Lab 4

Clint Valentine

Designing Optimal Harvesting Regimes

First we will use a function to remove disconnected nodes from the food webs downloaded at the below locations.

```r
# Rows are consumed by columns
library(igraph)
library(fmsb)
```

```
## Warning: package 'fmsb' was built under R version 3.1.3
```

```r
source("http://faraway.neu.edu/data/cb.R")
rm.solo <- function (adj.matrix) {
  adj.matrix <- as.matrix(adj.matrix)
  loc <- which(rowSums(adj.matrix) == 0  & colSums(adj.matrix) == 0)
  adj.matrix <- adj.matrix[-loc, -loc]
  return(adj.matrix)
}


host <- 'http://faraway.neu.edu/data/foodwebs/'

benguela <- rm.solo(read.table(paste(host, 'benguela.txt', sep='')))
britishgrasslands <- rm.solo(read.table(paste(host, 'british-grasslands.txt', sep='')))
cantoncreek <- rm.solo(read.table(paste(host, 'canton-creek.txt', sep='')))
chesapeakebay <- rm.solo(read.table(paste(host, 'chesapeake-bay.txt', sep='')))
coachella <- rm.solo(read.table(paste(host, 'coachella.txt', sep='')))
scotchbroom <- rm.solo(read.table(paste(host, 'scotch-broom.txt', sep='')))
skipwithpond <- rm.solo(read.table(paste(host, 'skipwith-pond.txt', sep='')))
stmarks <- rm.solo(read.table(paste(host, 'st-marks.txt', sep='')))
stonystream <- rm.solo(read.table(paste(host, 'stony-stream.txt', sep='')))

webs <- list('Benguela'=benguela, 'British Grasslands'=britishgrasslands,
             'Canton Creek'=cantoncreek, 'Chesapeakebay'=chesapeakebay,
             'Coachella'=coachella,'Scotchbroom'=scotchbroom,
             'Skipwith Pond'=skipwithpond, 'St. Marks'=stmarks,
             'Stony Stream'=stonystream)


report.adjacency <- function (adj.matrix){
  if (ncol(adj.matrix) == nrow(adj.matrix)) {
    S <- nrow(adj.matrix)
  } else {
    return('Matrix not Square')
  }

  L <- sum(adj.matrix == 1)
  C <- L/(S*S)
```

```r
  avg.degree <- mean(degree(graph.adjacency(adj.matrix)))
  l.G <- average.path.length(graph.adjacency(adj.matrix))

  basal <- length(which(rowSums(adj.matrix) == 0))/S
  intermediate <- length(which(rowSums(adj.matrix) != 0 &
                               colSums(adj.matrix) != 0))/S
  top <- length(which(colSums(adj.matrix) == 0))/S

  return(c(S=S, L=L, C=C, avg.degree=avg.degree, l.G=l.G, basal=basal,
           intermediate=intermediate, top=top ))
}

summ.foodwebs <- matrix(nrow=10, ncol=8,
                        dimnames=list(c(names(webs), 'Mean'),
                                      c('Species', 'Links', 'C', 'Avg. Deg.', 'Path Length',
                                        'Basal', 'Int.', 'Top')))

for (x in 1:length(webs)) {
  summ.foodwebs[x,] <- report.adjacency(webs[[x]])
}
summ.foodwebs['Mean', ] <- colMeans(summ.foodwebs, na.rm=TRUE)

radarchart(as.data.frame(summ.foodwebs), maxmin=FALSE, plty=1, pcol=cb,
           title='Radar Plot of Food Webs and Correlative Parameters')

legend(x='topleft', col=1:10, lty=1, legend=names(webs), cex=0.7)
```
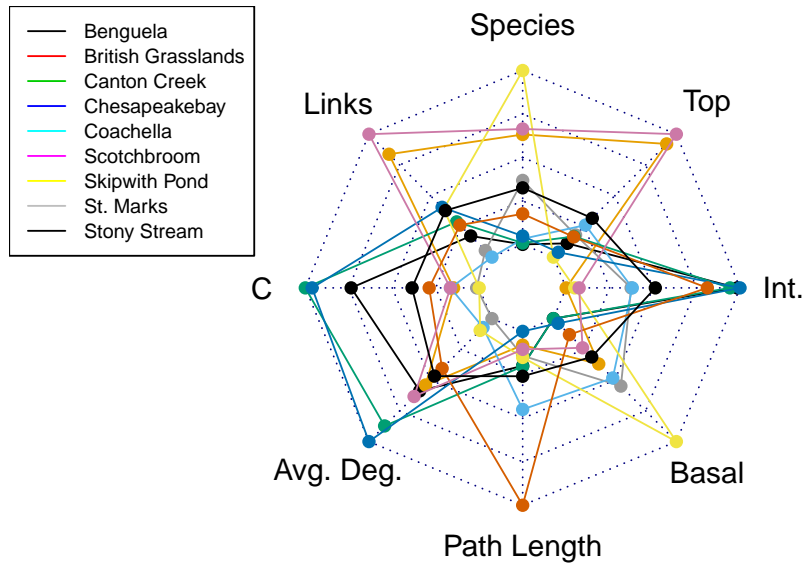
## Radar Plot of Food Webs and Correlative Parameters


```r
relations <- cor(summ.foodwebs[1:9,])

par(mfrow=c(3, 3), mar=c(1.1, 1, 4, 2), oma=c(5, 5, 5 ,0))
for (i in 1:length(webs)) {
  x <- degree.distribution(graph.adjacency(webs[[i]]))
  barplot(x, main=names(webs[i]), names.arg=0:(length(x)-1), yaxt='n')
  axis(2, las=2, line=-0.5)
}

mtext('Degree of Species Distribution', side=1, outer=1, line=2, font=2)
mtext('Frequency', side=2, outer=1, line=2.4, font=2)
mtext('Analysis of Empirical Food Webs', outer=1, line=2, cex=1.5)
```

