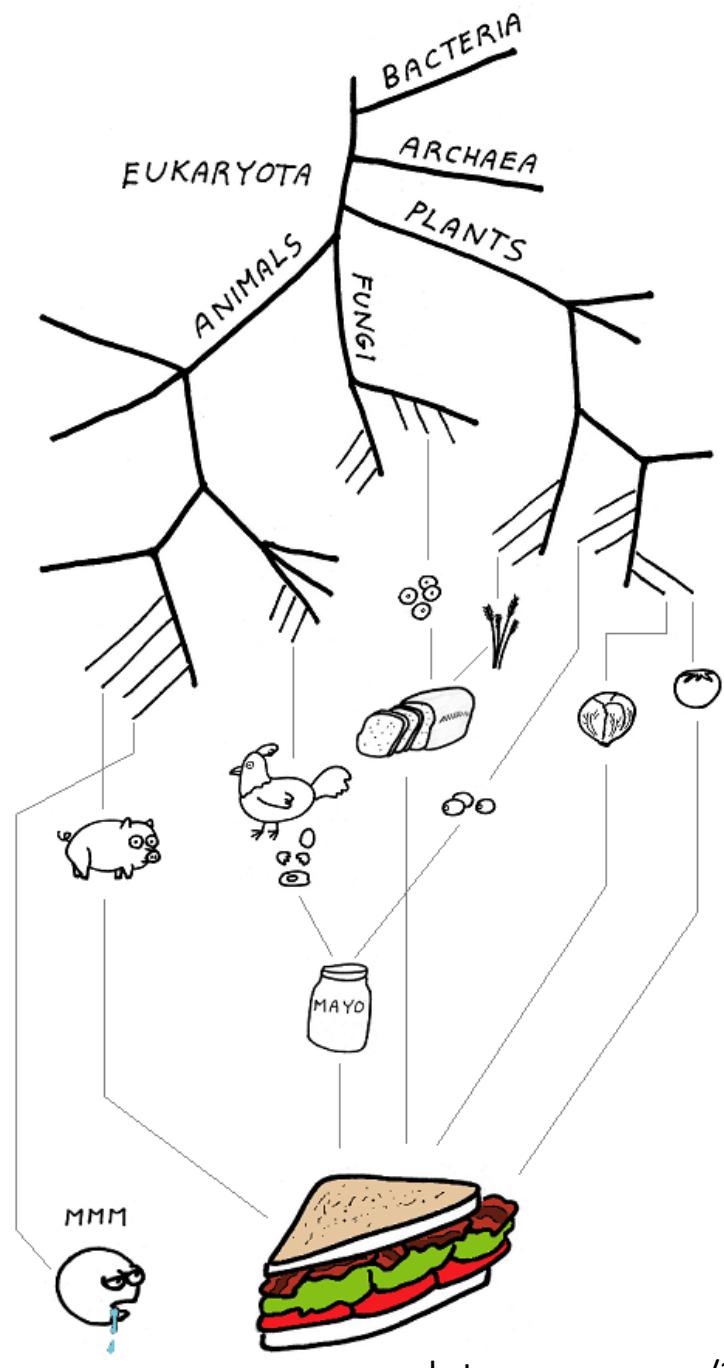


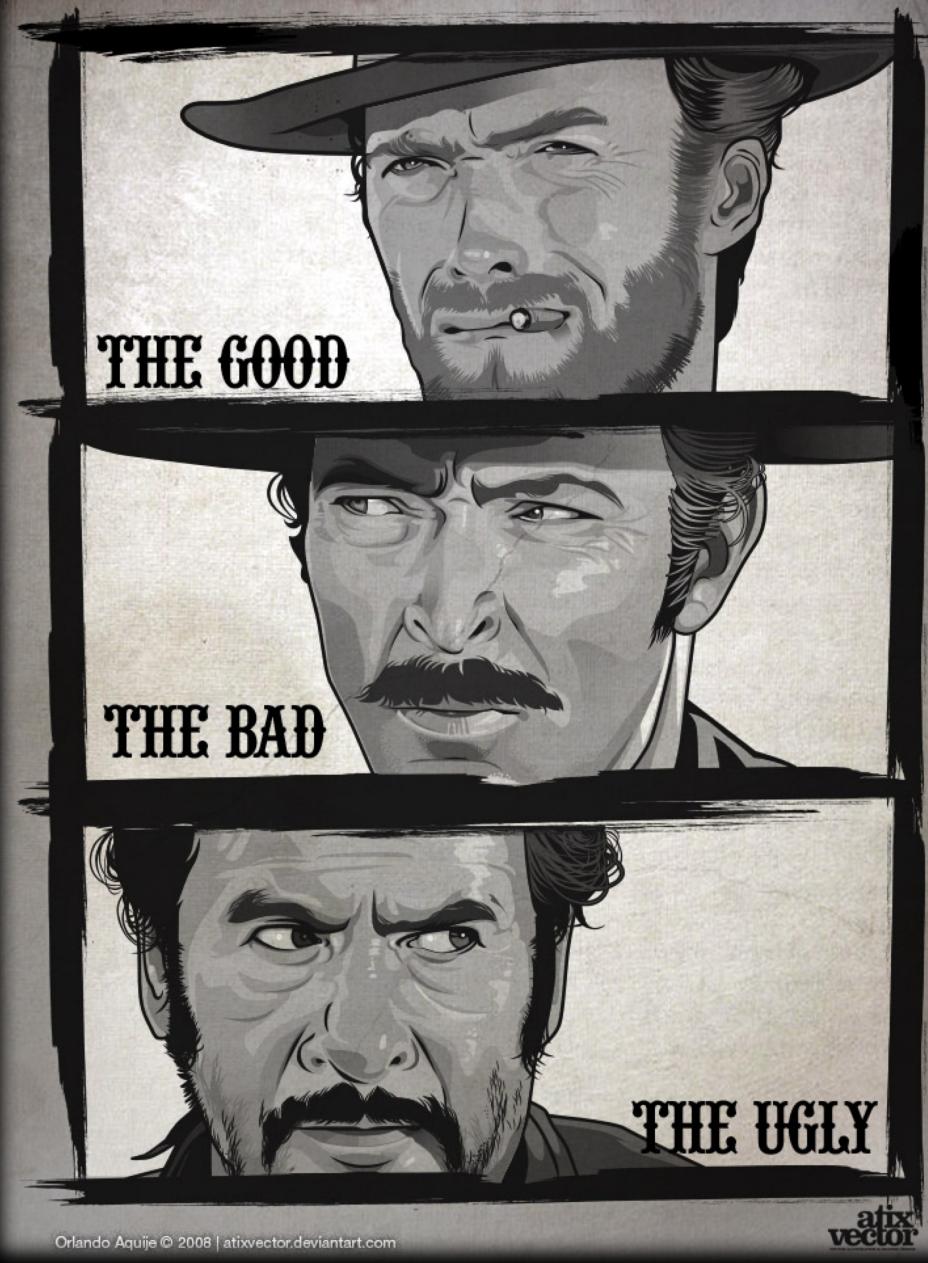
Eco-Evo Lunch

Yoav Ram

Feldman Lab
Stanford University
7 February, 2017



The Evolution of Stress-Induced Mutagenesis



Mutation rate evolution 101

Constant environment

- High mutation rates reduce *adaptedness* of populations
- The **reduction principle** - selection will reduce the mutation rate Liberman & Feldman 1986



Changing environment

- Natural selection favors *adaptability* – ability to adapt



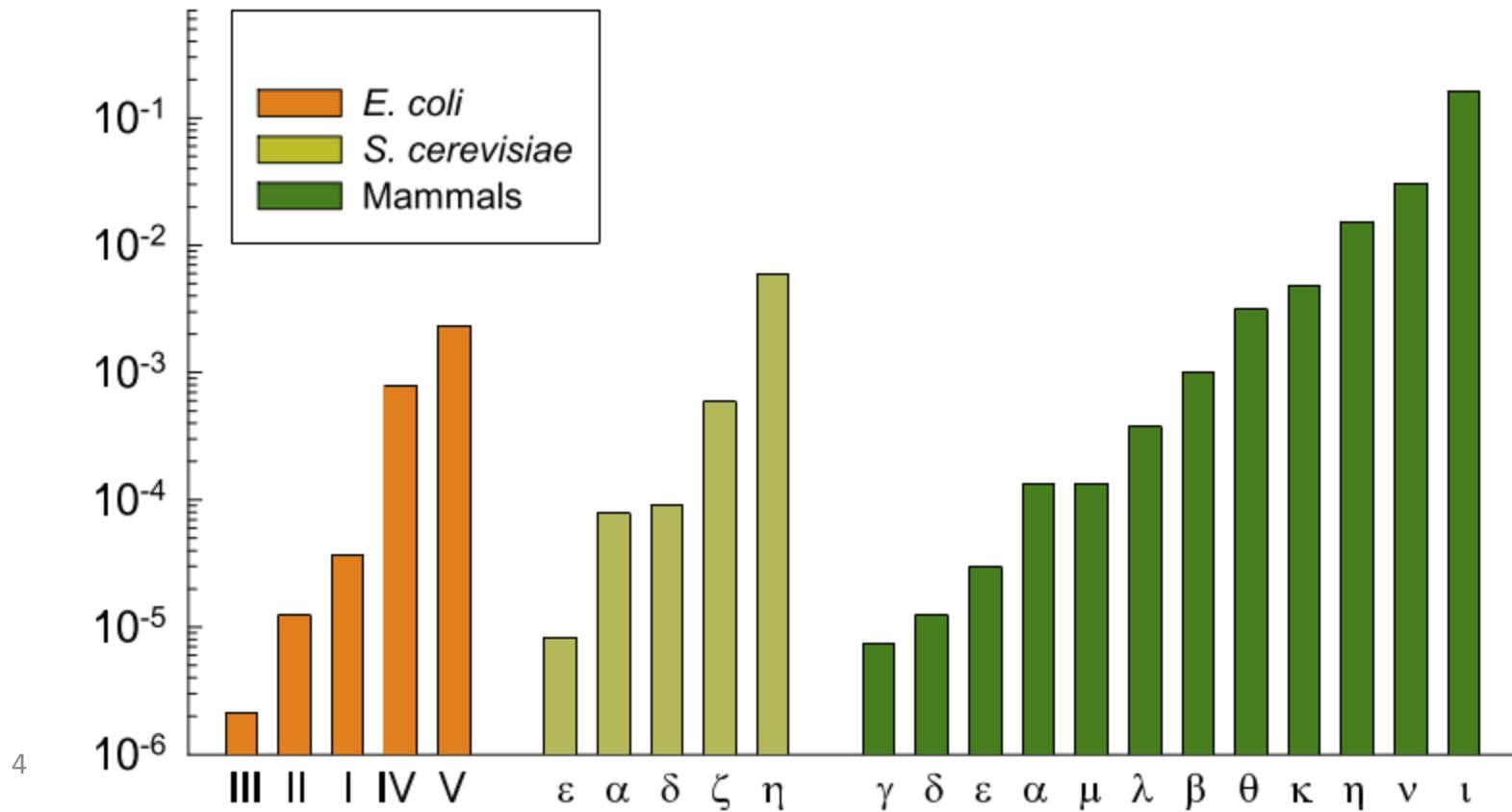
Trade-off

- The mutation rate must balance between *adaptability* and *adaptedness* Leigh 1973

