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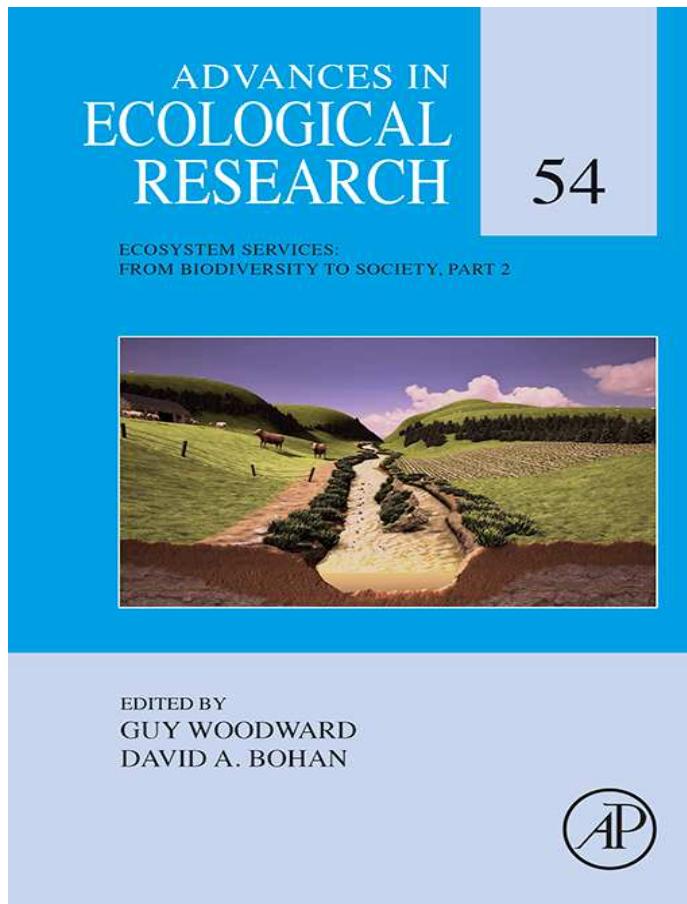
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The Visualisation of Ecological Networks, and Their Use as a Tool for Engagement, Advocacy and Management

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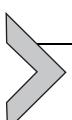
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Abstract

Ecological systems comprise of individuals and species interacting with each other and their environment, and these interactions combine to form complex networks. The maintenance of biodiversity and many ecosystem functions depend upon these ecological interactions. Humans, their crops and livestock can also be considered as part of these networks of interactions making network analysis valuable for considering the resilience of ecosystem services, i.e., the benefits we gain from nature. Networks are visually appealing and visualisation can attract attention and inform, both to communicate overall messages and provide comparisons between networks. There are many different approaches and layouts for visualising networks, but there is little research to help guide best practice. Ultimately though, best practice should be to ensure that messages are supported by evidence and clearly communicated with reference to the competence of the audience. Given the appeal of visualisations and the importance of networks in communicating the interdependence of species (including humans), ecological networks and their visualisation can be used to support excellent public engagement and can be used to enhance the value of citizen science, in which people actively contribute to scientific research. Network approaches could also be valuable for engagement with decision-makers and stakeholders, including their application to complex socio-economic systems, especially where co-production of network visualisations could provide evidence-based overviews of data. In summary, ecological networks and their visualisation are an important tool for scientific inquiry, communication and engagement with even greater potential than has currently been realised.



1. INTRODUCTION

We live in a time when nature is facing many threats; biodiversity is changing rapidly and many species are declining (Butchart et al., 2010; Loh et al., 2005). Many of the threats posed to nature are anthropogenic in origin and include direct threats, such as habitat loss or climate change, and indirect threats, such as the effects of over-exploitation cascading through ecosystems (Dirzo et al., 2014). The loss of populations and diversity should be a

concern in its own right because of the existence, or ‘intrinsic’, value of nature ([Secretariat of the Convention on Biological Diversity, 2001](#)), but in addition to this, there is increasing emphasis on the importance of nature for human existence and well-being ([Millennium Ecosystem Assessment, 2005](#)). Therefore, despite the fact that through industrialisation and urbanisation people are tending to be less personally engaged with nature ([Natural England, 2009](#); [Pergams and Zaradic, 2008](#)), people are benefitting from nature and ecosystems (e.g. in providing resources for development and economic growth), but also impacting upon them (due to the externalities arising from growth). In other words, humanity continues to be integrated in the networks of interactions between all other organisms.

A major challenge facing ecologists is effectively communicating the reliance of humanity on nature, so raising the importance of nature in public and political agendas, and thus influencing individuals and decision-makers ([Blackmore et al., 2013](#)). Ecological networks provide one potential powerful way to communicate these messages. Considering the interactions between entities (e.g. species or individual) helps to communicate the crux of ecology, i.e., the study of relationships of organisms with each other and their environment, and helps to demonstrate how humans, their crops and their livestock are integrated into the natural world ([Fig. 1B](#)). Here, we discuss the role of ecological networks and their visualisation as a tool for engagement through communication, citizen science (in which volunteers participate in the process of science; [Silvertown, 2009](#)) and evidence-based advocacy for decision-makers.

The idea that species exist in interrelationship with each other is not a new concept: Darwin iconically described an ‘entangled bank clothed with many plants of many kinds, with birds singing on the bushes, with various insects flitting about and with worms crawling through the damp earth’ ([Darwin, 1859](#)), and Charles Elton produced one of the first scientific visualisations of food webs ([Elton, 1927](#); [Fig. 1A](#)). Recently, the growth of multidisciplinary approaches in complexity science has made network analysis a powerful tool for research ([Newman, 2010](#)), and it has led to many important discoveries in ecological science (see [Section 2.1](#)). This has been supported by network visualisation, which is a valuable tool for data exploration and communication ([Fleischer and Hirsch, 2001](#)). Data visualisation, including visualisation of networks, makes use of the human visual system’s remarkable ability to efficiently and effectively interpret information, such as assessing patterns and identifying outliers. Therefore, data visualisation is increasingly being used by scientists as a tool for data

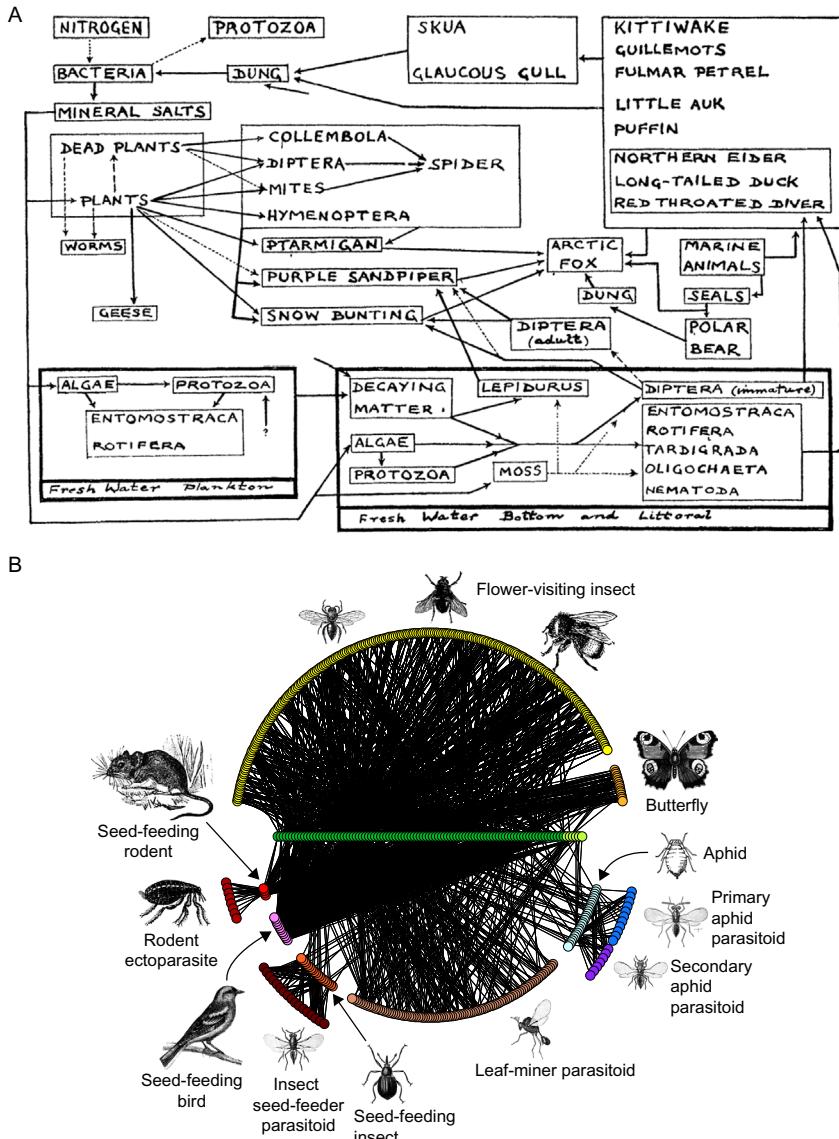


Figure 1 (A) An early scientific visualisation of a food web (described as a 'nitrogen cycle') reproduced from Elton (1927) and used with permission (© 1923 British Ecological Society). (B) A recent scientific visualisation of a network of ecological networks adapted from Pocock et al. (2012) and used with permission, showing how the crop plants (light green (light grey in the print version) circles) on which humans depend are part of a complex network of interactions including other plants (dark green (grey in the print version) circles) and many guilds of animals including potential ecosystem service providers such as flower-visiting insects (potential pollinators) and parasitoids (potential pest controllers), as well as many other species. The illustrations are used under licence from ClipartETC, see Bohan et al. (2013) for full acknowledgements.

exploration and communication (McInerney et al., 2014; Spiegelhalter et al., 2011; Tufte, 1983).

Here, we briefly review the importance of network approaches in ecology before exploring their visualisation and use as a communication tool. Specifically, we discuss the principles of data visualisation and how these need to be considered when selecting approaches and layouts to visualise networks. We then develop and consider this approach by examining the ways in which ecological networks (with varying degrees of complexity) have been used in public engagement and citizen science. Finally, we explore options for their use as a tool for engaging with decision-makers to inform policy and management.



