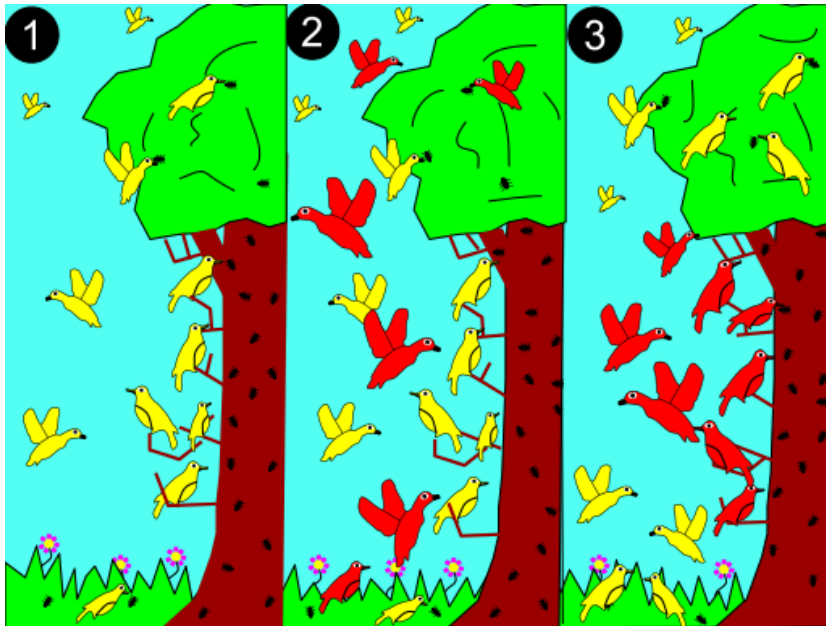


# Revisiting community ecology in the age of microbes: What can statistical physics contribute?



Pankaj Mehta

Collaborators: Nanxi Lu, Alvaro Sanchez, Josh Goldford, Madhu Advani, Guy Bunin  
Kirill Korolev, Daniel Segré

# Statistical physics + community ecology

## **Ecology+ Statistical Physics of Disordered systems**

Fisher + Mehta PNAS 2014

Fisher+Mehta PLoS One 2014

Dickens+Fisher+Mehta PRE 2016

Tikhonov Elife 2016

Tikhonov +Monasson PRL 2016

Bunin PRE 2016

Kessler +Shnerb PRE 2015

Posfai+Wingreen PRL 2017

## **Neutral theory:**

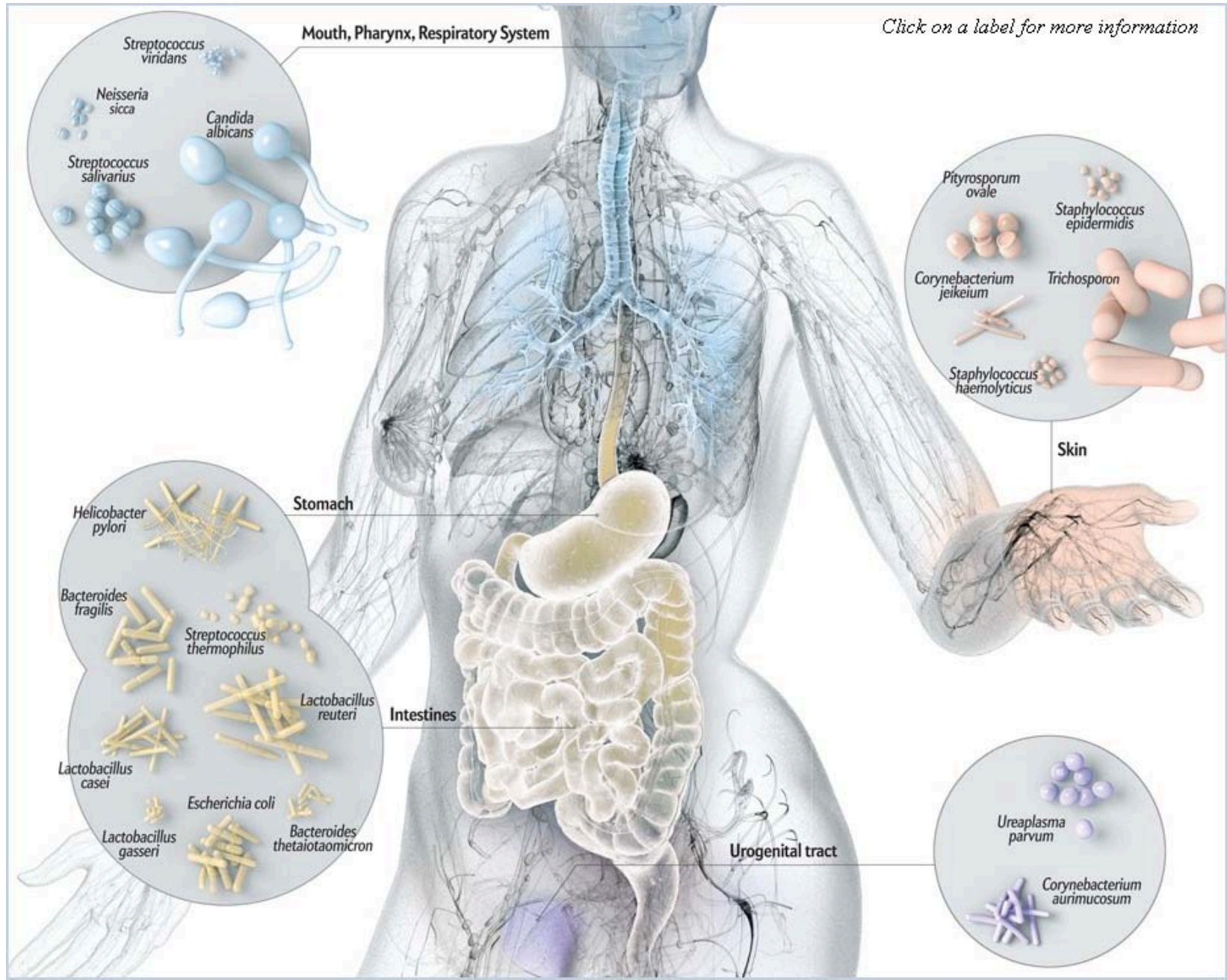
See review Azaele *et al.* Rev Mod Physics 88 (2016)

Shnerb group (Israel)

Volkov group (MD)

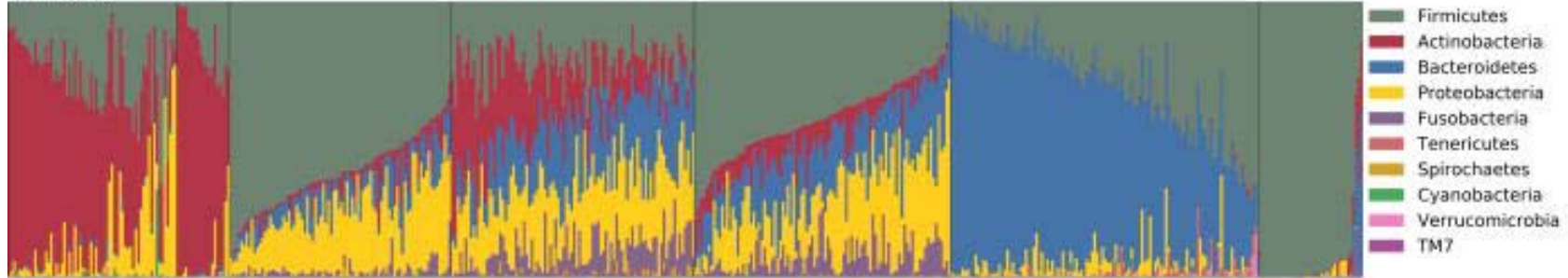
Maritan group (Padova, Italy)

# Microbial communities are diverse

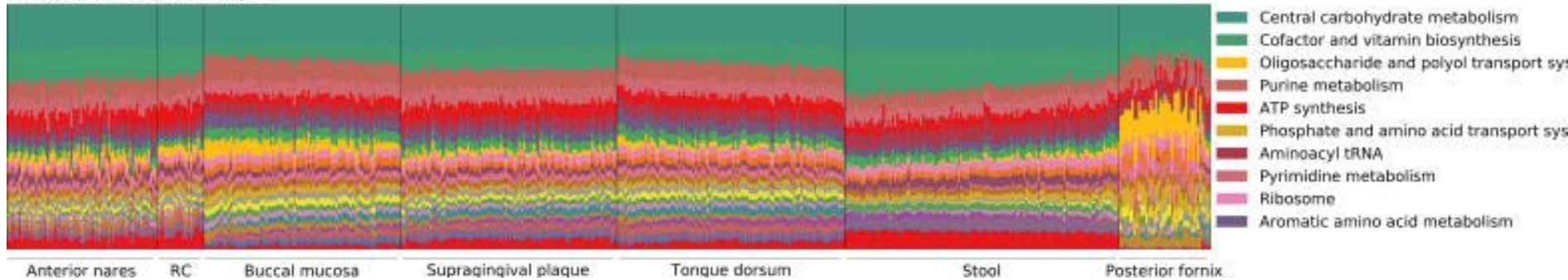


# Functional Convergence

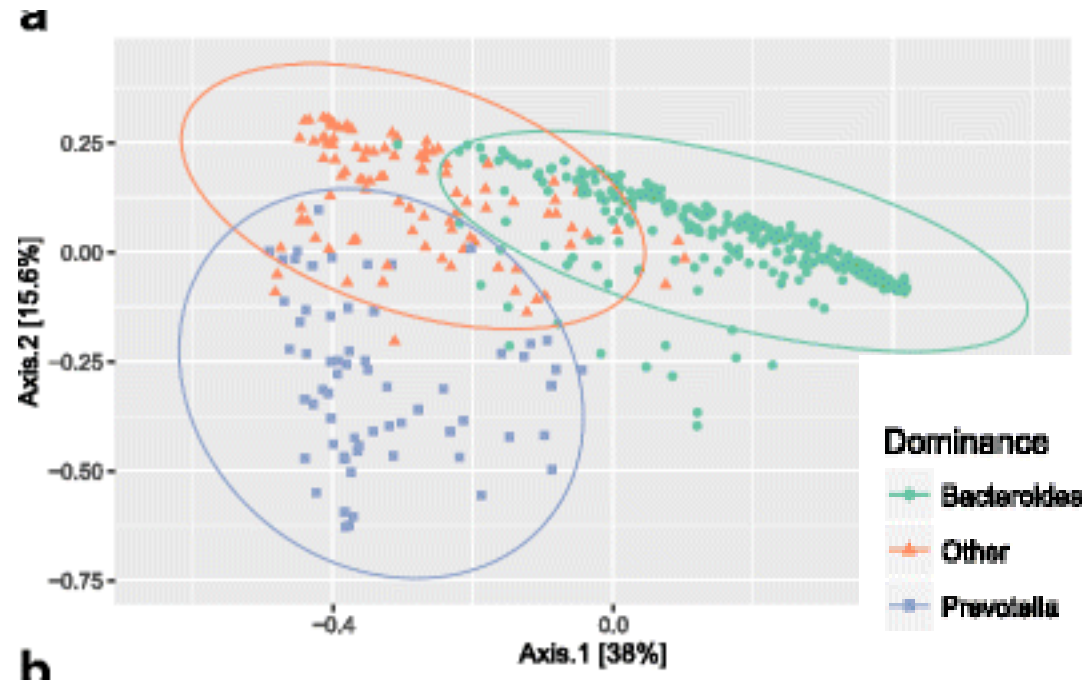
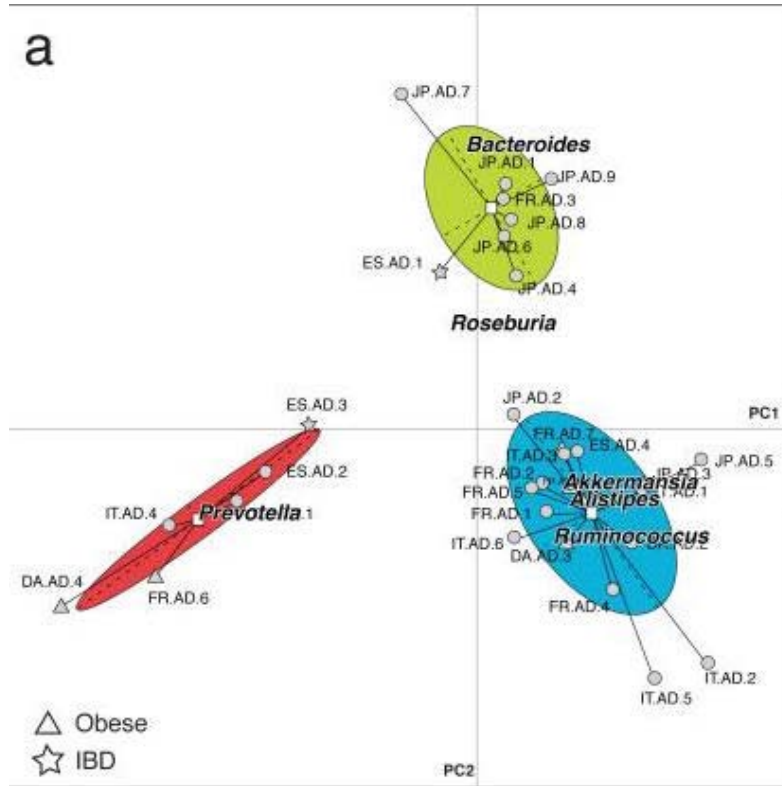
## A Phyla



