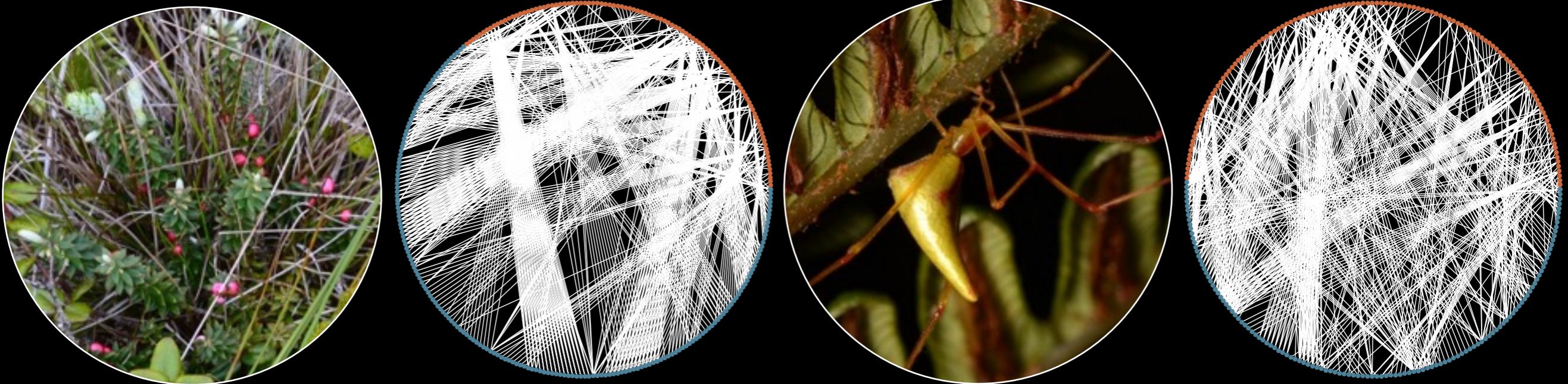


# Isolated islands untangle universal patterns at the nexus of macroevolution and macroecology

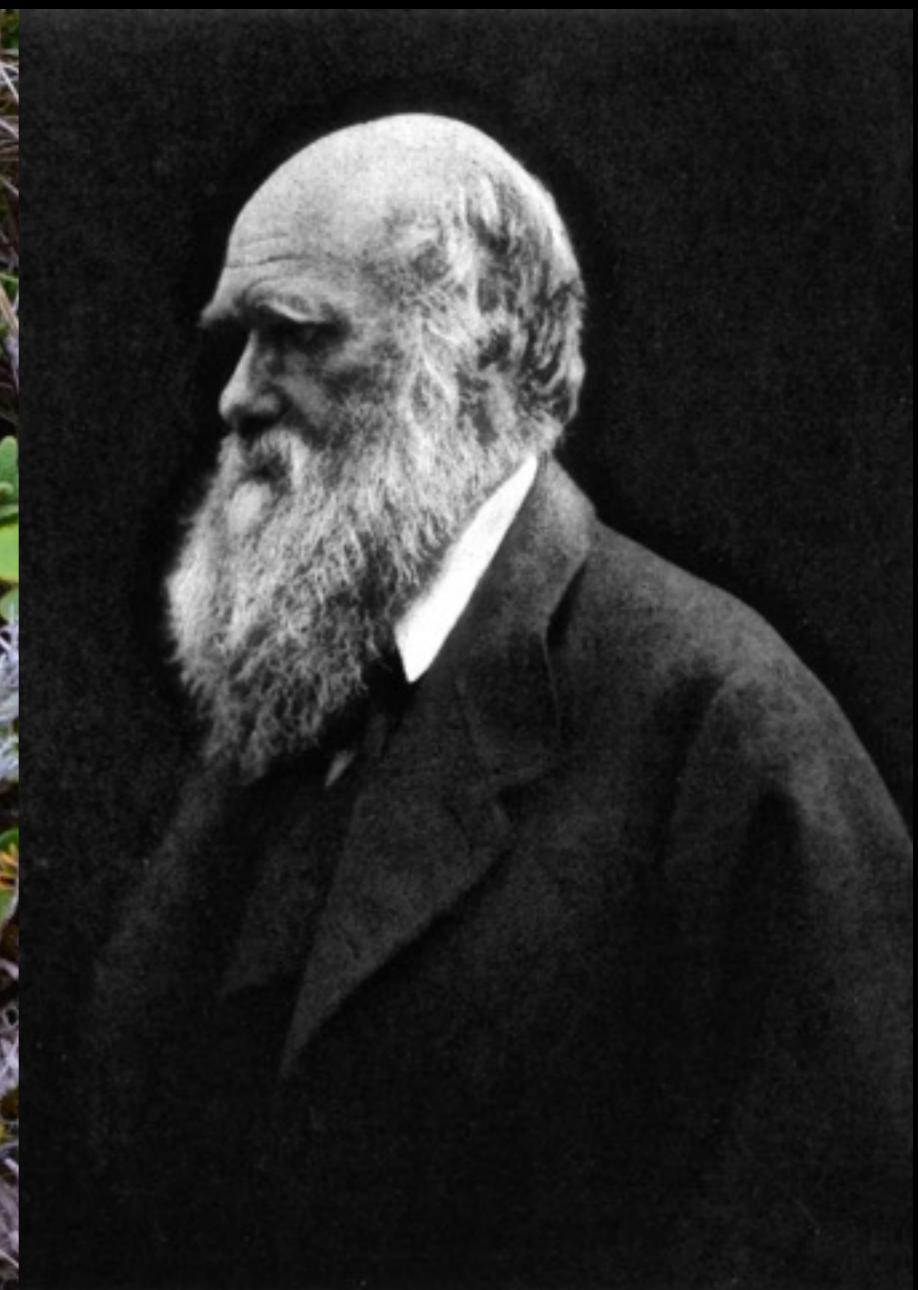


Andy Rominger

JY Lim, KR Goodman, J Harte, DS Gruner & RG Gillespie

Island Biology • 18 July 2016

# General biodiversity laws



# General biodiversity laws





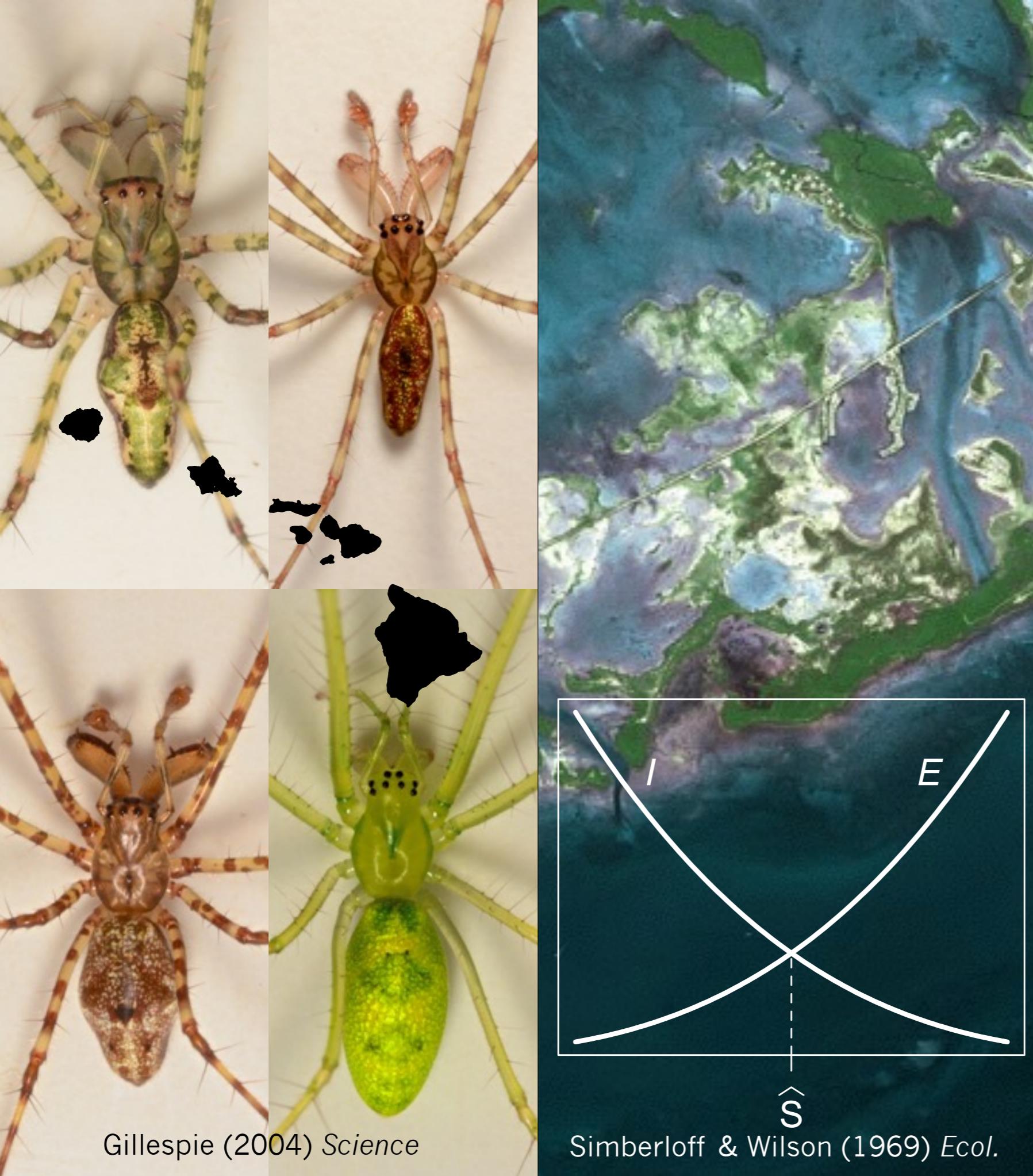
Gillespie (2004) Science



Gillespie (2004) *Science*



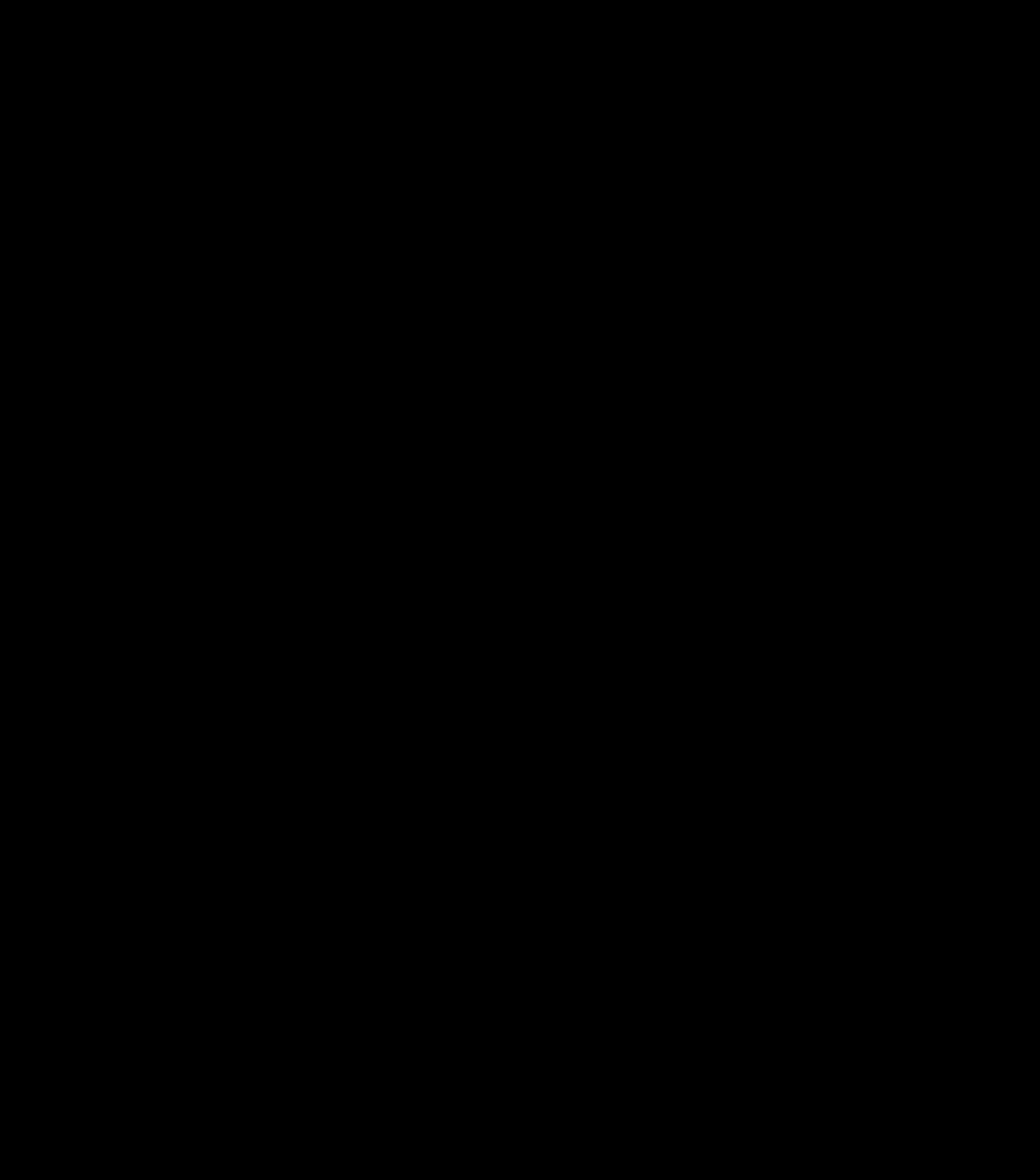
Simberloff & Wilson (1969) *Ecol.*



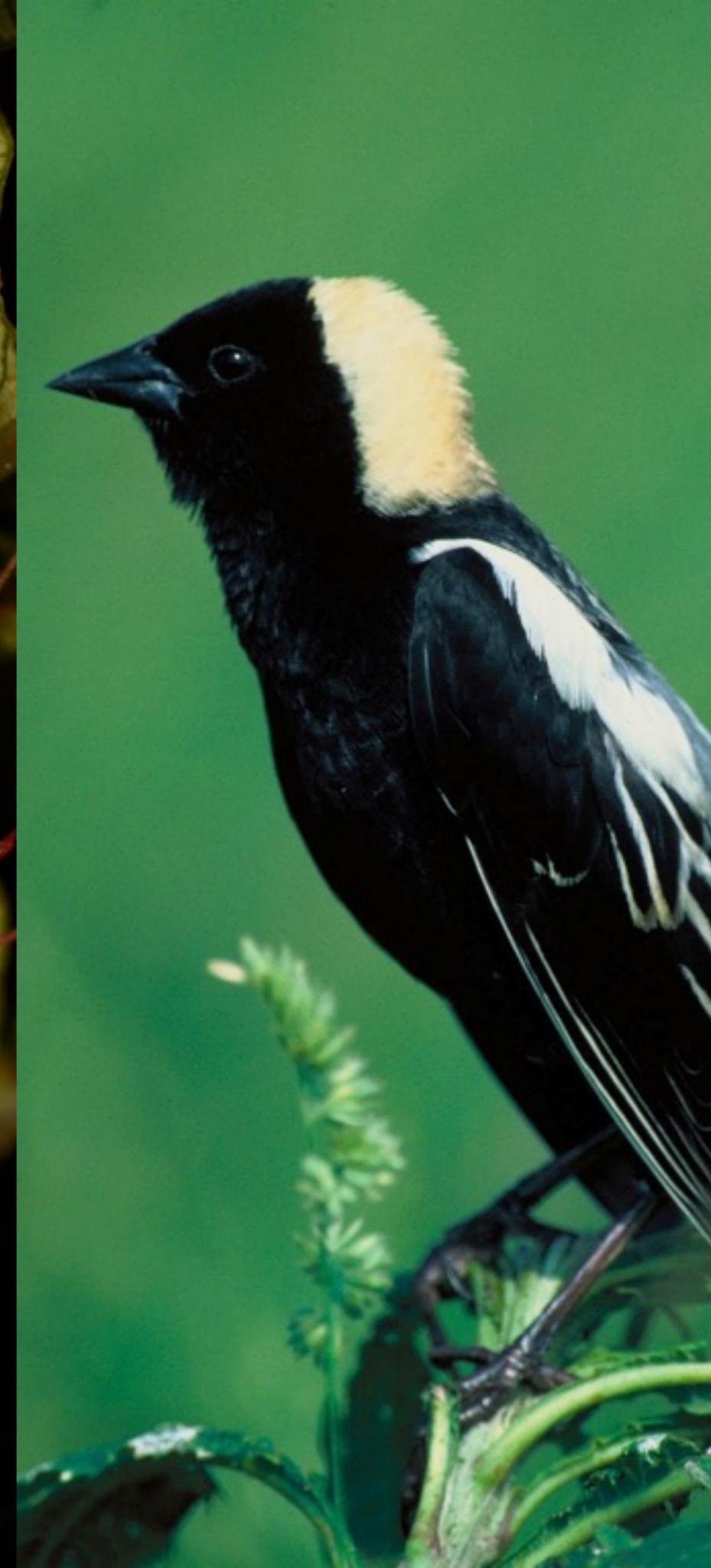
Simberloff & Wilson (1969) Ecol.

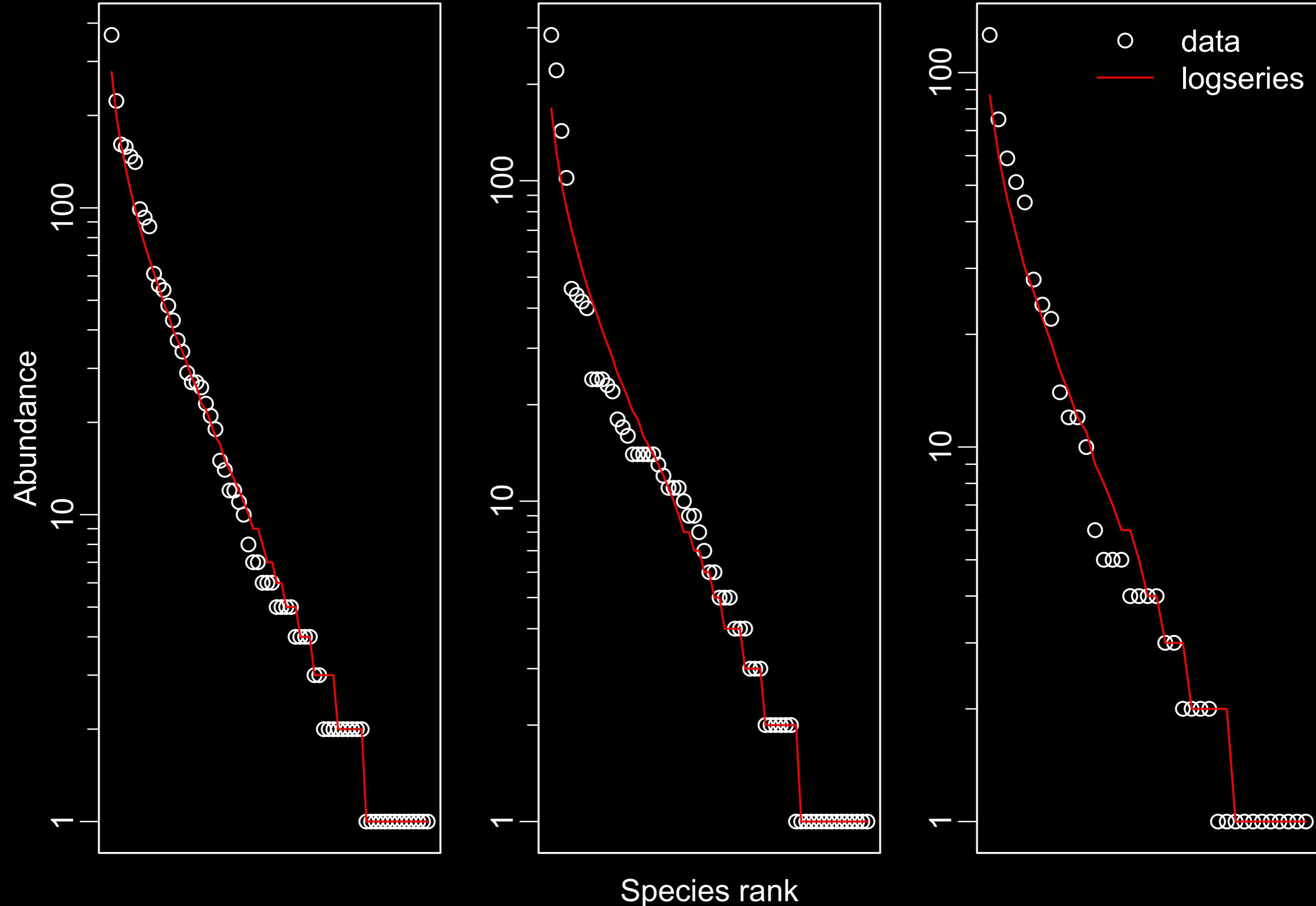


# Emergent similarity







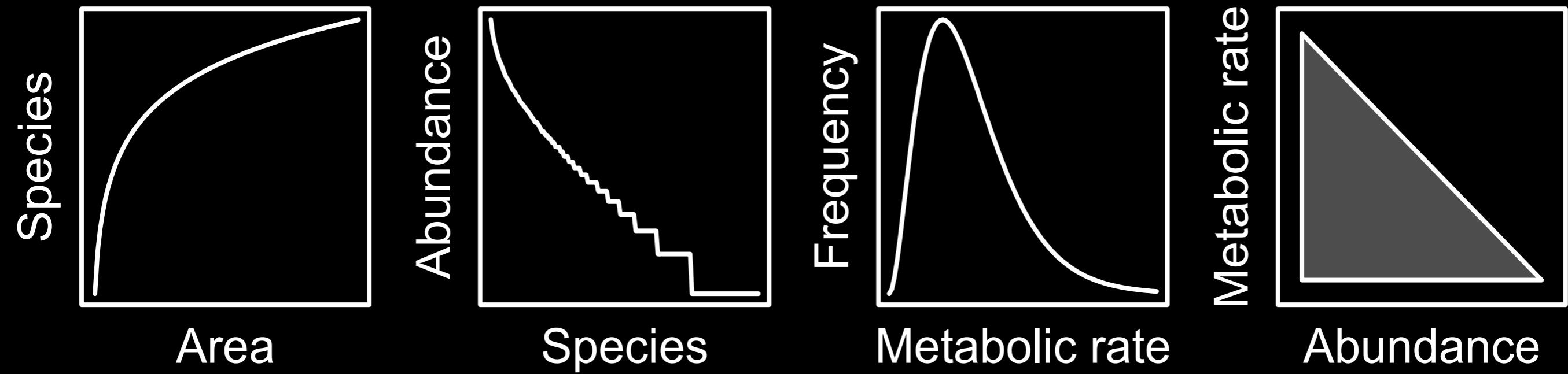


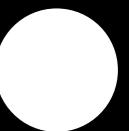
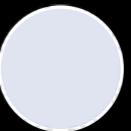
data from: [urbanforestmap.org](http://urbanforestmap.org)

