Seasonal community structure of benthic fish and invertebrates in two nearshore areas of British Columbia

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# Abstract:

# Introduction

Nearshore and inshore marine areas are important habitats for a diverse array of fishes. These can include commercially important fishes in all life history stages (references), as well as species that are not commercially important, but may have important ecological roles in the nearshore (references). Nearshore areas are increasingly utilized, not only for their capacity to produce consumable fish biomass, but for other human uses, such as energy development (references). In addition, temperate nearshore systems are likely to be impacted by the effects of climate change in the relatively near future (references). Defining seasonal patterns in fish communities will contribute to our ability to assess changes in nearshore fish communities and manage responses to both the observed changes and potential new threats.

The nearshore and inshore marine waters of British Columbia are important ecosystems, historically supporting harvests of fish by First Nations, and commercial and recreational fisheries (reference). Benthic species such as Pacific halibut and shrimps are harvested by all three types of fisheries, while other common species such as skates, sharks, forage fishes and ratfish are not widely utilized, but play important roles in the ecosystem. In addition, there are a few species, such as eulachon which are listed as threatened due to historical declines in abundance (reference). The relationships and interconnected-ness among these and the other species that inhabit nearshore and inshore marine waters in British Columbia are relatively unknown and unexplored. However, changes in the structure of nearshore fish communities can have broad implications for human use, as well as implications for the food webs and predator-prey relationships among the fish and invertebrate communities in this region.

To date, most of the information on nearshore fishes and invertebrates in British Columbia has been collected during summertime bottom-trawl surveys (references) meant to support stock assessment for commercially important species such as shrimps (references). Summertime tends to be the most common time for data collection in other systems as well (references). It is unclear if there are seasonal patterns in the structure of these ecosystems or whether the structure varies with changing oceanographic conditions caused by the highly variable seasonal changes that happen in the nearshore. It is also unclear if there are spatial patterns in nearshore assemblages that are consistent over seasonality and how much variability is present within an area of the coast relative to a larger coastwide region. The objectives of this study were to examine the seasonal and spatial structure of benthic fish and invertebrate communities in two areas of British Columbia. We compared the diversity of the catch among seasons and areas, clustered the communities by their similarity in species composition and catch, and examined the main environmental gradients (depth, temperature and salinity as determined by ROMS model output) that appeared to structure the communities. Additional goals were to identify indicator species for each of the communities and define the important gradients of change through multivariate analyses.

# Methods

## Study areas

The original goal of this survey was to estimate the seasonal abundance of eulachon (Thaleichthys pacificus) returning to river systems in northern British Columbia and the Fraser River in southern British Columbia, thus four areas were chosen for the study; Chatham Sound, the Strait of Juan de Fuca, Haro Strait and the southern Strait of Georgia (Figure 1). The Chatham Sound area is located on the northern coast of British Columbia (Figure 1). It was chosen based on its proximity to two large rivers (the Nass and Skeena rivers) that support significant eulachon runs (Hay et al. 1997). The Chatham Sound area is protected from the open ocean by a series of large and small islands. The area is approximately 25 km from east to west and 50 km from north to south. The Strait of Juan de Fuca area was between the tip of Washington state (U.S.A.) between Swiftsure Bank and Race Rocks at the southernmost tip of Vancouver Island in Canadian waters. This area was about 60 km by 10 km. The Haro Strait area was from Race Rocks to the mid-point of Galiano Island and the Strait of Georgia area was considered as the region between the mid-point of Galiano Island and Howe Sound north of the Fraser River mouth (Figure 1). These two areas were chosen because of their proximity and position as a migration corridor for eulachon returning to spawn in the Fraser River (Hay et al. 1997).

Species\_name CPUE  
11 Hydrolagus colliei 10000.48640  
7 Gadus chalcogrammus 2616.94180  
24 Squalus suckleyi 1358.94437  
17 Pandalopsis dispar 1295.64403  
10 Hippoglossoides elassodon 954.84129  
3 Atheresthes stomias 812.77367  
21 Parophrys vetulus 809.53130  
25 Thaleichthys pacificus 692.01589  
23 Raja rhina 583.00113  
14 Lyopsetta exilis 499.88294  
13 Lycodes pacificus 445.79219  
15 Merluccius productus 380.27450  
19 Pandalus jordani 349.31335  
16 Microstomus pacificus 291.02952  
5 Beringraja binoculata 290.66335  
9 Glyptocephalus zachirus 268.00583  
2 Anoplopoma fimbria 234.78183  
6 Clupea pallasii 152.69595  
18 Pandalus borealis 119.56366  
8 Gadus macrocephalus 72.04802  
22 Pectinidae 63.45363  
4 Bathyraja interrupta 63.16009  
20 Pandalus Platyceros 60.66700  
12 Lycodes brevipes 42.58756  
1 Actiniaria 41.03352

[1] 0.02581051

[1] 0.9034134

#### Number of sets by AreaGrouping  
#204 species total so 204 rows for each set  
#so number of sets = unique count by MONTH, YEAR, MAJOR\_STAT\_AREA\_CODE(or AreaGrouping)/204  
  
samples\_by\_month\_year\_area <- catch\_data %>%   
 group\_by(., AreaName, MONTH, YEAR) %>%  
 summarise(., number\_of\_sets = n()/204)

`summarise()` has grouped output by 'AreaName', 'MONTH'. You can override using  
the `.groups` argument.

samples\_by\_month\_year\_area <-samples\_by\_month\_year\_area %>%  
 arrange(., AreaName,YEAR)  
  
colnames(samples\_by\_month\_year\_area ) <- c("Area","Month", "Year","Total sets")  
  
# in wide format  
samples\_wide <-pivot\_wider(samples\_by\_month\_year\_area,   
 names\_from = Area,   
 values\_from = "Total sets")  
  
samples\_wide <- samples\_wide%>% arrange(., Year)  
samples\_wide\_tots<-sapply(samples\_wide[,3:6],FUN="sum",na.rm=TRUE)  
samples\_wide\_tots<-data.frame(Month="Total",Year=NA,'Chatham Sound'=samples\_wide\_tots[1],"Haro Strait"=samples\_wide\_tots[2],'Strait of Georgia'=samples\_wide\_tots[3],'Strait of Juan de Fuca'=samples\_wide\_tots[4])  
names(samples\_wide\_tots)<-names(samples\_wide)  
samples\_wide<-rbind(samples\_wide,samples\_wide\_tots)

Number of sets North vs South

Table 2. Mean CPUE of top 25 species by area

get top 25 species in long format

catch\_top25 <- catch\_data %>%   
 filter(., Species\_common\_name %in% c("Sea anemone",  
 "Sablefish",  
 "Arrowtooth flounder",  
 "Bering skate",  
 "Big skate",  
 "Pacific herring",  
 "Walleye pollock",  
 "Pacific cod",  
 "Rex sole",  
 "Flathead sole",  
 "Spotted ratfish",  
 "Shortfin eelpout",  
 "Blackbelly eelpout",  
 "Slender soles",  
 "North pacific hake",  
 "Pacific dover sole",  
 "Sidestripe shrimp",  
 "Northern shrimp",  
 "Pink shrimp",  
 "Spot prawn",  
 "English sole",  
 "Scallop",  
 "Longnose skate",  
 "Pacific spiny dogfish",  
 "Eulachon" ))  
  
# add log CPUE  
  
catch\_top25 <- catch\_top25 %>%   
 mutate(., log\_CPUE = log(CPUE+1), .after = CPUE)  
  
  
# mean CPUE north vs south  
  
mean\_CPUE\_top25\_north\_south <- catch\_top25 %>%  
 group\_by(., Species\_name, Species\_common\_name, MAJOR\_STAT\_AREA\_CODE)%>%  
 summarise(., mean\_CPUE = mean(CPUE))

`summarise()` has grouped output by 'Species\_name', 'Species\_common\_name'. You  
can override using the `.groups` argument.

mean\_CPUE\_top25\_north\_south <- pivot\_wider(mean\_CPUE\_top25\_north\_south,   
 names\_from = MAJOR\_STAT\_AREA\_CODE,   
 values\_from = mean\_CPUE)  
  
colnames(mean\_CPUE\_top25\_north\_south)<- c("Scientific Name", "Common Name",   
 "South CPUE", "North CPUE")  
  
export(mean\_CPUE\_top25\_north\_south, "mean\_CPUE\_top25\_north\_south.xlsx")  
  
  
# mean CPUE by area  
  
mean\_CPUE\_top25\_area <- catch\_top25 %>%  
 group\_by(., Species\_name, Species\_common\_name, AreaGrouping)%>%  
 summarise(., mean\_CPUE = mean(CPUE))

`summarise()` has grouped output by 'Species\_name', 'Species\_common\_name'. You  
can override using the `.groups` argument.

mean\_CPUE\_top25\_area <- pivot\_wider(mean\_CPUE\_top25\_area,   
 names\_from = AreaGrouping,   
 values\_from = mean\_CPUE)  
  
colnames(mean\_CPUE\_top25\_area)<- c("Scientific Name", "Common Name",   
 "A1 CPUE", "A2 CPUE",  
 "A3 CPUE", "A4 CPUE")  
  
export(mean\_CPUE\_top25\_area, "mean\_CPUE\_top25\_area.xlsx")

Figure 2. Proportion of catch for top species in stacked bar graphs by month and area

### by area   
  
CPUE\_by\_month\_area <- catch\_top25 %>%  
 group\_by(., Species\_common\_name, MONTH, AreaGrouping) %>%  
 summarise(., mean\_CPUE = mean(CPUE),  
 total\_CPUE = sum(CPUE),  
 mean\_log\_CPUE = mean(log\_CPUE))

`summarise()` has grouped output by 'Species\_common\_name', 'MONTH'. You can  
override using the `.groups` argument.

# add row for august to data frame for plotting  
  
aug\_row2 <- data.frame(Species\_common\_name = "Eulachon",  
 MONTH ="Aug",   
 AreaGrouping = "A1",  
 mean\_CPUE= 0,   
 total\_CPUE = 0,   
 mean\_log\_CPUE=0)  
  
CPUE\_by\_month\_area <- rbind(CPUE\_by\_month\_area, aug\_row2)  
  
  
CPUE\_by\_month\_area$MONTH<-factor(CPUE\_by\_month\_area$MONTH,  
 levels=c("Jan", "Feb", "Mar", "Apr",  
 "May", "Jun", "Jul","Aug",   
 "Sep", "Oct", "Nov", "Dec"))  
  
CPUE\_by\_month\_area$AreaGrouping<-factor(CPUE\_by\_month\_area$AreaGrouping,  
 labels=c("Strait of Juan de Fuca", "Haro Strait", "Strait of Georgia", "Chatham Sound"))  
  
  
# mean CPUE by month and area standardized to one   
  
ggplot(CPUE\_by\_month\_area )+  
 geom\_bar(aes(x=MONTH, y=mean\_CPUE, fill=Species\_common\_name),   
 stat = "identity", position = "fill")+  
 scale\_fill\_manual(values = mycolour) +  
 facet\_wrap(~AreaGrouping)+  
 labs(y= "Proportion", x= "Month", fill= "Species" )

Warning: Removed 1 rows containing missing values (`geom\_bar()`).

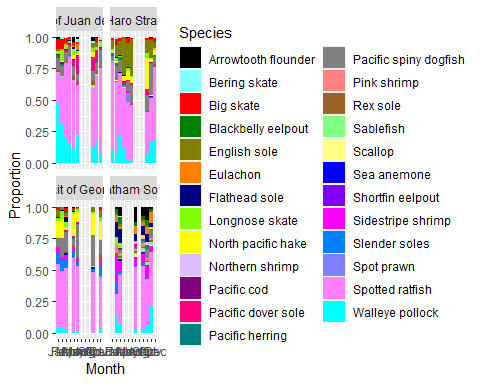


Figure 3. Correlation plot among species for co-occurrence in the trawl hauls

species\_cor <- cor(data.frame(catch\_wide\_log[,16:40]),use="complete.obs")  
  
round(species\_cor,2)

Sea.anemone Sablefish Arrowtooth.flounder Bering.skate  
Sea.anemone 1.00 0.15 -0.06 0.04  
Sablefish 0.15 1.00 0.32 0.00  
Arrowtooth.flounder -0.06 0.32 1.00 -0.04  
Bering.skate 0.04 0.00 -0.04 1.00  
Big.skate -0.08 -0.12 -0.20 0.17  
Pacific.herring -0.09 -0.15 -0.02 -0.03  
Walleye.pollock -0.06 -0.04 -0.04 0.14  
Pacific.cod -0.03 -0.07 -0.13 0.11  
Rex.sole 0.05 0.17 0.37 -0.03  
Flathead.sole -0.01 -0.02 0.41 -0.07  
Spotted.ratfish 0.01 -0.01 -0.03 0.09  
Shortfin.eelpout -0.01 0.06 0.32 -0.09  
Blackbelly.eelpout -0.03 0.09 0.43 -0.15  
Slender.soles 0.04 0.02 0.22 -0.25  
North.pacific.hake -0.04 -0.13 -0.30 -0.03  
Pacific.dover.sole 0.04 0.10 0.07 0.13  
Sidestripe.shrimp 0.14 0.14 0.34 -0.15  
Northern.shrimp 0.01 0.11 0.15 -0.07  
Pink.shrimp -0.01 0.19 0.43 -0.10  
Spot.prawn 0.14 0.03 0.07 -0.06  
English.sole -0.01 -0.11 -0.23 0.00  
Scallop -0.06 0.03 0.03 -0.01  
Longnose.skate -0.03 -0.08 -0.14 0.19  
Pacific.spiny.dogfish -0.10 -0.09 -0.16 0.16  
Eulachon -0.10 0.16 0.50 -0.05  
 Big.skate Pacific.herring Walleye.pollock Pacific.cod  
Sea.anemone -0.08 -0.09 -0.06 -0.03  
Sablefish -0.12 -0.15 -0.04 -0.07  
Arrowtooth.flounder -0.20 -0.02 -0.04 -0.13  
Bering.skate 0.17 -0.03 0.14 0.11  
Big.skate 1.00 0.16 0.22 0.05  
Pacific.herring 0.16 1.00 0.23 0.13  
Walleye.pollock 0.22 0.23 1.00 0.11  
Pacific.cod 0.05 0.13 0.11 1.00  
Rex.sole 0.05 -0.03 0.09 -0.08  
Flathead.sole -0.14 0.08 -0.01 -0.15  
Spotted.ratfish 0.06 -0.06 0.06 0.10  
Shortfin.eelpout -0.21 0.02 -0.07 -0.12  
Blackbelly.eelpout -0.25 0.00 -0.18 -0.20  
Slender.soles -0.24 -0.24 -0.31 -0.27  
North.pacific.hake 0.11 -0.14 -0.18 -0.01  
Pacific.dover.sole 0.05 -0.10 0.15 0.13  
Sidestripe.shrimp -0.25 -0.18 -0.26 -0.24  
Northern.shrimp -0.06 -0.03 -0.08 -0.14  
Pink.shrimp -0.24 0.00 -0.08 -0.17  
Spot.prawn -0.07 0.05 -0.03 -0.09  
English.sole 0.30 0.17 0.15 0.04  
Scallop -0.04 0.09 0.12 0.07  
Longnose.skate 0.14 -0.13 0.09 0.07  
Pacific.spiny.dogfish 0.16 -0.07 0.07 0.10  
Eulachon -0.10 0.02 0.09 -0.10  
 Rex.sole Flathead.sole Spotted.ratfish Shortfin.eelpout  
Sea.anemone 0.05 -0.01 0.01 -0.01  
Sablefish 0.17 -0.02 -0.01 0.06  
Arrowtooth.flounder 0.37 0.41 -0.03 0.32  
Bering.skate -0.03 -0.07 0.09 -0.09  
Big.skate 0.05 -0.14 0.06 -0.21  
Pacific.herring -0.03 0.08 -0.06 0.02  
Walleye.pollock 0.09 -0.01 0.06 -0.07  
Pacific.cod -0.08 -0.15 0.10 -0.12  
Rex.sole 1.00 0.26 -0.01 0.09  
Flathead.sole 0.26 1.00 -0.13 0.36  
Spotted.ratfish -0.01 -0.13 1.00 0.01  
Shortfin.eelpout 0.09 0.36 0.01 1.00  
Blackbelly.eelpout 0.24 0.55 -0.14 0.63  
Slender.soles 0.17 0.37 -0.05 0.36  
North.pacific.hake -0.24 -0.27 -0.01 -0.24  
Pacific.dover.sole 0.18 -0.05 0.17 -0.22  
Sidestripe.shrimp 0.21 0.36 0.01 0.42  
Northern.shrimp 0.03 0.11 -0.09 0.31  
Pink.shrimp 0.17 0.51 -0.12 0.54  
Spot.prawn 0.10 0.00 0.00 0.15  
English.sole 0.04 -0.09 0.05 -0.28  
Scallop -0.05 -0.11 0.14 -0.07  
Longnose.skate -0.06 -0.13 0.08 -0.14  
Pacific.spiny.dogfish -0.18 -0.21 0.07 -0.09  
Eulachon 0.31 0.44 0.00 0.42  
 Blackbelly.eelpout Slender.soles North.pacific.hake  
Sea.anemone -0.03 0.04 -0.04  
Sablefish 0.09 0.02 -0.13  
Arrowtooth.flounder 0.43 0.22 -0.30  
Bering.skate -0.15 -0.25 -0.03  
Big.skate -0.25 -0.24 0.11  
Pacific.herring 0.00 -0.24 -0.14  
Walleye.pollock -0.18 -0.31 -0.18  
Pacific.cod -0.20 -0.27 -0.01  
Rex.sole 0.24 0.17 -0.24  
Flathead.sole 0.55 0.37 -0.27  
Spotted.ratfish -0.14 -0.05 -0.01  
Shortfin.eelpout 0.63 0.36 -0.24  
Blackbelly.eelpout 1.00 0.59 -0.30  
Slender.soles 0.59 1.00 0.10  
North.pacific.hake -0.30 0.10 1.00  
Pacific.dover.sole -0.29 -0.29 0.05  
Sidestripe.shrimp 0.57 0.65 -0.11  
Northern.shrimp 0.29 0.27 -0.03  
Pink.shrimp 0.74 0.45 -0.36  
Spot.prawn 0.14 0.18 -0.05  
English.sole -0.33 -0.24 0.27  
Scallop -0.11 -0.20 -0.13  
Longnose.skate -0.19 0.03 0.20  
Pacific.spiny.dogfish -0.22 -0.13 0.31  
Eulachon 0.52 0.24 -0.36  
 Pacific.dover.sole Sidestripe.shrimp Northern.shrimp  
Sea.anemone 0.04 0.14 0.01  
Sablefish 0.10 0.14 0.11  
Arrowtooth.flounder 0.07 0.34 0.15  
Bering.skate 0.13 -0.15 -0.07  
Big.skate 0.05 -0.25 -0.06  
Pacific.herring -0.10 -0.18 -0.03  
Walleye.pollock 0.15 -0.26 -0.08  
Pacific.cod 0.13 -0.24 -0.14  
Rex.sole 0.18 0.21 0.03  
Flathead.sole -0.05 0.36 0.11  
Spotted.ratfish 0.17 0.01 -0.09  
Shortfin.eelpout -0.22 0.42 0.31  
Blackbelly.eelpout -0.29 0.57 0.29  
Slender.soles -0.29 0.65 0.27  
North.pacific.hake 0.05 -0.11 -0.03  
Pacific.dover.sole 1.00 -0.29 -0.28  
Sidestripe.shrimp -0.29 1.00 0.32  
Northern.shrimp -0.28 0.32 1.00  
Pink.shrimp -0.24 0.48 0.27  
Spot.prawn -0.19 0.31 0.28  
English.sole 0.17 -0.28 -0.10  
Scallop 0.12 -0.11 0.07  
Longnose.skate 0.04 -0.08 -0.04  
Pacific.spiny.dogfish 0.06 -0.22 0.01  
Eulachon -0.03 0.38 0.22  
 Pink.shrimp Spot.prawn English.sole Scallop  
Sea.anemone -0.01 0.14 -0.01 -0.06  
Sablefish 0.19 0.03 -0.11 0.03  
Arrowtooth.flounder 0.43 0.07 -0.23 0.03  
Bering.skate -0.10 -0.06 0.00 -0.01  
Big.skate -0.24 -0.07 0.30 -0.04  
Pacific.herring 0.00 0.05 0.17 0.09  
Walleye.pollock -0.08 -0.03 0.15 0.12  
Pacific.cod -0.17 -0.09 0.04 0.07  
Rex.sole 0.17 0.10 0.04 -0.05  
Flathead.sole 0.51 0.00 -0.09 -0.11  
Spotted.ratfish -0.12 0.00 0.05 0.14  
Shortfin.eelpout 0.54 0.15 -0.28 -0.07  
Blackbelly.eelpout 0.74 0.14 -0.33 -0.11  
Slender.soles 0.45 0.18 -0.24 -0.20  
North.pacific.hake -0.36 -0.05 0.27 -0.13  
Pacific.dover.sole -0.24 -0.19 0.17 0.12  
Sidestripe.shrimp 0.48 0.31 -0.28 -0.11  
Northern.shrimp 0.27 0.28 -0.10 0.07  
Pink.shrimp 1.00 0.16 -0.35 -0.07  
Spot.prawn 0.16 1.00 -0.11 0.16  
English.sole -0.35 -0.11 1.00 -0.03  
Scallop -0.07 0.16 -0.03 1.00  
Longnose.skate -0.23 -0.06 0.04 -0.06  
Pacific.spiny.dogfish -0.25 -0.08 0.15 -0.01  
Eulachon 0.48 -0.01 -0.21 -0.17  
 Longnose.skate Pacific.spiny.dogfish Eulachon  
Sea.anemone -0.03 -0.10 -0.10  
Sablefish -0.08 -0.09 0.16  
Arrowtooth.flounder -0.14 -0.16 0.50  
Bering.skate 0.19 0.16 -0.05  
Big.skate 0.14 0.16 -0.10  
Pacific.herring -0.13 -0.07 0.02  
Walleye.pollock 0.09 0.07 0.09  
Pacific.cod 0.07 0.10 -0.10  
Rex.sole -0.06 -0.18 0.31  
Flathead.sole -0.13 -0.21 0.44  
Spotted.ratfish 0.08 0.07 0.00  
Shortfin.eelpout -0.14 -0.09 0.42  
Blackbelly.eelpout -0.19 -0.22 0.52  
Slender.soles 0.03 -0.13 0.24  
North.pacific.hake 0.20 0.31 -0.36  
Pacific.dover.sole 0.04 0.06 -0.03  
Sidestripe.shrimp -0.08 -0.22 0.38  
Northern.shrimp -0.04 0.01 0.22  
Pink.shrimp -0.23 -0.25 0.48  
Spot.prawn -0.06 -0.08 -0.01  
English.sole 0.04 0.15 -0.21  
Scallop -0.06 -0.01 -0.17  
Longnose.skate 1.00 0.25 -0.14  
Pacific.spiny.dogfish 0.25 1.00 -0.09  
Eulachon -0.14 -0.09 1.00

png("Figure3.png",width=7,height=7,units="in",res=300)  
corrplot(species\_cor, tl.col = "black", tl.cex = 0.75,type="lower",method="color",outline=FALSE,diag=FALSE,order="FPC",mar=c(0,0,0,0),tl.srt=35)  
dev.off()

png   
 2

Table 4. Diversity measures by month and area

diversity\_data <- catch\_data %>%   
 mutate(., MONTH\_YEAR = format(as.Date(catch\_data$DATE,format="%Y-%m-%d")  
 ,"%b-%y"), .after = MONTH)  
  
