
Modelling Competition for Nutrients between Microbial Populations Growing on Solid Agar Surfaces

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ABSTRACT

Motivation: Growth rate is a major component of the evolutionary fitness of microbial organisms. When nutrients are plentiful, fast-growing strains come to dominate populations whereas slower-growing strains are wiped out. This makes growth rate an excellent (a useful) surrogate for the health of cells. Measuring the health of cells grown in different genetic backgrounds or environments can inform about genetic interaction and drug sensitivity. In high-throughput procedures such as QFA and SGA, arrays of microbial cultures are grown on solid agar plates and quantitative fitness estimates are determined from growth measurements. Diffusion of nutrients along gradients in nutrient density arising between fast- and slow-growing neighbours is likely to affect growth rate and fitness estimates. However, current analyses assume that cultures grow independently. We study data from QFA experiments growing *Saccharomyces cerevisiae* to test a mass action kinetic model of nutrient dependent growth and diffusion. We try to correct for competition to provide more accurate and precise fitness estimates.

Results: Don't know what to say yet.

Availability and Implementation: CANS, a Python package developed for the analysis in this paper, is freely available at <https://github.com/lwlss/CANS>.

1 INTRODUCTION

The bacteria *Escherichia Coli* and yeast *Saccharomyces cerevisiae* are unicellular organisms studied as a model prokaryote and eukaryote respectively. Bacteria and yeast grow in colonies, where cells may (be clones originating from a single cell or) belong to different genetic strains originating from different individual cells. In favourable conditions, growth is exponential and this makes growth rate a major component of fitness; faster growing strains quickly come to dominate the population. At a certain point growth becomes limited and a stationary phase is reached. For unicellular organisms, growth rate is equal to cell cycle progression rate and all of the genetic information must be copied before each division. As a result, evolutionary pressure has led to rapidly dividing organisms with compact genomes of essential genes. These genes have been conserved in other species over billions of years of evolution, which is, in part, what makes *E. Coli* and *S. cerevisiae* useful as model species. The eukaryote *S. cerevisiae*, is particularly useful for the study of other eukaryotes such as humans.

The growth rate of microbial organisms is measurable and is often used to determine fitness. In experiments, cell cultures are commonly grown in two types of medium: on the surface of a nutrient rich solid agar and in a liquid mixture

containing nutrients. (REMOVE: In spot tests (phenotypic array), cultures are pinned or inoculated on the surface of a solid agar containing nutrients. In liquid culture assays, cultures are mixed in a liquid medium containing nutrients.) In both cases cultures are incubated and growth is observed. Identical strains can grow differently between the two mediums and disagreement in fitness estimates is currently an issue Baryshnikova *et al.* (2010a) (I couldn't find a paper specifically talking about this issue but they have a correlation plot Fig2a where correlations are worse with a liquid culture study by Jasnos and Korona; in fact the Baryshnikova paper Fig3c seems to say that they had strong correlation in their "high-resolution liquid growth profiling study"). I do not focus on this issue and exclusively study fitness screens using solid agar.

Fitness estimates can be used to infer genetic interaction or drug response and high-throughput methods allow this to be conducted on a genome-wide scale (see e.g. Costanzo *et al.* (2010); Andrew *et al.* (2013)). In a typical genetic interaction screen a strain is made with a mutation in a query gene. Double mutants are created by introducing a second deletion in this strain. By comparing the growth of double mutants with a control containing a neutral deletion, genetic interactions can be inferred. If a strain is fitter than the control then the deletion is said to suppress the defect of the query gene. If a strain is less fit than the control then the deletion is said to enhance the defect of the query gene. Either scenario suggests that the two genes interact and have a related function. Due to redundancy, single deletions are often non-lethal. (Remove: Knock downs and conditional mutations can also be used.) This has allowed Costanzo *et al.* (2010) to explore genetic interactions for ~75% of the *S. cerevisiae* genome.

Synthetic Genetic Array (SGA) and Quantitative Fitness Analysis (QFA) are high-throughput methods for obtaining quantitative fitness estimates of microbial cultures grown on solid agar (Baryshnikova *et al.*, 2010b; Banks *et al.*, 2012). Typically one query gene and replicates of several deletions are pinned or inoculated in a rectangular array on a solid agar plate. Many plates with different query genes and deletions are grown in high-throughput to explore whole genomes. I study data from QFA which refers to quantitative estimation of fitness by measurement and fitting of growth curves. In a typical QFA procedure liquid cultures are inoculated onto solid agar (containing nutrients (already mentioned above)) in a 16x24 rectangular array of 384 spots. Inoculum density can be varied to capture more or less of the growth curve and the most dilute cultures are inoculated with ~100 starting cells (Addinall *et al.*, 2011). Plates are grown in incubation and removed to be photographed at timepoints throughout growth.

Photographs are of whole plates and growth typically covers several days to capture both the exponential and stationary growth phases. Colonyzer (Lawless *et al.*, 2010) processes optical density measurements in photographs to produce a timecourse of cell density estimates for each culture. In pasts analysis, the logistic growth model was independently fit to the timecourse of each culture and fitness estimates were defined in terms of parameters of this model: the growth constant r and carrying capacity K . In contrast, SGA typically uses a larger array of 1536 pinned cultures and a single endpoint assay of culture area to quantify growth. The differential form and solution of the logistic model (Verhulst, 1845) (probably don't need this reference) are given in Equations 1, where C represents cell density and C_{t_0} is cell density at time zero.

$$\dot{C} = rC \left(1 - \frac{C}{K}\right) \quad (1a)$$

$$C(t) = \frac{KC_{t_0}e^{rt}}{K + C_{t_0}(e^{rt} - 1)} \quad (1b)$$

The logistic model is a simple mechanistic model describing self-limiting growth and has a sigmoidal solution. Growth begins exponentially with rate rC and curtails as the population size increases and cells begin to compete for space and nutrients (remove: or interact in some other way). Cell density reaches a final carrying capacity K at the stationary phase. In QFA, nutrients must diffuse through agar to reach cells growing on the surface. It is plausible that the carrying capacity K represents the point at which nutrients either run out or growth becomes limited by the diffusion of nutrients and is approximately stationary. Fitting the logistic model to QFA data requires plate level or culture level parameters for C_{t_0} and culture level parameters for r and K making 769 or 1152 parameters per 384 culture plate.

//Could remove and just discuss MDR when I get to the results// The growth constant r could be used as a fitness measure. However, Addinall *et al.* (2011) define a more complicated fitness measure as the product of Maximum Doubling Rate (MDR) and Maximum Doubling Potential (MDP) which they calculate from logistic model parameters. MDR measures the doubling rate at the beginning of the exponential growth phase, when growth is fastest, and MDP is the number of divisions which a culture undergoes from inoculation to the stationary phase.

$$MDR = \frac{r}{\log\left(\frac{2(K-C_0)}{K-2C_0}\right)} \quad (2a)$$

$$MDP = \frac{\log\left(\frac{K}{C_0}\right)}{\log(2)} \quad (2b)$$

To improve the quality of fits, QFA now uses the generalised logistic model which requires an extra shape parameter for each culture. Standard and generalised logistic model r are not equivalent so comparison relies on MDR and MDP as fitness measures. The analysis of QFA data using both models is available through the QFA R package (Lawless *et al.*,

2016). //Could remove and just discuss MDR when I get to the results//

//Could remove//Addinall *et al.* (2011) used QFA and *S. cerevisiae* to screen for genes involved in telomere stability which is related to ageing and cancer and has implications for human health and disease. Hits from this study have been successfully followed to discover new biology (Holstein *et al.*, 2014). (To be honest I have no idea about the significance of what they found in this paper. We had a more general focus. If I have room I should probably try and sell the potential benefits and past successes of QFA a bit more to expand the motivation. Obviously I will mention the Addinall paper when I describe p15 in the methods.) //Could remove//

Since QFA aims to determine differences in the fitness of microbial strains from measurements of differences in growth, fast and slow growing cultures are often grown side-by-side. Figure 1 shows a section of a QFA plate from a study by Addinall *et al.* where this is the case. (Cultures were inoculated with approximately equal cell density but have grown at different rates to visibly different sizes after ~ 2.5 days.) It is likely that nutrients diffuse along gradients between fast and slow growing neighbours causing growth to appear faster or slower than if it were independent. Further support for such an effect comes from the experiment shown in Figure 2 where the same cultures are grown in alternate columns on two separate plates but with cultures added or removed from the neighbouring columns in between. Cultures in Figure 2a), where neighbours were removed, grew faster and larger (how much? I can look at the data myself) than the same cultures in Figure 2b), where neighbours were added. This suggests that an interaction between neighbours is present and may be affecting fitness estimates. Current QFA analysis using the logistic model assumes that cultures grow independently and ignores possible competition effects between neighbours. The sigmoidal curve of the logistic model poorly fits QFA data in many cases and this may be due to competition effects. I aim to fit a network model of nutrient dependent growth and diffusion to QFA data to try to correct for competition and increase the accuracy and precision of fitness estimates.

Could explain the difference in dilute and more concentrated cultures. In the image captions or elsewhere?

Could also talk about quorum sensing and ammonia when I get to competition.

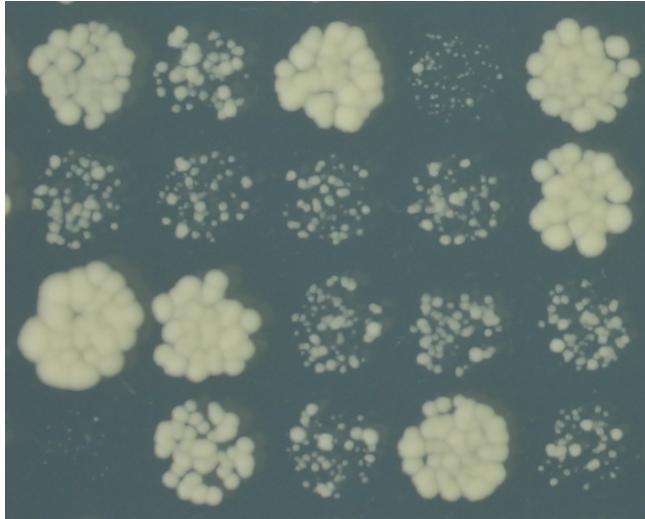


Figure 1: 4x5 section of a QFA plate. Taken from a 16x24 format solid agar plate inoculated with dilute *S. cerevisiae* cultures. Image captured at ~ 2.5 d after inoculation and incubation at 27°C .

