

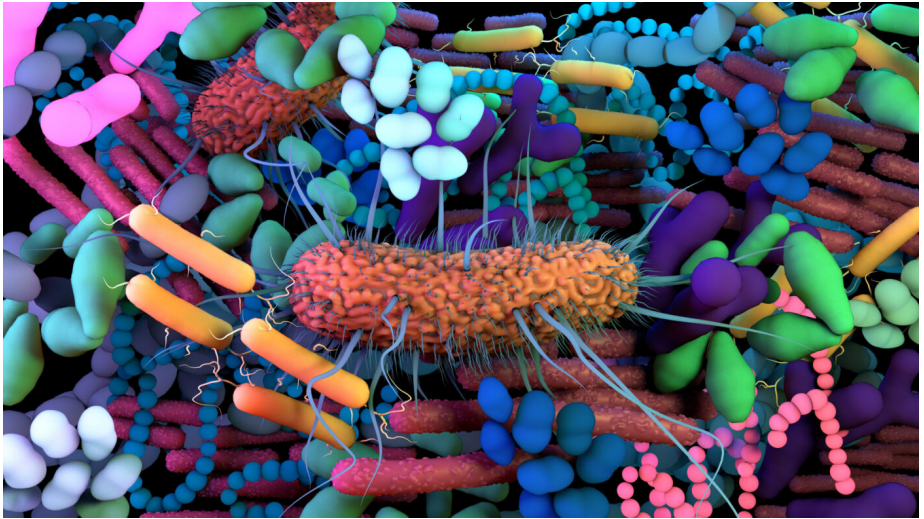
# Coexistence and diversity in a consumer resource model with a serial dilution setting

Samuele Pio Lipani

Physics and Astronomy department  
University of Padova

December 6, 2022

# Why many species coexist?



Martina Dal Bello , Hyunseok Lee , Akshit Goyal and Jeff Gore 

Joshua E. Goldford<sup>1,2\*</sup>, Nanxi Lu<sup>3\*</sup>, Djordje Bajić<sup>3</sup>, Sylvie Estrela<sup>3</sup>, Mikhail Tikhonov<sup>4,5</sup>, Alicia Sanchez-Gorostiaga<sup>3</sup>, Daniel Segre<sup>1,6,7</sup>, Pankaj Mehta<sup>1,7†</sup>, Alvaro Sanchez<sup>2,3†</sup>

# We can reproduce natural environments with experiments

nature  
ecology & evolution

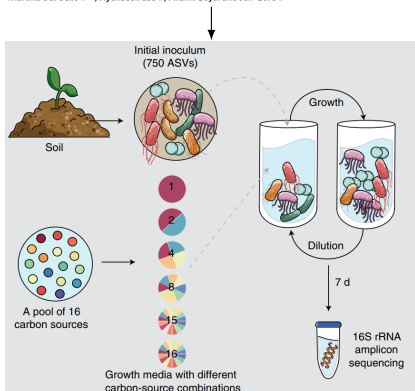
ARTICLES

<https://doi.org/10.1038/s41559-021-01535-8>

Check for updates

## Resource–diversity relationships in bacterial communities reflect the network structure of microbial metabolism

Martina Dal Bello<sup>1,2</sup>, Hyunseok Lee<sup>1</sup>, Akshit Goyal and Jeff Gore<sup>1,2</sup>

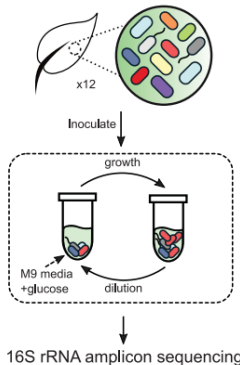


RESEARCH ARTICLE

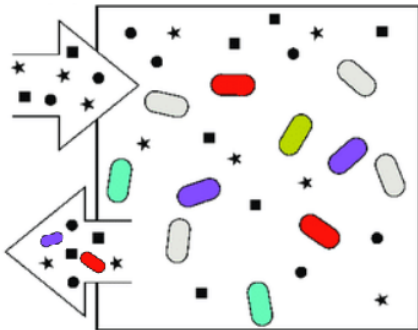
MICROBIOLOGY

## Emergent simplicity in microbial community assembly

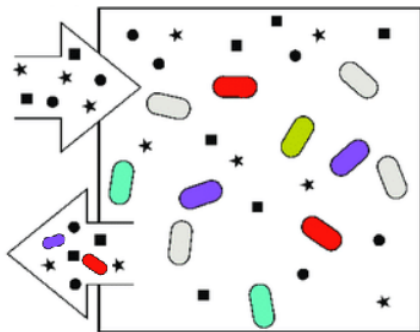
Joshua E. Goldford<sup>1,2</sup>, Nanxi Lu<sup>3</sup>, Djordje Bajić<sup>3</sup>, Sylvie Estrela<sup>2</sup>, Mikhail Tikhonov<sup>4,5</sup>, Alicia Sanchez-Gorostiaga<sup>3</sup>, Daniel Segrè<sup>1,6,7</sup>, Pankaj Mehta<sup>1,7</sup>, Alvaro Sanchez<sup>2,3</sup>



