

Coevolution leaves a stronger imprint on interactions than on community structure

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1 Coevolutionary dynamics act on both species and their interactions in
2 ways that shape ecological communities ^{1,2}. It remains unclear, how-
3 ever, how the structure of communities at larger spatial scales either
4 influences or is influenced by local coevolutionary processes ³, and how
5 mechanisms acting at these different scales feedback onto one another
6 ⁴. Here we show that, although species interactions vary substantially
7 over a continental gradient, the coevolutionary significance of individual
8 interactions is maintained across different scales. Notably, this occurs
9 despite the fact that observed community variation at the local scale
10 frequently tends to weaken or remove community-wide coevolutionary
11 signal. When considered in terms of the interplay between community
12 ecology and coevolutionary theory, our results demonstrate that indi-
13 vidual interactions are capable and likely to show a consistent signature
14 of past coevolution even when woven into communities that do not.

15 Ecological interactions often exert important selective pressures on the species
16 involved. For example, the phenologies of lodgepole pines and red crossbills re-

1 spond spatially to the presence of squirrels ⁵ and palm species undergo changes
2 in seed morphology in response to the extinction of bird dispersing their seeds
3 ⁶. Given that interactions are distributed in similar ways across communities, at
4 both the large ⁷ or small ⁸ scale, it can be argued that much ecological structure
5 is the end result of evolutionary or coevolutionary dynamics between species ^{9,10}.
6 Unfortunately, while the coevolutionary dynamic of pairs of interacting species
7 has been well described at macro ¹¹ and micro ¹² evolutionary timescales, most
8 attempts to understand how they cascade up to the levels of diversity of both
9 species and interactions found within empirical communities have been inconclu-
10 sive ¹³. Moreover, because coevolutionary dynamics are often presented as a key
11 driving force behind ecological structure across both time and space ¹⁴, it is crucial
12 to determine the scale at which they are both relevant and quantifiable.

13 Historically, the evidence for coevolution in taxonomically diverse communities
14 is quantified as the degree of matching between the phylogenies of two sets of
15 interacting organisms ¹⁵. This notion builds on the century-old idea that extant
16 species interact in a way similar to the way their ancestors did ¹⁶. Yet it is consid-
17 erably more restrictive than just phylogenetic conservation of species' interactions
18 ¹⁷, as it accounts for higher-order constraints. More explicitly, it is thought that
19 communities that have assembled by successive divergence events should display
20 phylogenetic congruence, that is (i) have similar phylogenetic trees and (ii) have
21 species at matching positions in the trees that tend to interact ¹⁸. On the other
22 hand, many ecological and evolutionary processes that occur locally are expected
23 to blur community-wide coevolutionary signal ¹⁹. One possible explanation is
24 that interactions can display substantial turnover at ecologically relevant tem-
25 poral and spatial scales ²⁰: the same two species can interact in different ways

1 under the effect of local environmental contingencies, spatial mismatch in species
2 phenologies, variations in population abundances, and chance events ²¹. It is un-
3 clear, however, whether these mechanisms influence how the coevolutionary signal
4 within individual interactions should vary across spatial scales.

5 To answer these questions, we study a dataset of interactions between rodents
6 and their ectoparasites from 51 sites across Western to Eastern Europe ²² (Meth-
7 ods Summary). This dataset is uniquely suited for this task as it represents
8 a paradigmatic system in which species-species interactions are thought to be
9 driven by macro-evolution and co-speciation events ²³, and coevolutionary signal
10 is indeed significant at the continental level ²⁴ ($p \leq 10^{-4}$; Methods Summary).
11 Importantly, it also provides spatial replication and variability at a scale large
12 enough to capture macro-ecological processes.

13 As host-macroparasites interactions are hypothesized to be both ecologically con-
14 strained and evolutionary conserved ²⁵, the congruence observed at the continen-
15 tal level sets the baseline for what would be expected in local communities. Of
16 course, if ecological mechanisms reduce coevolutionary signal, we should detect
17 coevolution at the continental scale but not locally. Noting that variation of in-
18 teractions can decrease congruence, we analyse the data at two different levels to
19 test these hypotheses: first, we use *regional* interaction data—which accounts for
20 different species composition across sites—and second, we use the *local* interaction
21 data—which also accounts for variation in the interactions between observed these
22 species (Methods Summary). Out of 51 sites, 35 show no signal of coevolution, 11
23 show significant coevolutionary signal when using the regional interactions, and
24 12 show significant coevolutionary signal using the local interactions (see *Supp.*

1 *Mat. 1* for network-level significance values).