Variability in mutation rates

Within individuals

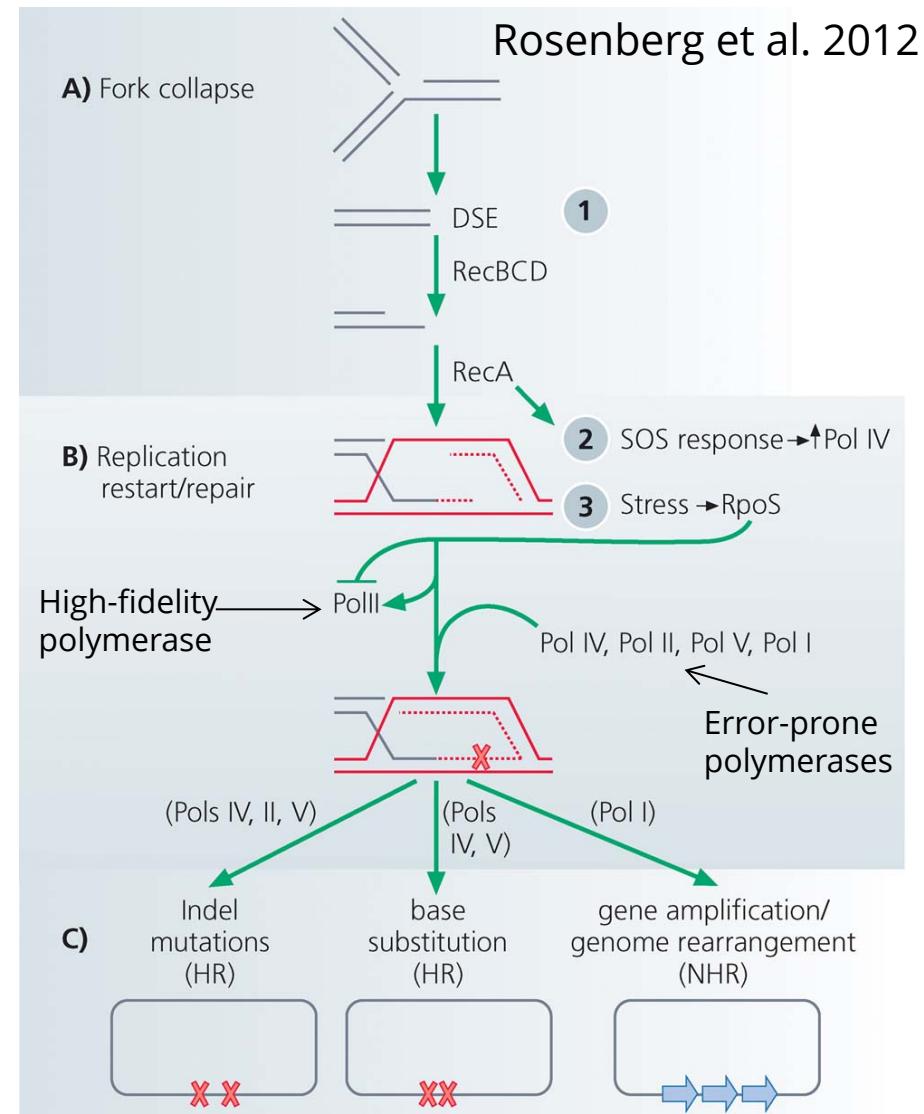
DNA polymerase error rate Lynch 2011



Stress-induced mutagenesis

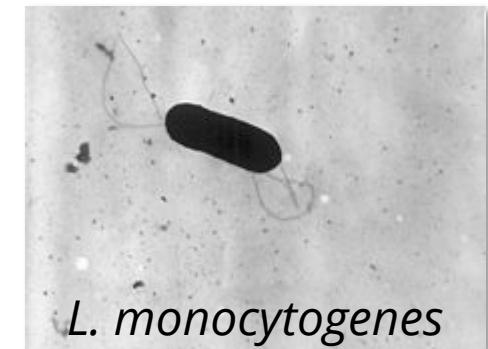
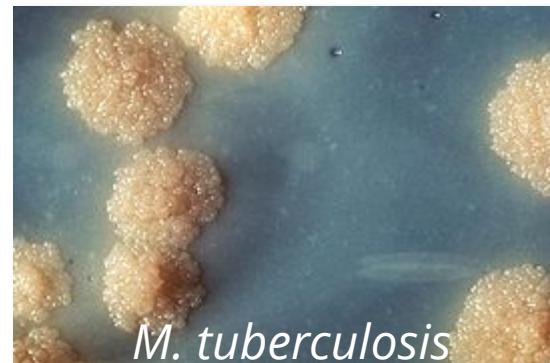
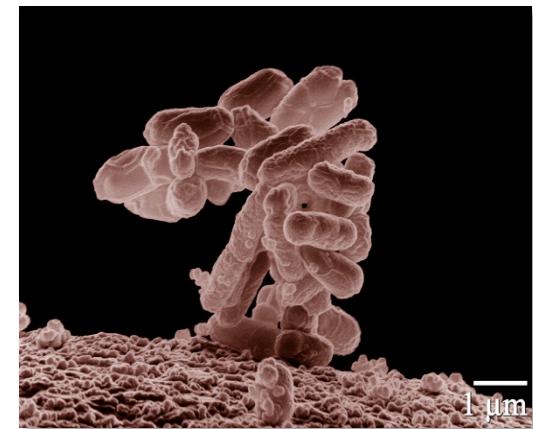
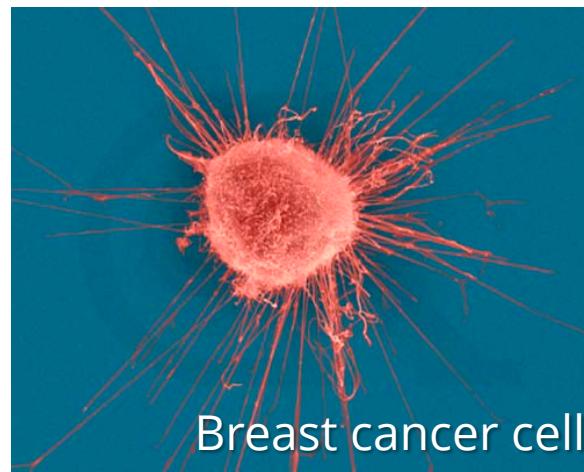
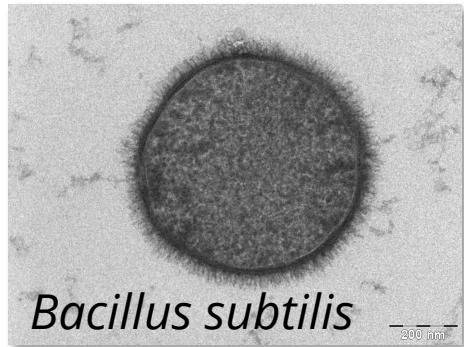
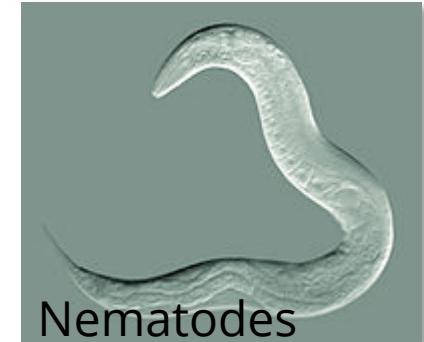
In *E. coli*:

- Error prone polymerase induced by stress responses:
 - SOS response
 - DNA damage
 - Starvation
- Mismatch repair system
- Other mechanisms:
 - Galhardo et al. 2007
 - Al Mamun, Science 2012





Evidence



Evolution of stress-induced mutagenesis

Null hypothesis

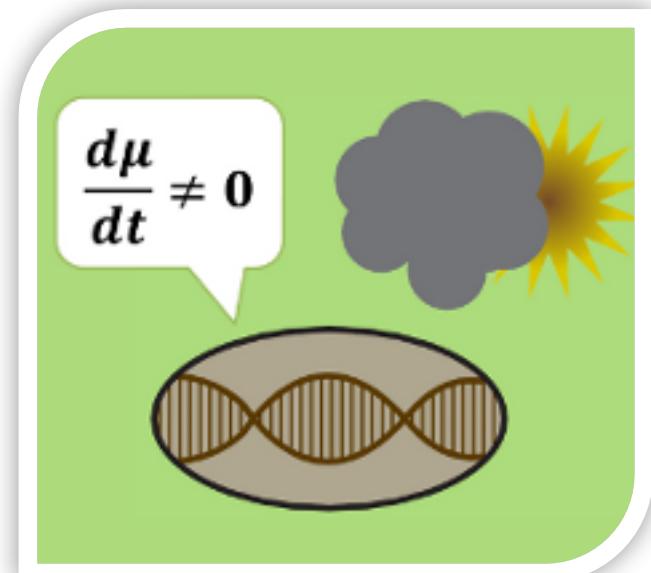
- Mutagenesis is the by-product of stress

Alternative non-adaptive hypotheses

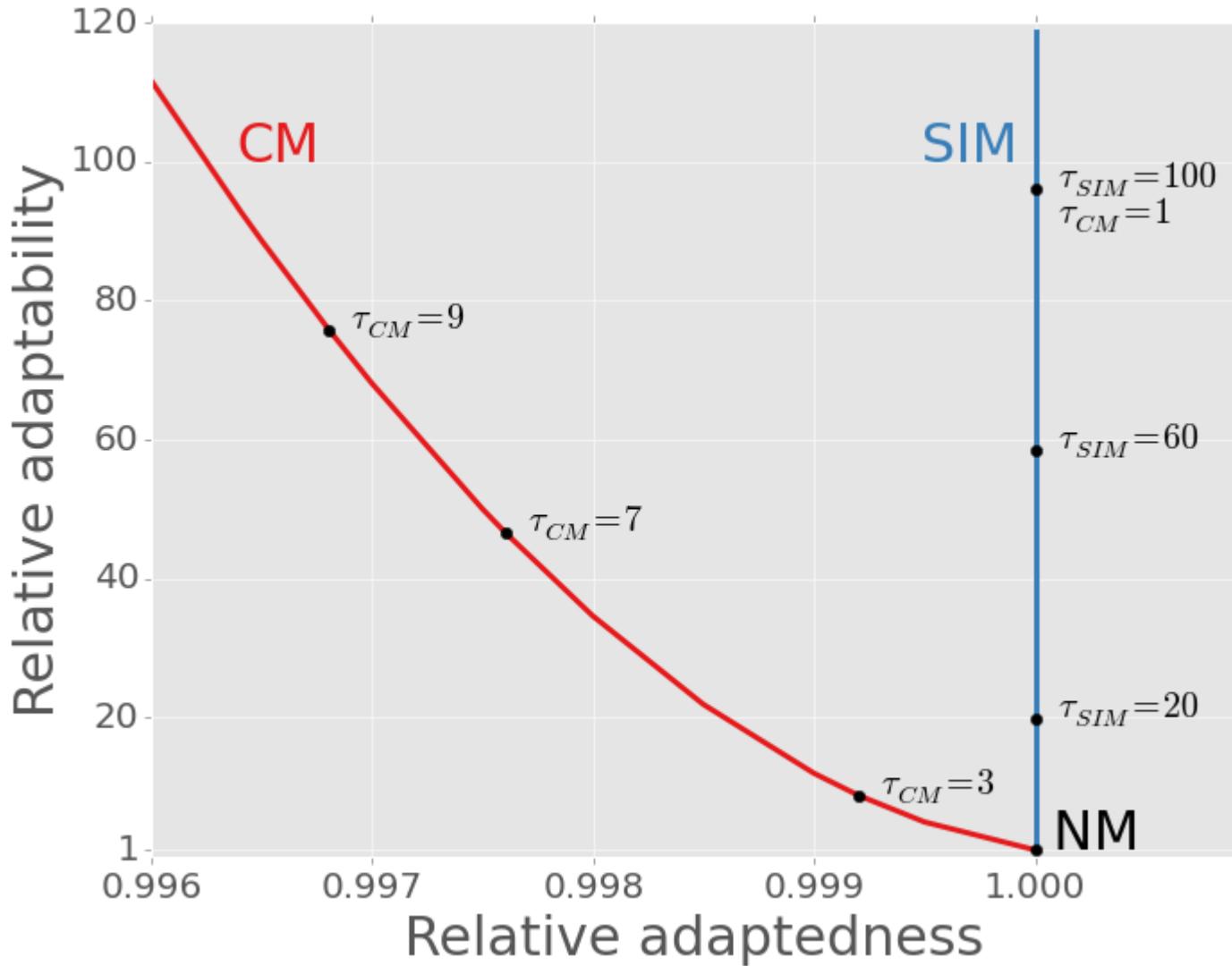
- Cost of replication fidelity
- Drift barrier hypothesis
- Pleiotropy