2. BENEFITS OF A NETWORK APPROACH IN ECOLOGY

2.1 How Network Approaches Are Used in Ecology

No organism lives in isolation but exists within complex networks of interactions among species. Pairwise interactions, such as competition and predation, have long been known to have a key role in ecology and evolutionary biology (Proulx et al., 2005), but the increase in the availability of both biological data and analytical methods has led to a dramatic increase in focus on networks in ecology (Heleno et al., 2014). The network approach in ecology is a useful way of considering ecosystems and their function: it is a holistic, system-wide and yet tractable approach to assess and understand whole ecosystems. Using this, we can describe the interactions between ecological entities (e.g. individuals or species) and can assess the emergent properties of the whole system (e.g. its stability, resilience to perturbation, robustness to the loss of nodes or efficiency of energy transfer). This provides an important theoretical approach for considering the maintenance of biodiversity and the stability of ecosystems (Bascompte and Jordano, 2007; Bascompte et al., 2006; Dunne et al., 2002; Jordano et al., 2002; May, 1973; Thébaud and Fontaine, 2010).

A network is, at its most basic, a set of entities called ‘nodes’, with pairs of nodes joined by ‘links’, thus creating a complex ‘network’. In community ecology, nodes in the network are usually species but could be individuals, populations, age classes or species aggregates. The links that connect them represent interactions. The link used in food webs represents a trophic link (e.g. one species feeding on another), but many different types of links can be considered, including mutualisms (pollination and seed dispersal), spatial proximity, disease transmission, interspecific competition, fluxes of energy,

biomass or nutrients, gene flow due to dispersal and so on (Ings et al., 2009; Kéfi et al., 2012). The combination of all these links results in ‘emergent properties’ of the system, i.e., properties that cannot be predicted by consideration of components and links individually. Emergent properties such as the network’s connectance, degree distribution, nestedness or modularity will affect the system’s resilience to perturbation (Bascompte et al., 2006; Thébaud and Fontaine, 2010; Tylianakis et al., 2010). Therefore, with the recent interest in research in the relationship of biodiversity to ecosystem function (Naeem et al., 2009), so linking network structure to ecological function is an active area of research (Hines et al., 2015; Thompson et al., 2012; Truchy et al., 2015).

By using network approaches, ecologists can also profit from sophisticated algorithms and general network theory developed in mathematics, physics, social sciences and computer science (Albert et al., 2000; Blüthgen et al., 2006; Montoya et al., 2006; Newman, 2003). Insights from ecological networks have, in turn, informed inference from networks in other systems, e.g., banking and commerce (May et al., 2008; Saavedra et al., 2011). Also, because network science is so multidisciplinary and a common language is used across disciplines, it also means that network approaches can be applied across the spatio-temporal scales and levels of complexity of socio-ecological systems (Hines et al., 2015; Mulder et al., 2015; Palomo et al., 2016).

2.2 The Importance of Interactions

The loss of interactions has been described as the most ‘insidious kind of extinction’ (Janzen, 1974). One of the reasons for this is that the loss (or gain) of interactions can be drivers of change. Even at the level of an individual species, its specialism or generalism (i.e. the ‘degree’ of the node in network terminology, which is defined as the number of links to or from a node) influences its sensitivity to change (Fisher and Owens, 2004). More generally, it is via individual interactions that impacts cascade through ecosystems. Measures such as network robustness, or properties such as connectance, describe the vulnerability of networks to the loss of particular species, and the cascading effects and feedbacks that can occur. Often these predictions are done via computer modelling (Dunne et al., 2002; Ostfeld and LoGiudice, 2003; Solé and Montoya, 2001; Staniczenko et al., 2010; Vieira and Almeida-Neto, 2015), although cascading effects have sometimes been empirically observed (Grinath et al., 2015; Knight et al., 2005). Specific perturbations, e.g., climate change or invasion by an exotic species, may

spread much faster through complex networks than had previously been thought (Montoya et al., 2009; Woodward et al., 2010). In addition, the loss of particular interactions, e.g., through phenological mismatch, has the potential to cause population declines (Miller-Rushing et al., 2010). One of the corollaries of a focus on interactions is that ‘important’ species within the network can be determined (Jordán et al., 2006; Libralato et al., 2006). These species are often referred to as ‘keystones’, i.e., those species that, through their interactions, are predicted to have disproportionately high impact on other species (Power et al., 1996) or are particularly sensitive to perturbation (Saavedra et al., 2011). Identifying these keystone species can support the efficient targeting of conservation resources.

While changes in interactions can be drivers of change in ecosystems, the assessment of interactions can also be used as an indicator of change (Gray et al., 2014) or a predictor of forthcoming change, e.g., using network metrics as early warning of tipping points (Dakos and Bascompte, 2014). Of course, because many ecosystem functions arise from interactions, networks can efficiently reveal changes in ecosystem function which may not be revealed by considering species assemblages alone (e.g. Tylianakis et al., 2007).

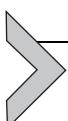
Ecosystem services are a particular type of ecosystem function with explicit value to humans (Millennium Ecosystem Assessment, 2005), and because many ecosystem functions are intrinsically linked to specific interactions, a network approach is useful for considering these ecosystem services (Losey and Vaughan, 2006). For example, insect pollination of crops is explicitly an interaction: a trophic interaction of the insect (usually) gaining a nectar or pollen reward and the mutualistic interaction of the plant benefitting by the transfer of pollen. Another example is the natural pest control of insects (a trophic interaction) by predatory insects or parasitoids. In both these examples, the benefit gained by the focal species can be placed in its wider context of the ‘supporting service’ provided by biodiversity by taking a network approach (Bohan et al., 2013; Memmott, 2009; Pocock et al., 2012). Overall, networks provide an ideal framework to explore the possible effects of global change and biodiversity loss on communities and ecosystems (Tylianakis et al., 2008), including the trade-offs between ecosystem services (Bennett et al., 2009; Bohan et al., 2013).

2.3 The Value of Network Visualisation for Researchers

Mathematical models, complex algorithms and statistical analysis are essential to fully understand the underlying complexity of a network (Bersier et al., 2002; Newman, 2003, 2004; Tylianakis et al., 2010).

However, these approaches can only provide a partial perspective at any instance in time: they allow researchers to address specific questions (e.g. ‘what is the level of connectance in this network?’ or ‘is this network nested?’). Complementing these analytical approaches is the use of visualisation as a tool for data exploration and hypothesis generation (Tukey, 1977). Visualisation benefits from the human brain’s incredible ability to assimilate visual information, to detect patterns and to detect outliers (Fig. 2). Visualisation also benefits from replacing calculations with ‘perceptual inference to improve comprehension, memory and decision making’ (McInerny et al., 2014), making it potentially effective in conveying information more effectively and efficiently than quantitative analysis and reporting alone (McInerny et al., 2014; Spiegelhalter et al., 2011). In order to use visualisations well, it is therefore necessary to consider the principles for data visualisation generally, and how they can be applied to network visualisation specifically.

In other words, visualisation is a powerful tool, but this means that for scientists, it should be treated carefully and handled with integrity (Spiegelhalter et al., 2011; Tufte, 1983). Here, we firstly discuss principles for data visualisation before going on to explore different methods for network visualisation. Later, we discuss how networks and their visualisation can be used as a tool for public engagement with science, for citizen science and for engagement with decision-makers.



3. VISUALISATION OF ECOLOGICAL NETWORKS: THE BALANCE OF SCIENTIFIC INTEGRITY, BEAUTY AND INTELLIGIBILITY

3.1 Principles of Data Visualisation

Thus far, we have discussed the ways in which ecological networks are an approach useful in providing a ‘whole systems’ perspective on ecology. The graphical presentation of networks is so inherently engaging and intuitively interpretable (at least at the level of illustrating nodes linked to other nodes) that visualisation is an essential aspect to any work with networks. There are many different ways of visualising networks, so it is pertinent to firstly review the principles of data visualisation before considering how these can be applied to networks.

Good, well-designed graphics are ‘far more effective than words’ at communicating messages from data (Tufte, 1983). Therefore, as computer

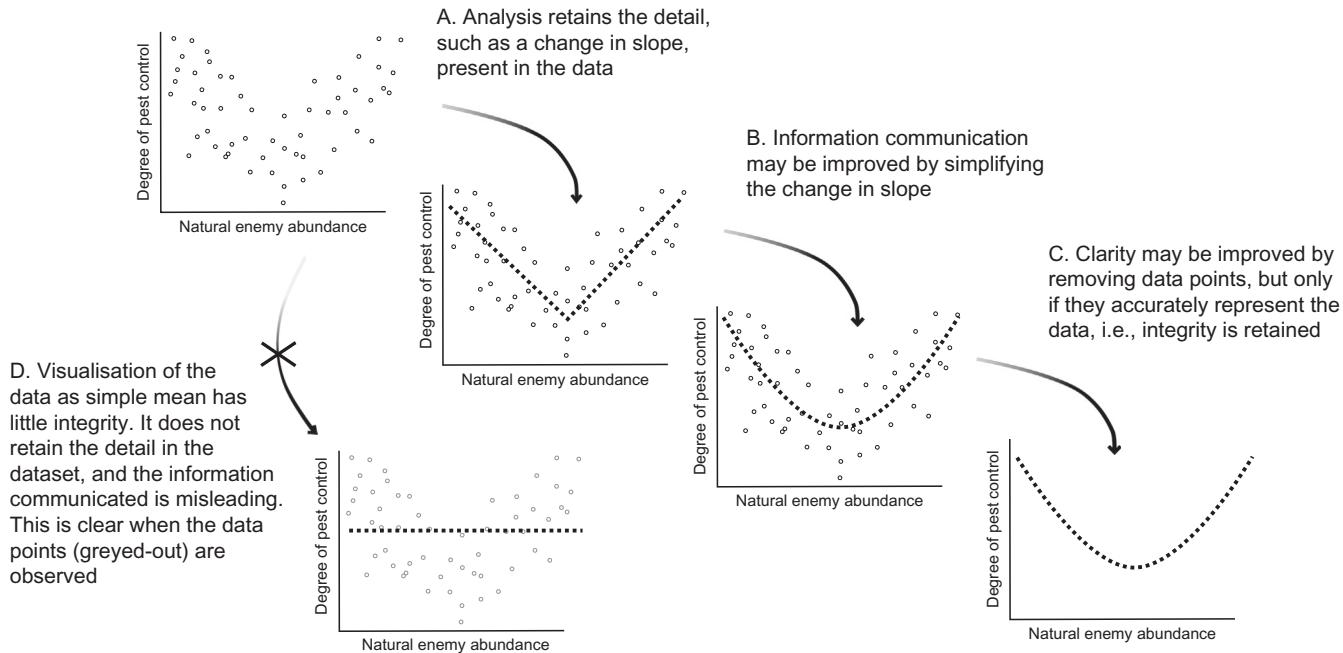


Figure 2 A simple schematic of a scatterplot visualisation to illustrate the process of producing visualisations which have graphical integrity. Given a dataset, such as that presented here for the relationship of rate of predation with natural enemy abundances, an analysis might suggest that the relationship would best be described using a segmented regression with a single breakpoint (A). (B) Researchers might decide that such a regression would be more simply represented as a single curve, losing details such as the slopes and position of the breakpoint. (C) This could be simplified further by presenting only a trend line. However, presenting both the data and the trend line allows misleading messages from data (D) to be identified.

programmes have made creating graphics increasingly straightforward, so visualisations have been used more frequently, such as in the use of ‘graphical abstracts’ of scientific papers and the use of ‘infographics’ by data journalists. Accompanying this has been increasing emphasis on best practice in data visualisation, as demonstrated by the series of articles published in *Nature Methods* (Kjærgaard, 2015). Presenting aesthetically appealing graphics is a very effective way of grabbing an audience’s attention. However, scientific visualisations go beyond graphically, or artistically, portraying information: good visualisations can be used to inform, persuade and convince (Spiegelhalter et al., 2011; Wong, 2012). Data visualisation is very suitable for highly complex datasets (such as networks) and ideal for data exploration by scientists (Wong, 2012).