## B Metabolic pathways



# “Clustering based on dominant family”

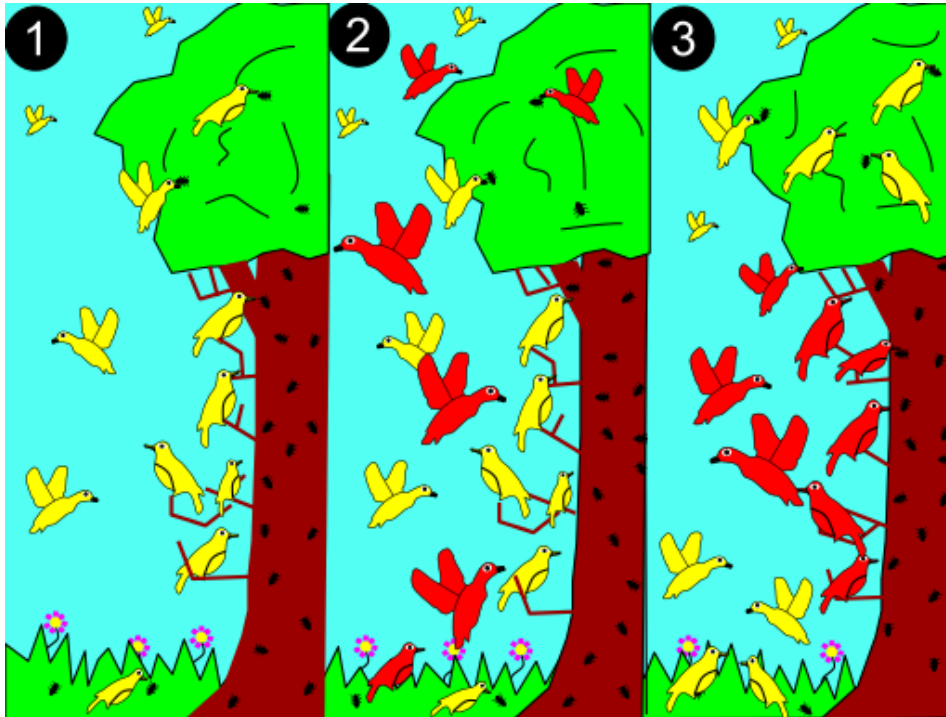


Nature 473, 174–180 (12 May 2011)

A Gorvitovskaia et al Microbiome 2016

How can we understand this mix between diversity  
and simplicity?

# Niche-based Theories



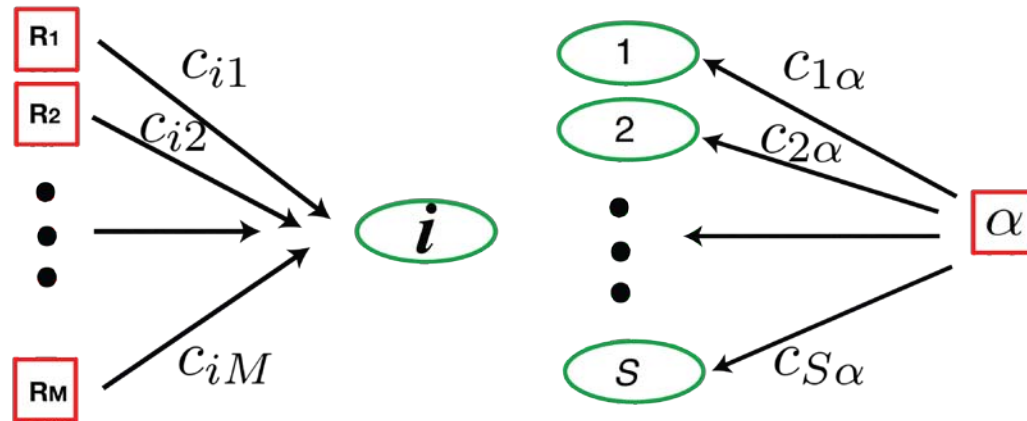
**Niche theory**- “Theory of competitive exclusion”; Tilman's  $R^*$  theory

**Mathematics:** Lotka –Volterra & MacArthur's consumer Resource model

**Central intuition:**

Number of species is strictly limited by number of limiting resources in environment

# MacArthur Consumer Resource Model



Canonical model:

$$\frac{1}{N_i} \frac{dN_i}{dt} = b_i \sum_{\alpha} (w_{\alpha} c_{i\alpha} R_{\alpha} - m_i)$$

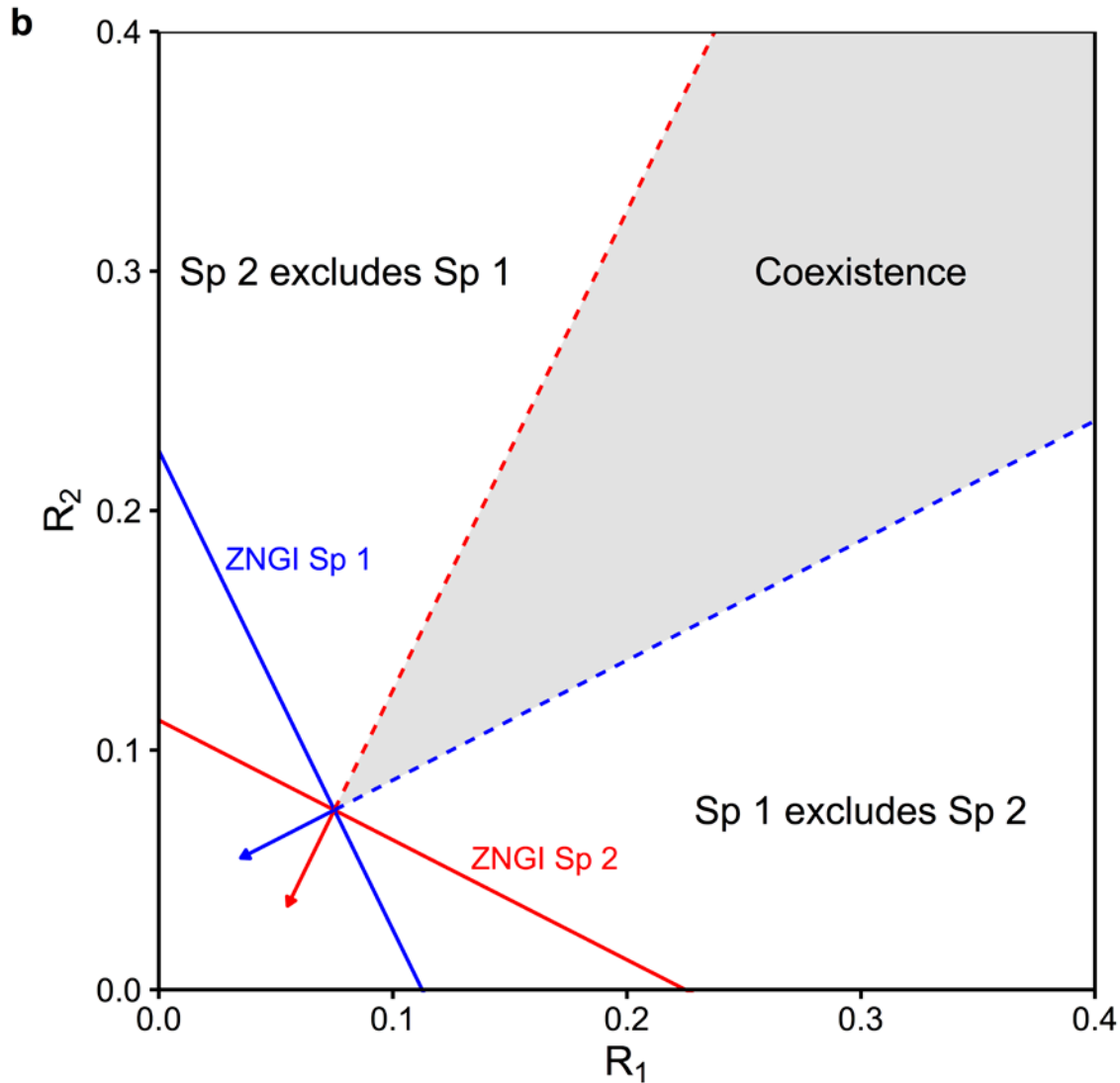
$$\frac{dR_{\beta}}{dt} = f_{\beta}(\mathbf{R}) - \sum_i c_{i\beta} R_{\beta} N_i$$

Fast dynamics: reduces to Lotka-Volterra equations

$$\frac{1}{N_i} \frac{dN_i}{dt} = K_i - N_i - \sum_j \alpha_{ij} N_j$$



Graphical intuitions from considering two species:



Letten, Ke, Fukami BioarXiv 2016

Each species must have its own “limiting resource” – (lowest  $R^*$  wins)

Suggests we need complex environments  
for diversity

[SPACE, TIME, PREDATION, EVOLUTION, ETC....]

# Limitations of Approaches

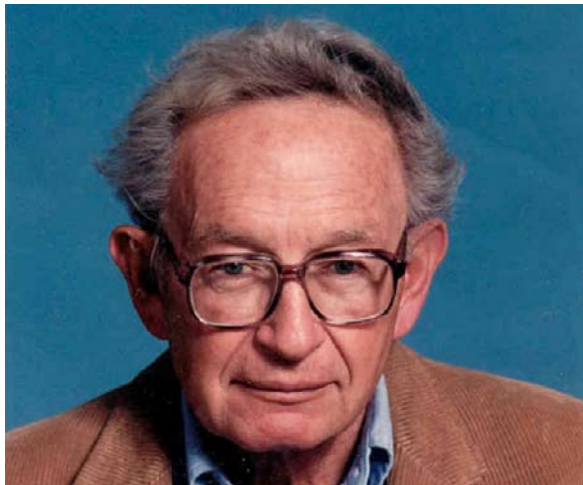
1. Not clear intuitions from few species scale up to complex ecosystems with many species --- emergence of new behaviors

4 August 1972, Volume 177, Number 4047

## More Is Different

Broken symmetry and the nature of the hierarchical structure of science.

