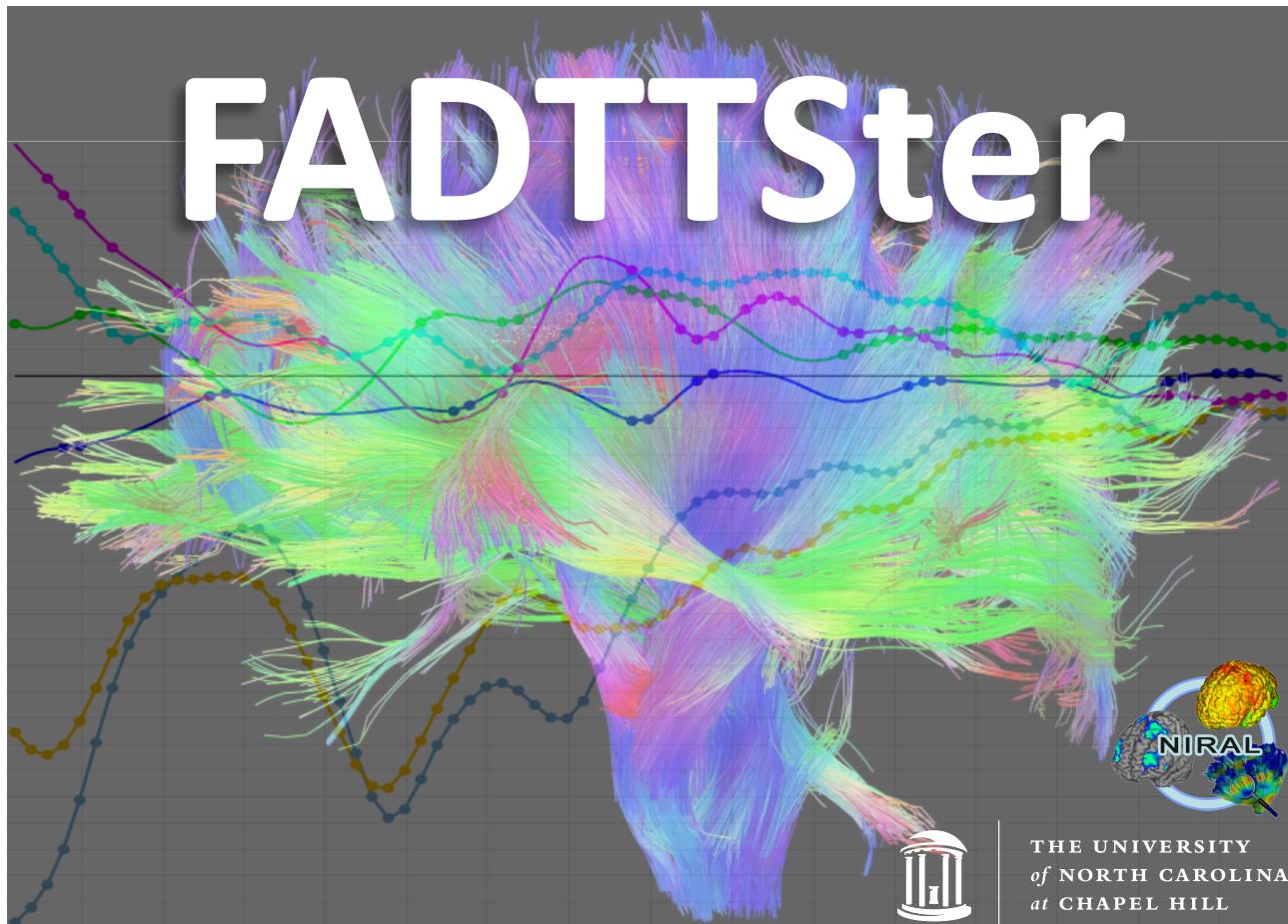


FADTTSter

User Guide



Last modifications made by Jean Noel on October 12, 2016

Contents

	Page
I Overview	3
A Why FADTTSter?	3
B What does FADTTSter do?	3
II Build instructions	5
A Requirements	5
B Build	5
C SuperBuild	5
III Start with FADTTSter	6
A Matlab script generation	6
1_ FADTTSter — GUI interface	6
a) Inputs tab	7
i. Add input files	8
ii. Edit input files	11
iii. Select covariates	15
b) Subjects tab	16
i. Add subjects	17
ii. Manage subjects	17
iii. Apply a QC threshold (FA file must be provided)	21
iv. Crop profile (FA file must be provided)	23
v. Remove subjects with <i>nan</i> values (FA file must be provided)	23
c) Execution tab	24
i. Adjuste settings and Matalb specifications	25
ii. Launch Matlab script generation	25
iii. Generated files	26
B Statistical data plotting	27
1_ Add plots	28
2_ Display plot	28
3_ Customize plot	36
a) Title/Axis/Legend Tab	37
b) Edition Tab	39

c) Special Features	41
4_ Save Plot	42
IV Advanced use of FADTTSter	43
A Configuration files	43
1_ Upload configurations to GUI	45
2_ Save configurations	46
B Plot settings	47
1_ Upload configurations to GUI	47
2_ Save configurations	47
C FADTTSter in command line	48
List of Figures	49
References	51

Part I

Overview

A Why FADTTSter?

The analysis of brain pathologies and development heavily relies on diffusion tensor imaging (DTI). Conventionally used to map the orientation of the white matter fiber tracts in the brain (Basser et al., 1994a,b), DTI uses the isotropic diffusion in cell bodies and spinal fluids and the anisotropic diffusion in axons comprising white matter (Feldman et al., 2010) to assess white matter (WM) integrity and maturation *in vivo*. Functional Analysis of Diffusion Tensor Tract Statistics (FADTTS) is a tool developed to outline the evolution of diffusion properties — axial diffusivity (AD), radial diffusivity (RD), mean diffusivity (MD) and fractional anisotropy (FA) — along white matter fiber tracts and their correlation with a set of covariates of interest, such as age or gender (Zhu et al., 2011). In the UNC-Utah NA-MIC DTI framework, an end-to-end toolset for atlas fiber tract based DTI analysis, the Matlab (MathWorks Inc, MA, USA) functions implemented in FADTTS (Kong) are used for the computation of the statistical data (Verde et al., 2014). However, coding knowledge is necessary to operate it, as the user needs to modify a Matlab script to make it fit each of her/his DTI studies. FADTTSter was first created to overcome this issue and make the statistical analysis accessible to any non-technical researcher. Now, FADTTSter is even more developed and features very useful options such as subjects management, profile cropping, data plotting, etc.

B What does FADTTSter do?

FADTTSter is a user-friendly version of FADTTS designed for users without coding skills. Its aim is to make FADTTS accessible to anyone. It can be divided in two major parts, each one working independently.

- **Matlab script generation:** A Matlab script and its mandatory inputs are automatically generated in a folder specific to the ongoing study, based on the information provided by the user (diffusion properties, subjects, qc threshold, nbr of permutations, p-value threshold, etc). Then, if specified, the script can be run on Matlab.
- **Statistical data plotting:** Enables the visualization of the data obtained after running the .m script. The statistical data plotting also allows the user to customize her/his results (tilte, axis, colors, etc).

FADTTSter is a command line based module as well as a GUI based tool. However, statistical data plotting is only available via the GUI interface.

FADTTSter entirely replaces FADTTS in the UNC-Utah NA-MIC DTI framework, during the statistical analysis of diffusion properties. It uses fiber bundle profiles obtained from *DTIAtlasFiberAnalyzer* (dti) as inputs and *MergeStatWithFiber* (mer) can use the outputs for brain visualization.

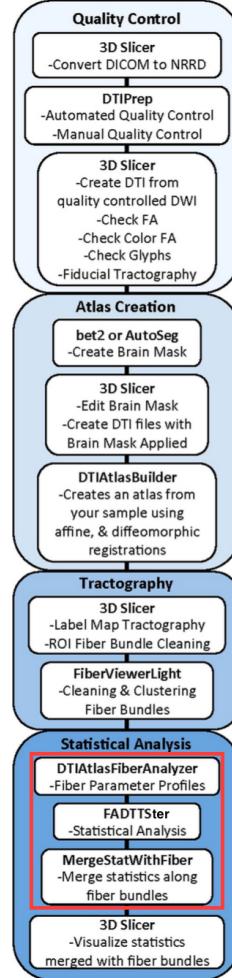


Figure 1: FADTTSter in the UNC-Utah NA-MIC DTI framework

Not only is FADTTSter practical, but it also enables any investigator to perform DTI analysis efficiently.

Part II

Build instructions

A Requirements

- Qt5
- SlicerExecutionModel
- VTK

B Build

1. Get files from Github:

```
$ git clone git@github.com:NIRALUser/FADTTSter.git
```

2. Make an out-of-source build directory:

```
$ mkdir ./FADTTSter-build  
$ cd FADTTSter-build
```

3. Configure the build:

```
$ ccmake .. /FADTTSter/src  
$ make
```

4. Get the executable:

```
$ ./bin/FADTTSter
```

C SuperBuild

To install FADTTSter and all its dependencies with a superBuild, refer to *UNC/Utah NAMIC DTI Fiber Analysis Framework*.

Part III

Start with FADTTSter

FADTTSter is made of two blocks: the *Matlab script generation* and the *statistical data plotting*. These parts work independently. They are both GUI based, but only the *Matlab script generation* can be run as a command line module. The following is a detailed presentation of FADTTSter and how to use it.

A Matlab script generation

The *Matlab script generation* is the reason why FADTTSter was originally developed. The idea was to “hide” every technical aspect for the writing of the Matlab script — used to generate the statistical data — with a user-friendly GUI interface. Subsequently, the tool was implemented with some options (subjects management, quality control, profile cropping, etc). Then FADTTSter was made available as a command line only based tool.

1_ FADTTSter — GUI interface

The *Matlab script generation* regroups the first three tabs of FADTTSter: *Inputs*, *Subjects* and *Execution*.



Figure 2: FADTTSter tabs used for *Matlab script generation*.

a) Inputs tab

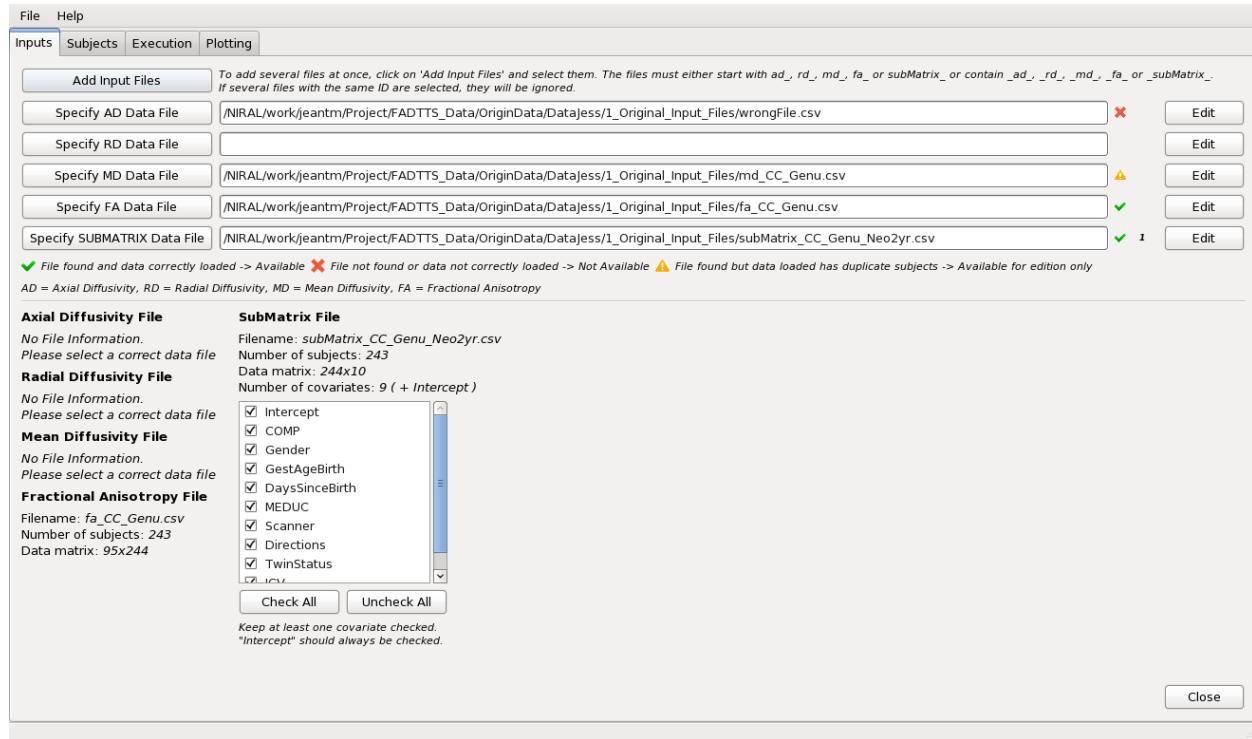


Figure 3: Inputs tab

The *Inputs* tab allows the user to set and edit the diffusion property files and the covariates file and set the covariates for the ongoing study.

i. Add input files

- Add several files at once:

1. Click on “Add Input Files”

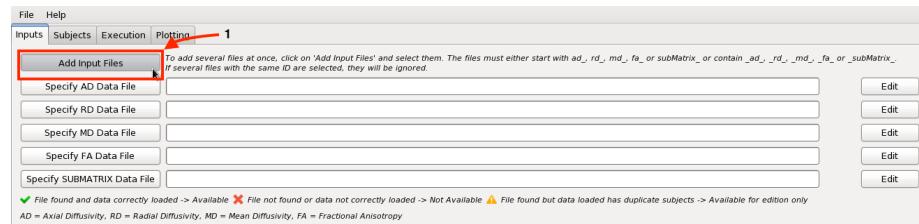


Figure 4: Adding input files

2. In the pop-up window displayed, browse to the folder containing the files you want to add
3. Select them
4. Click on “Open”

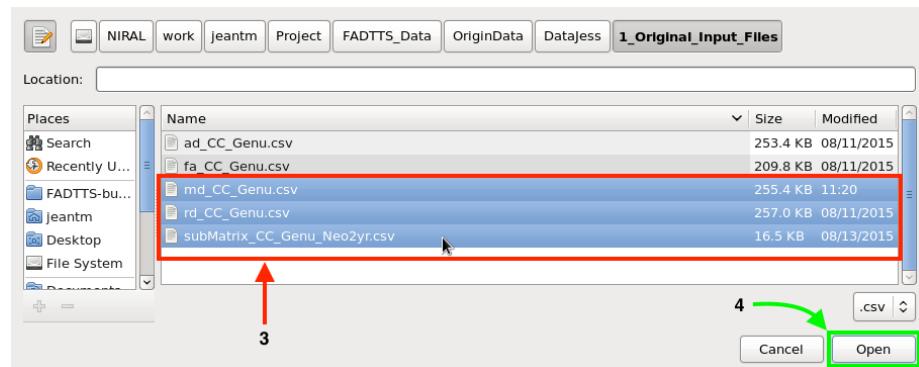


Figure 5: Pop-up window displayed to set multiple input files at once

Note:

- The default format for the input files is *.csv*.
- The selection is not case sensitive.

