COMMUNITY PHYLOGENETICS AND ECOSYSTEM FUNCTIONING

Phylogenetic patterns are not proxies of community assembly mechanisms (they are far better)

Pille Gerhold*,1, James F. Cahill Jr2, Marten Winter3, Igor V. Bartish4 and Andreas Prinzing5,6

1Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, 51005, Tartu, Estonia; 2Department of Biological Sciences, University of Alberta, Edmonton, AB, T6G 2E9 Canada; 3German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Deutscher Platz 5e, 04103, Leipzig, Germany; 4Department of Genetic Ecology, Institute of Botany, Academy of Sciences, CZ-25243, Pruhonice 1, Czech Republic; 5Research Unit “Écosystèmes Biodiversité, Evolution” («UMR 6553»), Centre National de la Recherche Scientifique, University Rennes 1, Campus Beaulieu, Bâtiment 14 A, 35042, Rennes, France; and 6Alterra, Wageningen UR (University & Research Centre), PO Box 47, NL-6700, AA Wageningen, The Netherlands

Summary

1. The subdiscipline of ‘community phylogenetics’ is rapidly growing and influencing thinking regarding community assembly. In particular, phylogenetic dispersion of co-occurring species within a community is commonly used as a proxy to identify which community assembly processes may have structured a particular community: phylogenetic clustering as a proxy for abiotic assembly, that is habitat filtering, and phylogenetic overdispersion as a proxy for biotic assembly, notably competition.

2. We challenge this approach by highlighting (typically) implicit assumptions that are, in reality, only weakly supported, including (i) phylogenetic dispersion reflects trait dispersion; (ii) a given ecological function can be performed only by a single trait state or combination of trait states; (iii) trait similarity causes enhanced competition; (iv) competition causes species exclusion; (v) communities are at equilibrium with processes of assembly having been completed; (vi) assembly through habitat filtering decreases in importance if assembly through competition increases, such that the relative balance of the two can be thus quantified by a single parameter; and (vii) observed phylogenetic dispersion is driven predominantly by local and present-day processes.

3. Moreover, technical sophistication of the phylogenetic-patterns-as-proxy approach trades off against sophistication in alternative, potentially more pertinent approaches to directly observe or manipulate assembly processes.

4. Despite concerns about using phylogenetic dispersion as a proxy for community assembly processes, we suggest there are underappreciated benefits of quantifying the phylogenetic structure of communities, including (i) understanding how coexistence leads to the macroevolutionary diversification of habitat lineage-pools (i.e. phylogenetic-patterns-as-result approach); and (ii) understanding the macroevolutionary contingency of habitat lineage-pools and how it affects present-day species coexistence in local communities (i.e. phylogenetic-patterns-as-cause approach).

5. We conclude that phylogenetic patterns may be little useful as proxy of community assembly. However, such patterns can prove useful to identify and test novel hypotheses on (i) how local coexistence may control macroevolution of the habitat lineage-pool, for example through competition among close relatives triggering displacement and diversification of characters, and (ii) how macroevolution within the habitat lineage-pool may control local coexistence of related species, for example through origin of close relatives that can potentially enter in competition.

Key-words: coexistence, competition, evolution, functional traits, habitat filtering, interactions, lineage-pool, macroevolutionary diversification, phylogeny
**Introduction**

Community ecologists have a long tradition of inferring mechanisms of community assembly from observed patterns of species occurrences. Though this inductive approach can lead to insights (e.g. Watt 1947; recent summary in Mittelbach 2012), ecologists also have a long tradition of pointing out when storytelling appears to go too far. Among the best known examples is Connell (1980) paper in which he brought the ‘ghost of competition past’ to the attention of ecologists, arguing that the commonly held notion of co-evolutionary shaping of competitors’ niches had surprisingly little direct support.

A core lesson taken from this episode in ecology’s history is that many stories can be told from the same ecological pattern, and without studying actual processes, pattern description can be of limited value for understanding mechanisms. Here, we suggest ecologists are presently heading down a similar path – this time in conjunction with new phylogenetic tools and more sophisticated statistical methodology.

Many ecologists use phylogenetic dispersion of co-occurring species *per se* to infer mechanisms of community assembly. Some of the recent examples of this approach are Diaz *et al.* (1999), Webb (2000) and Webb *et al.* (2002), see also Kembel (2009), though the underlying idea continues back to the application of taxonomic ratios (e.g. species/genus ratio) to infer ecological processes (Elton 1946). Combined, the studies suggest that observed patterns of phylogenetic dispersion found among co-occurring species within a community could be a suitable means by which one can understand the processes of community assembly, even if one is unable to specifically identify the traits, filters or species interactions operating in a particular location. Most notable is the idea that (A) abiotic assembly, that is habitat filtering (*sensu* Diaz *et al.*, 1999), results in phylogenetic clustering, as closely related species are more likely to possess the traits needed to survive under a given set of environmental conditions, and (B) biotic assembly, such as competition and other negative density-dependent interactions, results in phylogenetic overdispersion, because relatedness is assumed to increase trait similarity and the likelihood of competitive exclusion.

The number of such studies using phylogenetic dispersion of communities as a proxy for community assembly processes has increased exponentially (from 1 publication in 1997 to 5 publications in 2007 and 41 publications in 2014; see Fig. S1, Supporting information). We note that although many biotic assembly mechanisms other than competition, such as mutualism and facilitation, can structure natural communities, this ecological reality has not been fully integrated into the community phylogenetics approach (but see Elias *et al.* 2009; Sargent *et al.* 2011; Venail *et al.* 2014). Thus, here we focus on competition as the main biotic assembly mechanism.

Though the use of phylogenetic patterns as proxies of the processes of community assembly is rapidly increasing, there has also been an increase in critiques (e.g. Mayfield & Levine 2010; HilleRisLambers *et al.* 2012; Pavoine *et al.* 2013 challenging the use of assembly proxies in general). The concerns include spatial and temporal scale-dependency of phylogenetic patterns (Emerson & Gillespie 2008; Cavender-Bares *et al.* 2009) and lack of correlation between measures of phylogenetic dispersion and trait dispersion (Pavoine & Bonsall 2011; Srivastava *et al.* 2012; Pavoine *et al.* 2013; Swenson 2013), questioning the interpretation of assembly mechanisms using phylogenetic data.

