

Assembling my Network

The ecology is theoretical but the fun is real.

Network basics with R and igraph (part III of III)

Posted on [July 1, 2013](#)

In this third and final post in this little series of mine I want to bring it all together with my favorite kind of network, food webs. Thus I will be using a real food web to go over all the different tools and properties. Specifically I will be using the food web of the Otago Harbour, NZ intertidal zone (found [here](#)).

```

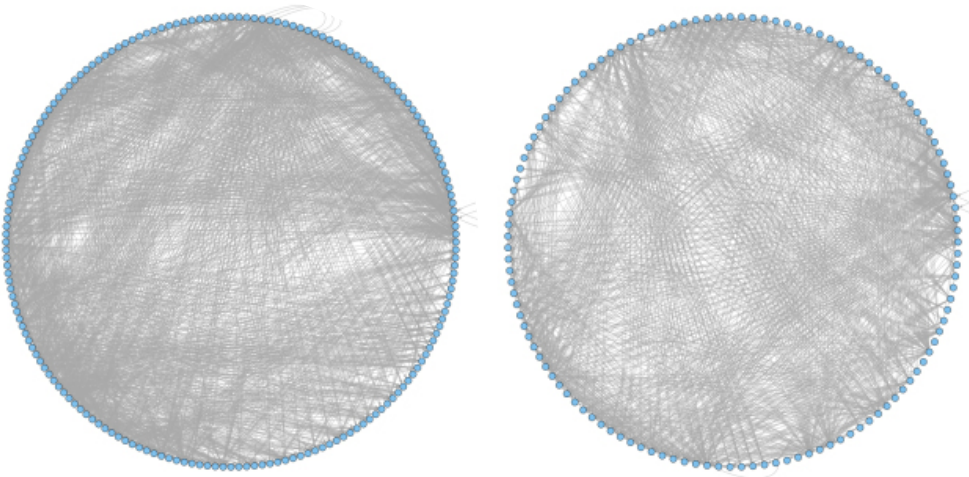
1 #####
2 #####
3 ####
4 #####          PART III: FOOD WEBS
5 #####
6 #####
7 #####
8 library(igraph)
9 library(NetIndices)
10 # Kim N. Mouritsen, Robert Poulin, John P. McLaughlin and David W. Thieltges. 2011.
11 # Food web including metazoan parasites for an intertidal ecosystem in New Zealand.
12 # Ecology 92:2006.
13
14 # Website: http://esapubs.org/archive/ecol/E092/173/
15
16 # Otago Harbour: intertidal mudflat
17 otago.links.data<-read.csv("~/Desktop/Projects/FoodwebAlpha/Data/Otago_Data_Links.csv")
18 otago.nodes.data<-read.csv("~/Desktop/Projects/FoodwebAlpha/Data/Otago_Data_Nodes.csv")
19
20 # Column names for data
21 colnames(otago.links.data)
22 colnames(otago.nodes.data)
23
24 # Convert the data into a graph object using the first 2 columns of the dataset as :
25 otago.graph<-graph.edgelist(as.matrix(otago.links.data[,1:2]))
26
27 # Create graph object of just predator prey links
28 otago.graph.p<-graph.edgelist(as.matrix(otago.links.data[1:1206,1:2]))
29
30 # Get the web into matrix form
31 otago.adjmatrix<-get.adjacency(otago.graph,sparse=F)
32 otago.adjmatrix.p<-get.adjacency(otago.graph.p,sparse=F)
33
34 # Get the basic network indices from the matrices with GenInd()
35 ind.otago<-GenInd(otago.adjmatrix)
36 ind.otago.p<-GenInd(otago.adjmatrix.p)
37
38 # Now to plot these two webs to get a feel for what we are dealing with
39
40 par(mar=c(.1,.1,.1,.1))
41 plot.igraph(otago.graph,vertex.label=NA,vertex.size=3,edge.arrow.size=.25,layout=lay
plot.igraph(otago.graph.p,vertex.label=NA,vertex.size=3,edge.arrow.size=.25,layout=

