The temporal assembly of plant-pollinator networks following restoration

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Abstract

TO BE RE-WRITTEN The structure of networks is related to ability of communities to maintain function in the face of species extinction. Understanding network structure and how it relates to network disassembly, therefore, is a priority for system-level conservation biology. We explore the assembly of plant-pollinator communities on native plant restorations in the Central Valley of California.

Introduction

Global change has created a severe biodiversity crisis, and as species are lost, so are their interactions (Dunn *et al.*, 2009; Barnosky *et al.*, 2011). Because mutualistic interactions are essential for maintaining the diversity their component guilds of species, these systems are particularly at risk from coextinction cascades. The nature of these cascades will depend on the interaction patterns within a community (Memmott *et al.*, 2004; Rezende *et al.*, 2007; Bascompte & Stouffer, 2009). Recovering the lost biodiversity and interactions through ecological restoration has become increasingly imperative, and a key restoration aim is to facilitate assembly of robust interaction networks (Menz *et al.*, 2010). We know little, however, about how to re-assemble interacting communities through restoration, or the process of ecological network assembly more generally.

The most widely explored mechanism of network assembly, preferential attachment (Barabási & Albert, 1999), predicts that a new species is more likely to interact with species that are already well-connected ("the rich-get-richer" principle, Barabási & Albert, 1999). In pollination systems — a particularly ubiquitous mutualism (Ollerton *et al.*, 2011; Klein *et al.*, 2007) — some studies have found support for this mechanism of assembly. Investigating the day-to-day, temporal assembly of a plant-pollinator network within a season, Olesen *et al.* (2008) found that new species tended to interact with already well-connected species, potentially because these species are either more abundant or more temporally persistent (Olesen *et al.*, 2008). In addition, using a space-for-time substitution to study primary succession along a glacier foreland, Albrecht *et al.* (2010) found some indication assembly was occurring through preferential attachment. Network nestedness, a pattern of interactions where a generalist core interacts with both specialist and generalist species, increased as the community aged (Albrecht *et al.*, 2010). Increasing nestedness could result from preferential attachment process where specialist species attach to the well-connected, generalist core.

In contrast to the ordered network build-up described by preferential attachment, significant reorganizations of interactions can punctuate assembly (Peel & Clauset, 2014). Such significant reorganizations of interactions, or changing points, are observed in social networks responding to abrupt shifts in the behavior of interactors (Peel & Clauset, 2014). In ecological communities, such shifts may occur if, as new species colonize, resident species change their interaction partners to optimize their foraging effort. In plant-pollinator communities, theory predicts pollinators optimize their use of floral resources to reduce interspecific competition and improve resource-use efficiency (Pyke, 1984; Valdovinos *et al.*, 2010, 2013; Albrecht *et al.*, 2010; Blüthgen *et al.*, 2007). No studies, however, have examined whether changing points occur during ecological network assembly, and how these changes relate to the behavior of the interactors.

Understanding network assembly is particularly relevant to ecological restoration, which is essentially 'applied succession' (Parker, 1997, e.g.,). In pollination systems, the time since an area was restored has been shown to affect the structure of networks (Forup *et al.*, 2008a,b; Devoto *et al.*, 2012), suggesting interactions are evolving as the community develops. Understanding the mechanisms of network assembly will help to guide community restoration.

Facilitating effective restoration of networks is especially imperative in areas where species interactions provide essential ecosystem services, such as crop pollination. In intensively managed agricultural landscapes, the demand for pollination services is the greatest (Kremen, 2008). However, honey bees, managed extensively around the world to provide crop pollination, are in global decline (Neumann & Carreck, 2010; van Engelsdorp *et al.*, 2009). In addition, native pollinators, which are capable of providing sufficient crop pollination (Kremen *et al.*, 2002; Winfree *et al.*, 2007; Kremen *et al.*, 2004), are in short supply because these landscapes make poor habitats for pollinator populations (Kremen *et al.*, 2002). To ensure provision the continued provision of ecosystem services and curb biodiversity loss, effective restoration of pollinators and their interactions in agricultural landscapes is critical.

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To promote pollinator services in agriculture, farmers are increasingly turning to the habitat restoration technique of planting strips of native plants along farm edges (hedgerows) to help provide habitat for pollinators without removing arable land from production. Hedgerows augment the richness, abundance and trait diversity of pollinators in agricultural landscapes(Morandin & Kremen, 2013; M'Gonigle *et al.*, 2015; Kremen & M'Gonigle, 2015; Ponisio *et al.*, 2015). In addition, hedgerows promote the persistence and colonization of floral resource specialists (M'Gonigle *et al.*, 2015). Little is known, however, about the assembly of the network following hedgerow restoration.

Using a long-term dataset of plant-pollinator communities assembling following hedgerow restoration in the highly simplified and intensively managed agricultural landscape of California's Central Valley, we explore the process of network development. We first determine whether the mechanism underlying network assembly is a smooth build up of interactions as would be predicted by preferential attachment, or punctuated by significant reorganizations of interactions (i.e., network changing points). Even with changing points in interaction organization, networks could still be assembling via preferential attachment if the network reorganizations were primarily driven the by peripheral, temporally variable species while a stable, well-connected core of species still persists. We test whether the species are most variable in their network position — and thus important contributors network reorganizations — are less persistent and connected species. To further explore the mechanisms underlying the temporal dynamics in the networks, we examine patterns in the species and interaction temporal turnover. Lastly, we investigate whether networks are assembling toward predictable interaction patterns, and the ramifications for the robustness of the networks to species extinction and cascading perturbations.

