

ANALYSIS OF FLENSBURG FJORD

ANIMAL NETWORK

SOCIAL NETWORK ANALYSIS

FINAL PROJECT REPORT

University of Florence, Academic Year 2020/2021

Author: Niccolò Ducci

Mat.: 7036789

1. INTRODUCTION

This Project is based on the Scientific Publication: **C. Dieter Zander, Neri Josten, Kim C. Detloff, Robert Poulin, John P. McLaughlin, and David W. Thieltges, 2011. “Food web including metazoan parasites for a brackish shallow water ecosystem in Germany and Denmark”, Ecology 92:2007.** The Researchers involved in this project built an ecological directed network of trophic¹ interaction between different species living in the Flensburg Fjord, through field sampling and supplemented with information from additional published sources and local expert knowledge. The resulting Data Set represents a food web for the Flensburg Fjord, a brackish shallow water inlet on the Baltic Sea, between Germany and Denmark.

The aim of this Project is to study a subset of the Flensburg Fjord Network, which excludes every organism that does not belong to the animal kingdom, using the theory and the techniques learned during the course to describe and understand its structure and main features. The software used to conduct this analysis are R (version 4.0.4, 2021-02-15) and

¹ **Trophic:** relating to feeding, any feeding relationship between organism and their surroundings, see also **Trophic Level.** **Source:** https://www.oxfordlearnersdictionaries.com/definition/american_english/trophic

Microsoft Excel. The main R packages utilized are: “igraph”, “igraphdata”, “ergm” and “Intergraph”.

2. DATA

The Dataset is divided into two excel files (CSV format), one for the nodes and one for the edges. The Node Dataset contains 180 nodes, each one representing an animal in one of its life-cycle stages or some functional/ taxonomic group (e.g., phytoplankton, macroalgae, and several groups of birds) lumped into a single node; this Dataset has also 46 nodal attributes. The Edge Dataset contains 1577 links which represents trophic interactions among the nodes; the links are then classified by type and by nodes involved, this Dataset has 19 edge attributes. The links are binary and directed, being 1 if there is a trophic interaction or 0 if there is no interaction, with the tie direction going from the feeder to the source of its feeding (e.g., gull feeds on fish so the tie goes from gull to fish).

All attributes of the two Datasets that presented more than 10 missing values were dropped; this threshold was decided subjectively. All the important variables (i.e., link type, species, life-cycle stage etc..) that described important feature of the network presented no missing values. The Node and the Edge Dataset, after the cleaning, presented 15 and 8 attributes respectively.

3. ANIMAL SUBGRAPH

The resulting Graph, created using R Studio, has 180 nodes, 1577 edges and 21 nodal and edge attributes. There are 2 self-loop edges that were deleted from the graph, the nodes involved are “Zooplankton” and “Meiofauna”, two groups of microscopical animals. The number of edges decreased to 1575. In order to ease computation, every node that does not belong to the animal kingdom was discarded. The resulting induced sub-graph has **172 nodes and 1416 directed edges**. There are no isolated nodes and no self-looping edges. The number of attributes remains 21. The animal sub-graph was used as the object of analysis

for this project. From now on the animal sub-graph will be referred to simply as “graph” to avoid cumbersomeness.

3.1 GRAPHICAL REPRESENTATION OF THE NETWORK

In this paragraph we take a first look at the graph. The graphical representation presented below, in *figure 1*, was obtained using an LGL² algorithm. Here we can see how the graph is connected, also there is a contrast between low connected peripheral nodes and highly