WARNING:

- Selected files must either start with *ID_* or contain *_ID_* (*ID* being *AD*, *RD*, *MD*, *FA* or *SUBMATRIX*)

- Selected files with the same *ID* are ignored.
(e.g. If you select the following files the files: *my_ad_file1.csv*, *AD_myfile2.csv*, *my_FA_file.csv* and *mySubmatrix_file.csv*, only *my_FA_file.csv* and *mySubmatrix_file.csv* will be added to the ongoing study.)

- **Add one file:**

1. Click on “Specify ID Data File”

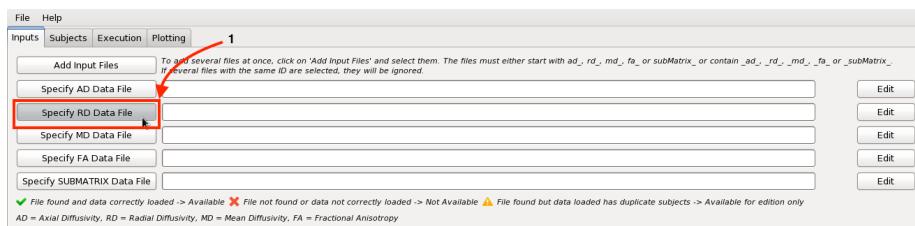


Figure 6: Adding one file using “Specify Data File” push button

2. In the pop-up window displayed, browse to the folder containing the file you want to add
3. Select it
4. Click on “Open” or double click on the file

Or

Give the absolute path to the file you want to add

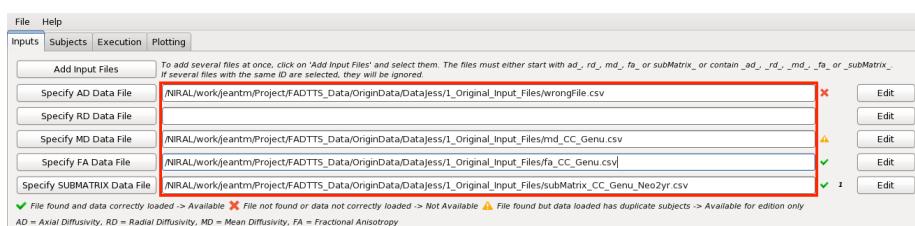


Figure 7: Adding one file specifying the absolute path

Note: Here, file name does not matter.

• File status and file information:



Figure 8: File status and file information after adding an input file

- File not found or data not correctly loaded → Ignored (1)
- File not provided (2)
- File found but data loaded has duplicate subjects → Available for edition only (2)
- File found and data correctly loaded → Available for the ongoing study (4)

The information provided contains:

- The file name
- The number of subjects found
- The size of the data matrix

In addition, for the covariates file, we have:

- The number of covariates found and their names
- The position of the column featuring the subjects

Note: All files must have the same data size. In other words, if an FA , a RD and a $SubMatrix$ file of respective data matrix size $M_{FA} \times N_{FA}$, $M_{RD} \times N_{RD}$ and $M_{SubMatrix} \times N_{SubMatrix}$, then we must have $M_{FA} = M_{RD} = N_{SubMatrix}$.

ii. Edit input files

The edition modifies the data loaded within the GUI but never the original data files.

- Start edition:

1. Click on “Edit”

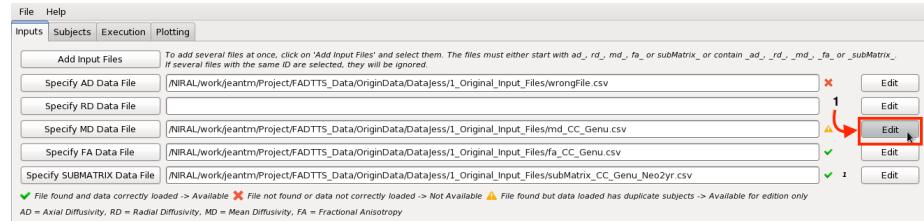


Figure 9: Editing an input file



Figure 10: Pop-up window displayed when file edition is unavailable (i.e. no data has been loaded (file not provided or not found))

2. Start the file edition

	1	2	3	4	5	6	7
1	Arc_length ...	neo-0004-2...	neo-0011-2...	neo-0012-2...	neo-0019-2...	neo-0029-3...	neo-0038-2...
2	-48.0514	0.00114087	0.00108696	0.00127783	0.00120734	0.00130956	0.00118406
3	-47.0514	0.00114113	0.00109276	0.00128372	0.00120994	0.00133207	0.00118723
4	-46.0514	0.00114663	0.00110083	0.00128555	0.00121011	0.00136825	0.00119025
5	-45.0514	0.00116706	0.00112183	0.00128378	0.00120562	0.00141746	0.00120257
6	-44.0514	0.00117682	0.00115025	0.00128564	0.00120192	0.00146816	0.00121711
7	-43.0514	0.00116688	0.00117234	0.00129035	0.0012031	0.0015076	0.00122463
8	-42.0514	0.00115034	0.00118564	0.00128572	0.00120912	0.00153192	0.00122573

Highlighted columns present -nan and/or nan values

 2 duplicate(s) found
 1

(a) Edition window displayed for a diffusion property file

	1	2	3	4	5	6	7
1	SUBJECT ID	COMP	Gender	GestAgeBirth	DaysSinceBi...	MEDUC	Scanner
2	neo-0004-2...	123	0	276	61	19	0
3	neo-0011-2...	105	0	283	12	15	0
4	neo-0012-2...	123	0	274	28	16	0
5	neo-0019-2...	119	0	275	15	25	0
6	neo-0029-3...	111	0	241	32	10	0
7	neo-0038-2...	110	1	279	28	18	0
8	neo-0042-2...	114	1	280	19	16	0

Highlighted columns present -nan and/or nan values

 1

(b) Edition window displayed for a covariates file

Figure 11: Edition windows available depending on the input file provided

- **Delete column(s)/row(s):**

1. Select column(s)/row(s) to delete
2. Click on “Delete column(s)”/“Delete row(s)”

Figure 12 shows a data grid with 8 rows and 7 columns. The first three columns (1, 2, 3) are highlighted with a red border. The fourth column (4) contains numerical values. The fifth column (5) contains text labels like 'neo-0004-2...'. The sixth column (6) contains numerical values. The seventh column (7) contains text labels like 'neo-0038-2...'. Below the grid is a toolbar with several buttons: 'Delete Selected Rows', 'Delete Selected Columns' (highlighted with a green box), 'Delete 2nd occurrences', 'Remove Duplicates' (highlighted with a green box), 'Save CSV File as ...', and 'Close'. A message 'Highlighted columns present -nan and/or nan values' is displayed above the toolbar. A message '2 duplicate(s) found' is displayed below the 'Remove Duplicates' button.

Figure 12: Deleting columns

- **Remove duplicates:**

- Click on “Remove Duplicates”

Figure 13 shows the same data grid and toolbar as Figure 12. The 'Remove Duplicates' button is highlighted with a green box. A green arrow points from the button to the number '2' indicating duplicate rows found.

Figure 13: Removing duplicates from data file

Note: Only second occurrences are deleted. Once applied, you cannot go back except by closing the editing window.

- ***nan* values (FA file only):**

Some data can be set as *nan* instead of a number. Should that be the case, the columns where at least one *nan* value is found are highlighted in a beautiful Carolina blue. It is the responsibility of the user to keep the data.

The screenshot shows a software interface for managing data files. At the top, there is a menu bar with 'File', 'Edit', 'View', 'Help', and 'About'. Below the menu is a toolbar with icons for opening, saving, and other file operations. The main area contains a table with 8 rows and 7 columns. The columns are labeled 1 through 7. Row 1 contains column headers: Arc_length ... T0008-1-1-1... T0008-1-2-1... T0008-2-1-1... T0008-2-2-1... T0011-1-2-1... T0017-1-1-1. Rows 2 through 8 contain numerical data. Columns 4, 5, and 6 are highlighted in blue, indicating they contain *nan* values. Below the table is a status bar with the message 'Highlighted columns present -nan and/or nan values'. Underneath the table are several buttons: 'Delete Selected Rows' (blue), 'Delete Selected Columns' (gray), 'Save CSV File as ...' (blue), 'Delete 2nd occurrences' (gray), 'Remove Duplicates' (gray), 'Specify subjects column' (dropdown menu with value 1), and 'Close' (button).

Figure 14: Nan values found in an FA file

- **Change subject column ID (covariates file only):**

- Set subjects column ID to the column where subjects are displayed

The screenshot shows a software interface for managing data files. At the top, there is a menu bar with 'File', 'Edit', 'View', 'Help', and 'About'. Below the menu is a toolbar with icons for opening, saving, and other file operations. The main area contains a table with 8 rows and 7 columns. The columns are labeled 1 through 7. Row 1 contains column headers: SUBJECT ID COMP Gender GestAgeBirth DaysSinceBi... MEDUC Scanner. Rows 2 through 8 contain subject identifiers and demographic data. Below the table is a status bar with the message 'Highlighted columns present -nan and/or nan values'. Underneath the table are several buttons: 'Delete Selected Rows' (blue), 'Delete Selected Columns' (gray), 'Save CSV File as ...' (blue), 'Delete 2nd occurrences' (gray), 'Remove Duplicates' (gray), 'Specify subjects column' (dropdown menu with value 1, currently active), and 'Close' (button). A cursor arrow points to the dropdown menu.

Figure 15: Setting column ID

Note: Usually, the subjects are in the first column. If so, this feature should not be used.

- **Save modifications:**

1. Click on “Save CSV File as ...”

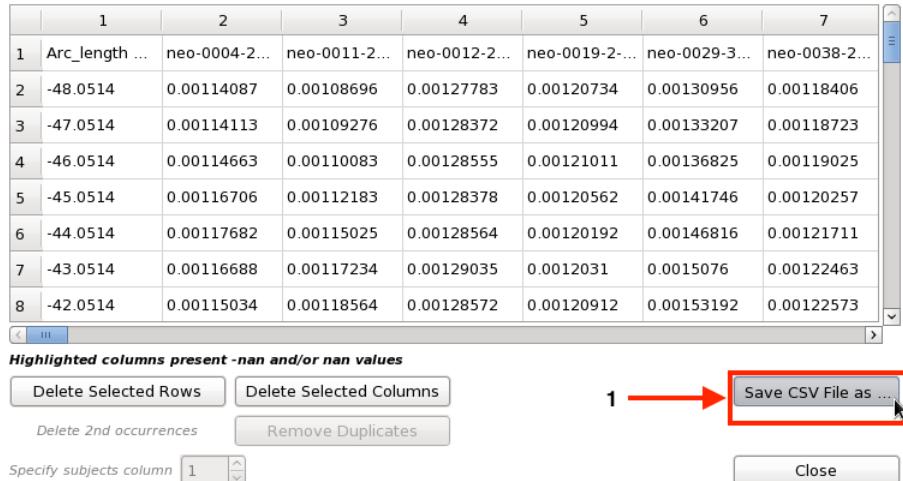


Figure 16: Save modifications after file edition

2. In the pop-up window displayed, browse to the folder where you want to save your modification
3. Rename the file if needed
4. Click on “Save”

Note:

- Make sure to save the file as a *.csv*
- If modifications are made AND saved, the path to the input file is automatically updated.
- If you close the edition window after making some modifications but without having saved them, the following pop-up will be displayed.

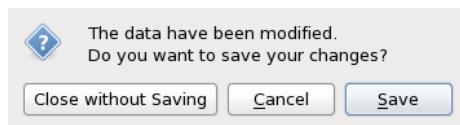


Figure 17: Closing pop-up displayed after modifications not saved

In that case you can:

- *Save* your modifications (cf previous point)
- *Discard* your modifications and go back to the main window with your data unchanged
- *Cancel* your decision and go back to the edition window

Note: As long as you do not write over the original file, it will remain unmodified, even if modification are applied.

iii. Select covariates

(Available only if a correct covariates file has been loaded)

- Click on a covariate to select/unselect it individually
- Click on “Check All”/“Uncheck All” to select/unselect all covariates

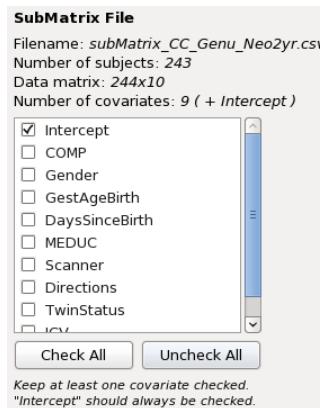


Figure 18: Toggle the covariates to add them to or remove them from the study

WARNING: *Intercept* should always be selected.

