

Visualizing metabolite fluxes on WikiPathways pathways using a PathVisio plugin

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Keywords

Wikipathways, Pathvisio

Abstract

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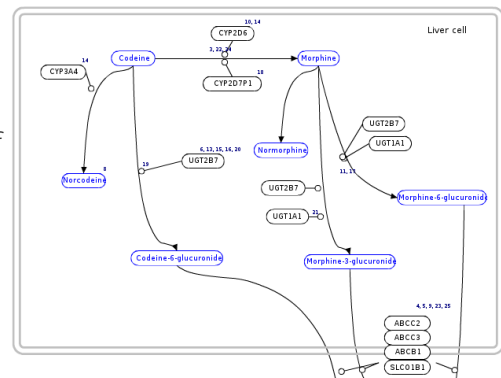
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Visualizing metabolite fluxes on WikiPathways pathways using a PathVisio plugin

Presenters: Anwasha Dutta (student in our group)

Date: Thursday March 29th 2012

Description: Biological pathways provide intuitive frameworks to integrate and co-analyze different kinds of biological data, such as system-wide transcriptomic, proteomic, and metabolomic measurements. While insightful, pathway analysis is generally limited to qualitative conclusions, and the analyses can only be as powerful as the curated annotations can enable. Using our open-source pathway analysis platform, PathVisio, we will bridge pathway analysis to the wealth of quantitative approaches already in development for metabolic network modeling, such as flux balance analysis and dynamic simulation. Our focus will be on the visualization of the modeling results, which will be critical for understanding how simulated models correlate with experimental measurements. The same biological processes that are visualized in pathways are also described by quantitative models. For example, the arrows that connect entities within metabolic pathways actually represent metabolite fluxes. The integration of large scale data analysis with modeled or measured fluxomics data, will help to gain more insights into the mechanism of the biological process.



The meeting is in **the BiGCaT course** room (1.302 In H1), UNS50 south wing 1th floor from **16.00 to 17.00**.