

# **Wrong Models in Ecology II**

**Patterns in Microbial Communities, Fluctuations and Environmental  
Stochasticity**

**Jacopo Grilli, Bengaluru 16/1/2025**



## Statistical ecology

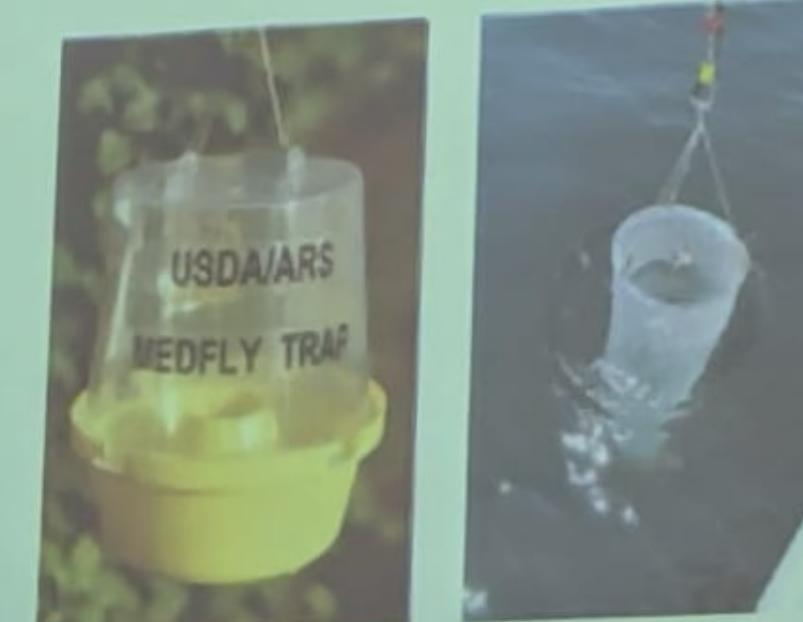
Predict species "fitness" (presence, abundance, reproduction, other measurements...) from environment & own traits

Ecological data

Controlled studies



Natural observation



Data matrix

Species	Sample					Descriptor			
	a	b	c	d	e	I	II	III	IV
1									
2									
3						Abundance data			
4									
5									
6									
7									

Factor	Sample					Descriptor			
	X	Y	Z	W		I	II	III	IV
X									
Y									
Z						Environment data			
W									

Tends to be noisy and sparse

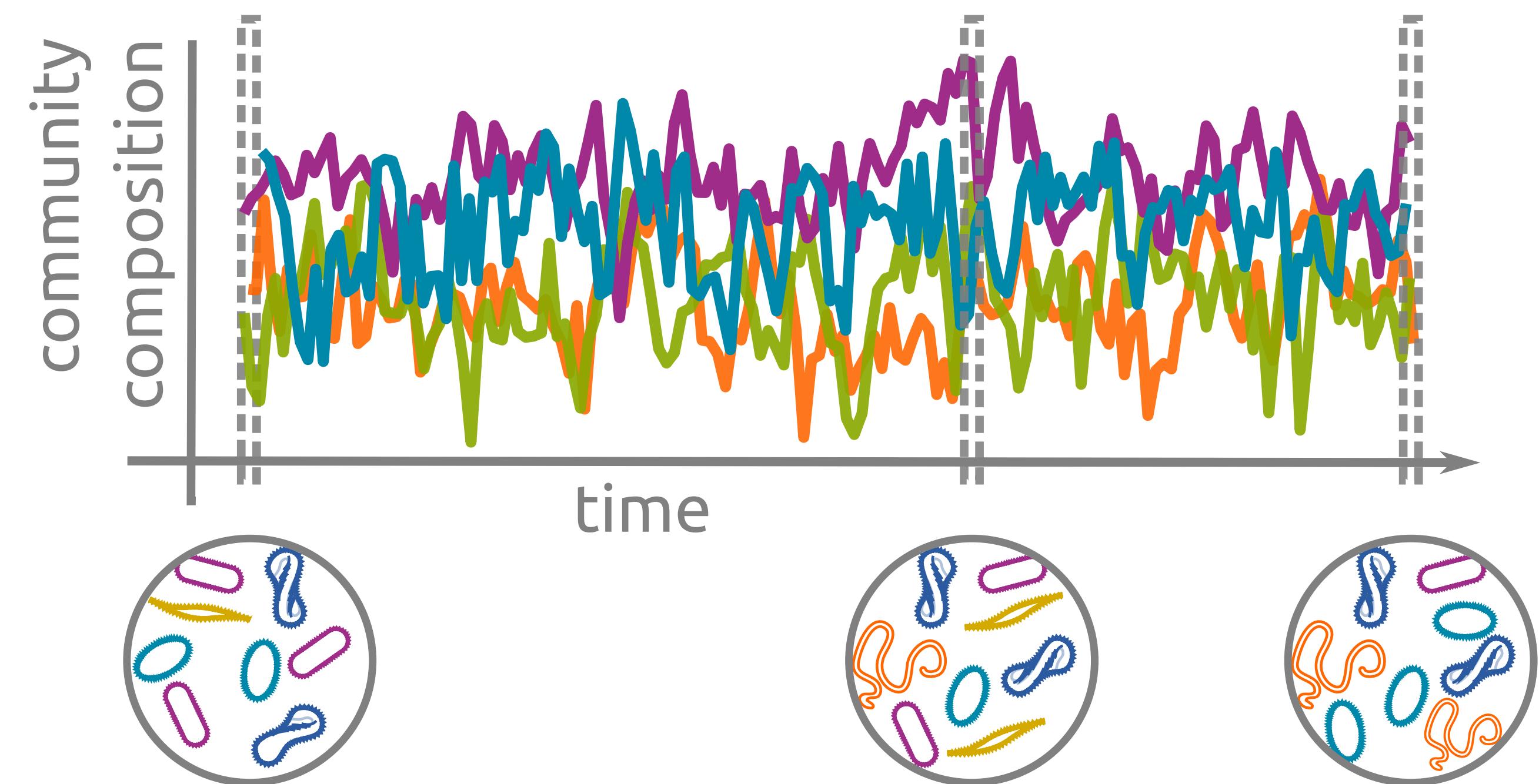
# Today

Species	Sample				
	a	b	c	d	e
1					
2					
3					
4					
5					
6					
7					

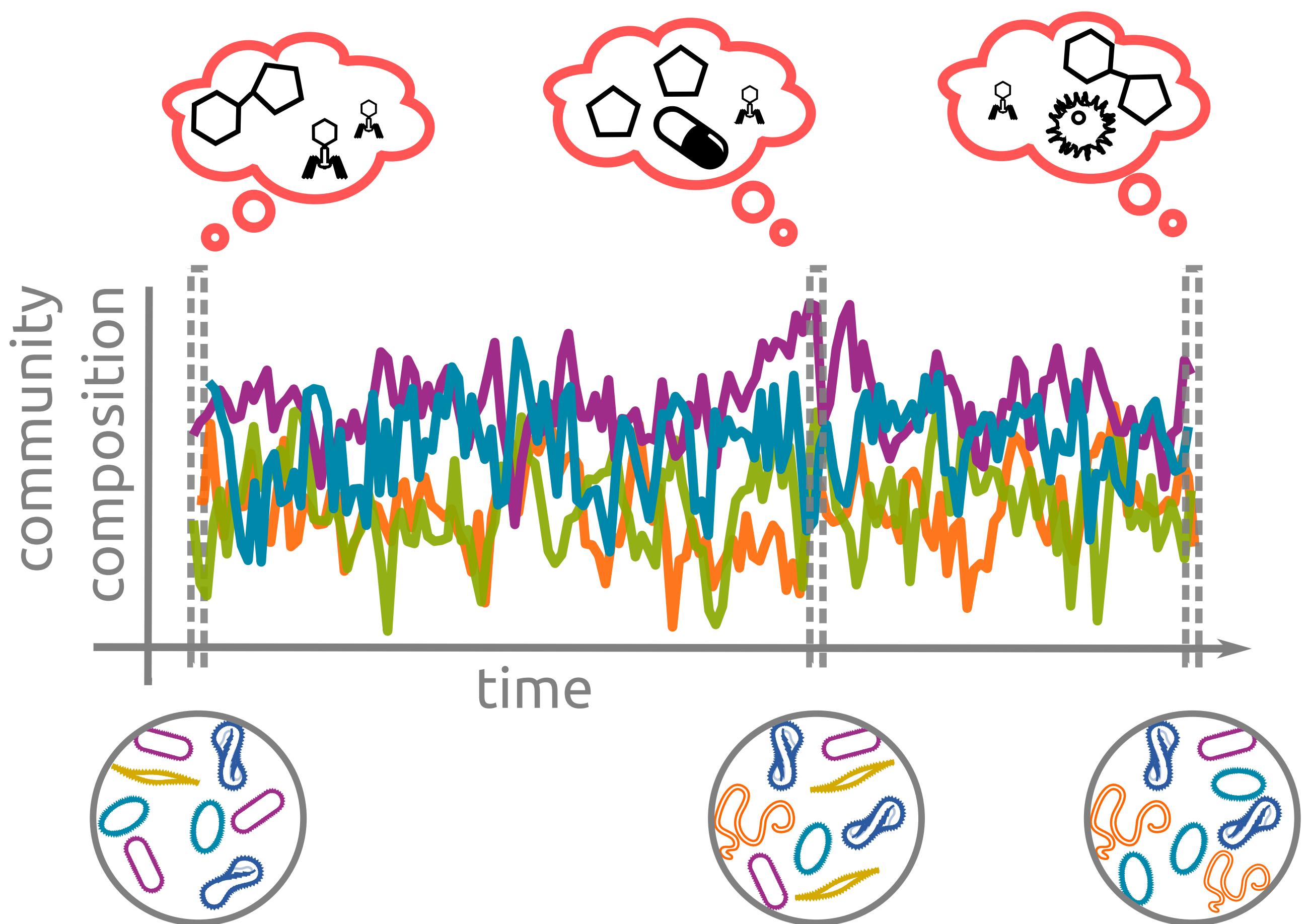
Tends to be noisy and sparse

# Data on Microbial Communities

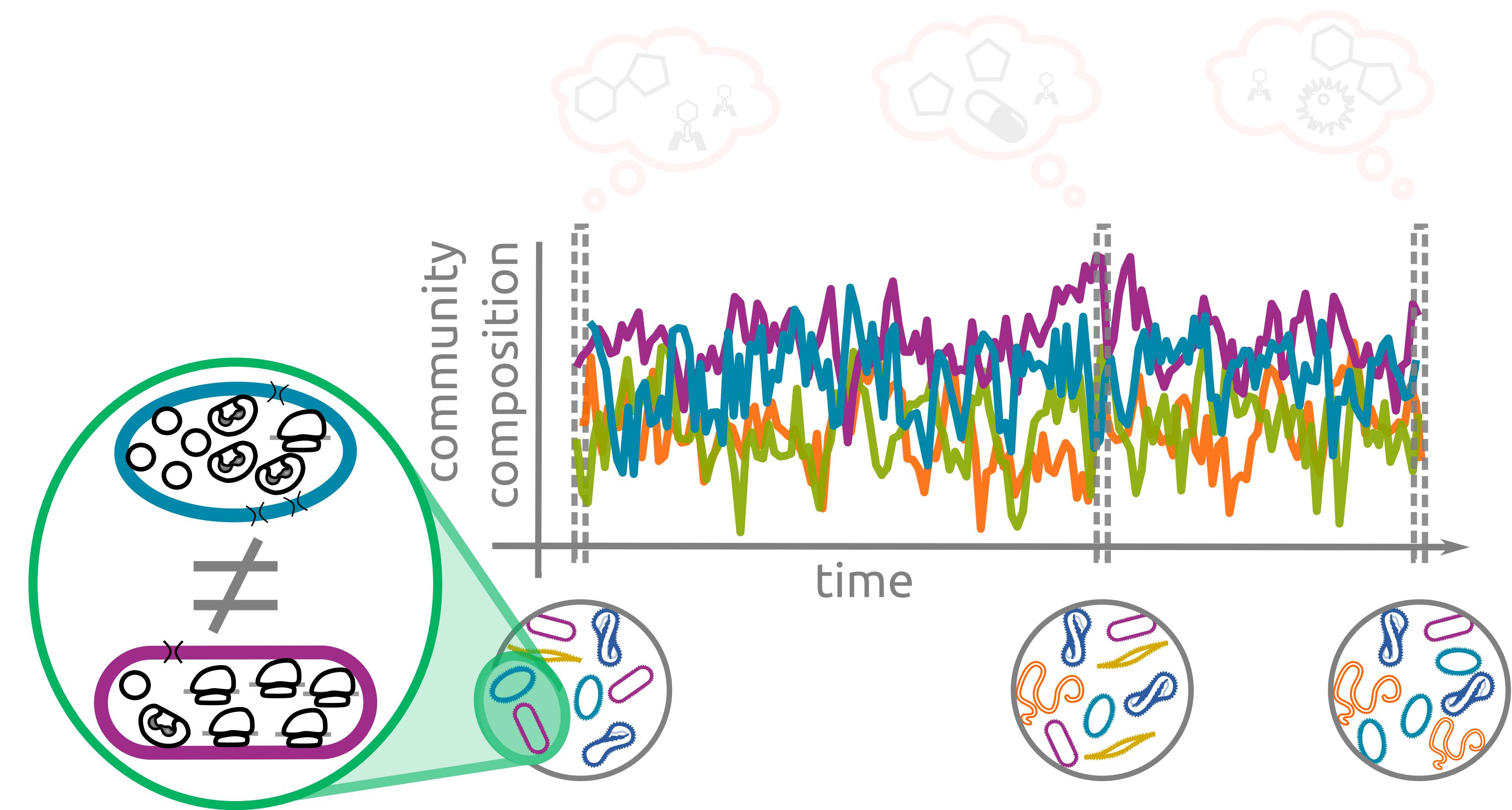
# The dynamics of communities is complex



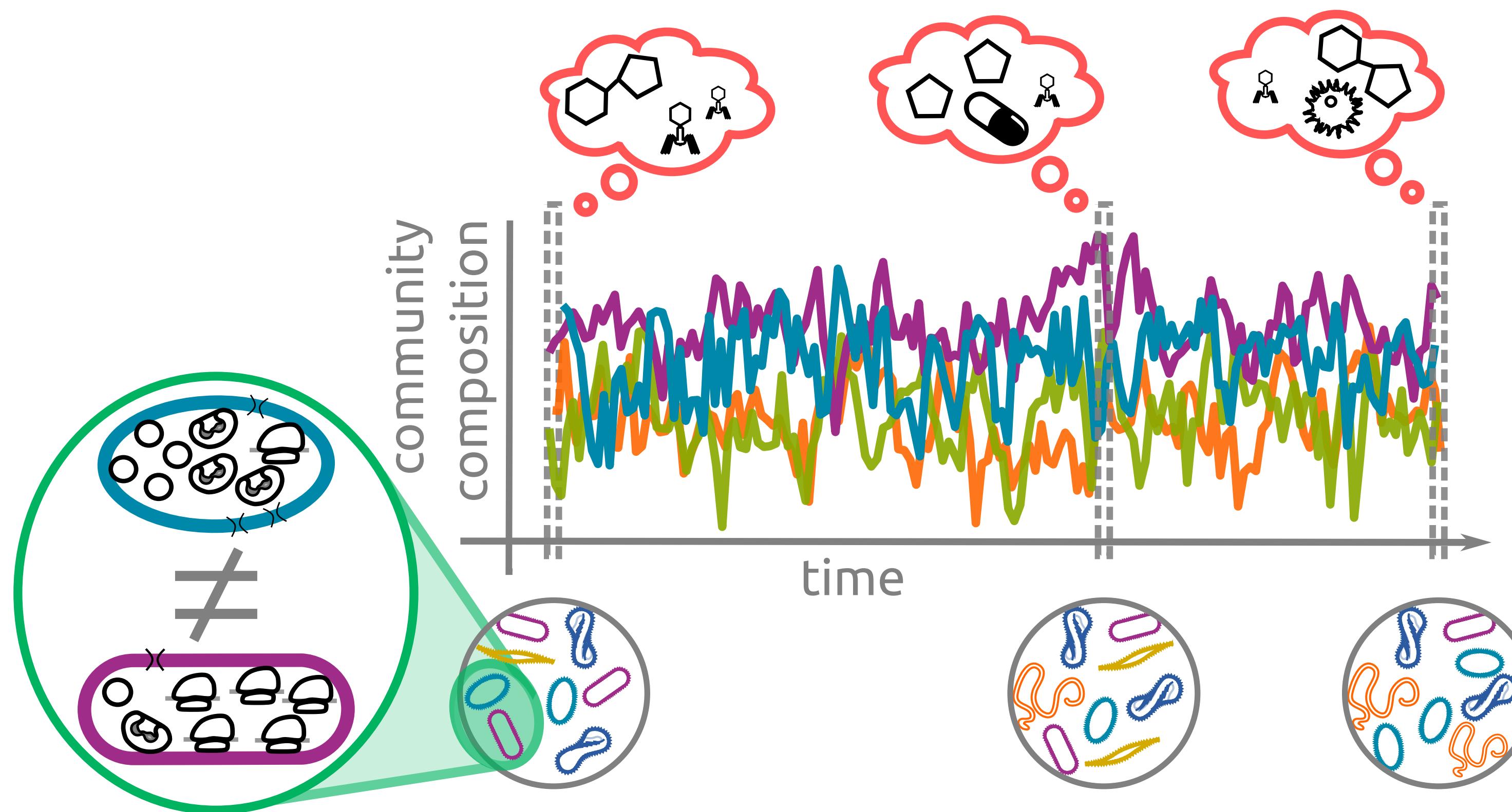
# because the environment is high-dimensional



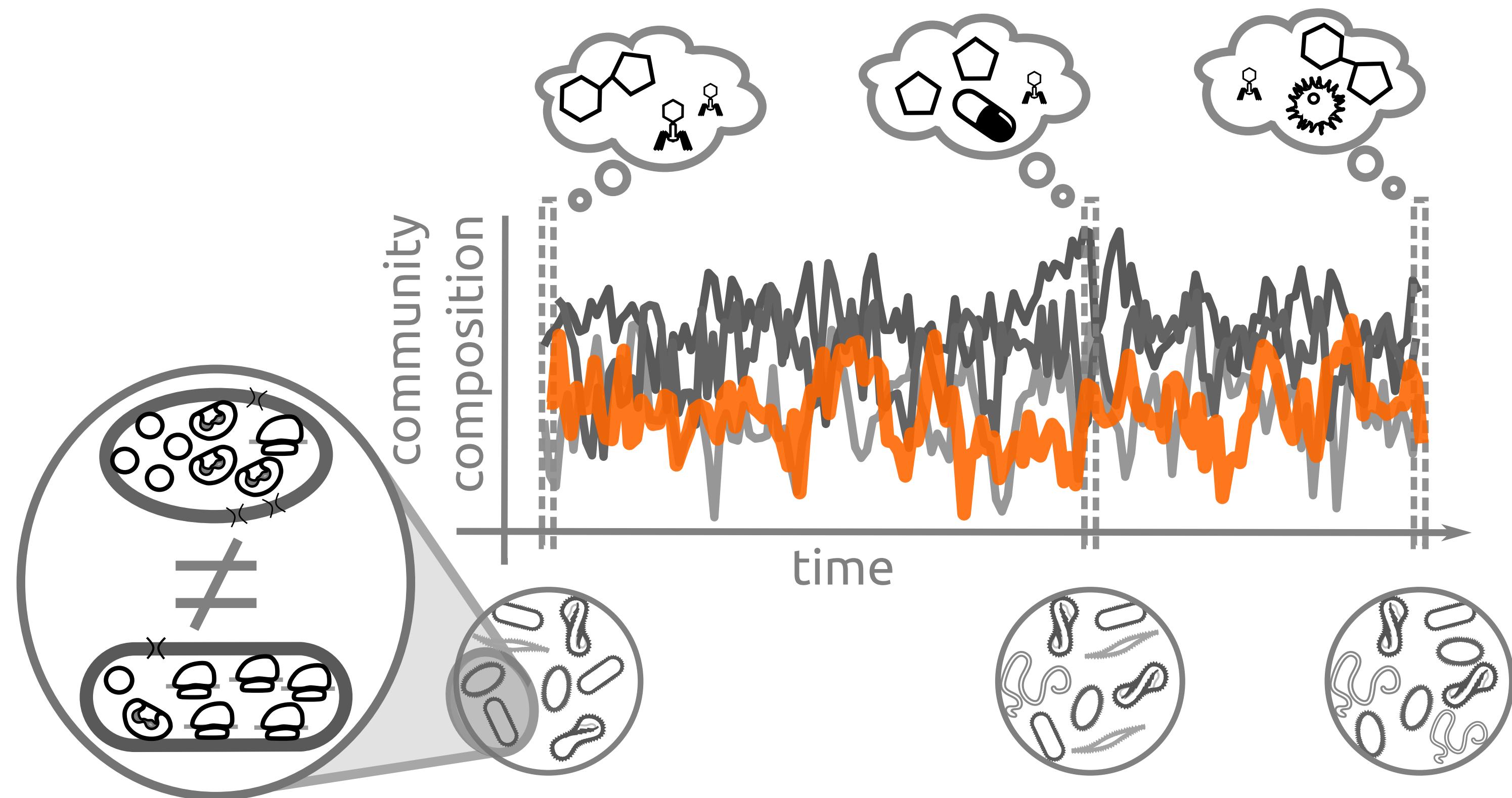
# because trait space is high-dimensional



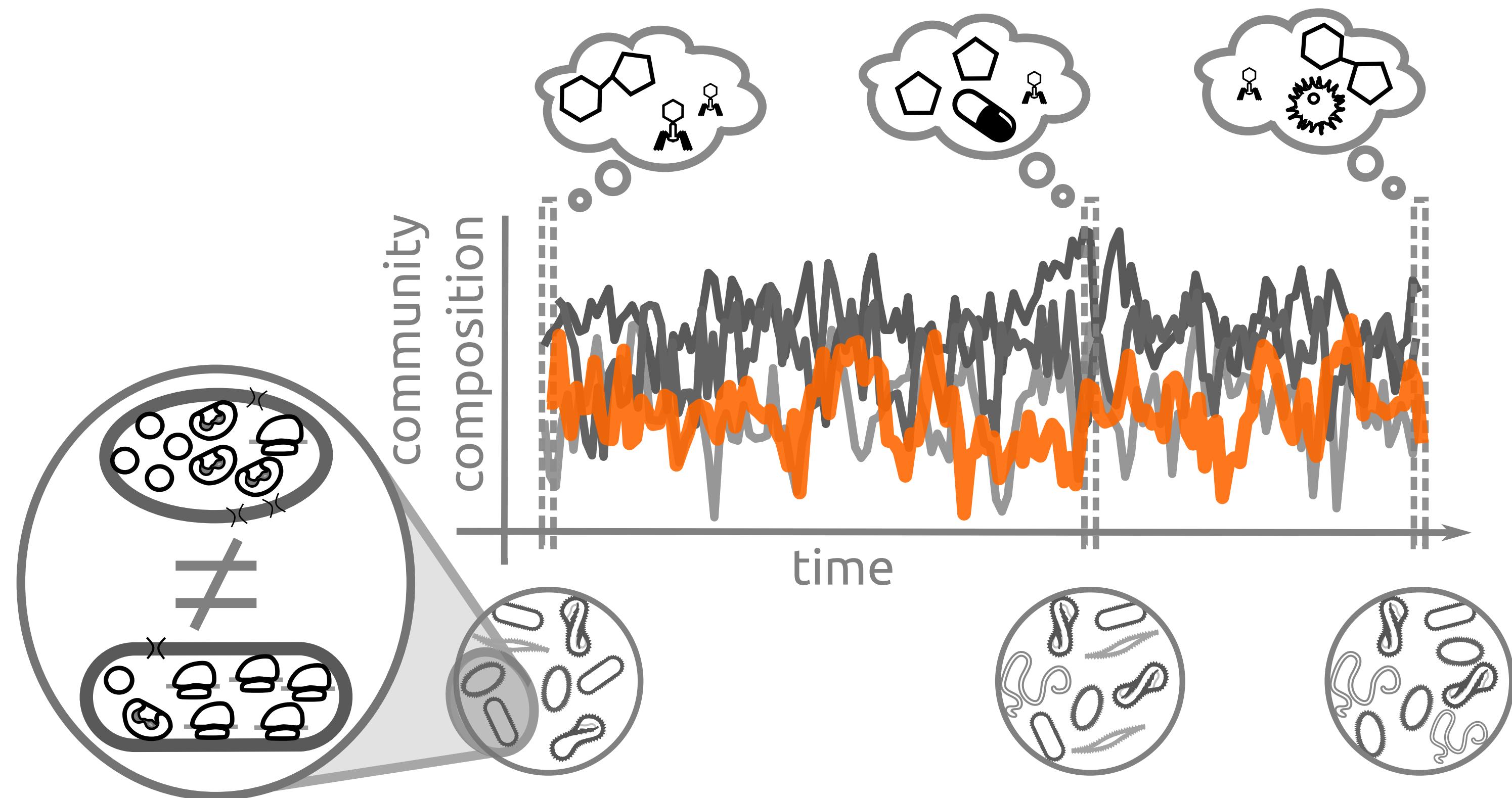
# what is the statistical structure of microbial community dynamics?



