Construction of system level kinetic model for gas fermenting acetogen *clostridium autoethanogenum*

Vishnuvardhan Mahamkali, Pedro A. Saa, Renato de Souza Pinto Lemgruber, Kaspar Valgepea, Lars Keld Nielsen, Esteban Marcellin*

Australian Institute for Bioengineering and Nanotechnology
The University of Queensland
Brisbane, Queensland, Australia

Acetogens are promising organisms for the production of chemicals from syngas (CO, H_2, and CO2) via gas fermentation using the Wood-Ljungdahl (W-L) pathway. Quantitative characterization of carbon, energy, and redox metabolism in the W-L pathway is required to guide the rational metabolic engineering of acetogens. Kinetic models have proven effective to understand and predict the metabolic states of cellular metabolism in a quantitative manner, despite their complexity. Kinetic models often involve a large number of heterogeneous non-linear parameters which are difficult to fit using the traditional Bayesian approaches. Several reports suggest that Approximate Bayesian Computation (ABC) overcome this limitation by sampling from an approximation of the posterior distribution without explicitly evaluating the likelihood function[1]. In the present study, we tried to explore the kinetic behaviour of enzymes in the W-L pathway using a core model consisting of reactions from the W-L pathway leading to the production of acetate, ethanol and 2,3-Butanediol. We have used a method developed by Saa & Nielsen[2] which is based on the ABC to sample the kinetic parameters of the model across different biomass conditions in continuous culture. We try to sample the distribution of parameters with respect to reference biomass condition, which also satisfies the other biomass conditions. We aim to find systems properties of the network (e.g., control structure) and key metabolic regulations. Finally, the framework can be used to predict missing allosteric interactions.

References

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