# combine month-year and area into one column  
  
#diversity\_data$area\_month <- paste(diversity\_data$AreaGrouping, diversity\_data$MONTH\_YEAR, sep=":")  
  
  
diversity\_data <- diversity\_data %>% group\_by(., MONTH, AreaGrouping,SEASON, EVENT\_ID, Species\_name) %>%  
 summarise(mean\_CPUE = mean(CPUE))

`summarise()` has grouped output by 'MONTH', 'AreaGrouping', 'SEASON',  
'EVENT\_ID'. You can override using the `.groups` argument.

diversity\_data<- pivot\_wider(diversity\_data, names\_from = Species\_name,   
 values\_from = mean\_CPUE)  
  
#diversity\_data\_rowname<- diversity\_data$area\_month  
  
#diversity\_data <- as.data.frame(diversity\_data,   
 # row.names =diversity\_data$area\_month)  
#diversity\_data <- as.data.frame(diversity\_data,  
 # row.names = diversity\_data$area\_month)  
  
#diversity\_data <- diversity\_data[,-1]  
  
# calculate diversity index  
  
diversity\_data$Simpson <- diversity(diversity\_data[,5:208], "simpson")  
diversity\_data$Shannon <- diversity(diversity\_data[,5:208], "shannon")  
  
H <- diversity(diversity\_data[,5:208])  
diversity\_data$Evenness <- H/log(specnumber(diversity\_data[,5:208]))  
  
diversity\_data$Richness<-specnumber(diversity\_data[,5:208])  
  
richness\_aov<-aov(Richness~AreaGrouping+SEASON+AreaGrouping\*SEASON,data=diversity\_data)  
richness\_aov

Call:  
 aov(formula = Richness ~ AreaGrouping + SEASON + AreaGrouping \*   
 SEASON, data = diversity\_data)  
  
Terms:  
 AreaGrouping SEASON AreaGrouping:SEASON Residuals  
Sum of Squares 1309.313 370.947 577.698 7772.054  
Deg. of Freedom 3 3 9 398  
  
Residual standard error: 4.419024  
Estimated effects may be unbalanced

summary(richness\_aov)

Df Sum Sq Mean Sq F value Pr(>F)   
AreaGrouping 3 1309 436.4 22.350 0.000000000000215 \*\*\*  
SEASON 3 371 123.6 6.332 0.000334 \*\*\*  
AreaGrouping:SEASON 9 578 64.2 3.287 0.000705 \*\*\*  
Residuals 398 7772 19.5   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

TukeyHSD(richness\_aov,which='AreaGrouping:SEASON')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Richness ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$`AreaGrouping:SEASON`  
 diff lwr upr p adj  
A2:Winter-A1:Winter 5.32051282 1.46248413 9.1785415 0.0003100  
A3:Winter-A1:Winter 5.06756757 1.16805351 8.9670816 0.0010499  
A4:Winter-A1:Winter 0.27777778 -4.39452699 4.9500825 1.0000000  
A1:Spring-A1:Winter -2.34444444 -6.09818278 1.4092939 0.7287967  
A2:Spring-A1:Winter 1.95161290 -2.10065042 6.0038762 0.9555028  
A3:Spring-A1:Winter 3.40000000 -1.13215752 7.9321575 0.4108211  
A4:Spring-A1:Winter 2.15517241 -1.96033533 6.2706802 0.9132234  
A1:Summer-A1:Winter -3.94444444 -9.83768061 1.9487917 0.6180386  
A2:Summer-A1:Winter 1.00000000 -5.16077776 7.1607778 0.9999999  
A3:Summer-A1:Winter 3.16666667 -2.72656950 9.0599028 0.8950873  
A4:Summer-A1:Winter 2.04838710 -2.00387622 6.1006504 0.9339206  
A1:Fall-A1:Winter 3.43750000 -1.40428757 8.2792876 0.5124432  
A2:Fall-A1:Winter 2.61111111 -3.28212505 8.5043473 0.9787340  
A3:Fall-A1:Winter 0.50000000 -8.79136346 9.7913635 1.0000000  
A4:Fall-A1:Winter 2.80952381 -0.61025311 6.2293007 0.2548918  
A3:Winter-A2:Winter -0.25294525 -3.74999155 3.2441010 1.0000000  
A4:Winter-A2:Winter -5.04273504 -9.38480307 -0.7006670 0.0072756  
A1:Spring-A2:Winter -7.66495726 -10.99867507 -4.3312395 0.0000000  
A2:Spring-A2:Winter -3.36889992 -7.03550065 0.2977008 0.1127603  
A3:Spring-A2:Winter -1.92051282 -6.11140469 2.2703791 0.9711004  
A4:Spring-A2:Winter -3.16534041 -6.90171926 0.5710384 0.2093179  
A1:Summer-A2:Winter -9.26495726 -14.89996884 -3.6299457 0.0000032  
A2:Summer-A2:Winter -4.32051282 -10.23475880 1.5937332 0.4597249  
A3:Summer-A2:Winter -2.15384615 -7.78885772 3.4811654 0.9950880  
A4:Summer-A2:Winter -3.27212572 -6.93872646 0.3944750 0.1432291  
A1:Fall-A2:Winter -1.88301282 -6.40695246 2.6409268 0.9882908  
A2:Fall-A2:Winter -2.70940171 -8.34441328 2.9256099 0.9561187  
A3:Fall-A2:Winter -4.82051282 -13.95027503 4.3092494 0.9077222  
A4:Fall-A2:Winter -2.51098901 -5.46361447 0.4416365 0.2039476  
A4:Winter-A3:Winter -4.78978979 -9.16875991 -0.4108197 0.0170877  
A1:Spring-A3:Winter -7.41201201 -10.79365347 -4.0303706 0.0000000  
A2:Spring-A3:Winter -3.11595466 -6.82618181 0.5942725 0.2217690  
A3:Spring-A3:Winter -1.66756757 -5.89668086 2.5615457 0.9932080  
A4:Spring-A3:Winter -2.91239515 -6.69159500 0.8668047 0.3622744  
A1:Summer-A3:Winter -9.01201201 -14.67550739 -3.3485166 0.0000085  
A2:Summer-A3:Winter -4.06756757 -10.00895883 1.8738237 0.5784094  
A3:Summer-A3:Winter -1.90090090 -7.56439628 3.7625945 0.9988260  
A4:Summer-A3:Winter -3.01918047 -6.72940762 0.6910467 0.2699486  
A1:Fall-A3:Winter -1.63006757 -6.18943752 2.9293024 0.9976113  
A2:Fall-A3:Winter -2.45645646 -8.11995184 3.2070389 0.9825772  
A3:Fall-A3:Winter -4.56756757 -13.71493782 4.5798027 0.9400776  
A4:Fall-A3:Winter -2.25804376 -5.26467338 0.7485859 0.4088077  
A1:Spring-A4:Winter -2.62222222 -6.87189525 1.6274508 0.7461620  
A2:Spring-A4:Winter 1.67383513 -2.84169446 6.1893647 0.9964570  
A3:Spring-A4:Winter 3.12222222 -1.82849704 8.0729415 0.7143985  
A4:Spring-A4:Winter 1.87739464 -2.69497602 6.4497653 0.9897684  
A1:Summer-A4:Winter -4.22222222 -10.44310656 1.9986621 0.5937371  
A2:Summer-A4:Winter 0.72222222 -5.75267948 7.1971239 1.0000000  
A3:Summer-A4:Winter 2.88888889 -3.33199544 9.1097732 0.9674880  
A4:Summer-A4:Winter 1.77060932 -2.74492027 6.2861389 0.9935873  
A1:Fall-A4:Winter 3.15972222 -2.07593211 8.3953766 0.7762014  
A2:Fall-A4:Winter 2.33333333 -3.88755100 8.5542177 0.9959793  
A3:Fall-A4:Winter 0.22222222 -9.28033556 9.7247800 1.0000000  
A4:Fall-A4:Winter 2.53174603 -1.42603663 6.4895287 0.6926079  
A2:Spring-A1:Spring 4.29605735 0.73935564 7.8527591 0.0038972  
A3:Spring-A1:Spring 5.74444444 1.64935704 9.8395318 0.0002126  
A4:Spring-A1:Spring 4.49961686 0.87102305 8.1282107 0.0024892  
A1:Summer-A1:Spring -1.60000000 -7.16412810 3.9641281 0.9998139  
A2:Summer-A1:Spring 3.34444444 -2.50230437 9.1911933 0.8389929  
A3:Summer-A1:Spring 5.51111111 -0.05301699 11.0752392 0.0553276  
A4:Summer-A1:Spring 4.39283154 0.83612983 7.9495333 0.0026696  
A1:Fall-A1:Spring 5.78194444 1.34660951 10.2172794 0.0009882  
A2:Fall-A1:Spring 4.95555556 -0.60857254 10.5196837 0.1455011  
A3:Fall-A1:Spring 2.84444444 -6.24173869 11.9306276 0.9994794  
A4:Fall-A1:Spring 5.15396825 2.33897922 7.9689573 0.0000001  
A3:Spring-A2:Spring 1.44838710 -2.92197071 5.8187449 0.9989853  
A4:Spring-A2:Spring 0.20355951 -3.73306082 4.1401798 1.0000000  
A1:Summer-A2:Spring -5.89605735 -11.66578941 -0.1263253 0.0394000  
A2:Summer-A2:Spring -0.95161290 -6.99435717 5.0911314 0.9999999  
A3:Summer-A2:Spring 1.21505376 -4.55467830 6.9847858 0.9999967  
A4:Summer-A2:Spring 0.09677419 -3.77367974 3.9672281 1.0000000  
A1:Fall-A2:Spring 1.48588710 -3.20479329 6.1765675 0.9994012  
A2:Fall-A2:Spring 0.65949821 -5.11023385 6.4292303 1.0000000  
A3:Fall-A2:Spring -1.45161290 -10.66513615 7.7619103 0.9999999  
A4:Fall-A2:Spring 0.85791091 -2.34434608 4.0601679 0.9999232  
A4:Spring-A3:Spring -1.24482759 -5.67388994 3.1842348 0.9998598  
A1:Summer-A3:Spring -7.34444444 -13.46076865 -1.2281202 0.0042938  
A2:Summer-A3:Spring -2.40000000 -8.77450955 3.9745095 0.9958140  
A3:Summer-A3:Spring -0.23333333 -6.34965754 5.8829909 1.0000000  
A4:Summer-A3:Spring -1.35161290 -5.72197071 3.0187449 0.9995496  
A1:Fall-A3:Spring 0.03750000 -5.07347802 5.1484780 1.0000000  
A2:Fall-A3:Spring -0.78888889 -6.90521310 5.3274353 1.0000000  
A3:Fall-A3:Spring -2.90000000 -12.33443821 6.5344382 0.9995814  
A4:Fall-A3:Spring -0.59047619 -4.38179042 3.2008380 1.0000000  
A1:Summer-A4:Spring -6.09961686 -11.91394176 -0.2852920 0.0290048  
A2:Summer-A4:Spring -1.15517241 -7.24050923 4.9301644 0.9999992  
A3:Summer-A4:Spring 1.01149425 -4.80283065 6.8258192 0.9999998  
A4:Summer-A4:Spring -0.10678532 -4.04340565 3.8298350 1.0000000  
A1:Fall-A4:Spring 1.28232759 -3.46309637 6.0277515 0.9999143  
A2:Fall-A4:Spring 0.45593870 -5.35838620 6.2702636 1.0000000  
A3:Fall-A4:Spring -1.65517241 -10.89668617 7.5863413 0.9999996  
A4:Fall-A4:Spring 0.65435140 -2.62757118 3.9362740 0.9999984  
A2:Summer-A1:Summer 4.94444444 -2.45988893 12.3487778 0.6219997  
A3:Summer-A1:Summer 7.11111111 -0.07214738 14.2943696 0.0556291  
A4:Summer-A1:Summer 5.99283154 0.22309948 11.7625636 0.0326571  
A1:Fall-A1:Summer 7.38194444 1.03278096 13.7311079 0.0071528  
A2:Fall-A1:Summer 6.55555556 -0.62770293 13.7388140 0.1194053  
A3:Fall-A1:Summer 4.44444444 -5.71421713 14.6031060 0.9810980  
A4:Fall-A1:Summer 6.75396825 1.40945291 12.0984836 0.0017747  
A3:Summer-A2:Summer 2.16666667 -5.23766670 9.5710000 0.9997694  
A4:Summer-A2:Summer 1.04838710 -4.99435717 7.0911314 0.9999998  
A1:Fall-A2:Summer 2.43750000 -4.16074425 9.0357442 0.9965855  
A2:Fall-A2:Summer 1.61111111 -5.79322226 9.0154445 0.9999949  
A3:Fall-A2:Summer -0.50000000 -10.81616960 9.8161696 1.0000000  
A4:Fall-A2:Summer 1.80952381 -3.82863142 7.4476790 0.9993015  
A4:Summer-A3:Summer -1.11827957 -6.88801163 4.6514525 0.9999989  
A1:Fall-A3:Summer 0.27083333 -6.07833015 6.6199968 1.0000000  
A2:Fall-A3:Summer -0.55555556 -7.73881404 6.6277029 1.0000000  
A3:Fall-A3:Summer -2.66666667 -12.82532824 7.4919949 0.9999407  
A4:Fall-A3:Summer -0.35714286 -5.70165820 4.9873725 1.0000000  
A1:Fall-A4:Summer 1.38911290 -3.30156749 6.0797933 0.9997331  
A2:Fall-A4:Summer 0.56272401 -5.20700805 6.3324561 1.0000000  
A3:Fall-A4:Summer -1.54838710 -10.76191034 7.6651361 0.9999999  
A4:Fall-A4:Summer 0.76113671 -2.44112027 3.9633937 0.9999836  
A2:Fall-A1:Fall -0.82638889 -7.17555237 5.5227746 1.0000000  
A3:Fall-A1:Fall -2.93750000 -12.52452662 6.6495266 0.9995971  
A4:Fall-A1:Fall -0.62797619 -4.78447937 3.5285270 1.0000000  
A3:Fall-A2:Fall -2.11111111 -12.26977269 8.0475505 0.9999973  
A4:Fall-A2:Fall 0.19841270 -5.14610264 5.5429280 1.0000000  
A4:Fall-A3:Fall 2.30952381 -6.64385805 11.2629057 0.9999526

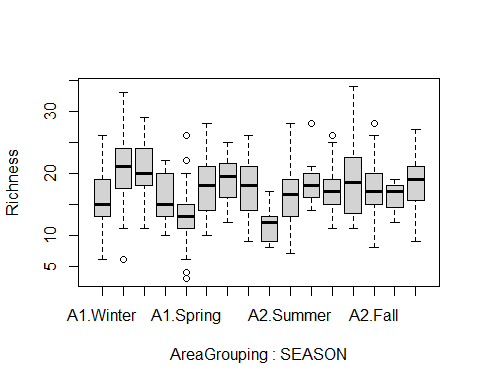
TukeyHSD(richness\_aov,which='AreaGrouping')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Richness ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$AreaGrouping  
 diff lwr upr p adj  
A2-A1 4.3383621 2.650789 6.0259348 0.0000000  
A3-A1 5.0335145 3.234171 6.8328577 0.0000000  
A4-A1 3.1612654 1.692850 4.6296808 0.0000003  
A3-A2 0.6951524 -1.142699 2.5330036 0.7633095  
A4-A2 -1.1770966 -2.692453 0.3382596 0.1881865  
A4-A3 -1.8722491 -3.511163 -0.2333352 0.0177895

TukeyHSD(richness\_aov,which='SEASON')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Richness ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$SEASON  
 diff lwr upr p adj  
Spring-Winter -1.82786524 -3.2848990 -0.37083148 0.0071499  
Summer-Winter -1.88853967 -3.7225036 -0.05457577 0.0407629  
Fall-Winter 0.06985929 -1.4280191 1.56773770 0.9993765  
Summer-Spring -0.06067444 -1.8827881 1.76143921 0.9997725  
Fall-Spring 1.89772453 0.4143789 3.38107016 0.0057771  
Fall-Summer 1.95839897 0.1034622 3.81333576 0.0339216

boxplot(Richness~AreaGrouping+SEASON,data=diversity\_data)



Simpson\_aov<-aov(Simpson~AreaGrouping+SEASON+AreaGrouping\*SEASON,data=diversity\_data)  
Simpson\_aov

Call:  
 aov(formula = Simpson ~ AreaGrouping + SEASON + AreaGrouping \*   
 SEASON, data = diversity\_data)  
  
Terms:  
 AreaGrouping SEASON AreaGrouping:SEASON Residuals  
Sum of Squares 0.649905 0.113687 0.434275 10.656278  
Deg. of Freedom 3 3 9 398  
  
Residual standard error: 0.1636294  
Estimated effects may be unbalanced

summary(Simpson\_aov)

Df Sum Sq Mean Sq F value Pr(>F)   
AreaGrouping 3 0.650 0.21664 8.091 0.0000304 \*\*\*  
SEASON 3 0.114 0.03790 1.415 0.2378   
AreaGrouping:SEASON 9 0.434 0.04825 1.802 0.0661 .   
Residuals 398 10.656 0.02677   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

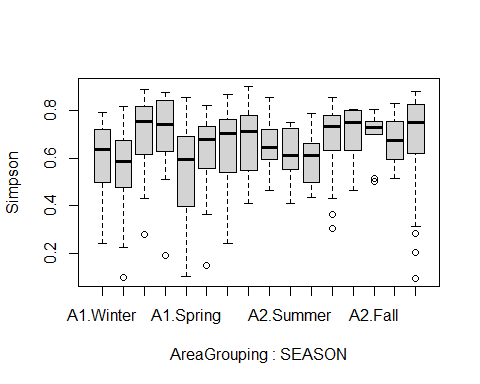
TukeyHSD(Simpson\_aov,which='AreaGrouping')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Simpson ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$AreaGrouping  
 diff lwr upr p adj  
A2-A1 0.006448568 -0.056039537 0.06893667 0.9933879  
A3-A1 0.069601123 0.002974338 0.13622791 0.0367178  
A4-A1 0.087025509 0.032652449 0.14139857 0.0002586  
A3-A2 0.063152556 -0.004900116 0.13120523 0.0798288  
A4-A2 0.080576941 0.024465737 0.13668815 0.0013747  
A4-A3 0.017424386 -0.043261960 0.07811073 0.8805573

