

# Practical Analysis of Ecological Networks

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# Introduction

(Delmas et al. 2018)

## 0.1 Why networks?

## 0.2 What this book is about

### 0.2.1 The structure of ecological networks

### 0.2.2 Best practices in ecological networks research

### 0.2.3 Programming

## 0.3 What this book is not about

### 0.3.1 The ecology of ecological networks

### 0.3.2 The foundation of network theory

There are a number of fantastic textbooks on network science, where the mathematics foundations of this field are laid out in a clear and comprehensive way.

### 0.3.3 Programming

## 0.4 How to read this book

### 0.4.1 The importance of primary literature

### 0.4.2 The importance of experimenting with code

This book involves *a lot* of computer code; in fact, it is mostly about writing computer code to analyse ecological networks. Although we rely extensively on a software package (Poisot et al. 2019) to do this, there will be many

applications where writing our own functions, or writing our own scripts, will be necessary. Copying and pasting this code, and running it exactly as presented here, is a terrible idea. Instead, we encourage readers to *adapt* the code to their own interests, uses, and questions.

How does one adapt code? **tk**

# 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? As such, a good understanding of the core concepts in ?? will be useful for this chapter.

To develop an intuition of why ecological networks differ, it is useful to think of them as sets. Not only does it allows defining a number of mathematical operations that will greatly simplify the notation, it also matches directly the formalism developped by Koleff, Gaston, and Lennon (2003) for the dissimilarity of presence-absence data, which we will follow throughout this chapter.

### 1.1 Pairwise network comparison

### 1.2 The metaweb

In the previous section, we have focused on the fact that different networks can share, or not, some of their species, and some of their interactions. This provided a powerful intuition to think about network dissimilarity in terms of  $\alpha$  and  $\beta$  diversity - but what about  $\gamma$ ? In this section, we will think about the "metaweb", defined by Dunne (2006) as the aggregation of all regional interactions in a series of related networks. In other words, we can define a metaweb as the recursive union of a collection of networks.

**1.2.1 Metaweb properties****1.2.2 Network distance to the metaweb****1.3 Multi-site network comparison**



## Chapter 2

# Motifs in ecological networks



## Chapter 3

# Nestedness and interaction overlap



## Chapter 4

# 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**

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