Should we build a macro-scale theory for coevolution? Nope.

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Coevolutionary dynamics acting on both species and their interactions are a key driving force behind the structure of ecological communities. The Geographic Mosaic Theory of Coevolution (GMTC) provides a spatial perspective to these dynamics by proposing the existence of feedbacks between local and regional scales. It remains unclear, however, how the structure of communities at larger spatial scales either influences or is influenced by local coevolutionary processes. Despite this, ecological networks are known to have an ecological structure, which suggest that coevolution may play a role in their evolutionary dynamics. Here we show that the coevolutionary significance of individual interactions is maintained when moving between the local and regional scale. Importantly, this oc-10 curs despite the fact that community variation at the local scale tends to weaken 11 or remove community-wide coevolutionary signal. This apparent mismatch be-12 tween our interaction-level and community-level results strongly suggests that interactions provide the correct scale to study coevolution at small spatial scales while communities are the relevant scale only at larger spatial extents. We provide a new perspective on the interplay between coevolutionary theory and community ecology, by establishing the organisational scales at which the different

- 1 theories have relevance. Although it has been tempting so far to understand how
- 2 coevolution relates to network structure, our results suggest that the way for-
- 3 ward is to understand how network structure may affect coevolution over space
- 4 instead.
- 5 Ecological interactions introduce selective pressures on the species involved. At
- 6 large organisational scales, this results in taxonomic boundaries delineating groups
- of interacting species 1, invariant structures in some ecological communities 2, and
- 8 conservatism of both the distribution of community modules 4 and the role of species
- 9 occupy within them ⁵. Although the evolutionary dynamics for a pair of interacting
- species has been well described ???, attempts to understand how these mechanisms
- cascade up to generate species diversity observed in large ecological networks have
- been unconclusive 6,7, despite the well known effect of antagonistic coevolution on
- genomic diversification ^{8,9}. The scales at which these diversities happen are hard
- to reconcile: coevolution is expressed within patches connected by gene-flow ^{10–12},
- whereas the species diversity of complex networks is typically observed at spatial
- scales matching the species distribution ^{13,14}. Because these scales differ by orders
- of magnitude, one must question the relevance of previous calls to scale the theory
- on coevolution up to multi-species systems covering large spatial extents ???.
- Network-based approaches ^{15,16}, on the other hand, were designed to study and
- describe species-rich systems. Previous empirical findings revealed the impact of
- evolutionary dynamics on overall network structure in food webs ^{1,17}, pollination
- networks ^{18,19}, and host-parasite networks ^{20,21}. Both micro ^{3,22} and macro ^{23,24} evo-
- ²³ lutionary dynamics have been measured or modelled in species-rich communities,
- but there is no understanding of how, or even of whether, local/micro-evolutionary

- and regional/macro-evolutionary feedback into one another. Another layer of com-
- 2 plexity is that ecological networks are known to vary in their structure over time and
- space ²⁵: the same two species will not interact in a consistent way locally, either be-
- 4 cause of local environmental contingencies, by chance, or because their phenolo-
- ⁵ gies do not positively covary in space ²⁶. As a consequence, *locally*, the evolutionary
- 6 signal on network structure is expected to be burried under much ecological noise,
- ⁷ and the effect of coevolution can only be inferred *regionally*.
- 8 In multi-species systems that typically span a large taxonomic range, coevolution is
- 9 often measured as the matching between the phylogenies of two sets of interacting
- organisms ^{20,27}. This build on the century-old ideas that extant species interact in a
- way similar to the way their ancestors did ²⁸. "Coevolved" systems should (i) have
- 12 approximately similar phylogenetic trees and (ii) species at matching positions in
- either trees should interact. It is not clear, however, how this idea relates to dynam-
- ics occurring at smaller scales ²⁹: many ecological and evolutionary processes that
- occur locally, or over small spatial scales, can disturb this expected structure. No-
- tably, it has been shown that species interactions are not consistent through space
- ¹⁷ Local loss of both interactions and species from the regional pool is most likely
- to result in observed communities that do not appear to have been shaped by co-
- 19 evolution.
- We use data on ectoparasites of rodents from Western to Eastern Europe 31 to test
- 21 the following four hypotheses. First, local species assemblages do not show evi-
- dence of coevolution even though the system has a whole does. Second, interaction-
- level coevolutionary signal is conserved. Third, interaction-level coevolutionary
- signal does not predict the spatial consistency of interactions. We do so by coupling

two novel methods: the PACO algorithm for detection of phylogenetic congruence

³², and a general framework for the variation of ecological networks ³⁰.

Local observations on the 51 localities (Supp. Mat. 1) are aggregated into a regional metanetwork ³⁰. The two phylogenetic trees have been rendered ultrametric. We use PACO³² to measure the congruence between trees knowing the matrix of interaction. PACO yields a network-level significance value for the likelihood that hosts and parasites have coevolved. For each local network, we measure the strength of coevolution using (i) only local observations and (ii) all possible interactions between local species (as known from the regional aggregation of all local networks). This allows us to separate the effect of species sorting (regional interactions) and interaction sorting (local interactions). At the regional scale, coevolutionary signal is extremely strong ($p \le 10^{-4}$), as established by previous analysis of this system ³³. Most local networks, on the other hand, show very little evidence of phylogenetic 13 congruence. Out of 51 local networks, 35 show no signal of coevolution, 11 show coevolution when using the regional interactions, and 12 show coevolution using 15 the local interactions (see *Supp. Mat. 1* for network-level significance values). **Fig**-16 ure?.