P. W. Anderson

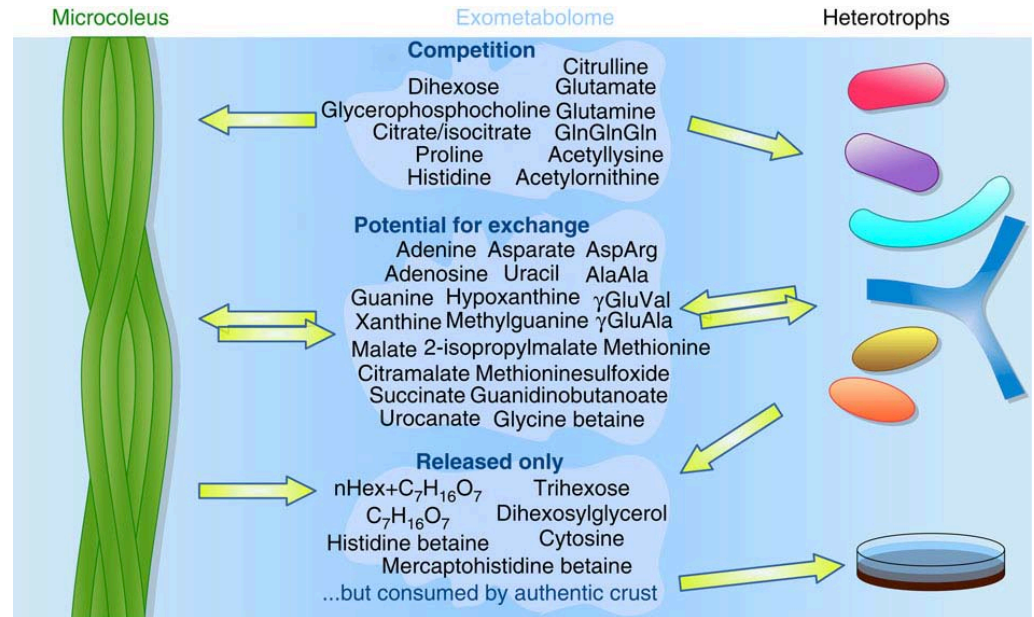
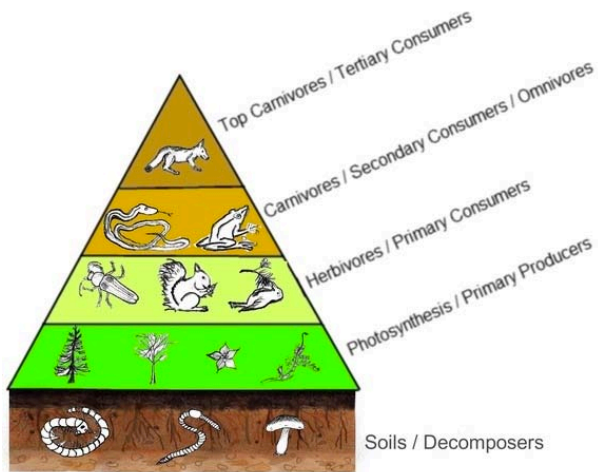


## SCIENCE

The constructionist hypothesis breaks down when confronted with the twin difficulties of scale and complexity. The behavior of large and complex aggregates of elementary particles, it turns out, is not to be understood in terms of a simple extrapolation of the properties of a few particles. Instead, at each level of complexity entirely new properties appear, and the understanding of the new behaviors requires research which I think is as fundamental in its nature as any other. That is, it

# Limitations of Approaches for Microbial Systems

## 2. Niche-based models assume trophic layer separation- no longer true in microbial world



# Statistical physics of MacArthur Consumer Resource Model



Madhu Advani  
Harvard

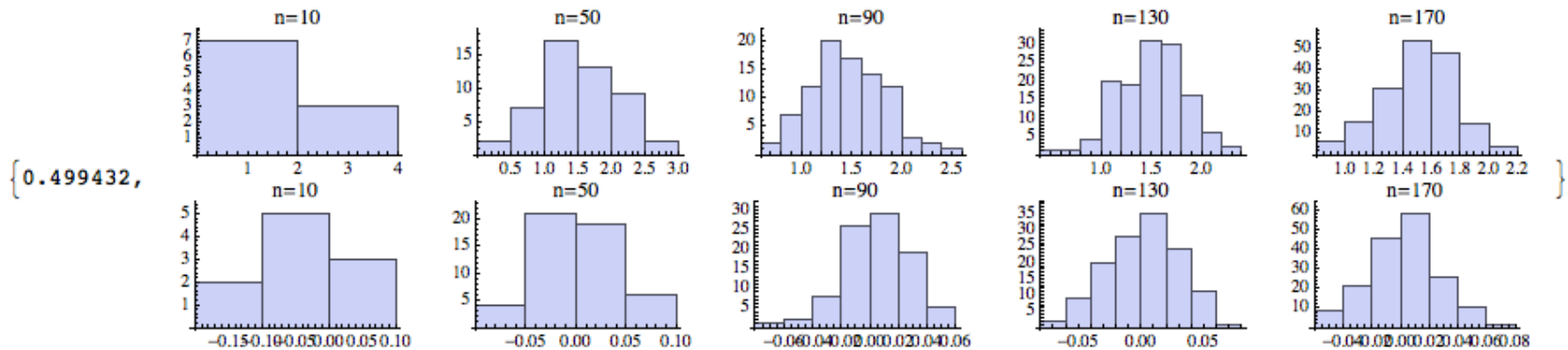


Guy Bunin  
Technion

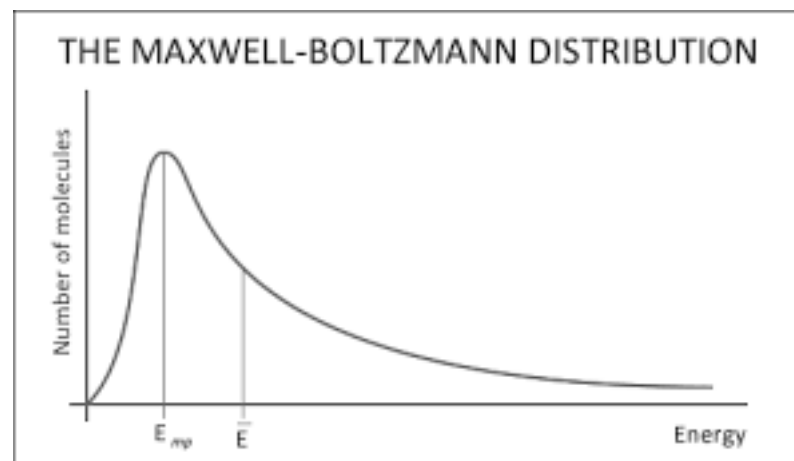
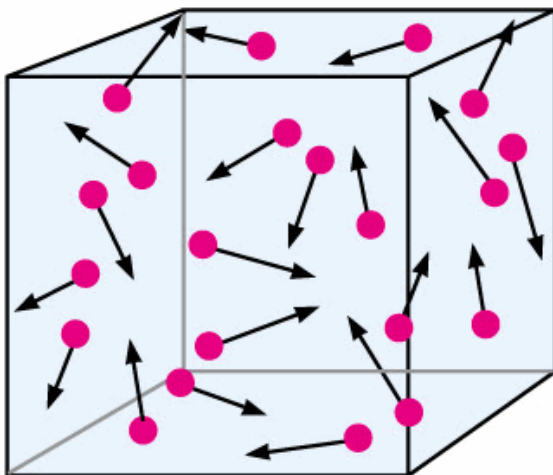
arXiv:1707.03957 / BioRxiv 162966

# Things are actually simpler for large systems

Central limit theorem applied to large systems with many degrees of freedom.



Price you pay: Talk about macroscopic quantities (pressure) and distributions

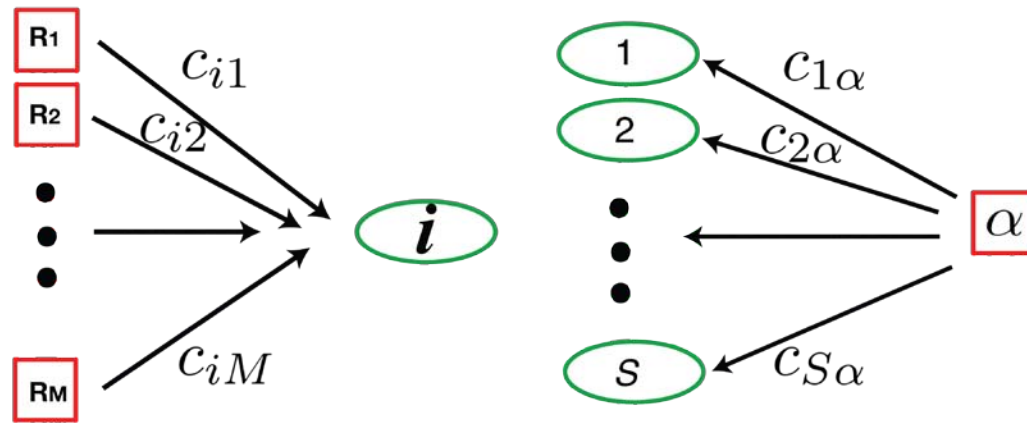
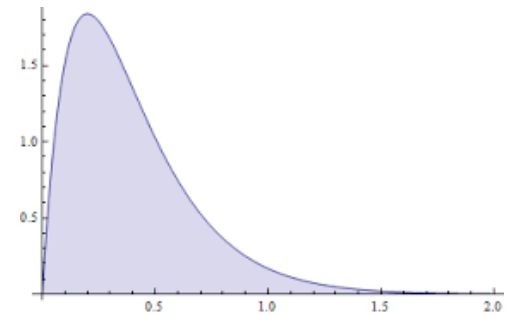
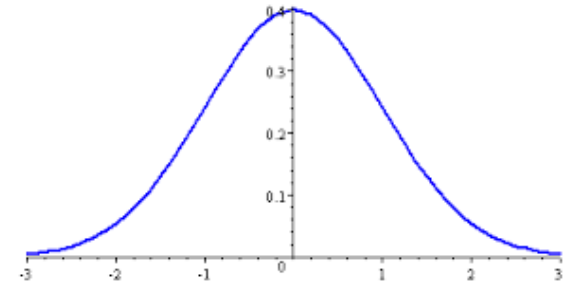


# A theory of large “typical ecosystems”

We will consider large ecosystems where  $S, M \gg 1$ . Draw parameters from random distribution (May 1973).

$$\frac{1}{N_i} \frac{dN_i}{dt} = b_i \sum_{\alpha} (w_{\alpha} c_{i\alpha} R_{\alpha} - m_i)$$

$$\frac{1}{R_{\alpha}} \frac{dR_{\alpha}}{dt} = K_{\alpha} - R_{\alpha} - \sum_i c_{i\alpha} N_i$$

