

<sub>1</sub> Non-linear models outperform linear models in

<sub>2</sub> predicting bacterial growth

<sub>3</sub> Uva Fung - Imperial College London

<sub>4</sub> Word count: 3131

## Abstract

Predicting bacterial growth is important in the food industry as the information can be used to determine food shelf life. Bacterial growth can be modelled using different approaches, which would influence the accuracy of the prediction. Here, I compared six models to identify the best one to be used in predicting bacterial growth. I also investigated if the use of multiple starting parameter values improved model fitting. This study show that non-linear models perform better than linear models. Gompertz model with multiple starting parameters have the highest number of converged datasets. Taking into account the significance of fitting, the Baranyi model is the best fitting one once the model successfully converges.

## 1 Introduction

The study of bacterial growth is important in food microbiology as it provides important information in determining shelf life and food safety [Zwietering et al., 1990]. The growth of bacteria over time can be separated into four phases: lag phase, exponential growth phase, stationary phase and dead phase [Wang et al., 2015], which can be modelled using different phenomenological and mechanistic approaches [Johnson and Omland, 2004, Peleg and Corradini, 2011]. Some simple phenomenological models only include time as the explanatory variable in predicting population growth. These models can be fitted quickly within a short period of time but with limited fitting accuracy. Other more complex ones, such as the Gompertz model, incorporates specific growth rate to improve goodness of fit. However, all phenomenological models only describe the pattern of bacterial growth and do not provide explanations on what causes the observed pattern [Peleg and Corradini,

2011]. Mechanistic models take into account additional biological parameters, such as growth rate, length of lag phase, initial and final population sizes, providing biological explanations on the observed patterns [Zwietering et al., 1990]. The starting values for parameters can be further searched for and adjusted during model fitting to obtain the optimal model. Some of the most popular mechanistic models include the Logistic model [Zwietering et al., 1990] and the Baranyi model [Baranyi and Roberts, 1994]. These models generally provide a better fit, but take a longer processing time and might not converge well depending on the starting parameters. The use of different models could have drastic differences in the predicted bacterial growth. This in turn could have a huge effect on the food industry, as models that predict bacterial growth poorly could cause wrong estimations of shelf life, leading to food wastage or hygiene and public health issues.

This study aims to identify the best model to be used in predicting bacterial growth across large empirical datasets. I will answer four questions:

- i) Which model has the highest number of successfully converged datasets?
- ii) Which model has the highest number of best fit across all datasets?
- ii) What is the time needed to fit each model?
- iv) Does the search for multiple starting parameter values increase the number of successful fitting in Gompertz and Baranyi models?

I hypothesized phenomenological models to spend a much shorter fitting time than mechanistic models because the latter has multiple biological parameters. I also expect the search for starting parameter values should increase the number of successful model fits in both Gompertz and Baranyi models, as this should increase the likelihood of sampling a starting parameter close enough for convergence. The best model will be determined based on the number of datasets successfully converged,

the number of datasets that are best fitted by the model, and the time needed to complete the model fitting process.

## 2 Methods

### Data collection

A total of 305 experimental datasets measuring bacterial growth over time were extracted from ten peer-reviewed published papers [Roth and Wheaton, 1962, Stannard et al., 1985, Phillips and Griffiths, 1987, Sivonen, 1990, Zwietering et al., 1990, Gill and DeLacy, 1991, Bae et al., 2014, Galarz et al., 2016, Bernhardt et al., 2018, Silva et al., 2018]. Each dataset recorded change in bacterial population size at different time points. These datasets consist of a combination of 45 different bacteria species grown in 18 different mediums at 17 different temperatures. A large range of species, mediums and temperatures were chosen in order to test that each model can be fitted to bacterial growth in different experimental settings.

### Data wrangling

Data wrangling and analysis were done in R (ver 3.6.3). Data was first filtered to remove data points with population size and time smaller than zero, as these represents incorrect measurements or error in data input. Datasets with fewer than 6 time points were also removed as the number of data points is too low for good quality model fitting.

