

MINERVA API and plugin architecture: new data visualization interfaces for disease maps

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Disease maps offer contextualized knowledge on disease mechanisms, which is indispensable for proper interpretation of high volumes of data generated by high throughput experiments, and available via numerous bioinformatics databases. Such interpretations become possible with proper data interfaces that allow to construct multiple information layers on top of disease maps. MINERVA (<http://r3lab.uni.lu/web/minerva-website/>), a standalone platform for web-based visual exploration of molecular diagrams, is developed with this goal in mind.

With the growth of the Disease Maps Community comes the demand for new visualization functionalities. Similarly, additional data interfaces are needed with more and more datasets becoming available, and with the advancing complexity of analysis required for interpretation. To address these needs, the MINERVA platform currently supports the Application Programming Interface (API), enabling automatization of a number of routines that were currently possible only via the user interface. The REST API of MINERVA automates such functionalities as: i) obtain elements and reactions of hosted maps; ii) list drugs, chemicals and miRNA targeting map elements; iii) upload data overlays to a given map. An important extension of the API enables custom JavaScript to interact with the respective MINERVA instance to retrieve its data and modify its visual state. This allows construction of custom plugins for advanced visualization, independent of the core functionality of MINERVA.

In the talk, we will discuss the REST API functionality of MINERVA and will demonstrate two extensions: i) a custom plugin facilitating the traversal of complex maps and ii) a new functionality for the visualization of structural information for the proteins participating in reactions shown via MINERVA. We will discuss future steps, by which the platform may support the Disease Maps Community better.