# Consumer resource model in continuous culture studies bacteria behavior



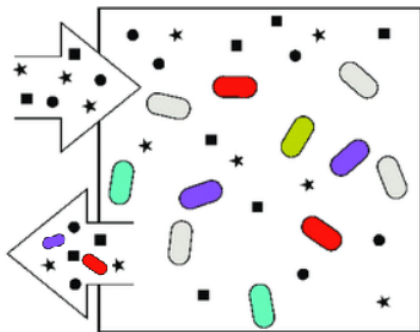
# Consumer resource model in continuous culture studies bacteria behavior



$$\dot{X}_i = X_i \left( \sum_{\alpha} a_{i\alpha} Y_{\alpha} - m_i \right) \quad \bullet$$

$$\dot{Y}_{\alpha} = K_{\alpha} - \omega_{\alpha} Y_{\alpha} - \sum_i X_i a_{i\alpha} Y_{\alpha} \quad \blacksquare$$

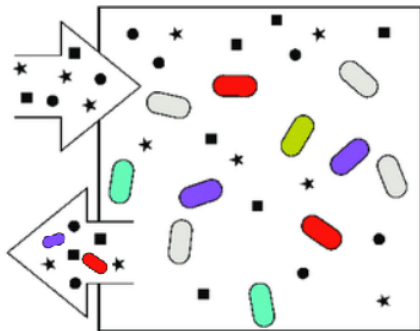
# Consumer resource model in continuous culture studies bacteria behavior



$$\dot{X}_i = X_i \left( \sum_{\alpha} a_{i\alpha} Y_{\alpha} - m_i \right) \quad \bullet$$

$$\dot{Y}_{\alpha} = K_{\alpha} - \omega_{\alpha} Y_{\alpha} - \sum_i X_i a_{i\alpha} Y_{\alpha} \quad \blacksquare$$

# Consumer resource model in continuous culture studies bacteria behavior

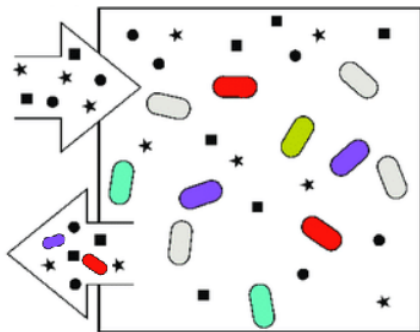


$$\dot{X}_i = X_i \left( \sum_{\alpha} a_{i\alpha} Y_{\alpha} - m_i \right) \quad \bullet$$

$$\dot{Y}_{\alpha} = K_{\alpha} - \omega_{\alpha} Y_{\alpha} - \sum_i X_i a_{i\alpha} Y_{\alpha} \quad \blacksquare$$



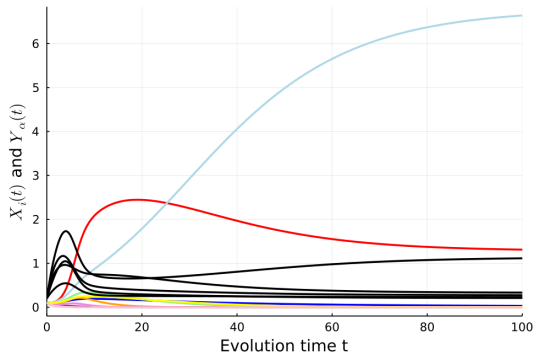
# Consumer resource model in continuous culture studies bacteria behavior



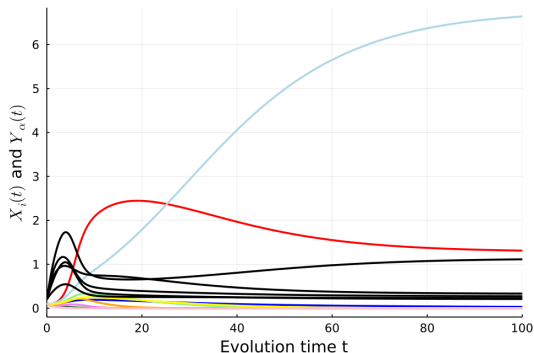
$$\dot{X}_i = X_i \left( \sum_{\alpha} \textcircled{a_{i\alpha}} Y_{\alpha} - m_i \right) \quad \bullet$$

$$\dot{Y}_{\alpha} = K_{\alpha} - \omega_{\alpha} Y_{\alpha} - \sum_i X_i \textcircled{a_{i\alpha}} Y_{\alpha} \quad \blacksquare$$

# What happens in chemostat setting?



# What happens in chemostat setting?



**P. Mehta, M. Advani,  
G. Bunin**

random consumer  
preferences  $a_{i\alpha}$

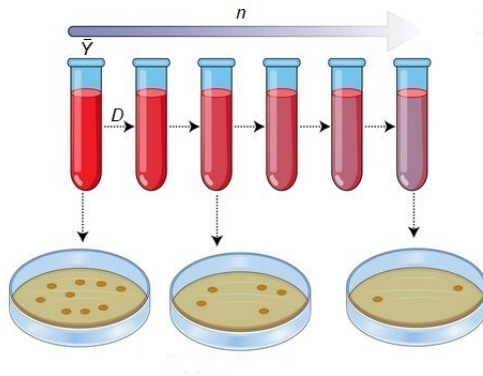
disordered systems  
techniques

$$\Phi^* \leq 1/2 \cdot M$$

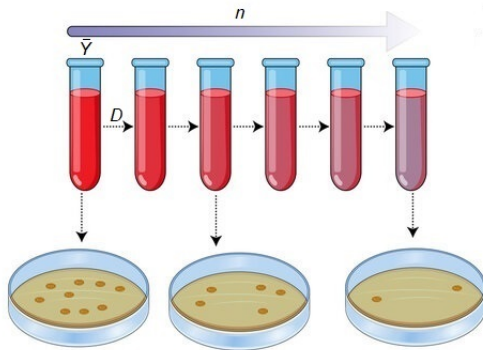
$\Phi^* = \#$  of species  
that survive