### Model fitting

For each dataset, I fitted six models: four phenomenological models (Ordinary Least Squares (OLS), Quadratic equation, Cubic equation, Gom-

80 pertz model) and two mechanistic models (Logistics model, Baranyi model).  
 81 Three models are fitted using the linear regression approach (OLS, Quadratic,  
 82 Cubic). The remaining three (Logistic, Gompertz, Baranyi) are fitted using  
 83 the non-linear least-squares (NLLS) approach, with parameters adjusted for  
 84 using the Levenberg-Marquardt algorithm. The three non-linear models are  
 85 chosen on the basis that they are the most popular models to be used in  
 86 predicting bacterial growth. The logistic model is chosen as it can model  
 87 complicated fluctuation patterns and chaos from a relatively a “simple” non-  
 88 linear process, while the Gompertz model is used across multiple disciplines  
 89 and can describe growth curves having a long or short lag time [Zwietering  
 90 et al., 1990]. The Baranyi model is applicable under dynamic conditions  
 91 with good fitting capacities [Poschet et al., 2005]. The equations used are  
 92 listed below. Notations in equations are as below: Time ( $t$ ), Population size  
 93 at time  $t$  ( $N_t$ ), Population size at time 0 ( $N_0$ ), population size at maximum  
 94 ( $K$ ), coefficients ( $m, a, b, c, d$ ), maximum specific growth rate ( $r$ ), time  
 95 when lag phase ends ( $t_{lag}$ ).

$$OLS : \log N_t = mt + c \quad (1)$$

$$Quadratic : \log N_t = a + bt + ct^2 \quad (2)$$

$$Cubic : \log N_t = a + bt + ct^2 + dt^3 \quad (3)$$

$$Logistic : N_t = \frac{N_0 K e^{rt}}{K + N_0 (e^{rt} - 1)} \quad (4)$$

$$Gompertz : \log N_t = N_0 + (K - N_0)e^{-e^{re^1}} \frac{t_{lag} - t}{(K - N_0)\log 10} + 1 \quad (5)$$

$$Baranyi : \log(N_t) = N_0 + rA(t) - \ln\left(1 + \frac{e^{rA(t)} - 1}{e^{(K-N_0)}}\right) \quad (6)$$

$$Baranyi : A(t) = t + \frac{1}{r}\ln(e^{-rt} + e^{-rt_{lag}} - e^{-r(t+t_{lag})}) \quad (7)$$

Each dataset consists of data to fit the three parameters ( $t$ ,  $N_0$ ,  $K$ ) using the graphical method [Holmström and Petersson, 2002]. Maximum specific growth rate ( $r$ ) was obtained from the slope estimate of the Ordinary Least Squares linear regression output. The time point of  $t_{lag}$  was determined as the time point prior to the greatest population increase within the first half of the experimental duration. In order to increase the likelihood of successful model fitting for Gompertz and Baranyi models, I further fitted both models with the addition of searching for multiple starting values for  $t_{lag}$ . The upper and lower ranges of  $t_{lag}$  was set as the first half of the experimental duration. This allowed the model to search for multiple starting values and iterates through them to determine the best fitting model. The fitted values, standard residuals and Akaike Information Criterion (AIC) scores were calculated for each model fitting.

#### Check for assumptions

After model fitting, I checked each model to see that the model fitted met the assumptions of homogeneity of variance and normality. For each model and dataset combination, I constructed residual vs fitted plots and Normal Q-Q plots. Datasets that did not fit the assumptions were removed

114 from the analysis. A total of 284 datasets remained for subsequent model  
115 comparison.

## 116 Model analysis

117 I first compared the number of successfully converged datasets for each  
118 of the five fitted mechanistic models. I then compared the AIC scores across  
119 all eight models to determine which model has the lowest AIC score for each  
120 dataset. AIC are relative scores used for comparison between models. If  
121 two models have a difference in AIC scores of 2 or more, then the model  
122 with a lower AIC score fits significantly better (Akaike, 1974). Thus in  
123 each dataset, the model that is significantly the best fitting one was also  
124 identified. The time taken for running each model fitting function was then  
125 tested.

