

A BIOINFORMATICS CHALLENGE TO DEPICT GENETIC VARIATION IN PATHWAY-BASED ANALYSIS

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Information on genetic variations (such as SNPs, indels, etc.) is currently not systematically evaluated in pathway analysis. Indeed, it is not yet possible to combine analysis, visualization, and interpretation of genetic variation and the consequent effects on gene/protein function, with regard to pathway dynamics. This project takes up the challenge to integrate the genetic information in a freely-available and open source software called PathVisio (www.pathvisio.org). PathVisio is a graphical tool for pathway-based analysis of results from biological experiments.

Genetic information (e.g. SNPs and their predicted functional effects, and Genome Wide Association Studies (GWAS) datasets) can be visualized on the corresponding pathway to facilitate meaningful interpretation. For this purpose, we defined the main steps of a visual design in PathVisio. The first step consists of linking genes to functional variants, and shows these in separate sections (the side panel in the figure). In the next step we perform pathway-visualization and -analysis of large genetic datasets. This permits visualization of significant polymorphisms in a dataset, and to evaluate their interactions within a single pathway or in a collection of pathways, for which we use WikiPathways (www.wikipathway.org). Finally, we investigate advanced tools to allow biological interpretation of gene-gene interactions affected by a specific variant. This step will capitalize on many existing tools and algorithms, which evaluate the expected effects of variants on gene expression, function of the resulting gene products and their interactions. We show the first and second steps of the visual design in PathVisio and would welcome suggestions.