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

Author: Daniel Boocock; Supervisor: Dr Conor Lawless

August 5, 2016

ABSTRACT

Motivation: The fitness of microbial strains can be estimated from the growth of cultures inoculated onto solid agar. In high-throughput procedures, an array of cultures is grown on the same agar plate and competition for nutrients between cultures is likely to affect growth. However, analysis assumes that cultures grow independently. We test a model of nutrient dependent growth and diffusion and try to correct for competition to provide more accurate and reliable fitness estimates.

Results: What should we say?

Availability and Implementation: CANS, a Python2 package developed for the analysis in this paper, is freely available from (github or PyPI).

Contact: daniel.boocock@protonmail.ch

1 INTRODUCTION

Dummy Lawless *et al.* (2010) citations (Heydari *et al.*, 2016) (Addinall *et al.*, 2008).

1.1 Subsection

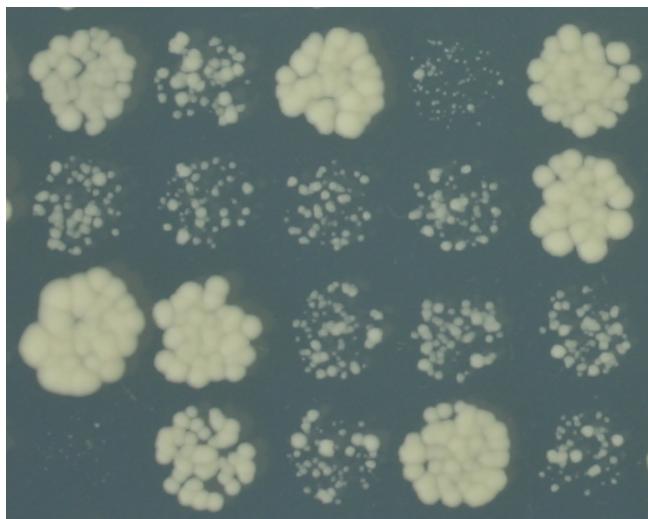


Figure 1: A section of a plate from a QFA experiment (Addinall *et al.*, 2011).

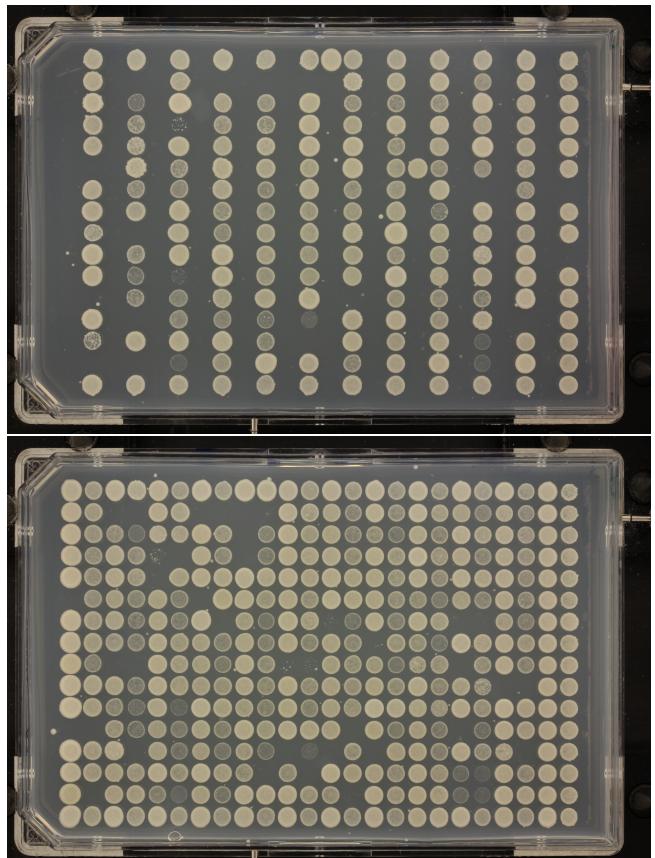


Figure 2: Images from an experiment designed to examine competition.