Creating good visualisations is about achieving a balance between clarity (e.g. removing extraneous information to permit inference from the data) and complexity (i.e. providing sufficient information to support detailed interpretation). By relying upon the ‘human visual system’s highly tuned ability to see patterns, spot trends and identify outliers’ (McInerny et al., 2014), good visualisations can communicate ‘several levels of detail [in a dataset] from a broad overview to the fine structure’ (Tufte, 1983). To give an example: a scatterplot with a line of best fit communicates both simple messages and the intricate detail about relationships between variables (Fig. 2A and B). Numerical description of the same dataset cannot communicate this so succinctly.

As graphical visualisation of data has become increasingly important in scientific communication, there has been increased research in the principles supporting good data visualisation and more sharing of good practice: from the adoption of good design principles (Evanko, 2013; McInerny et al., 2014; Spiegelhalter et al., 2011; Tufte, 1983; Wong, 2012) through to recommendations of colour palettes to use (Borland and Taylor, 2007; Brewer, 2015; Wong, 2010). Producing excellent visualisations requires artistic skill, but it also depends on quantitative, statistical skills so that the visualisation tells the truth (Tufte, 1983). In other words, it is absolutely essential for the creator to demonstrate ‘graphical integrity’ (Tufte, 1983) by showing the data honestly and avoiding the distortion of messages from the data. Therefore, good visualisations with high levels of beauty enable meanings of the data to be communicated more efficiently than via textual description and are aesthetically appealing. Poor visualisations, on the other hand, could mis-represent the data, be visually unappealing or, at worst, do both.

3.2 Applying Visualisation Principles to Networks

Network visualisations can be made to be very visually appealing. This is very clear with the growing interest in beautiful visualisations of networks produced and reproduced for mass public interest, showing how people interact via social media, computer servers are linked in the internet, genes interact in cells and so on (e.g. Börner, 2015; Lima, 2011). However, the audience is not restricted to the general public, and even in the relatively modest environment of peer-reviewed scientific publications, a network visualisation is often the pre-eminent figure within papers reporting the results of studies of empirical networks (Fig. 1B; Albrecht et al., 2014; Pocock et al., 2012; Toju et al., 2014; Wirta et al., 2014 and so on), presumably because it helps to disseminate the research to a wider audience and so generates further impact for the research.

It is helpful to consider approaches to network visualisation according to two interrelated concepts of aesthetic appeal and information content (Fig. 3). Aesthetic appeal is what makes a particular visualisation ‘attention-grabbing’. High aesthetic appeal will result both from the form of visualisation being applied, but also in the way in which the visualisation is created, drawing on the artistic and design skills of the communicator. While artistic skill will vary between people, applying data visualisation principles and best practice should help people to create good quality, eye-catching visualisations. The ‘information content’ is what we define as the ability for the observer draw inference about the information quickly and correctly (McGrath et al., 1996; Tufte, 1983). This information could be a broad message or information about the detail of the data. This concept is context specific because it depends on the message being communicated and the

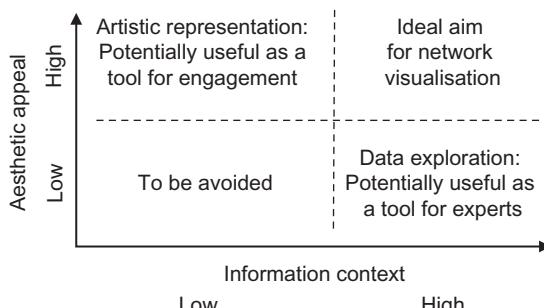


Figure 3 A simple schematic to represent the different approaches to visualising networks showing how aesthetic appeal and information content need to be considered with respect to the aim of the communicator and the audience.

aptitude and experience of the audience. High information content is therefore (at its best) a combination of clarity (of an overall message or pattern) and intricacy.

Visualisations with high aesthetic appeal are suitable for use to engage audiences, whether they are comprised of the general public, stakeholders or other scientists. In some cases, it may be appropriate to use network visualisations with lower information content to communicate a very simple overall message, such as the sheer complexity of a system. Visualisations with high information content are suitable as a scientific tool for data exploration, pattern detection and outlier detection; they may be useful and appropriate to use even if they have relatively low aesthetic appeal, i.e., are not immediately attention-grabbing. We suggest that the aspiration for network scientists should be to create network visualisations which are both aesthetically appealing and have high information content. For particularly important visualisations (e.g. those which support decision making or are for informing decision-makers; see [Section 6](#)), it is valuable to create visualisations in collaboration with skilled designers and the intended audience ([Börner et al., 2007](#); [McInerny et al., 2014](#)).

Ultimately, it is essential to be clear about the aims of the visualisation. We suggest that there are three broad reasons for visualising networks. The first aim is to graphically summarise a dataset. To put it bluntly, it is a way for scientists to visually boast about the size of the dataset and its complexity! This appears to have been one of the primary reasons for visualising networks to date. The main requirement for these visualisations is to be appealing and attention grabbing. The second aim is to communicate a specific message about the network either to the researcher (using the visualisation for data exploration) or to a wider audience. In these cases, it is necessary to choose a graphical layout which supports the clarity of this communication (see [Section 3.3](#)). The third aim is comparative: to use visualisation to communicate differences or changes in networks: this could be observed changes over time or space, or predicted changes in response to a particular perturbation.

3.3 Approaches for Visualising Networks

The reason for emphasising principles of network visualisation is that there are many different approaches to visualising networks: to give an example of this a range of approaches illustrating the same dataset are shown in [Fig. 4](#). There have been some attempts to create classifications of network visualisations ([Börner, 2015](#); [Lima, 2011](#)) and to understand how the layout

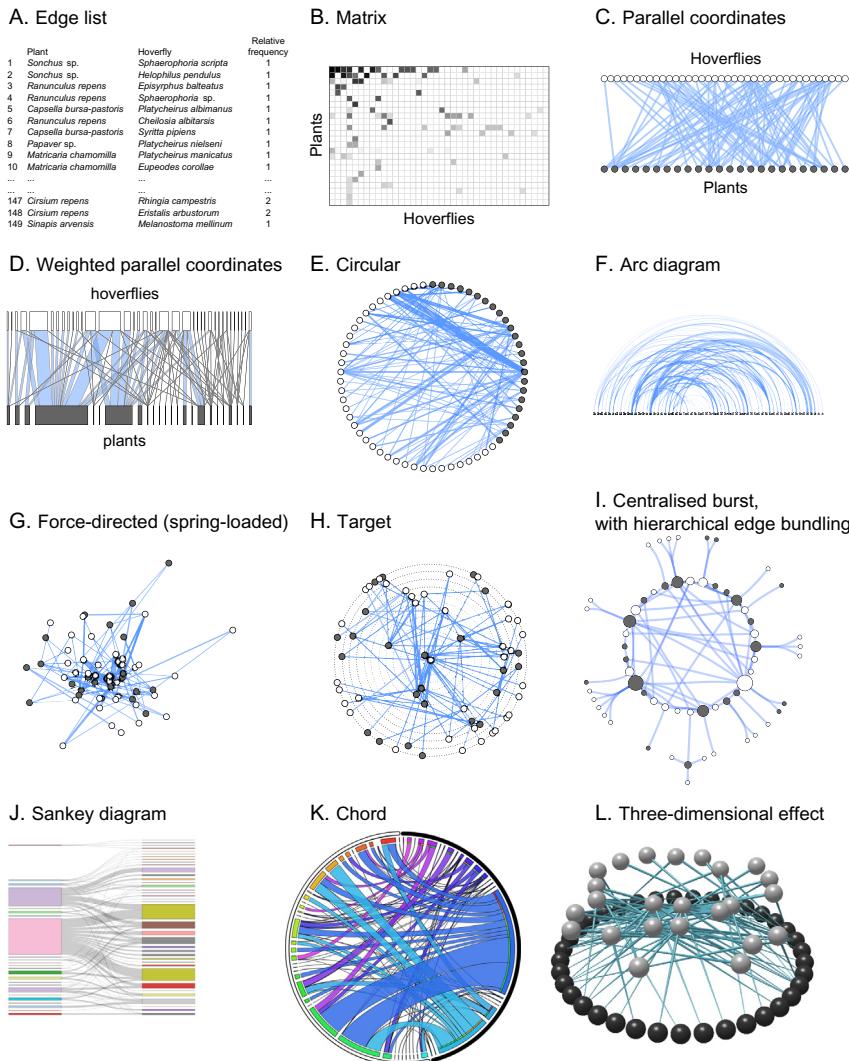


Figure 4 A range of network visualisation approaches all illustrating exactly the same network, namely, the subnetwork of hoverflies visiting flowers from Pocock et al. (2012). Of course, there is no 'correct' way of illustrating these data, so these illustrations represent a range of different visualisation approaches. The two basic forms of storing network information are the (A) edge list and (B) matrix. (B) Here, the rows and columns ordered to demonstrate nestedness and cells are shaded by relative frequency of the interactions. This bipartite network can be simply shown in a parallel coordinates plot (C) or its weighted equivalent (D). Nodes can be constrained in other ways, such as circular arrangements joined with straight lines (E) or linear arrangements joined with arced lines (F), or other combinations. Algorithms, such as the spring-loaded algorithm, can be used to optimise the position of nodes according to specific graph aesthetics (G).

