

## MPA\_25

Visualizing omics data in the OptFlux workbench

**Paulo Maia<sup>1</sup>, Paulo Vilaça<sup>1</sup>, Isabel Rocha<sup>2</sup> and Miguel Rocha<sup>2</sup>**

*<sup>1</sup>SilicoLife, Braga, Portugal*

*<sup>2</sup>University of Minho, Braga, Portugal*

OptFlux is an open-source and extensible workbench for Metabolic Engineering (ME) tasks. Since 2012, OptFlux adoption has been steadily increasing among users, making it one of the reference go-to platforms among the ME community. The workbench supports common ME tasks such as phenotype prediction for both wild-type and mutant genotypes, metabolic control analysis and pathway analysis as well as strain optimization procedures. Moreover, a visualization plug-in is included, allowing the navigation and edition of biochemical network layouts in a multitude of standard formats. This plug-in also allows the overlap of specific phenotypic conditions in the network layouts, providing an intuitive mechanism to explore and understand the associated flux distributions. Navigation between multiple layouts is also included.

However, for more specialized applications, such as the inclusion of experimental data, this framework was still lagging behind. In this work, the current visualization platform included in OptFlux is extended to support loading generic experimental data sources (e.g. transcript, protein, metabolite and flux measurements) and mapping it to the model information for posterior overlap with the layouts. The visualization features that will represent this data are also fully customizable. The inclusion of multiple conditions or time-dependent measurements is also supported for metabolite-associated data with intuitive bar-plots being displayed for immediate visual comparison. Finally, compound structural information from KEGG is also automatically downloaded and presented.