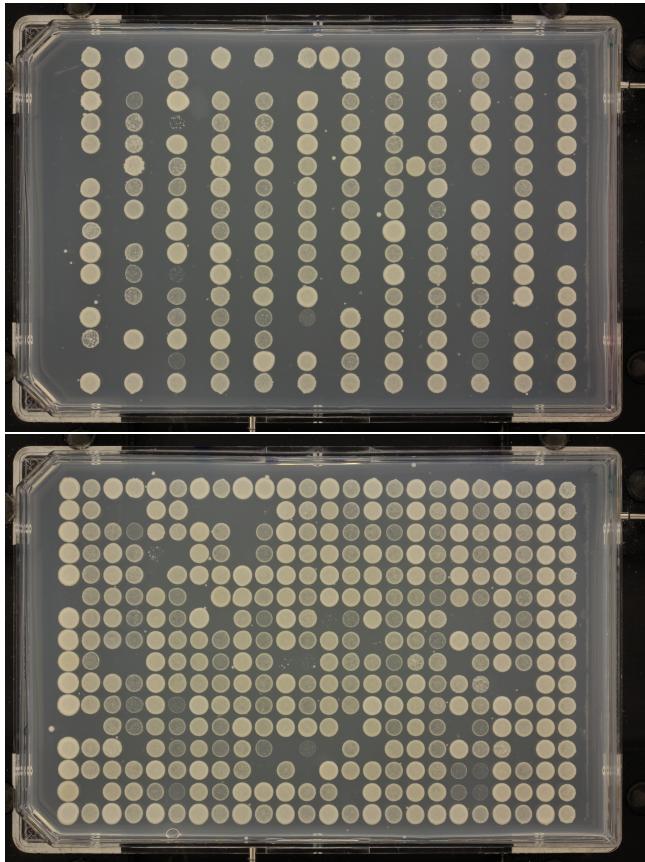


Figure 2: QFA experiment designed to examine competition. A) QFA plate inoculated with a more concentrated *S. Cerevisiae* inoculum (no cells inoculated on alternate columns). B) Same as in A, but with strains of similar growth rate inoculated in the positions missing in A.

Competition effects could be dealt with experimentally by randomising the location of cultures on repeated plates. This does not require explicit knowledge or modelling of the source of competition but reduces throughput, so, if possible,

a modelling approach is desirable. Poisoning of cultures by a signal molecule such as ethanol, which *S. cerevisiae* produces in the metabolism of sugars by fermentation, is another possible source of competition. QFA does not measure nutrients or signal, so if more than one source of competition exists, it becomes very difficult to fit a model and randomisation may be the best approach. QFA data for edge cultures is noisy due to reflections from plate edges. This is only partially corrected for by Colonyzer (Lawless *et al.*, 2010) and as a result data for edge cultures is usually discarded. Addinall *et al.* (2011) grow repeats of a neutral deletion in edge locations, rather than leaving them empty, because of concerns about competition. In an SGA study, Baryshnikova *et al.* (2010a) use statistical techniques to correct for competition between fast and slow growing neighbours in end-point assays of culture area. I hope that modelling competition for nutrients explicitly will better correct for competition using fewer repeats. QFA uses more information than SGA by fitting whole growth curves, rather than a single endpoint assay, so a modelling approach promises to be more powerful. Furthermore, modelling may identify and explain the source of competition. Simulation of an accurate model will allow comparison of experimental designs and exploration of ways to reduce competition effects.

//Diffusion Equation: I am probably going to have to repeat this when I get to the discussion so I could just leave until then.// Reo and Korolev (2014) use a diffusion equation model to simulate nutrient dependent growth of a single bacterial culture on a petri dish in two-dimensions. It would be too computationally intensive to fit a similar model to a full QFA plate in three-dimensions, especially if the model is to be used to process many plates from high-throughput experiments. Therefore, a simpler model of nutrient diffusion is required. //Diffusion Equation//

Lawless (link blog) proposed a model of nutrient dependent growth and competition (3,4), hereinafter the competition model, using mass action kinetics and network diffusion. A schematic of the model is drawn in Figure 3. He represents the nutrient dependent division of cells with the reaction equation,



where C is a cell, N is the amount of nutrient required for one cell division, and b is a rate constant for the reaction. (The identity of the limiting nutrient N is unknown but possible candidates are sugar and nitrogen.) He defines separate reactions (3) with growth constant b_i for each culture, indexed i , on a plate and uses mass action kinetics to derive rate equations for the amount of cells and nutrients associated with each culture, C_i and N_i . This gives the rate equation for C_i (4a) and the first term in the rate equation for N_i (4b).

$$\dot{C}_i = b_i N_i C_i, \quad (4a)$$

$$\dot{N}_i = -b_i N_i C_i - k_n \sum_{j \in \delta_i} (N_i - N_j). \quad (4b)$$

To arrive at the full competition model, he models the diffusion of nutrients along gradients between a culture i and its

closest neighbours δ_i by the second term in (4b), where k_n is a nutrient diffusion constant. This can also be expressed as a series of reactions of the form



and modelled with mass action kinetics. Unlike the logistic model (1), the competition model has no analytical solution, and must instead be solved numerically. If k_n is set to zero, the competition model reduces to the mass action equivalent of the logistic model, hereinafter the mass-action logistic model, (and has the same sigmoidal solution). (In this limit, parameters of the competition model can be converted in terms of parameters of the logistic model (see methods section)). When the competition model is fit to QFA data, C_i is observed and N_i is hidden. Inoculum density, C_{t_0} , is often below detectable levels. By assuming that inoculum density is the same for all cultures and that nutrients are distributed evenly throughout the agar at time zero, plate level initial values of cells and nutrients, C_{t_0} and N_{t_0} , can be used. k_n is assumed to be constant across the plate but must be inferred. There is a growth constant, b_i , for each of 384 cultures on a typical QFA plate making 387 parameters in total. The competition model shares more information between cultures and has less than half the number of parameters of either the standard or generalised logistic model (Banks *et al.*, 2012; Lawless *et al.*, 2016). (If I remove the section on MDR and the generalised logistic model above I will need to add a line of explanation here.)

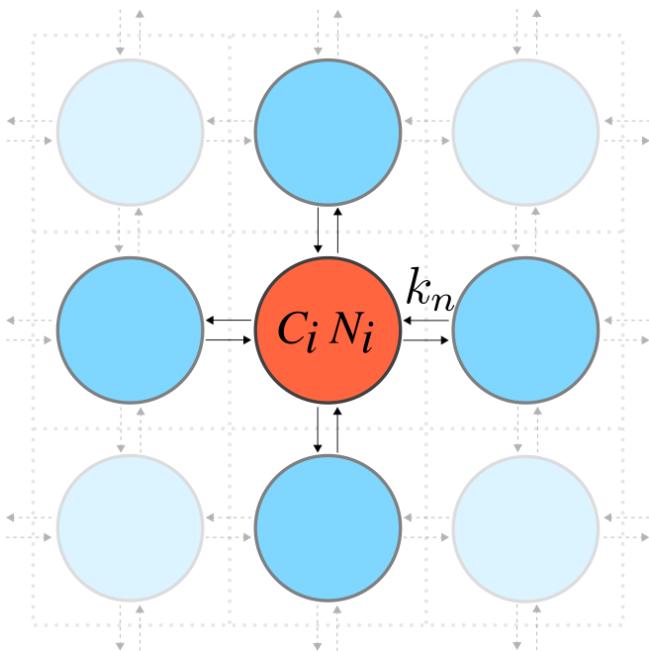


Figure 3: Schematic of the competition model. Each circle represents a culture, indexed i , growing in a rectangular array on the surface of a nutrient containing solid agar. Arrows represent a network of nutrient diffusion along gradients between cultures. C_i - amount of cells; N_i - amount of nutrients; k_n - plate level nutrient diffusion constant; darker blue circles δ_i - closest neighbours of culture i .

In QFA, populations begin with ~ 100 cells and quickly grow to reach thousands of cells so a deterministic approximation appears valid. Mass action kinetics applies to reactions in a well stirred mixture and is perhaps less valid for a culture growing on solid agar. However, a mass action approximation has been successful in other situations where this assumption is questionable: in the Lotka-Volterra model of predator-prey dynamics (Berryman, 1992) and in signalling and reaction models inside cells (Aldridge *et al.*, 2006; Chen *et al.*, 2010). The order of a reaction also affects the rate equation and the identity and quantity of the nutrient molecule in the (3) is unknown. Reaction (3) also assumes that all nutrients are converted to cells and includes no model of metabolism. I justify the use of the competition model because in the independent limit it has the same solution as the logistic model which has long been used to model microbial growth. Studying the competition model may help us to understand the nature of QFA experiments and, if some assumptions do not hold, it could be used as a first step in developing a more accurate model. Furthermore, collectively fitting the competition model involves a large number of parameters and data points and will require many simulations to be run. This necessitates the use of an approximate model for computational feasibility. This is especially true if the model is to be used in the analysis of high-throughput data. It is hoped that even an approximate model will be able to measure more reliable growth parameters and better estimate fitness. This will increase the power to infer genetic interaction and drug response which could lead to further discoveries. (For an example of a successful QFA study and follow up using the logistic model see Addinall *et al.* (2011) and Holstein *et al.* (2014)).

2 METHODS

2.1 CANS

To analyse QFA data using the competition model I developed the Python package CANS which can be used for model composition, model simulation, parameter inference, and visualisation of results. CANS accepts cell density timecourses for any size rectangular array. CANS can produce SBML models to document results of parameter inference or for independent validation. It is relatively simple to create and simulate new models involving reactions between species within cultures or between neighbouring cultures, and to fit these provided an initial guess. The CANS package is available at <https://github.com/lwlss/CANS>.

2.2 Solving and fitting

2.2.1 Solving

CANS numerically solves models using one of two methods. The first is slower and uses SciPy's `integrate.odeint` to solve models written in Python at user supplied timepoints. I vectorised code using NumPy to optimise solving of the competition model by this method. For solving a plate of 384 cultures with cell density observations at 10 unevenly spaced time points, I found that using the Python bindings for libRoadRunner was about 10 times faster. libRoadRunner requires models to be written in SBML so I wrote code using

the libSBML Python API to automatically generate SBML versions of the competition model for any size plate. Unlike SciPy's `odeint`, libRoadRunner only simulates at uniformly spaced timepoints. To fit QFA cell observations, which are not made at fixed time intervals, requires simulated cell amounts at the observed timepoints. For the analysis in (P15 section), where each timecourse has only 10 timepoints, I simulated sequentially between (pairs of) timepoints. This method was slower for the analysis in (Stripes section) where each timecourse had around 50 timepoints. To increase speed I used SciPy's `interpolate.splrep` to make a 5th order B-spline of cell density timecourses with smoothing condition $s = 1.0$. I evaluated the spline for cell density using SciPy's `interpolate splev` at 15 evenly spaced intervals from time zero to the time of the last QFA observation. I then solved these timecourses with one call to RoadRunner.`simulate`.

Table 1: Parameter bounds. Used for fitting the competition model to P15 and the Stripes and Filled plates. Bounds on N_{t_0} were applied to both $N_{t_0}^I$ and $N_{t_0}^E$ for internal and edge cultures. “guess” refers to the initial guess (see Section 2.4).

