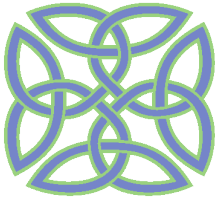


# Maximizing biological diversity

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## Where we're going

I'll show you a maximum entropy theorem...

... with entropy interpreted as biodiversity...

... but maybe you can interpret the theorem in other interesting ways.

### Plan:

1. Measuring biological diversity
2. The theorem
3. Examples and consequences
4. Unanswered questions

# *1. Measuring biological diversity*

*joint with Christina Cobbold*

## A spectrum of viewpoints on biodiversity

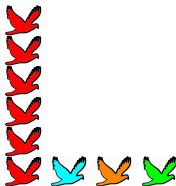
Conserving *species*  
is what matters

Rare species  
count for as much  
as common ones  
—every species is precious

Conserving *communities*  
is what matters

Common species  
are the really  
important ones  
—they shape the community

This →



← This

is more diverse than

is less diverse than

that →



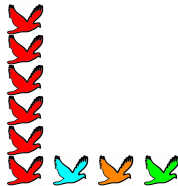
← that

# A spectrum of viewpoints on biodiversity

*Rare species are  
important*

*Rare species are  
unimportant*

This →



← This

is more diverse than

is less diverse than

that →



← that

# Quantifying diversity

model of  
community



**formula**

measure of  
diversity

# Quantifying diversity

similarity matrix  $Z$

model of  
community

# Quantifying diversity

## similarity matrix $Z$

$n \times n$  matrix ( $n$  = number of species)

$Z_{ij}$  = similarity between  $i$ th and  $j$ th species =  $Z_{ji}$

$$0 \leq Z_{ij} \leq 1 \text{ and } Z_{ii} = 1$$

totally  
dissimilar

identical

E.g.: Naive model:  $Z = \begin{pmatrix} 1 & 0 \\ \dots & \dots \\ 0 & 1 \end{pmatrix}$  (species have *nothing* in common)

E.g.: Genetic similarity.

E.g.: Taxonomic: e.g.  $Z_{ij} = \begin{cases} 1 & \text{if same species} \\ 0.7 & \text{if different species but same genus} \\ 0 & \text{otherwise.} \end{cases}$



