Human Brain Project

Project Title:	Human Brain Project
Sub-Project Title:	Medical Informatics Platform (SP8)

Document Title:	IP Web UI – User Guidelines V2.0 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 test. To be reviewed before the release.
Mihaela Damian CHUV Eva Miquel CHUV	v2	00/10/2016	Draft 2	Updated after the MIP v2 release.

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1. INTRODUCTION

The **Medical Informatics Platform** launched its first public release (v1) on 31st March 2016. The version 2 was released on 14th November 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 users are 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:

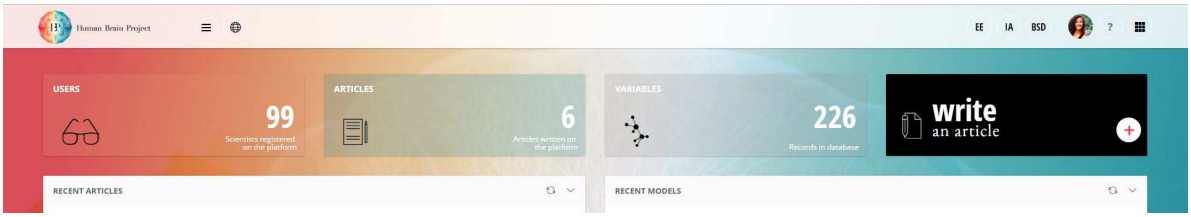
User Groups	E.g. User Subgroups	Internal/External (I/E)
CLINICIANS	Epidemiologists, Neuroclinicians	I+ E
RESEARCHERS	in Neurology, in Neuroimaging, in Pharmacology	I+ E
STATISTICIANS		I+ E
SCIENTIFIC DEVELOPERS	Method and Algorithm developers	I
PLATFORM DEVELOPER	Deploys tools and algorithms	I
MEDICAL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

2. MIP USER GUIDELINES

2.1. General navigation within the 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:

- **Epidemiological Exploration (EE)**
- **Interactive Analyses (IA)**
- **Biological Signatures of Diseases (BSD)**
- **Personal Profile**
- **Apps**

2.2. Exploration, Model and Experiment design

MIP proposes a series of user's services:

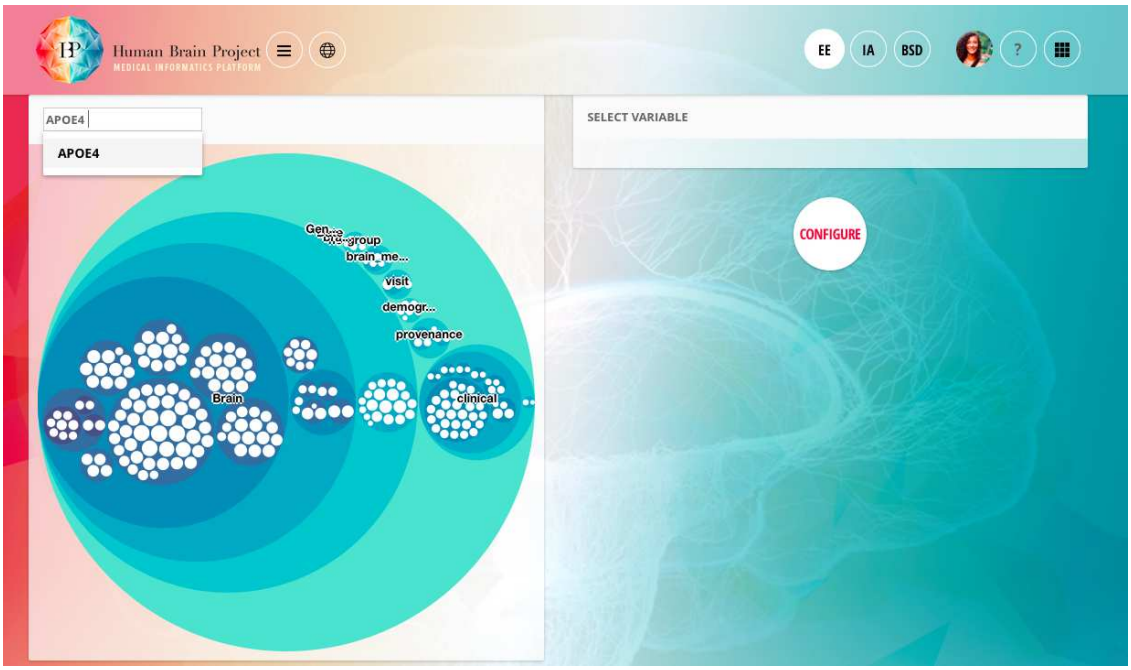
- **EE**: the Epidemiological Exploration – allowing you to browse though the variables released in the system and examine what data is available. Descriptive statistics will summarise this.
- **IA**: the Interactive Analyses – allowing you to design models
- **BSD**: the Biological Signatures of Disease – allowing you also to design experiments by applying algorithms to the models designed in IA.