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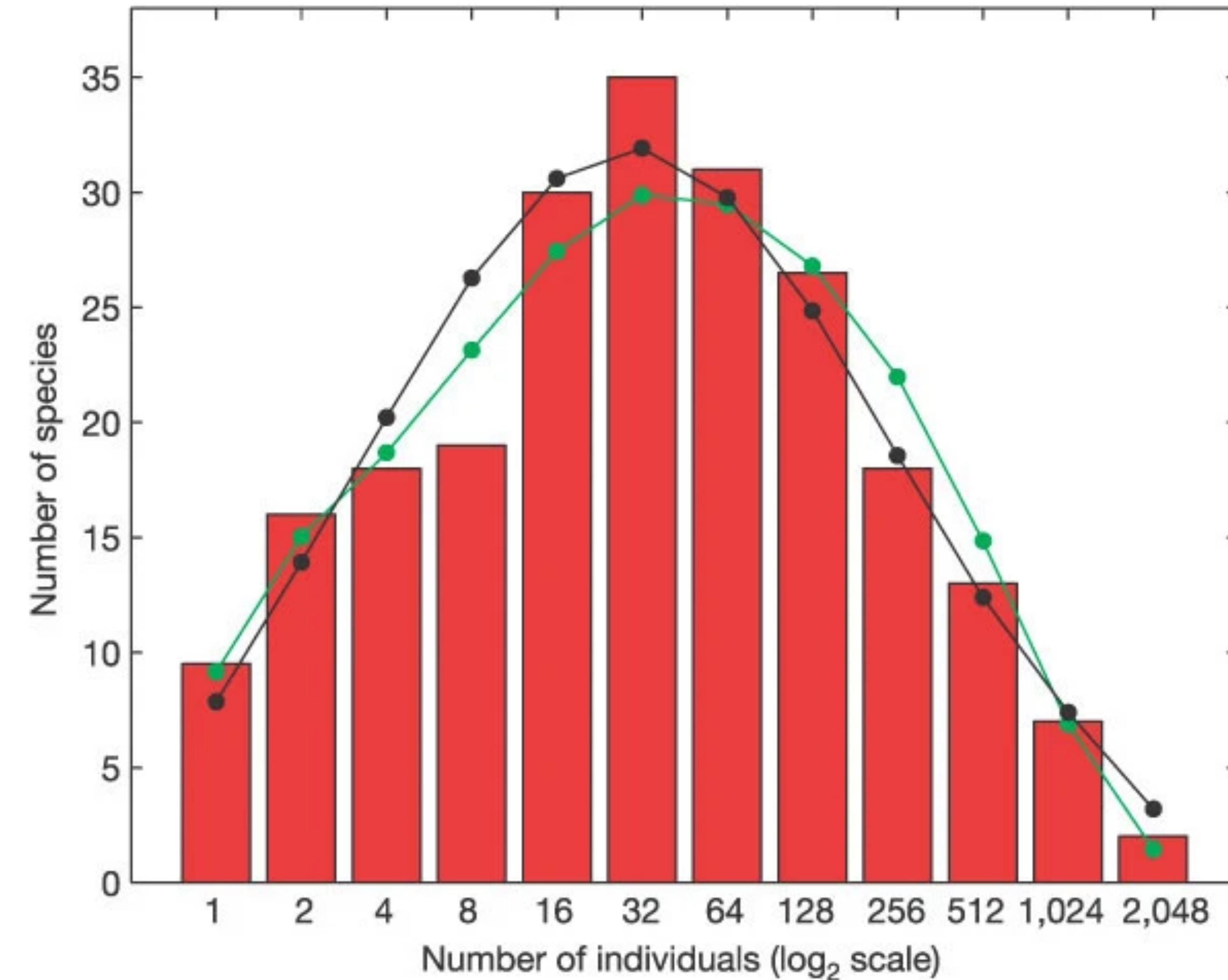
$$P(\text{community composition}; t) = ?$$

# A very basic phenomenology

There are many different “things” (species/types)

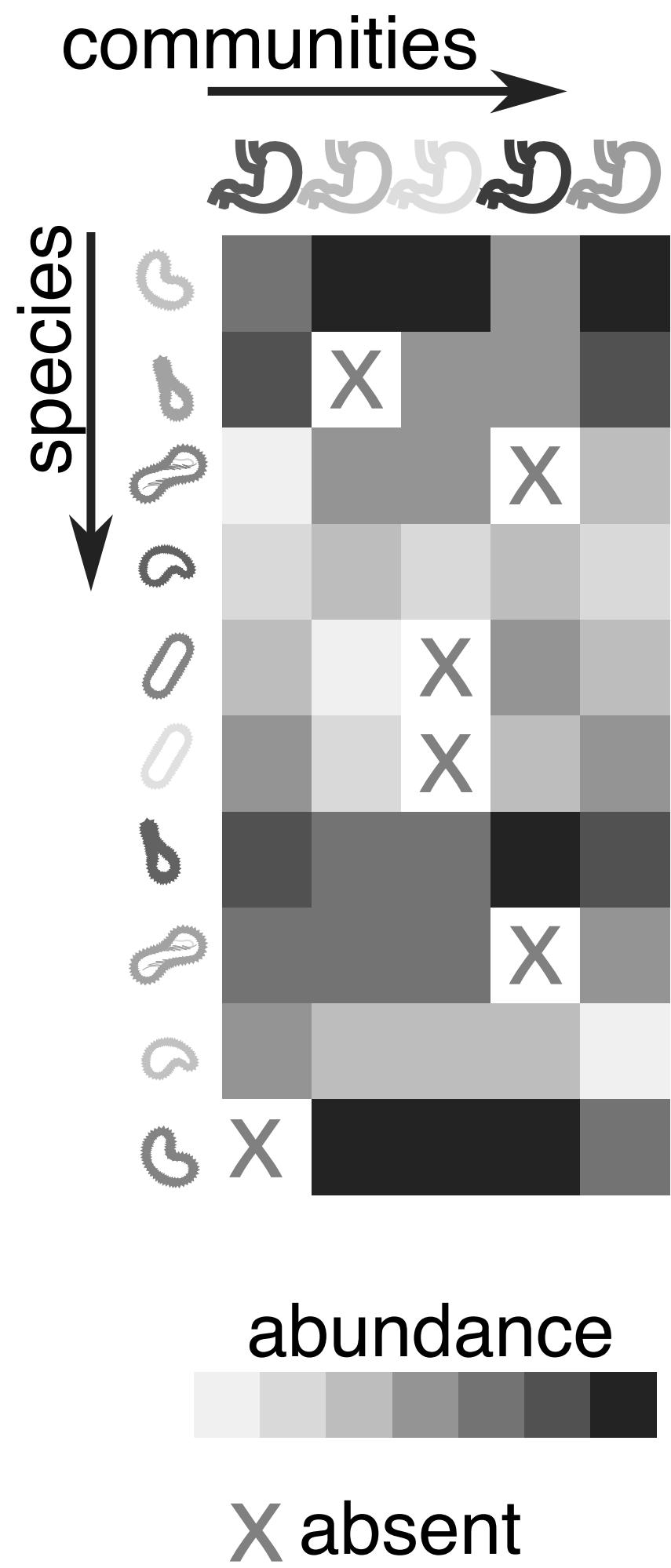
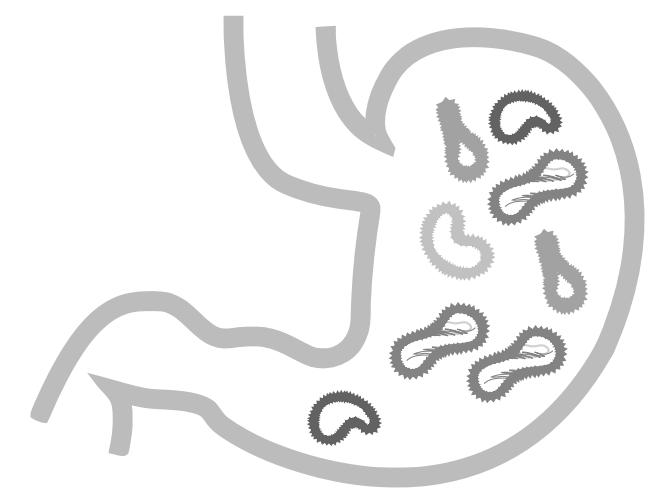
There are “common” and “rare” species

# Making the observation more quantitative

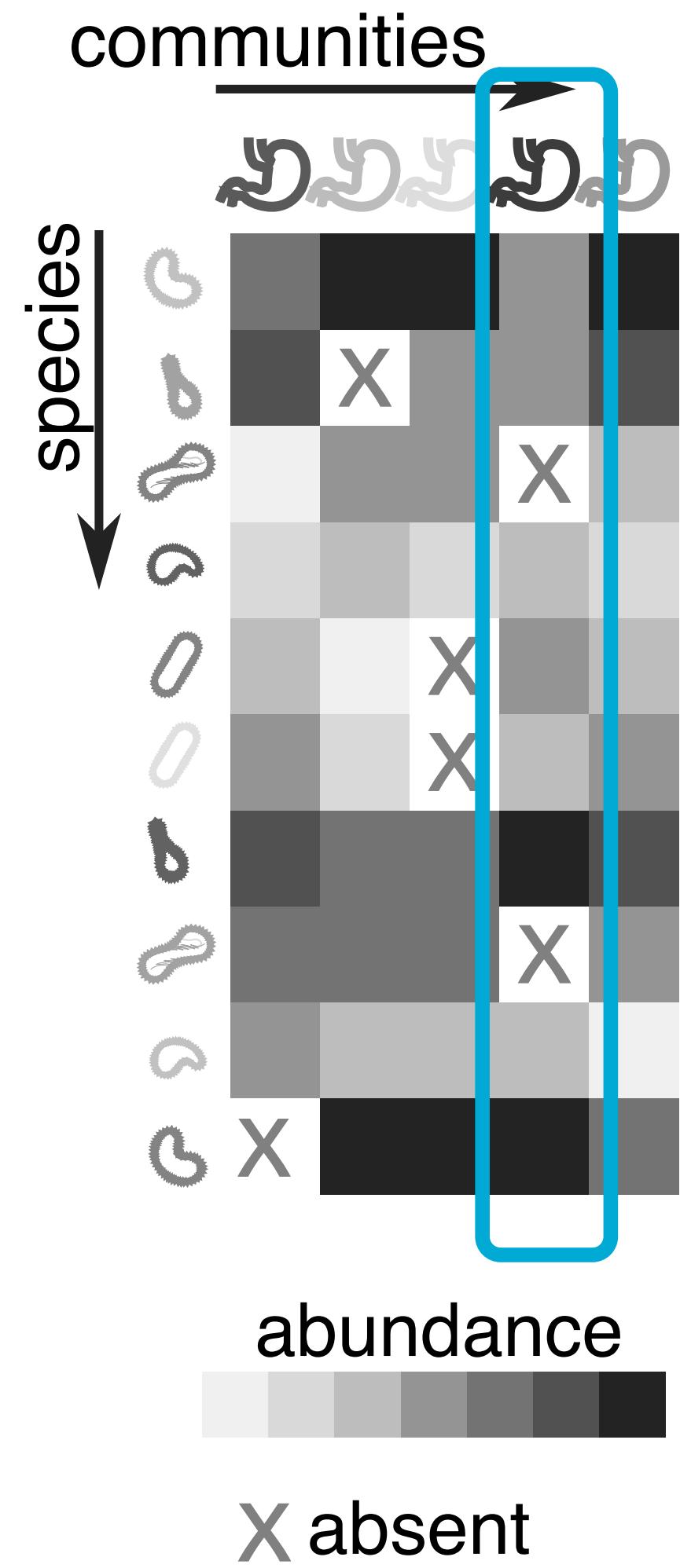
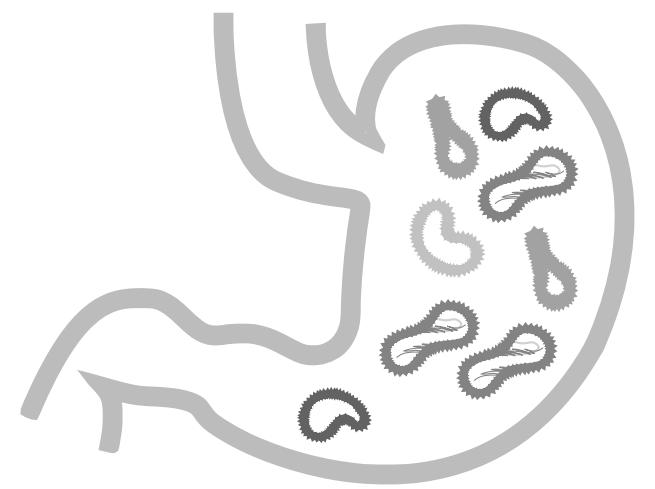


[Volkov et al., 2003]

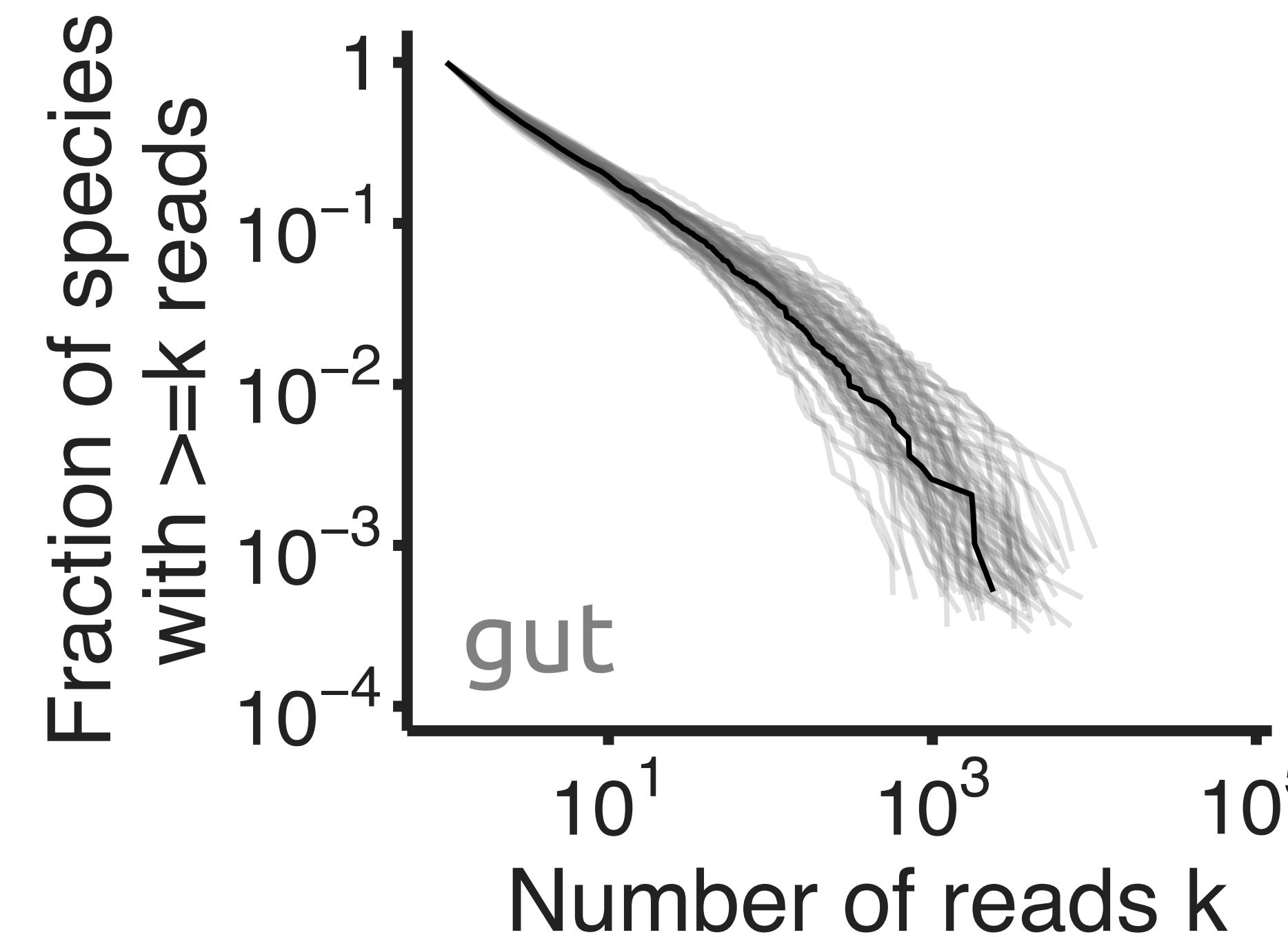
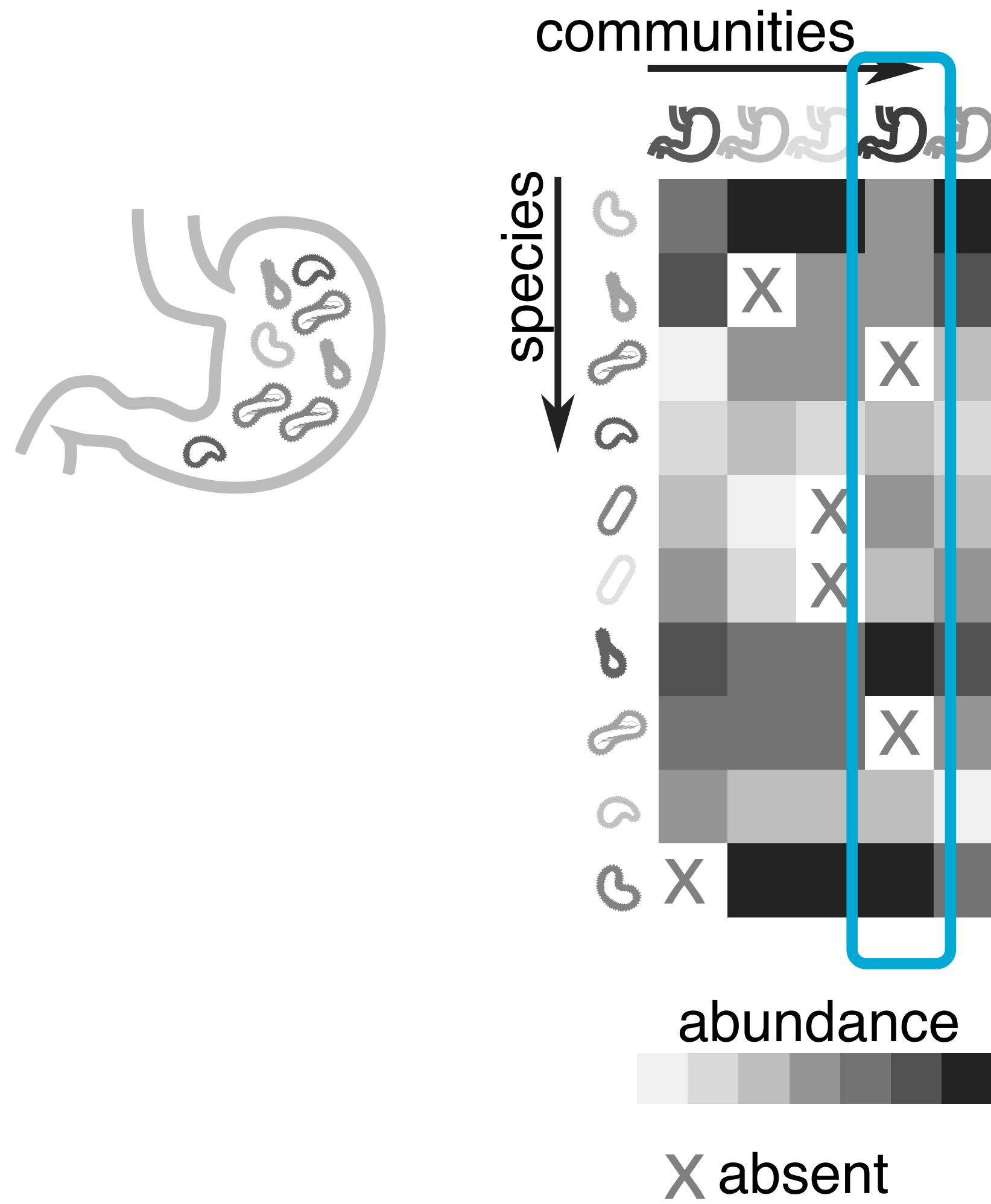
# Species Abundance distribution



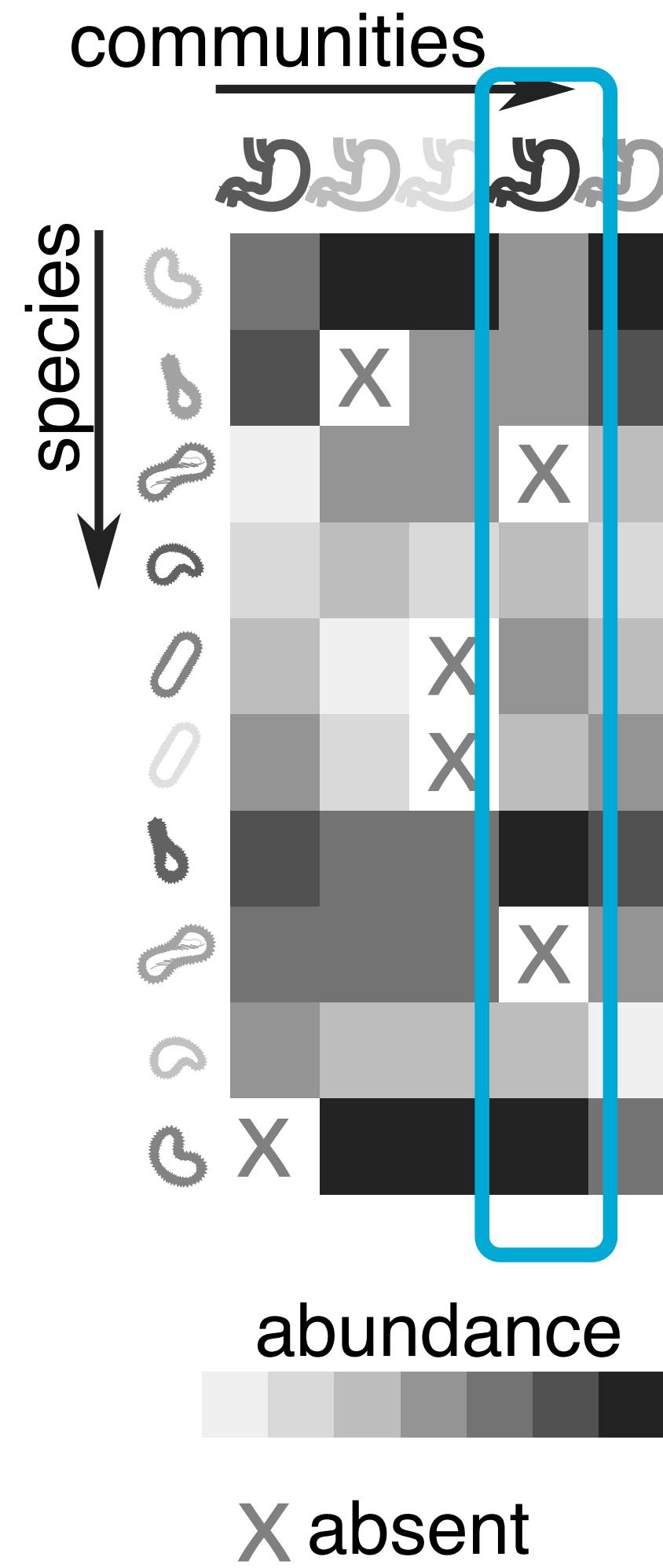
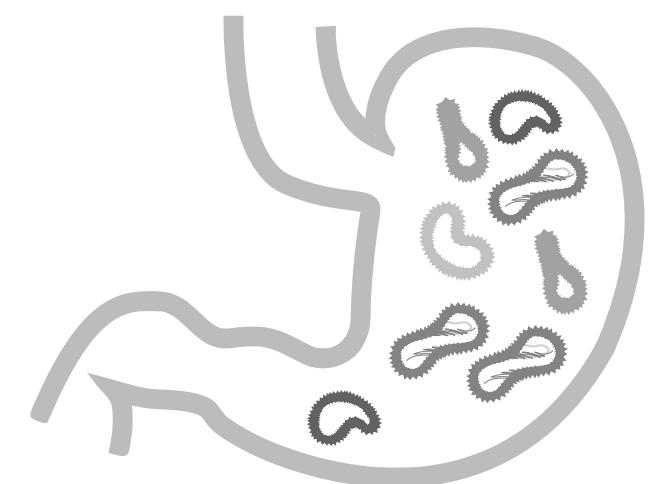
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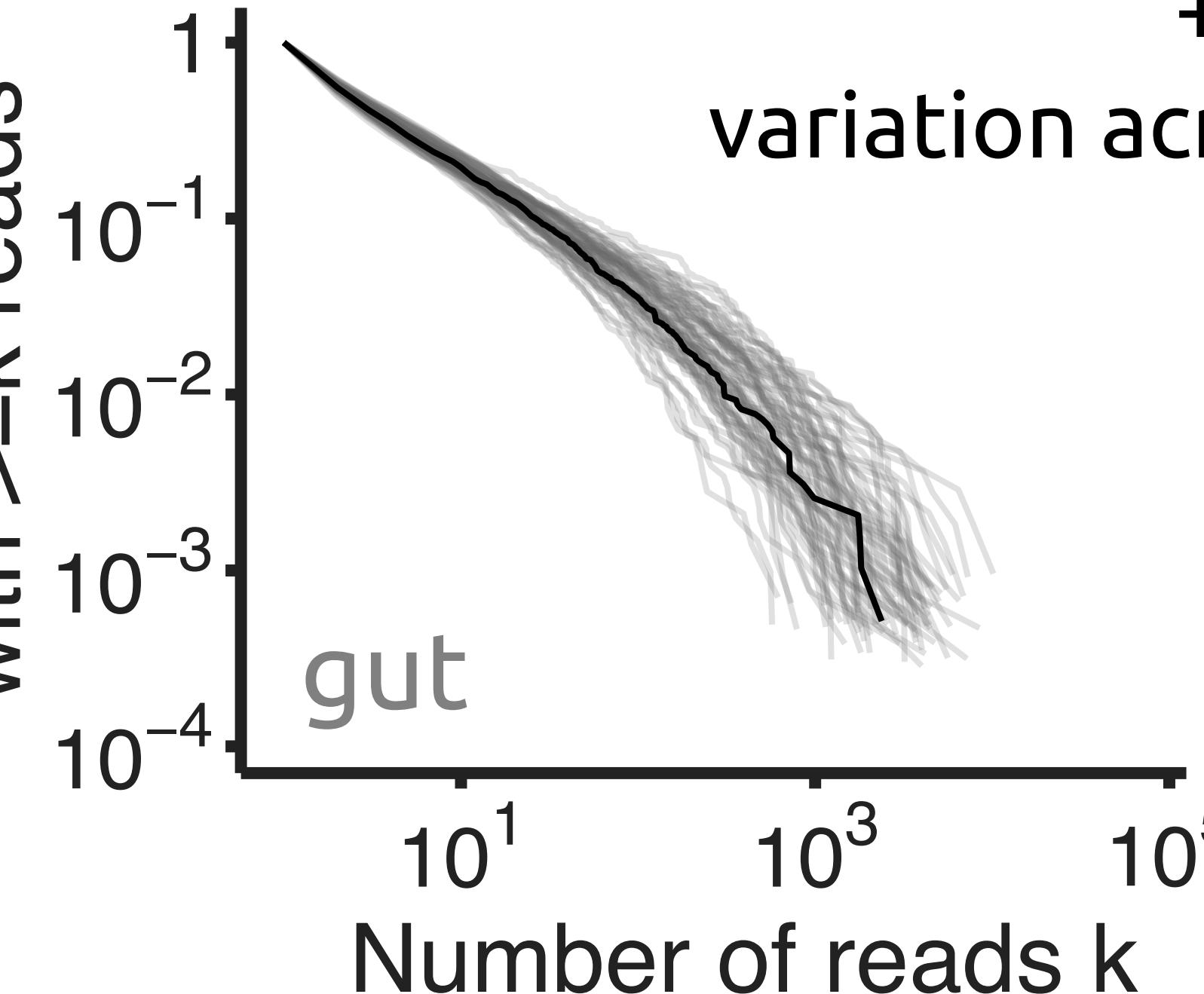
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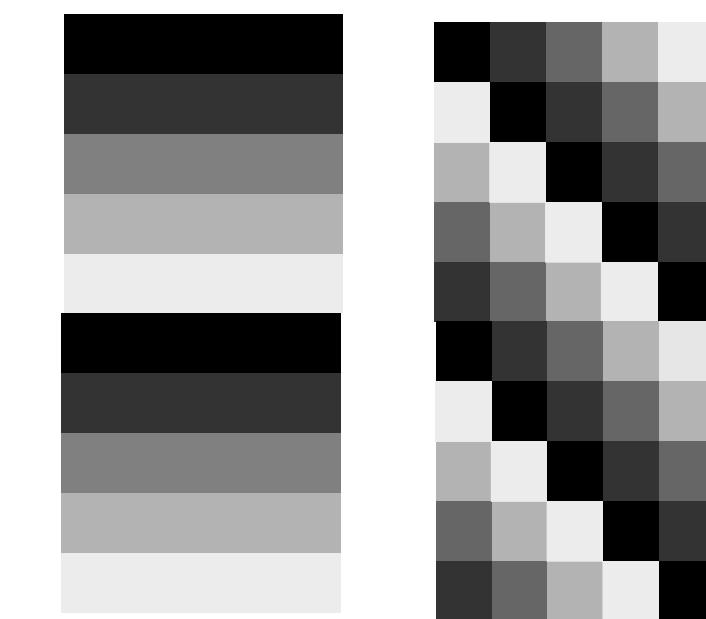
# Species Abundance distribution