Materials & Methods

Study sites and collection methods

We surveyed plant-pollinator interaction networks of assembling hedgerows (N=5), as well as in two types of non-assembling communities to serve as controls: unrestored, weedy field margins (N=19) and established hedgerows (greater than 10 years since planting, N=29). The sites were located in the Central Valley of California in Yolo, Colusa and Solano Counties. This area is composed of intensively managed agriculture – primarily monocultures of conventional row crops, vineyards and orchards. Hedgerows we planted along field margins where they do not remove valuable land from production. Plantings are between are ca. 3–6 m wide and approximately 350 m long, bordering large (ca. 30–hectare) crop fields. Hedgerows consist of native, perennial, shrub and tree plantings including *Rosa californica*, *Cercis occidentalis*, *Ceanothus spp.*, *Heteromeles arbutifolia*, *Sambucus mexicana*, *Eriogonum spp.*, *Baccharis spp.*, *Salvia spp.* and others (Kremen & M'Gonigle, 2015; M'Gonigle *et al.*, 2015). The mean distance between monitoring sites was 15 km, and the minimum distance between sites of the same type sampled in the same year was 2 km. The entire area surveyed spanned almost 300 km^2. The crop fields adjacent to all sites were similarly managed as intensive, high-input monoculture.

Monitoring began in 2006 and continued through 2015. Surveys of the assembling hedgerows began the year before the area was restored. For logistical reasons, no sampling of assembling hedgerows was conducted in 2010. Sites were sampled between two and five times per year (Tables S1-S3). In each round of sampling, the order in which sites were sampled was randomized. Surveys were conducted under sunny conditions when the temperature was above 21°C and wind speed was below 2.5 meters/second.

Flower-visitors to plants in hedgerows and unrestored controls were netted for one hour of active search time (the timer was paused when handling specimens). Honeybees (*Apis mellifera*) were

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not collected because their abundance is determined largely by hive placement by bee-keepers. All other insect flower visitors that touched the reproductive parts of the flower were collected; however, here we focus only on wild bees and syrphids — the most abundant and effective pollinators in the system (representing 49 and 19 percent of records, respectively, C. Kremen, A. Klein and L. Morandin, unpublished data). Bee and syrphid specimens were identified to species (or morpho-species for some bee specimens in the genera *Nomada* and *Sphecodes*) by expert taxonomists.

Quantitative networks were generated for each site through time. To account for the unequal number of surveys between years (Tables S1-S3), we use the mean of the interactions between a pair of plants and pollinators across surveys within a year to represent intearction frequency.

Change point analysis

Identifying change points

We employed a change point detection method (Peel & Clauset, 2014) to identify fundamental reorganizations in large-scale interaction patterns. A change point is caused by a merge, split, fragmentation or formation of communities (also called modules or compartments). Change point detection methods have yet to be generalized to quantitative networks, so for this analysis we focused on qualitative (binary) networks. Following Peel & Clauset (2014), we first defined a probability distribution over the networks using the generalized hierarchical random graph model (GHRG). The GHRG model is able to capture both assortative and disassortative community structure patterns at all scales in the network (Peel & Clauset, 2014). A network G is composed of vertices V and edges $E \subseteq VV$. The GHRG model decomposes the N vertices into a series of nested groups, the relationships among which are represented by the dendrogram T. The tips of T are the vertices of G, and the probability that two vertices u and v connect is given by the parameter p_r.

127 The probability distribution of the network G thus defined as:

$$P(G|T, pr) = p_r^{E_r}(1 - p_r)^{N_r - E_r} \tag{1}$$

128 Where E_r is the observed number of edges between vertices with the common ancestor r, and N_r
129 is the total possible edges.

130 Using Bayesian posterior inference and techniques from phylogenetic tree reconstruction, we fit
131 the GHRG model to the networks (Peel & Clauset, 2014). This is accomplished by using a Markov
132 chain Monte Carlo (MCMC) procedure to first sample the posterior distribution of bipartitions,
133 from which a consensus tree is derived (Peel & Clauset, 2014). We use β distributions with the
134 hyperparameters $\alpha = \beta = 1$ to define priors for p_r.

135 Once the GHRG model has been fit to the networks, we determine whether a change point occurred
136 between two time slices. To detect a change point, we compare the fit of two models — one
137 where a change point occurred between two networks, and one where no change occurred —
138 using posterior Bayes factors. We chose a sliding window of length, w, of four, within which to
139 find change points. Larger windows allow for more gradual changes, and four was the maximum
140 possible with our maximum of nine years of data. Lastly, to calculate a p-value for the Bayes
141 factors, we use parametric bootstrapping to numerically estimate the null distribution (Peel &
142 Clauset, 2014). We emploied code published online by L. Peel for the change point analysis.
143 Analyses we conducted in Python 3.4.

144 We next test whether the change points occurring in maturing hedgerows were a component of
145 the assembly process or a product of environmental shifts that lead to network reorganizations
146 in all types of communities. We model the number of change points as successes and the total
147 number of years each site was sampled as trails, and use a generalized linear model with Binomial
148 error to test whether the probability of a change point occurring varied by site type. We used

149 standard techniques to determine whether the assumptions of the models were met for this and all

150 subsequent models. For the non-assembling hedgerows and weedy field margins, only sites with

151 five or greater survey years were included in this analysis. All statistical analysis were conducted

152 in R 3.2.3 (R Core Team, 2015).