```

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14 plot.igraph(otago.graph.p, vertex.label=NA, vertex.size=5, edge.arrow.size=.25, layout=

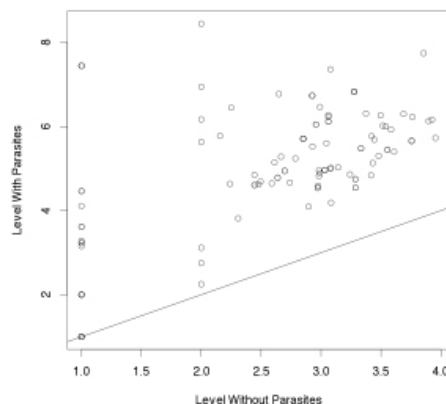
```



```

1 # The NetIndices package also has a function to get some of the trophic properties (
2 # TrophInd() takes in an adjacency matrix and gives an output of the trophic level (
3 # as well as an index of the degree of omnivory for each node
4
5 troph.otago<-TrophInd(otago.adjmatrix)
6 troph.otago.p<-TrophInd(otago.adjmatrix.p)
7
8 # An interesting aside, by adding parasites to the web it increases the trophic level
9 # this web.
10
11 plot(troph.otago[1:123,1]~troph.otago.p[,1],xlab="Level Without Parasites",ylab="Level
12 abline(a=0,b=1)

```



```

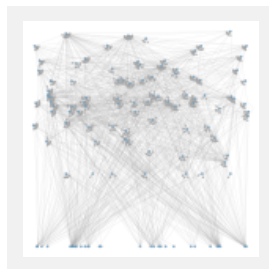
1 # An interesting use for this trophic level function is to then use trophic level as
2 # This way, I can plot the food web nodes according to trophic height. I think that
3 # of a food web, since you can gain more information about the trophic structure of
4 # glancing at the plot.
5
6 # First we need to create a two-column matrix identifying the x and y values for each
7 layout.matrix.1<-matrix(
8 nrow=length(V(otago.graph)), # Rows equal to the number of vertices
9 ncol=2
10 )

```

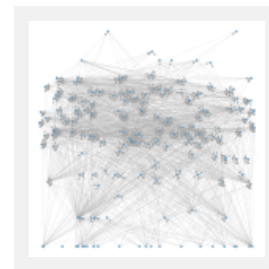
```

11 layout.matrix.1[,1]<-runif(length(V(otago.graph))) # randomly assign along x-axis
12 layout.matrix.1[,2]<-troph.otago$TL # y-axis value based on trophic level
13
14 layout.matrix.1p<-matrix(
15   nrow=length(V(otago.graph.p)), # Rows equal to the number of vertices
16   ncol=2
17 )
18 layout.matrix.1p[,1]<-runif(length(V(otago.graph.p)))
19 layout.matrix.1p[,2]<-troph.otago.p$TL
20
21 # Now we can use these matrices to define the layout instead of using the circle lay
22
23 par(mar=c(.1,.1,.1,.1),mfrow=c(1,2))
24
25 plot.igraph(otago.graph,
26   vertex.label.cex=.35,
27   vertex.size=3,
28   edge.arrow.size=.25,
29   layout=layout.matrix.1)
30
31 plot.igraph(otago.graph.p,
32   vertex.label.cex=.35,
33   vertex.size=3,
34   edge.arrow.size=.25,
35   layout=layout.matrix.1p)
36
37 # I am still working on the best way to plot the nodes along the x-axis. You may not
38 # runif() means that there is some chance that two nodes with the same trophic level
39 # will be right on top of one another

```



Without parasites



With parasites

