

Transcriptional robustness as a biological indicator of microbial process stability

About Us: The BIOSCALE group is situated within the Chemical Engineering (CIW) Faculty of the KIT. Our goal is to tackle challenges in bioprocess development with a novel and interdisciplinary approach involving bioprocess engineering, molecular biotechnology and data science. Our team envisions a biologically driven bioprocess development while applying cutting edge next generation sequencing technology and pioneering a harmonization of the molecular and technical nature of biotechnological processes.

Project: Microbial cells continuously adapt their gene expression to changing environmental and process conditions. While most studies focus on genes that respond strongly to such perturbations, much less is known about genes that maintain stable expression across a broad range of conditions. However, this transcriptional robustness may be particularly relevant for bioprocess development and scale-up, where cells experience changing and heterogeneous environments and stable biological reference points are needed. In this project, large-scale transcriptomics datasets will be used to systematically identify transcriptionally robust genes in *Corynebacterium glutamicum*. Beyond their quantitative classification, a major focus will be the functional interpretation of these patterns by analyzing associated metabolic pathways, cellular functions and regulatory characteristics. Robustness patterns will further be related to defined bioprocess perturbations to investigate which cellular functions remain stable despite changing process conditions and which become responsive. Comparative analyses of orthologous genes in *Escherichia coli* and other biotechnologically relevant bacterial species will address whether transcriptional robustness represents a conserved biological property or differs between organisms. By shifting the focus from what changes to also what remains stable, the project aims to provide a complementary perspective on cellular adaptation and explore the relevance of transcriptional robustness for bioprocess characterization and scale-up.

Your tasks:

- Identification and functional characterization of robust and variable genes
- Investigation of transcriptional responses to defined bioprocess perturbations
- Analysis of large-scale transcriptomics datasets
- Quantification and evaluation of transcriptional robustness in *Corynebacterium glutamicum*
- Comparative analysis with orthologous genes in *Escherichia coli* and other species

Your qualification:

- Background in bioinformatics, biology, biotechnology, bioengineering or similar
- Basic knowledge and interest in bioinformatics
- Programming experience in R and/or Python and familiarity with the command line are desirable but not mandatory
- Strong analytical thinking and interest in understanding biological mechanisms underlying transcriptional responses

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