



University  
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Boyd Orr Centre  
for Population and  
Ecosystem Health



# DIVERSITY

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# LOTS OF TYPES OF DIVERSITY

Alpha

Beta

Gamma

AND LOTS OF MEASURES OF DIVERSITY

Species  
richness

Shannon  
entropy

Simpson's  
index

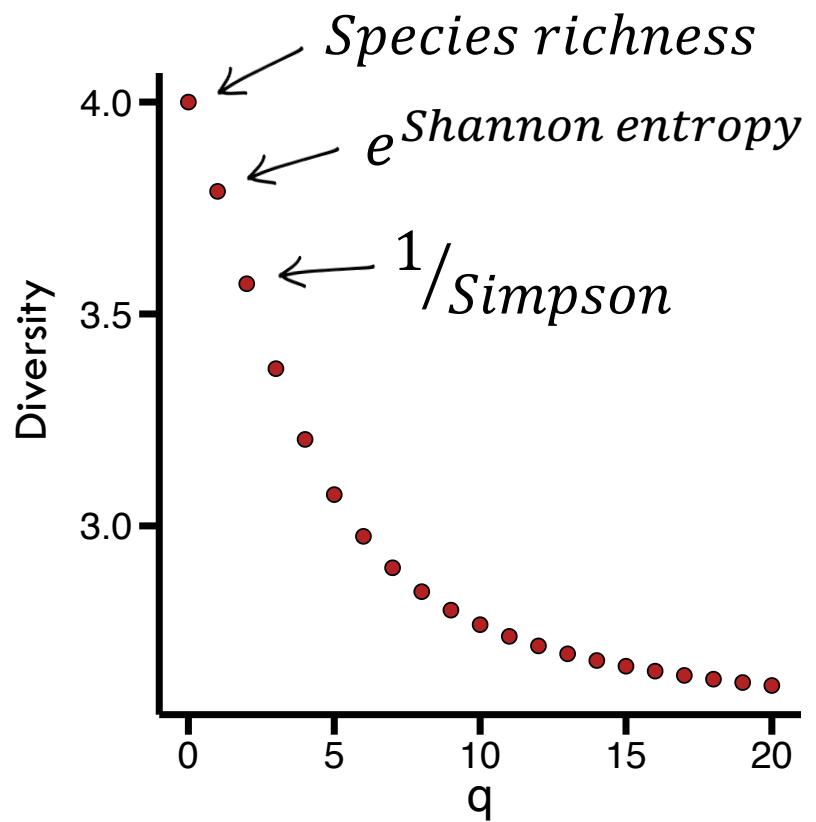
Berger-  
Parker

# HILL NUMBERS

Hill, M. (1973) Diversity and evenness... *Ecology* (54) 2: 427-32.

Jost, L. (2006) Entropy and diversity. *Oikos* (2) 2: 363-75.

$${}^q D(p) = M_{1-q}(p, p^{-1})$$

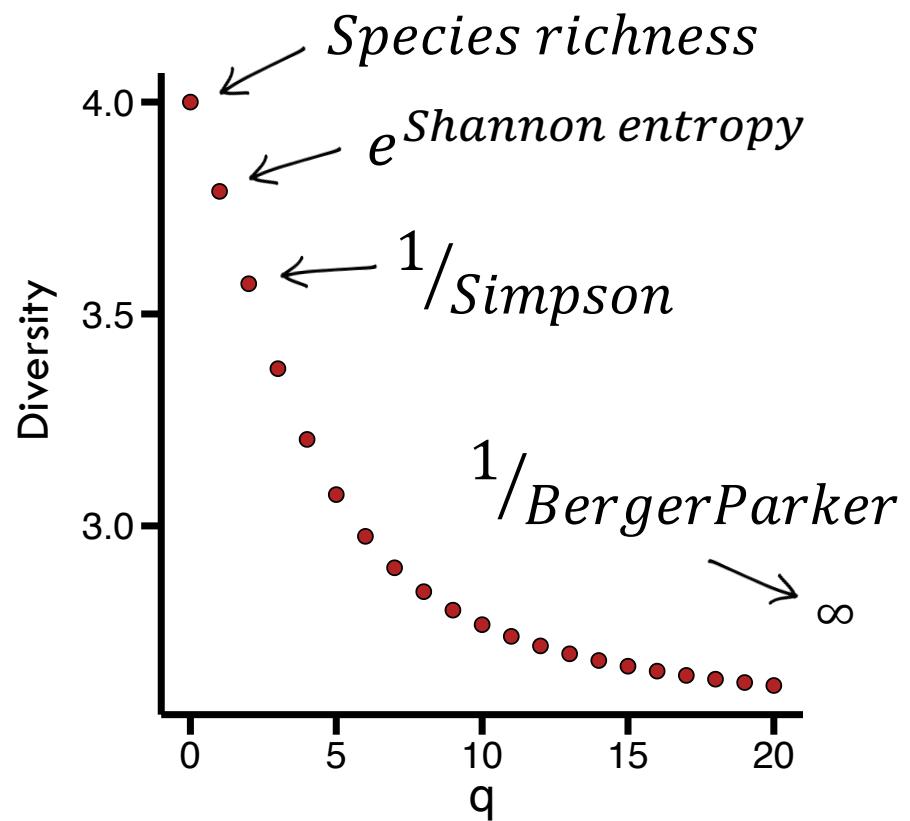
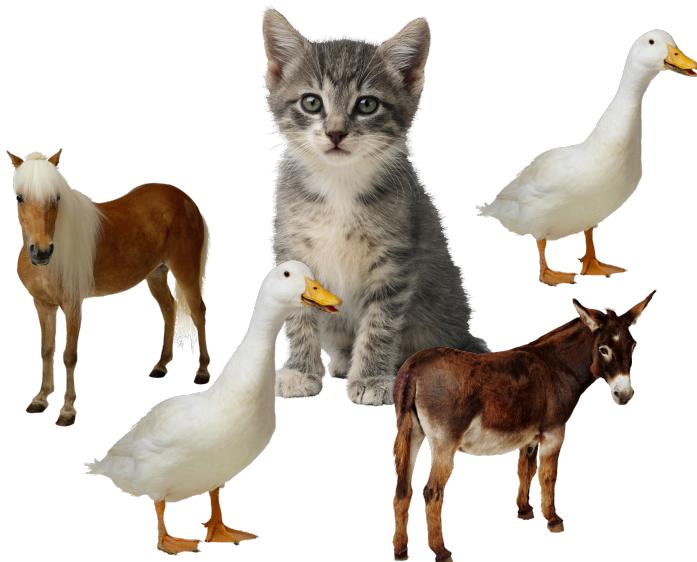


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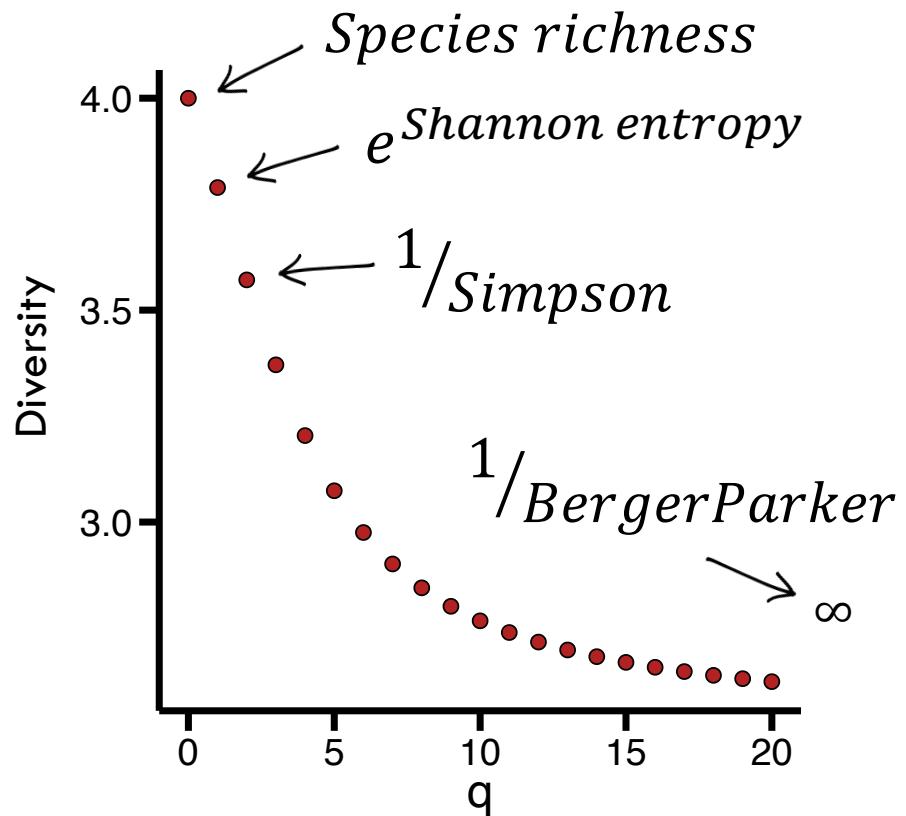


