Dependence of bacterial growth rate on dynamic temperature changes

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Abstract: Temperature is an important determinant of bacterial growth. While the dependence of bacterial growth on different temperatures has been well studied for many bacterial species, prediction of bacterial growth rate for dynamic temperature changes is relatively unclear. Here, the authors address this issue using a combination of experimental measurements of the growth, at the resolution of 5 min, of *Escherichia coli* and mathematical models. They measure growth curves at different temperatures and estimate model parameters to predict bacterial growth profiles subject to dynamic temperature changes. They compared these predicted growth profiles for various step-like temperature changes with experimental measurements using the coefficient of determination and mean square error and based on this comparison, ranked the different growth models, finding that the generalised logistic growth model gave the smallest error. They note that as the maximum specific growth increases the duration of this growth predominantly decreases. These results provide a basis to compute the dependence of the growth rate parameter in biomolecular circuits on dynamic temperatures and may be useful for designing biomolecular circuits that are robust to temperature.

1 Introduction

Environmental conditions affect almost all physical and biological processes. Ensuring robustness in performance during varying environmental conditions can be an important requirement in these processes. An example of this is robustness of oscillation period to temperature in designed circuits such as synthetic gene oscillators [1, 2]. Failing to respond to non-optimal temperature can cause cell death [3] as well as alter functional properties of biomolecular systems [4]. For this reason, to achieve desired performance of a synthetic circuit outside laboratory controlled environment, it is important to design temperature robustness. The performance of these designed gene circuits is largely affected by growth rate of the host organism such as bacteria [5–7]. Thus, bacterial growth rate is an important parameter and it is necessary to understand how this parameter depends on temperature. This can provide us important insight regarding role of temperature in these processes as well as can help design techniques to enhance robustness to temperature variations. In general from a mechanistic point of view how temperature dependence of different rates in a biomolecular system effect the final output is unclear [8]. However, phenomenological models have been used extensively in the context of food microbiology to predict bacterial growth when the temperature is fixed or changing [9–11].

Logistic growth models and its variants such as Richards model, the Gompertz model are widely used in describing bacterial growth [12]. In the classical logistic model the instantaneous population growth rate is proportional to both instantaneous population size and resource availability. Based on this, a generalised logistic growth model has been proposed where both instantaneous population size and resource availability can have scaling factors other than unity [13, 14]. The classical logistic model has also been updated in various articles, most notably by adding an additional multiplicative term representing the 'physiological state' of growth [15] or adding a multiplicative term representing very low rate of growth during lag phase [16]. Apart from logistic models, growth of bacterial culture has also been modelled by Monod relating population growth with concentration of nutrient [17]. All these models, often termed as primary models, are nonlinear in nature and have various parameters such as maximum specific growth rate, carrying capacity and lag time

which may depend on environmental conditions such as temperature.

The maximum specific growth rate of bacteria has claimed to be related to temperature according to Arrhenius equation and this relation has been studied in case of thermophilic *Bacillus* [18]. Ratkowsky *et al.* [19] proposed a square root law of temperature dependence of bacterial growth rate for temperature up to optimal temperature of growth and later modified this rule for the entire biokinetic temperature range [20]. Temperature dependence of these parameters has been compared using different models based on Arrhenius or square root law and especially the modified Ratkowsky model was found to be best for modelling temperature dependence of growth rate [21]. Ratkowsky and Arrhenius models are algebraic in nature and generally termed as secondary models. These secondary models of growth rate are used to predict bacterial growth when temperature is varying dynamically [22–24]. While temperature dependence of the parameter maximum specific growth rate has been much studied in literature, characterising the temperature dependence of other parameters in growth models should also be important. It has been proposed that the primary differential equation models can also be used as dynamic growth models when the temperature is changing, by replacing the constant model parameters as temperature-dependent parameters determined from fixed temperature experiments [25]. Additionally, there may also be trade-offs in bacterial growth profile occurring due to variation in temperature [26].

There are at least three interesting aspects of predicting a temperature dependent bacterial growth profile. One, it is possible to model bacterial growth using various standard models, but they may have different predictive capabilities when temperature changes. Two, effect of temperature changes can be different on various growth model parameters. Three, there may exist trade-offs in bacterial growth while the temperature is changing. Given these, prediction of bacterial growth subject to dynamic temperature changes is important to understand.