Note: “Uncheck All” will unselect all covariates but the *Intercept*.

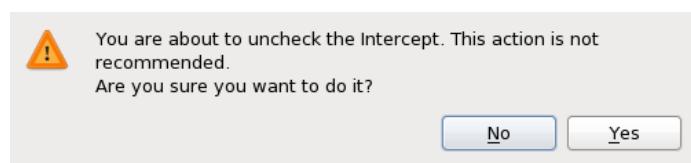


Figure 19: Unselecting the *Intercept* will result in displaying a warning pop-up

b) Subjects tab

The screenshot shows the 'Subjects' tab of a software application. The interface includes a menu bar with 'File' and 'Help', and tabs for 'Inputs', 'Subjects' (which is selected), 'Execution', and 'Plotting'. Below the tabs is a 'Subject List' section with a search bar and filter checkboxes for 'AD', 'RD', 'MD', 'FA', and 'SubMatrix'. A status bar indicates '225/225 subjects selected' and '225/261 matched'. To the right, a status bar shows '36/261 unmatched'. The main area displays a list of subject IDs, each preceded by a checkbox. The list is divided into two color-coded sections: a green section on the left containing 225 subjects and a red section on the right containing 36 unmatched subjects. At the bottom of the list are buttons for 'Check All Visible', 'Uncheck All Visible', 'Search:' (with a 'Case Sensitive' checkbox), 'Save Visible Checked Subjects as ...', and 'Profile Cropping' settings. A note at the bottom states: 'When QC threshold is based on population average, -nan and/or nan values can be found in the data. Then, nan values will appear as 0 when displayed and population average might be not go all the way along the arc length.'

Figure 20: Subjects tab

The *Subjects* tab allows the user to manage the subjects of the ongoing study. They can be added to/removed from the study individually or after setting a quality control (QC) threshold. Through this tab, the user can also crop the profile.

i. Add subjects

- From input files:

- Select the *ID* (*AD*, *MD*, *RD*, *FA* or *SUBMATRIX*) of the input file which subject list you want to add.



Figure 21: Adding subjects from input files

Note: Every input file provided in the *Inputs* tab is linked to a single diffusion property file (*AD*, *MD*, *RD* or *FA*) or to the covariates file (*SUBMATRIX*). Everytime an input file is correctly added and loaded, its selection is enabled in the *Subjects* tab.

- From external subject list:

1. Click on “Load List”



Figure 22: Adding a subjects from an external subject list

2. In the pop-up window displayed, browse to the folder containing the external subject list you want to add
3. Select it
4. Click on “Open” or double click on it

Note: Default format for the external subject list is *.txt*.

ii. Manage subjects

- Display:

Once the subjects have been added to the study from input files and/or an external subject list, they are sorted in two categories and displayed. The *matched subjects* are the subjects that have been found in all the subject lists provided. The *unmatched subjects* are the ones missing in at least one of the subject lists provided. Subjects within the *unmatched* group are automatically excluded from the study. Only the ones from the *matched* group can be added to the study at the user's convenience.

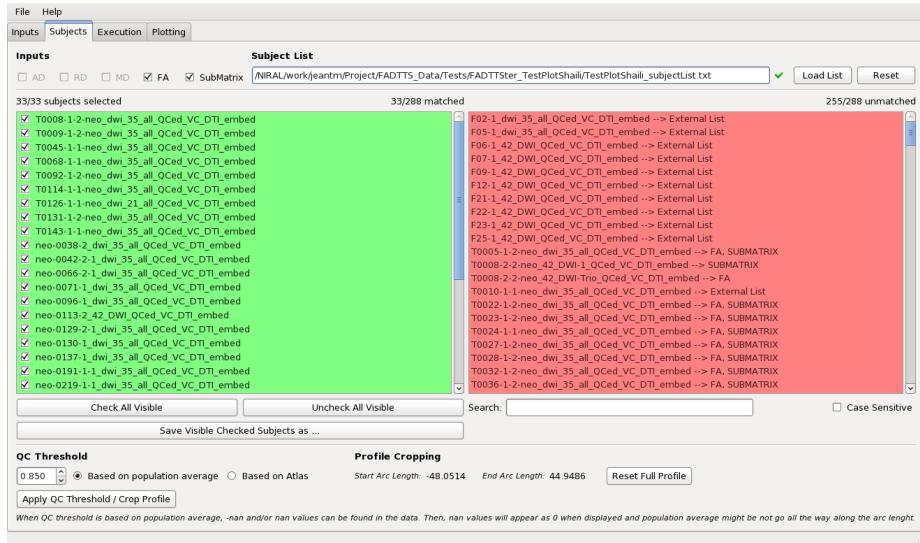


Figure 23: Subjects displayed regarding their occurrences in all subject lists provided

Note:

- In the *unmatched* window, subjects are displayed as follow:
 $subject_name \rightarrow occurrence\ 1, occurrence\ 2, \dots$
(e.g. Subjects are added from an *AD*, *RD* and *FA* file and an external subject list. If “Marcus_Paige” is found only in the *AD* file subject lists and in the external subject list, then it will be displayed in the *unmatched* window as: *Marcus_Paige* → *AD, external subject list*)
- On top of both display windows, information is provided about:
 - the number of subjects selected (*nbr of subjects selected / total nbr of matched subjects*)
 - the number of *matched* subjects (*nbr of matched subjects / total nbr of subjects*)
 - the number of *unmatched* subjects (*nbr of unmatched subjects / total nbr of subjects*)

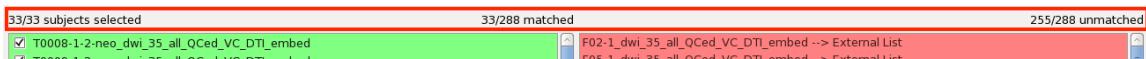


Figure 24: Information provided regarding the subjects displayed

- **Select subject:**

- Click on the subjects you want to add/remove

Or

- Click on “Check All Visible” / “Uncheck All Visible” to select/unselect all *visible subjects*



Figure 25: Selecting/unselecting a specific subject by clicking on it

- **Save subject list:**

1. Click on “Save Visible Checked Subjects as ...”
2. In the pop-up window displayed, browse to the folder where you want to save your subject list
3. Rename the file if needed
4. Click on “Save”



Figure 26: Save all subjects selected as one subject list

Note: Once you are done saving a subject list, you are asked if you want to use it right away for your study.

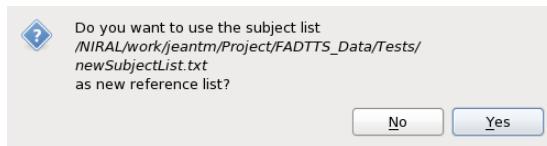


Figure 27: Use saved subject right away

- **Search for subject(s):**

– Fill the search bar

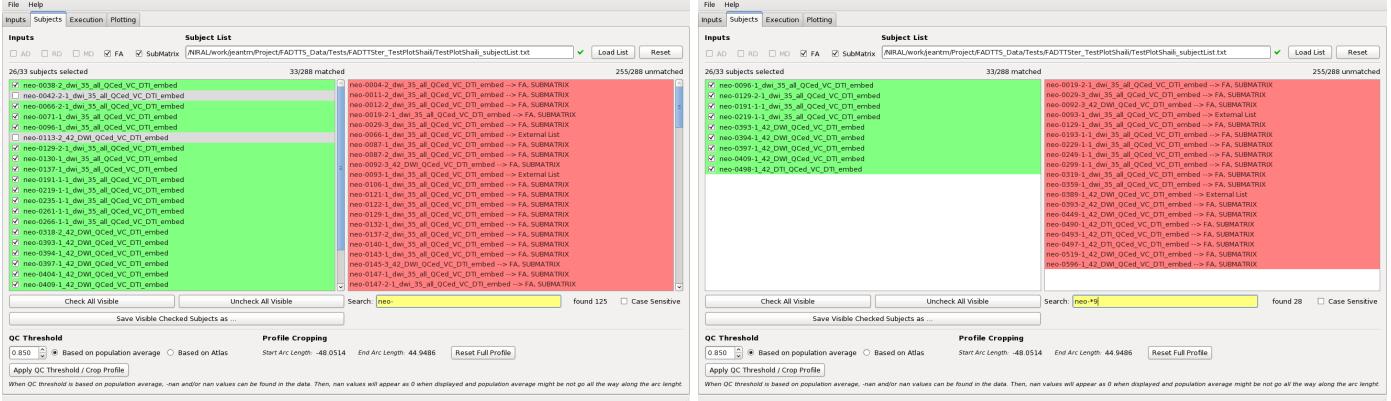


Figure 28: Searching for subjects

WARNING: A subject that does not fit the search remains checked as long as the user decides to modify its status. **Even if he is not displayed!**

Note:

- The search is done in both subjects' windows.
- The character * replaces any sequence of characters.
- As long as a search is ongoing, the search bar remains highlighted in yellow.

iii. Apply a QC threshold (FA file must be provided)

- Set QC threshold - *Subjects* tab

1. Set a value for the threshold (between 0 and 1)
2. Choose on what the threshold base
(Atlas can only be chosen if it is provided in the last column of the FA file)
3. Click on “Apply QC Threshold / Crop Profile”



Figure 29: Setting the QC threshold in the *Subjects* tab

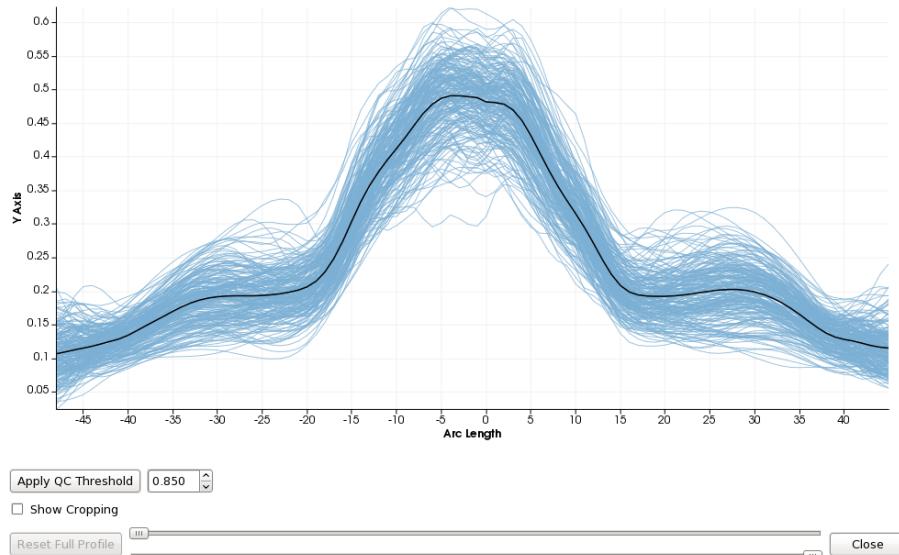


Figure 30: Pop-up window displayed to work on the QC threshold

- **Adjust QC threshold - pop-up window**

1. Adjust the QC threshold (value between 0 and 1)
2. See which subjects will be removed from the study

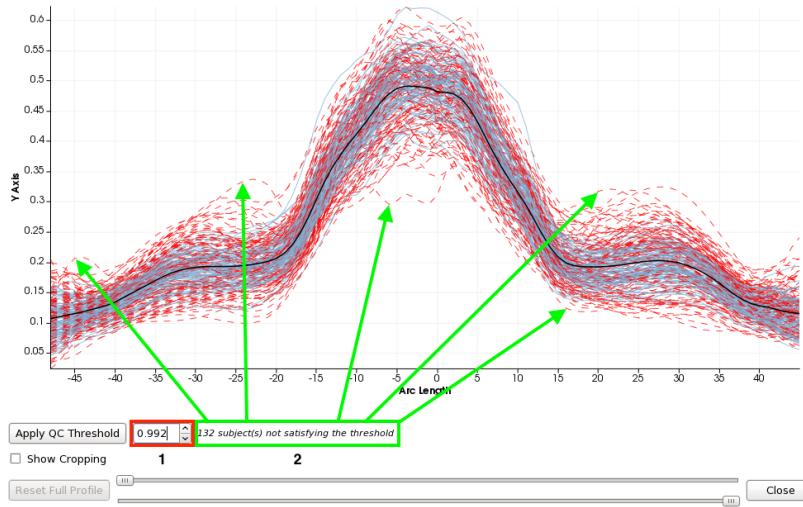


Figure 31: Adjusting the QC threshold

- **Apply QC threshold**

- Click on “Apply QC Threshold”

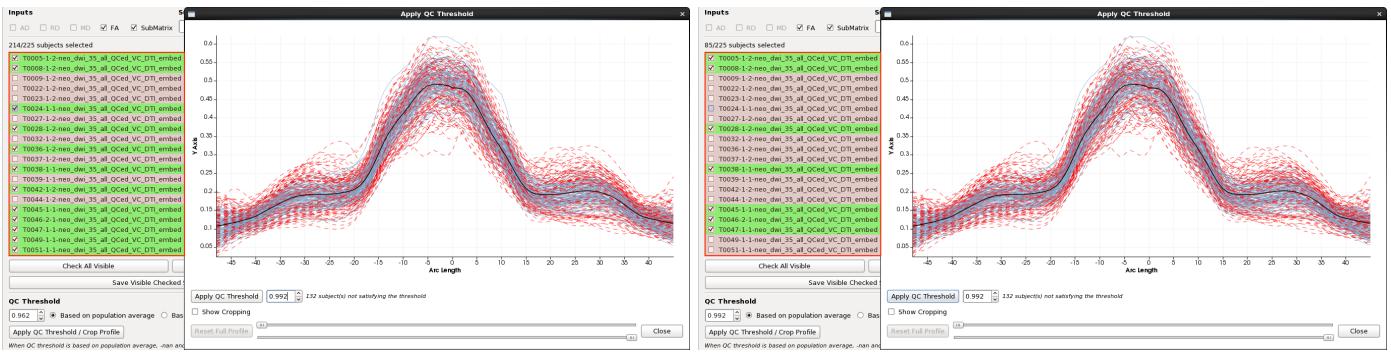


Figure 32: Apply a new QC threshold

Note: Applying a QC threshold results in unchecking all subjects that do not satisfy that QC threshold.