2 METHODS

2.1 Subsection

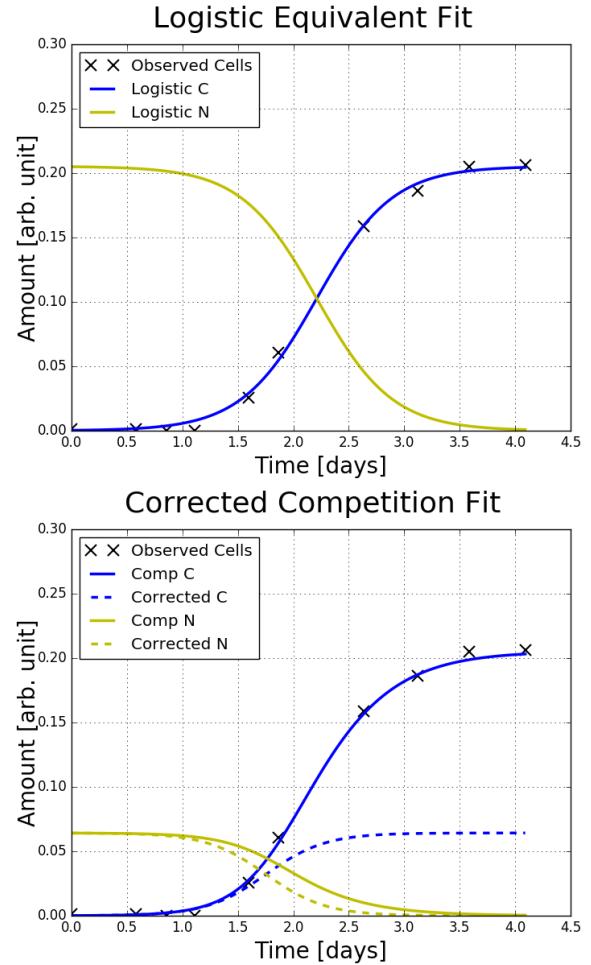


Figure 4: PUT KN VALUES (and r and K) ON THE PLOT. (Could even put obj fun values). Fits to culture (R10, C3) of P15 (Addinall et al., 2011) illustrating how the competition model can be seen as a correction to the logistic model. C - Cells; N - Nutrients. Top - Logistic Equivalent Fit; Bottom - Competition Fit (solid) and Corrected Logistic Equivalent Fit (dashed).

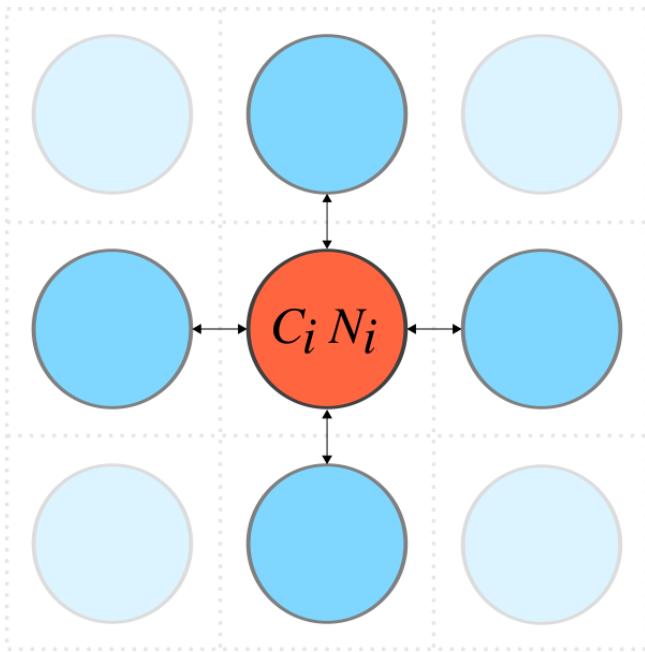


Figure 3: Schematic of the modelling approach. Each circle represents a culture, indexed i , on solid agar and arrows represent diffusion of nutrients. C_i - amount of cells; N_i - amount of nutrients; darker blue circles- neighbourhood δ_i .

3 RESULTS

(Palková et al., 1997)

3.1 Guessing

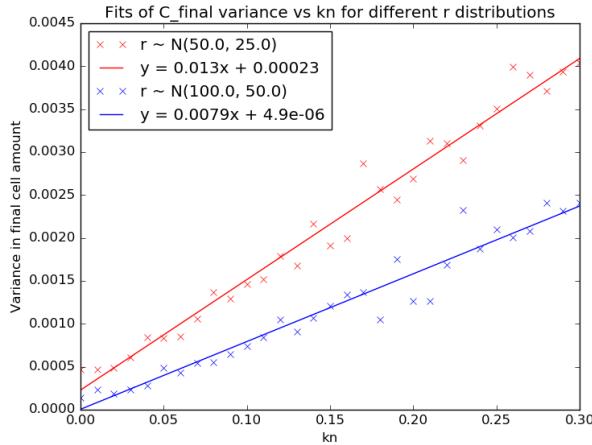


Figure 5: Guessing k_n from variation in final cell amounts.