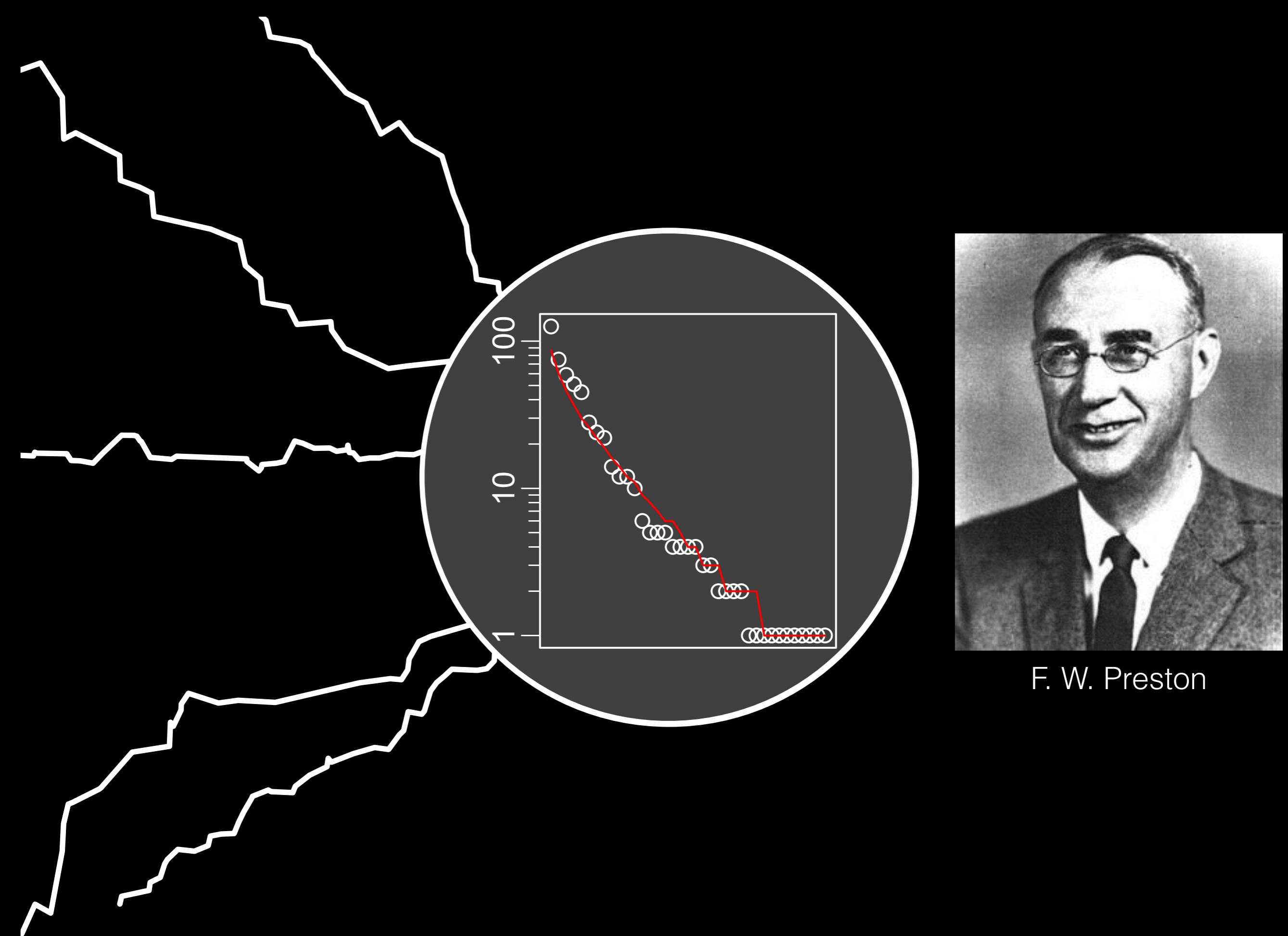
Gruner (2007) *Biol. J. Linn. Soc.*

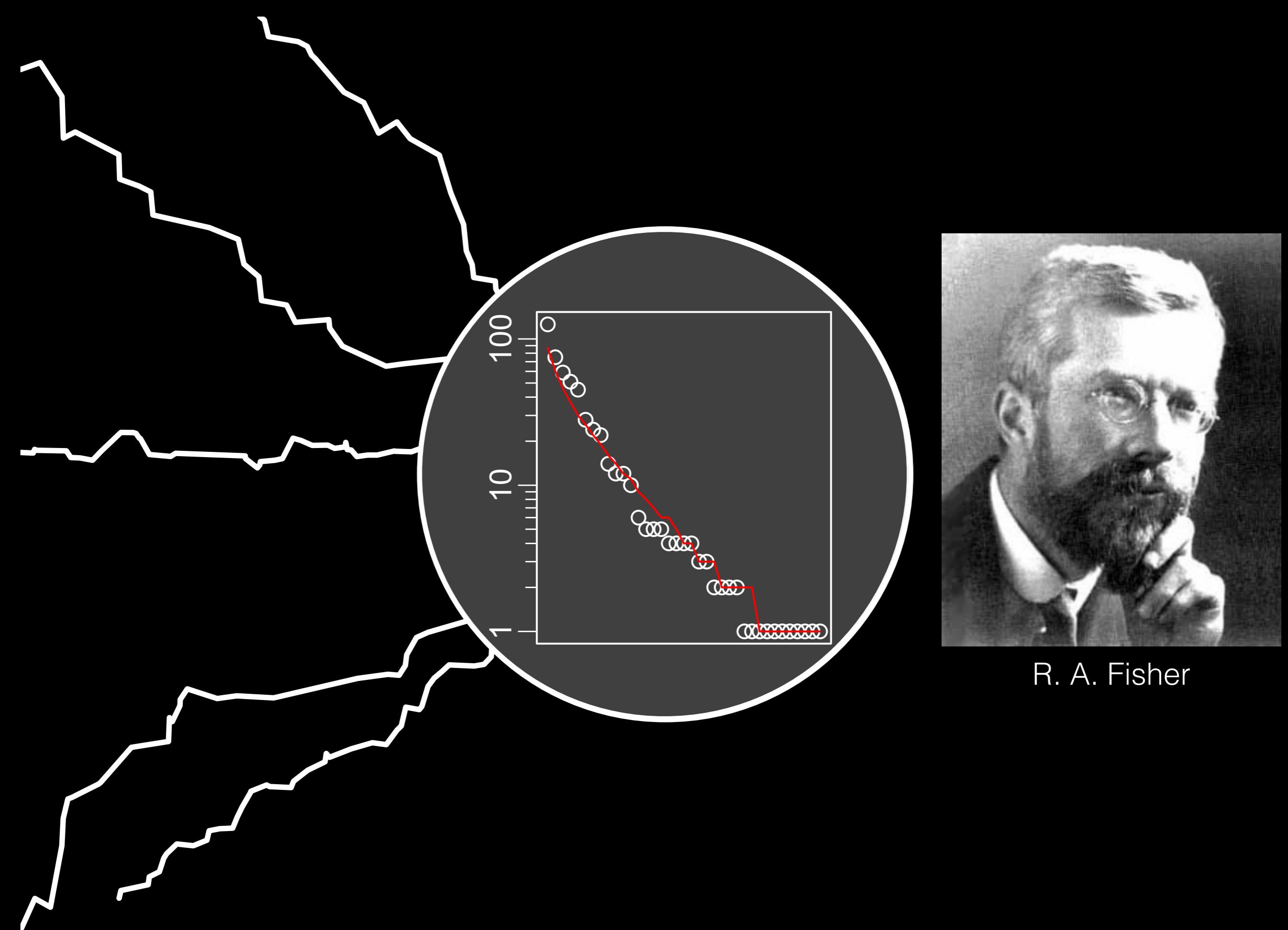
US Breeding Bird Survey

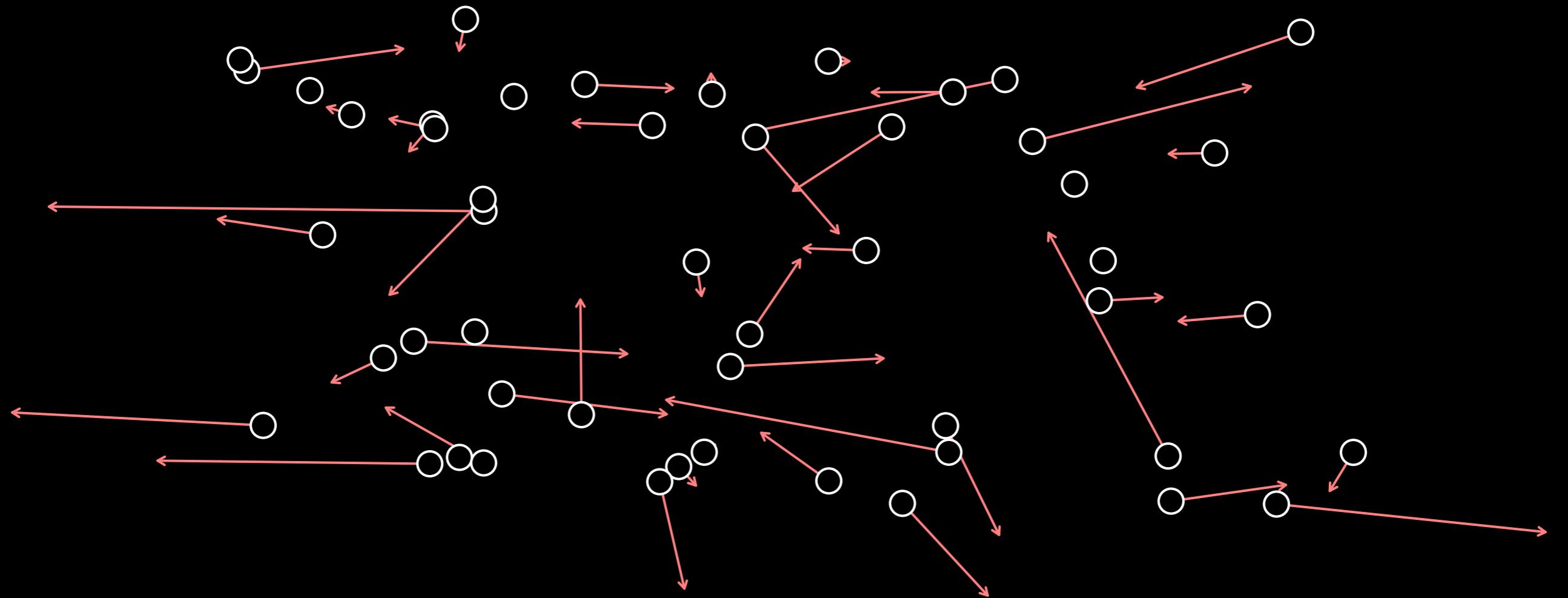
# General biodiversity laws



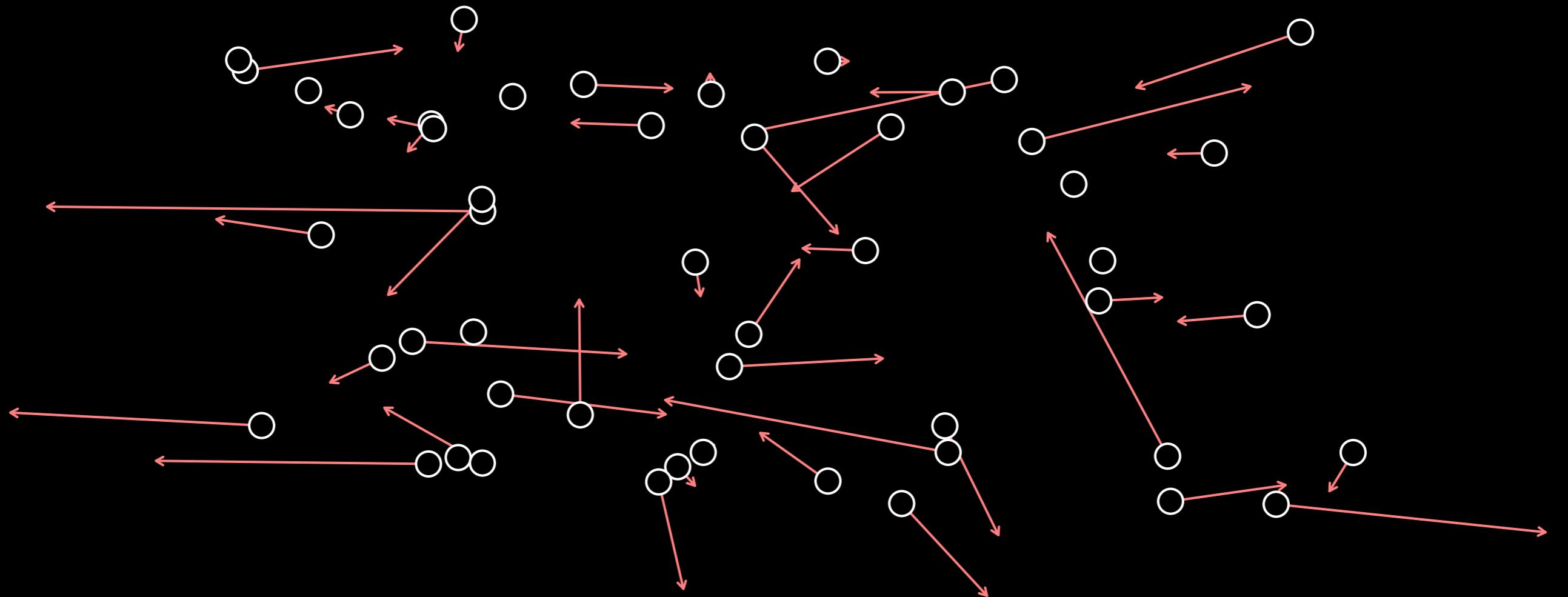




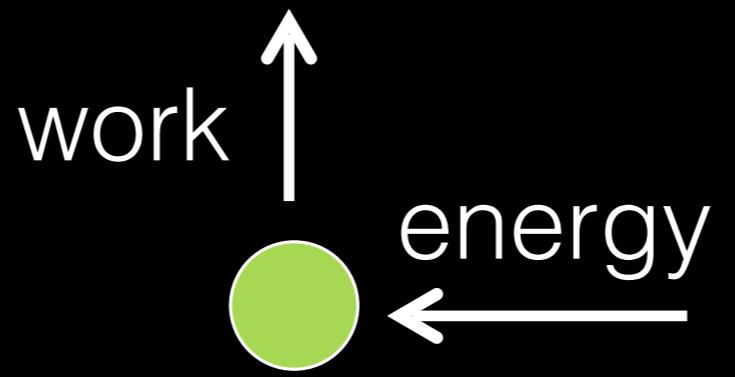


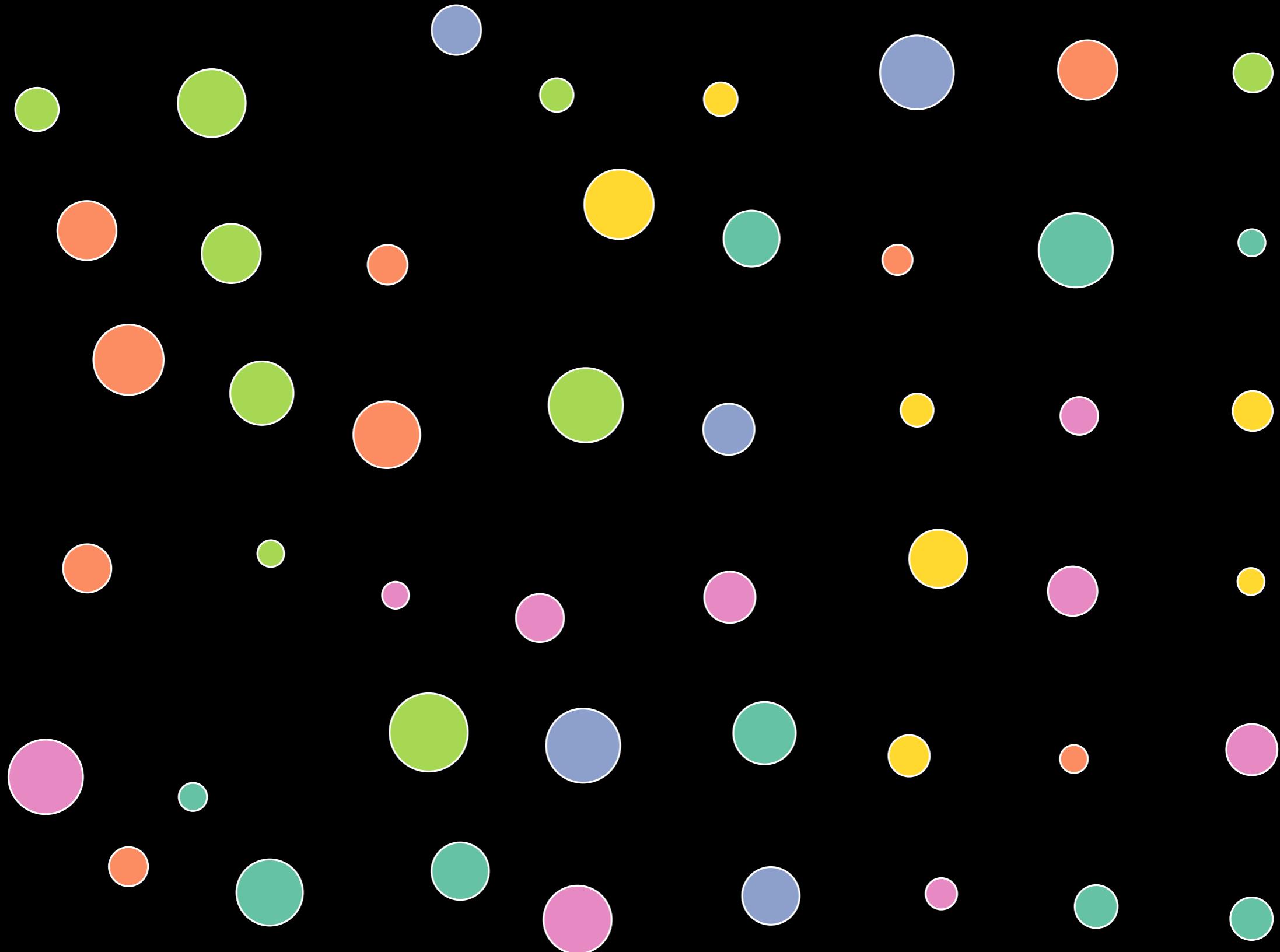


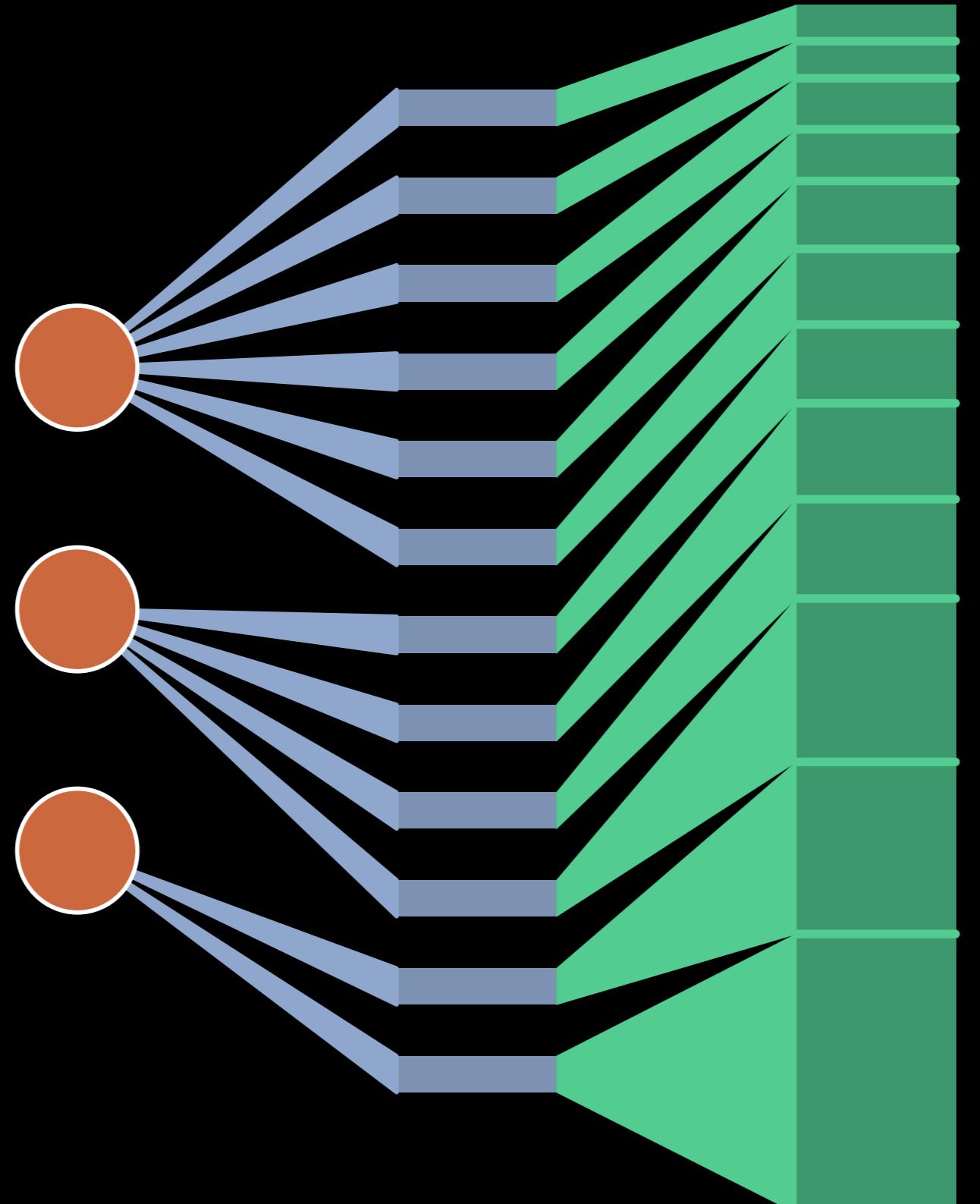
# Statistical constraint



~~t-test~~





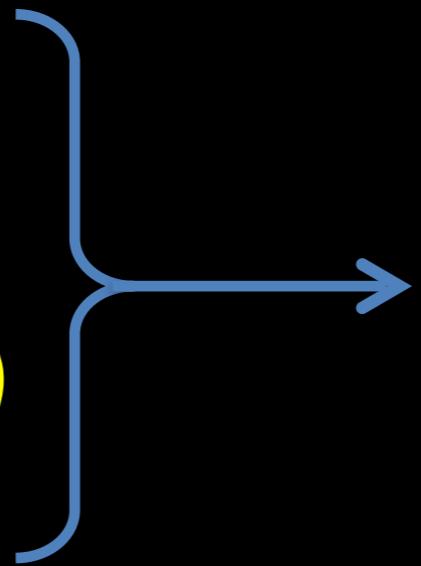


Species Individuals Energy

# Principle of Maximum Information Entropy

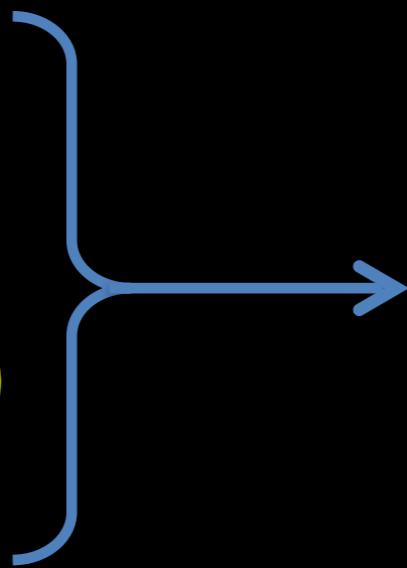
Known info  
*(‘state variables’)*

Known info  
(‘*state variables*’)



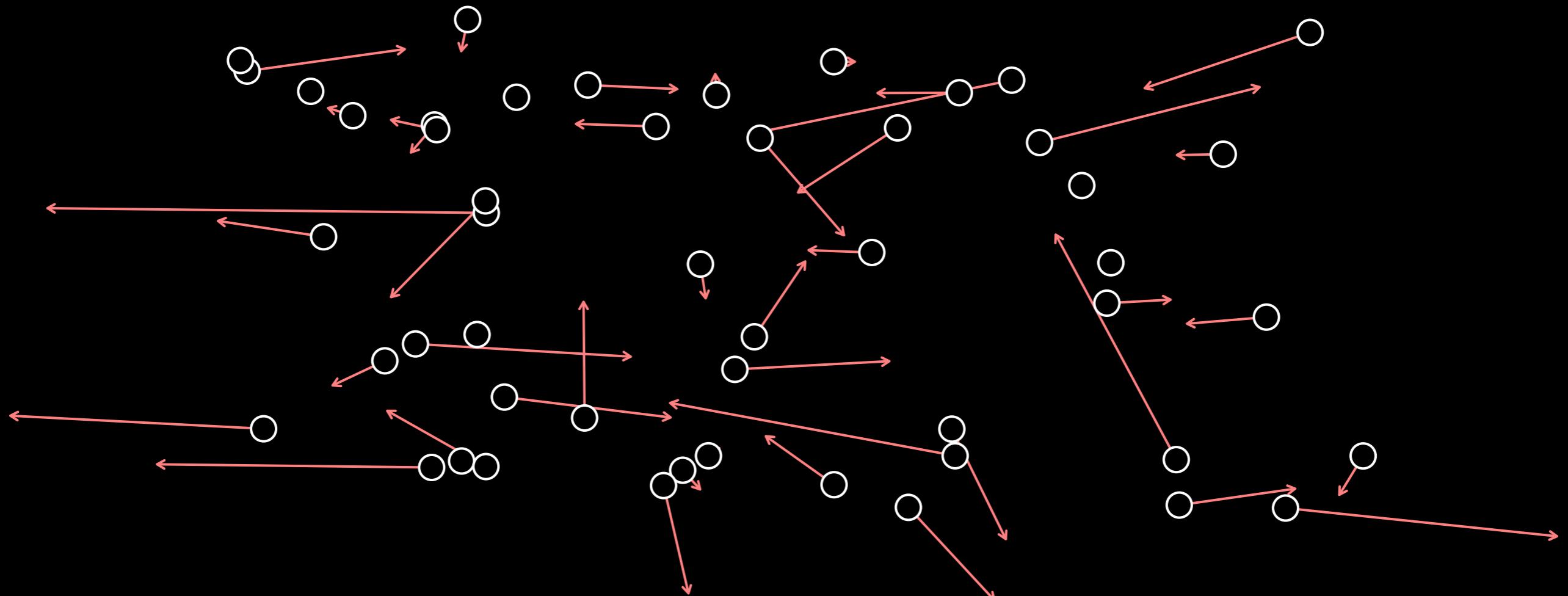
System  
probability  
distributions

Known info  
(‘*state variables*’)

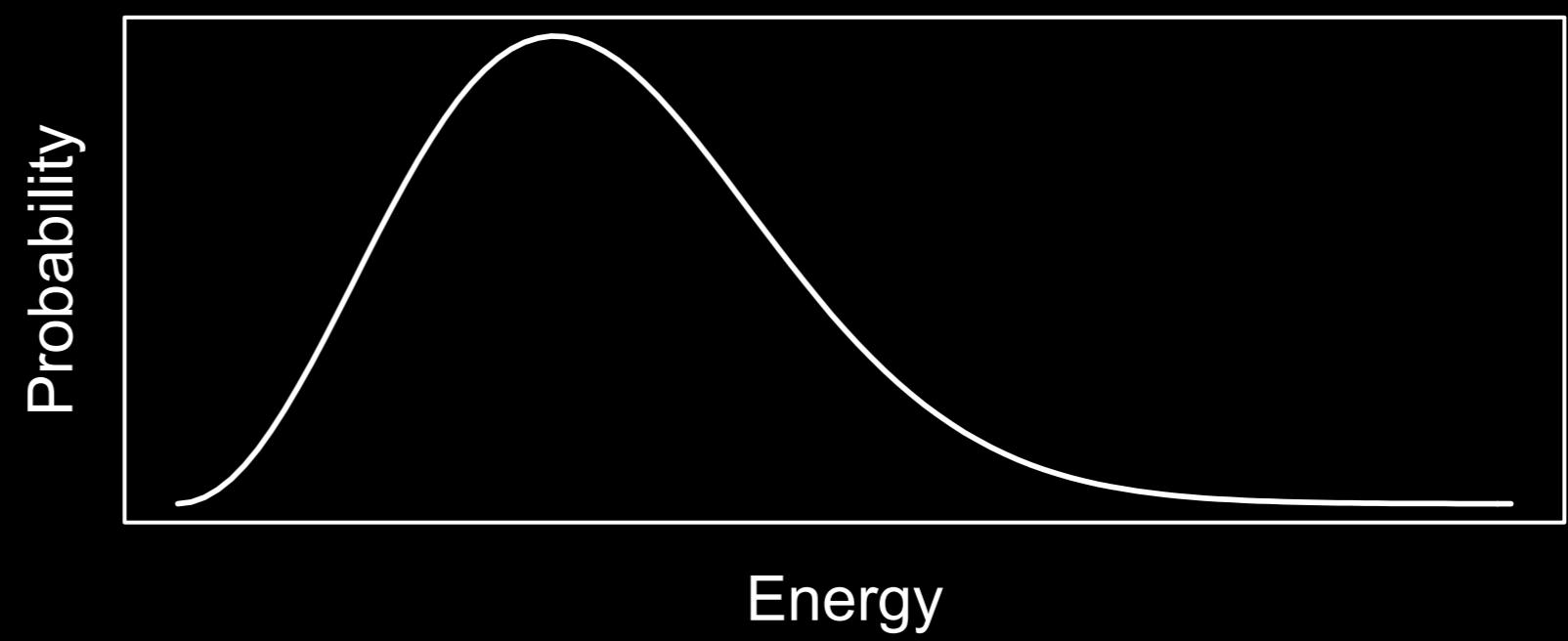


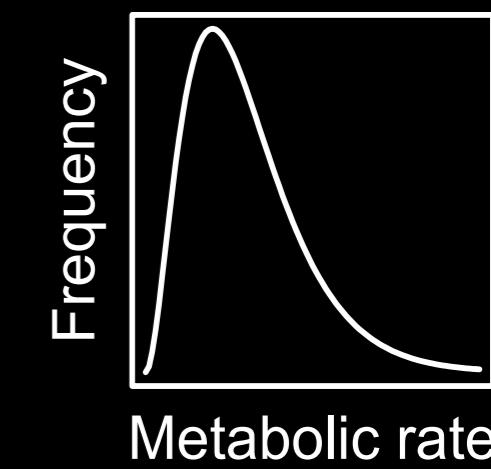
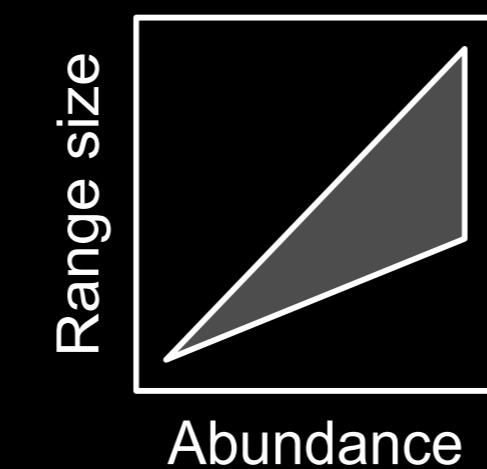
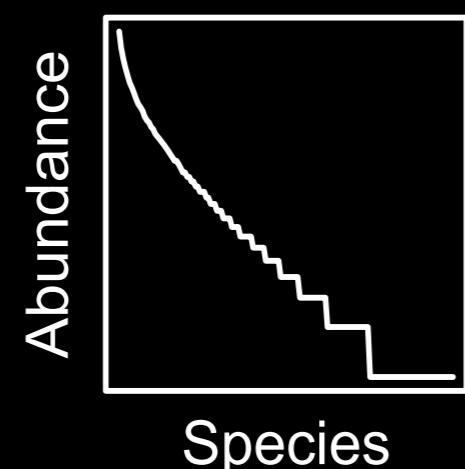
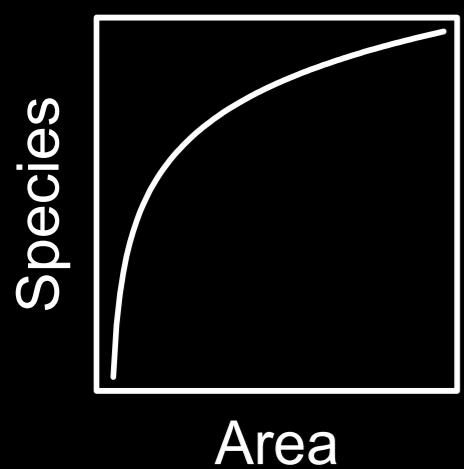
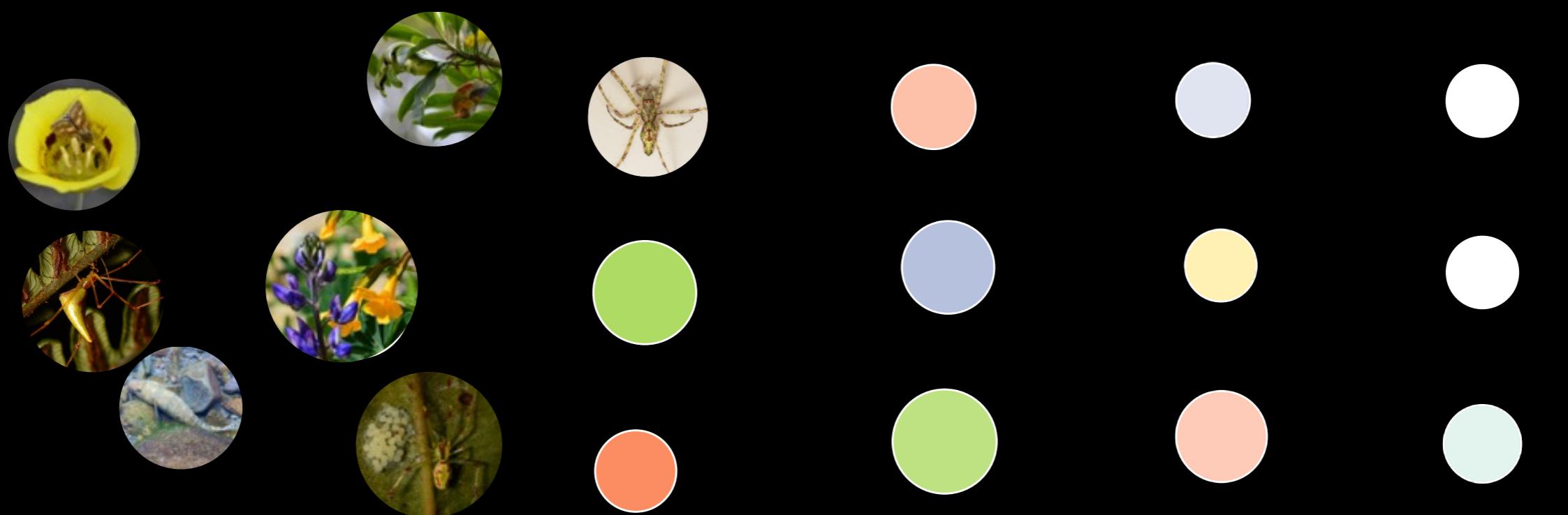
System  
probability  
distributions