## 126 Computing tools

127 Data wrangling, model fitting, assumption checking, model analysis and  
128 plotting were all done in R ver 3.6.3. Data wrangling was done using the *tidy-*  
129 *verse* package. Model fitting was done using *broom*, *stats*, *minpack.lm* and  
130 *nls.multstart* packages. Model fitting of OLS, quadratic and cubic equations  
131 was done using the *lm()* function in the *stats* package. Logistic, Gompertz  
132 and Baranyi models were fitted using the *nlsLM()* function in *minpack.lm*  
133 package, which uses the Leven-Marquardt algorithm to search for the best  
134 fitting model. Gompertz and Baranyi models with multiple starting pa-  
135 rameters were fitted using *nls\_multstart()* function in *nls.multstart* package.  
136 Run time for each function were tested using *system.time()* function. Graph  
137 plotting was done using *ggplot2* and *ggforce* packages.

Table 1: Number of datasets successfully converged by each non-linear model. NA refers to datasets that produce errors when fitted in the equation. Total number of datasets  $n = 284$ .

Models	No. successful datasets	No. failed datasets	NA
Logistic	282	1	1
Gompertz	158	98	28
Baranyi	90	4	190
Gompertz msp	184	35	149
Baranyi msp	80	8	196

### 138 3 Results

139 Among the five fitted non-linear models, the logistic model has the high-  
140 est number of successfully converged datasets and is fitted in 99.2% of the  
141 datasets (Table 1). Both Gompertz and Gompertz with multiple starting  
142 parameter values (Gompertz msp) successfully fitted a similar percentage of  
143 datasets, with 55.6% and 64.7% successful convergence respectively (Table  
144 1). The Baranyi model fitted the fewest number of datasets. Only 31.6%  
145 and 28.1% of datasets successfully converged using the Baranyi model and  
146 the Baranyi model with multiple starting values (Baranyi msp).

147 Among the eight models fitted, Gompertz msp model is best fitted to  
148 the greatest number of datasets based on lowest AIC scores (78) followed by  
149 the Baranyi model (71) (Table 2). The OLS model has the fewest number of  
150 best-fitting datasets. Only 2.4% of the total dataset returned the OLS model  
151 as the one with the lowest AIC. The use of multiple starting parameter values

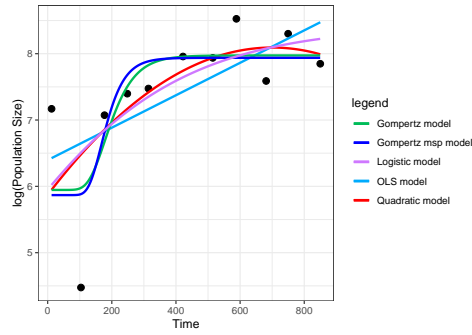


152 increases the number of datasets best fitted in the Gompertz msp model,  
153 but not in the Baranyi msp model (Table 2).

154       Once the significance in AIC scores is taken into account, I found that out  
155 of the total 284 datasets, 135 datasets were equally best fitted by more than  
156 one model (two or more models with an AIC score difference smaller than  
157 2) (Table 2; Fig. 1, Fig. 2). The remaining 149 datasets are significantly  
158 best fitted by a single model (Table 2; Fig. 3). Baranyi has the highest  
159 number of significantly best fitted datasets. When incorporating the number  
160 of successfully converged models, I found that the majority of the datasets  
161 successfully fitted by the Baranyi model return the Baranyi model as the  
162 one with the lowest AIC that fits significantly better than other models  
163 (Table 4). In contrast, only 5-8% of the datasets successfully fitted by the  
164 Logistic, Gompertz, Gompertz msp or Baranyi msp models returned these  
165 four models as the ones with significant best fit.