Here, we aim to predict bacterial growth curve for different temperature variations (Fig. 1). For this, we experimentally measured growth curves of *E. coli* MG1655 in the temperature range $29-37°C$, a typical choice of organism and temperature range in the context of biomolecular circuit design, and used standard mathematical models of growth such as the logistic
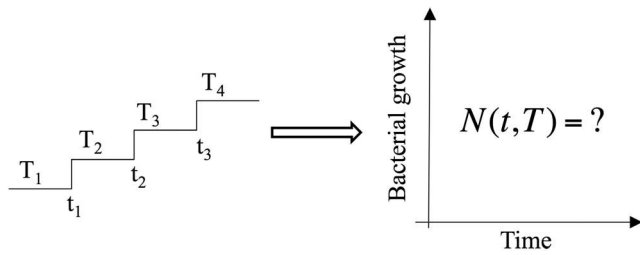
Fig. 1 *How to predict bacterial growth profile while temperature is varying with time ?*

Table 1 Mean of coefficient of variation for bacterial growth data recorded in the temperature range $29 - 37°C$ in LB media

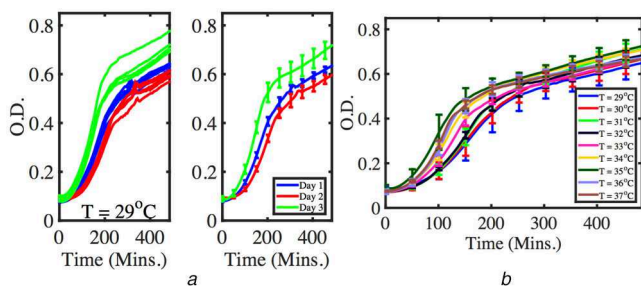| Temperature, °C	Day 1, %	Day 2, %	Day 3, %	Mean
29	3.8	4.5	7.5	5.3
30	2.6	1.8	1.6	2
31	4.5	2.7	1.9	3
32	3.6	2.6	2.5	2.9
33	1.6	2.5	2	2
34	3.7	4.6	1.4	3.2
35	5.9	1.1	3.3	3.4
36	5.4	6.9	5.7	5.6
37	2.3	1.2	2.4	2

Fig. 2 *Bacterial growth for E. coli MG1655 for different temperatures in LB media*

(a) Bacterial growth at 29°C in five different wells repeated for three days, *(b)* Mean bacterial growth with daily variation in the temperature range from $29 - 37°C$

growth model (also called Verhulst–Pearl model [27]) and its variants such as Richards model [28], Gompertz model [29], a generalised logistic growth model [13] and Monod's bacterial growth model [17]. We fit the growth curves to these models for each temperature to estimate the corresponding parameters finding that all models give a good fit to the data based on the coefficient of determination (R^2) and mean square error (MSE) in estimation with the generalised logistic growth model giving the best fit. Based on these parameter estimates, we predict the bacterial growth curve for dynamic temperature changes and experimentally verify the predictions, finding a good fit when the temperature is in the exponential phase of the bacterial growth. We note how the maximum growth rate increased with temperature in the temperature range considered, and was accompanied by a decrease in the duration of time for which the growth rate was near this maximum. These results should help investigation of temperature robustness in biomolecular circuit design and may help in analysing the dependence of bacterial growth to temperature that is important in the industry of food processing.

2 Methods

E. coli MG1655 is used in this study as it is the typical organism of choice for biomolecular circuit design. The growth rate was estimated using its optical density at 600 nm. The strain was grown overnight in Luria Bertrani (LB) media (HiMedia) at 37°C and subsequently diluted 1:50 in the same media. Effect of temperature

on bacterial growth rate in minimal media is briefly discussed and compared with LB media in Appendix 10.3. Measurements were performed in 96 well sterile tissue culture plates (Tarsons) and at different temperatures. A total of 200μl of the diluted culture was placed in a well and five such wells were measured. Measurements were taken in a platereader (Biotek Synergy H1) with double orbital shaking at 282 cpm for a total of 8 h at 5 min intervals. A well using just LB media was used to estimate background and this was subtracted from each measurement. The temperatures considered were 29, 30, 31, 32, 33, 34, 35, 36, and 37°C. The process was repeated for three separate days for each temperature. The data were analysed in MATLAB. In particular, the MATLAB nonlinear least square solver *lsqcurvefit* was used to estimate parameters.