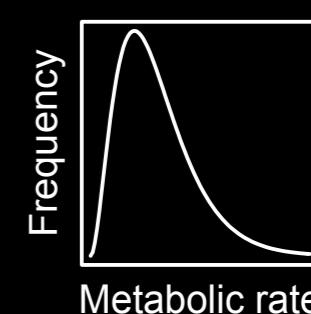
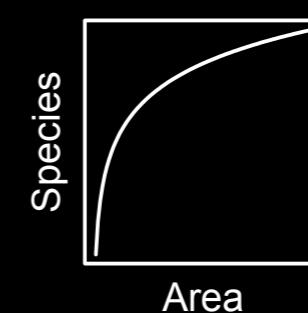
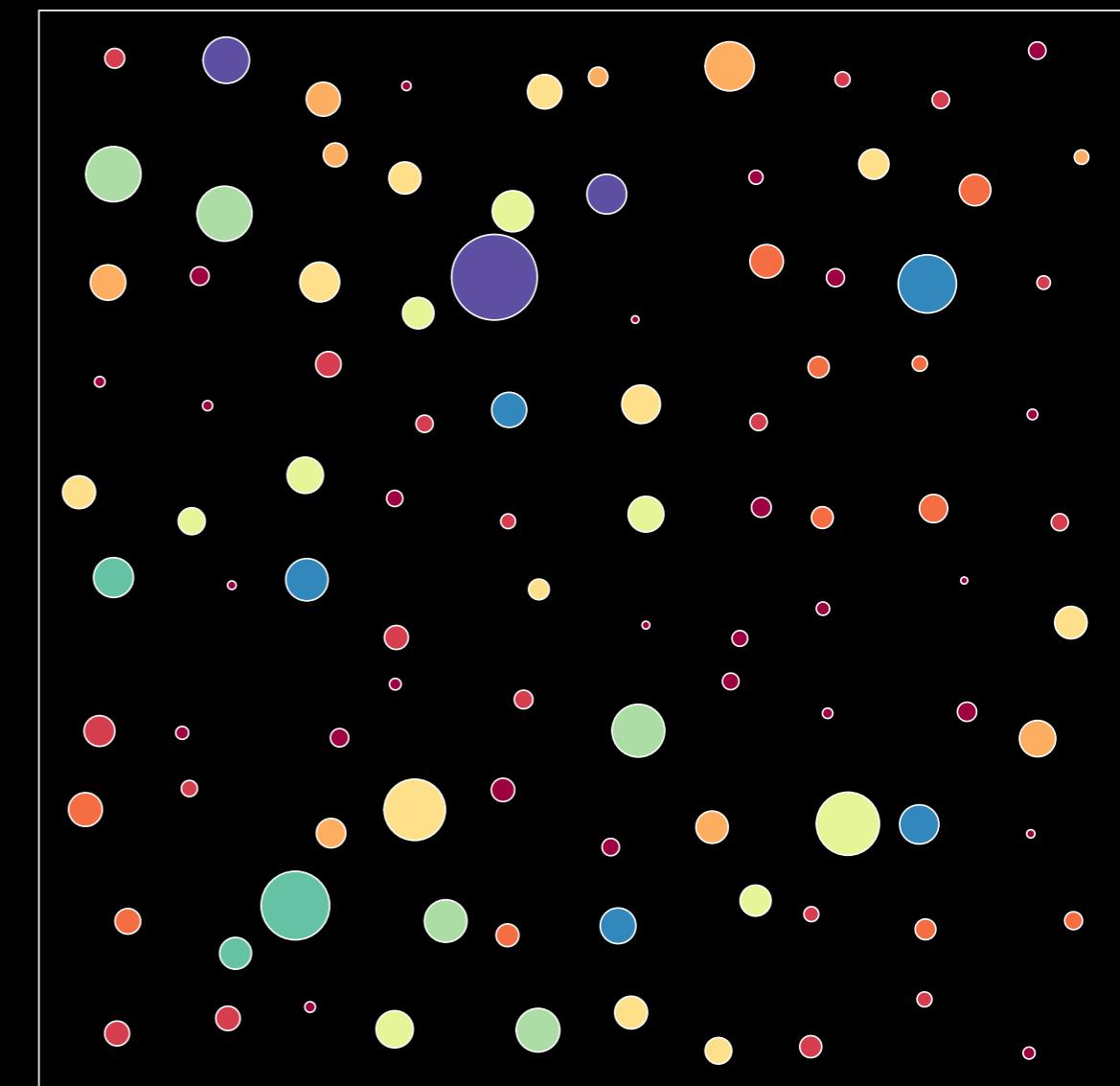
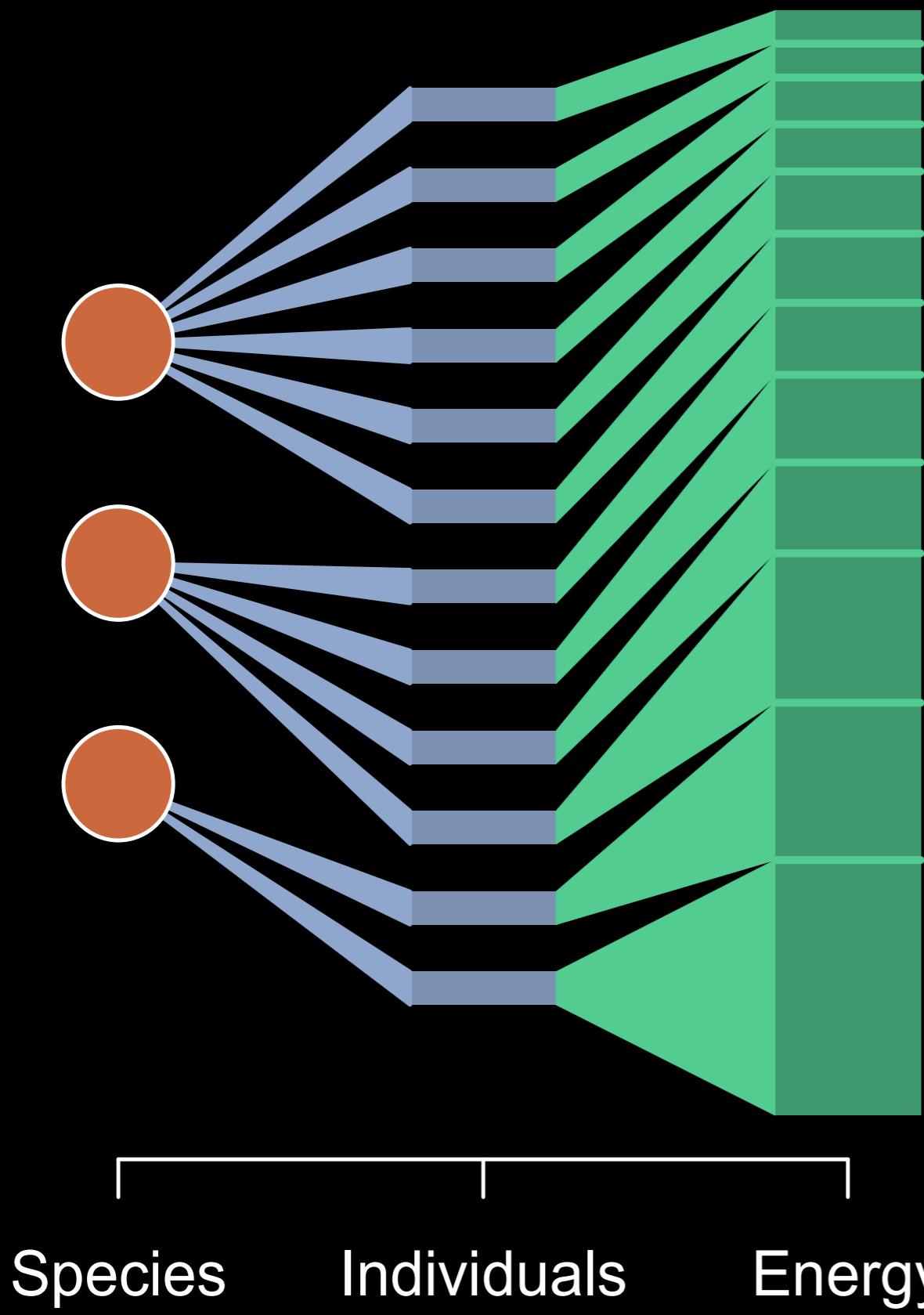
E. T. Jaynes





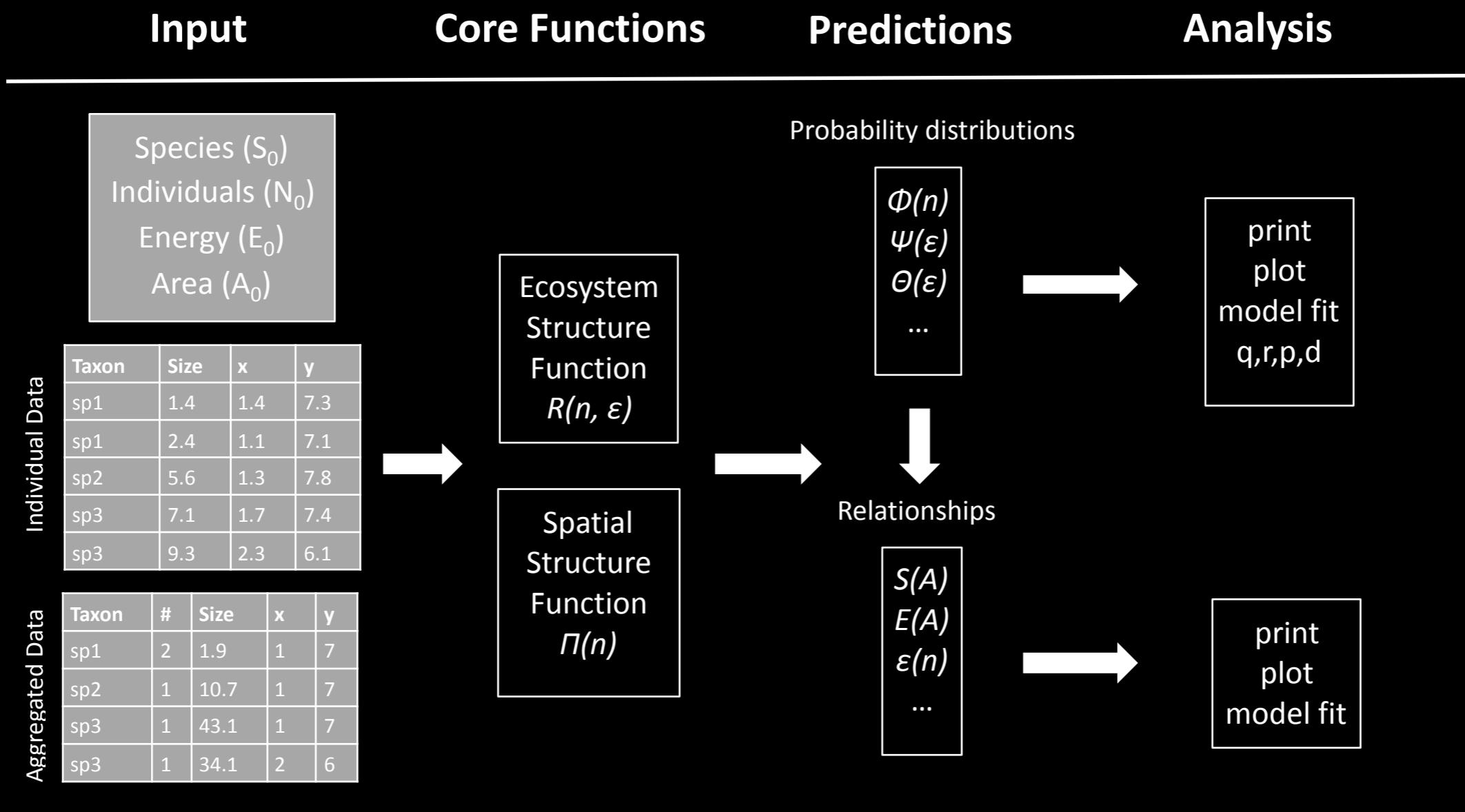
# Maximum Entropy Theory of Ecology

(Harte 2011)





# package: meterR



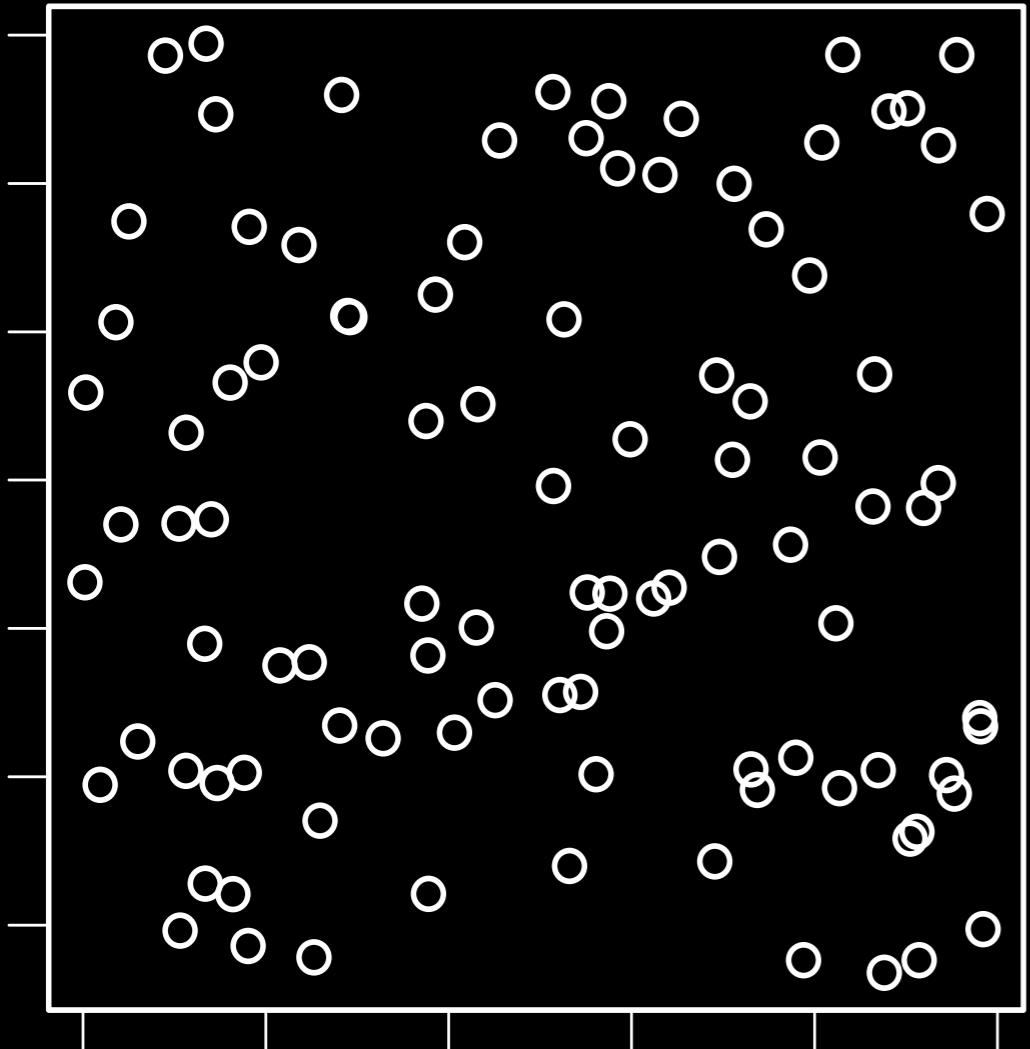
```
data(arth)  
data(anbo)
```

```
esf<-meteESF(spp,  
abund,  
power)  
ssf<-meteSSF(spp,  
abund,  
coords)
```

```
sad<-sad(esf)  
ipd<-ipd(esf)  
sipd<-sipd(esf)  
sar1<-downscaleSAR(esf)  
sar2<-  
meteSAR(spp,abund,  
x,y)  
etc.
```

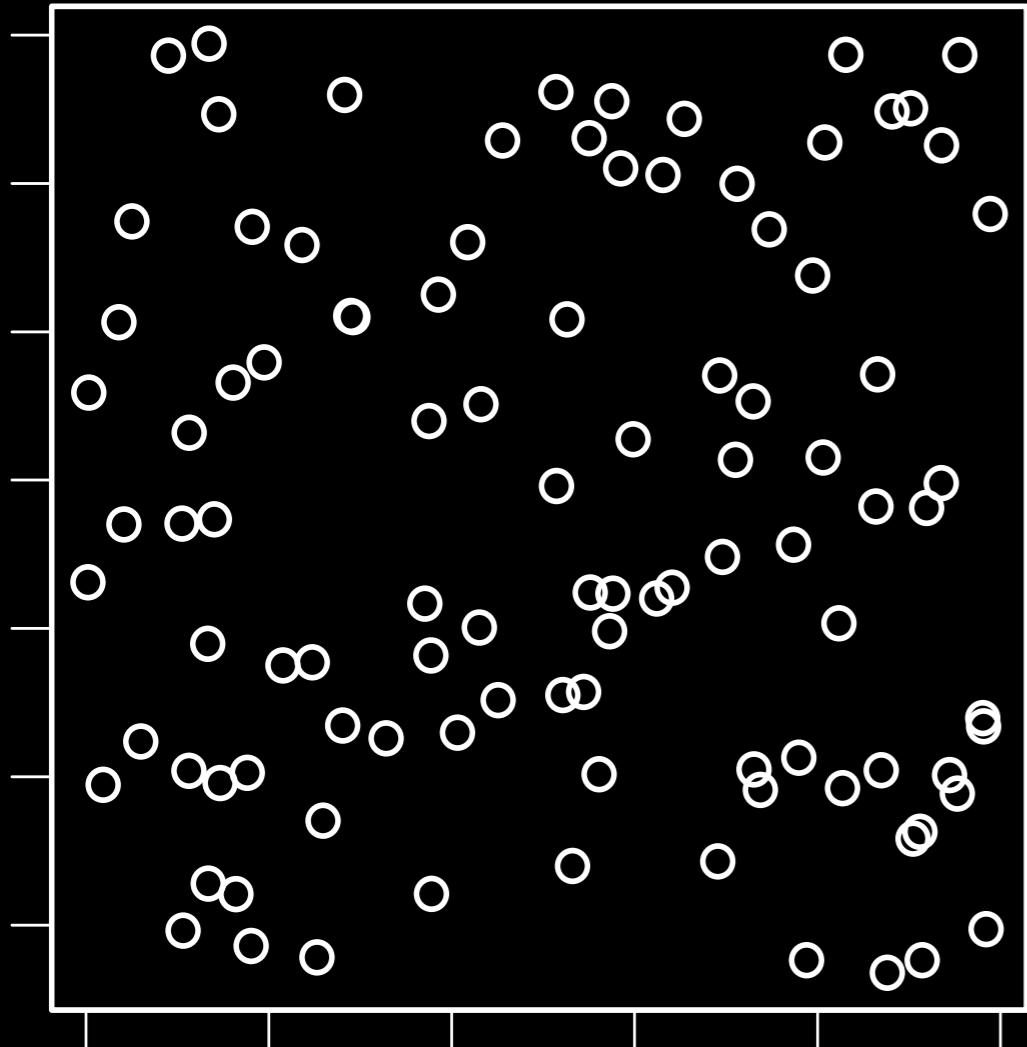
```
plot(sad)  
logLik(sad)  
mse(sad)  
sad$r()  
#simulation  
sad$q() #quantiles  
etc.
```

# Why test theory?

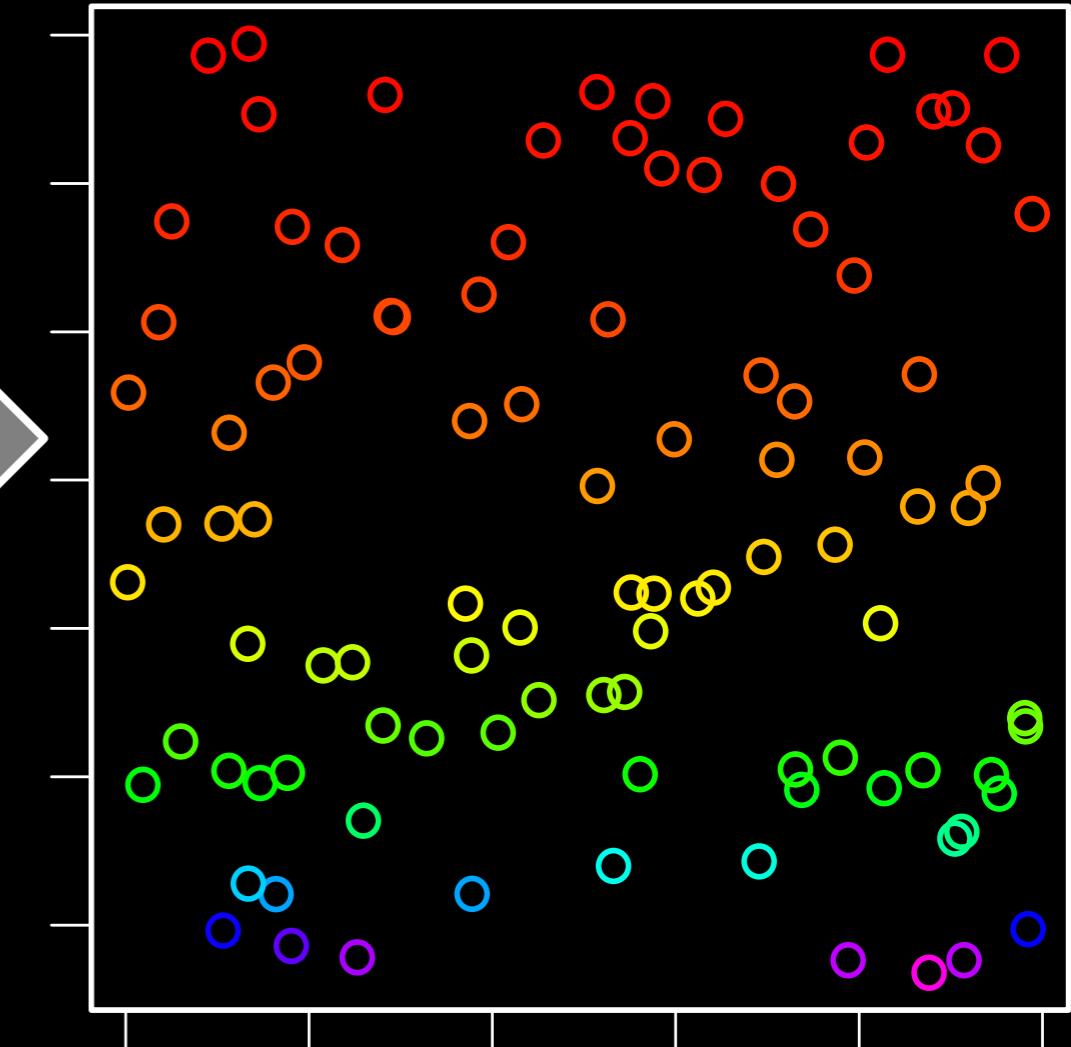
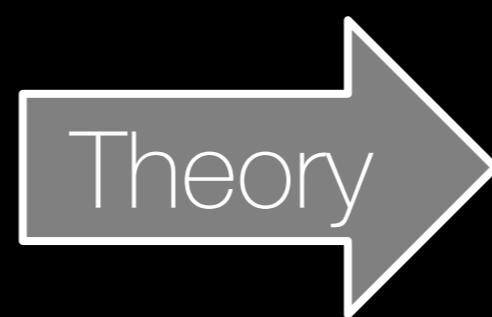


Mechanism AWOL

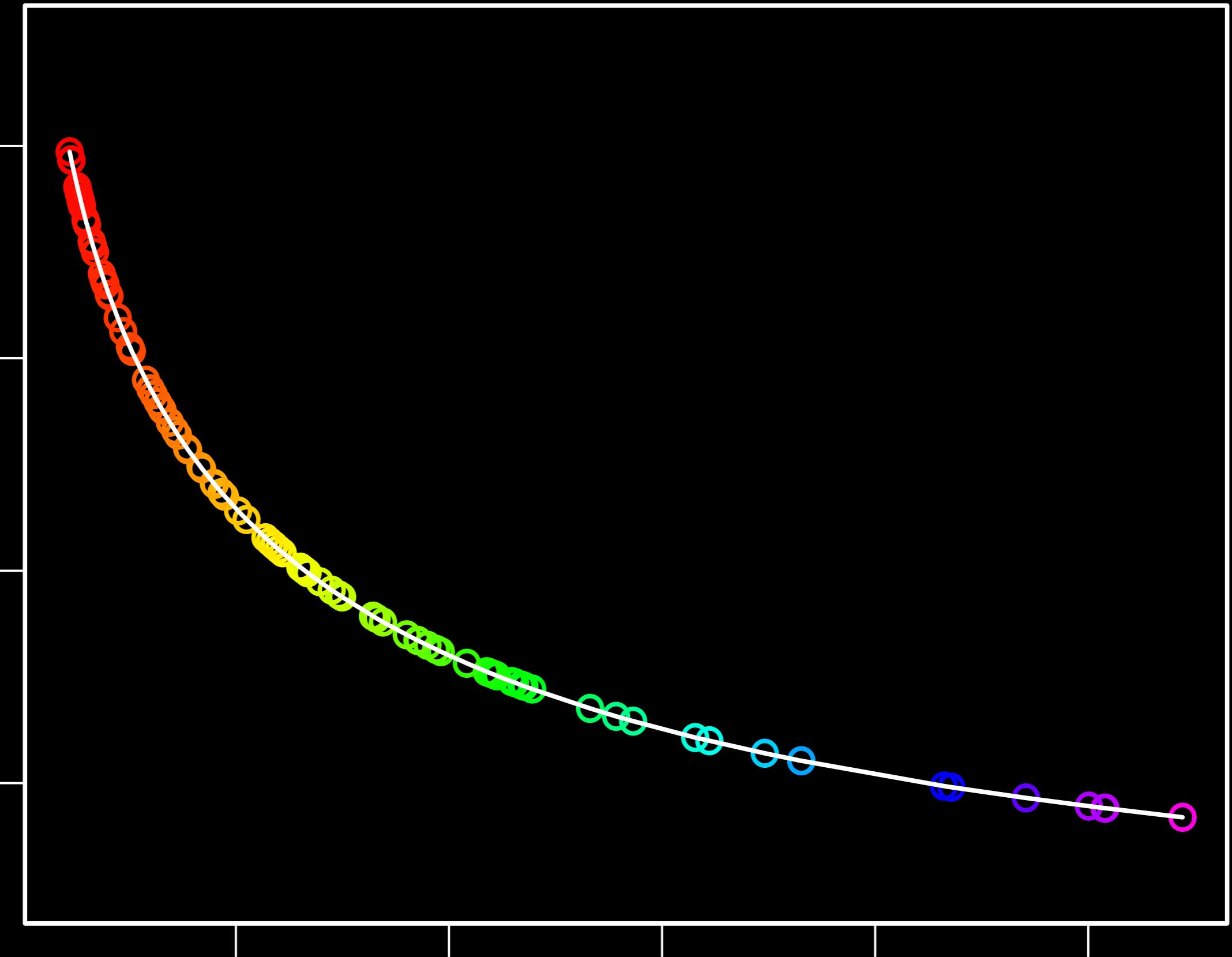
# Why test theory?