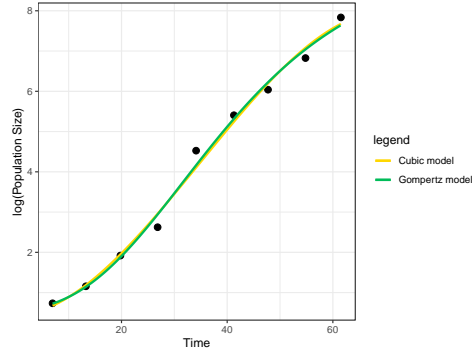
Table 2: Number of datasets best fitted by each model based on lowest AIC scores. Total number of datasets  $n = 284$ .

Model	No. datasets with lowest AIC	No. significantly best fitted datasets
OLS	5	0
Quadratic	14	3
Cubic	33	20
Logistic	52	25
Gompertz	15	12
Baranyi	73	73
Gompertz msp	85	12
Baranyi msp	7	4



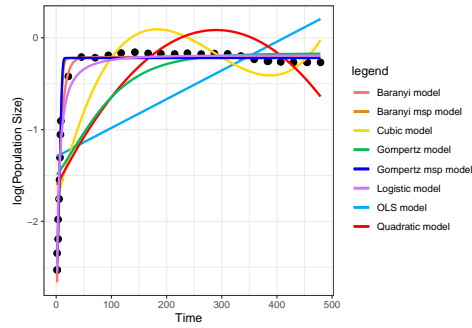
166

167 Fig 1: Model fitting in dataset ID277\_1. All the models fitted do not differ significantly  
 168 from each other and show a poor fit.



169

170 Fig 2: Model fitting in dataset ID259\_1. Both Cubic and Gompertz are equally the  
171 best fitting models.



172

173 Fig 3: Model fitting in dataset ID131\_1. The Baranyi model is significantly the best  
174 fitted model.

175 All three linear models (OLS, Quadratic, Cubic) have a similar user run  
176 time between 0.009 - 0.013s per dataset. The run time for non-linear models

Table 3: Percentage of significantly best fitted datasets relative to the total number of successfully converged datasets.

Model	No. datasets converged successfully	No. datasets significantly best fitted	% (No. significantly best-fitted datasets / No. successfully converged datasets)
Logistic	282	25	8.86%
Gompertz	158	12	7.59%
Baranyi	90	73	81.1%
Gompertz msp	184	12	6.52%
Baranyi msp	80	4	5%

Table 4: Time (in second) taken to fit each model and generate AIC outputs.

Model	User	System	Elapsed
OLS	0.013	0.001	0.015
Quadratic	0.012	0.001	0.017
Cubic	0.009	0.001	0.010
Logistic	0.021	0.006	0.028
Gompertz	0.113	0.034	0.155
Baranyi	0.040	0.009	0.052
Gompertz msp	3.057	0.874	5.667
Baranyi msp	7.692	1.861	13.285

177 is relatively longer (table 4). Among them, the logistic model takes the  
178 shortest time to run (0.021s), followed by Baranyi and the Gompertz model.  
179 The addition of multiple starting parameter values greatly increases the run  
180 time of Gompertz and Baranyi models to 3.057s and 7.692s respectively.

## 181 4 Discussion

182 This study aims to identify the best model in modelling bacterial growth  
183 across datasets, determined based on the number of successful convergence,  
184 the number of best fitted datasets and the time needed to fit the model.  
185 Among all non-linear models, the Logistic model has the highest percentage  
186 of successful convergence (99.2% of datasets), and the lowest percentage  
187 in the Baranyi msp model. One reason is that the Baranyi model has a  
188 more complex equation involving a logarithm term  $\ln(e^{-r*t} + e^{-r*t_{lag}} -$   
189  $e^{-r*(t+t_{lag})})$ . If the dataset produces a negative value, then the logarithmic  
190 function would not work and an error message would return [Wiscombe and  
191 Evans, 1977]. For example, a small growth rate, short lag period, and a long  
192 total time would lead to a negative value, in which taking its logarithmic  
193 term would return an error and the model cannot be fitted. Another reason  
194 is because the Baranyi model uses an additional parameter ( $t_{lag}$ ). The non-  
195 least square method works by searching for a combination of parameter  
196 values that is closest to the optimal least-squares solution with the smallest  
197 sum of squared residuals possible [See et al., 2018]. If the starting  $t_{lag}$  value  
198 is poorly estimated and too far off from the optimal value, then the model  
199 would fail to identify the optimal least-squares solution and cannot converge.  
200 This could be the case in this study as both Gompertz and Baranyi models  
201 incorporate an extra tlag parameter, while the Logistic model does not have  
202 this parameter.