Fraction of species  
with  $\geq k$  reads

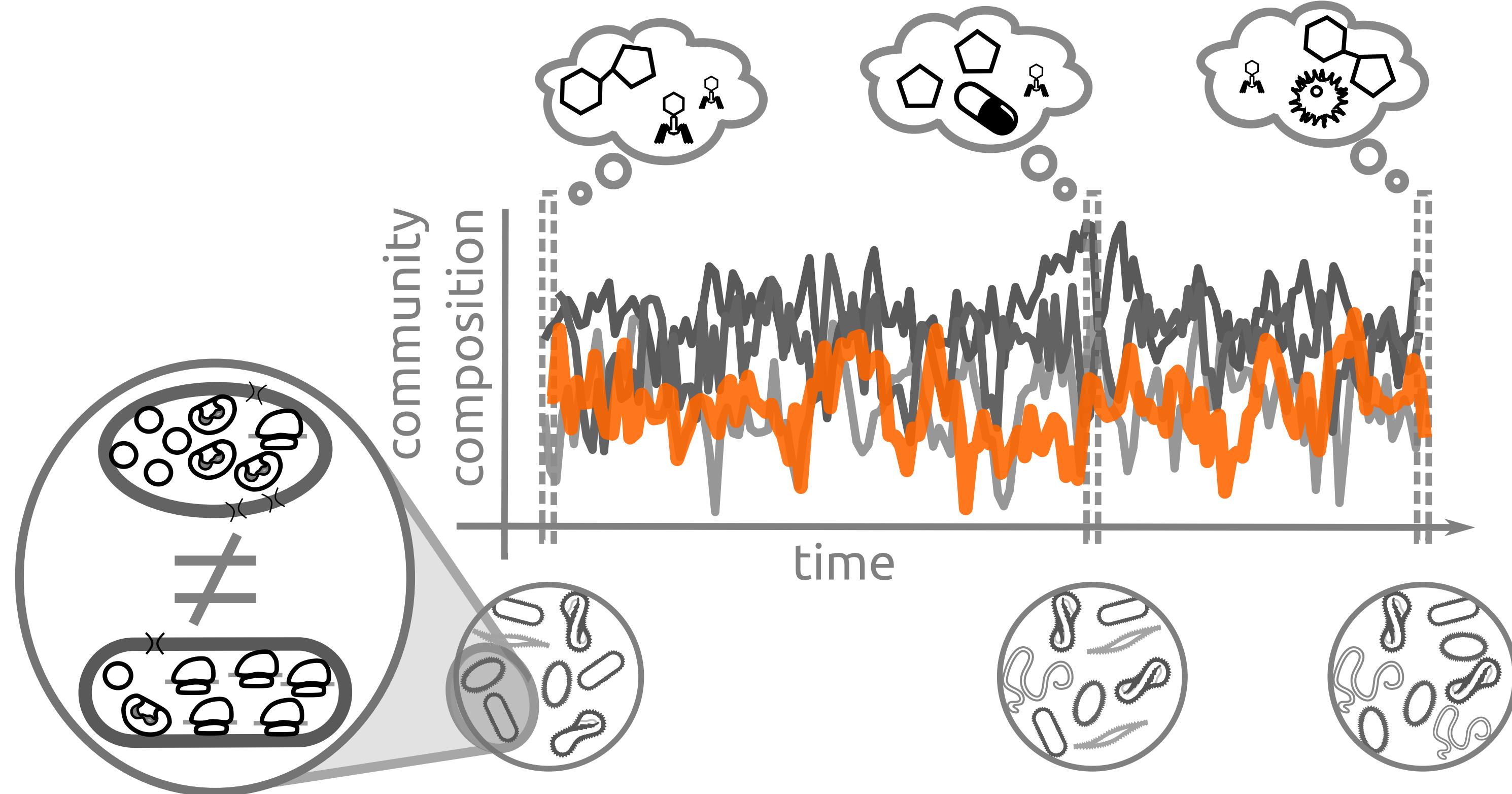


(sampling +)  
variation across communities  
+  
variation across species

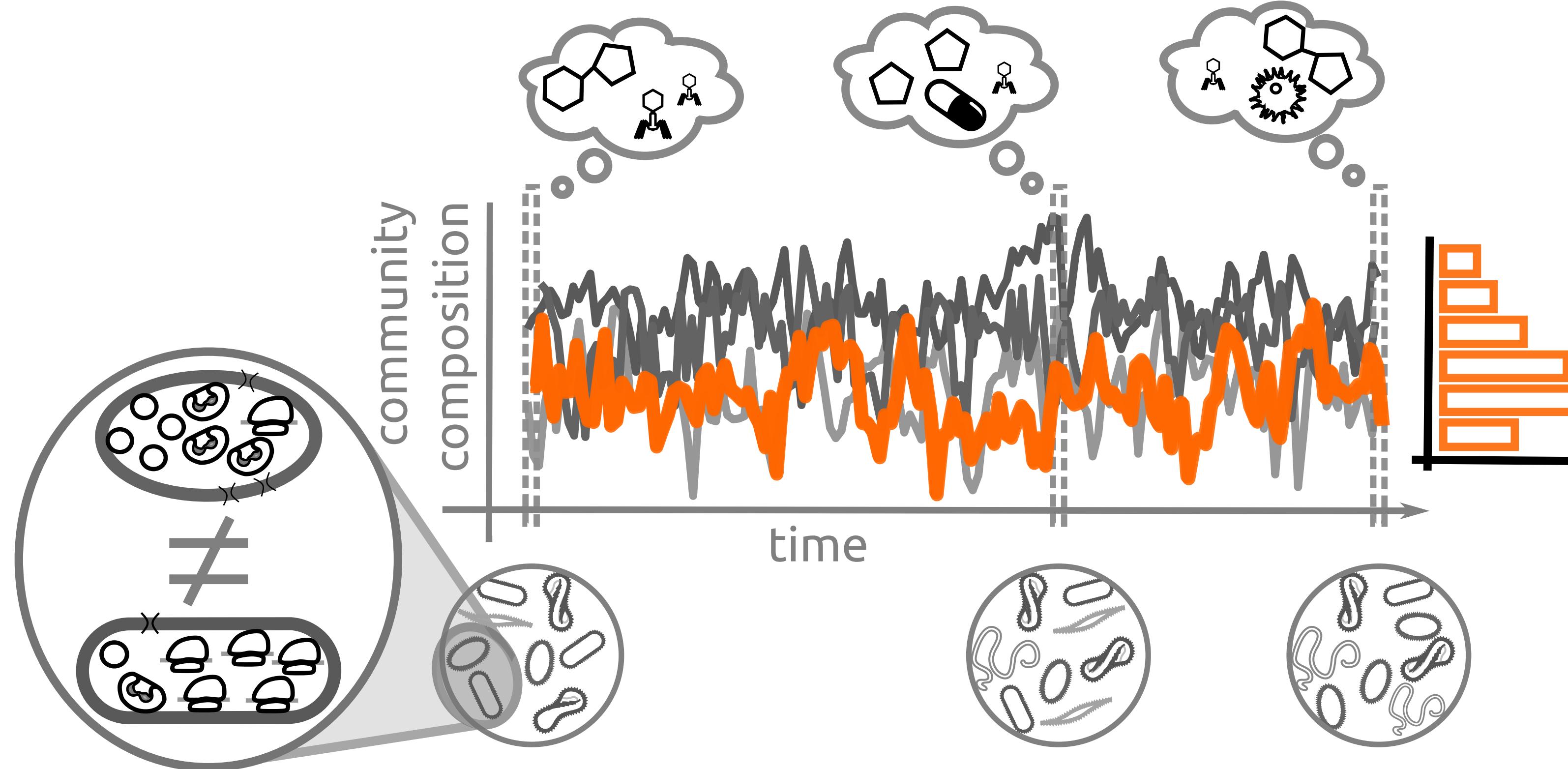


# **Abundance fluctuations are Gamma distr**

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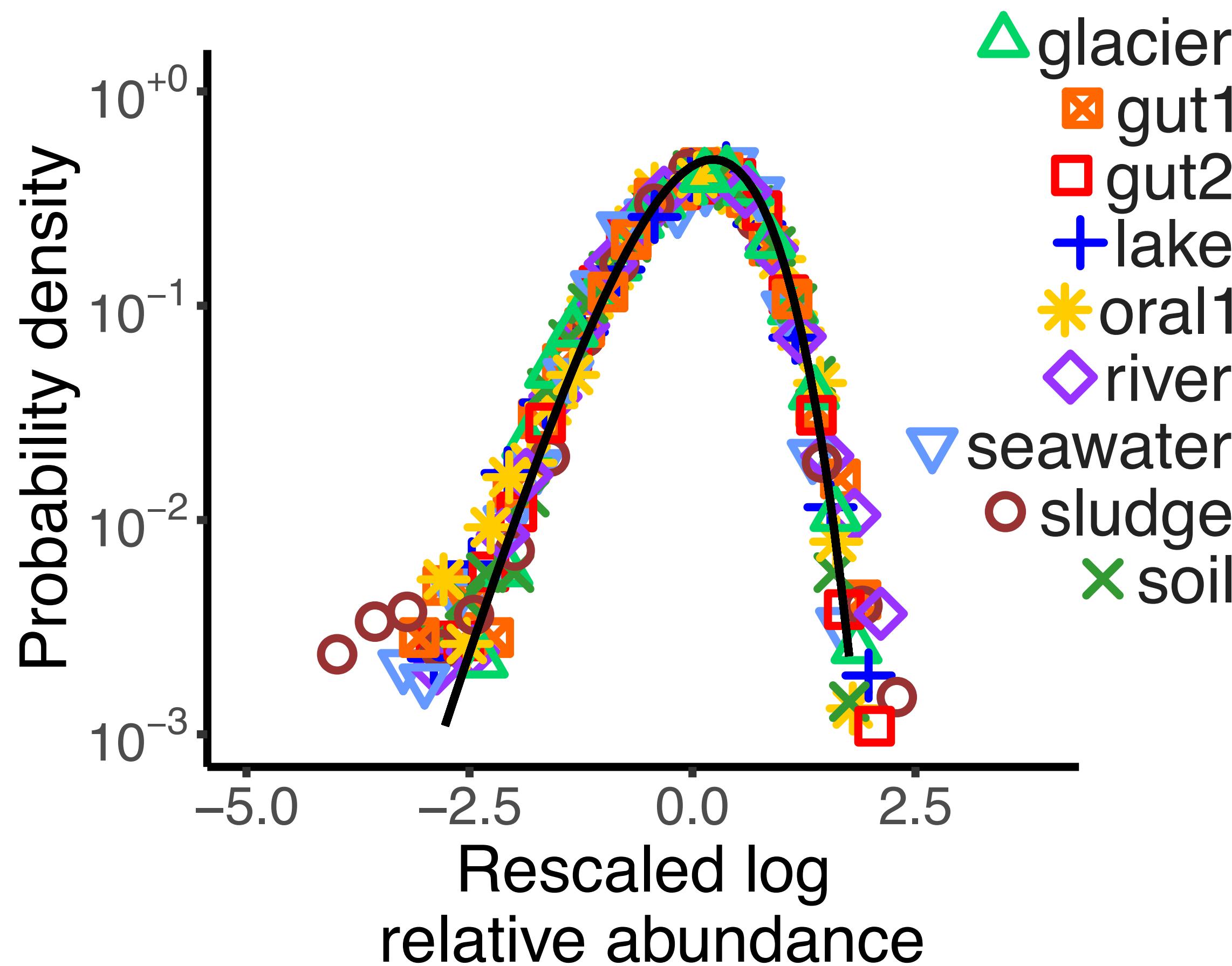
# Abundance fluctuations are Gamma distr



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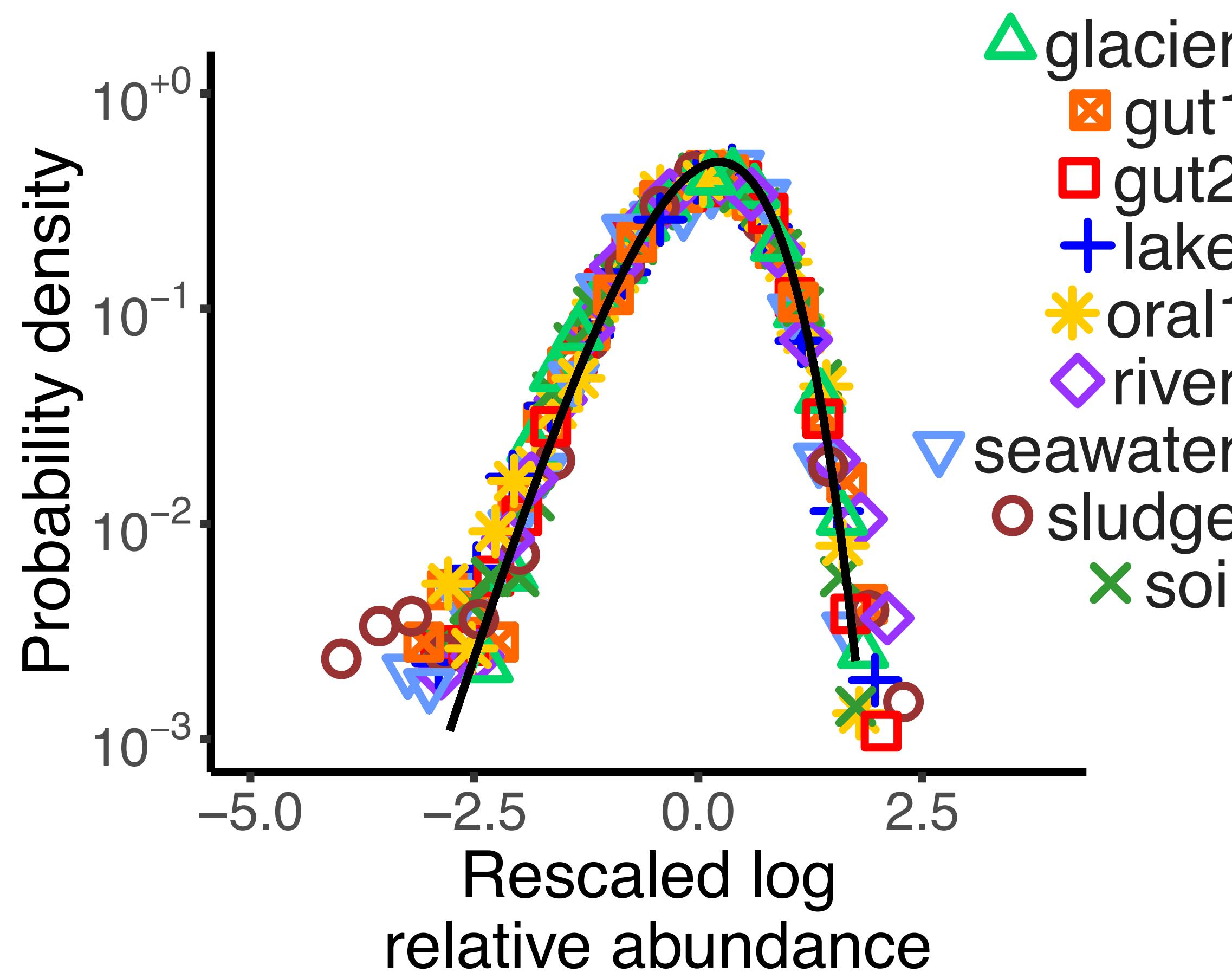
variation across communities  
for multiple environments



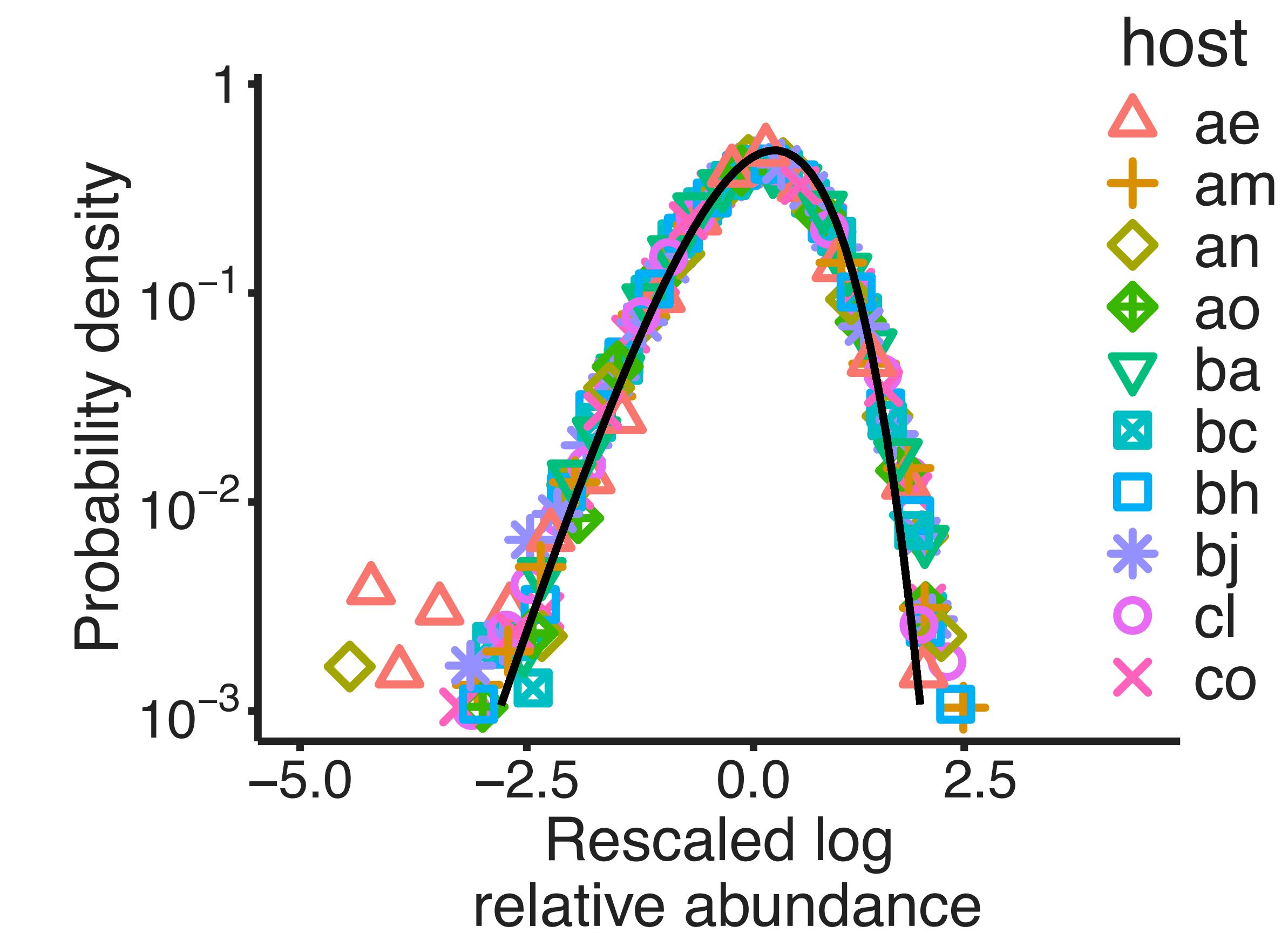
# Abundance fluctuations are Gamma distr