$M = \#$  of resources

# Experiments are performed in serial dilution

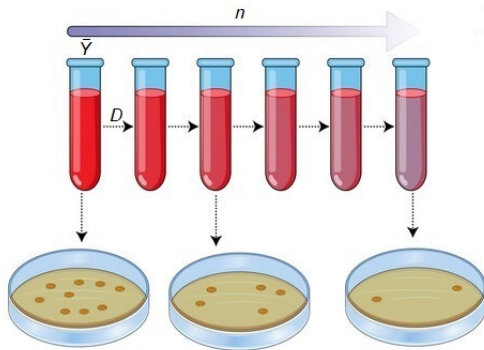


# Experiments are performed in serial dilution



$D$  = dilution factor

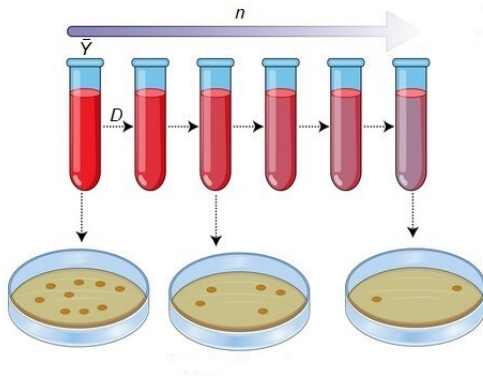
# Experiments are performed in serial dilution



$D$  = dilution factor

$n$  = number of dilution steps

# Experiments are performed in serial dilution



$D$  = dilution factor

$n$  = number of dilution steps

$\bar{Y}$  = resources replenished in each step

# Experiments and theoretical studies don't agree

## Problems

- *The majority of theoretical studies have been framed in the chemostat setting where resources are constantly restored flowing into the system*



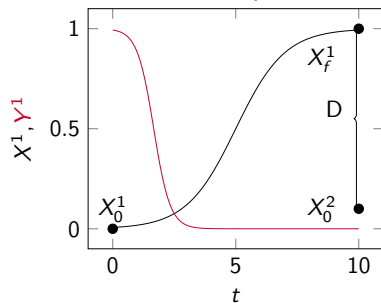
# Experiments and theoretical studies don't agree

## Problems

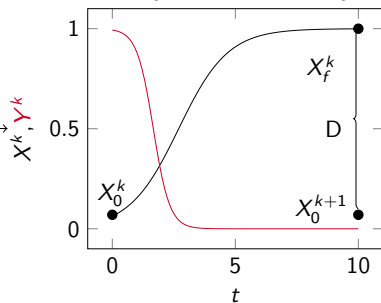
- *The majority of theoretical studies have been framed in the chemostat setting where resources are constantly restored flowing into the system*
- *Both experiments and natural communities are better described by serial dilution processes*

# What is a serial dilution process

First dilution cycle

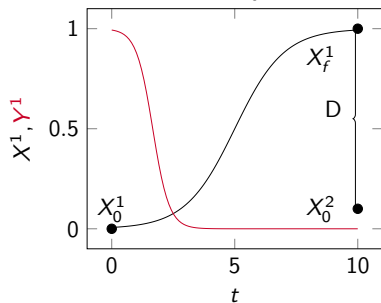


Steady state dilution cycle

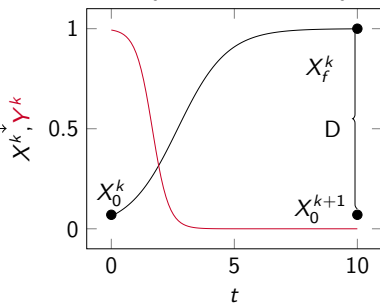


# What is a serial dilution process

First dilution cycle



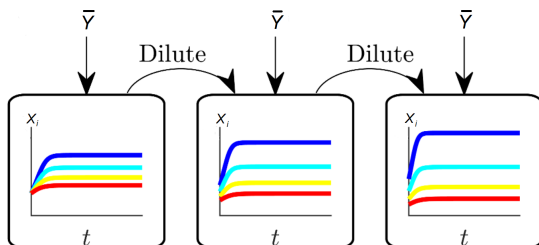
Steady state dilution cycle



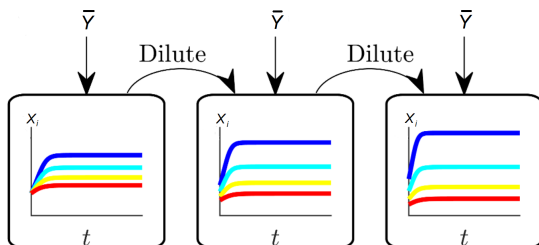
$$\dot{X}_i = X_i \sum_{\alpha=1}^M a_{i\alpha} Y_{\alpha}, \quad X_i^{k+1}(0) = \frac{X_i^k(t=10)}{D}$$

$$\dot{Y}_{\alpha} = -Y_{\alpha} \sum_{i=1}^X a_{i\alpha} X_i, \quad Y_{\alpha}^{k+1}(0) = \frac{Y_{\alpha}^k(t=10)}{D} + \bar{Y}_{\alpha}$$