iv. Crop profile (FA file must be provided)

1. Click on “Apply QC Threshold / Crop Profile”
2. Set range of study using the two sliding bars

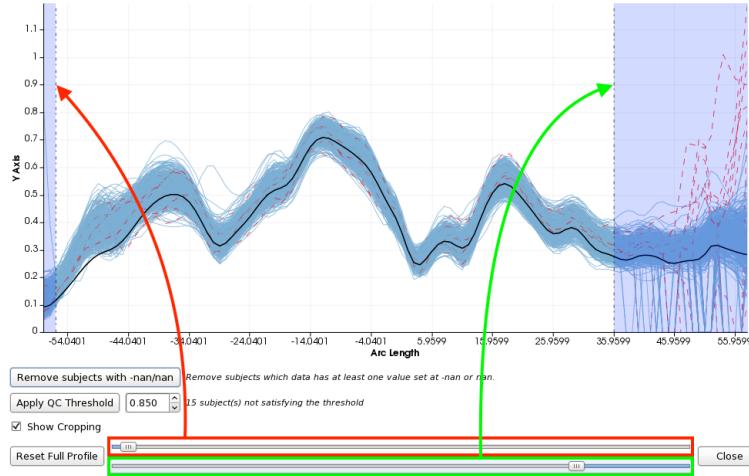


Figure 33: Adjusting the range of the study (highlighted zone are excluded)

v. Remove subjects with *nan* values (FA file must be provided)

1. Click on “Apply QC Threshold / Crop Profile”
2. If *nan* values are found, click on “Remove subjects with -nan/nan values”

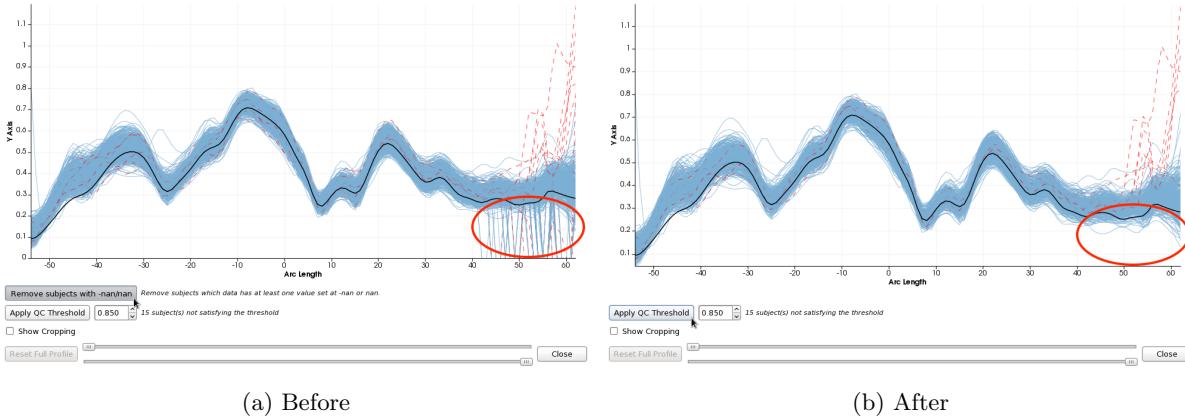


Figure 34: Removing *nan* values

c) Execution tab

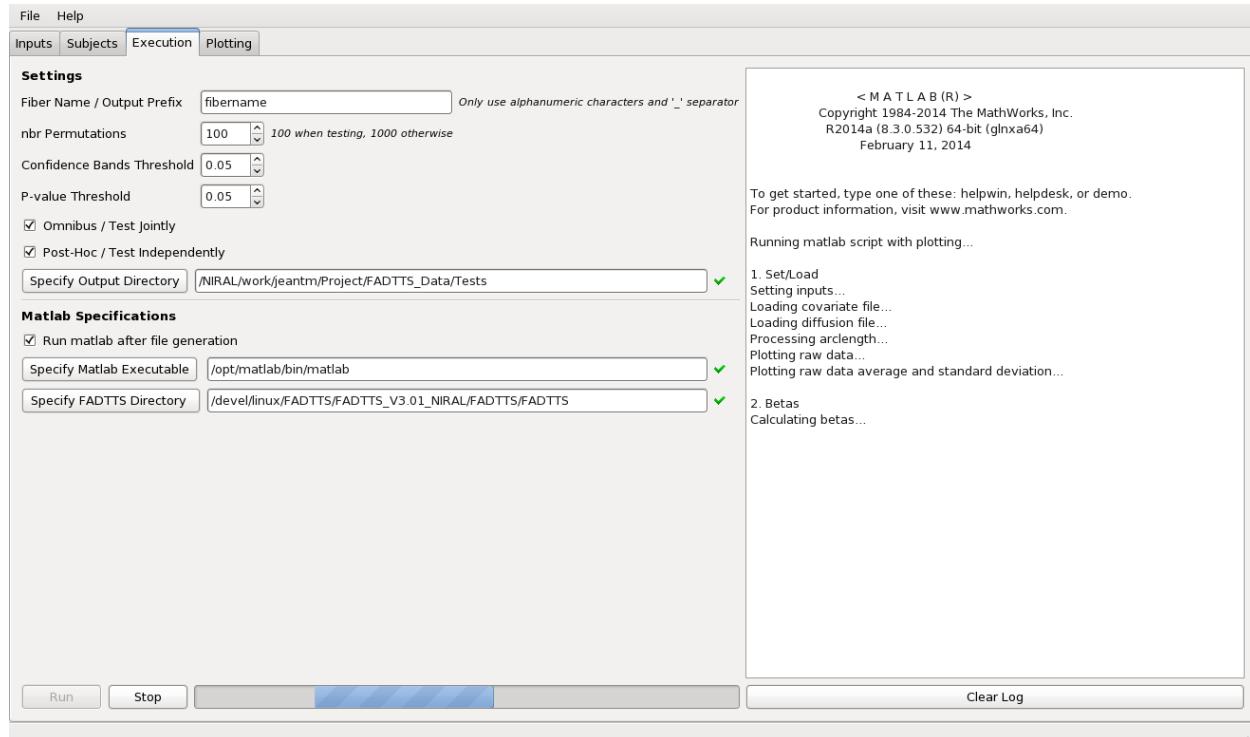


Figure 35: Execution tab

The *Execution* tab is where the user specifies the last information needed to run the *Matlab script generation* such as the fiber name, the number of permutations, the confidence bands threshold, the FADTTS directory (where the Matlab FADTTS function are defined on the system or killDevil), etc.

i. Adjuste settings and Matlab specifications

- Fiber name (Only use alphanumeric characters and “_” separator!)
- Number of permutations (value between 10 and 2000, usually 100 when testing, 1000 otherwise)
- Confidence band Threshold (value between 0 and 1)
- p-values threshold (value between 0 and 1)
- Omnibus
- Post-Hoc
- Output directory

ii. Launch Matlab script generation

1. Set FADTTS directory
2. If “Run Matlab after file generation” is checked, set a Matlab executable
3. Click on “Run”

WARNING:

- Matlab R2013b or later is needed to run the script!
- The computation of the script can be very long and use most of your computing power. We highly recommend that you launch your study on a remote server such as KillDevil instead of on your lab computer.

Note:

- You can follow the script computation in real time in the log window.
- Every file useful for the study is generated in the *Output directory* specified by the user. New input files are generated based on the quality control of subjects and fibers.

iii. Generated files

Every time FADTTSter is launched, you generate the following files:

- file1
- file2
- etc.

However, if you have decided to run the script once it has been generated, you have the following files in addition:

- file1
- file2
- etc.

B Statistical data plotting

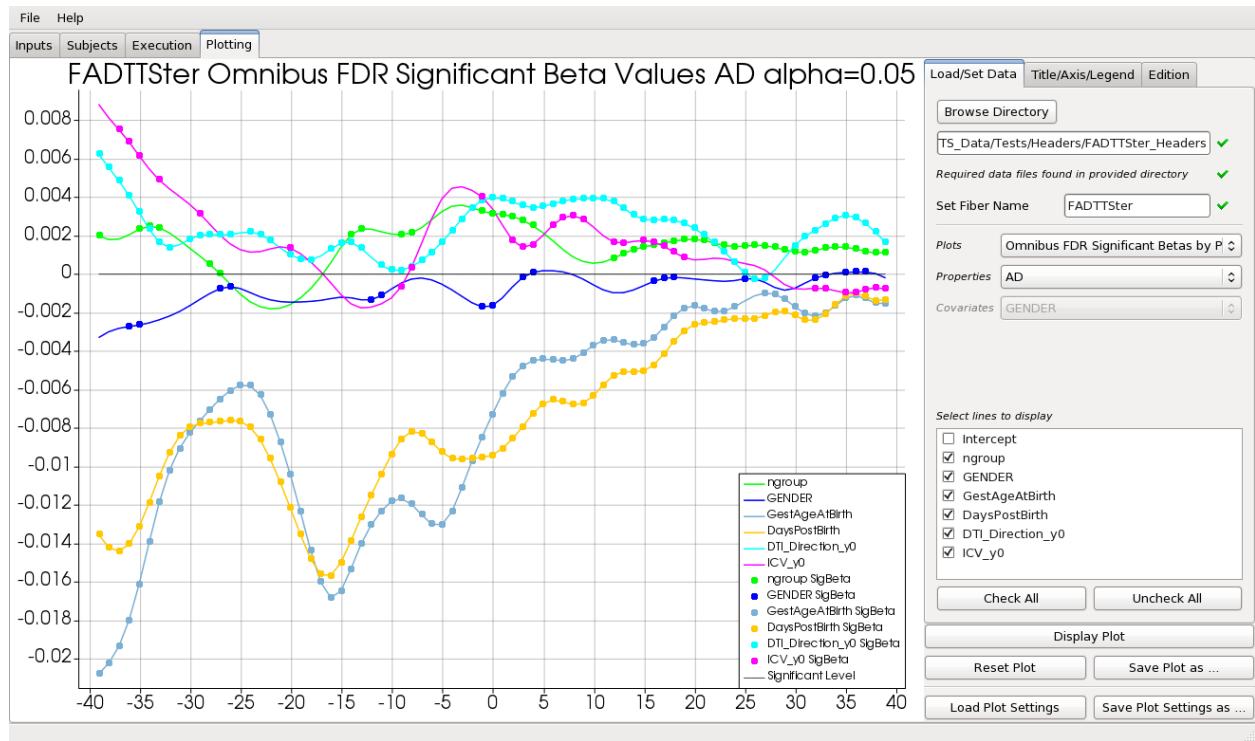


Figure 36: Plotting tab

The inputs generated and the data computed by running the Matlab script in the *Matlab script generation* process can be plotted within the GUI in its fourth and last tab: the Plotting Tab. It also allows customization of the plots.

1_ Add plots

- **Browsing:**

1. Click on “Browse Directory”
2. Browse to the folder containing the raw data files
3. Click on “Open”

- **Giving an absolute path**

Note:

- If the folder’s name is FADTTSter_*FiberName* then *FiberName* automatically extracted and set as the fiber name for the edition. Otherwise the user should set it. The fiber name can be modified at any time without any consequences.
- Once the directory containing the statistical data is set, the plotting becomes available only if the data files found in the directory enable a plot. Otherwise, even if the folder contains some data, the plotting will remain unavailable.