Adaptive hypothesis

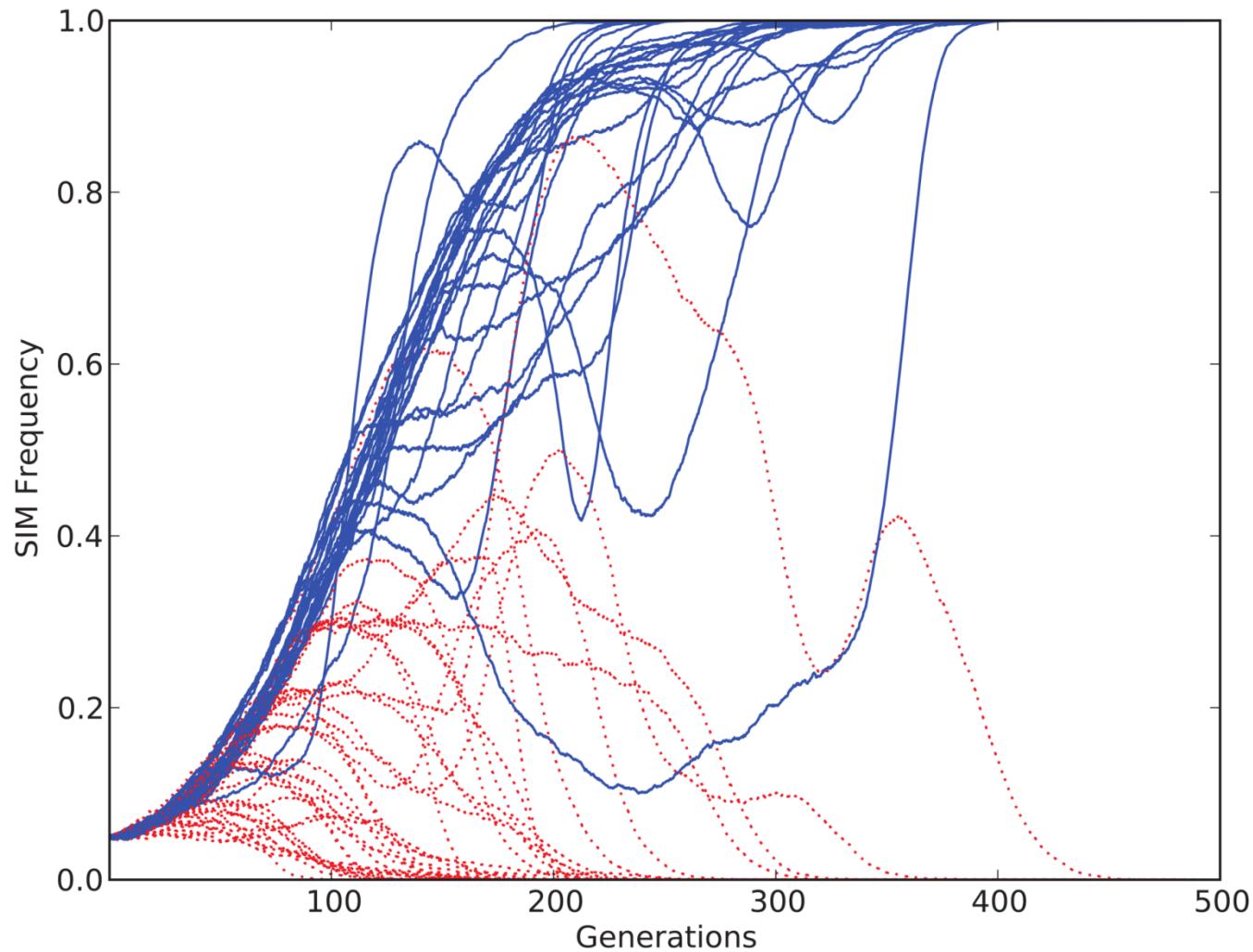
- 2nd order selection



SIM Breaks the *adaptability-adaptedness* trade-off



SIM wins competitions



Conclusions

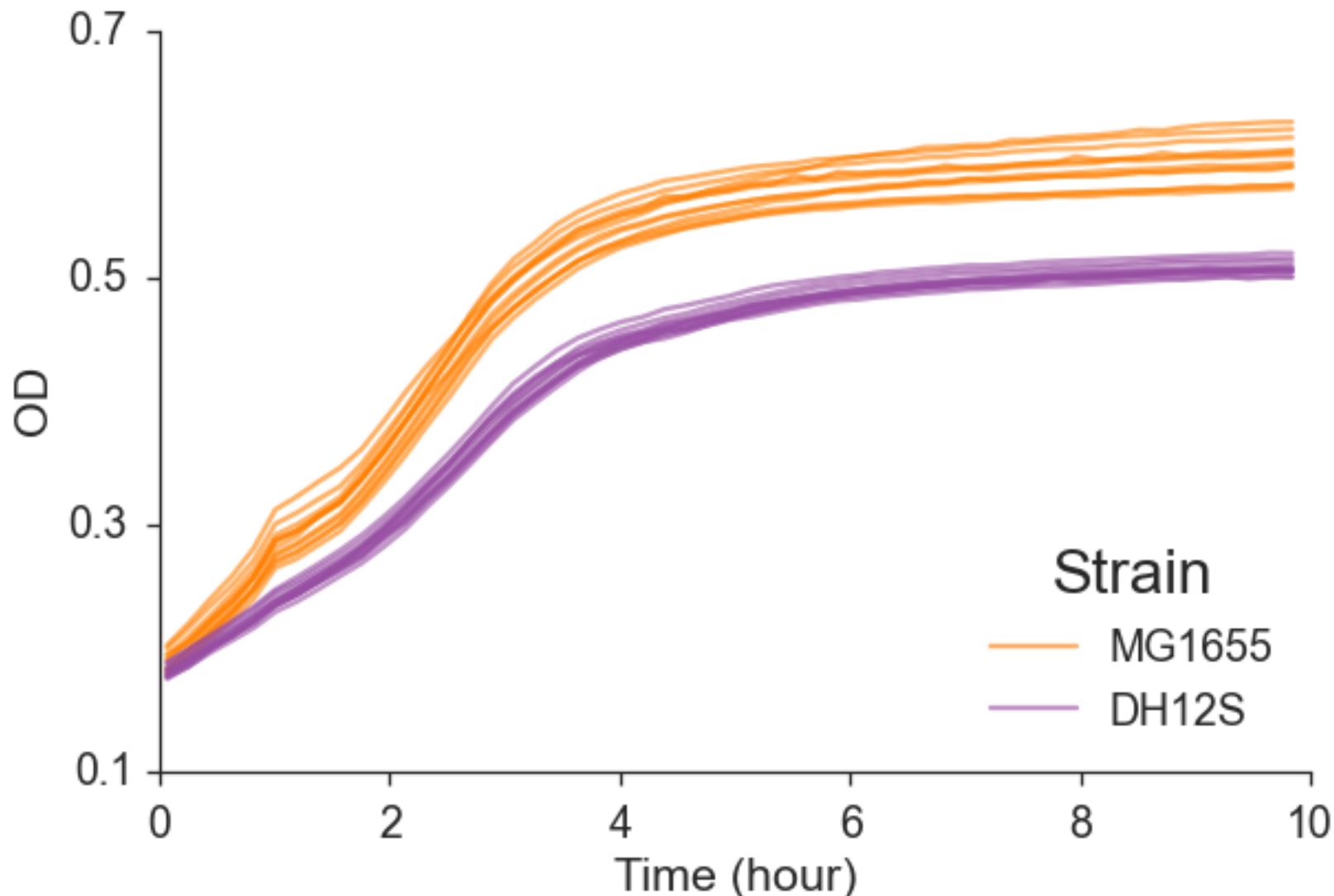
- **Stress-induced mutagenesis evolves:**
 - In constant & changing environments
- **2nd order selection** can lead to the evolution of stress-induced mutagenesis in asexual populations Ram & Hadany, Evolution 2012
- **More:**
- SIM & adaptive peak shifts Ram & Hadany, PRSB 2014
- SIM in presence of recombination in preparation
- SIM with of regulation errors in preparation

Predicting microbial growth in a mixed culture

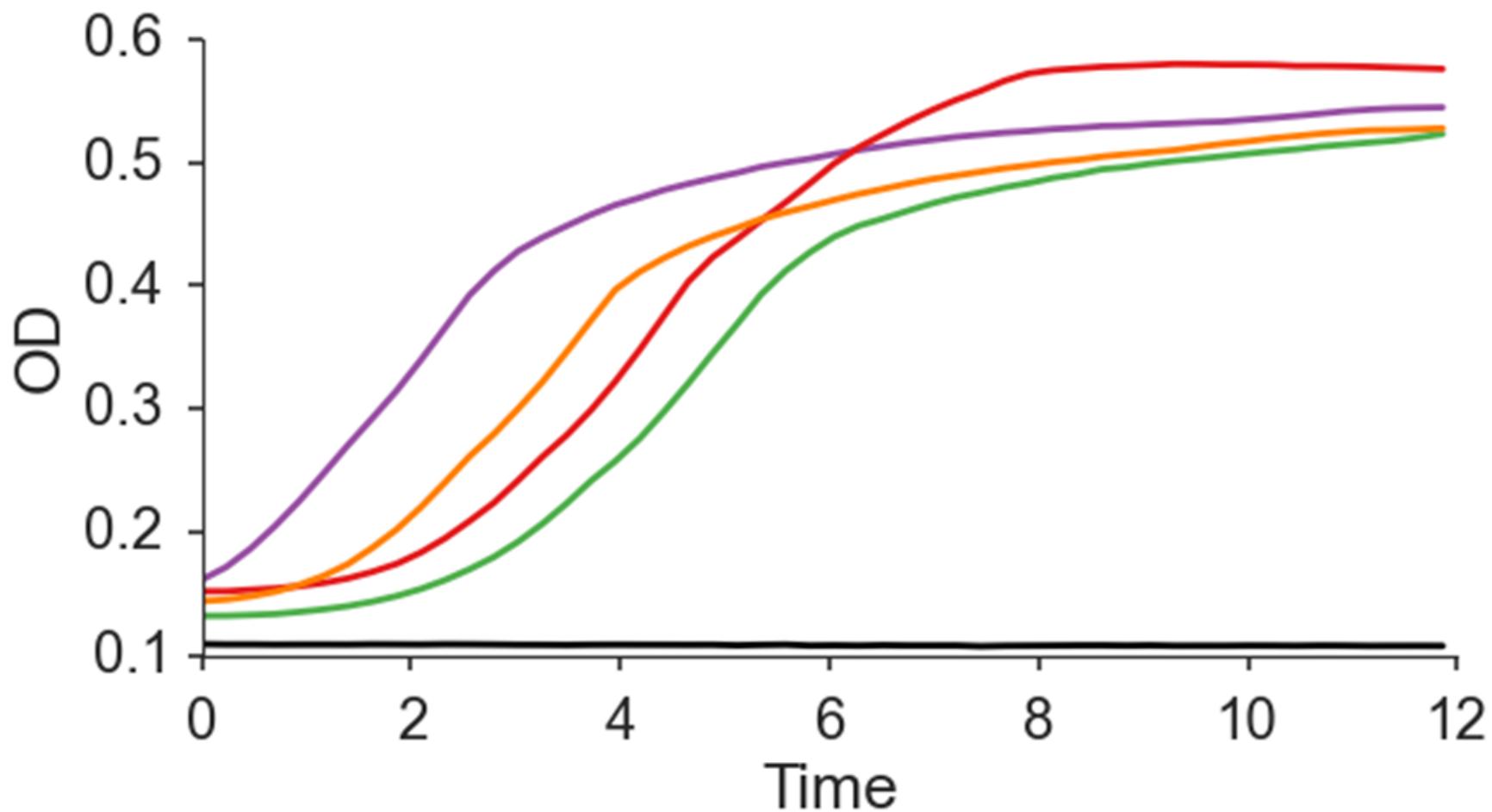
Yoav Ram

Feldman Lab @ Stanford

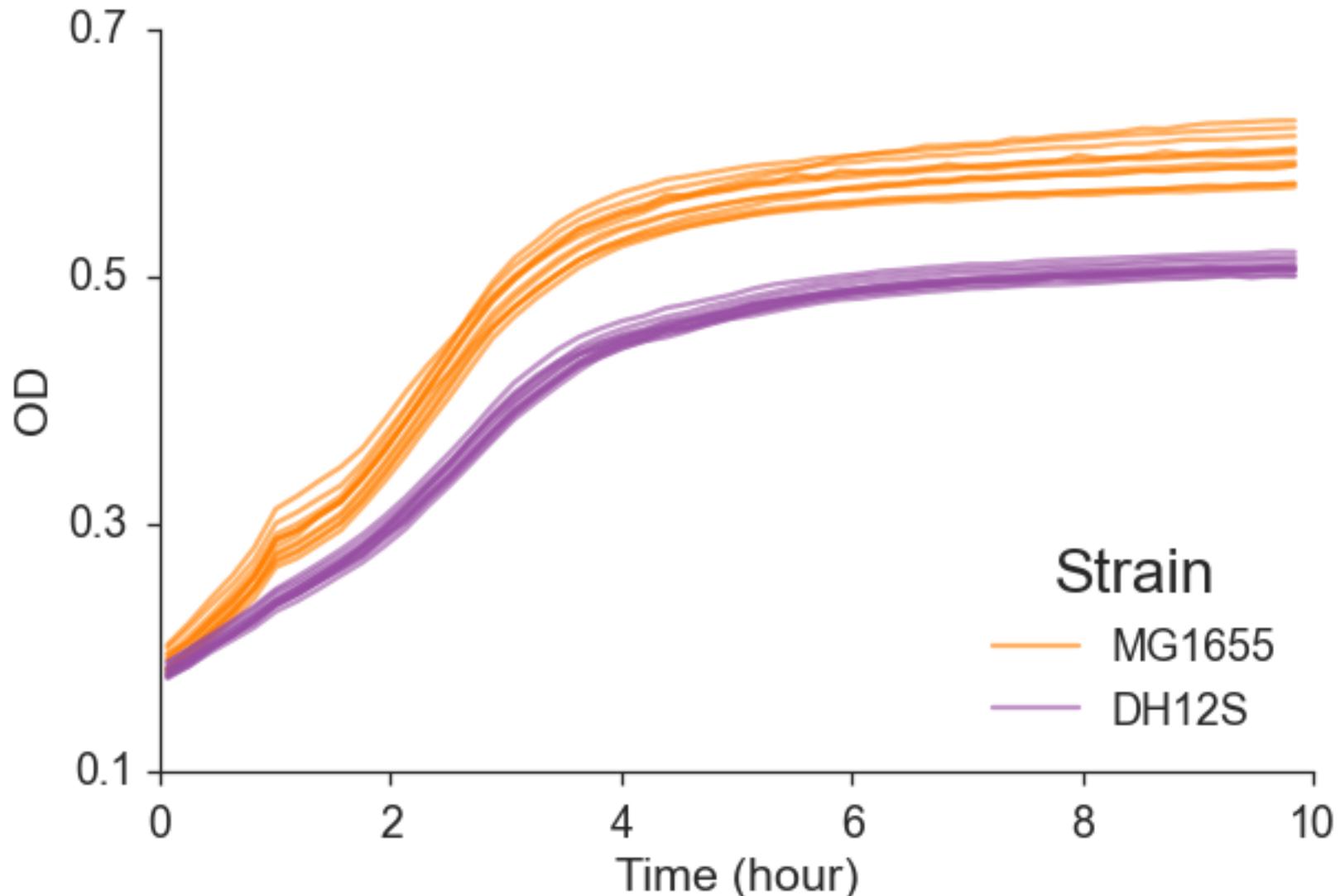
Which is fitter?



