*Title*

**Model-driven microbial engineering for chemical production**

*Contact*

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*Introduction*

Sustainable development requires environmental friendly and cost-effective production of energy and chemicals [1]. Microorganisms have been shown as powerful microbial cell factories to produce these bio-compounds. However, microorganisms can only achieve their maximum production capacities by metabolic engineering [1]. Among different approaches deploying in metabolic engineering, GEnome scale Metabolic models (GEMs) emerged to be useful in predicting genetic modification strategy with minimal experimental trial and error [2], [3].

*Goal*

In this project, GEMs are used to design genetic modification strategies to maximize the yield of interest chemicals. The approach aims to find and eliminate competed pathways, balance cofactors and increase precursors supply toward production of target compounds.

*Techniques*

GEMs for candidate microorganisms are downloaded from model repositories. Several strain design algorithms such as Optknock, Robustknock and MCSEnumeration will be used. Cobra Toolbox implemented in Matlab or Cobrapy implemented in Python is used to evaluate metabolic phenotypes.

***Literature***

[1] A. S. L. Hansen, R. M. Lennen, N. Sonnenschein, and M. J. Herrgård, "Systems biology solutions for biochemical production challenges," *Curr. Opin. Biotechnol.*, vol. 45, pp. 85–91, 2017.

[2] B. Kim, W. J. Kim, D. I. Kim, and S. Y. Lee, "Applications of genome-scale metabolic network model in metabolic engineering," *J. Ind. Microbiol. Biotechnol.*, vol. 42, no. 3, pp. 339–348, 2015.

[3] W. J. Kim, H. U. Kim, and S. Y. Lee, "Current state and applications of microbial genome-scale metabolic models," *Curr. Opin. Syst. Biol.*, vol. 2, pp. 10–18, 2017.