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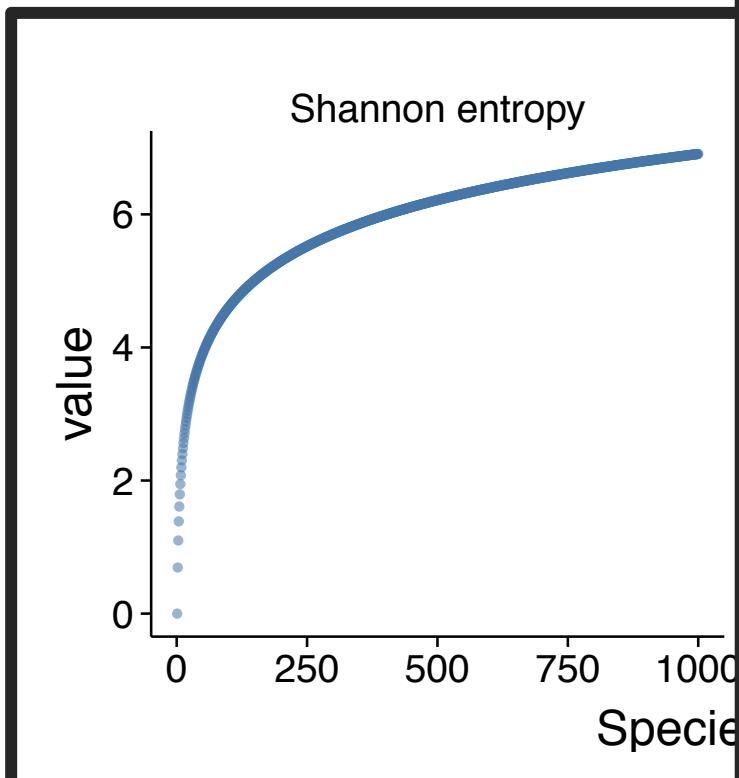
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$${}^q D(p) = M_{1-q}(p, p^{-1})$$



# EFFECTIVE NUMBERS



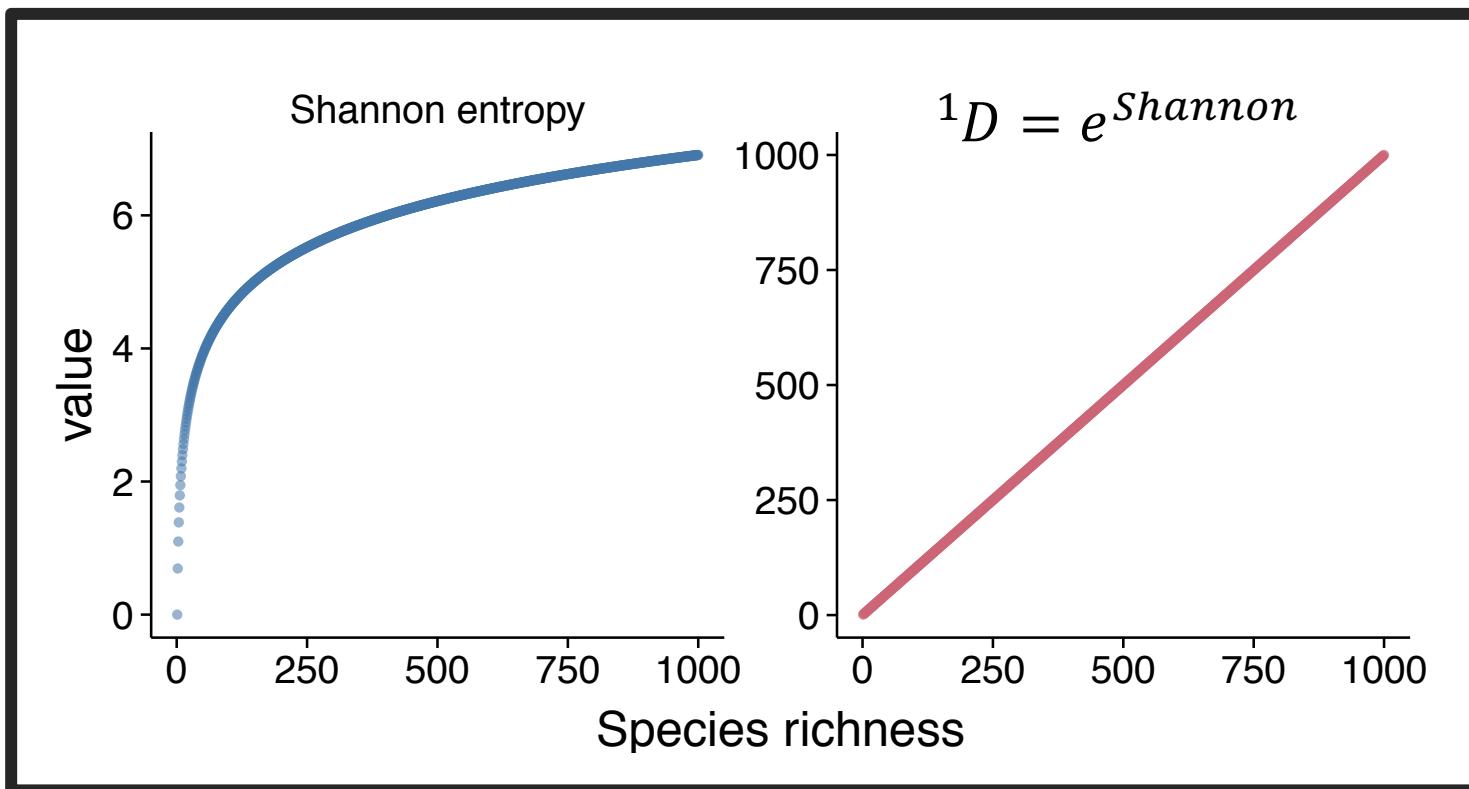
$$^qD(p) = M_{1-q}(p, p^{-1})$$

A		
sp 1	1	A
sp 1	1	A
sp 2	1	A
sp 1	1	A
sp 2	1	A
sp 3	1	A
sp 1	1	
sp 2	1	
sp 3	1	
sp 4	1	