Characteristics of species that contribute to change points

154 To further elucidate the nature of the change points, we examine the characteristics of the species

155 that contributed interaction reorganization. Some species remain in relatively similar network

156 positions through time, whereas others are more variable in their role and thus contribute more

157 strongly to network reorganization. We test the that more persistent species with the highest degree

158 are the most stable in their network position, as would be expected is the networks were assembling

159 via preferential attachment.

160 We calculate species persistence as the proprotion of surveys a plant or pollinator was observed.

161 Species observed consistently within and between years are thus maximally persistent. Weighted

162 species degree is calculated from interaction observations from an extensive dataset from Yolo

163 County (approx. 18000 interaction records) that included both the data included in this study and

164 additional data from sites where we collected flower visitors using the same methods (M'Gonigle

165 *et al.*, 2015; Ponisio *et al.*, 2015). To represent network position variability, we computed the

166 coefficient of variation of weighted closeness at each site through time. Closeness describes the

167 centrality of a species in the network by calculating path lengths to other vertices (species) in

168 the graph. We use linear mixed models to test whether the species closeness variability (log) is

169 related to the persistence or degree of that species (Bates *et al.*, 2014; Kuznetsova *et al.*, 2014).

170 We included random effects for species, as well as site. Because the degree and persistence of

171 pollinators was strongly correlated, ($\rho = 0.84$, p-value $< 2 * 10^{-16}$), we include each explanatory

172 variable in the model separately. Plant degree and persistent were not significantly correlated,

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but we use the same models as we did for the pollinators for consistency. A linear increase in closeness, as might be expected with assembly by preferential attachment, would also lead to a high variability in closeness scores, so we test whether closeness increases through time.

Species and interaction turnover

Reorganizations of network structure can be the result of species turnover or species changing their interaction partners (i.e., re-wiring). To better understand the mechanisms underlying the temporal dynamics of the assembling networks, we examined patterns of species and interaction turnover. Assembling networks may have higher rates of species turnover than non-assembling communities because new species are colonizing and establishing themselves (M'Gonigle *et al.*, 2015). Similarly, if pollinators try to maximize their foraging efficiency based on the species present, interactions may turnover more quickly than in established communities.

To estimate the temporal turnover of species and interactions, we use an approach similar to calculating spatial β-diversity. Instead of calculating the variation in community composition across sites within a year, however, we estimated turnover across years at a site. We first calculated the pairwise dissimilarity of species and interactions between years within each site using a dissimilarity estimator that incorporates abundances, while also accounting for unobserved records (Chao *et al.*, 2005). Dissimilarity estimates can be affected by the total number of species and individuals sampled at a site (e.g., Ponisio *et al.*, 2015). For example, the probability that two sites do not share any species is higher when there are few individuals at those sites. Following Ponisio *et al.* (2015), we use null models that constrained species richness to estimate the deviation of the observed dissimilarity from that which would be expected under a random community assembly process. With the corrected dissimilarity values, we then calculated the multivariate dispersion of community composition across years (Anderson *et al.*, 2011). In order to test whether assembling hedgerows had more turnover of species and interactions than non-assembling communities, the species and

interaction temporal turnover estimates were response variables in a linear mixed models with site type as an explanatory variable along with random effects for both year and site (Bates *et al.*, 2014; Kuznetsova *et al.*, 2014).

Though species may turnover across years, some groups of species may essentially replace each other if they fill similar roles in the network. At non-assembling communities, species turnover may overestimate the temporal changes in the networks if the interactions occurring in one year are similar to those in the next year when they are weighted by the similarity of their constituent species. We develop a method examine the temporal turnover of interactions weighted based on their similarity. We followed Ahn *et al.* (2010) algorithm to hierarchically cluster all the interactions (edges) across sites and years based on their similarity, and build a dendrogram. The interaction similarity is based how may plants and pollinators (vertices) two edges share (Ahn *et al.*, 2010; Kalinka & Tomancak, 2011). The more species edges shared in common, the shorter the branch length between them on the dendrogram. We next calculated the temporal turnover of interactions weighted by their similarity, as approximated by "phylogenetic" distance (Graham & Fine, 2008; Kembel *et al.*, 2010). When then use linear models to test whether the weighted turnover of interactions varied between assembling and non-assembling networks (Bates *et al.*, 2014; Kuznetsova *et al.*, 2014).

Temporal changes in interaction patterns

Network structure

Any changing points in network structure may contribute to the reorganization of the assembling networks into predictable interaction patterns. Pollination networks exhibit two main structural patterns — modularity (e.g., Olesen *et al.*, 2007) and nestedness (e.g., Bascompte *et al.*, 2006,

2003). In modular networks, interactions are insular, occurring within separate groups or "modules" more often than between modules. Communities in the network may fragment as the network assembles, enhancing modularity. Conversely, nested networks are like pyramid of interactions, where there are some species that interact with many species, other species that interact with a subset of those species, and so on. If species entering the network tend to interact with the generalist base of the network pyramid (i.e., via preferential attachment), nestedness would increase through time. Lastly, if the network is accumulating specialist species or species are beginning to limit their interaction niche breath as the network assembles, this would lead to an increase in the network-level specialization (Blüthgen *et al.*, 2006). To test whether network modularity, nestedness or specialization changed linearly with assembly, we use linear mixed models with the descriptive network metrics as the response variable, year of assembly as the explanatory variable, and random effects of site and year.