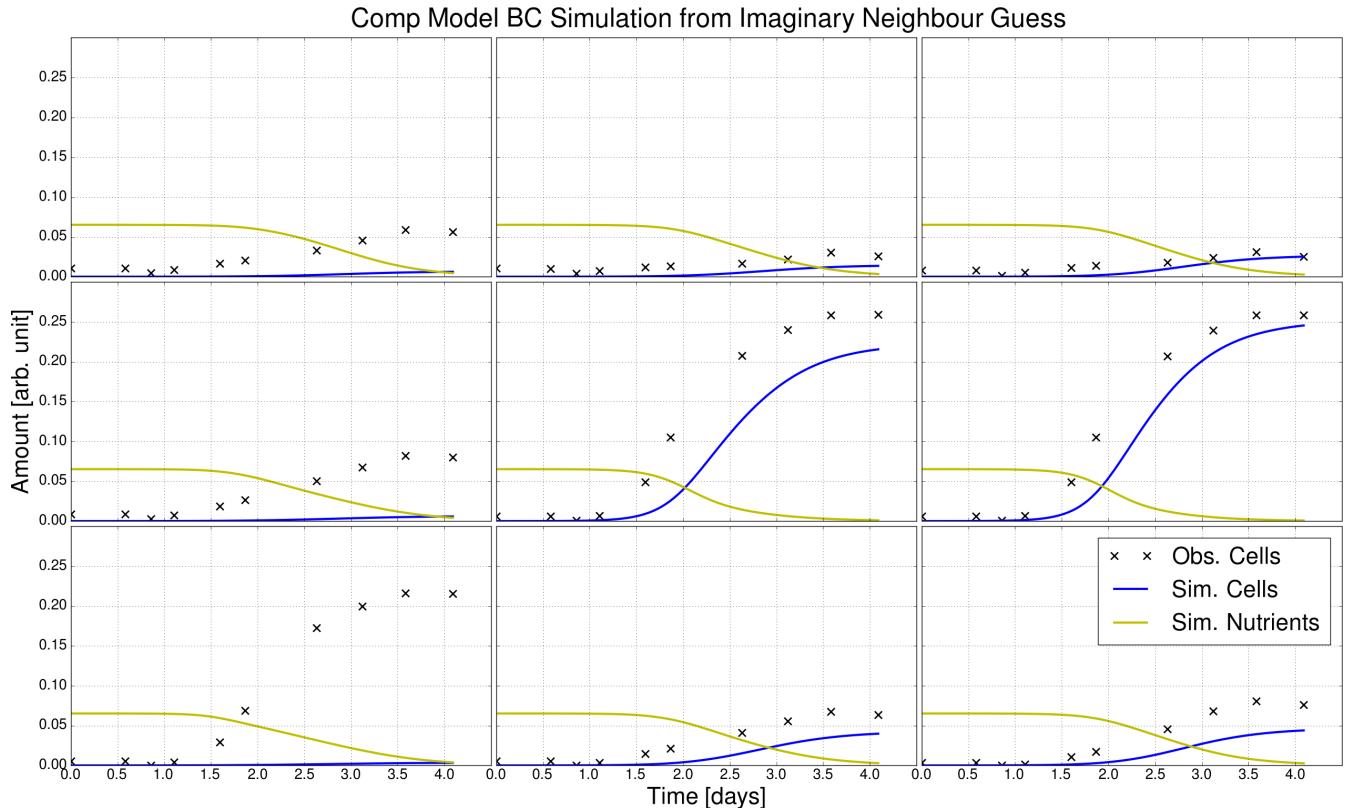


Figure 6: Comp Model BC simulation using parameters from Imaginary Neighbour guessing of P15 for cdc13-1 P15 at 27C (R5, C18). NOT TO GO HERE This method of guessing requires a b-guess to be supplied to fix the faster growing neighbour. I iterated through cell ratios. I iterated through a range of b guesses supplied at the plate level; running a different script with a C_0 guess, b_{guess} . It would probably have been better iterate through a list of b-guess values for each culture and choosing the estimated b value from the best fit of each culture. Guessing time is currently about four minutes which is fast compared to fitting which takes approximately three hours. However, this is unlikely to stop us from encountering local minima when we fit the Competition Model.

Scripts were run with combinations of the following values. `cellratios = np.logspace(-3, -5, num=5)` `fittype = ["imagineigh", "logeq"]` `zerokn = [True, False]`

Each script looped through the following array of b values which were supplied to the initial guesser and used at the plate level.

for b-guess in [35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 95, 100, 150]:

Each b-guess value is used to guess a complete set of b parameters for every culture in the plate. Each of these parameter sets is then used as an initial guess to Competition Model fitting. For the 13 b-guesses we must run 13 Competition Model fits. It would be better and more efficient to loop through the b-guesses at the culture level. Each culture still undergoes imaginary neighbour guessing with each of the 13 b-guess values, but now, for each culture, we choose just the b estimate from the best of the 13 fits. This will produce one set of b guesses which should be superior to any of the guesses attained when iterating through b-guess at the plate level. Then we only need to fit the Competition Model to 1 guess rather than 13. This will reduce

the number of scripts that need to be run in parallel, or the use of a finer grid over C_0 , and should make convergence faster. However, if using a gradient method we are still likely to encounter local minima from these guesses. Instead, this improvement could be considered when developing a genetic algorithm (if initial guesses are required) or if fitting using a brute force method with a fine grid of fixed plate level parameters. We will see later that with true plate level parameters fixed we can recover good estimates for b using a gradient method. It may be possible to evolve candidates of plate level parameters, fix these, and minimise using the current gradient method.

