



# Network analysis of phenological units to detect important species in plant-pollinator assemblages: can it inform conservation strategies?

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**Abstract:** Conservation of species is often focused either only on those that are endangered, or on maximising the number recorded on species lists. However, species share space and time with others, thus interacting and building frameworks of relationships that can be unravelled by community-level network analysis. It is these relationships that ultimately drive ecosystem function via the transfer of energy and nutrients. However interactions are rarely considered in conservation planning. Network analysis can be used to detect key species (“hubs”) that play an important role in cohesiveness of networks. We applied this approach to plant-pollinator communities on two montane Northern Apennine grasslands, paying special attention to the modules and the identity of hubs. We performed season-wide sampling and then focused the network analyses on time units consistent with plant phenology. After testing for significance of modules, only some modules were found to be significantly segregated from others. Thus, networks were organized around a structured core of modules with a set of companion species that were not organized into compartments. Using a network approach we obtained a list of important plant and pollinator species, including three Network Hubs of utmost importance, and other hubs of particular biogeographical interest. By having a lot of links and high partner diversity, hubs should convey stability to networks. Due to their role in the networks, taking into account such key species when considering the management of sites could help to preserve the greatest number of interactions and thus support many other species.

**Abbreviations:** PC– Pheno-Cluster; PCA–Principal Component Analysis.

**Nomenclature:** The Plant List (2013) for plants, Seifert (2004) for Hymenoptera: Formicidae and de Jong et al. (2014) for other insects.

## Introduction

Plant–pollinator interactions play a key functional role in ecosystems because they both facilitate the reproduction of plant species across generations (Ollerton et al. 2011) and also provide direct and indirect opportunities for animal feeding. However, these mainly mutualistic interactions could be disrupted by a range of factors including climate change (e.g., Hegland et al. 2009), land use alteration and changes in agriculture practices (e.g., Ollerton et al. 2014), lack of flower diversity, and increasing pathogens and pesticides (e.g., Goulson et al. 2015). It is likely that such factors are also threatening the pollination services provided (Tylianakis et al. 2010).

Baseline conservation assessments that include listing species diversity and/or the presence of endangered taxa in a given locality is a good first approximation. Nevertheless, species exist within a network of interactions with other species, and these interactions themselves are also in need of conservation (Janzen 1974, Tylianakis et al. 2010). Focusing

on complex networks where nodes (i.e., species) are connected by functional links such as herbivory, predation, seed dispersal and pollination, allows ecologists to understand the super-structure of these communities (e.g., modules of interacting species Olesen et al. 2007, Watts et al. 2016).

The idea of conserving of interactions is rather old (Janzen 1974), but in practice it has not yet been clarified how it should take place. Ecologists have suggested a number of network features that could be helpful to conservation biologists (Corbet 2000, Tylianakis et al. 2010, Kaiser-Bunbury and Blüthgen 2015). Their arguments mainly rely on (a) the ease of performing network analyses (Tylianakis et al. 2010, Kaiser-Bunbury and Blüthgen 2015), (b) a supposed relation between network indexes and stability/robustness against perturbations (Bascompte et al. 2006, Tylianakis et al. 2010, Santamaría et al. 2016), (c) the possibility of investigating species functional roles (niche) through interactions (Kaiser-Bunbury and Blüthgen 2015), (d) network’s species diversity, link distributions among species, and the classical relationship of diversity with stability and with functionality (Kaiser-

Bunbury and Blüthgen 2015). Therefore, network analyses have been suggested to be useful, but mainly for monitoring purposes (Tylianakis et al. 2010), such as checking an ecosystem's functioning after the restoration of a degraded habitat (Kaiser-Bunbury and Blüthgen 2015). However, conservation goes beyond just monitoring, but the ways in which network analyses could be further helpful for conservation are not presently clear.

The value of using a network approach to understand and conserve plant-pollinator interactions is hampered by both a limited geographic perspective (there are still large parts of the world that have never been studied) and the temporal resolution of most studies. Network ecologists have traditionally studied cumulative networks over long-periods of sampling, treating all interactions as simultaneous in their analysis. Alternatively, a single short period of sampling has been chosen as representative of the peak activity of the community, or because a target species is active. Either approach results into an over-simplified view because species in a community are dynamic both as to when they come into activity and how long they are active. More recent studies have divided the season into a-priori blocks of time of the same length, e.g., monthly (Basilio et al. 2006), every two-weeks (Kaiser-Bunbury et al. 2010), or even daily (Rasmussen et al. 2013). Nevertheless, such seasonal units are chosen arbitrarily and again there is a risk of obscuring the effects of species' phenology.

In this study, we aimed to assess how conservation practitioners could (1) define reliable seasonal units compatible with phenology; (2) interpret the structure of ecological networks and thus obtain insights on ecosystem functioning; (3) identify key species (hubs) and their features, that could possibly be the target of specific conservation actions, due to the role played by them in supporting others species by both direct and indirect interactions (Guimerà et al. 2007). We investigated the feasibility of these aims using season-wide sampling of flower visitors performed on two montane semi-dry grasslands differing in species composition in the Northern Apennine (Italian Peninsula). This work is the first of its type on such a southern European mountain chain.

