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Chapter 1

Comparing ecological networks

Although this might seem like a more advanced topic, comparing network is relatively easy in that it mostly involves enumerating elements – how many species, and how many interactions, are either unique to one, or shared by two networks?

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1.2 The metaweb

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Chapter 2

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The deeply flawed art of null hypothesis significance testing

Ecologists, like sadly a great majority of scientists, decide on the worthiness of an observation by ignoring their best judgement, decades of training in biology, and expertise; instead, we rely on whether some arbitrary value (the p-value) is lower than some even more arbitrary threshold (0.05). It all seems very *ad hoc* (it is). And yet, a surprising amount of literature on ecological networks attempts to decide whether some observed value of a network measure is "significant", and so it is with great reluctance that we will dedicate a chapter to this practice.

4.1 Fundamentals of network NHST

Null Hypothesis Significance Testing (NHST) for ecological networks strives to answer the following question: "if I observed the value f_0 for the measure f on a network $\mathbf{N}$, is it in the range of values expected by chance?". Most often, we want to refine this question by asking if the value is larger or smaller than we expect, and this is why this process usually involves a one-tailed one-sample t-test.

4.1.1 Generating a sample

Given a function f and a network $\mathbf{N}$, NHST requires to measure the distribution of possible values of $f(\mathbf{N})$. For most measures (all of them, in fact),

there is no direct expression of this distribution, and so we need to rely on an imperfect proxy: generating random networks. The exact models under which these models are generated is explained in section **TK**.

4.1.2 From the sample to the distribution

4.1.3 Estimating significance

4.2 Overview of the null models

4.3 An example using nestedness

4.4 Overview of the issues