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Design and Learn: Computational tools for guiding the development of a sustainable bioprocess

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Bio-based processes offer a solution to reduce reliance on polluting production processes and excessive land-use for food production. However, the design of such processes and effective microbial cell factories is hampered by the complexity of biological systems. The development of bioprocesses and microbial production strains can be accelerated by integrating concepts of resource allocation and condition-specific experimental datasets in metabolic models. To support the transition to a circular economy we focus on (1) the creation of innovative computational strategies for experiment design to streamline bioprocess development, and (2) the practical implementation of these methods on a hydrogen oxidizing bacteria to engineer a chassis capable of producing milk protein.

The first facet of our work involves the development of sophisticated computational methods to guide the design of experiments across all stages of bioprocess development, from initial concept to large-scale production. A central component is the establishment of an automated protein allocation model parametrization workflow. This workflow enables the seamless integration of diverse data sources, allowing for dynamic adjustments and optimization of protein allocation within the bioprocess.

The second aspect of our research focuses on the practical use of computational tools on *Xanthobacter sp. SoF1*, aiming to engineer this hydrogen oxidizing bacteria to produce milk protein from CO2 and N2. Our approach involves developing a metabolic model, making targeted genetic modifications, and optimizing pathways. By combining transcriptomics data with a protein allocation model, we design experiments to enhance milk protein production. This synergy between experimental design and computational models accelerates the optimization of bioprocess parameters for more efficient and sustainable production.

Consent

Yes

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