## Methods

### Study area

Sampling took place at 1650 m altitude on two semi-dry grasslands in the montane altitudinal belt of Mt. Lesima (1724 m a.s.l., 44°41'6" N 9°15'26" E, Northern Apennine, Fig. 1) which are subjected to different anthropogenic pressure and characterized by different plant composition despite being spatially adjacent (Barcella 2013). In the current study, *Sesleria pichiana* – *Laserpitium siler* community occurs on steep slopes with N-E exposure and not grazed; and the other, *Brachypodium rupestre* – *Festuca laevigata* community occurs on S-W slopes and is cattle grazed during the second half of the summer. According to Barcella (2013), both plant communities are important habitats for biodiversity as they belong to the Habitat 6210\* of Natura 2000 Network ("semi-natural dry grasslands and scrubland facies on calcareous substrates (*Festuco-Brometalia*) (\*important orchid sites)"). Neighbouring areas at lower altitudes are dominated by forests of the beech series *Trochiscantho nodiflori* – *Fago sylvaticae sigmetum* (Verde et al. 2010). The area surrounding the mountain has 1250–1500 mm average rainfall, 5 °C mean annual temperature and Temperate Oceanic Submediterranean bioclimate (Barcella 2013).

### Data collection

The sampling design was based on three fixed plots of 2.5 m × 2.5 m in each plant community during the summer season 2013. Each sampling plot was placed inside the area used to classify the vegetation in a previous study (Barcella 2013). In each plot, the insects visiting flowers and touching plant reproductive structures were captured with a net but without damaging the plants and put in labelled jars. Plots were sampled weekly, twice each sampling day, for 20 minutes each time. During each sampling day the starting plot was chosen at random. During the last three sampling dates, the *Brachypodium rupestre* – *Festuca laevigata* community was treated by intense grazing (no plants in flower were pre-



**Figure 1.** Sampling area in the Northern Apennine. From the left: Italy; sub-horizontal view on Oltrepò Pavese; vertical view of Mt. Lesima. In the latter, the polygon on the left refers to *Brachypodium rupestre* – *Festuca laevigata* community; the one on the right refers to *Sesleria pichiana* – *Laserpitium siler* community. Black diamonds are the sampling plots.

sent). Therefore, three new plots were defined in less grazed spots inside the same plant community.

Both plants and insects were recorded to species level in most cases. When such detail was impossible to reach due to difficult identification or unavailability of taxonomists, morpho-species were used for plants, such as *Ranunculus* spp. and *Galium* spp., and some specimens of Diptera, Hymenoptera: Ichneumonidae, and Lepidoptera: Micropterigidae.

At each date, the pollination units of each flowering species were counted inside the sampling plots. To do so, we considered both the arrangement of the single flower within an inflorescence and also pollinator behavior (Faegri and van der Pijl 1979). In detail, pollination unit was considered as the whole inflorescence if flowers were organized in a dense cluster with flowers opening sub-simultaneously, so that a medium-size insect pollinator would not need to fly between successive visits; pollination unit was the single flower if flowers were very separated within an inflorescence and had unsynchronized anthesis, so that a pollinator would have to fly between visits.

The two grasslands were different as regards richness of species within plant families, pollination-unit abundance and insect visits (Appendix Table A1, Appendix Figure A1).

#### Data analysis

*Detection of phenological units.* In each community, the flowering phenology was analyzed in order to identify time-units of plants flowering together, here called a “pheno-cluster”. We independently developed an approach similar to Fantinato et al. (2016). For each species, the number of pollination units (defined above) was calculated on each date to give the sequence of pollination units being produced over time. Pairwise Spearman correlations between the number of pollination units per date for each species were then calculated. Once two or more species were significantly correlated with each other (but not with other species), a new sequence representative of the correlated species was obtained by computing the mean value of their pollination-units on each date. The newly created variables were included in a cluster analysis with Bray-Curtis similarity index to detect pheno-clusters. The significance of the obtained pheno-clusters was tested by means of one-way PERMANOVA using the Bray-Curtis index of similarity (Anderson 2001), that is based on the formula

$$d_{jk} = 1 - \frac{\sum_i |x_{ji} - x_{ki}|}{\sum_i (x_{ji} + x_{ki})},$$

where  $x_{ji}$  (and  $x_{ki}$ ) are counts of species  $i$  in the sample  $j$  (and  $k$ ). The PAST 2.17 statistical software was used (Hammer et al. 2001).

*Detection of modules.* In each pheno-cluster, quantitative interaction matrices were analysed to detect modules, defined as groups of species that share most of the interactions. Quantitative matrices included count data, i.e., the number of individuals per insect species visiting a given plant species, as

suggested by Reitan and Nielsen (2016). The interacting species were re-arranged according to the QuanBiMo algorithm in the R package Bipartite v.2.03 (Dormann et al. 2008). This algorithm develops a dendrogram with species more likely to interact being grouped together. It optimises the outcome by random swaps of the branches with a simulated annealing Monte Carlo approach and by evaluating whether the newly swapped graph would be more likely than the former one.