TukeyHSD(Simpson\_aov,which='SEASON')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Simpson ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$SEASON  
 diff lwr upr p adj  
Spring-Winter -0.008154367 -0.06210598 0.04579725 0.9798486  
Summer-Winter 0.008047039 -0.05986169 0.07595577 0.9900735  
Fall-Winter 0.028639744 -0.02682428 0.08410377 0.5429447  
Summer-Spring 0.016201406 -0.05126853 0.08367134 0.9258180  
Fall-Spring 0.036794111 -0.01813179 0.09172001 0.3103501  
Fall-Summer 0.020592705 -0.04809262 0.08927803 0.8664138

boxplot(Simpson~AreaGrouping+SEASON,data=diversity\_data)



Shannon\_aov<-aov(Shannon~AreaGrouping+SEASON+AreaGrouping\*SEASON,data=diversity\_data)  
Shannon\_aov

Call:  
 aov(formula = Shannon ~ AreaGrouping + SEASON + AreaGrouping \*   
 SEASON, data = diversity\_data)  
  
Terms:  
 AreaGrouping SEASON AreaGrouping:SEASON Residuals  
Sum of Squares 8.75036 0.80531 2.67141 73.77700  
Deg. of Freedom 3 3 9 398  
  
Residual standard error: 0.4305454  
Estimated effects may be unbalanced

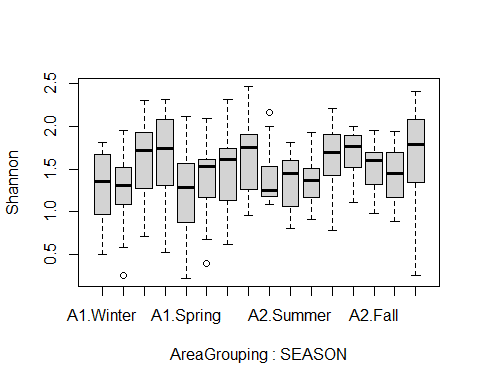
summary(Shannon\_aov)

Df Sum Sq Mean Sq F value Pr(>F)   
AreaGrouping 3 8.75 2.9168 15.735 0.00000000109 \*\*\*  
SEASON 3 0.81 0.2684 1.448 0.228   
AreaGrouping:SEASON 9 2.67 0.2968 1.601 0.113   
Residuals 398 73.78 0.1854   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

TukeyHSD(Shannon\_aov,which='AreaGrouping:SEASON')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Shannon ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$`AreaGrouping:SEASON`  
 diff lwr upr p adj  
A2:Winter-A1:Winter 0.00189437246 -0.373993259 0.377782004 1.0000000  
A3:Winter-A1:Winter 0.33643293747 -0.043496612 0.716362487 0.1521456  
A4:Winter-A1:Winter 0.35543154147 -0.099790986 0.810654069 0.3392238  
A1:Spring-A1:Winter -0.05693339148 -0.422660016 0.308793233 1.0000000  
A2:Spring-A1:Winter 0.09373586839 -0.301076038 0.488547775 0.9999838  
A3:Spring-A1:Winter 0.22943166073 -0.212136324 0.670999646 0.9182130  
A4:Spring-A1:Winter 0.37792063605 -0.023053173 0.778894445 0.0899913  
A1:Summer-A1:Winter 0.16794094866 -0.406236892 0.742118790 0.9997706  
A2:Summer-A1:Winter 0.06987913630 -0.530365275 0.670123548 1.0000000  
A3:Summer-A1:Winter 0.06717450503 -0.507003336 0.641352346 1.0000000  
A4:Summer-A1:Winter 0.35536964684 -0.039442260 0.750181553 0.1337718  
A1:Fall-A1:Winter 0.37898416806 -0.092751065 0.850719401 0.2907557  
A2:Fall-A1:Winter 0.22267023492 -0.351507606 0.796848076 0.9942820  
A3:Fall-A1:Winter 0.13946679729 -0.765790495 1.044724090 1.0000000  
A4:Fall-A1:Winter 0.38234299204 0.049154218 0.715531766 0.0087118  
A3:Winter-A2:Winter 0.33453856501 -0.006178562 0.675255692 0.0605471  
A4:Winter-A2:Winter 0.35353716901 -0.069510402 0.776584740 0.2290031  
A1:Spring-A2:Winter -0.05882776393 -0.383631800 0.265976272 0.9999996  
A2:Spring-A2:Winter 0.09184149593 -0.265395315 0.449078307 0.9999546  
A3:Spring-A2:Winter 0.22753728828 -0.180781194 0.635855771 0.8646275  
A4:Spring-A2:Winter 0.37602626359 0.011990972 0.740061555 0.0348365  
A1:Summer-A2:Winter 0.16604657620 -0.382972450 0.715065602 0.9996555  
A2:Summer-A2:Winter 0.06798476385 -0.508240063 0.644209591 1.0000000  
A3:Summer-A2:Winter 0.06528013257 -0.483738893 0.614299158 1.0000000  
A4:Summer-A2:Winter 0.35347527438 -0.003761537 0.710712085 0.0559144  
A1:Fall-A2:Winter 0.37708979561 -0.063677522 0.817857113 0.1957269  
A2:Fall-A2:Winter 0.22077586247 -0.328243163 0.769794888 0.9916999  
A3:Fall-A2:Winter 0.13757242483 -0.751940061 1.027084911 1.0000000  
A4:Fall-A2:Winter 0.38044861958 0.092774400 0.668122839 0.0007439  
A4:Winter-A3:Winter 0.01899860400 -0.407644337 0.445641545 1.0000000  
A1:Spring-A3:Winter -0.39336632895 -0.722839565 -0.063893093 0.0047139  
A2:Spring-A3:Winter -0.24269706908 -0.604184401 0.118790262 0.6127110  
A3:Spring-A3:Winter -0.10700127673 -0.519043671 0.305041118 0.9999483  
A4:Spring-A3:Winter 0.04148769858 -0.326719641 0.409695038 1.0000000  
A1:Summer-A3:Winter -0.16849198881 -0.720286192 0.383302214 0.9996134  
A2:Summer-A3:Winter -0.26655380117 -0.845423392 0.312315790 0.9698321  
A3:Summer-A3:Winter -0.26925843244 -0.821052635 0.282535770 0.9503466  
A4:Summer-A3:Winter 0.01893670937 -0.342550622 0.380424041 1.0000000  
A1:Fall-A3:Winter 0.04255123059 -0.401668062 0.486770523 1.0000000  
A2:Fall-A3:Winter -0.11376270255 -0.665556905 0.438031500 0.9999976  
A3:Fall-A3:Winter -0.19696614018 -1.088194178 0.694261897 0.9999938  
A4:Fall-A3:Winter 0.04591005457 -0.247025789 0.338845898 0.9999999  
A1:Spring-A4:Winter -0.41236493295 -0.826410462 0.001680596 0.0522133  
A2:Spring-A4:Winter -0.26169567309 -0.701643599 0.178252253 0.7945255  
A3:Spring-A4:Winter -0.12599988074 -0.608348325 0.356348564 0.9999443  
A4:Spring-A4:Winter 0.02248909458 -0.422996856 0.467975045 1.0000000  
A1:Summer-A4:Winter -0.18749059281 -0.793591186 0.418610001 0.9995484  
A2:Summer-A4:Winter -0.28555240517 -0.916401904 0.345297094 0.9741321  
A3:Summer-A4:Winter -0.28825703644 -0.894357630 0.317843557 0.9600102  
A4:Summer-A4:Winter -0.00006189463 -0.440009821 0.439886032 1.0000000  
A1:Fall-A4:Winter 0.02355262659 -0.486557035 0.533662288 1.0000000  
A2:Fall-A4:Winter -0.13276130655 -0.738861900 0.473339287 0.9999945  
A3:Fall-A4:Winter -0.21596474418 -1.141798693 0.709869205 0.9999872  
A4:Fall-A4:Winter 0.02691145057 -0.358695208 0.412518109 1.0000000  
A2:Spring-A1:Spring 0.15066925986 -0.195860092 0.497198612 0.9821706  
A3:Spring-A1:Spring 0.28636505221 -0.112619203 0.685349308 0.4923804  
A4:Spring-A1:Spring 0.43485402753 0.081320230 0.788387825 0.0028664  
A1:Summer-A1:Spring 0.22487434014 -0.317238511 0.766987191 0.9886789  
A2:Summer-A1:Spring 0.12681252778 -0.442836052 0.696461107 0.9999931  
A3:Summer-A1:Spring 0.12410789650 -0.418004955 0.666220748 0.9999900  
A4:Summer-A1:Spring 0.41230303831 0.065773686 0.758832391 0.0049838  
A1:Fall-A1:Spring 0.43591755954 0.003782996 0.868052123 0.0454990  
A2:Fall-A1:Spring 0.27960362640 -0.262509225 0.821716478 0.9226956  
A3:Fall-A1:Spring 0.19640018877 -0.688866390 1.081666768 0.9999934  
A4:Fall-A1:Spring 0.43927638351 0.165012078 0.713540689 0.0000071  
A3:Spring-A2:Spring 0.13569579235 -0.290108052 0.561499636 0.9993572  
A4:Spring-A2:Spring 0.28418476766 -0.099360045 0.667729581 0.4335942  
A1:Summer-A2:Spring 0.07420508027 -0.487939760 0.636349920 1.0000000  
A2:Summer-A2:Spring -0.02385673208 -0.612601143 0.564887679 1.0000000  
A3:Summer-A2:Spring -0.02656136336 -0.588706203 0.535583476 1.0000000  
A4:Summer-A2:Spring 0.26163377845 -0.115464444 0.638732001 0.5544619  
A1:Fall-A2:Spring 0.28524829968 -0.171764565 0.742261164 0.7297418  
A2:Fall-A2:Spring 0.12893436654 -0.433210473 0.691079206 0.9999898  
A3:Fall-A2:Spring 0.04573092891 -0.851942393 0.943404251 1.0000000  
A4:Fall-A2:Spring 0.28860712365 -0.023388688 0.600602936 0.1063748  
A4:Spring-A3:Spring 0.14848897532 -0.283034451 0.580012402 0.9984415  
A1:Summer-A3:Spring -0.06149071207 -0.657404015 0.534422591 1.0000000  
A2:Summer-A3:Spring -0.15955252443 -0.780620818 0.461515770 0.9999550  
A3:Summer-A3:Spring -0.16225715571 -0.758170459 0.433656148 0.9999057  
A4:Summer-A3:Spring 0.12593798610 -0.299865858 0.551741830 0.9997372  
A1:Fall-A3:Spring 0.14955250733 -0.348409943 0.647514958 0.9996835  
A2:Fall-A3:Spring -0.00676142581 -0.602674729 0.589151877 1.0000000  
A3:Fall-A3:Spring -0.08996486344 -1.009161925 0.829232198 1.0000000  
A4:Fall-A3:Spring 0.15291133130 -0.216476312 0.522298974 0.9889063  
A1:Summer-A4:Spring -0.20997968739 -0.776469206 0.356509831 0.9964586  
A2:Summer-A4:Spring -0.30804149975 -0.900935703 0.284852703 0.9182469  
A3:Summer-A4:Spring -0.31074613102 -0.877235650 0.255743388 0.8785338  
A4:Summer-A4:Spring -0.02255098921 -0.406095802 0.360993824 1.0000000  
A1:Fall-A4:Spring 0.00106353201 -0.461282996 0.463410060 1.0000000  
A2:Fall-A4:Spring -0.15525040113 -0.721739920 0.411239118 0.9998977  
A3:Fall-A4:Spring -0.23845383876 -1.138854276 0.661946598 0.9999336  
A4:Fall-A4:Spring 0.00442235599 -0.315335272 0.324179984 1.0000000  
A2:Summer-A1:Summer -0.09806181236 -0.819465814 0.623342189 1.0000000  
A3:Summer-A1:Summer -0.10076644363 -0.800631125 0.599098238 1.0000000  
A4:Summer-A1:Summer 0.18742869818 -0.374716142 0.749573538 0.9989123  
A1:Fall-A1:Summer 0.21104321940 -0.407555608 0.829642047 0.9985859  
A2:Fall-A1:Summer 0.05472928626 -0.645135395 0.754593968 1.0000000  
A3:Fall-A1:Summer -0.02847415137 -1.018232276 0.961283973 1.0000000  
A4:Fall-A1:Summer 0.21440204338 -0.306313943 0.735118030 0.9894802  
A3:Summer-A2:Summer -0.00270463128 -0.724108633 0.718699370 1.0000000  
A4:Summer-A2:Summer 0.28549051053 -0.303253901 0.874234922 0.9528753  
A1:Fall-A2:Summer 0.30910503176 -0.333761728 0.951971791 0.9561131  
A2:Fall-A2:Summer 0.15279109862 -0.568612903 0.874195100 0.9999965  
A3:Fall-A2:Summer 0.06958766099 -0.935516466 1.074691788 1.0000000  
A4:Fall-A2:Summer 0.31246385573 -0.236861457 0.861789168 0.8447725  
A4:Summer-A3:Summer 0.28819514181 -0.273949698 0.850339982 0.9262059  
A1:Fall-A3:Summer 0.31180966304 -0.306789165 0.930408491 0.9353917  
A2:Fall-A3:Summer 0.15549572990 -0.544368952 0.855360411 0.9999933  
A3:Fall-A3:Summer 0.07229229226 -0.917465832 1.062050417 1.0000000  
A4:Fall-A3:Summer 0.31516848701 -0.205547499 0.835884473 0.7723937  
A1:Fall-A4:Summer 0.02361452123 -0.433398343 0.480627386 1.0000000  
A2:Fall-A4:Summer -0.13269941191 -0.694844252 0.429445428 0.9999850  
A3:Fall-A4:Summer -0.21590284955 -1.113576172 0.681770473 0.9999809  
A4:Fall-A4:Summer 0.02697334520 -0.285022467 0.338969157 1.0000000  
A2:Fall-A1:Fall -0.15631393314 -0.774912761 0.462284895 0.9999636  
A3:Fall-A1:Fall -0.23951737077 -1.173581117 0.694546375 0.9999561  
A4:Fall-A1:Fall 0.00335882397 -0.401609169 0.408326817 1.0000000  
A3:Fall-A2:Fall -0.08320343763 -1.072961562 0.906554687 1.0000000  
A4:Fall-A2:Fall 0.15967275711 -0.361043229 0.680388743 0.9995933  
A4:Fall-A3:Fall 0.24287619474 -0.629451559 1.115203949 0.9998753

boxplot(Shannon~AreaGrouping+SEASON,data=diversity\_data)



Evenness\_aov<-aov(Evenness~AreaGrouping+SEASON+AreaGrouping\*SEASON,data=diversity\_data)  
Evenness\_aov

Call:  
 aov(formula = Evenness ~ AreaGrouping + SEASON + AreaGrouping \*   
 SEASON, data = diversity\_data)  
  
Terms:  
 AreaGrouping SEASON AreaGrouping:SEASON Residuals  
Sum of Squares 0.764789 0.052129 0.316376 7.634516  
Deg. of Freedom 3 3 9 398  
  
Residual standard error: 0.1384998  
Estimated effects may be unbalanced

summary(Evenness\_aov)

Df Sum Sq Mean Sq F value Pr(>F)   
AreaGrouping 3 0.765 0.25493 13.290 0.0000000277 \*\*\*  
SEASON 3 0.052 0.01738 0.906 0.4382   
AreaGrouping:SEASON 9 0.316 0.03515 1.833 0.0608 .   
Residuals 398 7.635 0.01918   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

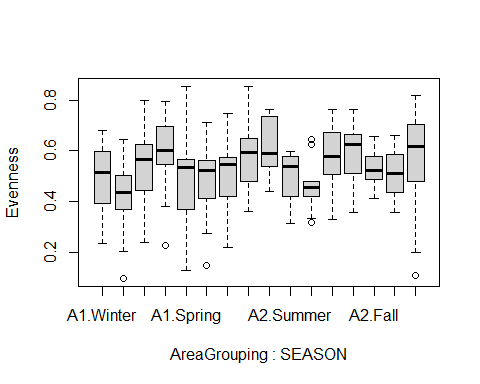
TukeyHSD(Evenness\_aov,which='AreaGrouping')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Evenness ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$AreaGrouping  
 diff lwr upr p adj  
A2-A1 -0.044287306 -0.097178741 0.008604128 0.1362897  
A3-A1 0.009819458 -0.046575056 0.066213972 0.9697547  
A4-A1 0.067171439 0.021148773 0.113194105 0.0010937  
A3-A2 0.054106764 -0.003494653 0.111708182 0.0743461  
A4-A2 0.111458746 0.063964873 0.158952618 0.0000000  
A4-A3 0.057351981 0.005985599 0.108718364 0.0216857

TukeyHSD(Evenness\_aov,which='SEASON')

Tukey multiple comparisons of means  
 95% family-wise confidence level  
  
Fit: aov(formula = Evenness ~ AreaGrouping + SEASON + AreaGrouping \* SEASON, data = diversity\_data)  
  
$SEASON  
 diff lwr upr p adj  
Spring-Winter 0.008184248 -0.03748170 0.05385019 0.9671654  
Summer-Winter 0.018700696 -0.03877889 0.07618028 0.8356549  
Fall-Winter 0.024162854 -0.02278323 0.07110894 0.5456905  
Summer-Spring 0.010516448 -0.04659173 0.06762463 0.9645379  
Fall-Spring 0.015978606 -0.03051200 0.06246921 0.8117794  
Fall-Summer 0.005462158 -0.05267475 0.06359907 0.9949874

boxplot(Evenness~AreaGrouping+SEASON,data=diversity\_data)



#diversity\_index <- data.frame(Shannon, Simpson, Evenness,   
 # row.names = diversity\_data\_rowname)  
  
#### species richness  
  
# compare species richness between areas

Figure 3. Bottom temperature, depth and salinity boxplots for distributions

Figure 5. Bray-curtis dissimilarity dendrograms between months and areas

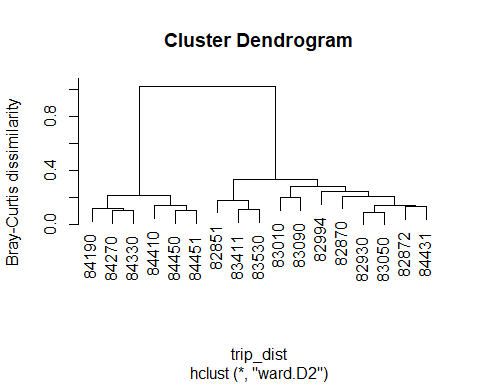
####### Cluster by trip #######  
  
# cluster analysis of top 25 species abundance across the 17 trips using the average   
# CPUE across all hauls of a cruise pooled together  
  
# adding year month values to dataset   
  
cluster\_top25 <- catch\_top25 %>%   
 mutate(., MONTH\_YEAR = format(as.Date(catch\_top25$DATE,format="%Y-%m-%d")  
 ,"%b-%y"), .after = MONTH)  
  
mean\_top25\_log <- cluster\_top25 %>%   
 group\_by(., TRIP\_ID, MAJOR\_STAT\_AREA\_CODE, Species\_common\_name, SEASON) %>%  
 summarise(., mean\_log\_CPUE = mean(log\_CPUE))

`summarise()` has grouped output by 'TRIP\_ID', 'MAJOR\_STAT\_AREA\_CODE',  
'Species\_common\_name'. You can override using the `.groups` argument.

mean\_top25\_log <- mean\_top25\_log %>%   
 pivot\_wider(., names\_from = Species\_common\_name, values\_from = mean\_log\_CPUE)   
  
  
# use trip ID as row names   
  
mean\_top25\_log <- as.data.frame(mean\_top25\_log, row.names = mean\_top25\_log$TRIP\_ID)  
mean\_top25\_log <- as.data.frame(mean\_top25\_log, row.names = mean\_top25\_log$TRIP\_ID)  
  
trip\_cluster\_data <- mean\_top25\_log[,-c(1:3)]  
  
# Hierarchical clustering by trip  
  
apply(trip\_cluster\_data, 1, sum)

82851 82870 82872 82930 82994 83010 83050 83090   
59.39264 62.79423 58.64533 65.20871 59.23182 52.13660 59.47539 48.22695   
 83411 83530 84190 84270 84330 84410 84431 84450   
55.97778 56.93672 72.29169 71.09294 73.98912 77.16230 56.92116 71.98369   
 84451   
68.55680

