Parkinson's disease map, an interactive map of molecular signaling.

Stephan Gebel[1], Marek Ostaszewski[1], Piotr Gawron[1], Reinhard Schneider[1], Rudi Balling[1]

[1]*Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Campus Belval, Luxembourg*

Recent developments in 'omics' technologies allow studying molecular pathogenesis/mechanisms of diseases in great detail. However, comprehensive interpretation of such data requires their integration with the existing body of knowledge on a given disease. The Luxembourg Centre for Systems Biomedicine has established technology and expertise supporting 'molecular disease maps' that allow the upload and interpretation of 'omics' data in the context of existing knowledge. The concept of molecular maps combines manually curated and high-quality knowledge repositories with bioinformatics tools. The new MINERVA platform is tailored for visualization and management of disease and molecular interaction maps (1). Its integrated tools allow for: automated annotation of elements and verification of the contents, visualisation via embedded Google Map application programming interface, export of the content, as image, network or computational model and combination with biomedical data analysis pipelines. Our pioneering Parkinson's disease (PD) map, developed together with the Systems Biology Institute (SBI) in Tokyo, Japan, makes the information from more than 1500 research articles and public databases available for interpretation in a molecular interaction map. The map is envisaged as a hub for the PD community to deal with rapidly increasing information on PD. To update and refine the map expert knowledge is collected by integrated feedback functions and on frequent workshops with field experts.
The freely accessible (http://pdmap.uni.lu) PD map give valuable insights for fundamental as well as translational researchers in academia, clinics and pharma industry and can be used as a blueprint for the development of other disease maps.

(1) Gawron, P., et al., (2016) MINERVA—a platform for visualization and curation of molecular interaction networks. npj Systems Biology and Applications (2), 16020; doi:10.1038/npjsba.2016.20.