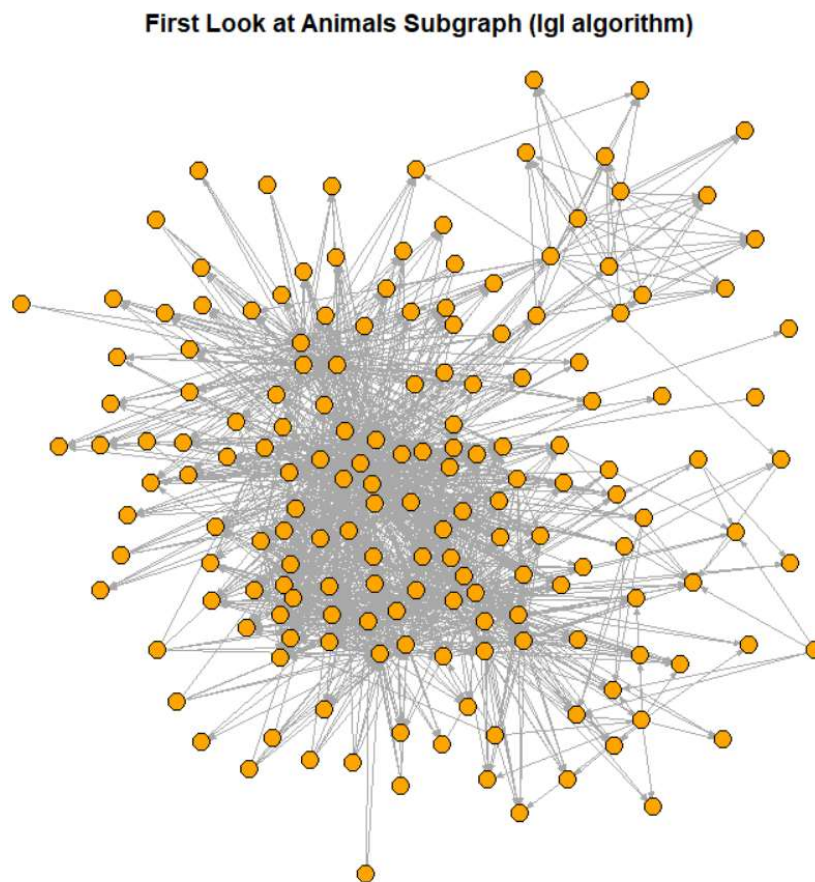


Figure 1

connected central nodes. From *figure 1* we get some insight on the structure of this ecological network, although this visualization is too messy to get any solid knowledge.

² **LGL**: Large Graph Layout, an algorithm aimed at visualizing large, connected graphs (“*igraph*” R package).

3.2 GRAPH COMPONENTS

This graph is connected, so we are only looking for strongly connected components³. There are only 2 strongly connected components that have a numerosity greater than one, that is all the other components are made of just one vertex. Of these two components one has 3 nodes while the other has 25 nodes, the former is composed of three parasitic animals while the latter is much more diverse, comprising birds, fishes and parasites.

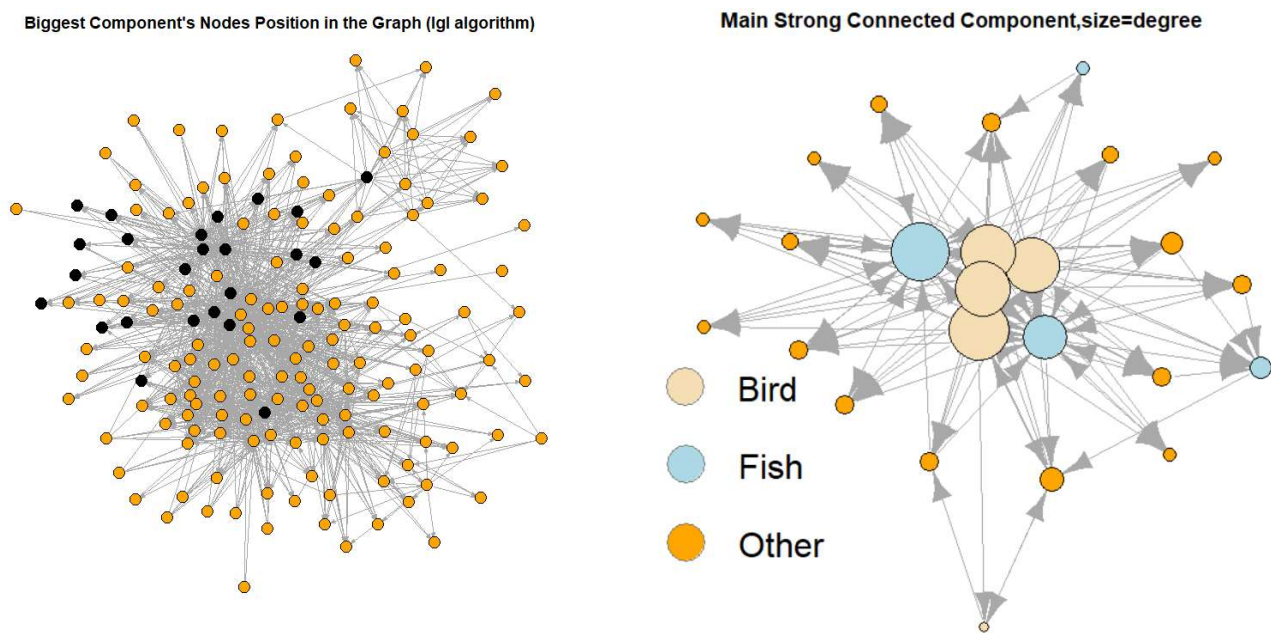


Figure 2

Figure 2 above is the visualization of the bigger component, along with its nodes position in the network; as we can see it contains a little ecosystem of various animals, it is interesting to note how birds and fishes, with some exceptions, are the most connected and central nodes, at least by degree. Other creatures play a much smaller role in terms of trophic interactions. The nodes involved in this component are very important for the network, in Figure 3 below there is a list of the ten most connected nodes by degree.

