Tutorial: MINERVA for visualization of disease maps

Piotr Gawron[1], Marek Ostaszewski[1]

Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Luxembourg, Luxembour[1]

The MINERVA platform (http://r3lab.uni.lu/web/minerva-website/) is used for visual exploration of molecular interaction diagrams and displaying them together with experimental data for interpretation. MINERVA supports several disease maps, including the Parkinson's disease map (pdmap.uni.lu). The functionalities of the platform allow for advanced annotation of uploaded diagrams, configuration of submaps or management of comments to hosted content. This tutorial will teach you how to upload and manage maps in MINERVA.

Tools to be presented:
You will be working with a running instance of MINERVA platform to upload your maps, learn how to:
- configure an advanced map (with submaps, graphical illustrations and pre-loaded datasets)
- configure automated annotators and verifications of the content
- manage users and their access to the platform
- manage comments to content on the map
- (for bioinformaticians) how to use MINERVA REST API and how to configure your own plugin

Technical requirements:
We will set up a sandbox instance of MINERVA for the needs of the tutorial. You will need:
- A laptop with access to the web and Chrome or Firefox browsers
- A CellDesigner software installed (http://celldesigner.org)
- Access to Newt Editor (http://newteditor.org)

After the tutorial, you will become familiar with the MINERVA platform and be able to use it for hosting and exploration of various molecular interaction networks. This may become useful not only for supporting disease maps, but other molecular maps you may want to construct and share.