Parameter	Lower Bound	Upper Bound
C_{t_0}	guess $\times 10^{-3}$	guess $\times 10^3$
N_{t_0}	guess / 2	guess x 2
k_n	0.0	10.0
b	0.0	None

Cultures at the edge of a plate have an advantage because they have access to a greater area of nutrients. I corrected for this using a separate parameter $N_{t_0}^E$ representing a higher initial amount of nutrients in edge cultures. In rate equations involving edge cultures, I scaled edge culture nutrient amount N_i by the ratio $N_{t_0}^I/N_{t_0}^E$, where $N_{t_0}^I$ is the amount of nutrients in internal cultures. The physical interpretation of this correction is that edge cultures have an extra supply of nutrients that can diffuse instantly into the reaction volume. This treatment reduced the error in cell density estimates for cultures one row or column inside the edge and resulted in better fits to internal cultures overall (see Table 2 or Section). Cell density measurements from edge cultures contain more noise due to reflections from plate walls (Lawless *et al.*, 2010). I collectively fit to all cultures and selected best fits based on only the fit to internal cultures.

(Could move to discussion but probably get rid) When fitting the competition model noise might be better dealt with by leaving edge cultures empty.

(Can go to results section or Stripes method section:) QFA data for the Stripes plate contained observations for cultures that were known to be empty. When fitting the competition model, I set growth constant b to zero for these cultures and removed them from fitting.

2.2.2 Fitting the competition model

I use QFA data after processing with Colonyzer (Lawless *et al.*, 2010). Colonyzer uses integrated optical density measurements in whole plate images as a proxy for cell density. I used [timecourses of] these cell density estimates, which have arbitrary units, throughout my analysis. I fit the competition model using a gradient method and made maximum likelihood estimates of parameters using a normal model of measurement error. For constrained minimisation I used the L-BFGS-B algorithm from SciPy's `integrate` package.

I determined stopping criteria so that parameters of full-plate simulated data sets, with a small amount of simulated noise, were recovered with high precision. To help the minimizer, I scaled C_{t_0} values by a factor of 10^5 to make parameter values closer in order of magnitude. I ran repeated fits using different parameter guesses for each plate (see Section (P15 and Stripes details)). I set bounds according to Table 1 and checked that best fits had no parameters at a boundary.

2.2.3 Fitting the logistic model

Fitting the mass action logistic model requires using culture level N_{t_0} and creating 383 extra parameters. The QFA R package (Lawless *et al.*, 2016) can fit the standard logistic model and has heuristic checks to correct a confounding of parameters that occurs when slow-growing cultures are dominated by noise. I did not have time to implement these checks for the mass action logistic model, so I instead fit the standard logistic model using the QFA R package. This is not equivalent because QFA R does not fit data collectively and instead uses a culture level C_0 . However, this is a useful comparison with a method of analysis currently used in QFA (see e.g. Addinall *et al.* (2011)). I do not expect much disagreement of fitness estimates with the mass action logistic model once heuristic checks are implemented. In contrast to the competition model, noisy data from edge cultures was discarded before fitting. I conduct model comparison between the competition and logistic models in sections (Results sections).

2.2.4 Data visualisation

(Do I really need this?) I created plotting functions to visualise fits and simulations of QFA timecourses and to compare the ranking of fitness estimates using the Python package matplotlib.

2.3 2.3 Parameter conversion

(Will move to the discussion: The identity of the nutrient molecule is unknown and it is not clear whether metabolism of the nutrient molecule will have a significant effect. If necessary a metabolism reaction could also be modelled.)

When k_n is set to zero, the competition model (4) reduces to the mass action logistic model which has the same sigmoidal solution as the standard logistic model. In this limit, it is possible to equate cells of both models and convert parameters using (6) (see Conor's blog for a derivation).

$$r_i = b_i(C_{t_0} + N_{t_0}) \quad (6a)$$

$$K = (C_{t_0} + N_{t_0}) \quad (6b)$$

The reaction equation of the competition model (3) assumes that all nutrients are converted to cells. This implies that all cultures starting with the same amount of nutrients reach the same final amount of cells. Therefore, to fit the mass action logistic model to QFA data, it is necessary to allow N_{t_0} to vary for each culture which is not physical and, in which case, the mass action logistic model has the same number of parameters (769) as the standard logistic model. (Probably repetition: When I fit the competition model I collectively fit the timecourses of all cultures on a plate using a plate level N_{t_0} and 387 parameters.) Figure 4 shows fits of a single culture on a larger 16x24 format plate using both models. This culture grew faster than its neighbours (not shown) and, according to the competition model, competed for more nutrients. Figure 4a shows the mass-action logistic model fit where N_{t_0} is estimated as being approximately equal to the final cell amount, or carrying capacity K . Figure 4b shows the competition model fit with a plate level N_{t_0} and $k_n > 0$. Resimulating with k_n set to zero gives the dashed mass action logistic model curves which are corrected for competition. We can therefore obtain the corrected logistic model r_i and K_i of these curves by converting from competition model estimates of b_i , C_{t_0} , and N_{t_0} . N.B. b is the same for both the solid and dashed curves in Figure 4b.

Competition model C_{t_0} and N_{t_0} are the same for all cultures on a plate. Therefore, by the conversion equations (6), all cultures on a plate have the same carrying capacity K and all $b_i \propto r_i$ by the same factor. Similarly, MDP is the same for all cultures and all $b_i \propto MDR_i$ by the same factor (see Equation 2). Therefore, b is equivalent to all common QFA fitness measures, r , MDR , and $MDR * MDP$ (see e.g. Addinall *et al.* (2011) and Lawless *et al.* (2016)). This makes b a very convenient fitness measure for the competition model; we need not convert to logistic model parameters to compare the fitness rankings of cultures on the same plate. To compare competition model fitness rankings between different plates we can of course use b . However, this is not

equivalent to comparing r or MDR as different plates may have different C_{t_0} and N_{t_0} .

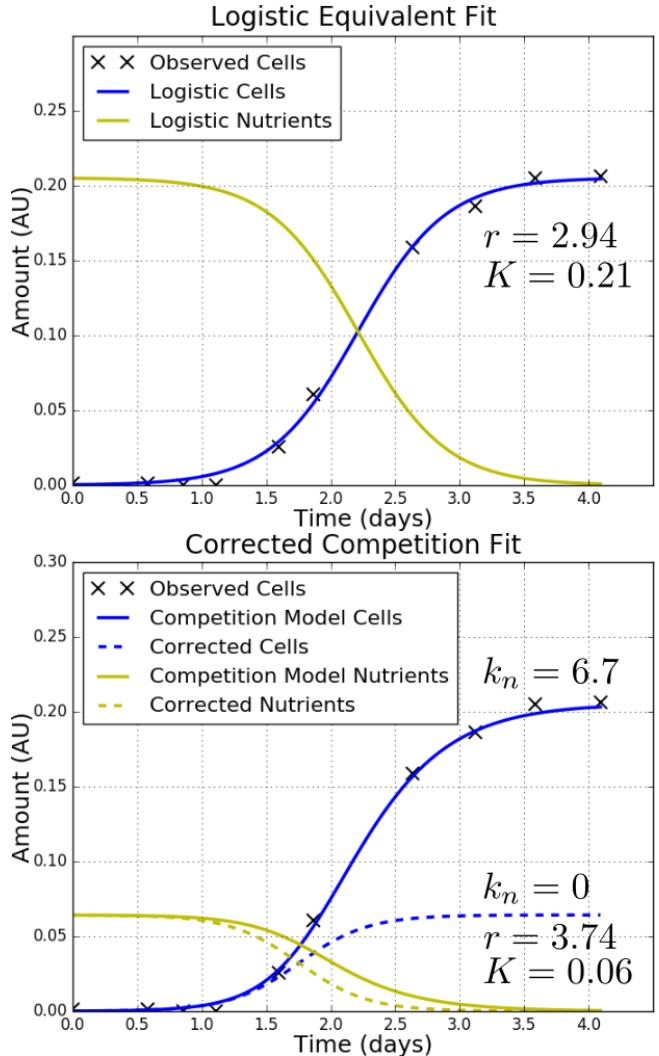


Figure 4: Using the competition model to correct for competition. Fits are to culture (R10, C3) of P15 which grew faster and reached a higher final cell density than its neighbours (not shown). According to the competition model, this is because this culture competed for more nutrients. To reach the same final cell density, the logistic equivalent model requires a higher amount of starting nutrients for this culture and a different amount for each neighbour. The correction to the competition model simulates how growth would have appeared without competition and allows us to return parameters r and K of the logistic model.

2.4 2.4 Making an initial guess

Achieving good fits of the competition model requires making a good initial guess. To fit the competition model to small simulated zones I could simply use many random parameter guesses. However, for fitting a full plate with 387 parameters the chance of any random guess being close to the “true” values is much smaller and more sophisticated guessing methods are required. I did not understand the disagreement between mass action logistic and competition model estimates of b which is only reduced when parameters are converted to logistic model r and K (see Section ??). Without this conver-

sion fitness rankings, using b , are inverted between the two models. I instead assumed that there was a more fundamental disagreement between models and developed the “Imaginary Neighbour Model” for guessing competition model b . This allowed good fits to be made. I did not have time to compare imaginary neighbour guessing with logistic model guessing so it is unclear which method is better.

2.4.1 2.4.1 Guessing initial amounts

Recall from the competition model reaction equations (3 and 5) that nutrients can only diffuse or be converted to cells. Thus, assuming that reactions are nearly complete at the end of cell observations and that $C_{t_0} \ll N_{t_0}$, the total initial amount of nutrients, N_{Tot} , can be estimated using,

$$N_{Tot} = n_I N_{t_0}^I + n_E N_{t_0}^E \approx C_F, \quad (7)$$

where C_F is the total of final cell measurements, n_I and n_E are the numbers of internal and edge cultures, and $N_{t_0}^I$ and $N_{t_0}^E$ are initial nutrient amounts for internal and edge cultures (see Section 2.2.2). Using (7) and an estimate for the ratio of area associated with edge cultures to area associated with internal cultures, $A_r = A^E/A^I = N_{t_0}^E/N_{t_0}^I$, I made guesses of $N_{t_0}^I$ and $N_{t_0}^E$ using,

$$\begin{aligned} N_{t_0}^I &= N_{Tot}/(n_I + n_E A_r) \\ N_{t_0}^E &= N_{Tot}/(n_I/A_r + n_E). \end{aligned} \quad (8)$$

When $A_r = 1$, (8) reduces to the initial nutrient guess for the one initial nutrient parameter model. I used $A_r = 1.4$. In QFA using dilute cultures, C_{t_0} falls below the level of detection. I did not estimate initial guesses of C_{t_0} and instead ran multiple fits over a range of C_{t_0} values in logspace. What was the range?

(Discussion: Recent work Herrmann and Lawless suggests that direct measures of C_{t_0} may not be reliable due to heterogeneity between inoculated cells; many inoculated cells don’t grow and only the fastest growing cells contribute significantly to the final population.)