2_ Display plot

Once the data is loaded, the user can choose to plot it. Here is how to do it:

1. Select the plot you want to display

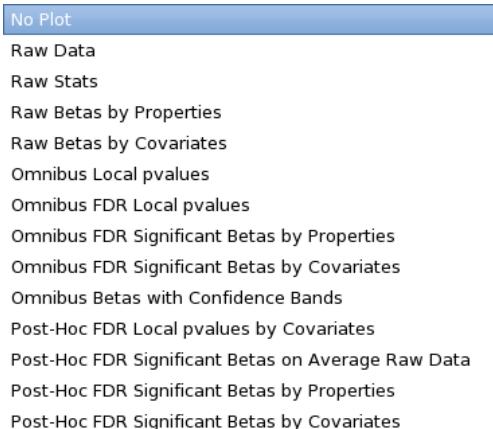


Figure 37: Plots available

2. Select a property – *AD*, *RD*, *MD* or *FA* – (only if needed)
3. Select a covariate (only if needed)
4. Click on “Display Plot”

All the plots are available are summarized below:

- **Raw Data**

Property→mandatory
Covariate→optional

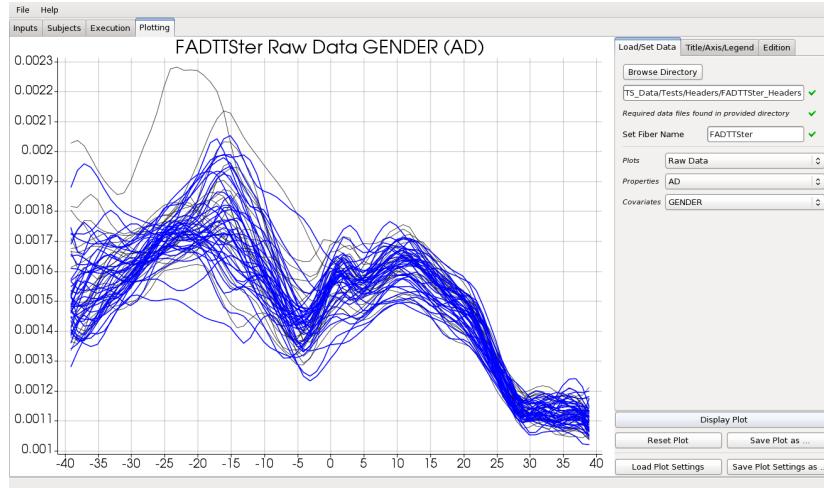


Figure 38: Plotting raw data

- **Raw Stats**

Property→mandatory
Covariate→optional

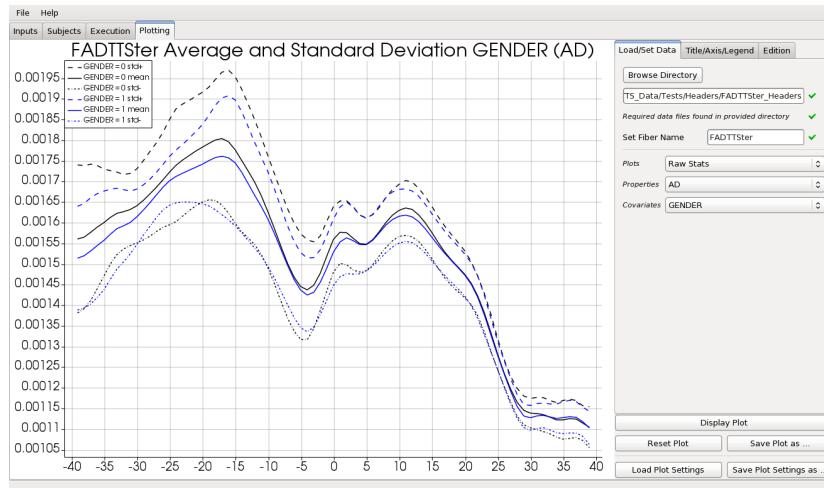


Figure 39: Plotting raw stats

- **Raw Betas by Properties**

Property→mandatory
Covariate→not required

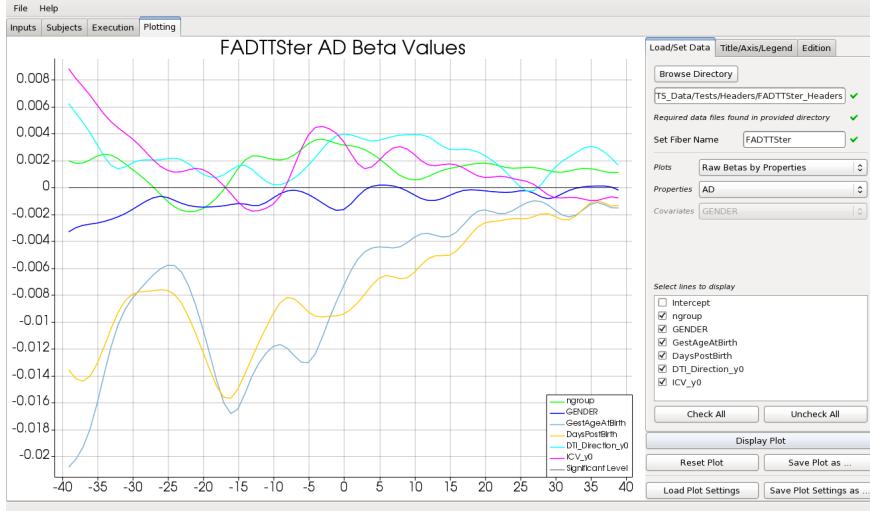


Figure 40: Plotting raw betas by properties

- **Raw Betas by Covariates**

Property→not required
Covariate→mandatory

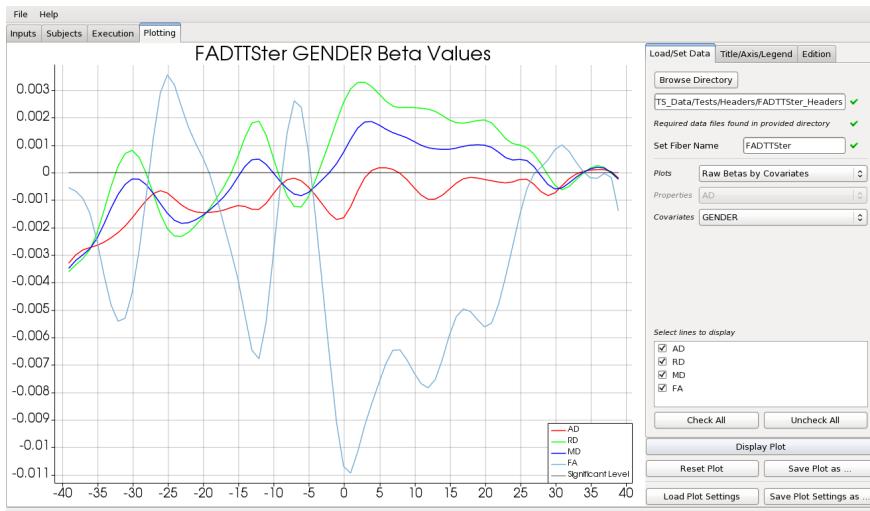


Figure 41: Plotting raw betas by covariates

- **Omnibus Local pvalues**

Property→not required

Covariate→not required

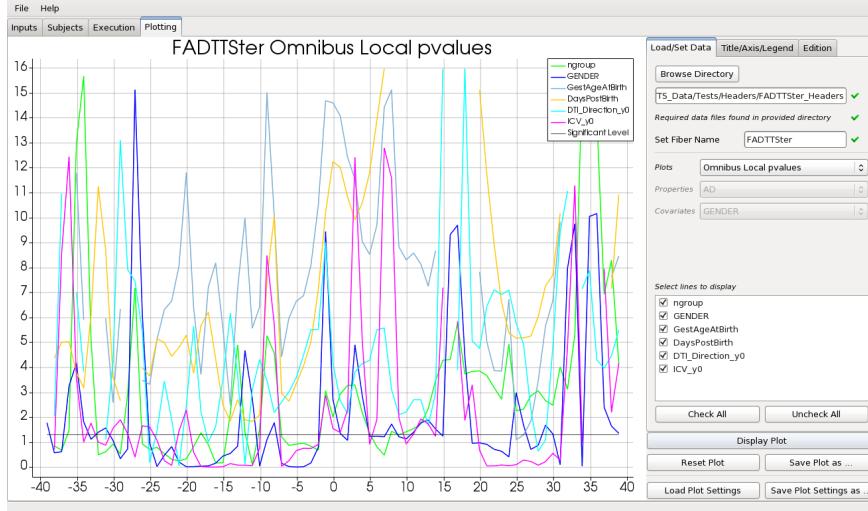


Figure 42: Plotting omnibus local pvalues

- **Omnibus FDR Local pvalues**

Property→not required

Covariate→not required

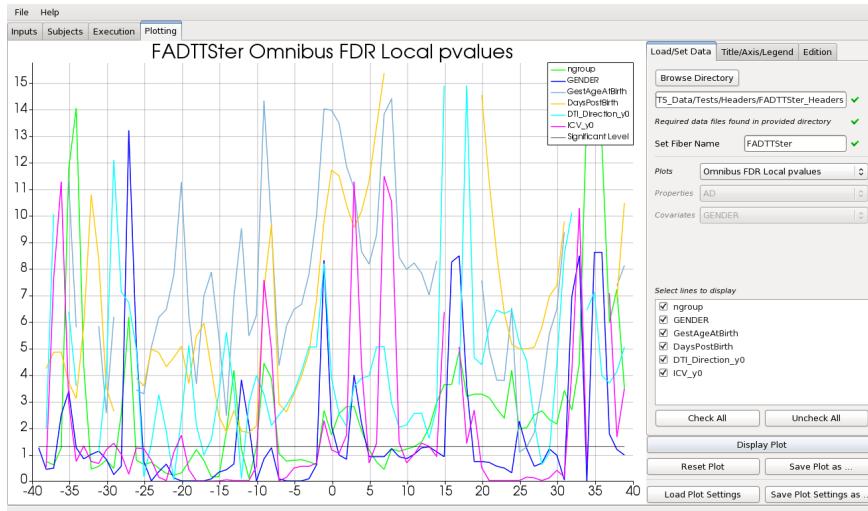


Figure 43: Plotting omnibus FDR local pvalues

- **Omnibus FDR Significant Betas by Properties**

Property→mandatory
Covariate→not required

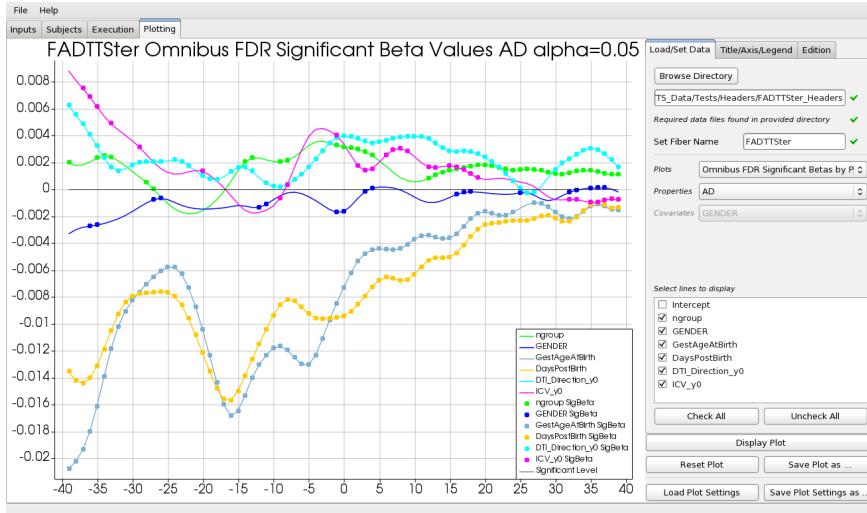


Figure 44: Plotting omnibus FDR significant betas by properties

- **Omnibus FDR Significant Betas by Covariates**

Property→not required
Covariate→mandatory

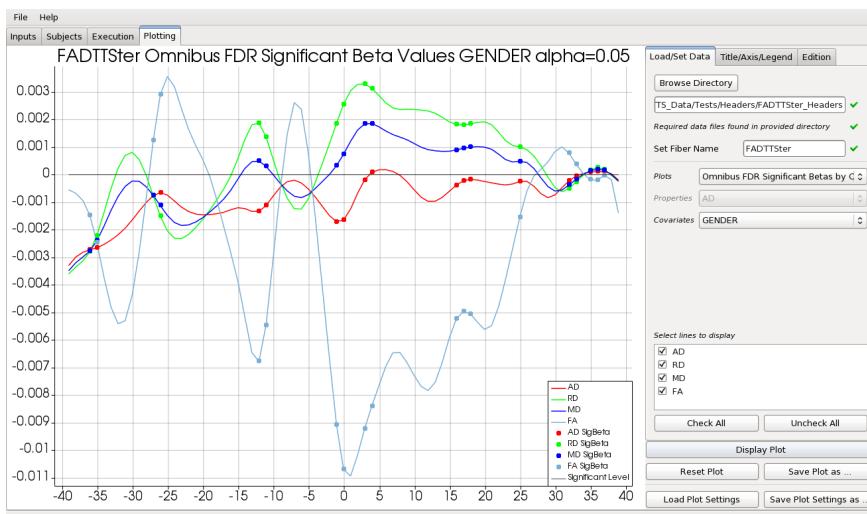


Figure 45: Plotting omnibus FDR significant betas by covariates

- **Omnibus Betas with Confidence Bands**

Property→mandatory

Covariate→optional

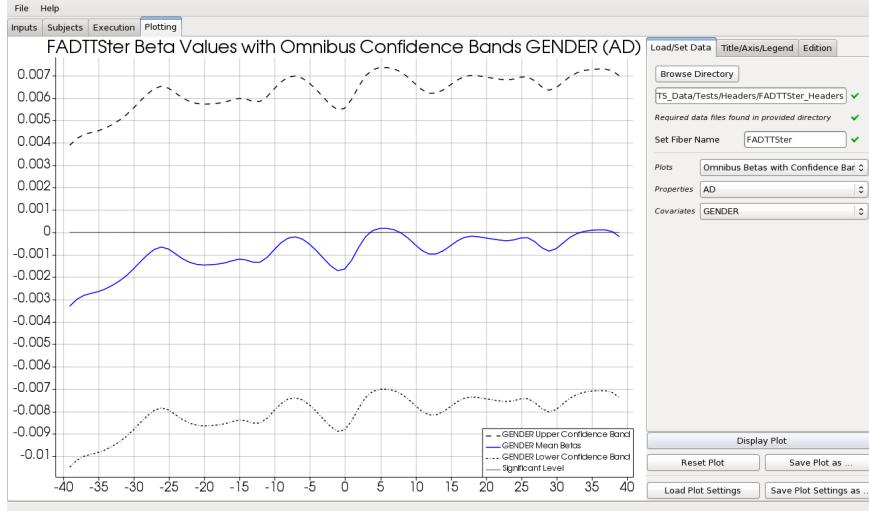


Figure 46: Plotting omnibus betas with confidence bands

- **Post-Hoc FDR Local pvalues by Covariates**

Property→not required

Covariate→mandatory

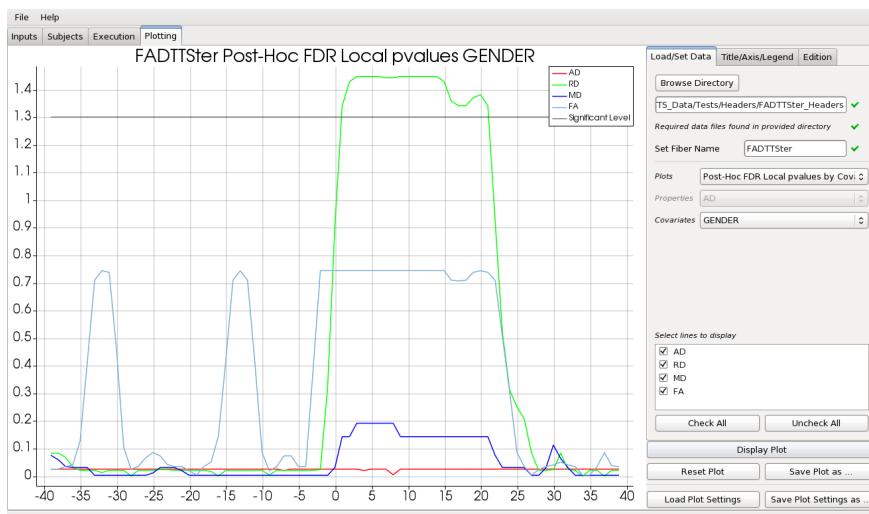


Figure 47: Plotting post-hoc FDR local pvalues by covariates

- **Post-Hoc FDR Significant Betas on Average Raw Data**

Property→mandatory

Covariate→optional

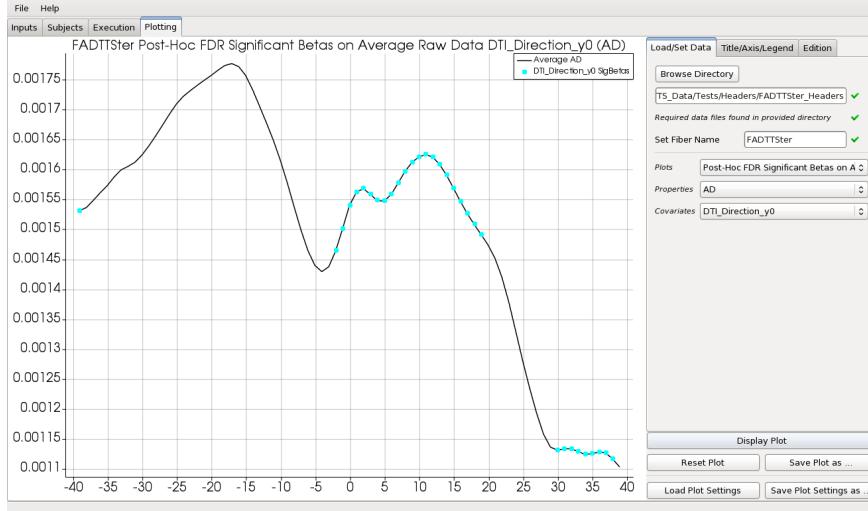


Figure 48: Plotting post-hoc FDR significant betas on average raw data

- **Post-Hoc FDR Significant Betas by Properties**

Property→mandatory

Covariate→not required

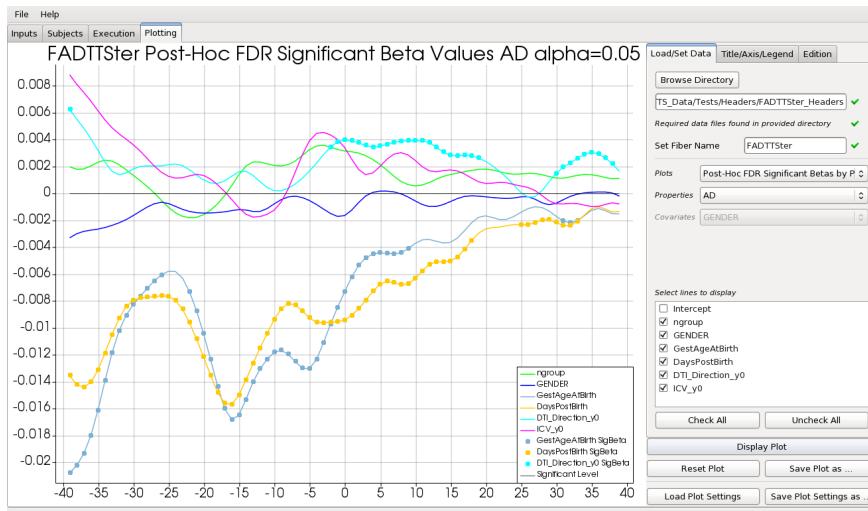


Figure 49: Plotting post-hoc FDR significant betas by properties

- **Post-Hoc FDR Significant Betas by Covariates**

Property→not required
Covariate→mandatory

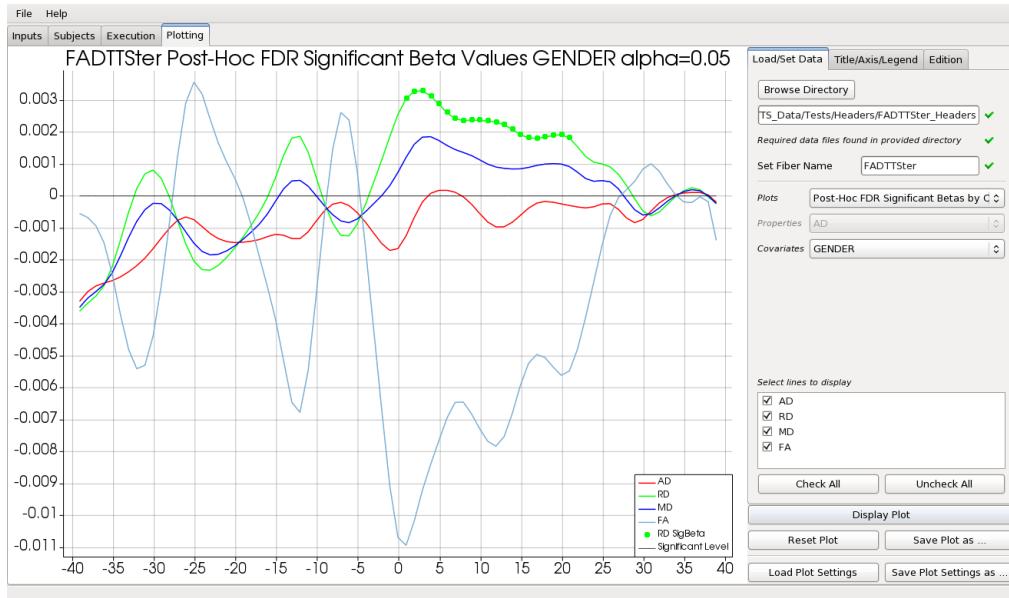


Figure 50: Plotting post-hoc FDR significant betas by covariates

3_ Customize plot

To customize the plots and enhance the results, the user can use the features available in the tabs *Title/Axis/Legend* and *Edition*.

<div style="border-bottom: 1px solid black; padding: 5px;"> Load/Set Data Title/Axis/Legend Edition </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Title <input type="checkbox"/> Use default title Title <input type="text"/> Size <input type="text" value="35.0"/> <input type="button" value="^"/> <input type="button" value="v"/> <input type="checkbox"/> Italic <input type="checkbox"/> Bold </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Axis <input checked="" type="checkbox"/> Grid On <input type="checkbox"/> Scientific notation <input type="checkbox"/> Use default axis names x Name <input type="text"/> y Name <input type="text"/> Size <input type="text" value="35.0"/> <input type="button" value="^"/> <input type="button" value="v"/> <input type="checkbox"/> Italic <input type="checkbox"/> Bold Label size <input type="text" value="20.0"/> <input type="button" value="^"/> <input type="button" value="v"/> <input type="checkbox"/> Set yMin <input type="text" value="-0.5000"/> <input type="button" value="^"/> <input type="button" value="v"/> <input type="checkbox"/> Set yMax <input type="text" value="0.5000"/> <input type="button" value="^"/> <input type="button" value="v"/> <i>If not specified, yMin and yMax will be automatically set.</i> </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Legend <input checked="" type="checkbox"/> Show Legend Position <input type="text" value="Top Left"/> <input type="button" value="^"/> <input type="button" value="v"/> </div> <div style="border-bottom: 1px solid black; padding: 5px; text-align: center;"> <input type="button" value="Display Plot"/> </div> <div style="border-bottom: 1px solid black; padding: 5px; text-align: center;"> <input type="button" value="Reset Plot"/> <input type="button" value="Save Plot as ..."