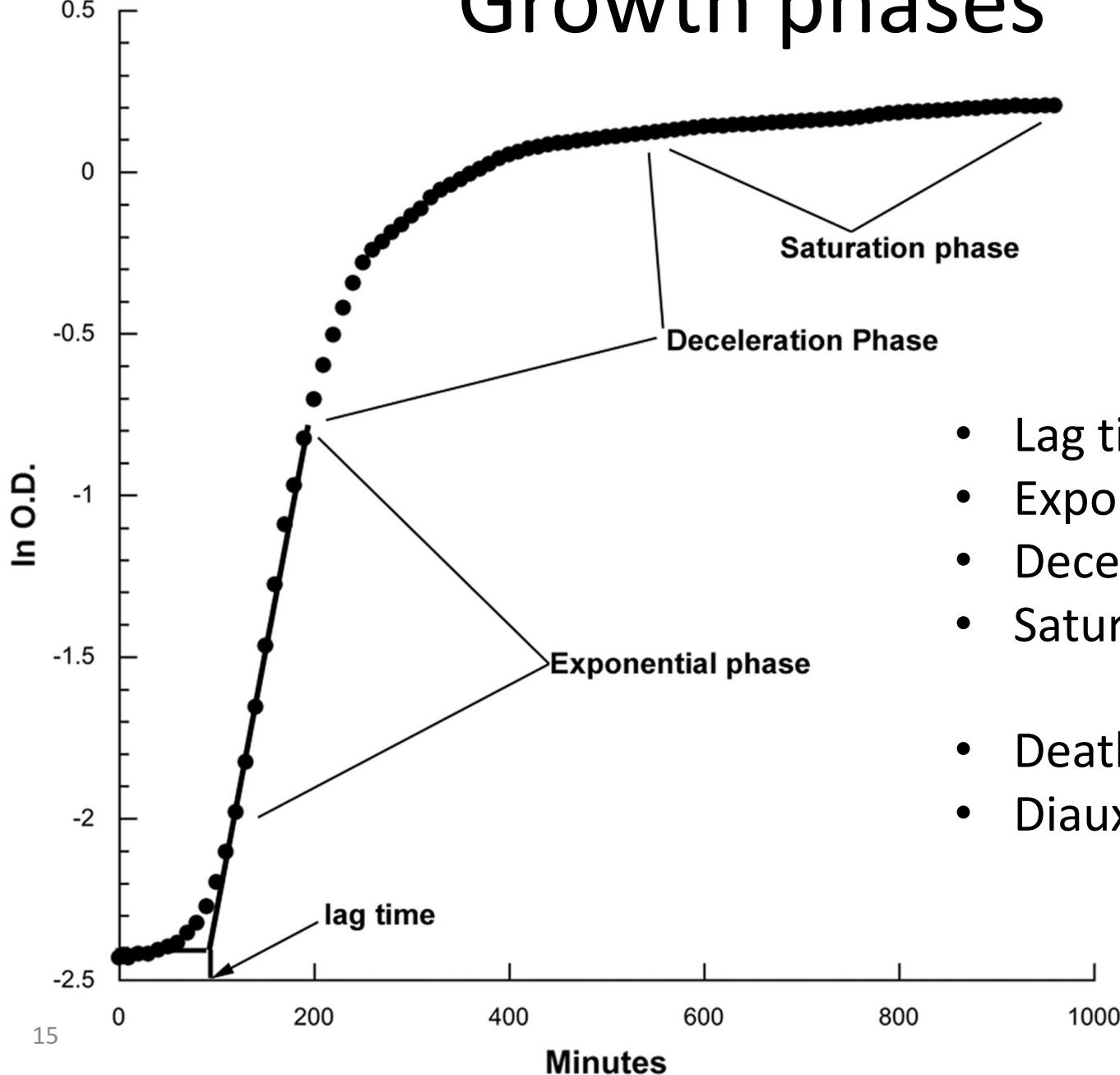
Which is fitter?



How much fitter???



Growth phases



Competition experiments

- Growth in a mixed culture
- Capture all relevant growth phases by direct competition
- Also captures direct interactions



Direct interactions



Cooperation (++)
bread & spread



Interference (--)
The opposite game



Spite (0-)
Quiet please



Parasitism (-)
Milk & Cookies



Charity (0+)
If I knew you were coming

Competition experiments

Strains must have a genotypic or phenotypic marker

- Fluorescence and flow cytometry

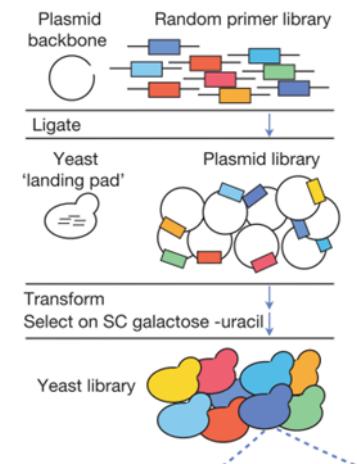
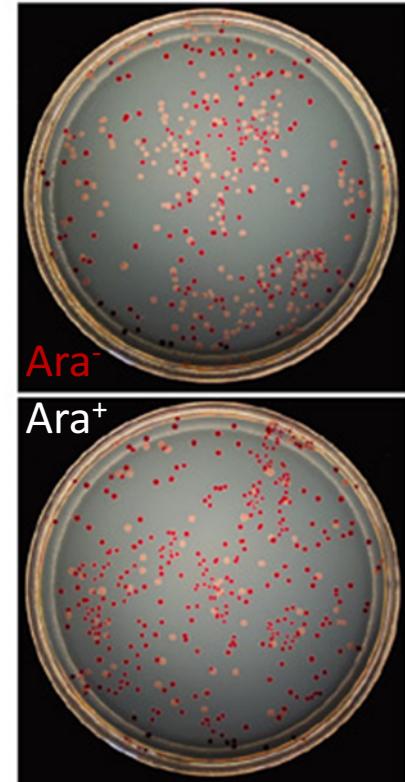
Gallet et al., Genetics 2012

- LTEE: arabinose utilization phenotype

Lenski et al., Am Nat 1991

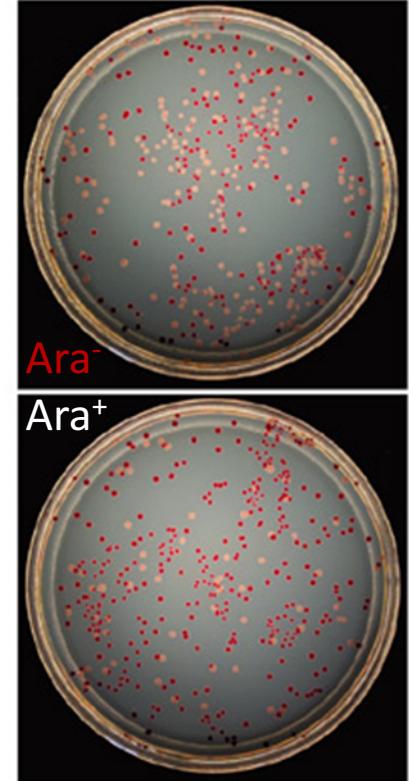
- Lineage tracking with deep sequencing

Bank et al., Evolution 2013; Levy et al., Nature 2015



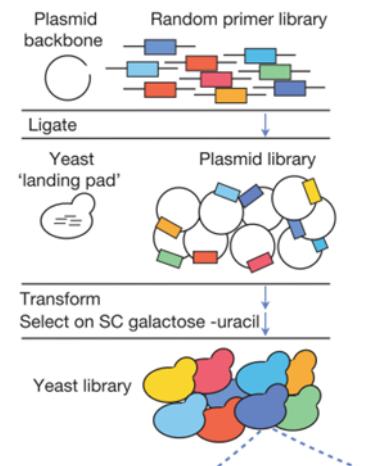
Competition experiments

Strains must have a genotypic or phenotypic marker



Laborious and Costly

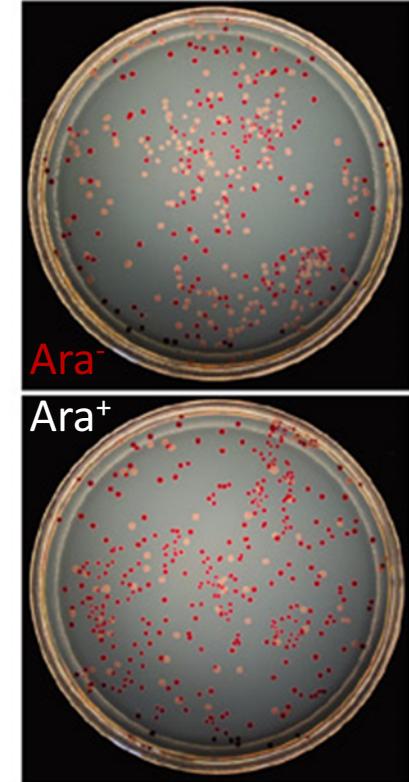
More so for non-model organisms



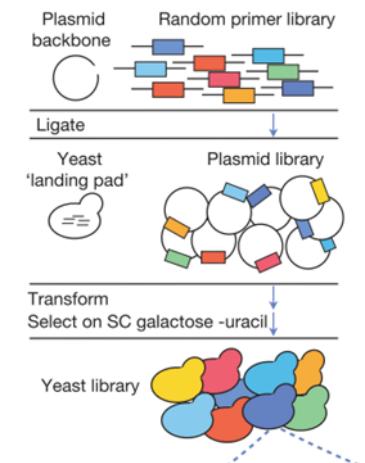
Competition experiments

Problem: Laborious and Costly

Our Solution: Computational framework that predicts competition results



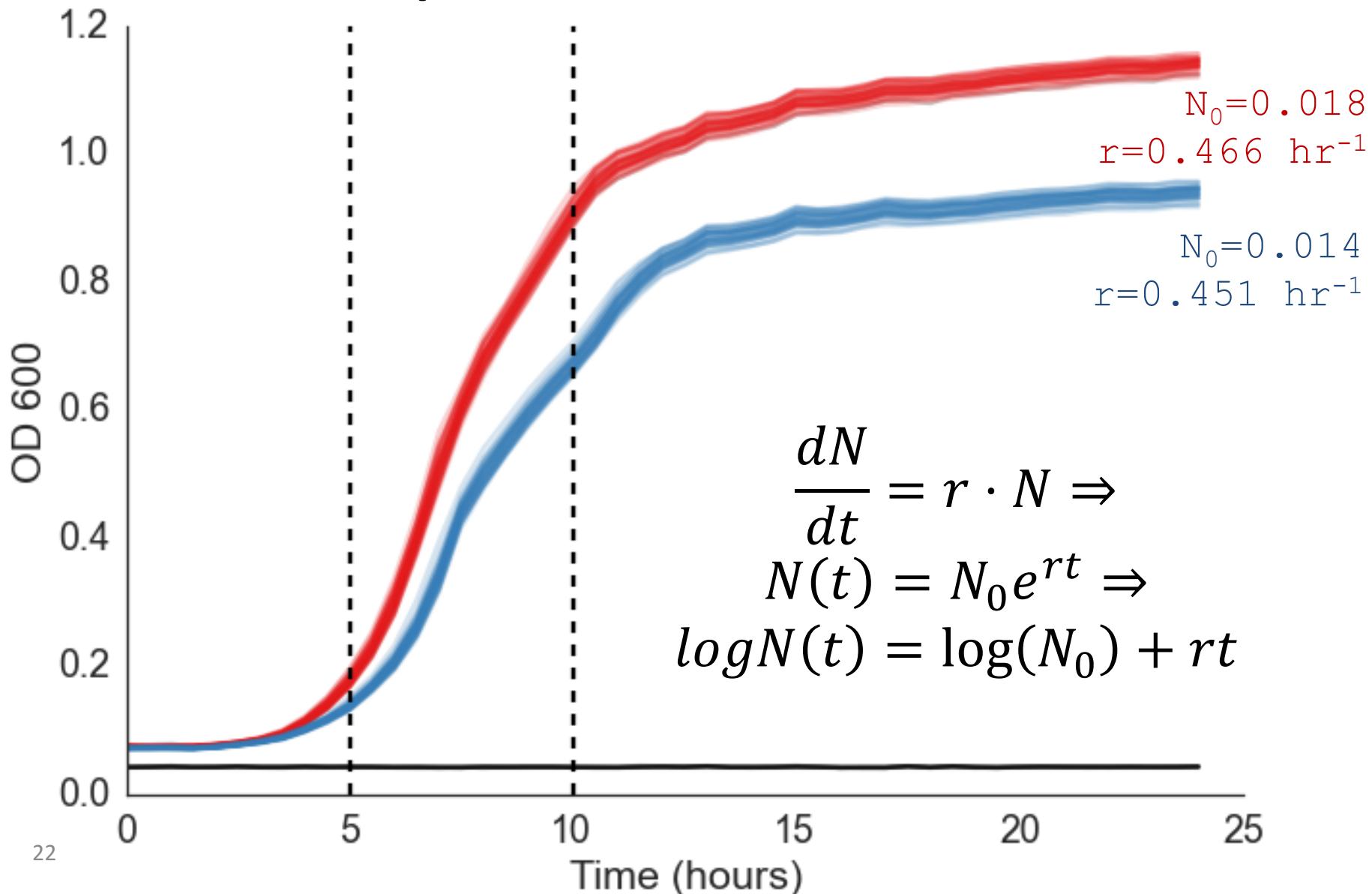
1. Fit growth models to growth curves
2. Predict competition results
3. Infer fitness



