CMEE lecture – Determining the structure of ecological networks

Monday 2nd March 2015

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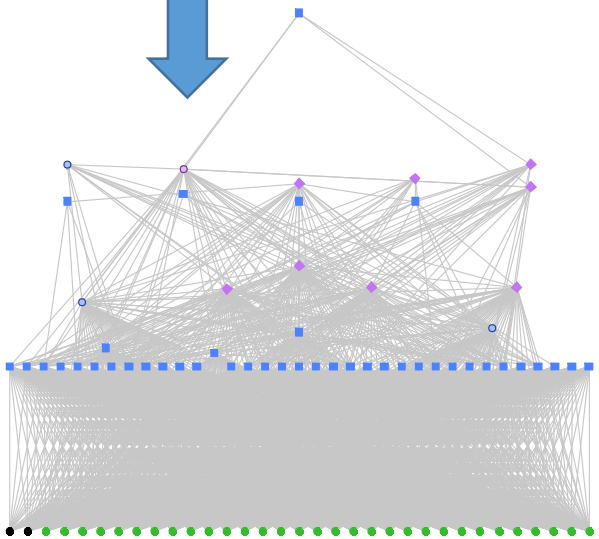
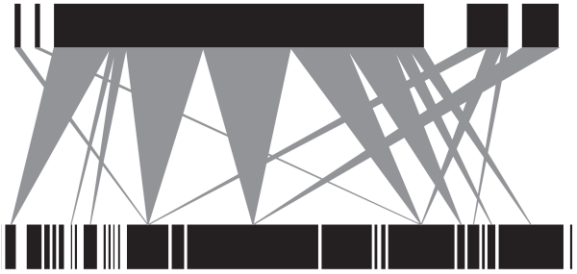
Ecological networks

Trophic networks

e.g.

- Food webs
- Host-parasite networks

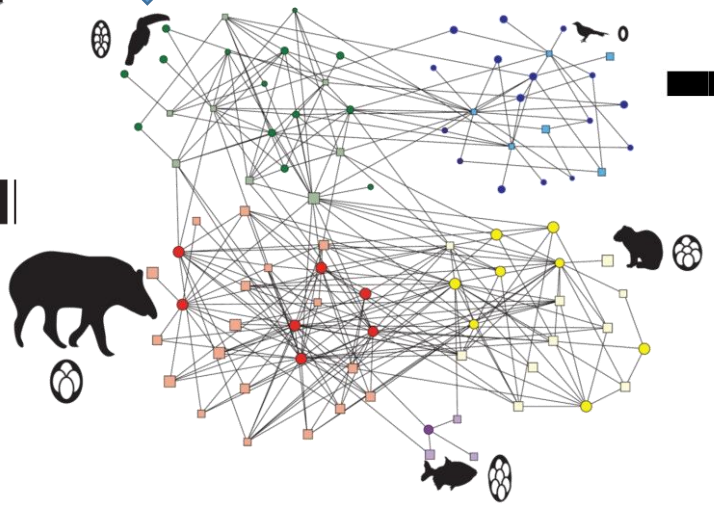


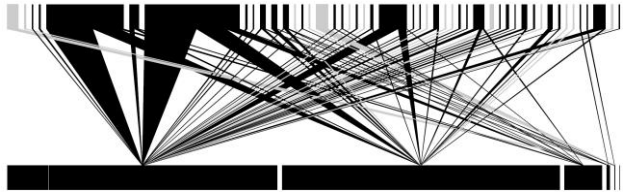


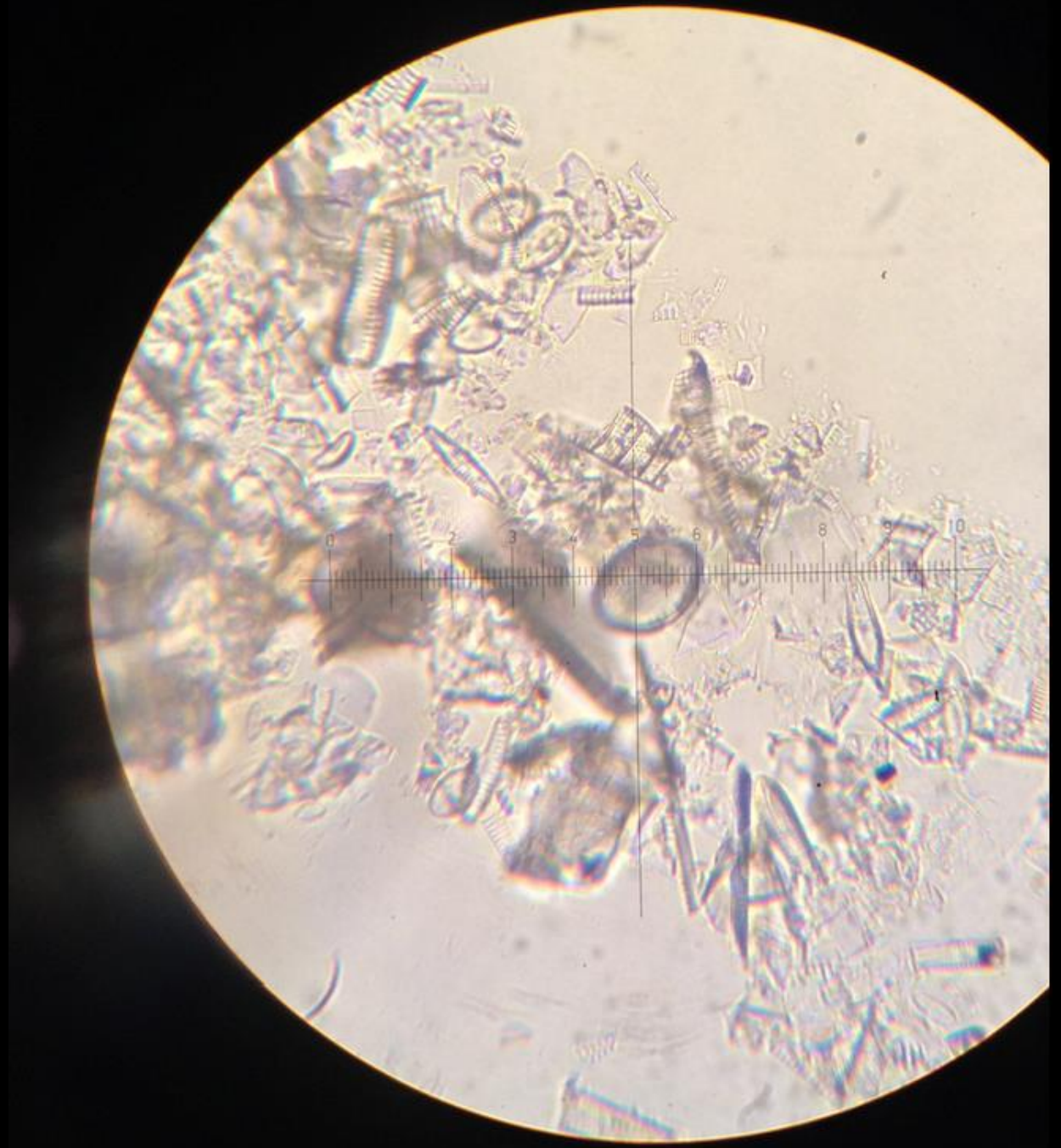
Mutualistic networks

e.g.

- Plant visitor networks
- Frugivore networks







Methods for constructing food webs

1. Gut contents analysis
   - Very slow and labour-intensive.
   - Rare interactions are often missed.
   - biased, e.g. soft bodied prey are missed.