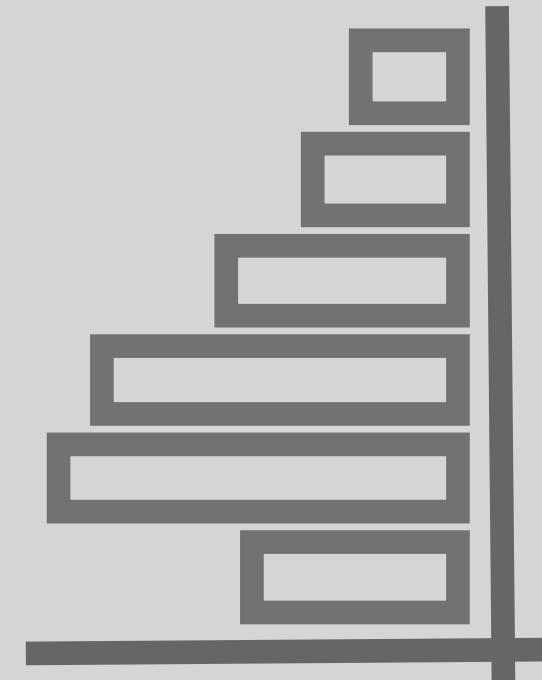
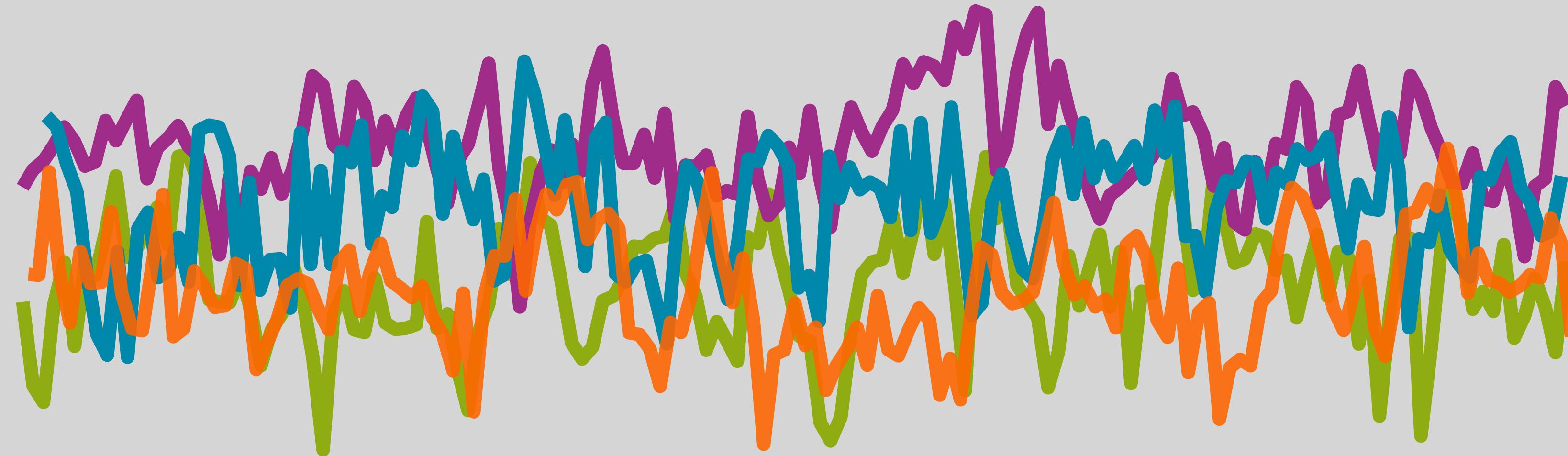


variation across communities  
for multiple environments

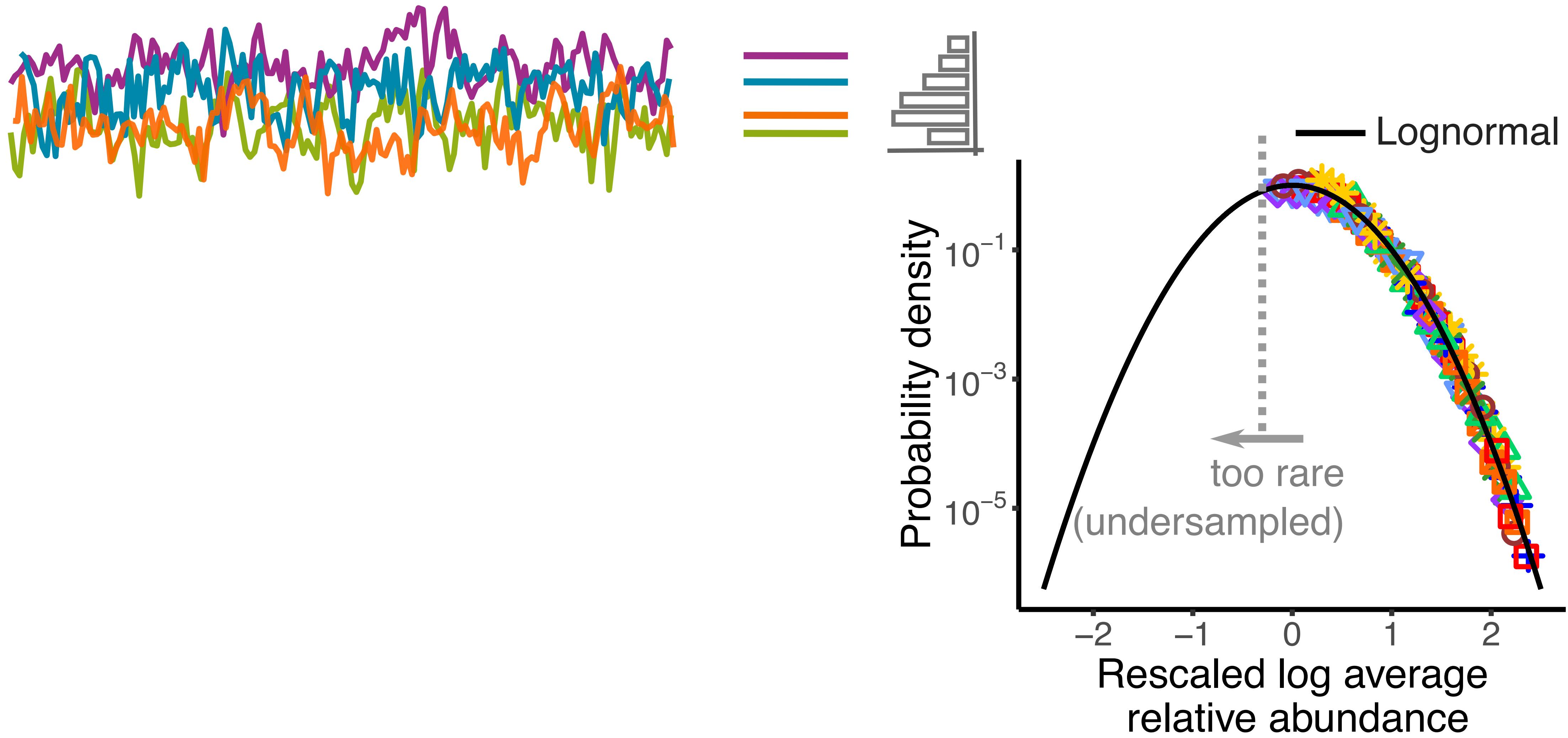


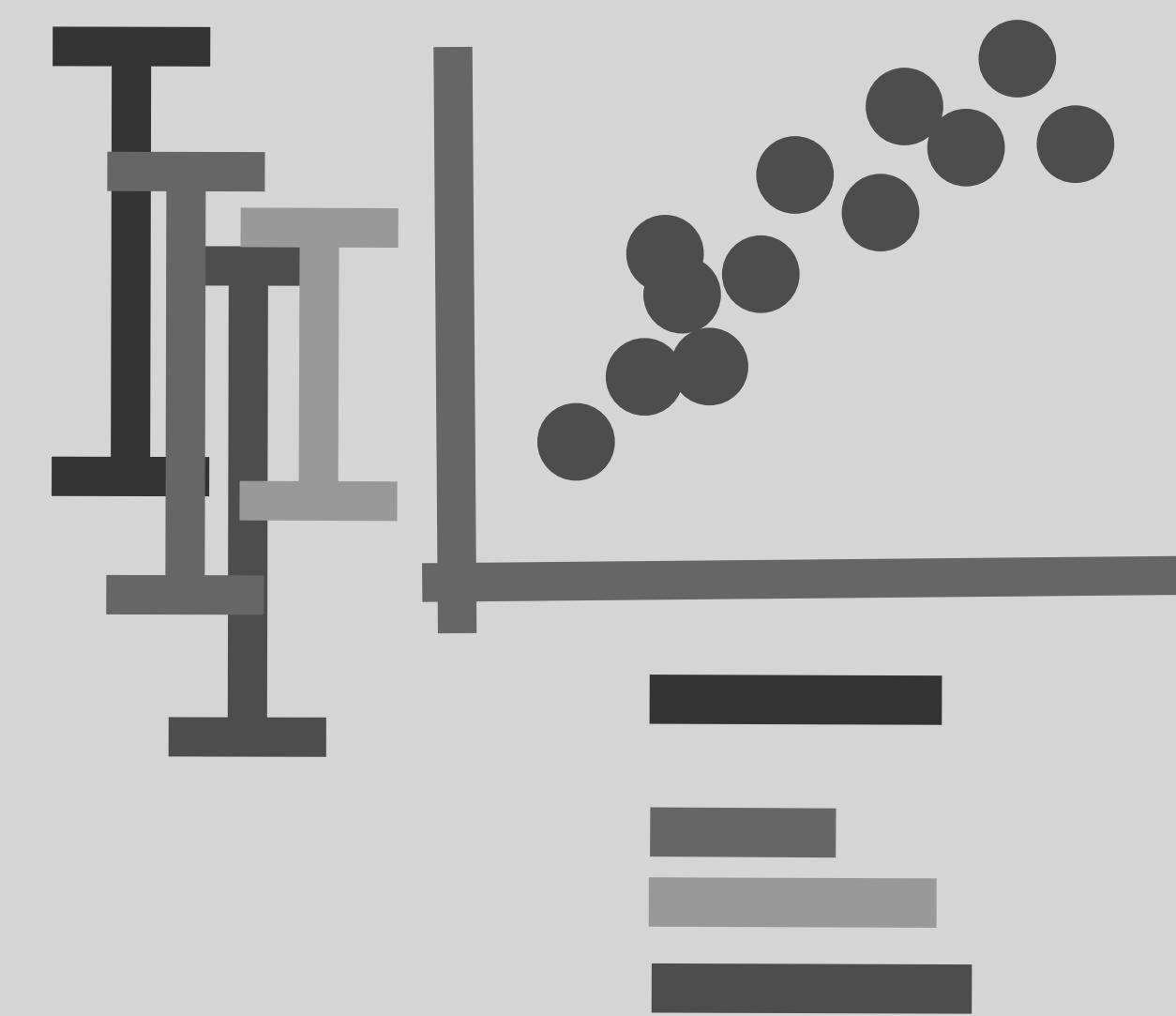
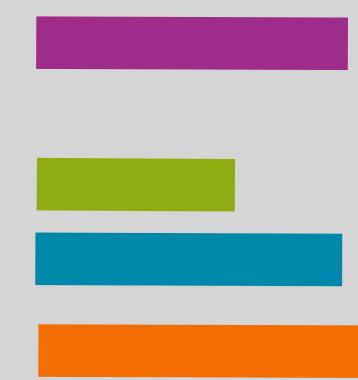
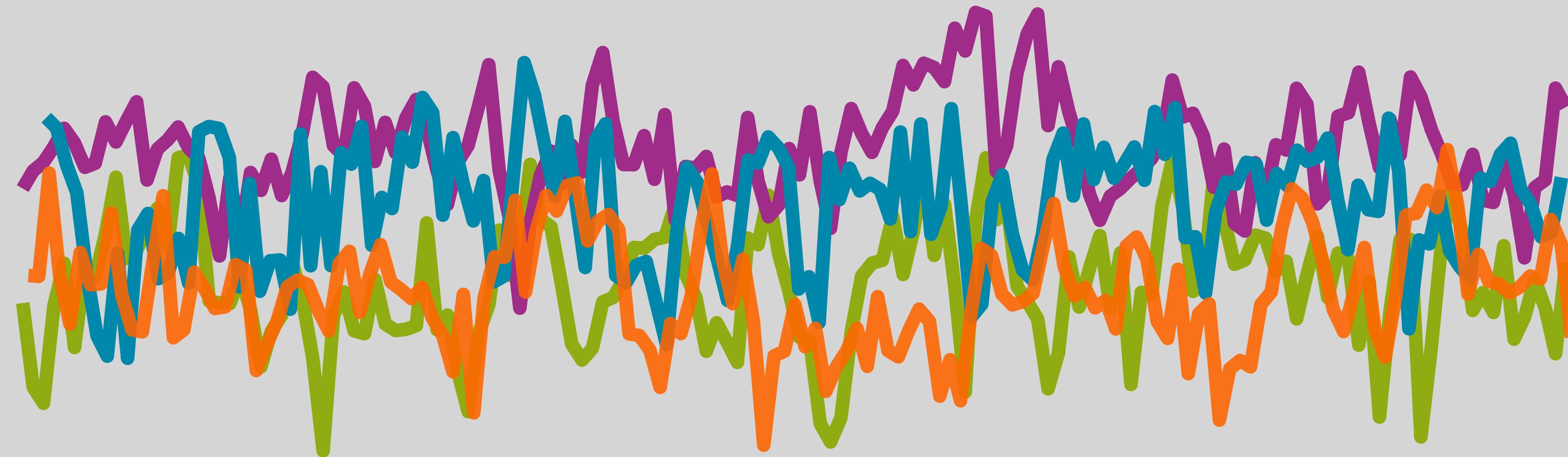
variation over time  
(human gut)



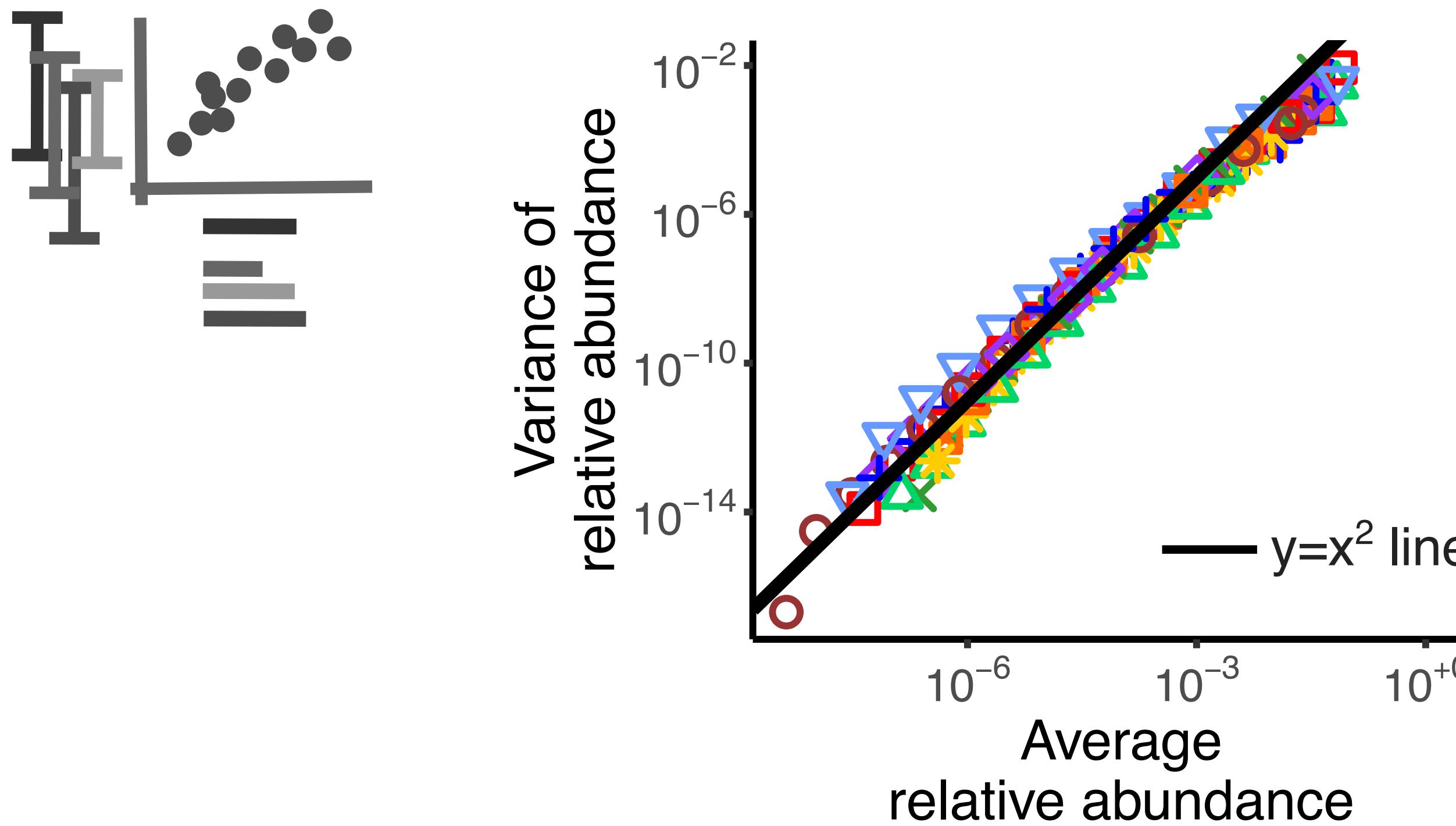
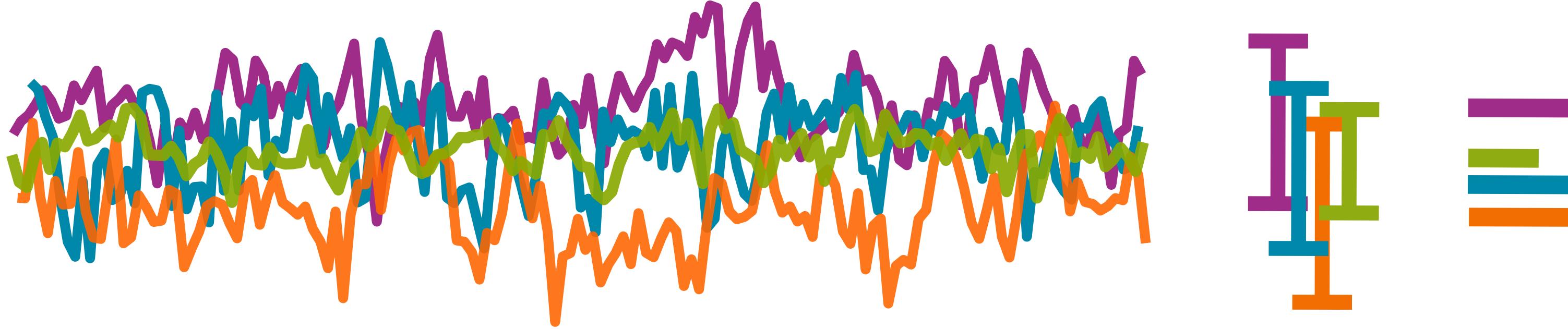


# Strong statistical regularities



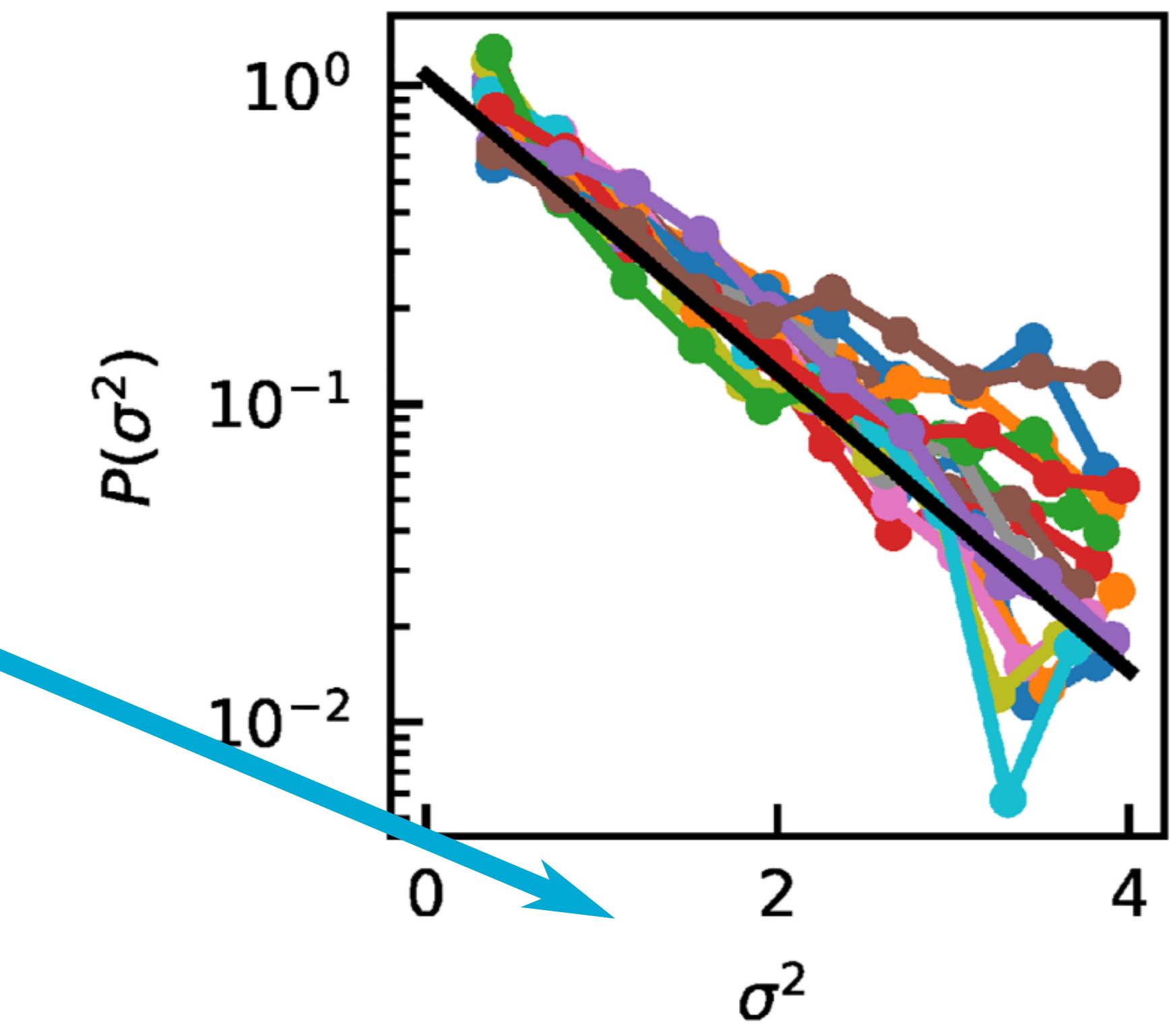
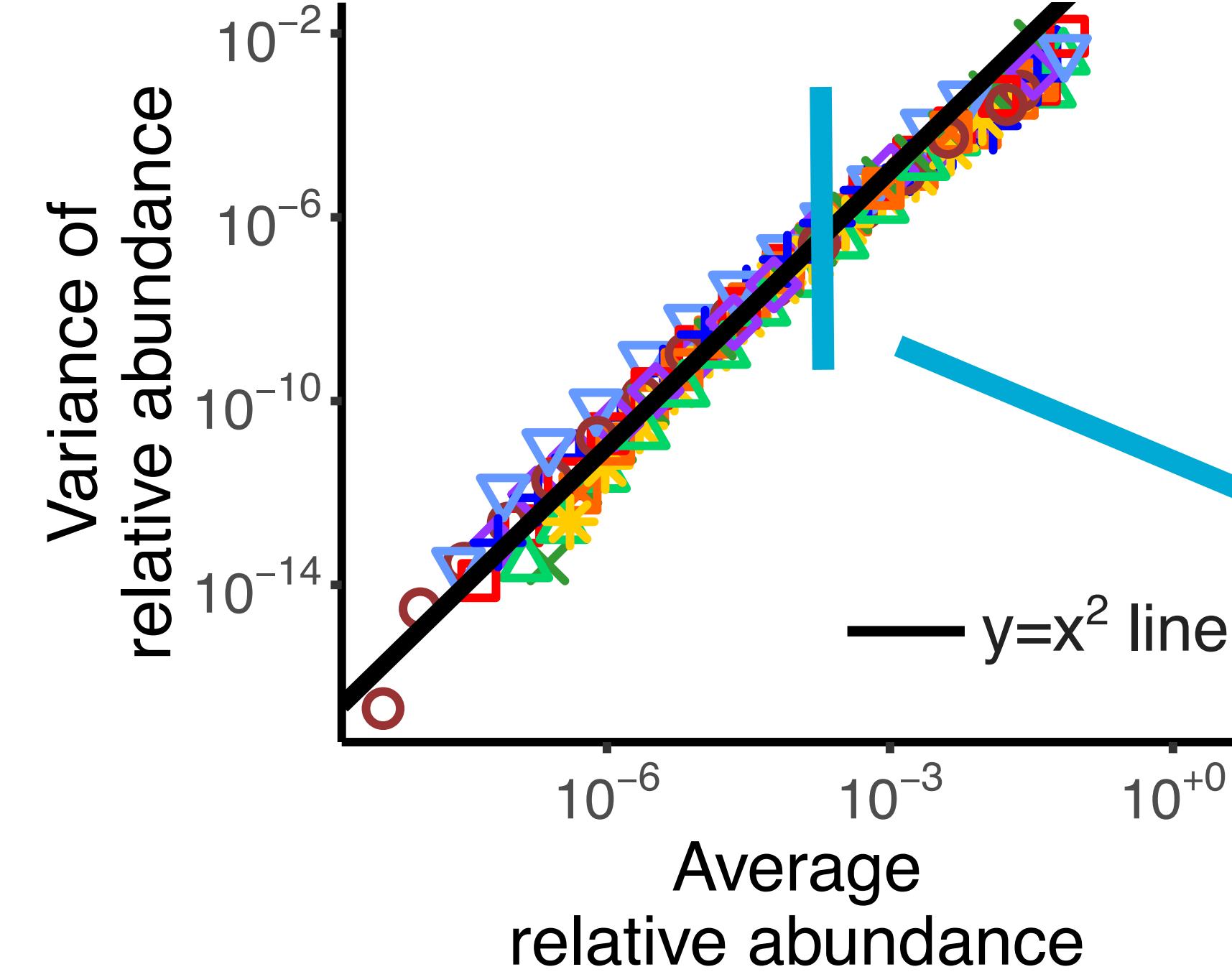
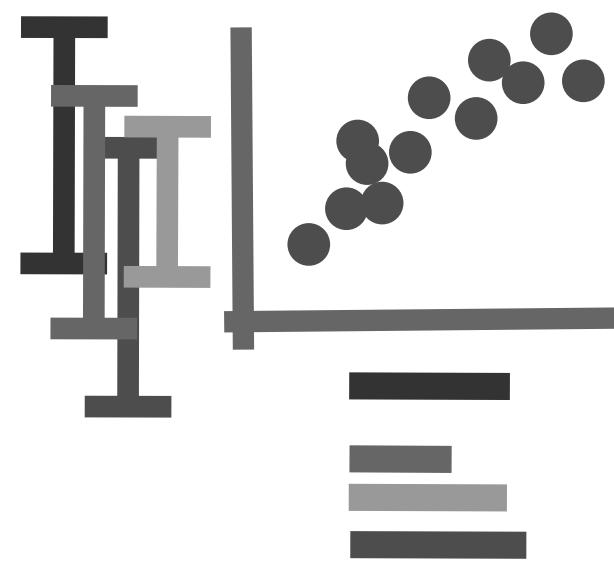
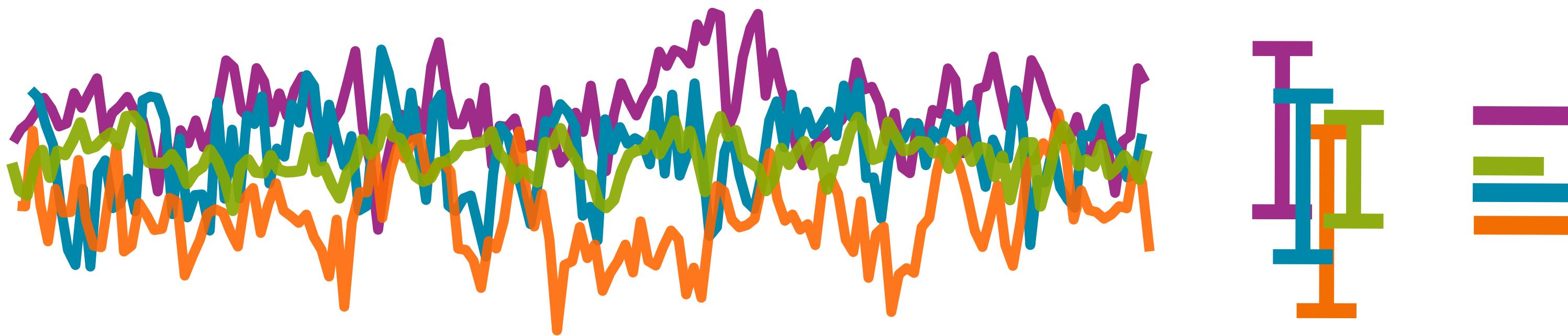