3.2 Competition Model Fitting to P15

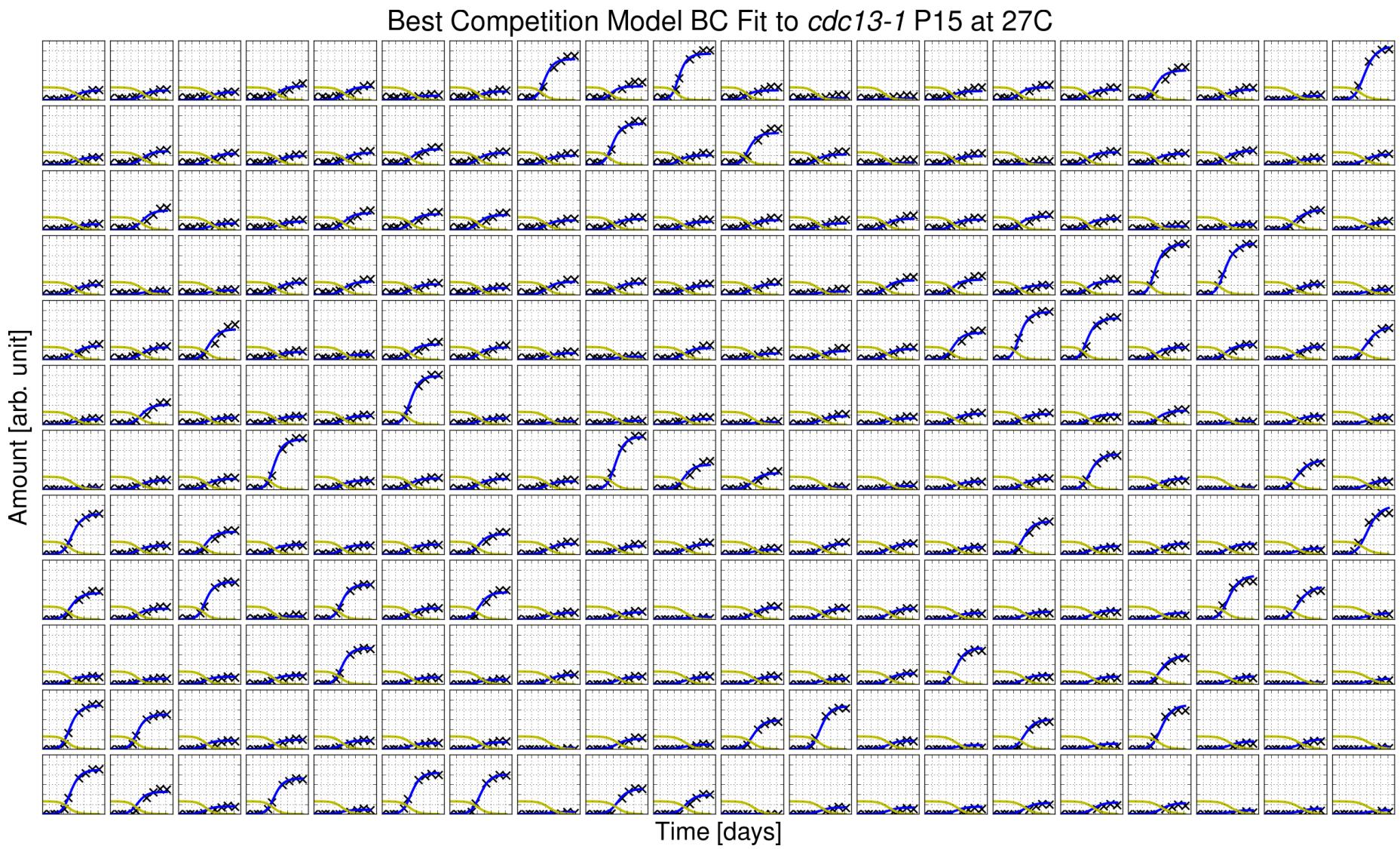


Figure 7: (R5, C18) P15 requires legend

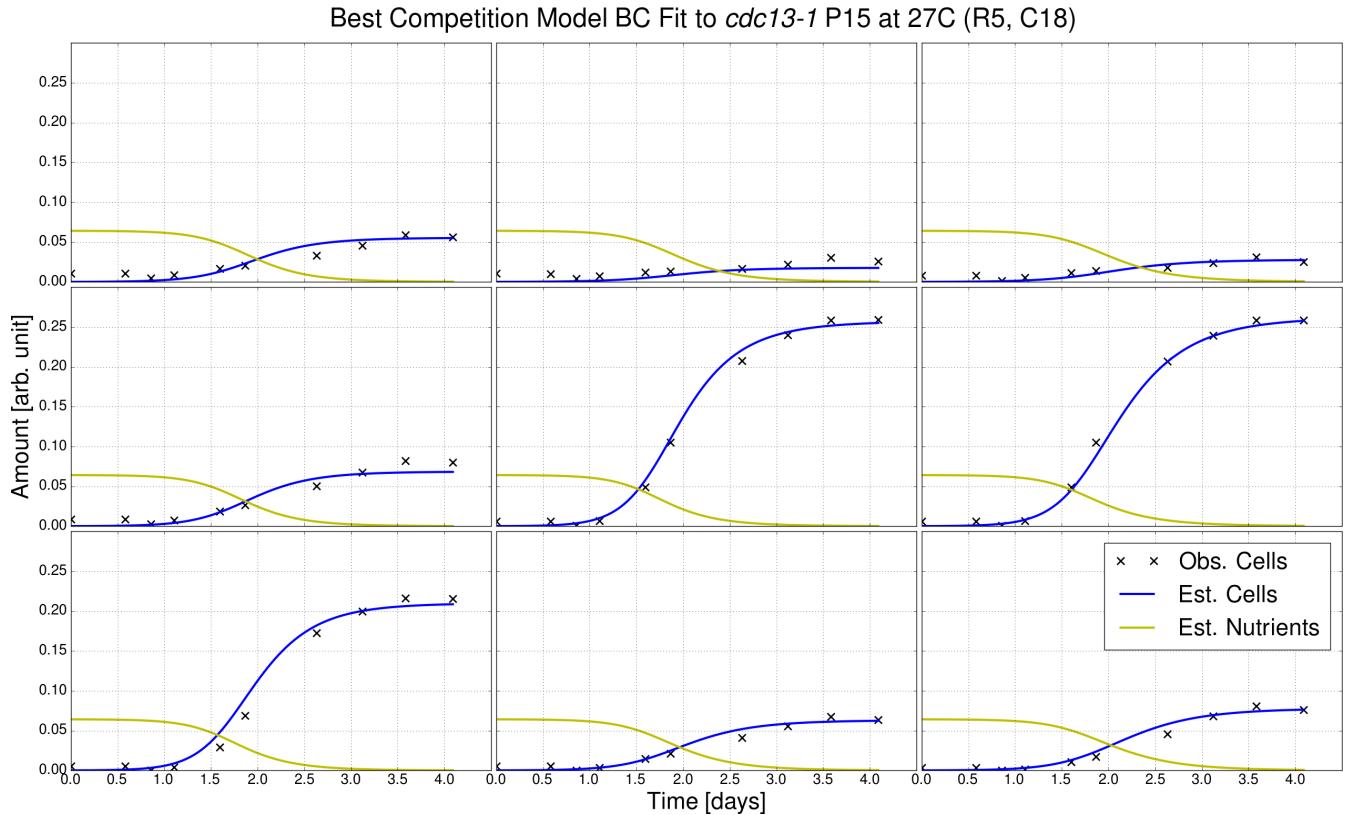


Figure 8: (R5, C18) P15

3.3 Evaluating the treatment of boundaries

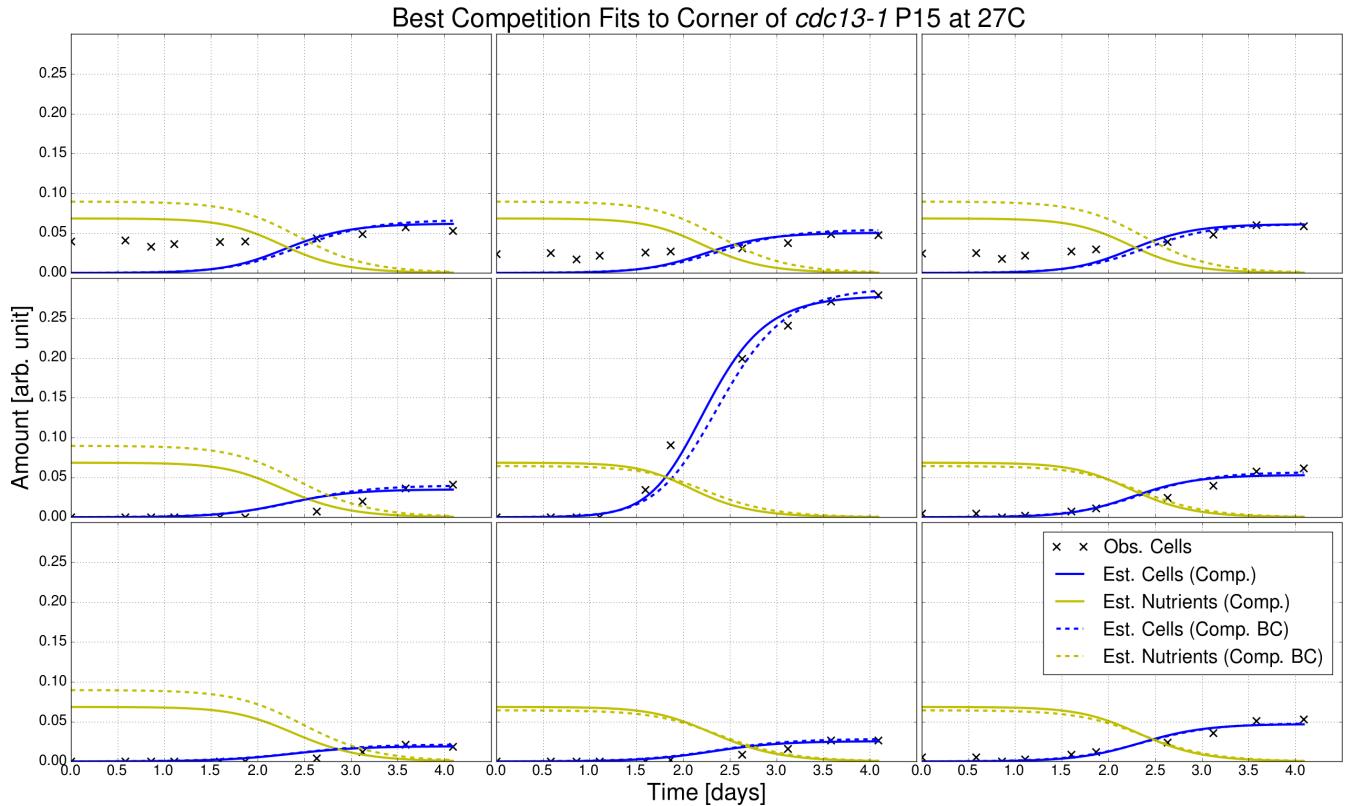


Figure 9: Top left corner of the Competition Model and Competition Model BC estimates for P15. NEED TO FIND OBJ FUN FOR DEPTH ONE AND TWO AND COMPARE TO AVG OBJ FUN FOR WHOLE PLATE (JUST DIVIDE BY 384). ALSO FIND COV FOR THE HIS3 EDGES.

