Human Brain Project

# Medical Informatics Platform User Manual

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| Summary: | Step-by-step guidelines on using the MIP.<br>Target audience: users of Medical Informatics Platform. |

**Versions, changes and contributors:**

| Version | Date | Status | Name of person | Change details |
|---|---|---|---|---|
| v1 | 29/02/2016 | Draft 1 | Mihaela Damian, CHUV | Created before the final test. To be reviewed before the release. |
| v2 | 01/10/2016 | Draft 2 | Mihaela Damian, CHUV<br>Eva Miquel, CHUV | Updated after the MIP v2 release. |
| v3 | 12/06/2018 | Draft 3 | Manuel Spuhler, CHUV | Updated with new workflows and screenshots. |
| … | | | | |

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# Medical Informatics Platform User Manual

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# 1. Introduction

The Medical Informatics Platform (MIP) aims to provide tools to the experts to analyse medical data and advance more rapidly in understanding the neurological and psychiatric diseases.

The users can access the platform via a Web UI (password restricted) where they can run exploratory data analyses, create and share analysis models, execute descriptive statistics, inferential statistics and machine-learning algorithms on user-defined analysis models, as well as collaboratively write articles.

**Target users**

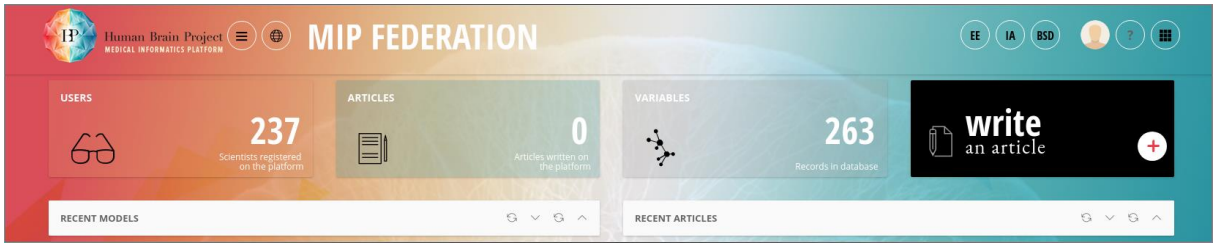
| User Groups | User subgroups |
|---|---|
| CLINICIANS | Epidemiologists, Neurologists |
| RESEARCHERS | in Neurology, Neuroimaging |
| STATISTICIANS | |
| SCIENTIFIC DEVELOPERS | Method and Algorithm developers |
| MIP PLATFORM DEVELOPERS | Deploy tools and algorithms |
| MEDICAL & RESEARCH WRITERS | |
| GENERAL PUBLIC | |

# 2. MIP User Guidelines

## 2.1 General Navigation with the MIP

After log-in, the platform opens with the main dashboard.

The dashboard shows a summary of statistics, users, available variables, as well as the latest three saved analysis models and articles (those of the current user or shared among all users). From here, the user may also start writing articles (description of data analyses performed).




At any time the user can return to this page by clicking on the HBP logo on the top left corner.

From the top banner, user can at any time access:

- **My Data**: personal dashboard displaying own work (saved analysis models and articles)
- **My Community**: all work labelled for sharing by any user within the MIP community
- **Functionalities**:
  - Epidemiological Exploration (**EE**)
  - Interactive Analyses (**IA**)
  - Biological Signatures of Diseases (**BSD**)
  - Personal Profile
  - Third-party web applications


## 2.2 Variables Exploration, Analysis Model and Experiment Design

The MIP provides the following functionalities:

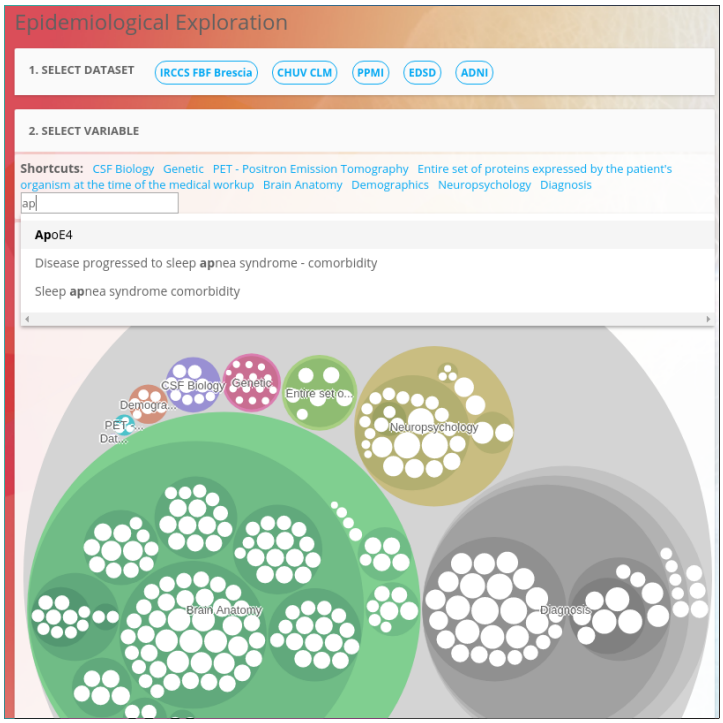
- **EE**: Epidemiological Exploration – allows exploration of the available variables, including visualisation of variables' types, selection of variables, visualisation of variables' descriptive information, and definition of analysis models (selection of response and explanatory variables for data analysis);
- **IA**: Interactive Analyses – provides descriptive summary statistics for the defined analysis models, in tabular and graphical formats;

- **BSD**: Biological Signatures of Disease – provides selection and configuration of data analysis algorithms – descriptive and inferential statistics, machine-learning and validation, using analysis models defined with IA functionality.

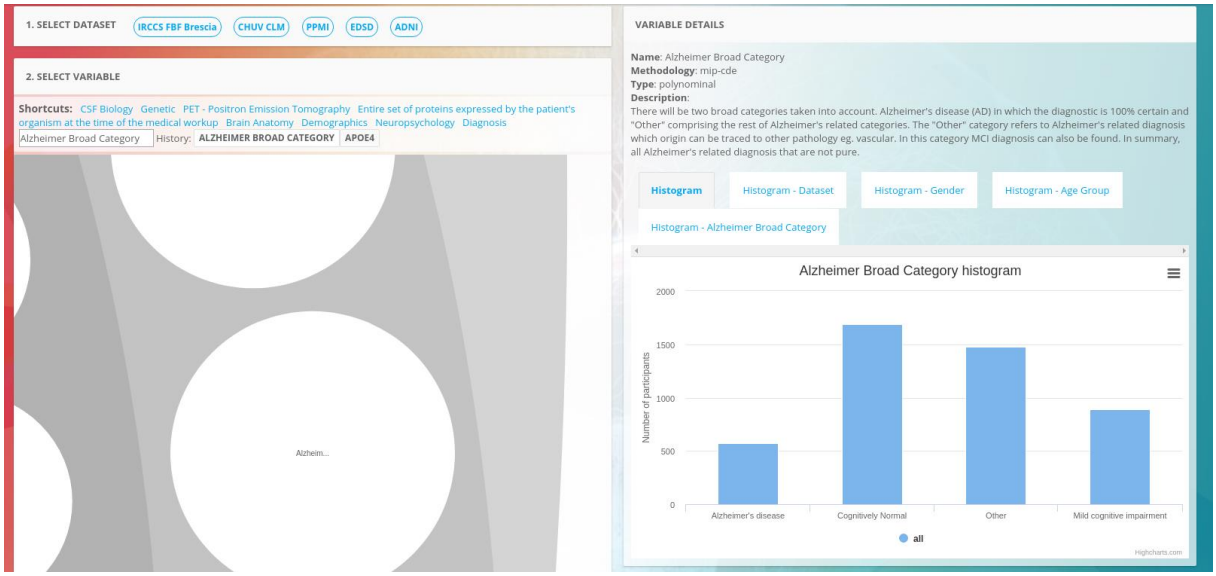
### *2.2.1 EE: Epidemiological Exploration*

The exploration of variables is done through their representation in a circle-pack design. We will call it the MIP Variable Space.