/> </div> <div style="padding: 5px; text-align: center;"> <input type="button" value="Load Plot Settings"/> <input type="button" value="Save Plot Settings as ..."/> </div>	<div style="border-bottom: 1px solid black; padding: 5px;"> Load/Set Data Title/Axis/Legend Edition </div> <div style="border-bottom: 1px solid black; padding: 5px;"> P-value Threshold <input type="text" value="0.05"/> <input type="button" value="^"/> <input type="button" value="v"/> </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Line Line Width <input type="text" value="1.50"/> <input type="button" value="^"/> <input type="button" value="v"/> Selected Line Color <input type="text" value="Red"/> <input type="button" value="^"/> <input type="button" value="v"/> </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Marker Marker Type <input type="text" value="Circle"/> <input type="button" value="^"/> <input type="button" value="v"/> Marker Size <input type="text" value="8.00"/> <input type="button" value="^"/> <input type="button" value="v"/> <small><input type="checkbox"/> Show positive betas in green, negative ones in red 'Post-Hoc FDR Sig Betas on Avg Raw Data' only</small> </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Properties AD <input type="text" value="Red"/> <input type="button" value="^"/> <input type="button" value="v"/> RD <input type="text" value="Lime"/> <input type="button" value="^"/> <input type="button" value="v"/> MD <input type="text" value="Blue"/> <input type="button" value="^"/> <input type="button" value="v"/> FA <input type="text" value="Carolina Blue"/> <input type="button" value="^"/> <input type="button" value="v"/> </div> <div style="border-bottom: 1px solid black; padding: 5px;"> Covariates Intercept <input type="text" value="Red"/> <input type="button" value="^"/> <input type="button" value="v"/> ngroup <input type="text" value="Lime"/> <input type="button" value="^"/> <input type="button" value="v"/> GENDER <input type="text" value="Blue"/> <input type="button" value="^"/> <input type="button" value="v"/> GestAgeAtBirth <input type="text" value="Carolina Blue"/> <input type="button" value="^"/> <input type="button" value="v"/> DaysPostBirth <input type="text" value="Yellow"/> <input type="button" value="^"/> <input type="button" value="v"/> DTI_Direction_y0 <input type="text" value="Cyan"/> <input type="button" value="^"/> <input type="button" value="v"/> ICV_y0 <input type="text" value="Magenta"/> <input type="button" value="^"/> <input type="button" value="v"/> </div> <div style="border-bottom: 1px solid black; padding: 5px; text-align: center;"> <input type="button" value="Display Plot"/> </div> <div style="border-bottom: 1px solid black; padding: 5px; text-align: center;"> <input type="button" value="Reset Plot"/> <input type="button" value="Save Plot as ..."/> </div> <div style="padding: 5px; text-align: center;"> <input type="button" value="Load Plot Settings"/> <input type="button" value="Save Plot Settings as ..."/> </div>
--	---

(a) Title/Axis/Legend tab

(b) Edition tab

Figure 51: Plot customization tabs

a) Title/Axis/Legend Tab

- Title

- *Use default title*: If checked, the title is automatically generated based on the plot displayed and the fiber name
- *Title*: Sets the title displayed (used only if *Use default title* is unchecked)
- *Size*: Sets the size of the title (value between 10 and 80)
- *Italic*: If checked, sets the title in italic
- *Bold*: If checked, makes the title bold

- Axis

- *Grid on*: Enables/disables the grid on the plotting area
- *Scientific notation*: Enables/disables the scientific notation for the axis
- *Use default axis names*: If checked, the axis names are automatically generated based on the plot displayed
- *x Names*: Sets the x axis name (used only if *Use default axis names* is disabled)
- *y Names*: Sets the y axis name (used only if *Use default axis names* is disabled)
- *Size*: Sets the size of the axis names (value between 10 and 80)
- *Italic*: If checked, sets the axis names in italic
- *Bold*: If checked, sets the axis names in bold
- *Label size*: Sets the size of the axis labels (value between 10 and 40)
- *Set yMin*: Enables/disables a minimum value for the y axis (value between -100 and 100)
- *Set yMax*: Enables/disables a maximum value for the y axis (value between -100 and 100)

- Legend

- *Show Legend*: Enables/disables the legend
- *Position*: Set the position of the legend on the plotting area
(*Top Left/Top Center/Top Right/Middle Left/Middle Center/Middle Right/Bottom Left/Bottom Center/Bottom Right*)