³ **Strongly Connected Components:** A group of vertices where for every pair of vertices there exists a directed path between them.

| | WorkingName | OrganismalGroup | ConsumerStrategyStage | degree(subg_strongComp) |
|-----|------------------------------|-----------------|-----------------------|-------------------------|
| 75 | Gulls | Bird | predator | 22 |
| 66 | Broad-nosed pipefish | Fish | predator | 21 |
| 71 | Cormorants | Bird | predator | 20 |
| 70 | Grebes/Loons | Bird | predator | 20 |
| 76 | Terns | Bird | predator | 20 |
| 64 | European flounder | Fish | predator | 16 |
| 165 | Contracaecum sp. / osculatum | Nematode | macroparasite | 9 |
| 68 | Sea stickleback | Fish | predator | 8 |
| 82 | Gyrodactylus spp. | Monogenean | macroparasite | 8 |
| 78 | Trichodina domergui | Protist | pathogen | 7 |

Figure 3 "Top ten Component's Nodes by Degree"

4. NETWORK STATISTICS

The Network statistics calculated are Density, Reciprocity, Transitivity and the odds ratio of Transitivity vs Reciprocity.

| NETWORK STATISTIC | VALUE |
|-------------------------|------------|
| Density | 0.04814361 |
| Reciprocity | 0.01129944 |
| Transitivity | 0.1892748 |
| OddsRatio | 4.615852 |
| Transitivity vs Density | |

Figure 4

Figure 4 shows these statistics. The first thing to be noted from these results is that the network is quite sparse, its density is very low. Reciprocity is almost absent with 99% of ties not being reciprocated: this was to be expected since a prey does not usually feed on its predator (e.g., a fish does not hunt gulls, a host does not infect a parasite, etc...). Transitivity

is quite large for a biological network⁴, indicating a tendency to form connections between nodes who share a common relation. Comparing Density and Transitivity in the form of an odds ratio tells us that the probability of observing a connection between nodes who share a common relation is 4.6 times higher than that of observing a relation between two randomly selected nodes.

4.1 ASSORTATIVITY

The Flensburg Fjord Graph has 15 nodal attributes, most of them are not useful for our purpose, while others are much more interesting. We focus on 4 main characteristics of interest: “Phylum”, “Organismal Group”, “Life-cycle” and a new binary variable called “Predator”, created from the variable “ConsumerStrategyStage”, which takes 1 if the node is a predator or 0 otherwise (e.g., non-feeding, parasite, etc...). We calculated the nominal version of the assortativity coefficient as it is shown in *Figure 5*.

| Node Attribute | Assortativity |
|-----------------|---------------|
| Phylum | -0.1604368 |
| Predator | -0.3491134 |
| Stage | -0.0490566 |
| OrganismalGroup | -0.1008899 |

Figure 5

As we can see there is a clear tendency toward disassortative mixing, every coefficient is negative. This can be explained by the fact that trophic interactions are more common between different species of animals, or between animals that have a different feeding strategy (e.g., hosts and parasites: rarely parasites infect other parasites), indeed only 40 out

⁴ This is a reference to the Textbook “Mark Newman - Networks (2018, Oxford University Press)” par. 7.3 page 185, where the author comments on the value of cluster coefficient for different types of networks.

of 1416 edges are between parasitic/non-feeding animals, while 423 edges are between predatory animals, leaving 953 mixed edges in terms of feeding strategy. The same could be said for life-cycle stage, keeping in mind that many animals have only 1 live-cycle stage.

5. NODAL STATISTICS

The Animal subset of the Flensburg Fjord Network has 172 nodes, in this paragraph we want to answer the question: which nodes are the most central/important for the Graph? It is important to stress that this is an ecological network of feeding relations between organisms (all animals in our case), this means that some centrality measurements may be more suitable than others to describe and analyse its features.

5.1 DEGREE CENTRALITY

Degree centrality is a measure of centrality based on the number of relations a node has: more connections to other nodes mean more importance and centrality. This kind of centrality measurement is useful in this setting, it allows us to see which animals are the most preyed upon/infected and which are the apex predators by checking respectively the number of in and out going ties.