# Strong statistical regularities

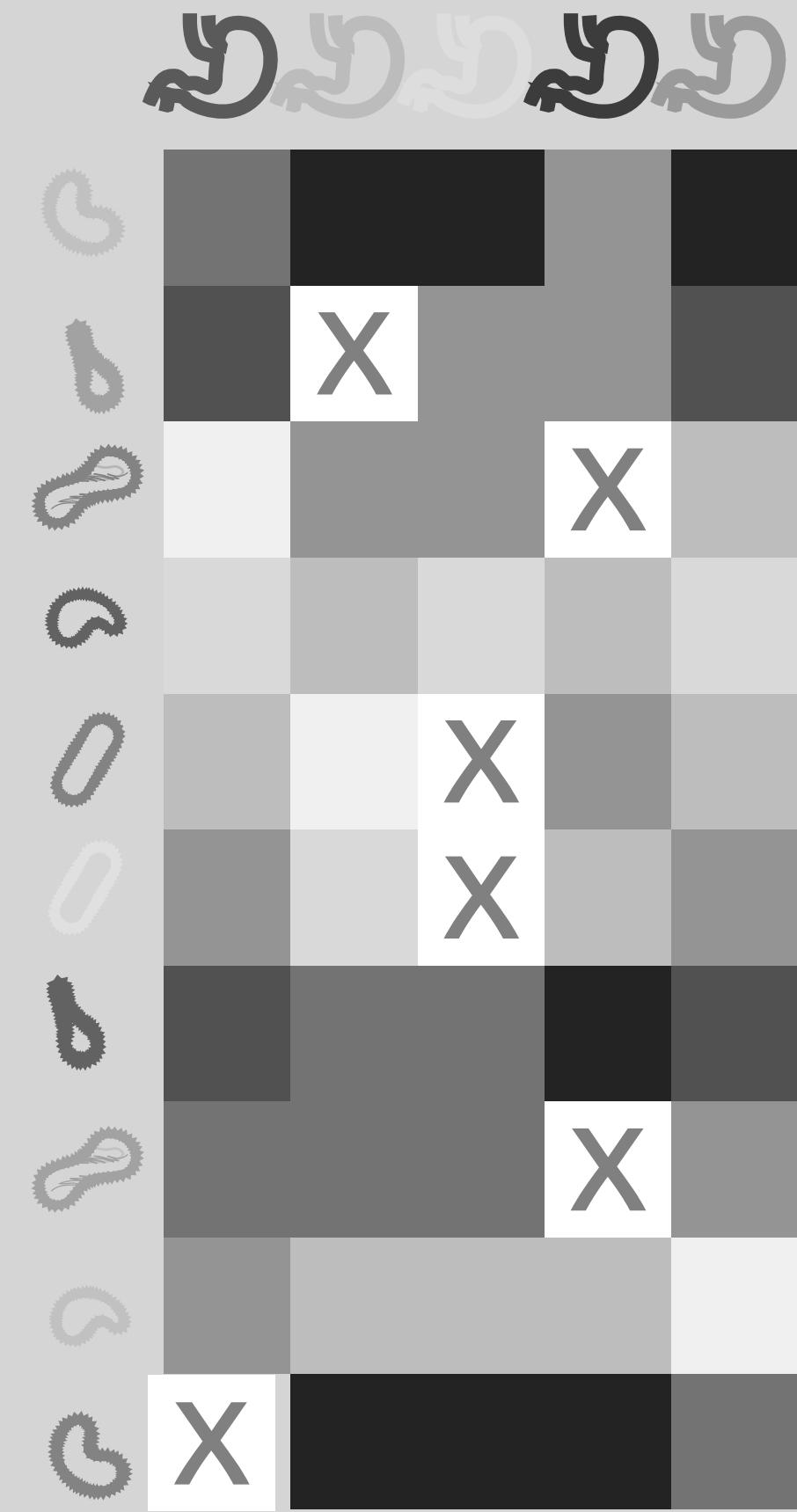
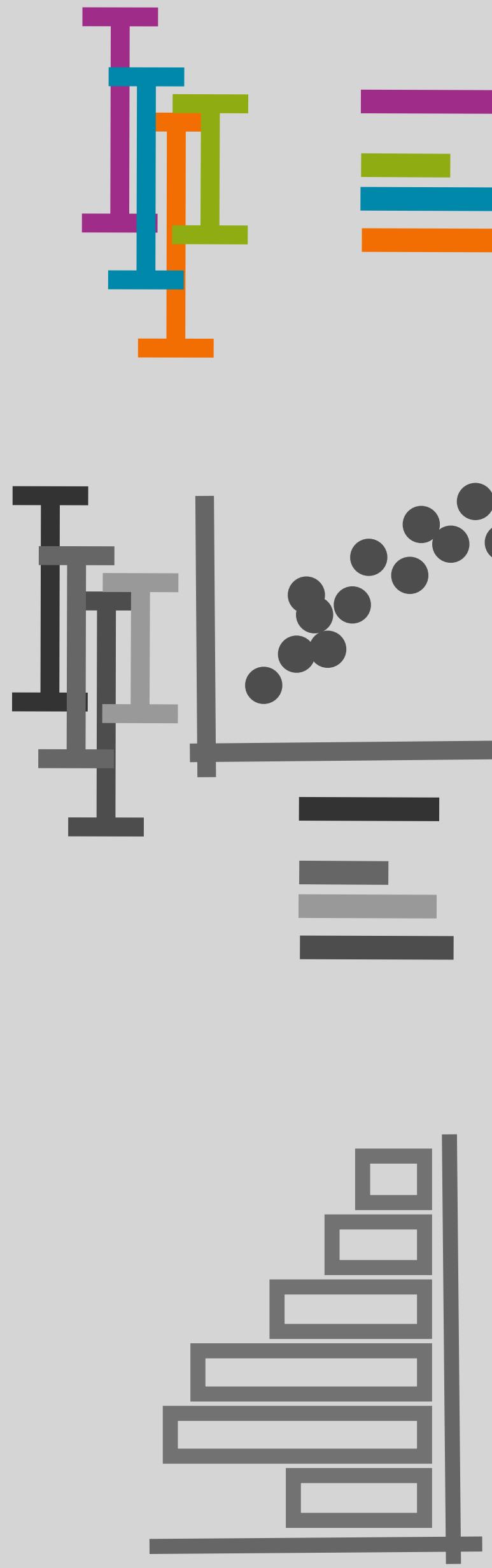


[Grilli, Nat Comm 2020, Zaoli and Grilli Sci Adv 2022]

# Strong statistical regularities



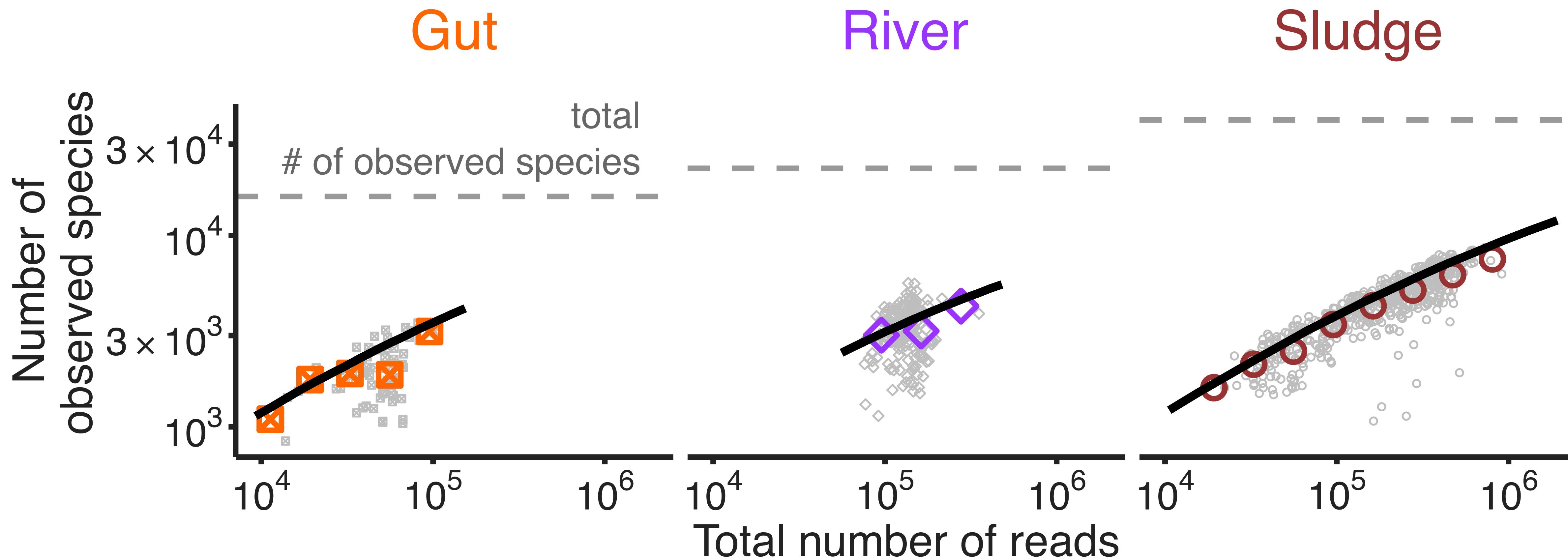
# generates



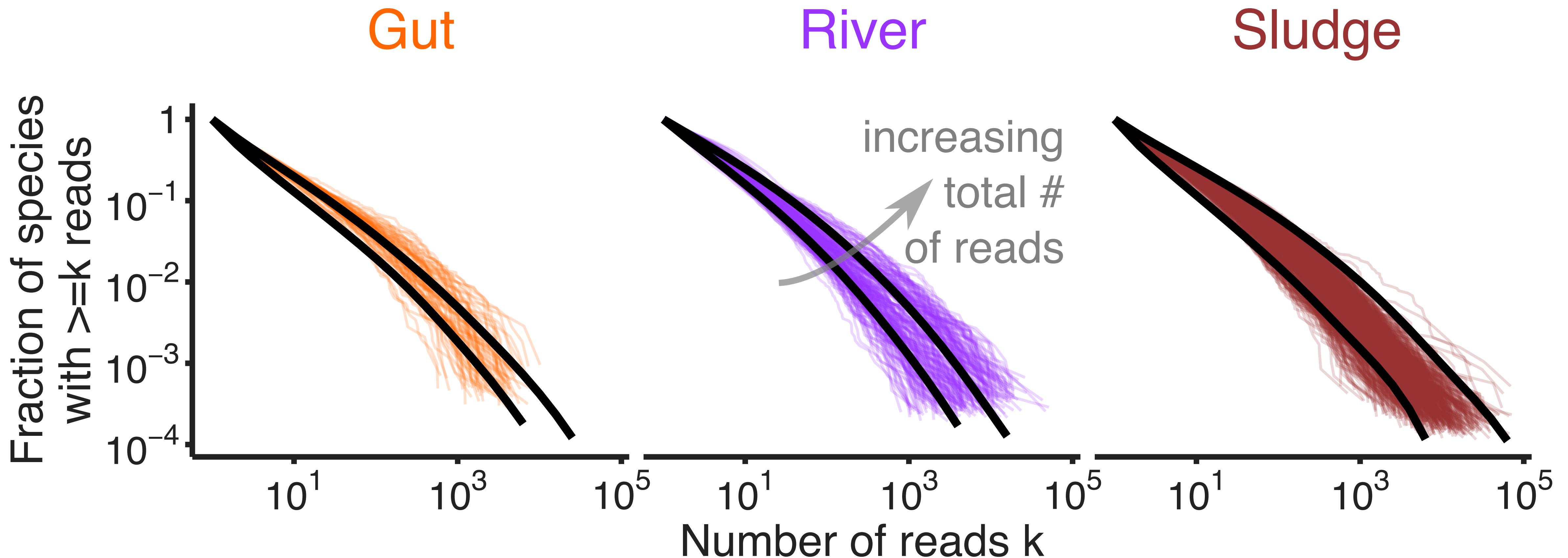
abundance

X absent

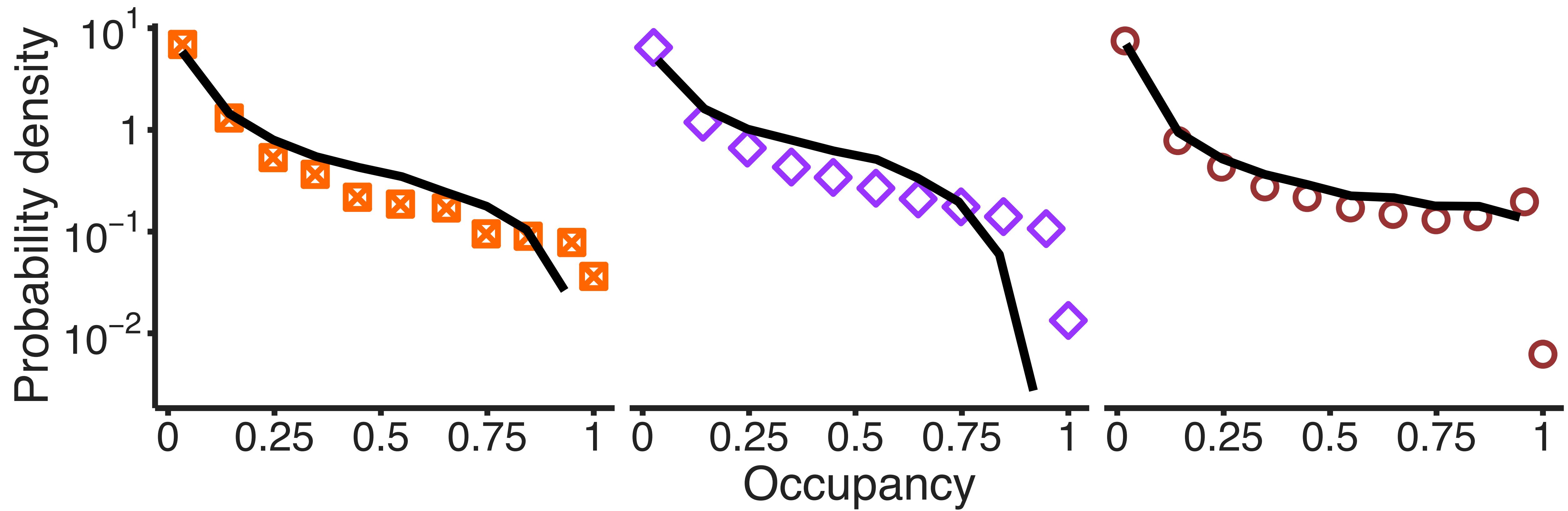
# From statistical regularities to other patterns



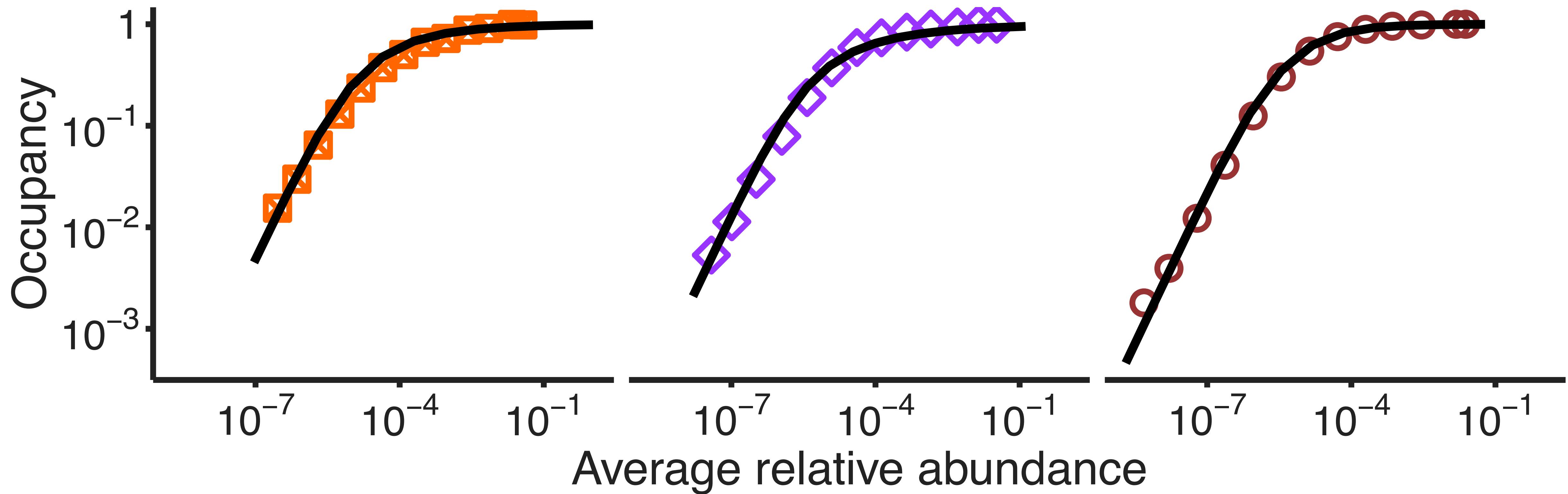
# From statistical regularities to other patterns

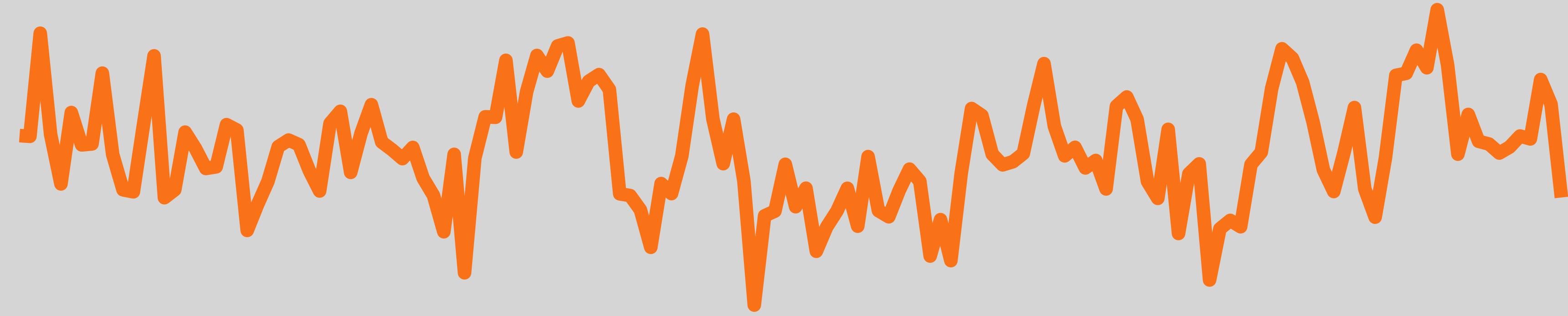


# From statistical regularities to other patterns



# From statistical regularities to other patterns





# Dynamics?

deterministic  
forces

$$\dot{x} = f(x) + \sqrt{D(x)}\xi(t)$$

stochastic  
forces

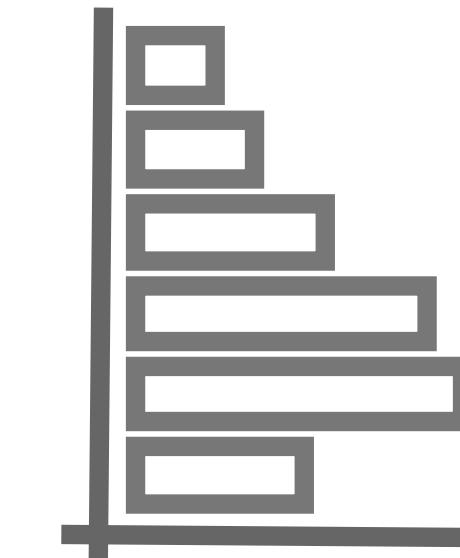
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at stationarity



~ gamma

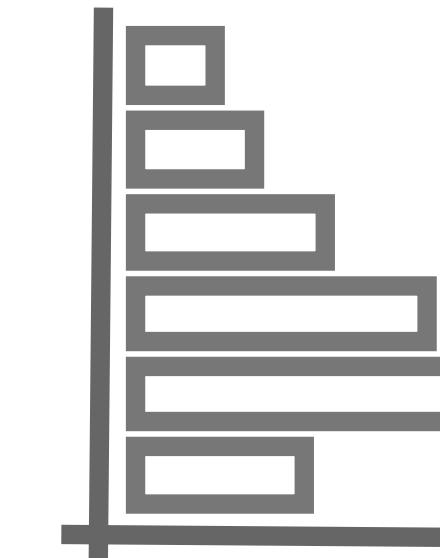
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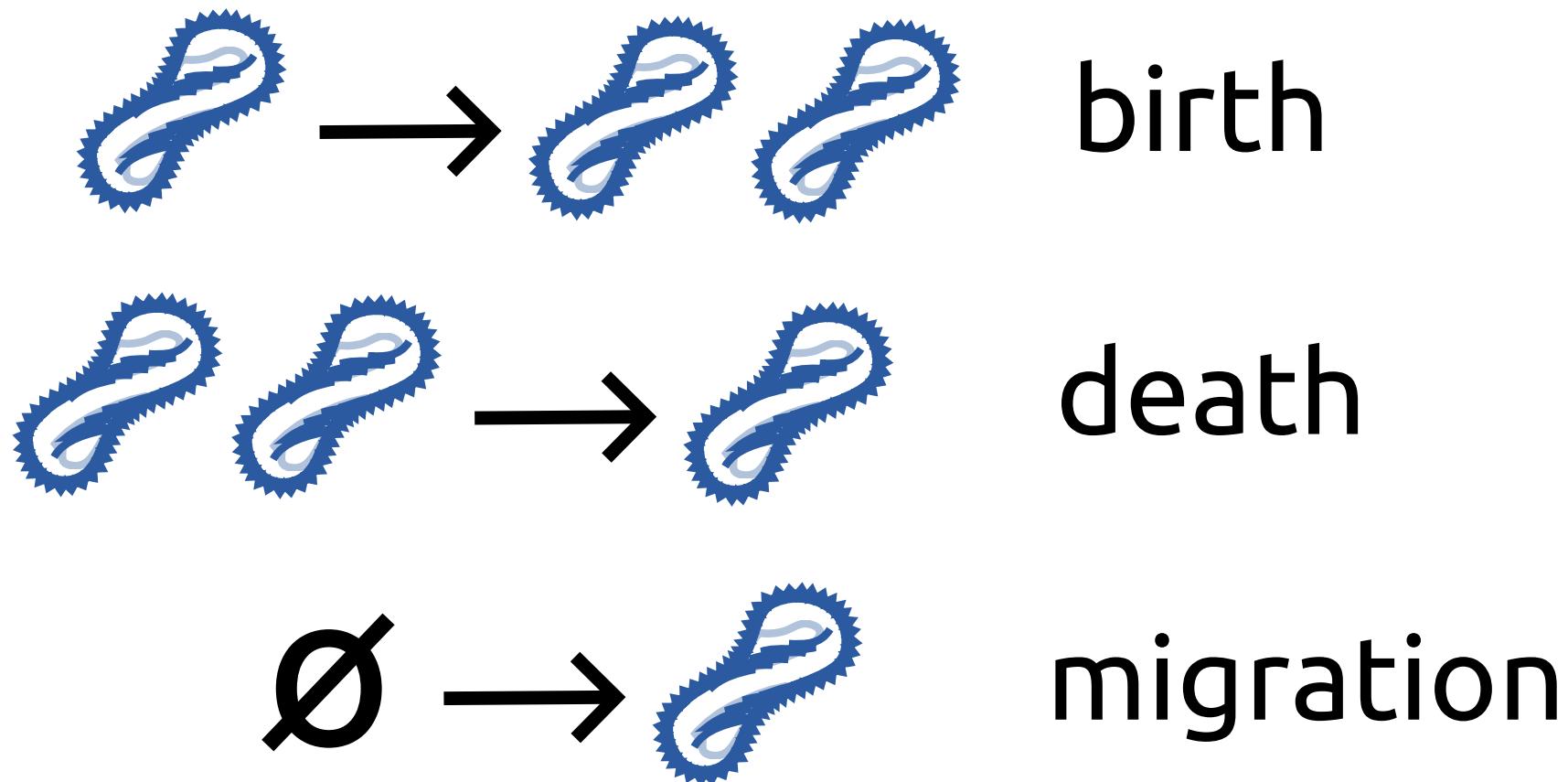


