# High-Throughput Non-Linnear Model Comparison of Bacterial Growth Curves: a Bayesian Approach

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Here's an abstract - it'll be about 200 words and a summary of all sections of the report s s

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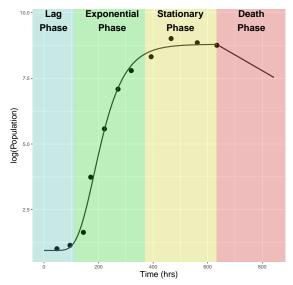


Figure 1: caption explaining the figure, and explaining how the models' parameters relate to the diagram

#### 3 1 Introduction

- 4 Understanding population growth is paramount in fields of study as far-flung as epidemiology,
- 5 climate science and even geopolitics. (Ozgul et al., 2010; Peleg, 1997) For decades a series of in-
- 6 creasibgly complex mathematical models have been used to explain trends in empirical population
- 7 growth data, and enable prediction. (Grijspeerdt & Vanrolleghem, 1999; Kingsland, 1982; Tjørve &
- 8 Tjørve, 2017) Those used for modelling bacterial growth largely rely on the same theory of bacterial
- 9 growth phases, shown in Figure 1.
- bacterial growth (Buchanan, 1918)
  - ((also mention the idea of modelling bio stuff as new or whatever (Transtrum & Qiu, 2016)))
- 12 (Kingsland, 1982)

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- This section will include background info on: (Baranyi et al., 1993; Posada & Buckley, 2004)
- population growth in general
  - the phases og bacterial population growth, using Figure 1 to help demonstrate
- the models I will be using and differences between them
- BIC for model Comparison, and why I chose it over other methods
- outline the hypothesis and aims

#### <sup>19</sup> 2 Methods

#### 20 **2.1** Data

include different measurement techniques, inc spectrometry.(Al-qadiri et al., 2008)

### 22 2.2 Computing Tools

- 23 contain in the Methods a sub-section called "Computing tools" which states briefly how each of
- 24 the scripting languages (bash, R, Python) was used and what packages within them were used and
- 25 a justification of why.

#### 26 2.3 Model Fitting

#### 27 2.4 Model Comparison

- 28 Here I will
- describe and explain the dataset
- possibly move the model and BIC stuff here from intro
- explain the process I took when fitting the models
- justify important decisions in code which may otherwise seem arbitrary, eg the starting

#### 33 Results

- start off using figure 2 and a table I can't work out how to use in latex to compare the models
- possibly also include a boxplot for BIC values of each model to visualise
- then use figures 3 and 4 to visualise the possibility of one model preforming better depending on temperature or medium or pop measuremnt method

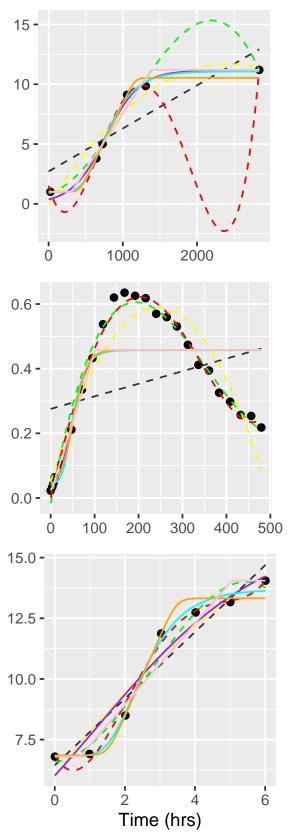


Figure 2: caption explaining the figure, and explaining the y axis (log of different units), which models we're looking at and what it tells us

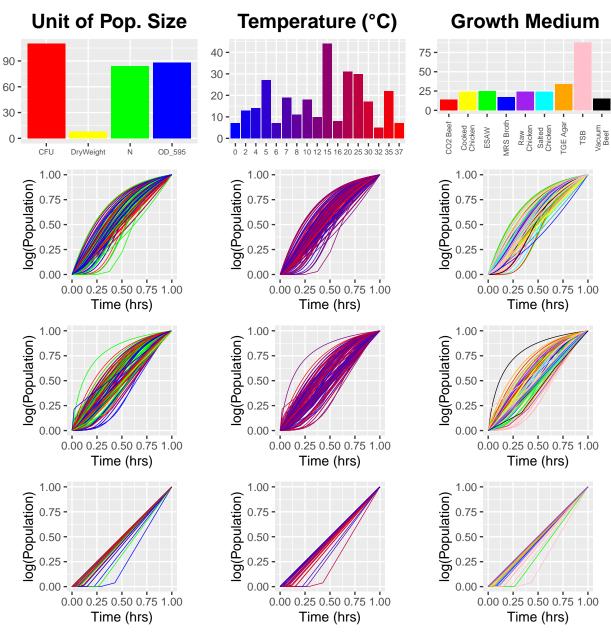


Figure 3: caption explaining the figure, including how it is all the regression lines from fitted models standardised to allow superimposition, and that barplots above act as legend, and which models are which