Top 5 nodes by IN-Degree Centrality

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | INdegree | INdegreeSTD |
|-----|------|--------------------|-----------------|-----------------------|----------|-------------|
| 77 | 21 | Hydrobia ulvae | Snail | predator | 29 | 0.1695906 |
| 46 | 59 | Common goby | Fish | predator | 28 | 0.1637427 |
| 76 | 20 | Hydrobia neglecta | Snail | predator | 28 | 0.1637427 |
| 78 | 19 | Hydrobia ventrosa | Snail | predator | 24 | 0.1403509 |
| 163 | 108 | Maritrema subdolum | Trematode | parasitic castrator | 24 | 0.1403509 |

Top 5 nodes by OUT-Degree Centrality

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | OUTdegree | OUTdegreeSTD |
|----|------|---------------------|-----------------|-----------------------|-----------|--------------|
| 19 | 75 | Gulls | Bird | predator | 101 | 0.5906433 |
| 41 | 41 | European green crab | Crab | predator | 66 | 0.3859649 |
| 16 | 71 | Cormorants | Bird | predator | 53 | 0.3099415 |
| 20 | 74 | Plovers | Bird | predator | 53 | 0.3099415 |
| 72 | 39 | Brown shrimp | Shrimp | predator | 53 | 0.3099415 |

Figure 6

Figure 6 shows the five most central nodes in terms of in and out degree. Out-degree values are much larger than the in-degree ones.

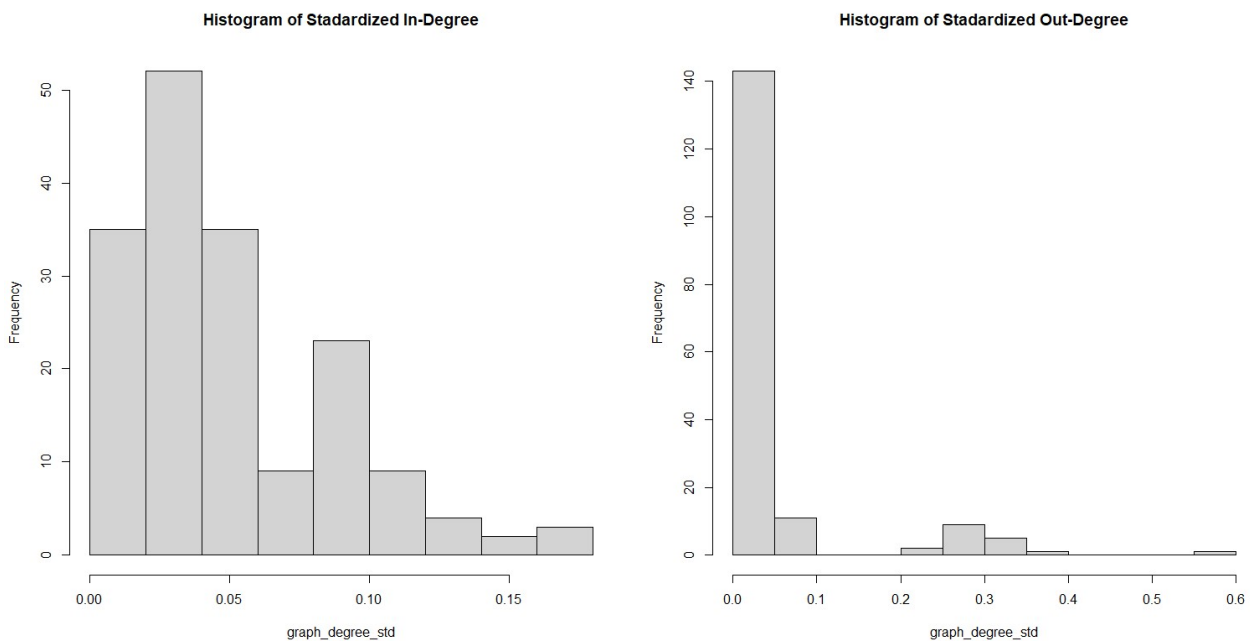


Figure 7

In Figure 7 we can see a comparison between the distribution of in-going and out-going degree centrality. The out-degree is almost zero for a large part of the nodes, while there is a small amount of very central nodes: these are the apex predators of this ecological niche, none of them is a parasite. This comparison highlights how, among Flensburg Fjord animals, being preyed upon/infected by is much more common than actively prey other animals.

5.2 OTHER MEASURES OF CENTRALITY

Other measures of centrality can be computed to check which nodes are central, but their interpretation for this kind of network is less useful compared to that of degree centrality.