# EFFECTIVE NUMBERS

$$^qD(p) = M_{1-q}(p, p^{-1})$$

Equivalent to the amount of **information gained in observing its result**

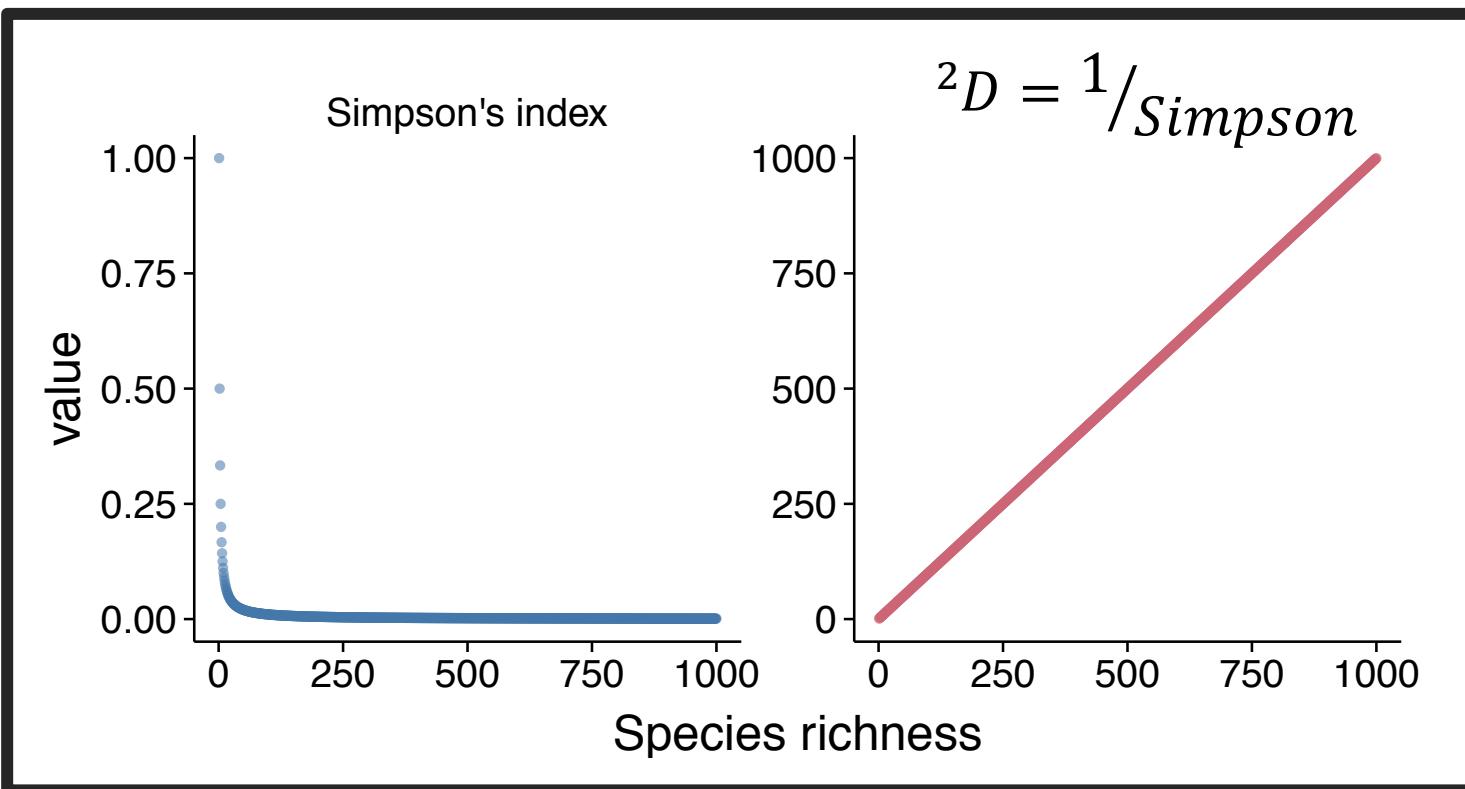


The **average uncertainty associated with predicting the species-identity of a single individual** in a sampling process

# EFFECTIVE NUMBERS

$$^q D(p) = M_{1-q}(p, p^{-1})$$

The number of equally common species in an equivalent community of equal diversity

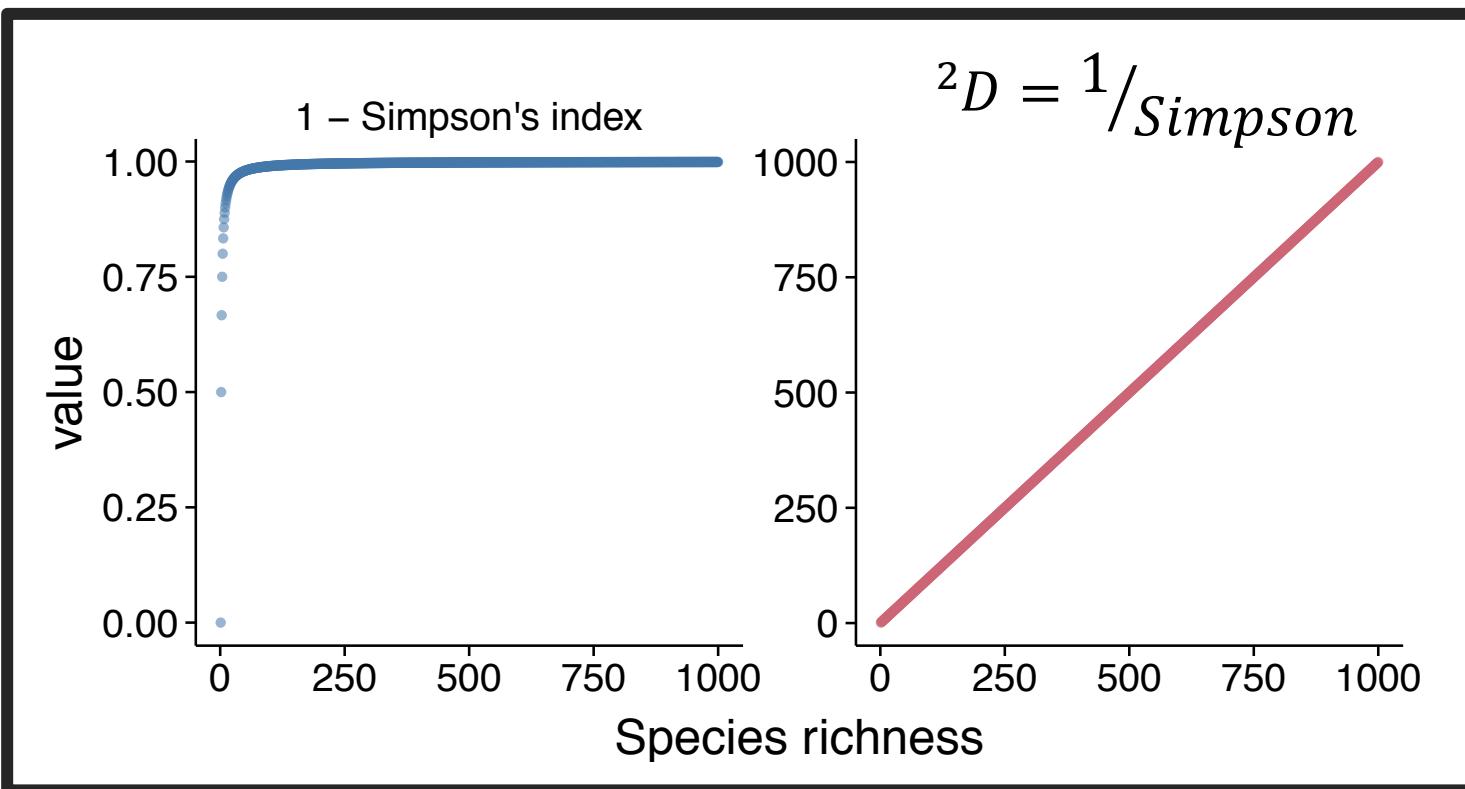


The **probability** with which two randomly selected individuals will **belong to the same species**

# EFFECTIVE NUMBERS

$$^qD(p) = M_{1-q}(p, p^{-1})$$

The number of equally common species in an equivalent community of equal diversity



The **probability** with which two randomly selected individuals will **belong to the different species**