You may start your work in EE and the system will lead you to the IA and BSD 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.

2.2.1. 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)



All variables have associated data in the system. Descriptive statistics are displayed on the right (see below): Summary, Histogram: x, Histogram-DX_bl, Histogram-x_Group, Histogram-PTGENDER, Histogram-APOE4.

You might stop your MIP exploration here, OR might decide to go further and ***configure a Model*** (or design a model). By configuring a model, you categorise the variables selected in the EE Variable Space into variables, covariables and groupings. You may also apply filters.

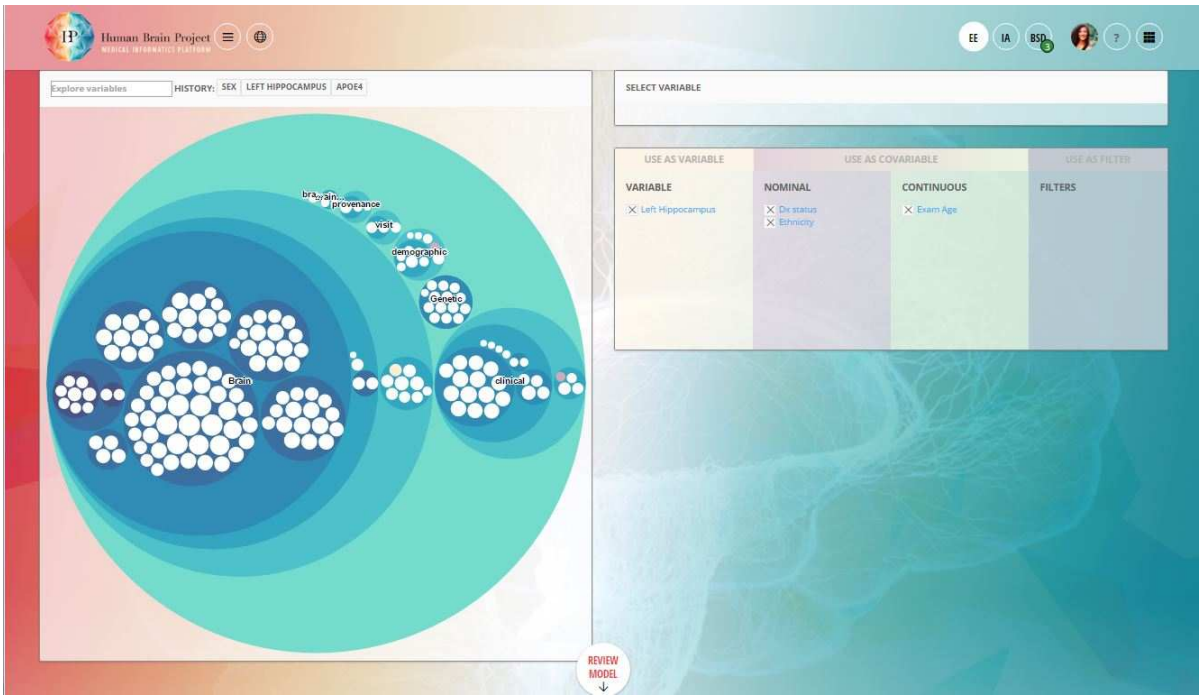
Configure a Model:

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 Status*, *Age at baseline* and *Sex* variables in EE and clicked "USE AS COVARIABLES". Then they will be classified as "NOMINAL" or "CONTINUOUS" automatically depending on their respective types.