Closeness centrality

CLOSENESS CENTRALITY

Collapsed ties

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | closOUT_std[ordALL[1:5]] |
|----|------|------------------|-----------------|-----------------------|--------------------------|
| 19 | 75 | Gulls | Bird | predator | 0.041184971 |
| 46 | 59 | Common goby | Fish | predator | 0.010847501 |
| 43 | 63 | Black goby | Fish | predator | 0.010733116 |
| 72 | 39 | Brown shrimp | Shrimp | predator | 0.008403361 |
| 54 | 61 | Two-spotted goby | Fish | predator | 0.010848877 |

Path from vertex

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | closOUT_std[ordOUT[1:5]] |
|-----|------|-------------------------|-----------------|-----------------------|--------------------------|
| 101 | 107 | Maritrema subdolum | Trematode | macroparasite | 0.04969486 |
| 89 | 103 | Cerc. microphall. No. 4 | Trematode | macroparasite | 0.04963716 |
| 95 | 83 | Himasthla continua | Trematode | macroparasite | 0.04963716 |
| 96 | 87 | Himasthla interrupta | Trematode | macroparasite | 0.04963716 |
| 97 | 91 | Himasthla militaris | Trematode | macroparasite | 0.04963716 |

Path to vertex

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | closIN_std[ordIN[1:5]] |
|-----|------|-----------------------|-----------------|-----------------------|------------------------|
| 110 | 7 | Zooplankton | Zooplankton | predator | 0.01268828 |
| 77 | 21 | Hydrobia ulvae | Snail | predator | 0.01213799 |
| 76 | 20 | Hydrobia neglecta | Snail | predator | 0.01213713 |
| 112 | 97 | Cryptocotyle concavum | Trematode | non-feeding | 0.01207457 |
| 113 | 101 | Cryptocotyle lingua | Trematode | non-feeding | 0.01207457 |

Figure 8, Top 5 nodes by standardized Closeness Centrality, 3 versions

Closeness centrality, *Figure 8*, is divided in three methods of calculation: one for paths from the vertex, one for paths to the vertex and one who does not account for the direction of the ties. There is some similarity with degree centrality: gulls and brown shrimps are present in the first closeness calculation method. In the last two methods, this centrality measure seems to privilege parasites over free-living creature: this might be because parasites infect nodes that have a lot of ties and are thus able to reach every other node faster.

Betweenness centrality

The betweenness centrality of a node “n” is defined as the fraction of geodesic paths between every other node that involves node “n”.

| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | bt_centr_std[bt_ord_std[1:5]] |
|----|------|------------------------------|-----------------|-----------------------|-------------------------------|
| 19 | 75 | Gulls | Bird | predator | 0.04630128 |
| 63 | 165 | Contracaecum sp. / osculatum | Nematode | macroparasite | 0.04358564 |
| 46 | 59 | Common goby | Fish | predator | 0.04110716 |
| 48 | 64 | European flounder | Fish | predator | 0.03544413 |
| 44 | 66 | Broad-nosed pipefish | Fish | predator | 0.02863118 |

Figure 9, Top 5 nodes by standardized Betweenness Centrality

Figure 9 shows the five most central nodes according to betweenness centrality. Gulls and Common Gobies are the only two nodes present here that are also present in both the Degree

centrality and the collapsed-ties type of Closeness centrality, meaning that these two nodes are important and central for the network.

Eigenvector centrality

This measure of centrality assigns high values to nodes that have many neighbours or important neighbours or both.

| Standardized Eigenvector Centrality | | | | | |
|-------------------------------------|------|--------------------------|-----------------|-----------------------|-------------------------------------|
| | name | WorkingName | OrganismalGroup | ConsumerStrategyStage | ei_centr_std[ord_ei_centr_std[1:5]] |
| 77 | 21 | Hydrobia ulvae | Snail | predator | 1.0000000 |
| 76 | 20 | Hydrobia neglecta | Snail | predator | 0.9681440 |
| 78 | 19 | Hydrobia ventrosa | Snail | predator | 0.7026373 |
| 163 | 108 | Maritrema subdolum | Trematode | parasitic castrator | 0.4777012 |
| 164 | 112 | Microphallus claviformis | Trematode | parasitic castrator | 0.4638297 |

Figure 10, Top 5 nodes by Standardized Eigenvector centrality

Figure 10 reports the top five nodes by Standardized Eigenvector centrality (i.e., every value is divided by the largest value observed). Here we can find some nodes that have already been encountered: the three *Hydrobia* species and *Maritrema subdolum* are also the most central vertices in both In-Degree and path-to-vertex Closeness centrality.