3.4 Agreement of b rankings

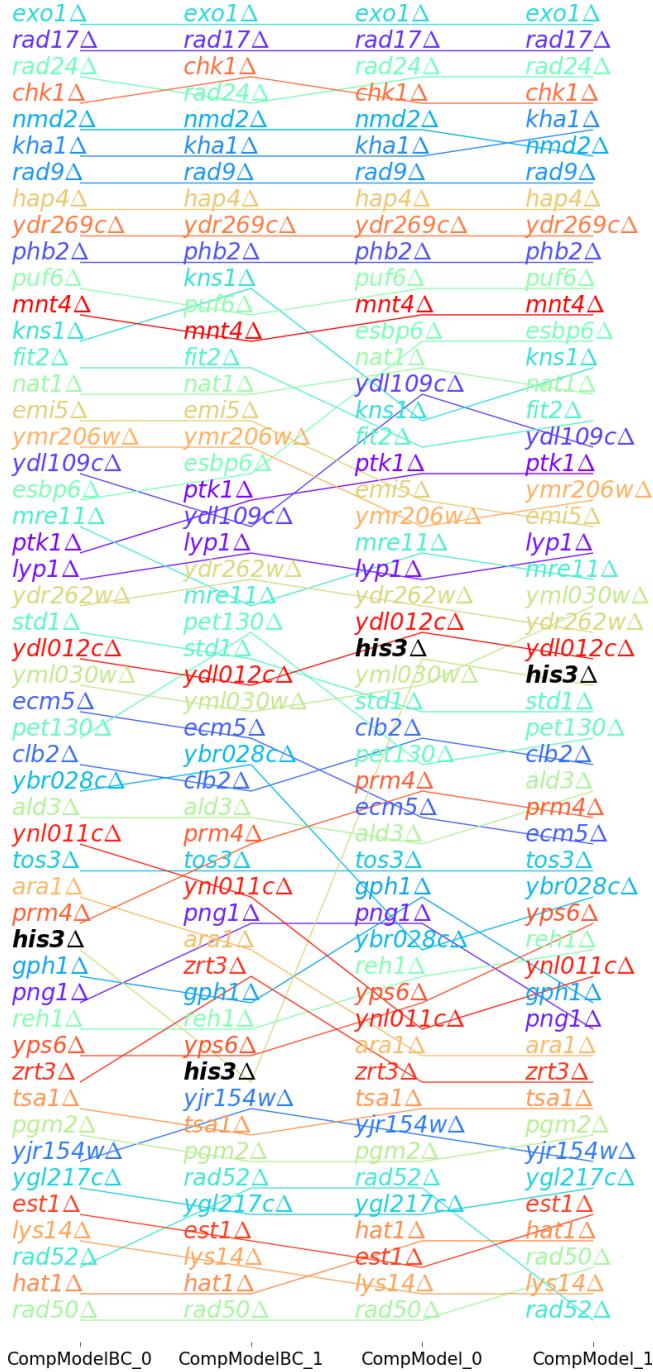


Figure 10: Comparison of *b* ranking for best five Competition Model fits P15. Includes HIS3 from edge cultures (could separate or exclude these).

3.5 Comparison of fitness ranking



Figure 11: *r* correlations for Comp Model BC, QFA R logistic, and logistic equivalent P15. INSTEAD GO WITH MDR AND USE GENERALIZED LOGISTIC MODEL AS WELL? ADD P-VALUES.

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.

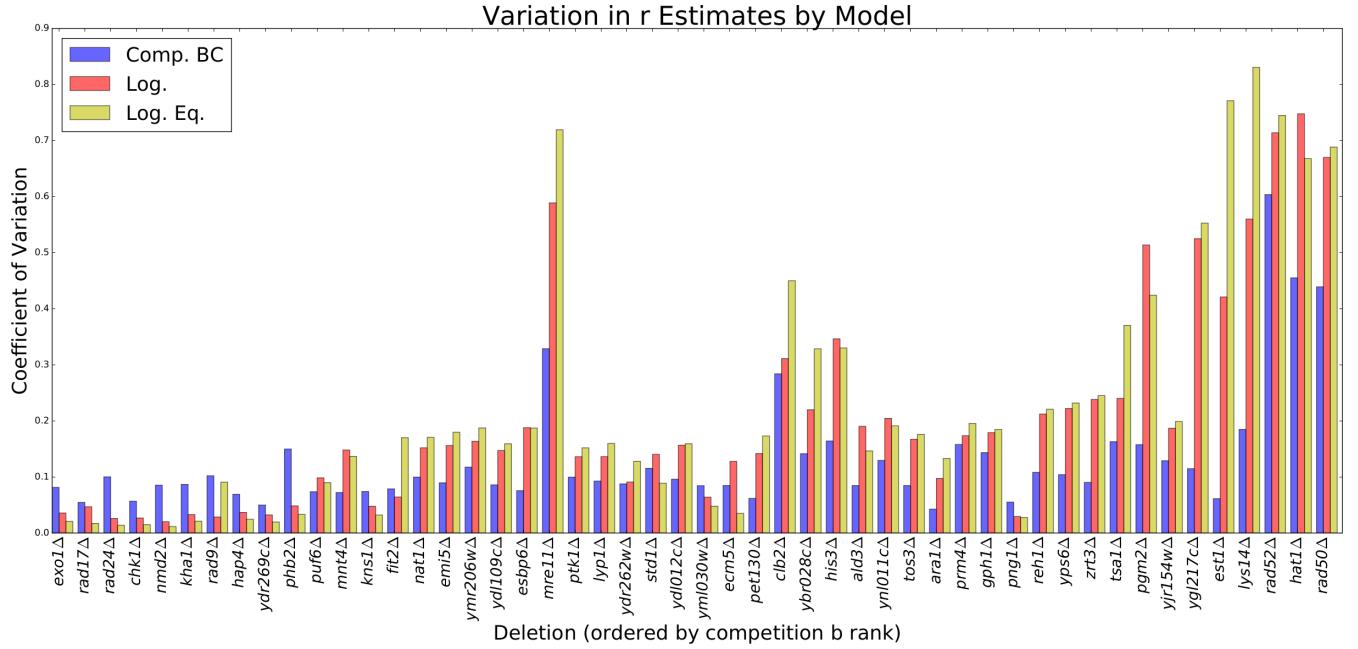


Figure 12: Coefficient of variation of r estimates from fits of the Competition Model BC, the QFA R Logistic Model, and the Logistic Equivalent Model to P15.

