

# Incorporating Trait Information in Population Growth Models: a Lotka-Volterra example

HTML Slides: <https://fomotis.github.io/researchday/>



# Introduction

# Traits and its Importance

- Traits are simply put characteristics (genetic and/or phenotypic) of a species.
- Traits can influence the survival of a species.



Peppered moths survival during the industrial evolution in Britain.

- Could fetch you an article in [BBC](#) and [New York Times](#).

# Traits (Cont.)

- Traits are measured per individual for each species. Thus,

$$M = \begin{pmatrix} b_{11} & \cdots & b_{1m} \\ \vdots & \vdots & \vdots \\ b_{n1} & \cdots & b_{nm} \end{pmatrix}$$

- Longitudinal measurements are also possible. This is especially done if evolution is of interest.

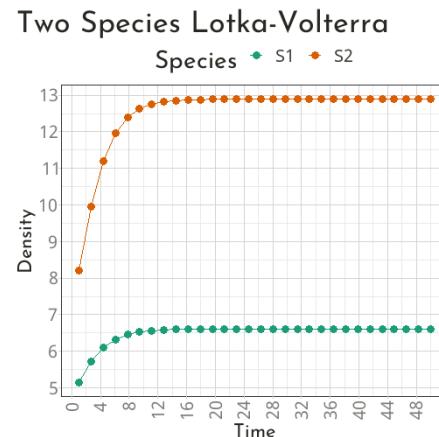
# Characterising Population Growth (Lotka-Volterra Model)

$$\frac{dN}{dt} = \text{diag}(N)(R - AN)$$

- Two Species Case

$$\begin{pmatrix} \frac{dN_1}{dt} \\ \frac{dN_2}{dt} \end{pmatrix} = \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \left[ \begin{pmatrix} r_1 \\ r_2 \end{pmatrix} - \begin{pmatrix} \alpha_{11} & \alpha_{12} \\ \alpha_{21} & \alpha_{22} \end{pmatrix} \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \right]$$

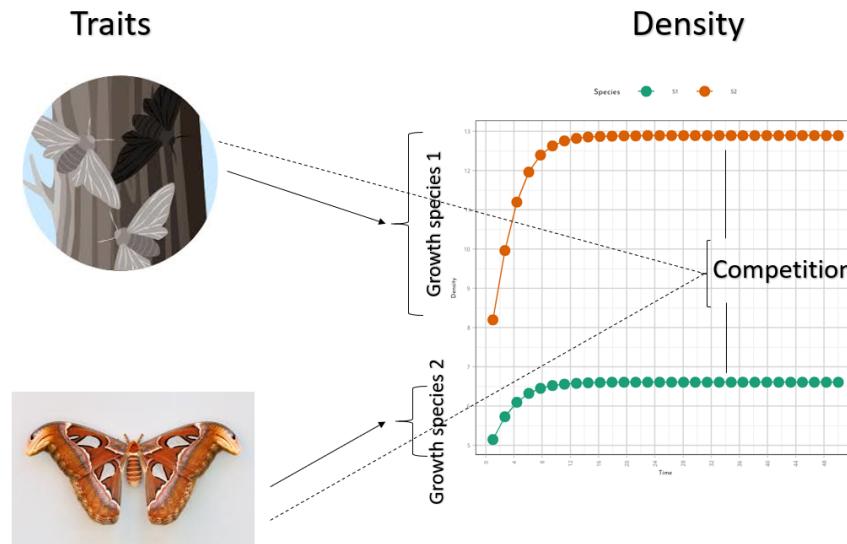
- $R$  is a vector of  $r$ 's growth rates.
- $A$  is a matrix of  $\alpha$ 's
  - $\alpha_{ij}, i = j$  are intraspecific interaction/competition.
  - $\alpha_{ij}, i \neq j$  are interspecific interaction/competition.



# Motivating the problem

# Ecological Questions of Interest

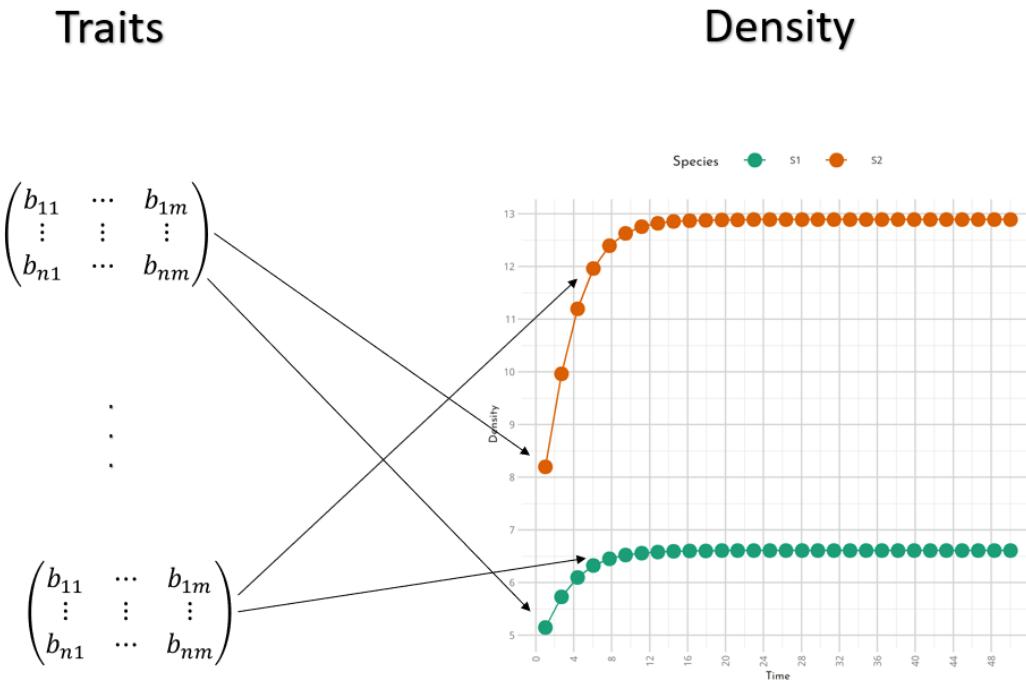
- Broader Question: what role do traits play in biodiversity dynamics?
- Specific Question: what is the role of traits in **growth, competition** and co-existence of species?



Effects of Interest.