To analyse the statistical variability, the percentage of variation in 5 well measurements for each day and temperature are calculated by the mean of the coefficient of variation (standard deviation/mean) for each time point and found to be at most 7.5% (Table 1). Possible biases in bacterial growth experiments in plates include edge effects which are thought to be minimised in Biotek Synergy H1 microplate reader because it has both top and bottom heaters. Batch effects are minimised by doing the experiment from the same strain of *E. coli* MG1655 in similar ambient conditions in same laboratory and the medium used (LB) is manufactured in the same batch by HiMedia.

3 Estimation of growth parameters and their temperature dependence

We experimentally measure the growth curves of *E. coli* MG1655 in the temperature range $29 - 37°C$ in 1°C increments (Fig. 2, described in Section 2 on Methods). These data were fit to the standard growth models such as the Verhulst–Pearl model, Richards model, Gompertz model, a generalised logistic growth model, and Monod's bacterial growth model. The equations for these models are shown in Appendix 10.1. We used nonlinear least squares to estimate the parameters at each temperature. These are plotted in Fig. 3. For the Verhulst–Pearl model, Richards model, and the Gompertz model, the integrated form is used for parameter estimation. For the generalised logistic growth model and Monod's model, as no explicit solution available, the solution is numerically integrated and used for parameter estimation.

We observe that all models give a high goodness of fit based on the coefficient of determination, R^2 ($R^2 > 0.95$, Table 2, defined in Appendix 10.2). The generalised logistic growth model gives the best fit (lowest MSE and highest R^2, Table 2) possibly because all other logistic models can be a special case of this model. We observe that the parameter representing maximum specific growth rate (r) increases with increasing temperature (Fig. 3*b*) for all the models used and the parameter signifying carrying capacity (K) remains almost constant to this temperature range (Fig. 3*c*). Other parameters have an increasing or decreasing dependence on temperature (Fig. 3*d*).

4 Prediction of bacterial growth for temperature changes

To understand the predictive capability of these models, here we used them to predict growth curves when the temperature changes with time. For this, we simulated the models with parameters estimated above in such a way that the parameters at a specific time duration corresponded to the temperature at that time duration. This is similar to the previous ways of predicting growth, when temperature changes that were used in other contexts [22, 30, 31]. We performed this procedure for various step changes in temperature as well as for a staircase variation in temperature. To test these predictions, we performed experiments where the growing bacteria were subjected to temperature changes as in the simulations.

We first compared the predicted growth for a step change in temperature using two sets of parameter with the growth predicted with one parameter set corresponding only to the initial temperature (Fig. 4). We find that the predicted growth profile is
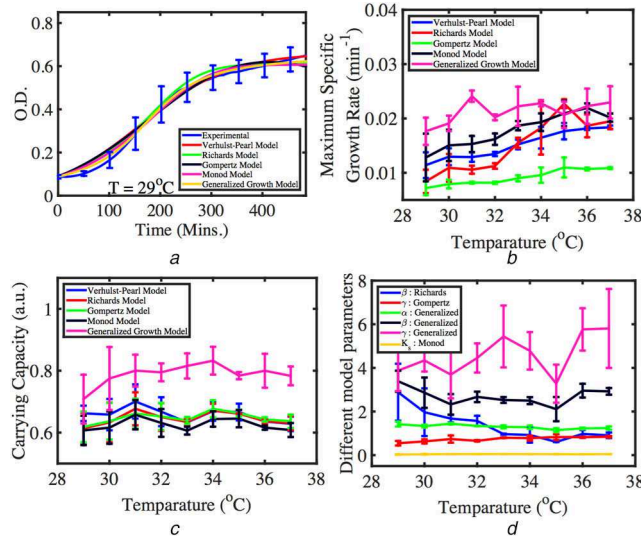
Fig. 3 *Different models for bacterial growth fitted to data*
(a) Comparison of different growth models fitted to experimental bacterial growth data at 29°C, *(b)* Estimated maximum specific growth rate for different models at individual temperatures, *(c)* Estimated carrying capacity for different models at individual temperatures, *(d)* Estimated values of different model parameters other than the maximum specific growth rate and carrying capacity at individual temperatures