(Continued)

influences the interpretability of the network (Huang and Eades, 2005; Purchase, 2000; Ware et al., 2002), but the development of visualisation approaches continues to be a rapidly developing field (Beck et al., 2014; Gibson et al., 2012; Pienta et al., 2015; Wilkinson, 2008).

In most cases, networks are visualised with nodes as polygons (typically circles or rectangles) and links as connecting lines (the major exception to this being the matrix representation of networks in which nodes are rows and columns, and links are intersecting cells; Fig. 4B). The layouts in Fig. 4 differ in the way that nodes and links are visualised. The position of nodes may be constrained to be placed as points or arcs in a circle or concentric rings, or points or rectangles on lines; they may be freely placed in two-dimensional space according to an algorithm or they may be laid over geospatial maps. As well as spatial position, other continuously varying or discrete attributes of the node can be communicated by size, shading or colour. These attributes include intrinsic traits of the node, e.g., trophic level, taxonomic identity or abundance, as well as those which are network specific, e.g., the number of links it has (i.e. the node degree). Similarly, links between nodes can communicate information via width, shading or colour, and they may be straight or curved. The choice of the specific layout and its attributes can be important in affecting the aesthetic appeal and the information content of visualisation, i.e., its ability for the visualisation to be interpreted accurately. As Fleischer and Hirsch (2001) describe: ‘graph [i.e. network] drawing is not a single well-defined problem, but an art, namely, the art of describing what a nice drawing of a graph means in the context of a particular application’.

One of the popular approaches of visualising networks is the use of algorithms, especially for the force-directed family of layouts (e.g. Fig. 4G; Gibson et al., 2012), such as those based on repulsion (Fruchterman and Reingold, 1991) or spring embedding (Kamada and Kawai, 1989). These algorithms have been optimised in different ways to meet particular criteria of speed or efficiency. Algorithms are designed according to specific ‘graph aesthetic criteria’, e.g., minimising the proportion of non-crossing links or

Figure 4—Cont'd In this target plot (H), the nodes are placed in concentric circles depending on their degree (higher degree nodes being placed towards the centre), whereas in the centralised burst plot (I), nodes are placed in circles so as to emphasise the nestedness of the network, and this is further emphasised by the use of edge bundling. Other more visually complex plots can also be produced including the ‘Sankey’ diagram which, here, is a snapshot of an interactive graphic (J), a chord plot with links coloured by the node (K) and a three-dimensional ball-and-stick plot (L).

maximising its symmetry (Gibson et al., 2012; Huang et al., 2013; Purchase, 2000). Even the examples in Fig. 4 where node position is partly constrained, e.g., in parallel coordinate or target plots, graph aesthetic criteria such as minimising line crossing can be applied (as in Fig. 4D, H and I; Dormann et al., 2009).

As well as contributing to the visual appeal, these graph aesthetics influence the interpretability of the graph, which for a given situation and audience is what we describe as its ‘information content’ (Fig. 3). This has been an active area of research (Fleischer and Hirsch, 2001; Gibson et al., 2012; Huang, 2007; Huang et al., 2013; Purchase, 2000; Ware et al., 2002) including using eye-tracking technology (Huang and Eades, 2005). Thus far, research has focussed on relatively small networks and metrics which can be verified by hand, such as shortest paths between pairs of nodes. We contend that it is much harder to accurately describe network-level properties from visualisations of larger networks (Newman, 2003). Therefore, researchers need good, evidence-based information (which is currently lacking) on how to draw networks to communicate different properties. The choice of the layout approach and its attributes is important because no approach is free from bias in terms of the information communicated: there is no fixed *a priori* idea of what is a good, or even ‘optimal’ layout (Fleischer and Hirsch, 2001), because it depends on the message being communicated. Of course, the information in the network is itself multivariate and can be summarised in many different ways (Kaiser-Bunbury and Blüthgen, 2015; Tylianakis et al., 2010). Within a single visualisation approach, the appearance of the network can vary dramatically depending on attributes of the layout (Fig. 5A–C). We recommend that researchers explore how different layouts and algorithms appear to communicate different messages and which appear to best match the evidence-based messages sought to be communicated. Throughout this process, it is important to continue to have ‘graphical integrity’ (Tufte, 1983) by having a quantitative evidence base for the message being communicated.

Increasingly elaborate and complex (and hence comprehensive) visualisations can make patterns difficult to see (Gramazio et al., 2014). In many cases, networks are drawn to illustrate every node and link. Incidentally, one of the beneficial aspects of network visualisations is that many of them are scalable, so that similar approaches and issues are relevant whether there are a dozen, a thousand or millions of nodes and links, e.g., Colomer-de-Simón et al. (2013), and also Albert et al. (2000) compared to Tu (2000). However, sometimes aggregating nodes or edges can support more effective communication, especially for very large networks (Börner et al., 2007), for

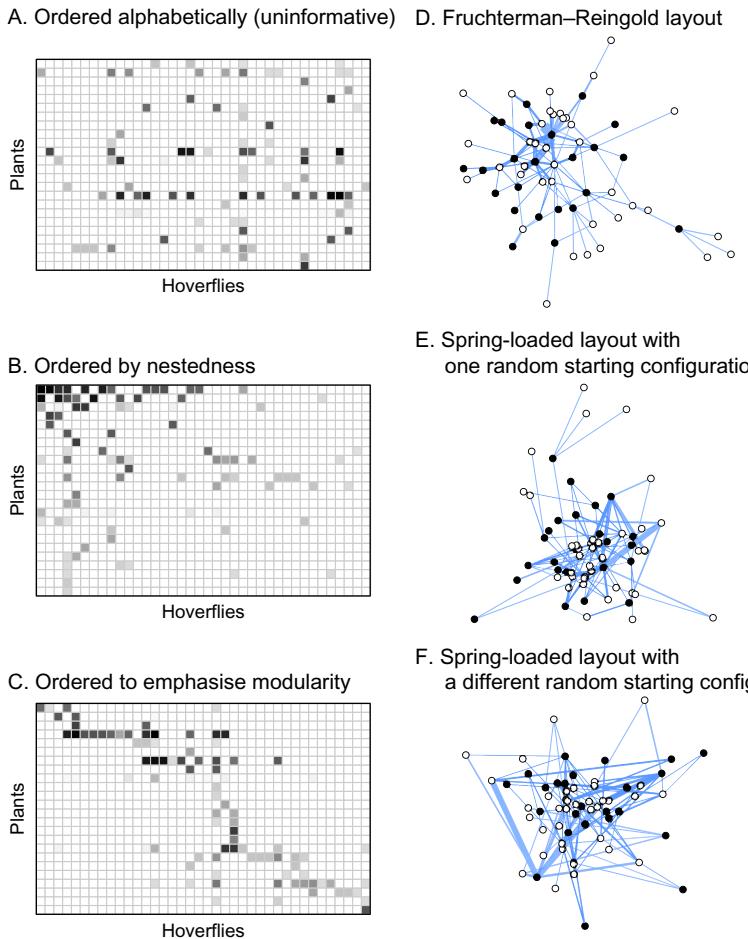


Figure 5 Network visualisation approaches can also be affected by the attributes of the specific visualisation. Here, the same network data as that illustrated in Fig. 4 can be visualised in different ways to emphasise different properties, such as nestedness and modularity (A–C). There is no single ‘correct’ way to visualise these networks, but networks could (in theory) be drawn in such a way that they communicate messages which are not supported by analysis of these data. This mis-communication could be unintentional, but the creator of the visualisation needs to demonstrate ‘graphic integrity’ to ensure that the message communicated through the visualisation is supported by the data themselves. Differences between (D) and (E) are due to the algorithm used to draw the layout, whereas differences between (E) and (F) are entirely due to the different random starting configurations.

example, [Olesen et al. \(2007\)](#) aggregated nodes at the level of the ‘module’ to show between-module relationships more clearly. Hierarchical edge bundling ([Fig. 4I](#)) is a popular way of aggregating edges to make clearer overall patterns in the network ([Holten, 2006; Pienta et al., 2015](#)). Also, the principle of ‘small multiples’ can be used, i.e., separating out patterns of interest ([McInerny and Krzywinski, 2015](#)), for example, highlighting subnetworks (called ego networks) around a focal node within the whole network ([Pienta et al., 2015](#)).

Recent criticism has suggested that some visualisation approaches have low information content, e.g., describing force-directed diagrams ([Figs. 4G and 5D–F](#)) disparagingly as ‘hairballs’ because it is argued that they are so hard to interpret effectively ([Krzywinski et al., 2012](#)). Some approaches can also hide or obscure information that may be of interest, e.g., at the centre of a force-directed layout ([Fig. 4G](#)) or at the back of a three-dimensional representation of a network ([Fig. 4L](#)). The appearance of visualisations is sometimes very sensitive to particular conditions. For instance, the final version of some force-directed layouts depends upon the random starting conditions ([Fig. 5E and F](#)). More importantly, the layout is often highly sensitive to the network structure, i.e., removing nodes or links can result in a very different configuration of the layout, making comparisons across networks impossible ([Bender-deMoll and McFarland, 2006](#)). Therefore, there has been recent development in approaches to support the comparison of networks, for example, with tools such as Circos ([Krzywinski et al., 2009](#); as applied in [Patel et al., 2015](#)), hive plots ([Krzywinski et al., 2012](#)) or user defined layouts ([Evans et al., 2013](#)). In these cases, the layout of the network, in particular the position of the nodes, is constrained and so both repeatable and consistent, making network visualisations comparable ([Fig. 6](#)). Hive plots, in particular, are very flexible, so the axes and the position of nodes on axes can be decided by the user ([Fig. 6C](#)); this means that they do require the viewer to be familiar with the approach to gain the most information from the visualisation ([Krzywinski et al., 2012](#)).