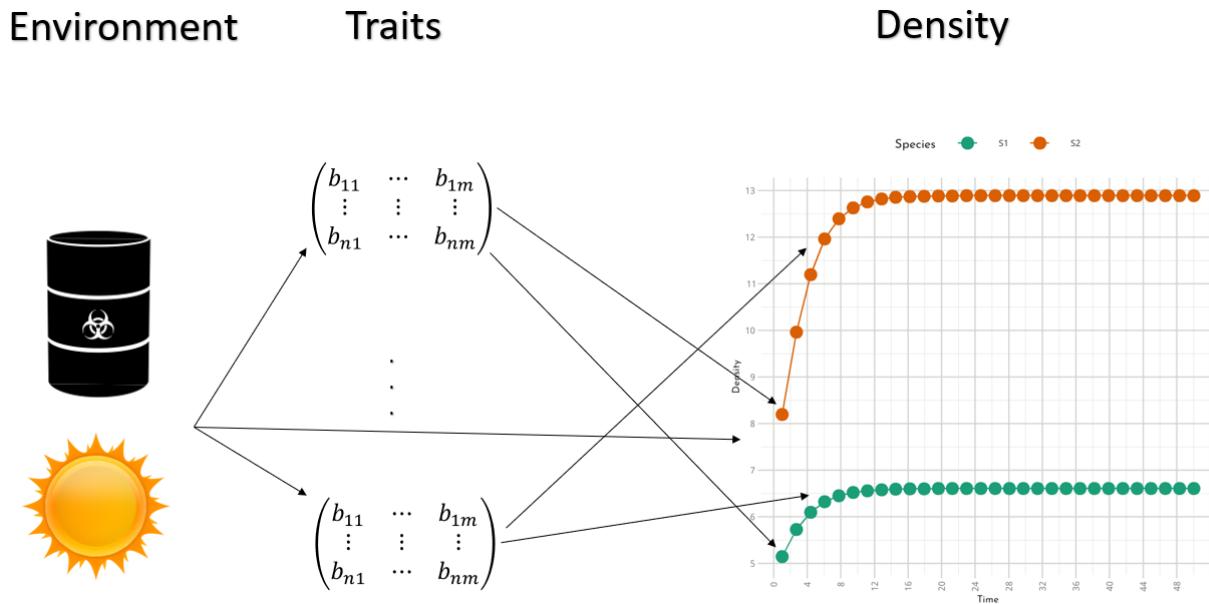
# The Modeling Challenge

- Connecting a vector/matrix of trait values to density points such that the ecological questions are answered.



# An Added Layer

- What about environmental factors?

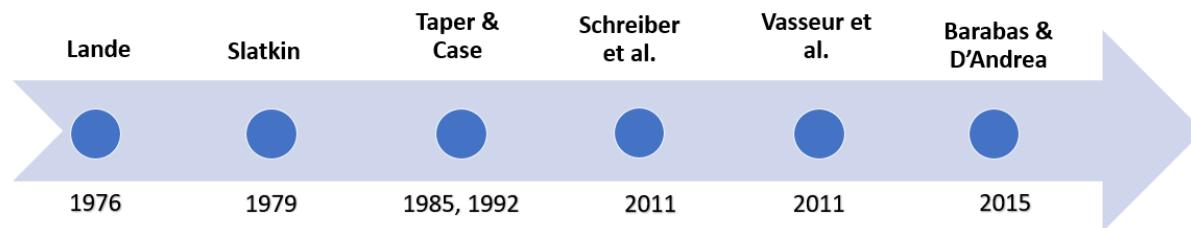


Possible Effects

# **Existing methods**

# A Quick Literature Dive

- The focus is on character displacement approach to trait based ecology.



Publication timeline for character displacement approach to trait based ecology

# Quantitative Genetic Lotka-Volterra (Barabas et al. 2015)

- Let  $T(t)$  be a trait vector measured at  $t$ ,  $T(t) \sim N(\mu(t), \sigma^2)$

$$\frac{dN_i(t)}{dt} = N_i(t) \int r_i(N, p, z, t) p_i(z, t) dz$$

$$r_i(N, p, z, t) = b(z) - \sum_{j=1}^S N_j(t) \int a(z, z') p_j(z', t) dz'$$

$$\frac{dN_i(t)}{dt} = N_i(t) \left( b_i(t) - \sum_{j=1}^S \alpha_{ij}(t) N_j(t) \right)$$

$$b_i(t) = \int p_i(z, t) b(z) dz$$

$$\alpha_{ij}(t) = \int \int p_i(z, t) a(z, z') p_j(z', t) dz' dz$$

- $a(z, z')$  and  $b(z)$  are appropriately chosen functions to describe interaction and intrinsic growth rate.

# Interaction Kernel $a(z, z')$ and Growth Rate $b(z)$

- If  $a(z, z') = \exp\left(-\frac{(z-z')^2}{\omega^2}\right)$  then,

$$\begin{aligned}\alpha_{ij}(t) &= \int \int p_i(z, t) a(z, z') p_j(z', t) dz' dz \\ &= \frac{w}{\sqrt{2\sigma_i^2 + 2\sigma_j^2 + w^2}} \exp\left(-\frac{(\mu_i(t) - \mu_j(t))^2}{2\sigma_i^2 + 2\sigma_j^2 + w^2}\right)\end{aligned}$$

- Note that,  $\alpha_{ij} = \frac{w}{\sqrt{4\sigma_i^2 + w^2}}$ , when  $i = j$
- If  $b(z) = r_i$ ,  $-\infty < z < \infty$  then,

$$b_i(t) = \int p_i(z, t) b(z) dz = r_i$$

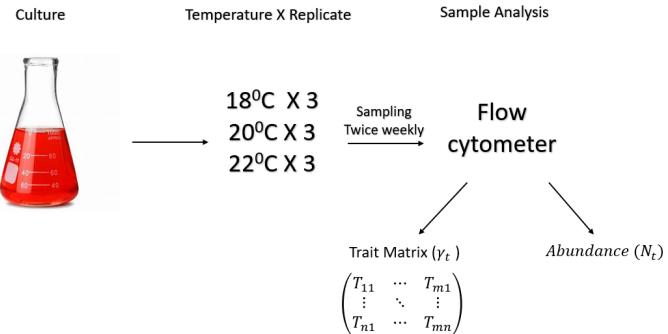
# Quantitative Genetic Lotka-Volterra (Two Species)

$$\begin{pmatrix} \frac{dN_1}{dt} \\ \frac{dN_2}{dt} \end{pmatrix} = \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \left[ \begin{pmatrix} r_1 \\ r_2 \end{pmatrix} - \begin{pmatrix} \alpha_{11} & \alpha_{12} \\ \alpha_{21} & \alpha_{22} \end{pmatrix} \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \right]$$