We use NODF (weighted or unweighted) to evaluate network nestedness (Almeida-Neto *et al.*, 2008). NODF evaluates whether species with fewer partners interact with subsets of partners with which more connected species interact (Almeida-Neto *et al.*, 2008). To estimate modularity, we use a hierarchical clustering algorithm (Newman & Girvan, 2004; Csardi & Nepusz, 2006). We calculated standardized z-scores so that nestedness and modularity metrics could be compared between communities. The z-scores were calculated by generating an ensemble of 999 randomly assembled communities, subtracting the mean of the statistic calculated across these communities from the observed value, and then dividing by the standard deviation. To assemble random communities, we reshuffled the interactions between species but fixed the total number of interactions, species and the distribution of the interaction frequencies (Galeano *et al.*, 2009). Lastly, Network specialization was measured using H2, which estimate the deviation of the observed interaction frequency between plants and pollinators from a null expectation where all partners interact in proportion to their abundances (Blüthgen *et al.*, 2006). It ranges from 0 for generalized networks to 1 for specialized networks.

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Network robustness

Lastly, we test the changes in interaction patterns associated with network assembly affect the robustness of the network to species loss and to cascading perturbations. Following Memmott *et al.* (2004), we simulate the extinction of plant species the subsequent extinction cascades of pollinator species. Because the reproduction of plant species if facilitated by active restoration efforts, it is unlikely the extinction of pollinators would affect plant populations in the hedgerows. However, plants ceasing to bloom, for example in response to drought, will likely affect the pollinators that depend on them. Plants species were eliminated based on their degree or abundance, and the number of pollinators that secondarily went extinct is calculated. The area below the extinction curve is an estimate of network robustness (Dormann *et al.*, 2008).

We also explored how the robustness to cascading perturbations changed as community assembled, using algebraic connectivity — the second smallest eigenvalue of the Laplacian matrix (Fiedler, 1973) — as a proxy for network robustness (Gaiarsa et al., submitted). Algebraic connectivity is related to how difficult it is to turn a network into completely disconnected groups of vertexs, or species (Costa *et al.*, 2007) — the larger the algebraic connectivity, the more robust a network is to cascading perturbations (Gaiarsa et al., submitted), and the harder it is to break the community into isolated groups of species.

Results

Over eight years and 747 samples, we collected and identified $19,547$ wild bees and syrphids comprising 173 species from 50 genera. We observed $1,521$ unique interactions between plants and pollinators.

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Change point analysis

Identifying change points

The majority (76%) of the sites tests underwent at least one significant reorganization of interactions (Fig. 1). All five of the assembling hedgerows experienced changing points, whereas only 40% and 81% of non-assembling hedgerows and field margins, respectively, underwent significant interaction reorganizations. Assembling hedgerows experienced significantly more changing points than the non-assembling networks (difference in the odds ratios between assembling and non-assembling networks, 3.316, 95% CI $[1.314, 8.572]$, p-value= 0.0117). Network assembly following restoration is thus punctuated by more interaction reorganizations than would be expected by environmental shifts that would effect assembling and non-assembling networks equally.

Characteristics of species that contribute to change points

In contradiction to the predictions of assembly by preferential attachment, both pollinator persistence and degree were positively related to network position variability (estimate of the slope of closeness variability and persistence $\pm$ standard error of the estimate, 0.653 ± 0.225, p-value=0.009; slope of closeness variability and degree, 0.008 ± 0.002, p-value='0.002). Plant persistence and degree were not significantly related to network position variability (estimate of the slope of closeness variability and persistence $\pm$ standard error of the estimate, -2.063 ± 3.091, p-value=0.5; slope of closeness variability and degree, 0.0018 ± 0.002, p-value=0.3). The variability of species network position was not the result of closeness linearly increasing through time, and, in fact, plant and pollinator closeness decreased decreased slightly through time (Fig. S1, estimate of the slope of closeness through time $\pm$ standard error of the estimate, pollinators: -0.0003 ± 0.00005, p-value=$2.7 * 10^{-12}$; plants -0.007 ± 0.001, p-value=$1.4 * 10^{-6}$). Through statistically significant, the slopes are so slight they may not me biologically significant.

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Species and interaction turnover

The rates of species and interaction temporal turnover was consistent across assembling hedgerows, non-assembling hedgerows and field margins, though mature hedgerows has marginally significantly less species turnover than field margins (estimate $\pm$ standard error of the estimate of the difference in turnover between field margins and mature hedgerows, -0.0498 ± 0.026, p-value=0.058). When interactions where weighted by their similarity, both assembling and mature hedgerows had high rates of turnover than field margins (estimate $\pm$ standard error of the estimate of the difference in turnover between field margins and assembling hedgerows, 0.115 ± 0.027, p-value=0.0002; field margins and mature hedgerows, 0.082 ± 0.024, p-value=0.002).

Temporal changes in interaction patterns

Network structure

Network nestedness significantly increased with assembly (estimate of the slope of nestedness through time $\pm$ standard error of the estimate, 1.834 ± 0.6142, p-value=0.022, Fig. 4). Modularity decreased (Fig. 4), though the slope was not significantly different from zero (estimate of the slope of modularity through time $\pm$ standard error of the estimate, -0.524 ± 0.295, p-value=0.124). Specialization remained relatively constant (estimate of the slope of specialization through time $\pm$ standard error of the estimate, 0.003 ± 0.015, p-value=0.827).