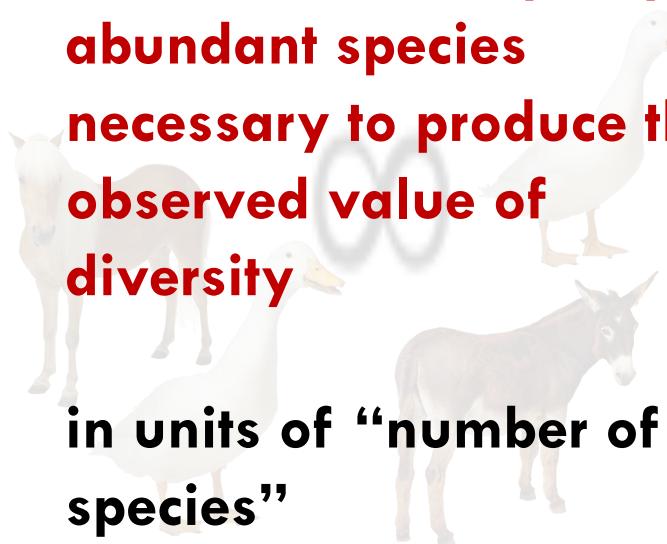
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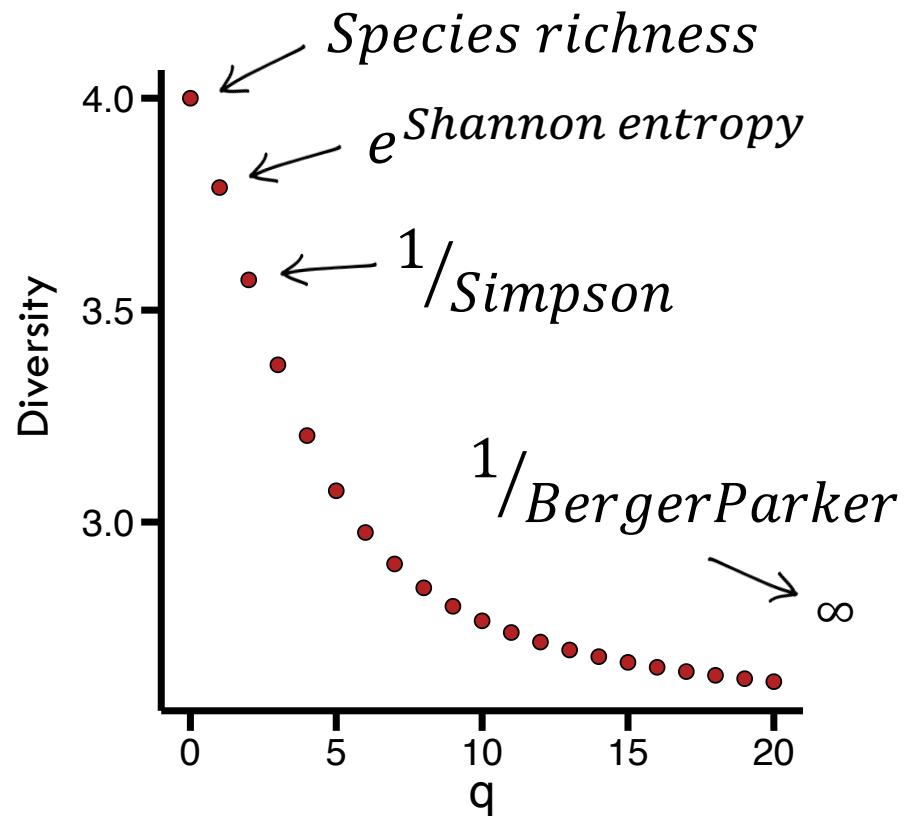
Jost, L. (2006) Entropy and diversity. *Oikos* (2) 2: 363-75.

$${}^q D(p) = M_{1-q}(p, p^{-1})$$

The number of equally abundant species necessary to produce the observed value of diversity

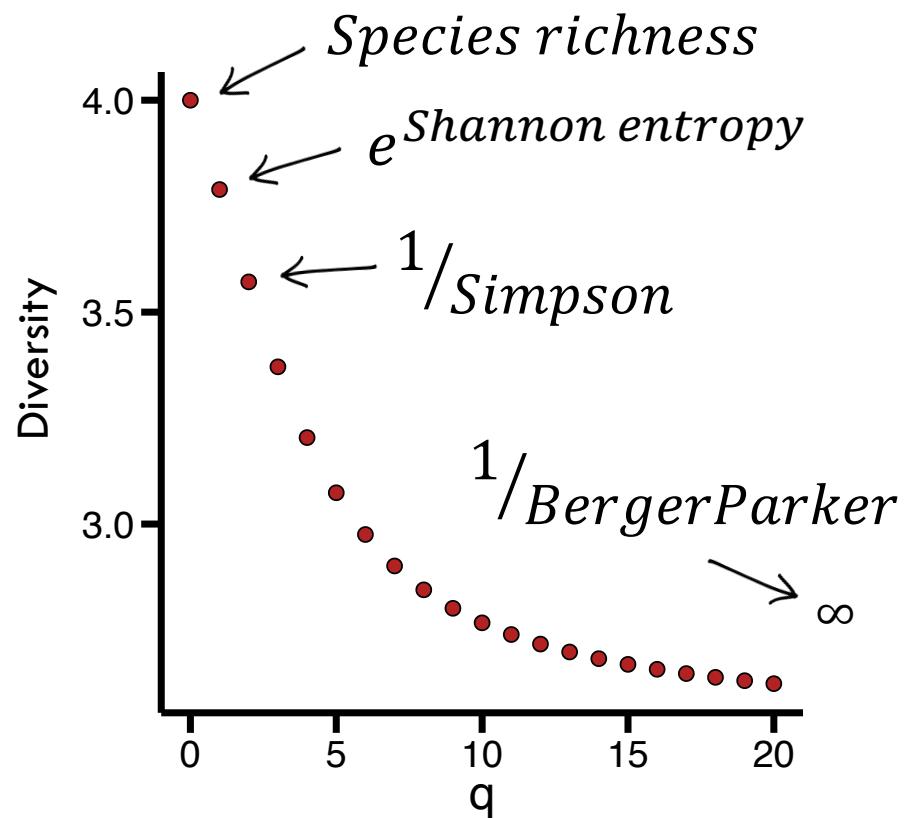
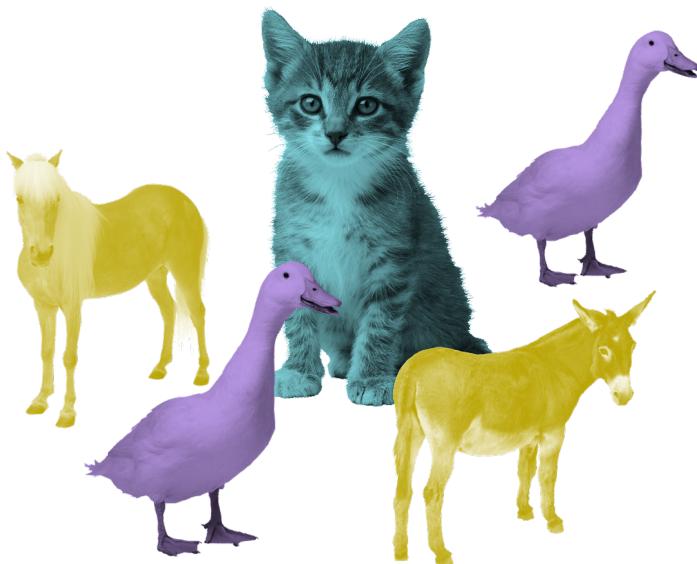


in units of “number of species”