203 Based on the lowest AIC scores, the Gompertz msp model gave the  
204 highest number of best fitted datasets followed by the Baranyi model. The  
205 linear models are generally poorly fitted than the non-linear ones because

the former does not take into account biological parameters (such as specific growth rate or lag phase), whereas these are included in the non-linear models [Peleg and Corradini, 2011]. Another reason is that the linear model fits the data points directly using linear regression, whereas the non-linear models are fitted using non-linear least squares, which would adjust parameter values to search for the best model. As a result, there is a higher chance for the best-fitted model to be identified using non-linear approaches.

However, when taking the relative difference in AIC scores between models into account, Baranyi model was the only model that is significantly better than all other models. All 73 datasets best fitted by the Baranyi model fit significantly better than other models based on a difference in AIC scores of 2 or more. For example, the Baranyi model is the best fitting one of all eight models in dataset 131\_1 (Fig. 3), as only the Baranyi model line passes through all data points. In contrast, the Gompertz msp model, which has the lowest AIC score in 85 datasets, only significantly best fits 12 datasets. One explanation is because the data fitted are of poor quality and did not show a distinctive lag, growth and stationary phase. For example, the data points in dataset 227\_1 (Fig. 1) are scattered and lack a clear growth phase. Thus in this dataset, none of the five fitted models (Gompertz, Gompertz msp, Logistic, OLS or Quadratic model) fits the data significantly better than others. Another possibility is that the data only captures part of the bacterial growth, such that it is also a good fit when implementing other models. An example is dataset 259\_1 (Fig. 2), which only records the growth phase of the bacteria. The resultant isothermal curves can be fitted by both cubic and the Gompertz model [Peleg and Corradini, 2011], and therefore both models best fit this dataset. It is also worth noting that in the Baranyi

232 model, 81.1% of the successfully converged datasets return Baranyi model  
233 as the best fitting one. This implies that once successfully converged, the  
234 Baranyi model generally is the best fitting model.

235 In line with my hypothesis, The use of non-linear least-square methods  
236 and multiple starting parameter values both increase the time needed to  
237 run the model. Unlike linear models which directly fit the parameters in  
238 the equation, extra time is needed in NLLS to adjust the parameters to  
239 search for the best combination of parameters [Kallehauge et al., 2016]. The  
240 inclusion of multiple starting parameters further increases the time needed,  
241 as additional time is needed to search for the best starting  $t_{lag}$  values. In  
242 particular, the Baranyi msp model takes more than twice the time to run  
243 than the Gompertz msp model. This is because the Baranyi has a more  
244 complex equation and therefore would take longer to compute.

245 The long time spent in Gompertz msp is compensated by the higher num-  
246 ber of successful convergence and the greater number of datasets fitted with  
247 the lowest AIC scores. However, after taking into account the significance  
248 of AIC between models, both Gompertz and Gompertz msp significantly  
249 fitted 12 datasets only. This suggests that the inclusion of multiple start-  
250 ing parameter values in the Gompertz model did not improve model fitting.  
251 This could be because the initial starting parameter value based on graphi-  
252 cal methods was not optimal [Holmström and Petersson, 2002], or that the  
253 Levenberg–Marquardt algorithm used in searching for the optimal model  
254 has limited searching ability and fail to identify more optimal parameter  
255 values for model fitting [Transtrum and Sethna, 2012]. The former can be  
256 improved by estimating using the geometrical sums method, which involves

