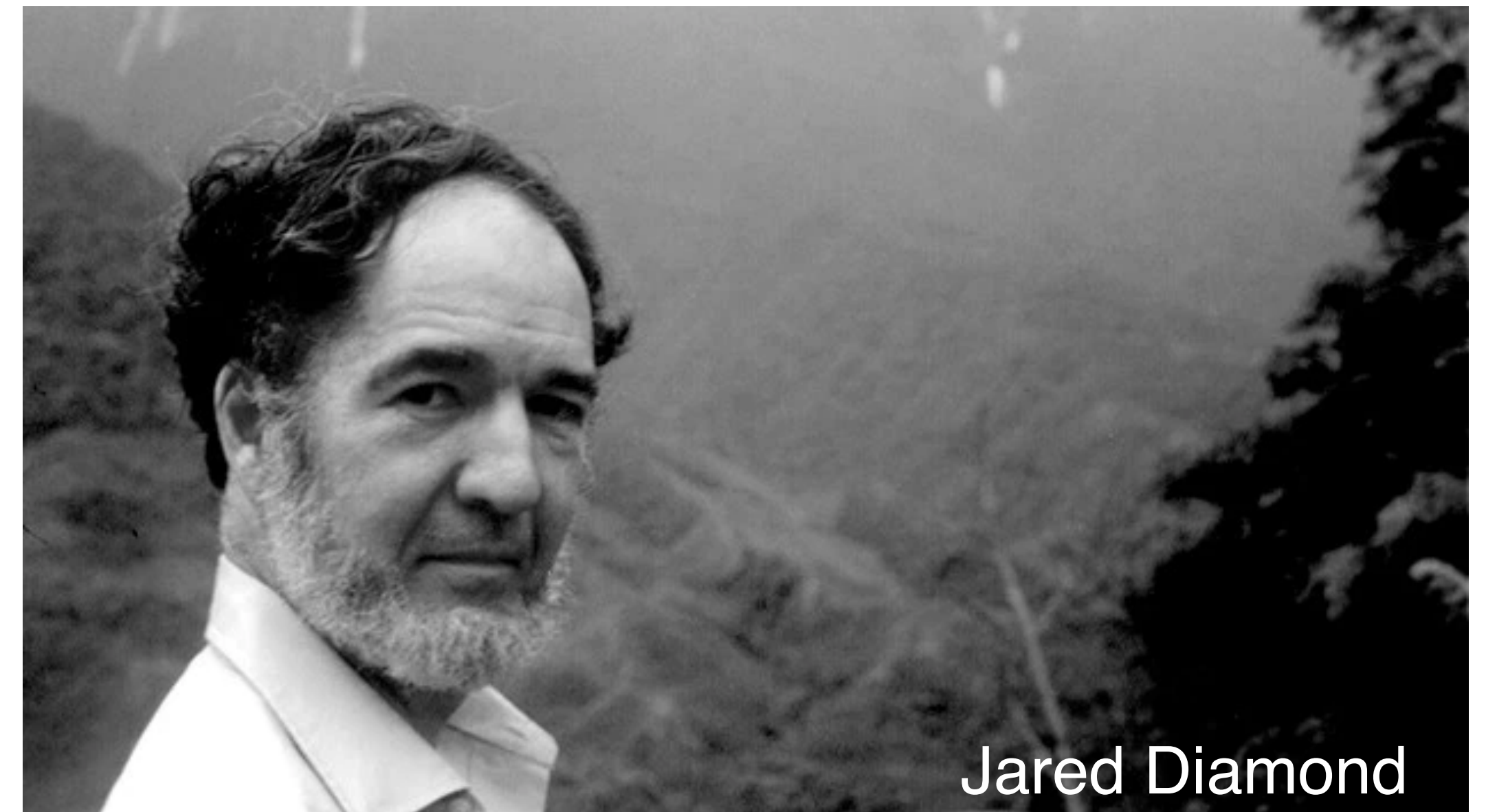


null models

foreword: a tale of islands



Jared Diamond

assembly rules: forbidden species combinations



Bismarck black myzomela
(found in 23 islands)