There are a number of ways to test the species composition and significance of modules (e.g., Martín González et al. 2012, Pozsgai et al. 2015). In our work, we followed Martín González et al. (2012), using the number of individuals per insect species visiting a given plant species as quantitative variable and modules as groups with a one-way PERMANOVA applying the Bray-Curtis similarity index (Anderson 2001). PAST 2.17 statistical software was used (Hammer et al. 2001).

*Network analysis.* For each pheno-cluster, network analysis was performed on quantitative interaction matrices (see above) to obtain the following network-level indexes. Connectance  $C$  is the proportion of realized links, calculated as

$$C = L/(I \times J) \quad (1)$$

where  $L$  is the number of interactions,  $I$  and  $J$  are the numbers of plant and animal species, respectively, and can vary from 0 to 1 (Blüthgen et al. 2006). Connectance is moderately sensitive to sampling effort (Rivera-Hutinel et al. 2012). Mainly for this reason, connectance appears to be less efficient in describing networks than other more robust indexes. Interaction diversity  $H'_2$  is a measure of generalization of network-level interactions independent to network size (Blüthgen et al. 2006). It is based on the two-dimensional Shannon entropy, which is computed as

$$H_2 = - \sum_{i=1}^r \sum_{j=1}^c (p_{ij} \times \ln p_{ij}), \quad (2.1)$$

where  $r$  and  $c$  refer to rows and columns of a contingency table of interactions between a plant species  $i$  and pollinator species  $j$ , and  $p_{ij}$  is the proportion of interactions in relation to the respective row total (Blüthgen et al. 2006). Its possible maximum and minimum are obtained from the distribution of interaction totals of the matrix.  $H'_2$  ranges between 0 (no specialization) and 1 (perfect specialisation), and it is calculated as follows

$$H'_2 = \frac{H_{2max} - H_2}{H_{2max} - H_{2min}} \quad (2.2)$$

(Blüthgen et al. 2006). Modularity  $Q$  for weighted matrices with the QuanBiMo algorithm (Dormann and Strauss 2014) is a measure of module-belonging, namely the species strength of being connected within a module. It is computed as follows

$$Q = \frac{1}{2m} \sum_{ij} (A_{ij} - K_{ij}) \delta(g_i, g_j), \quad (3)$$

where  $m = \sum_{i,j} A_{ij}$ ,  $K_{ij}$  refers to the marginal totals for rows and columns of a weighted interaction matrix  $A_{ij}$ ,  $g$  is a given module to which species  $i$  (or  $j$ ) is assigned to (Dormann and Strauss 2014).  $Q$  ranges from 0 to 1, the higher its value, the more segregated into modules is the network (Dormann and Strauss 2014). Due to its variation with network size, the modularity index was checked for significance following Dormann and Strauss (2014) by comparing the observed value with standardized z-scores of 100 quantitative null model expectations generated with *r2dtable* algorithm. For the computation of the above-mentioned indexes (1), (2.1), (2.2), (3), the R package *bipartite* v.2.03 was used. Finally, nestedness based on overlap and decreasing fill (NODF, Almeida-Neto et al. 2008) was computed using the software ANINHADO (Guimarães and Guimarães 2006). This measure is based on two properties: decreasing fill and paired overlap. In brief, in a matrix with  $n$  rows and  $m$  columns, it detects the degree of nestedness ( $N_p$ ) between pairs of columns and pairs of rows by comparing the marginal totals ("decreasing fill") and the percentage of filled ( $\neq 0$ ) matrix cells which are located at the same position ("paired overlap"),

$$NODF = \frac{\sum N_p}{\left[\frac{n(n-1)}{2}\right] + \left[\frac{m(m-1)}{2}\right]} \quad (4)$$

It ranges from zero (un-nested) to 100 (fully nested). The statistical significance of NODF was tested using 1000 random binary null models built by the *ER* algorithm, in which the presence or absence of interactions are randomly assigned.

*Key species.* The standardized among-module connectivity (c-values) and within-module degree (z-values) were computed at a species level for each pheno-cluster. The c-value is a measure of the contribution of a species in connecting species of the other modules, calculated as

$$c = 1 - \sum \left( \frac{k_{is}}{k_i} \right)^2 \quad (5)$$

where  $k_{is}$  is the number of links of species  $i$  to other species in module  $s$ , and  $k_i$  is its total amount of links (Guimerà and Amaral 2005); the z-value is a measure of the contribution of a species in connecting species of the same modules, calculated as

$$z = \frac{k_{it} - \bar{k}_{t_i}}{\sigma_{k_{t_i}}} \quad (6)$$

where  $k_{it}$  is links number of species  $i$  to species within its own module  $t$ ,  $\bar{k}_{t_i}$  is the links average of all species of module  $t$  and  $\sigma_{k_{t_i}}$  is its standard deviation (Guimerà and Amaral 2005). To detect key species, critical thresholds were found as 95% quantiles of null model distributions for c and z values, as shown by Dormann and Strauss (2014), computed from the 100 quantitative null models used to test the significance of modularity  $Q$  (Eq. 3).

