An approach towards the model construction of the microbial community dynamics in reactors

Pablo Ugalde-Salas, Jérôme Harmand, Elie Desmond-Le Quéméner

HAL Id: hal-04175116

https://hal.inrae.fr/hal-04175116

Submitted on 1 Aug 2023

An approach towards the model construction of the microbial community dynamics in reactors.

Pablo Ugalde-Salas[1], Jérôme Harmand[1], Elie Desmond-Le Quéméner[1] (elie.desmond-lequemener@inrae.fr)

[1]LBE, INRAE, Univ. Montpellier, 11100, Narbonne, France

In the context of continuously stirred reactors we explored the question of a mathematical model that could represent at the same time the microbial community and the substrates dynamics in which a number of parameters are obtained through the application of first principles from physics. In this line of thought each microbial species concentration represents a state variable of a dynamical system describing a chemostat.

The first parameters to identify are the microbial yields, which are obtained using reaction invariants and asymptotic observes coupled with first estimates based on thermodynamic modelling of microbial metabolism. Such an approach allows us to minimize the a priori knowledge usually necessary to compute such parameters. The second problem that arises is classifying the species in a functional group, that is assigning them one of the metabolisms that we presupposed are driving the process.

The third, and most challenging problem, is to find the growth function for each of the species depending on the state variables. It is well-documented that a single species on a substrate limited medium can be properly modelled by a Monod growth function or other substrate dependent expression such as the microbial transition state model derived from statistical physics and thermodynamics. However, when more species are added, microbial interactions matter and more complex growth expressions are needed to model the observed dynamics: this lies precisely beyond the actual state of a thermodynamic theory of growth of a microbial community.

In our approach to tackle this problem, we took a step back and studied the shape of such a growth function without assuming an explicit mathematical expression; we used optimal tracking on experimental data in a chemostat setting where a nitrification process was operated for over 500 days. Results indicate that species growth rates consisting of pulses and subsequent falls explain better the data than stable growth rates. This new approach provides a measure of how much one needs to deviate from a standard model to explain data and account for hidden parameters influencing growth such as microbial interactions.

Key words: Microbial community dynamics, chemostat theory, microbial classification, yield estimation, microbial interactions.