~ gamma

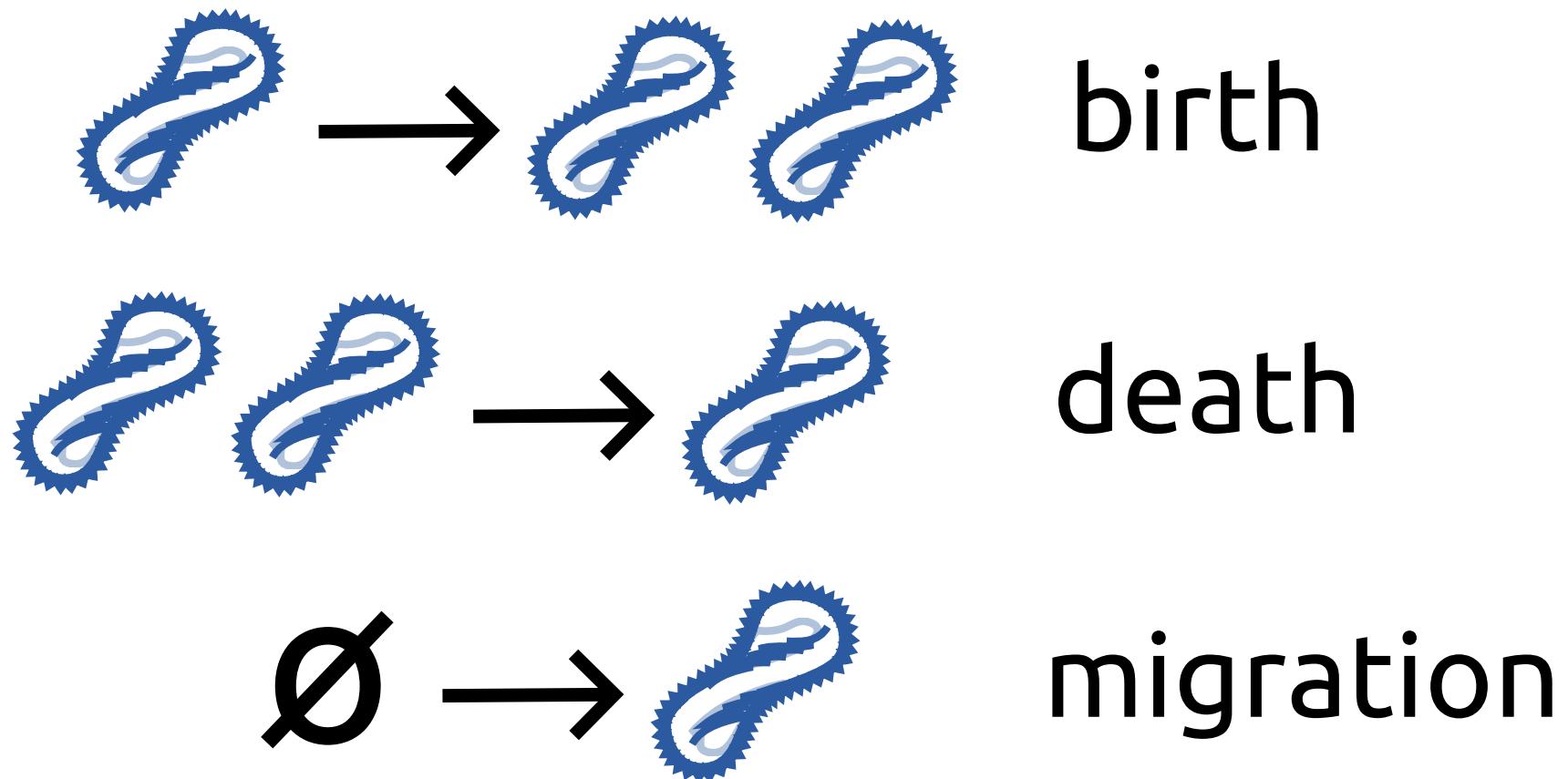
$$-\log D(x) + \int^x dz \frac{f(z)}{D(z)} = a - bx + c \log(x)$$

# **Two alternative models**

# Two alternative models



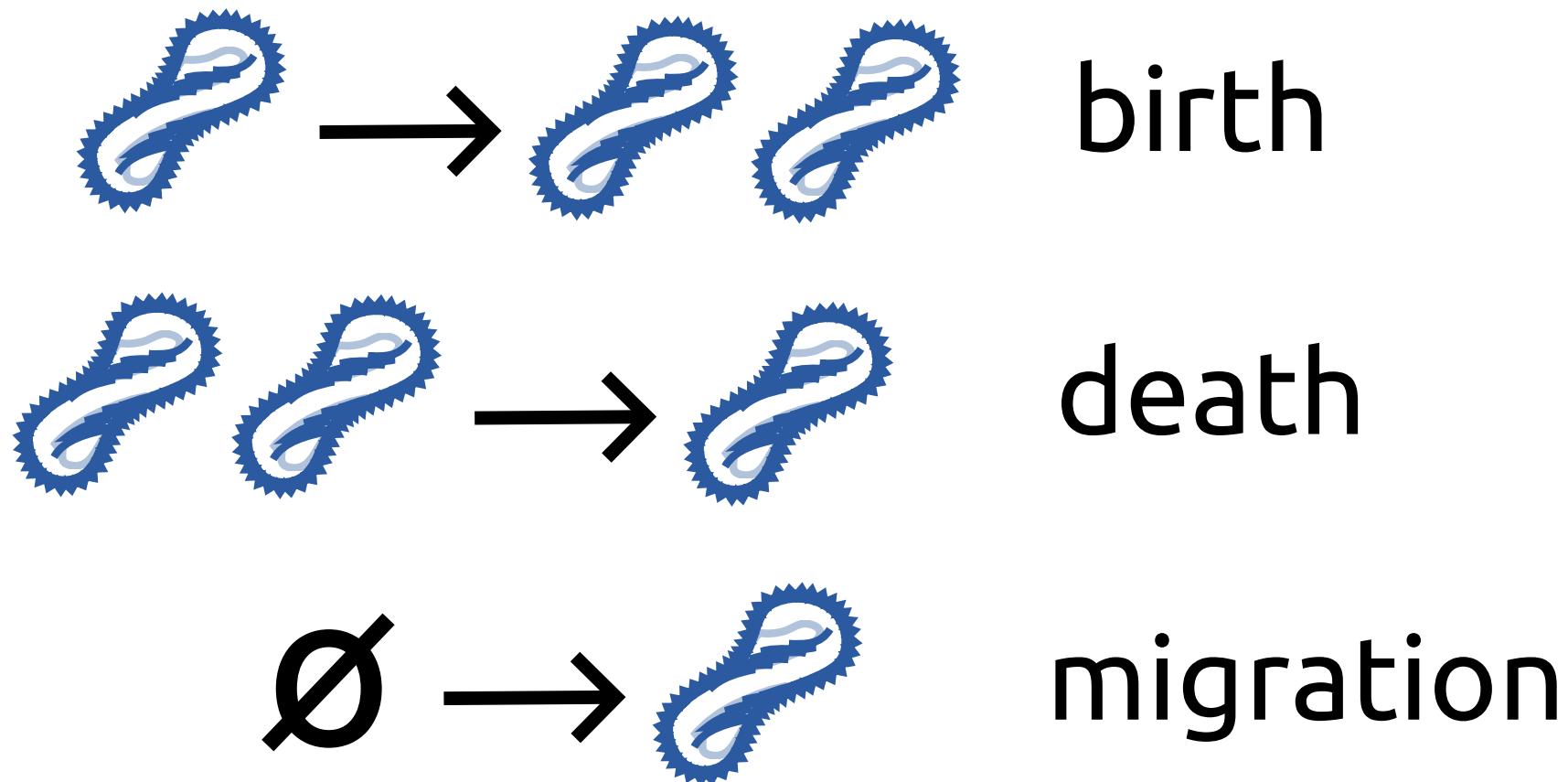
# Two alternative models



demographic  
stochasticity

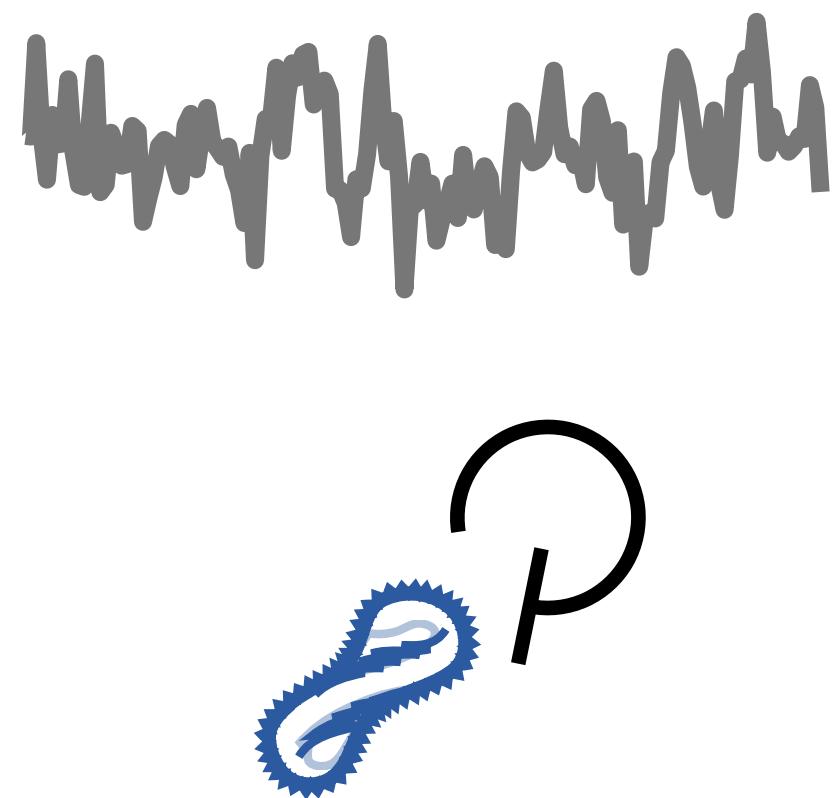
$$\dot{x} = -\frac{1}{\tau} (x^* - x) + \sqrt{\frac{\sigma}{\tau}} x \xi(t)$$

# Two alternative models



demographic  
stochasticity

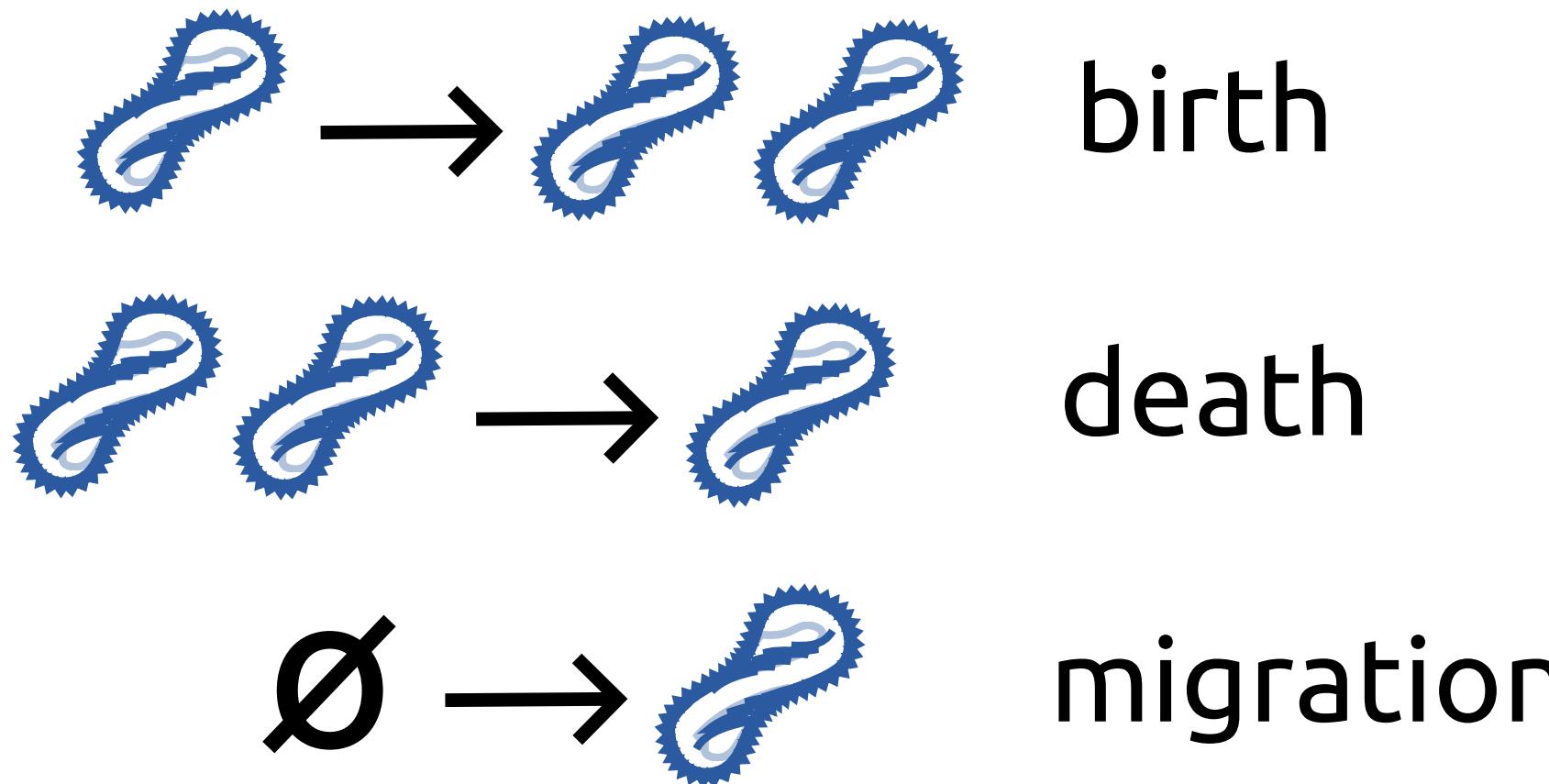
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fluctuating  
environment

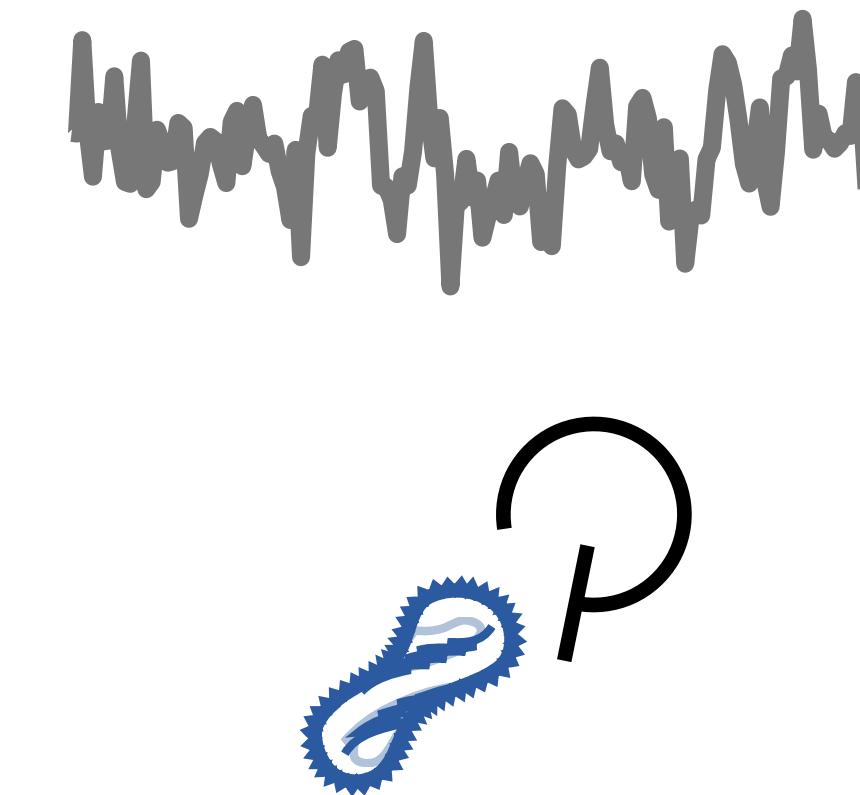
self-limited  
growth

# Two alternative models

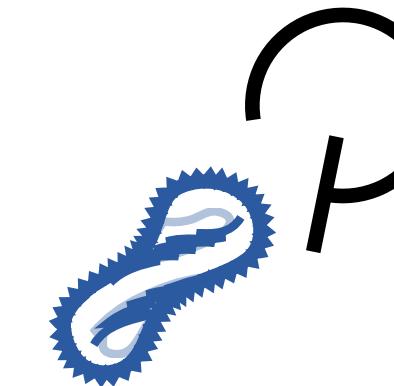


demographic  
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fluctuating  
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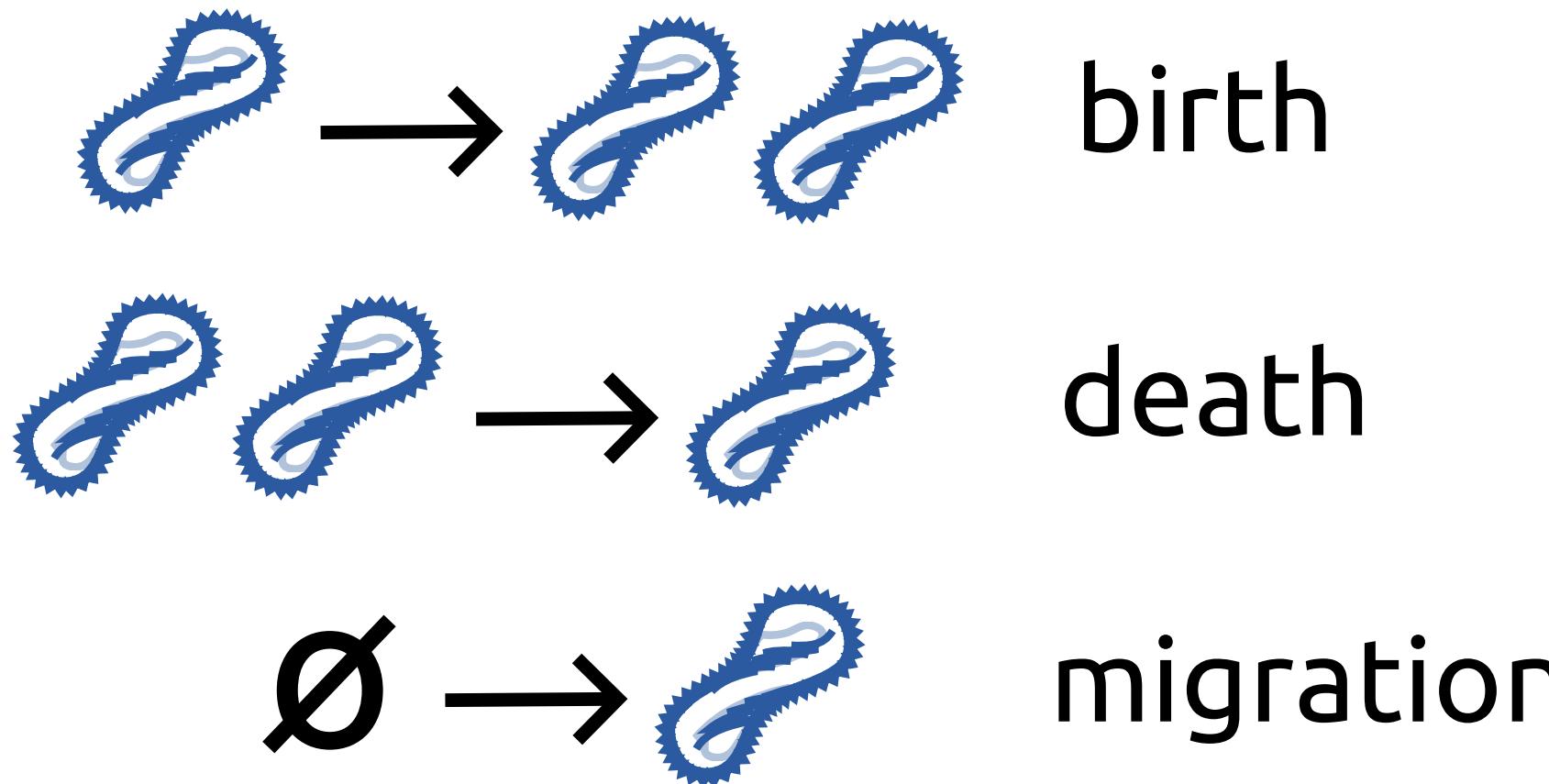


self-limited  
growth

environmental  
stochasticity

$$\dot{x} = \frac{x}{\tau} \left( 1 - \frac{x}{K} \right) + \sqrt{\frac{\sigma}{\tau}} x \xi(t)$$

# Two alternative models

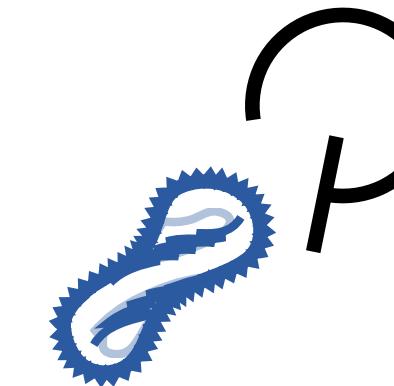


demographic  
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fluctuating  
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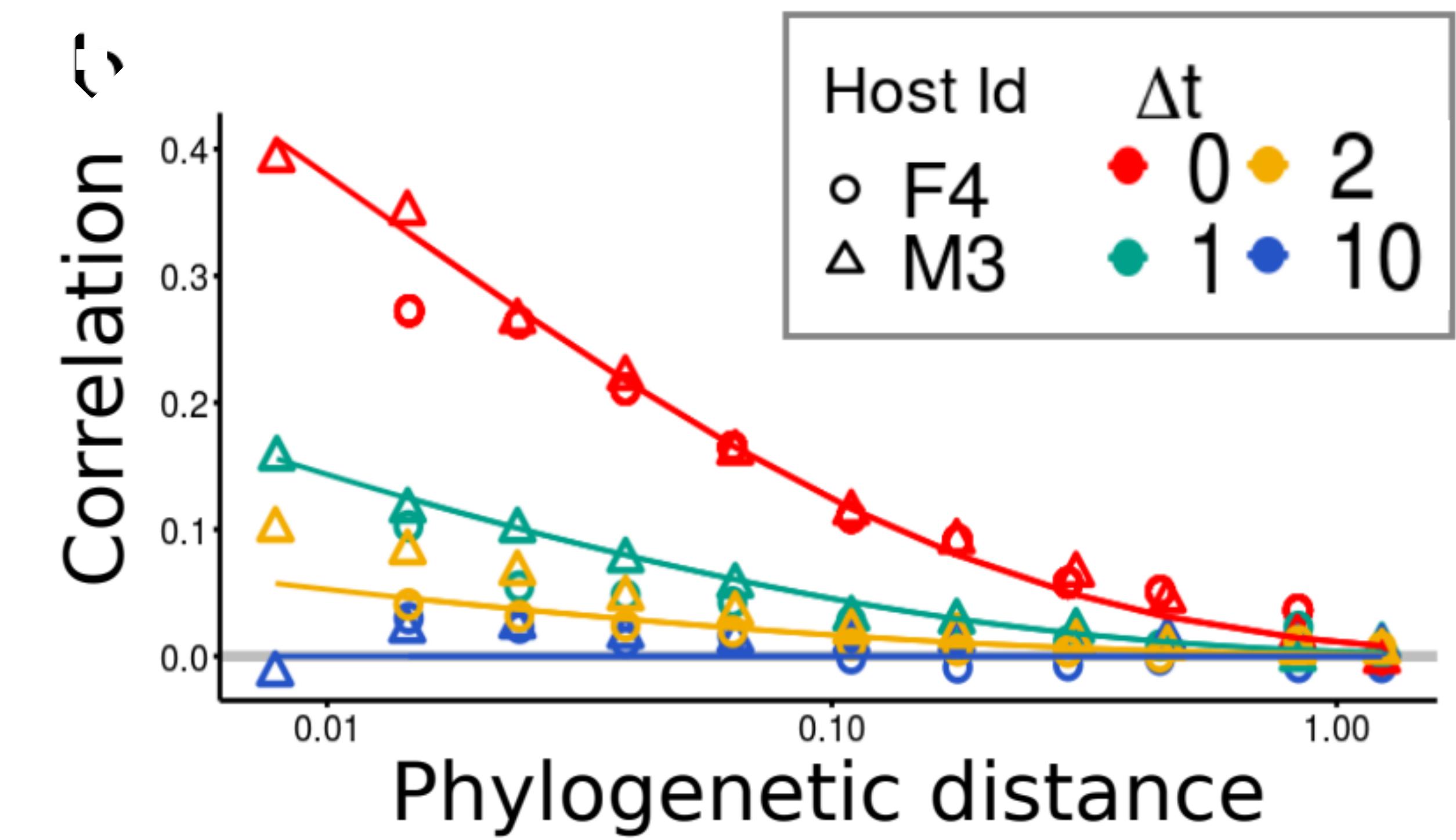
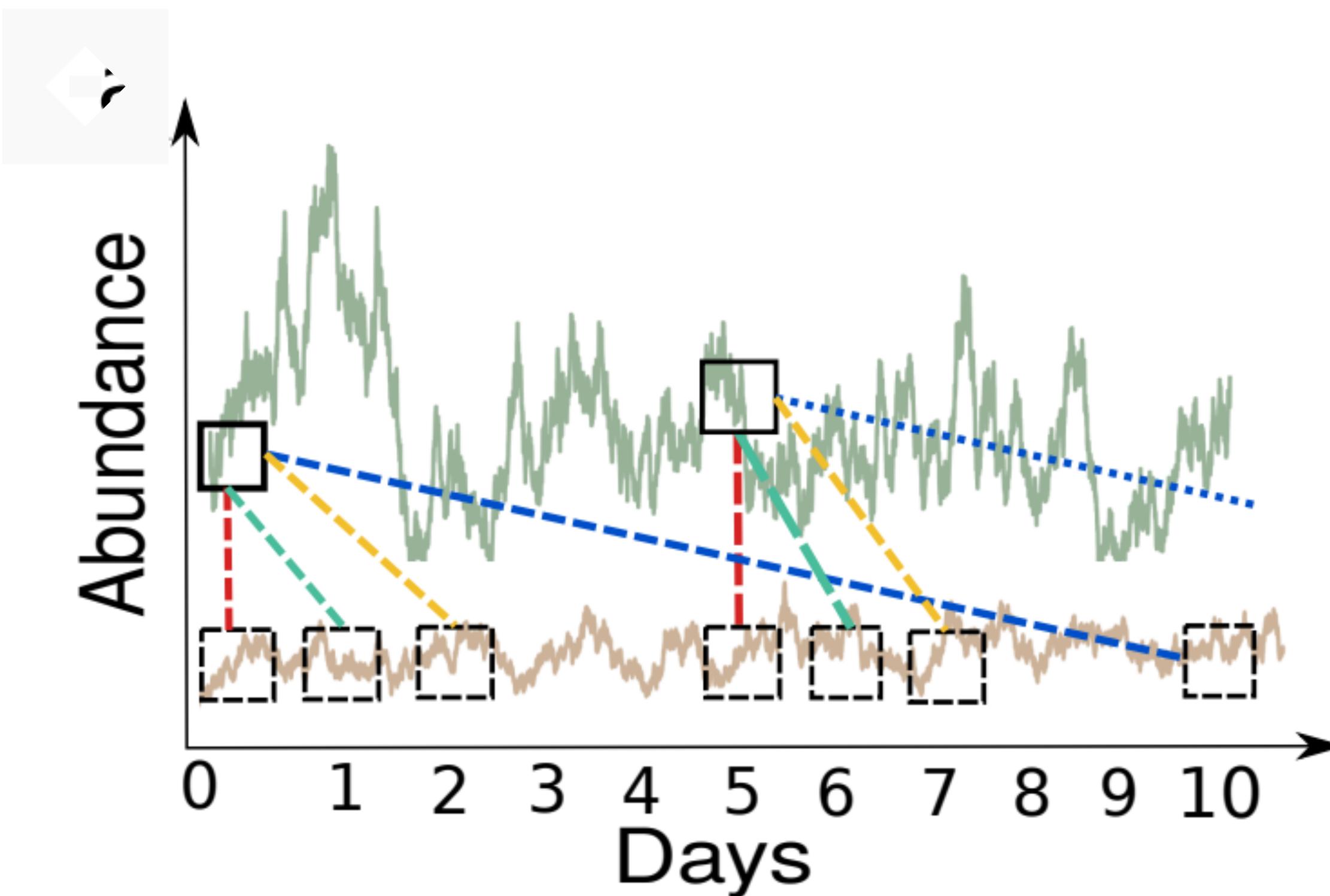


