Estimating the bacterial lag time: which model, which precision?

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The objective of this work was to explore the large number of bacterial growth models recently proposed in the field of predictive microbiology, concerning their capacity to give reliable estimates of the lag phase duration (lambda). We compared these models on the basis of their underlying biological explanations of the lag phenomenon, their mathematical formulation and their statistical fitting properties. Results show that a variety of biological interpretations of the lag phase exists, although different biological hypotheses sometimes converge to give identical mathematical equations. The fit of the different models provides relatively close lambda estimates, especially if we consider that the imprecision of the lambda estimates is generally larger than the differences between the models. In addition, the consistency of the lambda estimates closely depends on the quality of the dataset on which models were fitted.

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