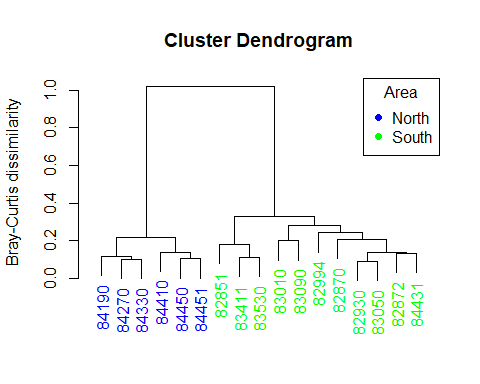
##### scale to 1? not done in other papers  
# Turn CPUE to relative abundance by dividing each value by sample total abundance  
  
#trip\_cluster\_data <- decostand(trip\_cluster\_data, method = "total")  
  
# check total abundance in each sample  
  
#apply(trip\_cluster\_data, 1, sum)  
  
  
# calculate Bray-Curtis distance among samples  
  
trip\_dist <- vegdist(trip\_cluster\_data, method = "bray")  
  
# cluster communities using average-linkage algorithm  
trip\_cluster <- hclust(trip\_dist, method = "ward.D2")  
  
# plot cluster diagram  
plot(trip\_cluster, ylab = "Bray-Curtis dissimilarity")



# cluster diagram coloured by area  
  
trip\_dend <- as.dendrogram(hclust(trip\_dist, method = "ward.D2"))  
  
order.dendrogram(trip\_dend)

[1] 11 12 13 14 16 17 1 9 10 6 8 5 2 4 7 3 15

labels\_colors(trip\_dend)<-north\_south\_colours[mean\_top25\_log$MAJOR\_STAT\_AREA\_CODE][order.dendrogram(trip\_dend)]  
  
plot(hang.dendrogram(trip\_dend, hang = 0.1), ylab = "Bray-Curtis dissimilarity", main = "Cluster Dendrogram")  
legend("topright", legend=c("North", "South"), title= "Area", pch=19,   
 col=c("blue", "green"))



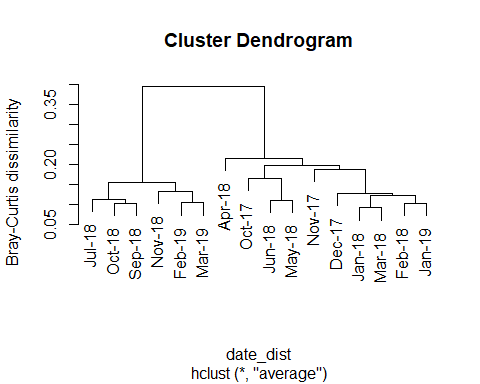
######### Cluster by trip using date #######  
  
mean\_top25\_log\_date <- cluster\_top25 %>%   
 group\_by(., MONTH\_YEAR, MAJOR\_STAT\_AREA\_CODE, Species\_common\_name) %>%  
 summarise(., mean\_log\_CPUE = mean(log\_CPUE))

`summarise()` has grouped output by 'MONTH\_YEAR', 'MAJOR\_STAT\_AREA\_CODE'. You  
can override using the `.groups` argument.

mean\_top25\_log\_date <- mean\_top25\_log\_date %>%   
 pivot\_wider(., names\_from = Species\_common\_name, values\_from = mean\_log\_CPUE)   
  
# use trip ID as row names   
  
mean\_top25\_log\_date <- as.data.frame(mean\_top25\_log\_date, row.names = mean\_top25\_log\_date$MONTH\_YEAR)  
mean\_top25\_log\_date <- as.data.frame(mean\_top25\_log\_date, row.names = mean\_top25\_log\_date$MONTH\_YEAR)  
  
date\_cluster\_data <- mean\_top25\_log\_date[,-c(1:2)]  
  
#Hierarchical clustering   
  
apply(date\_cluster\_data, 1, sum)

Apr-18 Dec-17 Feb-18 Feb-19 Jan-18 Jan-19 Jul-18 Jun-18   
48.22695 58.64533 56.27548 71.98369 65.20871 56.92116 72.29169 56.93672   
 Mar-18 Mar-19 May-18 Nov-17 Nov-18 Oct-17 Oct-18 Sep-18   
59.47539 68.55680 55.97778 62.79423 77.16230 59.39264 73.98912 71.09294

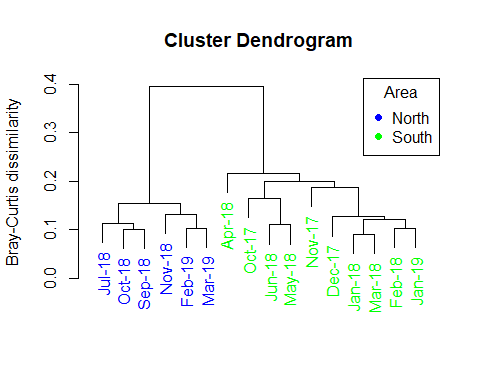
# Turn CPUE to relative abundance by dividing each value by sample total abundance  
  
#date\_cluster\_data <- decostand(date\_cluster\_data, method = "total")  
  
# check total abundance in each sample  
  
#apply(date\_cluster\_data, 1, sum)  
  
# calculate Bray-Curtis distance among samples  
  
date\_dist <- vegdist(date\_cluster\_data, method = "bray")  
  
# cluster communities using average-linkage algorithm  
date\_cluster <- hclust(date\_dist, method = "average")  
  
# plot cluster diagram  
plot(date\_cluster, ylab = "Bray-Curtis dissimilarity")



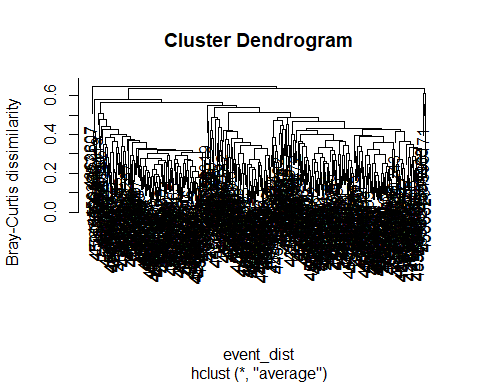
# cluster diagram coloured by area  
  
date\_dend <- as.dendrogram(hclust(date\_dist, method = "average"))  
  
order.dendrogram(date\_dend)

[1] 7 15 16 13 4 10 1 14 8 11 12 2 5 9 3 6

labels\_colors(date\_dend)<-north\_south\_colours[mean\_top25\_log\_date$MAJOR\_STAT\_AREA\_CODE][order.dendrogram(date\_dend)]  
  
plot(hang.dendrogram(date\_dend, hang = 0.1), ylab = "Bray-Curtis dissimilarity", main = "Cluster Dendrogram")  
legend("topright", legend=c("North", "South"), title= "Area", pch=19,   
 col=c("blue", "green"))



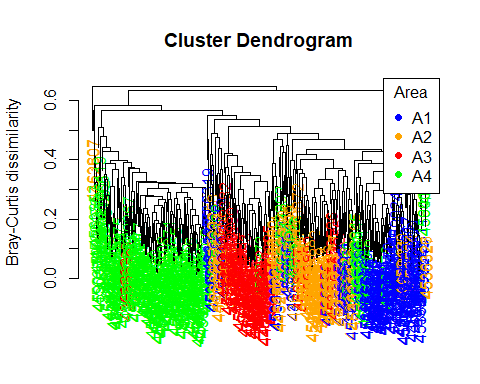
####### Cluster by event and area #######  
  
species\_cluster\_matrix\_area <- catch\_wide\_log[,-c(1,3:15)]  
  
cluster\_groups <- catch\_wide\_log[,c(2,9)]  
  
# use event ID as row names   
  
species\_cluster\_matrix <- as.data.frame(species\_cluster\_matrix\_area,   
 row.names = species\_cluster\_matrix\_area$EVENT\_ID)  
species\_cluster\_matrix <- as.data.frame(species\_cluster\_matrix,   
 row.names = species\_cluster\_matrix$EVENT\_ID)  
  
species\_cluster\_matrix <- species\_cluster\_matrix[,-1]  
  
  
# calculate Bray-Curtis distance among samples  
  
event\_dist <- vegdist(species\_cluster\_matrix, method = "bray")  
  
# cluster communities using average-linkage algorithm  
event\_cluster <- hclust(event\_dist, method = "average")  
  
# plot cluster diagram  
plot(event\_cluster, ylab = "Bray-Curtis dissimilarity")



# cluster diagram coloured by area  
  
event\_dend <- as.dendrogram(hclust(event\_dist, method = "average"))  
  
order.dendrogram(event\_dend)

[1] 3 89 268 319 396 267 320 321 254 373 397 414 369 309 286 287 398 265  
 [19] 251 394 288 400 232 226 227 231 311 412 252 255 230 233 293 292 294 272  
 [37] 331 411 229 303 38 237 118 385 370 392 410 381 117 384 285 408 234 409  
 [55] 389 402 380 243 250 332 336 335 379 260 313 387 258 315 262 390 368 316  
 [73] 295 317 279 329 330 298 241 300 302 242 326 271 314 327 244 238 274 235  
 [91] 290 283 306 289 225 249 263 291 278 261 259 264 266 275 328 324 334 239  
[109] 297 382 405 376 377 325 401 374 404 393 281 228 391 304 247 276 277 236  
[127] 273 240 406 299 305 246 282 407 333 375 378 308 371 280 386 403 149 28  
[145] 193 155 148 153 363 2 43 127 138 245 55 353 132 56 130 99 154 98  
[163] 347 180 6 211 212 173 178 36 167 171 214 87 354 355 75 63 122 352  
[181] 361 362 46 61 78 51 50 65 39 357 358 213 172 177 76 348 77 79  
[199] 116 119 8 45 85 49 84 80 356 284 120 125 126 83 86 42 182 217  
[217] 218 219 183 220 44 81 188 367 103 162 187 340 190 107 67 88 395 25  
[235] 388 100 26 134 163 253 40 203 136 215 399 62 32 19 37 337 339 23  
[253] 257 206 52 176 207 142 22 350 164 202 143 1 20 200 204 5 169 4  
[271] 35 110 111 31 33 29 73 345 74 343 53 69 346 70 72 34 108 224  
[289] 114 121 21 71 59 68 90 82 168 210 166 170 115 140 60 344 113 195  
[307] 205 144 341 64 137 151 102 342 161 372 141 158 112 104 150 139 106 109  
[325] 199 256 269 322 383 413 184 221 296 338 310 248 307 198 194 197 189 179  
[343] 186 270 133 159 7 11 15 16 222 17 223 12 13 9 18 101 364 365  
[361] 366 24 57 323 146 152 128 94 58 191 192 10 27 14 196 349 123 185  
[379] 47 95 48 124 54 30 359 360 96 129 97 201 131 135 145 66 41 91  
[397] 165 208 209 216 160 175 174 181 105 147 92 93 351 301 312 318 156 157

labels\_colors(event\_dend)<-area\_colours[catch\_wide\_log$AreaGrouping][order.dendrogram(event\_dend)]  
  
plot(hang.dendrogram(event\_dend), ylab = "Bray-Curtis dissimilarity",  
 main = "Cluster Dendrogram")  
legend("topright", legend=c("A1", "A2","A3","A4"), title= "Area", pch=19,   
 col=area\_colours)



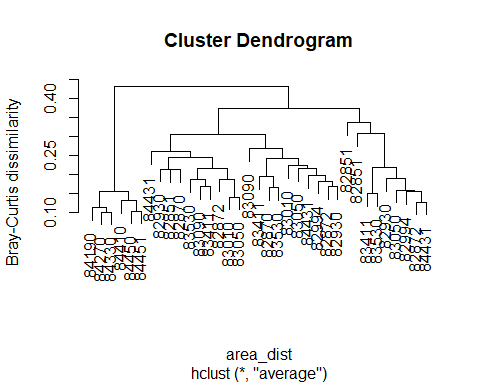
####### Cluster by trip and area #######  
  
# cluster analysis of top 25 species abundance across the 17 trips using the average   
# CPUE across all hauls of a cruise pooled together  
  
mean\_top25\_log\_area <- cluster\_top25 %>%   
 group\_by(., TRIP\_ID, AreaGrouping, Species\_common\_name) %>%  
 summarise(., mean\_log\_CPUE = mean(log\_CPUE))

`summarise()` has grouped output by 'TRIP\_ID', 'AreaGrouping'. You can override  
using the `.groups` argument.

mean\_top25\_log\_area <- mean\_top25\_log\_area %>%   
 pivot\_wider(., names\_from = Species\_common\_name, values\_from = mean\_log\_CPUE)   
  
  
# use trip ID as row names   
  
mean\_top25\_log\_area <- as.data.frame(mean\_top25\_log\_area,   
 row.names = mean\_top25\_log\_area$TRIP\_ID)  
mean\_top25\_log\_area <- as.data.frame(mean\_top25\_log\_area,   
 row.names = mean\_top25\_log\_area$TRIP\_ID)  
  
area\_cluster\_data <- mean\_top25\_log\_area[,-c(1:2)]  
  
# Hierarchical clustering by trip  
  
apply(area\_cluster\_data, 1, sum)

82851 82851 82851 82870 82870 82872 82872 82872   
70.33490 42.66862 41.56972 59.59400 65.99446 55.67464 56.32030 63.42444   
 82930 82930 82930 82994 82994 83010 83010 83050   
71.58263 63.38162 64.76241 65.90858 55.12305 53.35689 48.78079 64.68290   
 83050 83050 83090 83090 83411 83411 83411 83530   
51.89318 63.48621 46.17193 51.92598 57.98208 54.82925 53.11774 54.99956   
 83530 83530 84190 84270 84330 84410 84431 84431   
63.09796 53.39723 72.29169 71.09294 73.98912 77.16230 57.47859 56.54861   
 84431 84450 84451   
56.90512 71.98369 68.55680

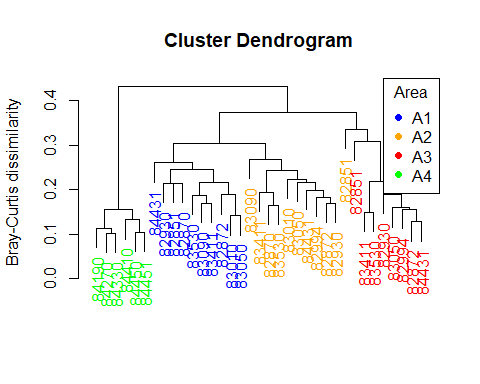
##### scale to 1? not done in other papers  
# Turn CPUE to relative abundance by dividing each value by sample total abundance  
  
#trip\_cluster\_data <- decostand(trip\_cluster\_data, method = "total")  
  
# check total abundance in each sample  
  
#apply(trip\_cluster\_data, 1, sum)  
  
  
# calculate Bray-Curtis distance among samples  
  
area\_dist <- vegdist(area\_cluster\_data, method = "bray")  
  
# cluster communities using average-linkage algorithm  
area\_cluster <- hclust(area\_dist, method = "average")  
  
# plot cluster diagram  
plot(area\_cluster, ylab = "Bray-Curtis dissimilarity")



# cluster diagram coloured by area  
  
area\_dend <- as.dendrogram(hclust(area\_dist, method = "average"))  
  
order.dendrogram(area\_dend)

[1] 27 28 29 30 34 35 31 9 1 4 24 19 21 6 14 16 20 22 5 25 15 17 32 12 7  
[26] 10 2 3 23 26 11 18 13 8 33

labels\_colors(area\_dend)<-area\_colours[mean\_top25\_log\_area$AreaGrouping][order.dendrogram(area\_dend)]  
  
plot(hang.dendrogram(area\_dend, hang = 0.1), ylab = "Bray-Curtis dissimilarity", main = "Cluster Dendrogram")  
legend("topright", legend=c("A1", "A2","A3","A4"), title= "Area", pch=19,   
 col=area\_colours)



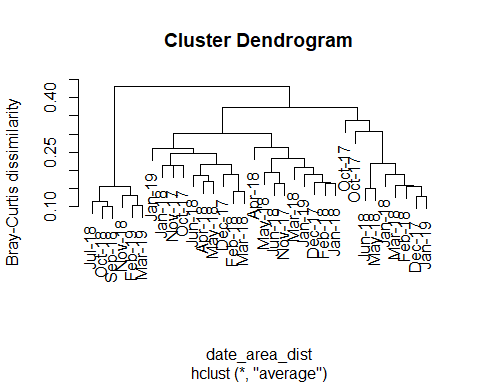
######### Cluster by trip and area using date #######  
  
mean\_top25\_log\_date\_area <- cluster\_top25 %>%   
 group\_by(., MONTH\_YEAR, AreaGrouping, Species\_common\_name) %>%  
 summarise(., mean\_log\_CPUE = mean(log\_CPUE))

`summarise()` has grouped output by 'MONTH\_YEAR', 'AreaGrouping'. You can  
override using the `.groups` argument.

mean\_top25\_log\_date\_area <- mean\_top25\_log\_date\_area %>%   
 pivot\_wider(., names\_from = Species\_common\_name, values\_from = mean\_log\_CPUE)   
  
# use trip ID as row names   
  
mean\_top25\_log\_date\_area <- as.data.frame(mean\_top25\_log\_date\_area,   
 row.names = mean\_top25\_log\_date\_area$MONTH\_YEAR)  
mean\_top25\_log\_date\_area <- as.data.frame(mean\_top25\_log\_date\_area,   
 row.names = mean\_top25\_log\_date\_area$MONTH\_YEAR)  
  
date\_area\_cluster\_data <- mean\_top25\_log\_date\_area[,-c(1:2)]  
  
#Hierarchical clustering   
  
apply(date\_area\_cluster\_data, 1, sum)

Apr-18 Apr-18 Dec-17 Dec-17 Dec-17 Feb-18 Feb-18 Feb-18   
46.17193 51.92598 55.67464 56.32030 63.42444 53.35689 60.19932 55.12305   
 Feb-19 Jan-18 Jan-18 Jan-18 Jan-19 Jan-19 Jan-19 Jul-18   
71.98369 71.58263 63.38162 64.76241 57.47859 56.54861 56.90512 72.29169   
 Jun-18 Jun-18 Jun-18 Mar-18 Mar-18 Mar-18 Mar-19 May-18   
54.99956 63.09796 53.39723 64.68290 51.89318 63.48621 68.55680 57.98208   
 May-18 May-18 Nov-17 Nov-17 Nov-18 Oct-17 Oct-17 Oct-17   
54.82925 53.11774 59.59400 65.99446 77.16230 70.33490 42.66862 41.56972   
 Oct-18 Sep-18   
73.98912 71.09294

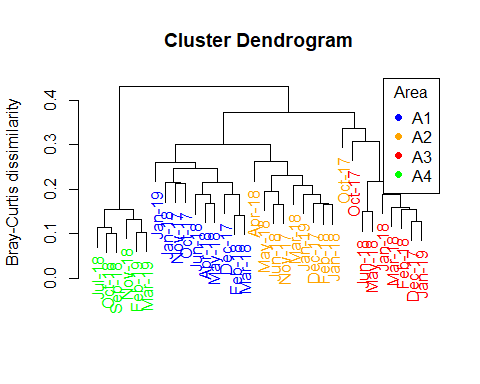
# Turn CPUE to relative abundance by dividing each value by sample total abundance  
  
#date\_cluster\_data <- decostand(date\_cluster\_data, method = "total")  
  
# check total abundance in each sample  
  
#apply(date\_cluster\_data, 1, sum)  
  
# calculate Bray-Curtis distance among samples  
  
date\_area\_dist <- vegdist(date\_area\_cluster\_data, method = "bray")  
  
# cluster communities using average-linkage algorithm  
date\_area\_cluster <- hclust(date\_area\_dist, method = "average")  
  
# plot cluster diagram  
plot(date\_area\_cluster, ylab = "Bray-Curtis dissimilarity")



# cluster diagram coloured by area  
  
date\_area\_dend <- as.dendrogram(hclust(date\_area\_dist, method = "average"))  
  
order.dendrogram(date\_area\_dend)

[1] 16 33 34 29 9 23 13 10 27 30 17 1 24 3 6 20 2 25 18 28 21 14 4 7 11  
[26] 31 32 19 26 12 22 8 5 15

labels\_colors(date\_area\_dend)<-area\_colours[mean\_top25\_log\_date\_area$AreaGrouping][order.dendrogram(date\_area\_dend)]  
  
plot(hang.dendrogram(date\_area\_dend, hang = 0.1), ylab = "Bray-Curtis dissimilarity", main = "Cluster Dendrogram")  
legend("topright", legend=c("A1", "A2","A3","A4"), title= "Area", pch=19,   
 col=area\_colours)



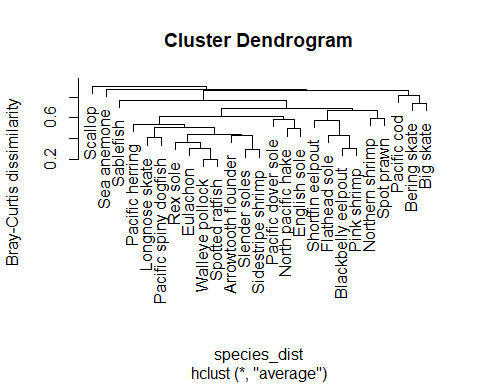
######### Cluster by species #######  
  
# cluster analysis of top 25 species CPUE across all events/halls   
# to examine which species had similar distributions among the hauls  
  
