

Bifurcation analysis of a model for cross-feeding in the chemostat

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Cross-feeding is a symbiotic relationship between microorganisms where one organism consumes metabolites produced by another. A recent mathematical model (Gudelj et al., 2016) for cross-feeding in a chemostat is based on empirical data on competing strains of *Escherichia coli* in a laboratory chemostat (Rosenzweig et al., 1994). The metabolism of glucose is assumed to follow two stages, 1. glycolysis and 2. tricarboxylic acid (TCA) cycle. Thereby the primary resource, glucose, is partially oxidized and forms an intermediate metabolite, which can in turn either be fully oxidized to carbon dioxide or excess quantities are secreted into the environment, and serve as secondary energy resource.

Both strains are able to grow on glucose and on the intermediate metabolite, but one of them specializes on glucose, and the other on the intermediate metabolite. The metabolite uptaken by the *E. coli* imposes a cost to cell growth. The model is parametrised to model the short-term dynamics of the competing strains, and predicts the existence of stable equilibria where the strains cross-feed for sufficiently large glucose concentrations. The ODE model for the chemostat dynamics is also of mathematical interest due to non-smooth derivatives of the concentration of the intermediate metabolite.

To better understand the bifurcation structure of the model and the appearance of cross-feeding equilibria, I perform analytically a bifurcation analysis for two particular sub-cases of the model, where the system of 6 ODEs is reduced to a system of 2 ODEs, and permits phase-plane analysis. These simpler cases retain to an extent the complex multistationarity of the full model.

References

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