Overall, there may be a number of often unspoken and ignored assumptions underlying the phylogenetic-patterns-as-proxy approach (Prinzinger *et al.* 2008; Cavender-Bares *et al.* 2009; Mayfield & Levine 2010; Srivastava *et al.* 2012), but so far there is no review that focuses on a systematic identification and evaluation of all these assumptions. We are also lacking a broad perspective for identifying the situations in which phylogenetic patterns within communities might be useful to identify hypotheses on (i) ecological factors driving lineage diversification and (ii) the effect of lineage diversification on coexistence (see Emerson & Gillespie 2008; Cavender-Bares *et al.* 2009; Mouquet *et al.* 2012 for possible scenarios of evolutionary community assembly or examples of ecological consequences of coexistence among related species).

Our goal in this study was to identify several hidden assumptions underlying the ‘phylogenetic-patterns-as-proxy’ approach (Fig. 1) and review their empirical support. We will show that these assumptions are typically weakly supported by existing data and in some cases they are also not consistent with modern coexistence theory (Assumptions). We also suggest that continued reliance on phylogenetic proxies for community assembly without incorporation of more mechanistic studies to ‘ground-truth’ the statistical pattern may lead to collateral damage to our understanding of processes (see Appendix S1, Supporting information). We will finally refer to future directions by exploring two alternative approaches on how processes of local assembly accumulate into diversification of entire phylogenetic lineages, and how phylogenetic diversification of lineages causes the observed patterns of local community assembly. In doing so, we will profit from prior approaches developed by evolutionary biologists and palaeo-ecologists (e.g., Boucot 1996; Brooks & McLennan 2002). While feedbacks of community processes on evolution have been described before (e.g. Cavender-Bares *et al.* 2009; HilleRisLambers *et al.* 2012), we will show that phylogenetic community structure can play an important role in testing these evolutionary hypotheses (Where to go: put evolution into community phylogenetics). For consistency, most of our examples come from plants, but the concepts and mechanisms we are talking about apply equally well outside the plant kingdom.
Assumptions (Fig. 1)

**Assumption 1: Phylogenetic Dispersion Reflects Dispersion of Phylogenetically Conserved Functional Traits**

Community assembly is assumed to be mediated via functional traits, and trait dispersion of a community is hence indicative of particular assembly processes. Phylogenetic dispersion is then used as a proxy for trait dispersion and the underlying assembly processes. However, we will outline below that closely related species co-occurring in a local community may not necessarily share similar functional traits, even if across an entire region they mostly do (Fig. 1, caveat of assumption 1).

Studies using phylogenetic relatedness as a proxy for trait dispersion often justify this by referring to phylogenetic niche conservatism; that is, species ecological niches and niche-related traits tend to be maintained between ancestors and descendants (e.g. Prinzing et al. 2001). We leave aside here the potential problem of mixing notions of similar traits (in ecology) with synapomorphic traits (in phylogeny Ridley 2003). We also note that the assumption does not require niche evolution to be constrained (Blomberg & Garland 2002; Münkemüller et al. 2012; Pan et al. 2014) or niche evolution to be slower than any theoretical evolutionary model such as Brownian motion (which may often not be the case possibly because selective environments themselves changed much faster than Brownian motion; e.g. Prinzing et al. 2014). It suffices that niches are more similar among closely related species than among distantly related species (i.e. ‘phylogenetic signal’ according to Losos 2008 or Münkemüller et al. In press). Support of niche conservatism seems dominant (Peterson 2011), but numerous counterexamples exist (Losos 2008; Mouquet et al. 2012). Niche evolution can be more labile or more conservative due to the convergence of niches between lineages or due to character displacement within lineages, and these can result from interactions among coexisting species, a link that we will further discuss in Where to go: put evolution into community phylogenetics.

However, what applies to a regional species pool does not necessarily apply to local communities, as the latter are typically small and possibly non-representative samples of a large pool (see Weiher et al. 2011 for the importance of such scaling). Tests for niche conservatism have usually occurred at regional scale only (but see Silvertown et al. 2006). Results at local scale may be different from those at regional scale: a single patch community containing a smaller range of niche conditions, trait values and lineages than an entire region (Willis et al. 2010). Across such limited ranges of niches, trait values and phylogenetic lineages, the relationship between phylogeographic distance and trait dissimilarity might disappear (Srivastava et al. 2012). In fact, all examples of studies failing to detect niche conservatism listed by Losos (2008) are within-genus comparisons, that is each covering a limited range of phylogenetic lineages. Additionally, in most lineages there is still a minority of species pairs that are dissimilar in traits and it might be specifically these dissimilar pairs that are selected into local communities (Prinzing et al. 2008). Finally, character displacement between coexisting, often congeneric species (known at least since Lack 1942) can result in the local loss of the regional correlation between phylogeographic distance and trait dissimilarity. Overall, even if across a region related species may tend to share similar traits and niches, dissimilar related species or similar non-related species might be filtered into a local community (Fig. 1).

The existing tests do not seem to support a blanket acceptance of the assumption ‘Increased local phylogenetic dispersion corresponds to increased local trait dispersion’. Silvertown et al. (2006) found no relationship between relatedness of species within communities and their local (alpha) niches, while Prinzing et al. (2008) found even a negative relationship for most niche axes and traits tested (see also Gerhold et al. 2011). Kluge & Kessler (2011) found no significant pattern of phylogenetic diversity along the elevation gradient, whereas functional-trait diversity did vary along the gradient. Spasojevic & Suding (2012) found also no correlation between phylogenetic and functional diversity along a stress-resource gradient (see also Purschke et al. 2013). In fact, Kraft et al. (2007) have shown that local phylogenetic overdispersion is indicative of a local trait overdispersion only if traits are very strongly conserved across the regional pool.

Overall, traits that are phylogenetically conserved across an entire major lineage or region can be phylogenetically convergent or divergent within a local community (Tofts & Silvertown 2000; Silvertown, Dodd & Gowing 2001; Prinzing et al. 2008). As a result, within a community trait dispersion does not necessarily increase, but may even decrease with phylogenetic dispersion (Fig. 1). This triggers many interesting questions such as which traits show positive and which show negative relationships (Silvertown et al. 2006). But it precludes simple application of phylogenetic distance as a proxy for trait distance, and thereby for negative interactions or filtering.