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   - Reliant on the quality of the data gathered from the literature.
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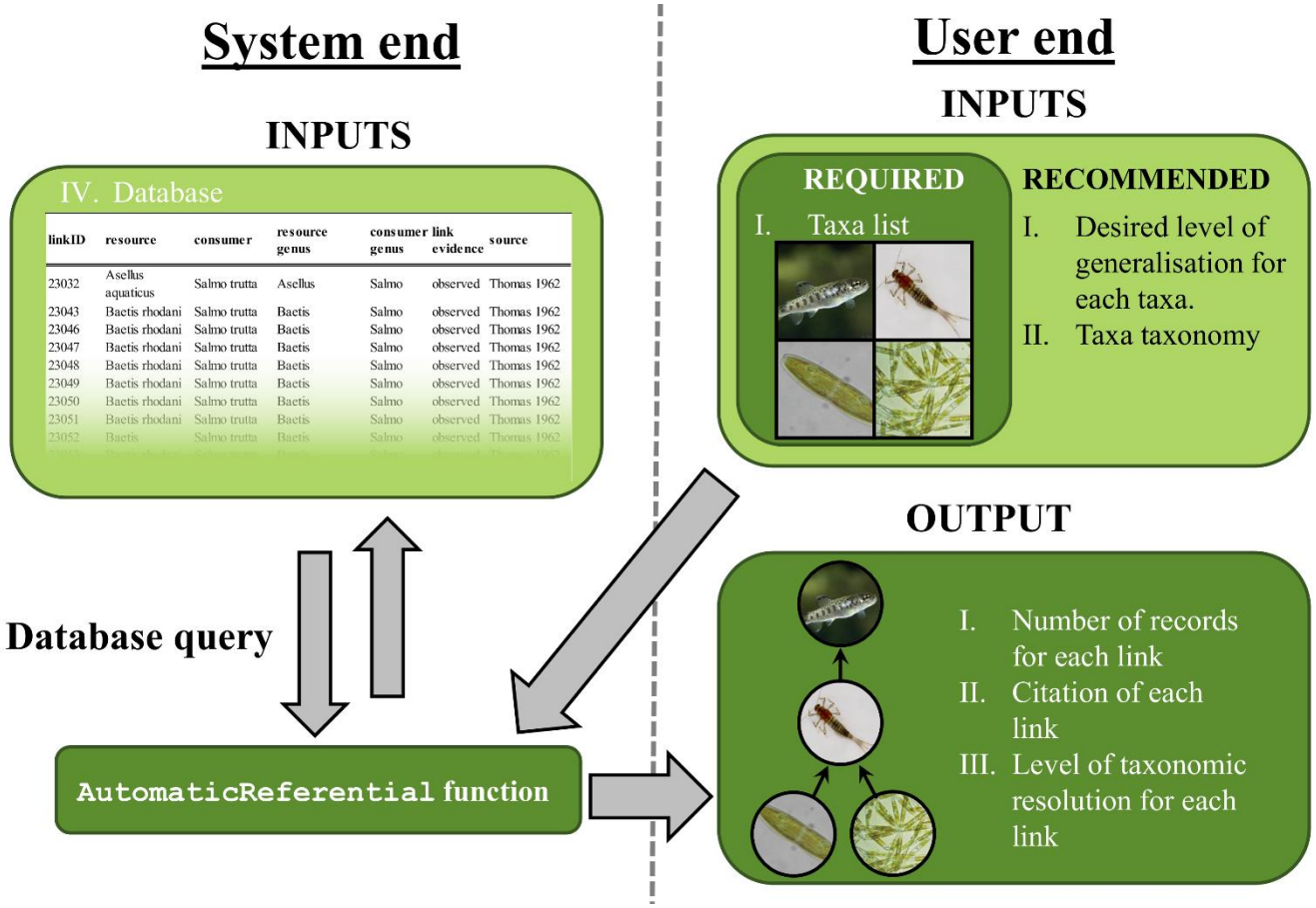
- Needs to be automated, which would allow networks to be repeated and queried by different researchers

The Automatic Referential method:

Searches for matches between a given species list and a given reference dataset.



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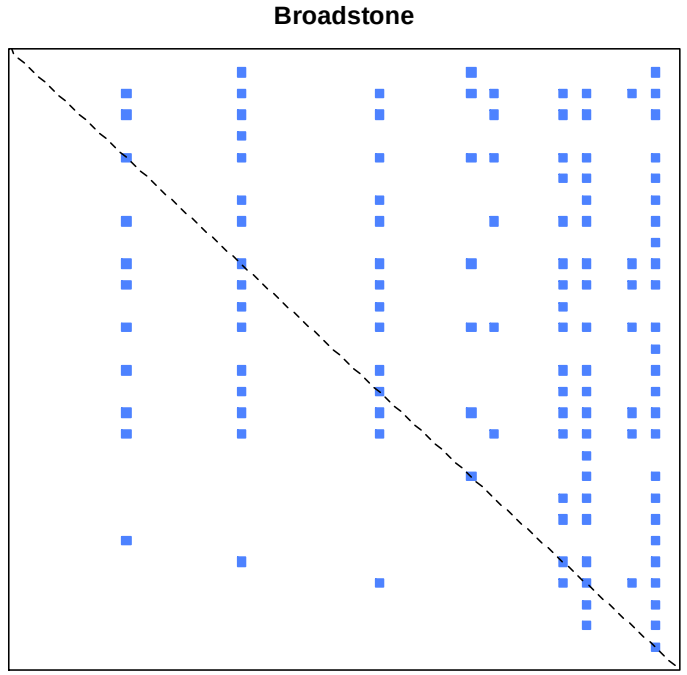
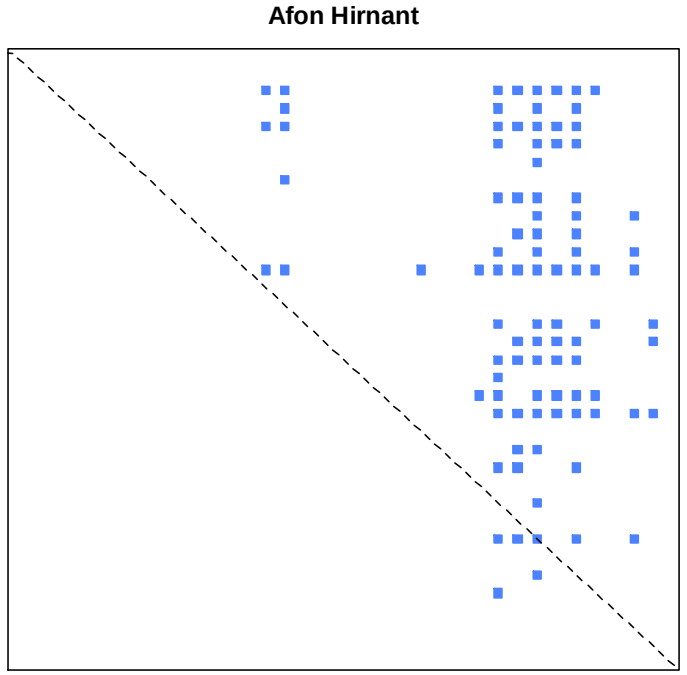
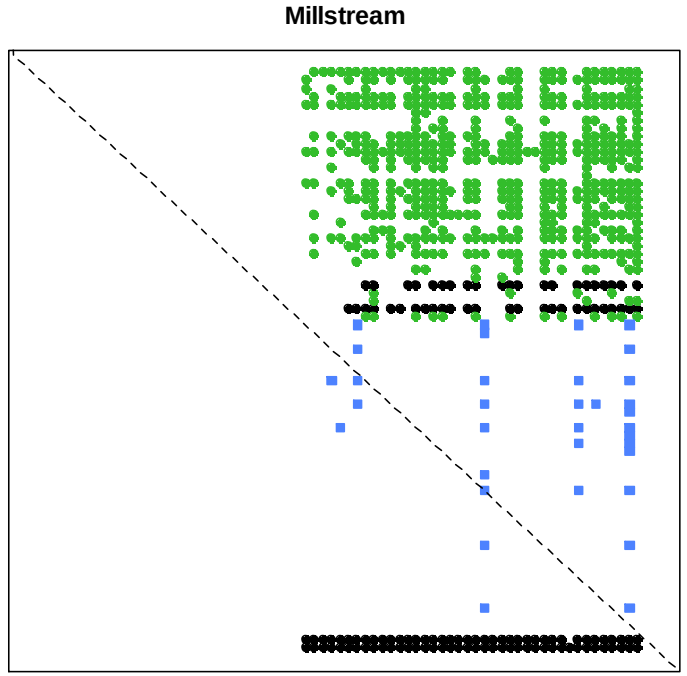
3. Deterministic models
   - Require prior knowledge of the structure of the network