Growth models



Exponential model



Exponential model

$$\frac{dN}{dt} = r \cdot N \Rightarrow N(t) = N_0 e^{rt} \Rightarrow \log N(t) = \log(N_0) + rt$$

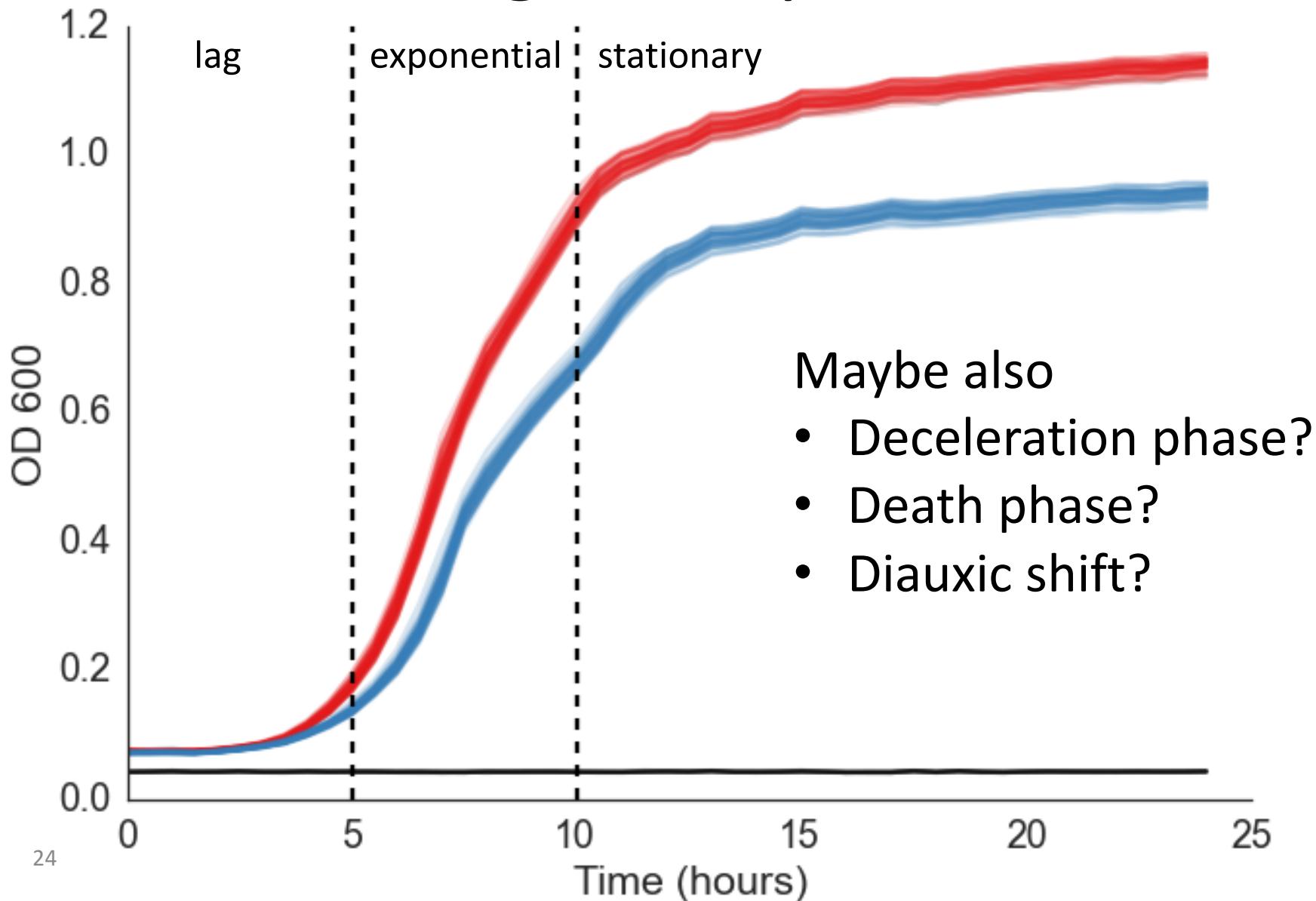
Traditional method says: $s = \textcolor{red}{r} - \textcolor{blue}{r} = 0.015 \text{ hr}^{-1}$

Can be converted to generations: $s_T = \frac{\textcolor{red}{r}-\textcolor{blue}{r}}{\textcolor{blue}{r}} \ln(2) \text{ gen}^{-1}$

Chevin 2011

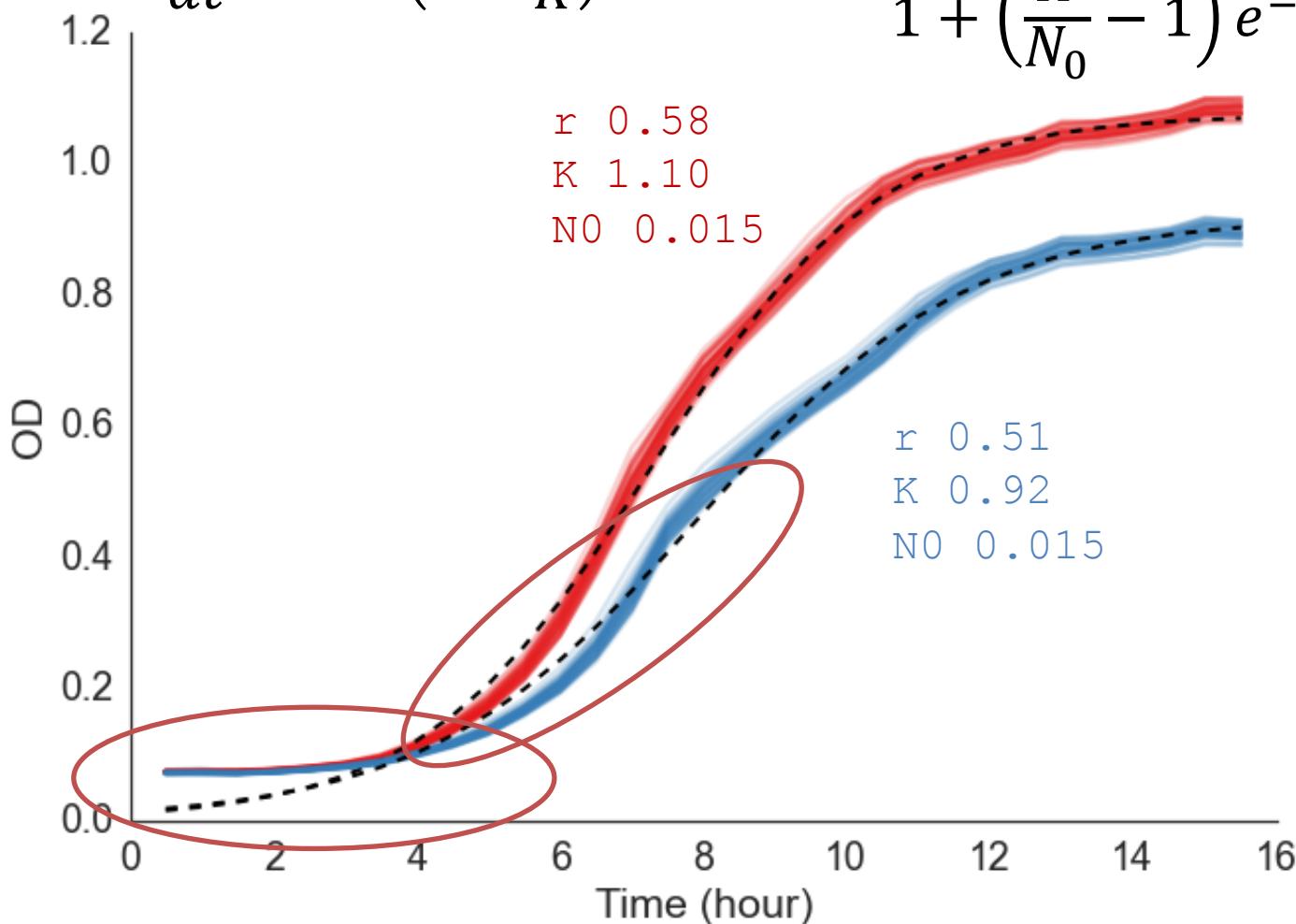
This analysis only captures one growth parameter ->
one growth phase

Three growth phases?



Logistic model

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right) \Rightarrow N(t) = \frac{K}{1 + \left(\frac{K}{N_0} - 1\right) e^{-rt}}$$



Logistic model: why?

Can be derived from resource consumption models.

Consumer growth:

$$\frac{dN}{dt} = \epsilon aRN$$

Abiotic resource with logistic growth:

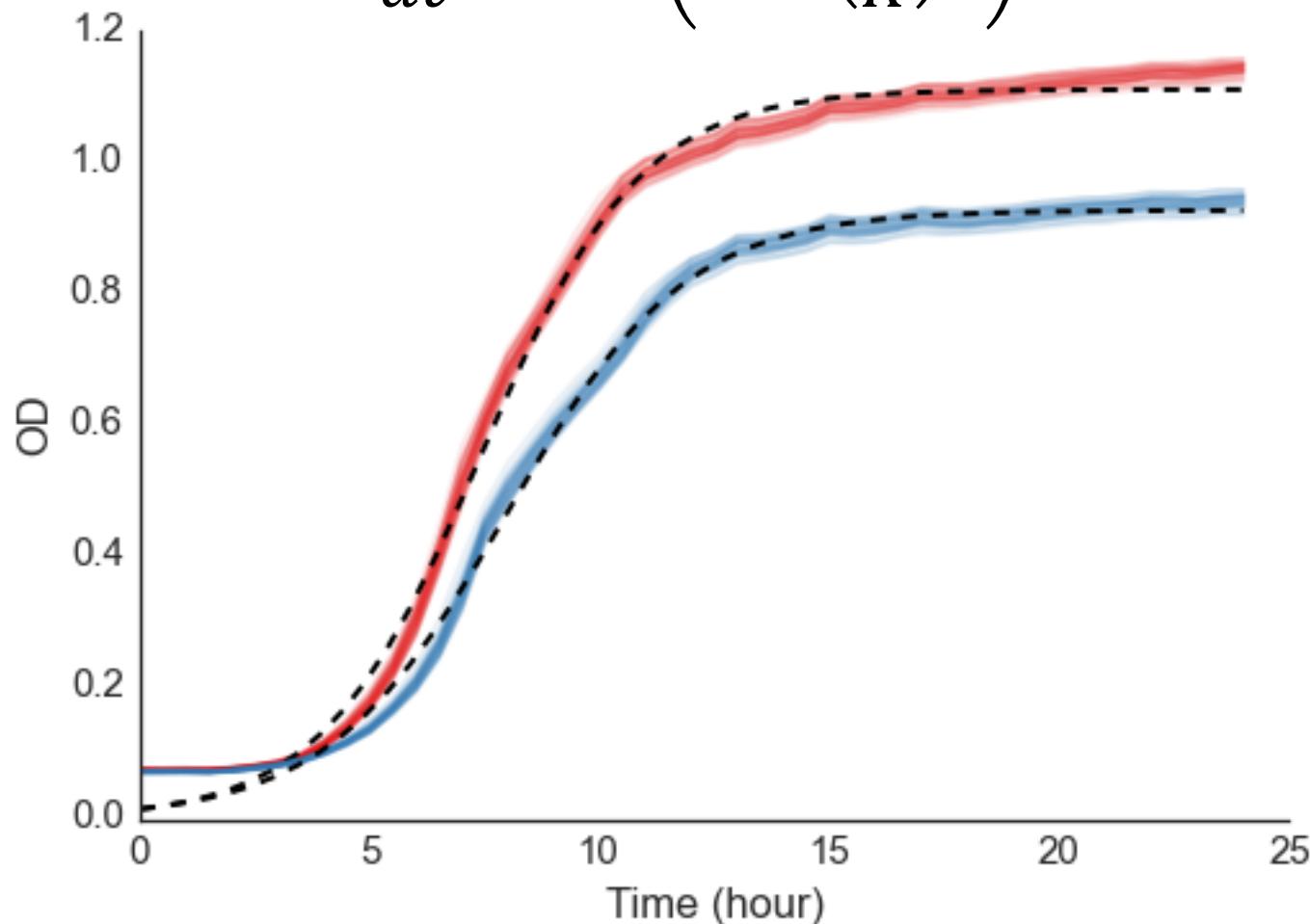
$$\frac{dR}{dt} = -aRN$$

Biotic resource with logistic growth:

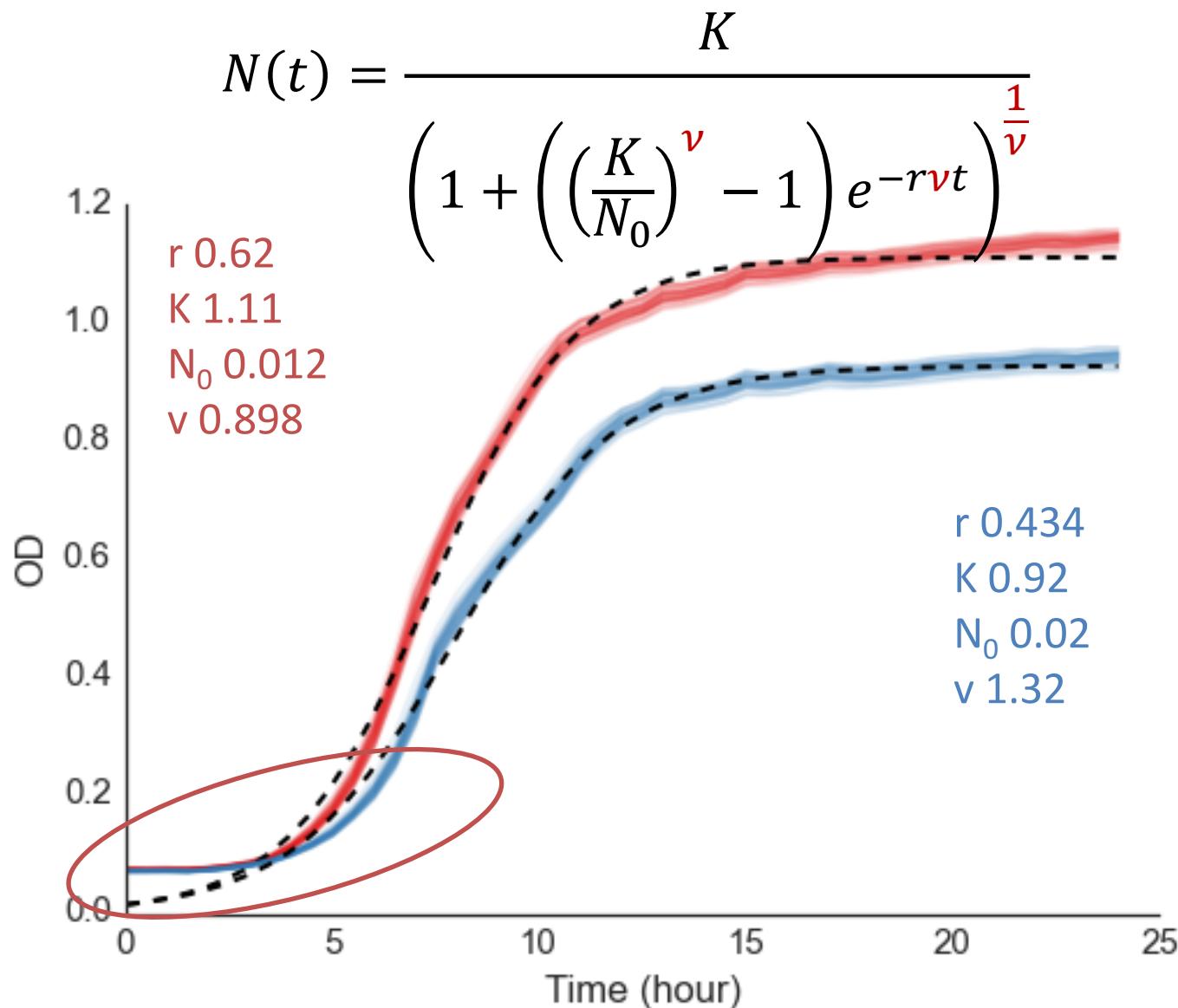
$$\frac{dR}{dt} = bR \left(1 - \frac{R}{K}\right) - aRN$$

Generalized logistic (Richards) model

$$\frac{dN}{dt} = rN \left(1 - \left(\frac{N}{K} \right)^{\nu} \right)$$



Generalized logistic (Richards) model



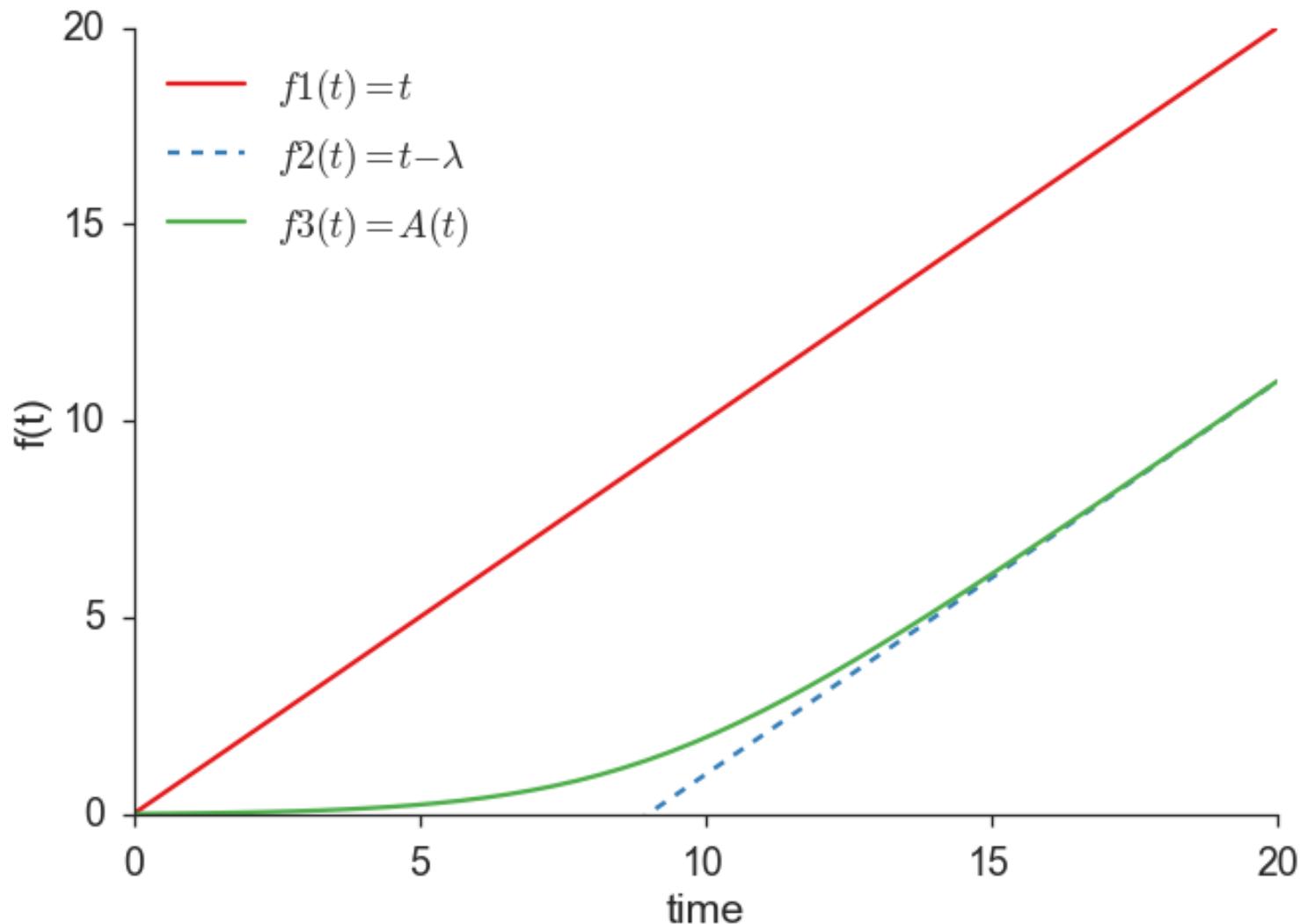
Baranyi-Roberts model

$$\frac{dN}{dt} = r\alpha(t)N \left(1 - \left(\frac{N}{K}\right)^{\nu}\right) \Rightarrow$$

$$N(t) = \frac{K}{\left(1 + \left(\left(\frac{K}{N_0}\right)^{\nu} - 1\right)e^{-r\nu A(t)}\right)^{\frac{1}{\nu}}}$$

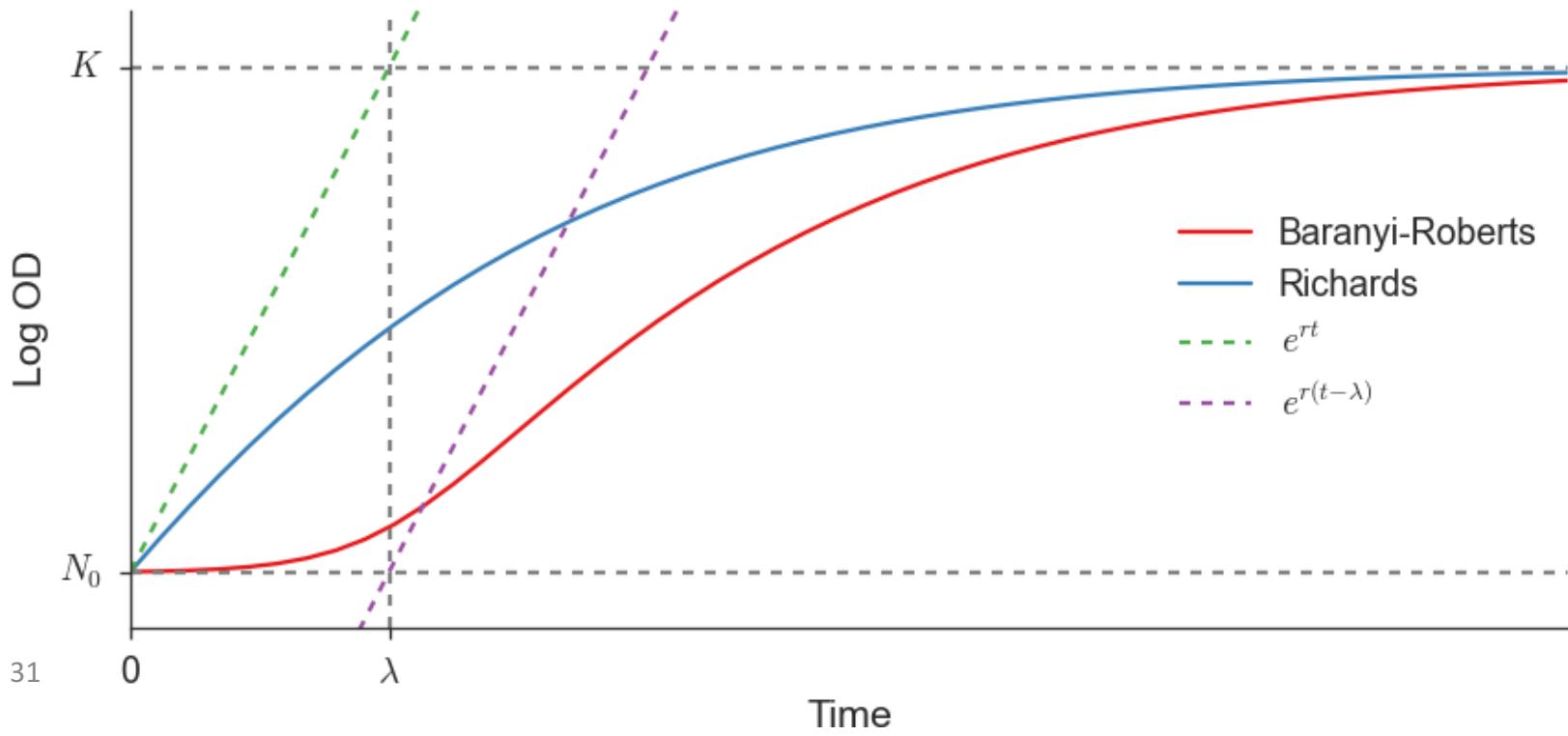
$$A(t) = \int_0^t \alpha(s)ds = t + \frac{1}{m} \log \left(\frac{e^{-mt} + q_0}{1 + q_0} \right)$$

Lag phase



Baranyi-Roberts model

$$N(t) = \frac{K}{\left(1 + \left(\left(\frac{K}{N_0}\right)^{\nu} - 1\right)e^{-r\nu A(t)}\right)^{\frac{1}{\nu}}}$$



Competition model

We extend the Baranyi-Roberts model for two strains:

$$\frac{dN_1}{dt} = r_1 \cdot \alpha_1(t) \cdot N_1 \left(1 - \frac{N_1^{\nu_1} + a_2 N_2^{\nu_2}}{K_1^{\nu_1}} \right)$$
$$\frac{dN_2}{dt} = r_2 \cdot \alpha_2(t) \cdot N_2 \left(1 - \frac{a_1 N_1^{\nu_1} + N_2^{\nu_2}}{K_2^{\nu_2}} \right)$$

- Focus on **resource competition**
- No direct interactions



Competitions model

$$\frac{dN_1}{dt} = r_1 \cdot \alpha_1(t) \cdot N_1 \left(1 - \frac{N_1^{\nu_1} + a_2 N_2^{\nu_2}}{K_1^{\nu_1}} \right)$$