5.3 NETWORK CENTRALIZATION

Network Centralization indices are used to see how central a graph is. High values, according to a certain centrality measure, mean that few nodes are very central while low values suggest that all nodes are almost equally central.

| Centralization Index | Value |
|------------------------------|-------------|
| Eigenvector Centralization | 0.4136262 |
| In-Degree Centralization | 0.1221572 |
| Out-Degree Centralization | 0.5456722 |
| Out-Closeness Centralization | 0.03406177 |
| In-Closeness Centralization | 0.003893666 |
| All-Closeness Centralization | 0.5630227 |
| Betweenness Centralization | 0.04402083 |

Figure 11

Figure 11 reports the network centrality index for every measure we have computed so far. These values vary a lot according to the type of centrality measure used. Overall, these indices seem to be affected by the way the direction of the ties was accounted for. The network has few important nodes when we consider out-going ties/paths, the same cannot be said for in-going ties/paths.

6. NETWORK MODELING

The aim of this chapter is to use the statistical models seen during the course to describe, make statistical inference and analyse the Flensburg Fjord Animal Graph. All the models presented here are the best in terms of AIC and BIC and were obtained through a process of trial and error. Parameters were estimated using a Monte Carlo Markov Chain Maximum Likelihood Approach with starting values equal to Maximum Pseudo Likelihood Estimates.

6.1 NETWORK MODELS

P1 Model

```
Call:
ergm(formula = net ~ edges + mutual + nodefactor("predator") +
      nodefactor("Stage ID") + nodematch("predator") + nodematch("Stage ID") +
      nodematch("Phylum") + nodefactor("Phylum"), control = control.ergm(seed = 1))

Iterations: 3 out of 20

Monte Carlo MLE Results:
```

| | Estimate | Std. Error | MCMC % | z value | Pr(> z) | |
|-----------------------------------|-----------|------------|--------|---------|----------|-----|
| edges | -11.01268 | 1.22827 | 0 | -8.966 | < 1e-04 | *** |
| mutual | -3.01119 | 0.35354 | 0 | -8.517 | < 1e-04 | *** |
| nodefactor.predator.1 | 2.46422 | 0.55694 | 0 | 4.425 | < 1e-04 | *** |
| nodefactor.Stage ID.2 | 4.10552 | 0.51240 | 0 | 8.012 | < 1e-04 | *** |
| nodefactor.Stage ID.3 | 2.78064 | 0.52673 | 0 | 5.279 | < 1e-04 | *** |
| nodefactor.Stage ID.4 | 3.34001 | 0.52287 | 0 | 6.388 | < 1e-04 | *** |
| nodematch.predator | -2.73244 | 0.48766 | 0 | -5.603 | < 1e-04 | *** |
| nodematch.Stage ID | 2.79055 | 0.50834 | 0 | 5.490 | < 1e-04 | *** |
| nodematch.Phylum | -1.60003 | 0.15321 | 0 | -10.443 | < 1e-04 | *** |
| nodefactor.Phylum.Annelida | 1.02813 | 0.46272 | 0 | 2.222 | 0.026287 | * |
| nodefactor.Phylum.Chelicerata | -0.96498 | 0.82168 | 0 | -1.174 | 0.240234 | |
| nodefactor.Phylum.Chordata | 3.29436 | 0.43847 | 0 | 7.513 | < 1e-04 | *** |
| nodefactor.Phylum.Ciliophora | 1.54637 | 0.41408 | 0 | 3.735 | 0.000188 | *** |
| nodefactor.Phylum.Crustacea | 1.10093 | 0.43611 | 0 | 2.524 | 0.011589 | * |
| nodefactor.Phylum.Echinodermata | 0.55060 | 0.58665 | 0 | 0.939 | 0.347959 | |
| nodefactor.Phylum.Hexapoda | -0.03266 | 0.63566 | 0 | -0.051 | 0.959023 | |
| nodefactor.Phylum.Mollusca | 1.71591 | 0.44093 | 0 | 3.892 | < 1e-04 | *** |
| nodefactor.Phylum.Nematoda | 0.06195 | 0.34412 | 0 | 0.180 | 0.857139 | |
| nodefactor.Phylum.Other | 0.67494 | 0.50305 | 0 | 1.342 | 0.179696 | |
| nodefactor.Phylum.Platyhelminthes | 0.62643 | 0.33273 | 0 | 1.883 | 0.059745 | . |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AIC: 8685    BIC: 8851    (Smaller is better.)
```

Figure 12, R output of the best p1 model

Figure 12 shows the R output of the best p1 model obtained. As we can see from the estimates there is a tendency against ties formation as well as less reciprocity than that expected by chance. Main and Homophily effects were added to the model, the three nodal attributes considered are Phylum, Predator and life-cycle Stage. The overall tendency seems to be against forming ties within the same category group except for the stage attribute.

Markov Graph Model