Network robustness

Assembly did not effect the robustness of the networks to species extinction when species where removed incrementally by degree (estimate of the slope of robustness through time $\pm$ standard error

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of the estimate, $6 * 10^{-5} \pm 4 * 10^{-3}$, p-value=0.987) or abundance (0.001 ± 0.003, p-value=0.65, Fig. 5).

In contrast, the robustness of networks to cascading perturbations, as measured by the algebraic connectivity of the network, increased as the network assembled (estimate of the slope of robustness through time $\pm$ standard error of the estimate, 0.6814 ± 0.272, p-value=0.042, Fig. 5).

Discussion

We show that the temporal assembly of plant-pollinator networks following restoration is a highly dynamic process where interactions often undergo significant reorganizations. These network organizations are unlikely to be a product of environmental forces alone because the network changing points in non-assembling communities are less frequent, and there are few consistent trends in when change points occurred across all sites. Several sites had changing points between year 2009 and 2011 (Fig. 1). In California, 2011 marked the beginning of a multi-year drought. In the assembling hedgerows were not sampled in 2010, so disentangling whether the changing points are due to skipping a year of assembly or the drought is not possible. Interestingly, most of the assembling hedgerows did not undergo a significant reorganization of interactions immediately the hedgerow was planted (i.e., the transition from weedy field margin to hedgerow). This result is consistent with the finding that in our study system, hedgerow restoration takes several years to have a significant impact on the plant-pollinator communities (Kremen and M'Gonigle, in prep).

Given that several changing points in network organization occurred during assembly, we next explored the species most likely responsible for the shifts in interaction patterns. Based on a preferential attachment-like mechanism, we expect that the most persistent and high degree species would remain stable in the network core during assembly, and would thus contribute the least to the changing points in network organization. Surprisingly however, we encountered the opposite:

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the species that were most variable in their network position and thus contributed most to network reorganizations where species with the highest degrees (i.e., most generalized) and persistence. For example, the five most ubiquitous species in our study landscape — *Halictus ligatus*, *Halictus tripartitus*, *Lasioglossum (Dialictus) incompletum*, and *Toxomerus marginatus* — were the only species that changed what module (i.e., community), and they were also present in across years in all of the assembling hedgerows. Because species degree and persistence were strongly correlated, it is difficult to disentangle the causal mechanism for why species with those characteristics are so variable in their network position. Generalized species may be able to better exploit the limited floral resources in the intensively managed agriculture landscape, and thus also most persistent. More persistent species also have longer phenologies, so they have the opportunity to visit many different flowers, resulting in a higher degree. Either way, our result suggests that adaptable species can change their network position to utilize the most advantageous floral resources available, which may depend on the other pollinator species that are present and the state of the floral resource. Thus given the opportunity and ability to use different resources, species will often change their network positions.

The frequent changing points in network organization, dynamic nature of the location of species in networks, and turnover of species and interactions all point to an assembly mechanism other than preferential attachment. Nestedness did increase with years post restoration, as would be expected if colonizing, specialist species attached to a central, generalist core Albrecht *et al.* (2010). With preferential attachment, however, we would also expect connectance and specialization to increase, and we found no such trends. The stable level of network-level specialization through the assembly process may be due to the increased colonization of specialized species (M'Gonigle *et al.*, 2015) accompanied by an increase in the diet breath of resident species. This would be expected if resident species were able to minimize their foraging time by expanding their diet breath as plant diversity increases with hedgerow maturation (Waser *et al.*, 1996; Pyke, 1984; Blüthgen *et al.*, 2007; Albrecht *et al.*, 2010). Such a change in pollinator behavior would also explain the increase

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358 in network nestedness.

359 The changes in network patterns with assembly also increased the robustness of the networks to
360 cascading perturbations – providing further evidence that hedgerows are valuable tool for promot-
361 ing species conservation and ecosystem provision in agricultural areas (M'Gonigle *et al.*, 2015;
362 Ponisio *et al.*, 2015; Kremen & M'Gonigle, 2015). Because the vulnerability of the network to
363 cascading perturbations, as measured by algebraic connectivity, is correlated with species richness,
364 the increase and plant and pollinator richness following restoration is at least partially responsible
365 for enhancing network robustness to cascading effects. The relationship between diversity and
366 stability in networks has been the subject of considerable debate (e.g., May, 1972; Pimm, 1984;
367 Montoya *et al.*, 2006). Our results provides one of the few empirical examples of how restoring
368 species diversity contributes to enhancing network stability. Though these hedgerows were de-
369 signed to promote floral resources across the growing season and not specifically to promote any
370 specific network properties (Menz *et al.*, 2010), the pollinators assembled into resilient interaction
371 patterns. With prior knowledge of the floral preferences of pollinators, future restoration efforts
372 may also be able to incorporate promoting network stability into planning efforts (M'Gonigle *et al.*,
373 2016)

374 Interestingly, however, the robustness of hedgerow communities to species loss did not change
375 with assembly. This is particularly surprising given the observed increase in nestedness, which
376 is often associated with an enhanced in robustness to extinction (Memmott *et al.*, 2004). It may
377 be that assembling hedgerows have not yet reached a sufficient level of nestedness to realize its
378 benefits. Nestedness of the assembling hedgerows, however, did not asymptote within the eight
379 years following restoration that the sites were surveyed, so hedgerow networks may eventually
380 reach sufficient levels of nestedness to gain the robustness advantage.