## Quantifying diversity

similarity matrix  $Z$

frequency distribution  $p$

model of  
community

## Quantifying diversity

similarity matrix  $Z$

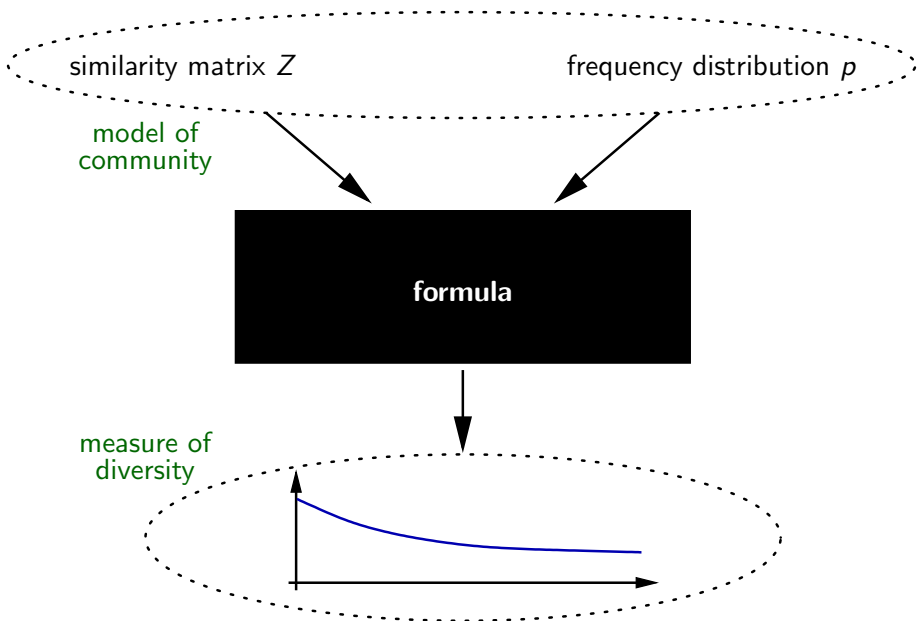
frequency distribution  $p$

$$p = \begin{pmatrix} p_1 \\ \vdots \\ p_n \end{pmatrix}$$

$p_i$  = relative frequency,  
or relative abundance,  
of the  $i$ th species

$$p_i \geq 0 \text{ and } \sum p_i = 1$$

# Quantifying diversity



# Quantifying diversity

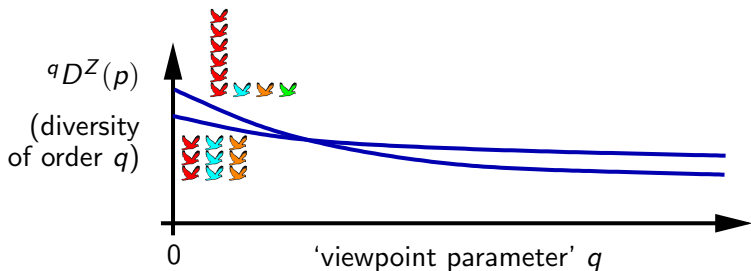
similarity matrix  $Z$

frequency distribution  $p$

$q = 0$ :  
rare species are  
important



$q = \infty$ :  
rare species are  
unimportant



# Quantifying diversity

similarity matrix  $Z$

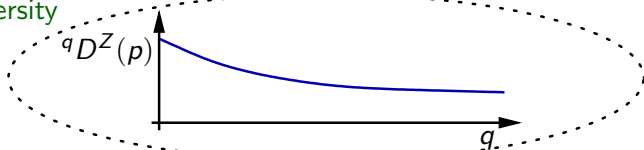
frequency distribution  $p$

model of  
community

The diversity of order  $q$  is

$${}^q D^Z(p) = \left( \sum_{i: p_i > 0} p_i(Zp)_i^{q-1} \right)^{\frac{1}{1-q}}$$

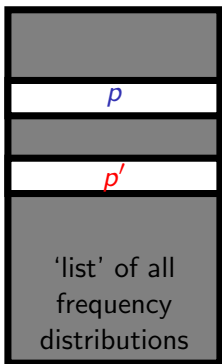
measure of  
diversity



# Visualizations

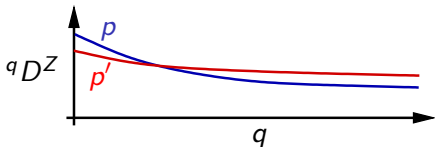
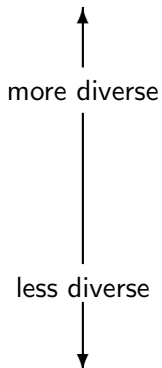
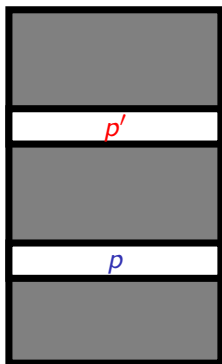
$$q = 0$$

(sensitive to rare species)



$$q = 10$$

(insensitive to rare species)



## 2. *The theorem*

# The central questions

Take a list of species, with known similarity matrix  $Z$ .

## Questions

- Which frequency distribution(s) maximize the diversity?
- What is the value of the maximum diversity?

Remember the birds!

In principle, the answers depend on the 'viewpoint parameter'  $q$ .



