Appendix A

# Data

## Data Sources

Three food webs were downloaded from the [Dryad Digital Repository](http://datadryad.org/resource/doi:10.5061/dryad.c213h) (Roopnarine & Hertog 2012a, 2012b). Another seven were available from [Ecological Archives](http://esapubs.org/Archive/search.php) (Hechinger et al. 2011; Mouritsen et al. 2011; Thieltges et al. 2011; Zander et al. 2011; Preston et al. 2012). Fourteen webs were provided by Jennifer Dunne of the [PEaCE Lab](http://peacelab.net/) (Baird & Ulanowicz 1989; Warren 1989; Polis 1991; Hall & Raffaelli 1991; Martinez 1991; Christensen & Pauly 1992; Havens 1992; Goldwasser & Roughgarden 1993; Opitz 1996; Waide & Reagan 1996; Yodzis 1998, 2000; Christian & Luczkovich 1999; Martinez et al. 1999; Memmott et al. 2000; Link 2002) that were analyzed in (Dunne et al. 2002, 2004). The remaining 26 food webs were downloaded from the [Interaction Web Database](http://www.nceas.ucsb.edu/interactionweb/html/thomps_towns.html) (Jaarsma et al. 1998; Townsend et al. 1998; Thompson & Townsend 1999, 2000, 2003, 2005; Thompson & Edwards 2001). We also used a subset of sixteen ecosystem networks provided by [Robert Ulanowicz through his website](http://www.cbl.umces.edu/~ulan), and used most recently in Ulanowicz et al. 2014.

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# Interaction strength

Required libraries

library(igraph)  
library(NetIndices)  
library(data.table)  
library(ggplot2)  
library(reshape2)

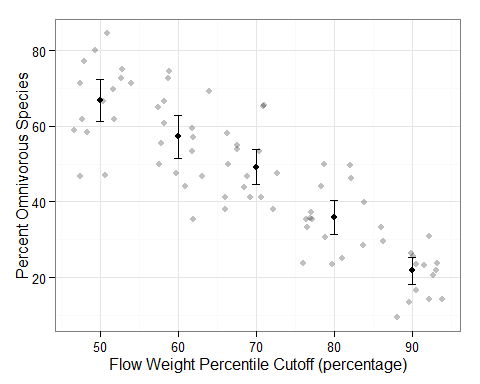
Import the Ulanowicz data

Determine the threshold flow weight above which we call "strong" interactions. Here we subset the Ulanowicz webs by taking just the top 50%, 40%, 30%, 20%, and 10%.

q50 <- sapply(ulanEDGE, function(x){quantile(x[,3], .5)})  
q60 <- sapply(ulanEDGE, function(x){quantile(x[,3], .6)})  
q70 <- sapply(ulanEDGE, function(x){quantile(x[,3], .7)})  
q80 <- sapply(ulanEDGE, function(x){quantile(x[,3], .8)})  
q90 <- sapply(ulanEDGE, function(x){quantile(x[,3], .9)})  
  
uEDGE.50 <- list()  
uEDGE.60 <- list()  
uEDGE.70 <- list()  
uEDGE.80 <- list()  
uEDGE.90 <- list()  
for(i in 1:length(ulanEDGE)){  
 uEDGE.50[[i]] <- ulanEDGE[[i]][which(ulanEDGE[[i]][,3] >= q50[i]),]  
 uEDGE.60[[i]] <- ulanEDGE[[i]][which(ulanEDGE[[i]][,3] >= q60[i]),]  
 uEDGE.70[[i]] <- ulanEDGE[[i]][which(ulanEDGE[[i]][,3] >= q70[i]),]  
 uEDGE.80[[i]] <- ulanEDGE[[i]][which(ulanEDGE[[i]][,3] >= q80[i]),]  
 uEDGE.90[[i]] <- ulanEDGE[[i]][which(ulanEDGE[[i]][,3] >= q90[i]),]  
}  
  