381 Plant-pollinator networks in general are highly dynamic, with high turnover of species and inter-
382 actions both within and between seasons (Burkle & Alarcón, 2011). Though our non-assembling

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communities experience fewer network reorganizations than the assembling hedgerows, 82% of field margins and 40% of mature hedgerows underwent at least one changing point in network structure. Pollinators are also highly opportunistic (Petanidou *et al.*, 2008; Vázquez, 2005; Albrecht *et al.*, 2010), though trait complementarity such as tongue length and corolla depth impose some biophysical limits to the interactions between plants and pollinators (Vázquez *et al.*, 2009; Vázquez *et al.*, 2009; Stang *et al.*, 2009, 2006; Santamaría & Rodríguez-Gironés, 2007). Such opportunism may buffer plant-pollinator communities from global change (e.g., Ramos-Jiliberto *et al.*, 2012; Kaiser-Bunbury *et al.*, 2010), but our limited understanding of the assembly of these communities impedes making such predictions (Vázquez *et al.*, 2009; Burkle & Alarcón, 2011). Unlike in the broader food web literature, we have few mechanistic models of mutualistic network assembly (Valdovinos *et al.*, 2013). In addition, the few that have been developed often borrow their mechanisms from competitive interactions, leading to inaccurate biological assumptions (Holland *et al.*, 2006). We need further development of mechanistic models of mutualistic system to generate testable predictions, along with empirical exploration of network assembly. Plant-pollinator communities and mutualisms in general are vital for the maintenance of biodiversity and the provision of essential ecosystem services. We must therefore understand the processes underlying their assembly to facilitate restoration and conservation.

