­Predicting competition results from growth curves

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# Abstract

Because pairwise competition experiments are laborious and expansive, many investigators do without them and use proxies of fitness such as growth rates. Here we propose a new method to predict the results of competition experiments from single strain growth curves.

# Introduction

## Growth curves

Growth curves are commonly used to estimate fitness in microbiology, genetics, and evolutionary biology. Growth curves are acquired by measuring the optical density (OD) of one or more populations of cells over varying time periods. The simplest way to estimate fitness from these curves is to infer the growth rate during the exponential growth phase. This is done by taking the log of the mean of the growth curves during the exponential growth phase and using linear regression to estimate the slope of the curves as a measure of the growth rate (Hall et al. 2014). Growth rates can indeed be proxies of the *selection coefficient s* (Chevin 2011), which is the standard way of measuring relative fitness in population genetics (Crow and Kimura 1970). But in many cases there are other growth phases that affect the selection coefficient in addition to the exponential growth phase: a lag phase, a deceleration phase, and a stationary phase. Indeed, it has been recently shown that the growth rate can be a poor estimate of relative fitness (Concepción-Acevedo et al. 2015).

## Pairwise competition experiments

Pairwise competition experiments can be used to infer fitness in a way that accounts for all growth phases. In competition experiments two strains are grown together in the same vessel – the strain of interest and a reference strain (for example, a mutant strain and a wildtype strain). The frequency of each strain is measured during the experiment [for example, using flow cytometry (Gallet et al. 2012)]. From the change in frequencies during the competition experiment investigators can estimate the selection coefficient of the strain of interest (Wiser and Lenski 2015). This is a much better method to estimate relative fitness, as it directly estimates fitness from frequencies change over time, rather than indirectly estimating it from proxy measures such as growth rates. However, competition experiments are more laborious than growth curves experiments and are typically more expansive, requiring the construction and assaying of genetic or phenotypic markers (Concepción-Acevedo et al. 2015 and references therein). Therefore, many investigators do without them and use proxies of fitness such as growth rates.

## Predicting competition results from growth curves

Here we propose a new framework for fitness inference. We fit growth models to growth curves data and use the fitted growth models to predict the results of competitions experiments. The predicted competitions can then be used instead of empirical ones to infer selection coefficients.

We implemented our method using an open source Python package that can be freely used and extended; in the future we intend to develop a user friendly web site that will allow other investigators to analyze growth curves (http://curveball.yoavram.com).

# Methods

Our method includes three stages: (i) fitting growth models to the growth curves data, (ii) using the fitted models to predict the results of competition assays, and (iii) inferring selection from the predicted competition results.

## Growth model

Because we are interested in several growth phases – the lag phase, the exponential phase, the deceleration phase, and the stationary phase – we use an extension of the classic logistic model, the Baranyi-Roberts model (Baranyi and Roberts 1994; Baranyi 1997).

The Baranyi-Roberts model is defined by the following one-species ordinary differential equation [see eqs. 1c, 3a, and 5a in (Baranyi and Roberts 1994)]:

(1a)

(1b)

(1c)

where is the population density, is the per capita growth rate, is time, is the adjustment function (see below), is the maximum density, and is a deceleration parameter.

The term is used to describe the deceleration in the growth of the population as it nears the maximum density. When the deceleration parameter is one (), the deceleration is the same as in the classic logistic model and the density at the time of the maximum growth rate is half the maximum density, . When or the density at the time of the maximum growth rate is higher or lower than , respectively.

The adjustment function is used to describe the adjustment of the population to a new environment. Typically, microorganisms are grown in overnight culture and diluted into fresh media for the growth curves experiment. Therefore, populations that are adjusted to stationary phase must now adjust to growth, and this takes some time. This adjustment phase is usually called the *lag phase*. The specific adjustment function we use here was suggested by Baranyi and Roberts (1994) due to being both computationally convenient and having a biological meaning: is the initial amount of some molecule (nutrient, enzyme, etc.) that is required for growth; is the rate in which this molecule is accumulated in the cell.