# Chemostat is a limit of serial dilution

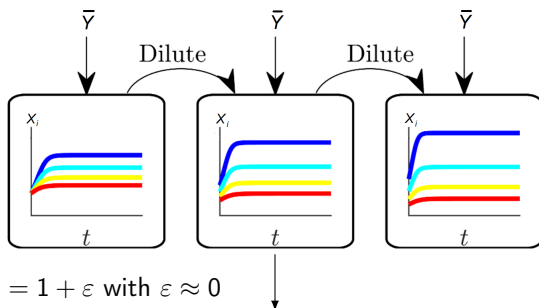


# Chemostat is a limit of serial dilution

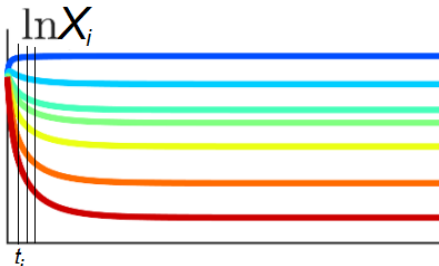


For  $t \approx \varepsilon$  and  $D = 1 + \varepsilon$  with  $\varepsilon \approx 0$

# Chemostat is a limit of serial dilution



For  $t \approx \varepsilon$  and  $D = 1 + \varepsilon$  with  $\varepsilon \approx 0$



# What is the setting of the model we are studying?

Constant replenish  $\bar{Y}_\alpha$

Dilution factor  $D \in [1.05, 100]$

Preferences  $a_{i\alpha} \sim \mathcal{U}(1 - \sigma, 1 + \sigma)$

$\sigma \in [10^{-3}, 0.5]$

Sparsity  $S \in \{0.1, 0\}$

# What is the setting of the model we are studying?

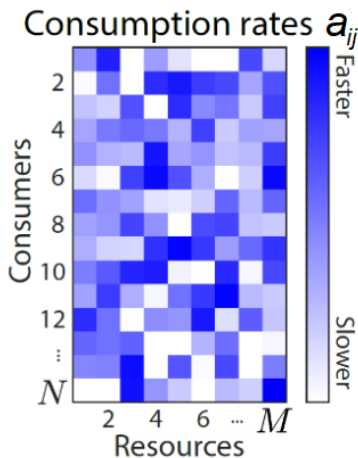
Constant replenish  $\bar{Y}_\alpha$

Dilution factor  $D \in [1.05, 100]$

Preferences  $a_{i\alpha} \sim \mathcal{U}(1 - \sigma, 1 + \sigma)$

$\sigma \in [10^{-3}, 0.5]$

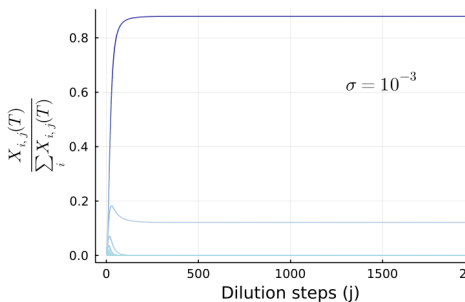
Sparsity  $S \in \{0.1, 0\}$



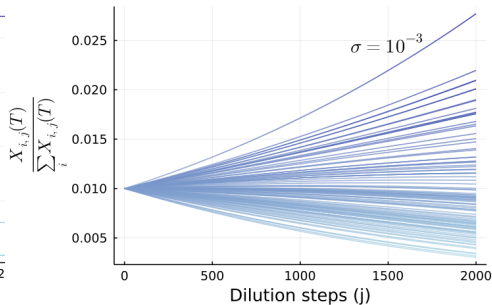


# Sparsity speeds up convergence

If we change the sparsity  $S$  and variability  $\sigma$  of  $a_{i\alpha}$  we find different convergence time scales

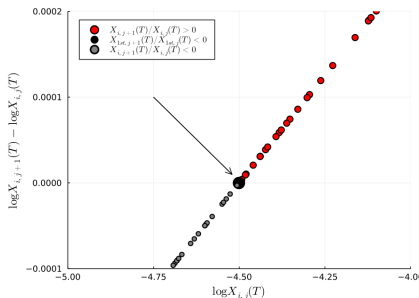


$S = 0.1$

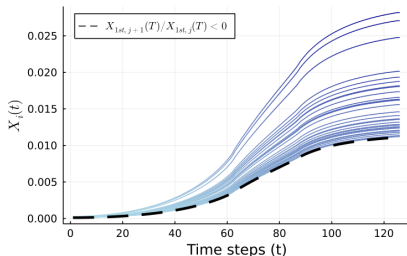
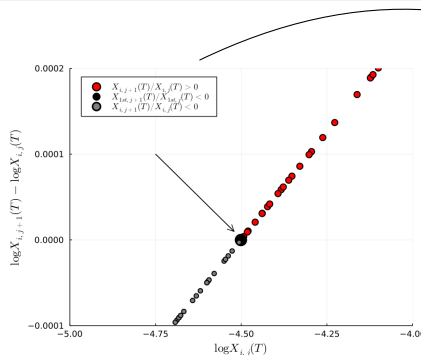