*Relationships between hubs and species diversity.* In order to relate both the among-module connectivity (c-values, Eq. 5) and the within-module participation (z-values, Eq. 6) with species-specific features, a PCA ordination was performed on the c- and z-values of insect species. We focused only on insects because, unlike the plants, they were present in all levels of the hubs hierarchy (see Table 2). This ordination was tested for a *post-hoc* correlation (and its significance tested after 10000 permutations) with the following species-specific features: degree  $N$ , that is the (normalized) number of links per species (Eq. 7); the specialization index  $d'$ , that is the species-specific counterpart of  $H'_2$  and recalls the Kullback-Leibler distance

$$d_i = \sum_{j=1}^c \left( p'_{ij} \ln \frac{p'_{ij}}{q_j} \right) \quad (8)$$

For a species  $i$ , this index compares  $p'_{ij}$ , the proportion of interactions (with a partner  $j$ ) considered in relation to the respective row total, with  $q_j$ , the partner  $j$  availability obtained as proportion of all its interactions in relation to the total number of interactions. Then,  $d'$  is the standardization between the possible maximum and minimum of  $d_i$  (Blüthgen et al. 2006), per-species Shannon diversity, that provides a measure of partner diversity for each species (Kaiser-Bunbury and Blüthgen 2015) calculated as

$$H = - \sum_{i=1}^S p_i \log_b p_i \quad (9)$$

where  $p_i$  is the proportion of interactions for a species  $i$  and  $S$  is the number of species. The PCA results and *post-hoc* correlation were obtained by the R package *vegan* v. 2.3, and the computation of the above-mentioned indexes from (5) to (9) was performed in the R package *bipartite* v.2.03.

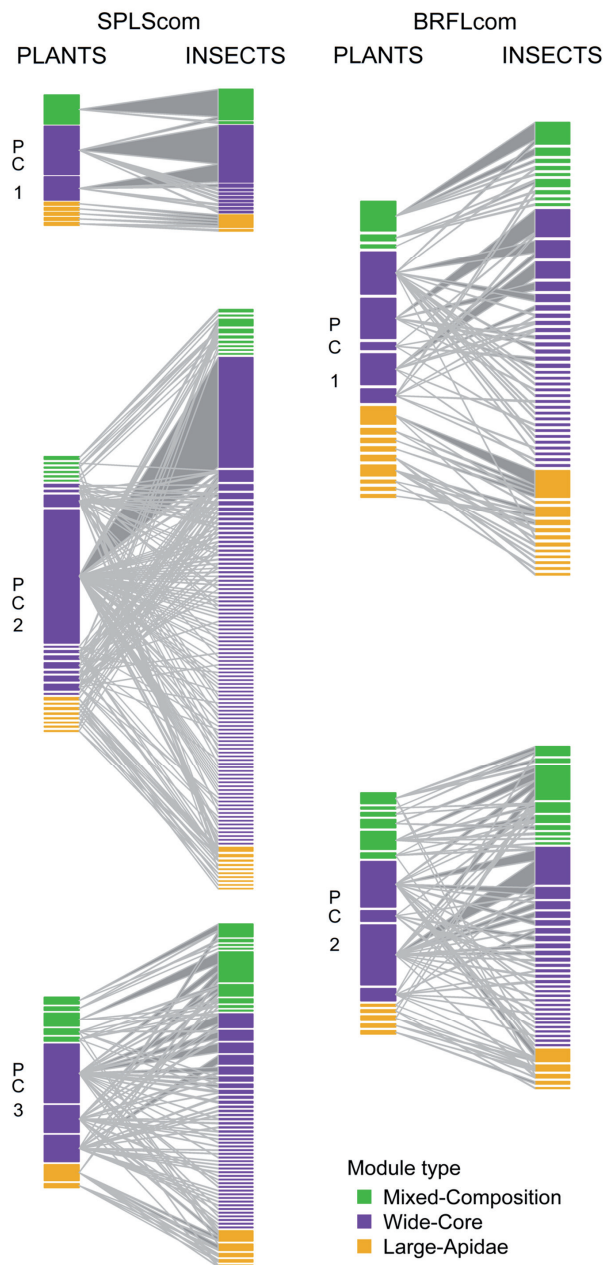
## Results

### *Topology of plant-pollinator networks*

The *Sesleria pichiana* – *Laserpitium siler* community had a higher number of interactions and greater species richness (1677 interactions, 34 plant species of 14 families and 145 insect species of 8 orders, 44 families, morpho-species included). In contrast, the *Brachypodium rupestre* – *Festuca laevigata* community was poorer (323 plant-pollinator interactions, 29 plant species of 16 families and 76 species of insects of 5 orders, 30 families, morpho-species included).

The *Sesleria pichiana* – *Laserpitium siler* community was organized into three pheno-clusters (PCs): (1) an initial short one of 2 weeks; (2) a longer central phase of 5 weeks; and (3) a final one of 2 weeks ( $F_{PC1-PC2} = 3.64$ ,  $p_{PC1-PC2} < 0.05$ ;  $F_{PC2-PC3} = 3.72$ ,  $p_{PC2-PC3} < 0.05$ ). In the *Brachypodium rupestre* – *Festuca laevigata* community, 2 significant pheno-clusters of respectively 5 and 4 weeks were identified ( $F_{PC1-PC2} = 5.61$ ;  $p_{PC1-PC2} < 0.01$ ).





