

Phenological models on microbial growth – which model is better and why?

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Abstract

Introduction

Phenological models are expected to fit data trends within its biological field. Yet due to different reasons, models developed and published from one sample may not fit the others. These reasons may be due to data variabilities, confounding factors, inaccurate assumptions or models being too-specific. This project is aimed at compare and contrast different published phenological models different microbial population growth data, which is a better one under what conditions. The hypotheses are:

- published phenological models are better than polynomials in describing microbial population data;
- appropriate phenological model(s) can be identified through distinguishable shapes of microbial population data; and
- parameters of data under each model is clustered, similar with dataset best-described by the same model but different from those described by other models.

Methods

Computing tools

R (ver 3.6.0)¹ was used with following packages: “ggplot2”² was used for visualisation; “reshape2”³ was used for converting dataset from wide to long format; “scales”⁴ was used for improve “ggplot” graphs data presentation; and “minpack.lm”⁵ was used for computing non-linear least square statistics for model comparisons.

Results

Discussion

Model fitness to real data and simplistic mathematics were favoured by both AIC⁶⁻⁸ and BIC^{6,9}. Apart from that, BIC also takes account of sample size effect^{6,9}. comparisons in different fields¹⁰⁻¹⁵

Conclusion

Code and Data Availability

All scripts and data used for this report were publicly available at GitHub.

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