User may also search for a variable by typing its name directly in the search box above the MIP Variable Space (see screen shot below, searching for APOE4 as an example)

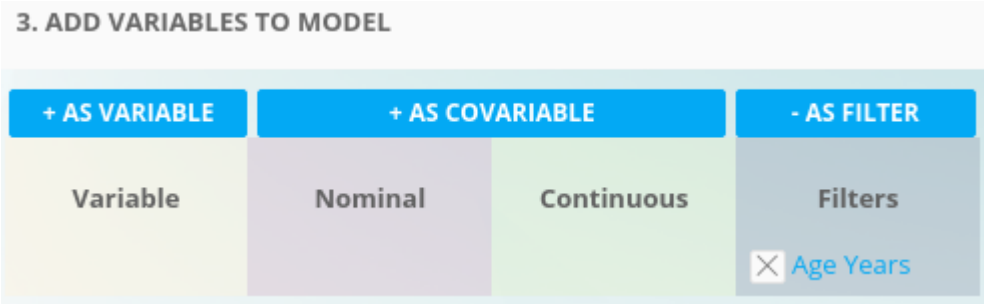



Some variables have descriptive information associated with it. They are displayed in the panel right of the MIP Variable Space (see next screenshot).




User may stop variables exploration here, or continue, to define an analysis model by selecting variables from the MIP Variable Space, as variable (response variable), co-variables (explanatory variables) and filters. It is possible to select a group of variables in one step. See screenshot below.

Variables used for setting up grouping and conditions should be selected as filter variables.




### 2.2.1.1 Define an Analysis Model

To define an analysis model, user needs to:

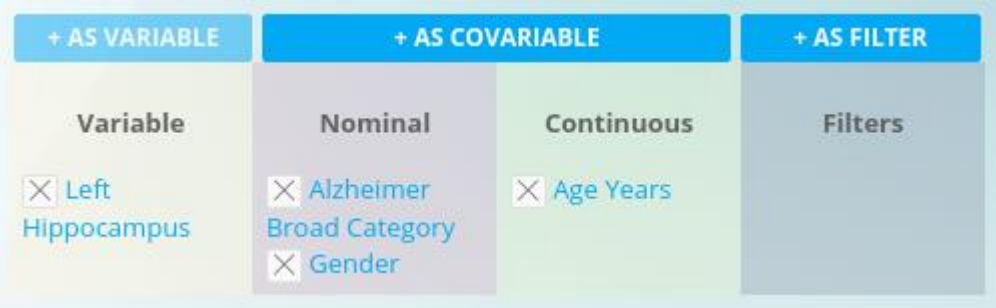
1. Search for the variables of interest in the MIP Variable Space, and click on the desired variable, or a group of variables.

Let's take an example: to predict changes in the volume of the Hippocampus in Alzheimer's disease, with respect to age and gender:

- Select the variable Left Hippocampus in the MIP Variable Space and then click on "+ AS VARIABLE" in the model table to define it as a response variable.

- Then select Age Years and Gender variables in EE and click "+ AS COVARIABLES", to define them as explanatory variables. Then do the same for Alzheimer Broad Category. Variables will be automatically classified as "NOMINAL" or "CONTINUOUS" depending on their respective types.

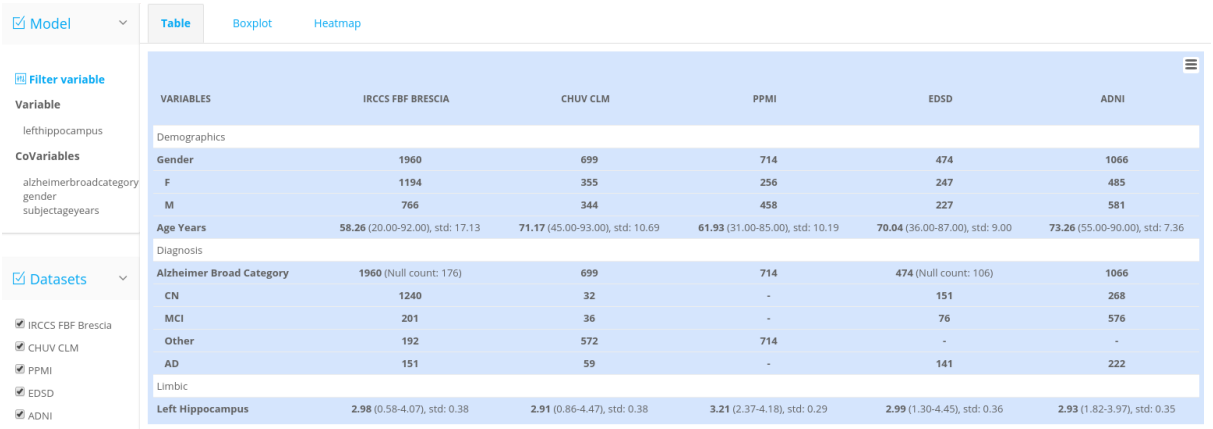
User may at any time remove variables from the Configuration table by clicking the "X" sign. Similarly, user may restore any previously searched variable from the "History" line.




