How well do different linear and nonlinear growth models fit to bacterial growth curves?

Sarah Dobson ,Imperial College London sld21@ic.ac.uk, Word Count: 2600

27th November 2021

1 Abstract

Microbial growth is a common cause of food spoilage and posioning. Mathmatical models that predict the rate of bacterial growth can be used to determine the shelf life of food products, minimise bacterial growth and optimise food production. Both linear and non-linear models have been used to predict growth curves across the literature, however which model is best at fitting bacteria growth curves is still debated. Using datasets from multiple published papers I compared two polynomial linear models: cubic and quadratic, with the three most popular non linear models, the Logistic, Gompertz and the Biryani Models, using AICc values to determine (1) whether linear or non linear models best predict bacterial growth curves and (2) which model best predicts bacterial growth overall. I found that the Gompertz model best fitted bacterial growth curves across the datasets but I could not determine whether linear or non linear models were superior at fitting bacterial growth curves due to convergence issues in the non linear models. Future studies should sample the starting parameters of non linear models in order to get a higher convergence rate.

2 Introduction

Microbial growth is a common cause of food spoilage and posioning (Peleg and Corradini, 2011). Food spoilage may be visible as the growth of slime colonies, textural changes, or off-odors and off-flavors (NRC 1985). Mathmatical models that correctly predict the rate of bacterial growth can be used to predict the shelf life of food products, minimise bacterial growth and optimise food production (Baranyi and Roberts, 1994). Bacterial growth can be separated into 4 phases as shown in Figure 1:

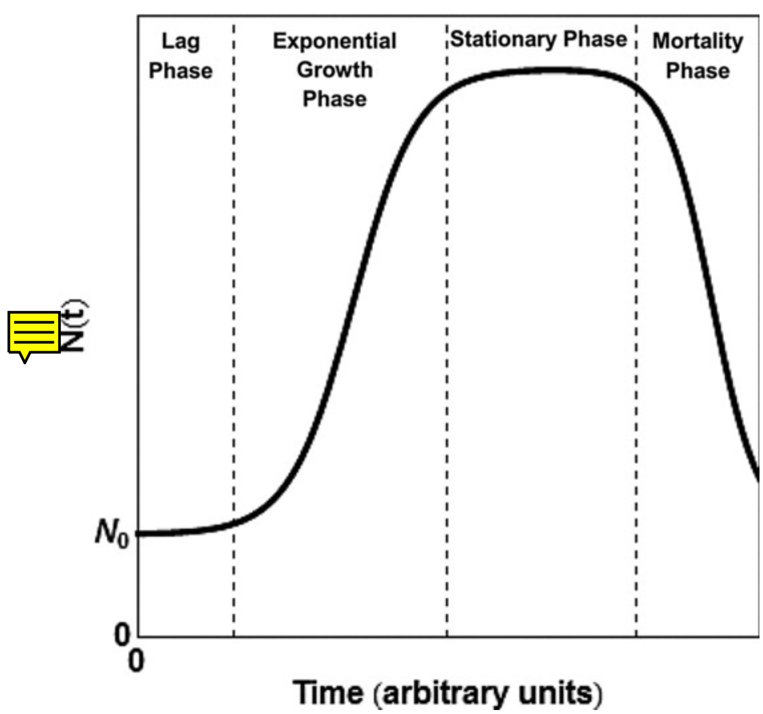


Figure 1: This diagram,taken from (Peleg and Corradini, 2011), shows the four phases of bacterial growth N_t over time: known all togather as the bacterial growth curve. (1) the lag phase: when bacteria are introduced to a new environmrnt or medium they do not initially grow and instead activate genes involved in better nutrient uptake from the new enviroment. (2)the exponential growth phase: acclimitisation to the new environemnt has been completed, and the bacteria starts to grow exponentially. (3)stationary phase: growth wavers as resources start to become limited, eg. competition for food and/or space. (4) death or mortality phase: as resources start to decline, the bacteria start to die off.

Over the years, a number of different models were used to attempt to predict bacterial growth. Two major types of model are used: linear and non linear. Linear models describe the direct relationship between growth and any explanaotry variables(in this case time) by using linear predictor functions whereas non linear models are fit to growth curves based on a minimum number of biologically relevent parameters (Grijspeerdt and Vanrolleghem, 1999).

Traditionally, microbial growth rates were measured by plotting population size against the time since innoculation and fitting a linear regression through the exponential growth phase (Baranyi and Roberts, 1994; Whiting and Cygnarowicz-Provost, 1992). However, this method only looks at predicting bacterial growth in the exponential growth phase and does not take into consideration the other phases which are also biologically relevant. For example, the duration of the lag phase determines how long food will last before becoming spoiled and in single cells determines when pathogenic cells can multiply to a poisoning concentration level (Baranyi et al., 2009; Baranyi and Roberts, 1994; Olofsson and Ma, 2011).