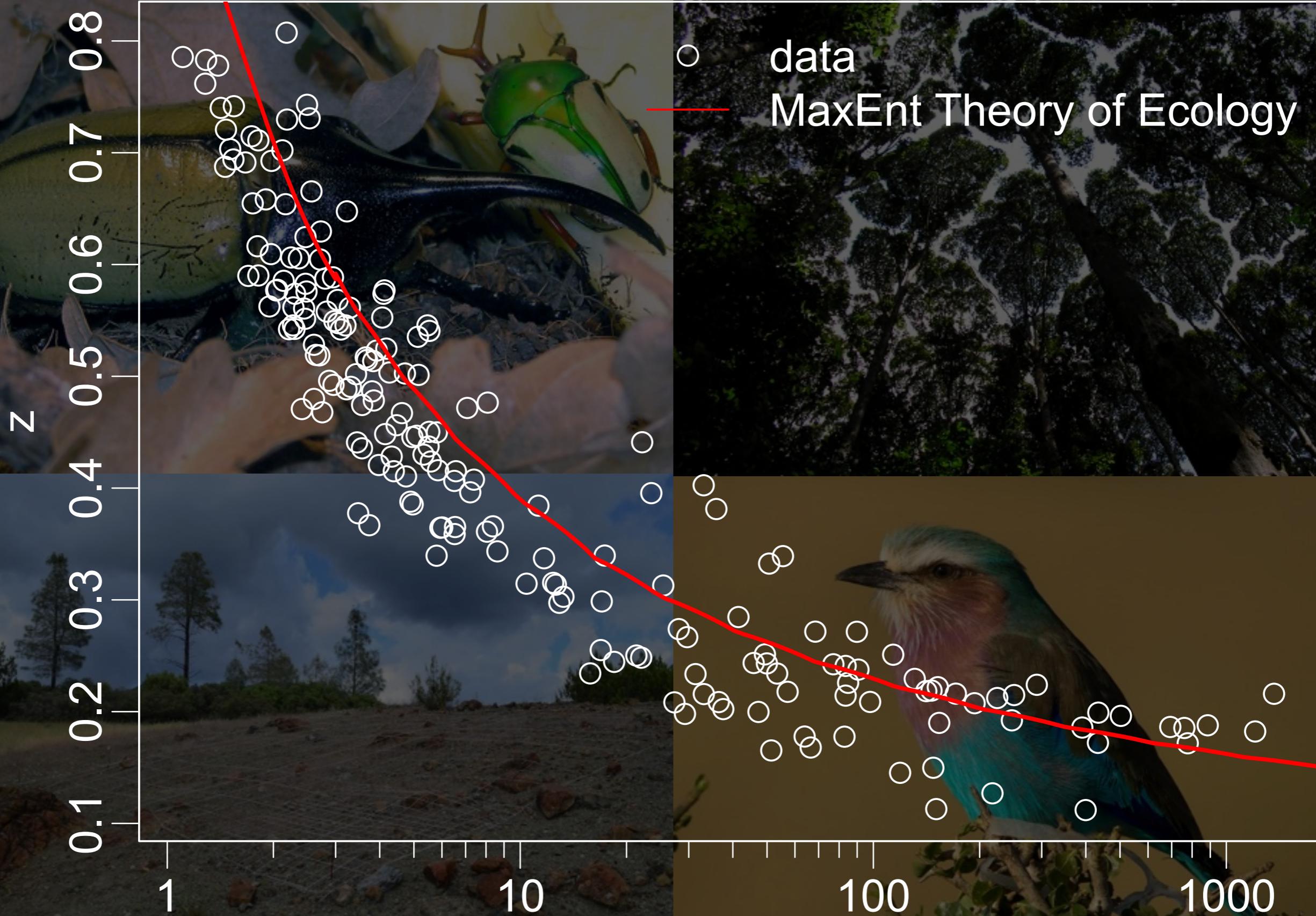


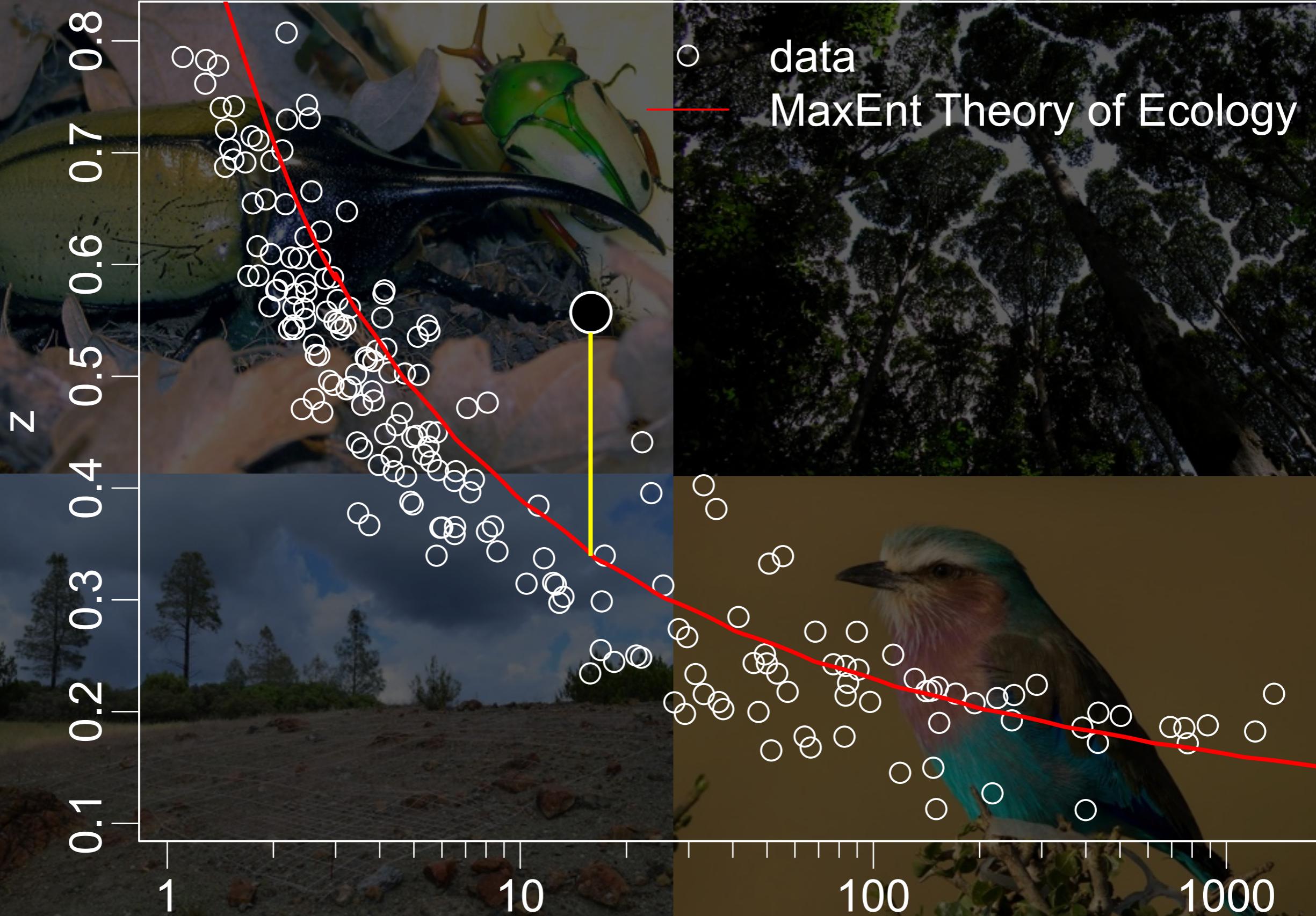
Mechanism AWOL

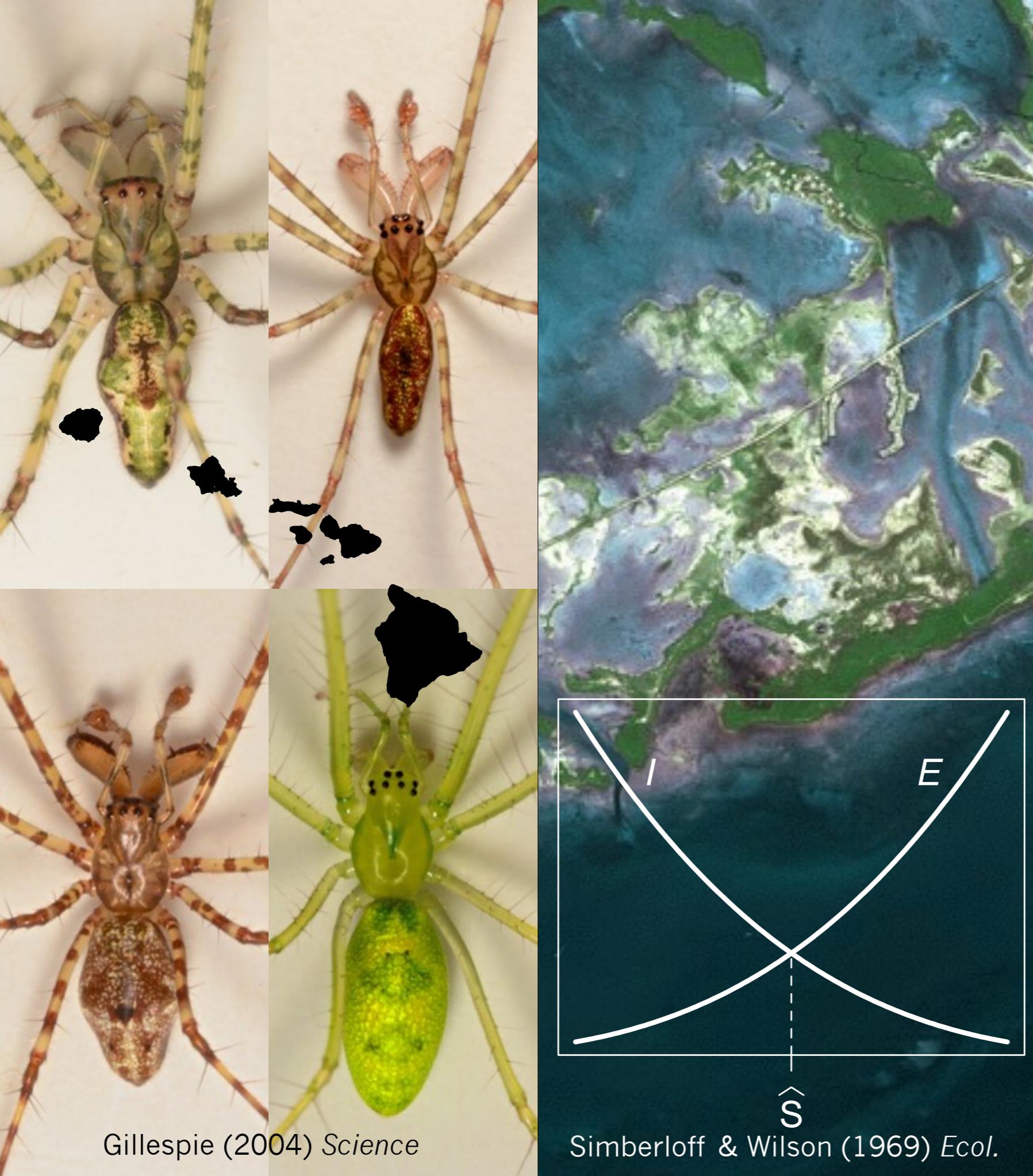


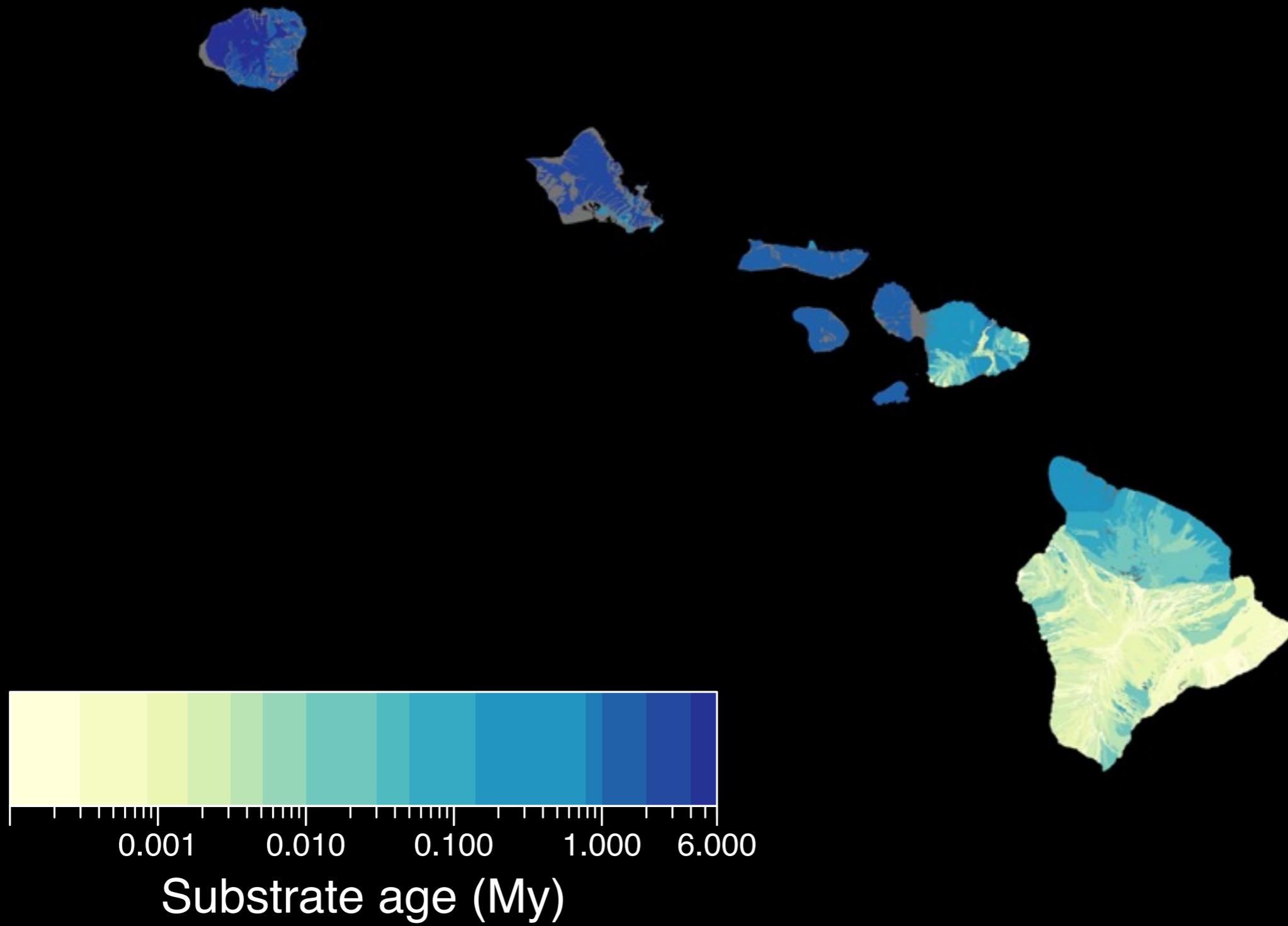
New insights





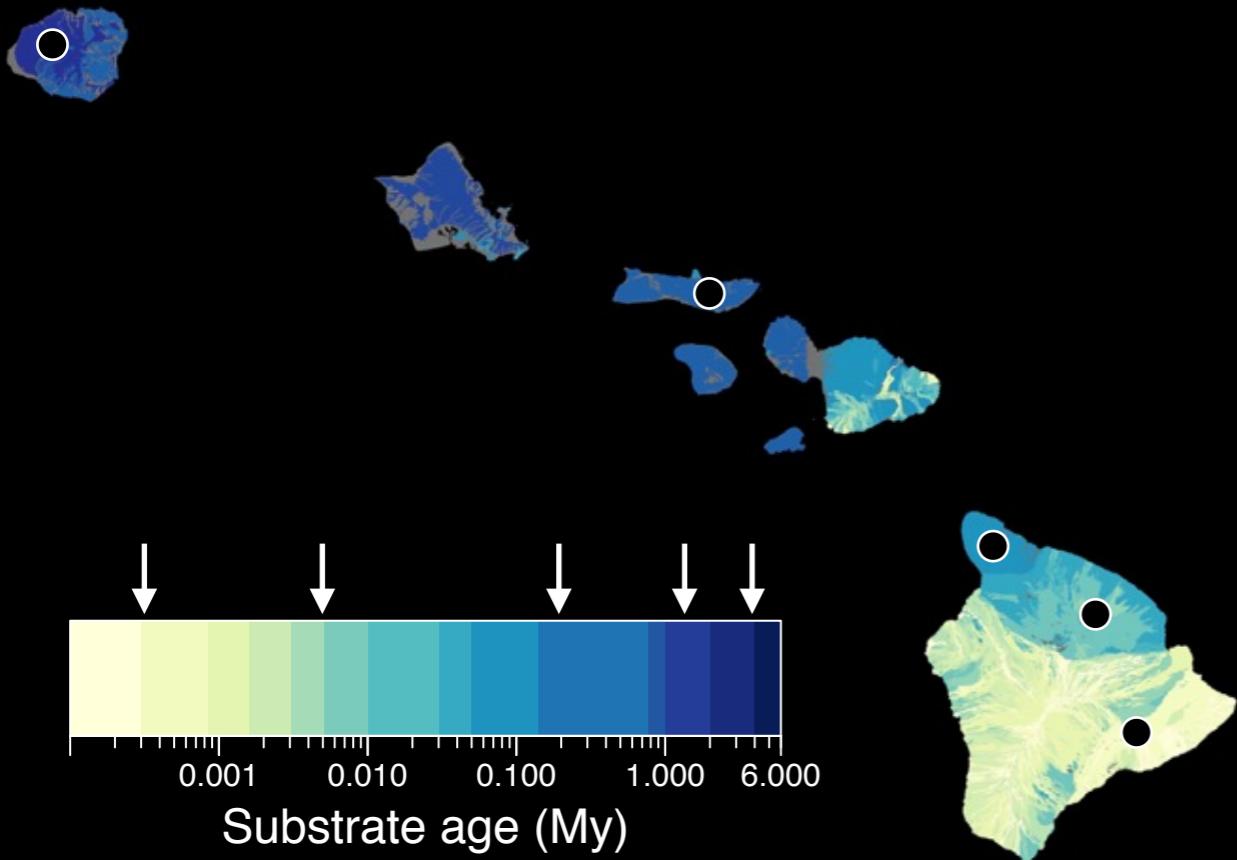








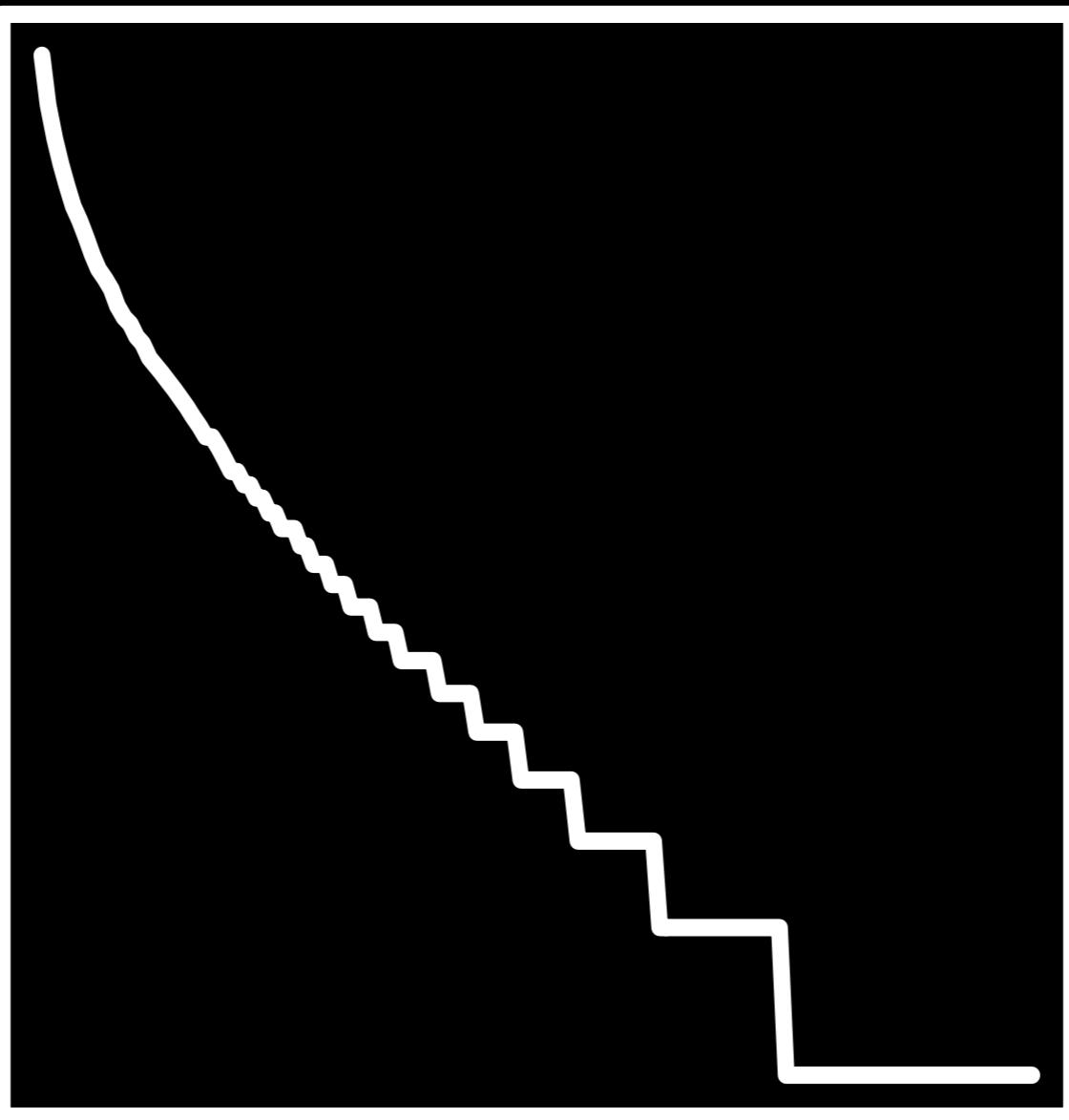
# Capturing evolving communities



15,997 arthropods collected

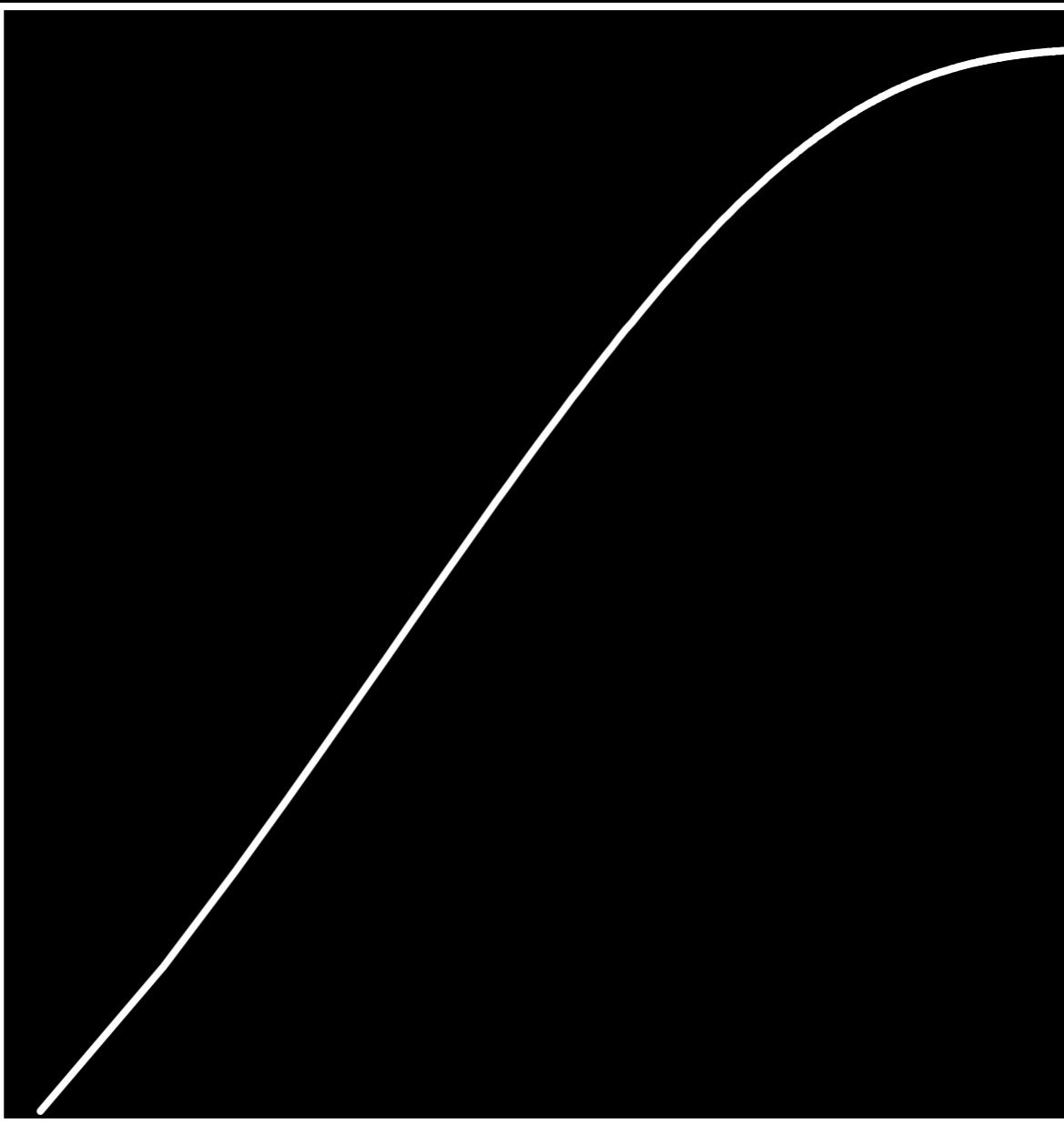


Abundance



Species

Cumulative density