2. When finished with analysis model definition, just click on the Review Model button at the bottom of the screen.

### *2.2.2 IA: Interactive Analysis*

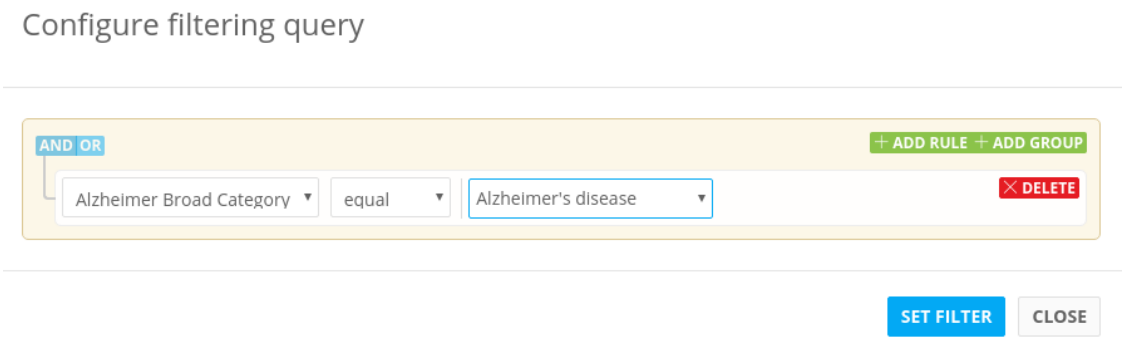
The analysis model is pre-populated with the statistical parameters of selected variables (variables and co-variables). Statistical description of the defined analysis model is provided in a table and in appropriate visualisations.




| VARIABLES | IRCCS FBF BRESCIA | CHUV CLM | PPMI | EDSD | ADNI |
|---|---|---|---|---|---|
| Demographics | | | | | |
| **Gender** | 1960 | 699 | 714 | 474 | 1066 |
| F | 1194 | 355 | 256 | 247 | 485 |
| M | 766 | 344 | 458 | 227 | 581 |
| **Age Years** | **58.26** (20.00-92.00), std: 17.13 | **71.17** (45.00-93.00), std: 10.69 | **61.93** (31.00-85.00), std: 10.19 | **70.04** (36.00-87.00), std: 9.00 | **73.26** (55.00-90.00), std: 7.36 |
| Diagnosis | | | | | |
| **Alzheimer Broad Category** | 1960 (Null count: 176) | 699 | 714 | 474 (Null count: 106) | 1066 |
| CN | 1240 | 32 | - | 151 | 268 |
| MCI | 201 | 36 | - | 76 | 576 |
| Other | 192 | 572 | 714 | - | - |
| AD | 151 | 59 | - | 141 | 222 |
| Limbic | | | | | |
| **Left Hippocampus** | **2.98** (0.58-4.07), std: 0.38 | **2.91** (0.86-4.47), std: 0.38 | **3.21** (2.37-4.18), std: 0.29 | **2.99** (1.30-4.45), std: 0.36 | **2.93** (1.82-3.97), std: 0.35 |

User can explore summary statistics of the defined analysis model by selecting/deselecting datasets, adding conditions (filters), and selecting visualisations.

To add conditions and grouping, click on the “filter variable” link on the left. That opens a pop-up window for configuring individual rules, their grouping and for selecting their combinations using “and/or” buttons. Conditional and grouping rules are applicable only to variables selected as “filter variables” in the EE functionality. See screenshot below.




After setting up grouping and conditional rules, the analysis model’s data is updated. Corresponding tabular and visual summary statistics reflect the analysis model changes.

