



Project Title:	Human Brain Project
Sub-Project Title:	Medical Informatics Platform (SP8)
Document Title:	MIP Web UI – User Guidelines V1.0 Public Release
Summary:	Step-by-step guidelines of how to use the MIP Web interface Audience: any users of Medical Informatics Platform

Versions, changes and contributors:

Authors	Version	Date	Status	Change details
Mihaela Damian, CHUV	v1	29/02/2016	Draft 1	Created before the final tests. To be reviewed before the release.

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1 Introduction

The Medical Informatics Platform launches its first public release (v1) on 31st March 2016.

This first release focuses on building a solid platform foundation so that any new features can be easily added in the coming months and years. The user will be able to access the platform via a Web UI (password restricted) where s/he can run exploratory analyses and create basic models and estimations, and save them for further review.

At M30 release - target users:

User Groups	E.g. User Subgroups	Internal/External (I/E)
CLINICIANS	Epidemiologists, Neuroclinicians	I + E
RESEARCHERS	in Neurology, in Neuroimaging, in Pharmacology	I + E
STATISTICIANS		I + E
SCIENTIFIC DEVELOPERS	Method and Algorithm developers	I
PLATFORM DEVELOPER	Deploys tools and algorithms	I
MEDICAL & RESEARCH WRITERS		I+E
GENERAL PUBLIC		I+E

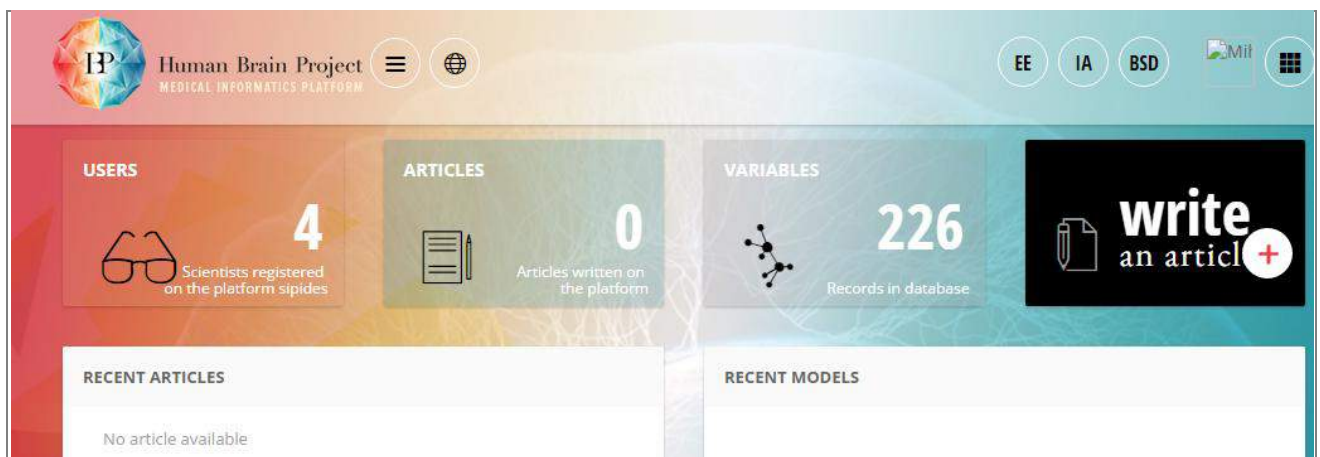
1. MIP User Guidelines

1.1 General navigation within MIP

Once you log in, the platform opens with the **main dashboard**.

The dashboard shows a live *summary of stats* (users, variables available, articles written), as well as the *latest three saved models and articles* (yours or of other users)

From here, you may also start **writing articles** (analyses' description) .



You may at any time come back to this page by clicking the HBP logo on the left top corner.