uGRAPH <- lapply(uEDGE.50, function(x){graph.edgelist(as.matrix(x[,1:2]))})  
uGRAPH6 <- lapply(uEDGE.60, function(x){graph.edgelist(as.matrix(x[,1:2]))})  
uGRAPH7 <- lapply(uEDGE.70, function(x){graph.edgelist(as.matrix(x[,1:2]))})  
uGRAPH8 <- lapply(uEDGE.80, function(x){graph.edgelist(as.matrix(x[,1:2]))})  
uGRAPH9 <- lapply(uEDGE.90, function(x){graph.edgelist(as.matrix(x[,1:2]))})  
  
uMAT <- lapply(uGRAPH, get.adjacency, sparse = F)  
uMAT6 <- lapply(uGRAPH6, get.adjacency, sparse = F)  
uMAT7 <- lapply(uGRAPH7, get.adjacency, sparse = F)  
uMAT8 <- lapply(uGRAPH8, get.adjacency, sparse = F)  
uMAT9 <- lapply(uGRAPH9, get.adjacency, sparse = F)

tind <- lapply(uMAT, TrophInd)  
tind6 <- lapply(uMAT6, TrophInd)  
tind7 <- lapply(uMAT7, TrophInd)  
tind8 <- lapply(uMAT8, TrophInd)  
tind9 <- lapply(uMAT9, TrophInd)  
  
prop.omn <- sapply(tind, function(x){(1 - sum(x$OI == 0)/nrow(x)) \* 100})  
prop.omn6 <- sapply(tind6, function(x){(1 - sum(x$OI == 0)/nrow(x)) \* 100})  
prop.omn7 <- sapply(tind7, function(x){(1 - sum(x$OI == 0)/nrow(x)) \* 100})  
prop.omn8 <- sapply(tind8, function(x){(1 - sum(x$OI == 0)/nrow(x)) \* 100})  
prop.omn9 <- sapply(tind9, function(x){(1 - sum(x$OI == 0)/nrow(x)) \* 100})  
  
p.omn <- matrix(c(prop.omn, prop.omn6, prop.omn7, prop.omn8, prop.omn9), ncol = 5)  
colnames(p.omn) <- seq(50, 90, 10)  
omn.dat <- data.frame(prop = seq(50, 90, 10), omn = colMeans(p.omn),   
 upper = apply(p.omn, 2,   
 function(x){mean(x) + 1.96 \* (sd(x)/sqrt(length(x)))}),   
 lower = apply(p.omn, 2,   
 function(x){mean(x) - 1.96 \* (sd(x)/sqrt(length(x)))}))

ggplot(omn.dat, aes(x = prop, y = omn)) + geom\_errorbar(aes(x = prop, ymax = upper, ymin = lower), width = 1) + geom\_point(data = data.frame(melt(p.omn)), aes(x = Var2, y = value), alpha = .25, position = "jitter") + geom\_point() + theme\_bw() + xlab("Flow Weight Percentile Cutoff (percentage)") + ylab("Percent Omnivorous Species")



**Figure A1** The proportion of omnivorous species in 15 ecosystem flow networks that have been subset by flow weight. Values along the x-axis represent removal of the bottom 50, 60, 70, 80, and 90 percentiles of flow weights. Data for making this figure is available from [<http://www.cbl.umces.edu/~ulan>](http://www.cbl.umces.edu/~ulan)

Note that there is still at least 20% omnivory even when only looking at the top 10% of interactions. We say "at least" because this simple analysis does not remove from consideration species who are disconnected from the web (i.e. they do not have any interactions whose flow is above the threshold).

# Code

All code here can also be found on [GitHub](https://github.com/jjborrelli/Food-Chain-Length)

Loading required packages

library(RCurl)  
library(igraph)  
library(reshape2)  
library(ggplot2)  
library(grid)  
library(data.table)  
library(devtools)  
library(NetIndices)

## Functions

The function analyze.eigen randomly fills a signed matrix and calculates the eigenvalue with the largest real part. This function takes in a sign matrix (a matrix of +1s, -1s, and 0s) and replaces the with values randomly drawn from predefined uniform distributions. This is the function used for the simple food webs.

analyze.eigen<-function(m){  
 for(i in 1:nrow(m)){  
 for (j in 1:nrow(m)){  
 ifelse(m[i,j]==1,m[i,j]<-runif(1,0,10),NA)  
 ifelse(m[i,j]==-1,m[i,j]<-runif(1,-1,0),NA)  
 }  
 }  
 for(i in 1:nrow(m)){  
 if(m[i,i]<0){m[i,i]<--1}  
 }  
 ev<-eigen(m)$values[1]  
 return(ev)  
}

The following functions are used for the random and niche model webs.