exclusion →



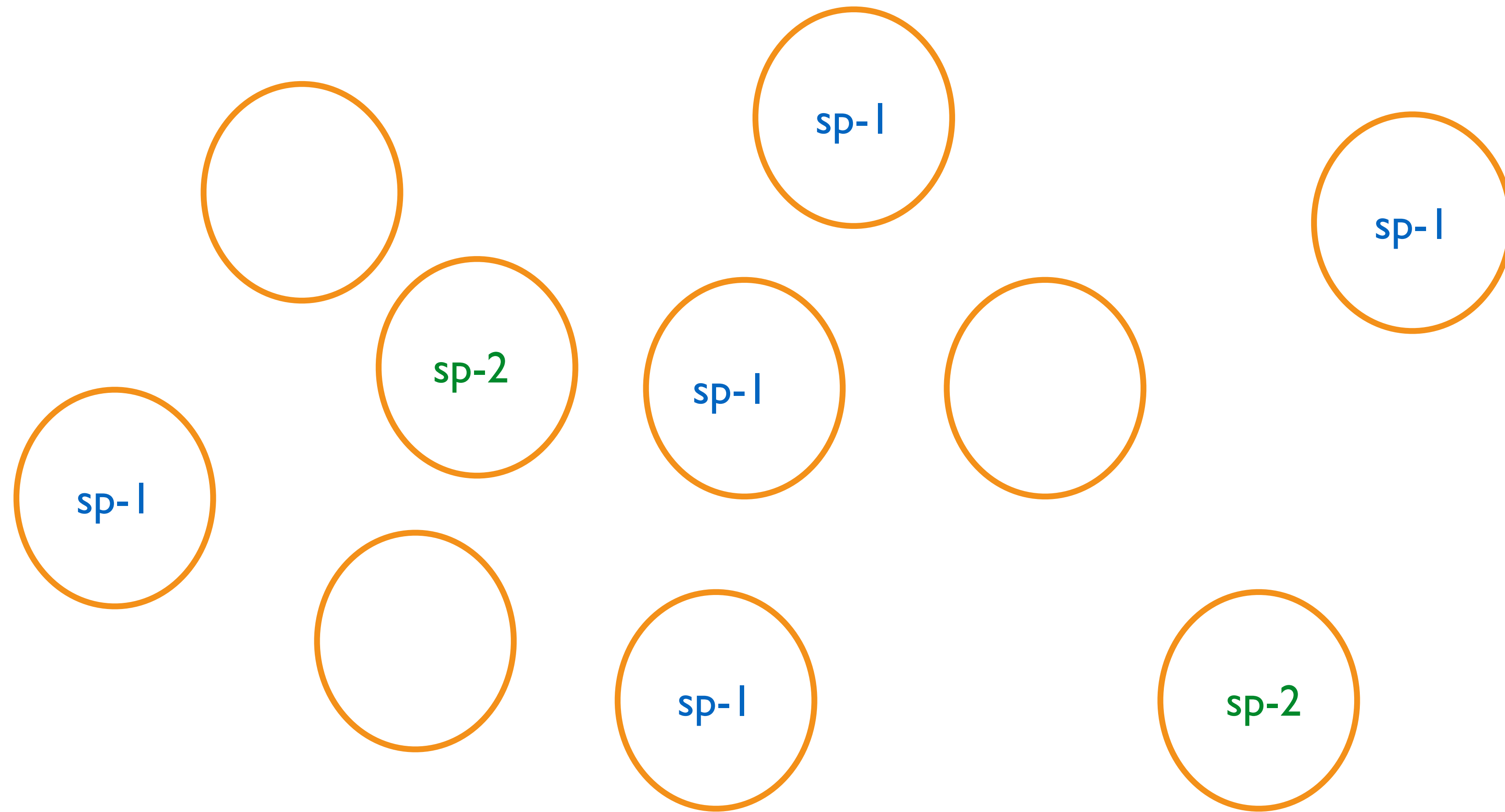
black sunbird
(found in 14 islands)