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).

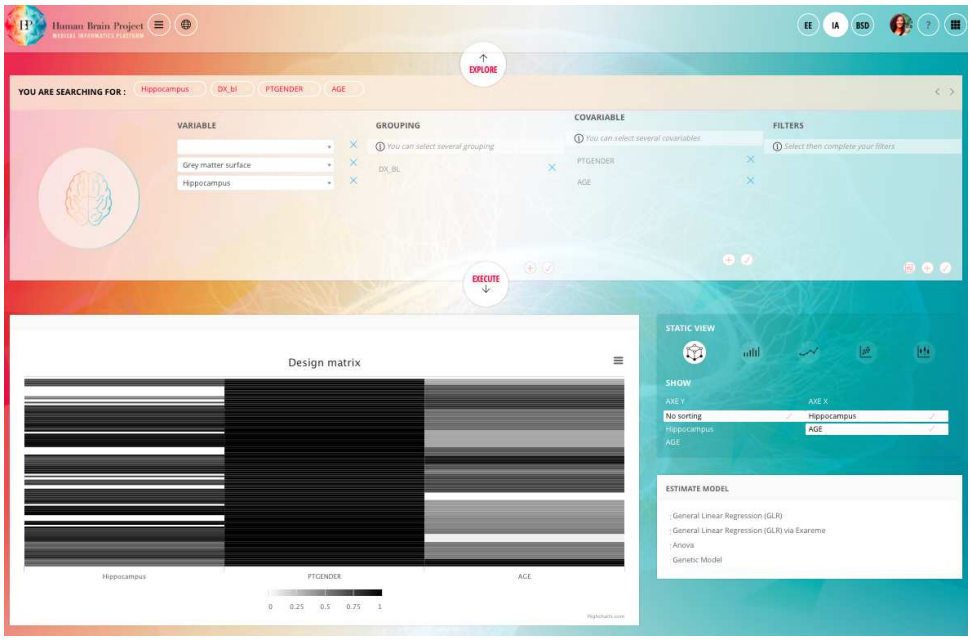


3. When happy with your configuration, just **click on Review Model** button at the bottom of the screen.

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.

2.2.2. 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 (*).

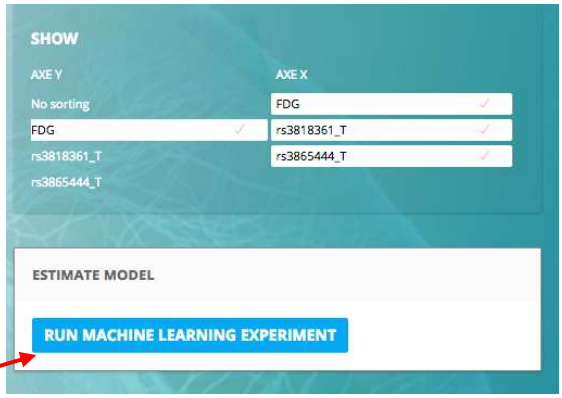
Note: to give you maximum flexibility, you may also access the IA section directly, without going through the EE.

If you want to apply Machine Learning Algorithms to your model above, please go to the next steep.