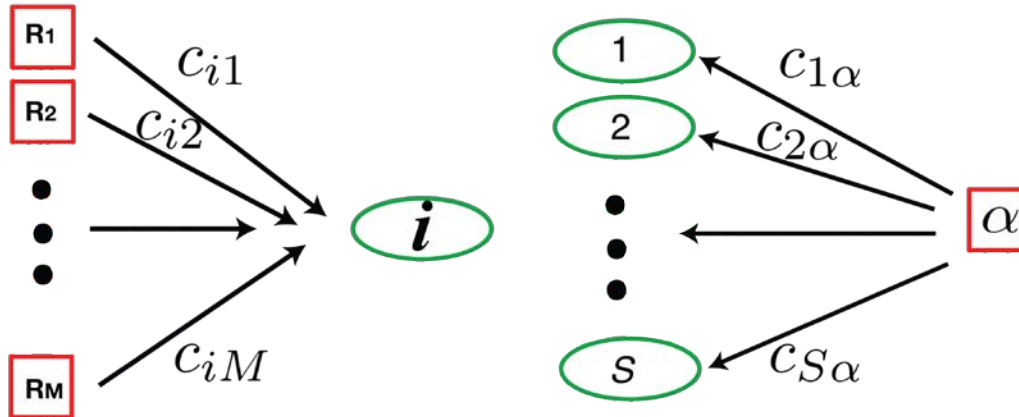
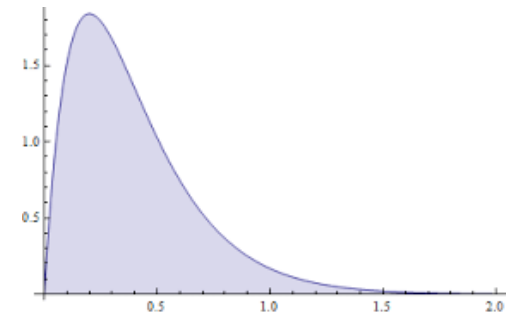
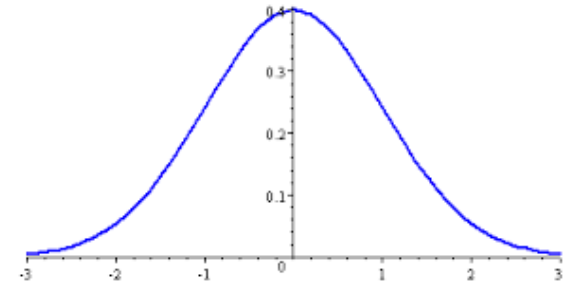


# A theory of large “typical ecosystems”

We will consider large ecosystems where  $S, M \gg 1$ . Draw parameters from random distribution (May 1973).

$$\frac{1}{N_i} \frac{dN_i}{dt} = g_i(\mathbf{R})$$

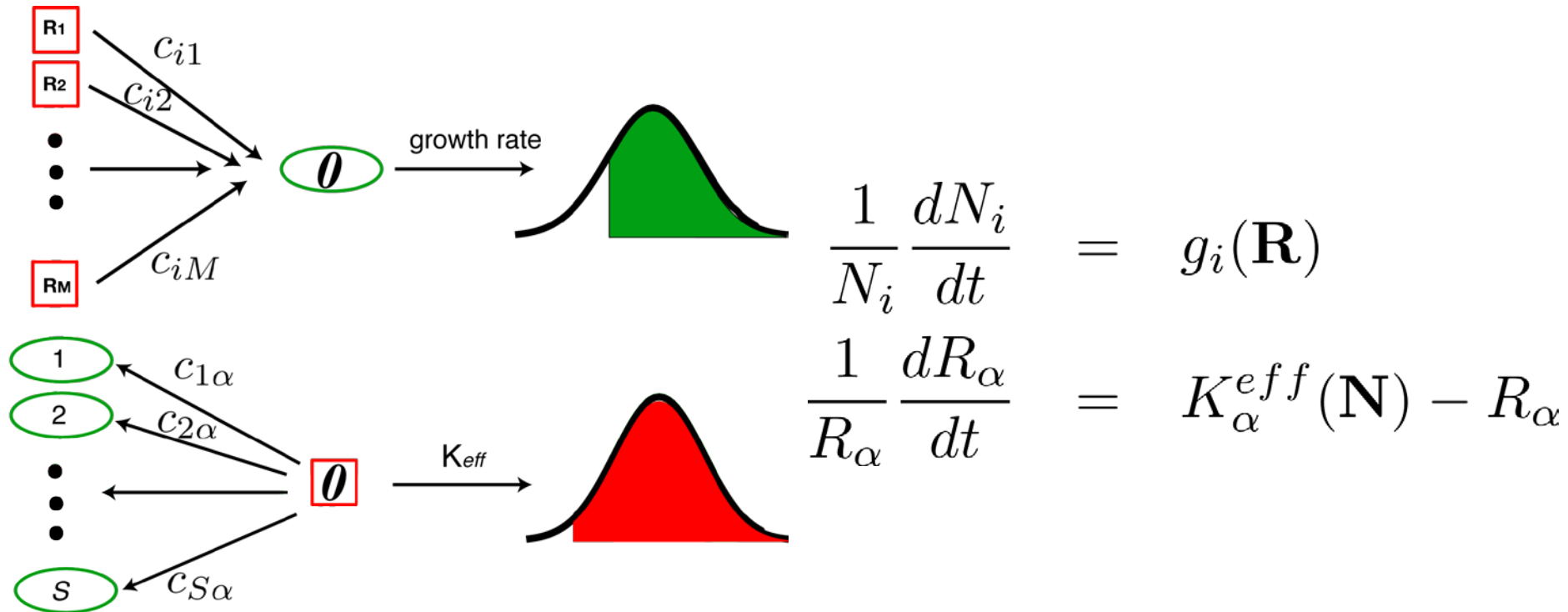
$$\frac{1}{R_\alpha} \frac{dR_\alpha}{dt} = K_\alpha^{eff}(\mathbf{N}) - R_\alpha$$





# Things are actually simpler for large ecosystems

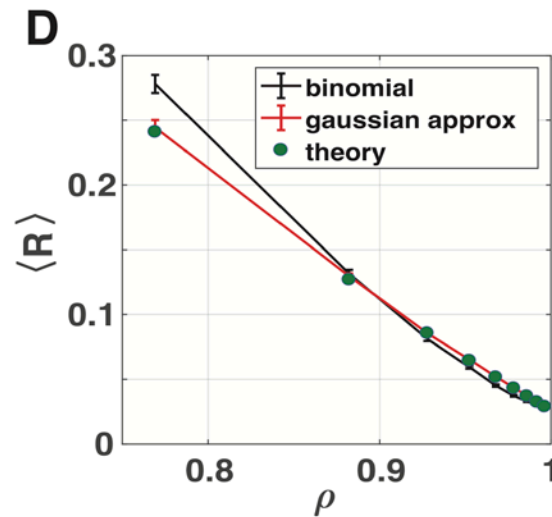
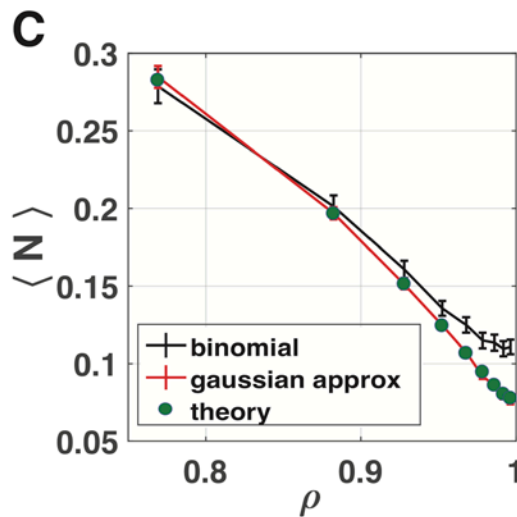
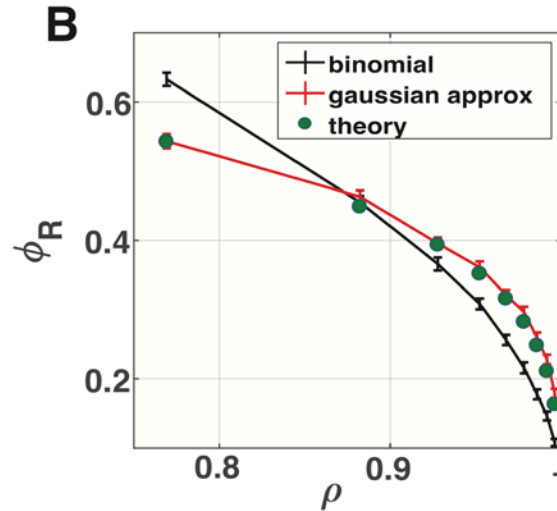
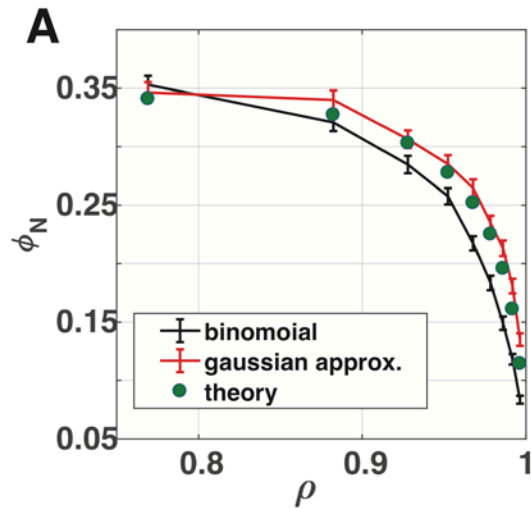
Pictorial of basic idea: Ask what happens when you add new species to the ecosystem (Levins + MacArthur 1967)



Use two-step cavity method to solve for “self-consistency” equations

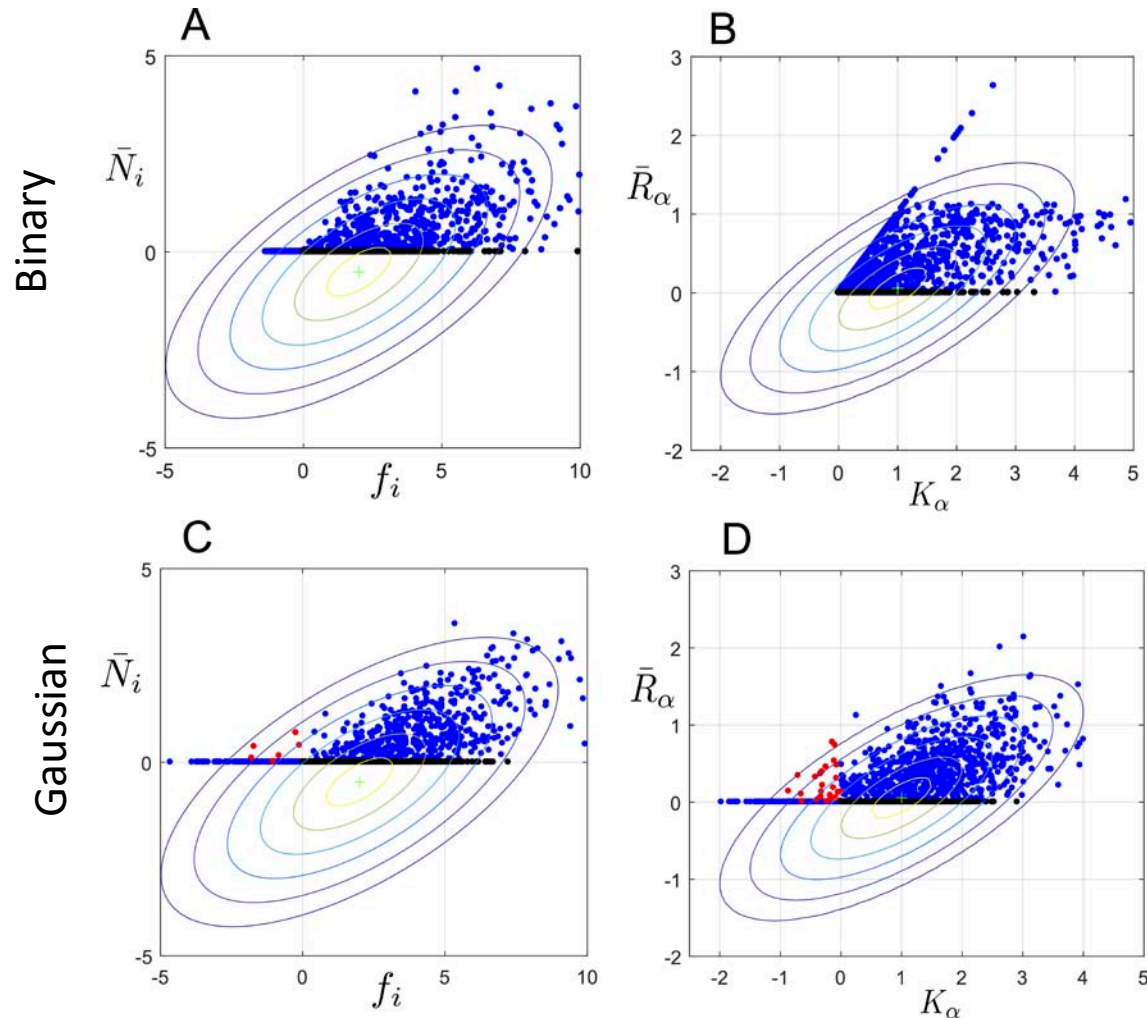
# Theory can predict numerical simulations