Daniel Simberloff

“In order to demonstrate that competition is responsible for the joint distributions of species, one would have to falsify a null hypothesis stating that the distributions are generated by the species randomly and individually colonizing an archipelago”

(Connor and Simberloff, 1979, *Ecology* **60**: 1132-1140)

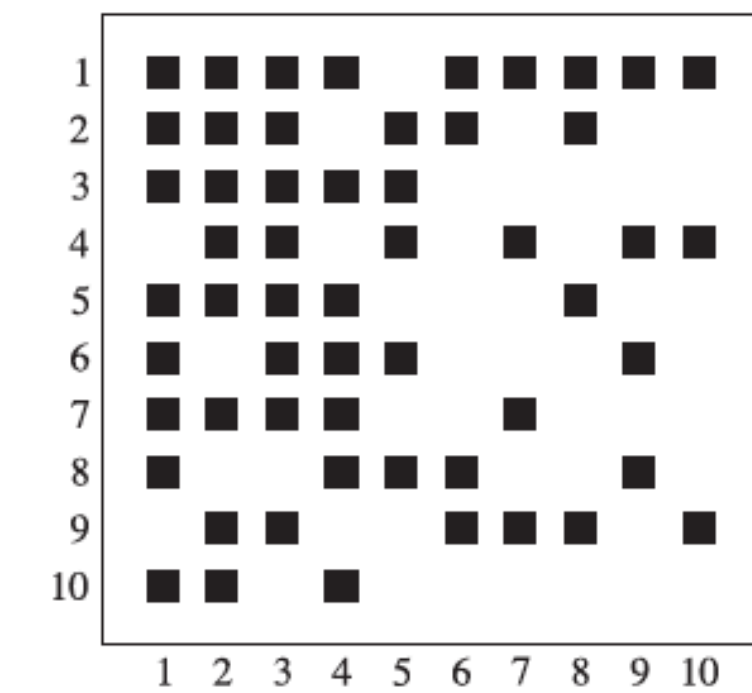
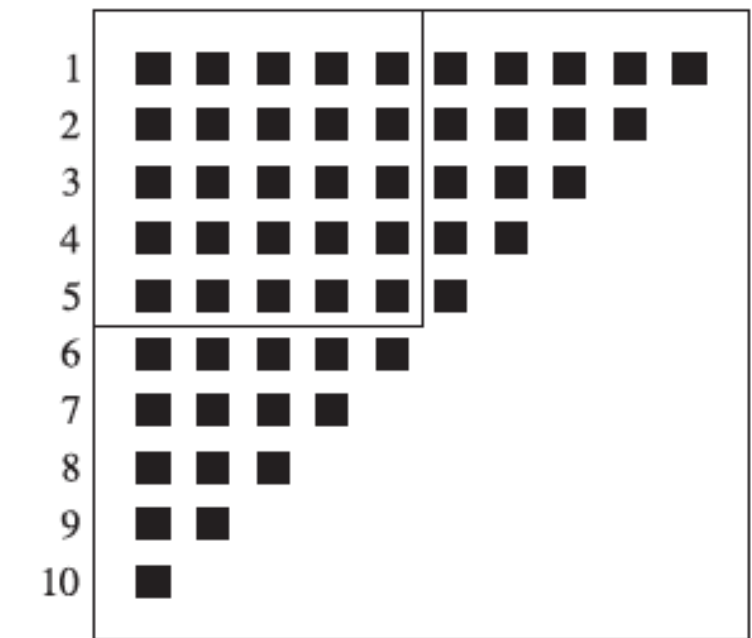
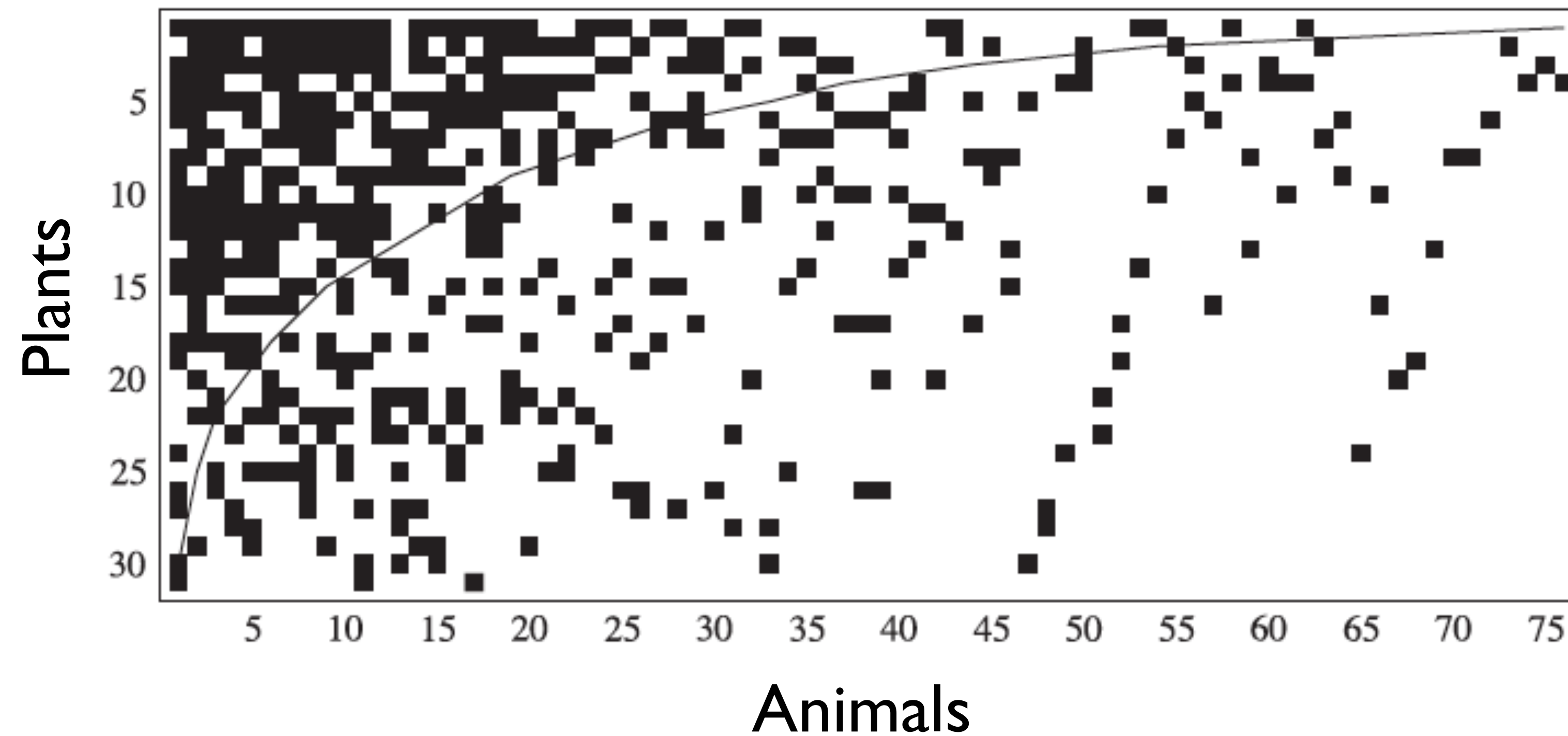


what is the expectation?

$N = 10$ islands; fraction sp-1 = 0.5; fraction sp-2 = 0.2

Probability of overlap if they are independent = $P_1 * P_2 = 0.1$

falsifying a null hypothesis in network research



$N = 0.74$, ... so what?

null models

a null model is an appropriate randomisation of the observed matrix intended to serve as a benchmark to assess the significance of a given pattern. It is a pattern-generating model that deliberately excludes a mechanism of interest, and so it serves to test whether the observed level of structure can be explained out of chance.

