

Ecological network analysis

Ecological network visualisation and analysis using the cheddar package in R

PART ONE – INTRODUCTION TO CHEDDAR

You will need to load the cheddar and igraph packages into R to begin.

We will work with some data that is already loaded into cheddar;

```
> data(pHwebs)
```

```
> pHwebs
```

A collection of 10 communities

Each element in a `CommunityCollection` is a Cheddar Community. Many of the usual list operations can be used.

```
> length(pHwebs)
```

```
[1] 10
```

```
> pHwebs[[1]]
```

Old Lodge containing 23 nodes and 137 trophic links

```
> names(pHwebs)
```

```
[1] "Old Lodge" "Afon Hafren" "Broadstone" "Dargall Lane"
```

```
[5] "Mosedal Beck" "Duddon Pike Beck" "Allt a'Mharcaidh" "Hardknott  
Gill"
```

```
[9] "Bere Stream" "Mill Stream"
```

Cheddar has many built in function that make analysing food webs easy, try using the `sapply()` and `NumberOfTrophicLinks()` function to extract the number of links in each of the communities.

There are three "accessor functions" in cheddar, that are used the most to extract information about the food webs being analysed. Let's try each one in turn;

```
> CPS(pHwebs[[1]])
```

```
> NPS(pHwebs[[1]])  
> TLPS(pHwebs[[1]])
```

To extract information about the collection for communities we use the slightly modified functions;

```
> collectionCPS(pHwebs)  
> collectionNPS(pHwebs)  
> collectionTLPS(pHwebs)
```

There is a lot you can do with these functions, and the various plotting functions contained within cheddar, for instance let's look at the 'trivariate plots'.

```
> par(mfrow=c(3,4))  
> for (community in pHwebs){  
+   PlotNvM(community)  
+ }
```

These plots have become a very popular method for displaying the flow of energy through a food web, from small abundant resources (producers – green) to large rare consumers (fish – pink) with the invertebrate (blue) community sitting in between. The scaling of these trivariate webs has been found to be very similar from a wide range of ecosystems (Woodward *et al.* 2005).

To obtain and plot the slope of this relationship we use

```
abline(lm(Log10N(community)~Log10M(community)))
```

the slope of this line gives an indication of the efficiency of the flow of energy through the food web.

Let's have a look at how the size of these networks vary with pH, use `collectionCPS()` to extract a vector containing the pH of each food web, and use `sapply()` and `NumberOfNodes()` to create a vector containing the size (number of species) of each network. Use these two vectors to assess how the size of these network vary with pH. Can you explain this relationship?

PART TWO

The distribution of links through an ecological network has implications for the stability of the network, and this in turn has implications for how we might expect a network to respond to

environmental stressors. There are various ways in which we can analyse the distribution of links within a network. One way is to characterise the degree distribution, use `PlotDegreeDistribution()` to visualise the distribution of links through each of the 10 webs. Can you see any differences between the webs?

Let's export our cheddar communities to igraph objects, use the following function to do that;

```
> ToIgraph <- function(community, weight=NULL)
{
  if(is.null(TLPS(community)))
  {
    stop('The community has no trophic links')
  }
  else
  {
    ttps <- TLPS(community, link.properties=weight)
    if(!is.null(weight))
    {
      ttps$weight <- ttps[,weight]
    }
    return (graph.data.frame(ttps,
      vertices=NPS(community),
      directed=TRUE))
  }
}
```

Use `NumberOfNodes()` and `NumberOfTrophicLinks()` to extract the number of vertices and edges from each food web, and use `erdos.renyi.game(n= , p.or.m= , type="gnm")` to generate a network with the same number of links and nodes as the food web, but with randomly distributed links, (remember – vertices is synonymous with nodes, edges is synonymous with links). Use `degree.distribution()` (because we are using igraph) to extract and plot the degree distribution of the random counterparts to each or the empirical food webs. Do you notice any differences between the random networks and food webs?

Some ecological networks are said to show ‘small world’ properties. Small world networks are characterised by two things; they have a higher clustering coefficient than expected, and short path lengths between nodes. Small world properties have been shown to influence the rate at which perturbations propagate through food webs (Montoya *et al.* 2006). Let’s test if these webs display these properties.

Calculate the clustering coefficient

Clustering coefficients measure the probability that nodes in a network cluster together. Put another way, if node A is connected to node B, and B is connected to C, what is the likelihood that A is also connected to C (forming a triangle)? Have a think about what this would mean in a food web context.

Use the `transitivity()` package in `igraph()` to create a vector containing the clustering coefficient of each network in our collection. Do the same for the Erdős–Rényi random networks. Plot these together and add the 1:1 line and use this to make inferences about the degree of clustering found in these food webs. Is the clustering found in these food webs less or more than that found in their random counterparts?

What do you think would happen if this were repeated on only the animal-animal interaction networks? i.e. no basal resources.

Average shortest path length

The shortest path between two nodes is the length (number of links) of the shortest path between the two, this is then averaged to get a global measure for the network. The average shortest path of a network is a measure of how many links there are connecting each node. This measure gives an indication of how quickly information will spread through a communications network, or how quickly news will spread through a social network. What do you think this measure means in terms of food webs?

Use `shortest.paths()` to calculate the mean shortest path length for each of the food webs. Hint: the path length between two nodes which are not connected is infinite, and makes no biological sense. Use `RemoveIsolatedNodes()` to fix this. Do the same for each web’s Erdős–Rényi random counterpart and plot these two vectors together again with the 1:1 line, use this to assess the average shortest path length in these food webs.

Over all do you think these webs show ‘small world’ properties?

Assessing the stability of networks

One way in which biologists assess the stability of networks is by calculating their 'robustness', this is usually defined as the proportion of species that need to be removed in order to result in the total loss of $\geq 50\%$ of species (i.e. primary removals plus secondary extinctions). Secondary extinctions occur when a species is left without any resources, hence resource species cannot go secondarily extinct (Dunne *et al.* 2002). Try using `RemoveNodes()` to write a function that will calculate this metric.

Assess if there is a relationship between robustness and network size, average shortest path, clustering.

References:

- Dunne, J.A., Williams, R.J. & Martinez, N.D. (2002). Network structure and biodiversity loss in food webs: robustness increases with connectance. *Ecology Letters*, **5**, 558–567.
- Montoya, J.M., Pimm, S.L. & Sole, R. V. (2006). Ecological networks and their fragility. *Nature*, **442**, 259–264.
- Woodward, G., Speirs, D.C. & Hildrew, A.G. (2005). Quantification and resolution of a complex, size-structured food web. *Advances in Ecological Research*, **36**, 85–135.