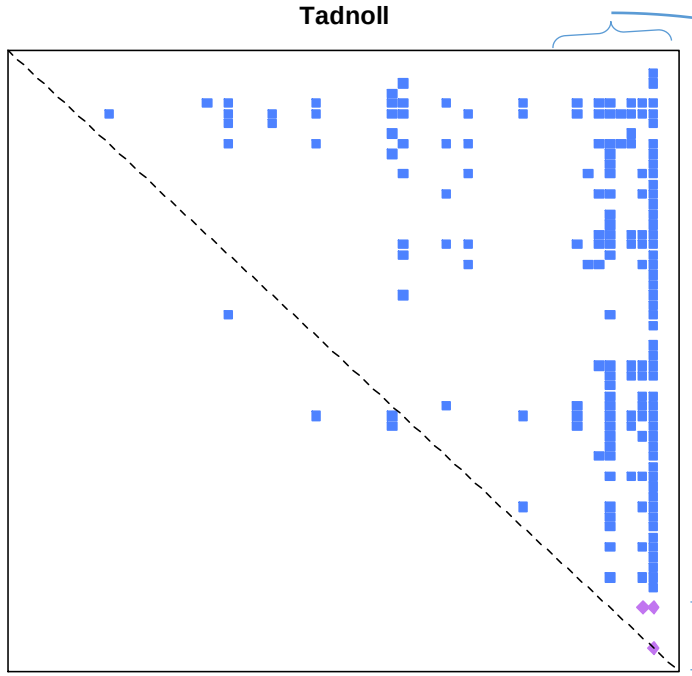
Empirical webs





Invertebrate-invertebrate interactions





Algae-invertebrates

Invertebrate-fish

detritus-invertebrates

Fish-fish

Interactions from the literature

Constructed a dataset of interactions from the literature:

- 20,823 pairwise trophic interactions
- from 51 different data sources
- 10,348 producer-animal links,
- 9,531 animal-animal links
- 944 detritus-animal links
- Up to date, consistent taxonomy

Deterministic models

- Allometric Diet Breadth Model (Petchey et al 2008)
- 3 simpler models based on body size (Allesina 2011)
  1. B_j-B_i (Difference model)
  2. B_i/B_j (Ratio model)
  3. $(B_j-B_i)(B_i/B_j)$ (Difference/Ratio model)

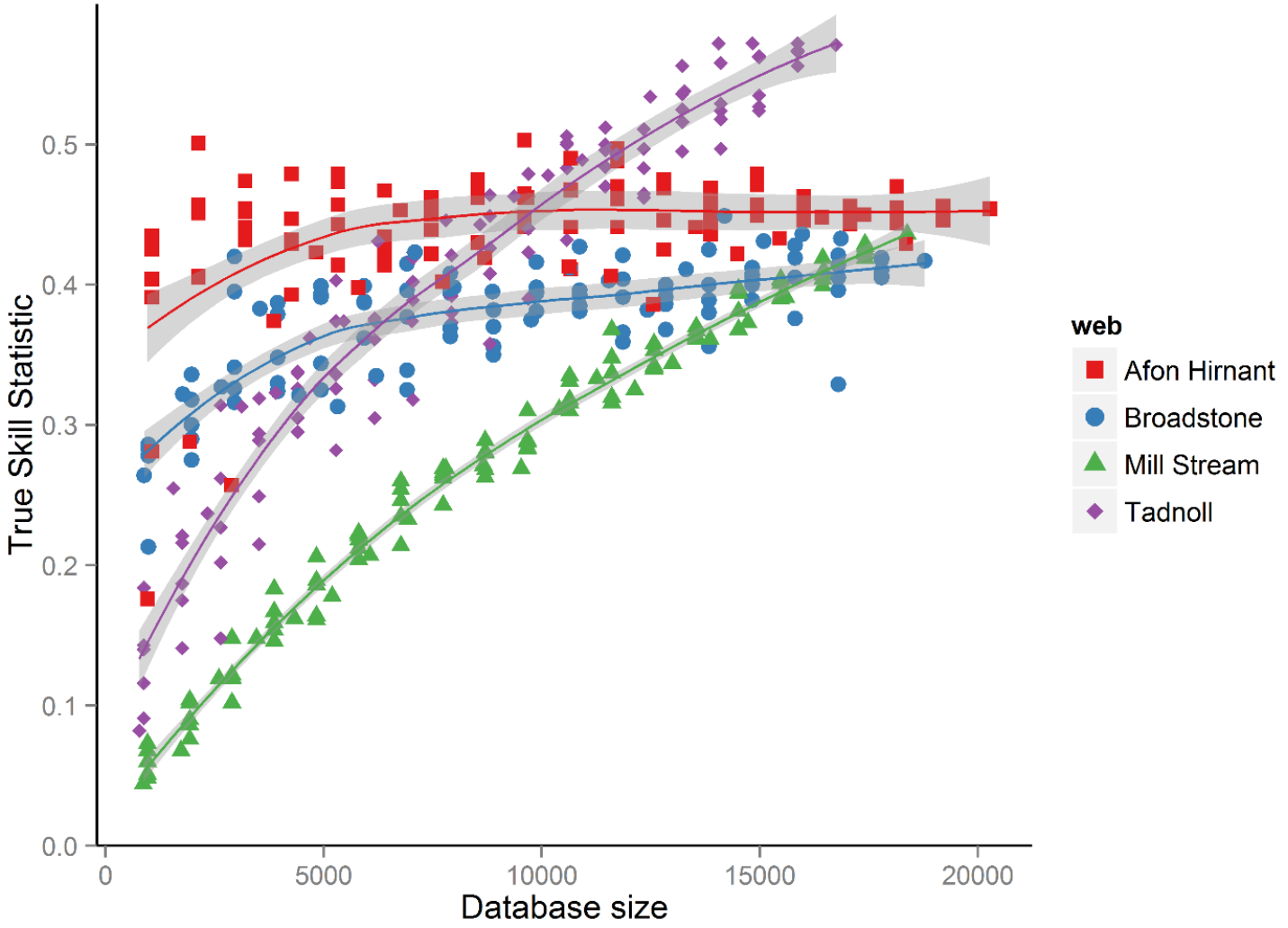
Measures of performance

- True Positive Rate (most commonly used) (a)
  - Links which were found empirically and were also predicted
- False Positive Rate (b)
  - Links which were predicted, but not found empirically
- False Negative Rate (c)
  - Links which were found empirically but not predicted
- True Negative Rate (d)
  - Links which were neither found empirically or predicted