**Figure 2.** Plant-pollinator networks of each phenological unit (PC) of each grassland (*Sesleria pichiana* - *Laserpitium siler* community = SPLScom, *Brachypodium rupestre* - *Festuca laevigata* community = BRFLcom). Each block represents a species, its size is proportional to the total number of interactions, line-width shows the abundance of interactions between the two linked partners.

A network analysis was performed on species interacting within the same pheno-cluster (Fig. 2). Connectance and nestedness were low in the networks. However, all network indexes varied highly between pheno-cluster (Table 1).

#### Modules of interacting species

A low number of modules was detected by the QuanBiMo algorithm, with a mean of 4.4 modules per pheno-cluster.

**Table 1.** Features of each phenological unit (pheno-cluster = PC) of each grassland (*Sesleria pichiana* - *Laserpitium siler* community = SPLScom, *Brachypodium rupestre* - *Festuca laevigata* community = BRFLcom). ‡ is significance of Modularity computed with 100 quantitative null models with r2dtable algorithm of Bipartite package for R. \* is for significance as  $p < 0.05$  with 1000 binary null-model with ER algorithm in ANINHADO.

	SPLScom			BRFLcom	
	PC 1	PC 2	PC 3	PC 1	PC 2
General features					
Length in weeks	2	5	2	5	4
Visited plants no. sp.	8	26	10	18	15
Visiting insect no. sp.	13	114	57	53	42
Network features					
Connectance	0.18	0.07	0.16	0.07	0.13
Q (modularity)	0.51‡	0.09‡	0.34‡	0.59‡	0.40‡
NODF (nestedness)	18.6	19.3*	22.3*	9.7	25.6*
$H'_2$	0.71	0.64	0.53	0.72	0.46

After testing for pair-wise significance of such modules, we found that several ones were not significantly distinct from the others (Appendix Table A2). Within significant modules, we detected recurrent members defined taxonomically, as follows. *Bombus* spp. (Hymenoptera: Apidae) visited mainly Fabaceae and Lamiaceae plants. Such modules could be called "Large-Apidae". A long array of insect species of many groups (Diptera, but also fewer Hymenoptera, Lepidoptera and Coleoptera) interacted with few plant species (e.g., Asteraceae, Apiaceae, Rosaceae, Ranunculaceae). Such latter modules could be called "Wide-core". The remaining species would belong to a "Mixed-composition" interacting group.

#### Among-module and within-module key species

Species values of among-module connectivity (c-values) and within-module participation (z-values) for pollinators and plants of both communities are shown in Fig. 3. Only a minor fraction of species is detectable. The taxonomic identities of key species are listed in Table 2. Following the categories given in Olesen et al. (2007), only insect species fitted the categories of "Network-Hub" (both high c- and z-values) and "Connectors" (high c-values). Instead, both insects and plants fitted the category of "Module-Hub" (high z-values). The remaining majority of species had both low c- and z-values and they were therefore categorized as "Peripherals". Finally, some species were multiple hubs as their role as key species changed depending on the phenological unit or on the community.

#### Relationships between hubs and species diversity

The PCA ordination axes explained species c- and z- values (PC1 = 92%, PC2 = 2.3%). Ordination scores were correlated with species links number  $N$  ( $r^2 = 0.57$ ,  $p < 0.001$ ) and partner diversity ( $r^2 = 0.63$ ,  $p < 0.001$ ), while they were moderately correlated with species-level specialization  $d'$  ( $r^2 = 0.13$ ,  $p < 0.001$ ). The ordination biplot (Fig. 4) shows that

**Table 2.** Taxonomic identity of Hub species of Figure 3, Hub type and belonging community are provided (*Sesleria pichiana* – *Laserpitium siler* community = SPLScom, *Brachypodium rupestre* – *Festuca laevigata* community = BRFLcom).

Plants	Family	Hub type	Community	Label in Fig. 3
<i>Lathyrus montanus</i>	Fabaceae	Module Hub	SPLScom	Pl.1
<i>Laserpitium siler</i>	Apiaceae	Module Hub	SPLScom	Pl.2
<i>Lotus corniculatus</i>	Fabaceae	Module Hub	BRFLcom	Pl.3
<i>Alchemilla glaucescens</i>	Rosaceae	Module Hub	BRFLcom	Pl.4
<i>Phyteuma ovatum</i>	Campanulaceae	Module Hub	BRFLcom	Pl.5
<i>Phyteuma scorzoniferolium</i>	Campanulaceae	Module Hub	BRFLcom	Pl.6
<i>Hypericum richeri</i>	Hypericaceae	Module Hub	BRFLcom	Pl.7
Insects	Order: Family	Hub type	Community	Label in Fig. 3
<i>Formica picea</i>	Hymenoptera: Formicidae	Module Hub	SPLScom; BRFLcom	In.1
<i>Chrysotoxum cautum</i>	Diptera: Syrphidae	Module Hub	SPLScom	In.2
<i>Chiastocheta lophota</i>	Diptera: Anthomyiidae	Module Hub	SPLScom; BRFLcom	In.3
<i>Botanophila</i> sp.	Diptera: Anthomyiidae	Module Hub	SPLScom	In.4
<i>Bombus soroeensis</i>	Hymenoptera: Apidae	Connector; Module Hub	SPLScom	In.5
<i>Bombus lapidarius</i>	Hymenoptera: Apidae	Module Hub	SPLScom	In.6
<i>Bombus rupestris</i>	Hymenoptera: Apidae	Network Hub; Connector; Module Hub	SPLScom; BRFLcom	In.7
<i>Micrinus heteromorphus</i>	Coleoptera: Malachiidae	Network Hub; Module Hub	SPLScom; BRFLcom	In.8
<i>Sepsis</i> sp.	Diptera: Sepsidae	Module Hub	SPLScom; BRFLcom	In.9
<i>Eristalis tenax</i>	Diptera: Syrphidae	Network Hub	SPLScom	In.10
<i>Episyrphus balteatus</i>	Diptera: Syrphidae	Connector	SPLScom	In.11
<i>Pieris brassicae</i>	Lepidoptera: Pieridae	Connector; Module Hub	SPLScom; BRFLcom	In.12
<i>Vanessa cardui</i>	Lepidoptera: Nymphalidae	Module Hub	SPLScom	In.13
<i>Bombus lucorum</i>	Hymenoptera: Apidae	Module Hub	BRFLcom	In.14