2 These results would appear to support the idea that macro-evolutionary pro-
3 cesses such as co-diversification can have consequences at the macro- ecological
4 level ²⁶ but may not in fact be detectable at finer spatial scales. On the other
5 hand, system-level differences say little about the behavior of individual inter-
6 actions, despite the fact most coevolutionary mechanisms act at the interaction
7 level ²⁷. As might be expected, we observe here that networks with interactions
8 that are important for coevolution at the continental scale indeed have more co-
9 evolutionary signal at the local and regional scales alike (Fig. 2A). Intriguingly,
10 we also find that the distribution of individual interactions' contributions to co-
11 evolution is strongly conserved, regardless of the scale at which the interactions
12 are quantified (Fig. 2B). Because interactions differ in their total contribution to
13 coevolution, this implies that their distribution across networks is what actually
14 drives differences in overall coevolutionary signal. Network-level coevolutionary
15 signal emerges directly from the properties of interactions and is not a property
16 of the network itself.

17 Beyond their contribution to coevolution, interactions also ultimately differ in
18 how frequently they vary when the species involved co-occur ^{28,29}. Once more, the
19 literature on host-parasite interactions usually assumes that the reason why some
20 interactions are more frequent is because they reflect a significant past history
21 of coevolution ³⁰. If this were true, we should observe a significant, positive
22 correlation between the probability of observing an interaction and the importance
23 of that interaction for coevolution at the continental scale (Methods Summary).
24 Surprisingly, we find that neither is true here since interactions that are important

1 for coevolution are not more conserved (Fig. 3).

2 Ultimately, coevolutionary signal varies across scale under the joint variation of
3 both species interactions and phylogenetic community structure, and so we expect
4 the contribution of each interaction to differ across scales too. Nonetheless, we
5 find that interactions that contribute strongly to coevolutionary signal at the con-
6 tinental scale *also* show a significant tendency to contribute strongly at the local
7 scale (Fig. 4). Remarkably, this result implies that the remnants of coevolution
8 are still locally detectable in *individual interactions* even though it does not leave
9 its imprint on most local networks.

10 Overall, the results of our analyses demonstrate that there is a sizeable gap be-
11 tween our current understanding of coevolution as the basis of multi-species in-
12 teractions and its applicability to ecological questions. Local networks show little
13 to no signal of coevolution and the strength of coevolution between two species
14 is a surprisingly poor predictor of how frequently they interact. In contrast to
15 the frequent assumption that phylogenetic structure is a key driver of community
16 structure ³¹, these data reveal that this impact is actually minimal at ecologi-
17 cally relevant spatial scales. Despite all the above, individual interactions are
18 able to maintain their coevolutionary signal even when the community they are
19 woven into does not. Thinking more broadly, these discrepancies provide a clear
20 roadmap for bridging the aforementioned gap between our appreciation of the role
21 of coevolution and its empirically measurable outcomes. Network structure is the
22 most parsimonious *mechanism* by which coevolution proceeds, not the imprint
23 coevolution leaves on ecological communities.

1 Methods Summary

2 We use data on observations of interactions between 121 species of rodents and
3 205 species of parasitic fleas in 51 locations across Europe ²² to build 51 species-
4 species interaction networks. Interactions were measured by combing rodents for
5 fleas, a method that gives high quality data as it has a high power of detection. To
6 account for differential sampling effort and across site variations in abundance, we
7 only study the networks' incidence matrices (presence and absence of interactions).