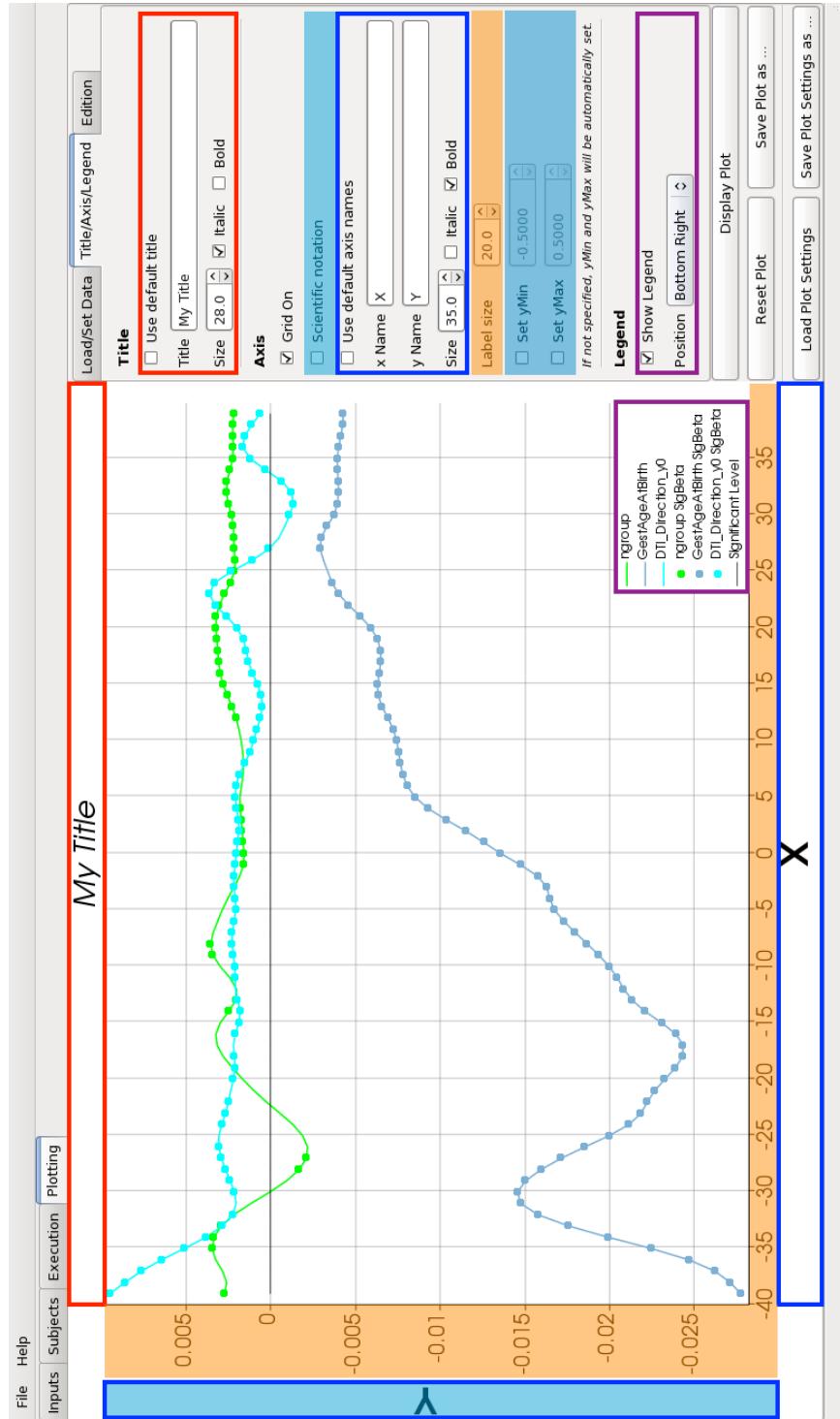


Figure 52: Plot customization (1/2)

b) Edition Tab

- **P-value threshold**

Sets the p-value threshold (value between 0 and 1)

- **Line**

- *Line Width*: Sets the line width (value between 0 and 1)

- *Color*: Sets the line color

- (*Red/Lime/Blue/Carolina Blue/ Yellow/Cyan/Magenta/Olive/Teal/Purple/Rosy Brown/Park Sea Green/ Corn Flower Blue/Maroon/Green/-Navy/Orange/Mint/Pink/Brown/Black*)

- **Marker**

- *Marker Type*: Sets the marker type
(*Circle/Cross/Diamond/Plus/Square*)

- *Color*: Sets the marker size (value between 4 and 20)

- *Show positive betas in green, negative ones in red*: This option is for *Post-Hoc FDR Significant Betas on Average Raw Data*. When enabled, positive betas are displayed in green, and negative ones in red. When disabled all betas have the same color.

- **Properties** Colors are automatically set to each property loaded. The user can change them if needed.

- (*Red/Lime/Blue/Carolina Blue/ Yellow/Cyan/Magenta/Olive/Teal/Purple/Rosy Brown/Park Sea Green/ Corn Flower Blue/Maroon/Green/-Navy/Orange/Mint/Pink/Brown/Black*)

- **Covariates**

- Colors are automatically set to each covariate loaded. The user can change them if needed.

- (*Red/Lime/Blue/Carolina Blue/ Yellow/Cyan/Magenta/Olive/Teal/Purple/Rosy Brown/Park Sea Green/ Corn Flower Blue/Maroon/Green/-Navy/Orange/Mint/Pink/Brown/Black*)

- The label of each covariate is extracted from the data file. If the user needs a more explicit one, it can be changed by simply writing the new label in the blank space on the third column. When no new label is provided, the orginal label is kept. To apply such modifications, the user must click on “Display Plot”.

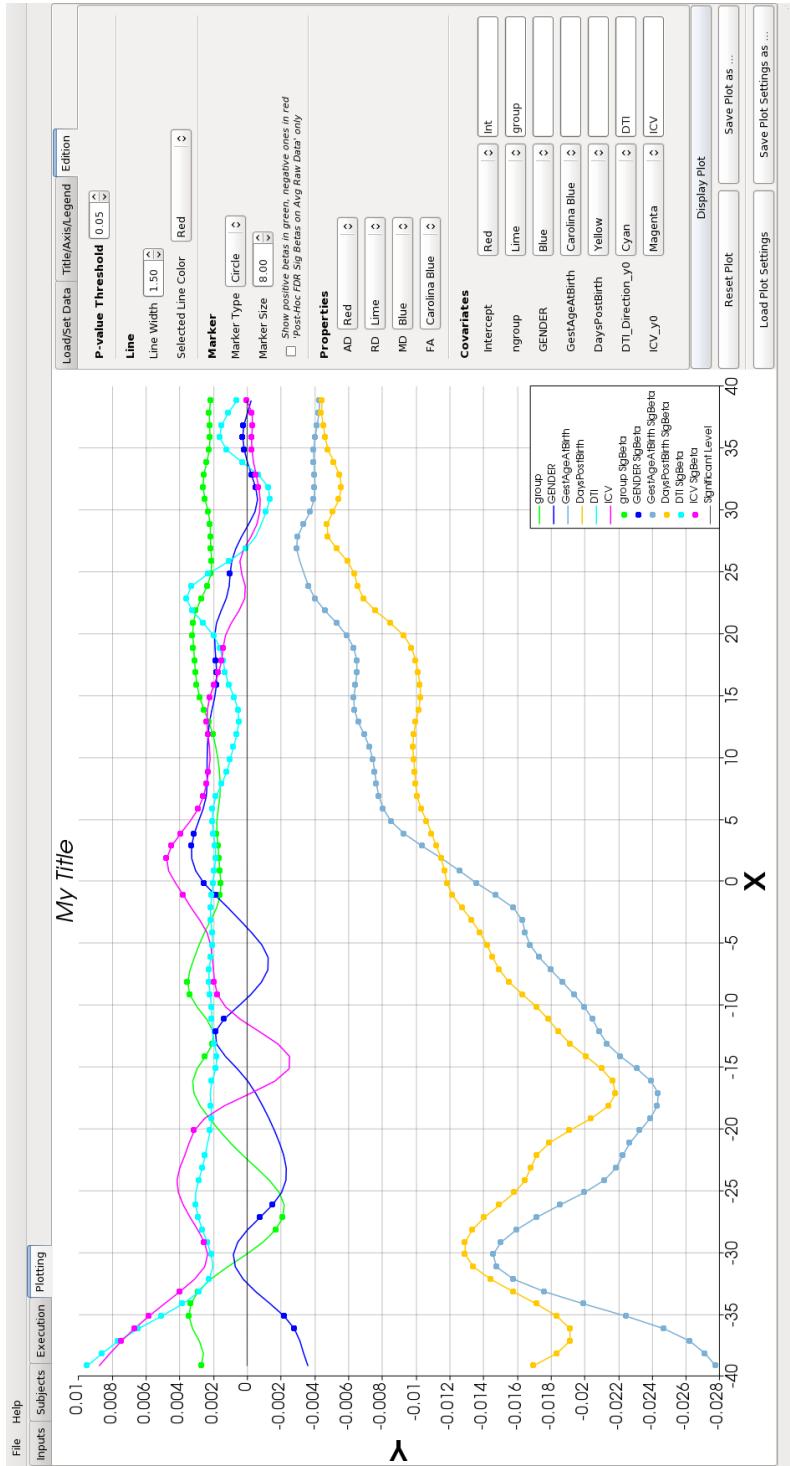


Figure 53: Plot customization (2/2)

c) Special Features

- **Select Lines**

When plotting the raw data, the user may select the lines displayed. If a line is selected, it is highlighted in red and the subject ID is displayed.

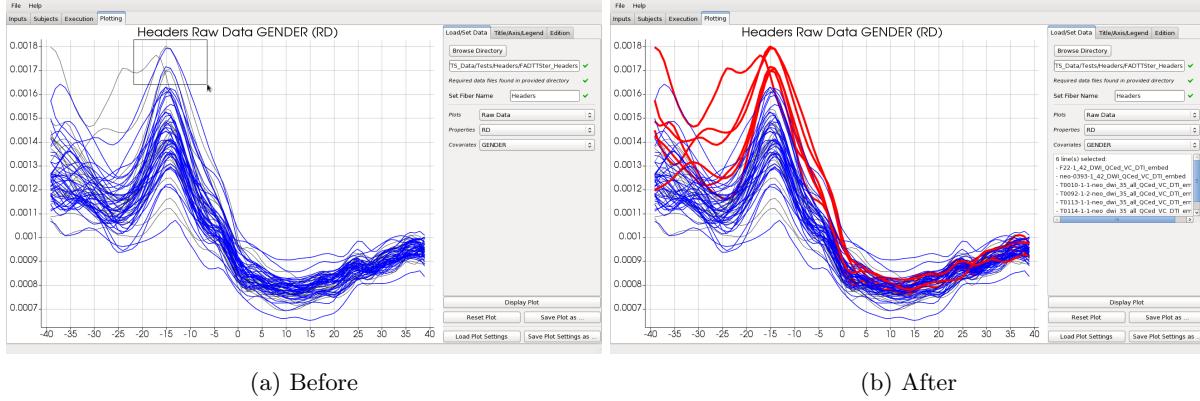


Figure 54: Line selection when plotting raw data

- **Choose properties/covariates to display**

Some plots give the option to choose the line to display. If this is the case, and if the user chooses to enable/disable some lines, the plotting area will automatically be updated.

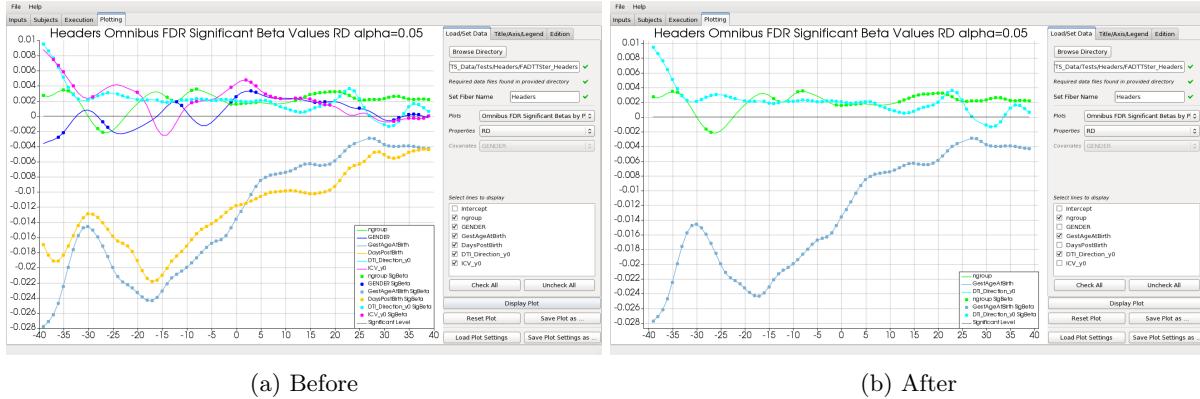


Figure 55: For some plots, the user can choose the lines to display

4_ Save Plot

1. Click on “Save Plot as . . .”
2. In the pop-up window displayed, browse to the folder where you want to save your plot
3. Rename the file if needed
4. Click on “Save”

Note: File are saved as a .eps.

Part IV

Advanced use of FADTTSter

The following sections will help you to use FADTTSter more efficiently with some very useful features.

A Configuration files

In order to prevent the user from entering the settings in the GUI over and over again, we can use the configuration files. The settings are split into two groups: *Para* and *Soft*. *Soft* rounds up all settings related to the software part while *Para* gathered the rest.