$$TSS = (ad - bc)/[(a + c)(b + d)]$$

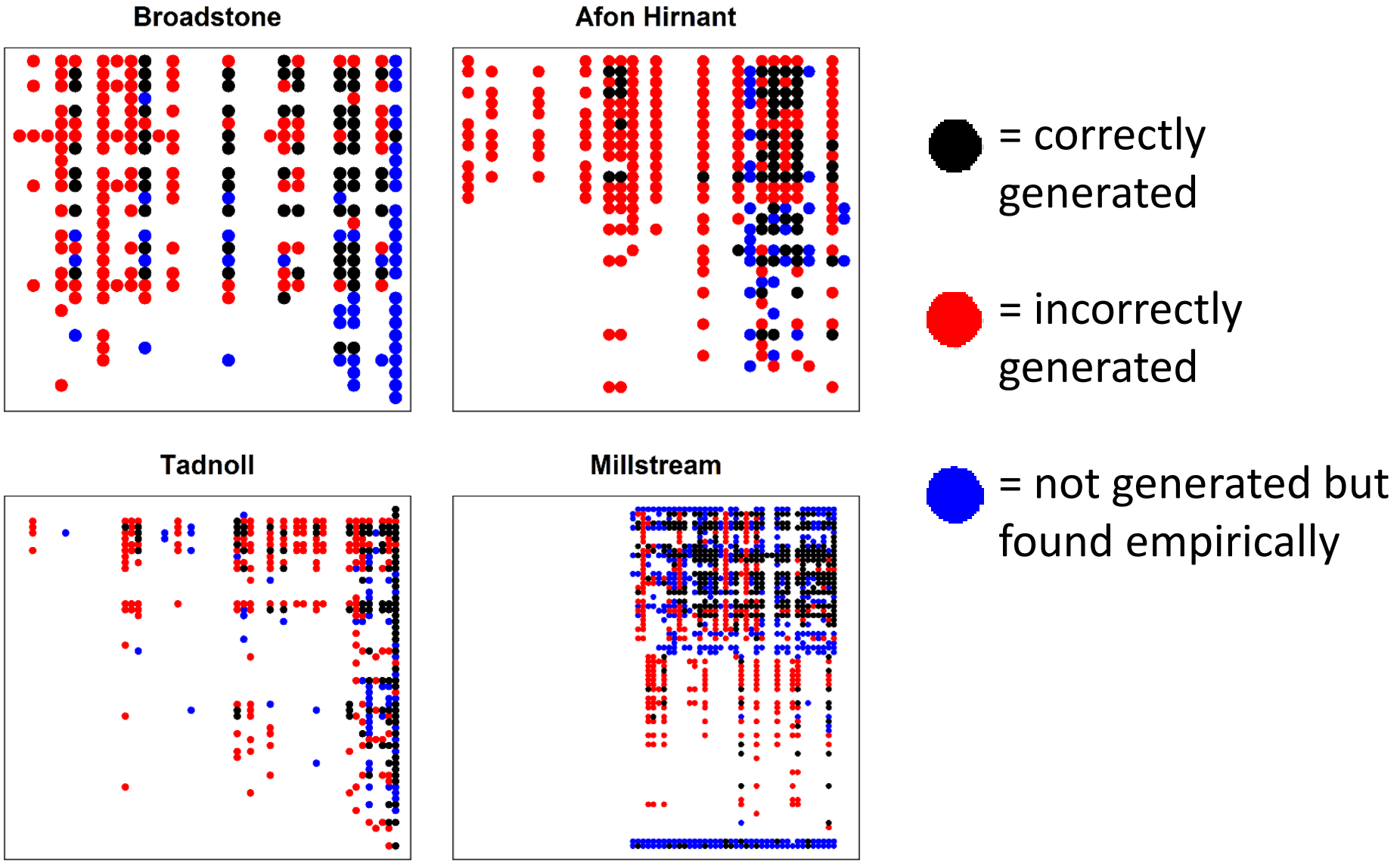
How is the quality of the food webs generated by the AR method impacted by the quality of the reference dataset?

The quality of the generated food webs improved as the quality of the dataset improved



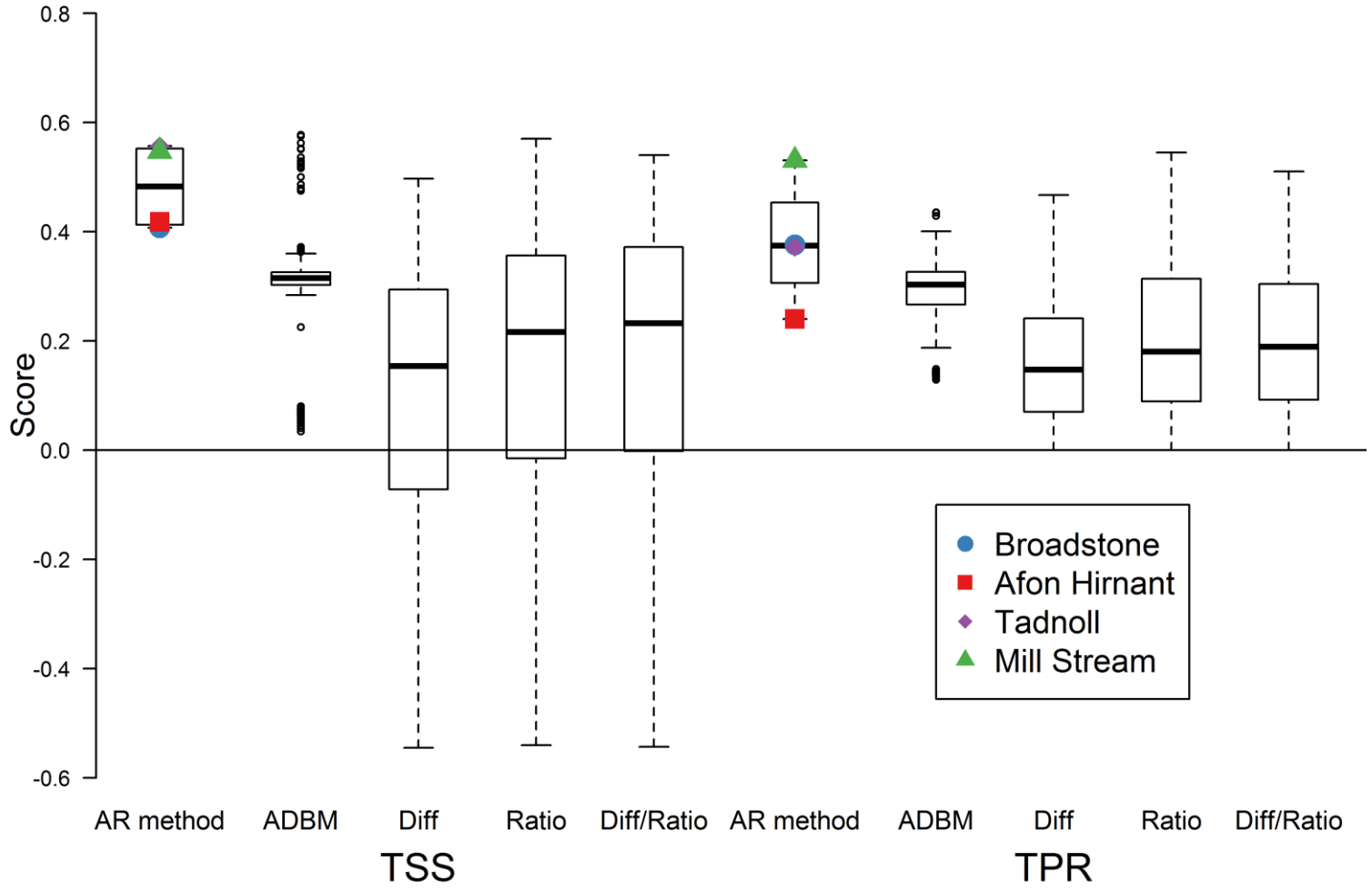
Does the AR method generate realistic food webs compared with the empirical data?