I. equiprequent null model

each cell ij has the same probability of having a “I” given by the total fraction of “I”s in the observed matrix

I	I	I	I	I
I	I	I		
I	I			
I				
I				

observed

	I		I	
I		I		I
	I		I	I
I	I			
		I	I	

randomization

$$\rho_{ij} = \frac{\text{total number of "I"s}}{\text{potential number of "I"s}} = \frac{12}{25} = 0.48$$

2. equiproquent column null model

the probability ρ_{ij} of drawing an interaction in cell ij is the fraction of “I”s in column j

$$\rho_{ij} = \begin{array}{l} \text{fraction of “I”s} \\ \text{in column } j \end{array} = \frac{1}{n} \sum_{i=1}^n M_{ij}$$

I	I	I		I
I	I	I		
I	I			
			I	
I				

observed

		I?		

randomization

$$\rho_{2,3} = \frac{2}{5} = 0.4$$

3. probabilistic cell null model

the probability ρ_{ij} of drawing an interaction in cell ij is proportional to the degree of both row i and column j

fraction of "I"s in row i fraction of "I"s in column j

$$\rho_{ij} = \frac{p_i + q_j}{2}$$

observed

$$\rho_{2,3} = \frac{3/5 + 2/5}{2} = 0.5$$

		?		

randomization

$$p_i = \frac{1}{n} \sum_{j=1}^n M_{ij} \quad q_j = \frac{1}{m} \sum_{i=1}^m M_{ij}$$

4. swap null model

it maintains exactly the number of “1”s in both rows and columns by sequentially reshuffling 2x2 sub matrices with the same row and column total as follows:

$$\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \longrightarrow \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$$