Analysis of Empirical Food Webs
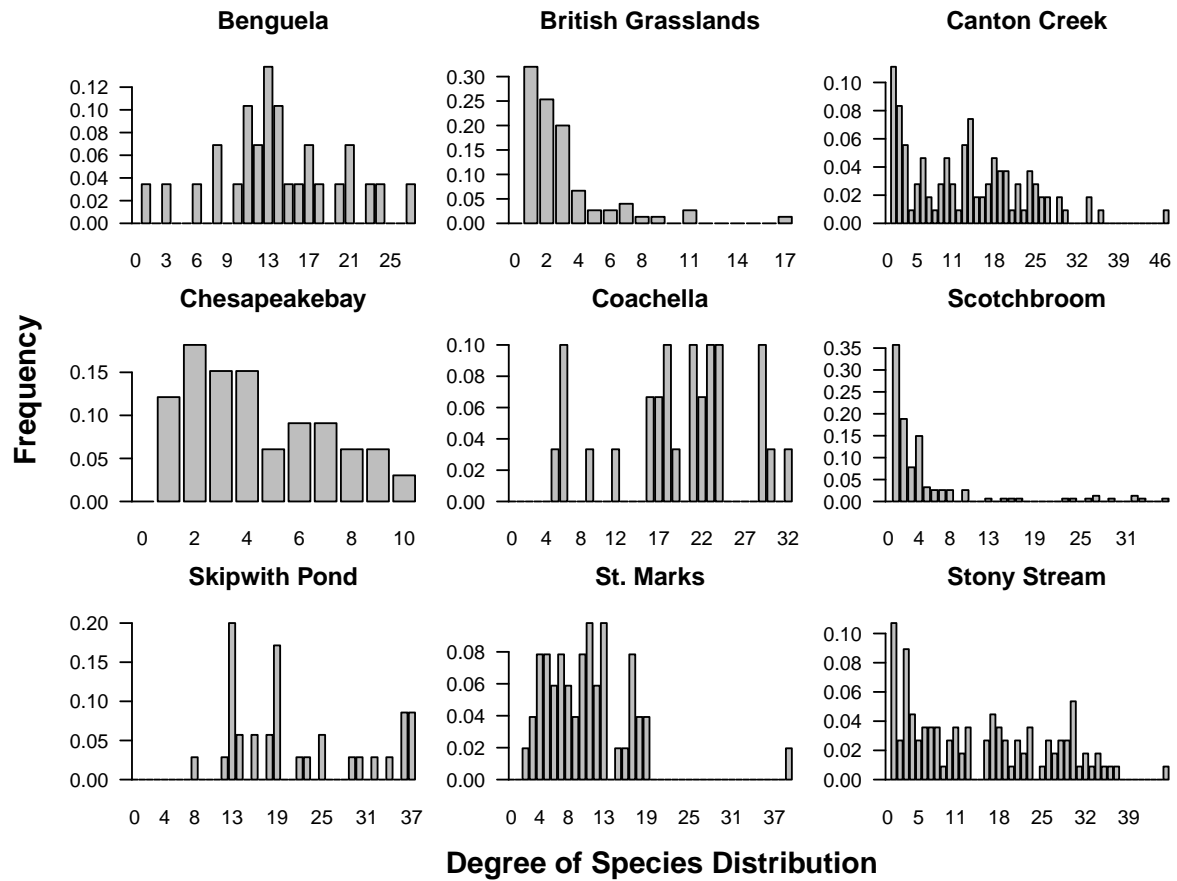
Comparing empirical and model food webs