The Baranyi-Roberts differential equation has a closed form solution:

(2a)

. (2b)

We use four forms of the Baranyi-Roberts model. The full model is described by eq. 2 and has six parameters. A five parameter form of the model has the deceleration parameter set to one, as in the classic logistic model. This form is useful because the reduced growth during the lag phase might sometimes be inferred as . A four parameter form of the model has no lag phase, with . This is also known as the Richards model or the generalized logistic model. This form of the model is useful in cases where there is no observed lag phase: either because the population adjusts very rapidly or because it is already adjusted prior to the growth experiment, usually by priming it in fresh media before the experiment. The fourth form is the classic logistic model, in which and .

## Model fitting and selection

We fit all four model forms to the mean growth curve of each strain using a least-squares procedure (Newville 2014). The standard deviation at each time point is used as weights for the least-squares procedure so that time points with lower variance are more heavily weighted and therefore better fitted.

We then calculate the Bayesian Information Criteria (BIC) of each model fit,

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where is the number of parameters of the model, is the number of time points , is the average density at time point , and is the expected density at time point according to the model. We select the model form with the lowest BIC.

As a sanity check, we also fit the data using a linear model () and check that the BIC of our selected model form is larger than the BIC of the linear model by at least 6 [See (Kass and Raftery 1995) for significance of BIC differences].

We repeat the model fitting procedure for the growth curves data of each strain to produce estimates for all six parameters as well as confidence intervals on these estimates.

## Competition prediction

We introduce the two-strain Baranyi-Roberts model, which, to the best of our knowledge, has not been used before:

(3a)

(3b)

(3c)

, (3d)

where is the value of parameter of strain which we get from the model fitting procedure. This equation system is then solved by numerical integration, resulting in a prediction of the competition dynamics.

This two-strain competition model explicitly assumes that all the interactions between the two strains can be attributed to *resource competition*. Therefore, all interactions are described by the deceleration of the growth rate of each strain in response to growth of the other strain. We do not however assume the same limiting resource or resource efficiency for both strains, as we use different maximum densities for each strain.

## Selection coefficient inference

Perhaps the most common method for estimating relative fitness or selection coefficients from pair-wise competition results is (Wiser and Lenski 2015):

(4)

where and are the densities of the strains and is time, usually chosen to be 24 hours.

# Discussion

We present a new computational method to predict the results of competitions between two strains from the separate growth curves of each strain.

This method should be very useful because growth curves experiments require much less effort and preparation than pair-wise competition assays (Concepción-Acevedo et al. 2015; Wiser and Lenski 2015; Hegreness et al. 2006; Gallet et al. 2012). As automatic 96-well microplate readers become more and more common in microbiology labs, growth curves experiments can be prepared in less than 30 minutes, after which the measurements are automatically collected by the automatic plate reader (Hall et al. 2014; Concepción-Acevedo et al. 2015).

Current methods for estimation of fitness from growth curves use the growth rate as a proxy of fitness. The growth rate and other proxies of fitness have several disadvantages: (i) they can't capture the full scope of effects contributing to differences in fitness; (ii) they are tough to compare between different studies and organisms; and (iii) they can't be used as parameters for population genetics models that test hypotheses and predict evolutionary dynamics. In contrast, our method integrates several growth phases into the fitness estimation, and our growth model can be extended to include other phases and factors of growth, such as biphasic growth and cell death.

The growth model that we use - the Baranyi-Roberts model - has a differential equation form and a closed form solution. Hence, it is highly useful for our method: the closed form is used to fit to growth curve data while the differential equation is used to predict the competition dynamics.

Our method assumes that the two strains interact solely via resource competition; that is, only through the factor . If the investigators know or suspect that additional interactions exist (*i.e.*, density-dependent interactions such as social or sexual selection, mutualism, and interference), our model can serve as a null hypothesis: the results of competition experiments can be compared to model predictions and a goodness of fit test can be used to decide if additional interactions are significant. Moreover, these additional interactions can be measured, either in terms of the difference in selection coefficients (between the coefficient calculated from the empirical results and coefficient calculated from the model prediction) or by fitting the empirical results to an extended model that includes density-dependent interactions (Masel 2014).

## Conclusions

We propose a new method to analyze growth curves, predict competition results, and estimate fitness. Our method is easy to use, has a clear biological interpretation, and can also be used as a null model for the interpretation of competition experiments.

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