2.2.3. BSD: Biological Signatures of Diseases

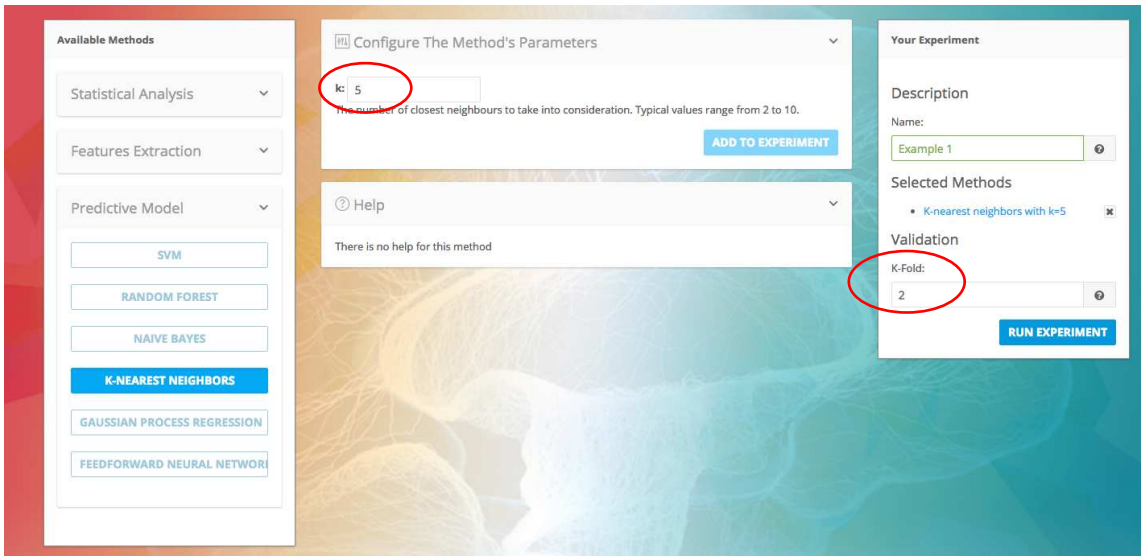
After designing and reviewing the model, you may decide to run Machine Learning Experiments. To create your Experiments, you will:

1- Click **Run Machine Learning Experiments** (see screenshot below)

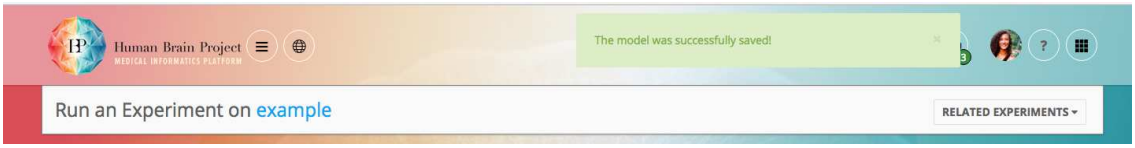


2- Add the parameters for running the experiment

3- Click RUN EXPERIMENT



4- Save your model: if you did not save already your model (*) at this point the system will ask you to do it.



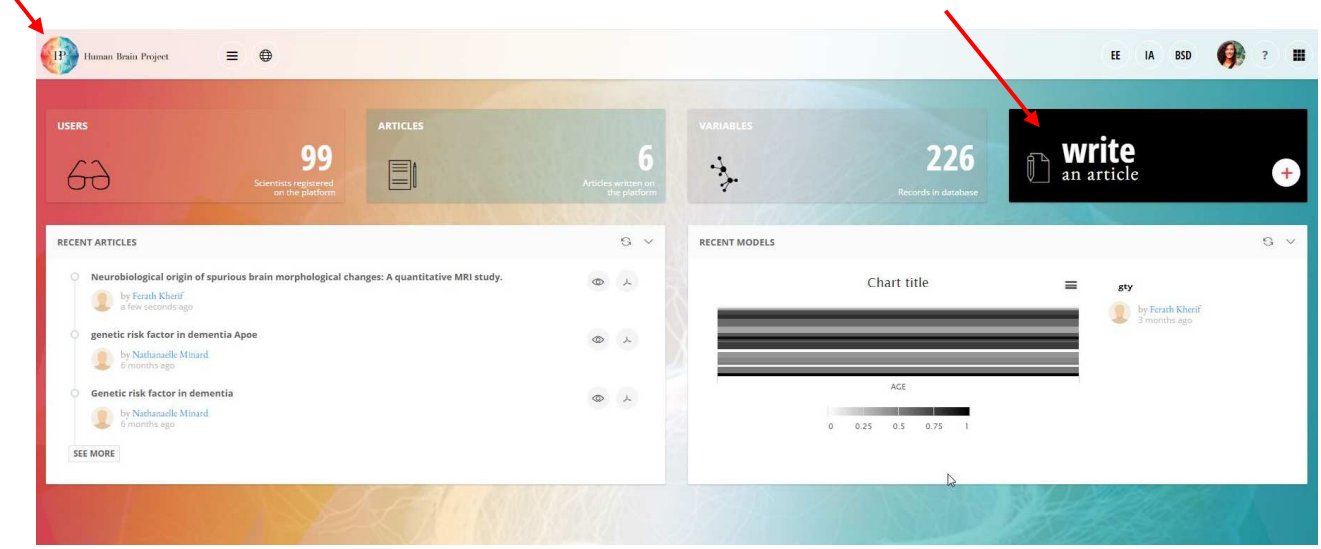
View result: a table detailed statistics is displayed for you.