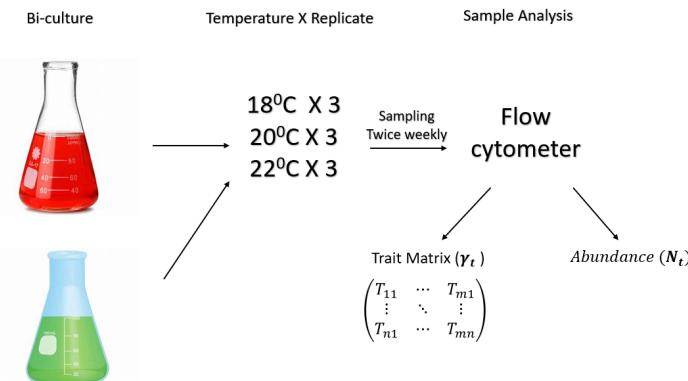
- $\alpha_{11} = \frac{w}{\sqrt{4\sigma_1^2+w^2}}$
- $\alpha_{12} = \alpha_{21} = \frac{w}{\sqrt{2\sigma_1^2+2\sigma_2^2+w^2}} \exp\left(-\frac{(\mu_1(t)-\mu_2(t))^2}{2\sigma_1^2+2\sigma_2^2+w^2}\right)$
- $\alpha_{22} = \frac{w}{\sqrt{4\sigma_2^2+w^2}}$

# Data and experiments

# Experiments

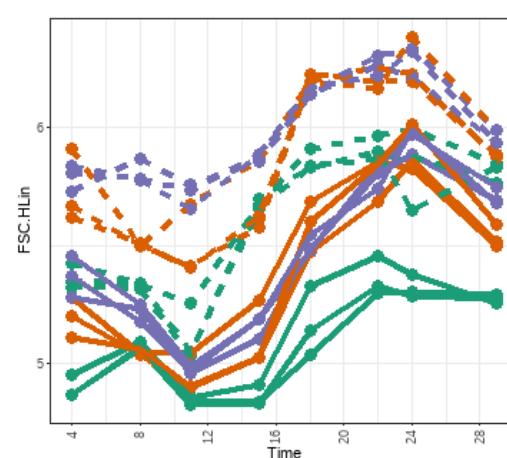
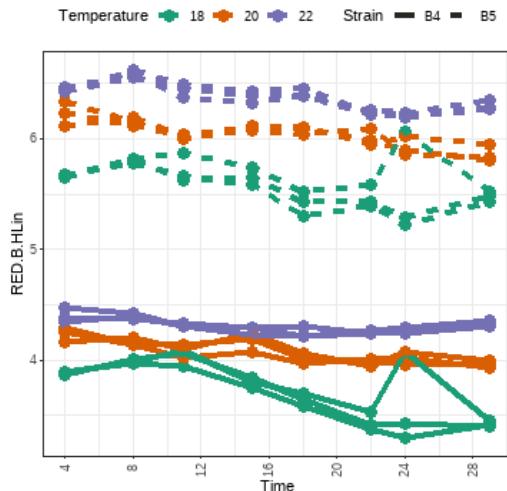
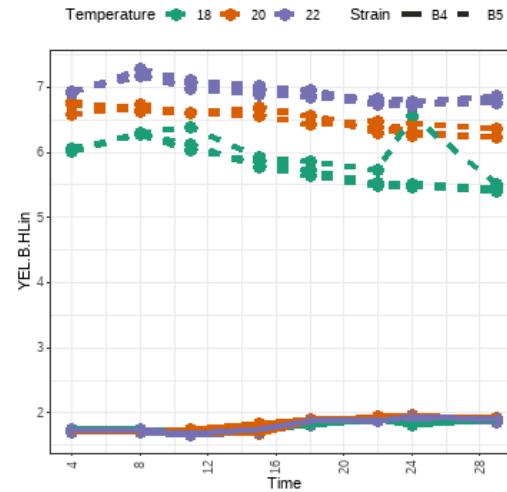
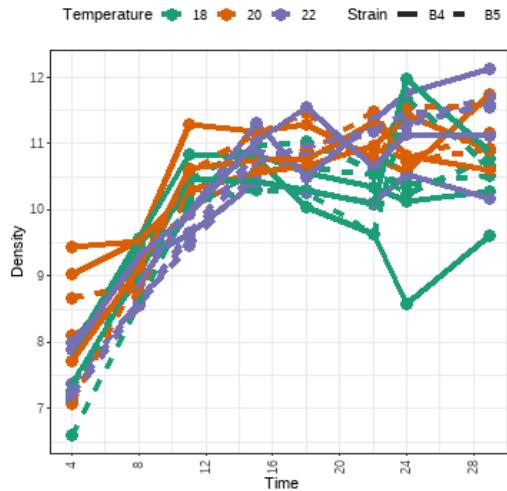


## Monoculture Experiment



## Biculture Experiment

# Data



# Fitting The Model

$$\begin{pmatrix} N_1 \\ N_2 \end{pmatrix} \sim MVN \left( \int \begin{pmatrix} \frac{dN_1}{dt} \\ \frac{dN_2}{dt} \end{pmatrix}, \Sigma \right)$$