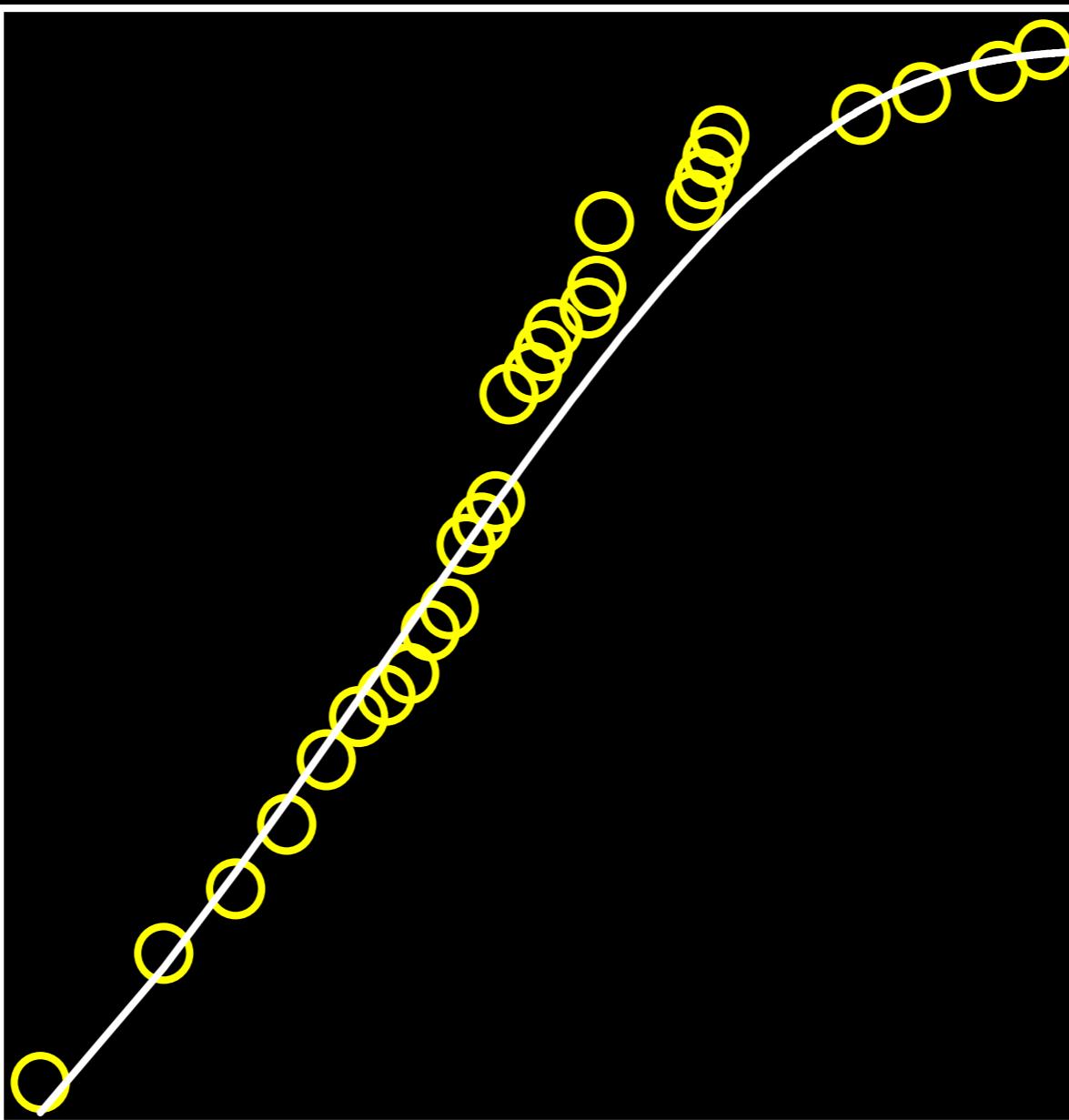


Abundance

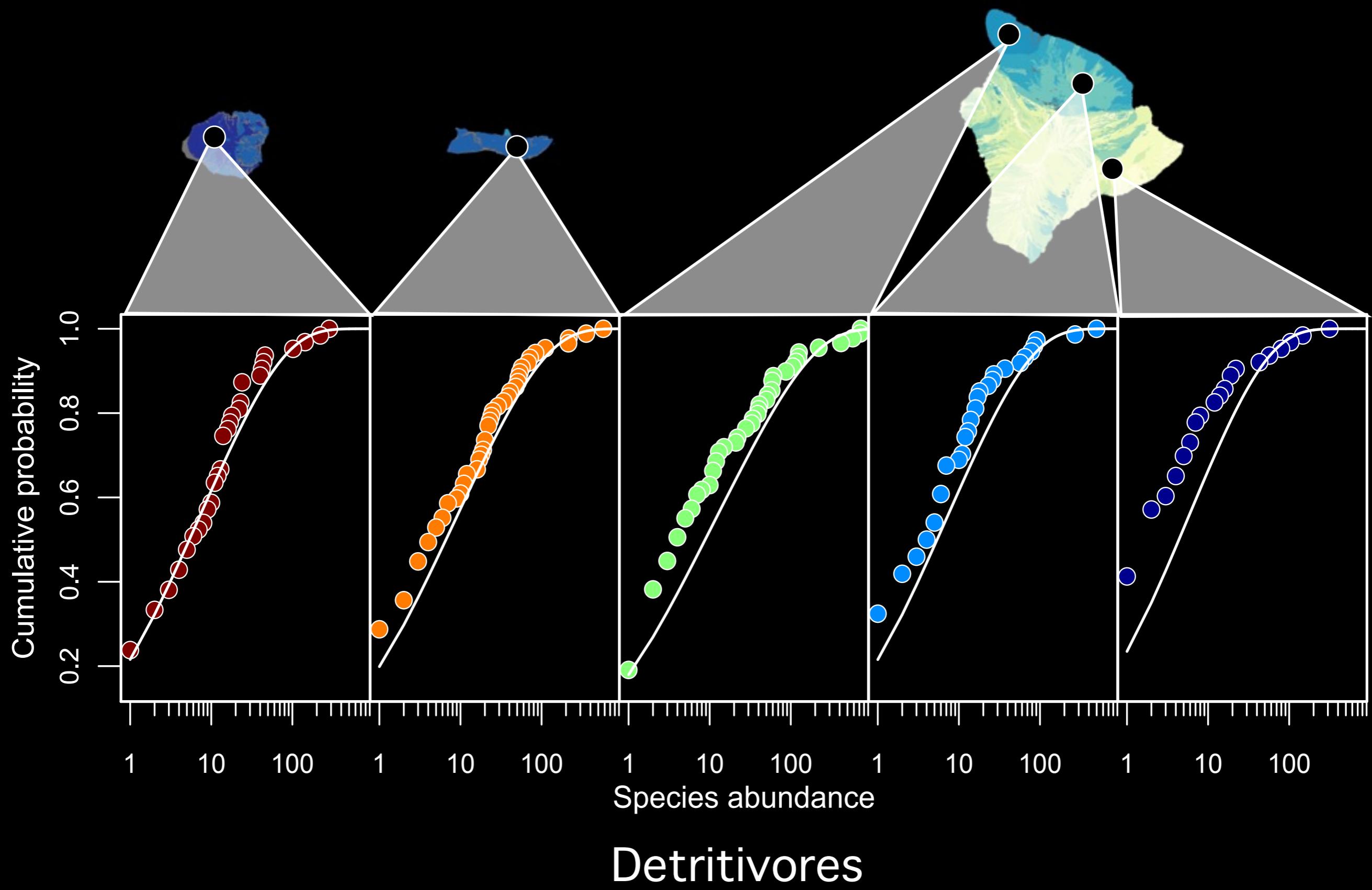
Theory

Cumulative density

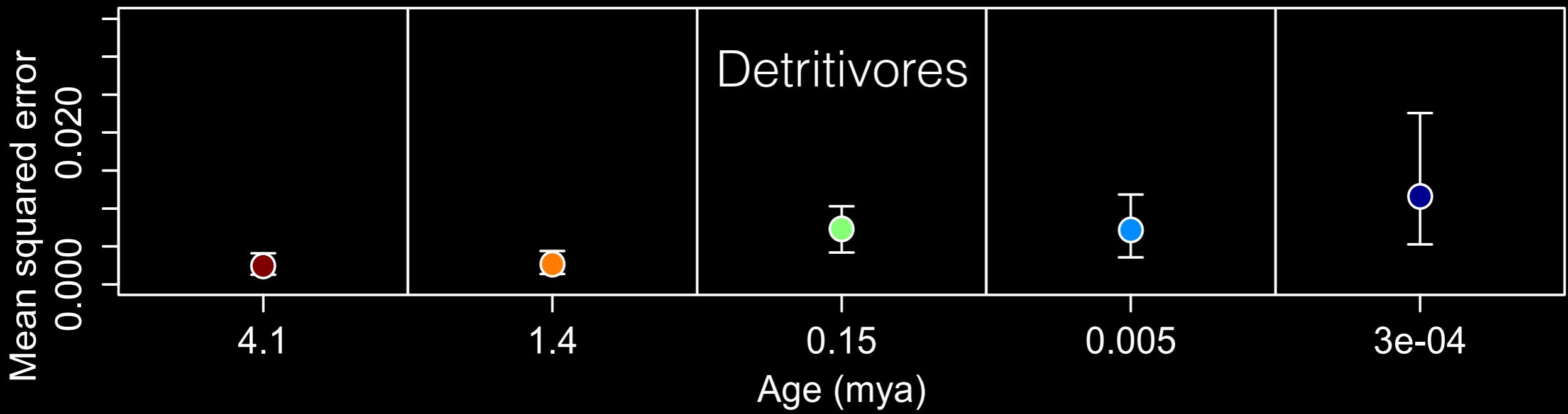
Abundance



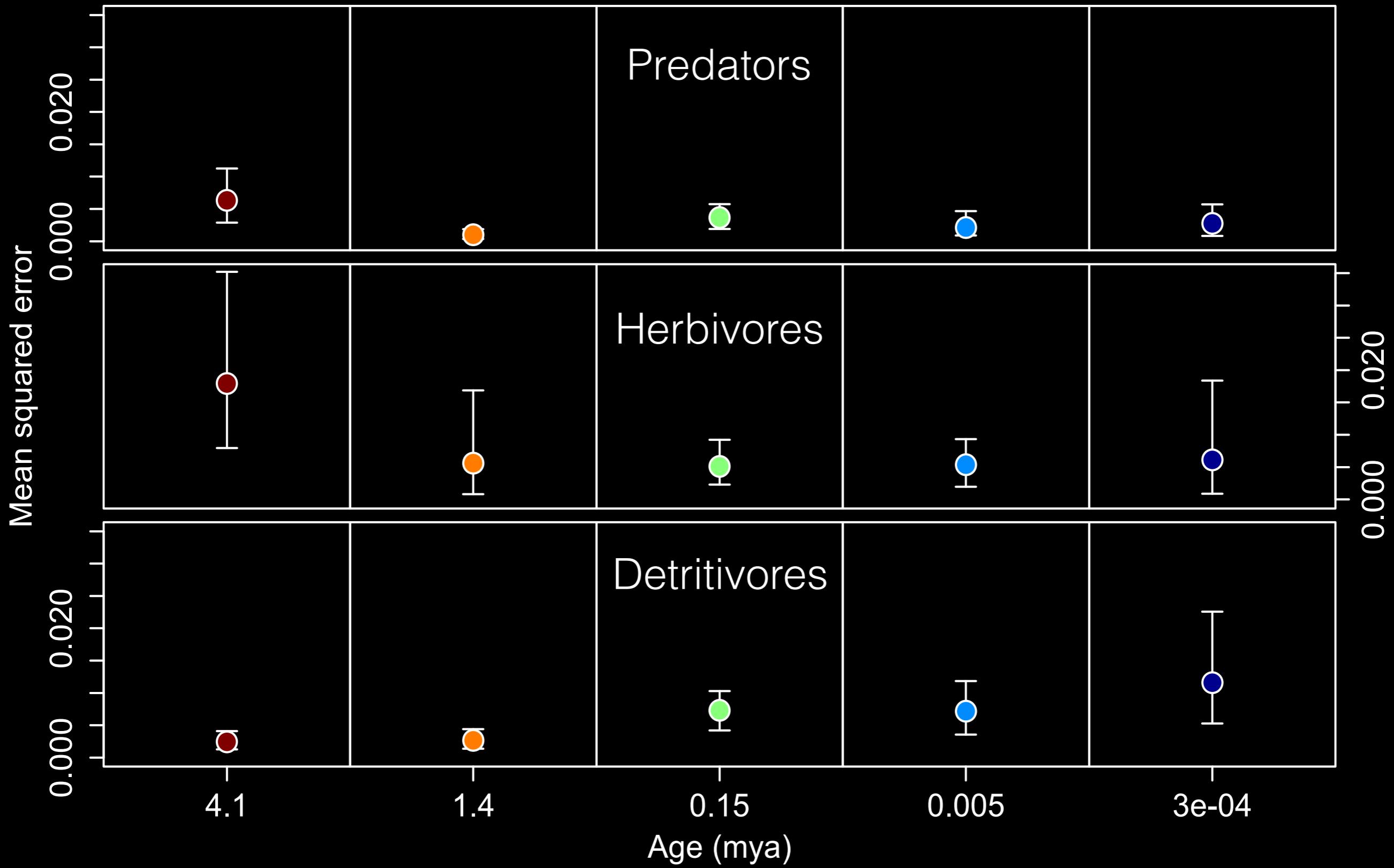
Theory  
Data



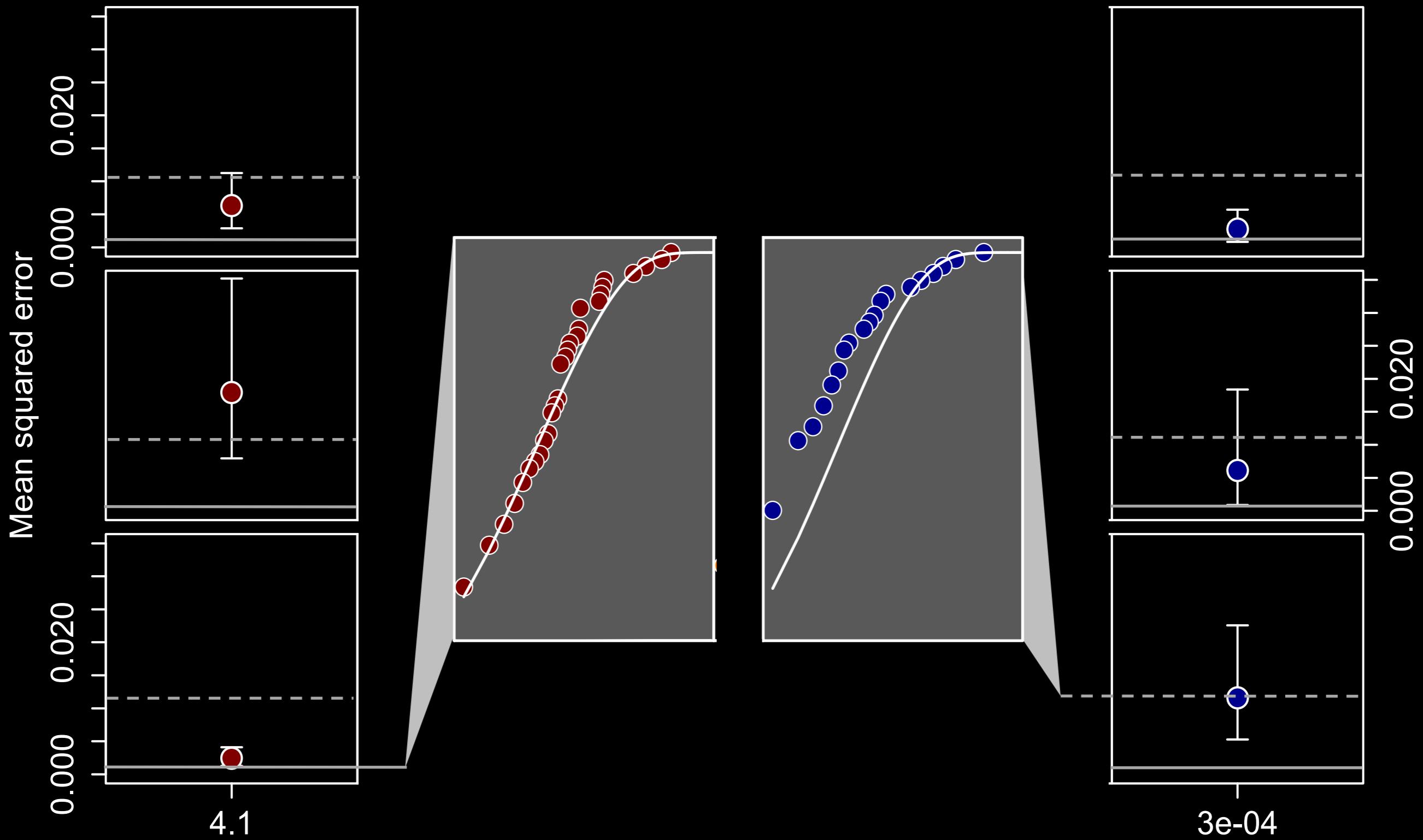
# Species abundance



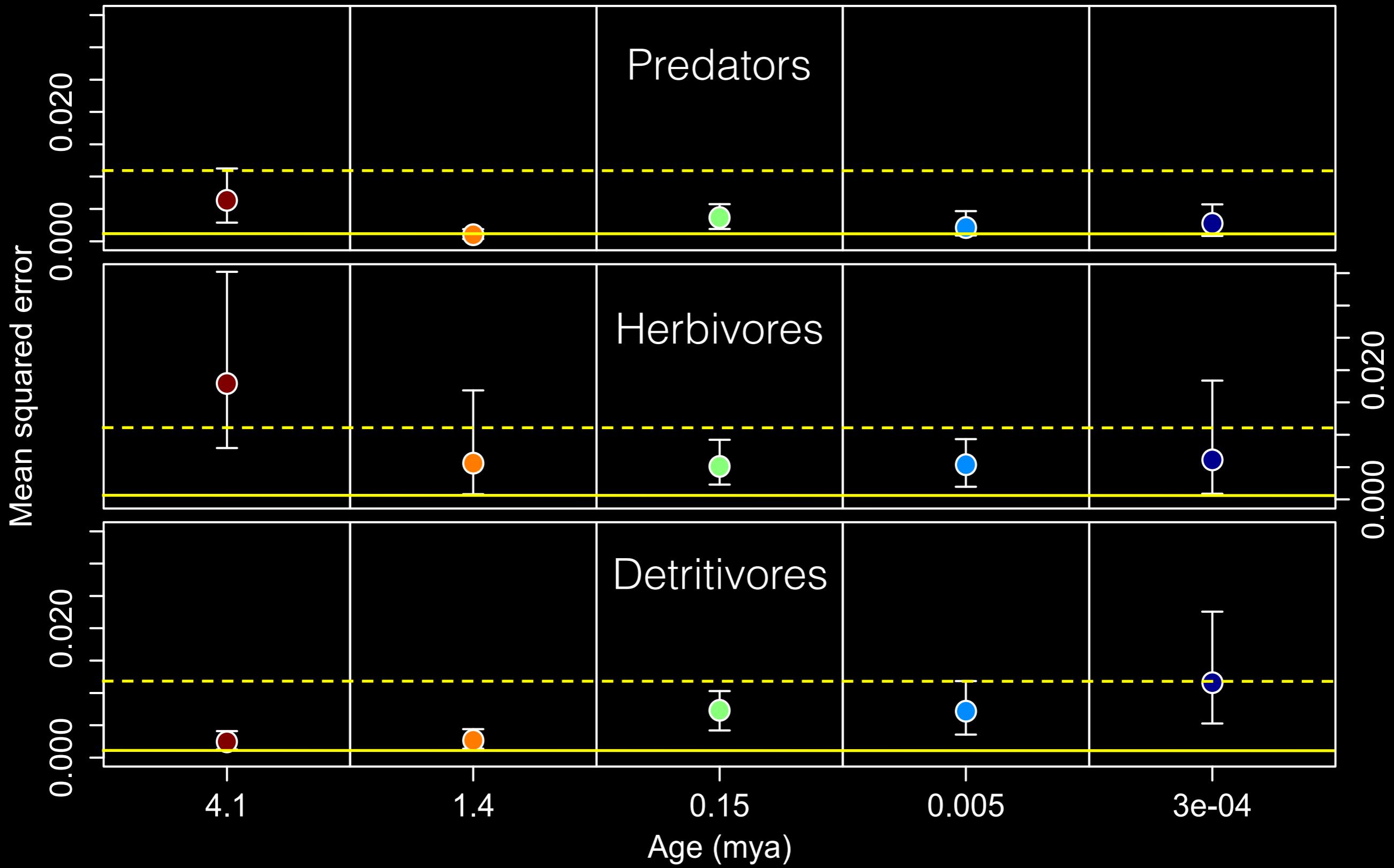
# Species abundance



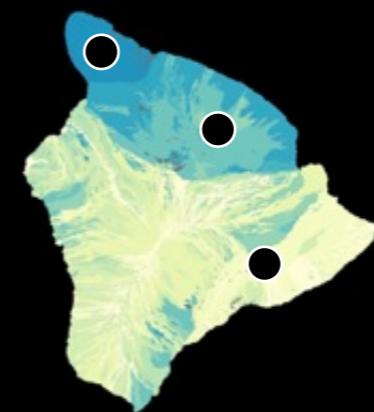
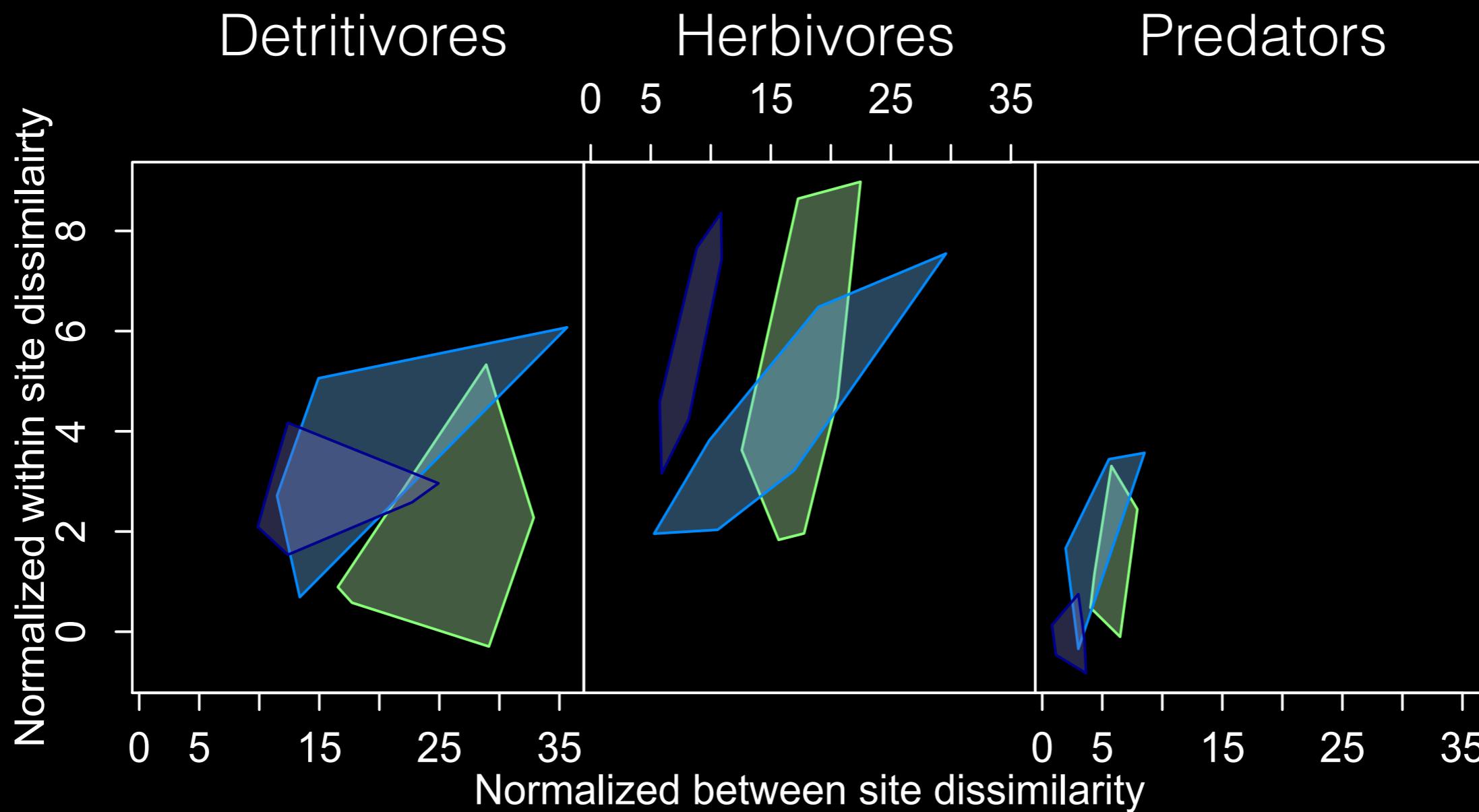
# Species abundance