3.1. Other MIP Functionality

3.1.1. Writing articles

1- Go to main **MIP Dashboard** (to do it, 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.

3.1.2. Accessing my Saved Articles and Models

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

- My Data – all my work, shared or unshared
- My Community – all my shared work

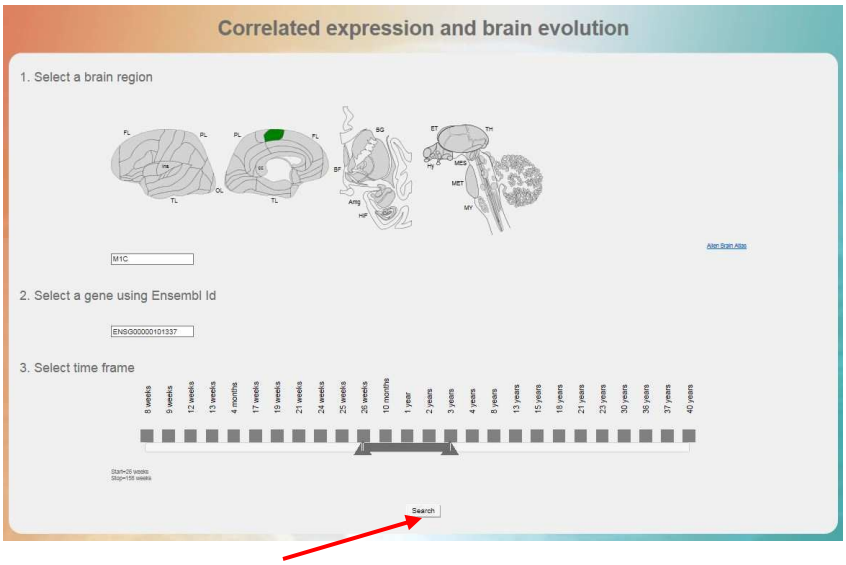
You can **preview** them, save them to a physical location or **open them for re-editing**.

3.1.3. Apps

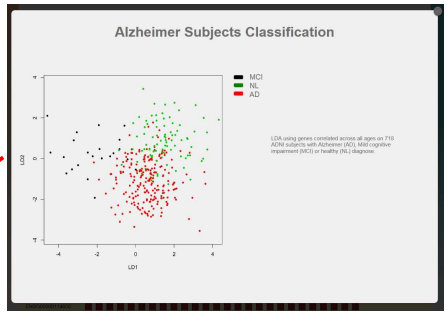
Gene Expression:

Choose a brain region, a gene and a time-frame to visualize gene expression and find correlations between them.

1. **Select** a brain region, a gene using Ensembl id and a time frame.
2. Click on **Search** to find the results



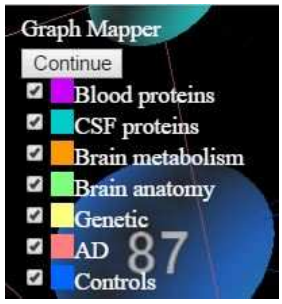
3. Once you have your Results, you could Download it and/ have an Alzheimer Subject Classification by clicking 



3D Biological Rules:

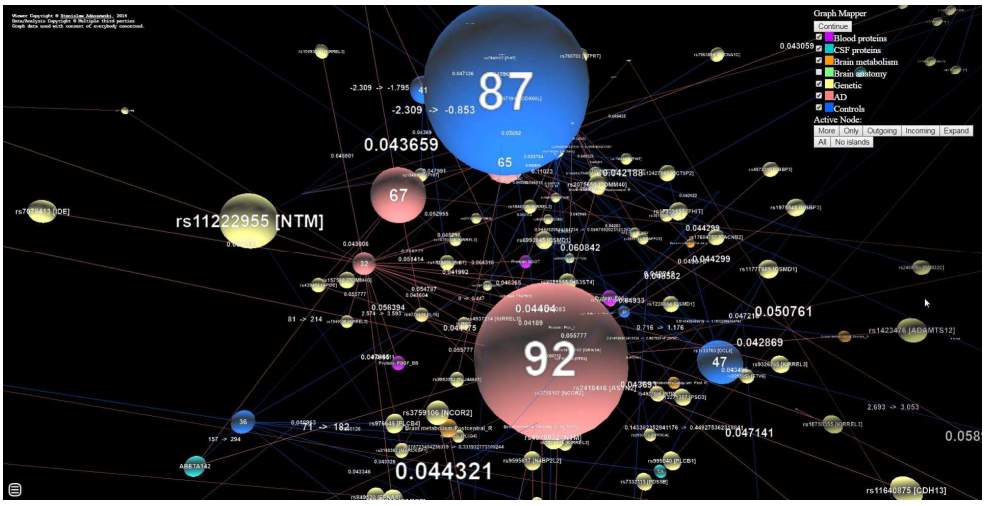
Navigate in a 3D world of variables.

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 such subgroups have the same underlying causes. 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 the AD subgroups and the **blue** spheres the healthy controls. The **number** in the sphere indicates the number of subjects belonging to the subgroups. The edges show the rules between the spheres and the variables that defined each subgroups.



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 it appear or disappear on the 3D world.

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

2D Biological Rules:

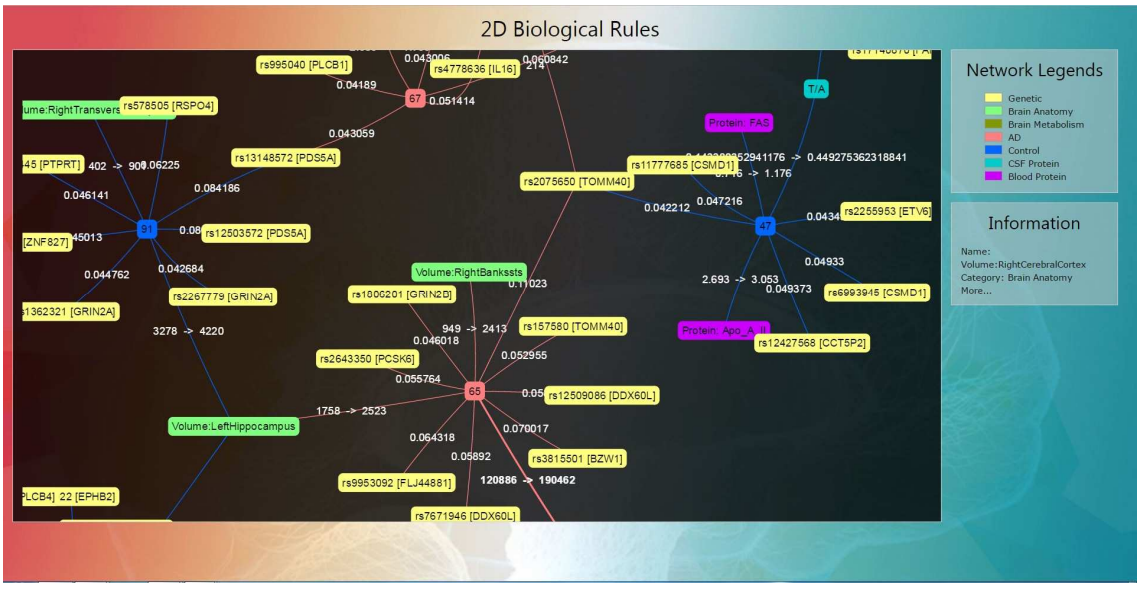
A graphical view of biological rules.

As the 3D application, 2D app 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 such subgroups have the same underlying causes. 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 site.

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



APPENDIX 1: EXPLORATION & MODEL DESIGN/CONFIGURE - PROCESS FLOW