2.4.2 2.4.2 Guessing b

To guess competition model b_i I used the imaginary neighbour model to quickly fit individual cultures. The model is based on the reaction and rate equations of the competition model (3–5) but tries to replicate the diffusion of nutrients into and out of a culture using imaginary fast and slow growing neighbours with different nutrient diffusion constants $k_{n,f}$ and $k_{n,s}$. The growth constants of the fast and slow growing cultures are b_f and b_s . A schematic of the model is drawn in Figure (ref). To fit the model to QFA data, I fixed C_{t_0} and $N_{t_0}^I$ for all cultures by the initial guesses (see Section 2.4.1); I fixed b_f at a range of different guesses, and fixed $b_s = 0$; I allowed b , $k_{n,f}$, and $k_{n,s}$ to vary. I determined the number, n , of each neighbour from the guess of $N_{t_0}^I$ and the range of final cell amounts, such that the culture with the highest observed final

cell density had enough slow growing neighbours to provide all of the nutrients necessary to reach this final cell density. I solved the imaginary neighbour model using SciPy’s `odeint`. I fit using a gradient method as in Section 2.2.2.

2.4.3 2.4.3 Guessing k_n

Simulations of the competition model using sets of b parameters drawn from different normal distributions have linear relationships between variance in final cell amount and nutrient diffusion constant k_n . I simulated guessed parameters C_0 , N_0 , and b_i with a range of different k_n values and used linear regression to parameterise the straight line. I then took the variance in final cell amount for real data and guessed k_n from the straight line.

Don’t think I need this figure. r->b and make titles bigger. Fitted k_n was much higher so I should probably resimulate over a bigger range. Only possibly to know in hindsight. I could also use the fitted parameters for this rather than drawing from a normal distribution.

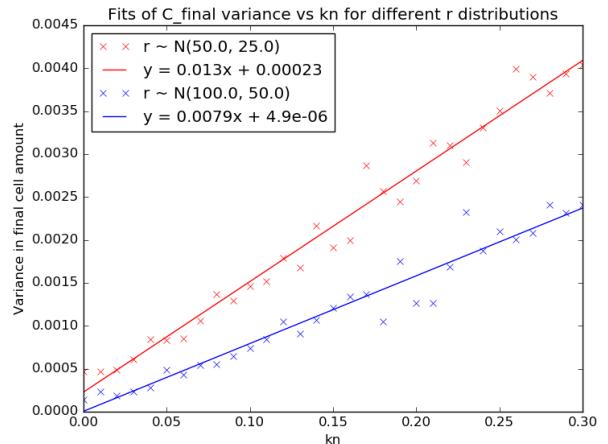


Figure 5: Guessing k_n from the variance in final cell amounts. The competition model is simulated for a 16x24 format plate using two random sets of culture-level b parameters drawn from different normal distributions. Each set of b parameters is simulated with a range of k_n parameter values. The variance in final cell density for all cultures is plotted against k_n for each simulation. Lines are shown for least squares fits to points from each set of b parameters.

2.5 2.5 Development of a genetic algorithm

2.6 2.6 Model comparison using a single QFA plate

2.7 2.7 Cross-plate calibration and validation

3 3 RESULTS

3.1 3.1 Guessing

N_0 estimated from average final cell amounts. See formula in code for two N_0 estimation.

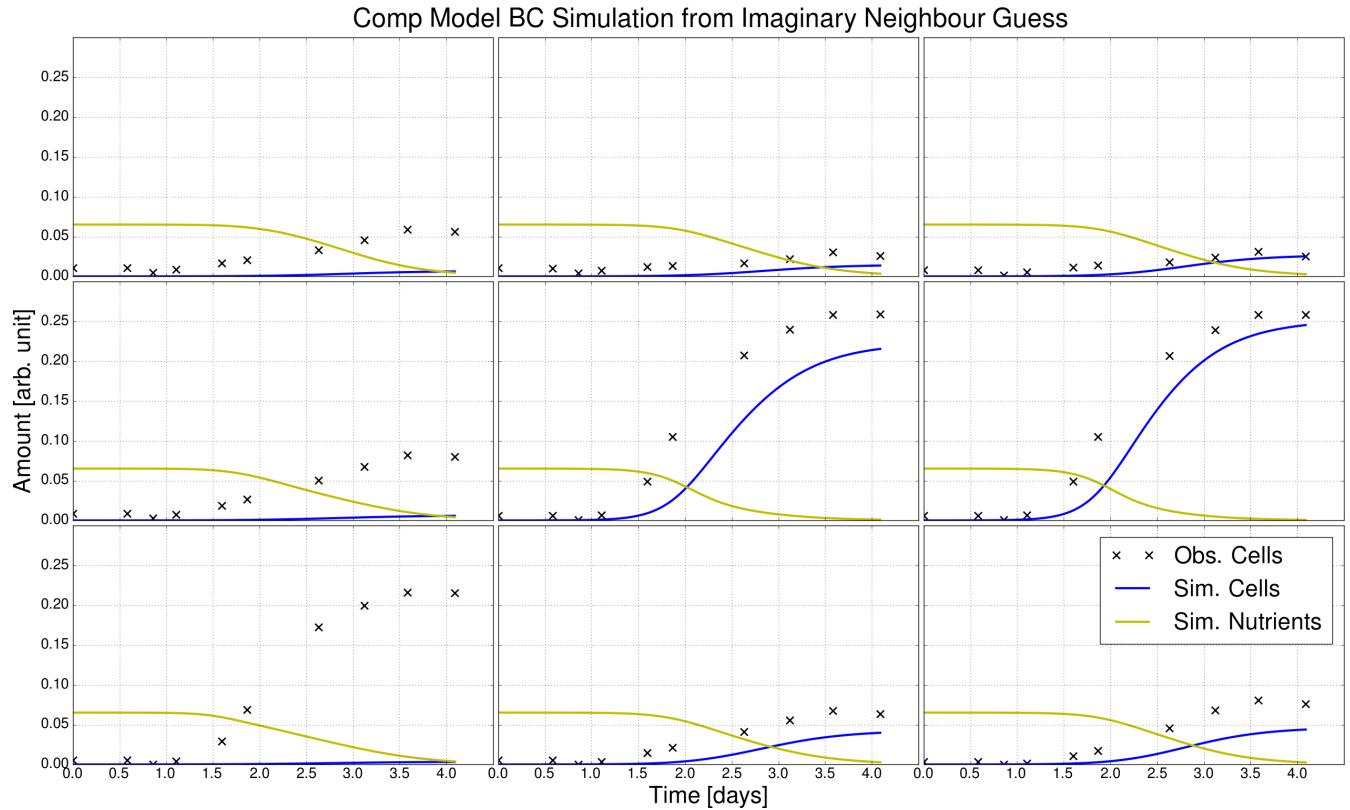


Figure 6: Competition model simulation using parameters from imaginary neighbour guessing. Shows a 3x3 zone with top-left coordinate (5, 18) from P15 with background cdc13-1 at 27°C.

3.2 Competition Model Fitting to P15

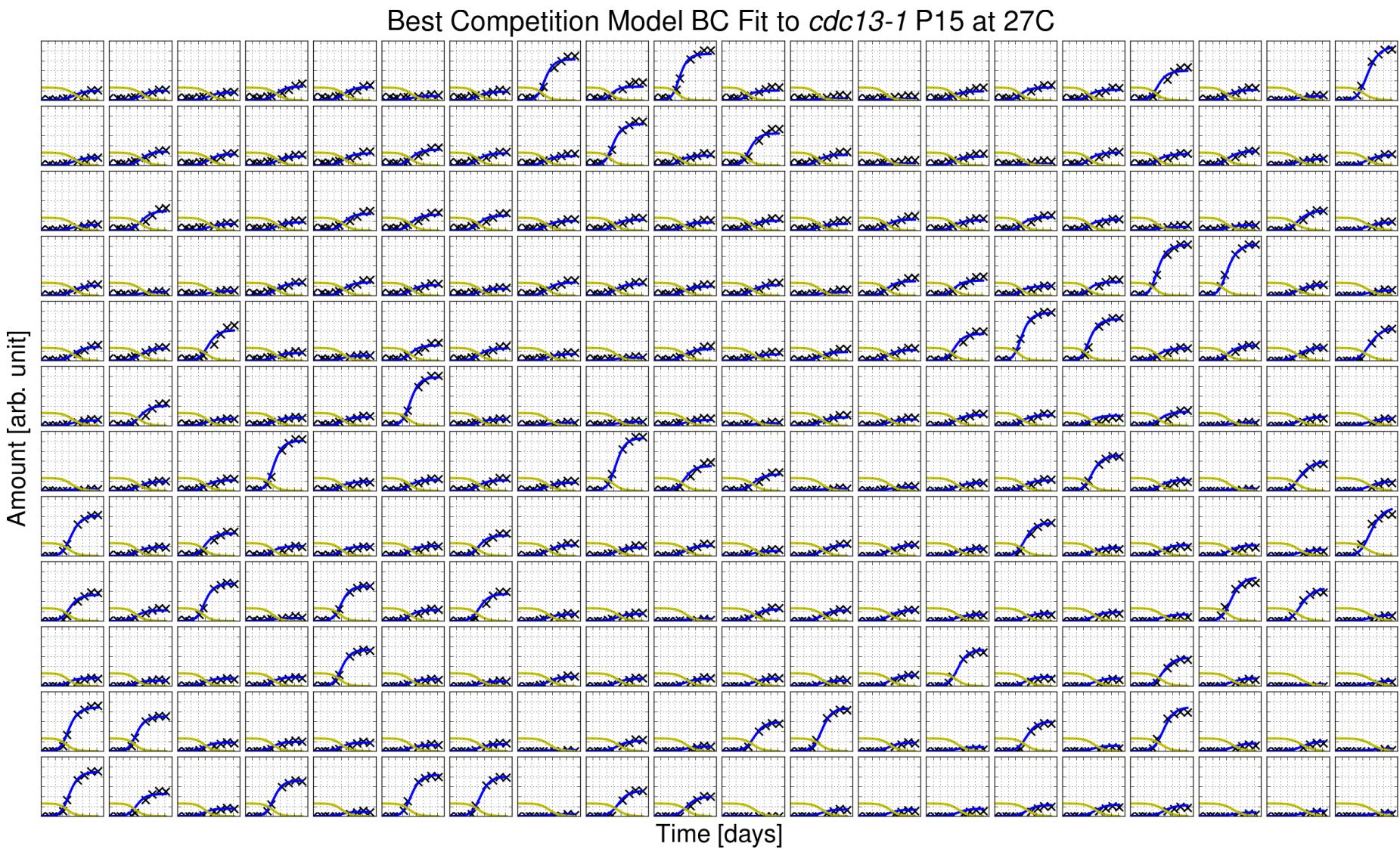


Figure 7: Fit of the competition model to a QFA plate. Data is for a 16x24 format plate (P15) with a background mutation *cdc13-1* incubated at 27°C. The plate contains 6 repeats of 50 genetic strains randomly arranged across the internal cultures. Repeats of a single strain are used for all edge cultures (removed in the plot). Model output for state variable, cell population size (blue curve), is fit to observed data (black crosses). Model predictions for unobserved variable (nutrient amount) are also plotted (yellow).