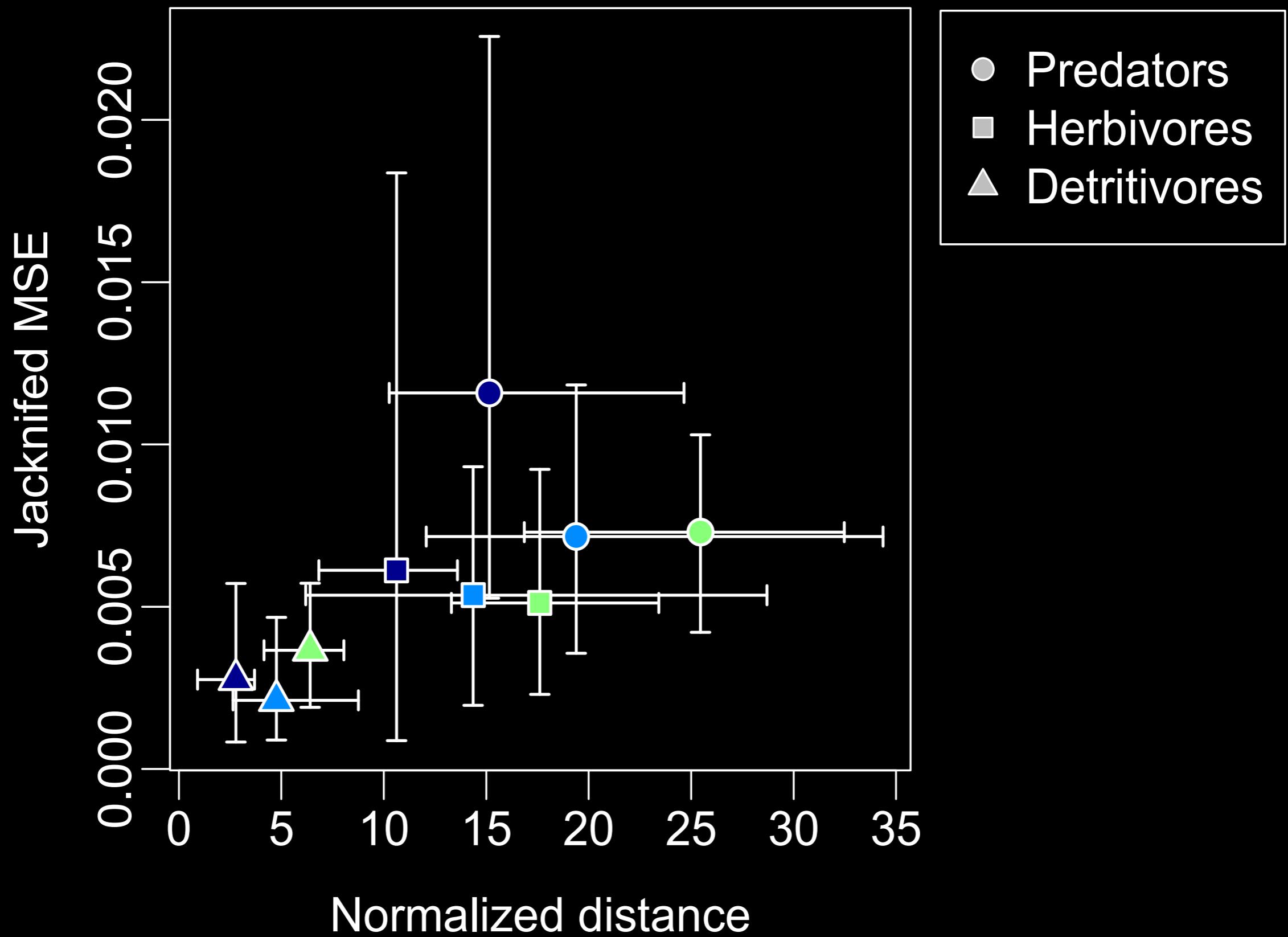
# Species abundance



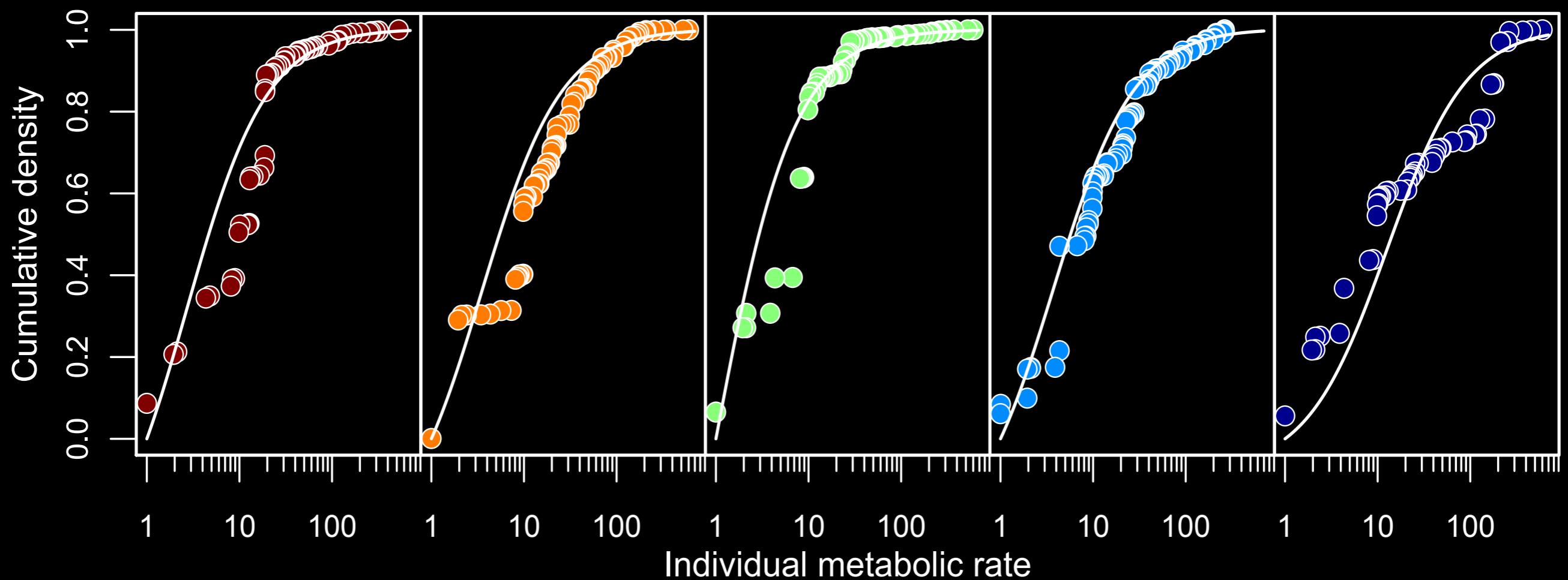
# Incomplete assembly



# Incomplete assembly

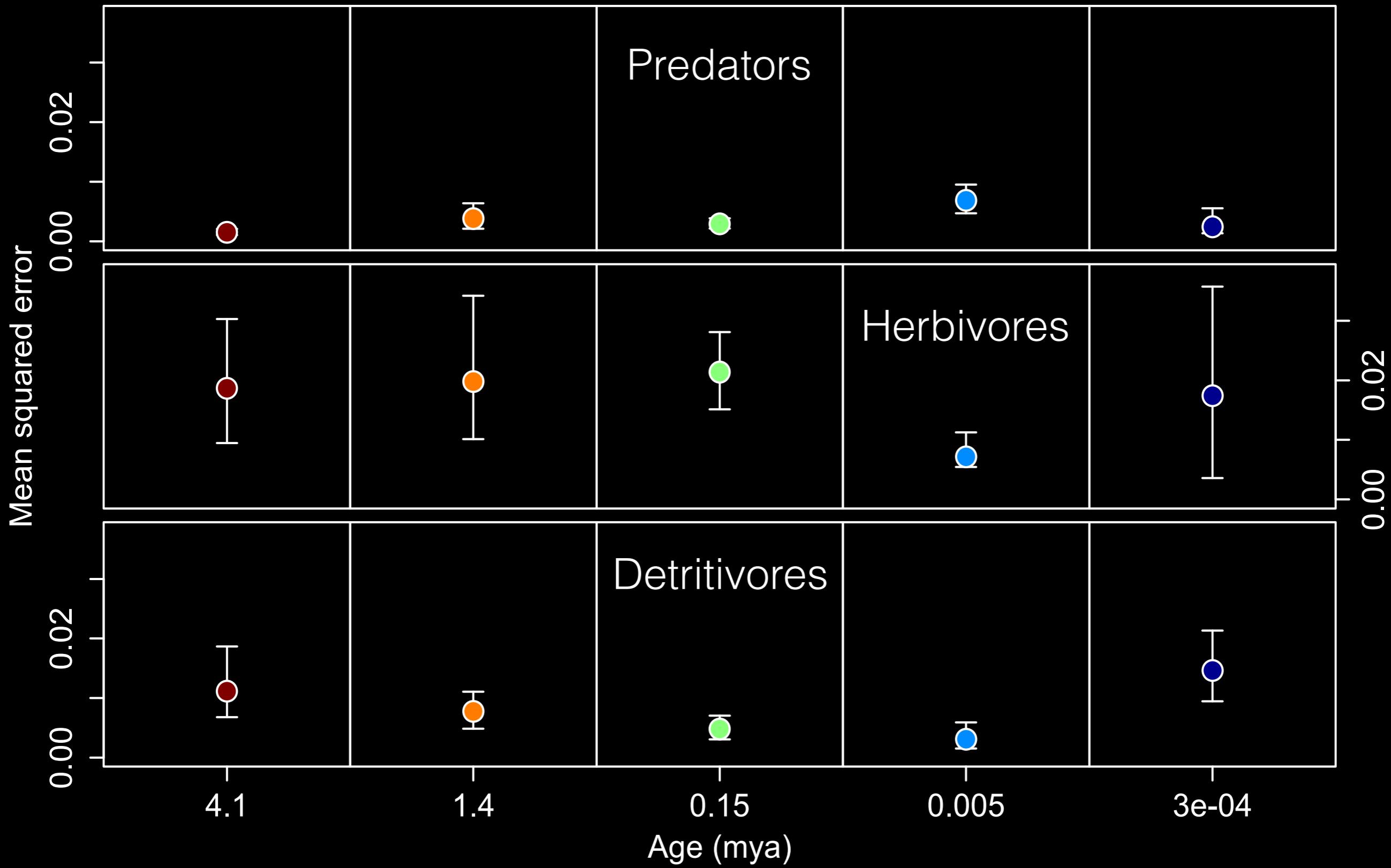


# Individual metabolic rate

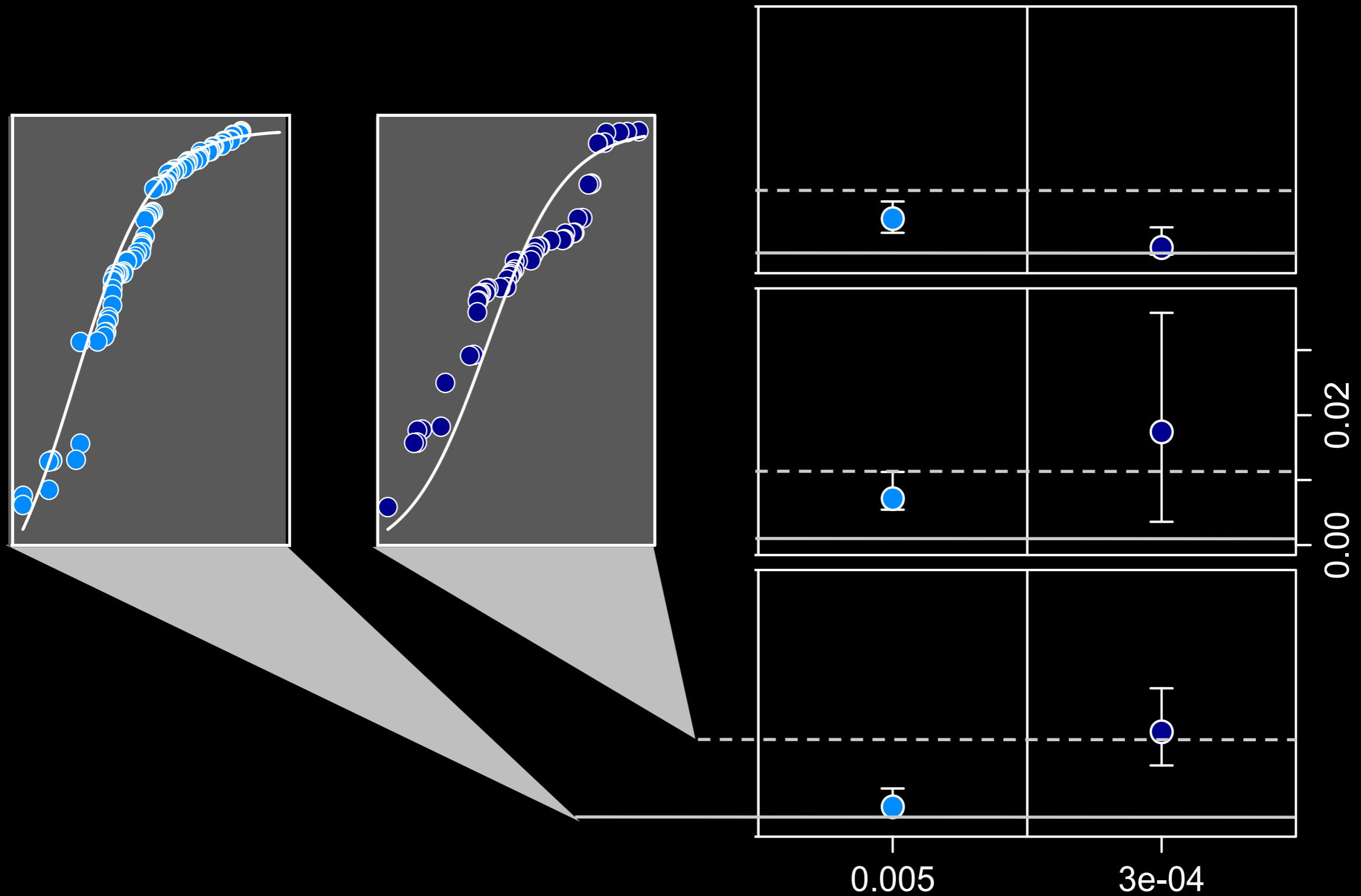


Detritivores

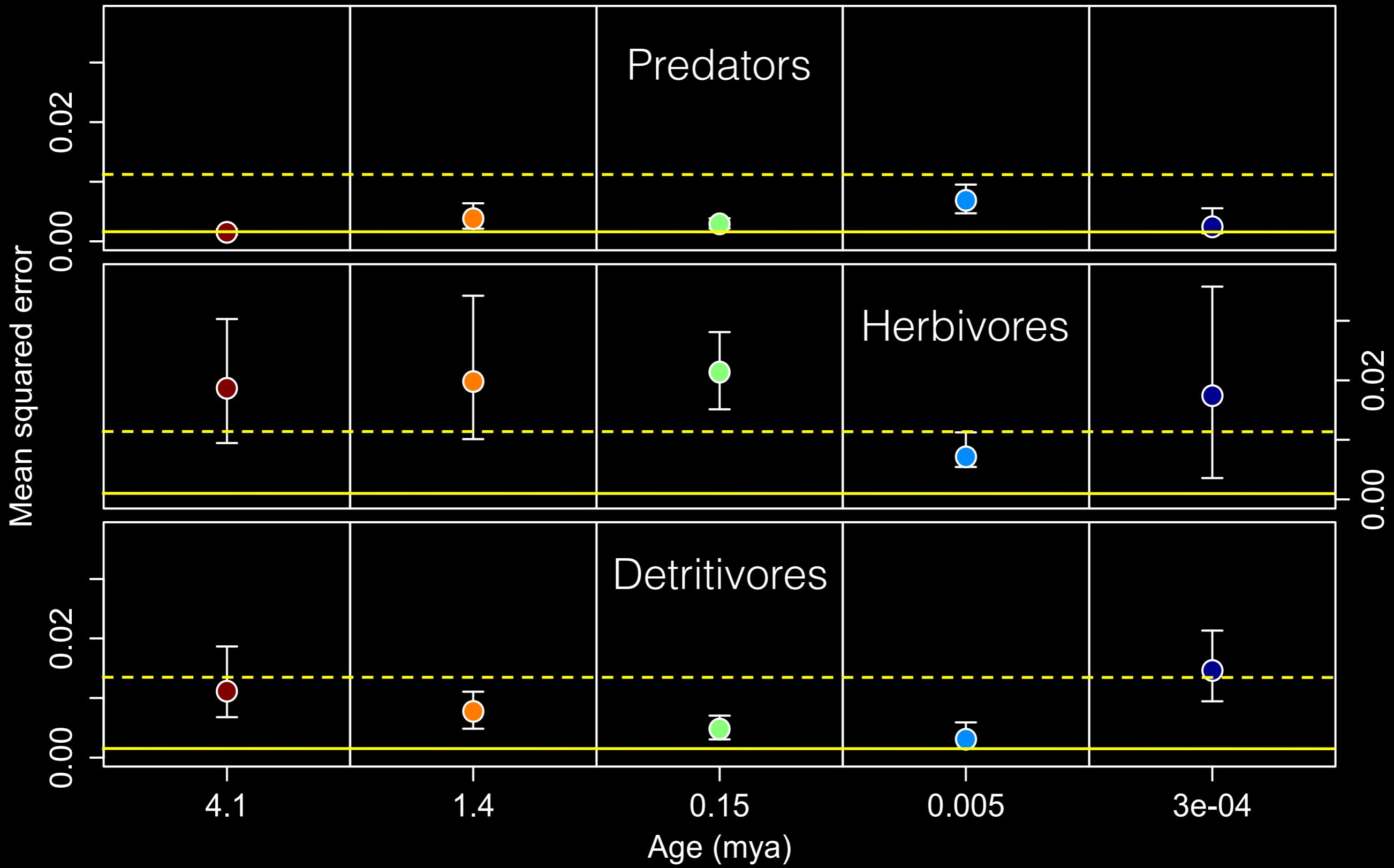
# Individual metabolic rate



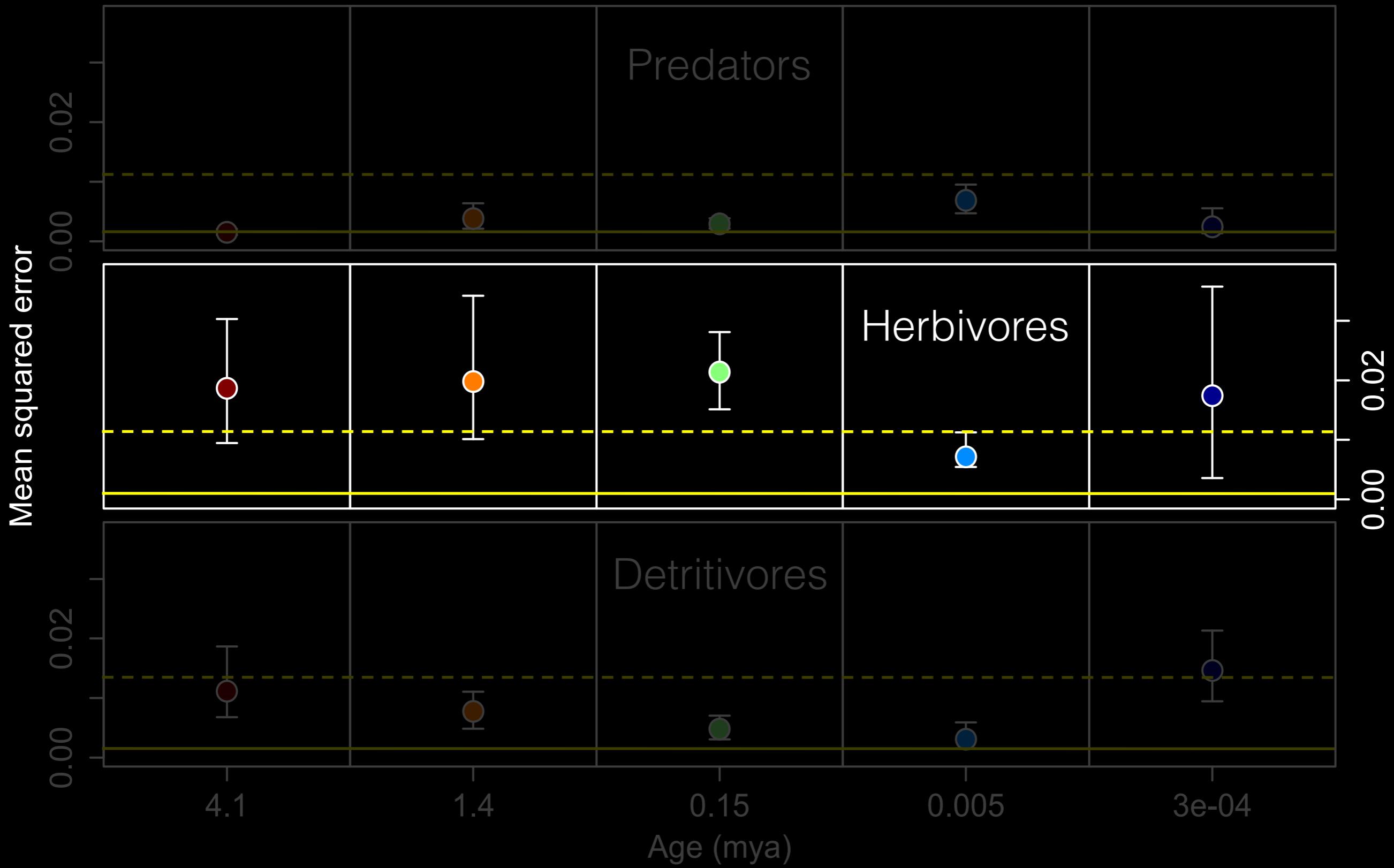
# Individual metabolic rate

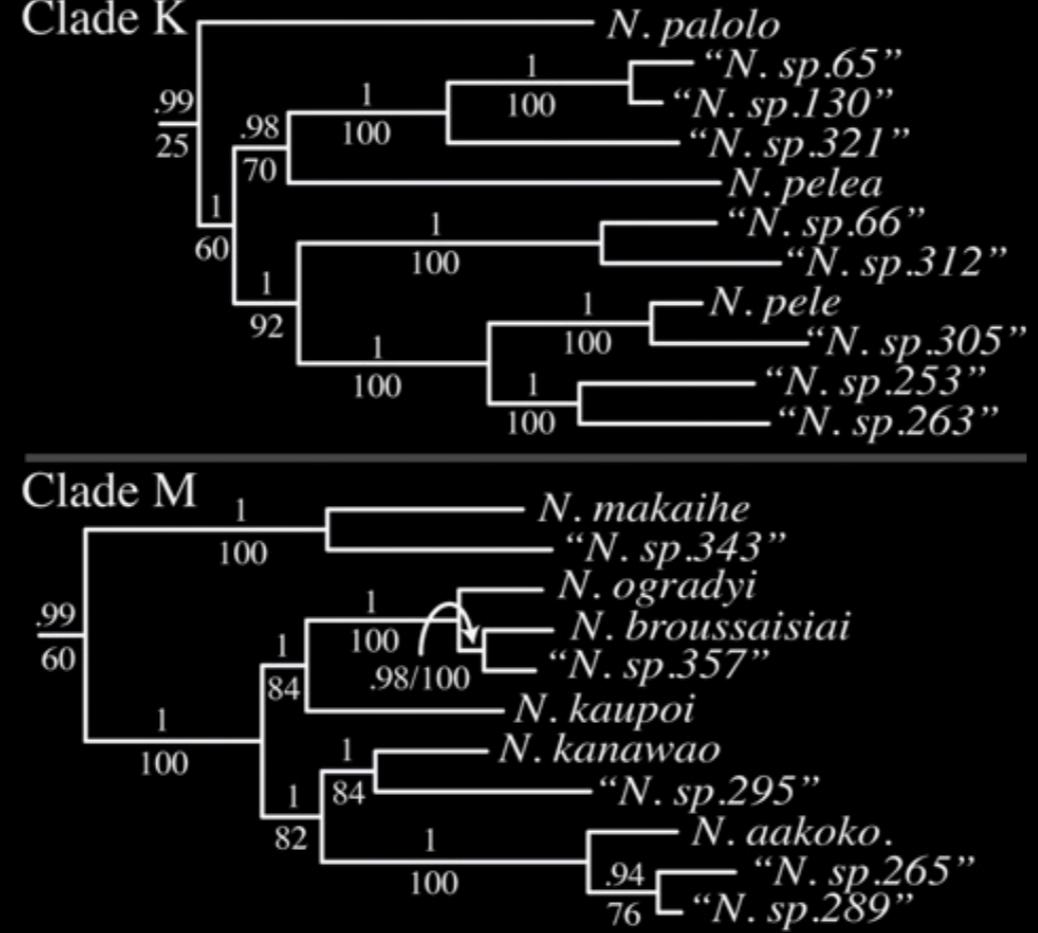
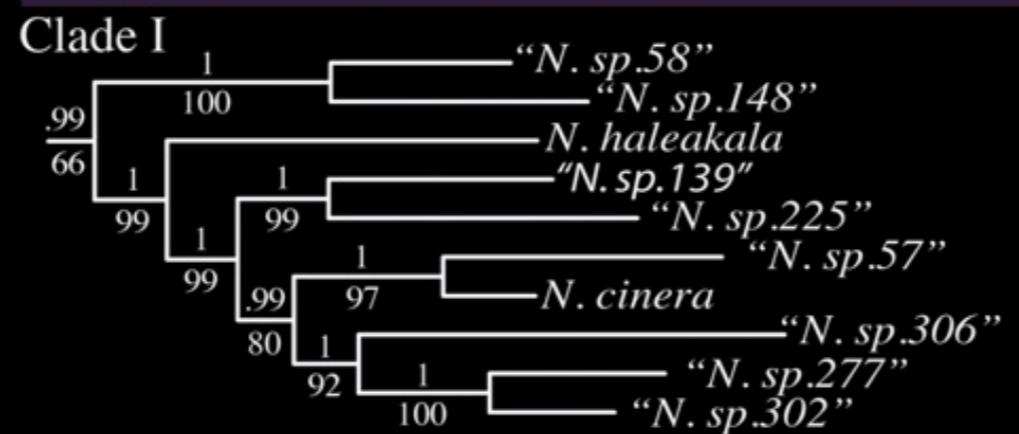
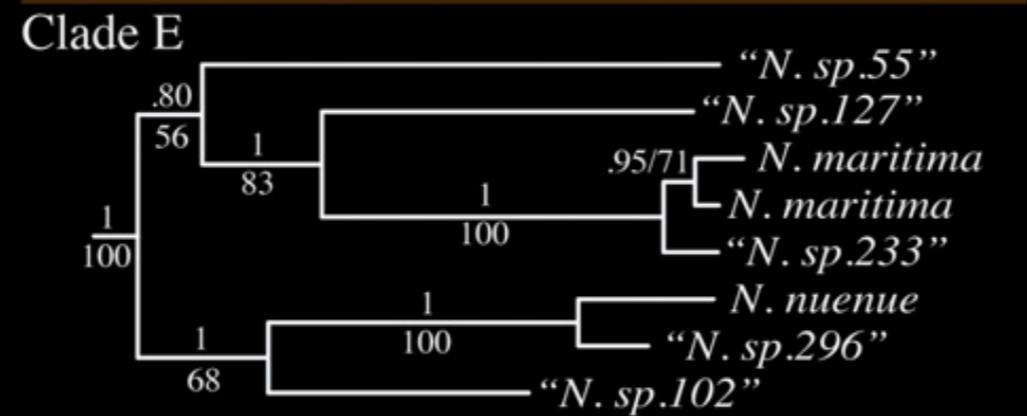


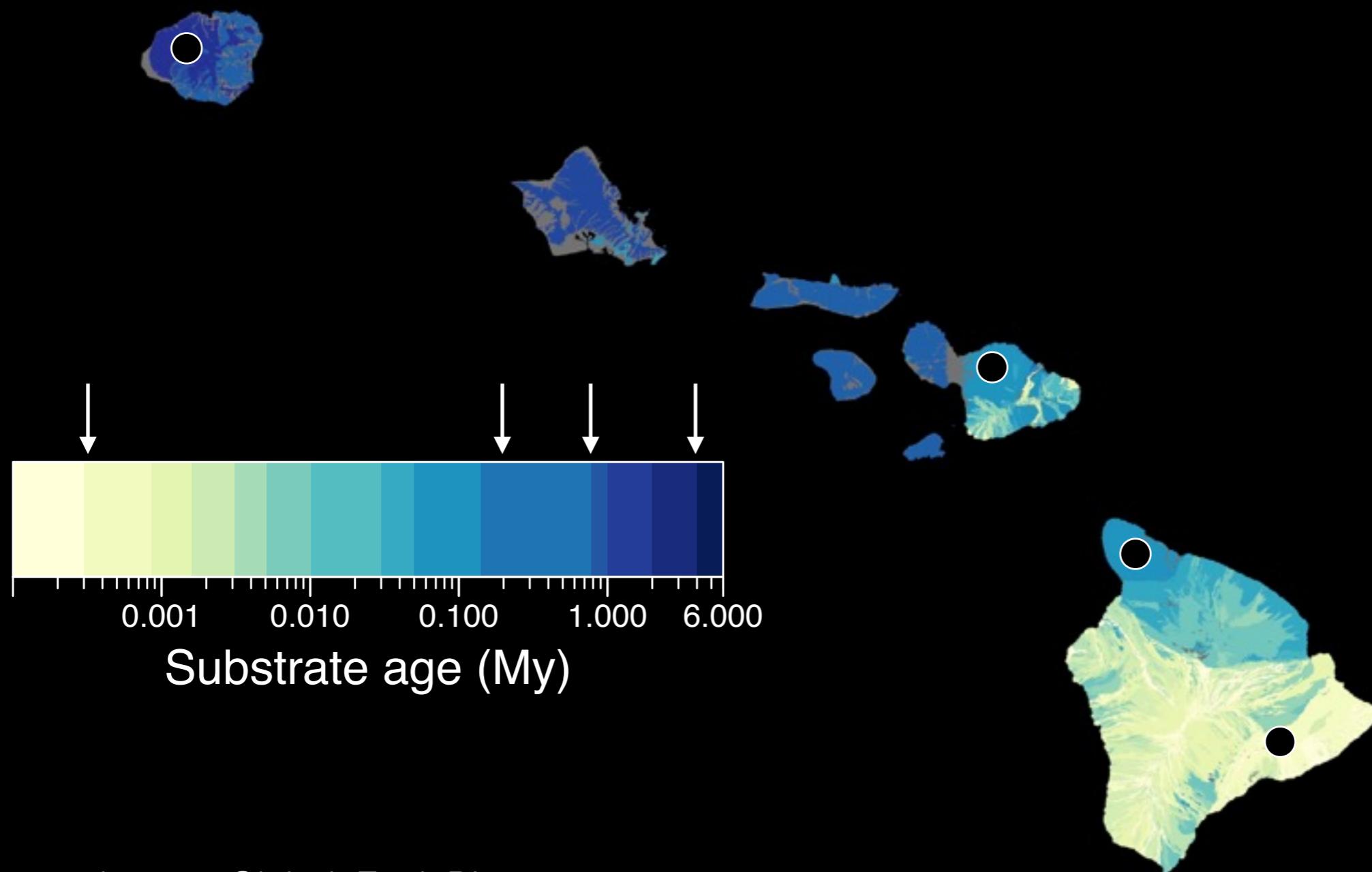
# Individual metabolic rate

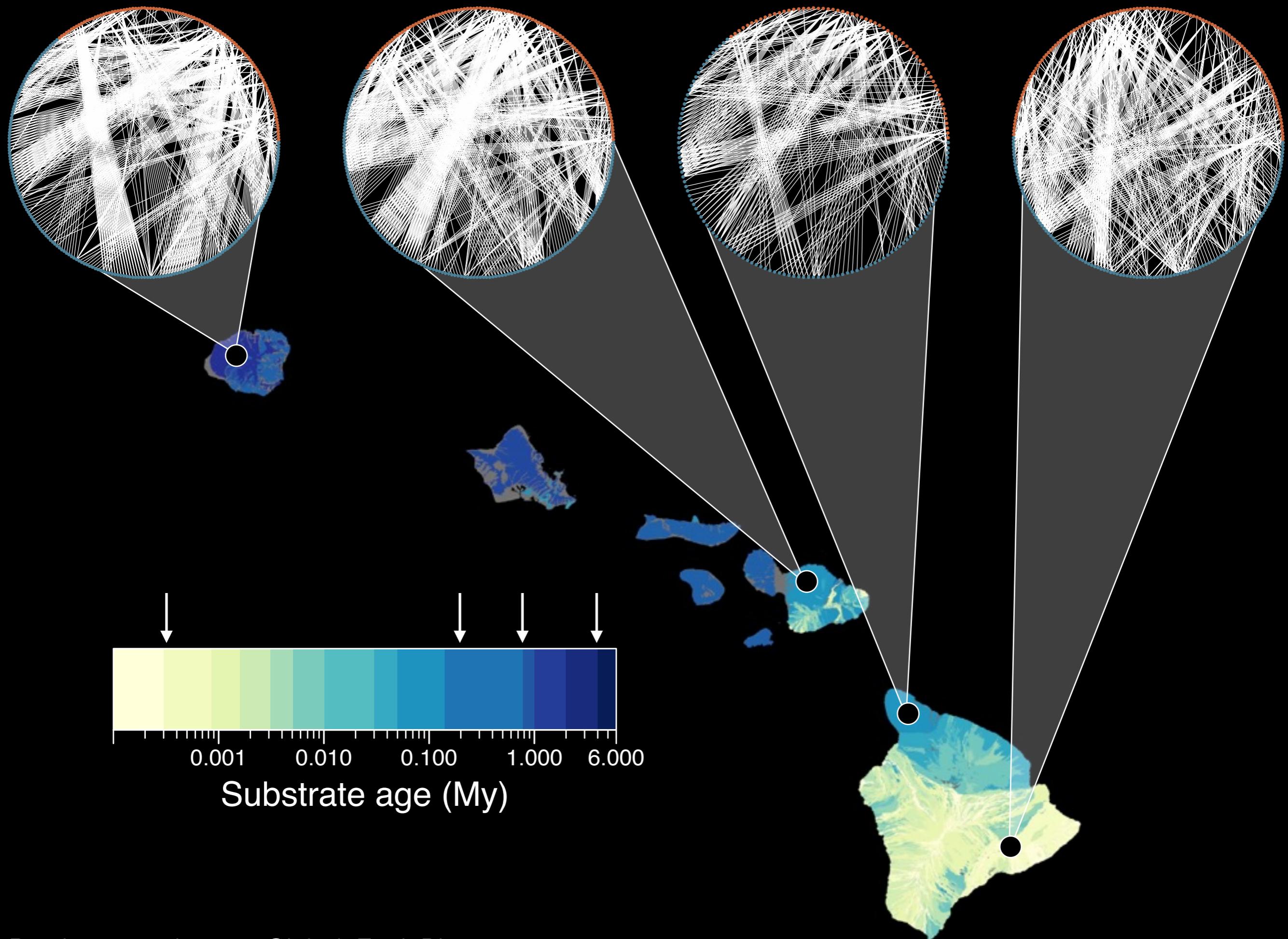


# Individual metabolic rate

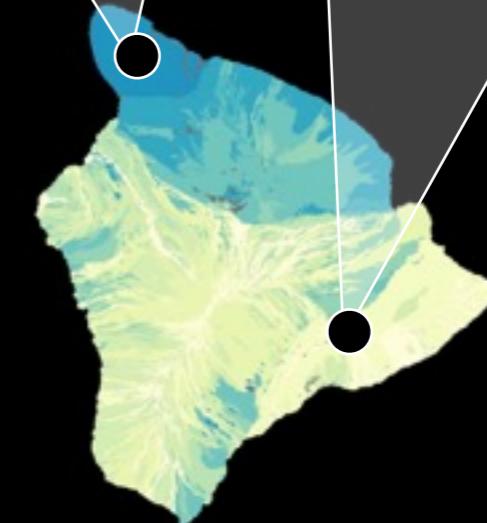
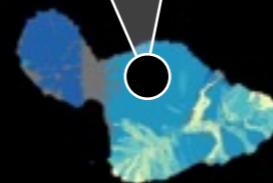
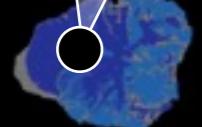
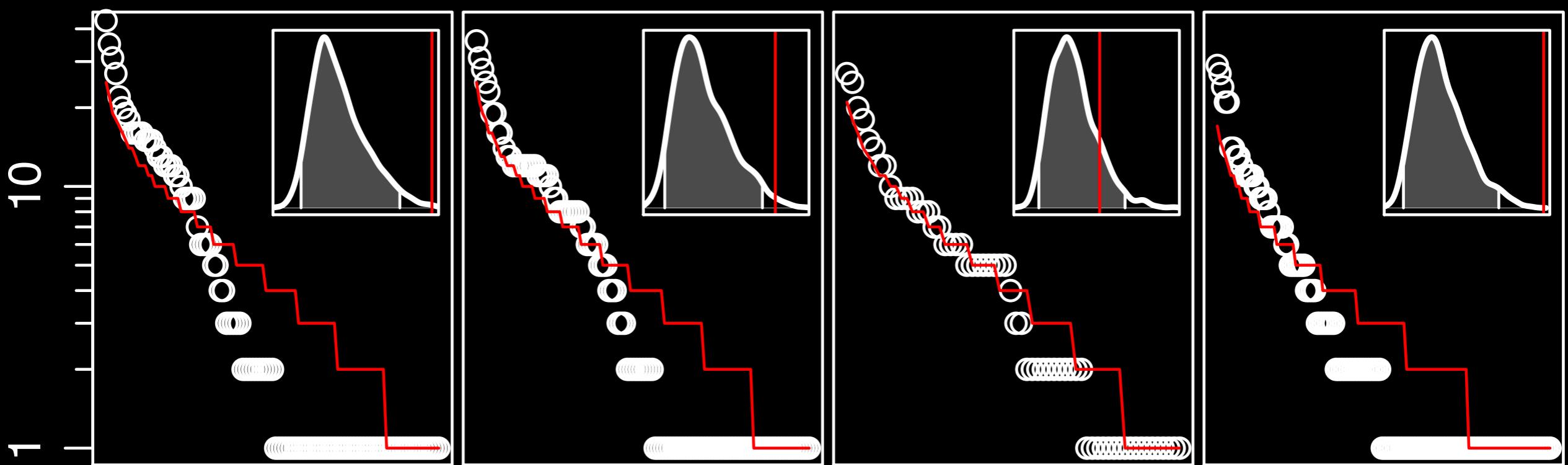