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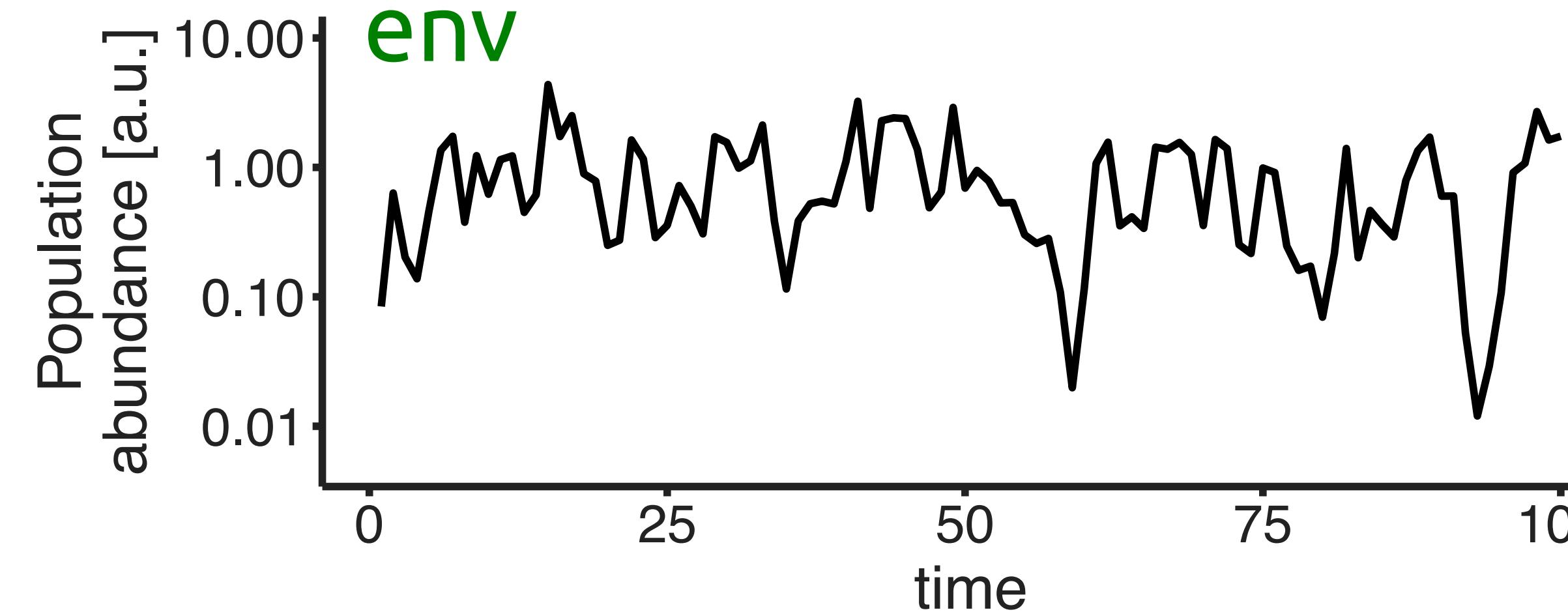
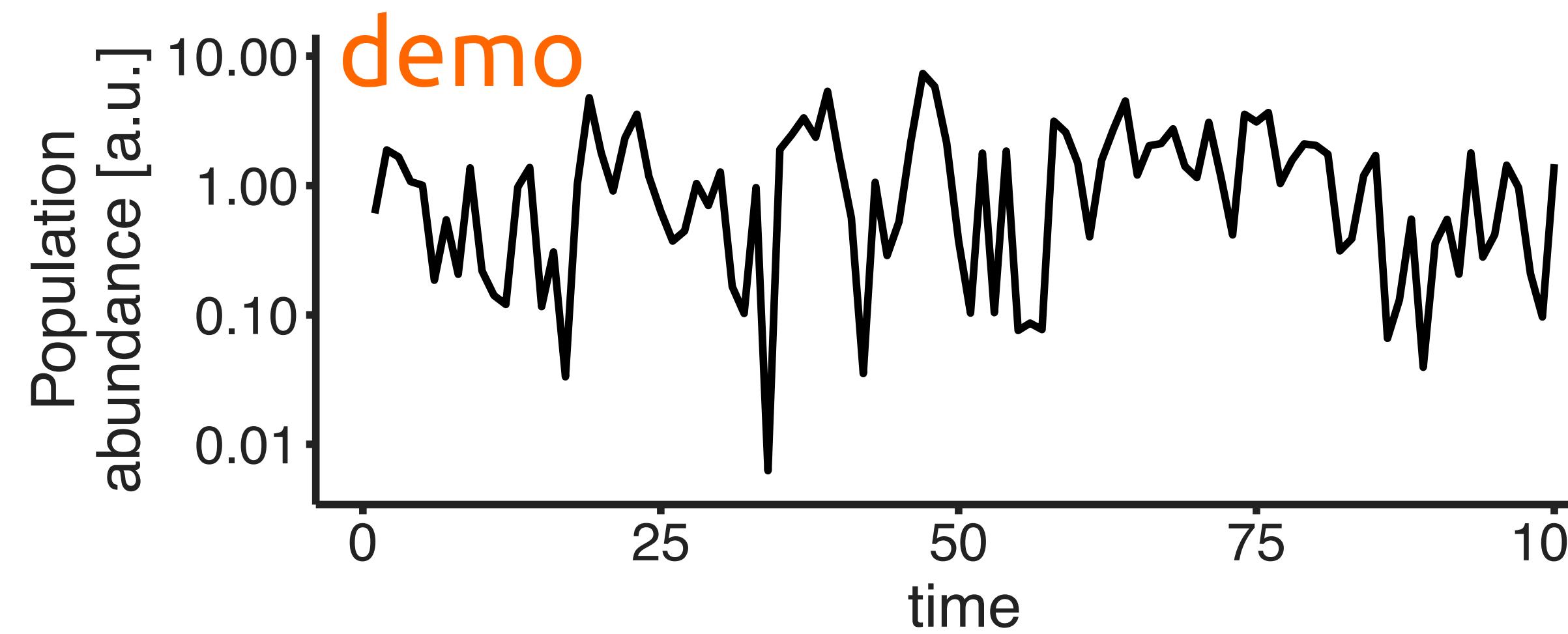
# Similar species are positively correlated consistently with environmental fluctuations



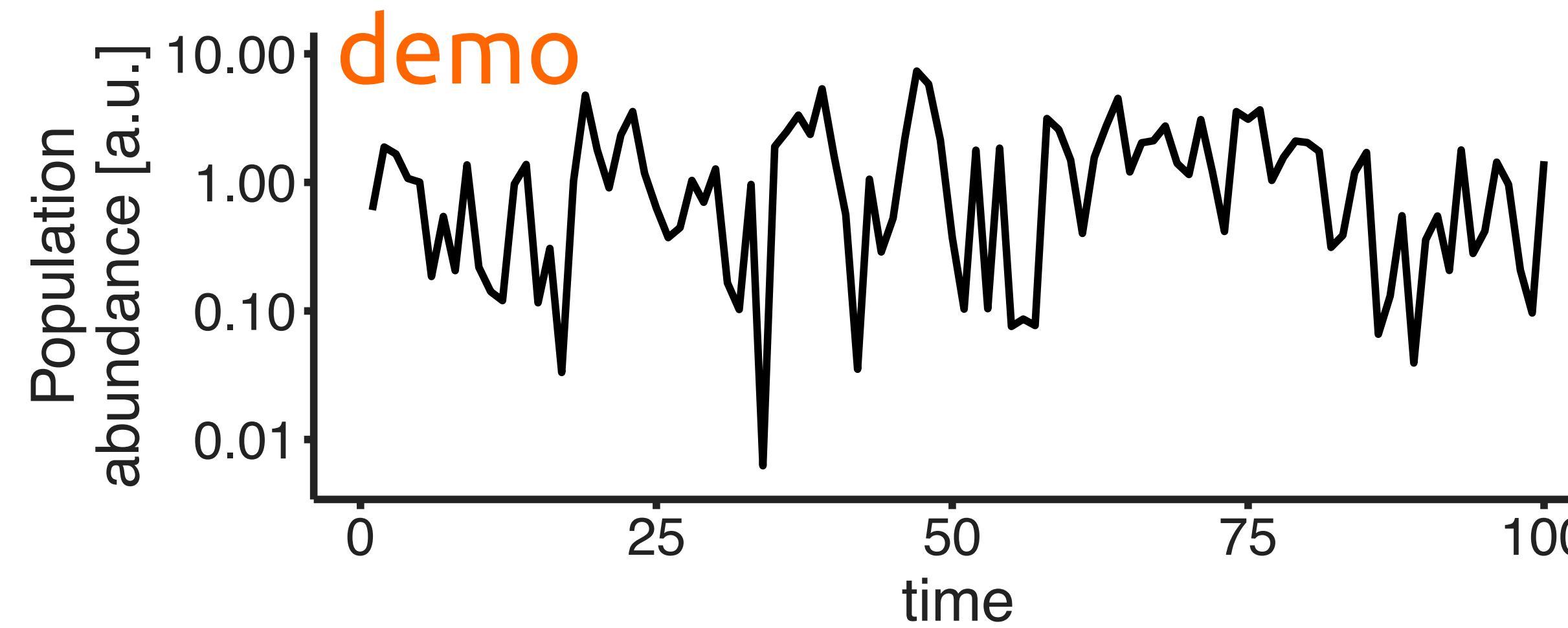
Sireci, Muñoz, Grilli PNAS 2023

**...indirect evidence  
what about dynamics?**

# How do we differentiate between trajectories



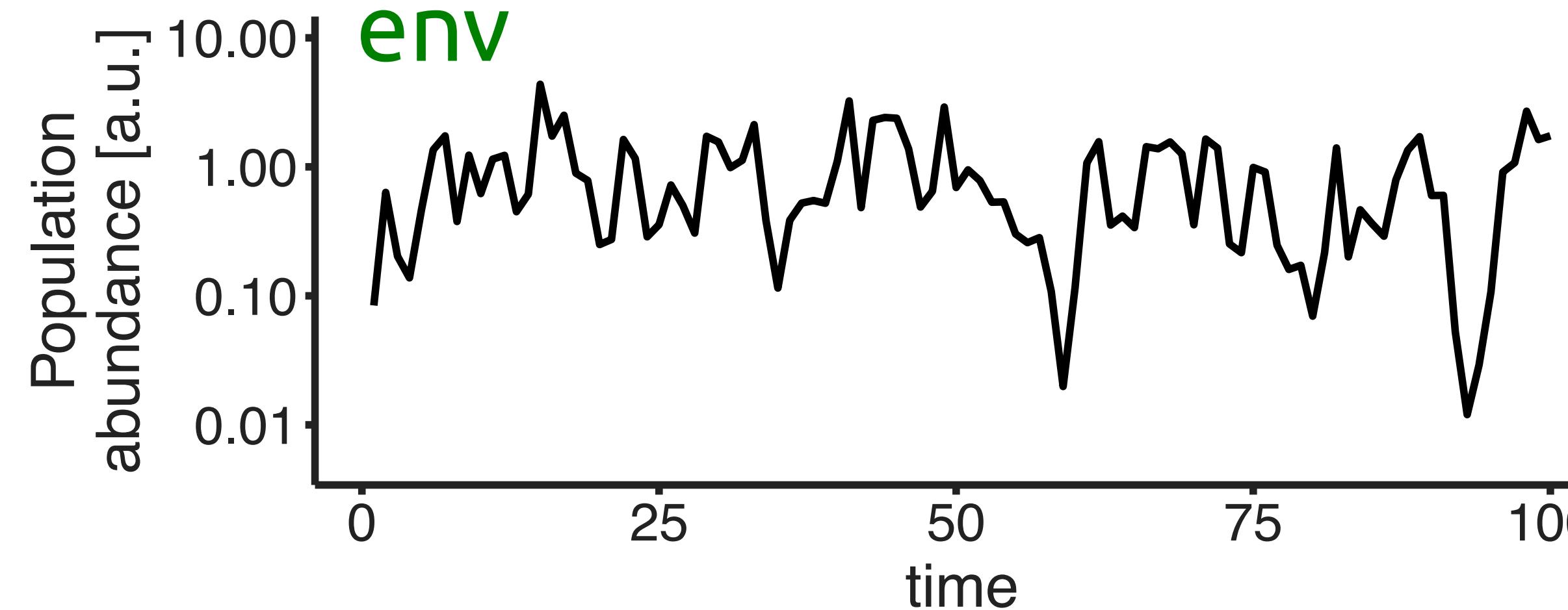
# How do we differentiate between trajectories



different

$$P(x, t + \tau | x_0, t)$$

same



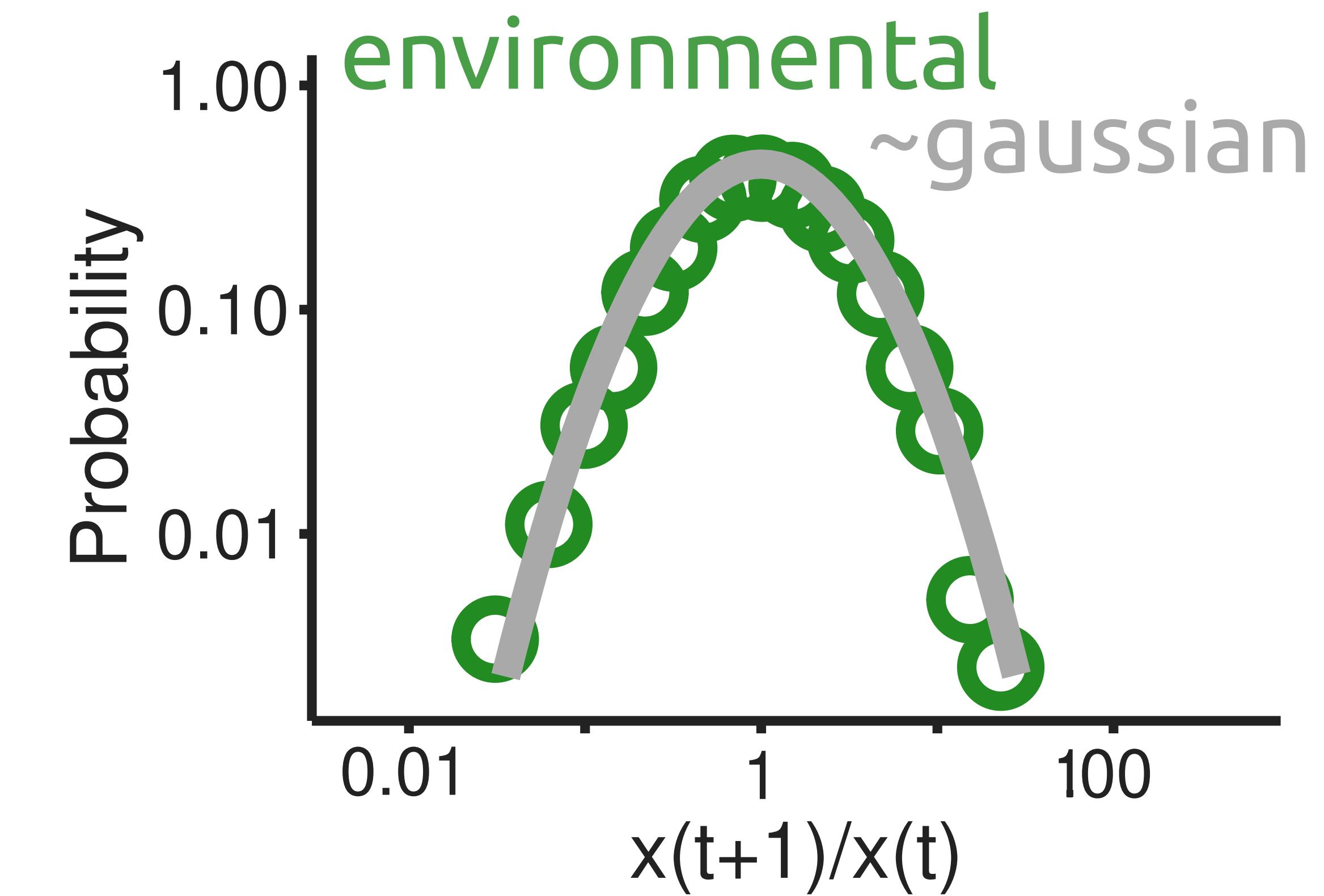
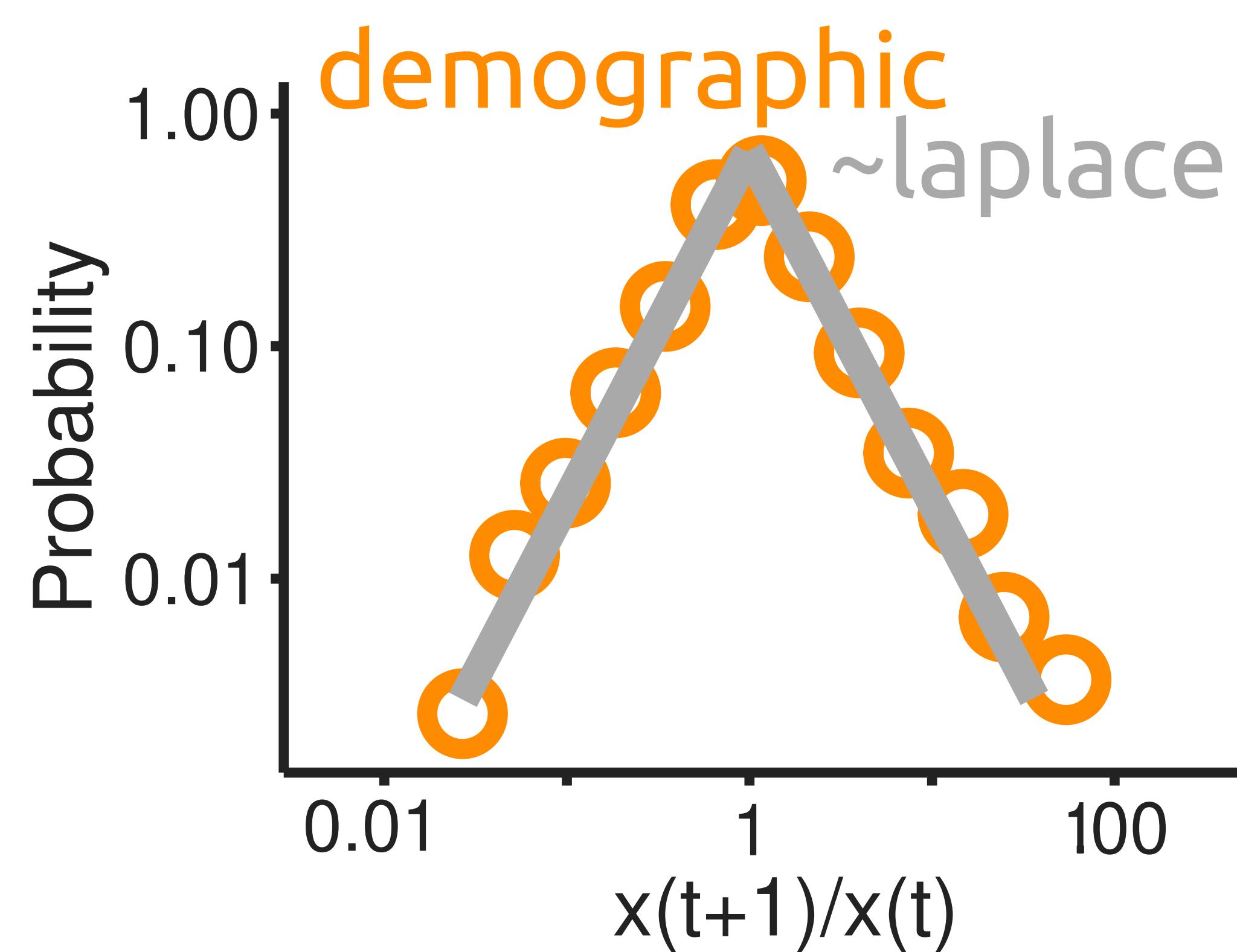
$$P^*(x) =$$

$$\lim_{t \rightarrow \infty} P(x, t | x_0, 0)$$

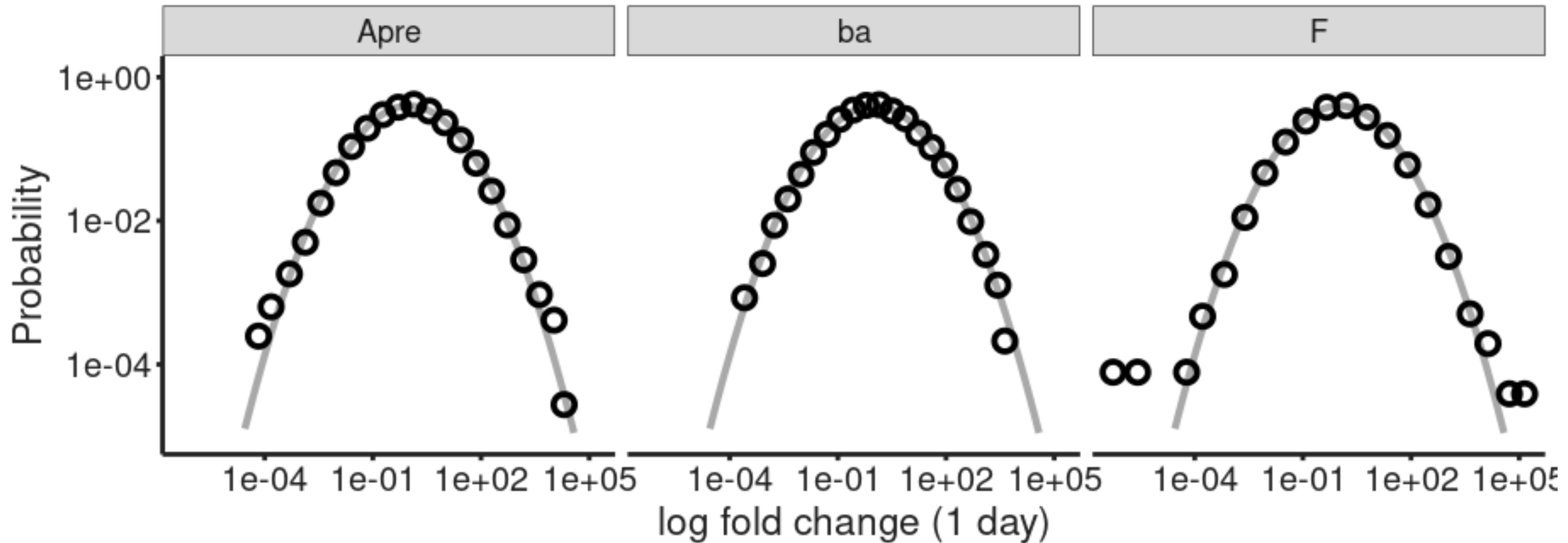
# Alternative predictions for log change distr