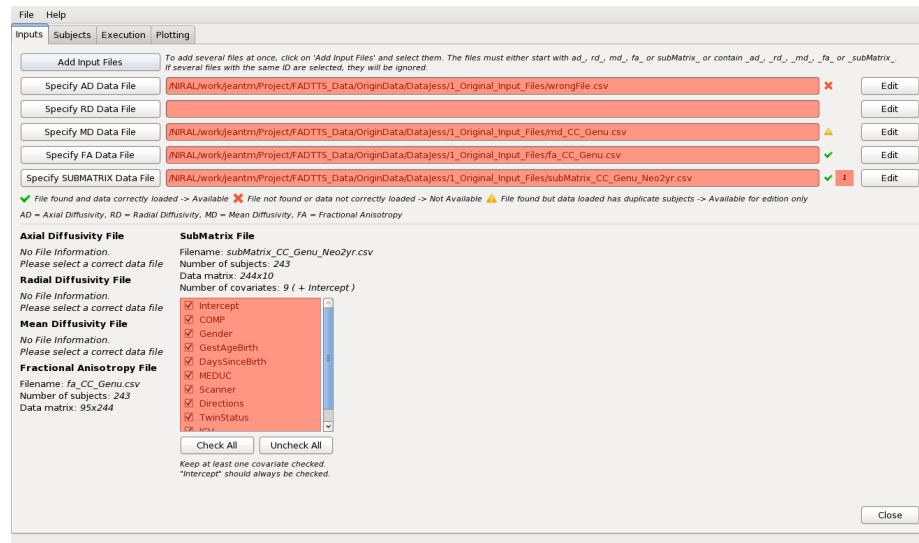


Figure 56: *Para* settings (red)

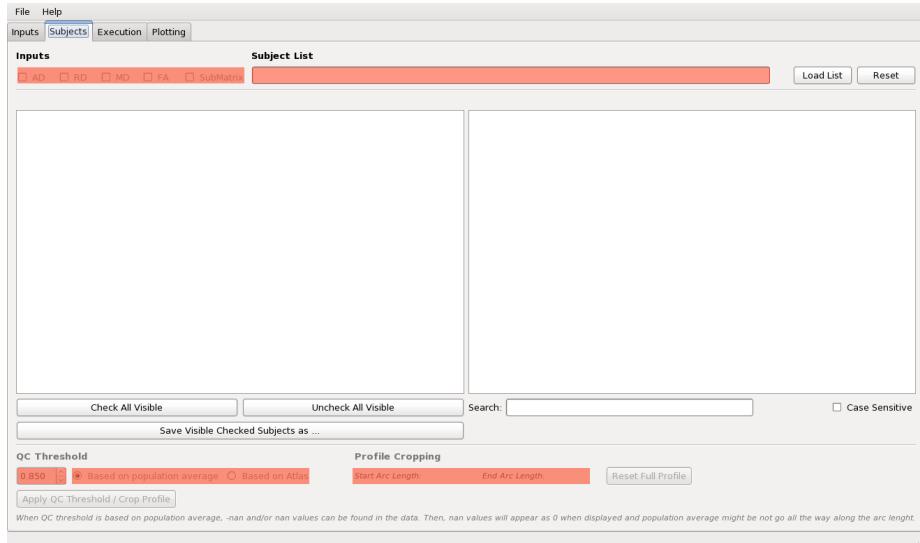


Figure 57: *Para* settings (red)

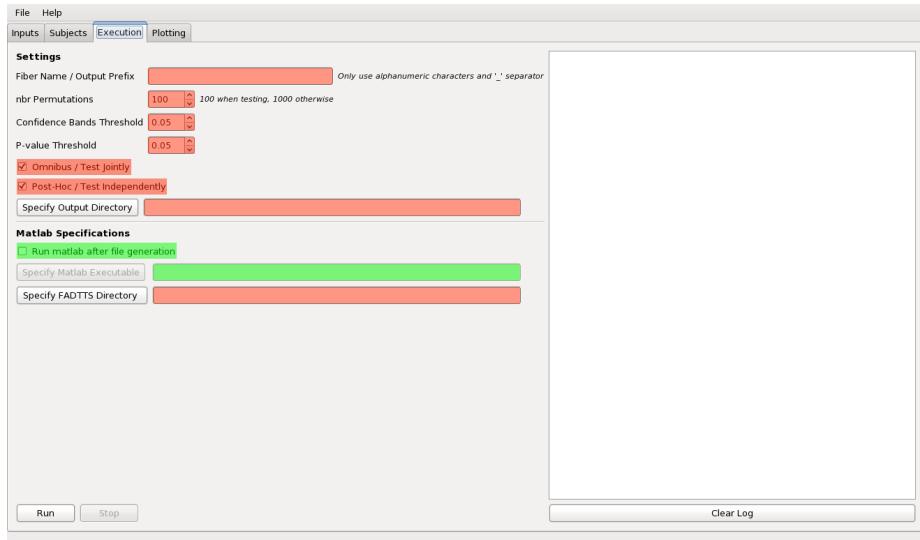


Figure 58: *Para* settings (red) and *Soft* settings (green) that can be set with the configuration files

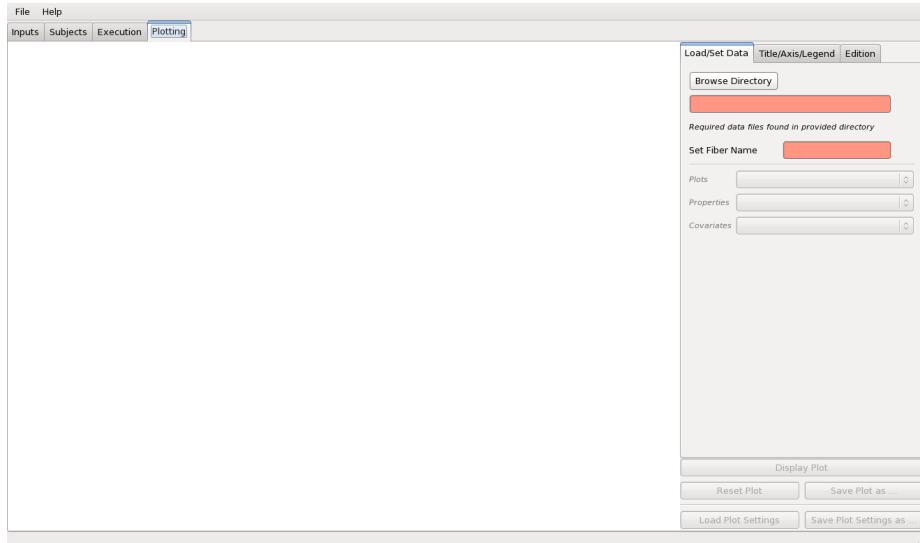


Figure 59: *Para* settings (red)

The configuration files are .json files. They have a very specific syntax. Templates for each configuration can be found [here](#).

1. Upload configurations to GUI

1. Click on “File”
2. Select “Load Parameters Configuration” or “Load Software Configuration” depending on what you want to add
3. Browse to the .json file containing the configuration wanted
4. Select it
5. Click on “Open”

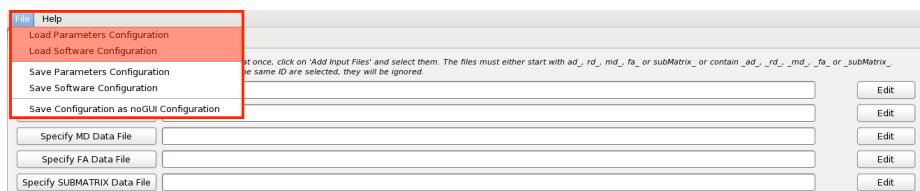


Figure 60: Load configuration files and add them to the GUI

2_ Save configurations

1. Click on “File”
2. Select “Save Parameters Configuration” or “Save Software Configuration” depending on what you want to save
3. Browse to the folder where you want to keep the configuration
4. Rename file if needed
5. Click on “Save”

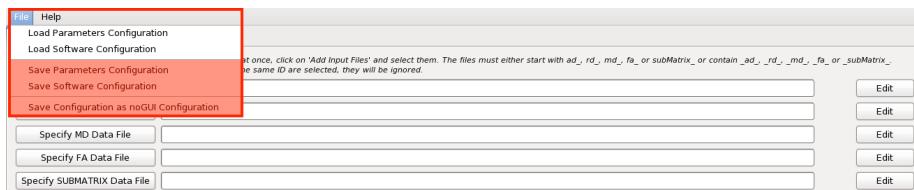


Figure 61: Save configurations

Note: “Save Configuration as noGUI Configuration” saves the configuration in such a way that it can be used to run FADTTSter without the GUI.

B Plot settings

To help the user to work efficiently on the visualization of the results, the same system of .json files exists for the plot settings. All the settings value can be saved and uploaded in the GUI for the plotting tab.

1_ Upload configurations to GUI

1. Click on “Load Plot Settings”
2. Browse to the .json file containing the plot settings wanted
3. Select it
4. Click on “Open”

2_ Save configurations

1. Click on “Save Plot Settings as ...”
2. Browse to the folder where you want to save the settings
3. Rename file if needed
4. Click on “Save”

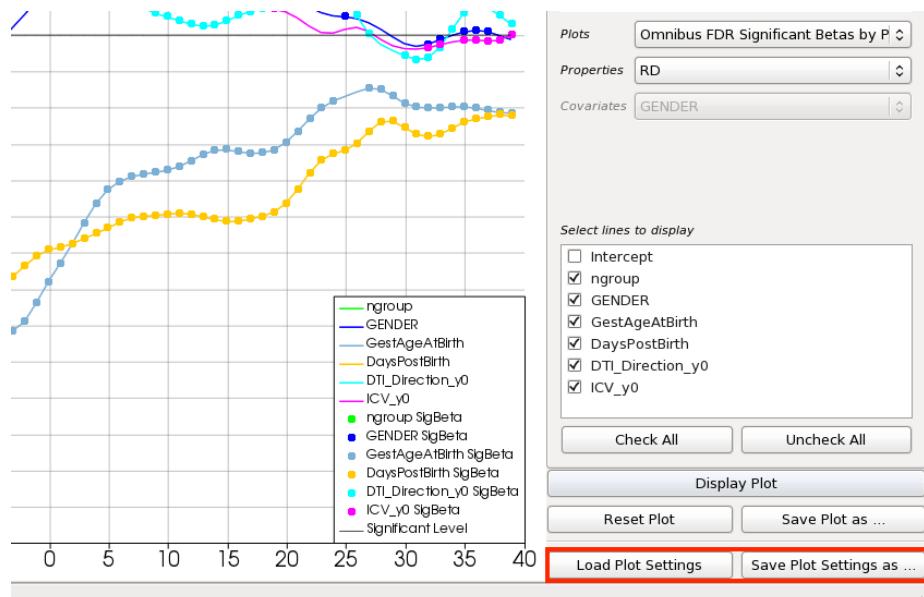


Figure 62: Load save plot settings

C FADTTSter in command line

FADTTSter can be launched with some options before the GUI is only in the terminal. Here some examples illustrating how to use them:

- Launch FADTTSter within a GUI:

```
$ FADTTSter [-d] [--softConfig] [--paraConfig]
```

[-d]: Path to a directory. When opening the GUI, a search will be made within the directory provided to find configuration files. If files are found, they will automatically be loaded to the GUI. Files must be named as following: **para*.json* or **Para*.json*, **soft*.json* or **Soft*.json* and **noGUI*.json* or **NoGUI*.json*.

[-softConfig]: Path to the .json file containing the software configuration. The configuration will automatically be loaded to the GUI.

[-paraConfig]: Path to the .json file containing the parameters configuration. The configuration will automatically be loaded to the GUI.

These parameters are independent of each other. However, if *[-d]* and *[-softConfig]* are used, the software configuration file provided by *[-softConfig]* will take over the one found in the directory provided by *[-d]*.

- Launch FADTTSter only using the terminal:

```
$ FADTTSter [--noGUI] [--noGUIConfig]
```

[-noGUI]: Indicates that the GUI should not be displayed.

[-noGUIConfig]: Path to the .json file containing the no-GUI configuration (parameters and software).

FADTTSter will be run with the information provided in the no-GUI configuration file. *[-noGUI]* and *[-noGUIConfig]* MUST be run together! Otherwise, FADTTSter cannot be computed.

List of Figures

1	FADTTSter in the UNC-Utah NA-MIC DTI framework	4
2	FADTTSter tabs used for <i>Matlab script generation</i>	6
3	Inputs tab	7
4	Adding input files	8
5	Pop-up window displayed to set multiple input files at once	8
6	Adding one file using “Specify Data File” push button	9
7	Adding one file specifying the absolute path	9
8	File status and file information after adding an input file	10
9	Editing an input file	11
10	Pop-up window displayed when file edition is unavailable (i.e. no data has been loaded (file not provided or not found)	11
11	Edition windows available depending on the input file provided	11
12	Deleting columns	12
13	Removing duplicates from data file	12
14	Nan values found in an FA file	13
15	Setting column ID	13
16	Save modifications after file edition	14
17	Closing pop-up displayed after modifications not saved	14
18	Toggle the covariates to add them to or remove them from the study	15
19	Unselecting the <i>Intercept</i> will result in displaying a warning pop-up	15
20	Subjects tab	16
21	Adding subjects from input files	17
22	Adding a subjects from an external subject list	17
23	Subjects displayed regarding their occurrences in all subject lists provided	18
24	Information provided regarding the subjects displayed	18
25	Selecting/unselecting a specific subject by clicking on it	19
26	Save all sujets selected as one subject list	19
27	Use saved subject right away	19
28	Searching for subjects	20
29	Setting the QC threshold in the <i>Subjects</i> tab	21
30	Pop-up window displayed to work on the QC threshold	21
31	Adjusting the QC threshold	22
32	Apply a new QC threshold	22
33	Adjusting the range of the study (highlighted zone are excluded)	23
34	Removing <i>nan</i> values	23
35	Execution tab	24
36	Plotting tab	27
37	Plots available	28
38	Plotting raw data	29
39	Plotting raw stats	29
40	Plotting raw betas by properties	30

41	Plotting raw betas by covariates	30
42	Plotting omnibus local pvalues	31
43	Plotting omnibus FDR local pvalues	31
44	Plotting omnibus FDR significant betas by properties	32
45	Plotting omnibus FDR significant betas by covariates	32
46	Plotting omnibus betas with confidence bands	33
47	Plotting post-hoc FDR local pvalues by covariates	33
48	Plotting post-hoc FDR significant betas on average raw data . . .	34
49	Plotting post-hoc FDR significant betas by properties	34
50	Plotting post-hoc FDR significant betas by covariates	35
51	Plot customization tabs	36
52	Plot customization (1/2)	38
53	Plot customization (2/2)	40
54	Line selection when plotting raw data	41
55	For some plots, the user can choose the lines to display	41
56	<i>Para</i> settings (red)	43
57	<i>Para</i> settings (red)	44
58	<i>Para</i> settings (red) and <i>Soft</i> settings (green) that can be set with the configuration files	44
59	<i>Para</i> settings (red)	45
60	Load configuration files and add them to the GUI	45
61	Save configurations	46
62	Load save plot settings	47

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