$S = 0$

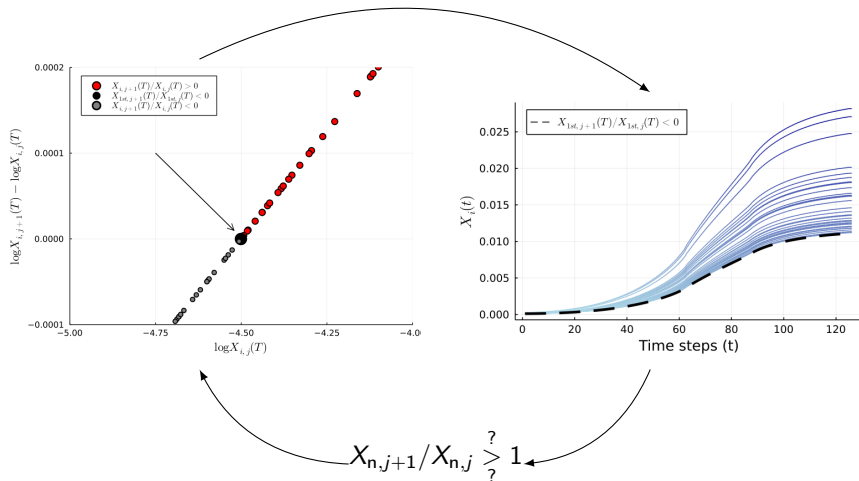
# Invasion analysis algorithm detects which species are going to extinction



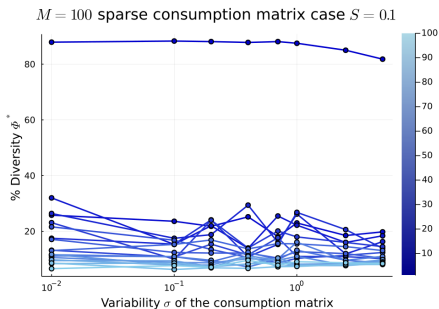
# Invasion analysis algorithm detects which species are going to extinction



# Invasion analysis algorithm detects which species are going to extinction



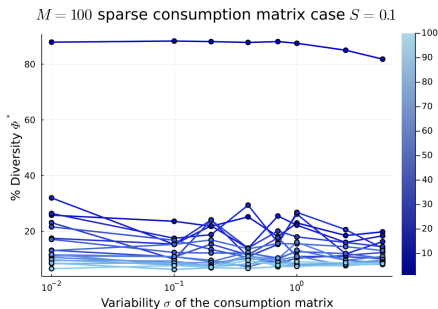
# Diversity curves behave differently with and without sparsity



Diversity  $\Phi^*(x) = \Phi^*(\sigma, x)$

stationarity ✓

# Diversity curves behave differently with and without sparsity

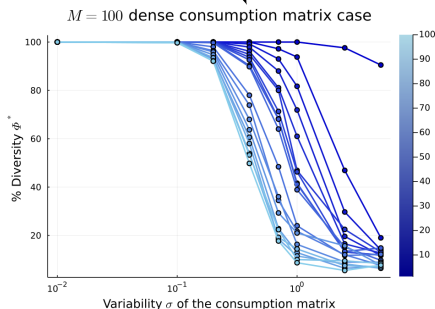


$$\text{Diversity } \Phi^*(x) = \Phi^*(\sigma, x)$$

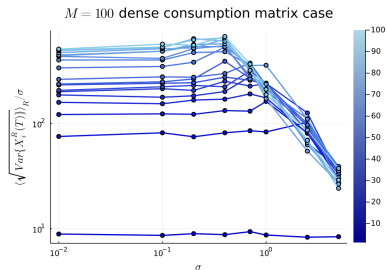
stationarity ✓

$$\text{Diversity } \Phi^*(x) = \Phi^*(\sigma, x)$$

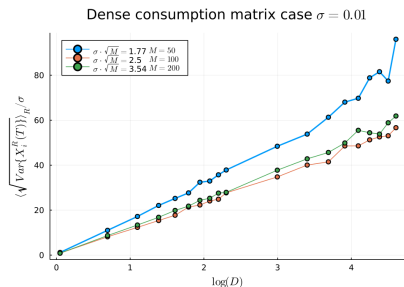
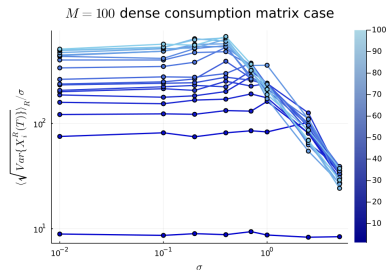
stationarity ✗