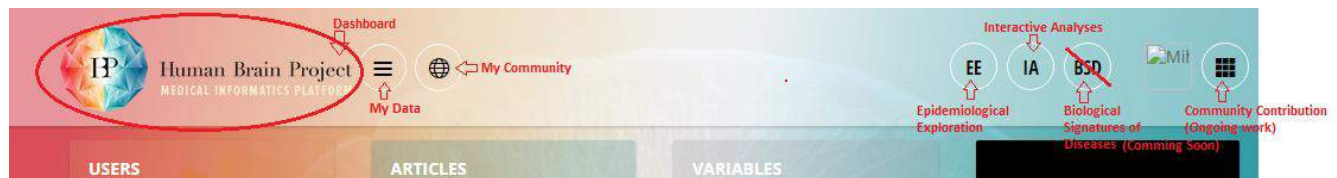
From the top banner, you may at any time access:

- My Data : your own personal dashboard, displaying *your own* work only (saved models and articles), shared or unshared
- My Community : your work and of the other users in the MIP community

as well as the user services:

- **Epidemiologica Exploration (EE)**
- **Interactive Analyses (IA)**
- Biological Signatures of Diseases (BSD) (Note: not yet deployed)
- **Personal Profile**
- Apps (Note: under development)

(see highlights in screenshot below)



1.2 Exploration, Model design and Estimation

MIP proposes a series of users services:

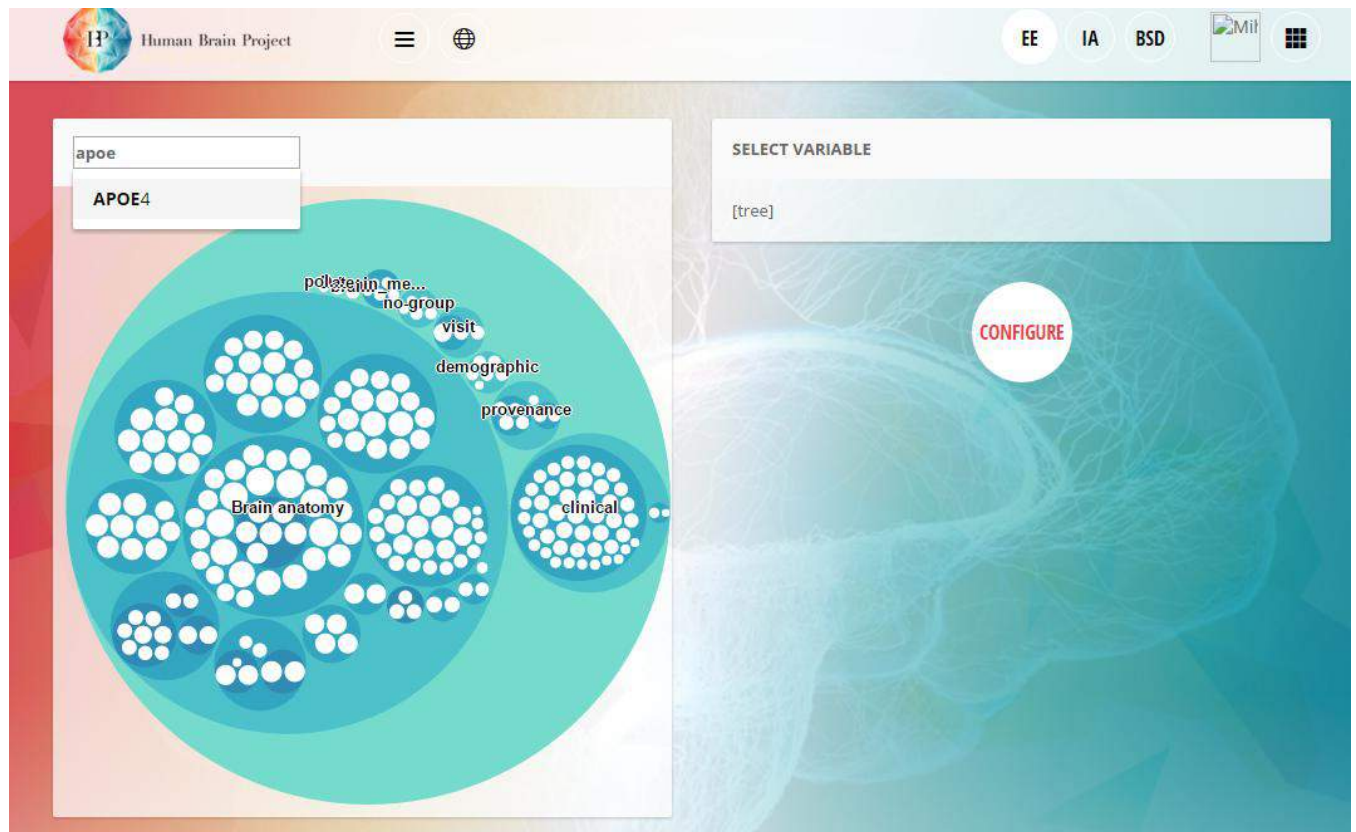
- EE : the Epidemiological Exploration – allowing you to browse though the variables released in the system and examine what data is available. Descriptive statistics will summarise this.
- IA : the Interactive Analyses : allowing you to design and estimate models.

