

# Population Dynamics Virtual Seminar



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## Using proteome structure to predict lag phase in microbial populations

When subject to sudden environmental changes, the population of microorganisms inside wastewater anaerobic digesters (AD) takes a significant amount of time to adjust.

The specific set of proteins a microorganism expresses (the proteome) depends on the growth conditions and substrates present and must be adapted when conditions change. This results in a slowdown or pause in growth known as a lag phase. We formulate a rational mechanistic model that predicts the duration of the lag phase based on the initial structure of the microorganism's proteome. Our model incorporates proteome partitioning and flux regulation with flux-balance achieved through changes to the size of precursor pools. Allocation of protein synthesis is regulated via regulation functions which mathematically optimise the growth rate.

We validate our modelling approach by application to the particular case of glucose-lactose diauxie of *E. coli* with model results capturing all principal features of the non-trivial growth curve.

Using the parameterised model we explore competition between populations in a changing environment with results comparing favourably with recent studies.

Our model presents a novel way to predict the lag phase, not only an important issue in wastewater treatment, but also significant in the wider context of studying bacterial growth.