specialization is mainly related to z values, while partner diversity and links tend to be more related to c values.

## Discussion

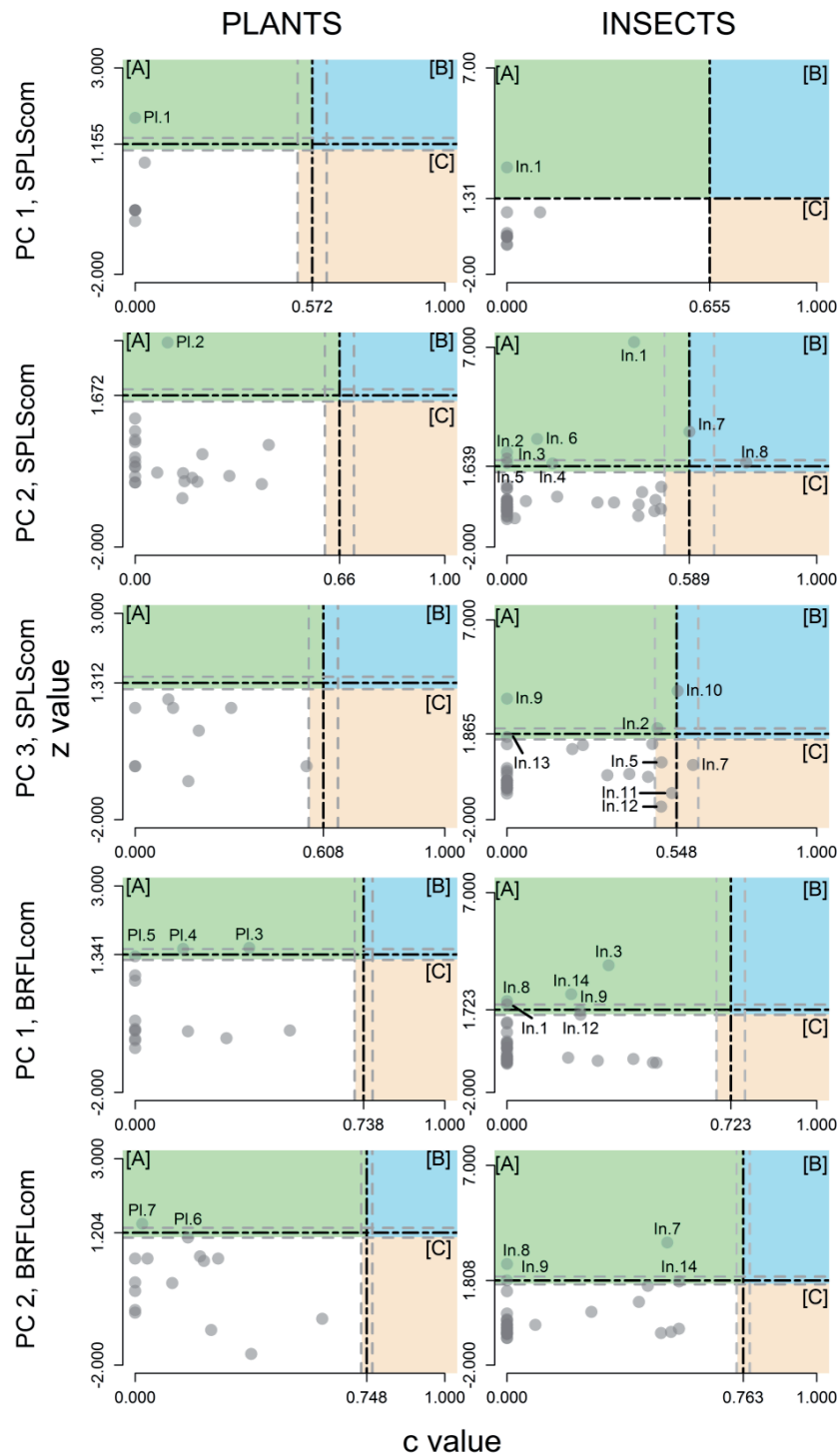
### *Ecology of montane plant-pollinator networks*

Montane ecosystems have received low attention from network ecologists even though altitude affects many factors that would influence foraging strategies and thus the communities (Miller-Struttman and Galen 2014, Watts et al. 2016). Despite that, it is possible to list some recurrent features. Variation of networks along altitudinal gradients might be due to the higher rate at which insect richness decreases (Viterbi et al. 2013) compared to that of flowers (Olesen and Jordano 2002). Accordingly, flower visitation has been found to decline along altitudinal gradients (Zhao et al. 2016), e.g., by over 50% between the lower and the upper alpine

belts (Arroyo et al. 1985). As a result of these patterns, connectance also progressively decreases with altitude (Olesen and Jordano 2002).