Various quantities as a function of the typical niche overlap



# Environmental engineering is a generic feature of large ecosystems

Properties in a diverse ecosystem are not the same as those of isolated individuals.



# Statistical physics of MacArthur Consumer Resource Model

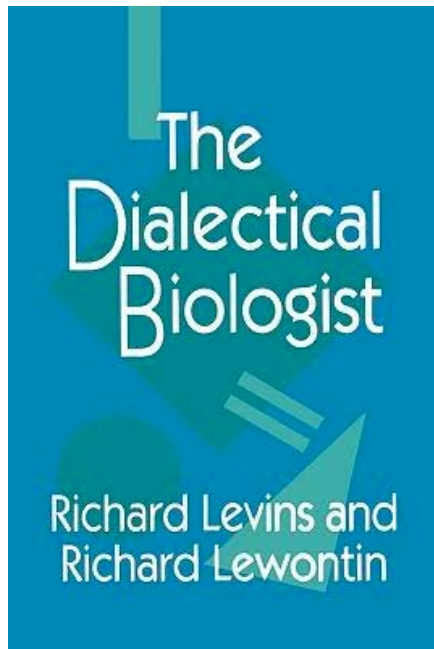


- Developed statistical mechanics of MacArthur Consumer Resource Model.
- Environmental engineering is a generic feature of diverse ecosystems.
- Properties of isolated individuals in isolation can differ significantly from those in complex ecosystems.
- **Practical implication:** Maybe its much easier to work directly with large ecosystems where you see “average” environment.

# Microbial Consumer Resource Model

Cross-feeding means **microbes construct their own environment.**

Implies we no longer think of organisms in fixed external environment

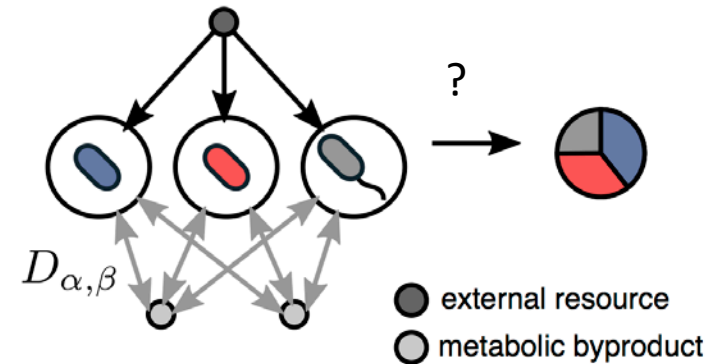
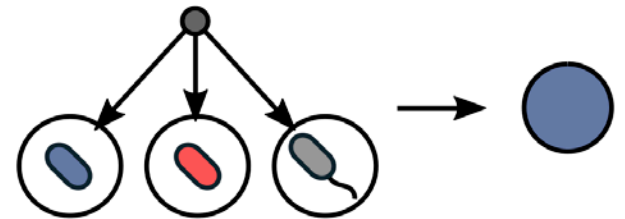


The incorporation of the organism as an active subject in its own ontogeny and in the construction of its own environment leads to a complex dialectical relationship of the elements in the triad of gene, environment, and organism. We have seen that the organism enters directly

# Microbial Consumer Resource Model

When microbes consume small molecule  
– they produce other molecules that can  
be consumed.

a.



$$\frac{1}{N_i} \frac{dN_i}{dt} = b_i \left[ \sum_{\alpha,\beta} D_{\alpha\beta}^i c_{i\beta} R_\beta w_{\alpha\beta} - m_i \right]$$

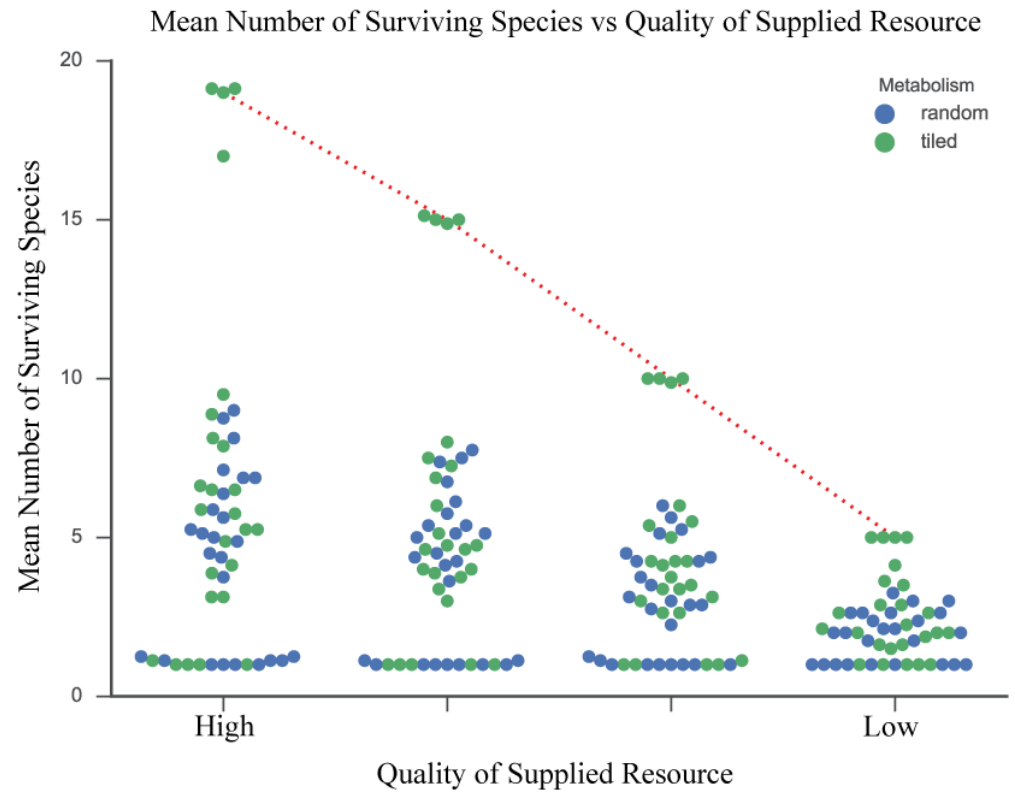
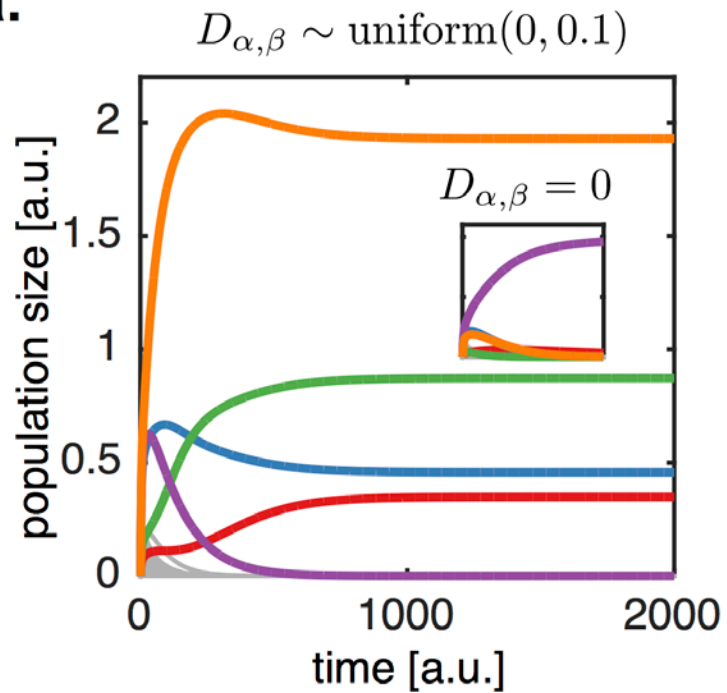
$$\frac{dR_\beta}{dt} = f_\beta(\vec{R}) - \sum_{i,\alpha} N_i D_{\alpha\beta}^i c_{i\beta} R_\beta + \sum_{i,\alpha} N_i D_{\beta\alpha}^i c_{i\alpha} R_\alpha$$

Depletion due to consumption

Production of resource  
(metabolic products)

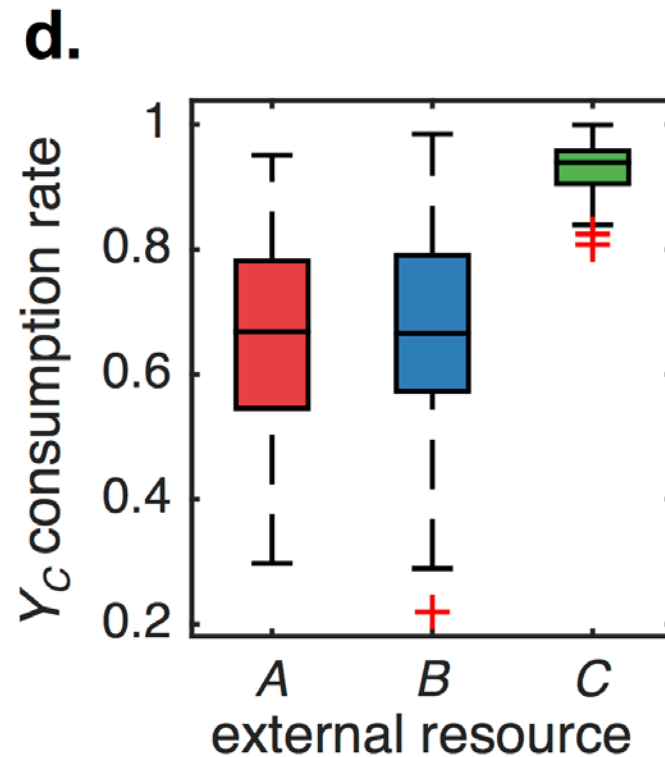
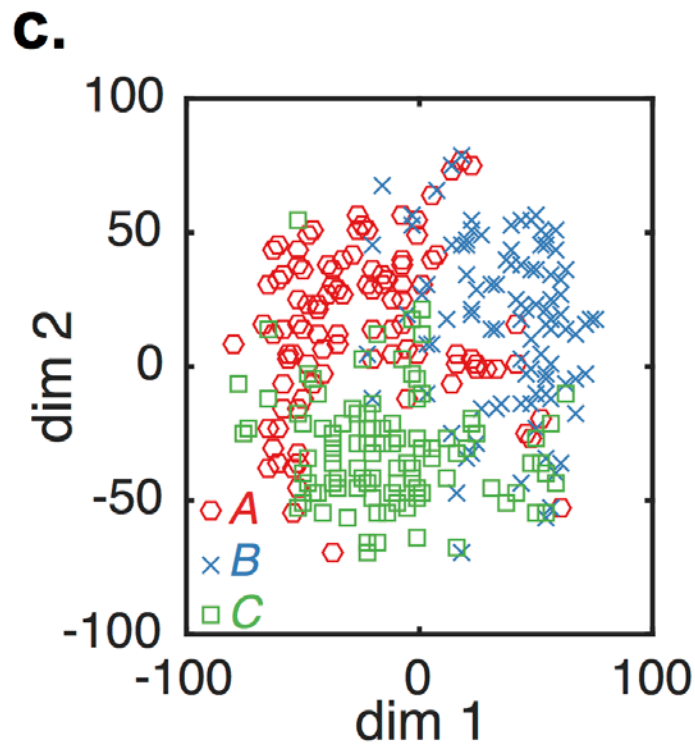
# Complex communities can coexist on a single resource

**a.**



# Structure of community shaped by external resource

The structure and “metagenomics” of community is shaped by external resource.