# filter event id and species CPUE  
  
species\_cluster\_data <- catch\_wide\_log[,-c(1,3:15)]  
  
# use event ID as row names   
  
species\_cluster\_data <- as.data.frame(species\_cluster\_data, row.names = species\_cluster\_data$EVENT\_ID)  
species\_cluster\_data <- as.data.frame(species\_cluster\_data, row.names = species\_cluster\_data$EVENT\_ID)  
  
species\_cluster\_data <- species\_cluster\_data[,-1]  
  
# transpose matrix   
  
species\_cluster\_data <- t(species\_cluster\_data)  
  
  
  
####### Hierarchical clustering ########  
  
apply(species\_cluster\_data, 1, sum)

Sea anemone Sablefish Arrowtooth flounder   
 183.5976 547.1076 1319.3593   
 Bering skate Big skate Pacific herring   
 317.3614 609.4460 1039.4643   
 Walleye pollock Pacific cod Rex sole   
 2391.4822 298.1008 1386.9613   
 Flathead sole Spotted ratfish Shortfin eelpout   
 1022.1668 3515.9994 304.5645   
 Blackbelly eelpout Slender soles North pacific hake   
 805.7899 1158.7098 992.4438   
 Pacific dover sole Sidestripe shrimp Northern shrimp   
 945.0828 1676.6647 501.3432   
 Pink shrimp Spot prawn English sole   
 689.2763 523.1920 1135.5061   
 Scallop Longnose skate Pacific spiny dogfish   
 145.7053 1292.7864 1796.9931   
 Eulachon   
 1546.6579

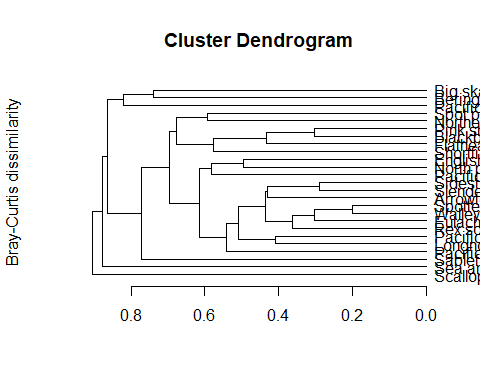
# convert the CPUE of each species from each event to the proportion of the total catch of  
# that species in all events during all trips of the study (relativizing by species totals)  
  
species\_cluster\_data <- decostand(species\_cluster\_data, method = "total")  
  
# check total abundance in each sample  
  
apply(species\_cluster\_data, 1, sum)

Sea anemone Sablefish Arrowtooth flounder   
 1 1 1   
 Bering skate Big skate Pacific herring   
 1 1 1   
 Walleye pollock Pacific cod Rex sole   
 1 1 1   
 Flathead sole Spotted ratfish Shortfin eelpout   
 1 1 1   
 Blackbelly eelpout Slender soles North pacific hake   
 1 1 1   
 Pacific dover sole Sidestripe shrimp Northern shrimp   
 1 1 1   
 Pink shrimp Spot prawn English sole   
 1 1 1   
 Scallop Longnose skate Pacific spiny dogfish   
 1 1 1   
 Eulachon   
 1

# calculate Bray-Curtis distance among species  
  
species\_dist <- vegdist(species\_cluster\_data, method = "bray")  
  
# cluster communities using average-linkage algorithm  
species\_cluster <- hclust(species\_dist, method = "average")  
  
# plot cluster diagram  
plot(species\_cluster, ylab = "Bray-Curtis dissimilarity")



# adjusted cluster diagram   
  
species\_dend <- as.dendrogram(hclust(species\_dist, method = "average"))  
  
plot(species\_dend, ylab = "Bray-Curtis dissimilarity",  
 main = "Cluster Dendrogram", horiz = TRUE)



cutree(species\_dend, k=9)

Sea anemone Sablefish Arrowtooth flounder   
 1 2 3   
 Bering skate Big skate Pacific herring   
 4 5 3   
 Walleye pollock Pacific cod Rex sole   
 3 6 3   
 Flathead sole Spotted ratfish Shortfin eelpout   
 7 3 7   
 Blackbelly eelpout Slender soles North pacific hake   
 7 3 3   
 Pacific dover sole Sidestripe shrimp Northern shrimp   
 3 3 8   
 Pink shrimp Spot prawn English sole   
 7 8 3   
 Scallop Longnose skate Pacific spiny dogfish   
 9 3 3   
 Eulachon   
 3

#====================================  
# indicator species analysis   
#====================================  
  
#trip\_km = kmeans(trip\_cluster\_data, centers=5)  
#groupskm = trip\_km$cluster  
#groupskm  
  
  
###### using area as groupings   
  
# filter event id and species CPUE  
  
species\_cluster\_matrix <- catch\_wide\_log[,-c(1,3:15)]  
  
cluster\_groups <- catch\_wide\_log[,c(2,9)]  
  
# use event ID as row names   
  
species\_cluster\_matrix <- as.data.frame(species\_cluster\_matrix,   
 row.names = species\_cluster\_matrix$EVENT\_ID)  
species\_cluster\_matrix <- as.data.frame(species\_cluster\_matrix,   
 row.names = species\_cluster\_matrix$EVENT\_ID)  
  
species\_cluster\_matrix <- species\_cluster\_matrix[,-1]  
  
  
indval\_area <- multipatt(species\_cluster\_matrix, cluster\_groups$AreaGrouping,   
 control = how(nperm=999))  
  
summary(indval\_area, indvalcomp=TRUE)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 25  
 Selected number of species: 18   
 Number of species associated to 1 group: 3   
 Number of species associated to 2 groups: 6   
 Number of species associated to 3 groups: 9   
  
 List of species associated to each combination:   
  
 Group A2 #sps. 1   
 A B stat p.value   
Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
  
 Group A4 #sps. 2   
 A B stat p.value   
Pink shrimp 0.8734 0.7407 0.804 0.001 \*\*\*  
Shortfin eelpout 0.9972 0.4568 0.675 0.001 \*\*\*  
  
 Group A1+A2 #sps. 2   
 A B stat p.value   
Bering skate 0.8888 0.2678 0.488 0.001 \*\*\*  
Pacific cod 0.8612 0.2295 0.445 0.001 \*\*\*  
  
 Group A1+A4 #sps. 2   
 A B stat p.value   
Arrowtooth flounder 0.7972 0.7093 0.752 0.001 \*\*\*  
Sablefish 0.7873 0.2868 0.475 0.001 \*\*\*  
  
 Group A3+A4 #sps. 2   
 A B stat p.value   
Slender soles 0.9261 0.8268 0.875 0.001 \*\*\*  
Blackbelly eelpout 0.9659 0.6364 0.784 0.001 \*\*\*  
  
 Group A1+A2+A3 #sps. 5   
 A B stat p.value   
North pacific hake 0.9681 0.6786 0.811 0.001 \*\*\*  
Pacific spiny dogfish 0.8506 0.7460 0.797 0.001 \*\*\*  
Longnose skate 0.8590 0.6587 0.752 0.001 \*\*\*  
English sole 0.8978 0.6111 0.741 0.001 \*\*\*  
Big skate 0.9737 0.3690 0.599 0.001 \*\*\*  
  
 Group A2+A3+A4 #sps. 4   
 A B stat p.value   
Sidestripe shrimp 0.9400 0.9245 0.932 0.001 \*\*\*  
Northern shrimp 0.9755 0.5252 0.716 0.001 \*\*\*  
Spot prawn 0.9272 0.5503 0.714 0.001 \*\*\*  
Sea anemone 0.9350 0.1792 0.409 0.010 \*\*   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# Component ‘A’ is the probability that the surveyed  
# site belongs to the target site group given the fact that the species has  
# been found. This conditional probability is called the specificity or positive  
# predictive value of the species as indicator of the site group. (2) Component  
#‘B’ is the probability of finding the species in sites belonging to the site group.  
# This second conditional probability is called the fidelity or sensitivity of the  
# species as indicator of the target site group.  
#http://www2.uaem.mx/r-mirror/web/packages/indicspecies/vignettes/indicspeciesTutorial.pdf  
  
  
summary(indval\_area, alpha=1)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 1  
  
 Total number of species: 25  
 Selected number of species: 18   
 Number of species associated to 1 group: 3   
 Number of species associated to 2 groups: 6   
 Number of species associated to 3 groups: 9   
  
 List of species associated to each combination:   
  
 Group A2 #sps. 1   
 stat p.value   
Scallop 0.472 0.001 \*\*\*  
  
 Group A4 #sps. 2   
 stat p.value   
Pink shrimp 0.804 0.001 \*\*\*  
Shortfin eelpout 0.675 0.001 \*\*\*  
  
 Group A1+A2 #sps. 2   
 stat p.value   
Bering skate 0.488 0.001 \*\*\*  
Pacific cod 0.445 0.001 \*\*\*  
  
 Group A1+A4 #sps. 2   
 stat p.value   
Arrowtooth flounder 0.752 0.001 \*\*\*  
Sablefish 0.475 0.001 \*\*\*  
  
 Group A3+A4 #sps. 2   
 stat p.value   
Slender soles 0.875 0.001 \*\*\*  
Blackbelly eelpout 0.784 0.001 \*\*\*  
  
 Group A1+A2+A3 #sps. 5   
 stat p.value   
North pacific hake 0.811 0.001 \*\*\*  
Pacific spiny dogfish 0.797 0.001 \*\*\*  
Longnose skate 0.752 0.001 \*\*\*  
English sole 0.741 0.001 \*\*\*  
Big skate 0.599 0.001 \*\*\*  
  
 Group A2+A3+A4 #sps. 4   
 stat p.value   
Sidestripe shrimp 0.932 0.001 \*\*\*  
Northern shrimp 0.716 0.001 \*\*\*  
Spot prawn 0.714 0.001 \*\*\*  
Sea anemone 0.409 0.010 \*\*   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# By setting alpha = 1 we say  
# we want to display the group to which each species is associated, regardless  
# of whether the association significant or not.  
# still gives 18 species so those species that occur in sites belonging to all groups  
# cannot be statistically tested, because there is no external group for comparison  
# 25-18=7 species associated with all sites  
  
indval\_area$sign

s.A1 s.A2 s.A3 s.A4 index stat p.value  
Sea anemone 0 1 1 1 14 0.4093908 0.010  
Sablefish 1 0 0 1 7 0.4751927 0.001  
Arrowtooth flounder 1 0 0 1 7 0.7519553 0.001  
Bering skate 1 1 0 0 5 0.4878480 0.001  
Big skate 1 1 1 0 11 0.5994511 0.001  
Pacific herring 1 1 1 1 15 0.7613870 NA  
Walleye pollock 1 1 1 1 15 0.9273098 NA  
Pacific cod 1 1 0 0 5 0.4445901 0.001  
Rex sole 1 1 1 1 15 0.8340577 NA  
Flathead sole 1 1 1 1 15 0.6370221 NA  
Spotted ratfish 1 1 1 1 15 0.9927272 NA  
Shortfin eelpout 0 0 0 1 4 0.6749077 0.001  
Blackbelly eelpout 0 0 1 1 10 0.7840107 0.001  
Slender soles 0 0 1 1 10 0.8750520 0.001  
North pacific hake 1 1 1 0 11 0.8105181 0.001  
Pacific dover sole 1 1 1 1 15 0.6464321 NA  
Sidestripe shrimp 0 1 1 1 14 0.9322257 0.001  
Northern shrimp 0 1 1 1 14 0.7157404 0.001  
Pink shrimp 0 0 0 1 4 0.8043489 0.001  
Spot prawn 0 1 1 1 14 0.7143147 0.001  
English sole 1 1 1 0 11 0.7406952 0.001  
Scallop 0 1 0 0 2 0.4716815 0.001  
Longnose skate 1 1 1 0 11 0.7522276 0.001  
Pacific spiny dogfish 1 1 1 0 11 0.7966024 0.001  
Eulachon 1 1 1 1 15 0.9022248 NA

# species with the highest IndVal corresponded to the set of all sites   
# as indicated by the NAs in the p.value column :   
# Pacific herring   
# Walleye pollock  
# Rex sole   
# Flathead sole   
# Spotted ratfish  
# Pacific dover sole  
# Eulachon   
  
### Indicator species analysis without site groups combinations  
  
indval\_single\_area <- multipatt(species\_cluster\_matrix, cluster\_groups$AreaGrouping,   
 duleg= TRUE, control = how(nperm=999))  
  
summary(indval\_single\_area)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 25  
 Selected number of species: 24   
 Number of species associated to 1 group: 24   
 Number of species associated to 2 groups: 0   
 Number of species associated to 3 groups: 0   
  
 List of species associated to each combination:   
  
 Group A1 #sps. 4   
 stat p.value   
Walleye pollock 0.568 0.001 \*\*\*  
Pacific dover sole 0.565 0.001 \*\*\*  
Pacific cod 0.417 0.001 \*\*\*  
Bering skate 0.374 0.001 \*\*\*  
  
 Group A2 #sps. 4   
 stat p.value   
English sole 0.617 0.001 \*\*\*  
Pacific herring 0.550 0.001 \*\*\*  
Scallop 0.472 0.001 \*\*\*  
Big skate 0.423 0.001 \*\*\*  
  
 Group A3 #sps. 7   
 stat p.value   
North pacific hake 0.709 0.001 \*\*\*  
Slender soles 0.700 0.001 \*\*\*  
Longnose skate 0.520 0.001 \*\*\*  
Pacific spiny dogfish 0.484 0.005 \*\*   
Northern shrimp 0.444 0.007 \*\*   
Spot prawn 0.440 0.038 \*   
Sea anemone 0.387 0.003 \*\*   
  
 Group A4 #sps. 9   
 stat p.value   
Pink shrimp 0.804 0.001 \*\*\*  
Blackbelly eelpout 0.767 0.001 \*\*\*  
Shortfin eelpout 0.675 0.001 \*\*\*  
Arrowtooth flounder 0.653 0.001 \*\*\*  
Sidestripe shrimp 0.629 0.001 \*\*\*  
Flathead sole 0.618 0.001 \*\*\*  
Eulachon 0.610 0.001 \*\*\*  
Rex sole 0.571 0.001 \*\*\*  
Sablefish 0.434 0.001 \*\*\*  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

summary(indval\_single\_area,indvalcomp=TRUE)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 25  
 Selected number of species: 24   
 Number of species associated to 1 group: 24   
 Number of species associated to 2 groups: 0   
 Number of species associated to 3 groups: 0   
  
 List of species associated to each combination:   
  
 Group A1 #sps. 4   
 A B stat p.value   
Walleye pollock 0.3291 0.9792 0.568 0.001 \*\*\*  
Pacific dover sole 0.4639 0.6875 0.565 0.001 \*\*\*  
Pacific cod 0.5975 0.2917 0.417 0.001 \*\*\*  
Bering skate 0.4977 0.2812 0.374 0.001 \*\*\*  
  
 Group A2 #sps. 4   
 A B stat p.value   
English sole 0.4670 0.8161 0.617 0.001 \*\*\*  
Pacific herring 0.3813 0.7931 0.550 0.001 \*\*\*  
Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
Big skate 0.4093 0.4368 0.423 0.001 \*\*\*  
  
 Group A3 #sps. 7   
 A B stat p.value   
North pacific hake 0.5171 0.9710 0.709 0.001 \*\*\*  
Slender soles 0.5209 0.9420 0.700 0.001 \*\*\*  
Longnose skate 0.3330 0.8116 0.520 0.001 \*\*\*  
Pacific spiny dogfish 0.2994 0.7826 0.484 0.005 \*\*   
Northern shrimp 0.3163 0.6232 0.444 0.007 \*\*   
Spot prawn 0.3036 0.6377 0.440 0.038 \*   
Sea anemone 0.4500 0.3333 0.387 0.003 \*\*   
  
 Group A4 #sps. 9   
 A B stat p.value   
Pink shrimp 0.8734 0.7407 0.804 0.001 \*\*\*  
Blackbelly eelpout 0.7879 0.7469 0.767 0.001 \*\*\*  
Shortfin eelpout 0.9972 0.4568 0.675 0.001 \*\*\*  
Arrowtooth flounder 0.5265 0.8086 0.653 0.001 \*\*\*  
Sidestripe shrimp 0.4299 0.9198 0.629 0.001 \*\*\*  
Flathead sole 0.5720 0.6667 0.618 0.001 \*\*\*  
Eulachon 0.4101 0.9074 0.610 0.001 \*\*\*  
Rex sole 0.3693 0.8827 0.571 0.001 \*\*\*  
Sablefish 0.5454 0.3457 0.434 0.001 \*\*\*  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

indval\_single\_area$sign

s.A1 s.A2 s.A3 s.A4 index stat p.value  
Sea anemone 0 0 1 0 3 0.3873051 0.003  
Sablefish 0 0 0 1 4 0.4342213 0.001  
Arrowtooth flounder 0 0 0 1 4 0.6525146 0.001  
Bering skate 1 0 0 0 1 0.3741486 0.001  
Big skate 0 1 0 0 2 0.4228359 0.001  
Pacific herring 0 1 0 0 2 0.5499003 0.001  
Walleye pollock 1 0 0 0 1 0.5677022 0.001  
Pacific cod 1 0 0 0 1 0.4174742 0.001  
Rex sole 0 0 0 1 4 0.5709605 0.001  
Flathead sole 0 0 0 1 4 0.6175228 0.001  
Spotted ratfish 1 0 0 0 1 0.5003824 0.834  
Shortfin eelpout 0 0 0 1 4 0.6749077 0.001  
Blackbelly eelpout 0 0 0 1 4 0.7671192 0.001  
Slender soles 0 0 1 0 3 0.7004759 0.001  
North pacific hake 0 0 1 0 3 0.7086309 0.001  
Pacific dover sole 1 0 0 0 1 0.5647538 0.001  
Sidestripe shrimp 0 0 0 1 4 0.6287904 0.001  
Northern shrimp 0 0 1 0 3 0.4439477 0.007  
Pink shrimp 0 0 0 1 4 0.8043489 0.001  
Spot prawn 0 0 1 0 3 0.4399982 0.038  
English sole 0 1 0 0 2 0.6173458 0.001  
Scallop 0 1 0 0 2 0.4716815 0.001  
Longnose skate 0 0 1 0 3 0.5199024 0.001  
Pacific spiny dogfish 0 0 1 0 3 0.4840695 0.005  
Eulachon 0 0 0 1 4 0.6099948 0.001

# only Spotted ratfish did not associate to a group  
  
### Restricting the order of site groups combinations  
  
# max 2 site combinations   
  
indval\_2\_area <- multipatt(species\_cluster\_matrix, cluster\_groups$AreaGrouping,   
 max.order = 2, control = how(nperm=999))  
  
summary(indval\_2\_area,indvalcomp=TRUE)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 25  
 Selected number of species: 24   
 Number of species associated to 1 group: 4   
 Number of species associated to 2 groups: 20   
 Number of species associated to 3 groups: 0   
  
 List of species associated to each combination:   
  
 Group A2 #sps. 1   
 A B stat p.value   
Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
  
 Group A4 #sps. 3   
 A B stat p.value   
Pink shrimp 0.8734 0.7407 0.804 0.001 \*\*\*  
Shortfin eelpout 0.9972 0.4568 0.675 0.001 \*\*\*  
Flathead sole 0.5720 0.6667 0.618 0.001 \*\*\*  
  
 Group A1+A2 #sps. 6   
 A B stat p.value   
Walleye pollock 0.6080 0.9508 0.760 0.001 \*\*\*  
Pacific herring 0.6806 0.7650 0.722 0.001 \*\*\*  
Pacific dover sole 0.6409 0.5410 0.589 0.001 \*\*\*  
Big skate 0.7621 0.4044 0.555 0.001 \*\*\*  
Bering skate 0.8888 0.2678 0.488 0.001 \*\*\*  
Pacific cod 0.8612 0.2295 0.445 0.001 \*\*\*  
  
 Group A1+A3 #sps. 2   
 A B stat p.value   
Pacific spiny dogfish 0.5901 0.7818 0.679 0.001 \*\*\*  
Longnose skate 0.6293 0.7212 0.674 0.001 \*\*\*  
  
 Group A1+A4 #sps. 4   
 A B stat p.value   
Eulachon 0.7072 0.9109 0.803 0.001 \*\*\*  
Arrowtooth flounder 0.7972 0.7093 0.752 0.001 \*\*\*  
Rex sole 0.6643 0.8023 0.730 0.001 \*\*\*  
Sablefish 0.7873 0.2868 0.475 0.001 \*\*\*  
  