**Assumption 2: A Single Ecological Function Can Only Be Performed by a Single Trait State or Combination of Trait States**

It is assumed that a given assembly process (i.e. habitat filtering) selects for one specific state of a trait (e.g. tall plants when light is limiting), or combination of correlated trait states (e.g. large plants and fast growth) realized in one particular lineage. Phylogenetic dispersion of a community is then assumed to indicate the corresponding assembly processes structuring the community. However, we will outline below that multiple (combinations of) traits may be equally appropriate to ‘solve an ecological problem’ (Fig. 1, caveat of assumption 2).
**Phylogenetic-patterns-as-proxy approach:**

<table>
<thead>
<tr>
<th>Assembly process</th>
<th>Habitat filtering</th>
<th>Competition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phylogeny</td>
<td>Community</td>
<td>Traits</td>
</tr>
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</table>

**Assumption 1:** Phylogeny reflects traits

**Caveat 1:** Community may select for related dissimilar species (or the inverse)

**Assumption 2:** A specific trait is needed for specific ecological function

**Caveat 2:** Multiple traits, occurring in multiple lineages, may serve the same function

**Assumption 3:** Trait similarity causes competition

**Caveat 3:** Trait similarity may facilitate coexistence

**Assumption 4:** Competition causes exclusion

**Caveat 4:** Competition may be symmetric and without losers or winners

**Assumption 5:** The system is at "rest"

**Caveat 5:** Not enough time has elapsed to lead to exclusion of species

**Assumption 6:** Habitat filtering and competition are alternative processes

**Caveat 6:** Habitat filtering and competition are independent, increase in parallel or mutually imply each other

**Assumption 7:** Community phylogenetic dispersion depends on local processes only

**Caveat 7:** Community phylogenetic dispersion reflects habitat species pools, not local processes

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**Phylogenetic-patterns-as-result approach:**

If « proxy » scenario is true:

<table>
<thead>
<tr>
<th>Habitat filtering</th>
<th>Competition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sympathy and habitat-niche convergence of closely related species</td>
<td>Sympathy and habitat-niche convergence of distantly related species</td>
</tr>
</tbody>
</table>

If « caveat » scenarios are true:

<table>
<thead>
<tr>
<th>Sympathy and trait divergence of closely related species</th>
<th>Sympathy and trait divergence of distantly related species</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sympathy and trait convergence of closely related species</td>
<td>Trait convergence of related species that are sympatric</td>
</tr>
<tr>
<td>Sympathy does not depend on relatedness</td>
<td>Joint evolution of traits related to competition and to tolerance to harsh abiotic environment</td>
</tr>
<tr>
<td>Sympathy of closely related species within particular habitat types</td>
<td>Sympathy of distantly related species in other habitat types</td>
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**Fig. 1.** Phylogenetic-patterns-as-proxy approach: the concept of using community phylogenetic dispersion as a proxy for ecological assembly processes (i.e. habitat filtering and competition), assumptions underlying the concept and the respective caveats. The arrows indicate the species that reach the communities (solid boxes) from their phylogenetic position or with their specific trait values. ‘Traits’ is short for ‘traits state’. Trait state ranges from small (small dots) to big values (big dots). = viable coexisting species; = coexisting species with reduced fitness due to competition. Phylogenetic-patterns-as-result approach: macroevolutionary patterns resulting from the assembly processes presented in the left part of the figure (see Table S1 for details).
For example, a diversity of traits can be associated with increased ability to competitively suppress neighbours. Competitive ability can be enhanced through increased dispersal distance among ramets (Semchenko et al. 2013), increased plant height (Gaudet & Keddy 1988), altered root growth (Wang et al. 2010) and potentially shifts in growth vs architectural traits (Herben & Goldberg 2014). Thus, though it may be possible to suggest that a given trait of a plant species will influence competitive dynamics, we find little reason to believe that focusing on a single trait within a community is sufficient to understand the role competition has played in the assembly of that community – as other critical traits may be overlooked.

Complexities such as those described above for trait–competition relationships are commonplace among trait–function relationships. For example, some plant species in arid environments can deal with prolonged drought through drought tolerance, involving traits such as slow growth rates and high water-use efficiency, while others use drought avoidance strategies, involving traits such as prolonged seed dormancy and rapid growth during rain events (Kozlowski & Pallardy 2002). Plants can respond to herbivory by avoidance, tolerance, resistance or by profiting from herbivores as mutualists (e.g. for dispersal), each related to a different set of traits (Tiffin 2000; Nunez-Farfán, Fornoni & Valverde 2007).

We acknowledge that there may be environmental conditions for which there is only a single appropriate trait, or to which each species may develop multiple trait responses, including one that is shared among species. Light limitation, for instance, will trigger height growth in most species, in addition to one of multiple other solutions such as early phenology or thin leaves (Larcher 2003). In such hypothetical cases, a single trait or a single phylogenetic lineage might dominate. However, in the bulk of the examples above, a single ecological problem can be resolved by fundamentally different traits or trait combinations, all potentially effective and evolutionarily stable. If these different trait solutions are represented by different phylogenetic lineages, we would not necessarily expect a given assembly process to cause any particular phylogenetic signal (Fig. 1, caveat of assumption 2).

ASSUMPTION 3: TRAIT SIMILARITY CAUSES ENHANCED COMPETITION

Drawing from both The Origin of Species (Darwin 1859) and limiting similarity theory (MacArthur & Levins 1967), a common assumption in community phylogenetics is that differences in competition-related traits reduce the strength of competition among species. Consequently, it is commonly assumed that phylogenetic overdispersion occurred because coexisting closely related species have more similar trait states (assumption 1), compete most intensely (this assumption) and exclude each other (below assumption 4; Webb et al. 2002). Below we will outline how trait similarity does not necessarily cause competition but it may even facilitate coexistence (Fig. 1, caveat of assumption 3).

Surprisingly, though there exist mountains of opinion, theory and conceptual papers discussing issues of trait similarity and competitive interactions (Webb 2000; Weih & Keddy 2001; de Bello et al. 2012), empirical studies have until recently been rare. The most comprehensive study addressing functional similarity and competition found that the strength of 275 interaction coefficients among potentially coexisting tree species was not related to functional similarity (Kunstler et al. 2012). Additional studies have tested the hypothesis that more closely related species should compete more strongly than more distantly related species (e.g. Burns & Strauss 2011). The current empirical focus on this question began with Cahill et al. (2008), in which they report little support for the competition–relatedness hypothesis. Venail et al. (2014) list 15 independent empirical studies since 2008 testing this hypothesis, finding full support in only four studies, mixed results in two and a lack of empirical support in nine of fifteen studies. We hence question the generality of this hypothesis, and recognize the potential impacts on the validity of the phylogenetic-patterns-as-proxy approach.