The ran.unif function fills in a sign structured matrix with random values drawn from a random uniform distribution. The impact of the prey on the predator population is drawn from a distribution between 0 and pred, while the impact of the predator on the prey is distributed between prey and 0.

ran.unif <- function(motmat, pred = 10, prey = -1, random = F){  
 newmat <- apply(motmat, c(1,2), function(x){  
 if(x==1){runif(1, 0, pred)}else if(x==-1){runif(1, prey, 0)} else{0}  
 })  
 if(random){  
 diag(newmat) <- runif(length(diag(newmat)), -1, 0)  
 }else{diag(newmat) <- -1}  
   
 return(newmat)  
}

The maxRE computes the largest eigenvalue and returns the real part.

maxRE <- function(rmat){  
 lam.max <- eigen(rmat)$values[which.max(Re(eigen(rmat)$values))]  
 return(lam.max)  
}

The eig.analysis function takes an imput of a list of matrices and randomly fills it according to ran.unif (above) n times and computes maxRE for each iteration.

eig.analysis <- function(n, matrices, params){  
 require(data.table)  
 dims <- dim(matrices[[1]])  
 cols <- length(matrices)  
 rows <- n  
 eigenMATRIX.re <- matrix(nrow = rows, ncol = cols)  
 eigenMATRIX.im <- matrix(nrow = rows, ncol = cols)  
 samps <- list()  
 for(i in 1:n){  
 ranmat <- lapply(matrices, ran.unif, pred = params[,1],  
 prey = params[,2], random = T)  
 sampvals <- matrix(nrow = length(ranmat), ncol = dims[1]^2)  
 for(j in 1:length(ranmat)){  
 sampvals[j,] <- ranmat[[j]]  
 }  
 eigs <- sapply(ranmat, maxRE)  
 eigenMATRIX.re[i,] <- Re(eigs)  
 eigenMATRIX.im[i,] <- Im(eigs)  
 samps[[i]] <- as.data.frame(sampvals)   
 }  
 svals <- cbind(web = rep(1:length(matrices), n), n = rep(1:n, each = cols), rbindlist(samps))  
 return(list(samples = svals, ematrix.re = eigenMATRIX.re, ematrix.im = eigenMATRIX.im))  
}

The conversion function takes in an adjacency matrix and converts it into sign matrix, assuming all interactions are predator/prey (+/-).

conversion <- function(tm){  
 for(i in 1:nrow(tm)){  
 for(j in 1:ncol(tm)){  
 if(tm[i,j] == 1){tm[j,i] <- -1}  
 }  
 }  
 return(tm)  
}

The randomWEBS function generates numweb random webs of S species and total interactions. The connectance of these webs would then be total/S^2. The chain parameter can be modified to change the maximum chain length in the web. For example, the default chain = 9 means that the webs have at least one chain of ten species.

randomWEBS <- function(S = 10, numweb = 200, chain = 9, total = 14){  
 require(NetIndices)  
 require(igraph)  
 mywebs <- list()  
 for(j in 1:numweb){  
   
 check <- 1  
 while(!check == 0){  
 myweb <- matrix(0, nrow = S, ncol = S)  
 for(i in 1:chain){  
 myweb[i,i+1] <- 1  
 }  
 tophalf <- which(myweb[upper.tri(myweb)] == 0)  
 newones <- sample(tophalf, total-chain)  
 myweb[upper.tri(myweb)][newones] <- 1  
 mywebs[[j]] <- myweb  
   
 indeg <- apply(myweb, 1, sum)  
 outdeg <- apply(myweb, 2, sum)  
 deg <- indeg + outdeg  
   
 if(sum(deg == 0) >= 1){check <- 1}else{check <- 0}  
   
 }  
   
 }  
 return(mywebs)  
}

The two functions below are the niche model (niche.model), and a function that uses the niche model code to generate a list of niche model food webs with a given connectance C and and number of species S (niche\_maker).