```

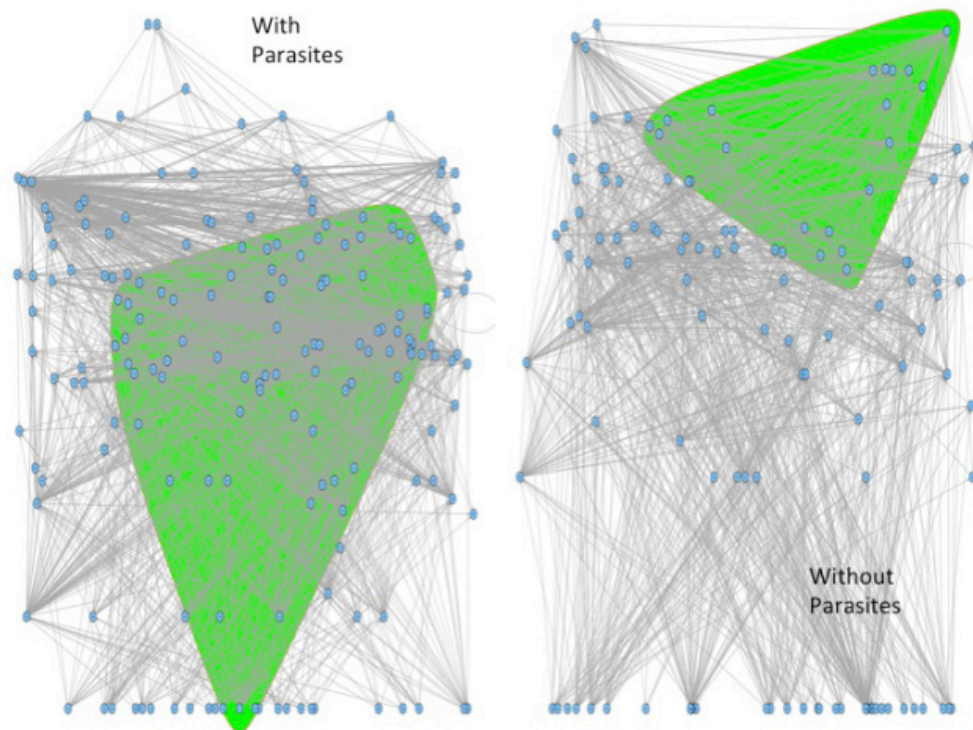
1 # It is also a bit interesting to see how the inclusion of parasites impacts commun:
2 wtc.otago<-walktrap.community(otago.graph)
3 wtc.otago.p<-walktrap.community(otago.graph.p)
4
5 par(mar=c(.1,.1,.1,.1),mfrow=c(1,2))
6
7 plot.igraph(otago.graph,
8   vertex.label.cex=.35,
9   vertex.size=3,
10  edge.arrow.size=.25,
11  layout=layout.matrix.1,
12
13  mark.groups=wtc.otago$membership,
14  mark.col="green")
15
16 plot.igraph(otago.graph.p,

```

```

16 vertex.label.cex=.35,
17 vertex.size=3,
18 edge.arrow.size=.25,
19 layout=layout.matrix.1p,
20 mark.groups=wtc.otago.p$membership,
21 mark.col="green")
22
23 # It is clear that the increase in the connectivity of the web with parasites has led
24 # a larger densely connected community

```



Webs with walktrap community shown in green

```

1 # It is clear that the increase in the connectivity of the web with parasites has led
2 # a larger densely connected community
3
4 # The degree distribution of a food web can tell us a lot about the amount of spec:
5 # generalization in the web (in degree), as well as vulnerability (out degree)
6
7 deg.otago<-degree(otago.graph)
8 deg.otago.p<-degree(otago.graph.p)
9
10 # Using the degree distribution gives a better way to visualize any differences
11 # Looking at the in degree tells us about how general the diets of consumers are
12 dd.otago.in<-degree.distribution(otago.graph,mode="in",cumulative=T)
13 dd.otago.in.p<-degree.distribution(otago.graph.p,mode="in",cumulative=T)
14
15 # Out degree is a measure of the vulnerability of organisms, telling us how many c
16 # eat each species.
17 dd.otago.out<-degree.distribution(otago.graph,mode="out",cumulative=T)
18 dd.otago.out.p<-degree.distribution(otago.graph.p,mode="out",cumulative=T)
19

```