Alternatives to the limiting similarity model predict that trait dissimilarity within a community may have different consequences on competition. Grime (2006) suggests that competition may be the strongest among species dissimilar in fitness-related traits such body size as there will be one stronger and one weaker competitor (see also Adler, HilleRisLambers & Levine 2007; Mayfield & Levine 2010; Narwani et al. 2013) (Fig. 1, assumption 2). Scheffer & van Nes (2006) suggest that among species similar in niche-related traits such as root length, competition is symmetric and no species will win over another, enhancing again coexistence among similar competitor species (see also Yan et al. 2012). The alternative models are endpoints of a continuous gradient of assembly scenarios (Adler, HilleRisLambers & Levine 2007). Moreover, trait similarity may increase processes alternative to competition such as predation pressure (Yguel et al. 2011) or facilitation or shared mutualisms (Elias et al. 2009; Sargent et al. 2011). Finally, Venail et al. (2014) suggest that not trait similarity or phylogenetic relatedness but species identity most strongly impacts competitive and facilitative interactions. Combined, we suggest the data supporting the limiting similarity model of plant competition are substantially more limited than one would imagine, given how widely this concept is used in modern community ecology. This should be a high priority for empirical studies.

ASSUMPTION 4: COMPETITION NECESSARILY CAUSES SPECIES EXCLUSION

It is commonly assumed that competition leads to exclusion of species and that the remaining species are then
phylogenetically overdispersed. However, we will outline below how competition may not always cause exclusion, but it may be without losers or winners (Fig. 1, caveat of assumption 4).

Gause’s competitive exclusion principle serves as the foundation for much of the current thinking on how competition may influence community assembly (Gause 1934). Despite substantial numbers of examples of how coexistence can be maintained even when competition occurs (e.g. temperature-dependent competitive abilities; Park 1954; etc.), community phylogenecist appear to have adopted the assumption that competition leads to exclusion. Further, it is assumed such exclusion will be non-random based upon evolutionary similarity (see assumption 3), resulting in phylogenetic overdispersion (i.e. limiting similarity sensu MacArthur & Levins 1967) or clustering (i.e. weaker competitor exclusion sensu Mayfield & Levine 2010).

Different observations have been used to argue in favour of competitive exclusion among closely related species. First, in forests, the adult trees in the canopy tend to be phylogenetically overdispersed in comparison with the young trees (Enquist, Haskell & Tiffney 2002; but see Violle et al. 2011). However, laboratory experiments suggest competitive exclusion of phylogenetic proximate species (e.g. Violle et al. 2011). However, laboratory communities inevitably are sampled from very small species pools (10 species in Violle et al. 2011) and hence better reflect any pattern of niche conservatism in the pool (assumption 1). Moreover, Petri dishes in the laboratory may render coexistence particularly difficult as spatial or temporal segregation of micro-habitat niches is rarely possible (Silvertown et al. 2006). In addition, even in the laboratory phylogenetic distance may be unrelated to coexistence (Best, Caulk & Stachowicz 2013; Narwani et al. 2013). The two existing studies that, in the field, compare competition to exclusion do not find any increase of phylogenetic dispersion with competition (Brunberg et al. 2012; Bennett et al. 2013). One possible explanation is that competition among closely related species is symmetric (e.g. among roots; Lamb & Cahill 2008) and hence causes no exclusion. Also, the outcome of competition among closely related species depends on the relative strength of the two types of species differences: while differences in competitive ability drive some species to dominance and others to elimination, niche differences stabilize species coexistence as individual fitness increases when species’ density decreases (Adler, HilleRisLambers & Levine 2007).

Overall, it appears that though competition can cause exclusion, exclusion is not a necessary consequence of competition (Fig. 1, caveat of assumption 4).

ASSUMPTION 5: THE SYSTEM IS AT ‘REST’ SUCH THAT THE PROCESS OF ASSEMBLY HAS PLAYED OUT

When community structure, such as phylogenetic dispersion, is interpreted as the result of community assembly processes, this implies that such processes operated both constantly and for a sufficiently long time (i.e. multiple years or generations) for community structure to respond. However, we will outline below that species communities are often at non-equilibrium and community structure only incompletely reflects assembly processes (Fig. 1, caveat of assumption 5).

Species losses or gains due to assembly processes typically happen only after shifts in species abundances and are hence slow (e.g. Booth & Grime 2003; Fig. 1). We often observe non-equilibrium communities, particularly if organisms are long-lived or if disturbances are frequent. Many systems are maintained in permanent non-equilibrium, for instance grasslands maintained by grazing (Fig. 1, caveats of assumption 5). As a result, despite strong competition among species in grasslands (Cahill et al. 2008), this competition may not leave a signature in species composition if grazing is sufficiently frequent (e.g. Zobel 1992). Moreover, Paine et al. (2012) found that different processes during different stages of succession may result in the same phylogenetic pattern within a community, reflecting different degrees to which the system is at rest. Gerhold et al. (2013) found assembly processes that are generally seen as mutually exclusive operating at different stages of assembly of the community. While dynamic, successional sequences have been studied using community phylogenies, the underlying assumption remained implicitly static: that strong interactions operate for sufficiently long time to lead to species exclusion and hence influence the patterns of phylogenetic diversity (e.g. Letcher 2010; Graham et al. 2012; Purschke et al. 2013).

Overall, studies on phylogenetic (and other) community structure are typically temporal ‘snapshots’, and we do not know whether they portray endpoints or transient dynamics, in particular in the presence of disturbances or long-lived species. Moreover, interpreting such snapshots of co-occurrence as coexistence is notoriously difficult due to spatial and temporal variability in population demography of the co-occurring species (Sipieński & McPeek 2010). Consequently, assumptions 1–4 can all be true, but there will be still no consistent, predictable changes in phylogenetic (or in any other) community structure due to a non-equilibrium state of the community.

ASSUMPTION 6: HABITAT FILTERING AND COMPETITION ARE ALTERNATIVE PROCESSES, NOT OPERATING TOGETHER NOR INTERACTING

Inferring the role of habitat filtering and competition from a single parameter (i.e. phylogenetic dispersion) only makes sense if the two processes are truly alternative – strong
filtering implies little competition and weak filtering corresponds to strong competition. However, we will show below that habitat filtering and competition may also be independent or mutually imply each other (Fig. 1, caveat of assumption 6).