You may start your work in EE and the system will lead you to the IA seamlessly, OR you can go straight to IA and design your model. You may find, however, that the EE exploration is easier for selecting the variables to go in the model.

1.2.1 EE: Epidemiological Exploration: user wants to explore the variables existent in MIP and the descriptive statistics of the associated data.

The exploration is done through the Circle-pack design. We will call it here the **MIP Variable Space**.

You may also search for the variable by typing directly in the *search box* above the Variable Space (see screen shot below, searching for APOE4 as an example)



Not all variables have associated data in the system yet. If they do, descriptive statistics are displayed on the right (see below). For the moment we only have counts, but more functions will be added soon.



You might stop your MIP exploration here, OR might decide to go further and **Design a Model** (or configure a model). By designing a model, you categorise the variables selected in the EE Variable Space into variables,

covariables and groupings. You may also apply filters.

Note: filter functionality does not work at the moment, but is scheduled to be delivered over the following months.

1.2.1.1 Designing a Model:

This section is helping you to configure your next step and it makes the transition to the Interactive Analyses.

To design/configure a model, you do:

- 1- **Click** on the **Configure** button, below the stats. A table shows up.
- 2- **Search for your variables** of interest and click on the category desired.

Let's take an example: say that we want to predict changes in the volume of the Hippocampus by considering the disease status at baseline, in rapport to age and gender.

For that we selected the variable *Hippocampus* in the Variable Space and (EE step above), then clicked on "USE AS VARIABLE" in the Configuration table. Then we selected *DX_bl* variable in EE and clicked "USE AS GROUPING". The same for *AGE* and *Gender*, but using them as covariables.

Optional: you may at any time **remove** the variables from the Configuration table by clicking the "X" sign.

Similarly, you may **restore** any previously searched variable from the "History" line (next to the search box, highlighted in picture below).

Measurement count	Min	Max	Average	Standard dev.
1,649	55.9	90.9	75.404	6.215

Summary | Histogram :AGE | Histogram :AGE-PTGENDER=Female | Histogram :AGE-PTGENDER=Male

USE AS VARIABLE	USE AS GROUPING	USE AS COVARIABLE	USE AS FILTER
VARIABLE X Hippocampus	GROUPING X DX_bl	COVARIABLE X PTGENDER X AGE	FILTERS