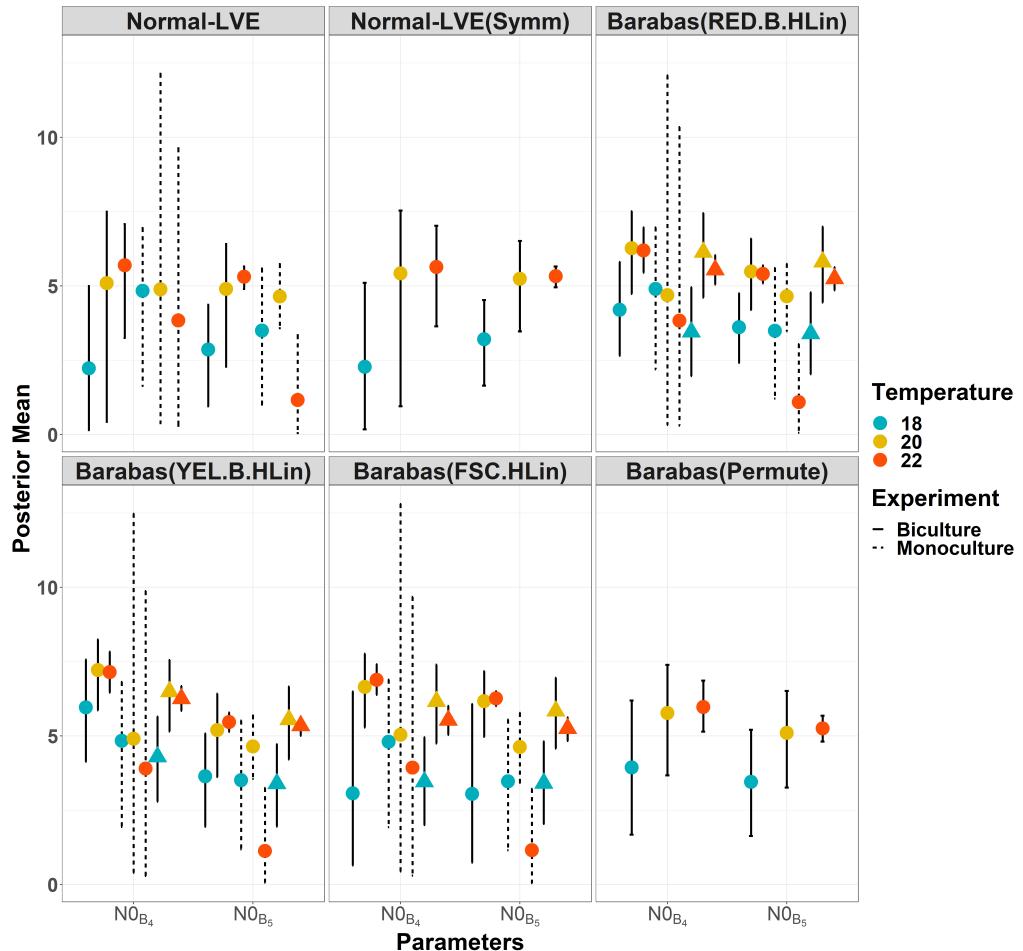
- $\Sigma = \begin{pmatrix} \sigma_1^2 & \rho\sigma_1\sigma_2 \\ \rho\sigma_1\sigma_2 & \sigma_2^2 \end{pmatrix}$
- $\hat{\alpha}_{12} = \frac{w}{\sqrt{2s_1^2+2s_2^2+w^2}} \exp\left\{-\frac{(\bar{z}_i(t)-\bar{z}_j(t))^2}{2s_1^2+2s_2^2+w^2}\right\}$ , thus  $\hat{\alpha}_{ii} = \frac{w}{\sqrt{4s_i^2+w^2}}$ ,  $i = 1, 2$
- $\bar{z}_i(t)$  is obtained by pooling  $\frac{\sum_{k=1}^{n(t)} z_{ik}}{n(t)}$  across replicates
- $s_1^2, s_j^2$  are obtained by pooling  $\frac{\sum_{k=1}^{n(t)} (z_{ik} - \bar{z}_i(t))^2}{n(t)-1}$  across replicates and  $t$
- For monoculture;  $\hat{\alpha}_{12} = 0$ ,  $\Sigma = \begin{pmatrix} \sigma_1^2 & 0 \\ 0 & \sigma_2^2 \end{pmatrix}$

# Fitting The Model (cont.)

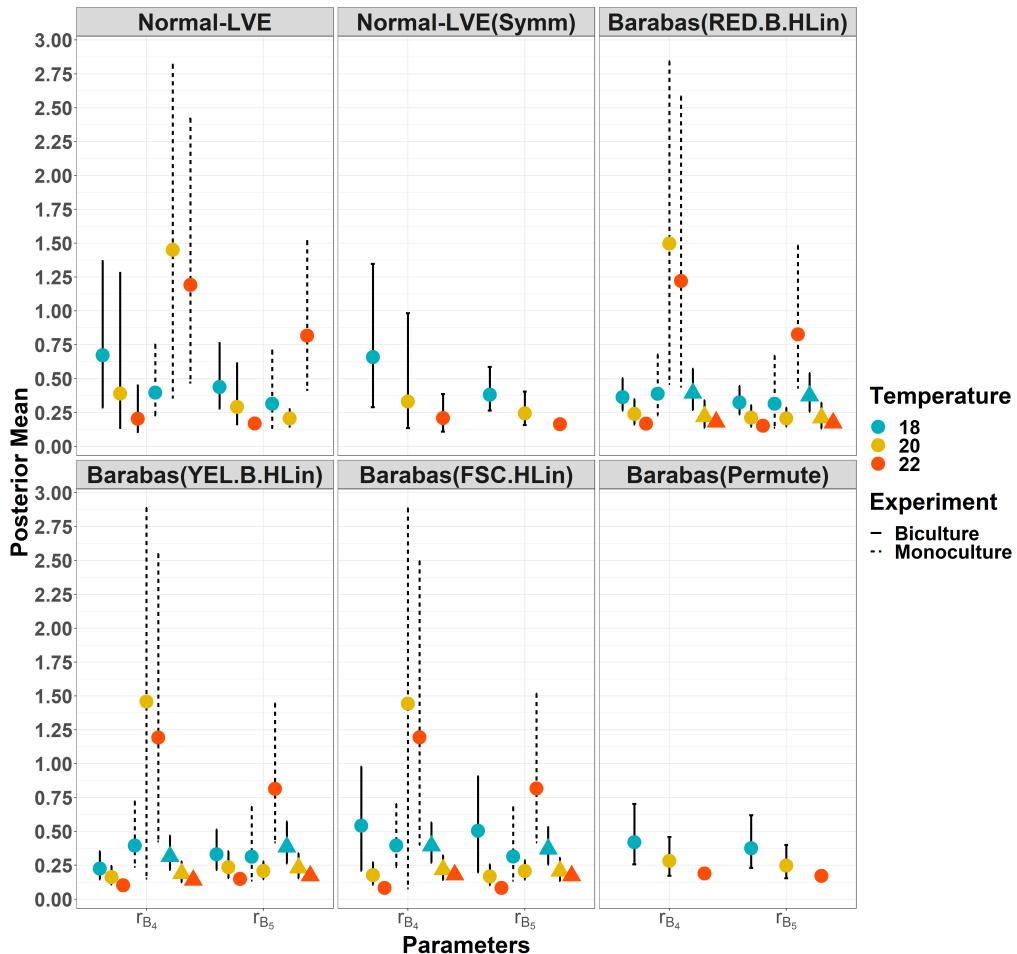
- **Normal-LVE**  $\Rightarrow \alpha_{ij}$  are parameters.
- **Symmetric-LVE**  $\Rightarrow \alpha_{ij} = \alpha_{ji}, i \neq j$
- **Barabas**  $\Rightarrow \alpha_{ij} = \frac{w}{\sqrt{2s_1^2+2s_2^2+w^2}} \exp\left\{-\frac{(\bar{z}_1(t)-\bar{z}_2(t))^2}{2s_1^2+2s_2^2+w^2}\right\}$
- **Barabas (Permute)**  $\Rightarrow \alpha_{ij}$  as in Barabas, but  $\bar{z}_i(t) = \bar{z}_i(t') \quad \forall \quad t \neq t'$ . Only for RED.B.HLin.