8 In our study, we define three scales for the network data and analysis— conti-
9 nental, regional, and local. The continental scale is the aggregated “metanetwork”
10 which includes all potential interactions between co-occurring species ²⁰ (*i.e.*, all
11 species and all their interactions across the 51 networks). Within each site, the
12 regional scale is given by the list of observed species and all their possible interac-
13 tions. Hence the regional networks are always a perfect subset of the continental
14 network. The local scale includes only the interactions that were actually observed
15 in the field at a given site. Therefore, the local and regional networks always in-
16 clude the same species, but the local network has only a subset (or, at most, an
17 exact match) of the interactions in the regional network. The spatial consistency
18 of every individual interaction is measured as the number of sites in which the
19 two species involved co-occur.

20 We quantified the coevolutionary signal in terms of the degree of matching be-
21 tween host and parasite phylogenies given knowledge of species interactions using
22 the *PACO* method ³², which is robust to variations in number of species. *PACO*
23 provides measures of both the network-level congruence (*i.e.*, is the network co-
24 evolved?) and the interaction-level signal (*i.e.*, what is the contribution of each

1 interaction to the overall coevolutionary signal?). We measured the phylogenetic
2 dissimilarity between two sites for hosts and parasites using PCD³³, a measure
3 that accounts for the dissimilarity of species, corrected for the phylogenetic dis-
4 tance between all species in the dataset. Since it is a requirement of the methods
5 we use here, the phylogenetic trees for hosts and parasites were rendered ultra-
6 metric (i.e., all species are at the same distance from the root).

7 References

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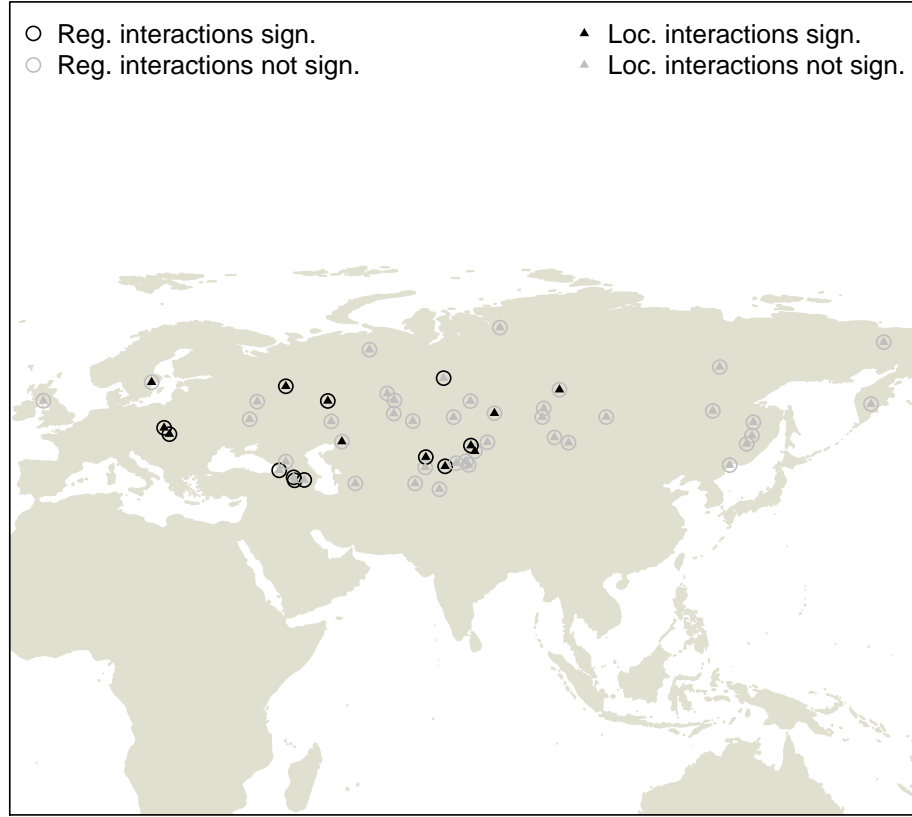


Figure 1: Spatial distribution of coevolutionary signal across the 51 sites. For each location, we indicate whether or not the structure of regional and local interaction networks is consistent with phylogenetic congruence. The color of the circle corresponds to regionally significant or nonsignificant (black and grey, respectively) while the color of the symbol within corresponds to locally significant or nonsignificant (black and grey, respectively).