$S = 0$ , species abundance distribution is a function of a rescaled variability  $s = \sigma \log D$

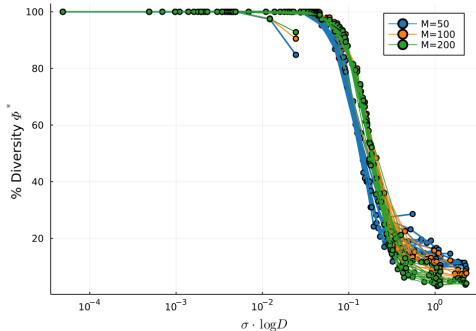
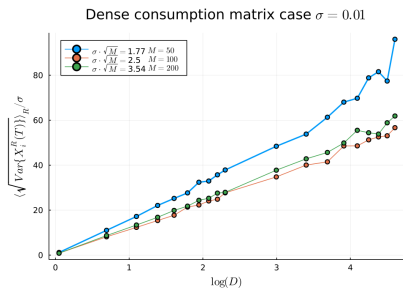
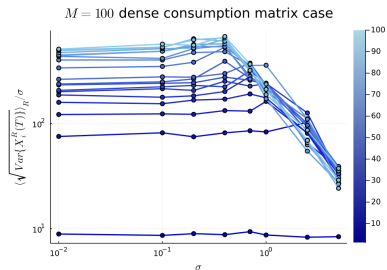


$S = 0$ , species abundance distribution is a function of a rescaled variability  $s = \sigma \log D$





$S = 0$ , species abundance distribution is a function of a rescaled variability  $s = \sigma \log D$



# Serial dilution model is influenced by many parameters

- Chemostat and serial dilution are different settings for describing the same natural environments

# Serial dilution model is influenced by many parameters

- Chemostat and serial dilution are different settings for describing the same natural environments
- Serial dilution is strongly influenced by the choice of the disorder of the consumption matrix and its sparsity

# Serial dilution model is influenced by many parameters

- Chemostat and serial dilution are different settings for describing the same natural environments
- Serial dilution is strongly influenced by the choice of the disorder of the consumption matrix and its sparsity
- Species abundance distribution can be written in terms of new quantities like a rescaled variability  $s = \sigma \log D$

# What are the future perspectives?

- We can compare different probability distributions to draw entries of  $a_{i\alpha}$  from

# What are the future perspectives?

- We can compare different probability distributions to draw entries of  $a_{i\alpha}$  from
- We can analyze how species preferences influence their role in the ecosystem, their final abundances in the SAD and its shape

# What are the future perspectives?

- We can compare different probability distributions to draw entries of  $a_{i\alpha}$  from
- We can analyze how species preferences influence their role in the ecosystem, their final abundances in the SAD and its shape
- Invasion analysis algorithm can be tested for large number of steps and different number of species to test its consistency

Thanks to:

**Prof. Samir Suweis**

**Prof. Jacopo Grilli**

**Dr. Matteo Sireci**



UNIVERSITÀ  
DEGLI STUDI  
DI PADOVA



The Abdus Salam  
**International Centre  
for Theoretical Physics**



# What happens for one species and one resource?

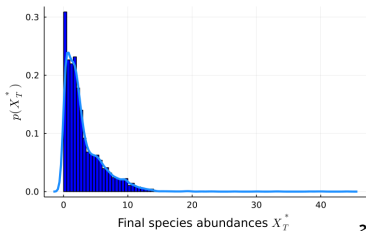
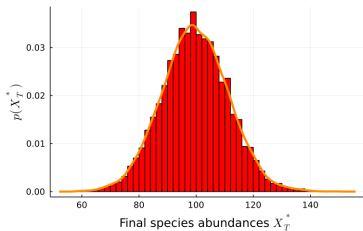
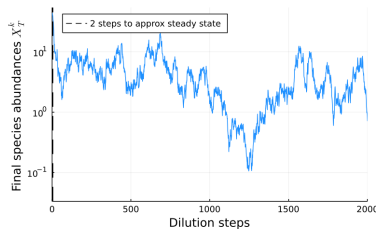
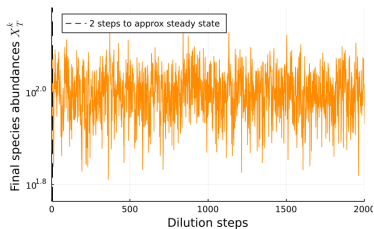
$$\dot{X} = XRY$$

$$\dot{Y} = -XRY$$

# What happens for one species and one resource?

$$\dot{X} = XRY$$

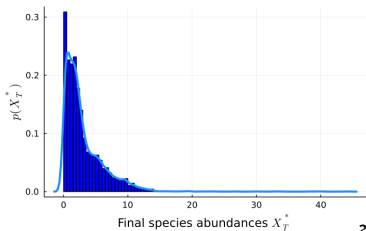
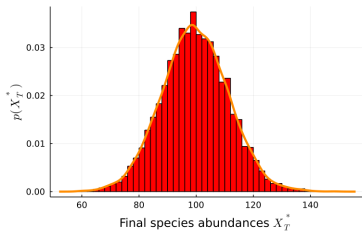
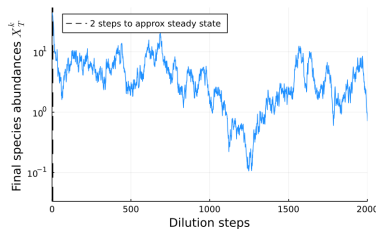
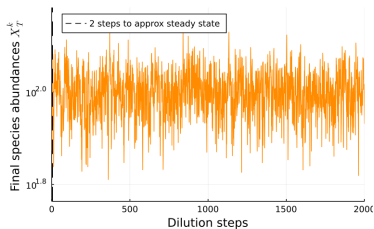
$$\dot{Y} = -XRY$$



