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.

Last revision: *February 27, 2023*

1 Introduction

2 Phylogenetic Signal testing for ecological network is important, but is hard.

3 Current methods work mostly for bipartite, or are model based.

4 We don't have a model for unipartite food webs.

5 So, here we propose a method based on Information Theory.

6 Dkl. Minimal Evolution. Interpretation as surprise.

7 Surprising species.

8 Methods

9 From phylogeny to distance matrix to distribution.

10 From ecological networks to distance matrix (through RDPG) to distribution.

11 Compute Dkl of the two distributions.

12 Permanova by reshuffling tips on tree.

13 Decomposition on species level.

14 Figure 1: diagram of method.

15 Data

16 Tanzania National Park

17 Marine food webs

18 Results

19 Tanzania National Park

20 Tanzania Surprising Species

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

22 Marine food webs

23 Marine surp spec

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

25 Conclusion

26 References