Acknowledgments

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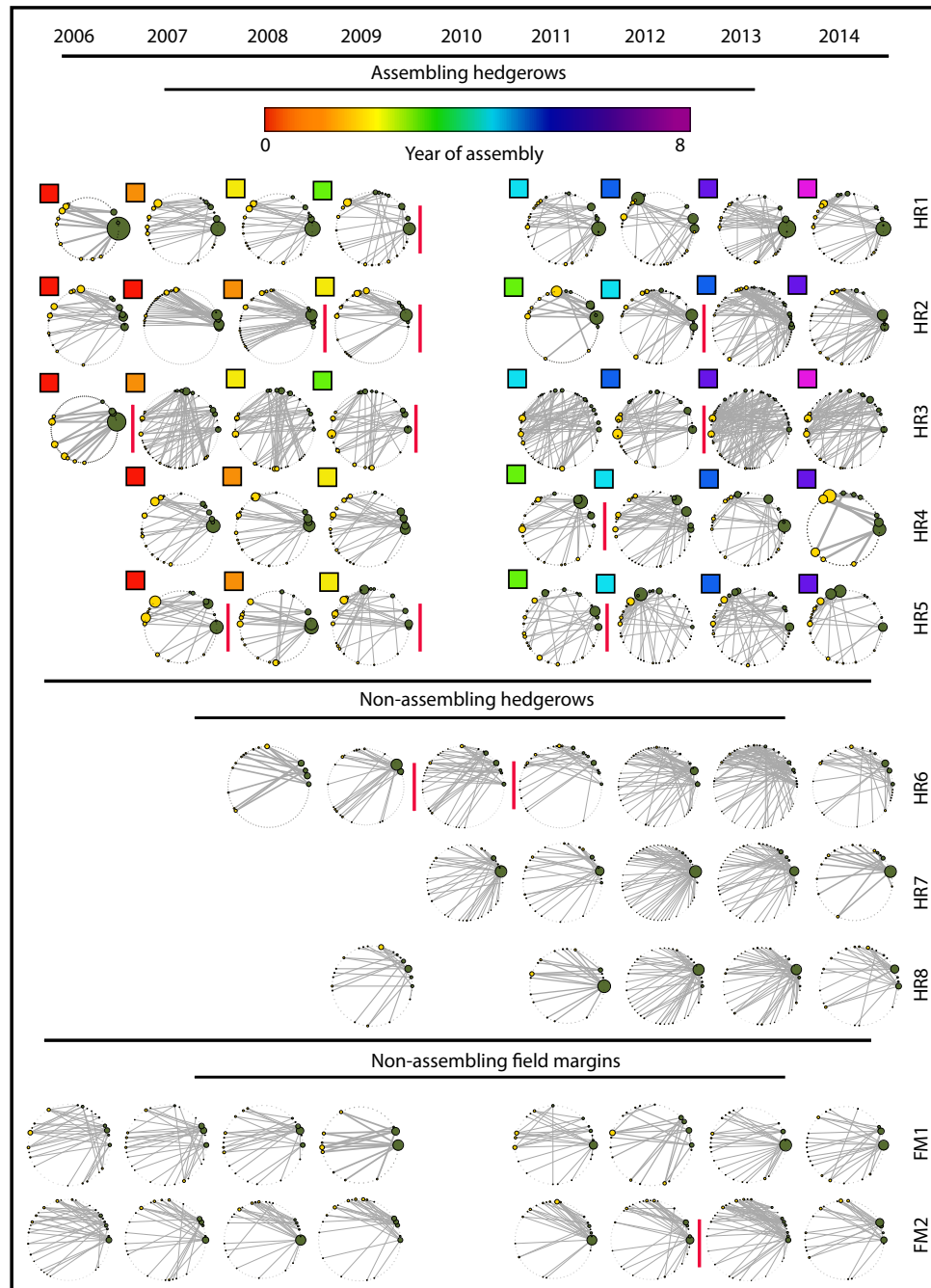
Figure 1: Assembling hedgerow networks had more changing points (vertical red lines) and non-assembling hedgerows and weedy field margins (a represented sample of non-assembling sites are depicted here). In each network, plants and pollinators are represented by green and yellow circles, respectively, weighted by their degree. Each species has has a consistent position in the network across years. In the assembling hedgerows, colored squares in the corner of each network represent the years post restoration.
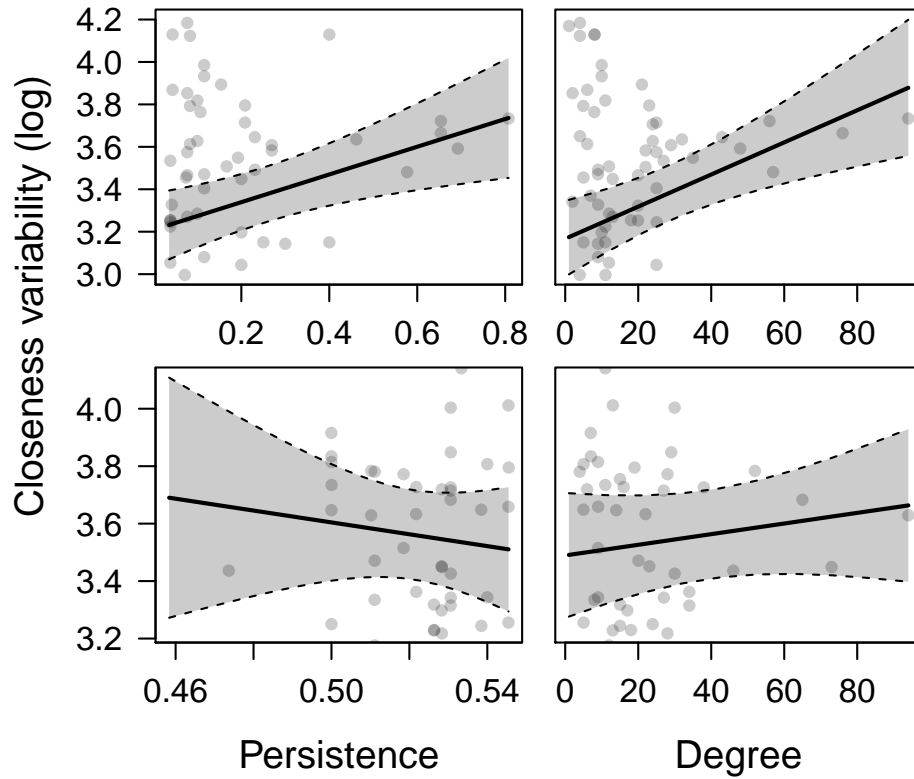
Figure 2: The coefficient of variation of network position, as represented by closeness, plotted against pollinator persistence and degree. Persistence and degree were positively related to network position variability in pollinators, but unrelated in plants. Points represents means for each species across sites. The solid line indicates the mean slope estimate and the dashed lines are the 95% confidence intervals around the estimate.
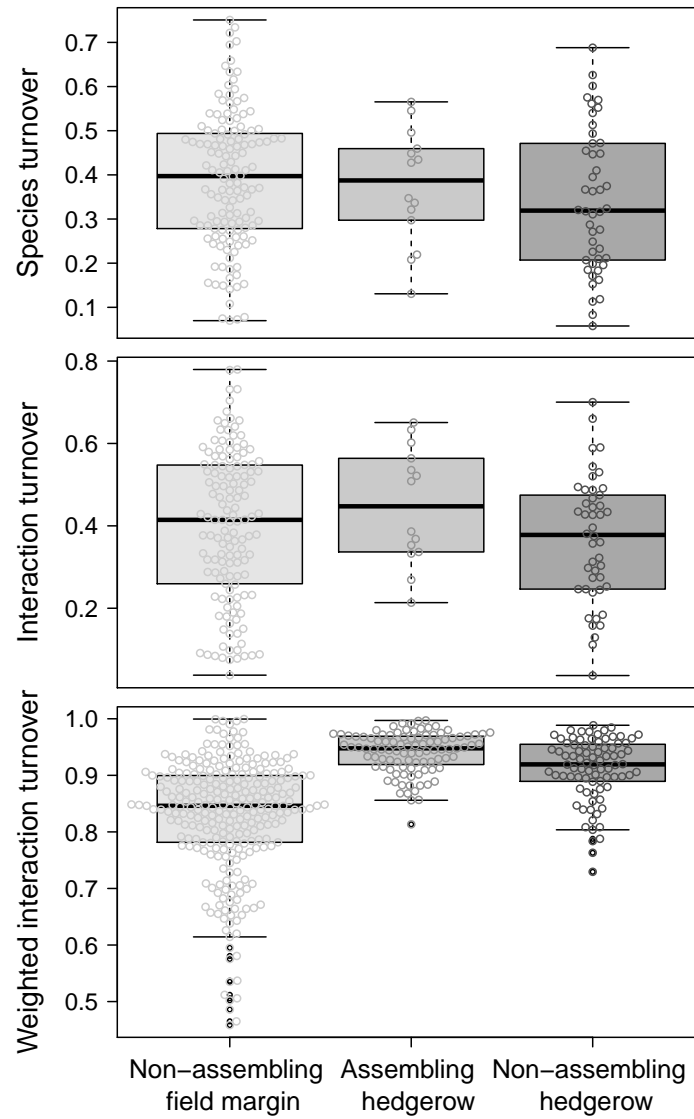
Figure 3: The pollinator species, interaction and weighted interactions turnover of plant-pollinator networks at non-assembling field margins sites, assembling hedgerows, and non-assembling, mature hedgerows. Rates of species and interaction turnover were similar