# Results

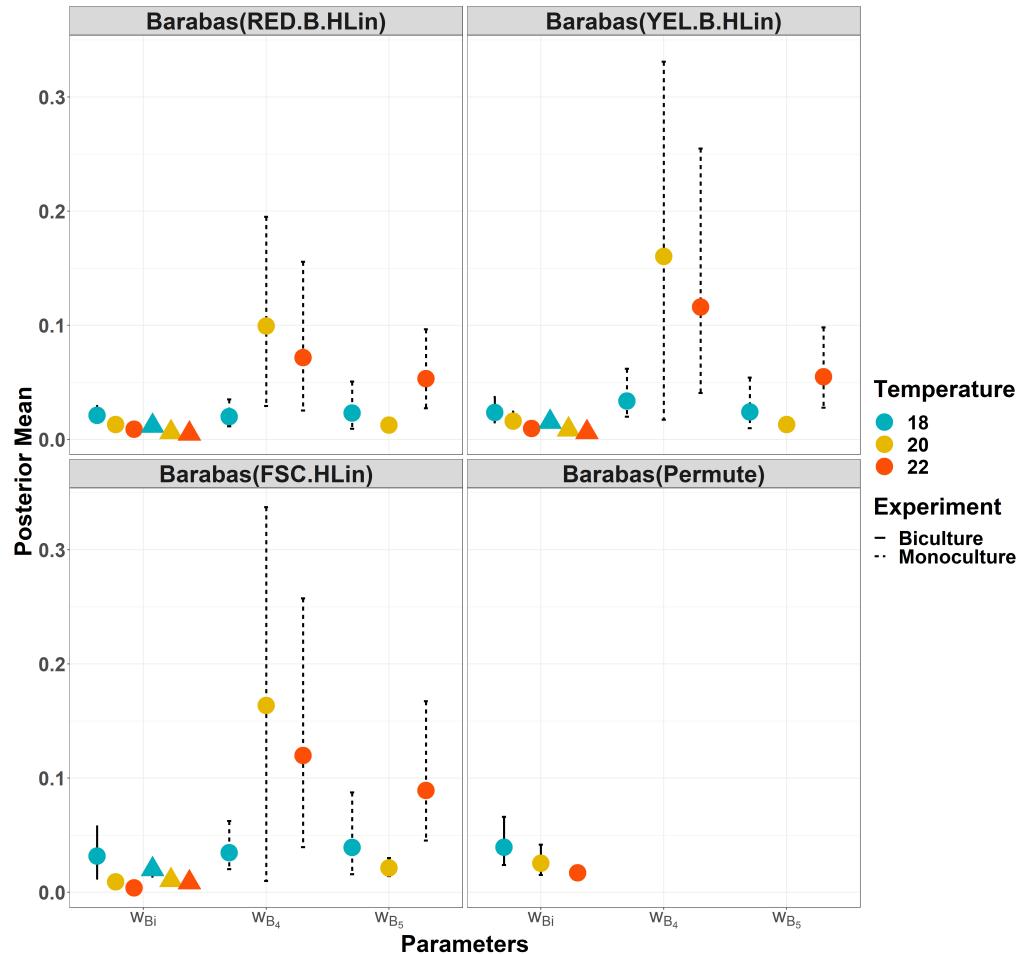
# Results ( $N'_0$ s)



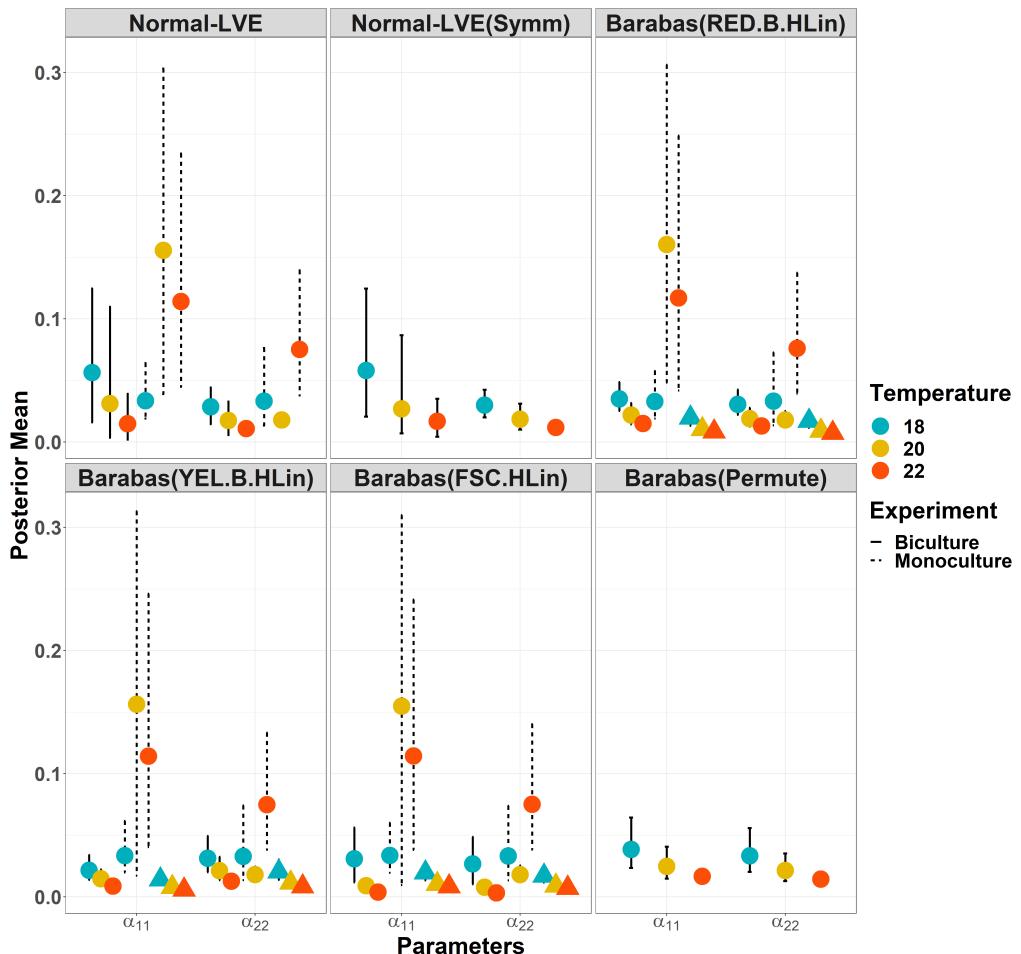
# Results ( $r's$ )