We acknowledge that studies using phylogenetic patterns as proxy of assembly tend to ask what is the relative importance of filtering and competition. The interpretation, however, tends to be absolute. To our knowledge, no study insists that the factor ranked as relatively less important might in fact still have a major absolute importance or that the factor ranked as relatively more important might still only have a minor absolute importance. These absolute magnitudes of filtering and competition effects on assembly may change independently; the situation of ‘no filtering, no competition’ might then result in a similar phylogenetic pattern of ‘strong filtering, strong competition’ (Fig. 1, caveat of assumption 6). Alternatively, filtering and competition may operate in parallel at larger and finer spatial scales, respectively (Helmus et al. 2007; Harmon-Threatt & Ackerly 2013; Parmentier et al. 2014), and may interact, too (Kraft et al. 2007). Habitat filtering can increase competition among the species suitable for the habitat (Kunstler et al. 2012). Also, increased habitat filtering of unadapted species may be confused with increased competitive exclusion (Grime 2006), when relying on trait or lineage dispersal (Mayfield & Levine 2010; Kunstler et al. 2012). Finally, differences in ecological niches (e.g. soil texture requirement) may permit coexistence between competitors, whereas differences in traits determining competitiveness and fitness (e.g. plant height in light competition) may lead to exclusion of either of the competitors (Chesson 2000; Adler, HilleRisLambers & Levine 2007). Hence, habitat filtering of niches might reinforce competitive exclusion, whereas habitat filtering of traits determining competitiveness may increase coexistence of competitors. No single trait or phylogenetic proxy can sort out this complexity.

ASSUMPTION 7: COMMUNITY PHYLOGENETIC DISPERSION DEPENDS ON LOCAL AND PRESENT-DAY PROCESSES ONLY; WITHOUT SUCH LOCAL PROCESSES, PHYLOGENETIC DISPERSION IS RANDOM

The structure of local communities, such as their phylogenetic dispersion, has been traditionally used to infer local processes of assembly. This implies that this structure only depends on local processes. However, we will show below that phylogenetic structure of a local community may reflect phylogenetic structure of the habitat type of this particular community rather than local assembly processes (Fig. 1, caveat of assumption 7).

Assembly of a community in a local habitat patch is influenced by dispersal, either short-distance dispersal from adjacent patches of other habitats or from refuges (‘mass effects’ in Leibold et al. 2004; post-glacial recolonizations in Leibold, Econom & Peres-Neto 2010) or by long-distance dispersal between patches of the same habitat type (‘species sorting’, and ‘patch dynamics’ at equilibrium in Leibold et al. 2004). Within-habitat type dispersal results in the formation of different species pools in different habitat types. Multiple studies have shown that such large-scale species pools of different habitats are characterized by different phylogenetic structures (e.g. Cavender-Bares, Keen & Miles 2006; Swenson et al. 2007; Cavender-Bares et al. 2009) – habitat species pools are in fact habitat lineage-pools (Pärtel 2002). Moreover, recent evidence suggests that the lineage-pool of a habitat type (e.g. grasslands) can influence the phylogenetic structure of local communities (Lessard et al. 2012). For example, in a habitat type occupied by lineages that have only relatively recently diversified, the lineage-pool is composed of more closely related species than expected by chance (Bartish et al. 2010). Past abundance of habitat types may drive present patterns of species diversity (Zobel et al. 2011) and possibly of phylogenetic diversity of habitat lineage-pools. Local communities within habitat patches are sampled from these habitat lineage-pools and can consequently reflect their macroevolutionary diversification (i.e. evolution at or above the level of species). This might result in phylogenetic overdispersion in communities of evolutionary old habitat types and clustering in communities of evolutionary young habitats (Fig. 1, caveat of assumption 7). To our knowledge, it has not been studied to which degree clustering of the habitat lineage-pool explains clustering of the communities in local habitat patches. We further develop this point in Where to go: put evolution into community phylogenetics.

There are multiple methodological approaches that may help identifying the effect of lineage-pools of habitats (Hardy 2008), and there are others permitting to filter them out (Hardy & Senterre 2007; Baraloto et al. 2012). However, in the next section we will show that the very differences between the phylogenetic structures of habitat lineage-pools are interesting in themselves as they connect local coexistence within habitat patches to the macroevolution of lineages. These differences deserve to be the focus of a research programme in itself instead of being used as covariables.

Where to go: put evolution into community phylogenetics

Despite an increasing number of pictures of Charles Darwin in conference presentations of community ecologists, the questions asked in many of these studies do not concern any evolutionary processes. Phylogeny is often used only as a proxy for aspects of ecology, though as stressed by Losos (2011), using phylogenetic approaches helps in finding patterns rather than identifying evolutionary (let alone ecological) processes. The obvious solution would be to use community phylogenetic dispersion not as a proxy for ecological processes, but to develop hypotheses on how phylogenetic diversification of lineages results from, or causes, community assembly. The phylogenetic-patterns-as-result
approach asks: Do particular assembly processes control the coexistence and adaptation of closely related species, and how do coexistence and adaptation of closely related species control patterns of phylogenetic diversification? The phylogenetic-patterns-as-cause approach asks: How do patterns of diversification of lineages control the phylogenetic structure of communities, and how does phylogenetic structure control assembly? We will develop both approaches.

If phylogenetic diversification and local coexistence interact, the widely held view of a distinction between macroevolutionary and ecological scale would no longer hold. For too long macroevolution has been thought to operate at a regional scale and ecological assembly at the scale of local patches within communities (Cornell & Lawton 1992; Lawton 1999), ignoring that these patches form networks of a given habitat often stretching across multiple regions. We are certainly not the first to think about these relationships between coexistence and diversification (e.g. Johnson & Stinchcombe 2007; Cavender-Bares et al. 2009; Cavender-Bares, Ackerly & Kozak 2012), but most of the existing studies are restricted in their coverage of concept or in their generality. Many studies are restricted to only one step in the chain connecting phylogenetic diversification and local coexistence (for instance to the relationship between openness of local communities to aliens and the phylogenetic dispersion of the communities, without further explaining the historical causes of phylogenetic dispersion; Gerhold et al. 2011). Other studies are restricted to cases of a single, minor lineage such as a genus (e.g. lizards in Glor et al. 2003), or to one particular environment (e.g. one extreme environment compared to others; Anacker et al. 2011). We believe that the existing methods to describe the phylogenetic structure of a large number of communities across a large taxon (such as fishes or angiosperms) and a large range of environments (such as all lakes in a region or an entire vegetation survey) provide a tool permitting to overcome these restrictions of case studies. Applied within the below approaches (and not as a proxy), these tools would permit eco-evolutionary analyses to cover the full range of lineages that species are facing within a community and the full range of environments that lineages are encountering throughout their evolution. In short, tools from community phylogenetics may help to identify interactions between diversification and coexistence. The fact that such studies are currently rare is unfortunately a collateral damage caused by current extensive focus on the phylogenetic-patterns-as-proxy, as we explain in Appendix S1.

