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Reconstructing genome-scale metabolic models with merlin: the *Ashbya gossypii* case study

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The reconstruction of genome-scale metabolic networks is an iterative process where information obtained from several data sources is combined to construct a preliminary set of reactions and boundaries. This process encompasses several steps, such as genome annotation; identification of the reactions; determination of the reaction stoichiometry; compartmentation and assignment of localization; determination of the biomass composition; determination of energy requirements; and finally definition of additional constraints [1]. *merlin* is a software tool, developed in-house, that implements semi-automatically several of these steps. *merlin* performs functional genomic annotations of lists of genes. *merlin* retrieves information of each homologue and automatically scores the results, allowing the user to change the selection, and dynamically (re-)annotate the genome. Afterwards, *merlin* allows the user to use KEGG metabolic data to build the reaction set expedites the transition from genome-scale data to SBML metabolic models, allowing the user to have a preliminary view of the biochemical network [2]. Although *Ashbya gossypii* has been known in the scientific community for 80 years (mainly as a plant pathogen) and in the industrial community for near 20 years (as a riboflavin producer), interest in this microorganism increased as a result of the publication of its genome sequence in 2004. *A. gossypii* grows well in waste vegetable oils and thus a cheap, environmental - friendly culture medium can be designed for growth and metabolite production. Taking advantage of these unique features, the development of a genome–scale metabolic model will help to develop *A. gossypii* as a cell factory organism.

References

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