# SIMILARITY

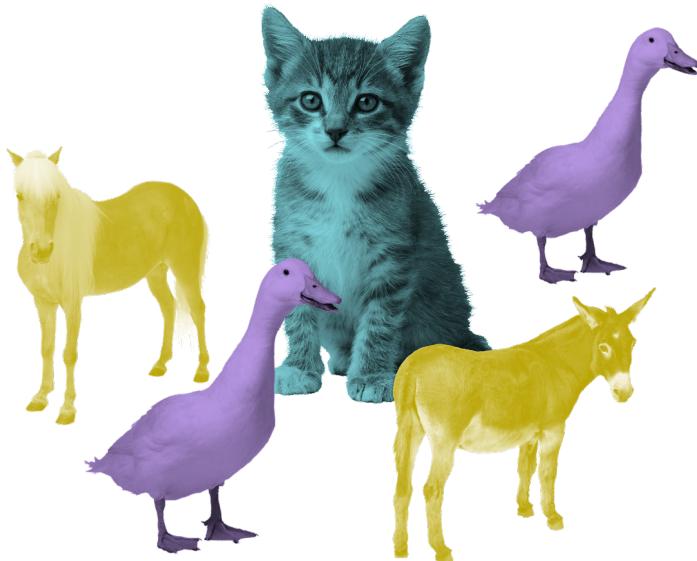
$${}^q D(p) = M_{1-q}(p, p^{-1})$$



# SIMILARITY

$${}^q D(\mathbf{p}) = M_{1-q}(\mathbf{p}, \mathbf{p}^{-1})$$

$${}^q D(\mathbf{p}) = M_{1-q}(\mathbf{p}, (\mathbf{Z}\mathbf{p})^{-1})$$

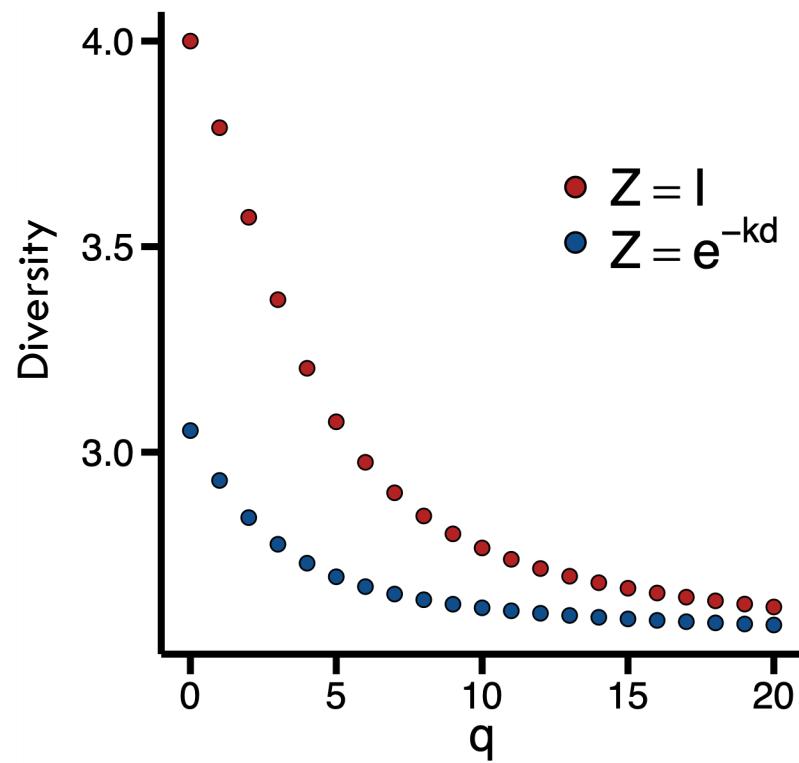
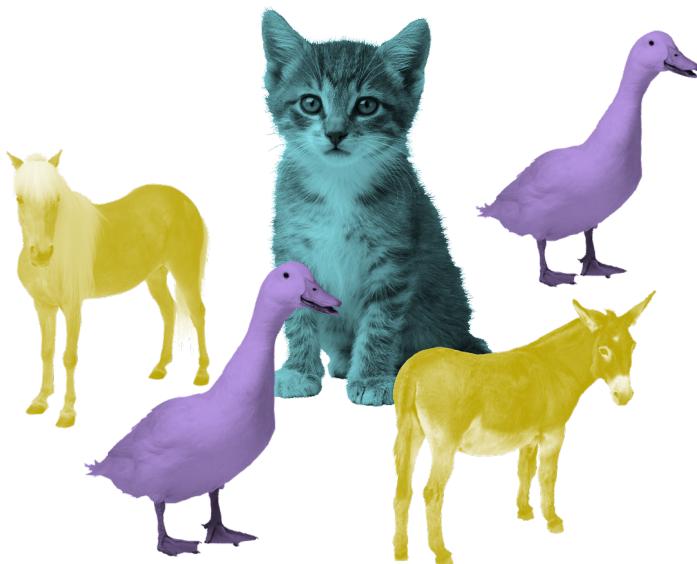


> Z

	ducks	cats	horses	donkeys
ducks	1	0	0.0	0.0
cats	0	1	0.0	0.0
horses	0	0	1.0	0.9
donkeys	0	0	0.9	1.0

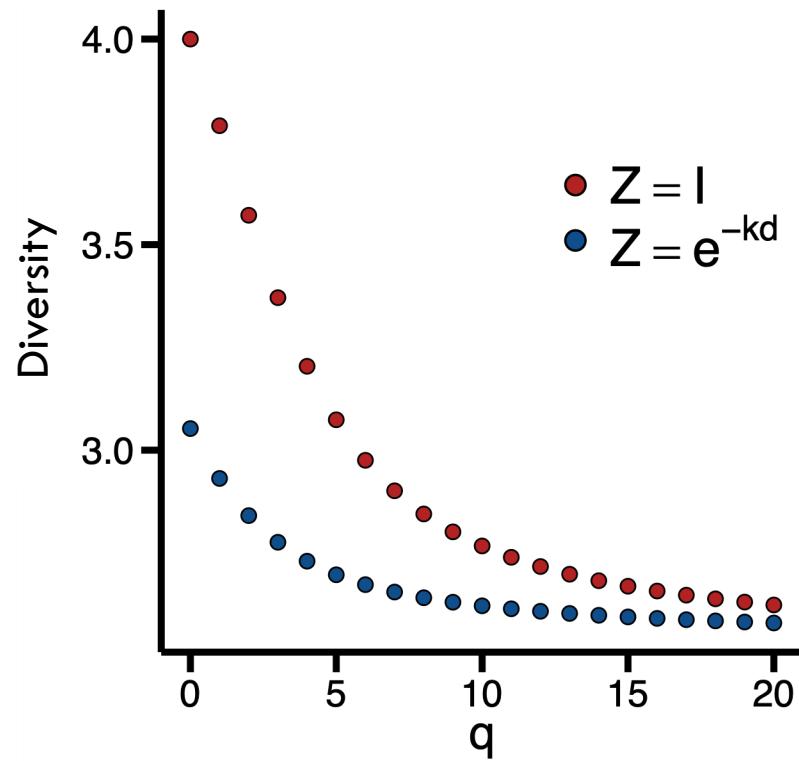
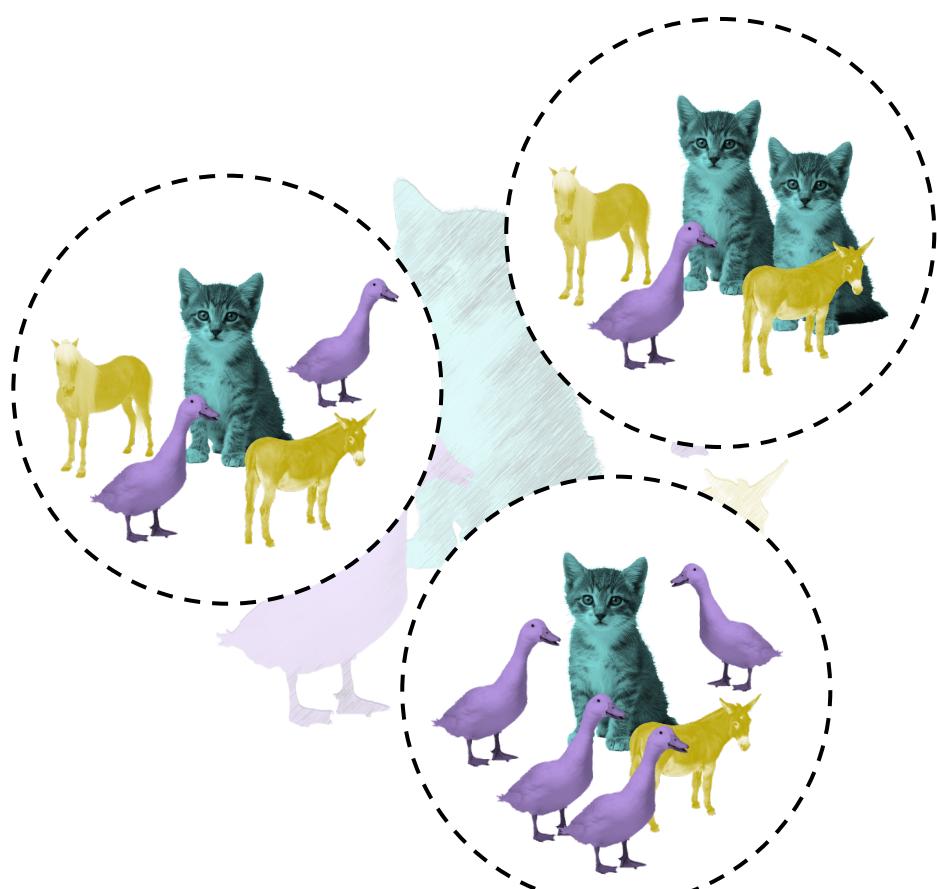
# SIMILARITY