3.4 Tools for Drawing Networks

Thus far, we have considered the diversity of network visualisations and the principles for visualising networks. We have focussed on principles to avoid being constrained by the availability of user-friendly software. However,

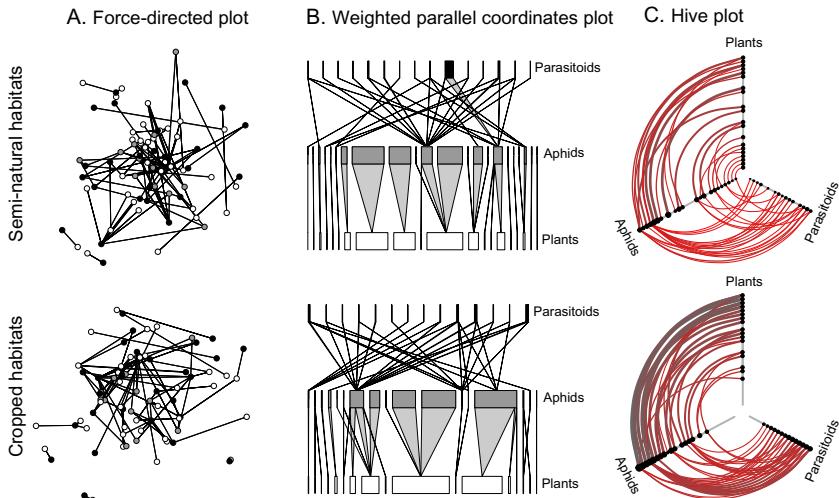


Figure 6 Some visualisation approaches are better than others at honestly communicating differences between networks. Here, we compare the plant–aphid–parasitoid networks from cropped and non-cropped land on a single farm (Evans et al., 2013; Pocock et al., 2012). (A) Force-directed networks do not allow direct comparisons to be made between these networks. (B) Weighted parallel coordinate plots allow some higher-level properties to be communicated such as changes in species richness and diversity. (C) Hive plots, with consistent positions of nodes, permit even more objective comparisons between the networks. The position of species is the same in the two hive plots; they are ordered by the rank of weighted degree in the combined network.

there are many different algorithms (Bender-deMoll and McFarland, 2006) and programmes (Gibson et al., 2012; Mehlan et al., 2013) available to support network visualisation. Many network ecologists use R (R Core Team, 2015) as a statistical and visualisation tool and several packages are available for network visualisation, notably: bipartite (Dormann et al., 2008), cheddar (Hudson et al., 2013), igraph (Csardi and Nepusz, 2006) and sna (Butts, 2014), and new packages are regularly released. Standalone packages such as Pajek (Batagelj and Mrvar, 2002), Gephi (Bastian et al., 2009), Cytoscape (Shannon, 2003), UCINET (Borgatti et al., 2002), SocNetV (Kalamaras, 2015) and GraphViz (Gansner and North, 2000) also provide graphical capabilities. Data-driven documents (D3) appear to be a growing approach for creating interactive data visualisations (Bostock et al., 2011). Although D3 is a programming language, and hence is a steep learning curve for ecologists used to R, some of the approaches are available in R via the networkD3 package (Gandrud et al., 2015).

3.5 Interactivity and Animation

So far, we have mostly focussed on two-dimensional, static visualisations of networks, but interactivity is an important aspect to visualisation (McInerny et al., 2014). Although this requires expertise, the creation of interactive network visualisations is increasingly accessible to many researchers using tools such as D3 (Bostock et al., 2011) or the ‘shiny’ package in the statistical program R (Chang et al., 2015). There are different ways in which network visualisations can be made interactive (reviewed by Pienta et al., 2015): they can allow users to access additional information, e.g., to obtain detailed attributes of user-selected nodes or links; they can allow users to sort and query the data, e.g., selecting subsets of the data or selecting the layout for visualising the network and they can allow users to visually query the data, e.g., by highlighting links from a node of interest. Interactivity can be combined with animation when users can select and drag nodes, seeing how the remainder of the network is dragged along (e.g. according to a force-directed algorithm) to follow the displaced node, which approximates to understanding the impact of perturbation of a selected node. This interactivity, especially combined with animation, makes the experience of assessing the data much more engaging, and so is likely to make it more memorable and a more powerful method of communication.

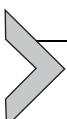
One strikingly good example of interactivity is CollaborationViz in which a static two-dimensional discussion of the results (in this case of analysis of a network of collaborations between biomedical researchers) was published in a peer-reviewed journal, with code and data openly available via a repository (Bian et al., 2014). Created in parallel to this is an animated, interactive visualisation of these data and analyses (<http://bianjiang.github.io/rcna/>). Other non-network examples include Gapminder World which is an interactive, animated data visualisation about global economics (<http://www.gapminder.org/world/>), People-Movin which provides a simpler interactive visualisation and is about human migration (<http://www.peoplemov.in>) and OneZoom which provides an interactive exploration of the tree of life, linking to databases of species traits and distributions (<http://www.onezoom.org/>). Using interactivity in this way is information-rich and engaging for audiences, although providing too much information could have the counter effect. Overall, interactivity appears to be a valuable approach for consideration in network visualisation.

3.6 Recommendations for Network Visualisation

Based on the assessment and discussion above, we therefore make recommendations about creating network visualisations.

- Be clear about the aim of the communication; is its primary purpose to be attention-grabbing or to communicate something more informative?
- Can you achieve the ideal of being both beautiful and informative?
- Aspire to make visualisations informative as well as illustrative: additional important attributes can often be included as variation in node or edge colour, size, shape or position, as long as this does not detract from the overall message.
- Provide full information about the creation of the visualisation. Defaults in programmes and automatic algorithms are not bias free, so state the detail used to construct the graphic, either by saving the script file or documenting programme options. (E.g. target and centralised burst plots look superficially similar but communicate very different messages about the data.) This will enable informed researchers to (1) replicate your visualisation and (2) interpret it in the light of potential biases of the approach used.

We have examined the importance of networks in ecology, the diverse ways in which they can be visualised, and the value of this as a tool for communication and engagement. Next, we discuss three areas in which such communication is valuable: public engagement, citizen science and in supporting decision-making.



4. ECOLOGICAL NETWORKS AS A TOOL FOR EFFECTIVE PUBLIC ENGAGEMENT

Public engagement with science and science communication are important activities supporting increased scientific literacy and democratisation of science (Bowater and Yeoman, 2013). In conservation science and ecology, communication is especially important because of the impetus of global threats to biodiversity and ecosystem services, but engagement with nature also impacts positively on individuals (Bowler et al., 2010). Arguably, one of the key messages that needs to be communicated to the general public is that people are part of the natural environment, not separated from it (Millennium Ecosystem Assessment, 2005). This naturally leads on to describing interdependence of species in food webs; an important concept used in science education (Hui, 2012). One way in which this has been illustrated is by drawing an analogy to the game of

'jenga' ([de Ruiter et al., 2005](#)) in which wooden blocks are balanced on top of each other to create a tower and players take turns to remove blocks. By removing enough blocks, the tower becomes precariously balanced and removal of one further block causes collapse of the tower; this is similar to the concept of 'robustness' in ecological network analysis ([Dunne et al., 2002](#)). Powerful though this description is as an analogy, two of the authors (M.J.O.P. and D.M.E.) developed this into a physical game in the Our Web of Life public engagement project. In this game, different animals and plants were drawn on the blocks, and the blocks were built into a tower, on top of which a doll was balanced. Playing the game involved removing the blocks one by one, to represent local species' extinctions, until the tower of blocks crashed down and the doll fell on the ground, to represent the way people could suffer from the loss of biodiversity ([Fig. 7A](#)). This game has been taken and played in many different locations, including a city centre shopping centre, the UK Houses of Parliament, school assemblies and science festivals. The message from the game is intuitive to the vast majority of audiences, and so this supports public engagement with science and the environment.

Of course, the analogy of a doll sitting on the tower built from animals and plants is partly flawed: people are an integral part of the environment with positive and negative impacts on the environment and nature, as well as gaining benefits from nature. Therefore, this game was accompanied by a poster display illustrating how people are an integral part of the environment

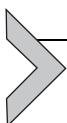


Figure 7 Examples of using network approaches in public engagement activities. (A) The game of 'biodiversity jenga' with accompanying display in the background; run here in a shopping centre in Bristol, UK as part of the 'Our Web of Life' science engagement project in 2010. (B) The plant–pollinator network puzzle; run here in a shopping centre in Didcot, UK as part of the 'Game Changer for Wildlife' science engagement project in 2015. Photo credits: (A) Dane Comerford and (B) Michael Pocock.

with the headline: ‘nature relies on us and we rely on nature’ (Fig. 7A). The visualisation of the simplified network was a way of effectively communicating the message that (i) people are not independent from nature, and (ii) nature itself is a complex network of interactions, so (iii) cascading effects could have unexpected indirect impacts, including on humans.

In another project, one of the authors (M.J.O.P.) developed a related activity in which puzzles were created from empirically observed plant–pollinator networks (Pocock, unpublished data). The network could be simplified to three types of flower species: one type were visited only by flies, another were only visited by bees, butterflies and day-flying moths, and the third type of flower species were visited by any of the insects (Fig. 7B). Players of the game at public events tried to recreate the complete network. This demonstrates, in a hands-on way, that pairwise interactions can be combined to create highly complex networks of interactions, thereby communicating the complexity of these plant–pollinator networks. Also, species could be removed one-by-one from the completed puzzle to predict cascading co-extinctions, which visually replicates the analysis of network ‘robustness’ for plant–pollinator networks (Memmott et al., 2004).

Finally, visualisation has been important in engaging people in a different aspect of network science, namely, disease transmission networks. A number of computer programmes have been produced which allow users to understand how disease spreads through contact networks, and some of these are presented as online games which give users the opportunity to implement various control strategies to see if they can eradicate the disease, e.g., the game Vax! (<http://vax.herokuapp.com/>). Similar online games allow participants to contribute to scientific knowledge, e.g., through problem solving (Cooper et al., 2010), and it would be fascinating to develop tools for engagement which also address relevant research questions about ecological networks.



5. ECOLOGICAL INTERACTIONS AND CITIZEN SCIENCE

5.1 Going Beyond Recording Species to Interactions

Citizen science is another way in which people can be engaged, by actively participating in the process of science (Pocock et al., 2015; Silvertown, 2009). Volunteer involvement through citizen science has a long history in ecology, and it allows records to be collected at large spatial extents over long time periods and at fine spatio-temporal resolutions, leading to excellent quality and important scientific research (Dickinson et al., 2010;

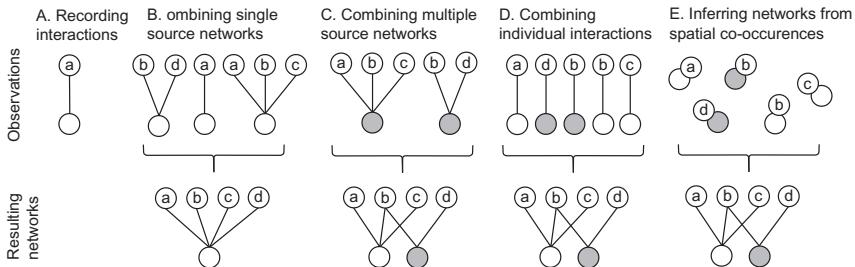


Figure 8 A representation of different ways in which citizen science data contributes to network construction.