PCA of community coefficients

$$\vec{\mathbf{R}}_{\alpha}^{\text{comm}} = \sum_{i\alpha} c_{i\alpha} \bar{N}_i$$



# Multiple communities in minimal environments

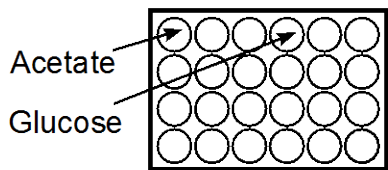
## Experimental tests:

Natural microbial ecosystems

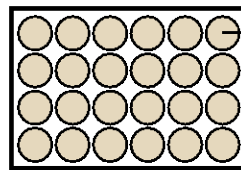


Harvest microbiome  
(place in PBS overnight, use buffer as inocula)

M9 salts + carbon source



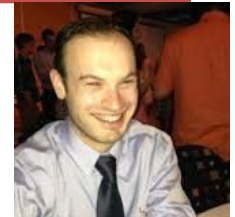
Grow for ~48 hours



Isolate genomic DNA  
Amplify/barcode 16s rRNA gene  
Next generation sequencing

10x  
Passage 1/100 culture  
into fresh media

Samples included:  
Leafs/soil of house plants, Soil  
outside house, Leafs/soil inside  
Rowland inst.



Josh Goldford



Nanxi Lu



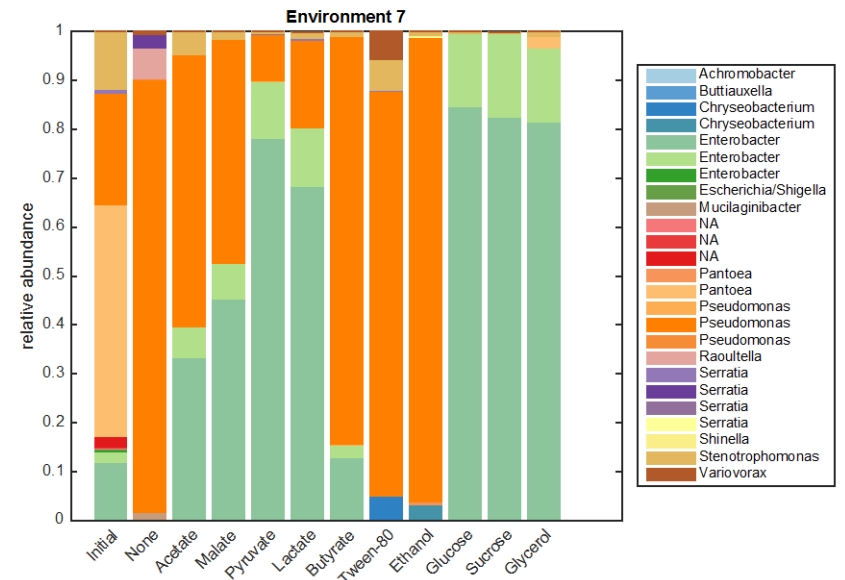
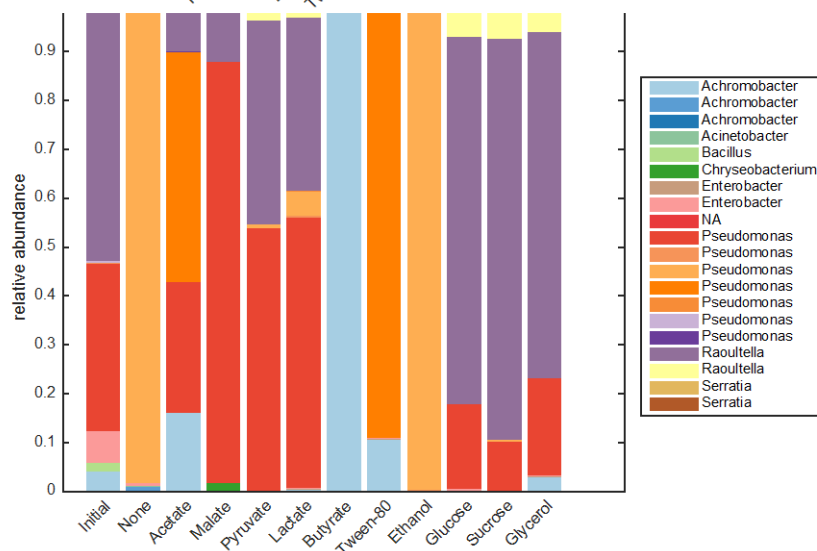
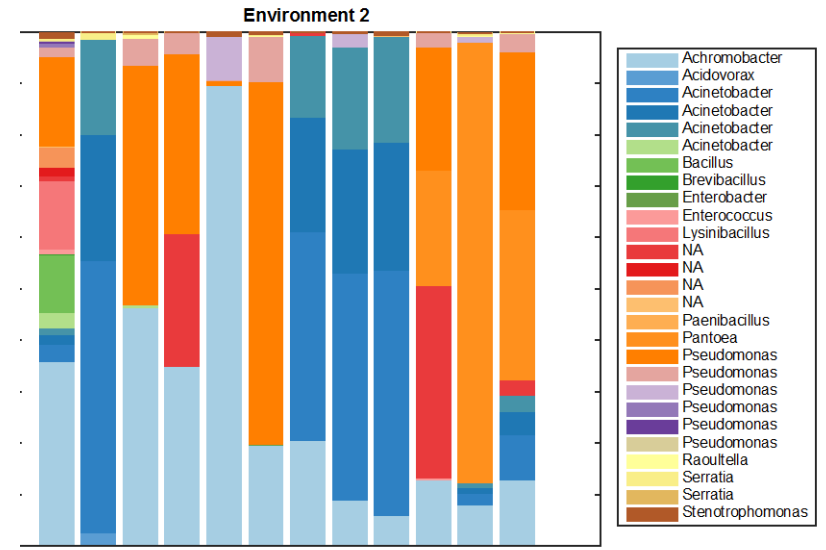
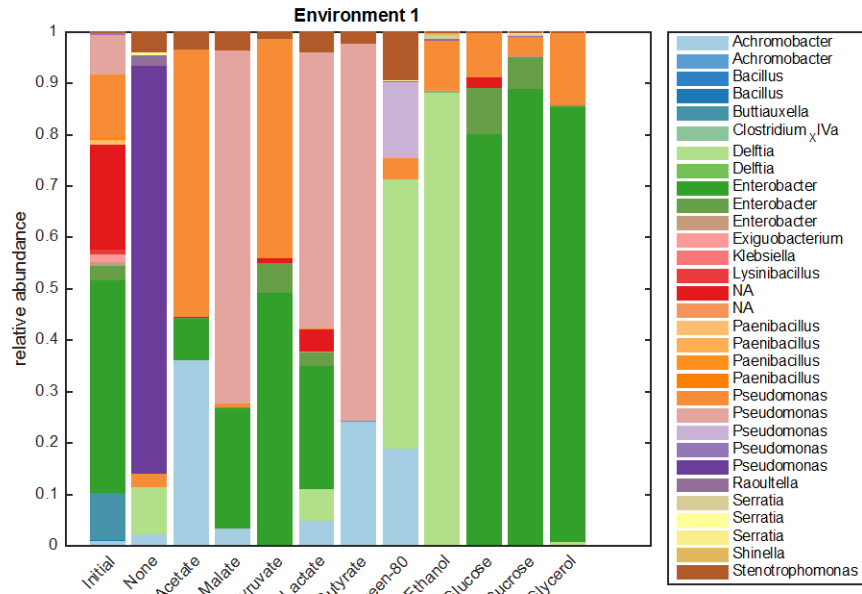
Alvaro Sanchez

Grow different natural communities in minimal environments with a single carbon sources

<b>Acetate</b>	Lactose	Melibiose	Tartrate	<b>Glycerol</b>
Benzoate	<b>Malate</b>	Trehalose	Decanoate	<b>Tween-80</b>
Formate	Mannitol	Raffinose	Dodecanoate	Methanol
Cellobiose	2-oxogutarate	Succinate	Myristate	<b>Ethanol</b>
Arabinose (D)	Maltose	Citrate	Hexanoate	1-Propanol
Arabinose (L)	Propionate	<b>Glucose</b>	<b>Butyrate</b>	1-Butanol
Glycolic acid	Inositol	Fructose	Ribose	Isoproponal
Glyoxylic acid	Fumerate	<b>Sucrose</b>	D-Sorbitol	<b>None</b>
Dulcitol	<b>Pyruvate</b>	Galactose	D-Salicin	
Oxalate	Rhamnose	<b>Lactate</b>	Adonitol	

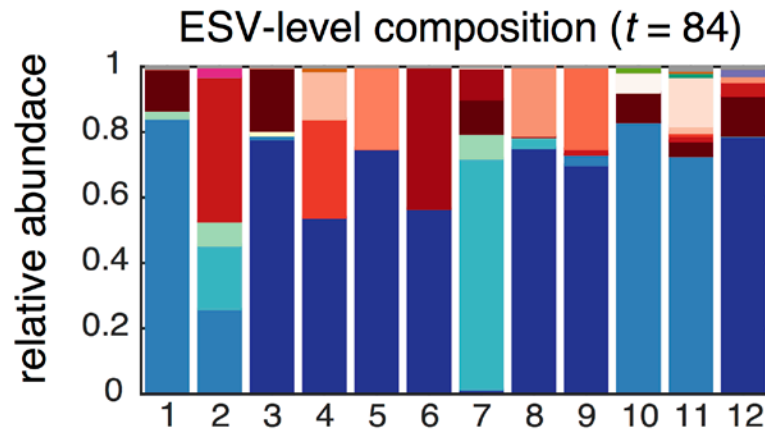
# Complex consortia in single resource environment

Complex consortia can grow on a single carbon source (seems to be generic!)



# Twelve distinct starting communities in glucose

c.