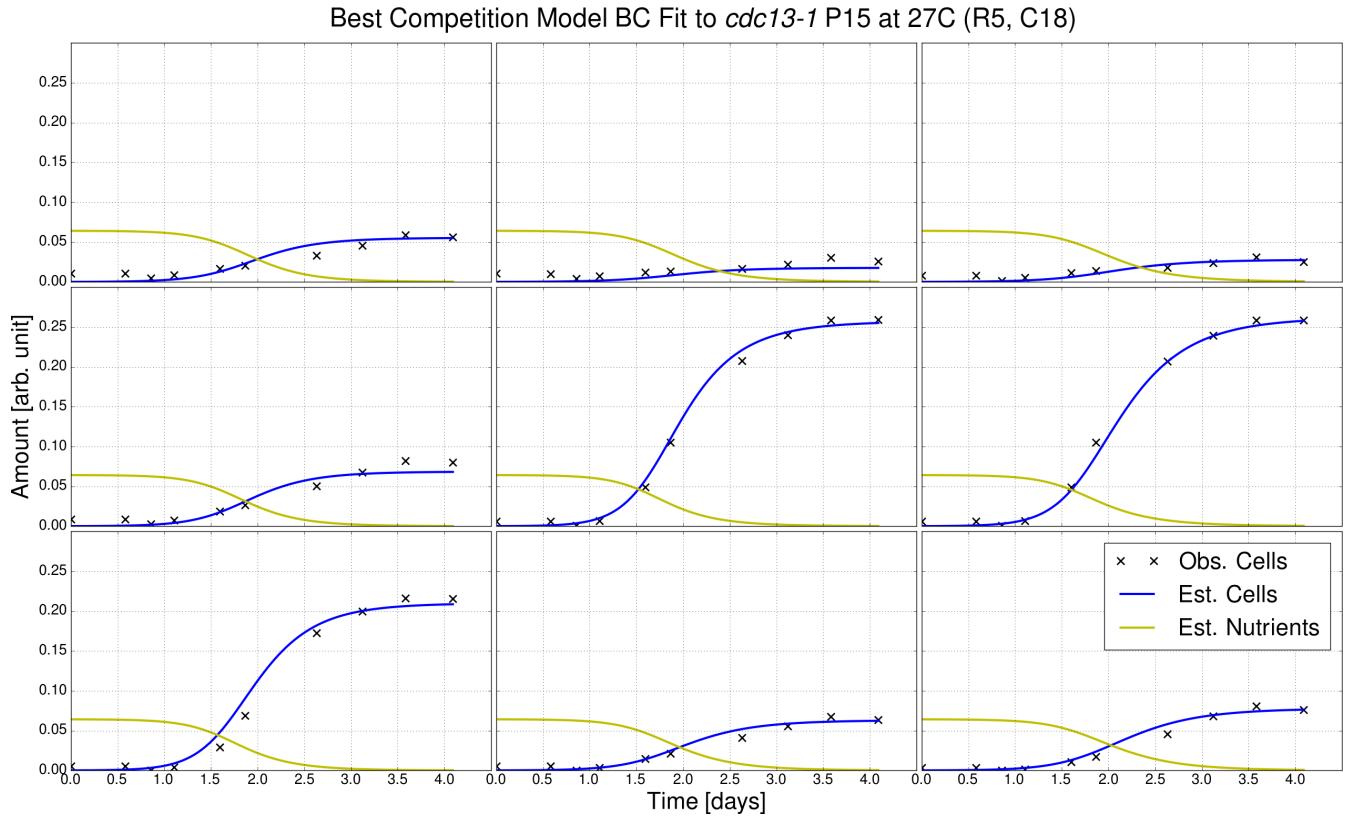


Figure 8: A 3x3 zone from Figure 7 with top-left coordinate (5, 18).

3.3 3.3 Evaluating the treatment of boundaries

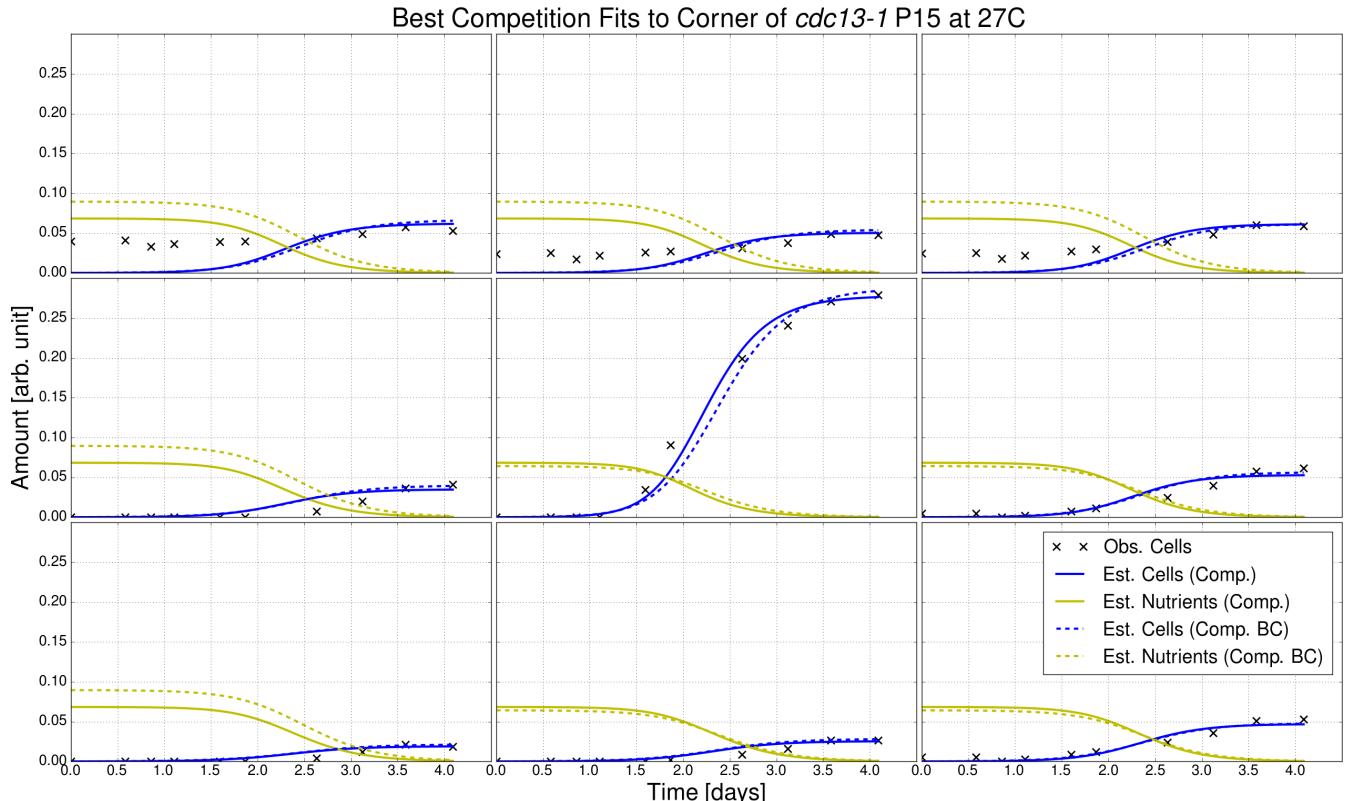


Figure 9: Treatment of boundary conditions in fits of the competition model. The top left corner of a 16x24 QFA plate fitted with two versions of the competition model, the first has a single initial nutrient amount for all cultures, the second has a separate initial nutrient amount for edge cultures.

Table 2: Average error in objective function for one or two N₀ parameter competition models. Values are for the same fits as in Figure 9 and have been scaled by 10⁴. Averages are for cultures belonging to the areas indicated by the column “Cultures”. “Next to edge” refers to cultures one in from the edge. “Internal” refers to all cultures but the edge.

Cultures	One N_0	Two N_0
Edge	35.9	36.5
Next to edge	9.54	7.98
Internal	6.67	6.30
All	12.4	12.2

Table 2

3.4 3.4 Agreement of b rankings

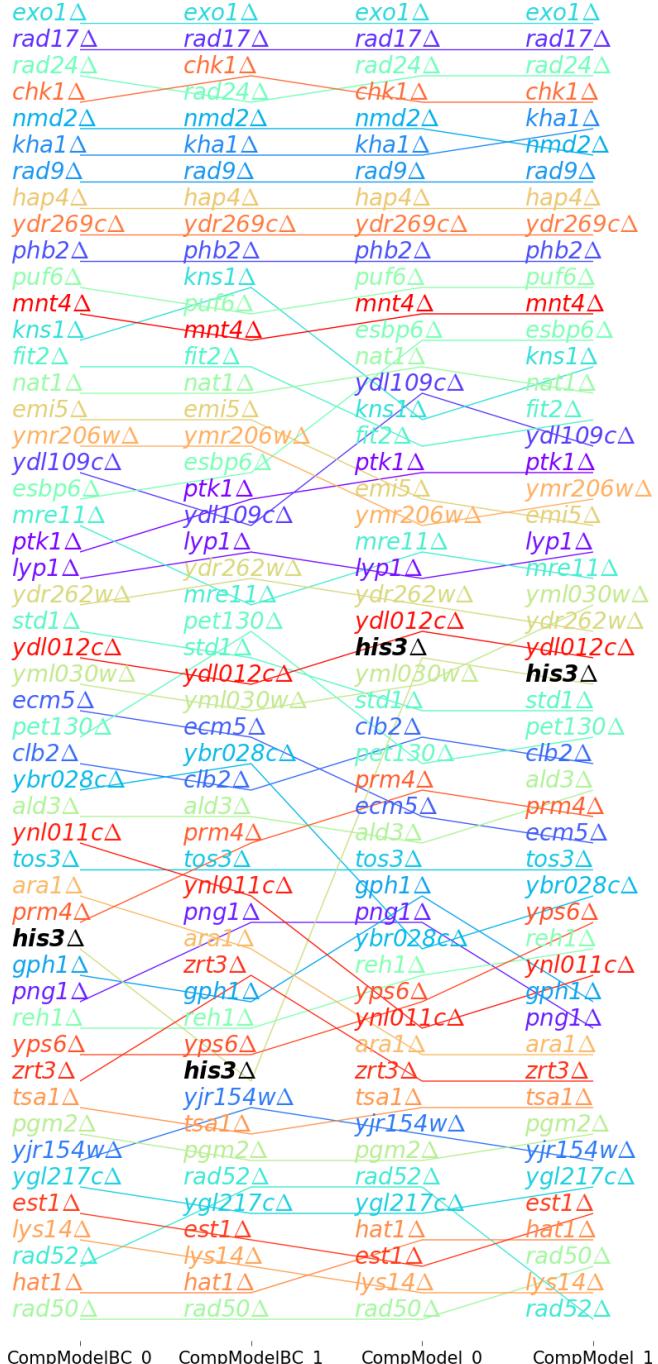


Figure 10: Comparison of b ranking for the best five competition model fits to P15. Ranking is calculated from the mean b estimate from the six repeats of each strain.

