

Master's Thesis: Theoretical investigation of the metabolic burden in *Pseudomonas putida* during the production of lycopene

Are you interested in synthetic biology, metabolic engineering, and systems microbiology? Join the professorship of systems biotechnology for an exciting master's thesis project where you will explore the cellular energy balance during heterologous production of valuable compounds!

Project Background:

Pseudomonas putida is a highly versatile and robust microbial host that has gained significant attention in biotechnology for the sustainable production of valuable chemicals. In this project, we aim to gain deeper insights into how the expression of a heterologous metabolic pathway affects the cellular physiology and metabolic balance of *P. putida*. As a model system, we focus on the biosynthesis of lycopene, a commercially important carotenoid widely used in the food, pharmaceutical, and cosmetic industries.

To achieve this, we have engineered different *P. putida* strains, each incorporating specific genetic modifications to support lycopene production. By comparing these strains' performance and metabolic responses, we seek to understand the metabolic burden imposed by heterologous production and identify strategies for improving yield while maintaining cellular health and growth efficiency. Ultimately, this knowledge will contribute to developing more robust microbial cell factories for industrial applications.

Project Description:

As part of this master's thesis project, you will conduct a theoretical study on the metabolic burden caused by the heterologous expression of a lycopene biosynthesis pathway in *P. putida*. Your tasks will include integrating the lycopene pathway into existing stoichiometric models of *P. putida* and performing flux balance analysis (FBA) to investigate its impact on the cellular metabolism. Additionally, you will explore the use of enzyme-constrained (ec) models to gain a more detailed understanding of metabolic limitations. Developing a coarse-grained model may also be part of the project. With the help of experimental data, the aim is to characterize the metabolic burden and eventually improve the lycopene production.

Your tasks will include:

- Model construction and analysis in MATLAB (COBRA Toolbox) / Python (COBRAPy)
- Integration of the lycopene pathway and analysis (FBA, FVA, dFBA, ...)
- Developing and testing an enzyme-constrained model
- Characterizing metabolic burden in lycopene production and identifying possible targets

Requirements:

- Solid background in microbiology, biotechnology, bioengineering, or a related field
- Basic knowledge of metabolic modeling concepts, such as stoichiometric models and flux balance analysis (FBA)
- Experience with programming (e.g., Python or MATLAB) and familiarity with metabolic modeling frameworks (e.g., COBRA Toolbox, cobrapy) is advantageous but not mandatory
- Interest in systems biology, metabolic engineering, and microbial physiology
- Ability to work independently

Start: From now

Language: German/ English

If you are motivated to work on a cutting-edge research project and expand your skills in computational biology, don't hesitate to contact Carina Meiners (c.meiners@tum.de) with your CV and your transcript of records.

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