The AR method generated realistic food webs



How does the performance of the AR method compare to deterministic models?

Without parameter optimisation the AR method out-performed deterministic models



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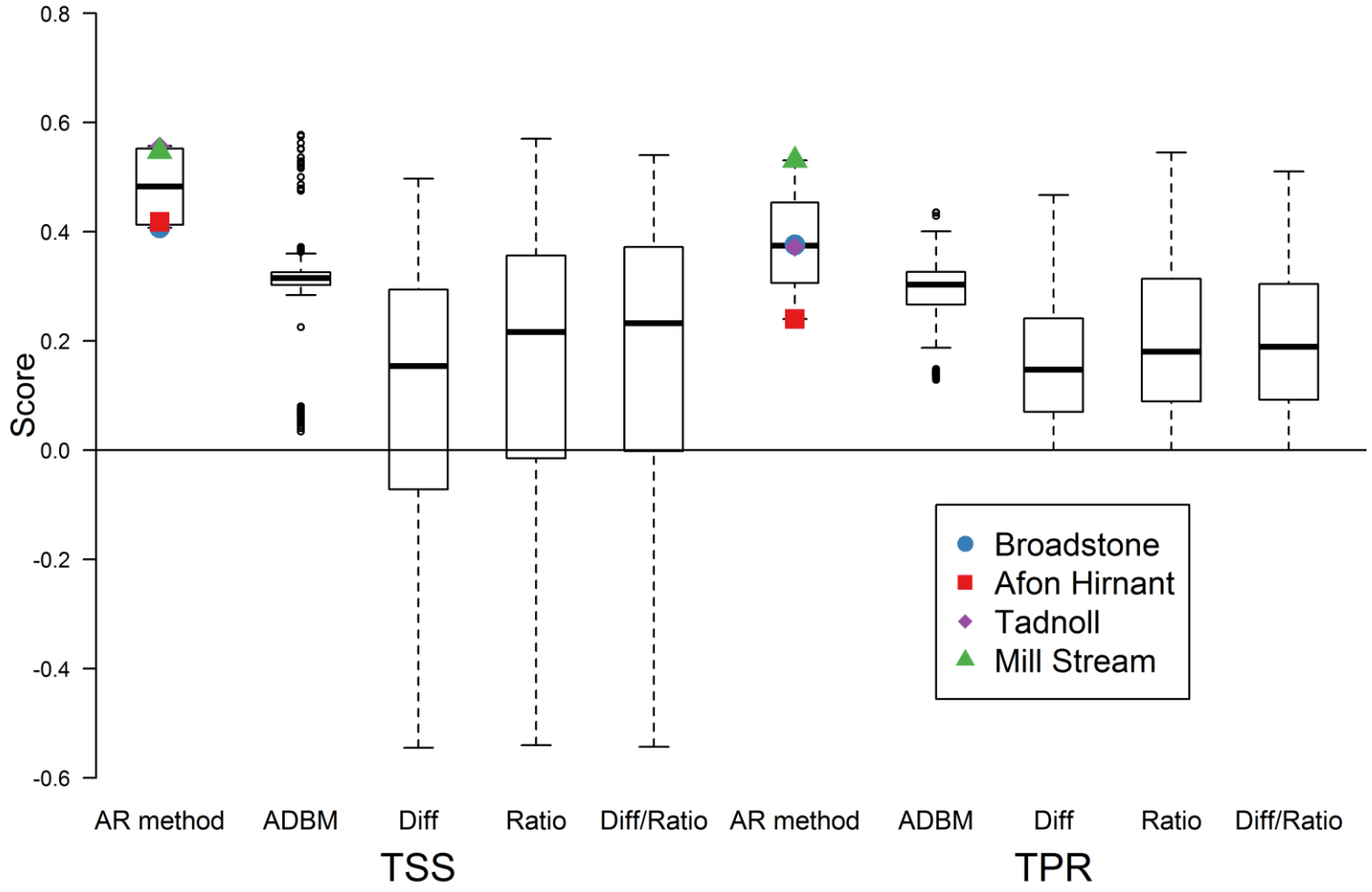

And some networks produced were very poor

Conclusions

- For predicting new networks, the AR method is the most appropriate approach
- However, combining this with deterministic models might produce the best quality predictions…