 Group A2+A3 #sps. 3   
 A B stat p.value   
North pacific hake 0.8086 0.8077 0.808 0.001 \*\*\*  
English sole 0.6919 0.6923 0.692 0.001 \*\*\*  
Northern shrimp 0.5915 0.6474 0.619 0.001 \*\*\*  
  
 Group A3+A4 #sps. 5   
 A B stat p.value   
Slender soles 0.9261 0.8268 0.875 0.001 \*\*\*  
Sidestripe shrimp 0.7665 0.9437 0.851 0.001 \*\*\*  
Blackbelly eelpout 0.9659 0.6364 0.784 0.001 \*\*\*  
Spot prawn 0.6069 0.5758 0.591 0.011 \*   
Sea anemone 0.7878 0.1991 0.396 0.004 \*\*   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# max 3 site combinations   
  
indval\_3\_area <- multipatt(species\_cluster\_matrix, cluster\_groups$AreaGrouping,   
 max.order = 3, control = how(nperm=999))  
  
summary(indval\_3\_area,indvalcomp=TRUE)

Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 25  
 Selected number of species: 24   
 Number of species associated to 1 group: 3   
 Number of species associated to 2 groups: 6   
 Number of species associated to 3 groups: 15   
  
 List of species associated to each combination:   
  
 Group A2 #sps. 1   
 A B stat p.value   
Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
  
 Group A4 #sps. 2   
 A B stat p.value   
Pink shrimp 0.8734 0.7407 0.804 0.001 \*\*\*  
Shortfin eelpout 0.9972 0.4568 0.675 0.001 \*\*\*  
  
 Group A1+A2 #sps. 2   
 A B stat p.value   
Bering skate 0.8888 0.2678 0.488 0.001 \*\*\*  
Pacific cod 0.8612 0.2295 0.445 0.001 \*\*\*  
  
 Group A1+A4 #sps. 2   
 A B stat p.value   
Arrowtooth flounder 0.7972 0.7093 0.752 0.001 \*\*\*  
Sablefish 0.7873 0.2868 0.475 0.002 \*\*   
  
 Group A3+A4 #sps. 2   
 A B stat p.value   
Slender soles 0.9261 0.8268 0.875 0.001 \*\*\*  
Blackbelly eelpout 0.9659 0.6364 0.784 0.001 \*\*\*  
  
 Group A1+A2+A3 #sps. 6   
 A B stat p.value   
North pacific hake 0.9681 0.6786 0.811 0.001 \*\*\*  
Pacific spiny dogfish 0.8506 0.7460 0.797 0.001 \*\*\*  
Longnose skate 0.8590 0.6587 0.752 0.001 \*\*\*  
English sole 0.8978 0.6111 0.741 0.001 \*\*\*  
Pacific dover sole 0.8114 0.4841 0.627 0.002 \*\*   
Big skate 0.9737 0.3690 0.599 0.001 \*\*\*  
  
 Group A1+A2+A4 #sps. 3   
 A B stat p.value   
Walleye pollock 0.8467 0.8812 0.864 0.001 \*\*\*  
Eulachon 0.8541 0.8522 0.853 0.001 \*\*\*  
Pacific herring 0.8915 0.6087 0.737 0.001 \*\*\*  
  
 Group A1+A3+A4 #sps. 1   
 A B stat p.value   
Rex sole 0.8518 0.7462 0.797 0.001 \*\*\*  
  
 Group A2+A3+A4 #sps. 5   
 A B stat p.value   
Sidestripe shrimp 0.9400 0.9245 0.932 0.001 \*\*\*  
Northern shrimp 0.9755 0.5252 0.716 0.001 \*\*\*  
Spot prawn 0.9272 0.5503 0.714 0.001 \*\*\*  
Flathead sole 0.8606 0.4560 0.626 0.001 \*\*\*  
Sea anemone 0.9350 0.1792 0.409 0.009 \*\*   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# combining species   
  
species\_comb = combinespecies(species\_cluster\_matrix, max.order = 2)$XC  
 dim(species\_comb)

[1] 414 325

indvalspcomb = multipatt(species\_comb, cluster\_groups$AreaGrouping, duleg = TRUE,  
 control = how(nperm=999))  
summary(indvalspcomb, indvalcomp = TRUE)

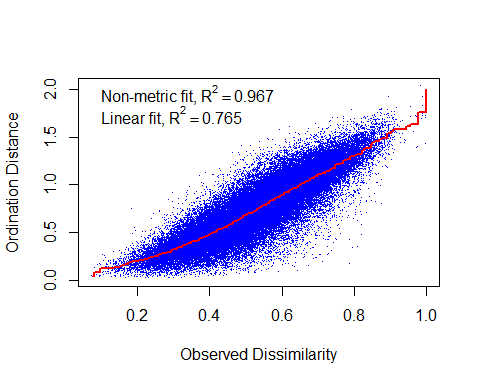
Multilevel pattern analysis  
 ---------------------------  
  
 Association function: IndVal.g  
 Significance level (alpha): 0.05  
  
 Total number of species: 325  
 Selected number of species: 289   
 Number of species associated to 1 group: 289   
 Number of species associated to 2 groups: 0   
 Number of species associated to 3 groups: 0   
  
 List of species associated to each combination:   
  
 Group A1 #sps. 63   
 A B stat p.value   
Walleye pollock+Pacific dover sole 0.54181 0.67708 0.606 0.001 \*\*\*  
Pacific dover sole+Eulachon 0.54502 0.63542 0.588 0.001 \*\*\*  
Walleye pollock 0.32914 0.97917 0.568 0.001 \*\*\*  
Spotted ratfish+Pacific dover sole 0.46400 0.68750 0.565 0.001 \*\*\*  
Pacific dover sole 0.46392 0.68750 0.565 0.001 \*\*\*  
Walleye pollock+Spotted ratfish 0.32738 0.96875 0.563 0.001 \*\*\*  
Walleye pollock+Eulachon 0.34671 0.89583 0.557 0.001 \*\*\*  
Walleye pollock+Pacific spiny dogfish 0.37784 0.77083 0.540 0.001 \*\*\*  
Pacific herring+Pacific dover sole 0.55601 0.51042 0.533 0.001 \*\*\*  
Pacific dover sole+Pacific spiny dogfish 0.50662 0.55208 0.529 0.001 \*\*\*  
Pacific spiny dogfish+Eulachon 0.37957 0.72917 0.526 0.001 \*\*\*  
Rex sole+Pacific dover sole 0.51249 0.51042 0.511 0.001 \*\*\*  
Pacific herring+Eulachon 0.36369 0.68750 0.500 0.001 \*\*\*  
Arrowtooth flounder+Pacific dover sole 0.54247 0.44792 0.493 0.001 \*\*\*  
Pacific herring+Pacific spiny dogfish 0.40007 0.60417 0.492 0.001 \*\*\*  
Walleye pollock+Longnose skate 0.36374 0.64583 0.485 0.002 \*\*   
Walleye pollock+Rex sole 0.34976 0.65625 0.479 0.007 \*\*   
Longnose skate+Eulachon 0.38236 0.59375 0.476 0.001 \*\*\*  
Pacific dover sole+Longnose skate 0.49365 0.44792 0.470 0.001 \*\*\*  
Pacific cod+Eulachon 0.74991 0.27083 0.451 0.001 \*\*\*  
Pacific cod+Pacific spiny dogfish 0.70760 0.28125 0.446 0.001 \*\*\*  
Pacific herring+Longnose skate 0.39331 0.50000 0.443 0.001 \*\*\*  
Pacific herring+Rex sole 0.36498 0.53125 0.440 0.001 \*\*\*  
Rex sole+Pacific spiny dogfish 0.36882 0.52083 0.438 0.001 \*\*\*  
Big skate+Pacific dover sole 0.62259 0.28125 0.418 0.001 \*\*\*  
Pacific cod+Spotted ratfish 0.59871 0.29167 0.418 0.001 \*\*\*  
Pacific cod 0.59755 0.29167 0.417 0.001 \*\*\*  
Walleye pollock+Pacific cod 0.61527 0.27083 0.408 0.001 \*\*\*  
Big skate+Rex sole 0.49924 0.33333 0.408 0.001 \*\*\*  
Big skate+Eulachon 0.45206 0.35417 0.400 0.001 \*\*\*  
Arrowtooth flounder+Longnose skate 0.40404 0.39583 0.400 0.001 \*\*\*  
Pacific cod+Longnose skate 0.72438 0.21875 0.398 0.001 \*\*\*  
Pacific dover sole+English sole 0.40697 0.38542 0.396 0.005 \*\*   
Arrowtooth flounder+Pacific spiny dogfish 0.36274 0.42708 0.394 0.009 \*\*   
Bering skate+Eulachon 0.61612 0.25000 0.392 0.001 \*\*\*  
Rex sole+Longnose skate 0.35183 0.43750 0.392 0.024 \*   
Bering skate+Walleye pollock 0.54337 0.28125 0.391 0.001 \*\*\*  
Rex sole+English sole 0.34216 0.43750 0.387 0.021 \*   
Pacific cod+Pacific dover sole 0.71574 0.20833 0.386 0.001 \*\*\*  
Bering skate+Pacific spiny dogfish 0.56538 0.26042 0.384 0.002 \*\*   
Arrowtooth flounder+English sole 0.43984 0.33333 0.383 0.002 \*\*   
North pacific hake+Pacific dover sole 0.37028 0.38542 0.378 0.003 \*\*   
Arrowtooth flounder+North pacific hake 0.43707 0.32292 0.376 0.001 \*\*\*  
Bering skate 0.49773 0.28125 0.374 0.001 \*\*\*  
Bering skate+Spotted ratfish 0.49773 0.28125 0.374 0.001 \*\*\*  
Pacific herring+Pacific cod 0.62925 0.21875 0.371 0.001 \*\*\*  
Bering skate+Pacific dover sole 0.68601 0.19792 0.368 0.002 \*\*   
Arrowtooth flounder+Big skate 0.56879 0.21875 0.353 0.001 \*\*\*  
Bering skate+Longnose skate 0.50185 0.21875 0.331 0.002 \*\*   
Pacific cod+Rex sole 0.64310 0.16667 0.327 0.001 \*\*\*  
Arrowtooth flounder+Bering skate 0.52095 0.16667 0.295 0.009 \*\*   
Pacific cod+Sidestripe shrimp 0.45249 0.18750 0.291 0.010 \*\*   
Arrowtooth flounder+Pacific cod 0.66934 0.12500 0.289 0.004 \*\*   
Sablefish+Pacific dover sole 0.46748 0.17708 0.288 0.011 \*   
Bering skate+Rex sole 0.52761 0.15625 0.287 0.012 \*   
Sablefish+North pacific hake 0.44383 0.16667 0.272 0.017 \*   
Pacific cod+North pacific hake 0.49393 0.14583 0.268 0.010 \*\*   
Sablefish+Longnose skate 0.41419 0.16667 0.263 0.038 \*   
Sablefish+English sole 0.45485 0.14583 0.258 0.029 \*   
Sablefish+Bering skate 0.72575 0.08333 0.246 0.003 \*\*   
Pacific cod+Flathead sole 0.65345 0.08333 0.233 0.012 \*   
Big skate+Pacific cod 0.54647 0.09375 0.226 0.017 \*   
Bering skate+Pacific cod 0.58344 0.07292 0.206 0.030 \*   
  
 Group A2 #sps. 59   
 A B stat p.value   
English sole 0.4670 0.8161 0.617 0.001 \*\*\*  
Spotted ratfish+English sole 0.4569 0.7931 0.602 0.001 \*\*\*  
Pacific herring+English sole 0.5437 0.6552 0.597 0.001 \*\*\*  
Walleye pollock+English sole 0.4611 0.7471 0.587 0.001 \*\*\*  
Sidestripe shrimp+English sole 0.4162 0.7471 0.558 0.001 \*\*\*  
Pacific herring+Walleye pollock 0.4017 0.7701 0.556 0.001 \*\*\*  
Pacific herring 0.3813 0.7931 0.550 0.001 \*\*\*  
Pacific herring+Northern shrimp 0.5116 0.5747 0.542 0.001 \*\*\*  
Pacific herring+Spotted ratfish 0.3769 0.7701 0.539 0.001 \*\*\*  
North pacific hake+English sole 0.4811 0.5977 0.536 0.001 \*\*\*  
English sole+Pacific spiny dogfish 0.4711 0.5977 0.531 0.001 \*\*\*  
Pacific herring+Sidestripe shrimp 0.3662 0.7126 0.511 0.001 \*\*\*  
Pacific herring+Scallop 0.7930 0.2989 0.487 0.001 \*\*\*  
Pacific herring+North pacific hake 0.4658 0.5057 0.485 0.001 \*\*\*  
Northern shrimp+Scallop 0.8639 0.2644 0.478 0.001 \*\*\*  
Walleye pollock+Scallop 0.7005 0.3218 0.475 0.001 \*\*\*  
Northern shrimp+English sole 0.4172 0.5402 0.475 0.001 \*\*\*  
Spotted ratfish+Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
Scallop 0.6675 0.3333 0.472 0.001 \*\*\*  
Walleye pollock+Northern shrimp 0.3347 0.6552 0.468 0.001 \*\*\*  
Pacific herring+Spot prawn 0.4972 0.4368 0.466 0.001 \*\*\*  
Big skate+English sole 0.5298 0.4023 0.462 0.001 \*\*\*  
Big skate+Northern shrimp 0.5394 0.3448 0.431 0.001 \*\*\*  
English sole+Longnose skate 0.4015 0.4598 0.430 0.001 \*\*\*  
Big skate+North pacific hake 0.5007 0.3678 0.429 0.001 \*\*\*  
Sidestripe shrimp+Scallop 0.7262 0.2529 0.429 0.001 \*\*\*  
Big skate+Pacific herring 0.4973 0.3678 0.428 0.001 \*\*\*  
Walleye pollock+Spot prawn 0.3872 0.4713 0.427 0.021 \*   
Spot prawn+English sole 0.5096 0.3563 0.426 0.002 \*\*   
Spot prawn+Scallop 0.7863 0.2299 0.425 0.001 \*\*\*  
Big skate+Spotted ratfish 0.4120 0.4368 0.424 0.001 \*\*\*  
Big skate 0.4093 0.4368 0.423 0.001 \*\*\*  
Big skate+Spot prawn 0.6704 0.2644 0.421 0.001 \*\*\*  
English sole+Scallop 0.7954 0.2184 0.417 0.001 \*\*\*  
English sole+Eulachon 0.3029 0.5517 0.409 0.011 \*   
Big skate+Sidestripe shrimp 0.4227 0.3908 0.406 0.002 \*\*   
Big skate+Walleye pollock 0.3941 0.4138 0.404 0.001 \*\*\*  
North pacific hake+Scallop 0.9243 0.1724 0.399 0.001 \*\*\*  
Bering skate+Northern shrimp 0.7697 0.1954 0.388 0.001 \*\*\*  
Scallop+Eulachon 0.6535 0.2299 0.388 0.001 \*\*\*  
Big skate+Scallop 1.0000 0.1379 0.371 0.001 \*\*\*  
Bering skate+English sole 0.6888 0.1954 0.367 0.001 \*\*\*  
Big skate+Pacific spiny dogfish 0.4097 0.3218 0.363 0.003 \*\*   
Scallop+Pacific spiny dogfish 0.6208 0.2069 0.358 0.001 \*\*\*  
Scallop+Longnose skate 0.7318 0.1724 0.355 0.001 \*\*\*  
Pacific dover sole+Northern shrimp 0.4656 0.2414 0.335 0.005 \*\*   
Bering skate+Scallop 0.9434 0.1149 0.329 0.001 \*\*\*  
Bering skate+Pacific herring 0.5464 0.1954 0.327 0.001 \*\*\*  
Big skate+Longnose skate 0.3821 0.2759 0.325 0.010 \*\*   
Bering skate+Sidestripe shrimp 0.4523 0.2299 0.322 0.009 \*\*   
Rex sole+Scallop 0.5402 0.1724 0.305 0.006 \*\*   
Pacific dover sole+Scallop 0.5326 0.1724 0.303 0.002 \*\*   
Flathead sole+English sole 0.3787 0.2414 0.302 0.049 \*   
Bering skate+Spot prawn 0.6621 0.1379 0.302 0.006 \*\*   
Bering skate+North pacific hake 0.5220 0.1494 0.279 0.008 \*\*   
Bering skate+Big skate 0.5047 0.1379 0.264 0.008 \*\*   
Flathead sole+Scallop 0.6410 0.1034 0.258 0.008 \*\*   
Pacific cod+English sole 0.4745 0.1379 0.256 0.024 \*   
Pink shrimp+Scallop 0.4970 0.1149 0.239 0.045 \*   
  
 Group A3 #sps. 60   
 A B stat p.value   
Slender soles+North pacific hake 0.8312 0.9130 0.871 0.001 \*\*\*  
North pacific hake+Sidestripe shrimp 0.6565 0.9710 0.798 0.001 \*\*\*  
Slender soles+Longnose skate 0.6614 0.7681 0.713 0.001 \*\*\*  
Spotted ratfish+North pacific hake 0.5176 0.9710 0.709 0.001 \*\*\*  
North pacific hake 0.5171 0.9710 0.709 0.001 \*\*\*  
Slender soles 0.5209 0.9420 0.700 0.001 \*\*\*  
Spotted ratfish+Slender soles 0.5198 0.9420 0.700 0.001 \*\*\*  
Slender soles+Sidestripe shrimp 0.5040 0.9420 0.689 0.001 \*\*\*  
Slender soles+Pacific spiny dogfish 0.6255 0.7391 0.680 0.001 \*\*\*  
North pacific hake+Longnose skate 0.5678 0.7826 0.667 0.001 \*\*\*  
North pacific hake+Northern shrimp 0.6400 0.6232 0.632 0.001 \*\*\*  
Sidestripe shrimp+Longnose skate 0.4823 0.8116 0.626 0.001 \*\*\*  
North pacific hake+Spot prawn 0.6110 0.6377 0.624 0.001 \*\*\*  
North pacific hake+Pacific spiny dogfish 0.5041 0.7681 0.622 0.001 \*\*\*  
Sidestripe shrimp+Pacific spiny dogfish 0.4306 0.7826 0.581 0.001 \*\*\*  
Slender soles+English sole 0.6134 0.5072 0.558 0.001 \*\*\*  
Slender soles+Spot prawn 0.5139 0.5797 0.546 0.001 \*\*\*  
Walleye pollock+Slender soles 0.4260 0.6957 0.544 0.001 \*\*\*  
Slender soles+Northern shrimp 0.4783 0.6087 0.540 0.001 \*\*\*  
Sea anemone+North pacific hake 0.8733 0.3333 0.540 0.001 \*\*\*  
Spotted ratfish+Longnose skate 0.3364 0.8116 0.523 0.001 \*\*\*  
Walleye pollock+North pacific hake 0.3747 0.7246 0.521 0.001 \*\*\*  
Longnose skate 0.3330 0.8116 0.520 0.001 \*\*\*  
Spot prawn+Longnose skate 0.4697 0.5507 0.509 0.001 \*\*\*  
Spotted ratfish+Pacific spiny dogfish 0.3005 0.7826 0.485 0.004 \*\*   
Blackbelly eelpout+North pacific hake 0.6478 0.3623 0.484 0.001 \*\*\*  
Pacific spiny dogfish 0.2994 0.7826 0.484 0.003 \*\*   
Northern shrimp+Longnose skate 0.4592 0.5072 0.483 0.001 \*\*\*  
Sidestripe shrimp+Spot prawn 0.3641 0.6377 0.482 0.002 \*\*   
Rex sole+North pacific hake 0.4441 0.5217 0.481 0.001 \*\*\*  
Sidestripe shrimp+Northern shrimp 0.3654 0.6232 0.477 0.001 \*\*\*  
Longnose skate+Pacific spiny dogfish 0.3511 0.6377 0.473 0.001 \*\*\*  
North pacific hake+Eulachon 0.3599 0.6087 0.468 0.001 \*\*\*  
Big skate+Slender soles 0.7618 0.2754 0.458 0.001 \*\*\*  
Sea anemone+Longnose skate 0.6388 0.3188 0.451 0.001 \*\*\*  
Sea anemone+Slender soles 0.6583 0.3043 0.448 0.001 \*\*\*  
Spotted ratfish+Northern shrimp 0.3211 0.6232 0.447 0.006 \*\*   
Northern shrimp 0.3163 0.6232 0.444 0.008 \*\*   
Spotted ratfish+Spot prawn 0.3082 0.6377 0.443 0.022 \*   
Spot prawn 0.3036 0.6377 0.440 0.034 \*   
Northern shrimp+Pacific spiny dogfish 0.3503 0.5072 0.422 0.002 \*\*   
Spot prawn+Pacific spiny dogfish 0.3500 0.4928 0.415 0.009 \*\*   
Sea anemone+Sidestripe shrimp 0.4737 0.3333 0.397 0.001 \*\*\*  
Northern shrimp+Spot prawn 0.3513 0.4493 0.397 0.007 \*\*   
Sea anemone+English sole 0.6612 0.2319 0.392 0.001 \*\*\*  
Sea anemone+Spotted ratfish 0.4520 0.3333 0.388 0.002 \*\*   
Sea anemone+Pacific spiny dogfish 0.6104 0.2464 0.388 0.001 \*\*\*  
Sea anemone 0.4500 0.3333 0.387 0.002 \*\*   
Sea anemone+Spot prawn 0.5082 0.2609 0.364 0.002 \*\*   
Slender soles+Pacific dover sole 0.4508 0.2899 0.361 0.003 \*\*   
Sea anemone+Northern shrimp 0.5518 0.1884 0.322 0.003 \*\*   
Sea anemone+Walleye pollock 0.3868 0.2609 0.318 0.010 \*\*   
Blackbelly eelpout+English sole 0.4307 0.2319 0.316 0.004 \*\*   
Big skate+Blackbelly eelpout 0.5968 0.1594 0.308 0.001 \*\*\*  
Sea anemone+Rex sole 0.4279 0.2174 0.305 0.014 \*   
Sea anemone+Pacific herring 0.4417 0.1884 0.288 0.009 \*\*   
Sea anemone+Eulachon 0.3548 0.2174 0.278 0.046 \*   
Sea anemone+Big skate 0.7504 0.1014 0.276 0.002 \*\*   
Sea anemone+Pacific dover sole 0.4920 0.1304 0.253 0.022 \*   
Sea anemone+Blackbelly eelpout 0.4037 0.1304 0.229 0.046 \*   
  
