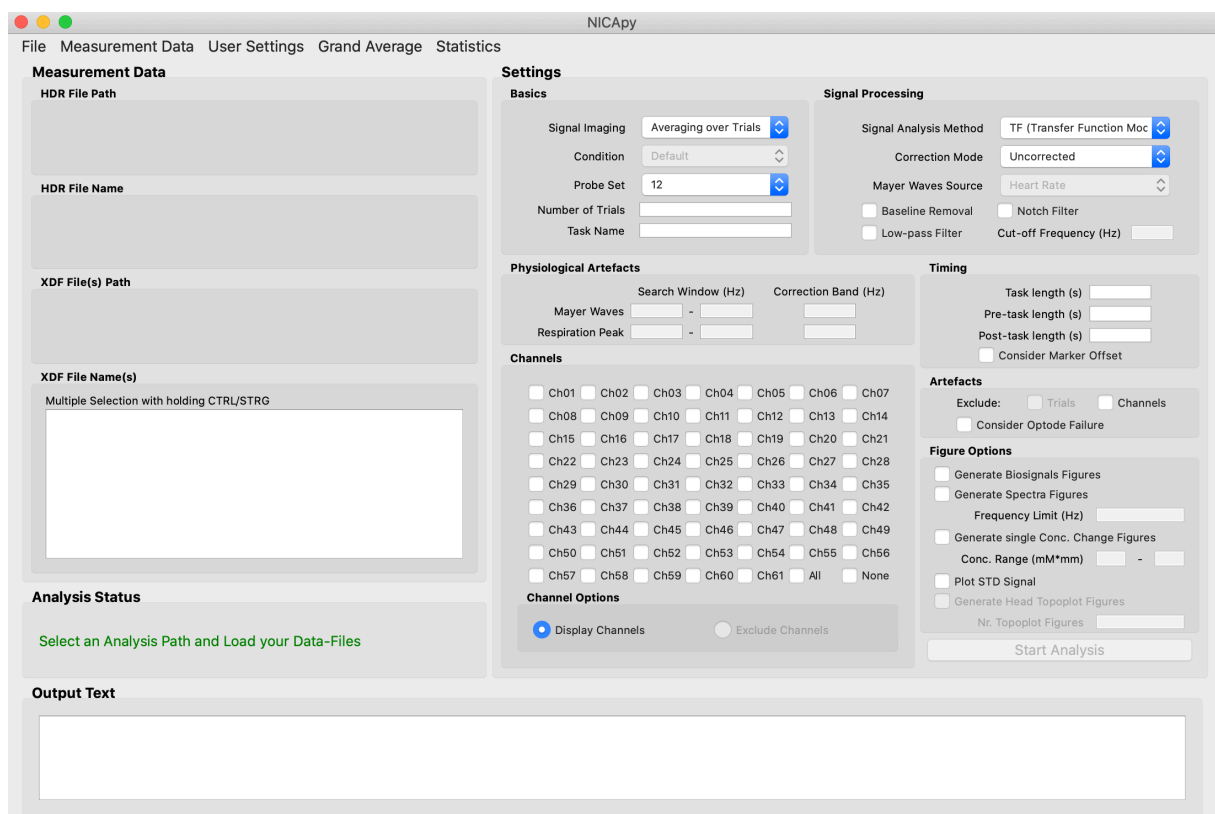


Figure 4: The GUI of NICApY presented to the user after successful start of NICApY

For performing a standard single analysis, the same steps have to be applied as in the MATLAB version of NICA. Load the files, define the conditions and their corresponding markers as used during the measurement, set all settings correctly and start the analysis.

For a Grand Average analysis, first the Start feature in the Grand Average menu has to be pressed, then the ROIs can be defined by entering the number of desired ROIs and the corresponding channels afterwards. Then an analysis path needs to be selected (same as at single analysis) and then the Start Analysis Button enables. By pressing the Start Analysis Button the files can be loaded through a file dialog. When all files are selected, press Cancel and the Grand Average analysis starts directly.

For performing a modified t-test, data resulting from a directly foregone single analysis can be used or a new \*.pickle file can be loaded. The application already checks if an foregone single analysis was performed and asks if that or a new file should be used for the modified t-test.

Settings for standard single analysis can be stored to a \*.json file by using the 'Save as' feature in the Settings menu. A stored settings file can be loaded by pressing 'Load' in the Settings menu and further selecting the desired file. Make sure the \*.json file is set up correctly if written by hand.

It is also useful to start NICApy from an IDE (e.g. PyCharm), not only when performing an analysis but especially while discovering the functionalities or debugging.

#### Note:

During the last testing section an error was discovered for some data files.

An error can occur when selecting 'Continuous' as Signal Imaging method in the Basics Groupbox. This is already not implemented completely correctly in the Matlab version of NICA and therefore, this should be corrected for future versions. This possible error in NICApy and NICA origin from the same cause. It was only discovered during the last sessions of testing.

It targets the calculation of the continuous signal for plotting in file comparespectra.m in NICA from line 79 – 111 and in file compare\_spectra.py in NICApy from line 95 – 121.

If further errors are detected, please feel free to report them to:

kris.unterhauser@hotmail.com