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- For predicting new networks, the AR method is the most appropriate approach
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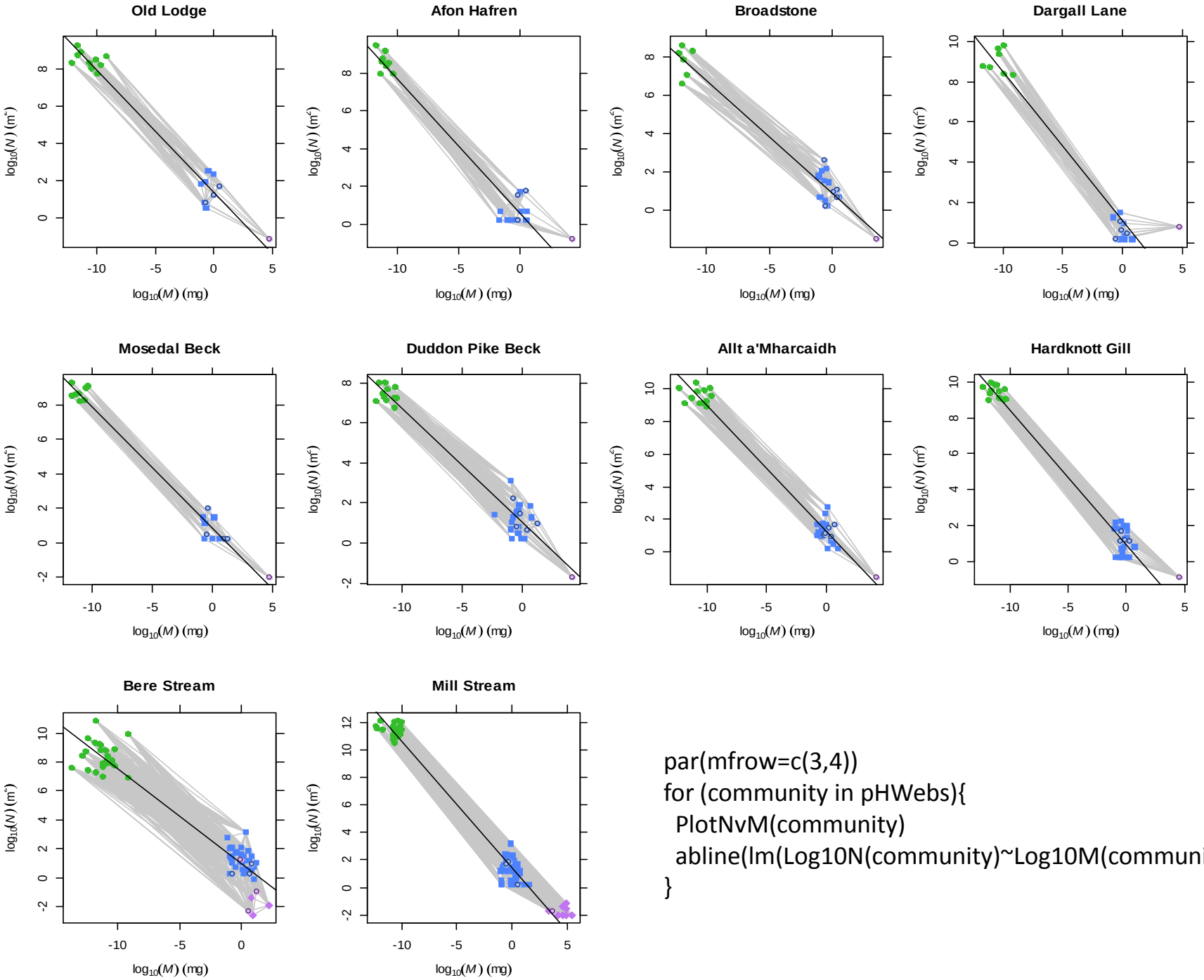
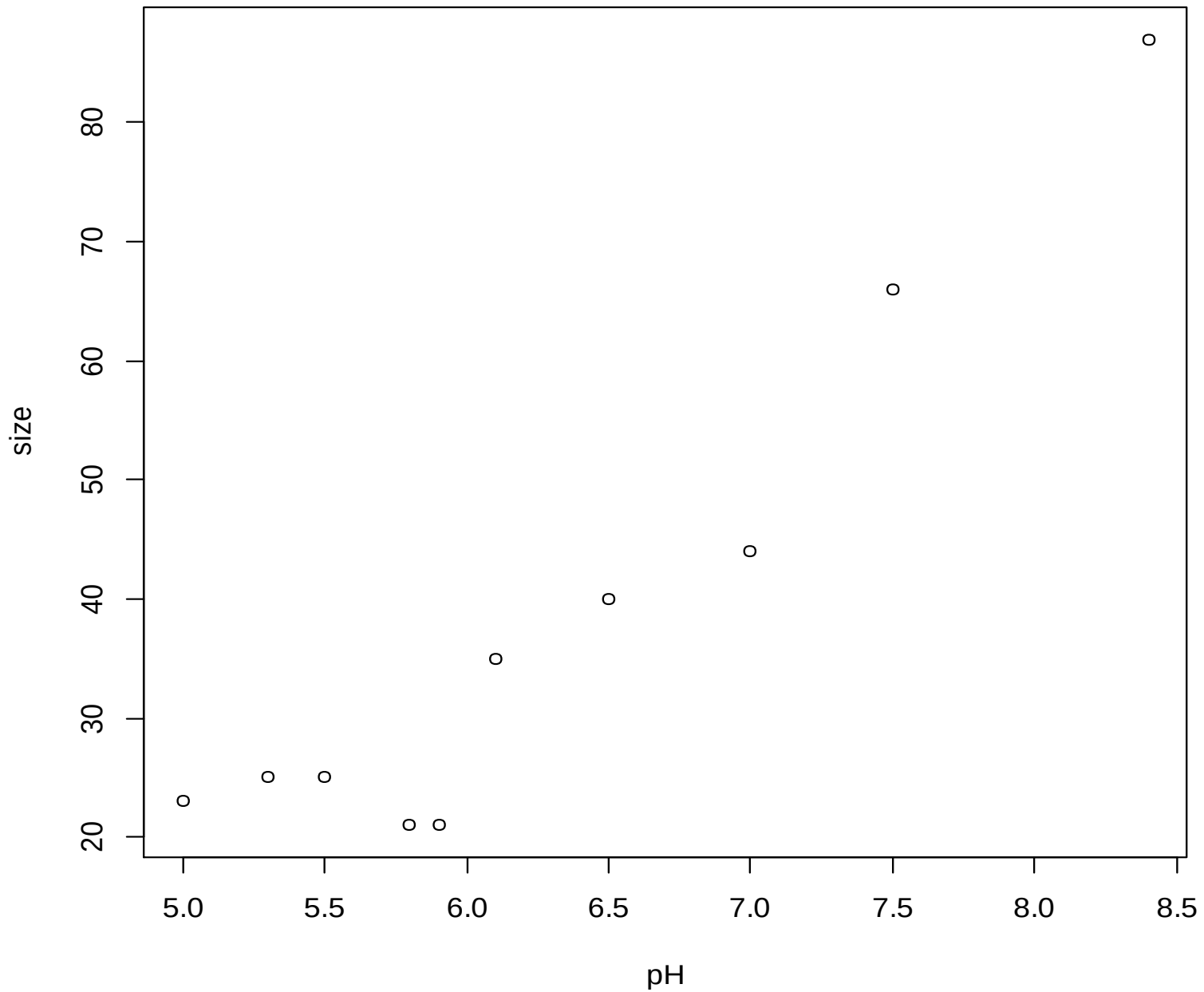
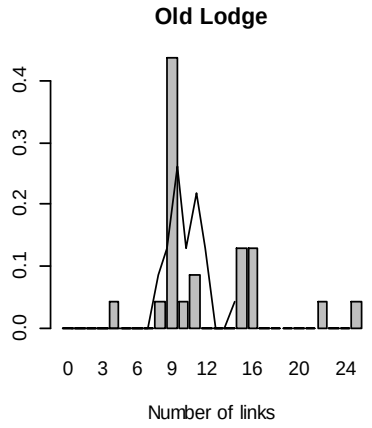
Any Questions?

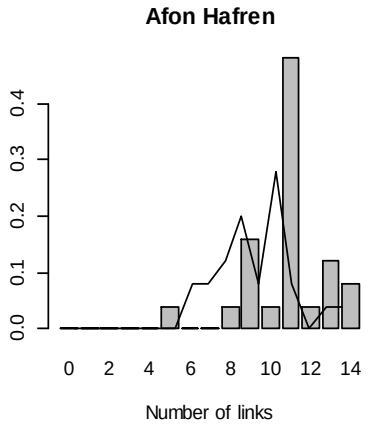


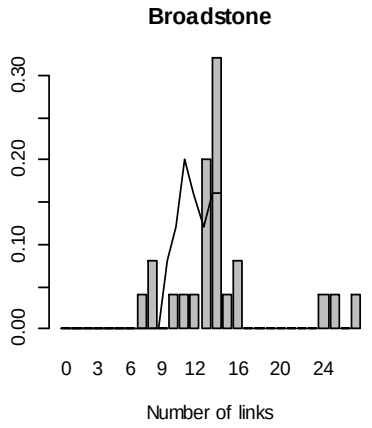

```
par(mfrow=c(3,4))
for (community in pHWebs){
 PlotNvM(community)
 abline(lm(Log10N(community)~Log10M(community)))
}
```

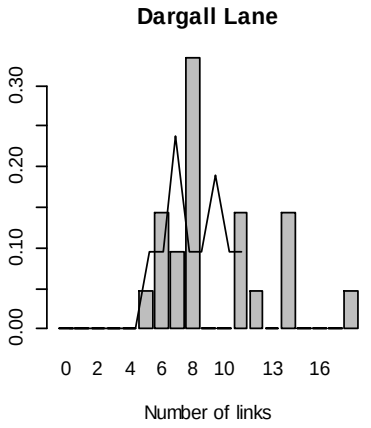


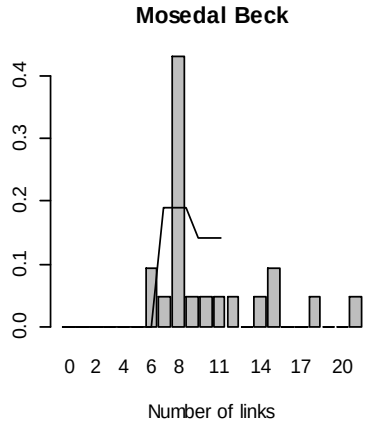

```
pH <- CollectionCPS(pHWebs)$pH
size <- sapply(pHWebs, 'NumberOfNodes')
plot(size~pH)
```