257 generalized interpolations [Holmström and Petersson, 2002]. The latter is  
 258 a common constraint in models with multiple parameters known as param-  
 259 eter evaporation [Transtrum et al., 2010]. In the Gompertz msp model, it  
 260 is possible that only a few parameter combinations are relevant to finding  
 261 the optimal model, whereas most other combinations do not return a better  
 262 fit. Therefore during model fitting, the Levenberg–Marquardt search algo-  
 263 rithm might get lost in regions of parameter space. The algorithm would  
 264 then push the parameters to infinite values without finding a good fit. Sim-  
 265 ilarly, the fewer number of successfully converged and best fitted datasets  
 266 in the Baranyi msp model could also be attributed to parameter evapo-  
 267 ration. It is suggested that the Leven-Marquardt search can be improved  
 268 by including corrections in the approximation of residuals [Transtrum and  
 269 Sethna, 2012]. Other search algorithms using hybrid Gauss–Newton (GN)  
 270 and quasi-Newton algorithms are recommended [Holmström and Petersson,  
 271 2002]. The use of Maximum Likelihood and Bayesian approaches in choos-  
 272 ing parameter searching for optimal model could also improve model fitting,  
 273 especially in datasets with small sample sizes [Zondervan-Zwijnenburg et al.,  
 274 2018].

275 To conclude, Gompertz model has the highest number of successful con-  
 276 vergence and best fit based on lowest AIC. However, taking into account the  
 277 significance of AIC scores, the Baranyi model is the best at fitting across  
 278 multiple datasets once successfully converged. Evidence from this study  
 279 does not support the use of multiple starting parameter values in Gompertz  
 280 or Baranyi models, due to the long run time and the lack of improvement  
 281 in data fitting. Future studies could focus on including multiple starting  
 282 values for more parameters (eg. specific growth rate), optimizing the search



method for starting parameter values, and adopt more advance search algorithms. Improvements in code vectorization could reduce the run time needed for models fitted with non-linear least-square methods.

## References

- [Bae et al., 2014] Bae, Y.-M., Zheng, L., Hyun, J.-E., Jung, K.-S., Heu, S., and Lee, S.-Y. (2014). Growth characteristics and biofilm formation of various spoilage bacteria isolated from fresh produce. *Journal of Food Science*, 79(10):M2072–2080.
- [Baranyi and Roberts, 1994] Baranyi, J. and Roberts, T. A. (1994). A dynamic approach to predicting bacterial growth in food. *International Journal of Food Microbiology*, 23(3):277–294.
- [Bernhardt et al., 2018] Bernhardt, J. R., Sunday, J. M., and O’Connor, M. I. (2018). Metabolic Theory and the Temperature-Size Rule Explain the Temperature Dependence of Population Carrying Capacity. *The American Naturalist*, 192(6):687–697.
- [Galarz et al., 2016] Galarz, L. A., Fonseca, G. G., and Prentice, C. (2016). Predicting bacterial growth in raw, salted, and cooked chicken breast fillets during storage. *Food Science and Technology International*, 22(6):461–474.
- [Gill and DeLacy, 1991] Gill, C. O. and DeLacy, K. M. (1991). Growth of *Escherichia coli* and *Salmonella typhimurium* on high-pH beef packed under vacuum or carbon dioxide. *International journal of food microbiology*, 13(1):21–30.

- 306 [Holmström and Petersson, 2002] Holmström, K. and Petersson, J. (2002).  
 307 A review of the parameter estimation problem of fitting positive expo-  
 308 nential sums to empirical data. *Applied Mathematics and Computation*,  
 309 126(1):31–61.
- 310 [Johnson and Omland, 2004] Johnson, J. B. and Omland, K. S. (2004).  
 311 Model selection in ecology and evolution. *Trends in Ecology & Evolu-*  
 312 *tion*, 19(2):101–108.
- 313 [Kallehauge et al., 2016] Kallehauge, J., Sourbron, S., Irving, B., Tanderup,  
 314 K., Schnabel, J., and Chappell, M. (2016). Comparison of linear and  
 315 nonlinear implementation of the compartmental tissue uptake model for  
 316 dynamic contrast-enhanced MRI: Linear Implementation of the Compart-  
 317 mental Tissue Uptake Model. *Magnetic Resonance in Medicine*, 77.
- 318 [Peleg and Corradini, 2011] Peleg, M. and Corradini, M. G. (2011). Micro-  
 319 bial Growth Curves: What the Models Tell Us and What They Cannot.  
 320 *Critical Reviews in Food Science and Nutrition*, 51(10):917–945.
- 321 [Phillips and Griffiths, 1987] Phillips, J. D. and Griffiths, M. (1987). The  
 322 relation between temperature and growth of bacteria in dairy products.  
 323 *Food Microbiology*, 4(2):173–185.
- 324 [Poschet et al., 2005] Poschet, F., Vereecken, K. M., Geeraerd, A. H.,  
 325 Nicolaï, B. M., and Van Impe, J. F. (2005). Analysis of a novel class of  
 326 predictive microbial growth models and application to coculture growth.  
 327 *International Journal of Food Microbiology*, 100(1):107–124.