Our networks were rather variable between pheno-clusters (Fig. 2, Table 1). Generally, connectance varied from low to medium levels of the typical range of altitudinal networks, the maximum value recorded at altitudes higher than 1500 m a.s.l. being about 0.3 (Olesen and Jordano 2002). Despite that, some links overlap between species, as given by the index  $H^2$ . Therefore, the ecological strategy of these networks swings between low and medium levels of generalization. At least a proportion of species is generalist and high-altitude pollination networks have not shown high specialization so far (Dupont et al. 2003, Fang and Huang 2012, Watts et al. 2016).

At higher elevations, the network nestedness decreases (Ramos-Jiliberto et al. 2010). Our networks also exhibited low levels of nestedness. These patterns suggest that (a) alti-



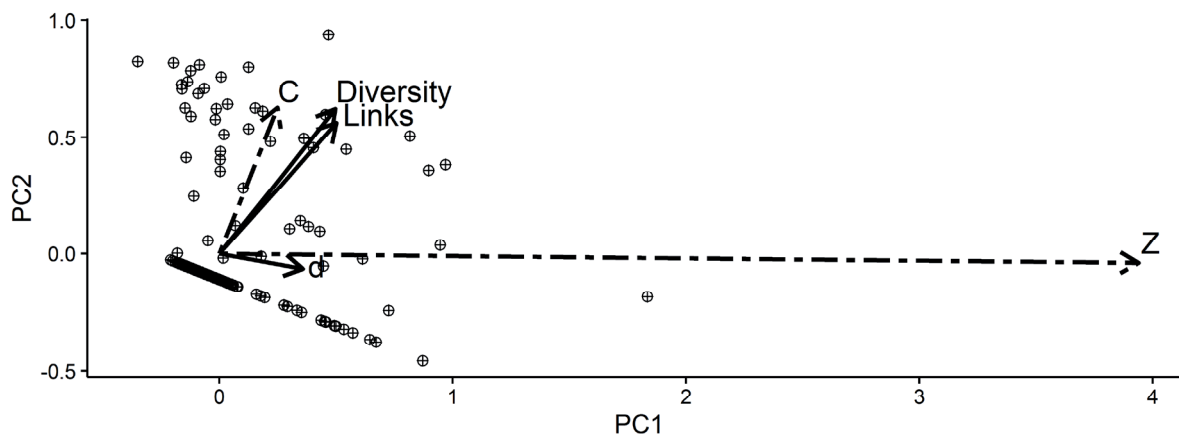
**Figure 3.** Among-module connectivity ( $c$ -) and within-module participation ( $z$ -) values for species of each phenological unit (PC) of both grasslands (*Sesleria pichiana* – *Laserpitium siler* community = SPLScom, *Brachypodium rupestre* – *Festuca laevigata* community = BRFLcom). Thresholds are 95% quantiles from 100 null models (mean in black  $\pm$  sd in grey). Plot areas refers to important roles as [A]: Module-hub, [B]: Network-hub, [C]: Connector. Species labels are listed in Table 2.

tudinal systems may be relatively fragile, assuming that network stability is increased by nestedness (Burgos et al. 2007); and (b) few species cover key roles in the network ("hub") (Jordano et al. 2006). In fact, key species were detected in rather low numbers in our systems (Fig. 3).

*Relationships between hubs and species diversity*

Network nodes within a given module are made more connected by Module Hubs, which would be those ones shar-

ing most of the interactions with other species of the same module (Martín González et al. 2010). In turn, Connectors share many links among various modules, thus connecting several compartments of the network (Guimerà and Amaral 2005). Network Hubs maximize both the within-module and the among-module connectivity (Olesen et al. 2007). Therefore, a hierarchy of important species can take place: within-module level, between-modules level or entire-network level. Without a network approach, this is an aspect of community ecology that would be undetected.



**Figure 4.** PCA biplot of insects' among-module connectivity ( $c$ -) and the within-module participation ( $z$ -) values. A *post-hoc* correlation was performed with Links (= number of links per species),  $d$  (= specialization index  $d'$ ) and diversity (= Shannon diversity). Variable arrows point to the direction of increasing gradient (most rapid change of the variable), their size is proportional to the  $r^2$  of the correlation with the ordination for the *post-hoc* variables (with the ordination-axes for  $c$ - and  $z$ - values).

Our hubs are a rather diverse set of species from different families (Table 2). However, being-a-Hub is related to some species-level features. Specialization index  $d'$  appears to be more related with  $z$ - values rather than with  $c$ -values (Fig. 4). This highlights that Module Hubs tend to be less generalist than other Hub types, as some interactions occur only within modules. Instead, higher-level Hubs link among various modules, with the result that they are more generalist.