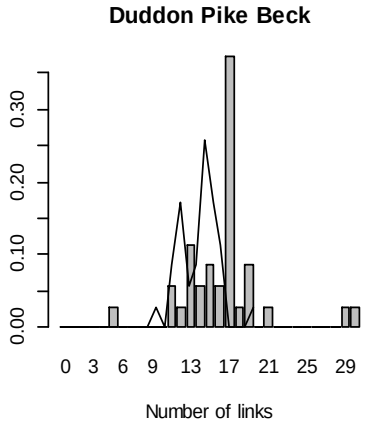


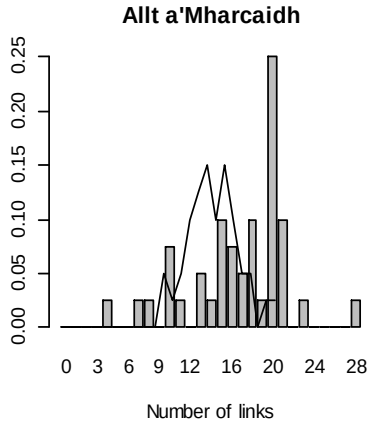


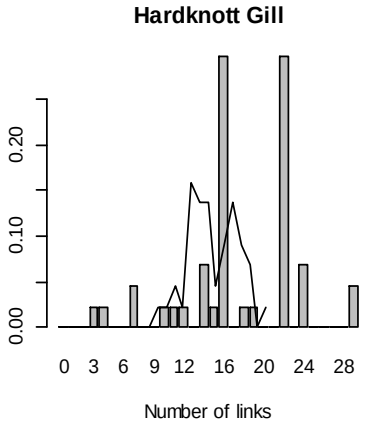


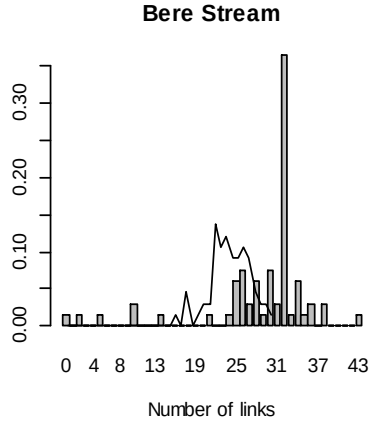


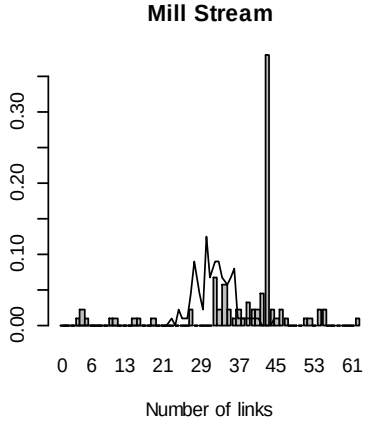




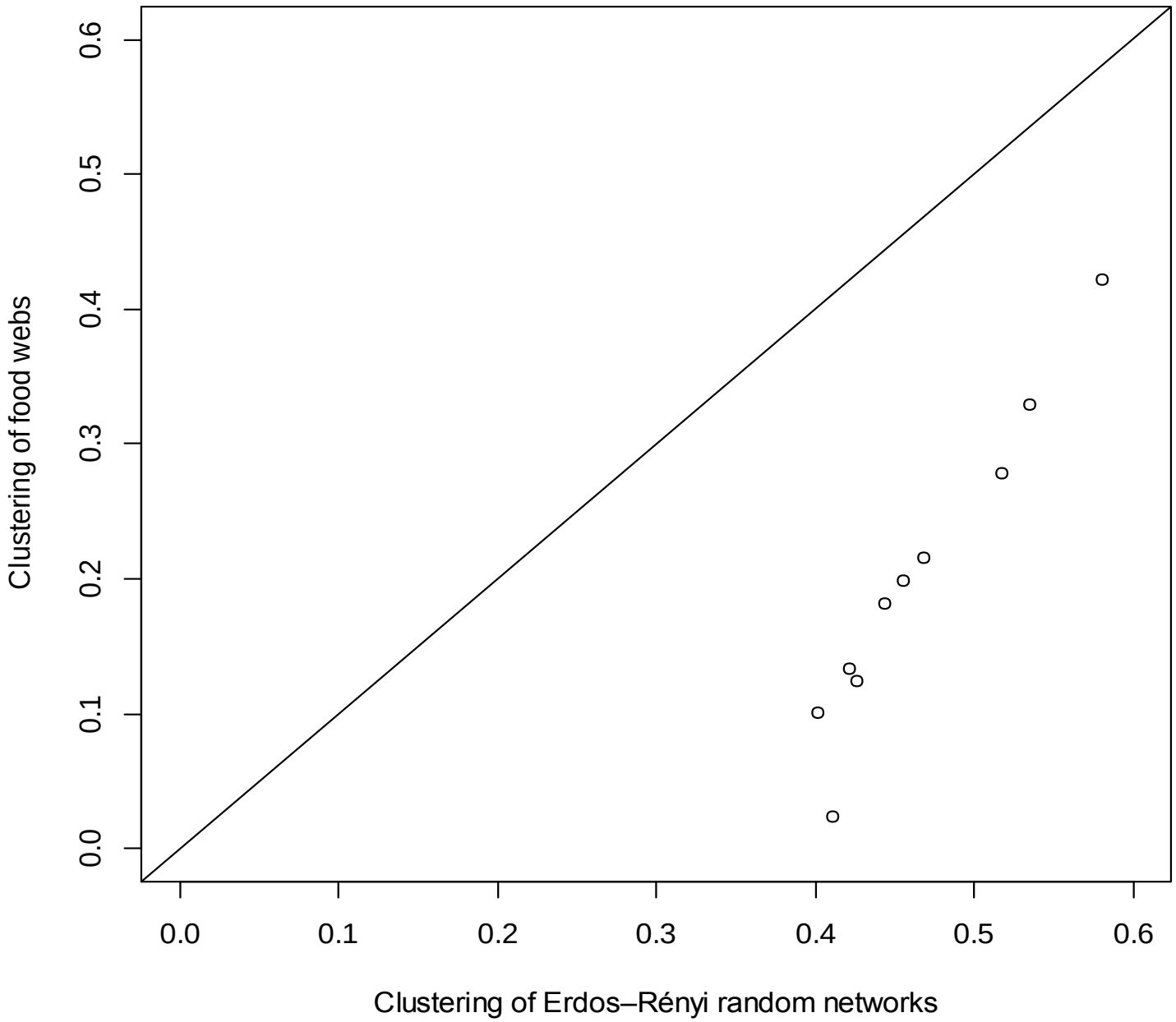




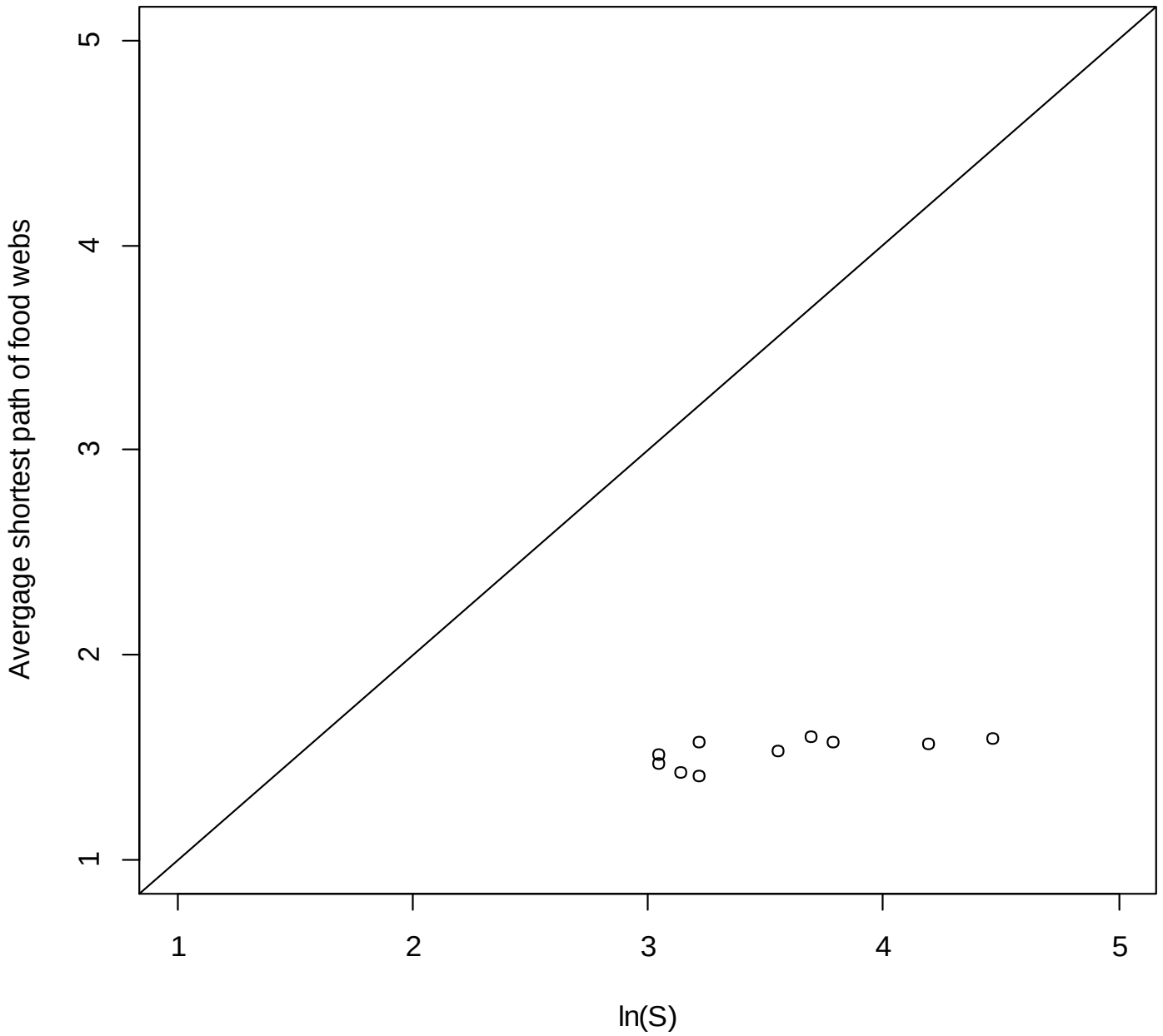




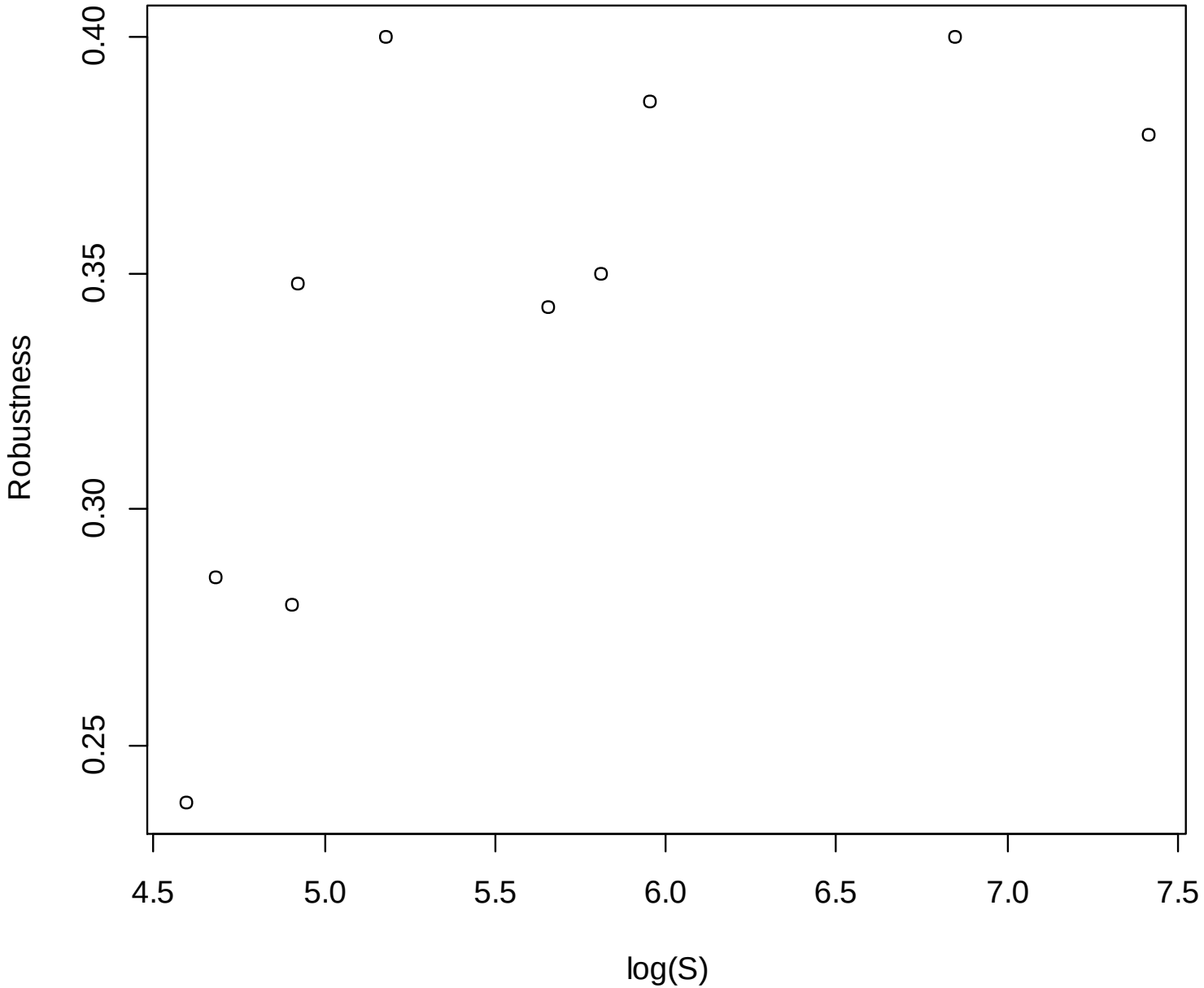

```
par(mfrow=c(3,4))
for (community in pHWebs){
  PlotDegreeDistribution(community, main=CPS(community)$title)
  g <- ToIgraph(community)
  n <- NumberOfNodes(community)
  m <- NumberOfTrophicLinks(community)
  ER <- erdos.renyi.game(n=n, p.or.m=m, type="gnm")
  points(degree.distribution(ER), type='l')
}
```




```
CC <- {}
ER.CC <- {}
for (community in pHWebs){
  g <- ToIgraph(community)
  CC <- c(CC, transitivity(g))
  n <- NumberOfNodes(community)
  m <- NumberOfTrophicLinks(community)
  ER <- erdos.renyi.game(n=n, p.or.m=m, type="gnm")
  ER.CC <- c(ER.CC, transitivity(ER))
}
plot(CC~ER.CC, ylim=c(0,0.6), xlim=c(0,0.6),
                ylab="Clustering of food webs",
                xlab="Clustering of Erdős–Rényi random networks")
abline(0,1)
```




```
SP <- {}
size <- {}
for (community in pHWebs){
  community <- RemoveIsolatedNodes(community)
  g <- ToIgraph(community)
  SP <- c(SP, mean(shortest.paths(g)))
 size <- c(size, NumberOfNodes(community))
}
plot(SP~log(size), ylim=c(1,5), xlim=c(1,5),
    ylab="Avergage shortest path of food webs",
    xlab="ln(S)")
abline(0,1)
```


Robustness
0.25
0.30
0.35
0.40
4.5
5.0
5.5
6.0
6.5
7.0
7.5
log(S)