Enterobacteriaceae

*Klebsiella*

*Enterobacter*

*Raoultella*

*Citrobacter*

*Klebsiella*

Alcaligenaceae

*Bordetella*

Comamonadaceae

*Delftia*

Moraxellaceae

*Acinetobacter*

Pseudomonadaceae

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Pseudomonas*

*Azomonas*

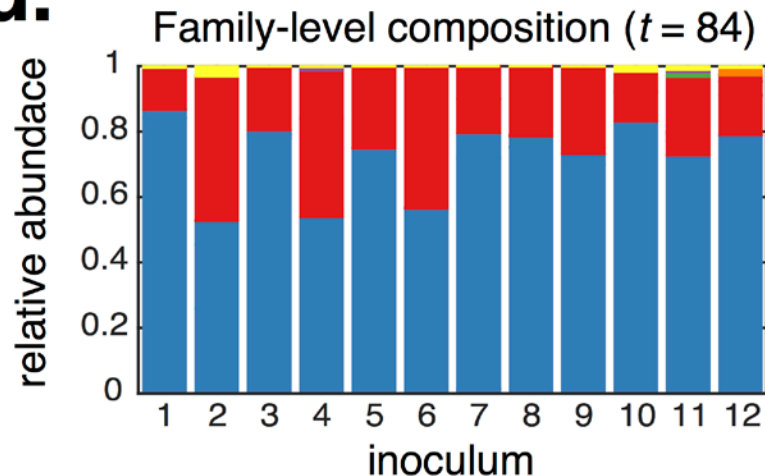
*Pseudomonas*

Xanthomonadaceae

*Stenotrophomonas*

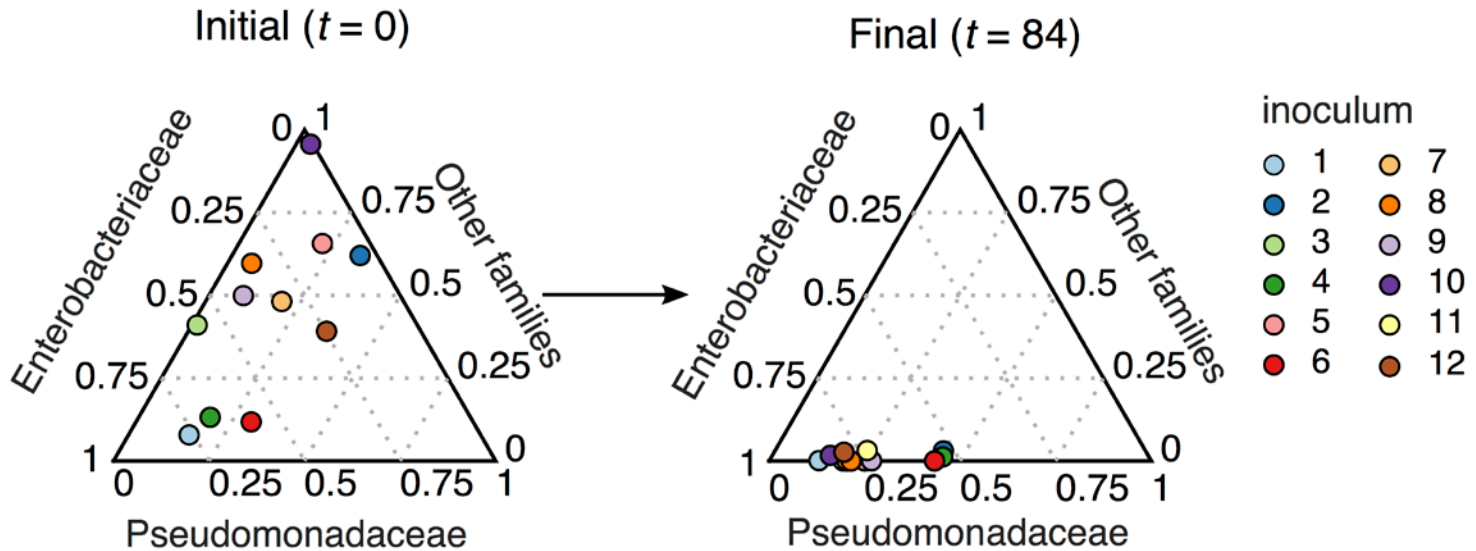
*Stenotrophomonas*

d.



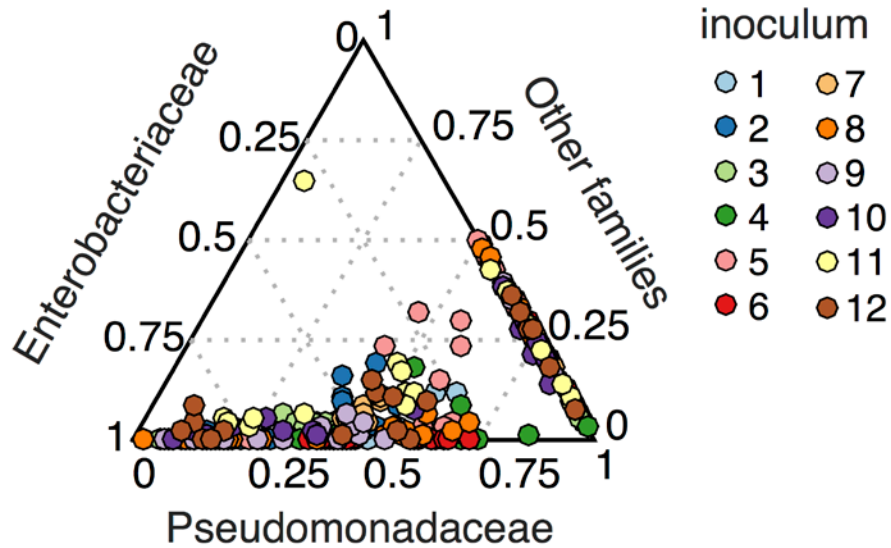
# Twelve distinct starting communities in glucose

e.