Table 2 Mean of coefficient of determination (R^2) and MSE between experimental data and different growth models at individual temperatures

| Temperature, °C	Verhulst–Pearl		Richard		Gompertz		Generalised logistic		Monod	
	R^2	MSE	R^2	MSE	R^2	MSE	R^2	MSE	R^2	MSE
29	0.980	0.0276	0.987	0.0225	0.978	0.0290	0.994	0.0147	0.983	0.0240
30	0.987	0.0232	0.990	0.0201	0.983	0.0264	0.996	0.0125	0.987	0.0227
31	0.987	0.0254	0.988	0.0237	0.965	0.0393	0.995	0.0154	0.985	0.0259
32	0.988	0.0235	0.989	0.0221	0.983	0.0275	0.995	0.0139	0.986	0.0241
33	0.985	0.0241	0.985	0.0241	0.981	0.0272	0.993	0.0160	0.978	0.0281
34	0.985	0.0254	0.985	0.0250	0.982	0.0282	0.993	0.0161	0.977	0.0303
35	0.973	0.0314	0.978	0.0289	0.978	0.0289	0.985	0.0224	0.957	0.0387
36	0.984	0.0245	0.985	0.0244	0.980	0.0278	0.994	0.0148	0.976	0.0294
37	0.983	0.0248	0.983	0.0247	0.979	0.0277	0.993	0.0153	0.974	0.0299
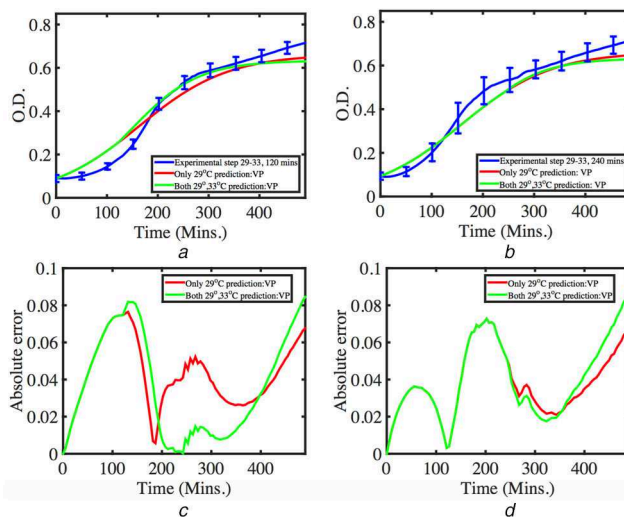
Fig. 4 *Predicted bacterial growth with and without using two sets of parameters of Verhulst–Pearl model for a step change in temperature. Blue line represents experimental growth with daily variation, red line signifies prediction with model parameters corresponding to lower temperature only and green line represents prediction using model parameters corresponding to both lower and upper temperature before and after application of step for*
(a) Step change in temperature from $29 - 33$°C at 120 min, *(b)* Step change in temperature from $29 - 33$°C at 240 min, *(c)* Absolute error in prediction when step is applied at 120 min, *(d)* Absolute error when step is applied at 240 min

closer to experimental one while using two sets of parameters for prediction when the step change is applied at *t*=120 min (Fig. 4*a*). When step change is applied at *t*=240 min, these two predictions are not significantly different (Fig. 4*b*), perhaps because at this time, bacterial growth is in the saturation region. The absolute error in prediction ($|x_i - \hat{x}_i|$) in both the cases (Figs. 4*c* and *d*) shows that the prediction using two sets of parameters is effective when step is applied at 120 min, during the exponential phase.
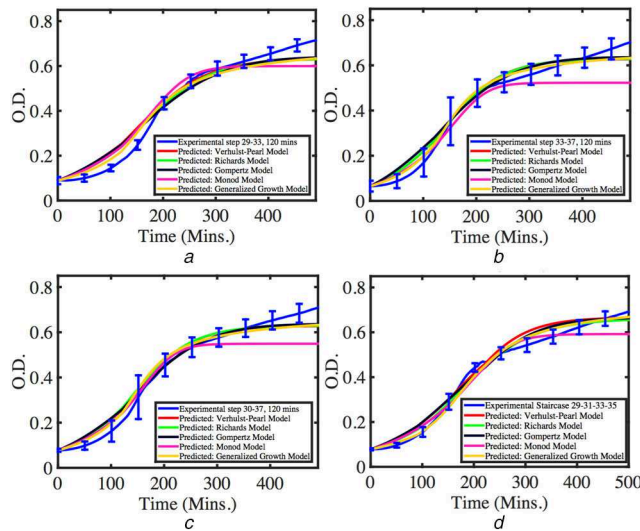
Fig. 5 *Predicted bacterial growth for dynamic variation in temperature*
(a) Experimental and predicted bacterial growth using different models when a step change from $29 - 33°C$ in temperature is applied at 120 min, *(b)* Experimental and predicted bacterial growth using different models when a step change from $33 - 37°C$ in temperature is applied at 120 min, *(c)* Experimental and predicted bacterial growth using different models when a step change from $30 - 37°C$ in temperature is applied at 120 min, *(d)* Experimental and predicted bacterial growth using different models when temperature is varied in a staircase fashion from $29 - 31 - 33 - 35°C$ at 90, 150 and 210 min, respectively