1	1	1	0	1
1	1	1		
1	1			
0			1	
1				

observed

0	1	1	1	1
1	1	1		
1	1			
1	1		0	
1				

randomization

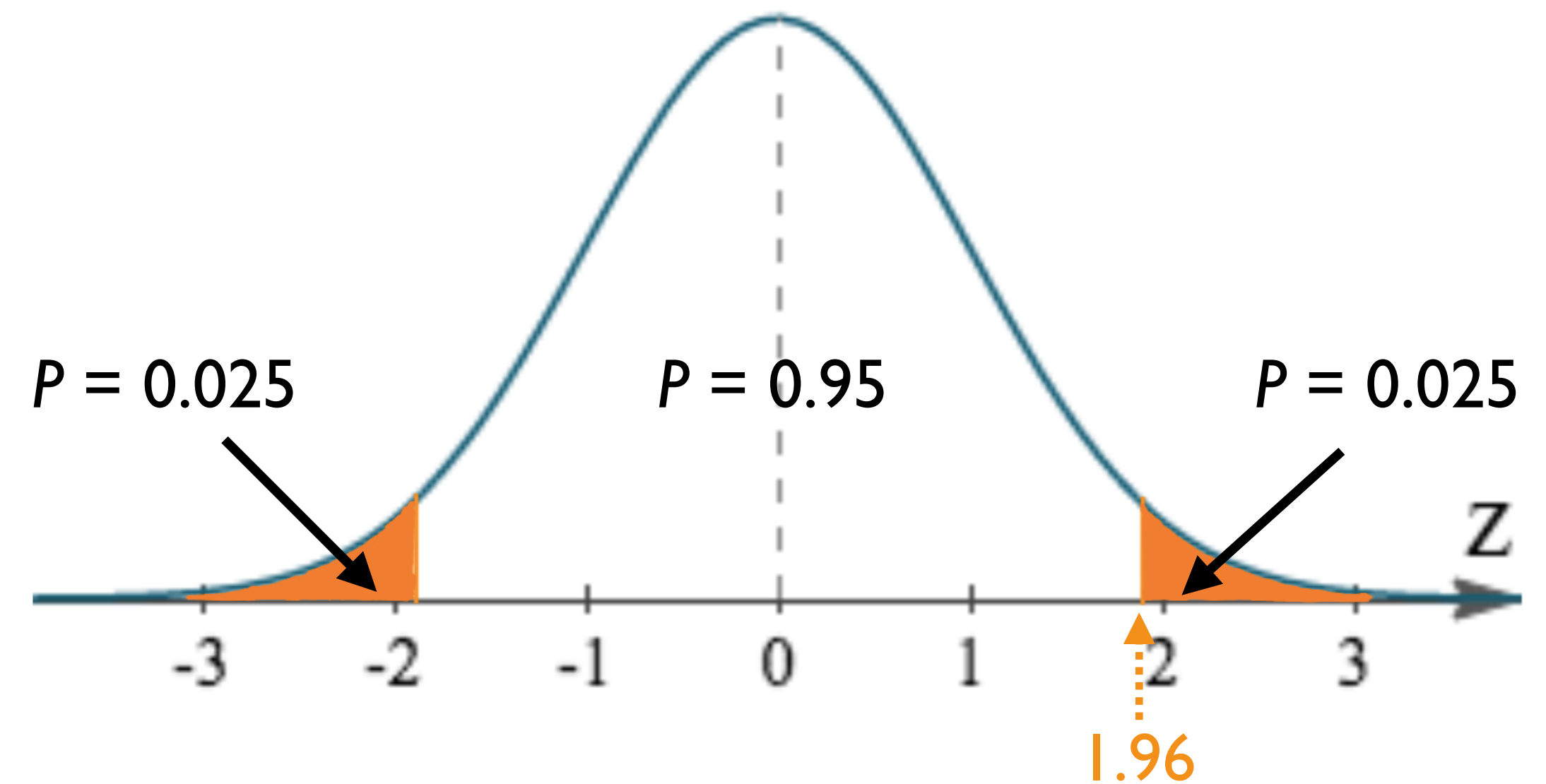
significance of a network pattern

observed value

average across replicates

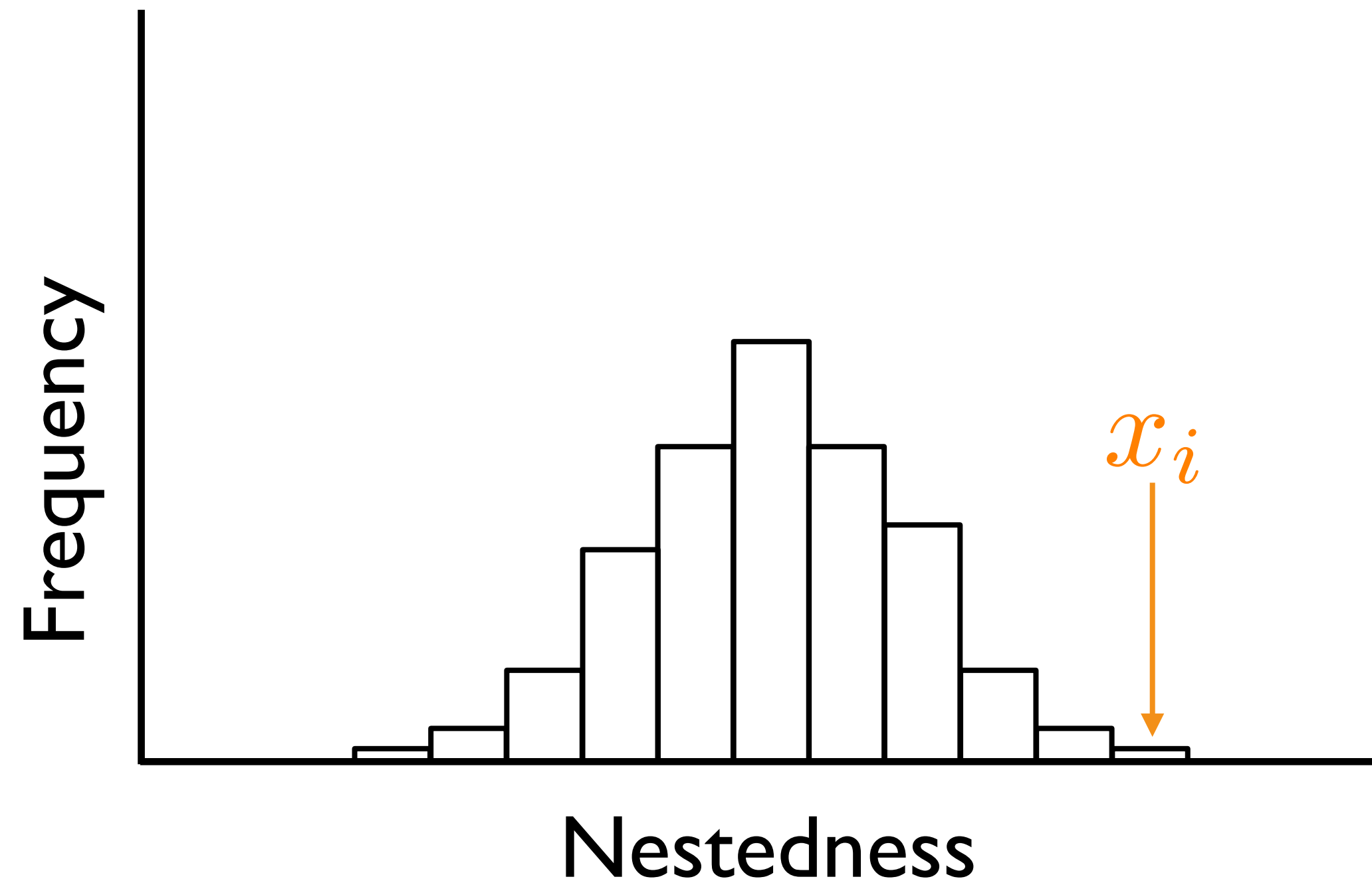
$$Z = \frac{x_i - \bar{x}}{\sigma}$$

standard deviation across replicates



- a z-score is a very useful statistic for calculating the probability of a value occurring within a normal distribution with a mean of 0 and a standard deviation of 1.
- a pattern is statistically significant ($P < 0.05$) if $Z > 1.96$

significance of a network pattern (II)



significance of nestedness (P -value): relative fraction of randomisations with a value of nestedness higher or equal than the observed one (e.g., 2 out of 100, $P = 0.02$)

which null model should one use?

- keep in mind what do we want to fix (e.g., only total number of “1”s, number of “1”s per rows, number of “1”s per rows and columns, ...)
- understand their goodness/limitations in the context of the trade-off between type I error (mistakenly rejecting a true null hypothesis) and type II error (mistakenly accepting a wrong null hypothesis)

hypothesis testing and type I vs type II error

null hypothesis (H_0) is

true

false

decision about null hypothesis (H_0)

accept

correct

type II error

probability = β

reject

type I error

probability = α

correct

Example:

H_0 : water is contaminated

H_1 : there is no contaminant

The type I error rate or significance level is the probability of rejecting the null hypothesis given that it is true. Often, the significance level is set to 0.05 (5%),

A type II error occurs when the null hypothesis is false, but erroneously fails to be rejected. The rate of the type II error is related to the power of a test.