niche.model<-function(S,C){  
 require(igraph)  
 connected = FALSE  
 while(!connected){   
 new.mat<-matrix(0,nrow=S,ncol=S)  
 ci<-vector()  
 niche<-runif(S,0,1)  
 r<-rbeta(S,1,((1/(2\*C))-1))\*niche  
   
 for(i in 1:S){  
 ci[i]<-runif(1,r[i]/2,niche[i])  
 }  
   
 r[which(niche==min(niche))]<-.00000001  
   
 for(i in 1:S){  
   
 for(j in 1:S){  
 if(niche[j]>(ci[i]-(.5\*r[i])) && niche[j]<(ci[i]+.5\*r[i])){  
 new.mat[j,i]<-1  
 }  
 }  
 }  
   
 new.mat<-new.mat[,order(apply(new.mat,2,sum))]  
   
 connected <- is.connected(graph.adjacency(new.mat))  
 }  
 return(new.mat)  
}  
  
niche\_maker <- function(n, S, C){  
 niche.list <- list()  
 for (i in 1:n){  
 niche.list[[i]]<- niche.model(S, C)  
 }  
 return(niche.list)  
}

The randomQSS function takes in a list of webs (as adjacency matrices) with the mywebs paramater, and a 1 row by 2 column matrix of parameters to feed into the eig.analysis function. It then outputs a list of two data frames. The first, web.dat contains information on quasi sign-stability, max, mean and median trophic level, standard deviation of trophic level, and the diameter (longest food chain) of the web. The second data frame, iter.dat contains information on each random sampling of each matrix. iter.dat has each sampled value for each link, and the real and imaginary parts of the largest eigenvalue.

randomQSS <- function(mywebs, params){  
 require(NetIndices)  
 require(igraph)  
   
 mywebs1 <- lapply(mywebs, conversion)  
 myweb.tl <- lapply(mywebs, TrophInd)  
 emat <- eig.analysis(1000, mywebs1, params)   
   
 qss <- apply(emat$ematrix.re, 2, function(x){sum(x<0)/1000})  
 maxtl <- sapply(myweb.tl, function(x){max(x$TL)})  
 meantl <- sapply(myweb.tl, function(x){mean(x$TL)})  
 medtl <- sapply(myweb.tl, function(x){median(x$TL)})  
 sdtl <- sapply(myweb.tl, function(x){sd(x$TL)})  
 diam <- sapply(lapply(mywebs, graph.adjacency), diameter)  
   
 web.dat <- data.frame(qss, diam, maxtl, meantl, medtl, sdtl)  
 iter.dat <- cbind(par = rep(paste(params, collapse = "\_"), nrow(emat$samples)),  
 emat$samples, reals = as.vector(emat$ematrix.re),  
 im = as.vector(emat$ematrix.im))  
   
 return(list(web.dat, iter.dat))  
}

The getQSS function is the main function for the simulation, putting together all previous functions. The webiter, maxchain, and totalINT paramaters are fed into the functions that generate the food webs. The params parameter should be a matrix with two columns, one for the impact of the prey on the predator, and one for the impact of the predator on the prey. This function is designed to run in parallel, and will run a set of webs on each core. The output is written to file according to filepath. This function will generate either random webs or niche model webs according to whether niche is TRUE or FALSE. It calls a separate script robustnessFUNC.R that holds the functions described above and allows each node of the cluster to complete the analysis.

getQSS <- function(webiter = 100, maxchain = 9, totalINT = 14, params, filepath, niche = FALSE){  
 require(doSNOW)  
 require(parallel)  
 require(data.table)  
   
 #make the cluster  
 cl <- makeCluster(detectCores()-1)  
 registerDoSNOW(cl)  
   