 Group A4 #sps. 107   
 A B stat p.value   
Pink shrimp 0.87342 0.74074 0.804 0.001 \*\*\*  
Spotted ratfish+Pink shrimp 0.87115 0.73457 0.800 0.001 \*\*\*  
Sidestripe shrimp+Pink shrimp 0.90880 0.70370 0.800 0.001 \*\*\*  
Pink shrimp+Eulachon 0.90855 0.69753 0.796 0.001 \*\*\*  
Blackbelly eelpout+Pink shrimp 0.98020 0.62963 0.786 0.001 \*\*\*  
Slender soles+Pink shrimp 0.94904 0.64198 0.781 0.001 \*\*\*  
Blackbelly eelpout+Eulachon 0.83612 0.71605 0.774 0.001 \*\*\*  
Arrowtooth flounder+Pink shrimp 0.94184 0.62963 0.770 0.001 \*\*\*  
Blackbelly eelpout 0.78787 0.74691 0.767 0.001 \*\*\*  
Rex sole+Pink shrimp 0.89717 0.64815 0.763 0.001 \*\*\*  
Spotted ratfish+Blackbelly eelpout 0.78440 0.74074 0.762 0.001 \*\*\*  
Arrowtooth flounder+Blackbelly eelpout 0.88091 0.64198 0.752 0.001 \*\*\*  
Blackbelly eelpout+Sidestripe shrimp 0.77018 0.70988 0.739 0.001 \*\*\*  
Flathead sole+Pink shrimp 0.97060 0.54938 0.730 0.001 \*\*\*  
Arrowtooth flounder+Sidestripe shrimp 0.70219 0.75926 0.730 0.001 \*\*\*  
Flathead sole+Blackbelly eelpout 0.88913 0.58025 0.718 0.001 \*\*\*  
Blackbelly eelpout+Slender soles 0.76230 0.66667 0.713 0.001 \*\*\*  
Walleye pollock+Pink shrimp 0.84682 0.59877 0.712 0.001 \*\*\*  
Arrowtooth flounder+Slender soles 0.75474 0.66049 0.706 0.001 \*\*\*  
Rex sole+Blackbelly eelpout 0.76091 0.65432 0.706 0.001 \*\*\*  
Walleye pollock+Blackbelly eelpout 0.79028 0.59259 0.684 0.001 \*\*\*  
Sidestripe shrimp+Eulachon 0.54508 0.85802 0.684 0.001 \*\*\*  
Shortfin eelpout+Blackbelly eelpout 1.00000 0.45679 0.676 0.001 \*\*\*  
Spotted ratfish+Shortfin eelpout 0.99718 0.45679 0.675 0.001 \*\*\*  
Shortfin eelpout 0.99718 0.45679 0.675 0.001 \*\*\*  
Slender soles+Eulachon 0.61951 0.72840 0.672 0.001 \*\*\*  
Shortfin eelpout+Sidestripe shrimp 0.99704 0.45062 0.670 0.001 \*\*\*  
Arrowtooth flounder+Eulachon 0.58721 0.75309 0.665 0.001 \*\*\*  
Shortfin eelpout+Eulachon 1.00000 0.43827 0.662 0.001 \*\*\*  
Arrowtooth flounder 0.52653 0.80864 0.653 0.001 \*\*\*  
Flathead sole+Slender soles 0.72278 0.58642 0.651 0.001 \*\*\*  
Arrowtooth flounder+Flathead sole 0.73035 0.58025 0.651 0.001 \*\*\*  
Shortfin eelpout+Slender soles 0.99675 0.41358 0.642 0.001 \*\*\*  
Arrowtooth flounder+Spotted ratfish 0.51895 0.79012 0.640 0.001 \*\*\*  
Rex sole+Sidestripe shrimp 0.49339 0.81481 0.634 0.001 \*\*\*  
Shortfin eelpout+Pink shrimp 0.99643 0.40123 0.632 0.001 \*\*\*  
Rex sole+Shortfin eelpout 0.99590 0.40123 0.632 0.001 \*\*\*  
Sidestripe shrimp 0.42987 0.91975 0.629 0.001 \*\*\*  
Flathead sole+Sidestripe shrimp 0.63416 0.61728 0.626 0.001 \*\*\*  
Spotted ratfish+Sidestripe shrimp 0.42353 0.91358 0.622 0.001 \*\*\*  
Arrowtooth flounder+Rex sole 0.53051 0.72222 0.619 0.001 \*\*\*  
Flathead sole 0.57200 0.66667 0.618 0.001 \*\*\*  
Rex sole+Slender soles 0.54128 0.70370 0.617 0.001 \*\*\*  
Flathead sole+Eulachon 0.60126 0.62963 0.615 0.001 \*\*\*  
Arrowtooth flounder+Shortfin eelpout 1.00000 0.37654 0.614 0.001 \*\*\*  
Flathead sole+Spotted ratfish 0.56928 0.65432 0.610 0.001 \*\*\*  
Eulachon 0.41006 0.90741 0.610 0.001 \*\*\*  
Spotted ratfish+Eulachon 0.40640 0.90123 0.605 0.001 \*\*\*  
Walleye pollock+Shortfin eelpout 0.99633 0.36420 0.602 0.001 \*\*\*  
Rex sole+Eulachon 0.44787 0.80247 0.599 0.001 \*\*\*  
Rex sole+Flathead sole 0.58638 0.58642 0.586 0.001 \*\*\*  
Flathead sole+Shortfin eelpout 1.00000 0.33333 0.577 0.001 \*\*\*  
Rex sole 0.36931 0.88272 0.571 0.001 \*\*\*  
Pink shrimp+Spot prawn 0.75866 0.42593 0.568 0.001 \*\*\*  
Blackbelly eelpout+Spot prawn 0.74840 0.42593 0.565 0.001 \*\*\*  
Rex sole+Spotted ratfish 0.36794 0.86420 0.564 0.001 \*\*\*  
Walleye pollock+Sidestripe shrimp 0.41205 0.73457 0.550 0.001 \*\*\*  
Shortfin eelpout+Spot prawn 0.99204 0.30247 0.548 0.001 \*\*\*  
Arrowtooth flounder+Walleye pollock 0.45797 0.63580 0.540 0.001 \*\*\*  
Pacific herring+Blackbelly eelpout 0.76972 0.37037 0.534 0.001 \*\*\*  
Blackbelly eelpout+Northern shrimp 0.78588 0.35802 0.530 0.001 \*\*\*  
Walleye pollock+Flathead sole 0.49668 0.55556 0.525 0.001 \*\*\*  
Pacific herring+Pink shrimp 0.75744 0.35802 0.521 0.001 \*\*\*  
Shortfin eelpout+Northern shrimp 0.99352 0.27160 0.519 0.001 \*\*\*  
Arrowtooth flounder+Spot prawn 0.58477 0.45679 0.517 0.001 \*\*\*  
Pink shrimp+Pacific spiny dogfish 0.80880 0.32716 0.514 0.001 \*\*\*  
Flathead sole+Spot prawn 0.67453 0.37654 0.504 0.001 \*\*\*  
Northern shrimp+Pink shrimp 0.76121 0.32099 0.494 0.001 \*\*\*  
Sablefish+Sidestripe shrimp 0.76680 0.30864 0.486 0.001 \*\*\*  
Sablefish+Pink shrimp 0.89919 0.25926 0.483 0.001 \*\*\*  
Spot prawn+Eulachon 0.45640 0.50617 0.481 0.001 \*\*\*  
Sablefish+Blackbelly eelpout 1.00000 0.22840 0.478 0.001 \*\*\*  
Arrowtooth flounder+Northern shrimp 0.65351 0.34568 0.475 0.001 \*\*\*  
Blackbelly eelpout+Pacific spiny dogfish 0.66440 0.33333 0.471 0.001 \*\*\*  
Shortfin eelpout+Pacific spiny dogfish 0.99429 0.21605 0.463 0.001 \*\*\*  
Sablefish+Eulachon 0.66128 0.31481 0.456 0.001 \*\*\*  
Rex sole+Spot prawn 0.41301 0.50000 0.454 0.001 \*\*\*  
Pacific herring+Shortfin eelpout 0.99350 0.20370 0.450 0.001 \*\*\*  
Northern shrimp+Eulachon 0.50116 0.39506 0.445 0.003 \*\*   
Sablefish+Arrowtooth flounder 0.64076 0.29630 0.436 0.001 \*\*\*  
Pacific herring+Slender soles 0.52074 0.36420 0.435 0.001 \*\*\*  
Sablefish 0.54544 0.34568 0.434 0.001 \*\*\*  
Sablefish+Slender soles 0.77306 0.24074 0.431 0.001 \*\*\*  
Sablefish+Rex sole 0.59326 0.30247 0.424 0.001 \*\*\*  
Sablefish+Spotted ratfish 0.53093 0.33333 0.421 0.001 \*\*\*  
Flathead sole+Northern shrimp 0.63742 0.26543 0.411 0.001 \*\*\*  
Pacific dover sole+Pink shrimp 0.84907 0.19753 0.410 0.001 \*\*\*  
Arrowtooth flounder+Pacific herring 0.43351 0.38272 0.407 0.002 \*\*   
Pink shrimp+Longnose skate 0.72931 0.21605 0.397 0.001 \*\*\*  
Pacific herring+Flathead sole 0.45592 0.32716 0.386 0.001 \*\*\*  
Rex sole+Northern shrimp 0.41078 0.35802 0.383 0.031 \*   
Shortfin eelpout+Longnose skate 0.99065 0.14815 0.383 0.001 \*\*\*  
Sablefish+Shortfin eelpout 1.00000 0.14198 0.377 0.001 \*\*\*  
Blackbelly eelpout+Longnose skate 0.58841 0.23457 0.372 0.002 \*\*   
Sablefish+Flathead sole 0.74800 0.17901 0.366 0.001 \*\*\*  
Sablefish+Northern shrimp 0.77481 0.16049 0.353 0.001 \*\*\*  
Flathead sole+Pacific spiny dogfish 0.40971 0.28395 0.341 0.023 \*   
Sablefish+Walleye pollock 0.45338 0.25309 0.339 0.006 \*\*   
Sablefish+Spot prawn 0.55669 0.17901 0.316 0.001 \*\*\*  
Blackbelly eelpout+Pacific dover sole 0.63933 0.15432 0.314 0.001 \*\*\*  
Shortfin eelpout+Pacific dover sole 1.00000 0.07407 0.272 0.002 \*\*   
Sea anemone+Pink shrimp 0.76007 0.08642 0.256 0.028 \*   
Sea anemone+Sablefish 0.74707 0.08025 0.245 0.005 \*\*   
Sea anemone+Shortfin eelpout 1.00000 0.04938 0.222 0.008 \*\*   
Shortfin eelpout+North pacific hake 0.97276 0.04938 0.219 0.014 \*   
Bering skate+Blackbelly eelpout 0.80920 0.05556 0.212 0.041 \*   
Bering skate+Shortfin eelpout 1.00000 0.03086 0.176 0.034 \*   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Figure 6. NMDS plots of species with secondary temperature, depth axes

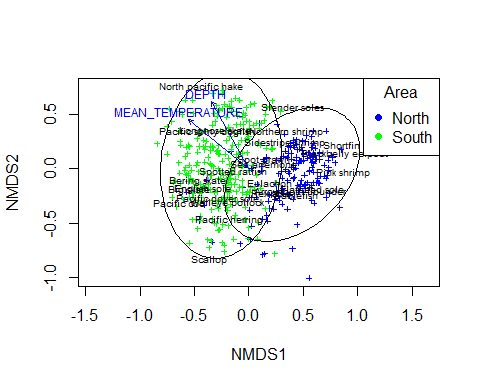
####### ordination ########  
  
# The metaMDS function automatically transforms data and checks solution  
# robustness  
  
event\_mds <- metaMDS(species\_cluster\_matrix, dist = "bray", trymax = 150, k=3,  
 maxit = 300)

Wisconsin double standardization  
Run 0 stress 0.1831461   
Run 1 stress 0.1830192   
... New best solution  
... Procrustes: rmse 0.008089038 max resid 0.06725604   
Run 2 stress 0.1856368   
Run 3 stress 0.1838528   
Run 4 stress 0.183463   
... Procrustes: rmse 0.01132381 max resid 0.06857591   
Run 5 stress 0.1858399   
Run 6 stress 0.1849387   
Run 7 stress 0.1858217   
Run 8 stress 0.1834194   
... Procrustes: rmse 0.007918695 max resid 0.06737851   
Run 9 stress 0.1830799   
... Procrustes: rmse 0.005844129 max resid 0.06614451   
Run 10 stress 0.1835746   
Run 11 stress 0.1831384   
... Procrustes: rmse 0.008212218 max resid 0.06664911   
Run 12 stress 0.1830307   
... Procrustes: rmse 0.001461372 max resid 0.01527989   
Run 13 stress 0.1832192   
... Procrustes: rmse 0.008840473 max resid 0.06790593   
Run 14 stress 0.185173   
Run 15 stress 0.183087   
... Procrustes: rmse 0.005772146 max resid 0.06621977   
Run 16 stress 0.1863546   
Run 17 stress 0.1832311   
... Procrustes: rmse 0.01027115 max resid 0.06799713   
Run 18 stress 0.1855063   
Run 19 stress 0.1857775   
Run 20 stress 0.1849415   
Run 21 stress 0.1830212   
... Procrustes: rmse 0.0003797808 max resid 0.003443174   
... Similar to previous best  
\*\*\* Best solution repeated 1 times

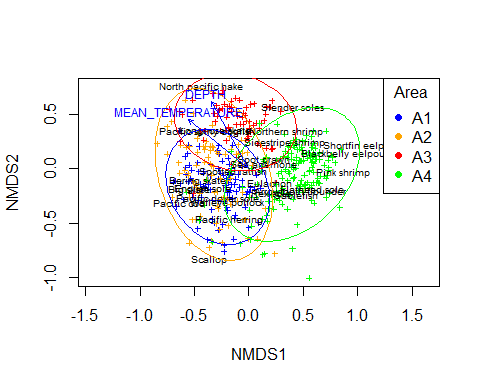
# Assess goodness of ordination fit (stress plot)  
stressplot(event\_mds)



# colour plot north vs south  
  
blank\_mds<- ordiplot(event\_mds, type = "n")  
points(blank\_mds, "sites", col = "blue",   
 select=catch\_wide\_log$MAJOR\_STAT\_AREA\_CODE=="8", pch=3, cex=0.5)  
points(blank\_mds, "sites", col = "green",   
 select=catch\_wide\_log$MAJOR\_STAT\_AREA\_CODE=="1", pch=3, cex=0.5)  
text(blank\_mds, "species", col = "black", cex=0.6)  
  
ordiellipse(blank\_mds, catch\_wide\_log$MAJOR\_STAT\_AREA\_CODE, conf = 0.95, label = FALSE)  
  
legend("topright", legend=c("North", "South"), title= "Area", pch=19,   
 col=c("blue", "green"))  
  
# add temp and depth axes to the plot  
  
plot(envfit(blank\_mds, catch\_wide\_log[, 14:15]), cex = 0.75)



# colour plot by area with ellipse  
  
blank\_mds<- ordiplot(event\_mds, type = "n")  
points(blank\_mds, "sites", col = "blue",   
 select=catch\_wide\_log$AreaGrouping=="A1", pch=3, cex=0.5)  
points(blank\_mds, "sites", col = "orange",   
 select=catch\_wide\_log$AreaGrouping=="A2", pch=3, cex=0.5)  
points(blank\_mds, "sites", col = "red",   
 select=catch\_wide\_log$AreaGrouping=="A3", pch=3, cex=0.5)  
points(blank\_mds, "sites", col = "green",   
 select=catch\_wide\_log$AreaGrouping=="A4", pch=3, cex=0.5)  
text(blank\_mds, "species", col = "black", cex=0.6)  
  
ordiellipse(blank\_mds, catch\_wide\_log$AreaGrouping, conf = 0.95,   
 label = FALSE, col = area\_colours)  
legend("topright", legend=c("A1", "A2", "A3", "A4"), title= "Area", pch=19,   
 col=area\_colours)  
# add temp and depth axes to the plot  
  
plot(envfit(blank\_mds, catch\_wide\_log[, 14:15]), cex = 0.75)



##### filter by area - A1 #####  
  
# set plot window to display all 4 area graphs at the same time  
par(mfrow=c(2,2))  
  
a1\_data <- catch\_wide\_log %>% filter(., AreaGrouping=="A1")  
   
NMDS\_a1 <- a1\_data[,-c(1,3:15)]  
  
# use event ID as row names   
  
NMDS\_a1 <- as.data.frame(NMDS\_a1, row.names = NMDS\_a1$EVENT\_ID)  
NMDS\_a1 <- as.data.frame(NMDS\_a1, row.names = NMDS\_a1$EVENT\_ID)  
  
NMDS\_a1 <- NMDS\_a1[,-1]  
  
# The metaMDS function automatically transforms data and checks solution  
# robustness  
  
mds\_a1 <- metaMDS(NMDS\_a1, dist = "bray", trymax = 150, k=3,  
 maxit = 300)

Wisconsin double standardization  
Run 0 stress 0.1633165   
Run 1 stress 0.1665194   
Run 2 stress 0.1671616   
Run 3 stress 0.1653596   
Run 4 stress 0.167638   
Run 5 stress 0.1633163   
... New best solution  
... Procrustes: rmse 0.0001864116 max resid 0.0009203104   
... Similar to previous best  
Run 6 stress 0.1633163   
... New best solution  
... Procrustes: rmse 0.0004453384 max resid 0.002317095   
... Similar to previous best  
Run 7 stress 0.1753692   
Run 8 stress 0.1657558   
Run 9 stress 0.165364   
Run 10 stress 0.1657741   
Run 11 stress 0.1657749   
Run 12 stress 0.1633161   
... New best solution  
... Procrustes: rmse 0.000189373 max resid 0.001058951   
... Similar to previous best  
Run 13 stress 0.1633162   
... Procrustes: rmse 0.0001200042 max resid 0.0005257066   
... Similar to previous best  
Run 14 stress 0.1633166   
... Procrustes: rmse 0.0006018302 max resid 0.003115366   
... Similar to previous best  
Run 15 stress 0.1633162   
... Procrustes: rmse 0.0004801185 max resid 0.002621434   
... Similar to previous best  
Run 16 stress 0.1672283   
Run 17 stress 0.1657556   
Run 18 stress 0.1653601   
Run 19 stress 0.163316   
... New best solution  
... Procrustes: rmse 0.0001604557 max resid 0.0007524413   
... Similar to previous best  
Run 20 stress 0.1672275   
\*\*\* Best solution repeated 1 times

# Assess goodness of ordination fit (stress plot)  
  
#stressplot(mds\_a1)  
  
# layering the plot   
  
blank\_mds\_a1<- ordiplot(mds\_a1, type = "n")  
points(blank\_mds\_a1, "sites", col = "blue",   
 select=a1\_data$SEASON=="Winter", pch=3, cex=0.5)  
points(blank\_mds\_a1, "sites", col = "orange",   
 select=a1\_data$SEASON=="Spring", pch=3, cex=0.5)  
points(blank\_mds\_a1, "sites", col = "red",   
 select=a1\_data$SEASON=="Summer", pch=3, cex=0.5)  
points(blank\_mds\_a1, "sites", col = "green",   
 select=a1\_data$SEASON=="Fall", pch=3, cex=0.5)  
text(blank\_mds\_a1, "species", col = "black", cex=0.6)  
  
  
ordiellipse(blank\_mds\_a1, a1\_data$SEASON,   
 conf = 0.95, label = FALSE, col = season\_colours)  
  
legend("topright", legend=c("Winter", "Spring", "Summer", "Fall"), title= "Season", pch=19,   
 col=season\_colours)  
title(main = "A1")  
  