328 [Roth and Wheaton, 1962] Roth, N. G. and Wheaton, R. (1962). Conti-  
329 nuity of psychrophilic and mesophilic growth characteristics in the genus  
330 *Arthrobacter*. *Journal of Bacteriology*, 83:551–555.

331 [See et al., 2018] See, J. J., Jamaian, S. S., Salleh, R. M., Nor, M. E.,  
332 and Aman, F. (2018). Parameter estimation of Monod model by the  
333 Least-Squares method for microalgae *Botryococcus Braunii* sp. *Journal*  
334 *of Physics: Conference Series*, 995:012026.

335 [Silva et al., 2018] Silva, A., Longhi, D., Dalcanton, F., and Aragão, G.  
336 (2018). Modelling the growth of lactic acid bacteria at different temper-  
337 atures. B. *Brazilian Archives of Biology and Technology*, 61.

338 [Sivonen, 1990] Sivonen, K. (1990). Effects of light, temperature, nitrate,  
339 orthophosphate, and bacteria on growth of and hepatotoxin production  
340 by *Oscillatoria agardhii* strains. *Applied and Environmental Microbiology*,  
341 56(9):2658–2666.

342 [Stannard et al., 1985] Stannard, C. J., Williams, A. P., and Gibbs, P. A.  
343 (1985). Temperature/growth relationships for psychrotrophic food-  
344 spoilage bacteria. *Food Microbiology*, 2(2):115–122.

345 [Transtrum et al., 2010] Transtrum, M. K., Machta, B. B., and Sethna, J. P.  
346 (2010). Why are Nonlinear Fits to Data so Challenging? *Physical Review*  
347 *Letters*, 104(6):060201. Publisher: American Physical Society.

348 [Transtrum and Sethna, 2012] Transtrum, M. K. and Sethna, J. P. (2012).  
349 Improvements to the Levenberg-Marquardt algorithm for nonlinear least-  
350 squares minimization. *arXiv:1201.5885 [physics]*.

- 351 [Wang et al., 2015] Wang, L., Fan, D., Chen, W., and Terentjev, E. M.  
352 (2015). Bacterial growth, detachment and cell size control on polyethylene  
353 terephthalate surfaces. *Scientific Reports*, 5(1):15159.
- 354 [Wiscombe and Evans, 1977] Wiscombe, W. J. and Evans, J. W. (1977).  
355 Exponential-sum fitting of radiative transmission functions. *Journal of*  
356 *Computational Physics*, 24(4):416–444.
- 357 [Zondervan-Zwijnenburg et al., 2018] Zondervan-Zwijnenburg, M., Depaoli,  
358 S., Peeters, M., and Schoot, R. (2018). Pushing the Limits: The Perfor-  
359 mance of Maximum Likelihood and Bayesian Estimation With Small and  
360 Unbalanced Samples in a Latent Growth Model. *Methodology*, 15:1–13.
- 361 [Zwietering et al., 1990] Zwietering, M. H., Jongenburger, I., Rombouts,  
362 F. M., and van 't Riet, K. (1990). Modeling of the Bacterial Growth  
363 Curve. *Applied and Environmental Microbiology*, 56(6):1875–1881.