3.7 Cross-plate validation

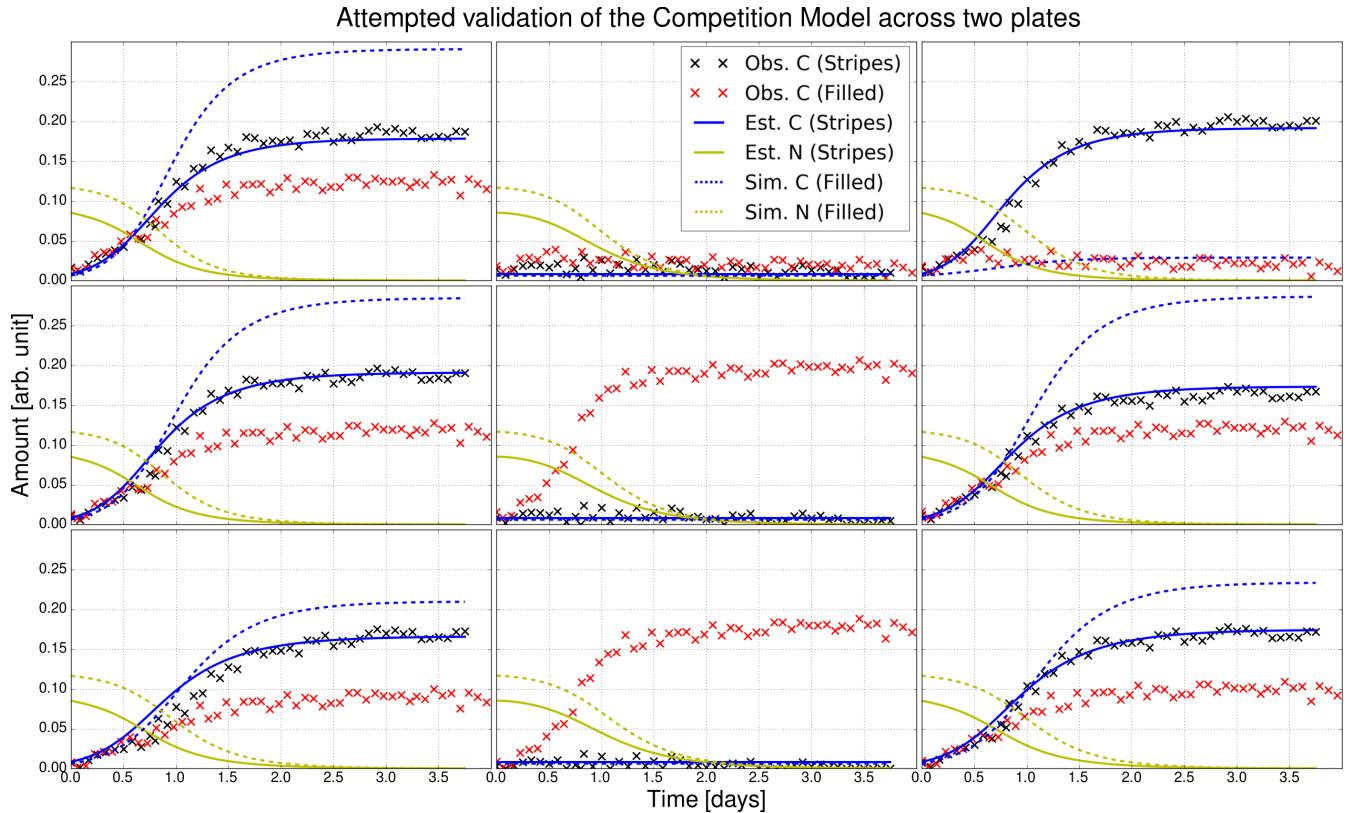


Figure 13: (R9, C10) top-right probable pinning mistake. Bottom-left not close to any such mistake. This is quite an extreme step between experiments. Perhaps we could have tried validating against weaker growing cultures rather than none.

3.8 Towards a genetic algorithm

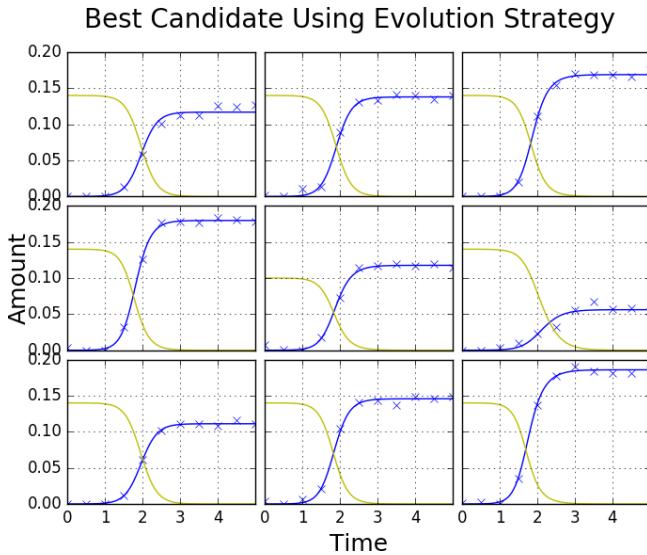


Figure 14: Genetic algorithm fit to a 3x3 simulation. MIGHT TAKE A LITTLE BIT OF WORK TO REPRODUCE AND COULD USE PARAMETERS FROM THE BEST P15 FIT RATHER THAN JUST PICKING/RANDOMIZING. NEED TO CHECK THAT PLATE LEVEL PARAMETERS WERE ALSO EVOLVED.