3.5 3.5 Comparison of fitness ranking

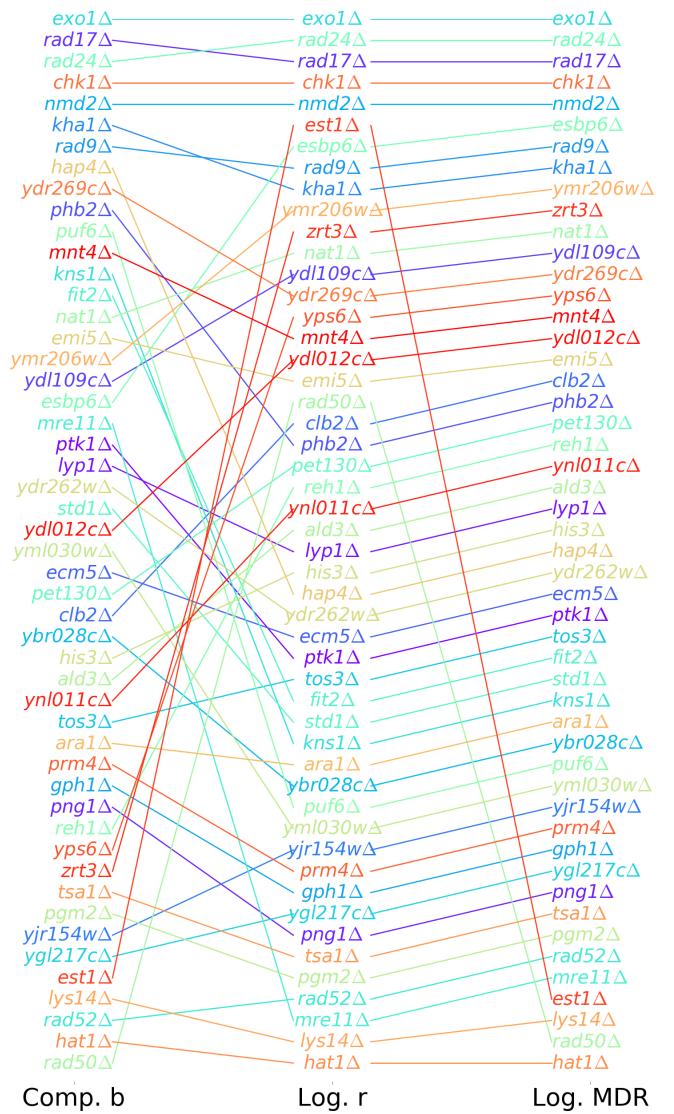
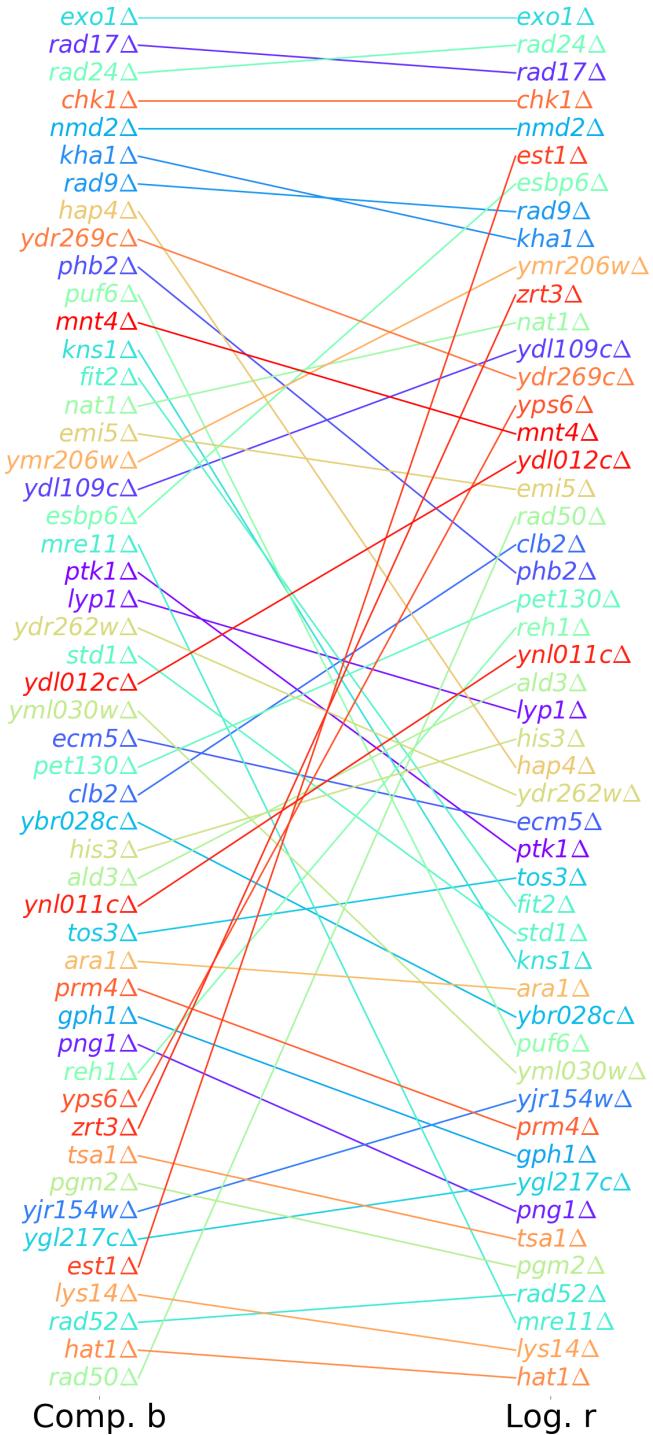


Figure 11: Comparison of r ranking for fits of the competition and logistic model to P15. Competition model r was converted from b, N_0 , and C_0 from the best competition model estimate. Logistic r was taken from fits using the QFA R package which makes heuristic checks for slow growing cultures.



3.6 Comparison of Variation in Fitness Estimates

Use repeats on plate 15 (6 per deletion) to calculate coefficient of variation (COV) of estimated r or MDR.

Figure 12: Comparison of r ranking for fits of the competition and logistic model to P15. Fitnesses of genetic strains are ranked most to least fit from top to bottom. Competition model r was converted from b , N_0 , and C_0 from the best competition model estimate. Logistic r and MDR were taken from logistic model fits using the QFA R package which makes heuristic checks for slow growing cultures.

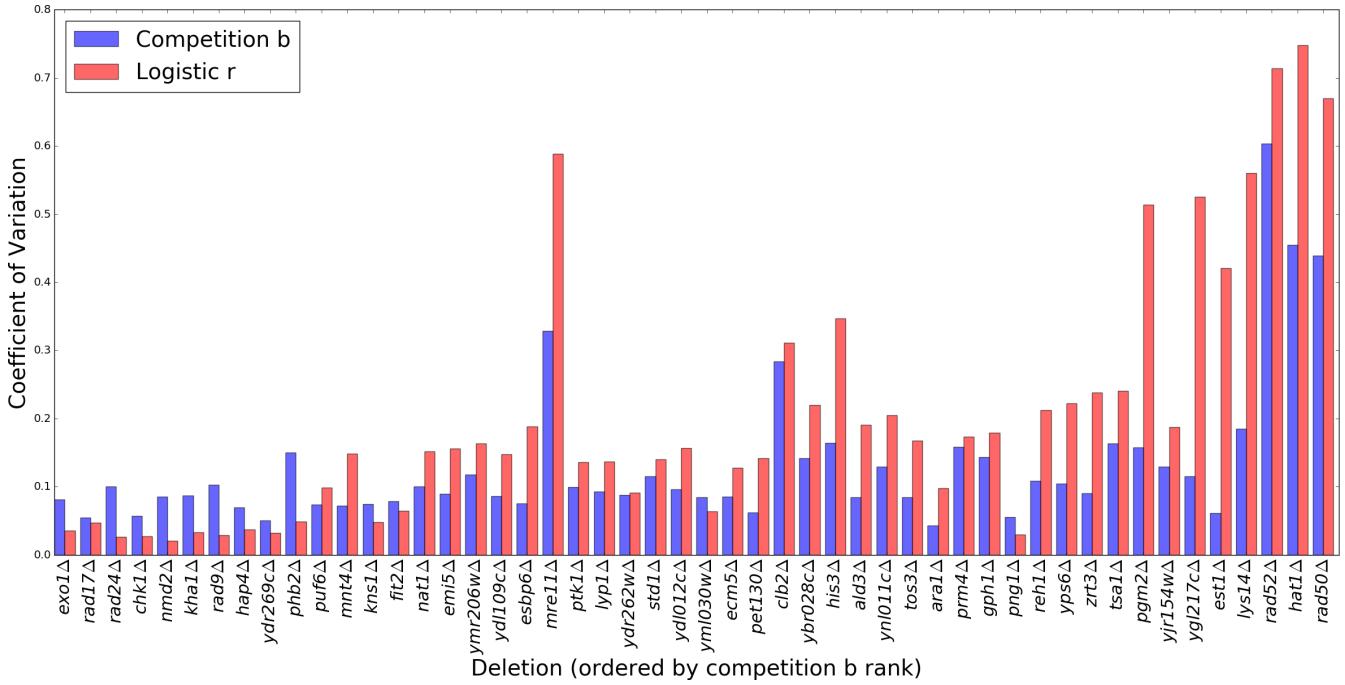


Figure 13: Coefficient of variation of r estimates. Strains are ordered left to right along the horizontal axis by highest to lowest competition model r ranking. Fits are for the competition model, the QFA R logistic model, and the logistic equivalent model.