Table 3 Mean of coefficient of determination (R^2) and MSE between experimental and predicted bacterial growth profiles for different growth models subjected to dynamic temperature variation

Step/staircase, °C	Verhulst–Pearl		Richard		Gompertz		Generalised logistic		Monod	
	R^2	MSE	R^2	MSE	R^2	MSE	R^2	MSE	R^2	MSE
29–33	0.959	0.046	0.966	0.041	0.962	0.044	0.970	0.039	0.949	0.048
33–37	0.975	0.034	0.975	0.033	0.973	0.035	0.985	0.026	0.883	0.079
30–37	0.972	0.036	0.970	0.037	0.976	0.033	0.976	0.033	0.910	0.071
29–31–33–35	0.972	0.035	0.987	0.024	0.978	0.03	0.988	0.023	0.966	0.038

Table 4 Empirical model for temperature variation in the parameters r (maximum specific growth rate), β and γ of generalised logistic growth model with R^2 and MSE goodness of fit metrics. Parameters $K = 0.8$ and $\alpha = 1.294$ are constant

Parameter	p_1	p_2	p_3	R^2	MSE
r	−0.0001	0.0072	−0.1074	0.884	0.001
β	0.0406	−2.676	46.6	0.852	0.136
γ	0.0544	−3.363	56.26	0.992	0.099

Next, we measured the growth curves for a step change in temperature from 29 to 33°C (Fig. 5*a*), from 33 to 37°C (Fig. 5*b*), and from 30 to 37°C (Fig. 5*c*), for steps applied at 120 min as well as for a temperature change applied in a staircase fashion from 29 to 31°C to 33 to 35°C with steps applied at 90, 150, and 210 min, respectively (Fig. 5*d*). We compared these to the mathematical predictions. We found that the coefficient of determination between the computational prediction and experimental measurement is high (≥ 0.95, Table 3) except two cases using Monod's model. The MSE in estimation is the lowest for the generalised logistic growth model in the case of changing as well (Table 3).

We conclude that this approach provides good predictive results to investigate the temperature dependence of growth rate in these contexts.

5 Empirical model of parameter variation with temperature

To predict bacterial growth subject to dynamic temperature variations, it is convenient to model parameter variations as function of temperature as suggested in [25]. For this, we can formulate empirical models from the parameter estimates obtained in Section 3. To illustrate this, we choose parameter estimates of the generalised logistic growth model at 30, 32, 34 and 36°C to be known. The parameters K (carrying capacity) and α remain almost constant when the temperature varies and are set to the mean

estimate at 30, 32, 34 and 36°C, that is 0.8 and 1.294, respectively. To obtain an empirical model for the rest of the parameters we fit a quadratic polynomial ($f(T) = p_1 T^2 + p_2 T + p_3$) to the known estimates for each parameter using MATLAB *fit* command (Table 4). We note that the quadratic polynomial model assumed in this case is purely empirical and a similar square-root model was proposed by Ratkowsky *et al.* to model variations in maximum specific growth rate with temperature [19]. Alternatively, Arrhenius equation gives the temperature dependence of chemical reaction rates and reaction rate has been replaced in this equation by bacterial growth rate to find its temperature dependence in various literature. This assumption has drawn criticism because bacterial growth involves several enzymes and substrates and a single rate determining equation may not be correct [19]. In our case the Arrhenius equation for temperature dependence of growth rate ($r = Ae^{-(E/RT)}$) has a poorer fit ($R^2 = 0.770$) compared to this empirical quadratic polynomial model ($R^2 = 0.884$, Table 4).