However, linear polynomial models, using a cubic or quadratic equation, could potentially capture the delayed start of population growth in the lag phase, decreasing momentum of the stationary phase and decline of the death phase. They are also commonly used to assess growth curves in other research fields such as plant growth (Jane et al., 2019). Linear models are also easy to run, interperate and (Grimm et al., 2011). It is possible that bacterial growth is better captured by nonlinear models. Growth rates do not change linearly or reach a maximum point like polynomial models (Jane et al., 2019). However, they are not as robust as linear models (Buchanan et al., 1997).

Over the years, many studies have used different models to fit bacterial growth curves, with differing conclusions. Therefore, there is significant disagreement in literature on which model is the best for predicting bacterial growth curves and selecting a model to use often appears to be subjective (Pla et al., 2015). Determining which of the models predicts bacterial growth best can be determined by model selection, where competing models are directly compared to each other and ranked by determining the relative support in the observed data for each model (Johnson and Omland, 2004).

Therefore I will compare two polynomial linear models: cubic and quadratic, with three of the most popular non linear models for predicting bacterial growth (Pla et al., 2015): the logistic model, the Gompertz Model and the Baranyi Model. I will fit all of these models across multiple datasets of bacterial growth over time. Using model selection, I will determine (1) whether linear or non linear models best predict bacterial growth curves and (2) out of all the models used which one best predicts bacterial growth.

3 Methods

3.1 Computing Tools

All of the data wrangling, model fitting and plotting was completed in R version 3.6.3. I wrangled the data and fitted the models using the tidyverse package (Wickham, 2017), which provided an easy and innutive way to filter and manipulate data and apply model fittins across each dataset. I fitted the linear models using the lm functionin in base R. I fitted the nonlinear models using NLLS (Non linear least squares) using the package minpack.lm (Elzhov et al., 2016) which uses non linear least squares to fit data to models with a slight modification to the LevenbergMarquardt algorithm, which creates a more robustness structure that handles less optimal starting parameter values. I calculated the AICc values using the package MuMIn (Barton and Barton, 2015) which easily streamlines the information-theoretic model selection and carries model averaging based on information criteria. I pulled model ouputs into dataframes using the package broom (Robinson, 2014), which made report resulting, creating plots and working with large numbers of models easy. I used a bash script to wrangle the data, fit models, plot the ouputs and compile the results into this pdf file. Bash allows me to easily sequentially run each script with minial coding.

3.2 Data Manipulation

I used Datasets from 10 peer-reviewed research papers to test model fits. These datatsets included populations of different bacterial species recorded over time in varying environmental conditions. Therefore, seperate datasets used to test model fits were defined by the paper the dataset came from, the species of bacteria used, temperature the bacteria were grown at, medium the bacteria were grown and the replicate number if the experiment was replicated. This gave a total of 305 datasets. The sample size of each dataset ranged from 3 to 151. I removed datasets with less than 8 datapoints as the models may have trouble fitting small sample sizes. I also removed negative population size and time measurements from datasets because these measurements are biologically impossible and were likely the result of a recording error.

3.3 Model fitting

For each dataset I fitted a quadratic regression linear model and a cubic regression linear model in R version 3.6.3. The log population size was the response with the time since innoculation as the explanatory variable. For the quadratic and cubic models time was fitted as a quadratic and cubic affects respectively. All models were checked for goodness of fit and that the assumptions for linear models were met.

All linear models were fit using a non linear least squares method (NLLS) using the package min.pack.lm (Elzhov et al., 2016) in R version 3.6.3. NLLS fits models to data by minimizing the squared differences between observed and predicted values (Johnson and Omland, 2004). Each model was run with 1000 iterations, the starting values used for each model are specified below. All model were checked for goodness of fit and that the assumptions for non linear models were met.

For my first nonlinear model I fitted each dataset to a logisitc model (Verhulst, 1838) with the following equation:

$$N_t = \frac{N_0 K_e^{rt}}{K + N0(e^{rt} - 1)} \quad (1)$$

N_t is the population size at time t, t is the time since innoculation, N_0 is the initial size of the bacteria population, K is the carrying capacity (ie. the maximum population size that the bacteria can achieve) and r is the maximum growth rate (the fastest that the bacteria population grows in a given time frame). I used K, N_0 and r as starting parameters. For each dataset, K was calculated by determining the maximum population size reached, N_0 was calculated by determining the population size at the first datapoint and r was determined by calculating the slope of the log of the population size against time via linear regression.

The second model is a revised Gompertz model (Grijspeerdt and Vanrolleghem, 1999). The gompertz model was fitted to each dataset using the following equation:

$$log(N_t) = log(N_0) + (log(K) - log(N_0)e^{-e*(r*e(1)*\frac{t_{lag}-t}{log(K)-log(N_0)*log10}} + 1 \quad (2)$$

The defintions for N_t, t, N_0,K and r are the same as the logisitic model above. t_{lag} is the amount of time the population spends in the lag phase. In the gompertz model r is the tangent to the infection point while t_{lag} intercepts this tangent on the x-axis. For each dataset, K was calculated by determining the maximum log population size reached, logN_0 was calculated by determining the log population size at the first datapoint, r was determined by calculating the slope of the log of the population size against time via linear regression and t_{lag} was calculated using the furtherest time point away from the intial time point where there was no growth in population size. r was calculated using the same methods described for the logistic model.