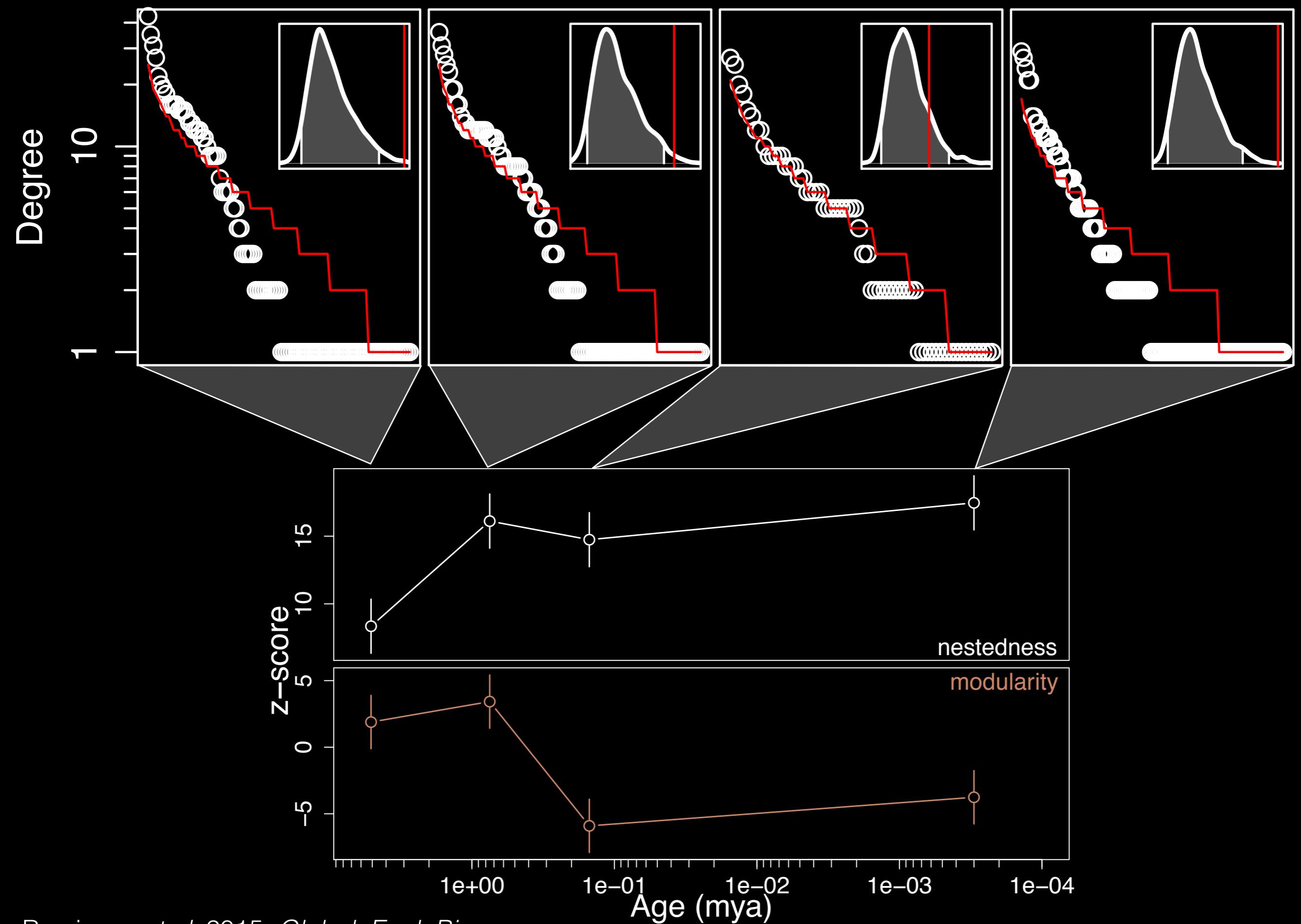




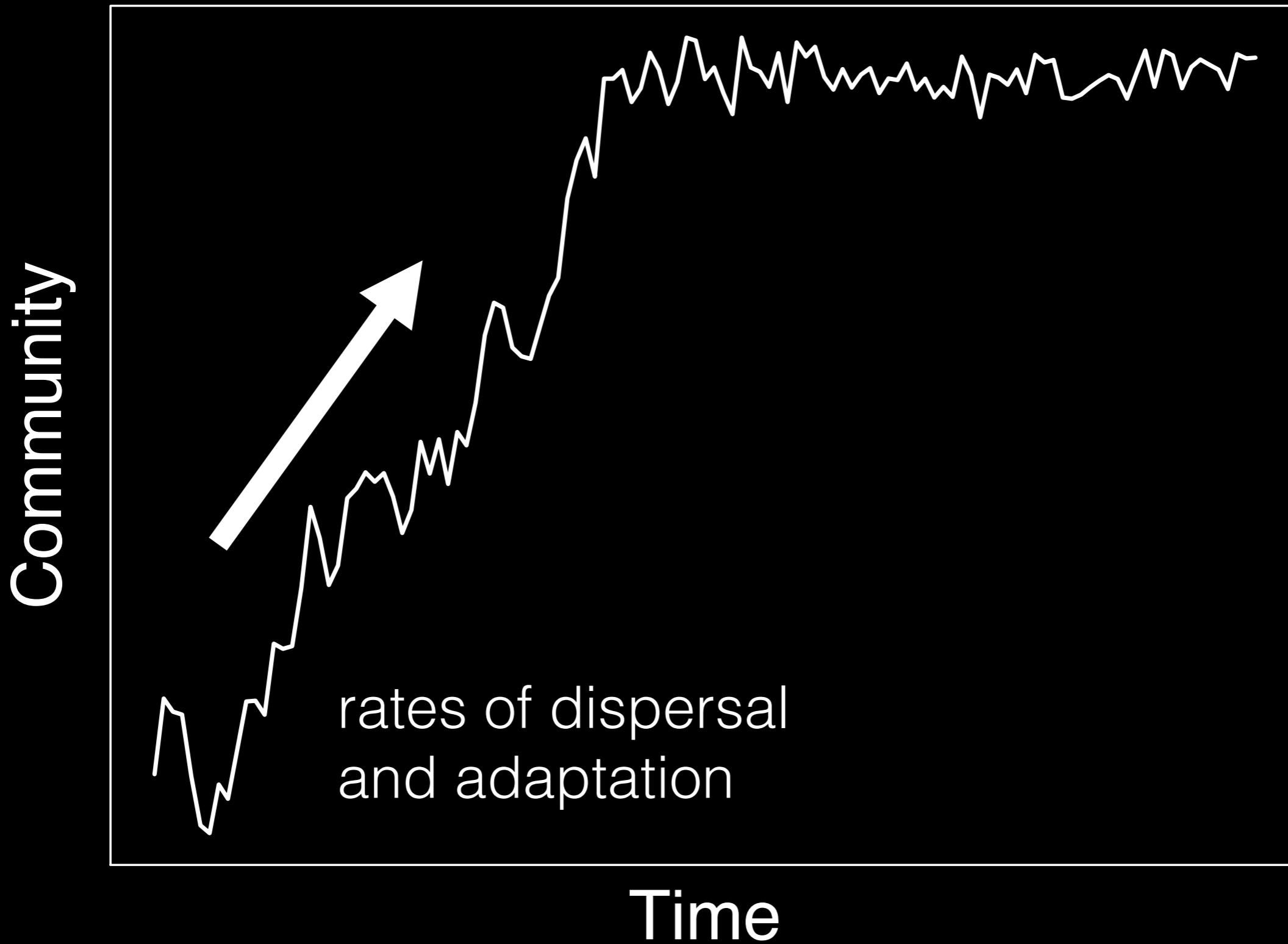


Degree

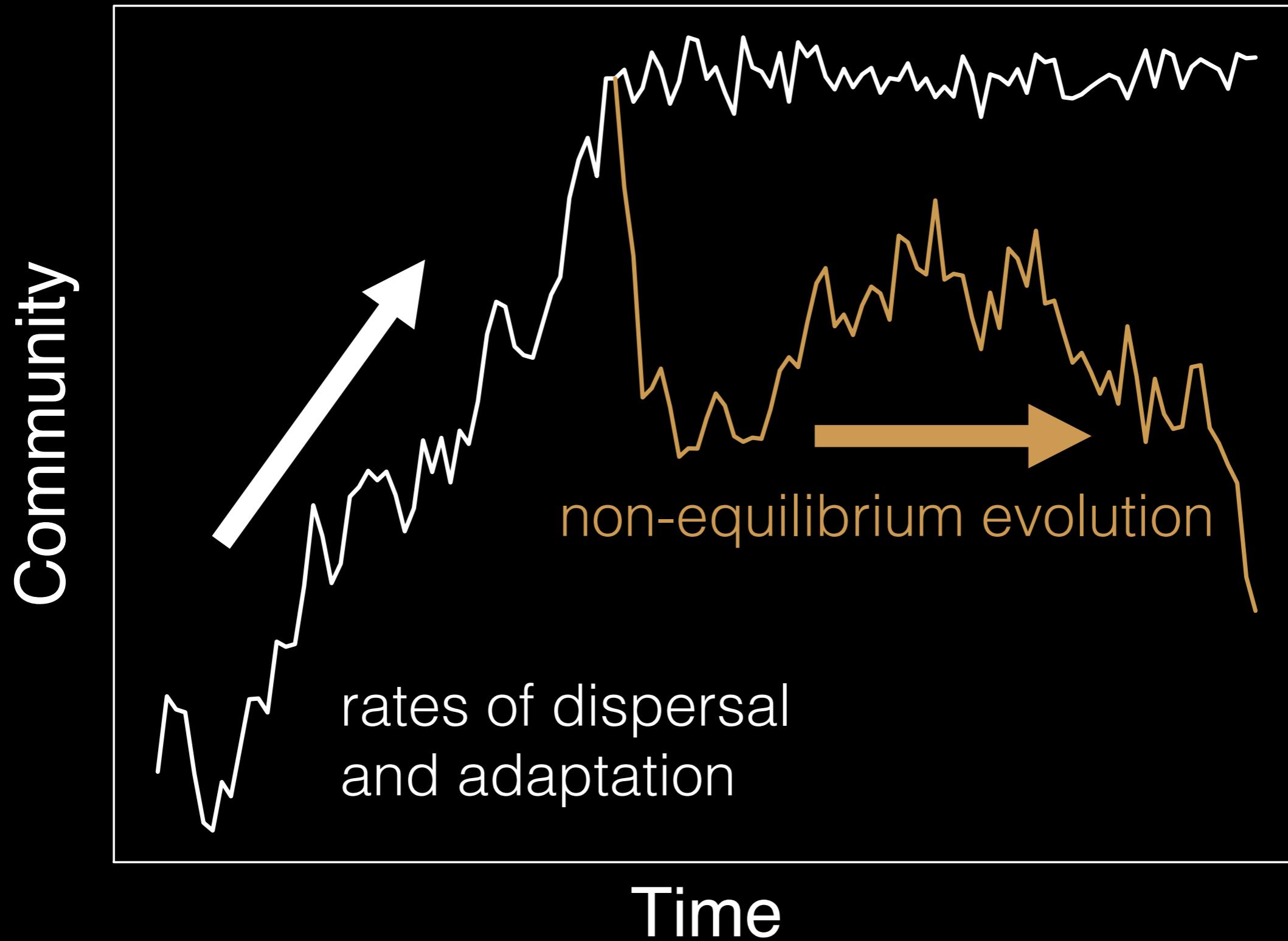




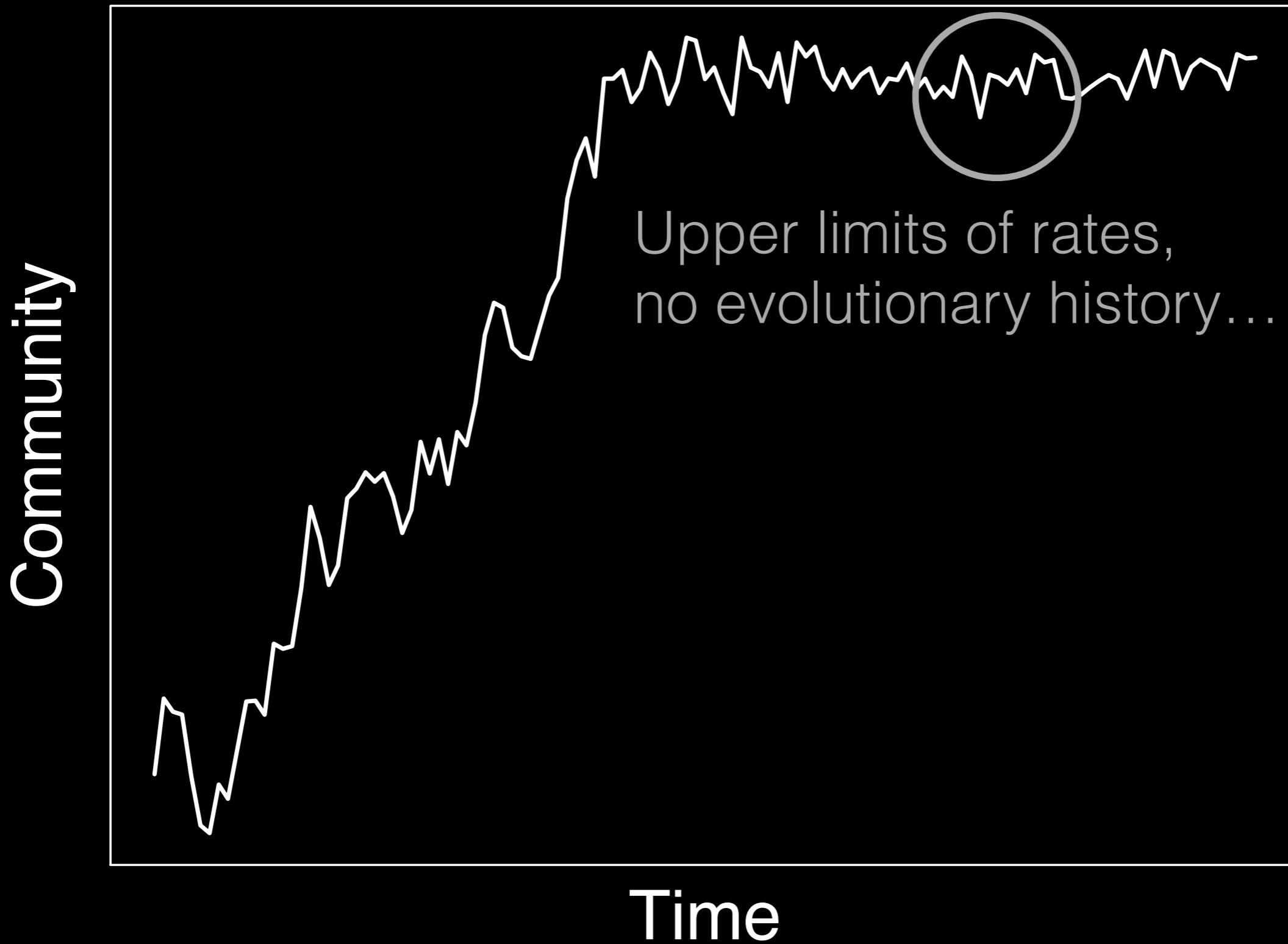
# Importance of memory



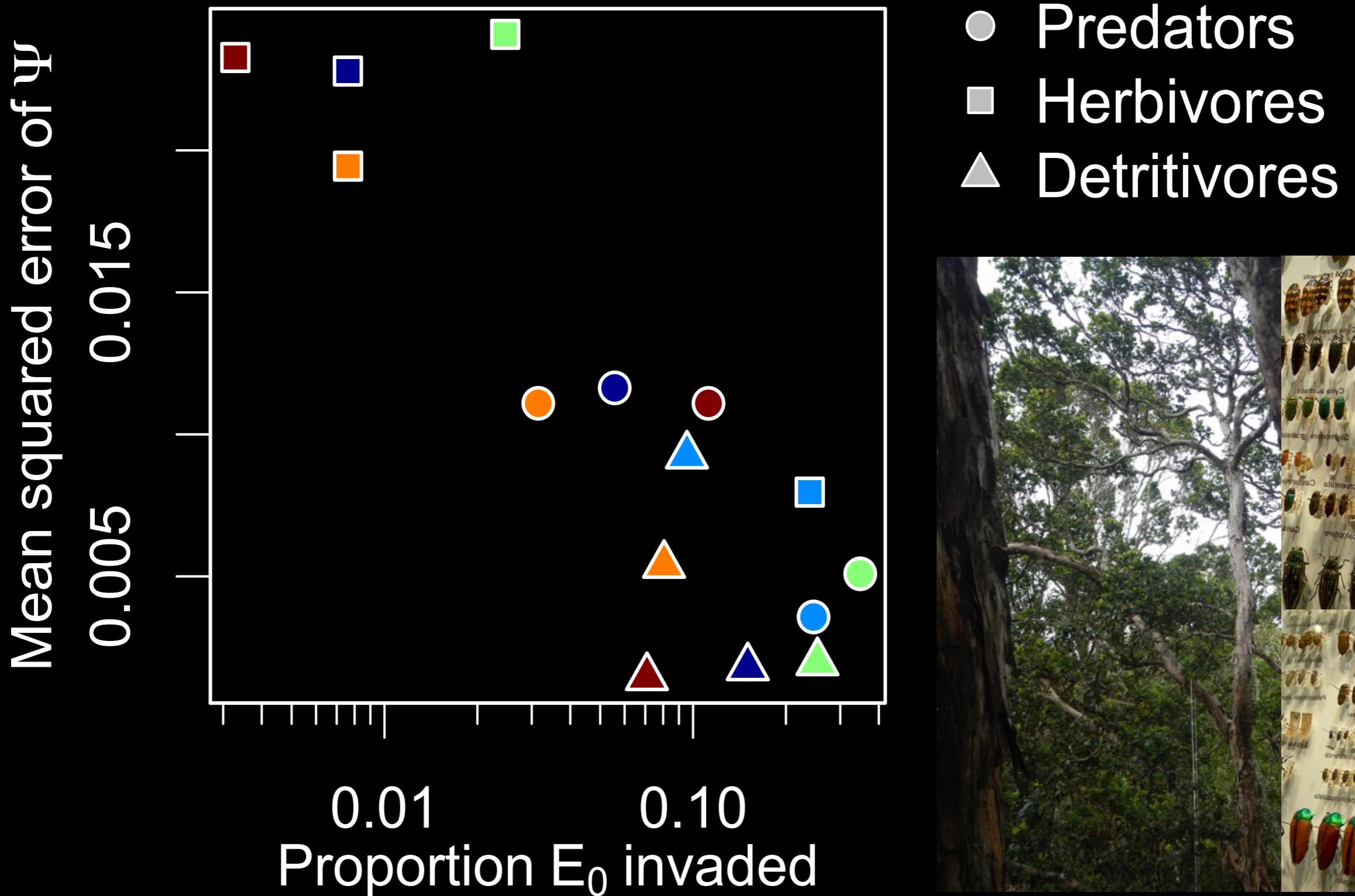
# Importance of memory



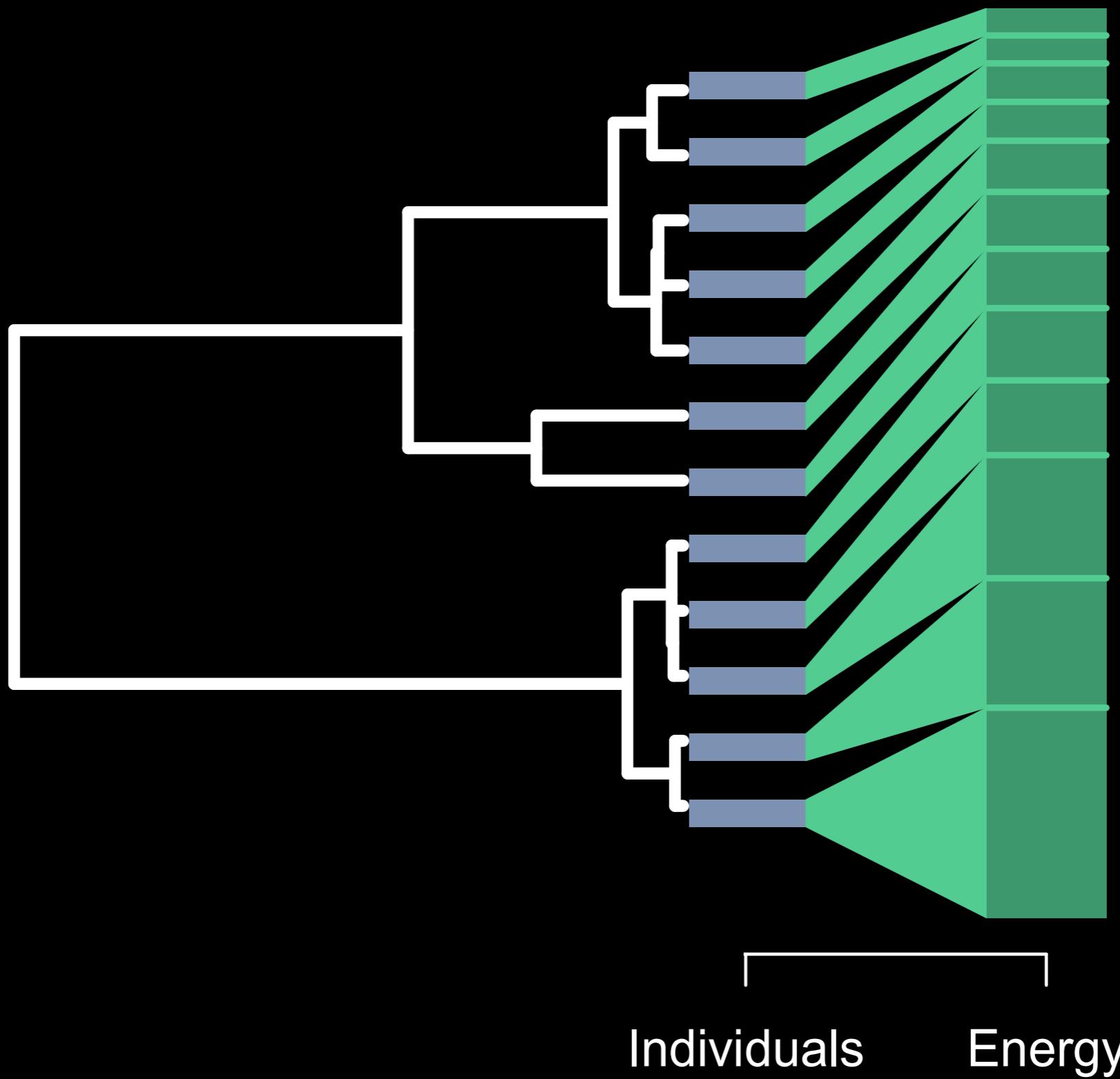
# Importance of memory



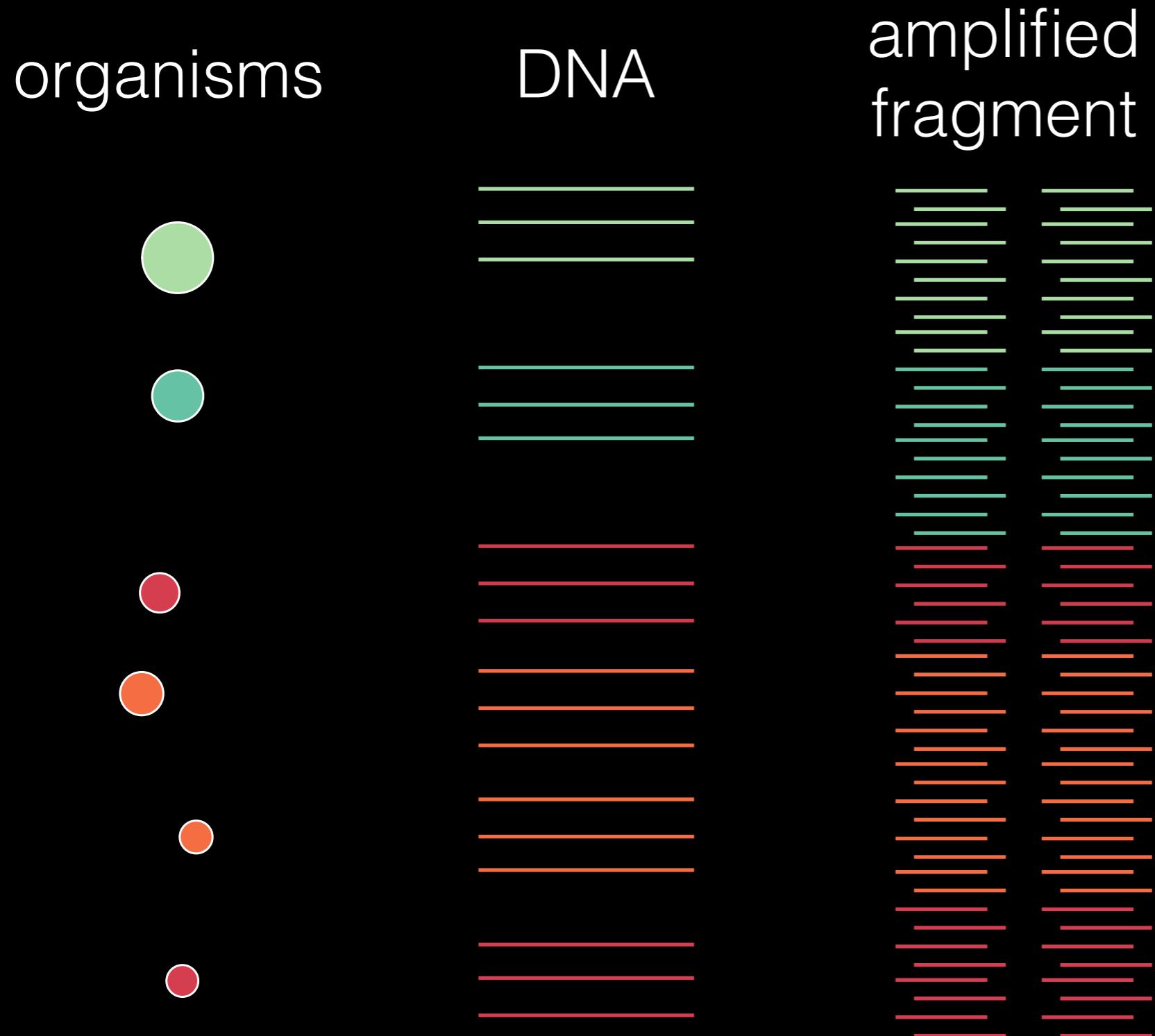
# Importance of history



# Importance of history



# High throughput ecology

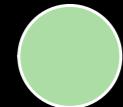


# High throughput ecology

organisms

DNA

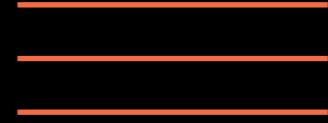
amplified  
fragment



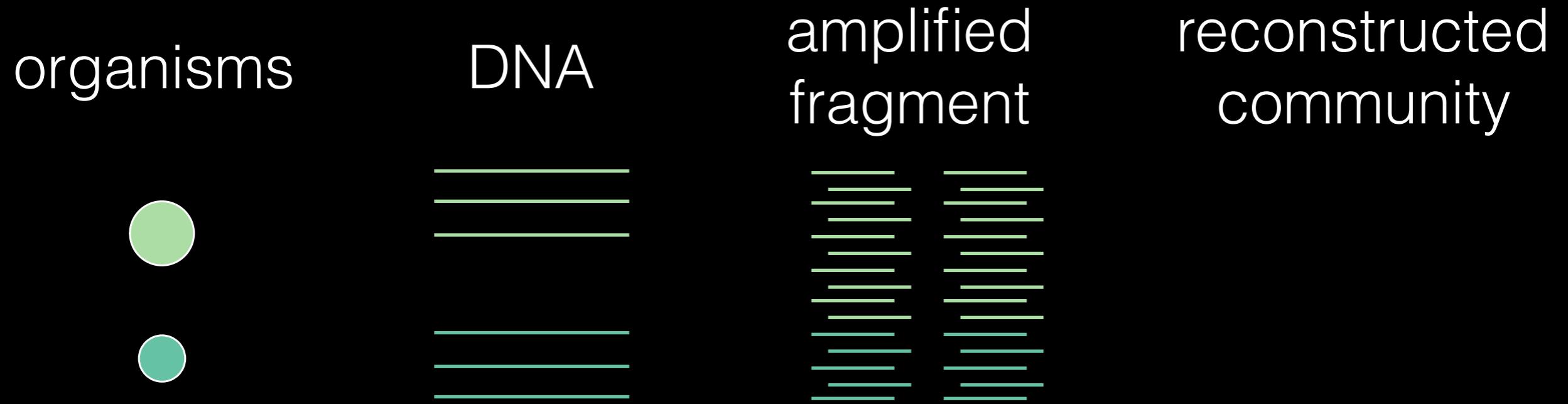
Henrik Krehenwinkel  
Sy 15b. Ev4.



Invertebrate evolution on  
islands  
Wednesday, 20 July



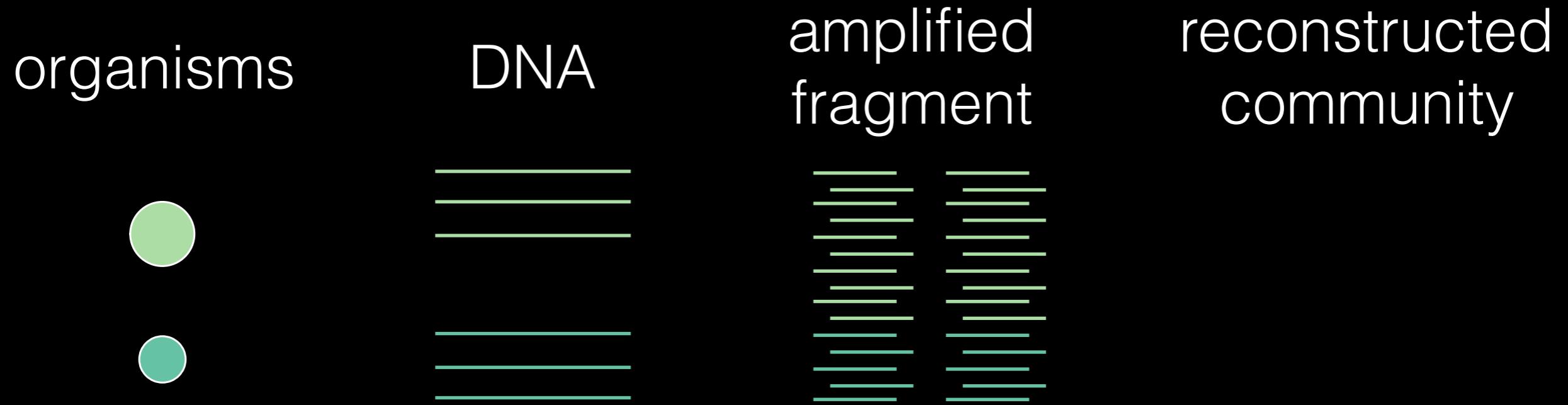
# High throughput ecology



$$\mathbb{P}(\text{comm} \mid \text{data}) =$$

$$\int_{\text{samp}} \frac{\mathbb{P}(\text{real data} \mid \text{sampling, ideal data}) \mathbb{P}(\text{ideal data} \mid \text{comm}) \mathbb{P}(\text{comm, sampling})}{\mathbb{P}(\text{data})} d\theta_{\text{samp}}$$

# High throughput ecology

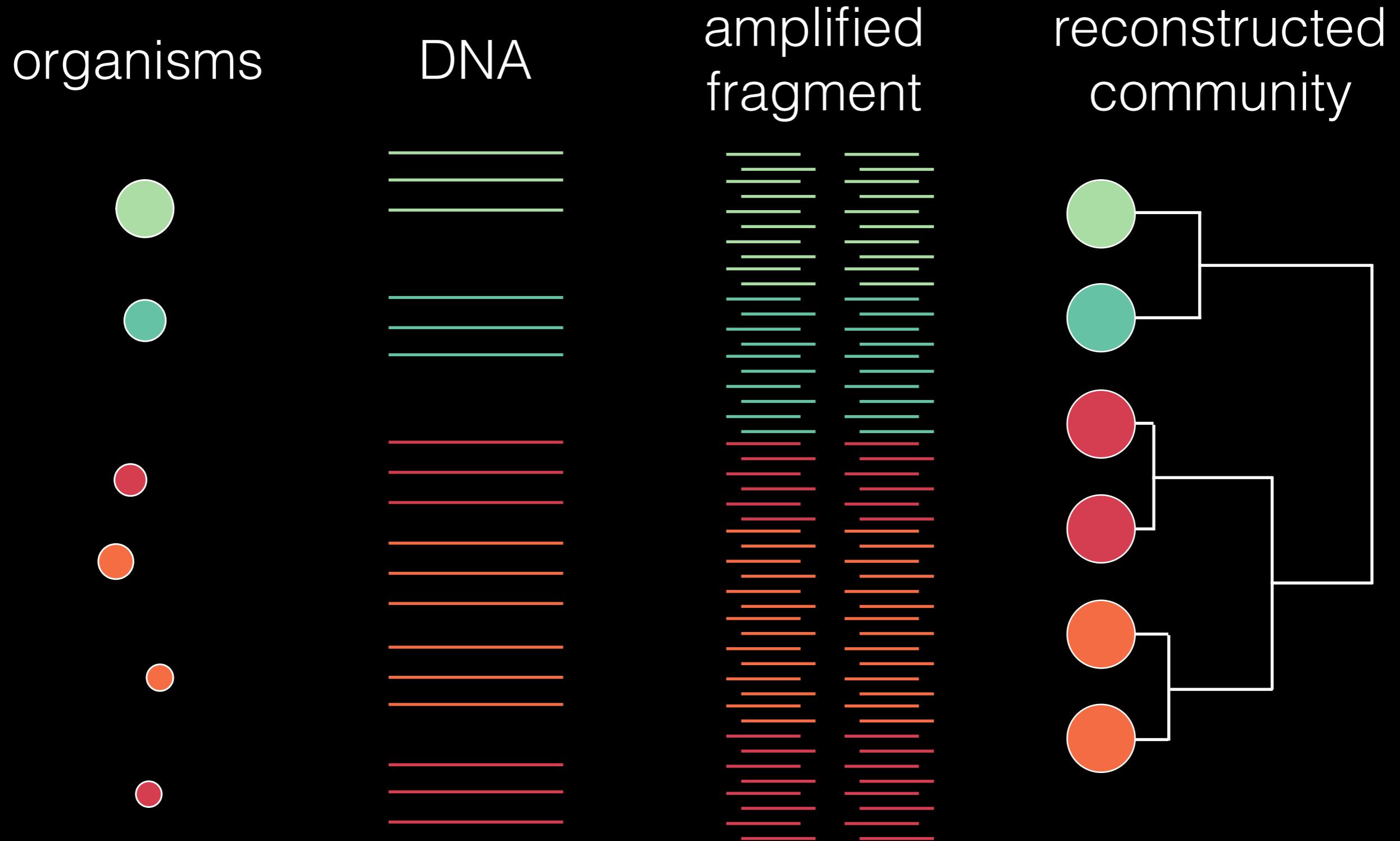


$$\mathbb{P}(\text{comm} \mid \text{data}) =$$

$$\int_{\text{samp}} \frac{\mathbb{P}(\text{real data} \mid \text{sampling, ideal data}) \mathbb{P}(\text{ideal data} \mid \text{comm}) \mathbb{P}(\text{comm, sampling})}{\mathbb{P}(\text{data})} d\theta_{\text{samp}}$$

Andy Rominger  
WS – iDigBio, Digitized natural history collections  
Tuesday 19 July