**PHYLOGENETIC-PATTERNS-AS-RESULT: HOW ECOLOGICAL COEXISTENCE CAN AFFECT MACROEVOLUTIONARY PROCESSES**

**Interactions influence macroevolutionary diversification**

Species interactions are known to affect diversification: competition may trigger speciation, lineage diversification or the origin of dissimilar swarms of similar species (Scheffer & van Nes 2006; Moen & Wiens 2009; Rabosky et al. 2011); arms races with natural enemies may trigger speciation (e.g. Smith & Benkman 2007; Benkman, Parchman & Mezquida 2010) and lineage diversification (Vermeij 2011); and the same is true for mutualist interactions (Herrera & Pellmyr 2002; Janson et al. 2008; but see Smith et al. 2008); notably between natives and invading non-native species, Vellend et al. 2007). In plants, such interactions with locally coexisting species may in part explain the abundance of local speciations (Givnish 2010). Moreover, some key innovations that characterize entire lineages are likely the outcome of such interactions (such as defensive silicas in grasses; e.g. Massey, Ennos & Hartley 2006). There is however, to our knowledge, no consistent theory spanning the entire range from local coexistence to macroevolutionary diversification (but see Bruun & Ejrnæs 2006).

**Community structure influences interactions and hence macroevolutionary diversification**

The presence of many species in a community can induce many interactions and possibly trigger the origin of even more species (Emerson & Kolm 2005; but see Cadena et al. 2005). Specifically, coexistence among closely related species can trigger character displacement to reduce competition intensity (Dayan & Simberloff 2005), or character convergence to reduce competition asymmetry (Scheffer & van Nes 2006). The former can accelerate character diversification within lineages, which in turn can, potentially, contribute to a reduction in niche conservatism (Ackerly 2009). The latter can do the opposite. Predation on coexisting closely related butterflies of repellent taste leads to convergence of warning signals (Elias et al. 2009) or escaping behaviours (Stoks & McPeek 2006). Enemy release of hosts growing in a phylogenetically distant neighbourhood (above references) might facilitate the host’s colonization of such neighbourhoods and promote niche diversification (Yguel et al. 2014). Finally, closely related species often interact by hybridization. Hybridization in turn is one of the major evolutionary forces of diversification, creating species of increased genetic diversity (with strong potential ecological consequences, e.g. McArt, Cook-Patton & Thaler 2012), and hybridization of plant hosts may trigger the speciation of phytophages (Evans et al. 2008).

**Habitat type controls community structure, interactions and hence diversification**

The importance of the various above-mentioned species interactions can vary strongly between communities of different habitat types and taxa. For example, the intensity of competition or the number of trophic levels might increase in communities in habitats of high soil fertility (Oksanen et al. 1981). The long-term implications of such habitat-specific interactions within communities for lineage diversification have so far rarely been searched, probably due to supposed ephemeral nature of local communities.
However, local communities are connected into persistent networks (e.g. all calcareous, temperate prairies of the planet) maintaining persistent habitat lineage-pools. Within-community ecological processes affecting natural selection and drift can ultimately scale up to macroevolutionary diversifications of entire lineage-pools of habitats (see e.g. Zobel et al. 2011). This evolutionary diversification of the habitat lineage-pools will then be reflected in local communities sampled from these pools. In some fields of evolutionary ecology, such as plant–pollinator interactions, this reflection is trivial. In other fields of ecology, this reflection remains unrecognized. If habitats differ in local assembly processes, and local assembly processes can scale up to the evolutionary diversification of the lineage-pool of that habitat, this creates differences in diversification of lineage-pools among habitat types. We will outline in the next section some examples how these differences can be studied.

**Turning assumptions and caveats of the phylogenetic-patterns-as-proxy approach into hypotheses of the phylogenetic-patterns-as-result approach**

As an example of a testable set of hypotheses on how coexistence can affect macroevolution, we come back to the above set of assumptions made by the phylogenetic-patterns-as-proxy approach. Instead of making assumptions about assembly processes, we can ask how these processes explain phylogenetic patterns of evolutionary interest. For example, should one find (instead of assume) that strong habitat filtering indeed decreases phylogenetic dispersion in specific habitats, then we can hypothesize occurrence of sympathy and niche convergence among closely related species in these habitats (Fig. 1, right part; see Table S1, Supporting information for details). Also, should one find (instead of assume) that in specific habitats strong competition results in increased phylogenetic dispersion, then we can hypothesize occurrence of sympathy and habitat-niche convergence among distant relatives and allopatry and niche divergence of closely related species in these habitats (Fig. 1, right part). We also suggest a phylogenetic-patterns-as-result hypothesis for each of the seven assumptions listed in Chapter II (Fig. 1). We stress that each of these hypotheses describes what theory predicts as a consequence of a given assembly process. This assembly process would have to be demonstrated (and not inferred) a priori using the approaches outlined in Table S1. The hypothesis then makes objective, testable predictions. Overall, the phylogenetic-patterns-as-result approach can contribute to explaining patterns of prime interest to evolutionary biologists, such as the major variation in sympathy or in habitat niche between related species, ranging from virtually total overlap to total mutual exclusiveness (Barraclough & Nee 2001).

The interaction between macroevolutionary diversification and coexistence, however, is not one-way. In the next section, we will treat the opposite direction, how phylogenetic patterns can be a cause of ecological coexistence. Obviously, these two directions of the interaction are mutually non-exclusive and may actually mutually reinforce each other.

