

Surprising Species: the trace of evolution in food webs through the lenses of information theory

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Detecting and analysing the role of macro-evolutionary processes in the structure of ecological networks is challenging, particularly for unipartite food webs. Current methods are either model-based, or relying on linear interactions, and provide limited information on the role of single species. Here, we propose a novel approach, building on Information Theory and providing a meaningful interpretation in terms of Minimal Evolution, to test for phylogenetic signal in unipartite food webs. Moreover, we show how that can be used to identify surprising species: species that have an unexpected peculiar ecological role, given their evolutionary history. We apply our methodology to two large food webs, and discuss the results.

Keywords:
Ecological Networks
Phylogenetic Signal
Information Theory

1

Introduction

Phylogenetic Signal testing for ecological network is important, but is hard.
Current methods work mostly for bipartite, or are model based.
We don't have a model for unipartite food webs.
So, here we propose a method based on Information Theory.
Dkl. Minimal Evolution. Interpretation as surprise.
Surprising species.

2

Methods

From phylogeny to distance matrix to distribution.
From ecological networks to distance matrix (through RDPG) to distribution.
Compute Dkl of the two distributions.
Permanova by reshuffling tips on tree.
Decomposition on species level.
Figure 1: diagram of method.

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Data

Tanzania National Park

Marine food webs

4 _____

Results

Tanzania National Park

Tanzania Surprising Species

Figure 2: permanova test || suprise of species || inlet of most suprising species.

Marine food webs

Marine surp spec

Figure 3: permanova test || suprise of species || inlet of most suprising species

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Conclusion

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References