 RESULT <- foreach(i = 1:maxchain) %dopar% {  
 source("C:/Users/jjborrelli/Desktop/GitHub/Food-Chain-Length/robustnessFUNC.R")  
   
 #cat(i, "\n")  
 if(!niche){  
 rwebs <- randomWEBS(S = 10, numweb = webiter, chain = i, total = totalINT)  
 }else{  
 rwebs <- niche\_maker(15, 10, totalINT)  
 }  
   
 rqss <- list()  
 for(j in 1:nrow(params)){  
 rqss[[j]] <- randomQSS(mywebs = rwebs, params = params[j,1:2])  
   
 rqss[[j]][[1]] <- cbind(C = rep(totalINT, nrow(rqss[[j]][[1]])),  
 mxch = rep(i, nrow(rqss[[j]][[1]])),   
 rqss[[j]][[1]],  
 par = rep(paste(params[j,], collapse = "/"),  
 nrow(rqss[[j]][[1]])))  
   
 rqss[[j]][[2]] <- cbind(C = rep(totalINT, nrow(rqss[[j]][[2]])),   
 mxch = rep(i, nrow(rqss[[j]][[2]])),  
 rqss[[j]][[2]],  
 par = rep(paste(params[j,], collapse = "/"),  
 nrow(rqss[[j]][[2]])))  
 cat("--", j, "\n")  
 }  
 rqss <- unlist(rqss, recursive = F)  
 web.dat.ls <- rbindlist(rqss[seq(1, length(rqss), 2)])  
 iter.dat.ls <- rbindlist(rqss[seq(2, length(rqss), 2)])  
   
 return(list(web.dat.ls, iter.dat.ls))  
   
 }  
   
 stopCluster(cl)  
   
  
 RESULT <- unlist(RESULT, recursive = F)  
 chain.data <- rbindlist(RESULT[seq(1, length(RESULT), 2)])  
 iter.data <- rbindlist(RESULT[seq(2, length(RESULT), 2)])  
 rm(RESULT)  
 write.csv(chain.data, file = paste(filepath, "/webdata-",   
 totalINT, ".csv", sep = ""),  
 row.names = F)  
   
 #Code to generate dataframes of sampled matrices (note this can create very large files)  
 #write.csv(iter.data, file = paste(filepath, "/iterdata-",   
 # totalINT, ".csv", sep = ""),  
 # row.names = F)  
   
 return(chain.data)  
}

## Simulations

### Simple webs

The code below will create the sign matrix structure for each perturbed chain of 2, 3, 4, 5, and 6 levels. A -1 indicates the impact of a predator on its prey (negative), while a 1 indicates the impact of the prey on the predator (positive).

sign2<-matrix(c(-1,-1,1,0),nrow=2,ncol=2)  
diag(sign2)<--1  
  
sign3<-matrix(c(-1,-1,-1,1,0,-1,1,1,0),nrow=3,ncol=3)  
diag(sign3)<--1  
  
sign4<-matrix(nrow=4,ncol=4)  
sign4[lower.tri(sign4)]<--1  
sign4[upper.tri(sign4)]<-1  
diag(sign4)<--1  
  
sign5<-matrix(nrow=5,ncol=5)  
sign5[lower.tri(sign5)]<--1  
sign5[upper.tri(sign5)]<-1  
diag(sign5)<--1  
  
sign6<-matrix(nrow=6,ncol=6)  
sign6[lower.tri(sign6)]<--1  
sign6[upper.tri(sign6)]<-1  
diag(sign6)<--1

These matrices are combined into a list for simplicity:

sign.matrices<-list(sign2,sign3,sign4,sign5,sign6)  
names(sign.matrices)<-c("2 sp","3 sp","4 sp","5 sp","6 sp")  
sign.matrices

The following code applies the analyze.eigen function to each of the 5 sign matrices created above. It then stores the max(Re(lambda)), or the eigen value with the largest real part in the eigenvalues list. Quasi sign-stability (qss) can then be calculated by determining the proportion of the max(Re(lambda)) that are negative out of the 10000 that are calculated.