(Hochachka et al., 2012; Miller-Rushing et al., 2012). Much citizen science in ecology has been about making records of species' occurrences. This is vital in understanding how species respond to environmental threats, such as habitat loss or climate change and has been well discussed elsewhere. Here, we explore the different approaches by which citizen science can combine with network approaches (Fig. 8).

The simplest approach is to make it explicit that an interaction is being recorded. For some taxa, host-associate interactions are entirely species specific, e.g., in gall-forming organisms or monophagous herbivorous insects, so that recording the feeding stage of the consumer implies the presence of the host (Stewart et al., 2015). Alternatively, the recording of disease (Bartel et al., 2011; Hochachka and Dhondt, 2000) is actually recording a disease-host interaction. Recording interactions can be made even more explicit, e.g., rearing parasitoids from leaf-mining insects (Pocock and Evans, 2014) or inviting people to record entomopathetic fungi on ladybirds (<http://www.brc.ac.uk/irecord/enter-Hesperiomyces-records>). However, although these examples go beyond recording species occurrences to recording interactions, they are not fully network approaches (Fig. 8A).

Another approach is recording species associated with a focal species (Fig. 8B). This approach has been particularly used in citizen science projects on pollinators, with standardised sampling at a single species of plants (e.g. a 'phytometer' or 'lure' plant), such as in the Great Sunflower Project (Oberhauser and LeBuhn, 2012). Although this can act as a way of using interactions for standardised monitoring of abundance or diversity, it does not lead to a fully networked approach.

5.2 Combining 'Source Webs' into Networks: Spipoll

Spipoll is a citizen science-based monitoring scheme of plant–pollinator interactions across France involving two of the authors (C.F. and R.J.).

Through the project people sample individual 'source webs' made of a plant and its flower visitors, by following a standardised protocol. Ultimately, these source webs can be combined to create flower-visitor networks (Fig. 9C). The first step of the protocol is to take pictures of every different insect visiting the flowers of a freely chosen plant over a specific time (at least 20 min). The second step is to identify each insect photographed to the level of a morphospecies, according to a reference classification of 630 animal taxa via a specifically designed computer aided identification tool (spipoll.snv.jussieu.fr/mkey/mkey-spipoll.html). The proposed morphospecies vary in their taxonomic resolutions since most French flower visitors cannot be identified at the species level from photos. Photographs of the plant and its flower visitors, identified to morphospecies, are uploaded to the project Website (www.spipoll.org) along with time and location of the sampling (Fig. 9A).

Since 2010, more than 16,050 source webs have been sampled by 1037 observers, representing a sampling effort of 9306 observation hours (Fig. 9B). These data can, with appropriate statistical methods, be used to investigate the response of flower-visitor richness, and to some extent composition, to environmental variables (Deguines et al., 2012). The results can then be visualised, e.g., to show how urban land-use affects the flower visitor richness of a specific plant (Fig. 9C). In this case, there was lower mean species richness in urbanised areas but also a change in composition to a higher probability of presence of honey bees and a lower average richness of syrphids in urbanised areas. The source webs can also be assembled to generate bipartite networks, illustrating the observed interactions averaged across large territories and through time (e.g. Fig. 9D). In addition to exemplifying the complexity of species interactions within ecological systems, such an approach paves the way for a macro-ecological perspective on species interactions and interaction networks, which is a recently emerging field in need of appropriate data (Violle et al., 2014).

In addition to enabling research in network ecology, citizen science projects like Spipoll link together a community of observers who increase their identification skills and engagement with nature. Although not easily quantifiable, such observers' empowerment might contribute to raising public awareness on pollination issues, as exemplified by these quotes from participants: 'j'essaye de véhiculer que quoiqu'il arrive, les plantes sauvages sont moins méchantes que les produits chimiques' ['I tell people that having wild plants is better than spraying them with chemicals'], or from a local mayor: 'on tente la gestion différenciée et le 0 phyto maintenant' ['we now undertake sympathetic management without use of herbicides'].

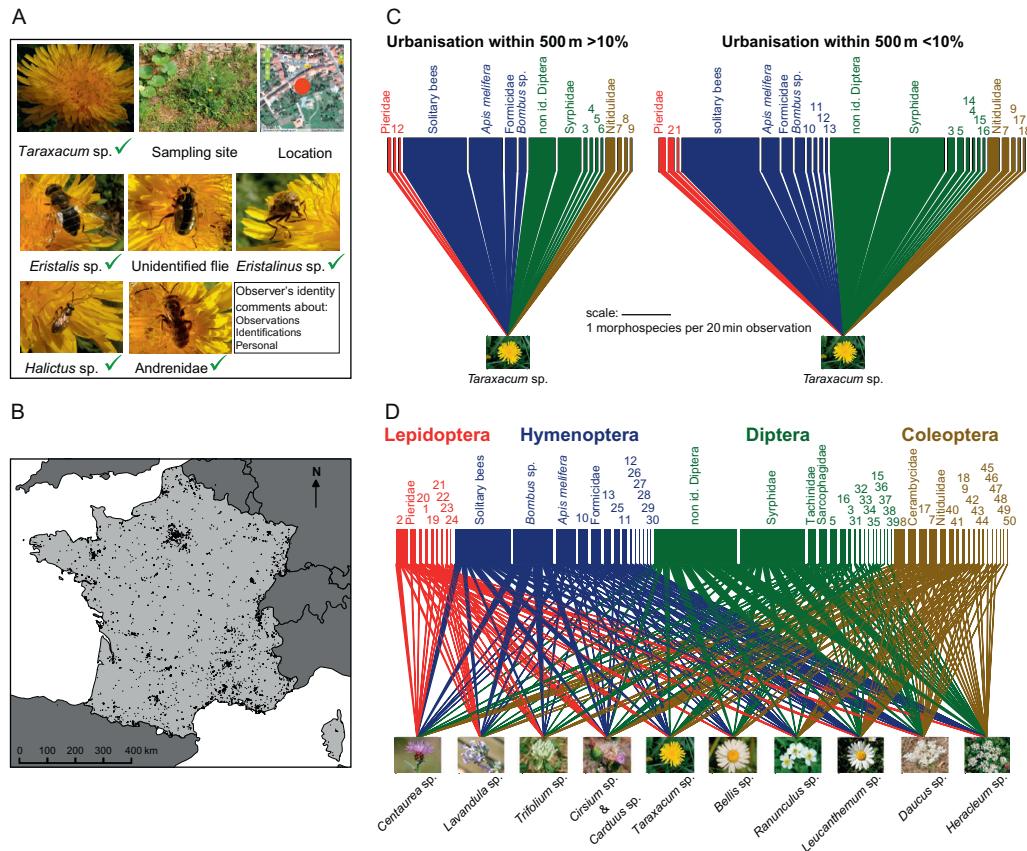


Figure 9 See legend on next page.

5.3 Combining Individual Interactions into Whole Networks: DBIF and iSpot

Although in the long history of wildlife recording most records are of species' occurrences (Pocock et al., 2015), there have been collections of records of interactions, especially trophic interactions of phytophagous insects. In the UK, these records have been collated in the Database of Insect Feeding interactions (DBIF; accessible at <http://www.brc.ac.uk/dbif/>) (Smith and Roy, 2008; Ward, 1988). Currently, DBIF contains about 47,000 interactions for over 9300 invertebrate taxa and 5700 plant taxa. In addition to this, recorders belonging to individual recording communities have also collected information on interactions, for example, in the UK: bee–flower interactions recorded by members of the Bees, Wasps and Ants Recording Society and collated in the species accounts in the published distribution atlases (Edwards and Roy, 2009), fungus–plant associations recorded through the British Mycological Society and available to view on their Website (<http://www.fieldmycology.net/FRDBI/assoc.asp>), and invertebrate–microhabitat associations, as recorded by woodlouse recorders (Harding and Sutton, 1985).

One particular scheme in which interactions can be recorded and visualised is iSpot (<http://www.ispotnature.org>), which involves two of the authors (M.H. and J.S.). iSpot is a social network that enables participants to share photographs of any kind of wildlife with an online community of naturalists who help each other identify what they have seen. The

Figure 9 (A) Content of a sampling unit of Spipoll, namely a plant associated with observed flower-visitors at a given place and time, and during a controlled sampling time. The observations are documented by one picture of the sampling site, one of the flower and one per observed flower-visitor morphospecies. The observer also provides a name for each of the observed taxa, according to a reference classification adapted for picture-based identification. Observations are then discussed among observers, and identification progressively validated and detailed by a combined involvement of observers and experts. The identifications with a green (grey in the print version) tick are validated. (B) Location of the about 16,050 Spipoll sampling points. At each site, represented by black dots, one source web has been monitored for 20 min or more (for detailed protocol, see Deguines et al., 2012). (C) Average species richness and composition for a 20 min observation session, represented as source webs linking *Taraxacum* sp. to its flower-visitors, for locations with more or less than 10% of urban land use in a 500 m buffer around the sampling points, respectively, left and right. These were assembled from the 308 sampling units of 20 min performed on *Taraxacum* sp. The width of the upper boxes is proportional to the observed average morphospecies richness of a given taxa. The same scale is used for both source webs. (D) Bipartite interaction network made from the merging of 10 source webs, from the most commonly sampled plant genus across France. See Appendix B for details and photo credits.

Website operates globally but has the largest number of participants in South Africa and in Great Britain. At the time of writing, 55,000 registered users have collectively submitted more than half a million observations of more than 30,000 taxa, the majority of which have been identified to the level of species (Silvertown et al., 2015). In 2013, iSpot introduced the facility to display and record ecological interactions and several thousand have been collated in the UK and South Africa since then (Fig. 10). Individuals who post photographs of a plant or insect species are shown images of those species known to interact with it. This was initially populated with information from DBIF and has been augmented by interactions recorded through iSpot.

The form that participants use to submit interaction data allows a limited set of interaction types in order to encourage people to describe what they had seen as objectively as possible. Thus, for example, it is possible to report that an insect A was seen visiting plant B but not that insect A was pollinating plant B, since the effectiveness of pollination cannot be directly witnessed from a flower visit alone. We show a comparison between the interactions reported from the UK and South Africa in Fig. 10. Although the iSpot community in South Africa is much smaller than the one in Britain, they were more active in recording interactions and the ecological networks formed by the species that were reported were also considerably more complex in South Africa (Fig. 11). Currently, the resulting networks are a small sample of the potential ecological interactions. However, already previously unrecorded interactions have been observed, for example, 10 of the observed interactions of leaf-miners with plants in the UK (28% of the total) were not present in DBIF, and 2 of these 10 had apparently not been previously documented anywhere (Charles Godfray, personal communication).