$$r = \log \left( x(t + \tau)/x(t) \right)$$

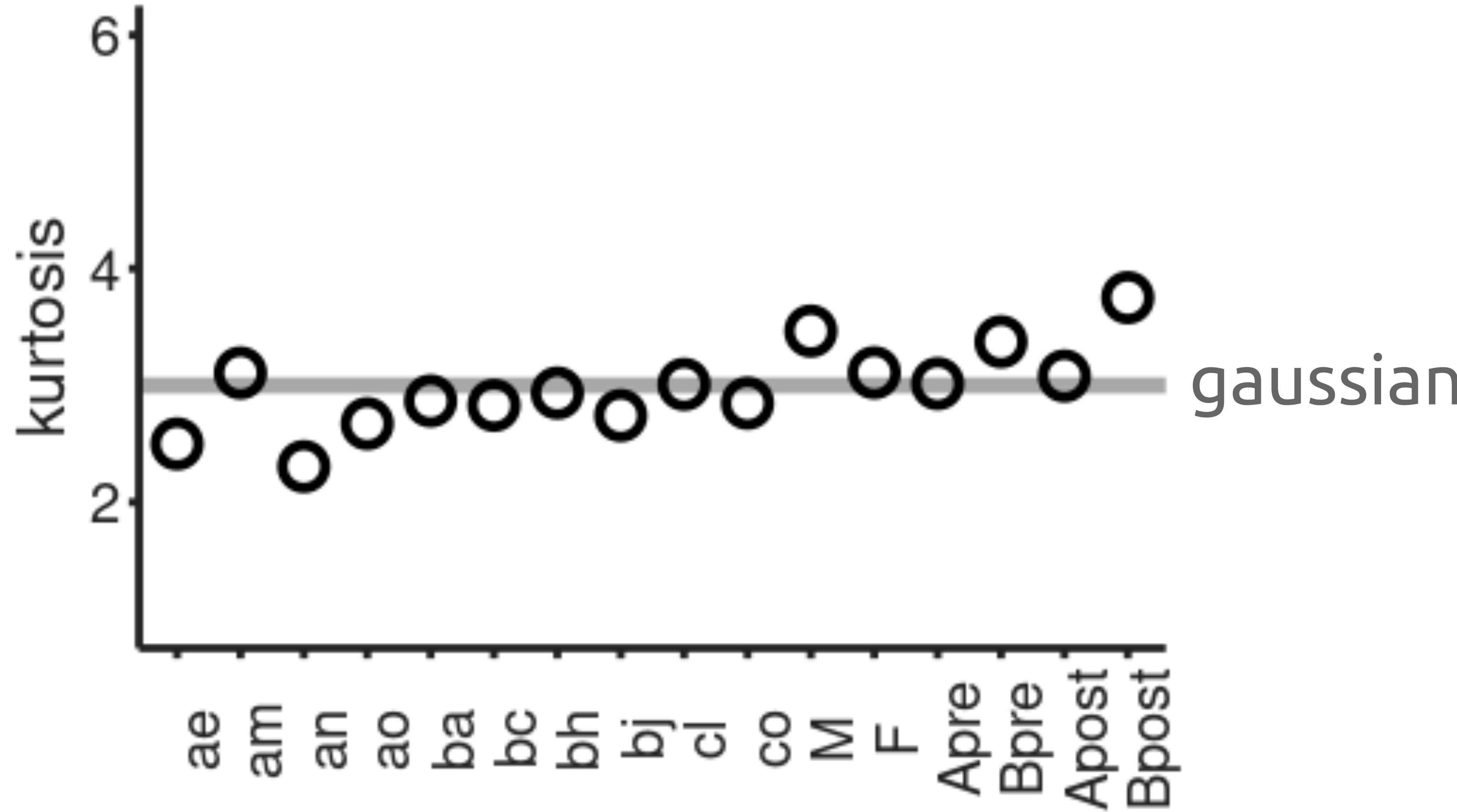
$$P^*(r) = ?$$



# Log-rate change is Gaussian in data

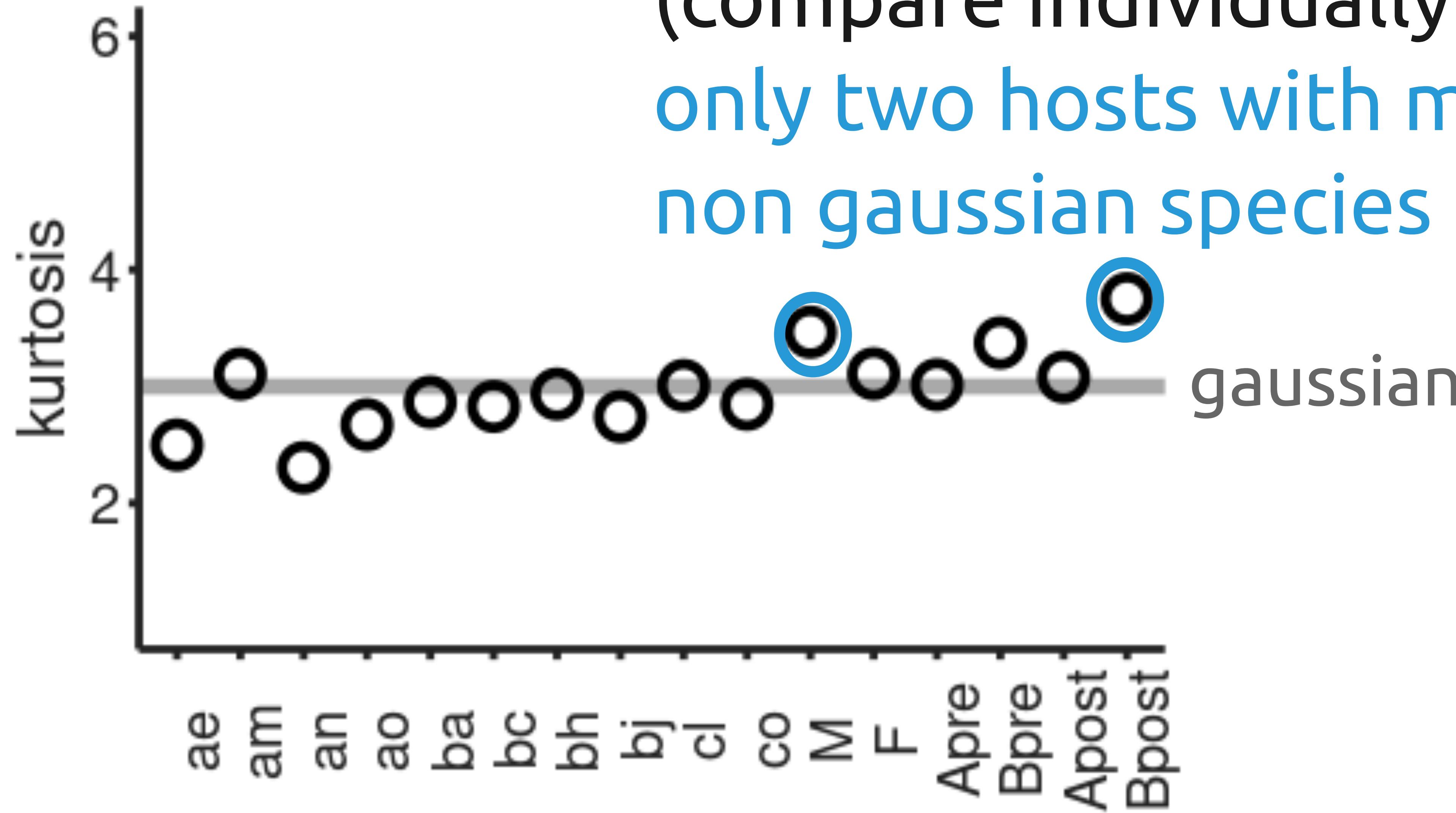


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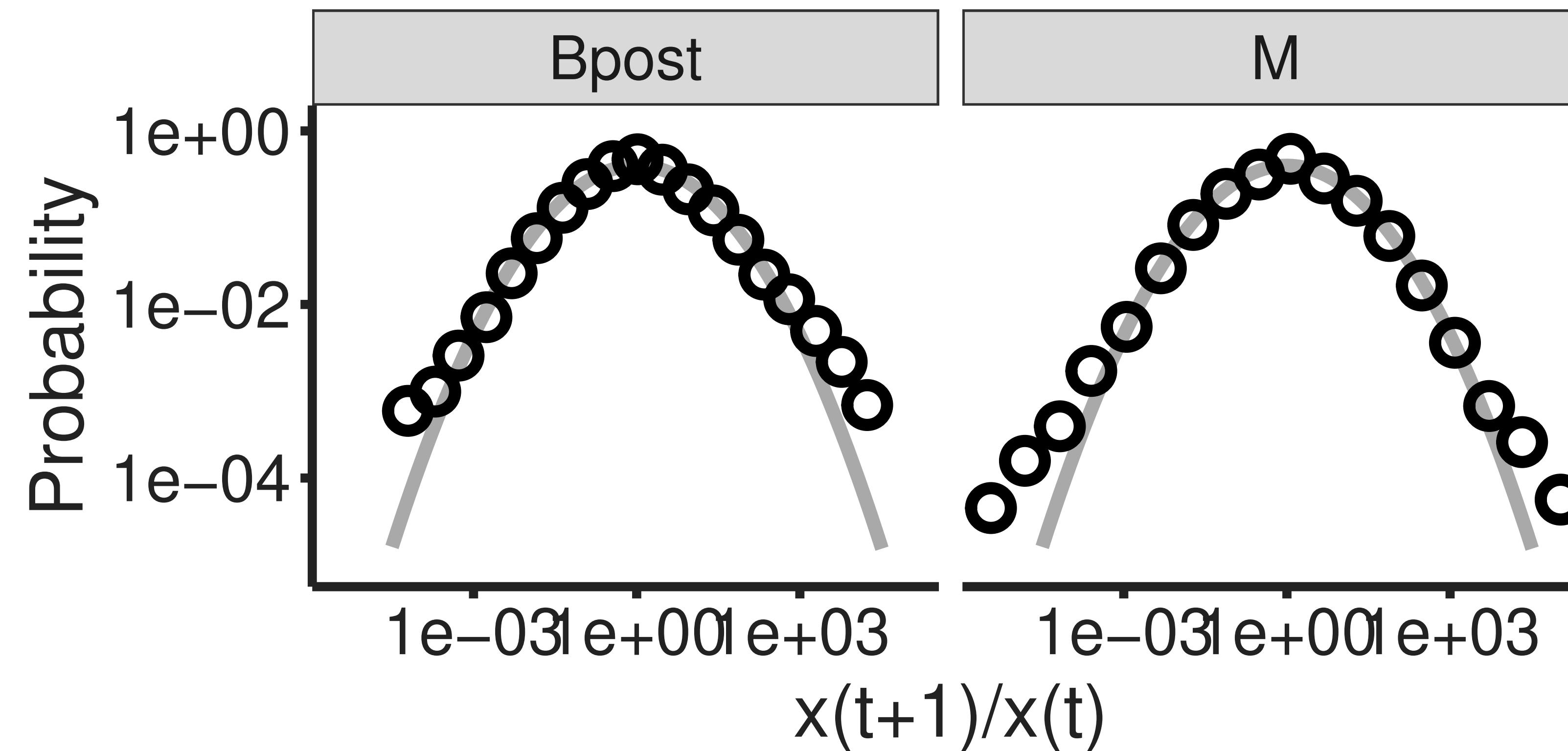


# Log-rate change is Gaussian in data

(compare individually per sp)  
only two hosts with more  
non gaussian species

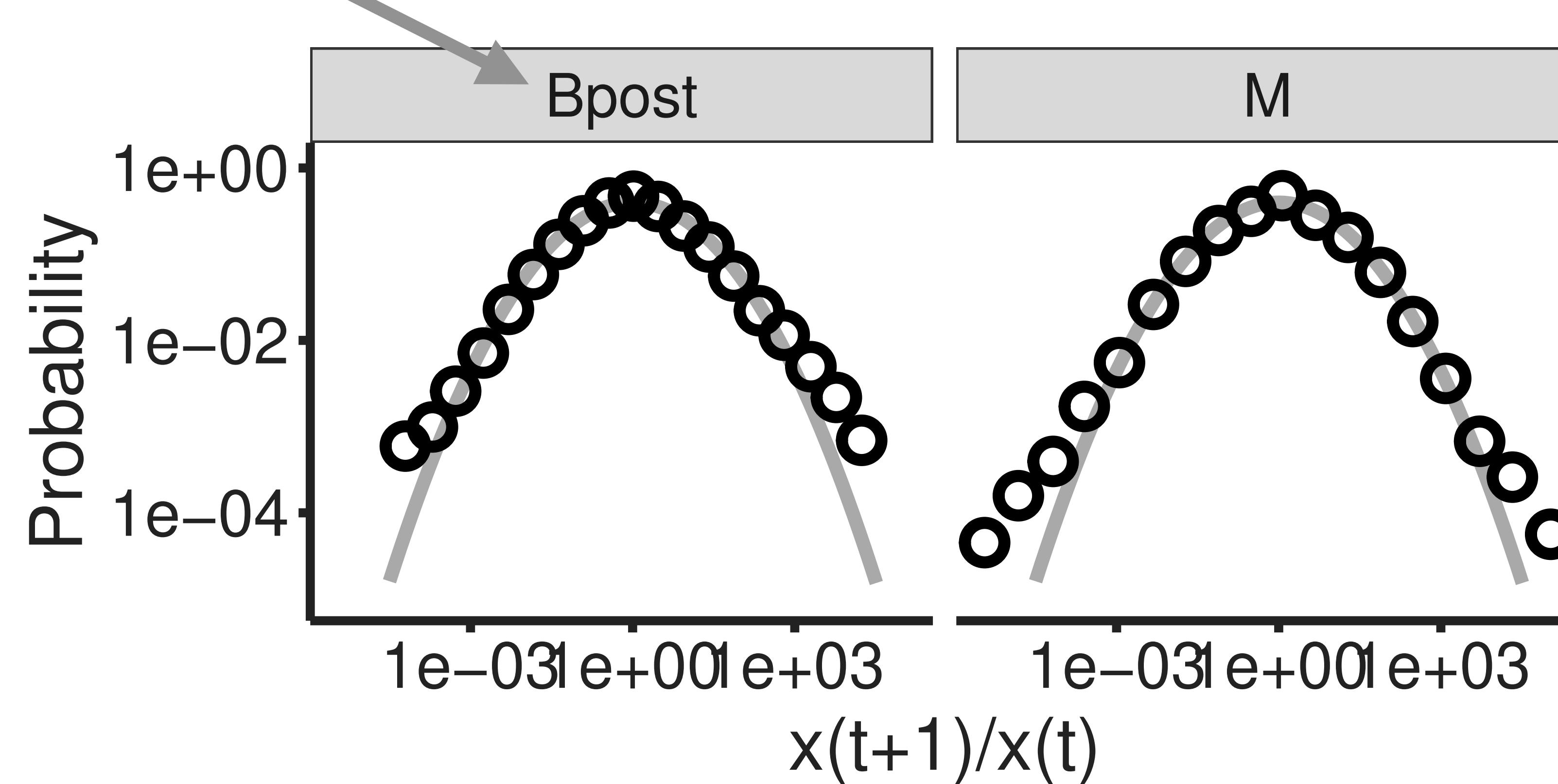


# Two hosts have non-gaussian log-fold changes

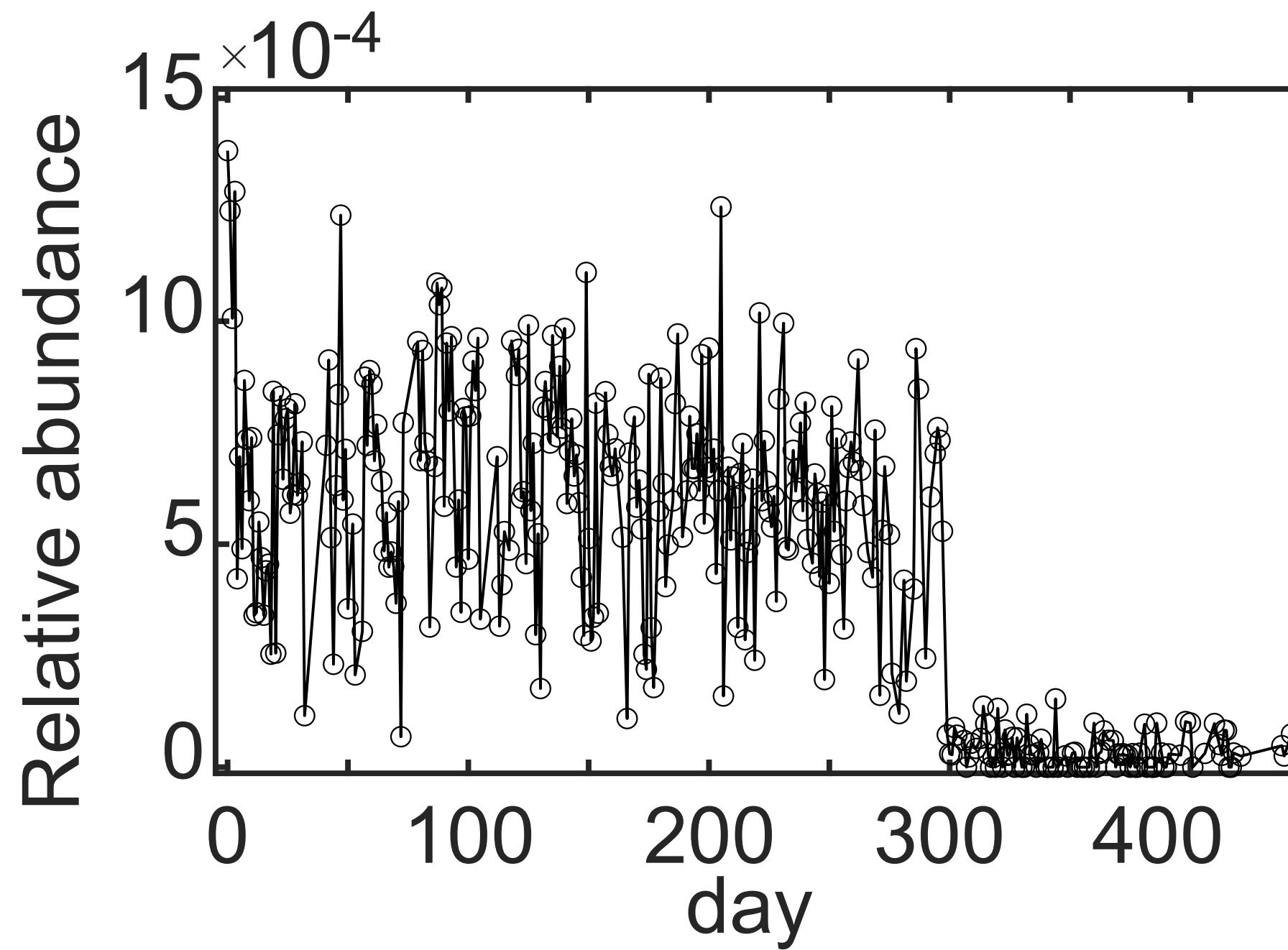


# Two hosts have non-gaussian log-fold changes

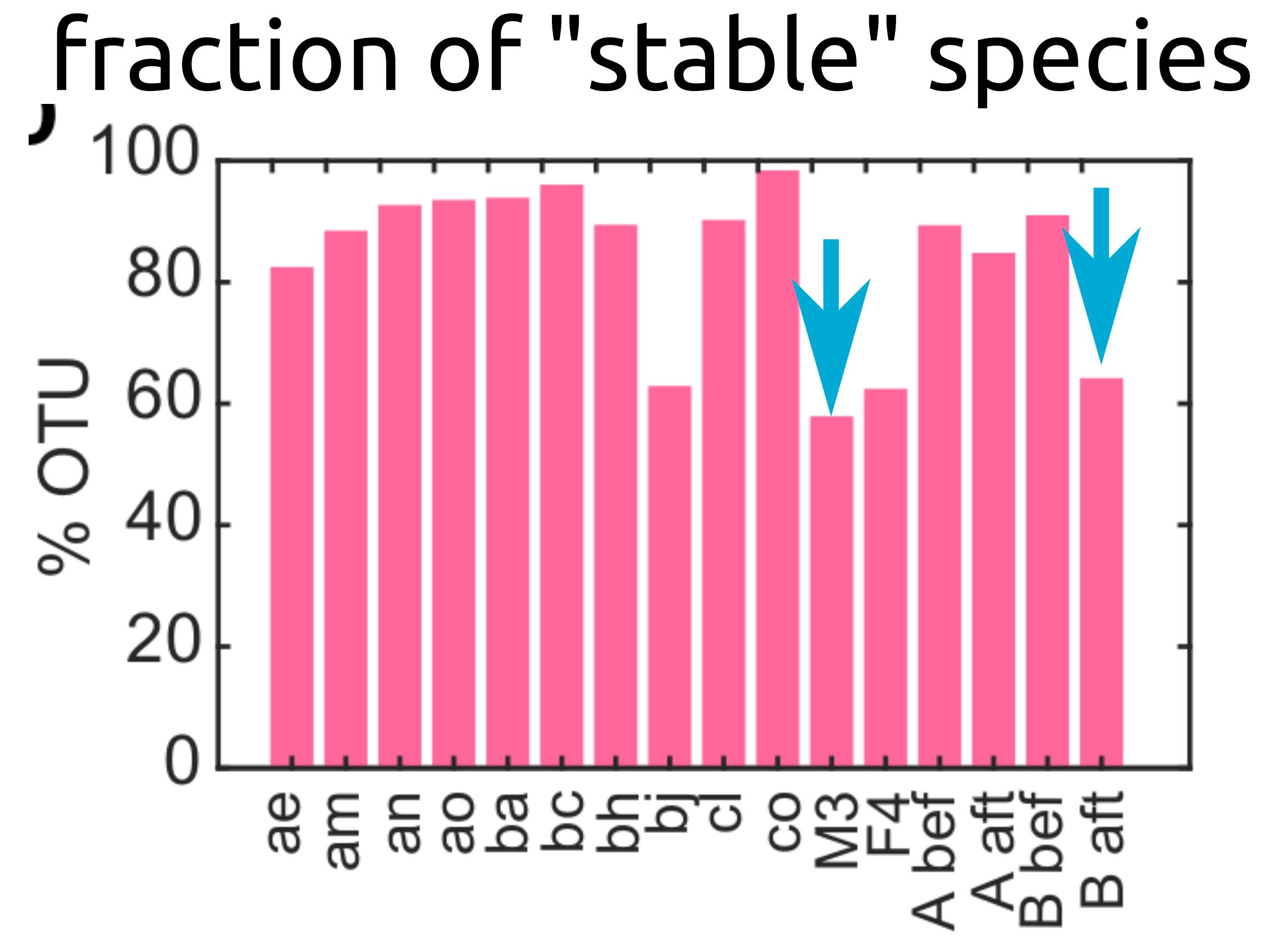
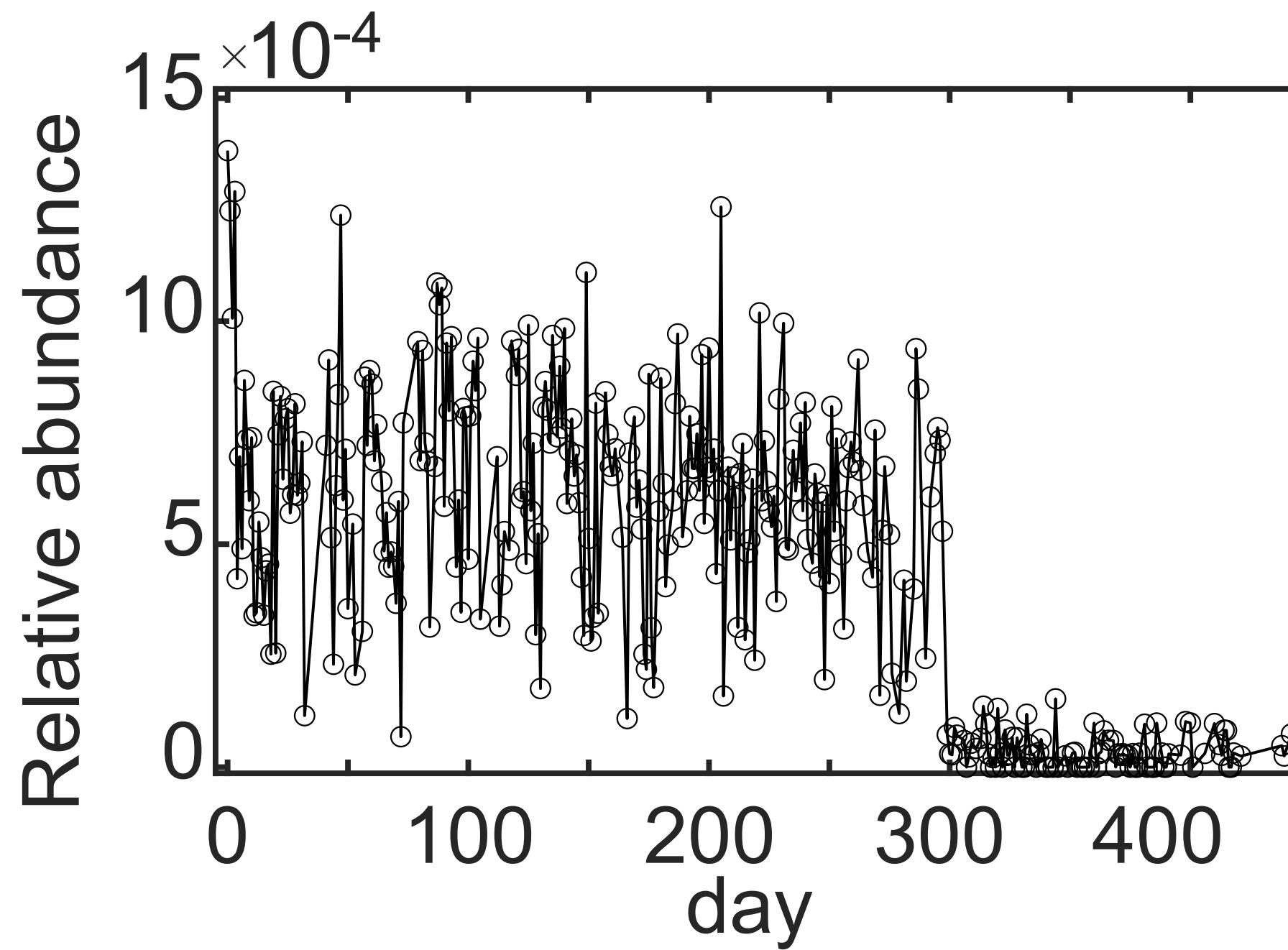
post salmonella infection



# There exist unstable species on long timescales



# There exist unstable species on long timescales



# Removing unstable species recover gaussianity