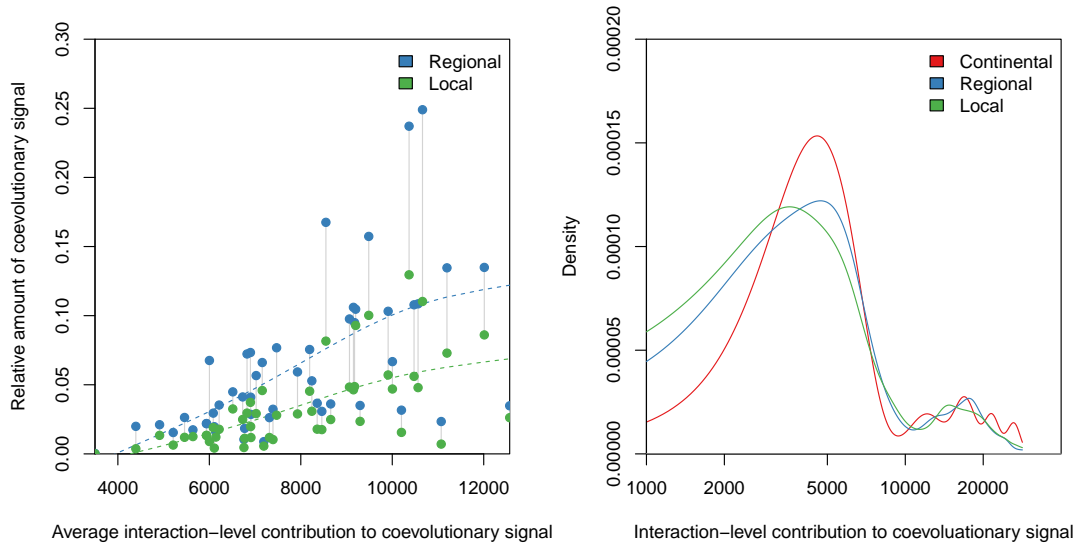


Figure 2: Distribution of coevolutionary signal at the network and interaction level. **A** Networks that have lower coevolutionary signal are made of interactions that contribute little to coevolution at the continental scale. **B** Interactions in the local, regional, and continental scale have equal contributions to coevolution.