```
Call:
ergm(formula = net ~ edges + mutual + ostar(2) + ostar(3) + +gwodegree(decay = log(1.3),
  fixed = TRUE) + nodefactor("predator") + nodefactor("Stage ID") +
  nodefactor("Phylum") + nodematch("predator") + nodematch("Stage ID") +
  nodematch("Phylum"), control = control.ergm(seed = 1))

Iterations: 16 out of 20
Monte Carlo MLE Results:
```

| | Estimate | Std. Error | MCMC % | z value | Pr(> z) | |
|-----------------------------------|------------|------------|--------|----------|----------|-----|
| edges | -1.063e+01 | 5.218e-02 | 63 | -203.677 | <1e-04 | *** |
| mutual | -2.196e+00 | 1.085e-02 | 82 | -202.275 | <1e-04 | *** |
| ostar2 | 6.723e-02 | 4.324e-03 | 0 | 15.549 | <1e-04 | *** |
| ostar3 | -7.694e-04 | 1.055e-04 | 1 | -7.290 | <1e-04 | *** |
| gwodeg.fixed.0.262364264467491 | -1.289e+00 | 1.157e-02 | 41 | -111.401 | <1e-04 | *** |
| nodefactor.predator.1 | 2.398e+00 | 3.710e-02 | 18 | 64.630 | <1e-04 | *** |
| nodefactor.Stage ID.2 | 3.769e+00 | 4.524e-02 | 8 | 83.330 | <1e-04 | *** |
| nodefactor.Stage ID.3 | 2.635e+00 | 4.079e-02 | 12 | 64.601 | <1e-04 | *** |
| nodefactor.Stage ID.4 | 3.152e+00 | 3.528e-02 | 15 | 89.317 | <1e-04 | *** |
| nodefactor.Phylum.Annelida | 8.612e-01 | 2.284e-02 | 87 | 37.710 | <1e-04 | *** |
| nodefactor.Phylum.Chelicerata | -9.472e-01 | 3.618e-02 | 99 | -26.181 | <1e-04 | *** |
| nodefactor.Phylum.Chordata | 1.670e+00 | 5.410e-02 | 8 | 30.862 | <1e-04 | *** |
| nodefactor.Phylum.Ciliophora | 1.368e+00 | 2.152e-02 | 92 | 63.580 | <1e-04 | *** |
| nodefactor.Phylum.Crustacea | 9.165e-01 | 5.246e-02 | 9 | 17.471 | <1e-04 | *** |
| nodefactor.Phylum.Echinodermata | 4.348e-01 | 2.745e-02 | 98 | 15.843 | <1e-04 | *** |
| nodefactor.Phylum.Hexapoda | -1.825e-02 | 2.977e-02 | 97 | -0.613 | 0.540 | |
| nodefactor.Phylum.Mollusca | 1.368e+00 | 4.653e-02 | 11 | 29.395 | <1e-04 | *** |
| nodefactor.Phylum.Nematoda | 3.256e-03 | 2.918e-02 | 20 | 0.112 | 0.911 | |
| nodefactor.Phylum.Other | 5.596e-01 | 2.378e-02 | 94 | 23.537 | <1e-04 | *** |
| nodefactor.Phylum.Platyhelminthes | 5.204e-01 | 3.595e-02 | 12 | 14.476 | <1e-04 | *** |
| nodematch.predator | -2.676e+00 | 3.098e-02 | 16 | -86.365 | <1e-04 | *** |
| nodematch.Stage ID | 2.643e+00 | 4.726e-02 | 7 | 55.931 | <1e-04 | *** |
| nodematch.Phylum | -1.038e+00 | 2.187e-02 | 6 | -47.446 | <1e-04 | *** |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
AIC: 7647    BIC: 7837    (Smaller is better.)
```

Figure 13, R output of the best Markov Graph Model

Figure 13 shows the output of the best Markov Model obtained. Fitting the data to a Markov Model was difficult due to degeneracy issues, to solve this problem an alternating k-star term was added. The resulting parameters effects are consistent with those of the p1 model. The out-star parameters have opposite effects, and the alternating k-term seems to indicate uniformity among nodes in terms of out-degree centrality.