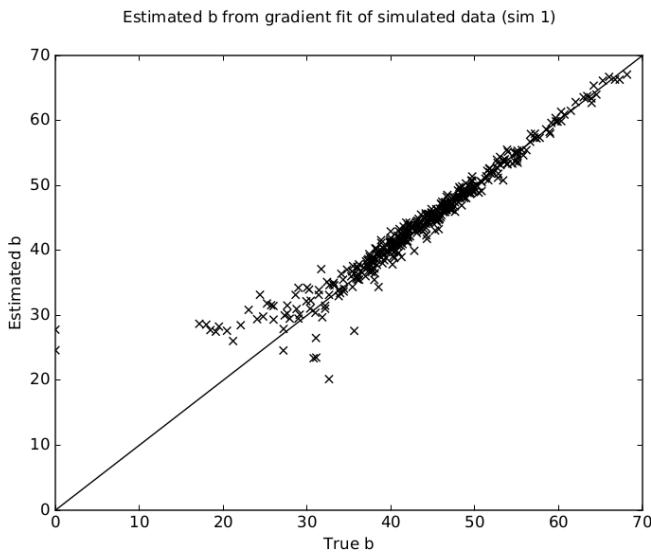


Figure 15: Recovery of true b values from a gradient method with fixed plate level parameters. I simulated timecourses from the best five (which model? all BC?) fits to p15, fixed the true plate level parameters, and used a gradient method to recover b . This plot shows the worst case from the five sets of values.

4 DISCUSSION

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 be-

cause 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.

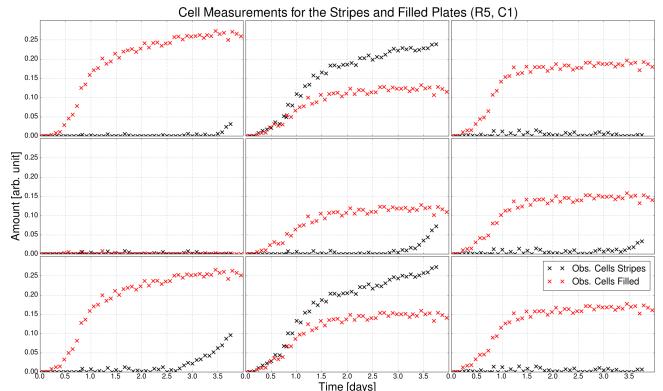


Figure 16: Observed cells for (R5, C1) 3x3 zone of Stripes and Filled plates showing (for Stripes data) slow growing cultures starting to grow after faster growing cultures have reached the stationary phase.

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 petri-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.//

Reo and Korolev (2014) simulate nutrient dependent growth of a single bacterial culture on a petri dish in two-dimensions using the diffusion equation and Neumann and Dirichlet boundary conditions. They create a sink for nutrients from culture growth and equate the flux of nutrients through the 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 for the nutrient sink and culture growth. Simulating or fitting this model could help us learn more about diffusion in QFA experiments. I am interested to know whether growth becomes diffusion limited at some time-point (before nutrients are fully depleted) and what area of nutrients a culture can access within this time. It is probably unfeasible to use such a detailed model to fit a whole

plate because of the computational time this would take. However, if necessary, it may be possible to use a finer grid to increase compartmentalisation of nutrients. 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. 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.//

The composition of nutrients (sugars, nitrogen, etc.) in QFQ agars follows a traditional recipe 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 better if we knew the identity of the limiting nutrient and could ensure that it is always the same molecule. This could be achieved using a different formula of agar.

We could have designed the stripes validation experiment better. Rather than filling the gaps with cultures which were not grown on the stripes plate, and for which we had no b estimates, we could have repeated the cultures from 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 used stripes and filled plates with drastic differences. This is a stern test of the competition model. 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) the cultures surrounding the edge may be very different from each other and this makes accurate fitting difficult. As a result we need to use larger zones are more difficult to work with. If we could surround small 3x3 and 4x4 zones with an empty ring then we would only need to consider the net flux of nutrients into or out of the zone and not the variation cultures surrounding the zone. We could also surround with an identical strain to reduce net flux although then we would have to consider biological variance.

//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 comes 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 the effect by taking cells to be inoculated 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. There is still the issue of heterogeneity if not all of these cells grow as starting cell density would then effectively be lower than the measured value.

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//

REFERENCES

- Addinall, S.G. *et al.* (2008) A genomewide suppressor and enhancer analysis of *cdc13-1* reveals varied cellular processes influencing telomere capping in *Saccharomyces cerevisiae*. *Genetics*, **180**, 4, 2251–2266.
- Addinall, S.G. *et al.* (2011) Quantitative fitness analysis shows that nmd proteins and many other protein complexes suppress or enhance distinct telomere cap defects. *PLoS Genet*, **7**, 4, 1–16.
- Heydari, J. *et al.* (2016) Bayesian hierarchical modelling for inferring genetic interactions in yeast. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, **65**, 3, 367–393.
- Lawless, C. *et al.* (2010) Colonyzer: automated quantification of micro-organism growth characteristics on solid agar. *BMC Bioinformatics*, **11**, 1, 1–12.
- Palková, Z. *et al.* (1997) Ammonia mediates communication between yeast colonies. *Nature*, **390**, 6659, 532–536.