eigenvalues<-list()  
qss<-list()  
for(i in 1:5){  
 eigenvalues[[i]]<-replicate(10000,analyze.eigen(sign.matrices[[i]]))  
 qss[[i]]<-sum(Re(eigenvalues[[i]])<0)/10000  
}  
  
names(eigenvalues)<-c("2 sp","3 sp","4 sp","5 sp","6 sp")  
names(qss)<-c("2 sp","3 sp","4 sp","5 sp", "6 sp")  
qss

### Random and niche model webs

Set the parameters for the simulation, and the desired levels of connectance.

pars <- data.frame(pred = c(10, 10, 10, 5, 5, 5, 1, 1, 1), prey = c(-1, -5, -10, -1, -5, -10, -1, -5, -10))  
ints <- c(12, 16, 20, 24, 28)

Use the getQSS function to create webs and determine quasi sign-stability for a range of parameters.

**For random webs**

for(con in 1:length(ints)){  
 getQSS(25, maxchain =7, totalINT = ints[con], params = pars,   
 filepath = myfilepath1, niche = F)  
 cat(con/length(ints)\*100, "%", "\n")  
}

**For niche model webs**

for(con in 1:length(ints)){  
 getQSS(25, maxchain =7, totalINT = ints[con]/100, params = pars,   
 filepath = myfilepath2, niche = T)  
 cat(con/length(ints)\*100, "%", "\n")  
}

## Figures

### Figure 1

#### Figure 1a

path <- getURL("https://raw.githubusercontent.com/jjborrelli/Food-Chain-Length/master/Tables/webDiameters.csv",  
 ssl.verifypeer=0L, followlocation=1L)  
  
web.diameters <- read.csv(text = path, row.names = 1)  
  
diam.plot <- ggplot(web.diameters, aes(x = Diameter + 1))  
diam.plot <- diam.plot + geom\_histogram(binwidth = 1)  
diam.plot <- diam.plot + theme(axis.title.x = element\_text(size = 20))  
diam.plot <- diam.plot + theme(axis.title.y = element\_text(size = 20))  
diam.plot <- diam.plot + theme(axis.text.x = element\_text(size = 15))  
diam.plot <- diam.plot + theme(axis.text.y = element\_text(size = 15))  
diam.plot <- diam.plot + scale\_y\_continuous(name = "Density", limits = c(0,.55))  
diam.plot <- diam.plot + scale\_x\_continuous(name = "Longest Chain Length", breaks = 0:9) + theme\_bw()

#### Figure 1b

path2 <- getURL("https://raw.githubusercontent.com/jjborrelli/Food-Chain-Length/master/Tables/NodeProperties.csv", ssl.verifypeer=0L, followlocation=1L)  
trophic.properties <- read.csv(text = path2, row.names = 1)  
  
consumers <- which(round(trophic.properties$TL, 6) >= 2)  
  
# ggplot of distribution of trophic positions equal or higher than 2  
tc.plot <- ggplot(trophic.properties[consumers,], aes(x = TL)) + theme\_bw()  
tc.plot <- tc.plot + geom\_histogram(binwidth = 1) + xlab("Trophic Position") + ylab("Density")  
tc.plot <- tc.plot + scale\_x\_continuous(limits = c(2,6),name = "Trophic Position") + scale\_y\_continuous(name = "Density", limits = c(0,.55))  
tc.plot

### Figure 2

The simple web matrices can be visualized with the following code (note: requires the igraph library):

But first the sign matrices need to be converted to graph objects

graph.chains<-lapply(sign.matrices, graph.adjacency)

The layout is defined for each node of each chain:

twospec2<-matrix(c(1,1,  
 2,2),nrow=2,ncol=2,byrow=T)  
threespec2<-matrix(c(1,1,  
 3,1,  
 2,2),nrow=3,ncol=2,byrow=T)  
fourspec2<-matrix(c(1,1,  
 2,2,  
 0,2,  
 1,3),nrow=4,ncol=2,byrow=T)  
fivespec2<-matrix(c(2,1,  
 3,2,  
 1,2,  
 3,3,  
 1,3),nrow=5,ncol=2,byrow=T)  
sixspec2<-matrix(c(2,1,  
 3,2,  
 1,2,  
 3,3,  
 1,3,  
 2,4),nrow=6,ncol=2,byrow=T)  
  
layouts<-list(twospec2,threespec2,fourspec2,fivespec2,sixspec2)