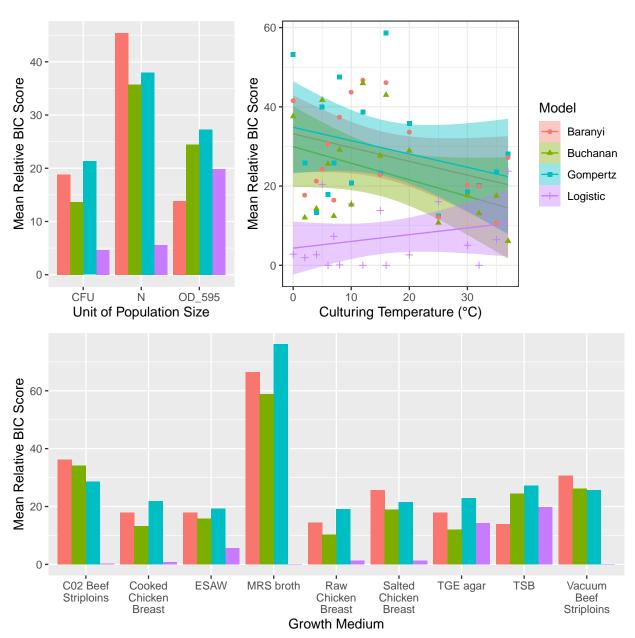


Figure 4: caption explaining the figure, and that colours for each model is concistent throughout.

### 38 4 Discussion

- use results to determine best model(s)
- $\bullet$  explore whether covariables make a difference
- mention death phase, think about models which account for that, possibly suggest splines
- $\bullet$  discuss possibiltiy of accounting for the 3 covariables in the formulae multivariate regression
- more on that later!
- discuss how this all fits with my initial aims and hypotheses

#### 5 References

- Al-qadiri, H. M., Al-alami, N. I., Lin, M., Al-holy, M., Cavinato, A. G., & Rasco, B. a. (2008).

  Fourier Transform Infrared Spectroscopy and Multivariate Analysis. *Journal of Rapid Meth-ods & Automation in Microbiology*, 16, 73–89.
- Baranyi, J., Roberts, T. A., & McClure, P. (1993). A non-autonomous differential equation to model bacterial growth. Food Microbiology, 10(1), 43–59. https://doi.org/10.1006/fmic.1993.1005
- Buchanan, R. E. (1918). Life Phases in a Bacterial Culture. The Journal of Infectious Diseases, 23(2), 109–125.
- Grijspeerdt, K., & Vanrolleghem, P. (1999). Estimating the parameters of the Baranyi model for bacterial growth. *Food Microbiology*, 16(6), 593–605. https://doi.org/10.1006/fmic.1999. 0285
- Kingsland, S. (1982). The Refractory Model: The Logistic Curve and the History of Population
   Ecology. The Quarterly Review of Biology, 57(1), 29–52.
- Ozgul, A., Childs, D. Z., Oli, M. K., Armitage, K. B., Blumstein, D. T., Olson, L. E., Tuljapurkar, S., & Coulson, T. (2010). Coupled dynamics of body mass and population growth in response to environmental change. *Nature*, 466 (7305), 482–485. https://doi.org/10.1038/nature09210
- Peleg, M. (1997). Modeling Microbial Populations with the Original and Modified Versions of the Continuous and Discrete Logistic Equations. *Critical Reviews in Food Science and Nutrition*, 37(5), 471–490. https://doi.org/10.1080/10408399709527785
- Posada, D., & Buckley, T. R. (2004). Model selection and model averaging in phylogenetics: Advantages of akaike information criterion and bayesian approaches over likelihood ratio tests.

  Systematic Biology, 53(5), 793–808. https://doi.org/10.1080/10635150490522304
- Tjørve, K. M., & Tjørve, E. (2017). The use of Gompertz models in growth analyses, and new Gompertz-model approach: An addition to the Unified-Richards family. *PLoS ONE*, 12(6), 1–17. https://doi.org/10.1371/journal.pone.0178691
- Transtrum, M. K., & Qiu, P. (2016). Bridging Mechanistic and Phenomenological Models of Complex Biological Systems. *PLoS Computational Biology*, 12(5)arXiv 1509.06278, 1–34. https://doi.org/10.1371/journal.pcbi.1004915