

Beyond Differential Gene Expression: Exploring the Energetic Costs of Gene Expression

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 in response to changing environmental and process conditions. When comparing two or more conditions using transcriptomic analyses, most studies focus on identifying differentially expressed genes (DEGs). While these statistical approaches reveal significant changes in gene expression, they do not directly account for the biological costs associated with these changes.

In this project, we want to introduce an additional perspective: How much energy does a microbial cell invest in adapting its gene expression? For example, a small change in the expression of a very large protein might require more cellular resources than a large change in a small protein. To investigate this, we aim to estimate the bioenergetic costs associated with changes in gene expression, considering nucleotide and amino acid biosynthesis as well as the transcription and translation processes themselves, expressed in ATP equivalents.

As a model organism, we work with *Corynebacterium glutamicum*, a well-established industrial workhorse widely used for the production of amino acids and other biotechnologically relevant compounds. Using existing transcriptomic datasets, we aim to explore whether the genes showing the strongest changes in expression are also those associated with the highest energetic costs, providing a new perspective on how microbial cells allocate their resources.

Your tasks:

- Literature research on the bioenergetic costs of gene expression in microorganisms
- Development of a computational approach to estimate the energetic costs of transcription and translation
- Comparison of conventional differential gene expression analyses with the estimated energetic costs
- Visualization and biological interpretation of the results

Your qualification:

- Background in bioinformatics, biology, biotechnology, bioengineering or similar
- Interest in microbial physiology, metabolism, and working with biological datasets
- Programming experience in R and/or Python are desirable but not mandatory
- Strong analytical thinking and interest in understanding biological mechanisms underlying transcriptional responses

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