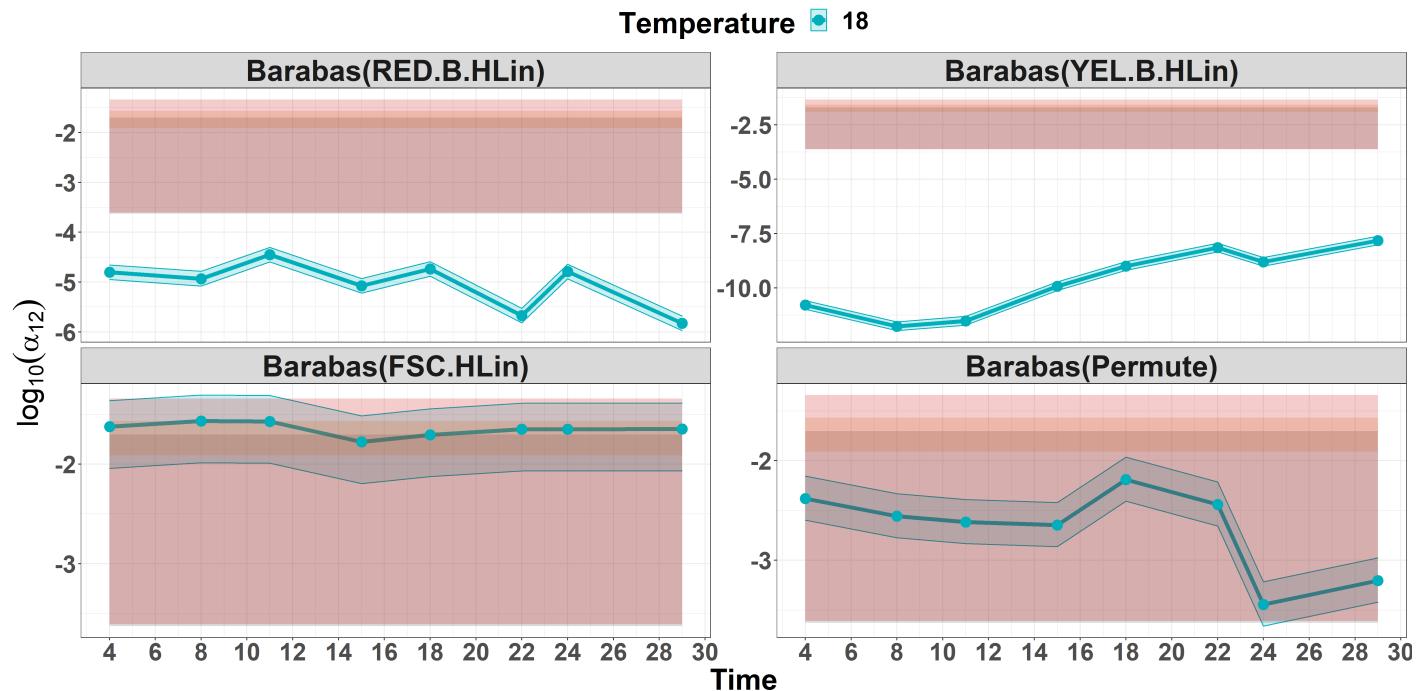
# Results ( $w$ )



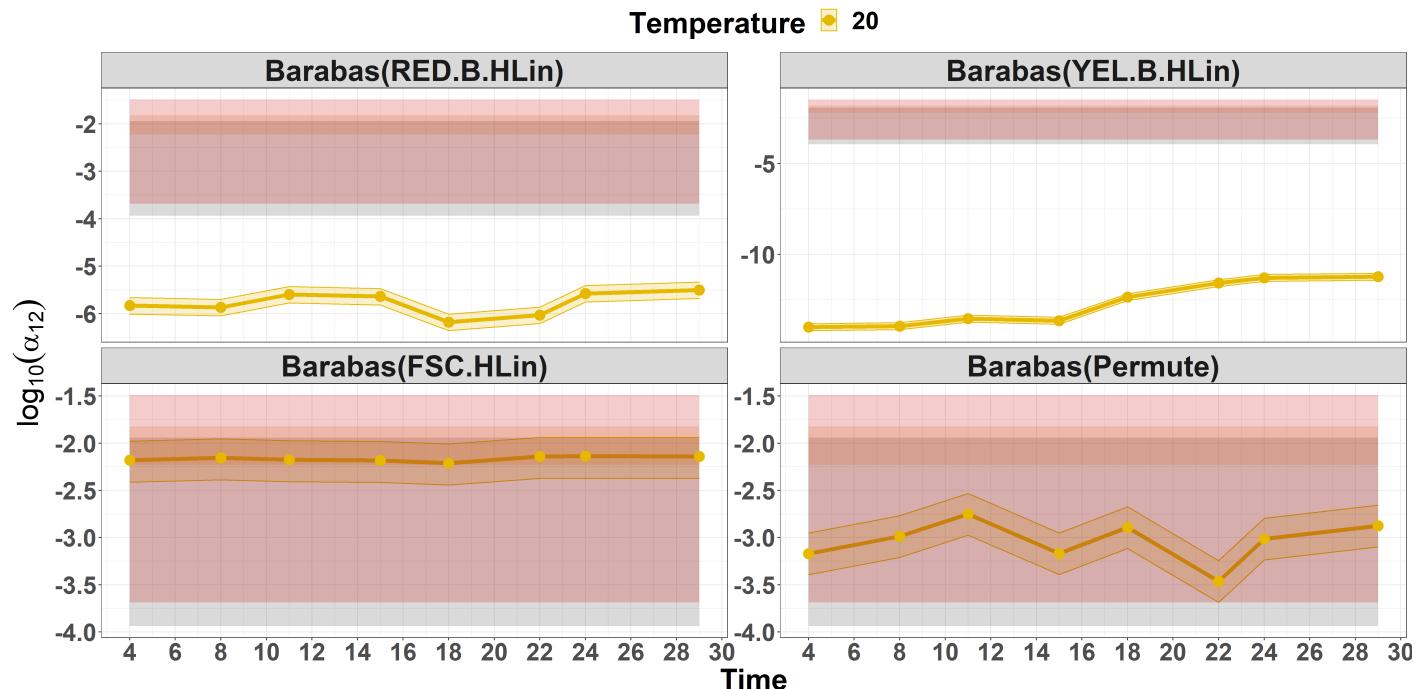
# Results ( $\alpha_{ij}, i = j$ )