As  $z$ - and  $c$ - values were highly correlated with partner diversity and degree, hubs have a high number of partners and links. This matches other pollination networks, in which hubs interact with about half of the visiting species (Martín González et al. 2010). Moreover, higher partner diversity of a Hub has been related to wider resource/partner usage (Kaiser-Bunbury and Blüthgen 2015). This relates hubs to the classical stability view on species diversity, as wider resource usage decreases the need for specific resources to survive (Kaiser-Bunbury and Blüthgen 2015). Such diversity also relates to the functionality of the system and in fact when hubs are selectively removed, networks break down faster than removing random nodes (Albert et al. 2000, Jeong et al. 2001). So, empirical evidence clearly shows that Network Hubs provide stability to the entire system, with also moderate contribution of Connectors (Reis et al. 2014), while the loss of Module Hubs is likely to result in module fragmentation. Therefore, it is clear that the cohesiveness of the system is provided by such a hierarchy (Olesen et al. 2007).

#### Modules of interacting species

Instead of species tightly enclosed into modules, as commonly found (Olesen et al. 2007, Martín González et al. 2012, Larson et al. 2014) we obtained a more variable structure. The networks of our study showed an unorganized plethora of companion nodes, such as the species in non-significant modules, interacting with a well-structured core, the significant "Large-Apidae" and "Wide-Core" modules. Such a core would be consistent in time despite the year-to-year turnover of spe-

cies in the networks and its taxonomic composition also matches other temperate altitudinal systems (Fang and Huang 2012).

#### Why phenological units are useful

Within each plant community, we obtained independent networks that resulted from the detection of phenological units. Previously, network ecologists have typically overlooked the time component (but see Valverde et al. 2016), though more recent studies have divided the season into a-priori time periods of the same length (Basilio et al. 2006, Kaiser-Bunbury et al. 2010, Rasmussen et al. 2013). On one hand, the latter is a useful approach in order to shed light on the dynamics of systems across time. On the other hand, the risk of obscuring species' phenologies might take place and it might also affect the independency of each unit. Therefore, phenological units are useful to network analyses at least for three reasons. Firstly, such an approach is consistent with the phenology of species, as they have strong effects on interaction networks (Martín González et al. 2012, Valverde et al. 2016). Secondly, it might be useful to replicate networks in time instead of in space in order to obtain independent plant-pollinator networks from a low number of sites. Thirdly, applied to conservation, it allows one to monitor the entire season, and thus identify key species consistently with seasonal dynamics.

#### Conclusions

In this study, three insect species were shown to be important for the entire network by being Network Hubs: *Bombus rupestris* (Hymenoptera: Apidae), *Micrinus heteromorphus* (Coleoptera: Malachiidae) and *Eristalis tenax* (Diptera: Syrphidae). Moreover, four important taxa were also distinctive from a biogeographical perspective, being Alps endemics occurring out of the known range (the above mentioned Malachiidae) or South-European orophytes occurring only in specific sectors of the Alps and Apennines where



they are not present together (*Phyteuma ovatum*, *Phyteuma scorzonerifolium* and *Hypericum richeri*). They might be considered for conservation for their double role under both network and biogeographical perspectives, as also suggested by Paraskevopoulou et al. (2015) in benthic networks. Thus, some species, either common or regionally rare, might turn out to be important for the conservation of other species. Some of the identified hubs could need specific protection, perhaps according to their life histories or known threats (Corbet 2000, Kaiser-Bunbury and Blüthgen 2015).

As suggested by Corbet (2000), conserving networks would necessarily imply that we (a) identify the modules; (b) identify the hubs that sustain them; (c) assess their vulnerability. In these terms, previous work has successfully identified those invasive species that should be management priorities by sharing the interaction module with a rare native species of conservationist interest (Larson et al. 2014). Therefore, practitioners should consider species not only as mere lists but also view them within the framework of their interactions, and the work of Larson et al. (2014) provides a good example of its application and feasibility.

As we found that some modules are not reliable units, we also suggest that conservation of networks should not only focus on modules but should consider identifying the whole hierarchy of hubs (not only those of the modules).

Network analyses are useful for monitoring robustness and ecosystem functioning. Given the role played by phenology in the interactions, the entire season should be studied in order to cover the seasonal dynamics; in this work we showed how to deal with such a task, namely identifying reliable seasonal units. Moreover, it could also inform the conservation of habitats by helping the planning and scheduling of specific management actions. This may be particularly important when key plant or insect species are subjected to disturbance through inappropriate habitat management such as grazing and mowing at the wrong time (Tarrant et al. 2013).

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## Electronic supplement

**Table A1.** Main plant families of the two plant communities (*Sesleria pichiana* – *Laserpitium siler* community, *Brachypodium rupestre* – *Festuca laevigata* community).

**Table A2.** Pairwise statistics between modules each phenological unit (PC) for both grasslands.

**Figure A1.** Functional groups expressed as absolute percentage, plants referring to location of nectar in the corolla and insects referring to pseudo-taxonomic groups.

The file may be downloaded from [www.akademai.com](http://www.akademai.com).