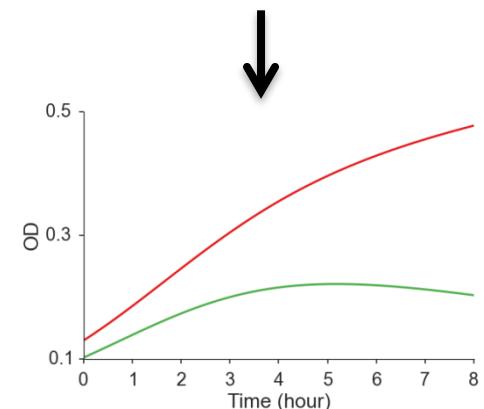
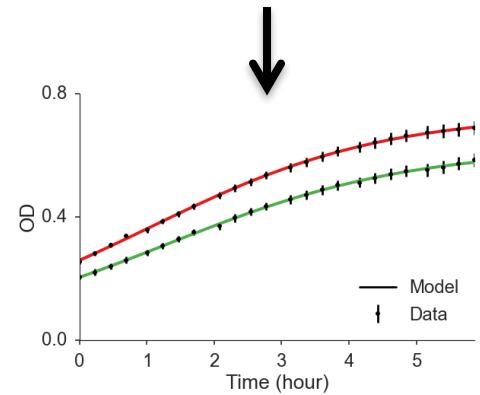
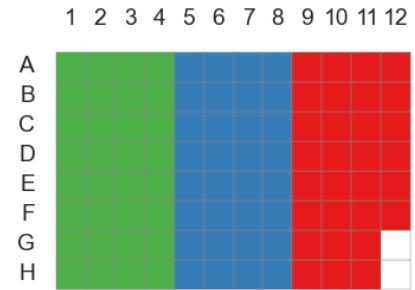
$$\frac{dN_2}{dt} = r_2 \cdot \alpha_2(t) \cdot N_2 \left(1 - \frac{a_1 N_1^{\nu_1} + N_2^{\nu_2}}{K_2^{\nu_2}} \right)$$

- Estimate a_1 and a_2 by fitting $N_1 + N_2$ total OD in mixed culture
- Infer N_1 and N_2 by solving model

Testing the predictive framework

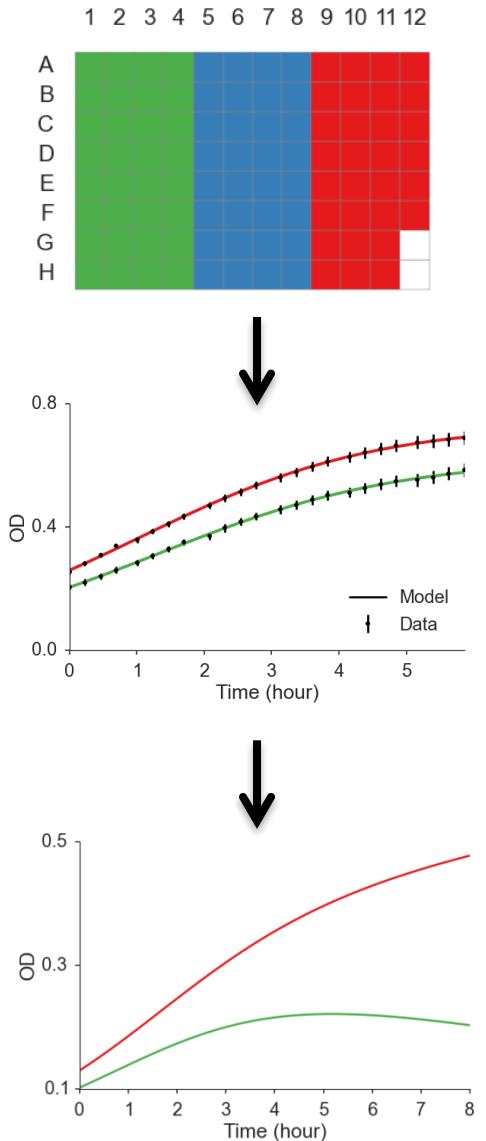
Testing the predictive framework

- Two *E. coli* strains with fluorescent proteins (**GFP**, **RFP**)
- Growth in mono- and mixed culture
- Measure OD over time
- Fit growth model
- Predict competition results from fitted growth models
- Validate predictions using pairwise competition experiments
- Use fluorescence to measure frequencies over time



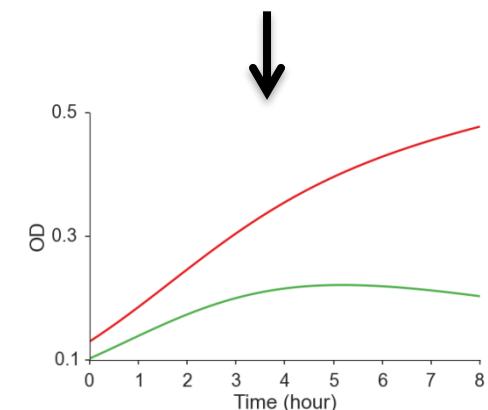
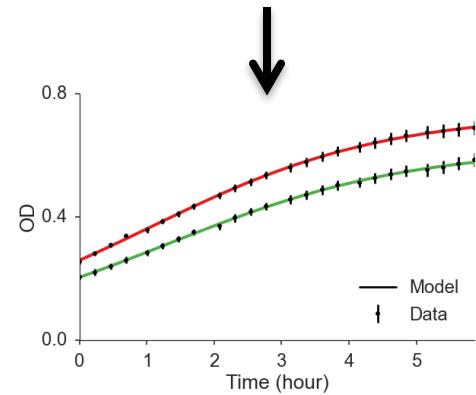
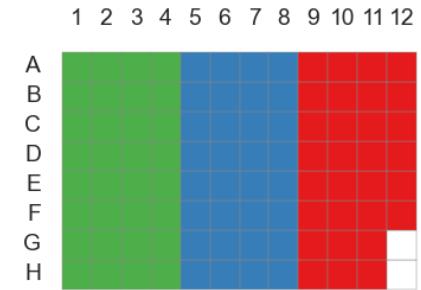
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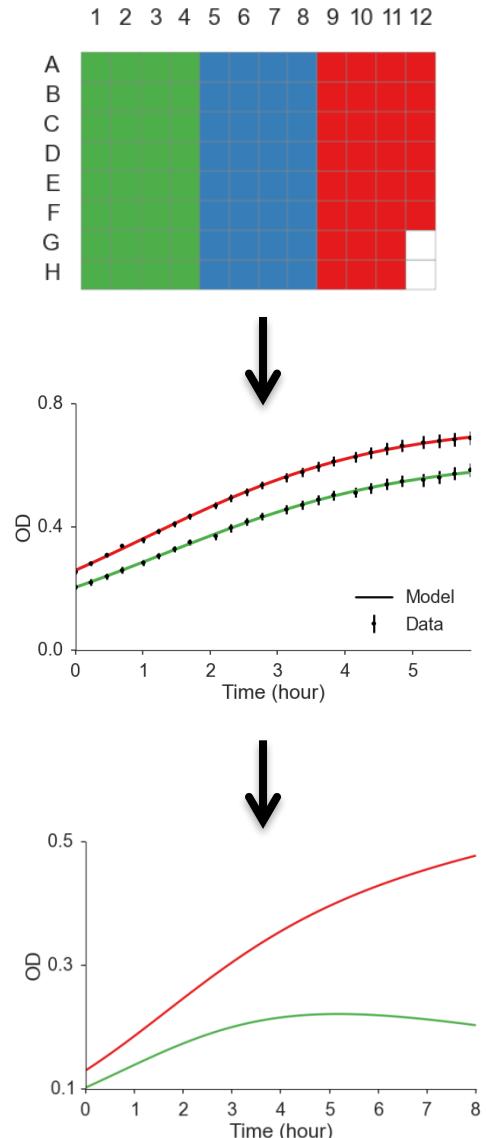
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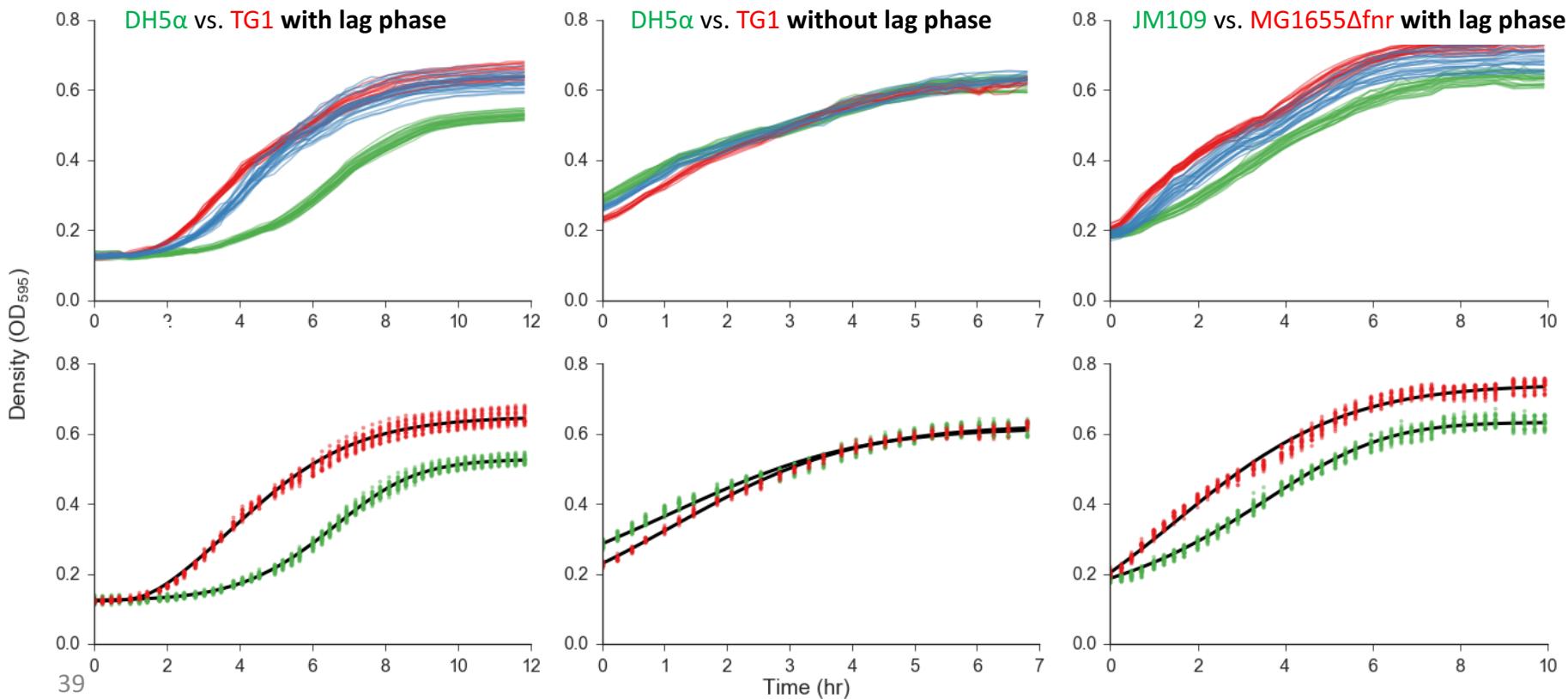
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Growth curves data

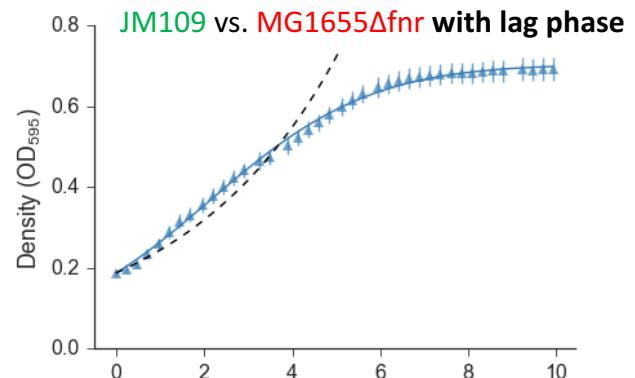
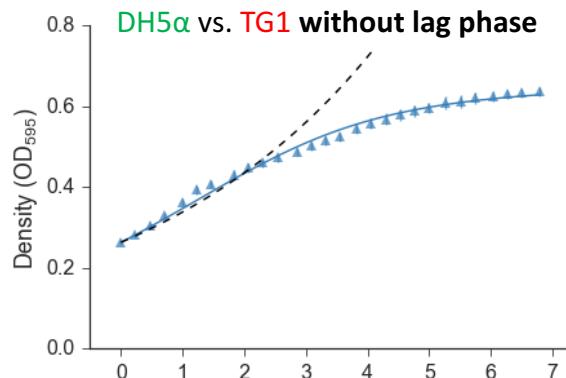
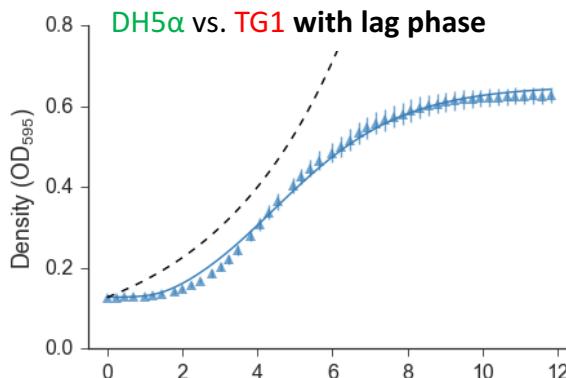
Top: Data from 3 experiments with *E. coli*