**PHYLOGENETIC-PATTERNS-AS-CAUSE: HOW MACROEVOLUTIONARY PROCESSES CAN AFFECT INTERACTIONS AMONG COEXISTING SPECIES**

Macroevolution within habitat lineage-pools constrains phylogenetic dispersion of local communities

The phylogenetic structure of a local community is often understood as being constrained by the phylogenetic structure of the regional lineage-pool (Ricklefs & Schluter 1993), which is hence used as a null model to study community phylogenetic structure. However, the habitat lineage-pool may be no less important than the regional lineage-pool (Pärtel 2002). Usually, habitats have been considered as being nested within regions, which implies that they are younger than the regions. However, there is no reason for such a nested hierarchy of habitats within regions. In fact, the ‘global’ lineage-pool of a habitat type may be more important than the regional lineage-pool across all habitat types in determining community phylogenetic structure (Fig. 2). For instance, the phylogenetic relatedness of plant species in two grassland communities on two distinct continents can be higher than the phylogenetic relatedness of a grassland and a forest patch on the same continent, even though macroecological studies often pool such distinct habitat types across grid cells (Winter et al. 2009). In fact, Ortega et al. (1997) found that across the Canary archipelago in the Atlantic Ocean lineages seem to be more capable of jumping between islands than between habitat types, that is vegetation zones (note that smaller organisms might perceive habitats at a scale much finer than vegetation zones, e.g. litter, tree trunks and tree canopies; Prinzing & Woas 2003). Similarities among communities of the same habitat type on different continents are further increased by the unprecedented introduction of non-native species in all places of the world (Wintert et al. 2009), combined with the tendency of species to maintain their habitat niche after introduction (e.g. Petitpierre et al. 2012).

While local communities are ephemeral, habitat types and their lineage-pools can persist for geological time periods. Hence, species compositions in contemporary communities of a given habitat type might correspond to lineage-pools of that habitat type even for millions of years. Indeed, relationships between biota and environments have been found to persist across millions of years despite temporary disintegration of these relationships for thousands or few million years (Boucot 1996). Palaeoecologists have even suggested that lineage-pools will reassemble after temporal disappearance and reappearance of the habitat type (DiMichele et al. 2004). Many of the present habitats may appear at first sight unique and recent, given the strong and dynamic impact of recent quaternary climate changes and human transformation. However,
Phylogenies and community assembly

Fig. 2. Conceptual figure of phylogenetic structures of communities in different habitats (squares: grasslands, triangle: forest, star: swamp) and on different continents. Lineage-pools of habitats (solid circle) may encompass similar sets of phylogenetic lineages, while the lineage-pool of a region (dashed circle) encompasses different sets of lineages. This indicates that evolution of lineages has been more strongly constrained by habitat type across regions than by region across habitat types.

many of the dynamic, present environmental impacts on habitats may trigger environmental constraints that have existed in other forms already in earlier geological epochs. Artificial ponds or live-stocking, for example, can trigger submerged and grazed conditions colonized by lineages adapted to these conditions since many million years (Antonelli et al. 2011). Ultimately, this may explain why we tend to find particular past phylogenetic lineages in particular present-day habitats (e.g. Prinzing et al. 2001).

Often being formed during millions of years, lineage-pools of distinct habitat types possess distinct evolutionary histories which are inevitably reflected in the phylogenetic structure of contemporary communities sampled from these lineage-pools. The maximum age of many lineages has been found to be linked to the age of habitat types, which is particularly straightforward if the lineages themselves physically construct these habitat types such as trees constructing forest habitats (Wang et al. 2009). Hence, lineage-pools of ancient habitat types may have diversified for a long period. Moist or aquatic habitats, for instance, are more ancient than Angiosperms (Wing & Boucher 1998), contrary to, for instance, habitats dominated by grazing of large mammals (Behrens-meyer et al. 1992). As a possible result, aquatic habitats today show a phylogenetic overdispersion of incumbent Angiosperm species pools (Bartish et al. 2010). Evolutionary young habitat types, in contrast, have undergone rapid recent diversification and are phylogenetically clustered. For instance, dry open habitats can be relatively recent in the history of Angiosperms and may have acted as arena of the recent radiation, for example of the Mediterranean flora with only very limited immigration of lineages from more ancient habitats (Ackerly 2003; Bartish et al. 2010), or fynbos compared to subtropical thicket in South African vegetation (Procheş et al. 2006). As a result, contemporary communities of the evolutionary old habitat types can draw their constituent species from a wider range of major, old lineages than the communities of the young habitat types (see also Gerhold et al. 2008). Consequently, phylogenetic dispersion may be much higher in local communities of evolutionary older than in younger habitat types. Similar ideas have been discussed by Wiens & Donoghue (2004) for tropical vs. temperate habitats and have recently been expanded to different altitudinal levels at square kilometres resolution (Hutter, Guayasamin & Wiens 2013). To our knowledge, these ideas have not yet been applied to at the scale of habitats differentiated in local patches of only hundreds of square metres, the scale most community ecologists study.

Phylogenetic dispersion of a local community might hence be the result of macroevolutionary diversification in lineage-pools of habitat types, instead of or in addition to ongoing assembly processes (Hubert et al. 2011). There is, however, still an alternative scenario of evolutionary community assembly not involving conserved lineage-pools: on remote oceanic islands, closely related species might overcome niche conservatism and adapt to new habitats in order to colonize empty niches (Emerson & Gillespie 2008; for similar phenomena in urban ‘island’ of artificial habitats, see for instance Domihue & Lambert 2014). We can hypothesize that such a scenario is more likely when niche conservatism is low and dispersal is a limiting factor in determining community phylogenetic structure.

Phylogenetic dispersion of a local community being the result of macroevolutionary diversification of the corresponding habitat lineage-pool contradicts above assumption of the proxy approach. However, it also triggers a number of interesting new questions. First, we can ask whether age and rate of diversification within a given habitat type influence present structure of the lineage-pool of the habitat and of the local communities within the habitat. Such a relationship implies that the lineage-pool of a present habitat results to a large degree from diversification within this or similar habitats, and indeed this appears likely, for instance, in elevational habitat zonations (Hutter, Guayasamin & Wiens 2013). Early diversification will be represented by high mean phylogenetic distances among species, whereas a high rate of diversification will be represented by low distances among closely related species. These two distances are standard parameters used in community phylogeny (Webb et al. 2002), but without possible macroevolutionary interpretation so far. Secondly, we can ask how patterns of macroevolutionary diversification may affect the microecological coexistence mechanisms in local communities. Below we will give some examples of possible effects of phylogenetic pattern on local coexistence. Our goal was not to provide a compact body of theory but to demonstrate that searching for effects of phylogenetic pattern on local coexistence can be pertinent in many fields in ecology. We stress that in none of the examples we use community phylogenies as a proxy, and hence, they do not suffer from the problems of the proxy approach outlined in Assumptions.
Example 1: does phylogenetic clustering of local communities increase character displacement? Character displacement represents the divergence of trait states of competing species too similar to one another could not coexist without diverging (Dayan & Simberloff 2005). Ecologists have long searched for, and found, character displacement among some closely related species (Lack 1942), albeit in general the phenomenon may be only moderately frequent (Stuart & Losos 2013). We should thus find character displacement in phylogenetically clustered communities rather than in overdispersed communities. This was found recently for plant communities (Prinzing et al. 2008), but the evidence had accumulated for a long time. For instance, Becerra (2007) observed that species in the plant genus *Bursera* possess more dissimilar defence chemicals if they locally coexist than if they do not. We admit that it can be methodologically challenging to confirm character displacement in one trait among other traits which possibly serve the same ecological function (see assumption 2 in Assumptions).