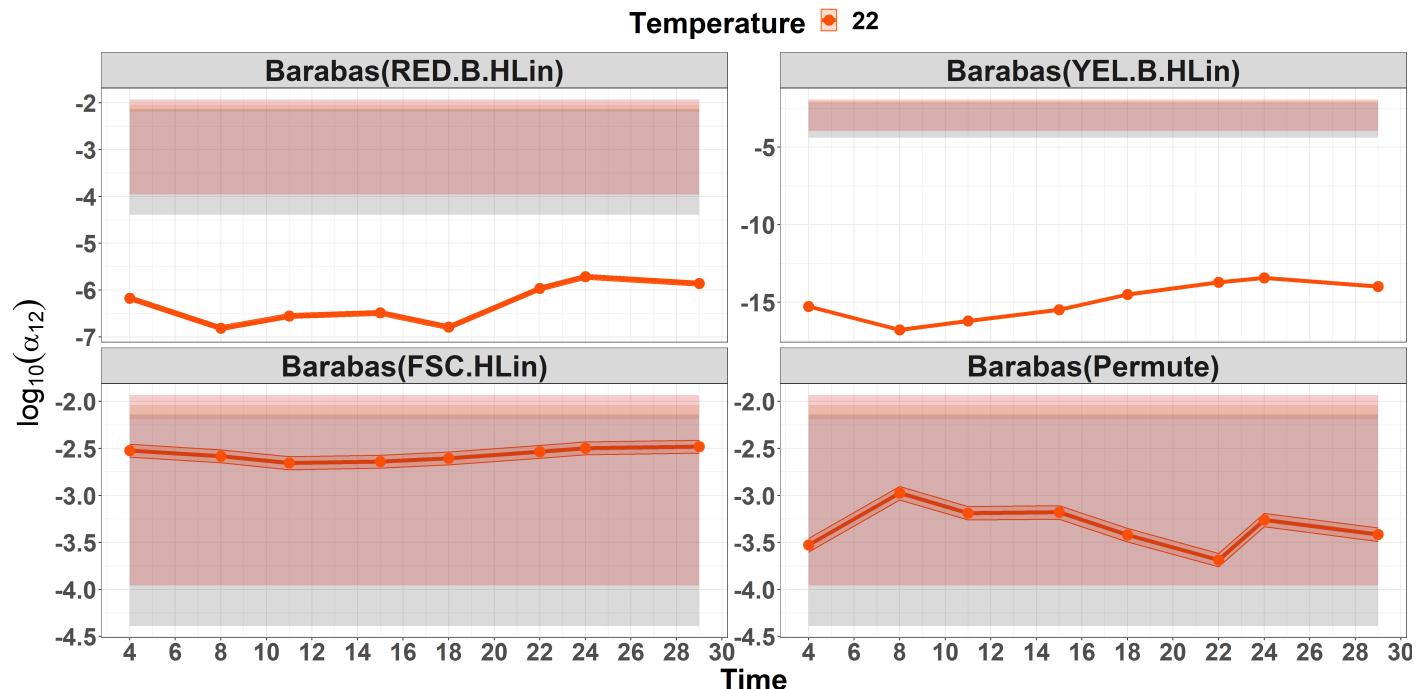
# Results ( $\alpha_{ij}, i \neq j$ )



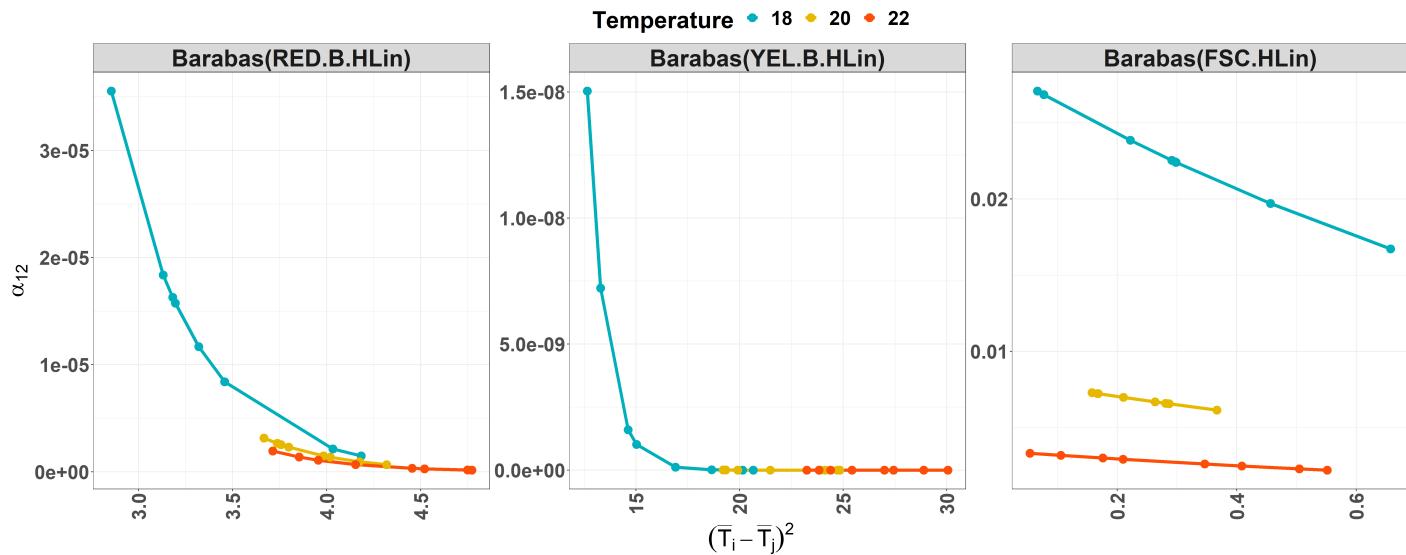
# Results ( $\alpha_{ij}, i \neq j$ )