between site types. However, when interactions where weighted by their uniqueness, both hedgerow types had higher turnover that unrestored field margins. Boxplots represent medians (black horizontal line) first and third quartiles (box perimeter) and extremes (whiskers).
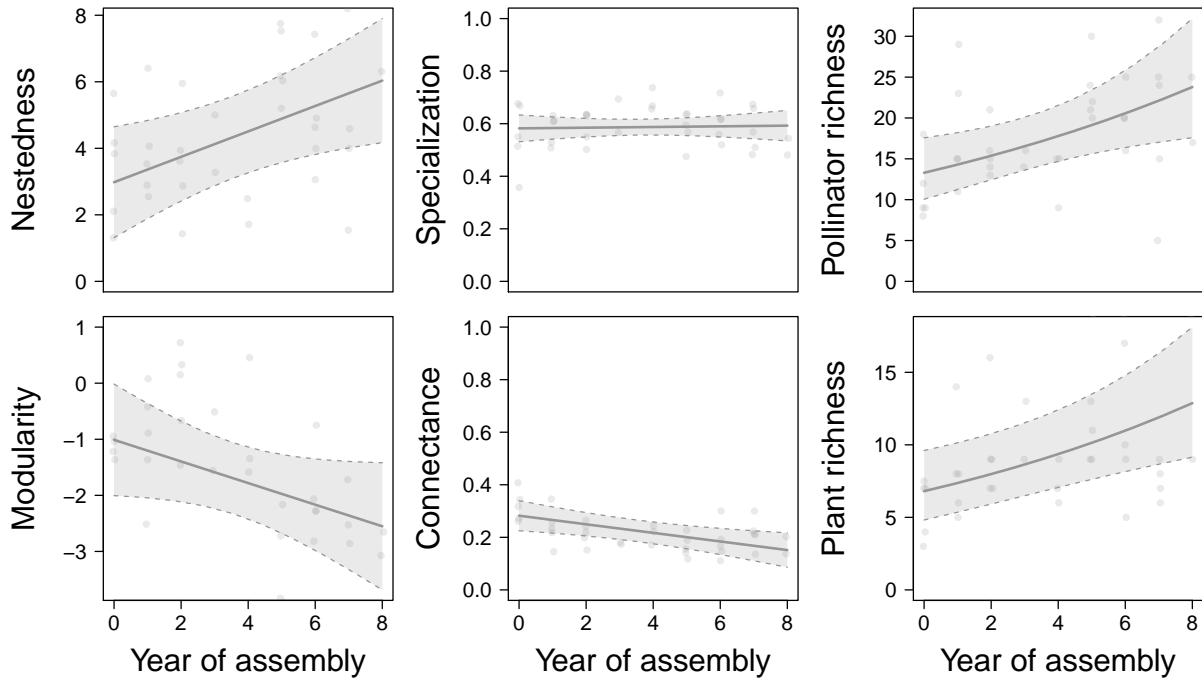
Figure 4: The change in nestedness, modularity, specialization and connectance as the networks assemble. The left panels represent *z*-scores. Scores greater than ~ 2 or less than ~ -2 are significantly more or less structured than randomly assembled networks. Points are the value for each site at each year of assembly. The solid line indicates the mean slope estimate and the dashed lines are the 95% confidence intervals around the estimate.
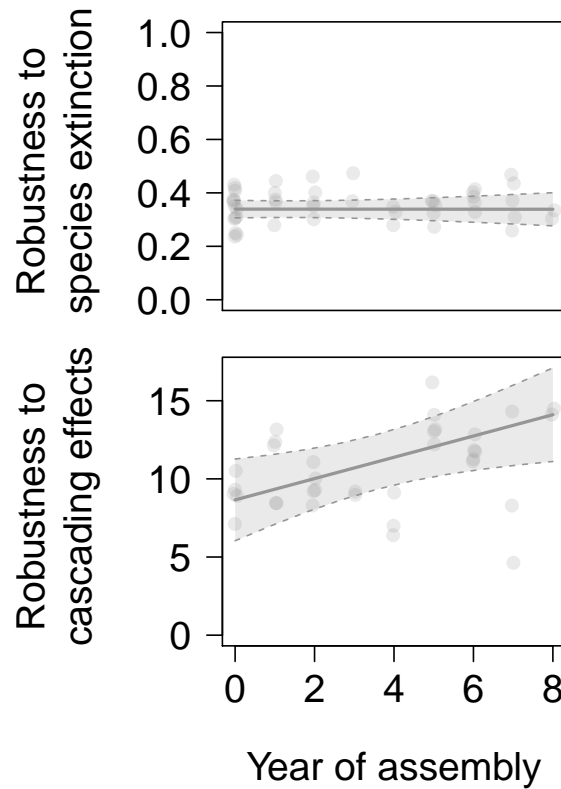
Figure 5: The robustness of networks to species extinction and to cascading perturbations. The robustness to species extinction is measured by incrementally removing species by degree, through removing species by abundance did not yield qualitatively different results. The robustness of networks to cascading perturbations is measured as the algebraic connectivity, the second smallest eigenvalue of the Laplacian matrix. Points are the value for each site at each year of assembly. The solid line indicates the mean slope estimate and the dashed lines are the 95% confidence intervals around the estimate.