This suggests that macro-evolutionary processes (such as co-diversification) have 18 consequences at the macro-ecological level 34, but may not be detected at finer spatial scales due to a stronger effect of ecological processes locally. PACO permits the 20 analysis of how strongly each interaction contribute to coevolution, in a way that 21 is as independent as possible from other interactions. As interactions vary only in-22 sofar that there are some locations in which they do not happen, we expect that the overall contribution of interactions will be the same in the local and regional

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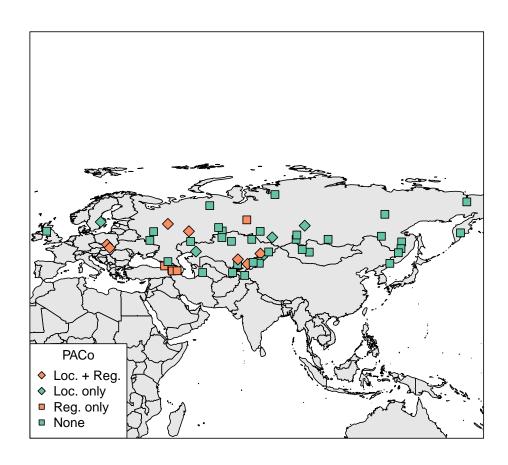


Figure 1: figure1

- networks. For the 5 networks that show evidences of coevolution accounting both
- ² for species and interactions sorting, we measured the contribution of each inter-
- action locally, and compared it to its contribution to the regional network. Results
- are presented in **FIG**.

5 Point 2 – Interactions respond locally to micro-processes

- Review of mechanisms involved in interactions locally: neutrality and trait-
- 7 based mechanisms

18

- Key refs: Oikos paper, Canard, Olesen, Combes
- These mechanism can only *filter* from a pool of regional interactions
- Key refs: Biol Lett paper, Olito & Fox, Lounnas, ...
- Key points: i) even though they will change the network-level signal, contribution of interactions should not vary locally vs. regionally ii) this is the expectation because (a) past knowledge about motifs/evolution and (b) interactions are the unit in which selection takes place, not networks
- Illustration: distribution of the significance in each interaction locally (measured vs. metaweb) vs. in the regional network.

17 Point 3 – The spatial replication of networks is imperfect

Ecological processes = sorting of interactions + species

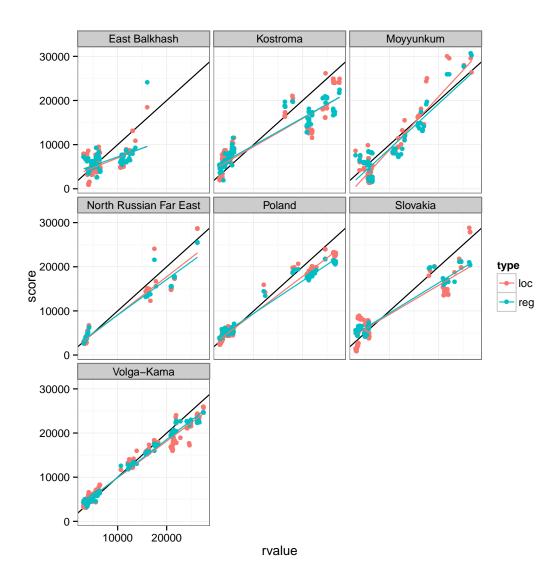


Figure 2: figure2

- Key refs: Ecol Lett -div
- Key points: observation of interactions result from filtering through two pro-
- cesses, and not clear they are related to past coevolution = we expect a loss
- 4 of signal locally
- Illustration: jacknife score vs. observed/possible : there is no relationship
- between how important an interaction is (coevo) and how frequent it will be.
- suggests that ecological >> evolutionary drivers of local network structure
- This is caused by local ecological processes, but also influences local evolu-
- 9 tionary dynamics
- Key refs: Gomulkiewicz, Hochberg, Benkman, Siepilski
- Key points: i) Opportunity to integrate more network theory to understand
- between-sites differences ii) Even though coevo theory recognized variation
- in effects, very little attention to variation in presence/absence of int and its
- implications

15 Conclusions

- Need to bridge ecological networks with co-evolution (understand the im-
- pact of ecology vs. evolution in the local observations)
- Main advance: coevolutionary dynamics are important at the continental/regional
- scale, much less at the local scale

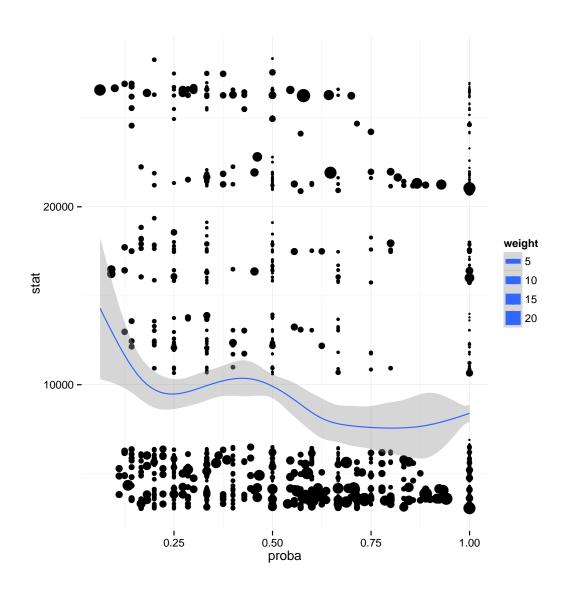


Figure 3: figure3

- Focus on datasets that are spatially replicated, with as good as possible phy logenies. Ref Buckley, Hearkel.
- Currently local variability is not accounted for by statistical methods, need to
 do a better job. See Desdevises chapter on ParaFit 2.0.
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