The third linear model is the Baranyi Model (Baranyi and Roberts, 1994) which is based on the concept that the rate of bacterial growth is controlled by the rate of a 'bottleneck' biochemical reaction (Buchanan et al., 1997). I fitted the data in each dataset to the Baranyi model using the two equations below taken from (Pla et al., 2015). I inserted the equation for N_t into places were N_t appeared in the equation for logN_t.

$$Equation1 : log(N_t) = N_0 + r * A * N_t * t - ln(1 + \frac{e^{r*N_0*t} - 1}{e^{(K-N_0)}} \quad (3)$$

$$Equation2 : N_t = t - \frac{1}{r} * ln * (e^{-r*t} + e^{-r*t_{lag}} - e^{-r(t+t_{lag})}) \quad (4)$$

The defintions for N_t, t, N_0,K, r (and t_{lag} are the same as the gompertz model.

3.4 Comparing Models

I compared how well each model across fitted the data across each dataset by calculating their small sample unbiased Akaike information criterion (AICc) values using the package MuMIN (Barton and Barton, 2015) in R. AICc values are ideal for comparing between models as they consider both fit and complexity of the models, and correct biases for more complex models (Johnson and Omland, 2004). AICc also corrects bias for small sample sizes, and should be used when the total number of samples divided by the number of parameters is less than 40 (Johnson and Omland, 2004). This is the case for the majority of the datasets. The best fiting model for each dataset was assigned with the model with the lowest AICc. The best fitting model across all the datasets was determined by considering how many times each model successfully converged and the number of times each model had the lowest AICc across all datasets and the total number datasets where they successfully ran.

4 Results

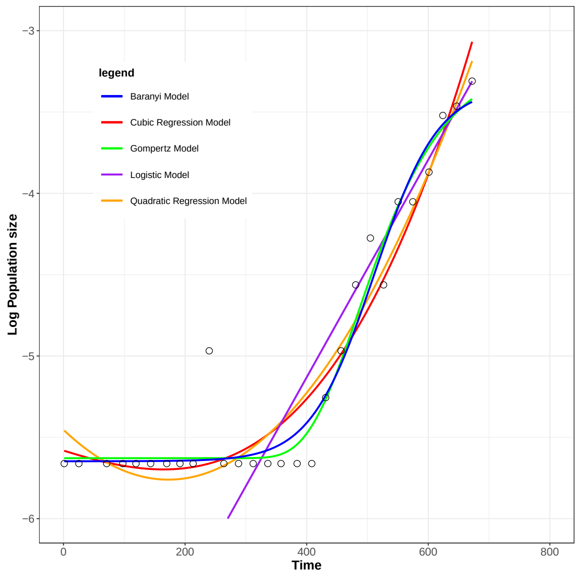
In total I fitted each model to 228 datasets. Ranigng from 8 to 151 data points, with 23823 data points across all datasets. Model diagnostics showed that the datasets fit the assumptions for NLLS analysis. A list of all the model AICc and the best fitting model for each dataset can be found in table S1. A list of how many times each model had the lowest AICc and successfully converged across all the datasets are found in Table 1.

The quadratic and cubic linear models converged across the most datasets at 100%, while the logistic, gompertz and baranyi models converged in 97%, 56% and 11% of the datasets respectively (Table 1). Only 4 of the 228 datasets had successful runs with all models. The quadratic and cubic linear models had the best model fit for 25.4% and 23.3% of the datasets respectively. The logisitc model was the best fit for 16.7% of the datasets were the model converged, and 16.2% overall. The baranyi model was the best fit for 19.2% of the datasets where the model converged and 2.2% overall. The gompertz model had the highest number of best fits both across the datasets where the model converged at 58.5% and across all datasets at 32.9%. In total, linear models and non linear models were the best fit for 48.6% and 51.4% of the datasets respectviely. ON average the linear and nonlinear models had a best model fit of 55.5% and 39% respectively. Plotting model

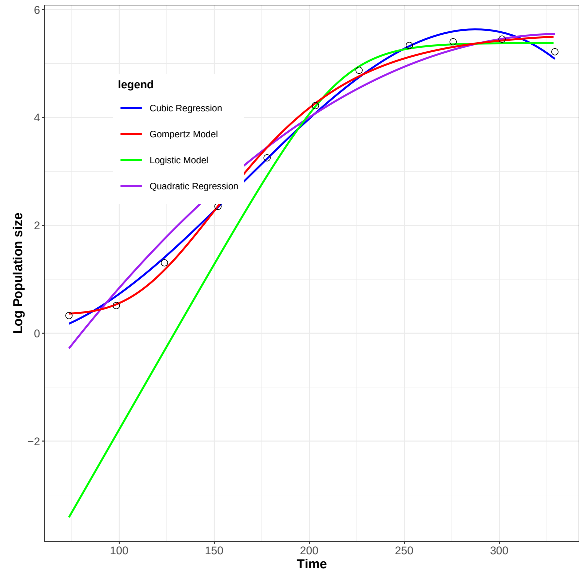
Table 1: A list of the number times each model was the best fit and successfully converged across all 228 datasets