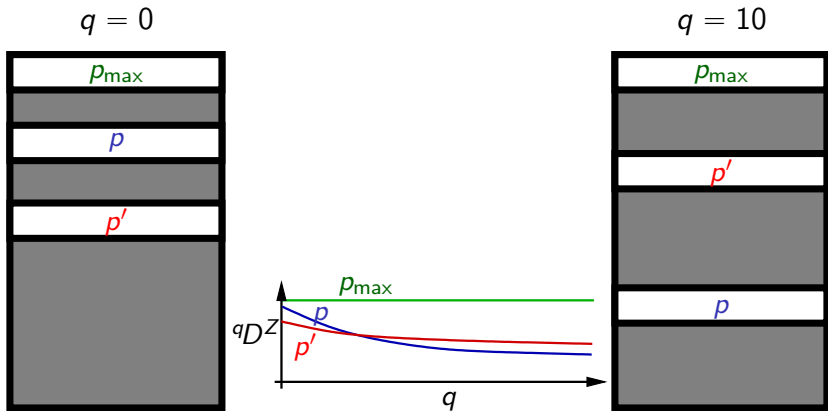
# The solution

Theorem (2009) Neither answer depends on  $q$ . That is,

- There is a single frequency distribution  $p_{\max}$  that maximizes diversity of all orders  $q$  simultaneously ( $0 \leq q \leq \infty$ )  
—a ‘best of all possible worlds’.
- The maximum diversity,  ${}^q D^Z(p_{\max})$ , is the same for all  $q$ .

The proof of the theorem gives a construction of  $p_{\max}$ .

## How is that possible?



Different values of the viewpoint parameter  $q$  produce different judgements on which distributions are more diverse than which others.

*But there is a single distribution  $p_{\max}$  that is optimal for all  $q$ .*

### *3. Examples and consequences*

## The naive model

Put

$$Z_{ij} = \begin{cases} 1 & \text{if } i = j, \\ 0 & \text{if } i \neq j. \end{cases}$$

(Then  ${}^qD^Z(\rho)$  is exponential of Rényi entropy.)

The maximizing distribution is uniform: every species has equal abundance.

Why? Can prove it directly, or reason as follows:

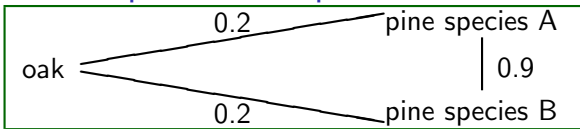
One corollary of the theorem is that if a distribution is maximizing for *some*  $q > 0$ , then it is maximizing for *all*  $q$ .

We know that the uniform distribution maximizes the Shannon entropy ( $q = 1$ ).

It follows that the uniform distribution maximizes all the Rényi entropies.

## A three-species example

$$Z = \begin{pmatrix} 1 & 0.2 & 0.2 \\ 0.2 & 1 & 0.9 \\ 0.2 & 0.9 & 1 \end{pmatrix}$$



Which frequency distribution maximizes the diversity?

Not this:

	0.333...
0.333...	
	0.333...

Or this:

	0.25
0.5	
	0.25

In fact, it's this:

	0.26
0.48	
	0.26

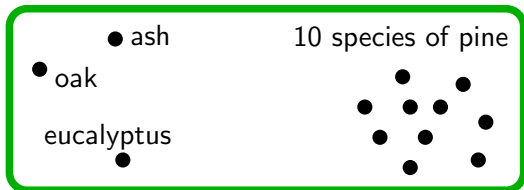
This distribution maximizes diversity for *all*  $q$ , with constant value 1.703....

## Properties of maximizing distributions

- There can be more than one maximizing distribution.
- A maximizing distribution can eliminate some species entirely.

*How can that be?*

To understand, run time backwards. . .

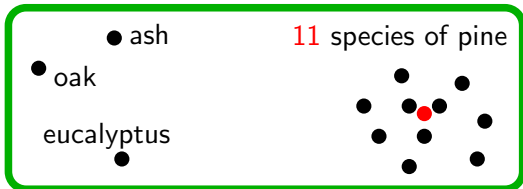


## Properties of maximizing distributions

- There can be more than one maximizing distribution.
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*How can that be?*

To understand, run time backwards. . .



Introducing an 11th species of pine *decreases* diversity.

So if we start with a forest containing all 11 pine species, eliminating the 11th will *increase* diversity.

## Computing the maximizing distribution

Start with an  $n \times n$  similarity matrix  $Z$ .