$${}^q D(\mathbf{p}) = M_{1-q}(\mathbf{p}, (\mathbf{Z}\mathbf{p})^{-1})$$



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# PARTITIONING DIVERSITY

## Metacommunity diversity

$${}^q\bar{A}^Z = M_{1-q}(\mathbf{w}, {}^q\bar{\alpha}_j^Z)$$

Normalised alpha: average similarity-sensitive **diversity** of subcommunities  
 (norm\_meta\_alpha)

$${}^qR^Z = M_{1-q}(\mathbf{w}, {}^q\rho_j^Z)$$

Raw beta (reversed): average **redundancy** of subcommunities (raw\_meta\_rho)

$${}^q\bar{R}^Z = M_{1-q}(\mathbf{w}, {}^q\bar{\rho}_j^Z)$$

Normalised beta (reversed): average **representativeness** of subcommunities  
 (norm\_meta\_rho)

$${}^qB^Z = M_{1-q}(\mathbf{w}, {}^q\beta_j^Z)$$

Raw beta: average **distinctiveness** of subcommunities (raw\_meta\_beta)

$${}^q\bar{B}^Z = M_{1-q}(\mathbf{w}, {}^q\bar{\beta}_j^Z)$$

Normalised beta: **effective number of distinct subcommunities** (norm\_meta\_beta)

$${}^qG^Z = M_{1-q}(\mathbf{w}, {}^q\gamma_j^Z)$$

Gamma: **metacommunity** similarity-sensitive diversity (meta\_gamma)

## Subcommunity diversity

$${}^q\bar{\alpha}_j^Z = M_{1-q}\left(\bar{\mathbf{P}}_{.j}, (\mathbf{Z}\bar{\mathbf{P}}_j)^{-1}\right)$$

Normalised alpha: similarity sensitive **diversity** of subcommunity  $j$  in isolation  
 (norm\_sub\_alpha)

$${}^q\rho_j^Z = M_{1-q}\left(\bar{\mathbf{P}}_{.j}, (\mathbf{Z}\mathbf{p})_i/(\mathbf{Z}\bar{\mathbf{P}}_j)_i\right)$$

Raw beta (reversed): **redundancy** of subcommunity  $j$  (raw\_sub\_rho)

$${}^q\bar{\rho}_j^Z = M_{1-q}\left(\bar{\mathbf{P}}_{.j}, (\mathbf{Z}\mathbf{p})_i/(\mathbf{Z}\bar{\mathbf{P}}_j)_i\right)$$

Normalised beta (reversed): **representativeness** of subcommunity  $j$  (norm\_sub\_rho)

$${}^q\beta_j^Z = 1/{}^q\rho_j^Z$$

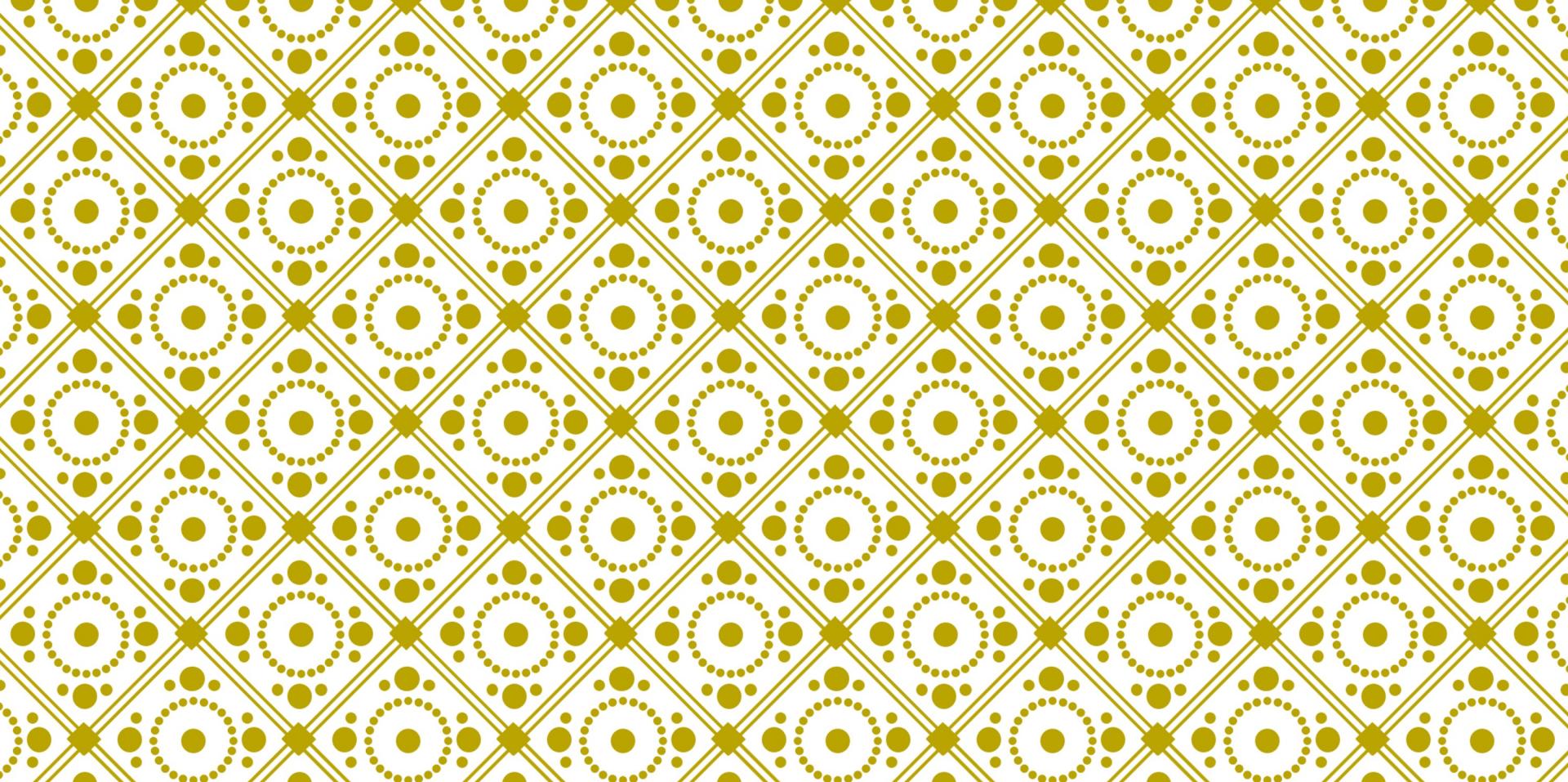
Raw beta: **distinctiveness** of subcommunity  $j$  (raw\_sub\_beta)

$${}^q\bar{\beta}_j^Z = 1/{}^q\bar{\rho}_j^Z$$

Normalised beta: estimate of **effective number of distinct subcommunities**  
 (norm\_sub\_beta)

$${}^q\gamma_j^Z = M_{1-q}\left(\bar{\mathbf{P}}_{.j}, (\mathbf{Z}\mathbf{p})_i^{-1}\right)$$

Gamma: **contribution** per individual toward metacommunity diversity (sub\_gamma)



# BIODIVERSITY



Barro-Colorado  
Island Forest census  
plot

# BARRO-COLORADO ISLAND FOREST CENSUS PLOT

The screenshot shows the RStudio interface with two data frames open:

- pmatrix:** This data frame contains the following data:

	grid.001.001
<i>Abarema_macradenia</i>	0.000000e+00
<i>Acacia_melanoceras</i>	0.000000e+00
<i>Acalypha_diversifolia</i>	1.274941e-05
<i>Acalypha_macrostachya</i>	4.249803e-06
<i>Adelia_triloba</i>	0.000000e+00
<i>Aegiphila_panamensis</i>	0.000000e+00

Showing 1 to 6 of 323 entries

- Z.matrix:** This data frame contains the following data:

	Abarema_macradenia	Acacia_melanoceras
<i>Abarema_macradenia</i>	1	0
<i>Acacia_melanoceras</i>	0	1
<i>Acalypha_diversifolia</i>	0	0
<i>Acalypha_macrostachya</i>	0	0
<i>Adelia_triloba</i>	0	0
<i>Aegiphila_panamensis</i>	0	0

Showing 1 to 6 of 323 entries

# BARRO-COLORADO ISLAND FOREST CENSUS PLOT

Metacommunity = 50 ha forest plot

Subcommunities = 1250 [20×20 m] quadrats

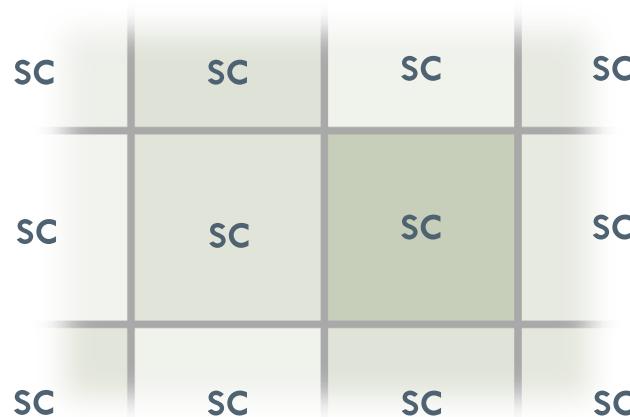
Spatial biodiversity: Seventh census (2010)

Naïve-species similarity, all species are completely  
distinct:  $Z = I$

# BARRO-COLORADO ISLAND FOREST CENSUS PLOT

Spatial

2010:

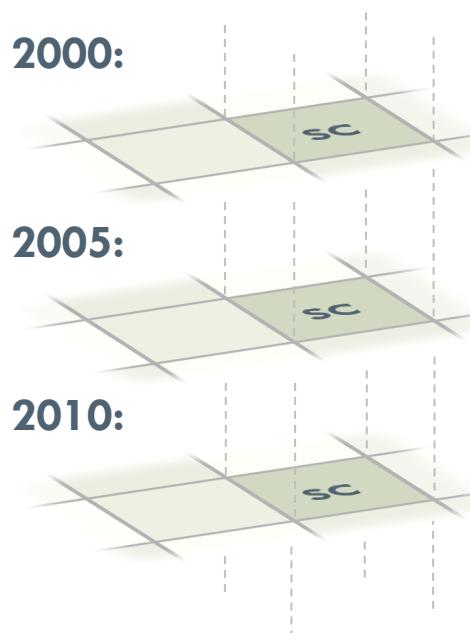


Temporal

2000:

2005:

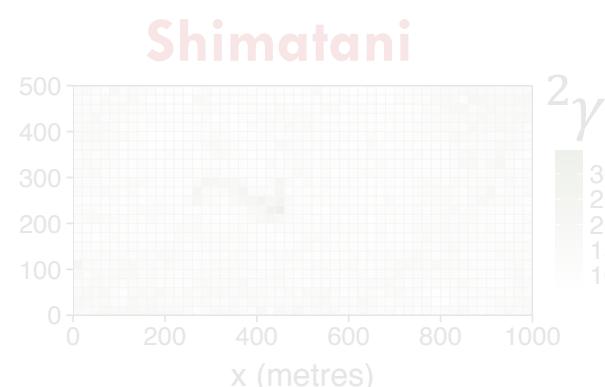
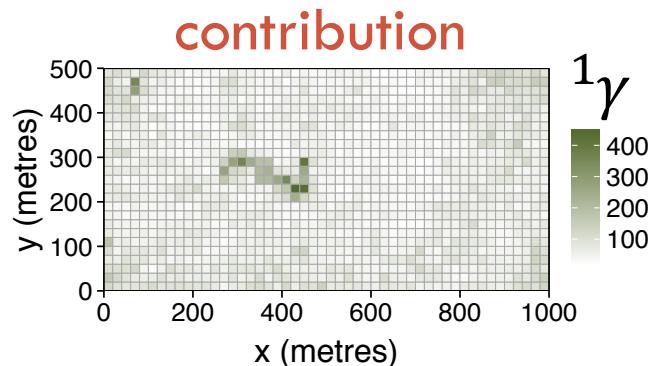
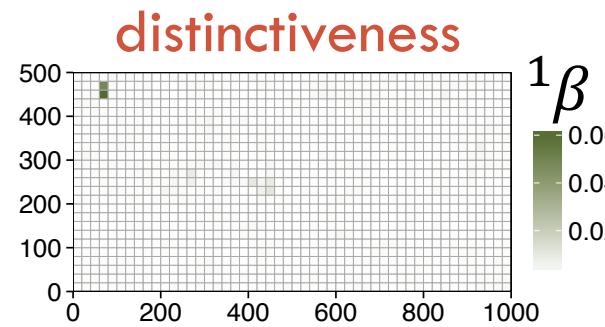
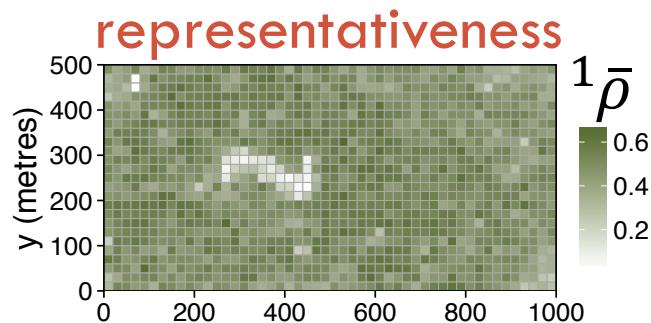
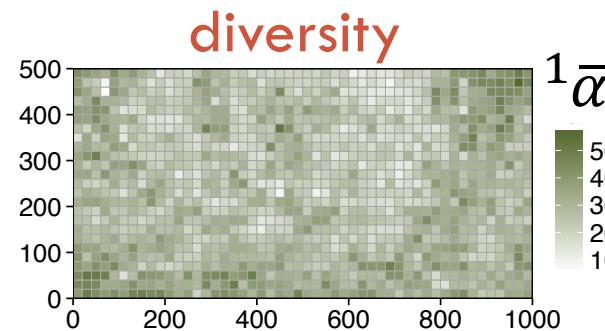
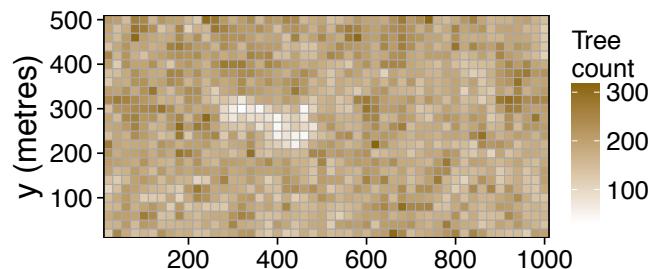
2010:



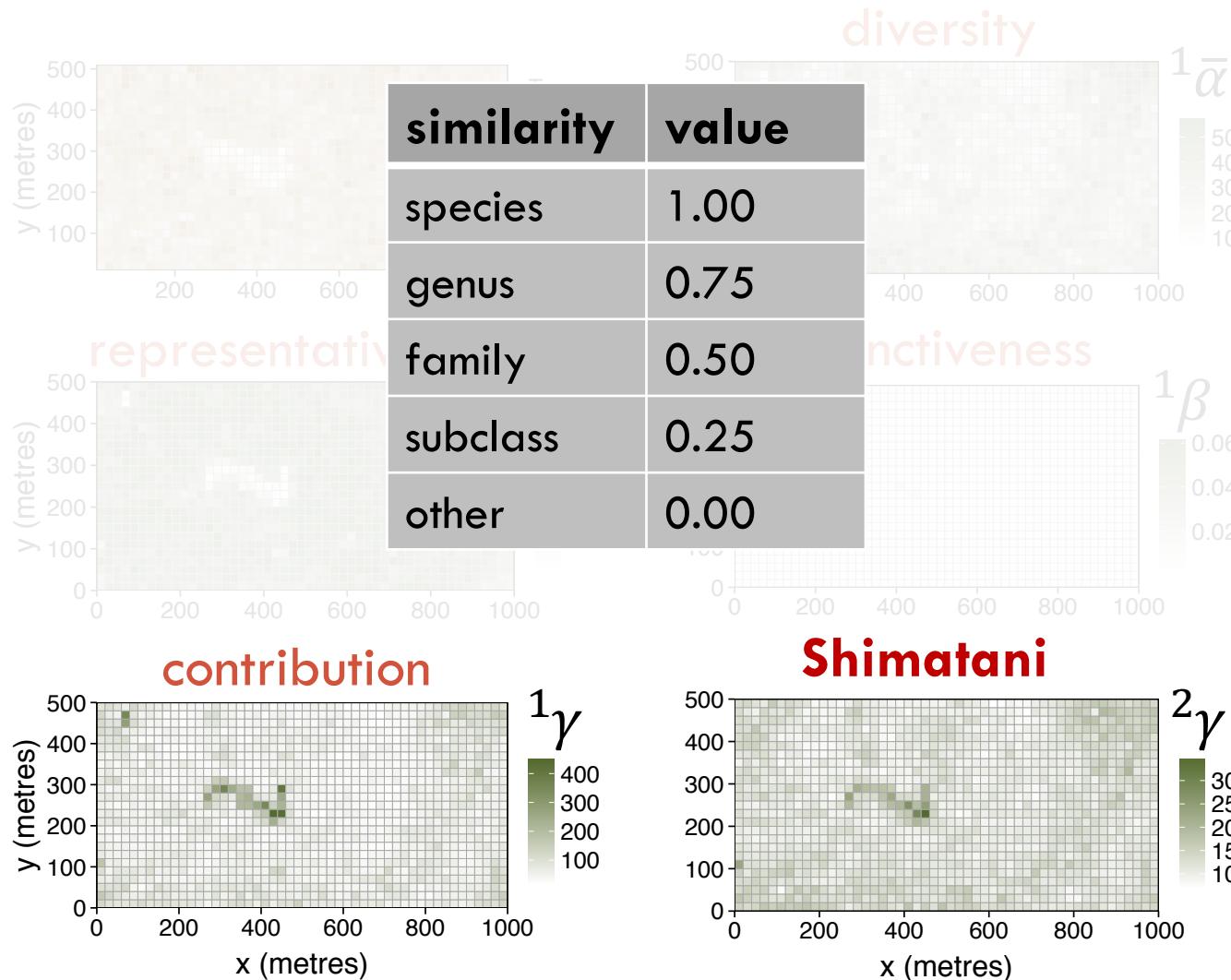
7 tree censuses

at approximately  
5-year intervals  
from 1981-2010

# SPATIAL BIODIVERSITY

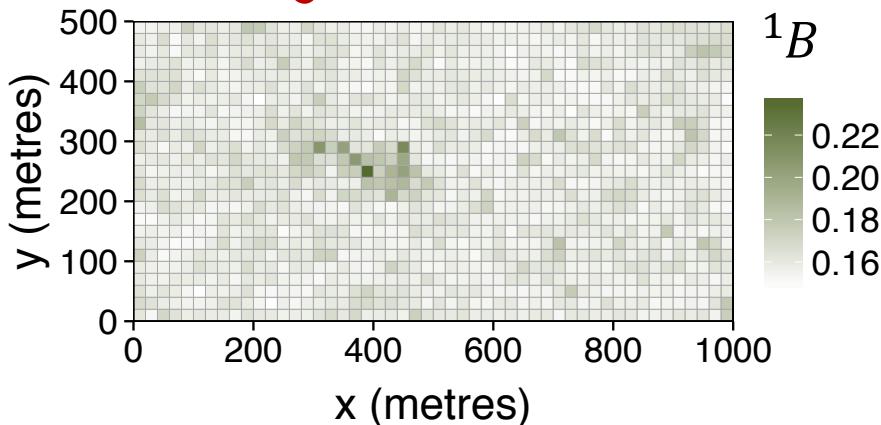


# TAXONOMIC DIVERSITY

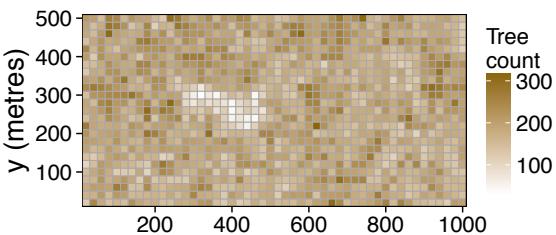


# TEMPORAL BIODIVERSITY

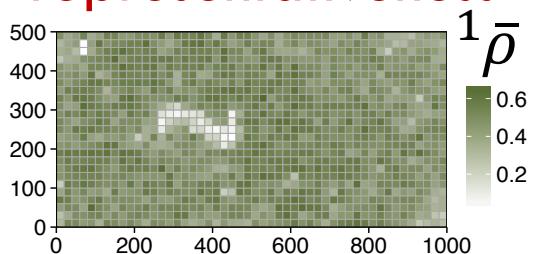
average distinctiveness



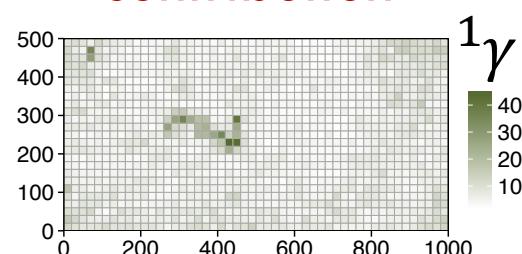
81/82



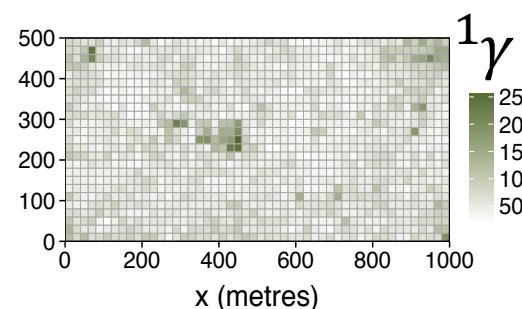
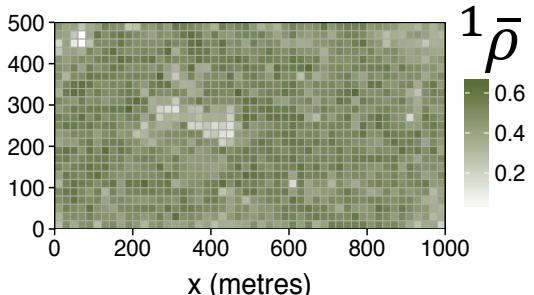
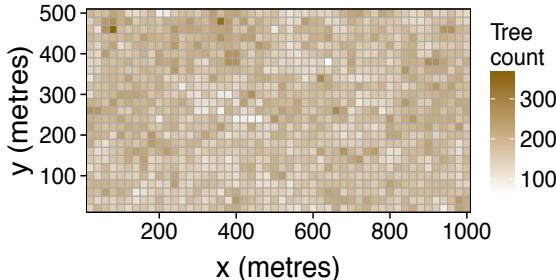
representativeness



contribution



2010



# R PACKAGES

## ■ **rdiversity**

- Our package for diversity measurement
- Opinionated about the best way to measure diversity
- <https://github.com/boydorr/rdiversity>
- <http://boydorr.github.io/rdiversity>
- <https://cloud.r-project.org/web/packages/rdiversity/index.html>

## ■ **vegan**

- The most popular R package for diversity measurement
- A package that covers most popular ways of measuring diversity
- <https://github.com/vegandevs/vegan>
- <https://cran.r-project.org/web/packages/vegan/index.html>

See also:

## ■ **iNEXT**