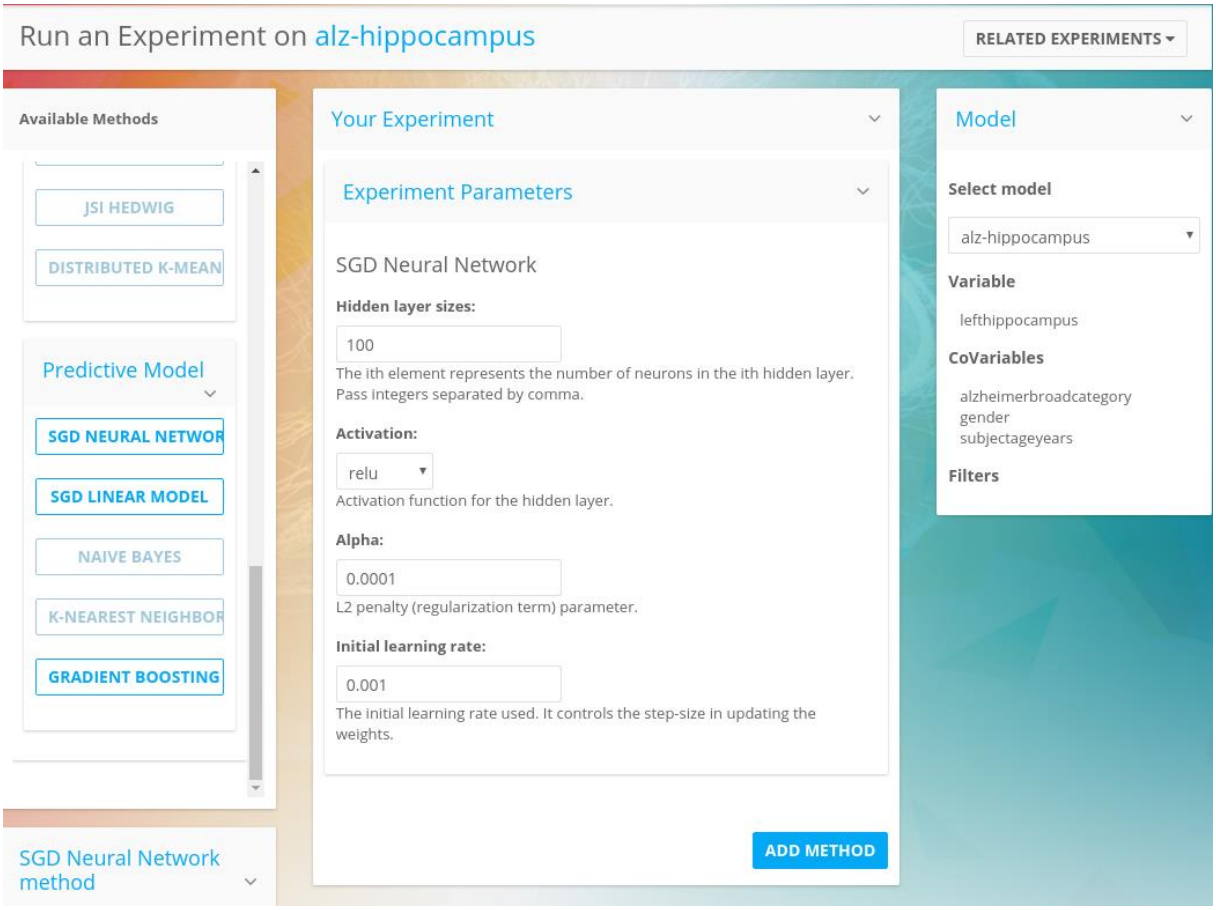
To perform an experiment, user needs to save the analysis model by giving it a name. He can also share it with the MIP community.


### *2.2.3 BSD: Biological Signatures of Diseases*

To configure the experiment:

1- Click “Run Machine Learning Experiment”, on the IA screen.


2- In the next BSD screen, choose a method among the “Available Methods”, see screenshot below.




3- For some methods user can configure parameters of the algorithm.

4- Click on “Add method” to add it to the methods selected for the experiment. Several methods can be added to an experiment.

5- User can choose to train and validate the experiment on various datasets. See screenshot below.


6- When ready to run the experiment, user needs to give it a name and then to click on RUN EXPERIMENT.

The results of the experiment are presented in textual, tabular or visual format depending on the type of methods chosen and their implementation.

