

## **Interactive web based curation of biological pathways with advanced layout and complexity management support**

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Alterations in human metabolism that we determine again and again in individuals with a certain illness, but not in healthy ones, give us hints about how that illness occurs. With the help of recently developed genomics techniques at a very large scale, one can easily discover such alterations. Even though such discovery is useful in deciding those at risk for the associated disease, it does not help in discovery of the cause of the disease. For exactly this reason, we need to research how our metabolism works and where and why it fails by constructing pathways or maps specific to diseases.

Thus, it is inevitable to develop an interactive web based editor for constructing pathways from scratch or modifying existing ones in a standard notation such as Systems Biology Graphical Notation (SBGN). It needs to feature inspection, search and highlight mechanisms as well as advanced diagramming tools such as grid and alignment guidelines. In addition, the tool should have full support for compound (nested) structures to represent cellular compartments, molecular complexes, and sub-pathways with proper automated layout. Furthermore, operations for hiding or collapsing currently irrelevant parts of a map and then gradually showing or expanding them on demand are especially useful when managing large maps. Finally, ability to overlay experimental data on these maps would be very useful.