# Results ( $\alpha_{ij}, i \neq j$ )

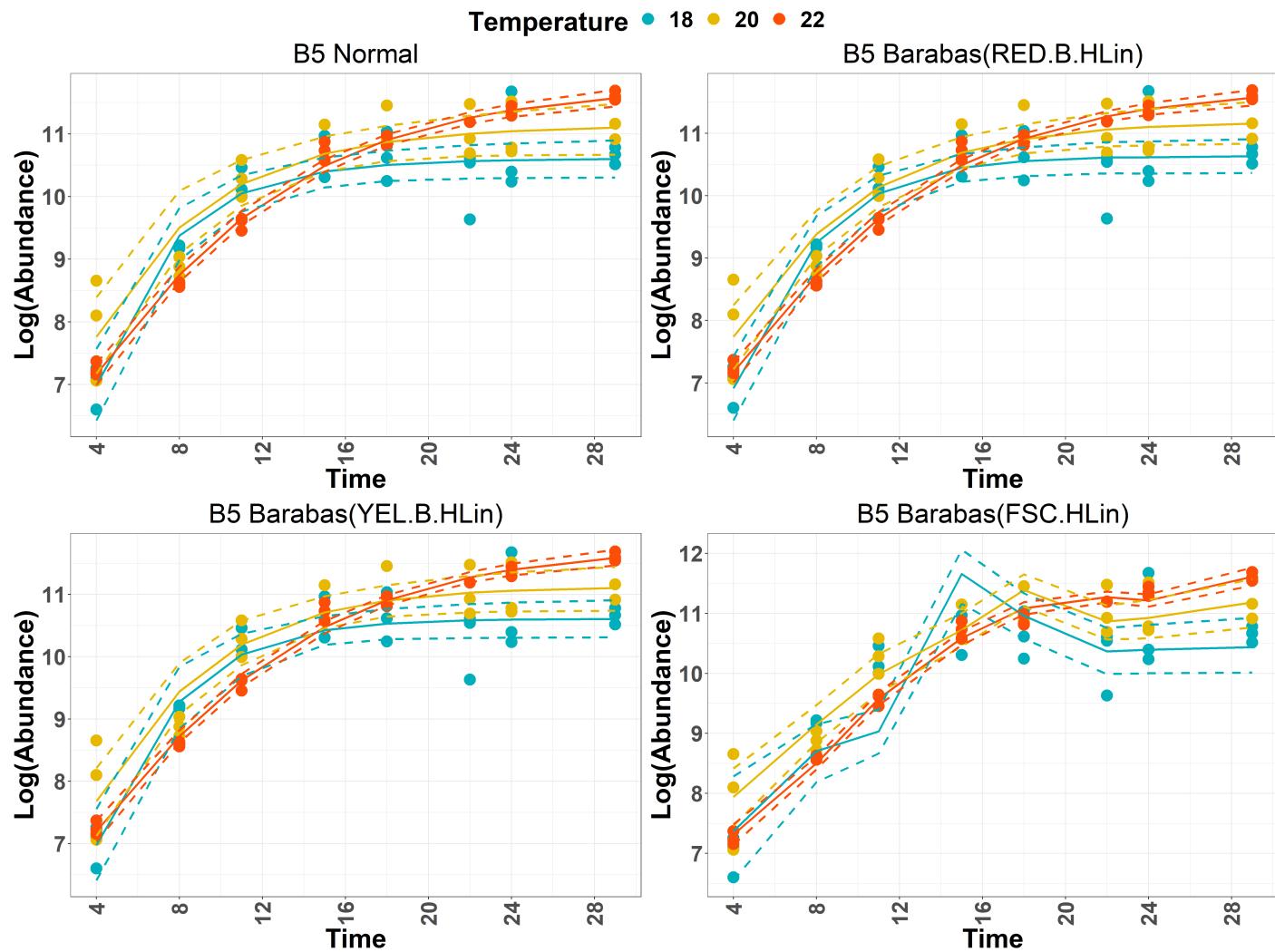


# Results ( $\alpha_{ij}, i \neq j$ )



# Model Prediction (B4s)

# Model Prediction (B5s)



# Model Comparison (Model Posterior Probabilities)

Temperature	Weights	Normal.LVE	Symmetric.LVE	Brabas.RED.B.HLin.	Barabas.YEL.B.HLin.	Barabas.FSC.HLin.	Barabas.Permute.
18	pbma	0.152	0.165	0.666	0.017	0.000	0.000
18	BB	0.175	0.175	0.575	0.018	0.011	0.046
18	stacking	0.000	0.000	0.864	0.000	0.000	0.135
20	pbma	0.009	0.045	0.486	0.170	0.267	0.023
20	BB	0.011	0.048	0.374	0.202	0.321	0.044
20	stacking	0.000	0.000	0.531	0.054	0.415	0.000
22	pbma	0.058	0.079	0.618	0.112	0.131	0.003
22	BB	0.050	0.066	0.409	0.154	0.317	0.005
22	stacking	0.000	0.000	0.418	0.169	0.413	0.000

Note:

Model Posterior probabilities computed using different weights.

BB=Bayesian Bootstrap

pbma=Pseudo Bayesian Model Averaging

# On-going work

## Some Things to Consider

- $b(z) = r_i, -\infty < z < \infty$  ?
- What about the uncertainty about  $\frac{\sum_{k=1}^{n(t)} z_{ik}}{n(t)}$  ?

## Other Growth Functions

- Uniform growth: 
$$\begin{cases} b(z) = \gamma, \kappa < z < \kappa + 2\gamma \\ 0, \text{otherwise} \end{cases}$$
- Quadratic growth: 
$$\begin{cases} \gamma^2 - (z - \kappa - \gamma)^2, \kappa < z < \kappa + 2\gamma \\ 0, \text{otherwise} \end{cases}$$
- Triangular growth: 
$$\begin{cases} \gamma - |z - \kappa - \gamma|, \kappa < z < \kappa + 2\gamma \\ 0, \text{otherwise} \end{cases}$$

# Questions & Suggestions 😊