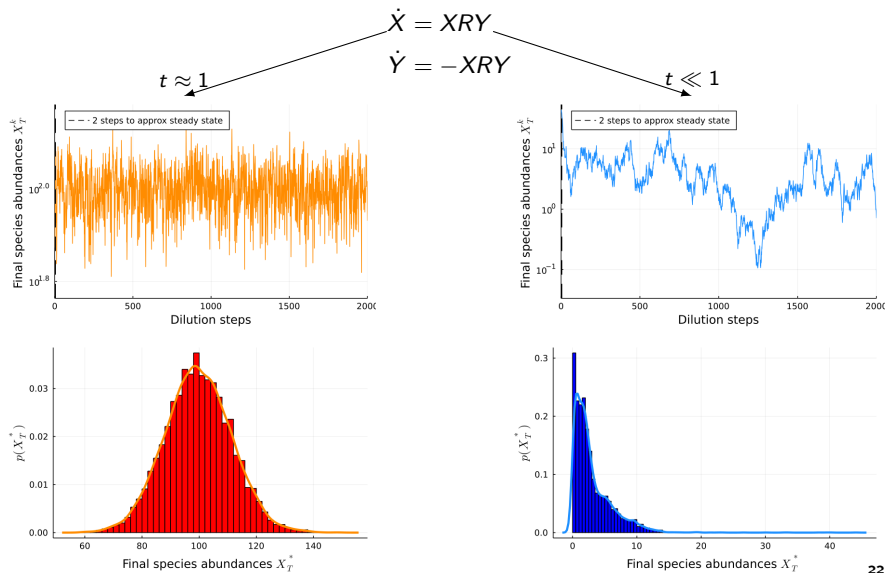
# What happens for one species and one resource?

$$\begin{aligned}\dot{X} &= XRY \\ \dot{Y} &= -XRY\end{aligned}$$

$t \approx 1$



# What happens for one species and one resource?



# Mean species abundance grows logistically

$$\dot{\bar{X}}(t) = \bar{X}(t) \sum_{\alpha=1}^M a_{i\alpha} Y_{\alpha}(t)$$

$$\dot{\bar{X}}(t) = \bar{X}(t) \left( \mu \bar{Y}(t) + \sum_{\alpha=1}^M d_{i\alpha} Y_{\alpha}(t) \right)$$

$$\dot{\bar{X}}(t) = \bar{X}(t) (\mu \bar{Y}(t) + \xi_i) \quad \forall i = 1, \dots, S$$

If

$$B = \gamma^*(\bar{Y}(\tau) + \bar{X}(T)) = \gamma^*(\bar{Y}(t) + \bar{X}(t))$$

$$\bar{Y}(t) = \bar{X}(T) - \bar{X}(t)$$

# Mean species abundance grows logistically

$$\dot{\bar{X}}(t) = \bar{X}(t) \sum_{\alpha=1}^M a_{i\alpha} Y_{\alpha}(t)$$

$$\dot{\bar{X}}(t) = \bar{X}(t) \left( \mu \bar{Y}(t) + \sum_{\alpha=1}^M d_{i\alpha} Y_{\alpha}(t) \right)$$

$$\dot{\bar{X}}(t) = \bar{X}(t) (\mu \bar{Y}(t) + \xi_i) \quad \forall i = 1, \dots, S$$

If

$$B = \gamma^*(\bar{Y}(T) + \bar{X}(T)) = \gamma^*(\bar{Y}(t) + \bar{X}(t))$$

$$\bar{Y}(t) = \bar{X}(T) - \bar{X}(t)$$

Then

$$\dot{\bar{X}}(t) = \mu \bar{X}(t) (\bar{X}(T) - \bar{X}(t)) + \bar{X}(t) \xi_i$$

# Numerical proof sustaining mean abd. logistic growth

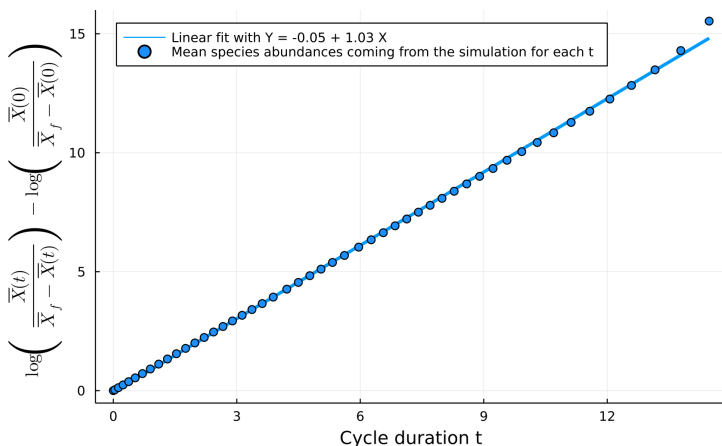
If  $\bar{X}(t)\xi$  is a subleading term then

$$\dot{\bar{X}}(t) = \mu \bar{X}(t) (\bar{X}_f - \bar{X}(t)) + \mathcal{O}(1/M)$$