Next, we verify the predictive capability of these secondary empirical models by comparing the prediction with measured growth curves for a step change in temperature from 29 to 33°C (Fig. 6), from 33 to 37°C (Fig. 6*b*), and from 30 to 37°C (Fig. 6), for steps applied at 120 min as well as for a temperature change applied in a staircase fashion from 29 to 31°C, from 31 to 33°C, and from 33 to 35°C with steps applied at 90, 150, and 210 min, respectively (Fig. 6*d*). For this, we solve the differential equation of generalised logistic growth model (Appendix 10.1) replacing the
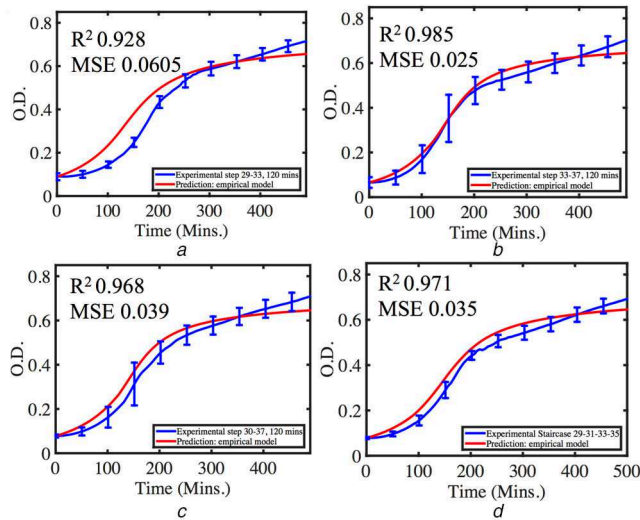
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Fig. 6 *Predicted bacterial growth using empirical models of parameter variations with temperature. Experimental and predicted bacterial growth when a step change from*

(a) $29 - 33°C$ in temperature is applied at 120 min, *(b)* from $33 - 37°C$ in temperature is applied at 120 min, *(c)* from $30 - 37°C$ in temperature is applied at 120 min and, *(d)* When temperature is varied in a staircase fashion from $29 - 31 - 33 - 35°C$ at 90, 150 and 210 min, respectively
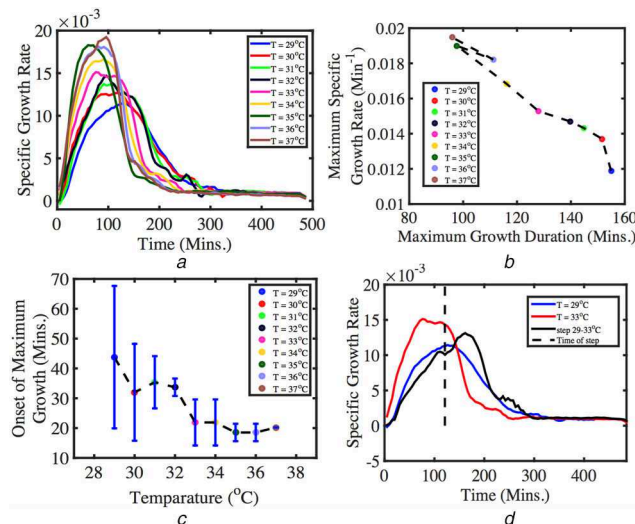

Fig. 7 *Trade-off between maximum specific growth rate and duration of maximum growth*
(a) Specific growth rate curves in the temperature range from 29 to 37°C. Growth rate is calculated from the mean of first difference of growth data and smoothened using MATLAB *smooth* function, *(b)* Maximum specific growth rate and duration of maximum growth in the temperature range, *(c)* Time required to reach 50% of maximum growth for the first time as temperature is varied, *(d)* Change in the specific growth rate curve as step temperature is applied from 29 to 33°C at 120 min

constant parameters with these empirical models. We find that the predicted bacterial growth matches well with experimental growth curves with $R^2 > 0.92$.