- Computing the maximizing distribution(s) takes  $2^n$  steps.
- But each step is fast. E.g. can do 25 species in a few seconds.
- And that's for *arbitrary* similarity matrices  $Z$ .  
For some *special* types of  $Z$ , the computation is near-instant.



## Tree-based similarity matrices

Suppose we define similarity via a taxonomic or phylogenetic tree.

### Example

Put

$$Z_{ij} = \begin{cases} 1 & \text{if same species } (i = j) \\ 0.7 & \text{if different species but same genus} \\ 0.3 & \text{if different genera but same family} \\ 0 & \text{otherwise.} \end{cases}$$

Then:

- There's a unique maximizing distribution  $p_{\max}$ .
- It eliminates no species; that is,  $(p_{\max})_i > 0$  for all  $i$ .

## *4. Unanswered questions*

## Why is the theorem true?

Why is there a *single frequency distribution* that maximizes diversity from all viewpoints simultaneously?

- We can prove it. . .
- And it's easy in the naive case where  $Z$  is the identity (Rényi entropies). Then the maximizing distribution is uniform.

But we lack intuition as to why it's true in general.

## What about maximization under constraints?

The theorem concerns maximization of diversity without constraints.

For some constraints, the theorem fails: there is no distribution that maximizes diversity for all  $q$  simultaneously.

Under which types of constraint *can* we maximize diversity for all  $q$  simultaneously?

## What is the significance of the maximum diversity itself?

The theorem also says that the maximum diversity is independent of the choice of viewpoint parameter  $q$ .

So, any similarity matrix  $Z$  ('list of species') gives rise to a number,  $D_{\max}(Z) = {}^q D^Z(p_{\max})$ , which does not depend on the choice of  $q$ .

What does  $D_{\max}(Z)$  mean?

It has geometric significance. . .

ways better behaved. For a compact (not necessarily positive definite) metric space  $A$ , the maximum diversity of  $A$  is

$$(4.3) \quad |A|_+ = \sup_{\mu \in P(A)} \left( \int \int e^{-d(a,b)} d\mu(a) d\mu(b) \right)^{-1}, \quad (\text{Mark Meckes})$$

where  $P(A)$  denotes the space of Borel probability measures on  $A$ . By renormalization, this

equivalence (7.1) of packing and covering numbers. When  $\overline{\dim}_{\text{Mink}} A = \underline{\dim}_{\text{Mink}} A$ , or equivalently  $\lim_{\varepsilon \rightarrow 0^+} \frac{\log N(A, \varepsilon)}{\log(1/\varepsilon)}$  exists, the Minkowski dimension  $\dim_{\text{Mink}} A$  is equal to this limit.

The upper, lower, and ordinary diversity dimension of an arbitrary compact metric space  $A$  are defined analogously to magnitude dimensions, using the maximum diversity

How else can it be understood?

## What are the biological implications of the theorem?

The theorem is fundamentally a maximum entropy theorem.

Interpreting entropy as diversity, it says there's a 'best of all possible worlds' (if we think diversity is good).

But there are other biological interpretations of entropy!

*Under those interpretations, what does the theorem tell us?*

# *Summary*

# Summary

- - There is a one-parameter family of diversity measures,  $({}^qD^Z(p))_{0 \leq q \leq \infty}$ , generalizing Rényi (and Shannon) entropy.
  - They take into account not only the frequencies  $p_i$  of the species, but also the inter-species **similarities** ( $Z_{ij}$ ).
- - Different values of the parameter  $q$  correspond to different **viewpoints** on the relative importance of rare/common species.
  - Different values of  $q$  produce different judgements on which communities are more diverse.
- Nevertheless:
  - Given a similarity matrix  $Z$ , there's a single frequency distribution  $p_{\max}$  that maximizes diversity **from all viewpoints  $q$  simultaneously**.
  - Moreover, the maximum diversity value  ${}^qD^Z(p_{\max})$  is the same for all  $q$ .
- Still, we don't fully understand:
  - **why** the theorem is true
  - **what** its biological implications are.