REVIEW MODEL

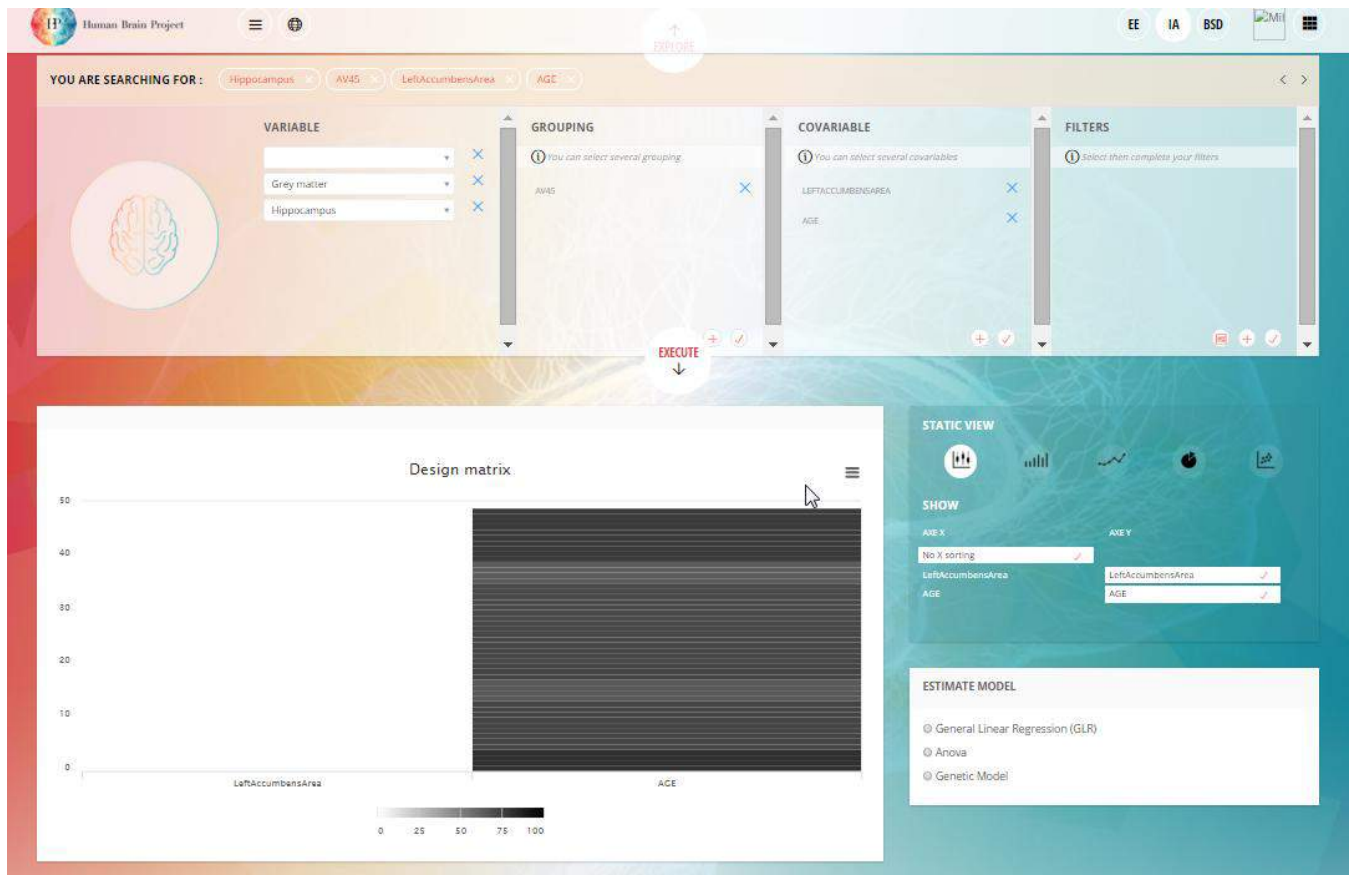
Note: Please note that in current release Filters do not work. They will be implemented in the coming releases.

- 3- When happy with your configuration, just **click on Review Model** button at the bottom of the screen.