3.7 Cross-plate validation

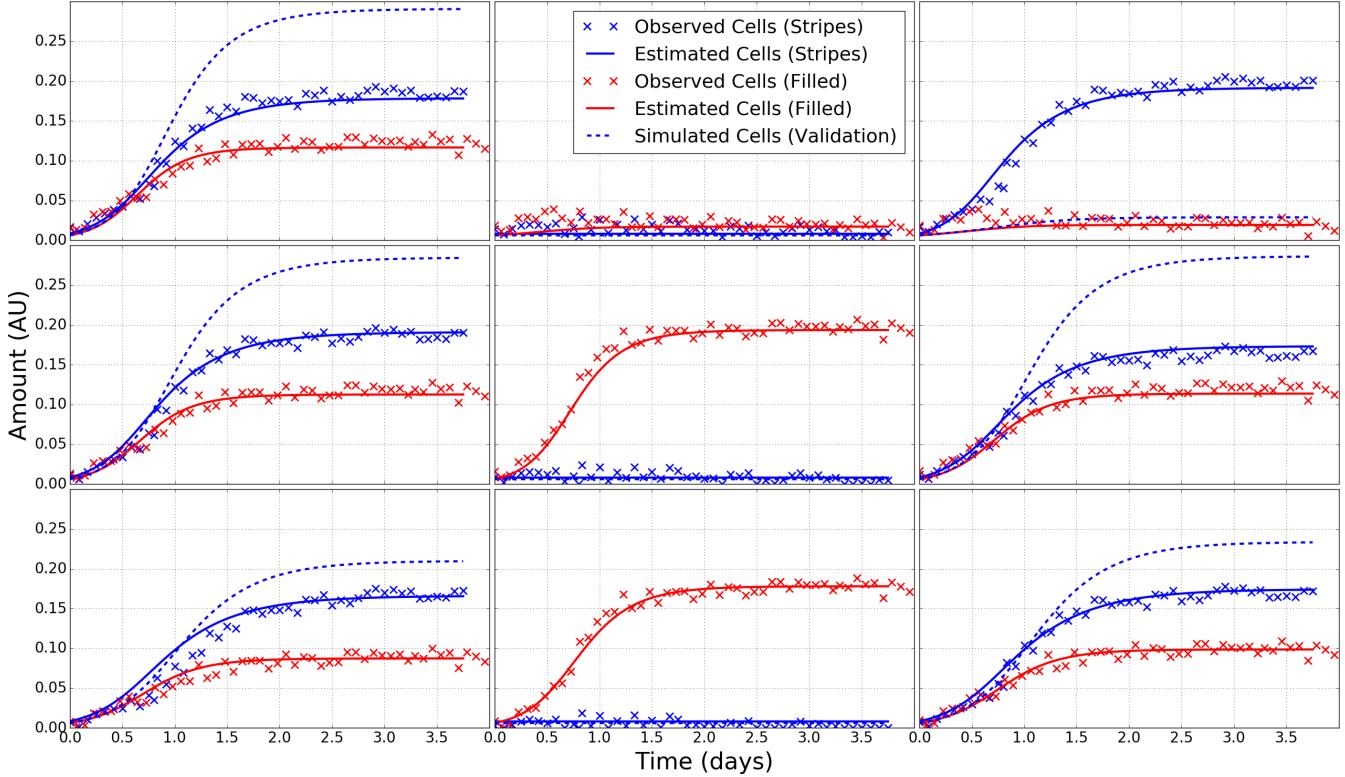


Figure 14: Calibration and validation of the competition model. I fit the competition model to the 16x24 format “Stripes” and “Filled” plates in Figure 2. The plot shows cell measurements and estimates for both plates for a 3x3 section with top left coordinates (R9, C10). I took the parameters estimates for the “Filled” plate (calibration) and set growth constant, b , to zero for cultures in the empty columns of the “Stripes” plate. I then simulated using these parameters to produce the dashed blue curve (validation). If the model is working correctly, the dashed blue curve should resemble the “Stripes” data (blue crosses).

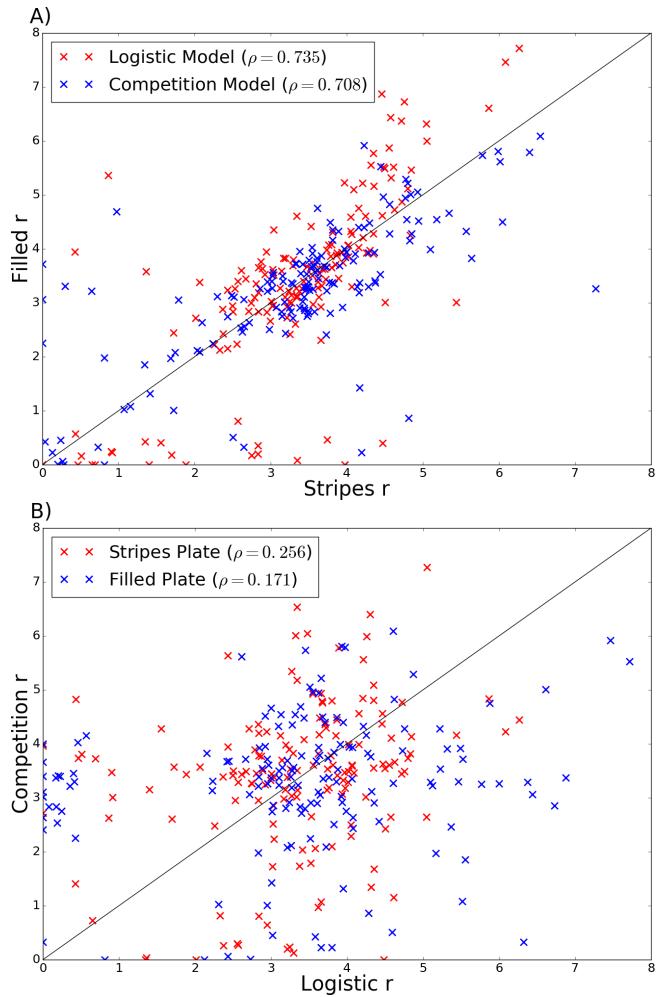


Figure 15: Correlation of r estimates for “Stripes” and “Filled” plates. A) Correlation of r estimates between plates for logistic and competition models. B) Correlation of r estimates between logistic and competition models for both plates. I fit the competition model and independent model to the “Stripes” and “Filled” plates in Figure 2. I converted competition model b to logistic model r . I only used data for cultures that were common between the two plates common and removed edge cultures. The Pearson correlation coefficient, ρ , is shown in the legends. The line $y = x$ is also plotted.

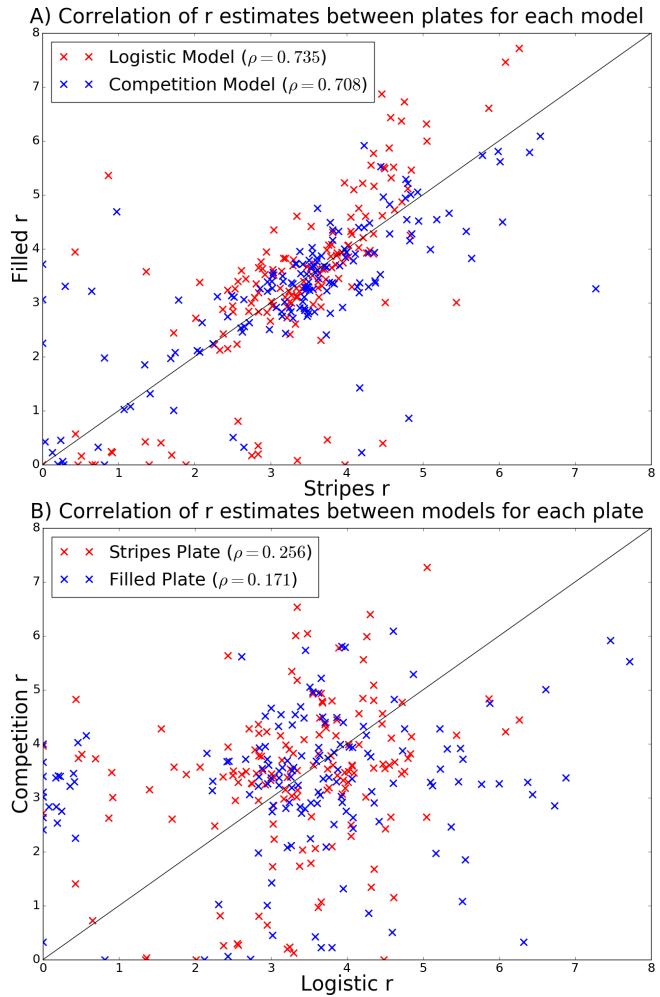


Figure 16: Correlation of r estimates for “Stripes” and “Filled” plates. I fit the competition model and independent model to the “Stripes” and “Filled” plates in Figure 2. I converted competition model b to logistic model r . I only used data for cultures that were common between the two plates common and removed edge cultures. The Pearson correlation coefficient, ρ , is shown in the legends. The line $y = x$ is also plotted.

3.8 Towards a genetic algorithm

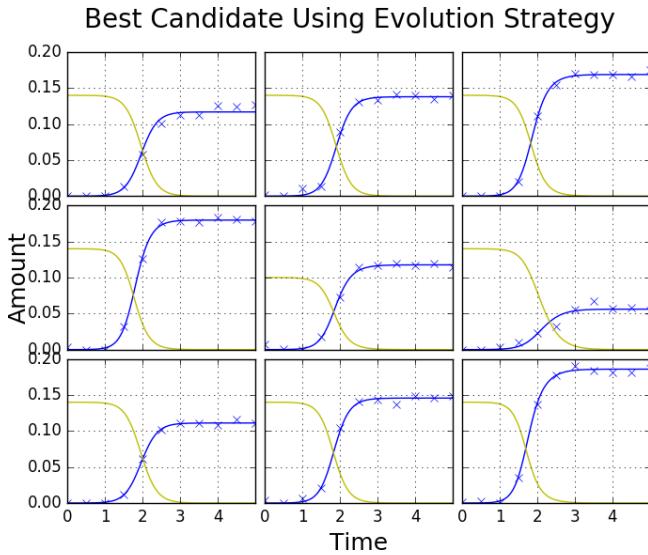


Figure 17: Genetic algorithm fit to a 3x3 simulation. MIGHT TAKE A LITTLE BIT OF WORK TO REPRODUCE AND COULD USE PARAMETERS FROM THE BEST P15 FIT RATHER THAN JUST PICKING/RANDOMIZING. NEED TO CHECK THAT PLATE LEVEL PARAMETERS WERE ALSO EVOLVED.

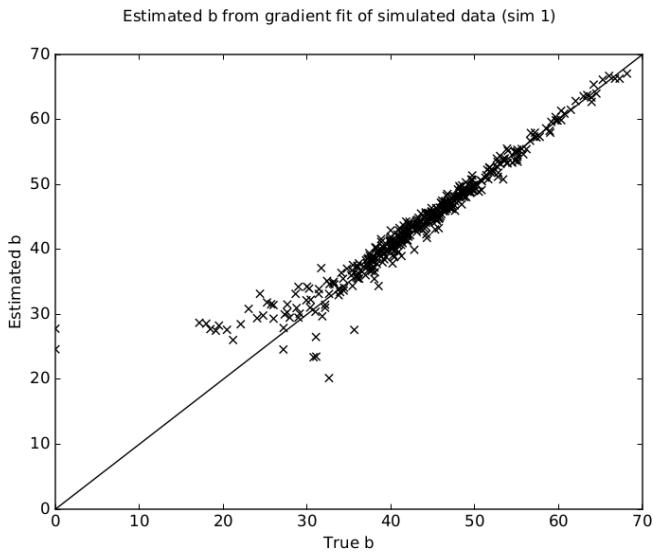


Figure 18: Recovery of true b values from a gradient method with fixed plate level parameters. I simulated timecourses from the best five (which model? all BC?) fits to p15, fixed the true plate level parameters, and used a gradient method to recover b . This plot shows the worst case from the five sets of values.