Model	Best Model Count	Convergence Count
Quadratic	58	228
Cubic	53	228
Logisitc	37	221
Gompertz	75	128
Baranyi	5	26

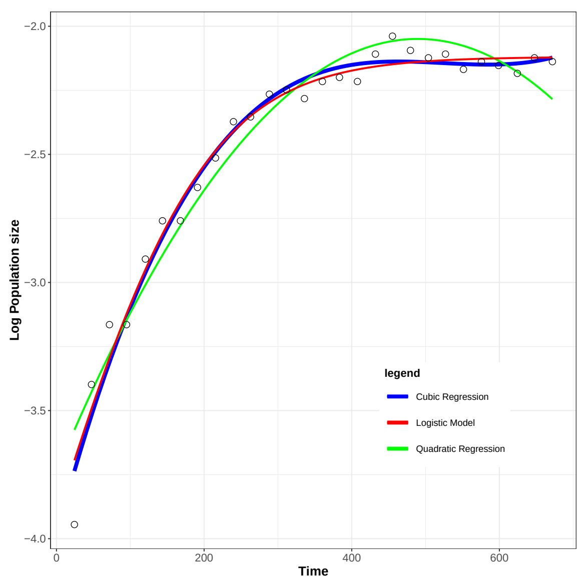
outputs for each dataset visualised how well the models fit the data. Examples of the plotted predicted lines for each dataset are shown in figure 2.



(a) Plots the change in log population size over time for dataset 245_1 where every model successfully converged. Each line represents a different model. Each datapoint represents individual samples from the dataset.



(b) Plots the change in log population size over time for dataset '196_1', where every model except baranyi successfully converged. Eaah line represents a different model. Each datapoint represents individual samples fromm the dataset.



(c) Plots the change in log population size over time for dataset 230_1,, where only the quadratic, cubic and logisitc models uccessfully converged. Each line represents a different model. Each datapoint represents individual samples from the dataset.

Figure 2: shows plots of the predicted lines for each model across selected datasets

5 Discussion

I found that while non linear models were the best fitting models fits across more datasets than linear models, on average the linear models accounted for more best model fits than the non linear models. Further examination also reveals that across some datasets, the AICc values of the Gompertz, Quadratic and Cubic models had a difference of less than 2 in (Table S1). An AICc difference of less than 2 is not significantly different and AICcs wihtin that range should all be considered the best fit (Akaike, 1998).

None of the non-linear model managed to converge across all datasets. A lack of model convergence suggests that the models are not a good fit to the data. However, the model parameters are based on theoretical phases in closed habitats, which rely on the datasets recording population growth from start to end (Grijspeerdt and Vanrolleghem, 1999), and that there is sufficient information recorded for each phase (Buchanan et al., 1997). The death phase is rarely recorded in the datasets and across the literature (Peleg and Corradini, 2011), and recording issues and stochastic events can lead to a lack of data for other phases (Peleg and Corradini, 2011; Pla et al., 2015).This could make it more difficult for nonlinear models to fit to the data (Buchanan et al., 1997). For example the Figures 2C shows model fittings for a dataset where there is a lack of a lag and death phase and the Gompertz and Baranyi models never converged. A lack of a lag phase (and death phase for Baranyi) may have made the model difficult to the fit to the data. However, the convergence issues of the nonlinear models may be solved by random sampling of the starting parameters, where in each iteration of the model the starting parameters are randomly chosen from a defined range. Sampling of the parameters would possibly allow for all of the nonlinear models to converge and determine if non linear models can be used across the datasets.

I found that the Gompertz model had the most best model fits across all the datasets at 32.9% despite only converging across just over half the datasets. The Gompertz model is widely used across the literature (Tjørve and Tjørve, 2017) and has been shown to more accurately describe bacterial growth rates than many other models (Grijspeerdt and Vanrolleghem, 1999; Pla et al., 2015). This may be because of Gompertz model's consideration of the inflection point in bacterial growth, which cah help to accurately describe the lag phase (Baranyi and Roberts, 1994). Figures 2A and 2B show that the Gompertz model fits the lag phase accurately compared to the cubic and quadratic regression in this data set. The quadratic and cubic regression models had the second and third most best model fits across all the datasets, similar numbers of best model fits across the dataset. Linear models are more robust than the non linear models, especially in datasets with smaller samples sizes and minimal data, which has also been the case for previous studies (Baranyi and Roberts, 1994). Many datasets in this study had less than 10 samples. Despite converging in over 95% of datasets the logistic model had the second lowest number of best fits across all datasets and the lowest in datasets where it converged. Studeis have shown that the logistic model does not accurately describe bacterial growth (Smith et al., 2007) and is often outcompeted by other non linear models pla2015comparison. The poor performance of the Baranyi model was unexpected as other studies have shown that it more accurately describes bacterial growth data compared to the Gompertz model due to its more mechanistic definition of a lag period (Baranyi et al., 1993; Baranyi and Roberts, 1994; Pla et al., 2015). The Baranyi's ability to converge may have been affected by the logistics of the datasets as mentioned in the previous paragraph.