This will automatically take you to the *IA (Interactive Analyses)* section, showing you the results of your model design – the **Design Matrix** as default visualisation. See below.

1.2.2 IA: Interactive Analyses:

You arrive here from the EE section (see above), in which case the design model is pre-populated with the variables already selected.



You can easily switch between the visualisation options on the right-hand side panel – highlighted below in red.

You may also remove and read variables from the axis. The model view will be refreshed.



If you wish, you may **save your model** (by giving it a name) at this point and **share** it with the MIP community – as below.

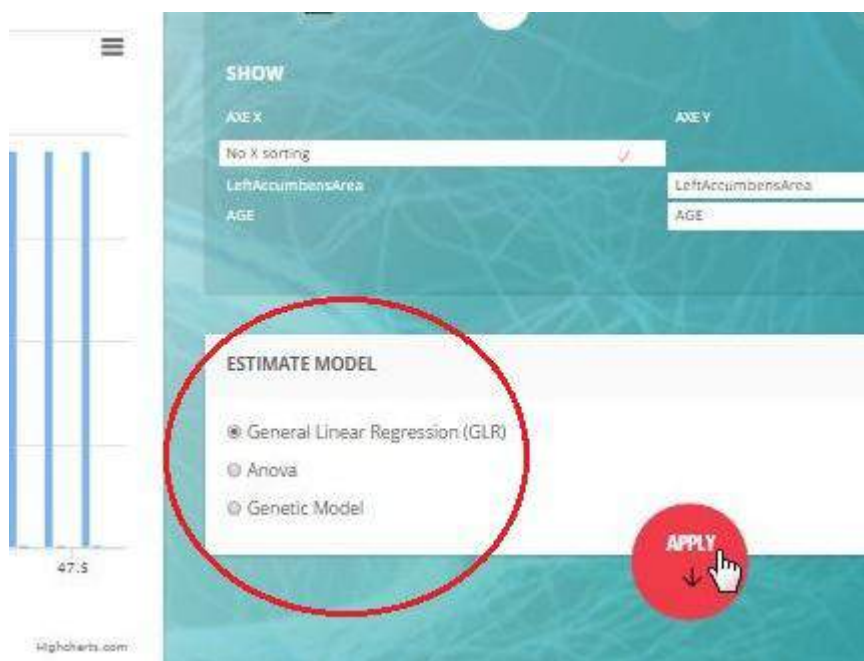


Note: to give you maximum flexibility, you may also access the IA section directly, without going through the EE.

