Visualizing metabolite fluxes on wikipathways pathways using a PathVisio plugin

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Biological pathways provide intuitive frameworks to integrate and co-analyze different kinds of biological data, such as system-wide transcriptomic, proteomic, and metabolomic measurements. Our open-source pathway analysis platform, PathVisio, currently allows visualization of data on the nodes of the pathway models, i.e., genes, proteins, metabolites etc. The EdgeVisualization plugin in development, will allow the visualization of experimental data on the edges of the pathways, i.e., reactions, interactions etc. 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 proposed integrated visualization will have several important impacts on the field:
- makes modeling results more accessible and interpretable to biologists who wish to learn from them
- enables researchers who develop flux modeling approaches to better improve and distribute their models
- facilitates new ways to explore effects on mechanism, such as genetic effects.

Flux data from published literature: http://rsta.royalsocietypublishing.org/content/369/1954/4295.short
*Note: The fluxes for the reactions between 1,3-Bisphospho-D-glycerate -> 3-Phosphoglycerate and 3-Phosphoglycerate -> 2-Phosphoglycerate were defined in the opposite (upward) direction which becomes clear from the visualization. Those would probably be adjusted in the next modeling stage

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www.pathvisio.org
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