In my study I investigated whether linear or non linear models were better at fitting bacteiral growth curves by fitting quadratic, cubic, logisitc, gompertz and baranyi models to 228 datasets which recorded bacterial growth overtime by comparing AICc values. I also determined which individual model best fitted the 228 datasets. I found that Gompertz model had the best fit across the largest number of datsets. I found that non linear models were marginally better than linear models. Howevever, convergence issues in non-linear models and a difference in AICc values of less than 2 between linear and non-linear models in some datasets suggest that linear models could fit to bacterial growth curves just as well, or even better, than non linear models. Due to these convergence issues, I can not determine whether linear or non linear models are better or whather Gompertz is the best model for fitting bacterial for growth curves. Those interested in determing the best model for predicitng bacterial growth with nonlinear models should sample each model's starting parameters in order to increase convergence.

References

Akaike, H. (1998). A bayesian analysis of the minimum aic procedure. In *Selected Papers of Hirotugu Akaike*, pages 275–280. Springer.

Baranyi, J., George, S. M., and Kutalik, Z. (2009). Parameter estimation for the distribution of single cell lag times. *Journal of theoretical biology*, 259(1):24–30.

Baranyi, J., McClure, P., Sutherland, J., and Roberts, T. (1993). Modeling bacterial growth responses. *Journal of industrial microbiology and biotechnology*, 12(3-5):190–194.

Baranyi, J. and Roberts, T. A. (1994). A dynamic approach to predicting bacterial growth in food. *International journal of food microbiology*, 23(3-4):277–294.

Barton, K. and Barton, M. K. (2015). Package 'mumin'. *Version*, 1(18):439.

Buchanan, R., Whiting, R., and Damert, W. (1997). When is simple good enough: a comparison of the gompertz, baranyi, and three-phase linear models for fitting bacterial growth curves. *Food microbiology*, 14(4):313–326.

Elzhov, T. V., Mullen, K. M., Spiess, A.-N., Bolker, B., Mullen, M. K. M., and Suggests, M. (2016). Package 'minpack. lm'. *Title R Interface Levenberg-Marquardt Nonlinear Least-Sq. Algorithm Found MINPACK Plus Support Bounds*.

Grijspeerdt, K. and Vanrolleghem, P. (1999). Estimating the parameters of the baranyi model for bacterial growth. *Food microbiology*, 16(6):593–605.

Grimm, K. J., Ram, N., and Hamagami, F. (2011). Nonlinear growth curves in developmental research. *Child development*, 82(5):1357–1371.

Jane, S. A., Fernandes, F. A., Silva, E. M., Muniz, J. A., and Fernandes, T. J. (2019). Comparison of polynomial and nonlinear models on description of pepper growth. *Revista Brasileira de Ciências Agrárias*, 14(4):1–7.

Johnson, J. B. and Omland, K. S. (2004). Model selection in ecology and evolution. *Trends in ecology & evolution*, 19(2):101–108.

Olofsson, P. and Ma, X. (2011). Modeling and estimating bacterial lag phase. *Mathematical biosciences*, 234(2):127–131.

Peleg, M. and Corradini, M. G. (2011). Microbial growth curves: what the models tell us and what they cannot. *Critical reviews in food science and nutrition*, 51(10):917–945.

Pla, M.-L., Oltra, S., Esteban, M.-D., Andreu, S., and Palop, A. (2015). Comparison of primary models to predict microbial growth by the plate count and absorbance methods. *BioMed research international*, 2015.

Robinson, D. (2014). broom: An r package for converting statistical analysis objects into tidy data frames. *arXiv preprint arXiv:1412.3565.*

Smith, H. et al. (2007). Bacterial growth. *Arizona State University*, 14.

Tjørve, K. M. and 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):e0178691.

Verhulst, P.-F. (1838). Notice sur la loi que la population suit dans son accroissement. *Corresp. Math. Phys.*, 10:113–126.

Whiting, R. and Cygnarowicz-Provost, M. (1992). A quantitative model for bacterial growth and decline. *Food Microbiology*, 9(4):269–277.

Wickham, H. (2017). The tidyverse. *R package ver*, 1(1):836.

6 Appendix

Table S1: List of model AICcs and best fitting models for each dataset.

Rep_ID	Cubic_AICc	Quadratic_AICc	Log_AICc	Gom_AICc	Bar_AICc	Best_model
100_1	25.74	45.38	218	21.21	NA	Gompertz
101_1	24.11	42.87	207.13	27.95	NA	Cubic
102_1	13.37	10.75	153.86	21.93	NA	Quadratic
103_1	26.3	39.88	177.97	15.45	NA	Gompertz
104_1	23.94	23.33	136.5	12.7	NA	Gompertz
105_1	18.23	24.47	NA	17.48	NA	Gompertz
106_1	27.84	31.33	144.4	6.47	NA	Gompertz
107_1	8.06	14.73	174.81	18.16	NA	Cubic
108_1	40.06	25	NA	32.94	NA	Quadratic
109_1	25.8	19.82	71.74	19.06	NA	Gompertz
110_1	4.38	3.7	118.42	2.17	NA	Gompertz
111_1	2.64	24.19	130.01	13.26	NA	Cubic
112_1	13.33	30.42	60.81	21.12	NA	Cubic
113_1	28.57	26.36	94.29	2.95	NA	Gompertz
114_1	40.71	35.73	118.95	2.36	NA	Gompertz
115_1	14.48	16.04	NA	14.06	NA	Gompertz
116_1	36.21	32.12	74.94	33.63	NA	Quadratic
118_1	16.1	11.53	NA	23.94	NA	Quadratic
119_1	28.26	20.61	NA	26.54	NA	Quadratic
124_1	10.76	32.66	165.8	2.79	NA	Gompertz
125_1	12.29	28.5	173.28	9.07	NA	Gompertz
126_1	7.42	21.36	101.89	9.46	NA	Cubic