Example 2: does phylogenetic clustering of local communities increase or decrease invisibility (Fig. 3b)? Successful establishment of aliens may be more likely for aliens with no close relatives in the recipient native community, due to lack of competitive exclusion (‘Darwin’s naturalization hypothesis’; Strauss, Webb & Salamin 2006; Parker et al. 2012), but the opposite has also been found (reviewed in Thuiller et al. 2010 and Maitner et al. 2012). Everything else being equal, an alien is more likely to face related natives in a recipient community representing many phylogenetic lineages than in a phylogenetically clustered community representing only few lineages. The latter should thus be more open to aliens than the former. This is what Gerhold et al. (2011) observed, albeit palaeo-ecological scenarios indicate the opposite (e.g. DiMichele & Bateman 1996). Gerhold et al. suggest that phylogenetically clustered communities are sampled from ‘naive’ habitat lineage-pools that have been closed to immigration from distant lineages during the evolutionary past (environmental islands; Ackerly 2003) rendering these communities open to aliens today (Fig. 3b).

Example 3: does phylogenetic clustering of local communities increase enemy pressure? Natural enemies such as phytophages or parasitoids tend to be neither specialized on a single host species nor completely generalist, but specialized on a set of closely related hosts (‘oligophages’; Strong, Lawton & Southwood 1984). In a phylogenetically clustered community, coexisting species are closely related and are hence likely to exchange more natural enemies than in a phylogenetically overdispersed community (Jactel & Brockerhoff 2007; Yguel et al. 2011). Consequently, higher evolutionary proximity instead of contemporary spatial proximity of neighbouring plants may drastically increase phytophagy (Yguel et al. 2011; Parker et al. 2012) and constrain phytophage community assembly (Vialatte et al. 2010). Inversely, hosts in phylogenetically overdispersed communities tend to be surrounded by phylogenetically distant neighbours and hence might profit from reduced pressure by natural enemies.

Example 4: does phylogenetic clustering of local communities increase or decrease mutualism and facilitation? Mutualistic or facilitative interactions between species are often the result of complementary capacities of the involved species, reflecting complementary traits, which are often expressed in distantly related species. Coexisting distantly related species are hence considered more likely to be complementary and to engage in mutualism than coexisting closely related species (Verdu et al. 2009; Valiente-Banuet & Verdu 2013; but see Venail et al. 2014 who found no effect). In that case, species profit from growing

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**Fig. 3.** (a) Phylogenetic-patterns-as-result approach: An example of ecological coexistence affecting macroevolutionary diversification – for example, interaction between preys and predators may result in selection, extinction and speciation (e.g. Smith & Benkman 2007) and finally macroevolutionary diversification of some lineages and disappearance of others (Vermeij 2011). Communities with less predators (e.g. due to lower prey abundances or due to higher numbers of top predators) would not lead to these patterns of predator-induced prey diversification. These processes are classical at the level of predator–prey interactions, but might also operate at the level of competitive or other interactions. (b) Phylogenetic-patterns-as-cause approach: An example of macroevolutionary diversification affecting ecological coexistence in local communities – for example receptiveness to invasions. These diversifications and assembly processes are classical at the level of regional lineage-pools of spatially isolated islands but might also operate at the level of distinct lineage-pools (environmental islands *sensu* Ackerly 2003; see e.g. Gerhold et al. 2011).
in communities composed of distantly related species. However, mutualism/facilitation may also result from similarity, in particular when mediated via a third species. Elias et al. (2009) and Sargent et al. (2011) show that closely related neighbours can benefit from each other by mutually repulsing of shared predators or attracting shared pollinators (Chapter II). These species hence profit from growing in communities composed of closely related species.

We acknowledge that both approaches, phylogenetic-patterns-as-result and phylogenetic-patterns-as-cause, are methodologically challenging. The biggest challenge is probably to sort out cause and effect. We see four promising approaches that have been suggested in the literature to infer causal relationships, but stress that none of them is a perfect cure. First, we increasingly need in situ, local observational and experimental studies of the processes inferred from phylogenetic patterns (Losos 2011; Weber & Agrawal 2012). The performance of species needs to be studied in the presence of closely or distantly related species (e.g. Venail et al. 2014), ‘Performance’ includes reproductive output and abundance but also characters permitting to avoid competitors (e.g. self-thinning), lack of resources (high C/N), or pathologies (grazing, necrosis). Such direct tests will only cover subsets of the phylogeny and short time periods, and may hence be non-representative for patterns of coexistence and phylogenetic diversification in the geological past when macroevolution happened. However, these tests are the only way to really manipulate processes, even if most manipulations will affect multiple processes at a time (HilleRisLambers et al. 2012). Secondly, when studying whether patterns of coexistence are consistent with the predictions of hypotheses, we should increasingly follow coexistence through time over many years. This would truly permit identifying causes and consequences for community assembly. Underexploited tools to do so are permanent-plot data bases as available from forestry, for instance (e.g. Joyce & Rehfeldt 2013). Thirdly, when studying patterns of coexistence across phylogenetic trees, reconstructing the temporal order at which patterns of diversification and of coexistence occur is important to identify what is cause, that is comes early, and what might be effect, that is comes late (e.g. Brooks & McLennan 2002; Moen, Smith & Wiens 2009). Finally, we suggest profiting from the experiments that nature has already replicated, such as the impact of herbivore-plant coevolution on plant community structure. Proceedings of the National Academy of Sciences of the United States of America, 106, 19699–19706. This study does not use data, but additional Supporting Information may be found in the online version of this article.

**References**


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**Supporting Information**

Additional Supporting information may be found in the online version of this article:

**Appendix S1** Possible detriments of the phylogenetic-patterns-as-proxy approach to other approaches in community ecology.

**Fig. S1** Number of publications using the phylogenetic-patterns-as-proxy approach.

**Table S1** Hypotheses of phylogenetic-patterns-as-result approach.