```

20 # And finally the degree ("all") simply tells us about how well connected that species
21 # within the network
22 dd.otago<-degree.distribution(otago.graph,mode="all",cumulative=T)
23 dd.otago.p<-degree.distribution(otago.graph.p,mode="all",cumulative=T)
24
25 par(mfrow=c(2,2))
26 plot(dd.otago.in,xlim=c(0,80))
27 plot(dd.otago.out,xlim=c(0,80))
28 plot(dd.otago.in.p,xlim=c(0,80))
29 plot(dd.otago.out.p,xlim=c(0,80))
30
31 power.fit<-power.law.fit(deg.otago)
32 power.fit.p<-power.law.fit(deg.otago.p)
33
34 par(mfrow=c(1,2))
35 plot(dd.otago,log="xy")
36 lines(1:180,10*(1:180)^((-power.fit$alpha)+1))
37
38 plot(dd.otago.p,log="xy")
39 lines(1:100,10*(1:100)^((-power.fit.p$alpha)+1))
40
41 # I can look at the diameter of the two versions of the web
42 # For food webs the diameter is going to be the longest food chain
43
44 # since energy only flows in one direction, the diameter will read from
45 # basal species to top predator.
46
47 get.diameter(otago.graph)
48 get.diameter(otago.graph.p)
49
50 # I think that here it is interesting to note that the diameter of the predator-prey
51 # food web (which we expect to be smaller) is not a subset of the diameter for the
52 # larger parasites included network
53
54 # The next few properties are all related to the small world-ness of the network:
55
56 transitivity(otago.graph)
57 transitivity(otago.graph.p)
58
59 # Betweenness is the number of shortest paths going through a specified node or edge
60
61 otago.between<-betweenness(otago.graph)
62 otago.between.p<-betweenness(otago.graph.p)
63
64 plot(otago.between[1:123]~otago.between.p)
65 abline(a=0,b=1)
66
67 otago.edge.between<-edge.betweenness(otago.graph)
68 otago.edge.between.p<-edge.betweenness(otago.graph.p)
69
70 closeness(otago.graph)
71
72 # Here are the adjacency matrices for each of the 13 subgraphs again
73 s1<-matrix(c(0,1,0,0,0,1,0,0,0),nrow=3,ncol=3)
74 s2<-matrix(c(0,1,1,0,0,1,0,0,0),nrow=3,ncol=3)
75 s3<-matrix(c(0,1,0,0,0,1,1,0,0),nrow=3,ncol=3)
76 s4<-matrix(c(0,0,1,0,0,1,0,0,0),nrow=3,ncol=3)
77 s5<-matrix(c(0,1,1,0,0,0,0,0,0),nrow=3,ncol=3)
78 d2<-matrix(c(0,1,1,1,0,1,0,0,0),nrow=3,ncol=3)