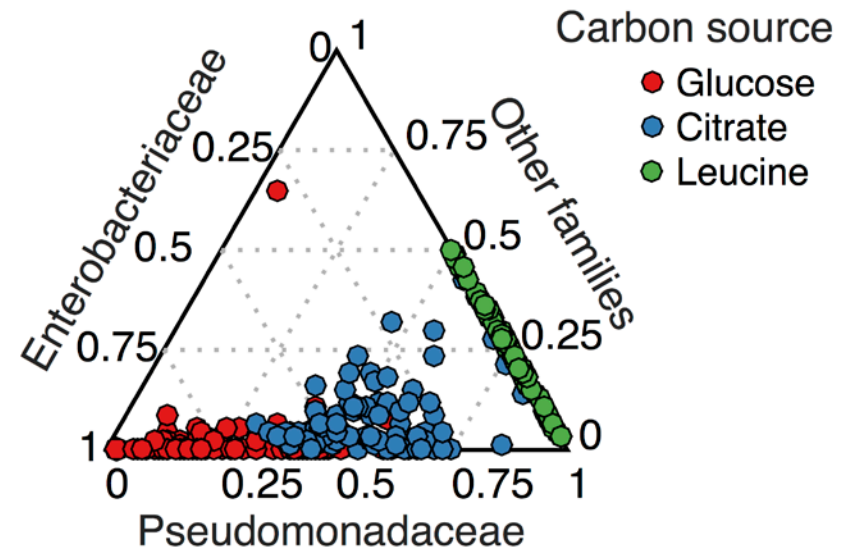


# Twelve distinct starting communities in multiple carbon sources

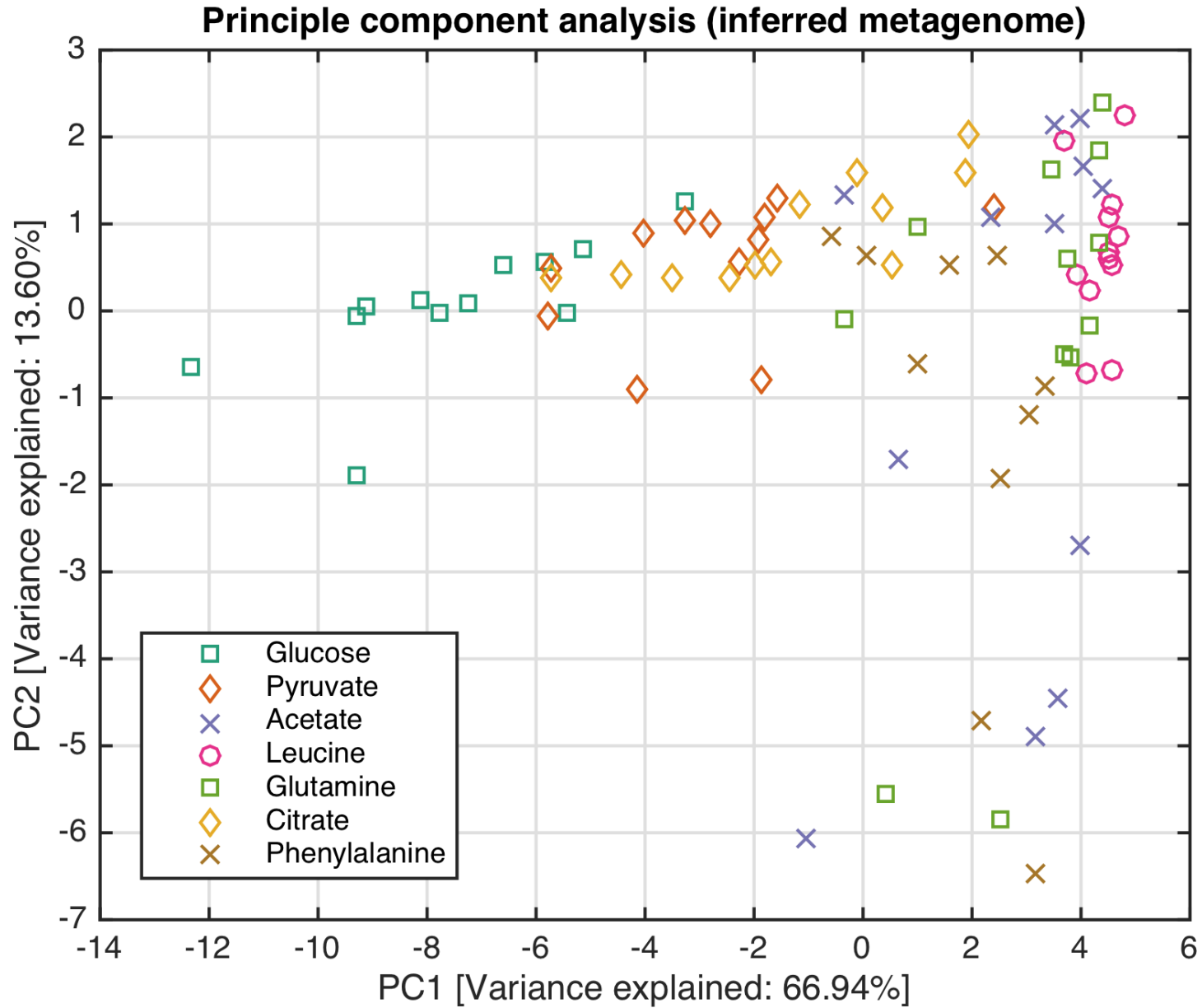
**a.**



**b.**



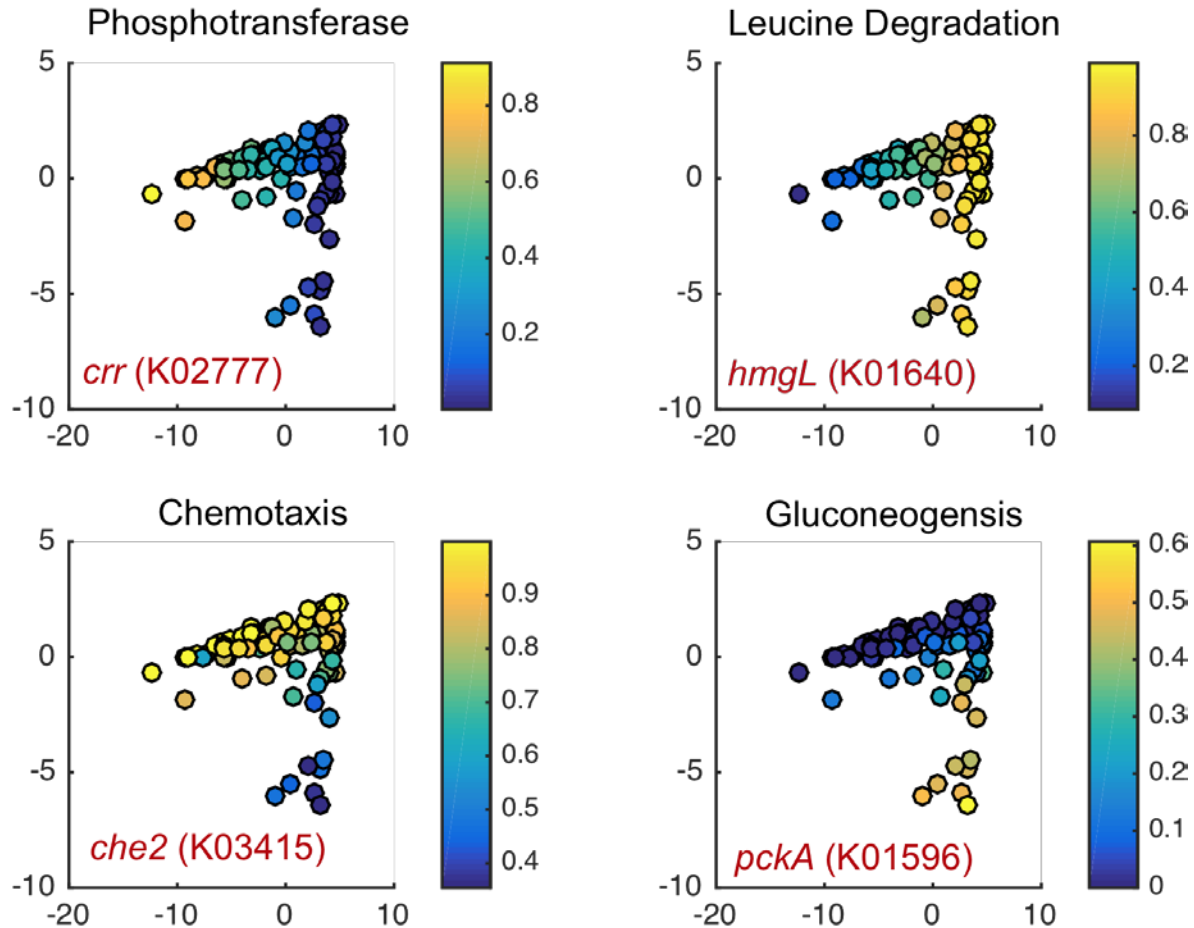
# Co-existence is metabolically mediated



# Co-existence is metabolically mediated

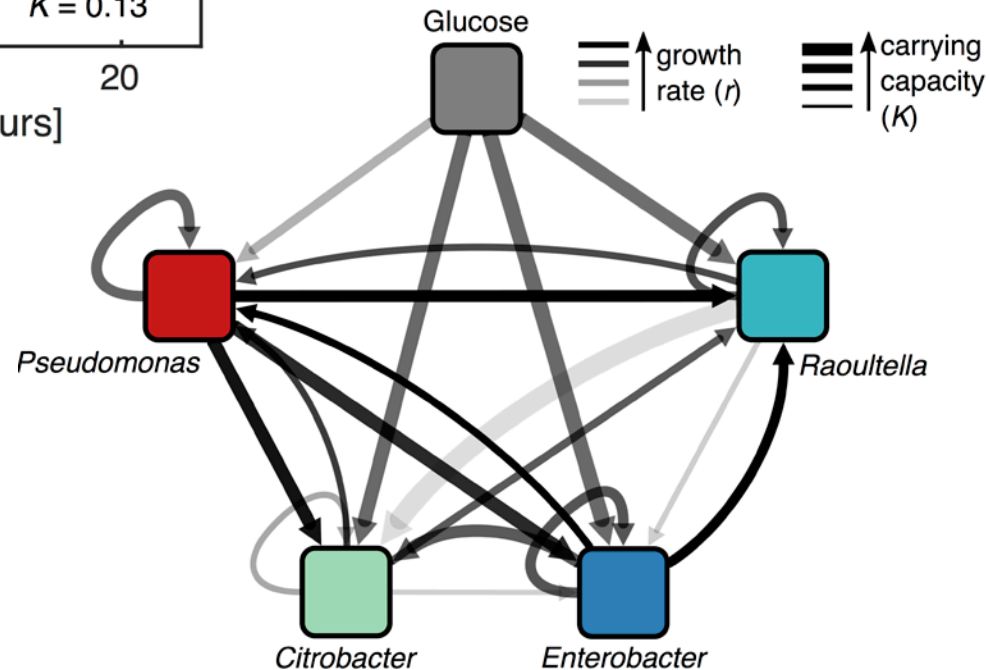
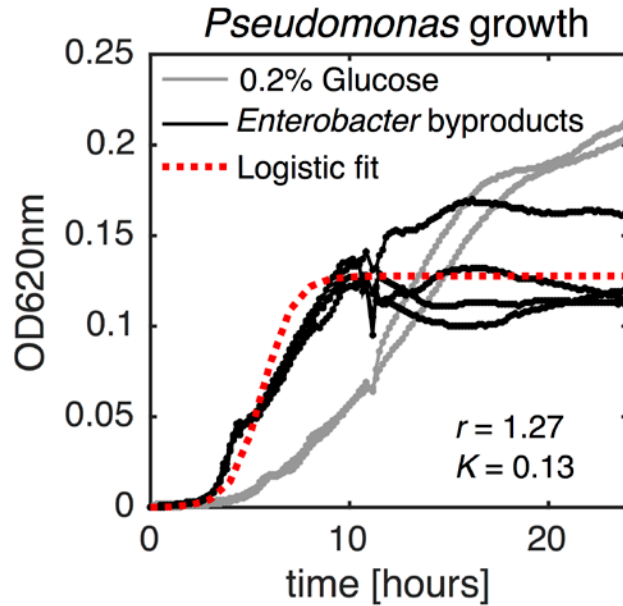
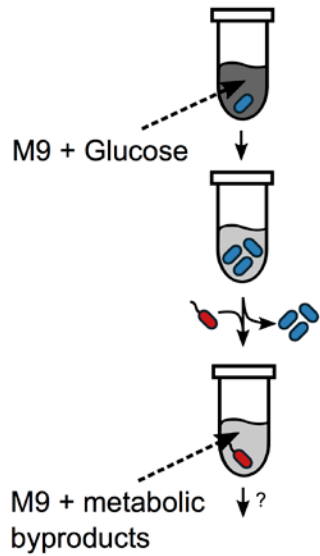
PCA 1- Glycolysis versus fermentation

PCA 2- Gluconeogenesis (Biofilm formation?)





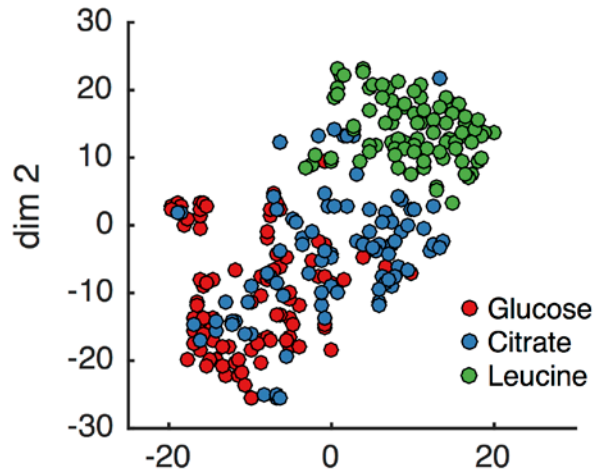
# Cross-feeding is generic between species



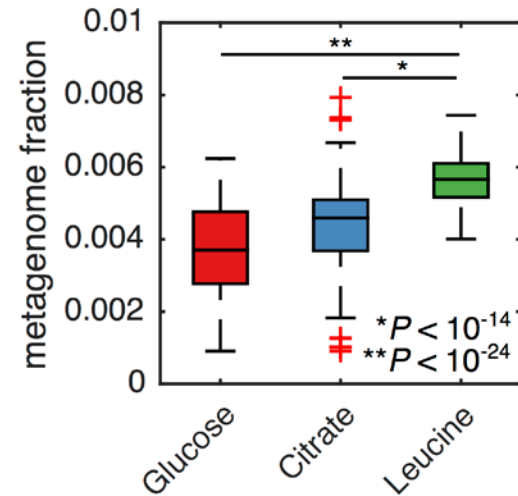
# External resources shape community structure

## Experiments

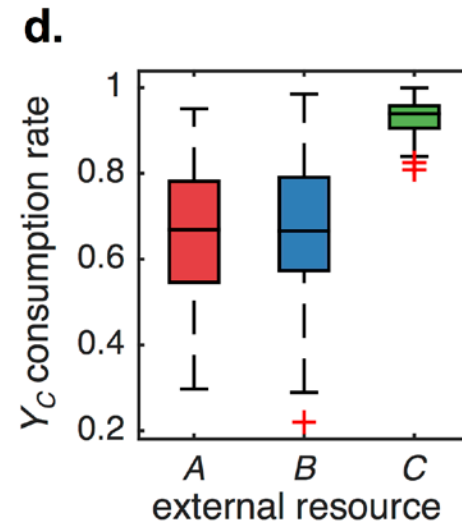
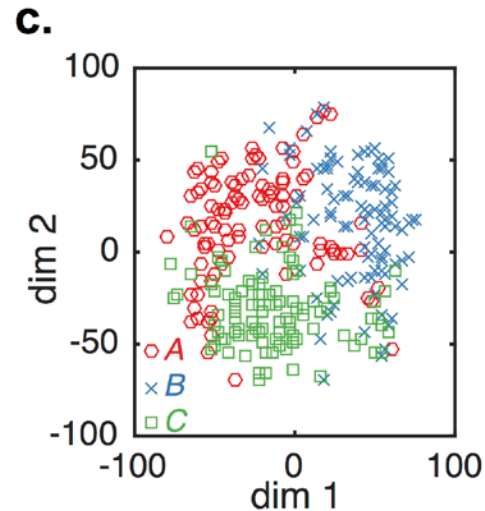
**c.** tSNE on PICRUSt metagenomes



**d.** Leucine Degradation (M00036)



## Theory



# Microbial Consumer Resource Model

- Introduce Microbial Consumer Resource Model to include cross-feeding
- Leads to qualitatively different behaviors — single externally supplied resource can sustain multispecies microbial ecosystems
- Bacteria construct their “own niches” — need to think about environment and species together on equal footing
- “Emergent Simplicity” — all these properties seem to be typical.
- Much more: thermodynamic limitations, ecological principles, what sets limits on diversity etc. and of course experimental analysis.

# Acknowledgements

POSTDOC OPENINGS !!!



Joshua Goldford



Alvaro Sanchez



Nanxi Lu

Charles Fisher

Guy Bunin

Madhu Advani

Benjamin Dickens

Daniel Segrè

Mehta Group



Kirill Korolev



Cui Wenping

Funding:

SIMONS FOUNDATION



# Co-existence is metabolically mediated

PCA by log-relative abundance shows clustering by sugar source