127_1	21.1	31.91	166.54	13.47	NA	Gompertz
128_1	11.15	12.42	121.17	6.79	NA	Gompertz
129_1	24.07	24.09	79.02	24.55	NA	Cubic
130_1	149.84	153.47	114.16	NA	NA	Logistic
131_1	135.51	138.88	NA	136.41	NA	Cubic
132_1	14.55	23.01	161.51	4.24	NA	Gompertz
133_1	9.85	7.68	181.07	3.48	NA	Gompertz
134_1	7.55	7.76	86.84	22.97	NA	Cubic
135_1	42.65	31.46	89.29	20.27	NA	Gompertz
136_1	35.46	23.48	90.52	26.8	NA	Quadratic
137_1	33.83	29.61	80.15	26.91	NA	Gompertz
139_1	35.26	24.33	101.96	15.66	NA	Gompertz
141_1	27.02	46.73	NA	NA	NA	Cubic
143_1	38.65	29.04	87.46	22.68	NA	Gompertz
144_1	44.55	31.79	74.37	NA	NA	Quadratic
145_1	36.13	34.59	97.61	NA	NA	Quadratic
146_1	54.34	62.8	39.1	NA	NA	Logistic
147_1	33.76	30.24	NA	5.89	NA	Gompertz
148_1	38.87	39.56	174.45	13.3	NA	Gompertz
149_1	23.53	22.71	51.24	12.21	NA	Gompertz
150_1	53.93	41.96	107.37	49.31	NA	Quadratic
152_1	33.77	33.63	NA	1.13	NA	Gompertz
153_1	114.87	118.62	NA	114.97	NA	Cubic
154_1	125.73	126.69	NA	NA	NA	Cubic
155_1	111.57	115.18	81.39	NA	NA	Logistic
156_1	20.2	18.82	162.28	2.92	NA	Gompertz
157_1	40.43	35.85	130.68	0.34	NA	Gompertz
158_1	4.37	1.38	113.82	12.38	NA	Quadratic
159_1	20.29	34.72	126.81	3.43	NA	Gompertz
160_1	31.72	25.45	183.22	23.75	NA	Gompertz
161_1	24.15	24.76	149.61	13.86	NA	Gompertz
162_1	5.64	14.27	NA	8.86	NA	Cubic
163_1	5.69	13.16	73.11	32.61	31.57	Cubic
164_1	4.56	2.38	64.6	NA	NA	Quadratic
165_1	56.82	64.25	58.94	NA	NA	Cubic
166_1	4.95	27.52	NA	NA	NA	Cubic
167_1	18.16	32.07	NA	NA	7.96	Baranyi
168_1	22.8	8.62	108.02	NA	NA	Quadratic
169_1	1.75	26.78	1.76	NA	11.88	Cubic
170_1	13.11	27.7	5.24	NA	30.09	Logistic
171_1	37.48	53.34	3.96	NA	17.74	Logistic
172_1	42.14	56.64	3.83	NA	20.93	Logistic
173_1	48.05	55.5	91.8	NA	NA	Cubic
174_1	40.48	50.58	5.87	NA	NA	Logistic
175_1	63.88	70.37	3.12	NA	NA	Logistic
176_1	61.36	75.49	2.29	NA	NA	Logistic
177_1	46.5	63.78	16.08	NA	NA	Logistic
178_1	58.2	71.58	1.25	NA	82.42	Logistic
179_1	54.47	68.19	11.65	NA	20.91	Logistic
180_1	31.98	53.32	69.56	NA	NA	Cubic
181_1	30.77	44.26	119.65	NA	NA	Cubic
182_1	23.06	42.6	119.76	NA	NA	Cubic
183_1	39.17	47.83	48.69	NA	NA	Cubic
184_1	46.78	57.18	34.82	NA	NA	Logistic
185_1	21.52	23.63	41.62	NA	NA	Cubic
186_1	20.01	24.11	24.36	NA	NA	Cubic
187_1	30.27	31.88	21.1	NA	NA	Logistic
188_1	27.5	34.09	67.02	NA	NA	Cubic
189_1	41.8	44.05	78.74	NA	NA	Cubic
190_1	27.16	28.13	46.35	NA	NA	Cubic