Social Circuit Model

```
Call:
ergm(formula = net ~ edges + mutual + nodefactor("predator") +
      nodefactor("Stage ID") + nodematch("predator") + nodematch("Stage ID") +
      nodefactor("Phylum") + nodematch("Phylum") + dgwesp(fixed = T,
      type = "ISP") + dgwdsp(fixed = T, type = "OSP"), control = control.ergm(seed = 1))

Iterations: 15 out of 20
Monte Carlo MLE Results:
```

| | Estimate | Std. Error | MCMC % | z value | Pr(> z) | |
|-----------------------------------|-----------|------------|--------|---------|----------|-----|
| edges | -9.500895 | 1.167472 | 0 | -8.138 | < 1e-04 | *** |
| mutual | -2.268632 | 0.367539 | 0 | -6.172 | < 1e-04 | *** |
| nodefactor.predator.1 | 2.625247 | 0.553015 | 0 | 4.747 | < 1e-04 | *** |
| nodefactor.Stage ID.2 | 4.051442 | 0.509213 | 0 | 7.956 | < 1e-04 | *** |
| nodefactor.Stage ID.3 | 2.787788 | 0.532803 | 0 | 5.232 | < 1e-04 | *** |
| nodefactor.Stage ID.4 | 3.475252 | 0.523005 | 0 | 6.645 | < 1e-04 | *** |
| nodematch.predator | -2.686282 | 0.492103 | 0 | -5.459 | < 1e-04 | *** |
| nodematch.Stage ID | 2.771997 | 0.509625 | 0 | 5.439 | < 1e-04 | *** |
| nodefactor.Phylum.Annelida | 1.056829 | 0.487179 | 0 | 2.169 | 0.03006 | * |
| nodefactor.Phylum.Chelicerata | -1.276689 | 0.973444 | 0 | -1.312 | 0.18968 | |
| nodefactor.Phylum.Chordata | 2.579143 | 0.455175 | 0 | 5.666 | < 1e-04 | *** |
| nodefactor.Phylum.Ciliophora | 1.682166 | 0.424526 | 0 | 3.962 | < 1e-04 | *** |
| nodefactor.Phylum.Crustacea | 1.083193 | 0.449719 | 0 | 2.409 | 0.01601 | * |
| nodefactor.Phylum.Echinodermata | 0.612377 | 0.536524 | 0 | 1.141 | 0.25371 | |
| nodefactor.Phylum.Hexapoda | -0.089792 | 0.707879 | 0 | -0.127 | 0.89906 | |
| nodefactor.Phylum.Mollusca | 1.350883 | 0.449982 | 0 | 3.002 | 0.00268 | ** |
| nodefactor.Phylum.Nematoda | 0.127863 | 0.354062 | 0 | 0.361 | 0.71800 | |
| nodefactor.Phylum.Other | 0.811368 | 0.520789 | 0 | 1.558 | 0.11924 | |
| nodefactor.Phylum.Platyhelminthes | 0.564770 | 0.345982 | 0 | 1.632 | 0.10260 | |
| nodematch.Phylum | -0.798877 | 0.135794 | 0 | -5.883 | < 1e-04 | *** |
| gwesp.ISP.fixed.0 | -0.178385 | 0.024191 | 0 | -7.374 | < 1e-04 | *** |
| gwdsp.OSP.fixed.0 | -0.208026 | 0.009041 | 0 | -23.008 | < 1e-04 | *** |

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

AIC: 7470    BIC: 7652    (Smaller is better.)
```

Figure 14, R output of the best social circuit model

Figure 14 shows the results for the best social circuit model in terms of AIC and BIC. The nodal statistic parameters of homophily and main effect are similar to those of other model types, as well as the edges and mutual parameters. The last two parameters of Figure 14 indicate, respectively, the tendency towards forming triangles and k-2 paths; both these parameters are negative, meaning that there is a tendency against cluster formation and that we observe less triangles and k-2 paths than what we would expect by chance. Overall, this model is the best in terms of AIC and BIC.

7. REFERENCES

C. Dieter Zander, Neri Josten, Kim C. Detloff, Robert Poulin, John P. McLaughlin, and David W. Thielges, 2011. *"Food web including metazoan parasites for a brackish shallow water ecosystem in Germany and Denmark"*, Ecology 92:2007

"Network visualization with R" PolNet 2016 Workshop, St. Louis, MO Katherine Ognyanova, Rutgers University Web: www.kateto.net, Twitter: [ognyanova](https://twitter.com/ognyanova)

Mark Newman – *"Networks (2018, Oxford University Press)"*