4 DISCUSSION

//Noise affecting competition model//

I also had some thoughts about why the competition model might have higher variance. The competition model has to deal with noise of the slowest growing cultures which affects both plate level parameter estimates and the b estimates of faster growing neighbours. I.e. sharing plate level parameters gives us more information about slower growing cultures but adds noise to our estimates of faster growing cultures. For

the logistic model, each growth curve is fit independently and so fast growing cultures are less affected by noise and may have less variance than competition model estimates. Conversely slow-growing cultures are dominated by noise and this requires us to use heuristic checks (accuracy is actually affected more than precision). This may be why we see more variance in the b estimates of fast growing cultures from the competition but less for medium and slow growing (probably also less overall). If we had a plate with no very slow growing cultures dominated by noise perhaps we would see less variance in the fastest growers from the competition model. We could probably use the filled plate to check this.

In light of heterogeneity. For independent fits may start with inoculum density below the level of detection and take time zero the time when cells first reach some observable level. I.e. different t_0 for each culture.

(Wait until discussion: Recent work by Herrmann and Lawless - issues with plate level C_{t_0} - Could approximate cells as not starting to grow until levels become detectable at t_i (OK if assume only small diffusion before this point)).

Possible to have fast nutrient limited diffusion without nutrinet competition and poisoning by ethanol. Separable.

Fitness ranking from competition model fits may be better than from logistic model fits (Will comparing stripes rankings reveal anythin?). However, we cannot quantitatively compare fitness estimates between plates because we are not finding global minima. Work has begun to develop a genetic algorithm to do so. I am not convinced that this will succeed because growth is systematically overestimated when we move from the filled to striped plate for all of the current best parameter solutions. This suggests an issue with the modelling approach; below I suggest ways in which this could be improved. In any case, qualitative cross-plate validation using order of fitness ranking may still be better (for the competition model).

The first thing to notice about QFA data - from P15, the striped plate, and the filled plate - is the characteristic endpoint in growth on each plate (experiments could be designed to study variation in timescales over regions of a plate by inoculating cultures in columns left-to-right according to fitness). This suggests a plate-level or region-level growth-limiting effect. // Could this conceivably be an experimental limitation such as the drying out of an agar plate over time? // Comparison of the striped and filled data, shows that cultures grow larger when neighbours are removed and this suggests a direct interaction between cultures. The strongest candidates are competition for nutrients and growth limiting signalling such as ethanol poisoning. It is possible that other growth limiting effects may exist and could confound any attempt to fit a model which accounts for just one of these. It makes sense to investigate each likely effect in turn to determine its contribution and to start by validating the independent limit.

Spots can grow after a long time. Must be nutrients remaining or an encroachment? I have an image for the stripes plate showing cultures growing and believe after a very late stage. I need to check the data images but this may just be encroachment of another culture.

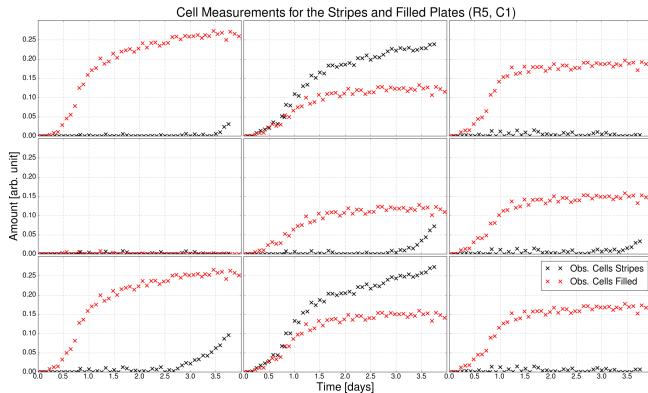


Figure 19: Observed cells for (R5, C1) 3x3 zone of Stripes and Filled plates showing (for Stripes data) slow growing cultures starting to grow after faster growing cultures have reached the stationary phase.

We have only studied data where cultures are grown in an array on solid agar where we cannot validate the independent limit. In this limit, our model says that nutrients can only be converted to cells and all cultures starting with the same amount of nutrients will reach the same final cell density. This ignores metabolism which may differ between strains. Cell arrest could also limit growth (and this may occur in different strains at different rates). If present, differences in such effects could account entirely for differences in final cell density. However, they are unlikely to be the only effect, because this would not lead to the observed characteristic endpoint in growth. Using one-culture spot tests (in a perte-dish on agar?) or liquid cultures we can grow cultures independently and validate the independent limit. A current issue with methods for estimating fitness, is that identical strains grow differently on agar or in liquid culture leading to different fitness rankings (cite). This problem need not affect our validation as we can simply define a culture to have different parameters for growth in either medium. A greater difference may be caused by the dimensionality of the environment. Mass action kinetics is derived for reactions in a three-dimensional (gas or fluid?) (Guldberg and Waage C.M. Guldberg and P. Waage, Studies Concerning Affinity, C. M. Forhandlinger: Videnskabs-Selskabet i Christiana (1864), 35) and this approximation is more valid for liquid cultures than for cultures spotted onto a surface. I suggest to study first the more ideal case of liquid cultures and later see if the model holds for cultures grown on a surface. If it does not, it may be necessary to use a fractal kinetics model (I have references for this from the proposal) or, if the reaction is diffusion limited, consider a more detailed model of nutrient diffusion.

// Model equations for metabolism//

Our model splits the agar into a grid with volume discretised per culture. In the stripes validation, we overestimate the effect of diffusion when neighbouring cultures are removed. I believe that we are not accurately capturing the point at which growth becomes diffusion limited and that nutrients are well approximated as being evenly distributed within the spatial scales that we model. A diffusion equation model could capture the local distribution of nutrients around a culture when the stationary phase is reached. Reo and Korolev (2014) use

the diffusion equation (with Neumann and Dirichlet boundary conditions) to simulate nutrient dependent growth of a single bacterial culture on a perte dish in two-dimensions. They create a sink for nutrients from culture growth and equate the flux of nutrients through culture area with the rate of increase in culture size. They model culture area as varying and keep culture density constant. We may instead keep culture area constant, allow culture density to vary, and use our mass action kinetic model (eq no.) for the nutrient sink and culture growth. Simulating or fitting this model could help us learn more about diffusion in QFA experiments. It is probably computationally unfeasible to use such a detailed model to fit a whole plate. However, if necessary, it may be possible to use a finer grid to increase compartmentalisation of nutrients to capture spatial heterogeneity in the distribution of nutrients around a culture and the effect of diffusion limited growth. This could extend the validity of the competition model over a larger range of variability in culture growth rates (for instance when some cultures are left empty and others are very fast growing.)

It would also be useful to determine experimentally how nutrients are distributed throughout the agar at the stationary phase. Gaps could be left in an array of cultures and only inoculated once the stationary phase is reached. If they grow then nutrients remain. (Sill require simulations to see distribution across depth). This could be extended by growing a single column of identical strains and, after the stationary stage has been reached, inoculating identical strains on the same plate at different distances from the row.

//Talk about an improvement to the imaginary neighbour model.//

Nutrients (sugars, nitrogen, etc.) in QFQ agars are of a standard composition, designed to reduce the excess of any single nutrient (check QFA paper and cite). ((background) What is the nutrient? Nitrogen is only used to build molecules for new cells, whereas sugars are also used for metabolism.) For modelling nutrient limited growth, especially across plates, it would be useful to know the identity of the limiting nutrient and ensure that it is always the same. We could achieve this using a different formula of agar.

The design of the stripes validation experiment could be improved. Rather than filling gaps with cultures not present on the stripes plate, and for which we have no b estimates, we could fill with repeats of the cultures already present on the stripes plate. (I'm not sure it makes any difference actually whether we validate from one direction to the other). It would also have been helpful to have repeats to study differences in COV between the competition and independent models. In order to make sure that competition effects were present in data, we made a drastic change between the stripes and filled plates. This provides a stern validation. The model assumes that competition effects are present whenever there is a difference in final cell amounts between cultures. We could have first validated the model against a smaller change, by varying between slower and faster growing cultures rather than none and very strong growing cultures. If the model works well between such plates it may work well for the majority

of QFA experiments which typically have smaller differences between cultures than the data we study. If we did want to test the in an extreme case we could have inoculated fast growing cultures next certain strains and not others to try to induce a change in ranking for which the competition model might compensate better than the logistic model.

//Signalling//

If we find that competition for nutrients is not a significant effect, for instance if growth becomes diffusion limited before nutrients from neighbours can be accessed, then we could instead model signalling by ethanol as the interaction effect. This may be modelled similarly to how we are already modelling nutrient diffusion.

//Signalling equation//

If there is any combination of competition, metabolism, signalling, or arrest contributing significantly to differences in the growth of cultures and the interaction between neighbours then it will be difficult to separate them when fitting a model to data. We may have to develop ways to calibrate effects in isolation (e.g. by adding/measuring ethanol?) and use this information when fitting to high-throughput data.

It is quicker to fit to small zones of a plate but as these have a larger proportion of edge cultures boundary conditions become important. In current data (e.g. P15), different cultures surround the edge and this makes accurate fitting difficult. As a result we must work with larger zones that take longer to analyse. We could surround small 3x3 and 4x4 zones with an empty ring and only need to consider net flux of nutrients across the boundary and not local variation due to different cultures surrounding the zone. We could also surround with the same, low-variance, strain to reduce net flux.

//Stochastic effects//

Unpublished work by Hermann and Lawless has investigated heterogeneity between cell lines within single QFA spots. They have found that a single or small number of extremely fast growing cell-lines come to dominate the population of a single culture. The implication is that cultures with a lower starting cell densities are likely to have greater variance between repeats. We could use higher starting cell concentrations to reduce this variance but then we study less of the growth phase. It may be possible to reduce heterogeneity by inoculating from the exponential growth phase rather than the stationary phase and still study full growth curves. (Unless mean population growth constant is being studied...) Starting cell densities should ideally be as close to the lowest resolvable level as possible.

//Ways to measure C_0 // There is a confounding effect between initial cell density and b value with may justify using initial cell densities slightly above the minimum detectable level. Heterogeneity within cultures is an issue again here and cell density would effectively be lower than the measured value, e.g., if most inoculated cells are dead or slow growing.

To fit growth curves more accurately QFA has begun using the generalised logistic model (cite). Fitness estimates (MDR*MDP or MDR?) from this model have higher coefficient of variation than those from either the standard logistic or competition model. (accuracy and precision? Could for

instance a step function be less variable than the standard logistic model?) Although the fits to data are qualitatively worse, it may be advisable to revert to the standard logistic model.

The logistic model requires different K parameters (N_0 for log. eq.) to be fit for each culture. The competition model shares information about N_0 between cultures and therefore has 383 fewer parameters for a full plate (Could this also explain the higher variance for the fastest growers?). For the slowest growing cultures, noise is more dominant and there is a confounding effect between r and K. To deal with this, the QFA R package uses heuristic checks. In the case of *est1Δ*, this has led to a dramatic disagreement in estimated fitness with the competition model. The estimate from (which model)? agrees better with existing biological knowledge (/independent spot experiments?). (Is the competition model then useful?)

//QFA R is fixing C_0 rather than fitting (I used a grid)//
//Improvement to imaginary neighbour guessing//

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