Bottom: Monoculture data with fitted growth models



Growth curves data

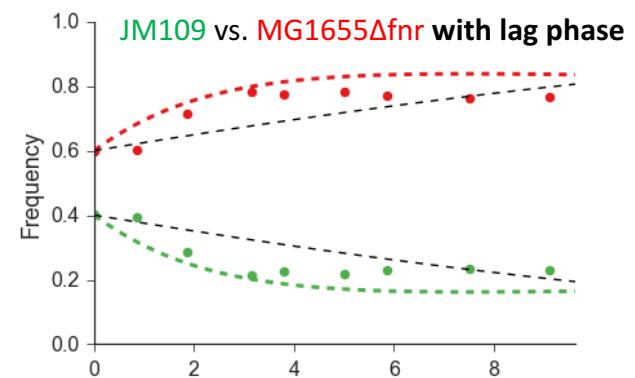
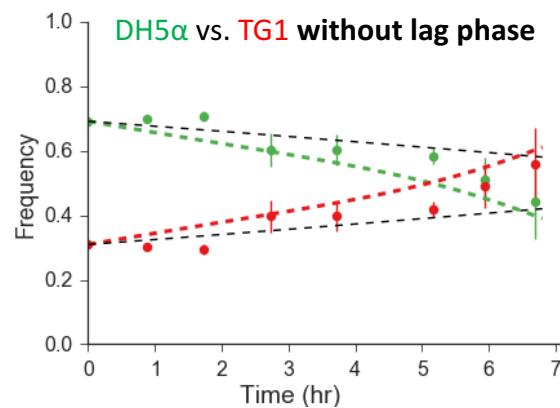
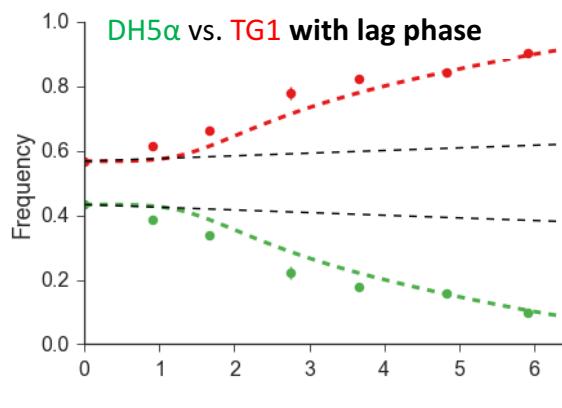
Mixed culture data with fitted competition models



*Dashed lines are fitted exponential models

Competition prediction

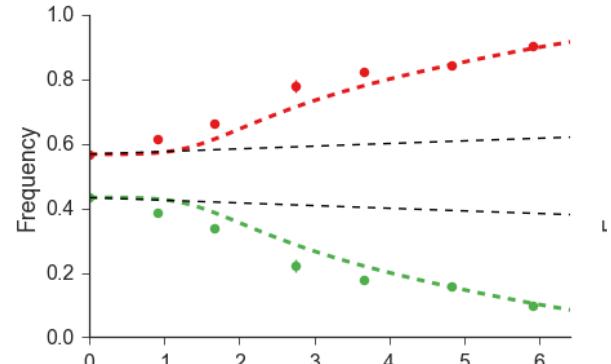
Dashed: competition model prediction
Markers: flow cytometry data



*Dashed lines are exponential models prediction

Summary

1. Fit growth models to growth curves
2. Predict competition results
3. Infer fitness



Collaborators:

Eynat Dellus-Gur, Maayan Bibi, Uri Obolski, Judith Berman,
Lilach Hadany (Tel-Aviv University)

Preprint:

Ram et al. Predicting microbial relative growth in a mixed culture from growth curve data. bioRxiv, doi:[10.1101/022640](https://doi.org/10.1101/022640)

Software website: curveball.yoavram.com

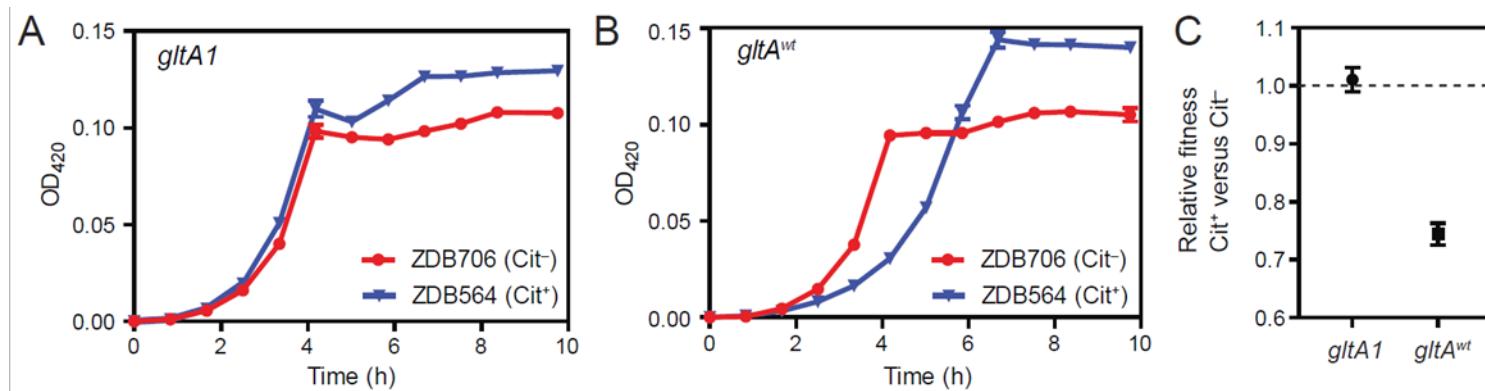
Test case: Citrate utilization in *E. coli*

Quandt et al., eLife 2015;10.7554/eLife.09696 (Barrick lab)

- mutations in the *gltA* gene - encodes citrate synthase (CS)
- before and after *E. coli* evolved to grow aerobically on citrate (Cit^+)
- first *gltA* mutation increases CS activity, beneficial for growth on acetate
- contributed to preserving the rudimentary Cit^+ trait from extinction
- Cit^+ then refined by more mutations
- The potentiating *gltA* mutation became deleterious to fitness
- beneficial *gltA* mutations evolved to reduced CS activity

Test case: Citrate utilization in *E. coli*

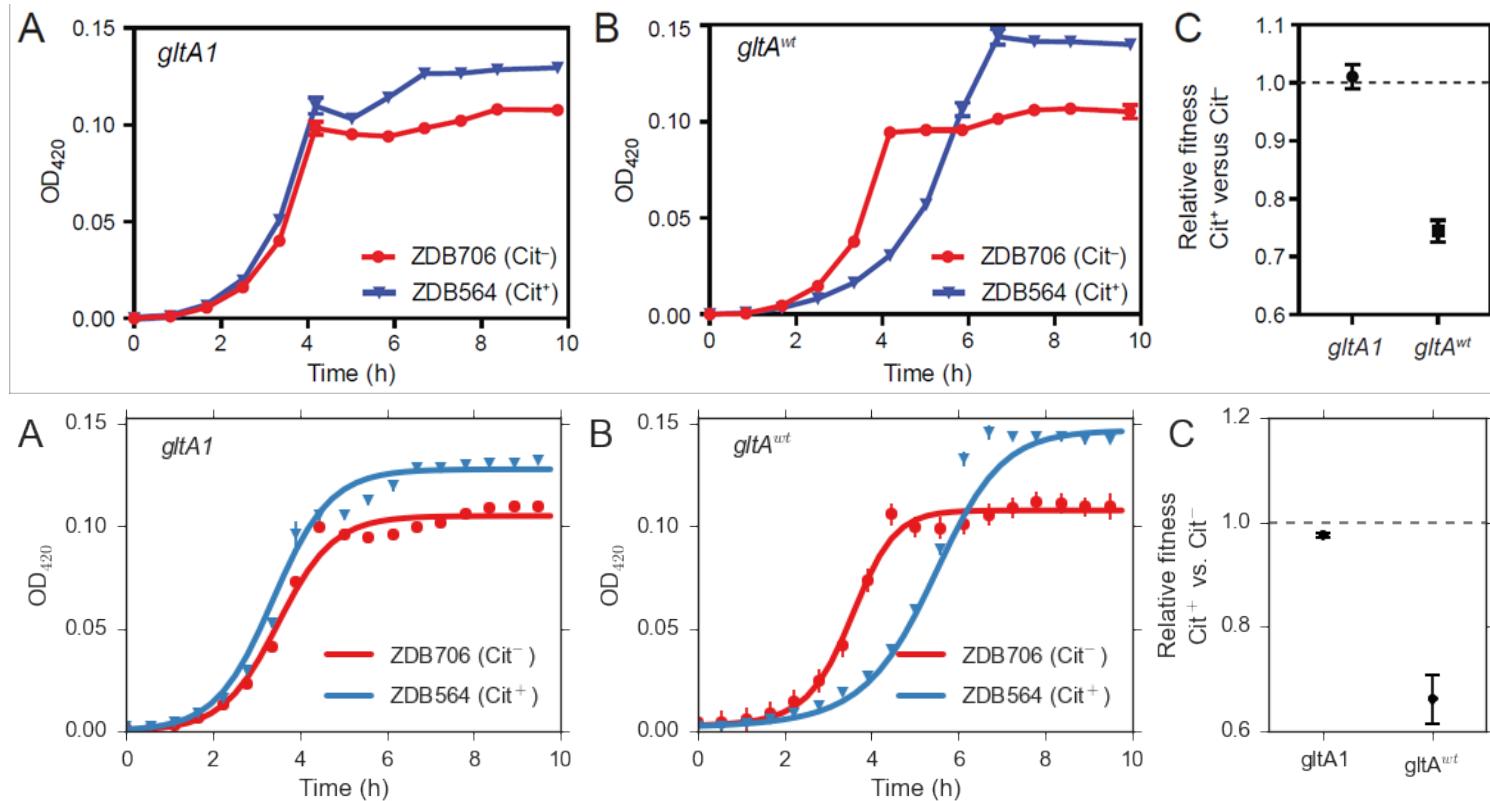
Figure 4:



- A) Early Cit⁺ and Cit⁻ revertant with *gltA1* mutation: Cit⁺ has higher K
- B) Early Cit⁺ and Cit⁻ revertant with wildtype *gltA*: Cit⁻ has shorter lag and lower K
- C) Relative fitness Cit⁺ vs. Cit⁻ from competition assays

Test case: Citrate utilization in *E. coli*

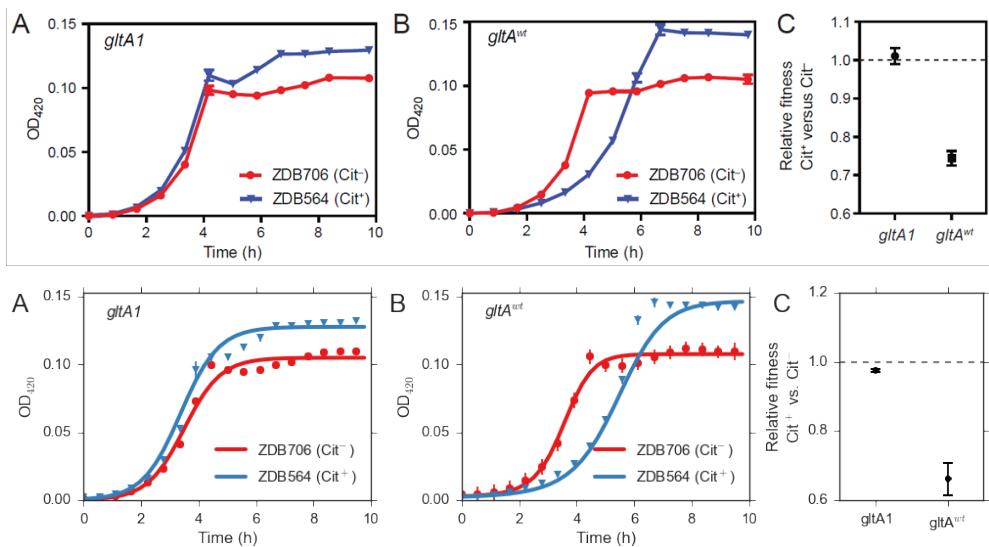
Fig. 4 from Quandt et al., 2015



Reproduce Fig. 4 with *Curveball* using only growth curves data

Test case: Citrate utilization in *E. coli*

Fig. 4 from Quandt et al., 2015



Reproduce Fig. 4 with Curveball

The discrepancy between panel **C** In the top and bottom figures can be explained by:

1. The model fits are not perfect, especially in Cit⁺ *gltA^{wt}*: there is a strange “bump” in the curves.
2. Competition and growth assays were done in different conditions: 100uL x 96 wells vs. 50mL flasks; x10 glucose concentration in growth assays.

Future directions

- Complex growth curves:
 - Bi-phasic growth:
 - Diauxic shift: glucose-ethanol, glucose-lactose etc.
 - Changing drug concentrations
 - Deep stationary phase
 - Cell death
- Null model for detection of direct interactions
- Predict adaptive evolution
- Interpret fitness differences

Acknowledgments

Collaborators on Curveball:

Hadany Lab

Lilach Hadany

Uri Obolski

Eynat Dellus-Gur

Berman Lab

Judith Berman

Maayan Bibi

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 github.com/yoavram

 www.yoavram.com



Israeli
Ministry
of Science &
Technology



Thank You!

Presentation: github.com/yoavram/EcoEvoLunch2017

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-  github.com/yoavram
-  www.yoavram.com