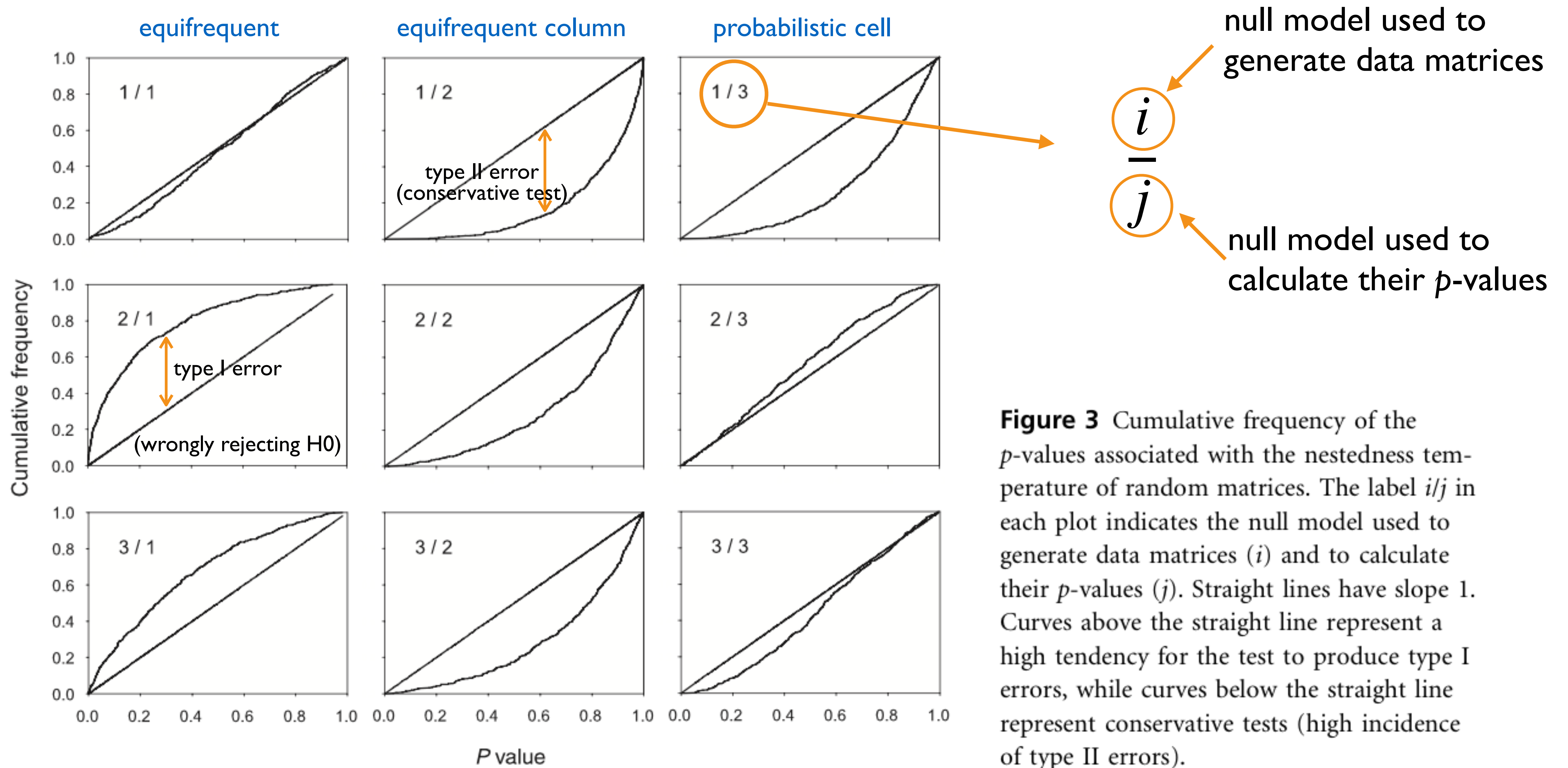


Figure 3 Cumulative frequency of the p -values associated with the nestedness temperature of random matrices. The label i/j in each plot indicates the null model used to generate data matrices (i) and to calculate their p -values (j). Straight lines have slope 1. Curves above the straight line represent a high tendency for the test to produce type I errors, while curves below the straight line represent conservative tests (high incidence of type II errors).

comparing across networks

$$z = \frac{x_i - \bar{x}}{\sigma}$$

- a z-score is a very useful statistic for normalising a value and therefore making it comparable across systems. The raw value of nestedness, for example, depends on matrix size, shape, and filling. It can not be compared across communities. Relative nestedness (z-score) can be used to compare across networks (not perfect, but good enough).