191_1	30.44	34.88	27.48	NA	NA	Logistic
192_1	32.61	37.38	3.02	NA	NA	Logistic
193_1	42.86	47.96	13.66	4.65	NA	Gompertz
194_1	39.41	43.25	31.73	NA	NA	Logistic
195_1	0.41	16.68	NA	NA	61.94	Cubic
196_1	46.55	46.64	62.11	NA	NA	Cubic
197_1	44.72	45.48	37.04	NA	NA	Logistic
198_1	40.83	49.07	8.31	6.27	NA	Gompertz
199_1	16.92	21.06	12.78	NA	11.18	Baranyi
200_1	30.46	30.95	11.85	NA	23.54	Logistic
201_1	42.85	39	45.13	22.42	NA	Gompertz
202_1	22.86	27.87	39.38	11.32	NA	Gompertz
203_1	22.21	26.3	15.78	NA	NA	Logistic
204_1	23.77	29.88	65.94	NA	NA	Cubic
205_1	17.92	20.52	49	NA	NA	Cubic
206_1	14.84	26.66	66.05	NA	NA	Cubic
207_1	30.17	33.04	45.46	NA	NA	Cubic
208_1	37.72	40.39	25.87	NA	NA	Logistic
209_1	37	40.99	11.05	NA	NA	Logistic
21_1	32.55	38.11	179.03	28.6	NA	Gompertz
210_1	75.36	74.72	23.9	NA	NA	Logistic
211_1	46.17	49.27	25.18	NA	NA	Logistic
212_1	36.4	35.47	23.35	NA	NA	Logistic
213_1	43.42	49.07	76.51	NA	NA	Cubic
214_1	42.68	47.96	0.61	NA	NA	Logistic
215_1	63.39	66.58	28.95	NA	NA	Logistic
216_1	53.64	55.94	17.21	NA	63.07	Logistic
217_1	48.17	48.28	14.76	NA	NA	Logistic
218_1	62.73	62.79	19.78	NA	NA	Logistic
219_1	52.26	51.48	14.66	NA	NA	Logistic
22_1	31.48	31.03	140.18	12.67	NA	Gompertz
220_1	61.56	65.47	9.69	NA	NA	Logistic
221_1	48.91	55.3	9.66	NA	NA	Logistic
222_1	44.19	48.03	1.33	NA	NA	Logistic
223_1	32.91	37.43	11.33	NA	NA	Logistic
224_1	39.16	43.66	103.16	NA	NA	Cubic
225_1	27.01	31.78	24.99	NA	NA	Logistic
226_1	34.95	39.24	71.05	NA	NA	Cubic
227_1	22.04	28.64	70.65	NA	NA	Cubic
228_1	20.07	28.96	26.99	NA	NA	Cubic
229_1	59.27	60.32	236.66	57.64	15.83	Baranyi
23_1	26.35	20.05	202.4	27.09	NA	Quadratic
230_1	59.05	39.01	138.9	NA	NA	Quadratic
231_1	43.53	16.92	140.77	NA	NA	Quadratic
232_1	62.95	59.94	252.66	NA	62.72	Quadratic
233_1	51.28	45.16	86.32	52.21	NA	Quadratic
234_1	38.06	5.32	169.06	NA	22.64	Quadratic
235_1	64.13	27.04	172.51	NA	87.83	Quadratic
236_1	63.63	44.09	189.11	NA	47.3	Quadratic
237_1	14.4	11.77	231.65	NA	32.67	Quadratic
238_1	44.23	45.03	245.01	NA	58.45	Cubic
239_1	4.1	17.57	38.6	NA	NA	Cubic
24_1	21.15	15.1	120.99	18.16	NA	Quadratic
240_1	43.02	0.52	155.39	NA	NA	Quadratic
241_1	17.09	15.6	233.58	NA	NA	Quadratic
242_1	4.28	45.54	142.27	NA	62.24	Cubic
243_1	31.06	54.94	22.97	NA	71.73	Logistic
244_1	8.89	46.17	13.12	NA	8.48	Baranyi
245_1	7.01	5.79	253.35	8.36	4.2	Baranyi
246_1	24.9	26.89	53.88	NA	40.75	Cubic