We anticipate that information about interactions collected by volunteers will continue to increase as this becomes easier for them to submit interactions. Also interactions are likely to be more diverse than species, for instance, one bee species seen 10 times only counts as one species, but it is likely to be visiting different flowers, equating to several different interactions. We suggest that this diversity could be motivating to volunteers to record interactions. As these data increase, they are likely to become as valuable a resource as information on species occurrences, and it will allow scientists to address important questions about the drivers and impacts of environmental change (Violle et al., 2014). This put the individual interaction from an observer in the bigger context of a network of interactions, and visualisation approaches will be important to support this research.

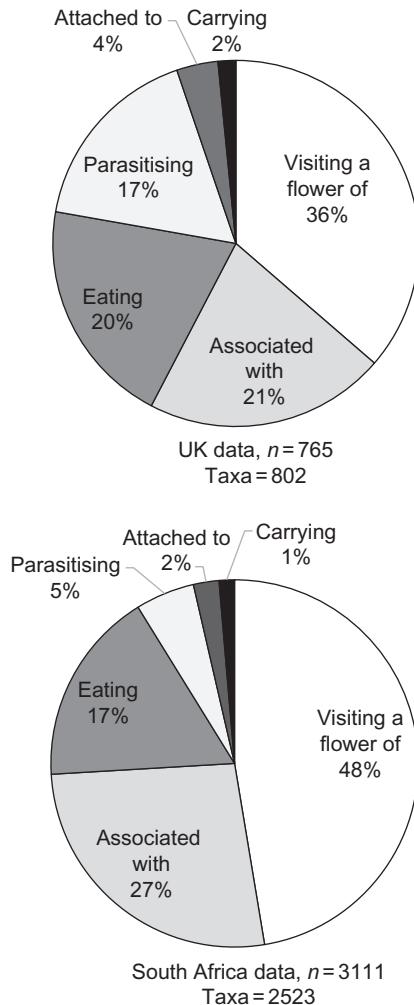


Figure 10 Summary of the interactions submitted to iSpot in the UK and South Africa since 2013, showing how flower visitors currently form the majority of reported interactions.

5.4 Inferring Networks from Abundance Data: Machine Learning Methods

Although we have emphasised ways in which participants in citizen science can record interactions, we are currently limited in many potential applications by the lack of data because the focus of many naturalists has, for a long time, been to record species occurrences (Pocock et al., 2015). However,

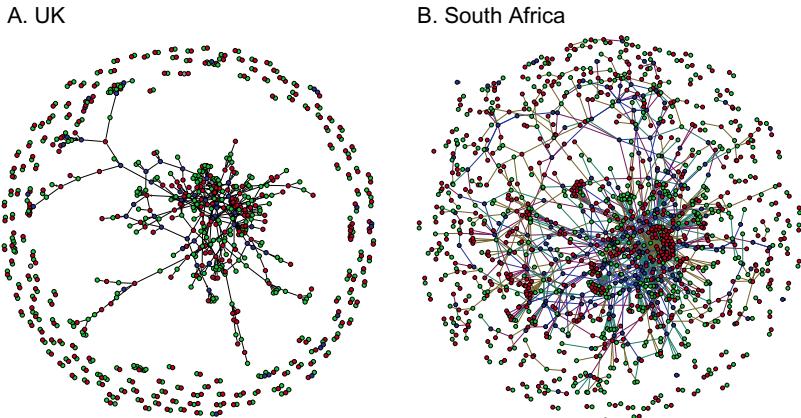


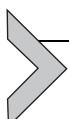
Figure 11 Associations between different species showing that as the number of reported interactions increase (here showing 765 interactions between 802 taxa in the UK vs. 3111 interactions between 2523 taxa in South Africa) the system changes from many isolated pairwise interactions to a well-connected network. Species are coloured by the status defined by the participant submitting the records and so do not necessarily have specific ecological meaning: 'interactors' are coloured green (light grey in the print version), 'interactees' are coloured red (grey in the print version) and those with both roles are coloured blue (grey in the print version).

species' co-occurrence can be used to infer interactions for the construction of networks, so adding value to the occurrence data already collected (Fig. 8E). Methods to infer network structure are considered in detail elsewhere (Faisal et al., 2010; Tamaddoni-Nezhad et al., 2012; Vacher et al., 2016); we briefly review them here because of their value for citizen science data.

One broad approach for inferring networks is statistical machine learning (reviewed and evaluated by Faisal et al., 2010). Bayesian networks are one method; they represent statistical dependencies between random variables (e.g. species and habitats) via the notion of conditional probabilities. Bayesian learning algorithms then use heuristic search methods to find a network configuration which best explains the observed data (e.g. co-occurrence or abundance). Bayesian networks have been used to reconstruct regulatory networks from gene expression data (e.g. Friedman et al., 2000) and species interactions from co-occurrence data (e.g. Aderhold et al., 2012; Milns et al., 2010). Gaussian Graphical Models are another statistical machine learning method. They can efficiently infer networks from large scale data but work on the assumption that the joint distribution of the data follows a multivariate Gaussian distribution; an assumption will usually not be met in ecological cases.

A second broad approach for inferring networks is logic-based machine learning, e.g., Inductive Logic Programming (ILP) (Muggleton, 1991). A key advantage of logic-based machine learning over the statistical methods is the possibility of integrating the existing knowledge into the learning process (e.g. general rules, such as predators being larger than prey). A form of ILP, called Abductive ILP, was used by Tamaddoni-Nezhad et al. (2013) and Bohan et al. (2011) to automatically generate species and functional food webs directly from ecological census data from 257 arable fields in the UK. Background knowledge on species size and functional groups informed the construction of a ‘logical model’ which was combined, via Abductive ILP, with observations of change in invertebrate numbers induced by management differences in the arable fields to generate a set of abductive hypotheses in the form of who ‘eats’ whom. In addition, probabilities can be assigned to hypothesised trophic links via Hypothesis Frequency Estimation (Tamaddoni-Nezhad et al., 2012). Text mining from the literature available on the internet can also be used to automatically corroborate, or reveal unexpected, hypotheses of trophic relationships (Tamaddoni-Nezhad et al., 2013).

As we have considered here, citizen science has great potential both to directly contribute to the collection of interaction data (Sections 5.2 and 5.3) and to permit networks to be constructed from occurrence data (Section 5.4). It is good to have these network data and to have people engaged (via participation in citizen science) with ideas of the importance of networks of interactions in species’ persistence, but the important final question we address is how ecological networks can be used to support action by stakeholders and decision-makers.



6. NETWORKS AS A TOOL FOR ENGAGEMENT WITH STAKEHOLDERS AND DECISION-MAKERS

We have discussed how network approaches can be useful when engaging with the public and when encouraging participation in research via citizen science. However, another important audience for engagement with research is stakeholders and decision-makers. Network approaches, and the accompanying network visualisations, may be potentially powerful tools for supporting engagement with decision-makers and in supporting transparency for decision-making and advocacy by stakeholders and policy-makers.

Policy-makers and practitioners need to make strategic decisions to managing ecosystems in the face of diverse demands and pressures. Their ability to do this partly depends on the quality and availability of information. One approach to do this is to reduce complexity, for example, through the use of indicators. This is an area in which ecological networks may be able to contribute to monitoring and evaluating the state of ecosystems, by simplifying the complexity of ecosystems into simple network metrics (Gray et al., 2014). This has been used in the ‘trophic level index’ to assess external pressures such as overfishing (Shannon et al., 2014). Despite this, it is important to recognise their limitations, and ecosystem-level models (and indices derived from them) are currently unlikely to be useful for providing numerical tactical advice on specific, applied policy questions, such as fisheries regulations (Heymans et al., 2014). Many indicators are retrospective, i.e., describing what has happened, but networks could be particularly useful (in theory, at least) in supporting the identification of indicators that are forward-looking, i.e., assessing ecosystem resilience (Spears et al., 2015; Truchy et al., 2015) or proximity to critical thresholds (Dakos and Bascompte, 2014).

Network approaches can also be used to better understand emergent properties and behaviour of whole systems, so providing an evidence base for decision-making. These approaches are increasingly being used as an approach to understand the causes and consequences of pollinator declines, i.e., explicitly recognising the importance of considering the whole system rather than just individual species, although the added-value of a network approach will vary according to the question and the system (Memmott, 2009). One example of this is the framework for considering the cascading effects of light pollution on moths and pollination (Macgregor et al., 2015). Another intriguing example is the application of ecological network approaches to the banking sector to explain its lack of resilience to perturbation (May et al., 2008).

Although the use of ecological networks by policy-makers in the environmental field has been limited, social networks have received a greater level of policy interest. Broadly, these are sectors where the policy interest is in social interactions among individuals and especially groups, and specifically relates to the flow of information between these groups. In this context, network analysis can provide insight to various actors and their relationships, and how they can exchange information to promote adaptation and find solutions to common challenges (Bharwani et al., 2013). Importantly, for policy-makers, it can help to identify critical points at which policy could be targeted for greatest impact. Social network analysis

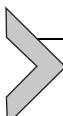
is valuable where interpersonal relationships are critical, as in relation to the exchange of evidence at the interface of research and policy. For example, there are many potential applications of social network analysis within the public health sector ([Luke and Harris, 2007](#)), even though its use at the policy level even in this sector is rare ([Shearer et al., 2014](#)). However, there could be scope for network analysis in informing the development of policies to reduce the risk of invasive pathogens through trade ([Hulme, 2009](#)), the disruption of illegal wildlife trade ([Patel et al., 2015](#)), or understanding the spread of various livestock diseases, although this has been analysis post-policy rather than to inform policy decisions (e.g. [Ortiz-Pelaez et al., 2006](#)).

It is recognised that policy decisions are taken in an increasingly complex policy environment ([Lindquist, 2011](#)), and ways of presenting evidence that can account for this complexity yet provide simple solutions are valued highly. In engaging with stakeholders, scientists need to balance simple summaries with detail, and visualisations are an effective way of achieving this (see [Fig. 2](#) and [Section 3.5](#)). Demonstrating its importance, the Australian government has a Policy Visualisation Network. This has been in place since 2012 and provides training for Government employees in visualisation techniques ([Department of Industry, 2012](#)). However, most Governments have not yet shown such commitment to the formal use of visualisation. As we have discussed in [Section 3](#), visualisation is especially valuable for networks, yet a scan of the visualisations available on a recent Website promoting visualisation in biological science ([BiVi, 2015](#)) suggests that only a very small proportion of visualisations in science relate to ecological networks, and the majority of these are for diseases.