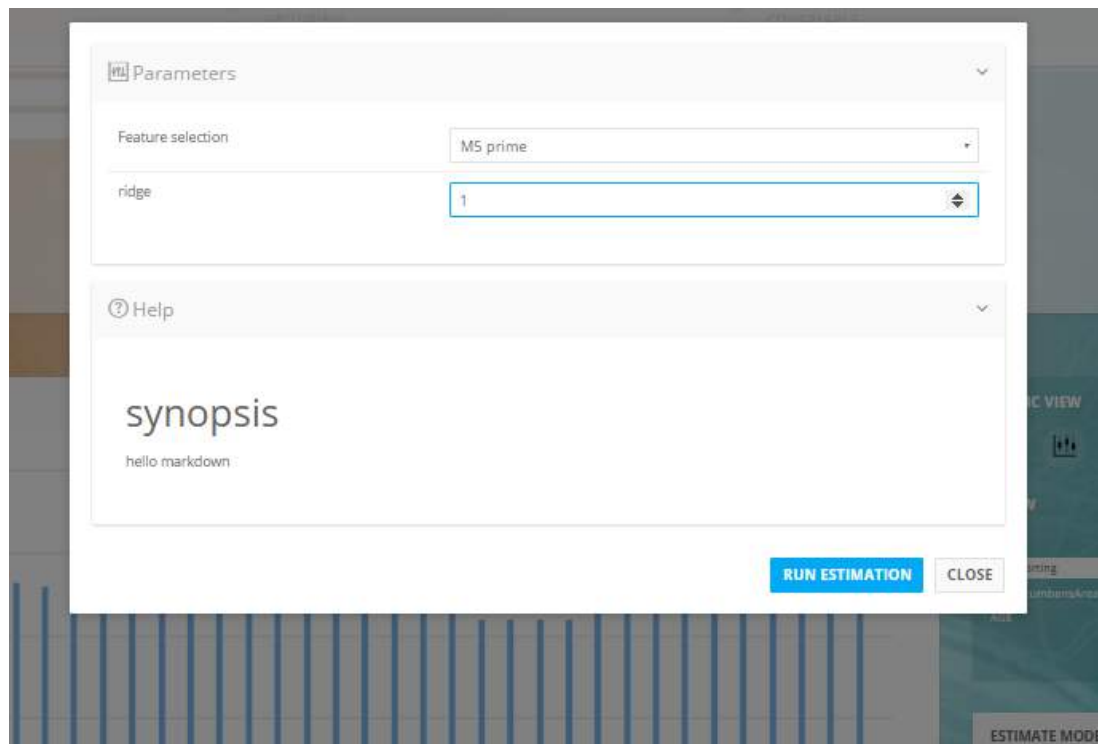
1.2.2.1 Estimate a Model: after designing and reviewing the model, you may decide to Estimate your model.

To Estimate the model you designed earlier, you will:

- 1- **select one of the methods** available in the MIP catalogue and
- 2- Click **Apply** (see screenshot below)



- 3- Enter the parameters for running the method:



- 4- **Click RUN ESTIMATION**
- 5- **View result:** a table detailed statistics is displayed for you.
- 6- Click **Close**, to close the estimation

Note: at this point, the functionality for saving the estimation results is not yet implemented. We will let you know when it will be done.

Other MIP functionality

1.3 Writing articles

- 1- **Go to main MIP Dashboard** (to do so click the HBP icon on the top left-hand side)



- 2- Click on **Write an Article**



3- **Write the article:** use the editor to add a title, abstract and content to your article.

You can also drag and drop results of your models (or others' if are shared) into the content of your article, from the left-hand side.

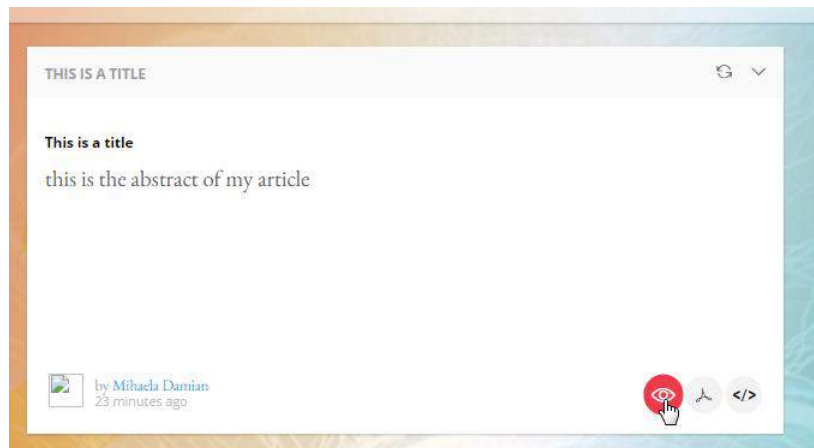
4- Give a **name** to your article, **save it** and optionally, **share it**.

1.4 Accessing my saved articles and models

You can at any time access your already written articles and saved models, either via:

1. My Data – all my work, shared or unshared
2. My Community – all my shared work

You can **preview** them, **save** them to a physical location or **open them for re-editing**.



Appendix 1: Exploration & Model Design/Configure - Process flow