247_1	33.54	0.92	184.4	NA	75.98	Quadratic
248_1	31.58	22.16	216.62	31.12	29.8	Quadratic
249_1	41.25	17.45	62.82	NA	NA	Quadratic
25_1	30.46	31.44	88.53	21.17	NA	Gompertz
250_1	52.77	12.27	81.04	NA	61.86	Quadratic
253_1	22.69	22.07	95.91	30.8	NA	Quadratic
26_1	24.24	22.07	92.7	30.27	NA	Quadratic
27_1	24.35	18.39	191.85	17.06	NA	Gompertz
28_1	12.38	6.11	127.03	12.35	NA	Quadratic
29_1	25.4	34.87	NA	29.48	NA	Cubic
30_1	34.85	38.44	NA	22.08	NA	Gompertz
31_1	30.41	34.58	148.97	24.63	NA	Gompertz
32_1	34.6	29.35	60.91	12.2	43.61	Gompertz
33_1	5.35	31.17	64.43	16.31	NA	Cubic
34_1	21.89	22.79	NA	24.48	NA	Cubic
35_1	35.25	30	NA	30.15	NA	Quadratic
36_1	20.47	12.29	NA	20.11	NA	Quadratic
41_1	27.06	43.54	NA	25.78	NA	Gompertz
42_1	23.64	45.4	157.57	22.41	NA	Gompertz
43_1	26.34	40.97	138.51	3.93	NA	Gompertz
44_1	10.1	32.44	113.51	2.2	NA	Gompertz
45_1	21.88	28.37	228.59	0.79	NA	Gompertz
45_2	33.6	32.48	NA	NA	NA	Quadratic
45_3	23.16	26.61	249.56	NA	NA	Cubic
45_4	31.57	33.84	NA	NA	NA	Cubic
45_5	18.49	26.92	237.65	NA	NA	Cubic
46_1	28.19	24.88	255.23	NA	NA	Quadratic
46_2	25.98	22.07	242.04	NA	NA	Quadratic
46_3	25.81	21.93	251.83	NA	NA	Quadratic
46_4	27.16	25.43	271.95	NA	NA	Quadratic
46_5	24.92	22.56	228.21	NA	NA	Quadratic
47_1	46.02	39.63	203.29	NA	NA	Quadratic
47_2	50.43	44.96	NA	NA	NA	Quadratic
47_3	46.67	40.93	212.51	40.73	NA	Gompertz
47_4	46.51	42.27	NA	37	NA	Gompertz
47_5	37.13	35.48	227.88	32.71	NA	Gompertz
48_1	44.67	39.36	201.61	36.67	NA	Gompertz
48_2	44.4	38.29	209.37	37.64	NA	Gompertz
48_3	30	25.04	207.94	23.64	NA	Gompertz
48_4	46.88	39.65	214.3	46.22	NA	Quadratic
48_5	37.9	19.24	183.9	30.91	NA	Quadratic
49_1	35.61	29.06	194.85	29.9	NA	Quadratic
49_2	10.17	14.49	194.77	9.72	NA	Gompertz
49_3	31.89	26.54	216.49	24.46	NA	Gompertz
49_4	40.03	32.75	206.98	32.08	NA	Gompertz
49_5	43.91	37.64	208.92	NA	NA	Quadratic
50_1	36.14	50.32	600.39	44.91	NA	Cubic
51_1	41.66	35.45	497.44	37.96	NA	Quadratic
52_1	38.62	34.5	560.56	39.08	NA	Quadratic
53_1	37.48	50.64	757.55	43.92	NA	Cubic
54_1	24.9	29.82	572.74	12.39	NA	Gompertz
55_1	30.97	28.4	NA	27.88	NA	Gompertz
56_1	35.37	40.73	663.92	38.85	NA	Cubic
57_1	39.67	35.07	492.92	36.08	NA	Quadratic
58_1	35.65	31.43	607.7	30.37	NA	Gompertz
59_1	29.64	34.91	574.01	33.13	NA	Cubic
60_1	26.1	23.02	NA	24.05	NA	Quadratic
61_1	29.3	30.18	531.04	25.89	NA	Gompertz
62_1	37.32	33.46	177.89	31.92	NA	Gompertz
63_1	16.9	6.89	132.03	16.06	NA	Quadratic

64_1	22.78	15.17	132.01	18.52	NA	Quadratic
65_1	34.17	32.29	660.91	21.7	NA	Gompertz
66_1	5.41	5.75	712.16	0.85	NA	Gompertz
67_1	257.94	268.54	2417.54	244.5	NA	Gompertz
68_1	132.01	129.84	1615.36	91.49	NA	Gompertz
69_1	99.27	109.51	1915.86	40.35	NA	Gompertz
7_1	14.73	3.91	159.02	14.92	NA	Quadratic
70_1	132.92	152.49	1658.56	60.81	NA	Gompertz
8_1	33.77	30.26	197.01	23.65	NA	Gompertz
80_1	29.97	32.53	118.67	20.61	NA	Gompertz
81_1	31.54	31.72	137.28	16.43	NA	Gompertz
82_1	26.58	30.16	163.48	9.64	NA	Gompertz
83_1	26.91	34.95	131.86	12.59	NA	Gompertz
84_1	31.23	23.48	123.09	28.53	NA	Quadratic
85_1	21.42	31.63	NA	26.88	NA	Cubic
86_1	20.2	20.2	157.7	20.98	NA	Quadratic
87_1	35.89	26.63	108.63	29.26	NA	Quadratic
88_1	16.43	30.82	85.24	12.78	NA	Gompertz
89_1	16.8	26.11	84.9	3.09	NA	Gompertz
90_1	36.69	29.8	120.77	17.92	NA	Gompertz
91_1	13.07	19.49	50.48	17.4	NA	Cubic
92_1	32.43	21.29	80.77	37.23	NA	Quadratic
93_1	34.39	24.7	NA	37.74	NA	Quadratic
94_1	22.29	18.9	111.92	16.17	NA	Gompertz
95_1	23.4	23.55	NA	19.72	NA	Gompertz
99_1	45.5	32.91	82.62	36.73	NA	Quadratic