To date, most visualisations and data-driven forms of communication have been tailored to specific stakeholder audiences and preferences, emphasising *a priori* particular disciplines, and levels of detail and information to communicate ([McInerny et al., 2014](#)). The danger of this community-specific approach to visualisation is that it can be exclusive, excluding some of the stakeholders. Our belief is that, in the future, visualisation could be used to provide a mechanism to solve problems through co-production of data visualisations, which should facilitate communication and discussion between stakeholder groups, especially for highly debated issues, where declarations and statements made by any one stakeholder group could be verified and critiqued by other stakeholders and the public. Guided by experts in visualisation and data, all stakeholders could work together to select visualisations that meet criteria for communication. Such a process for retaining integrity, by balancing beauty, detail and information ([Fig. 2](#)),

could yield visualisations that are interactive, both in terms of being directly query-able but also by incorporating models predicting ecosystem changes.

To date, there is little evidence that ecological network analysis has been instrumental in informing policy decisions, and despite its potential (e.g. discussed by [Tylianakis et al., 2010](#)), it remains at the fringe of scientific methodology that is applied to environmental management problems. Overall, though, we conclude that when engaging with policy-makers, (i) there is great potential for network approaches to be used to interpret data from complex socio-economic systems, and (ii) visualisation is a powerful tool to achieve this. With the growing expertise in network approaches and visualisation, we hope that these can be used in combination for more effective, evidence-based engagement with policy-makers and stakeholders in the future.



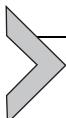
7. CONCLUSION

The network approach is a valuable tool for ecologists which is helping to revolutionise ecological science. However, networks are also a valuable tool for engagement. For public engagement, network approach can help people to better understand ecology as the system of interactions between species, and the place of humans within (not external to) these systems. For advocacy and decision-making, networks can be used as an approach for stakeholders to synthesise and incorporate complexity. One way of efficiently communicating messages about networks is via visualisation because networks are inherently visually appealing. There are many ways of visualising networks, and we recommend that much greater emphasis is given to the potential for visualisation to provide greater information content (rather than simply being used to grab people's attention). Altogether, networks and their visualisation are important tools for scientific inquiry, communication and engagement with potential for even greater benefits than have currently been realised.

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APPENDIX A. FURTHER INFORMATION ON THE PRODUCTION OF THE NETWORK FIGURES

Here, we briefly describe how we created the visualisations in Figs. 1, 4–6, and 11. As we have discussed in the main text (Section 3.4), there are many different standalone programmes available for drawing networks, and many packages within programmes such as R, Python or Matlab. Each programme and package has its own advantages and disadvantages, although there will be shared aspects among many of the approaches, enabling similar-looking visualisations to be produced via a variety of routes. There are regular changes in the availability of programmes and packages. Therefore, in describing the way we created these visualisations, we are not specifically recommending any approach, and not including an approach does not imply criticism.

Figure 1

Figure 1B was drawn with Pajek (Batagelj and Mrvar, 2002) with the coordinates of the nodes on arcs and node colour defined by the user. Species within each colour (different grey shades in the print version) group are ordered alphabetically (i.e. arbitrarily) rather than according to any graph aesthetic.

Figure 4

Except where otherwise stated, these figures were drawn in R 3.2.1 (R Core Team, 2015) using the packages ‘bipartite’ (Dormann et al., 2008) or ‘sna’ (Butts, 2014). Except where otherwise stated, the plants were drawn as filled polygons (coloured dark grey) and the hoverflies were drawn as open polygons (coloured white). In most cases, the lines represent interactions and the width of the line represents the observed frequency of the interaction. In many cases, the figures were exported in Portable Document Format (PDF) and imported as vectors into the illustration software ‘Inkscape’ (Inkscape, 2015) for tidying the figures.

(B) The matrices were drawn with the ‘visweb’ in the ‘bipartite’ package in R. The order of the rows and columns was determined by the ‘type’ argument, where ‘type=“nested”’, so the rows and columns are arranged in decreasing order of the total of their sums.

(C) The parallel coordinates plot was drawn with purpose-written code to draw nodes with the command ‘points’ and links with the command ‘segments’.

(D) The weighted coordinates plot was drawn with ‘plotweb’ in the ‘bipartite’ package in R, with the position of the nodes determined by the row and column coordinates of the first dimension of a correspondence analysis on the matrix (undertaken with ‘cca’ in the package ‘vegan’ ([Oksanen et al., 2015](#)) in R). This has the effect of minimising the number of overlapping lines.

(E) The circular plot was drawn with ‘gplot’ in the ‘sna’ package in R, with the argument ‘mode=“circle”’.

(F) The arcplot was drawn with ‘arcplot’ in the ‘arcdiagram’ package ([Sanchez, 2014](#)) in R.

(G) The force-directed layout was drawn with ‘gplot’ in the ‘sna’ package in R with the argument mode = ‘spring’ and default parameters used for this layout. Line widths were scaled by their abundance.

(H) The target plot was drawn with ‘gplot.target’ in the ‘sna’ package in R. The concentric rings represent the rank of the degree of each node (i.e. links to and from it) with the value of the degree (from the outside inwards, representing): {1,2,3,...,9,10,13,14}.

(I) The centralised burst plot with hierarchical edge bundling was drawn with the standalone programme ‘Cytoscape’ ([Shannon, 2003](#)) and by selecting appropriate parameters from the graphical user interface to create the desired layout.

(J) Sankey diagrams are usually used to show flow between different attributes at different levels, e.g., in food webs or organisational diagrams, although they can be used for bipartite networks. This Sankey diagram was drawn with ‘sankeyNetwork’ in ‘networkD3’ ([Gandrud et al., 2015](#)). ‘networkD3’ is an implementation of some of the network-drawing tools in D3 ([Bostock et al., 2011](#)) but within R. The result is an interactive visualisation in which the nodes can be moved within their trophic level and hovering a cursor causes the relevant links and/or nodes to be highlighted. [Figure 4J](#) is a static snapshot of the visualisation.

(K) The chord diagram was created using ‘Circos’ ([Krzywinski et al., 2009](#)), specifically the Circos Online implementation available at <http://circos.ca>

mkweb.bcgsc.ca/tableviewer/. Appropriate parameters were selected using the graphical user interface to create the desired layout.

(L) The three-dimensional effect layout was created with the standalone programme ‘Network3D’ ([Williams, 2010](#)). Appropriate parameters were selected using the graphical user interface to create the desired layout.

Figure 5

(A–C) The matrices were drawn with the ‘visweb’ in the ‘bipartite’ package in R. The order of the rows and columns was determined by the ‘type’ argument. (A) The argument type = ‘none’, so the rows and columns were arranged arbitrarily (according to alphabetical order). (B) The argument type = ‘nested’, so the rows and columns are arranged according to the row and column coordinates of the first dimension of a correspondence analysis on the matrix (undertaken with ‘cca’ in the package ‘vegan’ in R). (C) The argument type = ‘diagonal’, so the rows and columns are arranged with the highest number of interactions shown along the diagonal.

(D) The Fruchterman–Reingold layout was drawn with ‘gplot’ in ‘sna’ in R with the argument mode = ‘fruchtermanreingold’ and default parameters used. Line widths were scaled by their abundance.

(E–F) The spring-loaded layout was drawn with ‘gplot’ in ‘sna’ in R with the argument mode = ‘spring’ and default parameters used for this layout. Line widths were scaled by their abundance.

Figure 6

(A) The force-directed plot was drawn with ‘gplot’ in the ‘sna’ package in R using the ‘spring’ method. Nodes are coloured according to their trophic level: white = plants, grey = aphids, black = parasitoids.

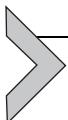
(B) The weighted parallel coordinates plot was drawn with ‘plotweb’ in the ‘bipartite’ package in R. The species are presented in the same order in each trophic level, and this order was obtained from the default option (method = ‘cca’) which minimises the number of crossing links. The width of the bars indicates the abundance of aphids (grey), links from plants (white) and abundance of parasitoids (black, increased by a factor of 10 compared to aphids). The plot was exported as a PDF and then imported to Inkscape for final tidying of the image.

(C) The hive plot was drawn with the R package ‘HiveR’ ([Hanson, 2015](#)). Species are ordered on each axis according to the rank of their weighted degree for the combined network. The width and darkness of

the lines are proportional to the log-scaled abundance of the interaction (narrow, red (grey in the print version) lines are low abundance, wide, dark grey lines are high abundance), and the size of the nodes for aphids and parasitoids is proportion to their log-transformed abundance.

Figure 11

The networks were drawn with Gephi (Bastian et al., 2009) with attributes selected by the user.



APPENDIX B. DETAIL AND PHOTO CREDITS FOR FIGURE 9

Numbers above the upper boxes of the webs correspond to the following taxa: 1, non-identified Lepidoptera; 2, Nymphalidae; 3, Bombyliidae; 4, Sarcophagidae; 5, Empididae; 6, Conopidae; 7, Cetoniidae; 8, Oedemeridae; 9, Curculionidae; 10, Ichneumonoidea; 11, Crabronidae; 12, non-identified Hymenoptera; 13, Tenthredinidae; 14, Calliphoridae; 15, Scatopsidae; 16, Sepsidae; 17, non-identified Coleoptera; 18, Chrysomelidae; 19, Lycaenidae; 20, Hesperiidae; 21, Zyginaeidae; 22, Sphingidae; 23, Papilionidae; 24, Noctuidae; 25, Vespoidea; 26, Gasteruptiidae; 27, Pompilidae; 28, Chrysidoidea; 29, Cephidae; 30, Sphecidae; 31, Muscidae; 32, Sciaridae; 33, Calliphoridae; 34, Chloropidae; 35, Stratiomyidae; 36, Tephritidae; 37, Conopidae; 38, Platystomatidae; 39, Tabanidae; 40, Mordellidae; 41, Dermestidae; 42, Dasytidae; 43, Cleridae; 44, Malachiidae; 45, Scraptiidae; 46, Cantharidae; 47, Elateridae; 48, Buprestidae; 49, Meloidae; 50, Tenebrionidae.

Photo credit: alain42820@spipoll, calin01@spipoll, cigale@spipoll, ascalaf07@spipoll, steed@spipoll, 46L@spipoll, cvd@spipoll, alaink@spipoll.

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