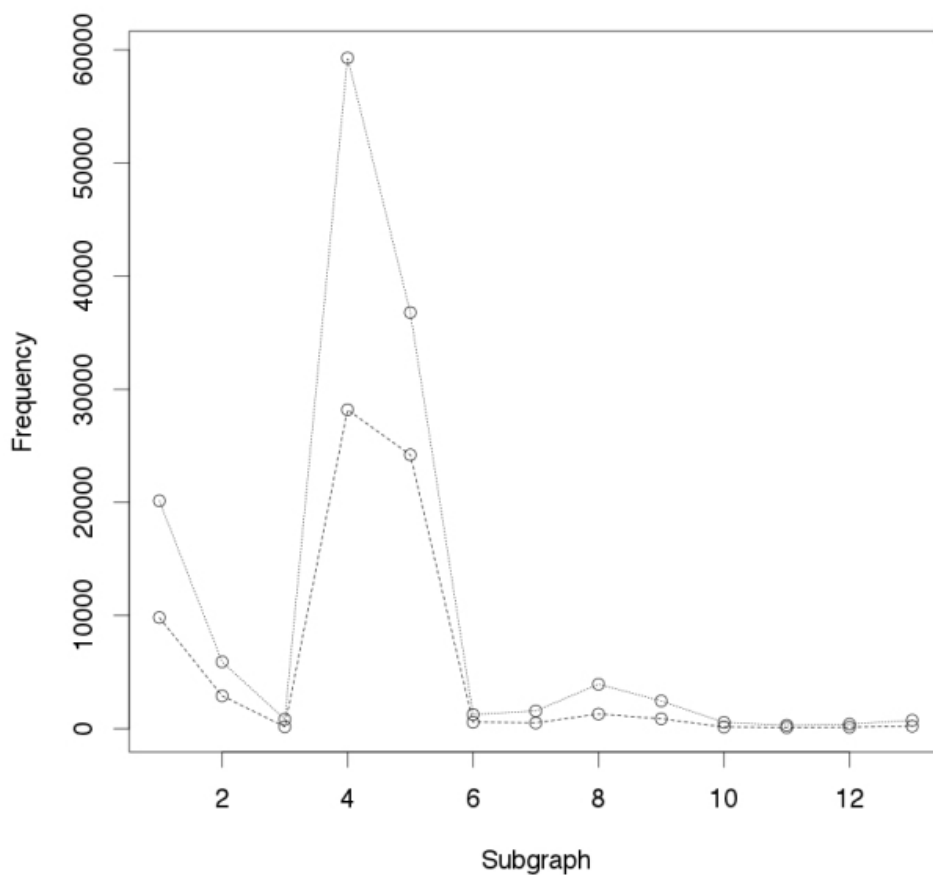
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78 d1<-matrix(c(0,1,1,0,0,1,0,1,0),nrow=3,ncol=3)
79 d3<-matrix(c(0,0,1,1,0,0,1,0,0),nrow=3,ncol=3)
80 d4<-matrix(c(0,0,0,1,0,1,0,1,0),nrow=3,ncol=3)
81 d5<-matrix(c(0,1,1,0,0,1,1,0,0),nrow=3,ncol=3)
82 d6<-matrix(c(0,1,1,1,0,1,1,1,0),nrow=3,ncol=3)
83 d7<-matrix(c(0,1,1,1,0,1,1,0,0),nrow=3,ncol=3)
84 d8<-matrix(c(0,1,1,1,0,0,1,0,0),nrow=3,ncol=3)

85
86 # Turn them into a convenient list
87 subgraph3.mat<-list(s1,s2,s3,s4,s5,d1,d2,d3,d4,d5,d6,d7,d8)
88 # And then into a list of graph objects
89 subgraph3.graph<-lapply(subgraph3.mat,graph.adjacency)
90
91 # Count the number of the 13 different 3-node subgraphs in the two webs
92 subgraph.freq.otago<-c()
93 subgraph.freq.otago.p<-c()
94 for(i in 1:13){
95   subgraph.freq.otago[i]<-
96   graph.count.subisomorphisms.vf2(otago.graph,subgraph3.graph[[i]])
97   subgraph.freq.otago.p[i]<-
98   graph.count.subisomorphisms.vf2(otago.graph.p,subgraph3.graph[[i]])
99 }
100
101 plot(subgraph.freq.otago,type="o",lty=3, xlab="Subgraph",ylab="Frequency")
102 points(subgraph.freq.otago.p,type="o",lty=2)
103
104 plot(subgraph.freq.otago~subgraph.freq.otago.p)
105 abline(a=0,b=1)

```

Frequencies of the 13 possible 3-node subgraphs

Note I did not spend a great deal of time on the degree distribution and the small world properties of the food web. I am planning different posts on these different properties that will explore them in greater detail. Mostly, as I was writing up this post I noticed that there were a few things that didn't match my expectations, and that there are a few other tools out there that give different answers. So be on the lookout for future posts about degree distributions and fitting a function to them, also for posts about the multitude of different tools that are supposedly all measuring the same thing (do they all give the same answer?).

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