6 Trade-off in bacterial growth

Trade-off mechanisms in bacteria are important to understand their diversity and competition [26]. Here, using the temporal data measured, we investigate possible trade-off in bacterial growth when temperature is varied which may arise due to fixed resources. For this, we compute specific growth rate curves for each temperature from first difference of experimental measurements, $(x_{i+1} - x_i)/x_i \Delta t$, where x_i is the bacterial growth measured at ith instant and Δt is the interval between two successive measurements. These curves are found to be pulse-shaped (Fig. 7*a*). The height and width of these pulse-shaped curves signify the maximum specific growth rate and duration of maximum growth, respectively. The duration of maximum growth is defined as the time required to reach maximum growth rate from 50% of maximum growth rate and then again fall to 50%. We find that the maximum specific growth rate increases with temperature whereas the duration of maximum growth decreases (Fig. 7*b*). Additionally, the time to reach 50% of maximum growth rate for

the first time has a decreasing trend as temperature increases (Fig. 7*c*). This observation is similar to the conjecture of Baranyi and Roberts [15] that the maximum specific growth rate and lag time is inversely proportional. In case of dynamic temperature variation, such as in applying a step change in temperature, maximum specific growth rate increases with corresponding decrease in duration for maximum growth (Fig. 7*d*, Table 5).

7 Discussion

As the growth rate is an important parameter in the functioning of natural and designed biomolecular circuits, investigating its dependence on temperature is an important problem in designing and assessing temperature robustness in biomolecular circuits. Bacterial growth rate is closely related to the performance of these synthetic constructs, and characterising dependence of bacterial growth rate on dynamic temperature changes is a first step towards this goal. Here, we use, experimental measurements of growth of *E. coli* MG1655 taken in temperature range $29 - 37°C$, a typical choice of organism and temperature range in such contexts, and a set of existing models of growth rate – Verhulst–Pearl model, Richards model, Gompertz model, a generalised growth model, Monod's bacterial growth model – to present three main results.

Table 5 Mean of maximum specific growth rate and duration of maximum growth computed from experimental measurements for constant and step change in temperature at 120 min

Temperature, °C (Constant or step change)	Maximum specific growth rate, min^{-1}	Duration of maximum growth, min
29	0.0119	154.93
30	0.0137	151.56
33	0.0153	127.98
37	0.0195	95.99
29–33	0.0131	133.88
33–37	0.0170	121.25
30–37	0.0159	116.20

First, we extract parameters from these models using the experimental data at different temperatures. Secondly, we use these parameters to predict the growth curve of bacteria subject to different temperature changes and verify the prediction experimentally, finding that all models give reasonably good results, with the generalised model being the best among those for the observed data. Thirdly, we note that the increase in maximum growth rate as temperature is increased in the range $29 - 37°C$ is simultaneous with a decrease in the duration for which this maximum growth rate persists.

The model-based prediction has proven to be beneficial for most dynamical systems and the dependence of these models on environmental factors is important to understand. Here, we have studied temperature dependence of different growth models and used this a priori information to predict bacterial growth profiles subjected to arbitrary temperature variations. This framework should help in prediction of growth while there is dynamic temperature variations.

8 Acknowledgments

9 References

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10 Appendix

10.1 Growth models

Different logistic [13] and bacterial growth models used are

(i) Verhulst–Pearl model:

$$\dot{N}(t) = rN(t)\left[1 - \frac{N(t)}{K}\right],$$
$$\Rightarrow N(t) = \frac{N(0)K}{N(0) + (K - N(0))\exp(-rt)}. \tag{1}$$

(ii) Richards model:

$$\dot{N}(t) = rN(t)\left[1 - \left(\frac{N(t)}{K}\right)^{\beta}\right],$$
$$\Rightarrow N(t) = \frac{N(0)K}{[N(0)^{\beta} + (K^{\beta} - N(0)^{\beta})\exp(-\beta rt)]^{1/\beta}}. \tag{2}$$