Setting the plotting options to highlight the longest chain in each web:

for(i in 1:5){  
 E(graph.chains[[i]])$color = "darkslategray4"  
 E(graph.chains[[i]], path = c(1:(i+1)))$color = "black"  
}

Create the plot

par(mfrow=c(5, 1),mar=c(.1, .1, .1, .1))  
for(i in 1:5){  
 plot.igraph(graph.chains[[i]], layout = layouts[[i]],  
 vertex.size = 40,  
 vertex.color = "white",  
 vertex.label.color = "black",  
 vertex.label.cex = .8,  
 edge.width = 1,  
 edge.arrow.size = .35,  
 frame = T,  
 margin = 0)  
}

### Figure 3

qss.plot <- qplot(2:6, unlist(qss), xlab = "Longest Chain Length", ylab = "Quasi Sign-Stability", margin = T)  
qss.plot <- qss.plot + geom\_point(size = 2)  
qss.plot <- qss.plot + geom\_line() + theme\_bw()  
qss.plot

### Figure 4

First import the data from the random webs

web.files <- list.files(path = filepath1, pattern = "web")  
temp.ls <- list()  
for(i in 1:length(web.files)){  
 temp.ls[[i]]<- fread(paste(filepath1,   
 web.files[i], sep = ""))  
}  
webdata <- rbindlist(temp.ls)  
webdata$C <- factor(webdata$C)  
  
# Formulas for upper and lower confidence limits  
sem.l <- function(x){mean(x) - 1.96\*sqrt(var(x)/length(x))}  
sem.u <- function(x){mean(x) + 1.96\*sqrt(var(x)/length(x))}  
  
sub1 <- subset(webdata, par == "1/-10" | par == "10/-1" | par == "1/-5" | par == "5/-1")  
sub2 <- subset(webdata, par == "5/-10" | par == "10/-5")  
sub3 <- subset(webdata, par == "1/-1" | par == "10/-10" | par == "5/-5")

Plots of the different subsets of data. The final plot is what appears in the paper.

ggplot(sub1, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(sub2, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(sub3, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(webdata, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")

### Figure 4

First import the data from the niche model webs

web.files <- list.files(path = filepath2, pattern = "web")  
temp.ls <- list()  
for(i in 1:length(web.files)){  
 temp.ls[[i]]<- fread(paste(filepath2,   
 web.files[i], sep = ""))  
}  
webdata <- rbindlist(temp.ls)  
webdata$C <- factor(webdata$C)  
  
# Formulas for upper and lower confidence limits  
sem.l <- function(x){mean(x) - 1.96\*sqrt(var(x)/length(x))}  
sem.u <- function(x){mean(x) + 1.96\*sqrt(var(x)/length(x))}  
  
sub1 <- subset(webdata, par == "1/-10" | par == "10/-1" | par == "1/-5" | par == "5/-1")  
sub2 <- subset(webdata, par == "5/-10" | par == "10/-5")  
sub3 <- subset(webdata, par == "1/-1" | par == "10/-10" | par == "5/-5")

Plots of the different subsets of data. The final plot is what appears in the paper.

ggplot(sub1, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(sub2, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(sub3, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")  
  
  
ggplot(webdata, aes(x = factor(diam+1), y = qss)) +   
 geom\_point(alpha = .25, position = position\_jitter(w=0.2), col = "grey58") +   
 stat\_summary(fun.y="mean", geom="point") +  
 stat\_summary(fun.ymin = sem.l, fun.y = "mean", fun.ymax = sem.u,  
 geom="errorbar", width = .2) +   
 facet\_grid(par~C) + theme\_bw() +  
 xlab("Longest Food Chain Length") + ylab("Quasi sign-stability")