

II11. Bioinformatics, Omics and Bionanotechnologies

P424. Towards the integration of regulatory networks with metabolic models

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Metabolism is present in every living being and for that reason understanding the mechanisms behind it is essential for comprehending the phenotypical behaviour of the organisms. Metabolic models reconstructed at genome scale level can provide in-depth comprehension of the metabolic processes within an organism, therefore emerging as one of the best strategies for studying these systems. Genome-scale metabolic models can be enriched with information from regulatory networks, such as gene expression data. Merging regulatory networks with metabolic models can help uncovering information that can be used for many applications, for example identifying potential drug targets.

In this work we propose developing bioinformatics tools capable of merging a genome-scale metabolic models with regulatory networks. A tool named CORAMI (Combination Of Regulatory And Metabolic Information) is being developed as a plugin for merlin software. A genome-scale metabolic model of *Saccharomyces cerevisiae* will be imported into merlin in order to collect the necessary metabolic data for CORAMI. Also, annotation data for metabolic genes will be integrated with regulatory genes in order to validate the integration and establish a correlation between these two models. Additionally, the regulatory network of *S. cerevisiae* chosen to be merged with the metabolic model was manual curated. Here we present the strategy for merging the two networks, which together can provide unique insights into *S. cerevisiae*'s phenotypical behaviour. In the future, several tools which will allow the user to explore the total potential of the plugin and retrieve more results for their studies will be developed.