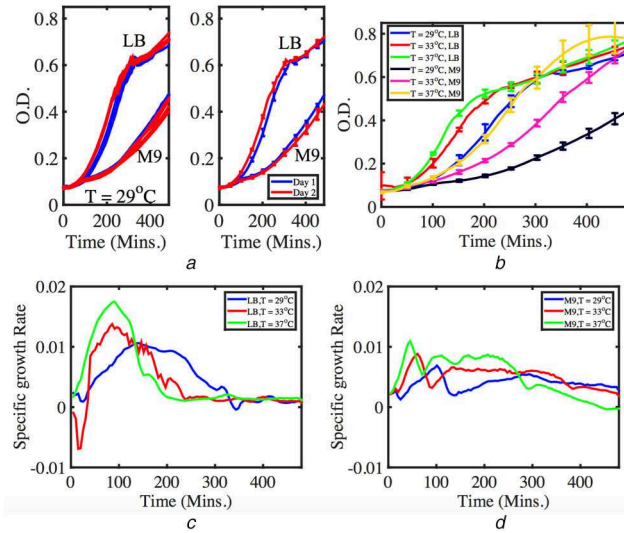*IET Syst. Biol.*, 2020, Vol. 14 Iss. 2, pp. 68-74

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Fig. 8 *Bacterial growth for E. coli MG1655 for different temperatures in LB media and M9 minimal media*
(a) Bacterial growth at 29°C in five different wells repeated for two days, *(b)* Mean bacterial growth with daily variation at 29, 33, and 37°C. Specific growth rate curves at 29, 33, and 37°C. Growth rate is calculated from the first difference of mean growth data and smoothened using MATLAB *smooth* function for *(c)* LB media, *(d)* M9 minimal media

(iii) Gompertz model:

$$\dot{N}(t) = rN(t)\left[\log\left(\frac{K}{N(t)}\right)\right]^{\gamma},$$

$$\Rightarrow N(t) = K\exp\left[-\left\{(\gamma-1)rt + \left[\ln\left(\frac{K}{N(0)}\right)\right]^{1-\gamma}\right\}^{1/(1-\gamma)}\right]. \tag{3}$$

(iv) Generalised logistic growth model:

$$\dot{N}(t) = rN(t)^{\alpha}\left[1 - \left(\frac{N(t)}{K}\right)^{\beta}\right]^{\gamma}, \tag{4}$$

(v) Monod's bacterial growth model:

$$\dot{N}(t) = N(t)\frac{rS(t)}{K_s + S(t)},$$

$$\dot{S}(t) = -\frac{1}{\Gamma}\frac{dN(t)}{dt}. \tag{5}$$

Here, $N(t)$ is the population concentration at time t, the parameters r and K are maximum specific growth rate and carrying capacity, respectively. In the Monod's model, $S(t)$ is the nutrient concentration at time t. The carrying capacity in Monod's model is given by $K = \Gamma S_0 + N_0$, where S_0 and N_0 are initial concentrations for the nutrient and bacterial population, respectively.

10.2 Coefficient of determination (R^2) and MSE

Coefficient of determination: Let the data be a sequence of real numbers, x_i and the estimate is $\hat{x}_i$, $i = 1, 2, \ldots, n$. The mean of the observed data is, $\bar{x} = 1/n \sum_{i=1}^{n} x_i$. The coefficient of Determination (R^2) is defined as [32]

$$R^2 = 1 - \frac{RSS}{TSS}, \tag{6}$$

where the residual sum of squares, $RSS = \sum_{i=1}^{n}(x_i - \hat{x}_i)^2$ and total sum of squares, $TSS = \sum_{i=1}^{n}(x_i - \bar{x})^2$.

Mean square error: The MSE is defined as

$$MSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - \hat{x}_i)^2}. \tag{7}$$

10.3 Temperature dependence of bacterial growth in minimal media

The strain was grown overnight in LB media at 37°C and subsequently diluted 1:50 in M9 minimal media supplemented with 0.2% casamino acid, 0.4% glucose, 100 mM thiamine, 1 M MgSO$_4$, 1 M CaCl$_2$ and the growth measurements are taken at 29, 33, and 37°C and the same is repeated for two days. For comparison, the same culture is grown together in LB media as well (Figs. 8*a* and *b*). We find that the maximum specific growth rate obtained from the first difference of growth data is lower, and the duration of maximum growth is higher in minimal media as compared to LB media (Figs. 8*c* and *d*). The tradeoff between maximum specific growth rate and duration of maximum growth is similar. Effect of temperature is magnified compared to LB media in the sense that overall growth is slower.