# Numerical proof sustaining mean abd. logistic growth

If  $\bar{X}(t)\xi$  is a subleading term then

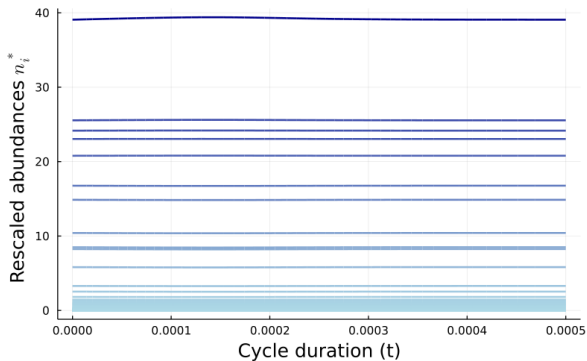
$$\dot{\bar{X}}(t) = \mu \bar{X}(t) (\bar{X}_f - \bar{X}(t)) + \mathcal{O}(1/M)$$



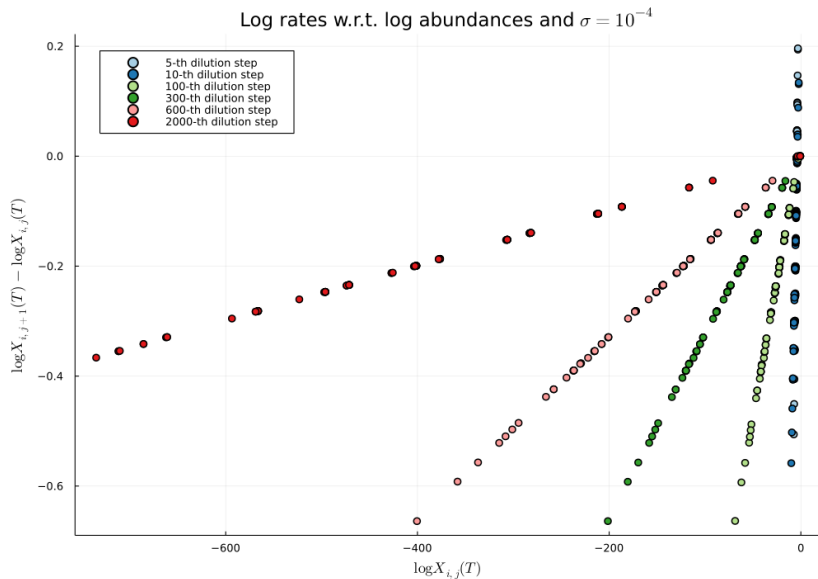


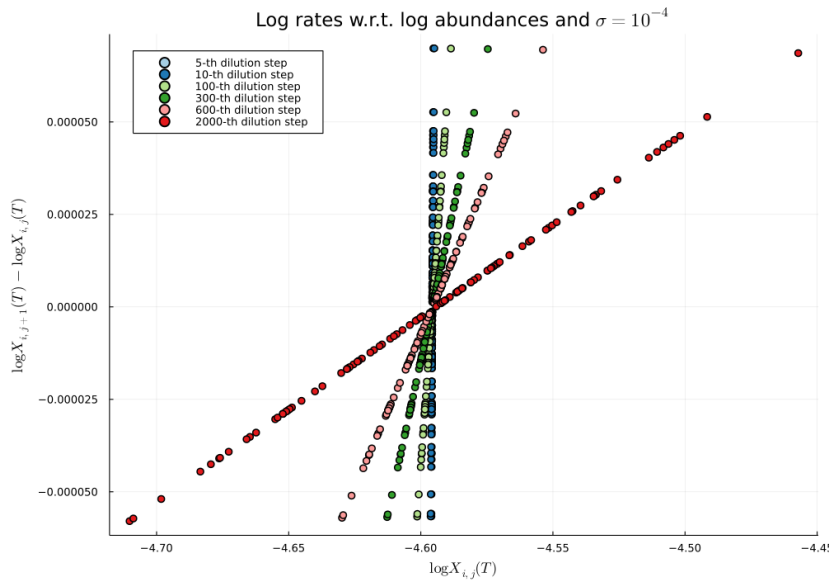
# Stability of rescaled abundances

Write  $X_i(t) = n_i(t)\bar{X}(t)$  and plot  $n_i(t)$  at stationarity



That means:  $X_i(t) = n_i^* \bar{X}_i(t)$  and  $\dot{X}_i(t) = n_i^* \dot{\bar{X}}(t)$

Growth rates  $S = 0.1$ 

Growth rates  $S = 0$ 

SADs depend on a rescaled variance  $s = \sigma \log D$

$$\Phi^*(s) = \int_0^\infty dx \, p(x|s)$$