# High throughput ecology



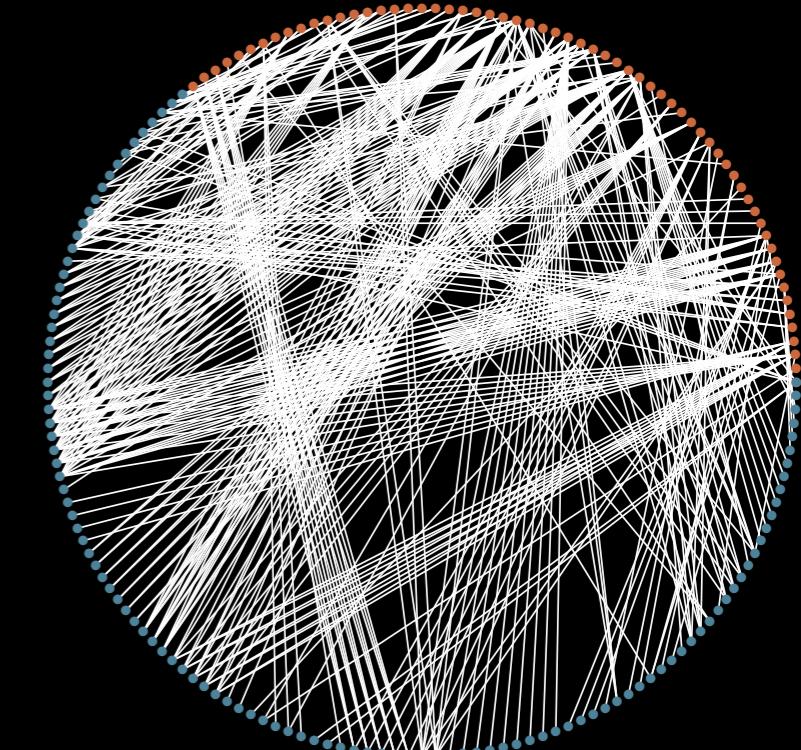
# High throughput ecology

organisms

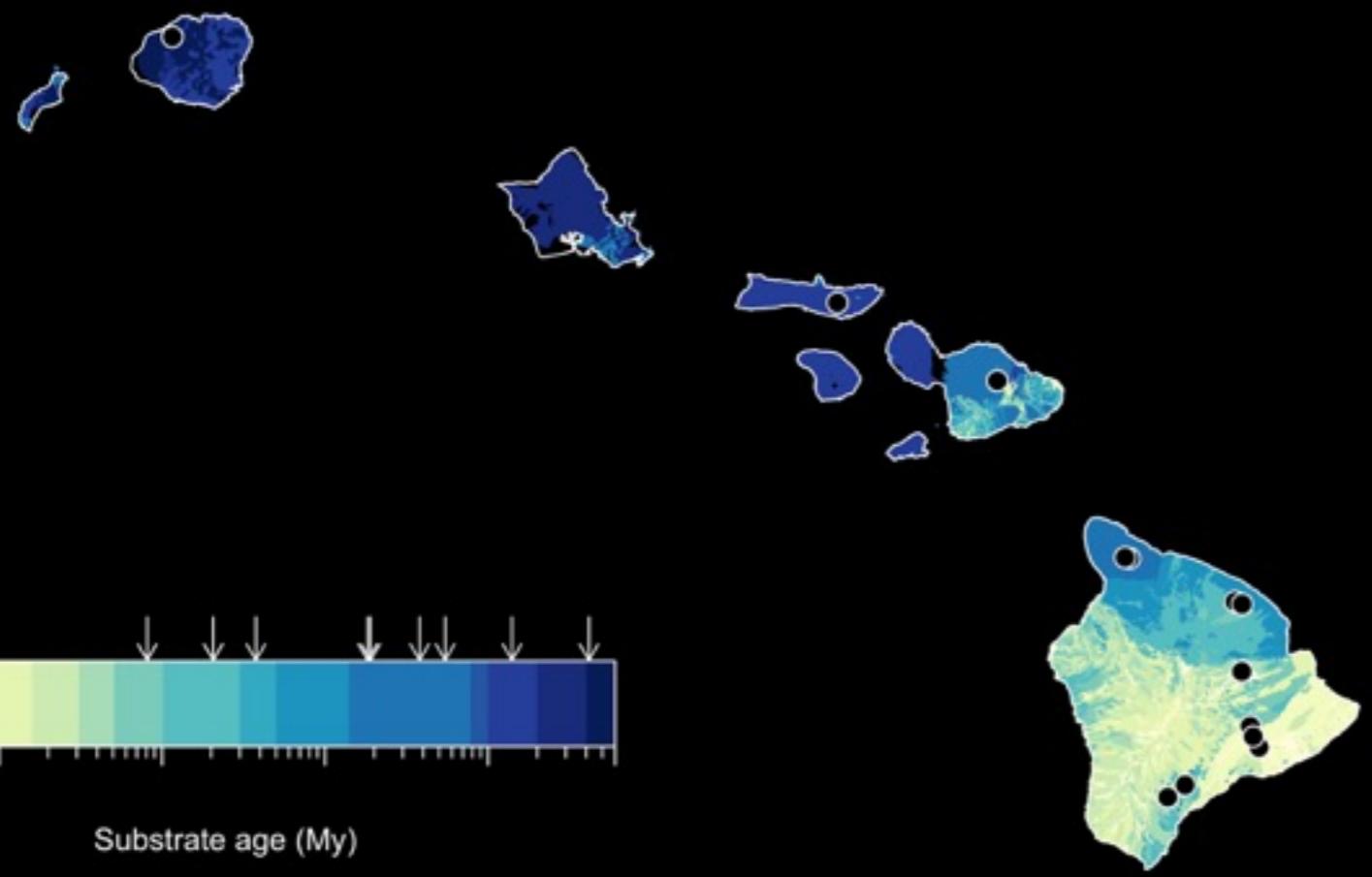
DNA

amplified  
fragment

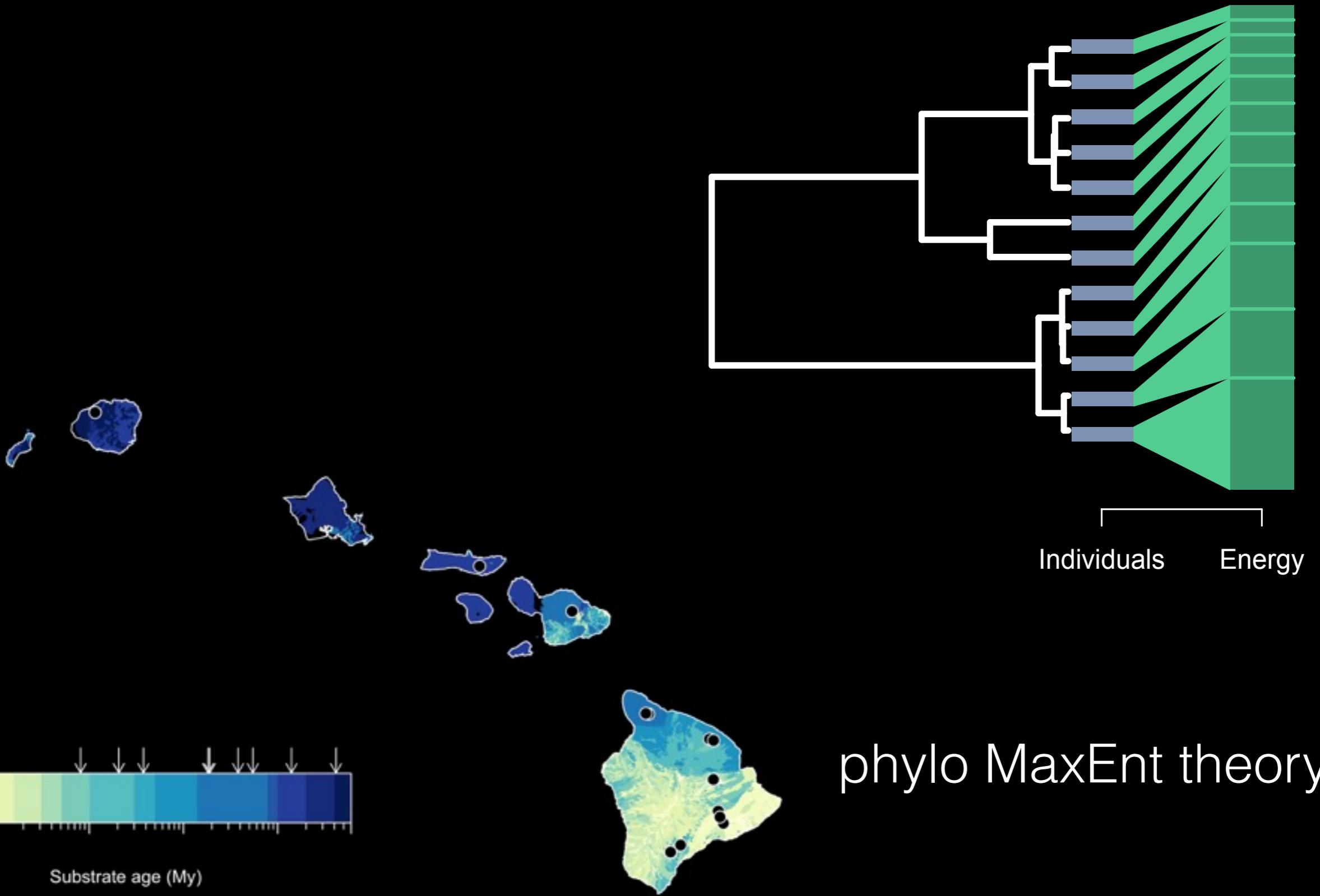
reconstructed  
community



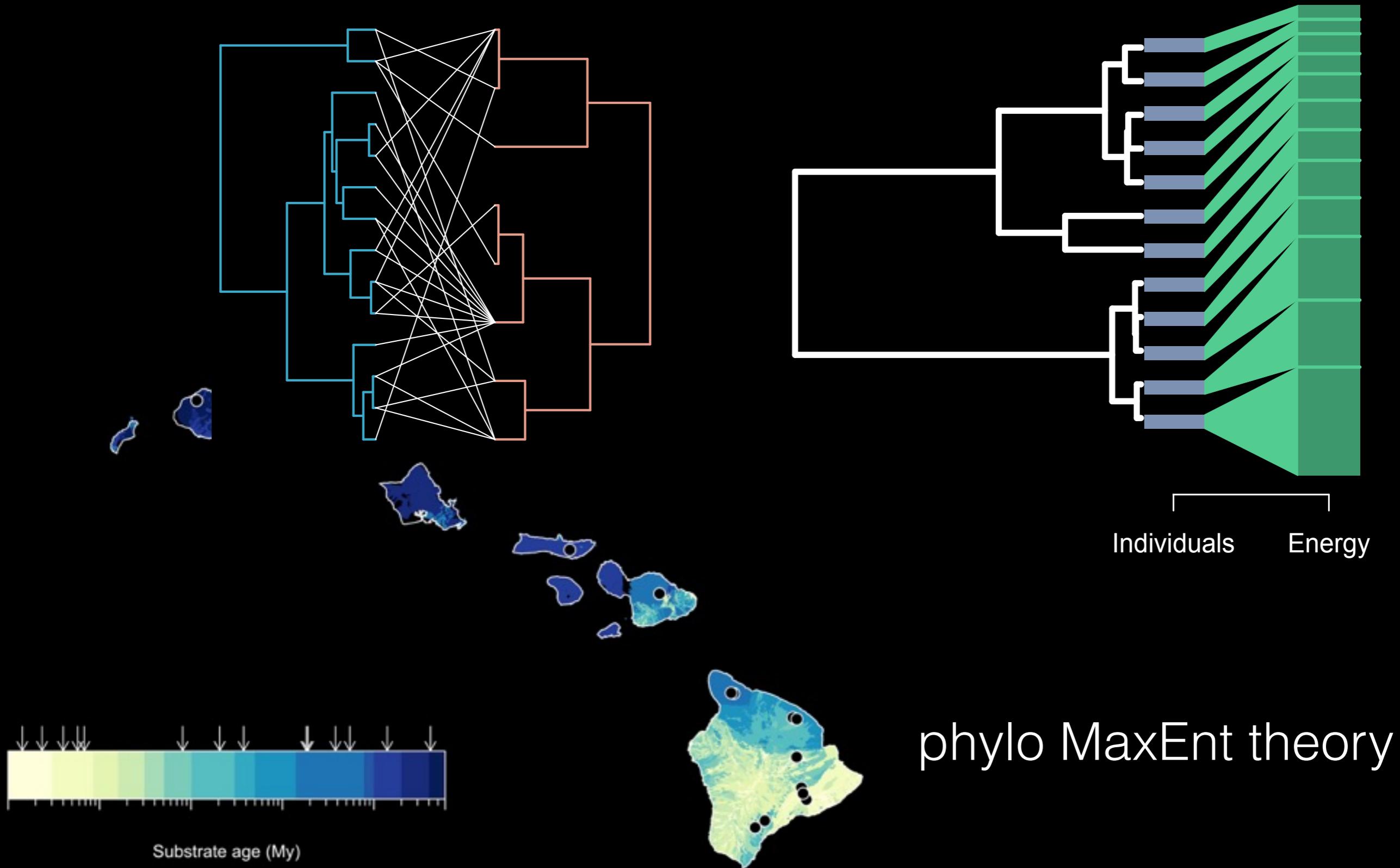
# High throughput ecology



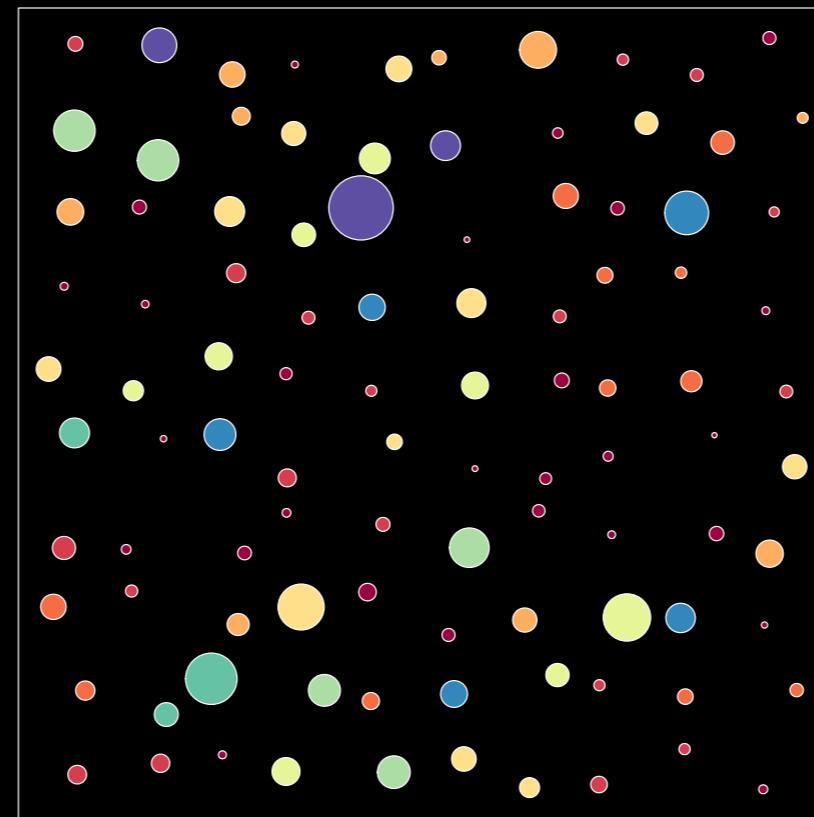
# High throughput ecology



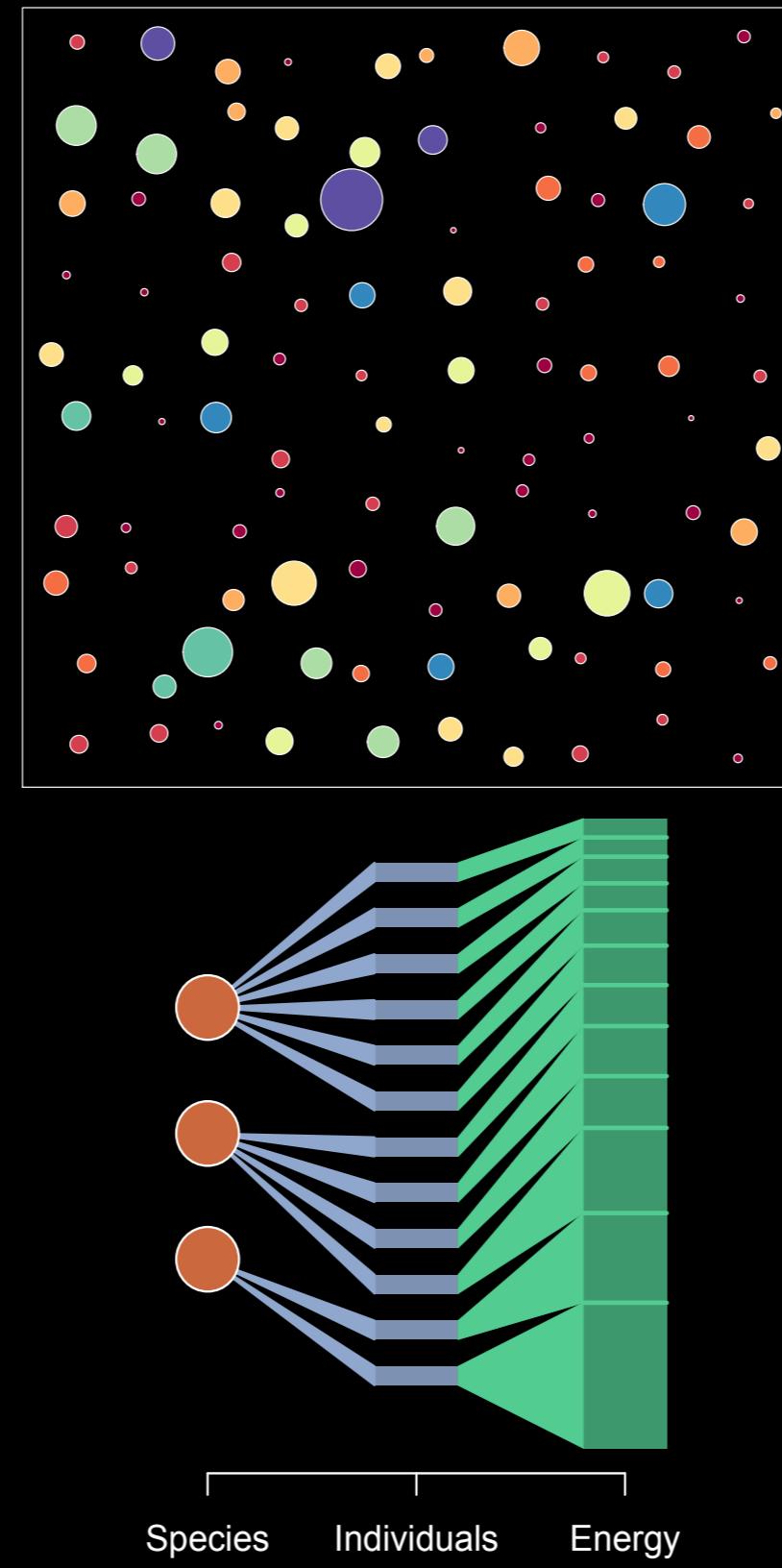
# High throughput ecology



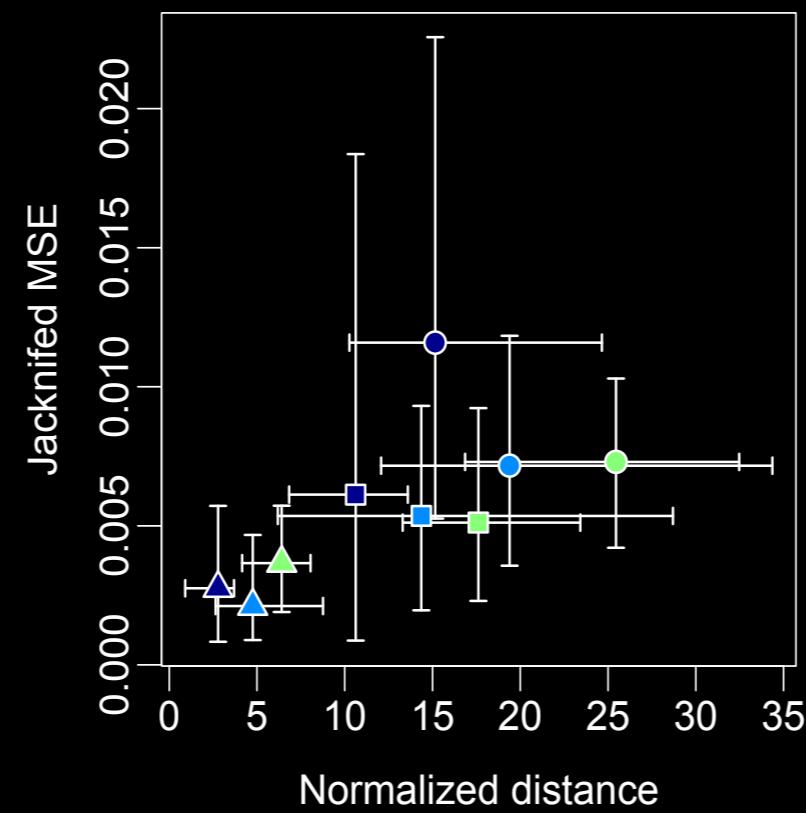
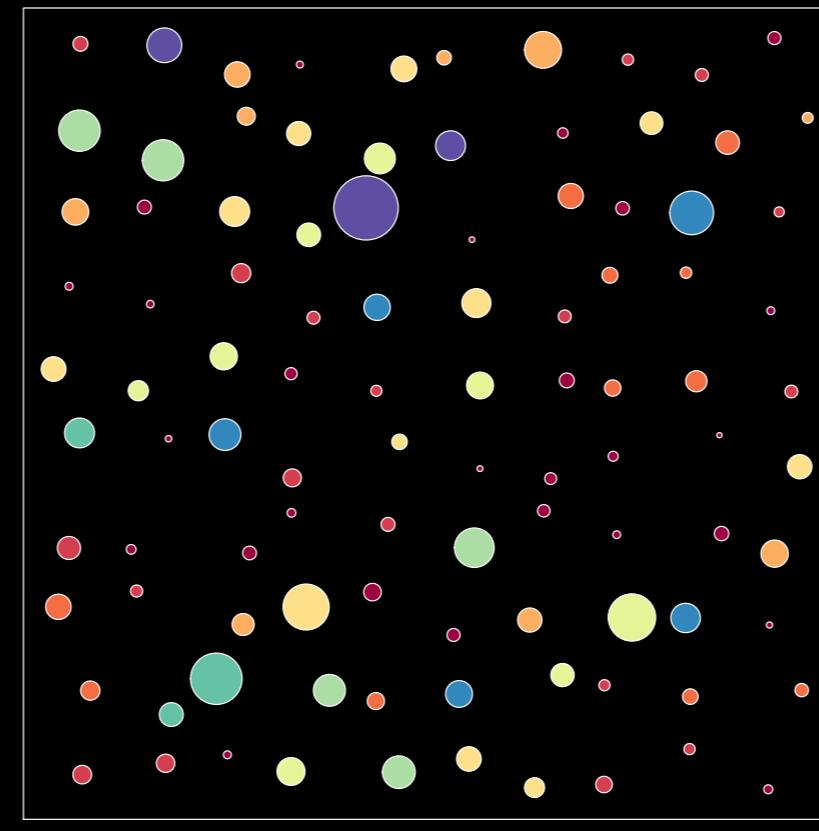
# What constrains biodiversity?



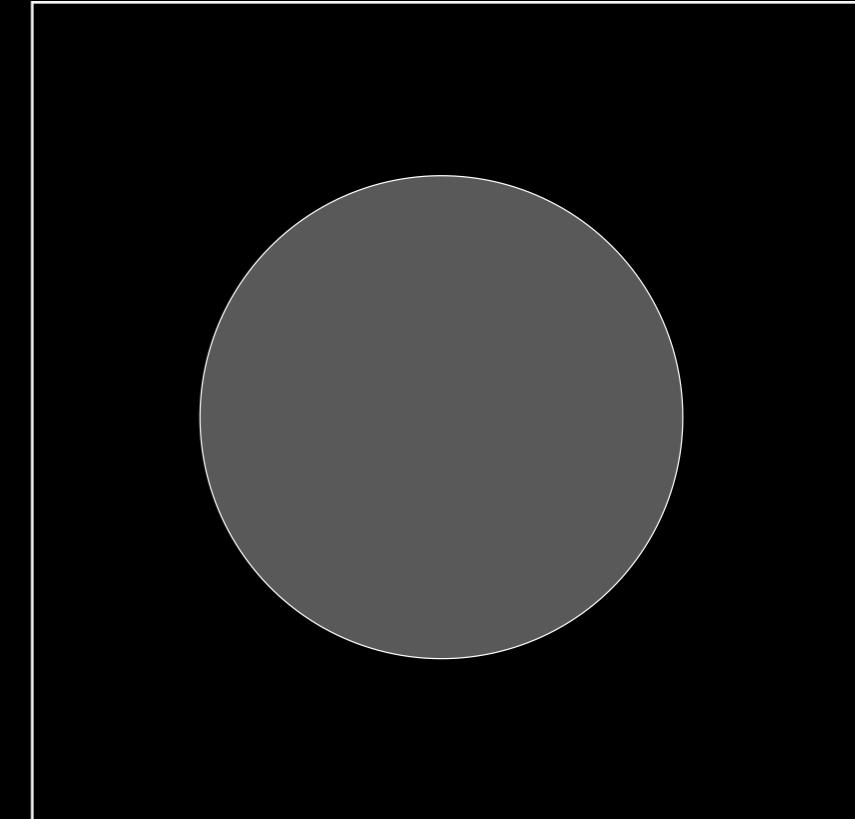
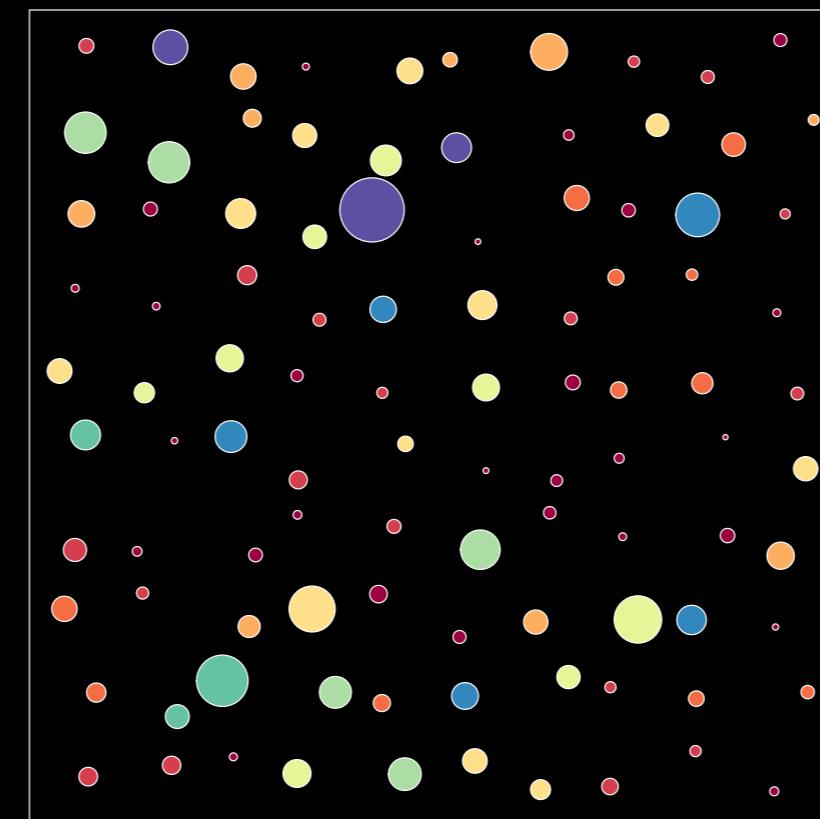
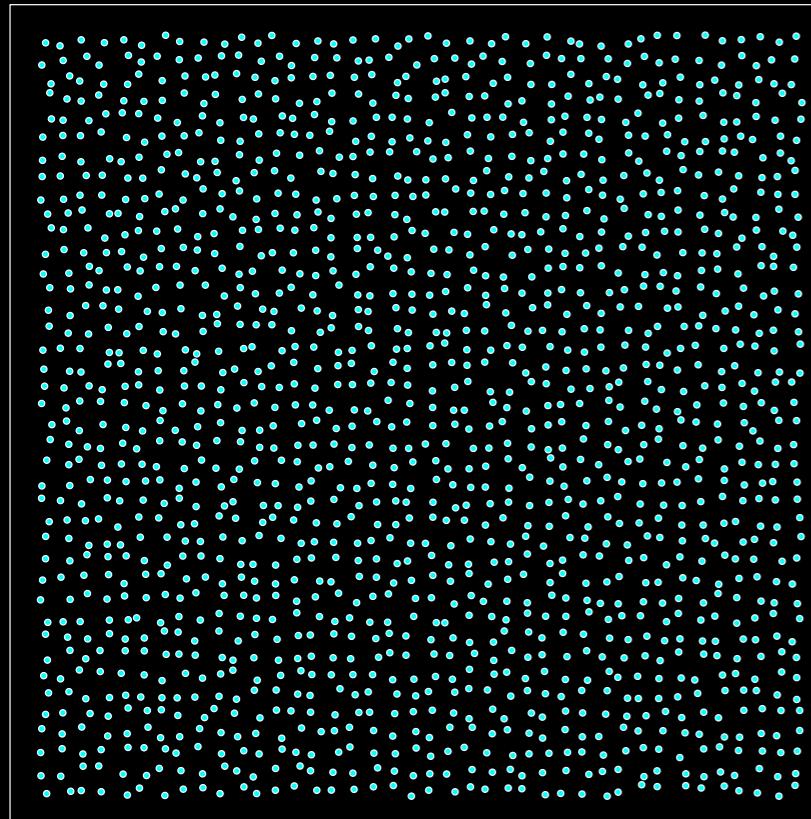
# What constrains biodiversity?



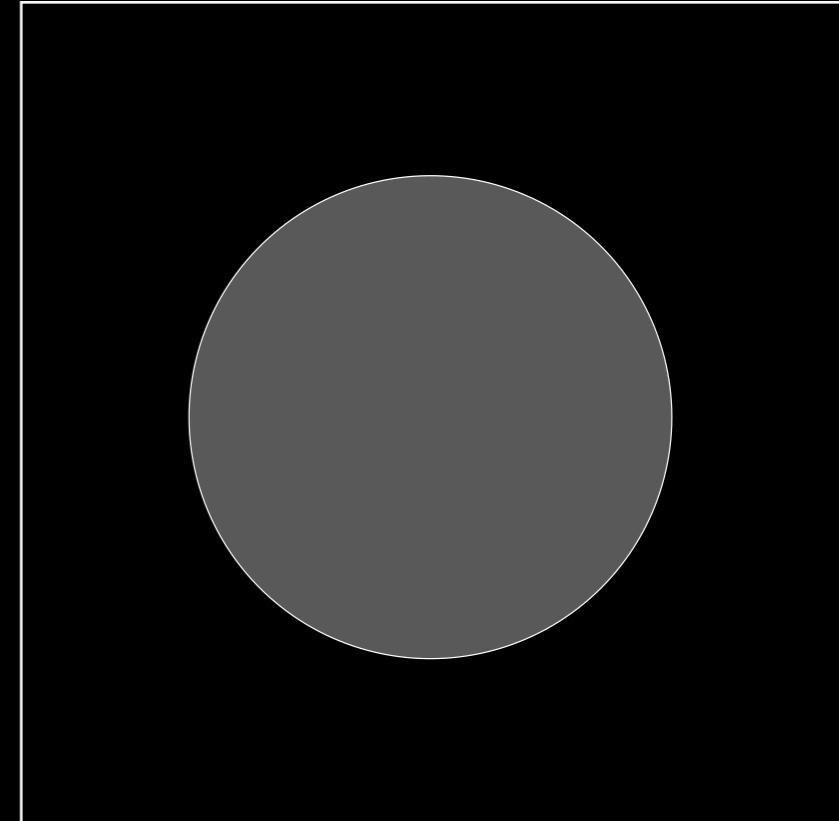
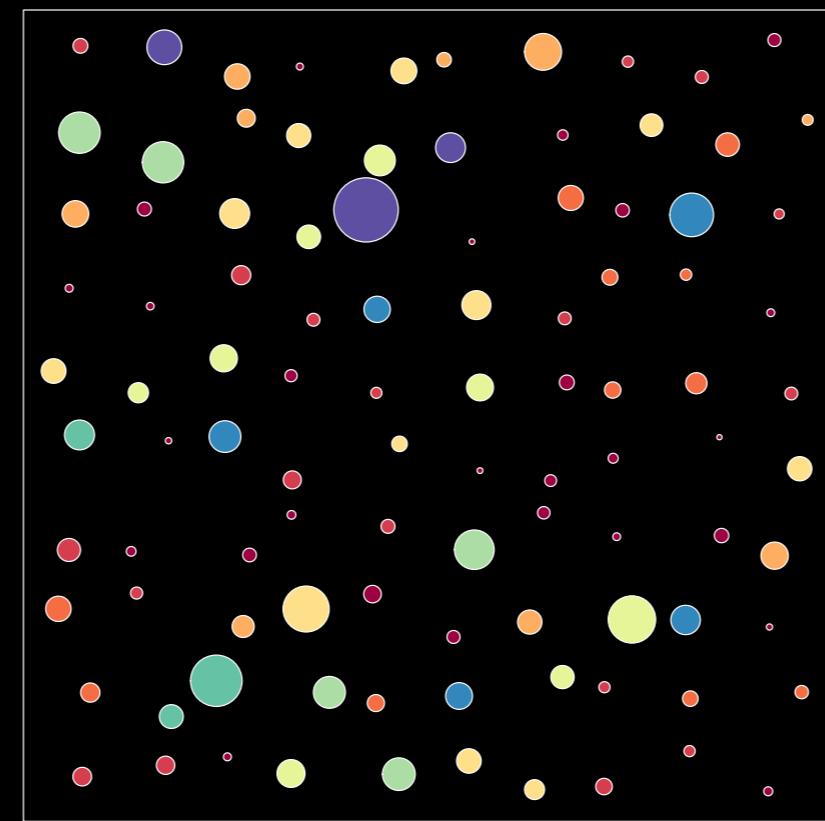
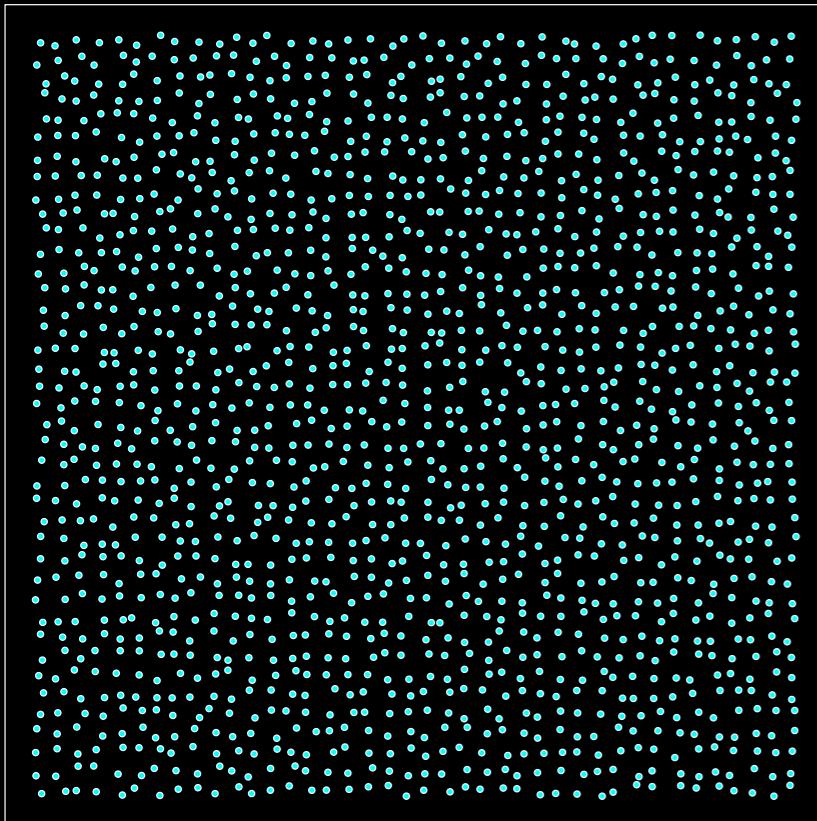
# What constrains biodiversity?



# What constrains biodiversity?



# What constrains biodiversity?



# Thank you!



J. Y. Lim



K. R. Goodman



D. S. Gruner



J. Harte



R. G. Gillespie



GORDON AND BETTY  
**MOORE**  
FOUNDATION



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[nature.berkeley.edu/~rominger](http://nature.berkeley.edu/~rominger)