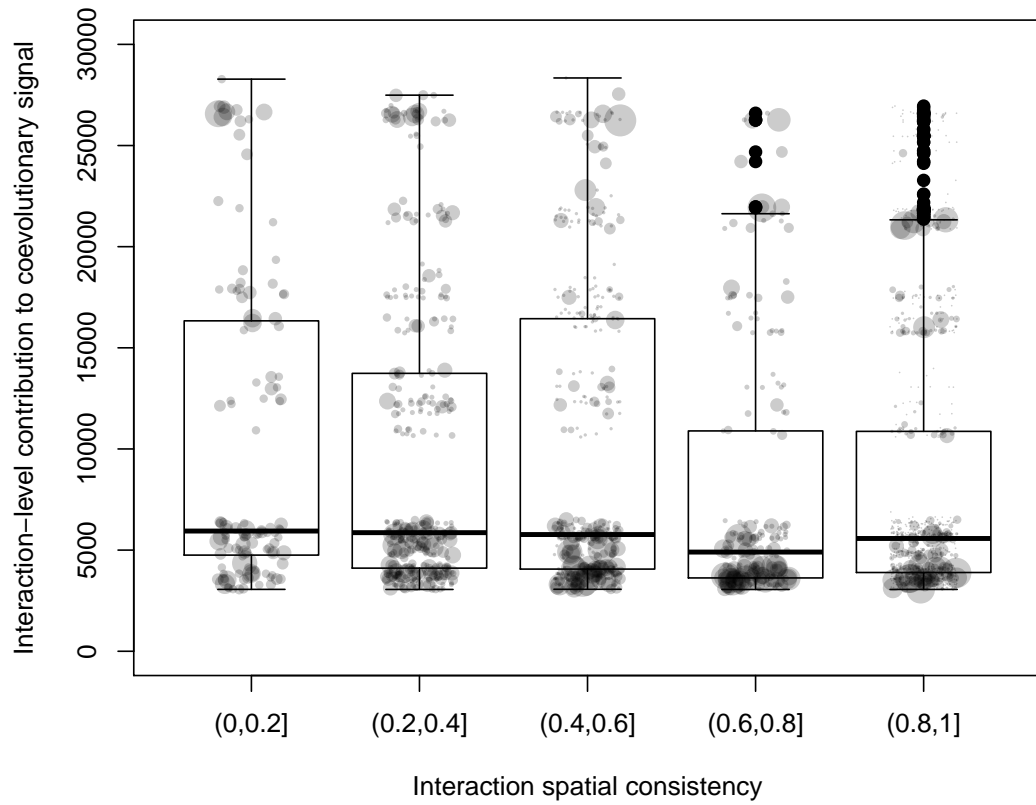


Figure 3: Lack of a relationship between the spatial consistency of an interaction and its importance for coevolution in the continental network. Spatial consistency is defined as the probability of observing an interaction between two species given that they were observed to co-occur.

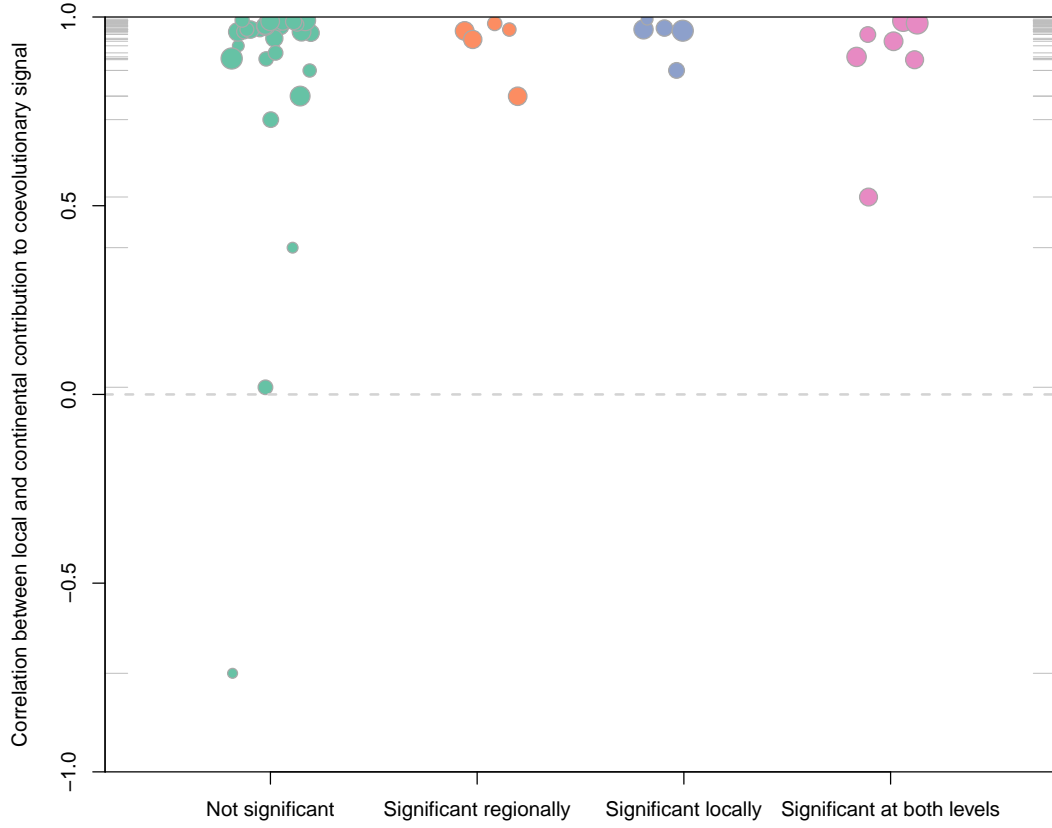


Figure 4: Correlation (Pearson’s statistic) between the interaction-level contribution to coevolutionary signal at the local and continental scales. All positive correlations are significant with $\alpha = 0.05$. The size of each dot represents the base 10 logarithm of the number of interactions (network size).

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