# 3. Other MIP Functionalities

### *3.1.1 Writing Articles*

1- Go to main MIP Dashboard (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;

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

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

### *3.1.2 Accessing my Saved Articles and Models*

User can at any time access the already written articles and saved analysis models, via:

- My Data – all own work, shared or unshared;
- My Community – all work shared within the MIP community;

User can preview articles, save them to a file system accessible from his computer or open them for re-editing.

### *3.1.3 Third Party Applications*

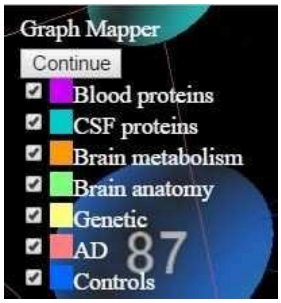
3rd Party Application are made by you, to provide some insights on specific models or visualisations.

#### 3.1.3.1 3D Biological Rules:

Navigate in a 3D world of variables.

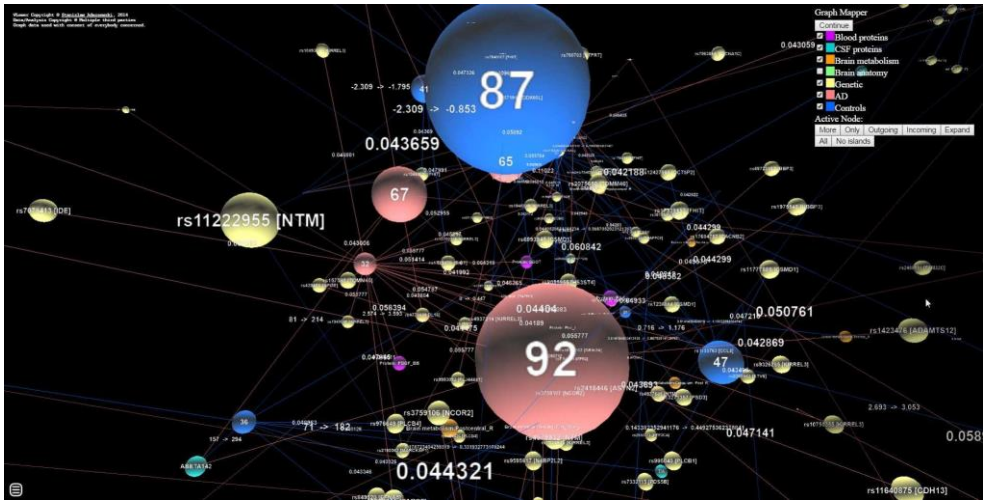
The 3D application shows the results of a rule-based clustering algorithm applied to Alzheimer's disease patients to identify homogeneous subgroups of patients. The hypothesis is that patients in each subgroup have the same underlying cause of the disease. The rule-based algorithm aims to explain the variability between individuals and describes a population by a group of "local over-densities".

These are defined as subspaces over combinations of variables: blood proteins (magenta), CSF proteins (aqua-blue), Brain metabolism (orange), brain anatomy (green)and genetic (yellow).




The red spheres represent AD subgroups and the blue ones healthy controls. The number in a sphere indicates the number of subjects belonging to the subgroup. The edges show rules between the spheres and variables that define each subgroup.

User can also use the left mouse button for rotation, the middle button for zoom and the right mouse button for translation.




User can select and deselect the different variables clicking on the variables tick to make them appear or disappear in the 3D world.

For the genetic variable click “More” to get additional information from the http://www.ensembl.org/ database.

### 3.1.3.2 2D Biological Rules

A graphical view of biological rules.


Like the 3D application, 2D application shows the results of a rule-based clustering algorithm applied to Alzheimer’s disease patients to identify homogeneous subgroups of patients. The hypothesis is that patients in each subgroup have the same underlying cause of the disease. The rule-based algorithm aims to explain the variability between individuals and describes a population by a group of “local over-densities”.

These are defined as subspaces over combinations of variables: genetic (yellow), brain anatomy (green), brain metabolism (orange), CSF proteins (aqua-blue) and blood proteins (magenta).

In this application user can select a variable on the 2D Map and get information on the right side.

The red spheres represent AD subgroups and the blue ones healthy controls. The number in a sphere indicates the number of subjects belonging to the subgroup. The edges show the rules between the spheres and the variables that define each subgroup.