# add temp and depth axis  
  
plot(envfit(blank\_mds\_a1, a1\_data[, 14:15]), cex = 0.75, col = "black")  
  
  
##### filter by area - A2 #####  
  
a2\_data <- catch\_wide\_log %>% filter(., AreaGrouping=="A2")  
  
NMDS\_a2 <- a2\_data[,-c(1,3:15)]  
  
# use event ID as row names   
  
NMDS\_a2 <- as.data.frame(NMDS\_a2, row.names = NMDS\_a2$EVENT\_ID)  
NMDS\_a2 <- as.data.frame(NMDS\_a2, row.names = NMDS\_a2$EVENT\_ID)  
  
NMDS\_a2 <- NMDS\_a2[,-1]  
  
# The metaMDS function automatically transforms data and checks solution  
# robustness  
  
mds\_a2 <- metaMDS(NMDS\_a2, dist = "bray", trymax = 150, k=3,  
 maxit = 300)

Wisconsin double standardization  
Run 0 stress 0.1736838   
Run 1 stress 0.173684   
... Procrustes: rmse 0.0003233156 max resid 0.001600407   
... Similar to previous best  
Run 2 stress 0.1736839   
... Procrustes: rmse 0.00009449634 max resid 0.0005076884   
... Similar to previous best  
Run 3 stress 0.1736837   
... New best solution  
... Procrustes: rmse 0.0002869186 max resid 0.001507546   
... Similar to previous best  
Run 4 stress 0.1736835   
... New best solution  
... Procrustes: rmse 0.0001167166 max resid 0.0004148589   
... Similar to previous best  
Run 5 stress 0.1736837   
... Procrustes: rmse 0.0001614124 max resid 0.0008977513   
... Similar to previous best  
Run 6 stress 0.1736836   
... Procrustes: rmse 0.00008407708 max resid 0.0004584594   
... Similar to previous best  
Run 7 stress 0.1736836   
... Procrustes: rmse 0.00006765789 max resid 0.0005312406   
... Similar to previous best  
Run 8 stress 0.1736835   
... New best solution  
... Procrustes: rmse 0.000065713 max resid 0.0003157528   
... Similar to previous best  
Run 9 stress 0.1736835   
... Procrustes: rmse 0.00003907231 max resid 0.0002062113   
... Similar to previous best  
Run 10 stress 0.1736836   
... Procrustes: rmse 0.0001122784 max resid 0.00052132   
... Similar to previous best  
Run 11 stress 0.1736835   
... Procrustes: rmse 0.00004539928 max resid 0.0002206647   
... Similar to previous best  
Run 12 stress 0.1736838   
... Procrustes: rmse 0.0001961034 max resid 0.001209601   
... Similar to previous best  
Run 13 stress 0.1736837   
... Procrustes: rmse 0.0001552311 max resid 0.0008814511   
... Similar to previous best  
Run 14 stress 0.1736835   
... Procrustes: rmse 0.00007699536 max resid 0.0004474224   
... Similar to previous best  
Run 15 stress 0.1736838   
... Procrustes: rmse 0.0001953443 max resid 0.001208352   
... Similar to previous best  
Run 16 stress 0.1736839   
... Procrustes: rmse 0.0002059647 max resid 0.001467329   
... Similar to previous best  
Run 17 stress 0.1736838   
... Procrustes: rmse 0.0002403995 max resid 0.001436682   
... Similar to previous best  
Run 18 stress 0.1736838   
... Procrustes: rmse 0.0002198582 max resid 0.001313814   
... Similar to previous best  
Run 19 stress 0.173684   
... Procrustes: rmse 0.0002762418 max resid 0.0016567   
... Similar to previous best  
Run 20 stress 0.1736839   
... Procrustes: rmse 0.000250446 max resid 0.001497254   
... Similar to previous best  
\*\*\* Best solution repeated 13 times

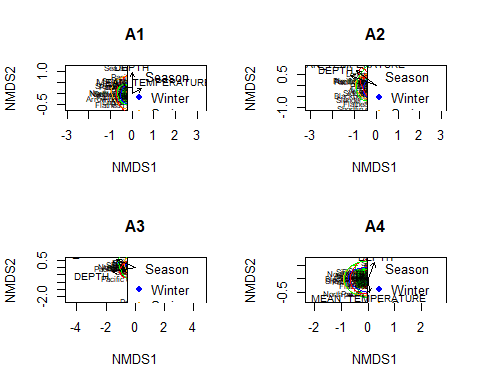
# Assess goodness of ordination fit (stress plot)  
  
#stressplot(mds\_a2)  
  
# layering the plot   
  
blank\_mds\_a2<- ordiplot(mds\_a2, type = "n")  
points(blank\_mds\_a2, "sites", col = "blue",   
 select=a2\_data$SEASON=="Winter", pch=3, cex=0.5)  
points(blank\_mds\_a2, "sites", col = "orange",   
 select=a2\_data$SEASON=="Spring", pch=3, cex=0.5)  
points(blank\_mds\_a2, "sites", col = "red",   
 select=a2\_data$SEASON=="Summer", pch=3, cex=0.5)  
points(blank\_mds\_a2, "sites", col = "green",   
 select=a2\_data$SEASON=="Fall", pch=3, cex=0.5)  
text(blank\_mds\_a2, "species", col = "black", cex=0.6)  
  
  
ordiellipse(blank\_mds\_a2, a2\_data$SEASON,   
 conf = 0.95, label = FALSE, col = season\_colours)  
  
legend("topright", legend=c("Winter", "Spring", "Summer", "Fall"), title= "Season", pch=19,   
 col=season\_colours)  
title(main = "A2")  
  
# add temp and depth axis  
  
plot(envfit(blank\_mds\_a2, a2\_data[, 14:15]), cex = 0.75, col = "black")  
  
  
##### filter by area - A3 #####  
  
a3\_data <- catch\_wide\_log %>% filter(., AreaGrouping=="A3")  
  
NMDS\_a3 <- a3\_data[,-c(1,3:15)]  
  
# use event ID as row names   
  
NMDS\_a3 <- as.data.frame(NMDS\_a3, row.names = NMDS\_a3$EVENT\_ID)  
NMDS\_a3 <- as.data.frame(NMDS\_a3, row.names = NMDS\_a3$EVENT\_ID)  
  
NMDS\_a3 <- NMDS\_a3[,-1]  
  
# The metaMDS function automatically transforms data and checks solution  
# robustness  
  
mds\_a3 <- metaMDS(NMDS\_a3, dist = "bray", trymax = 150, k=3,  
 maxit = 300)

Wisconsin double standardization  
Run 0 stress 0.1503781   
Run 1 stress 0.1517428   
Run 2 stress 0.151104   
Run 3 stress 0.1513039   
Run 4 stress 0.1507342   
... Procrustes: rmse 0.01903306 max resid 0.1073515   
Run 5 stress 0.1511034   
Run 6 stress 0.1503771   
... New best solution  
... Procrustes: rmse 0.0006148659 max resid 0.003090921   
... Similar to previous best  
Run 7 stress 0.151169   
Run 8 stress 0.1505821   
... Procrustes: rmse 0.01040827 max resid 0.0689458   
Run 9 stress 0.1506425   
... Procrustes: rmse 0.01147768 max resid 0.06423213   
Run 10 stress 0.150378   
... Procrustes: rmse 0.0007611143 max resid 0.004989206   
... Similar to previous best  
Run 11 stress 0.1513049   
Run 12 stress 0.1513046   
Run 13 stress 0.1507348   
... Procrustes: rmse 0.01915964 max resid 0.108726   
Run 14 stress 0.1507343   
... Procrustes: rmse 0.01912743 max resid 0.1085273   
Run 15 stress 0.151305   
Run 16 stress 0.1503771   
... Procrustes: rmse 0.00008748775 max resid 0.0004018372   
... Similar to previous best  
Run 17 stress 0.1507334   
... Procrustes: rmse 0.01892302 max resid 0.1071532   
Run 18 stress 0.1507336   
... Procrustes: rmse 0.0189882 max resid 0.10763   
Run 19 stress 0.1513036   
Run 20 stress 0.1511368   
\*\*\* Best solution repeated 3 times

# Assess goodness of ordination fit (stress plot)  
  
#stressplot(mds\_a3)  
  
# layering the plot   
  
blank\_mds\_a3<- ordiplot(mds\_a3, type = "n")  
points(blank\_mds\_a3, "sites", col = "blue",   
 select=a3\_data$SEASON=="Winter", pch=3, cex=0.5)  
points(blank\_mds\_a3, "sites", col = "orange",   
 select=a3\_data$SEASON=="Spring", pch=3, cex=0.5)  
points(blank\_mds\_a3, "sites", col = "red",   
 select=a3\_data$SEASON=="Summer", pch=3, cex=0.5)  
points(blank\_mds\_a3, "sites", col = "green",   
 select=a3\_data$SEASON=="Fall", pch=3, cex=0.5)  
text(blank\_mds\_a3, "species", col = "black", cex=0.6)  
  
  
ordiellipse(blank\_mds\_a3, a3\_data$SEASON,   
 conf = 0.95, label = FALSE, col = season\_colours)  
  
legend("topright", legend=c("Winter", "Spring", "Summer", "Fall"), title= "Season", pch=19,   
 col=season\_colours)  
title(main = "A3")  
  
# add temp and depth axis  
  
plot(envfit(blank\_mds\_a3, a3\_data[, 14:15]), cex = 0.75, col = "black")  
  
##### filter by area - A4 #####  
  
a4\_data <- catch\_wide\_log %>% filter(., AreaGrouping=="A4")  
  
NMDS\_a4 <- a4\_data[,-c(1,3:15)]  
  
# use event ID as row names   
  
NMDS\_a4 <- as.data.frame(NMDS\_a4, row.names = NMDS\_a4$EVENT\_ID)  
NMDS\_a4 <- as.data.frame(NMDS\_a4, row.names = NMDS\_a4$EVENT\_ID)  
  
NMDS\_a4 <- NMDS\_a4[,-1]  
  
# The metaMDS function automatically transforms data and checks solution  
# robustness  
  
mds\_a4 <- metaMDS(NMDS\_a4, dist = "bray", trymax = 150, k=3,  
 maxit = 300)

Wisconsin double standardization  
Run 0 stress 0.1746088   
Run 1 stress 0.1754063   
Run 2 stress 0.1748849   
... Procrustes: rmse 0.01097267 max resid 0.08617487   
Run 3 stress 0.1748858   
... Procrustes: rmse 0.01113809 max resid 0.08587522   
Run 4 stress 0.175103   
... Procrustes: rmse 0.0185311 max resid 0.2191954   
Run 5 stress 0.1754277   
Run 6 stress 0.1748869   
... Procrustes: rmse 0.01127873 max resid 0.08711166   
Run 7 stress 0.1748838   
... Procrustes: rmse 0.01068813 max resid 0.08650337   
Run 8 stress 0.175074   
... Procrustes: rmse 0.01588627 max resid 0.1859844   
Run 9 stress 0.175074   
... Procrustes: rmse 0.01569288 max resid 0.184629   
Run 10 stress 0.1750739   
... Procrustes: rmse 0.01592979 max resid 0.1859529   
Run 11 stress 0.1750749   
... Procrustes: rmse 0.01585656 max resid 0.1861901   
Run 12 stress 0.1748825   
... Procrustes: rmse 0.0102139 max resid 0.08471125   
Run 13 stress 0.1746081   
... New best solution  
... Procrustes: rmse 0.0004828547 max resid 0.002865026   
... Similar to previous best  
Run 14 stress 0.1754086   
Run 15 stress 0.1748945   
... Procrustes: rmse 0.01125895 max resid 0.08773832   
Run 16 stress 0.1750752   
... Procrustes: rmse 0.01578388 max resid 0.1852746   
Run 17 stress 0.1746093   
... Procrustes: rmse 0.0004995824 max resid 0.004749446   
... Similar to previous best  
Run 18 stress 0.1754106   
Run 19 stress 0.1758961   
Run 20 stress 0.174608   
... New best solution  
... Procrustes: rmse 0.0002827496 max resid 0.001826976   
... Similar to previous best  
\*\*\* Best solution repeated 1 times

# Assess goodness of ordination fit (stress plot)  
  
#stressplot(mds\_a4)  
  
# layering the plot   
  
blank\_mds\_a4<- ordiplot(mds\_a4, type = "n")  
points(blank\_mds\_a4, "sites", col = "blue",   
 select=a4\_data$SEASON=="Winter", pch=3, cex=0.5)  
points(blank\_mds\_a4, "sites", col = "orange",   
 select=a4\_data$SEASON=="Spring", pch=3, cex=0.5)  
points(blank\_mds\_a4, "sites", col = "red",   
 select=a4\_data$SEASON=="Summer", pch=3, cex=0.5)  
points(blank\_mds\_a4, "sites", col = "green",   
 select=a4\_data$SEASON=="Fall", pch=3, cex=0.5)  
text(blank\_mds\_a4, "species", col = "black", cex=0.6)  
  
  
ordiellipse(blank\_mds\_a4, a4\_data$SEASON,   
 conf = 0.95, label = FALSE, col = season\_colours)  
  
legend("topright", legend=c("Winter", "Spring", "Summer", "Fall"),   
 title= "Season", pch=19,col=season\_colours)  
title(main = "A4")  
  
# add temp and depth axis  
  
plot(envfit(blank\_mds\_a4, a4\_data[, 14:15]), cex = 0.75, col = "black")



par(mfrow=c(1,1))  
  
#==============================================================  
# Figure 7. Maps of showing cluster locations by month  
#==============================================================  
  
# A1 - no results   
  
B=strassoc(species\_cluster\_matrix, cluster=cluster\_groups$AreaGrouping ,func="B")  
 sel=which(B[,"A1"]>0.2)  
 sel

Arrowtooth flounder Bering skate Big skate   
 3 4 5   
 Pacific herring Walleye pollock Pacific cod   
 6 7 8   
 Rex sole Flathead sole Spotted ratfish   
 9 10 11   
 North pacific hake Pacific dover sole Sidestripe shrimp   
 15 16 17   
 Spot prawn English sole Longnose skate   
 20 21 23   
Pacific spiny dogfish Eulachon   
 24 25

sc= indicators(X=species\_cluster\_matrix[,sel],   
 cluster=cluster\_groups$AreaGrouping, group="A1", verbose=TRUE,  
 At=0.5, Bt=0.2)

Target site group: A1  
Number of candidate species: 17  
Number of sites: 414   
Size of the site group: 96   
Starting species 1 ... accepted combinations: 186   
Starting species 2 ... accepted combinations: 208   
Starting species 3 ... accepted combinations: 275   
Starting species 4 ... accepted combinations: 366   
Starting species 5 ... accepted combinations: 434   
Starting species 6 ... accepted combinations: 450   
Starting species 7 ... accepted combinations: 485   
Starting species 8 ... accepted combinations: 485   
Starting species 9 ... accepted combinations: 498   
Starting species 10 ... accepted combinations: 503   
Starting species 11 ... accepted combinations: 512   
Starting species 12 ... accepted combinations: 512   
Starting species 13 ... accepted combinations: 512   
Starting species 14 ... accepted combinations: 512   
Starting species 15 ... accepted combinations: 512   
Starting species 16 ... accepted combinations: 512   
Starting species 17 ... accepted combinations: 512   
Number of valid combinations: 512  
Number of remaining species: 14   
Calculating statistical significance (permutational test)...

print(sc, sqrtIVt = 0.6)

[1] A B sqrtIV p.value  
<0 rows> (or 0-length row.names)

# A2 - no results   
   
 B=strassoc(species\_cluster\_matrix, cluster=cluster\_groups$AreaGrouping ,func="B")  
 sel=which(B[,"A2"]>0.2)  
 sel

Arrowtooth flounder Bering skate Big skate   
 3 4 5   
 Pacific herring Walleye pollock Rex sole   
 6 7 9   
 Flathead sole Spotted ratfish Slender soles   
 10 11 14   
 North pacific hake Pacific dover sole Sidestripe shrimp   
 15 16 17   
 Northern shrimp Pink shrimp Spot prawn   
 18 19 20   
 English sole Scallop Longnose skate   
 21 22 23   
Pacific spiny dogfish Eulachon   
 24 25

sc= indicators(X=species\_cluster\_matrix[,sel],   
 cluster=cluster\_groups$AreaGrouping, group="A2", verbose=TRUE,  
 At=0.5, Bt=0.2)

Target site group: A2  
Number of candidate species: 20  
Number of sites: 414   
Size of the site group: 87   
Starting species 1 ... accepted combinations: 0   
Starting species 2 ... accepted combinations: 0   
Starting species 3 ... accepted combinations: 234   
Starting species 4 ... accepted combinations: 377   
Starting species 5 ... accepted combinations: 415   
Starting species 6 ... accepted combinations: 415   
Starting species 7 ... accepted combinations: 415   
Starting species 8 ... accepted combinations: 431   
Starting species 9 ... accepted combinations: 431   
Starting species 10 ... accepted combinations: 437   
Starting species 11 ... accepted combinations: 437   
Starting species 12 ... accepted combinations: 439   
Starting species 13 ... accepted combinations: 444   
Starting species 14 ... accepted combinations: 444   
Starting species 15 ... accepted combinations: 446   
Starting species 16 ... accepted combinations: 447   
Starting species 17 ... accepted combinations: 449   
Starting species 18 ... accepted combinations: 449   
Starting species 19 ... accepted combinations: 449   
Starting species 20 ... accepted combinations: 449   
Number of valid combinations: 449  
Number of remaining species: 15   
Calculating statistical significance (permutational test)...

print(sc, sqrtIVt = 0.6)

[1] A B sqrtIV p.value  
<0 rows> (or 0-length row.names)

# A3 - Spotted ratfish, Slender soles, North pacific hake, Sidestripe shrimp  
  
 B=strassoc(species\_cluster\_matrix, cluster=cluster\_groups$AreaGrouping ,func="B")  
 sel=which(B[,"A3"]>0.2)  
 sel

Sea anemone Arrowtooth flounder Big skate   
 1 3 5   
 Pacific herring Walleye pollock Rex sole   
 6 7 9   
 Flathead sole Spotted ratfish Blackbelly eelpout   
 10 11 13   
 Slender soles North pacific hake Pacific dover sole   
 14 15 16   
 Sidestripe shrimp Northern shrimp Spot prawn   
 17 18 20   
 English sole Longnose skate Pacific spiny dogfish   
 21 23 24   
 Eulachon   
 25

sc= indicators(X=species\_cluster\_matrix[,sel],   
 cluster=cluster\_groups$AreaGrouping, group="A3", verbose=TRUE,  
 At=0.5, Bt=0.2)

Target site group: A3  
Number of candidate species: 19  
Number of sites: 414   
Size of the site group: 69   
Starting species 1 ... accepted combinations: 149   
Starting species 2 ... accepted combinations: 149   
Starting species 3 ... accepted combinations: 223   
Starting species 4 ... accepted combinations: 264   
Starting species 5 ... accepted combinations: 356   
Starting species 6 ... accepted combinations: 470   
Starting species 7 ... accepted combinations: 470   
Starting species 8 ... accepted combinations: 579   
Starting species 9 ... accepted combinations: 614   
Starting species 10 ... accepted combinations: 726   
Starting species 11 ... accepted combinations: 779   
Starting species 12 ... accepted combinations: 779   
Starting species 13 ... accepted combinations: 779   
Starting species 14 ... accepted combinations: 779   
Starting species 15 ... accepted combinations: 779   
Starting species 16 ... accepted combinations: 779   
Starting species 17 ... accepted combinations: 779   
Starting species 18 ... accepted combinations: 779   
Starting species 19 ... accepted combinations: 779   
Number of valid combinations: 779  
Number of remaining species: 17   
Calculating statistical significance (permutational test)...

print(sc, sqrtIVt = 0.8)

A  
Slender soles+North pacific hake+Sidestripe shrimp 0.7482152  
Spotted ratfish+Slender soles+North pacific hake+Sidestripe shrimp 0.7481538  
Slender soles+North pacific hake 0.7461459  
Spotted ratfish+Slender soles+North pacific hake 0.7449586  
 B  
Slender soles+North pacific hake+Sidestripe shrimp 0.9130435  
Spotted ratfish+Slender soles+North pacific hake+Sidestripe shrimp 0.9130435  
Slender soles+North pacific hake 0.9130435  
Spotted ratfish+Slender soles+North pacific hake 0.9130435  
 sqrtIV  
Slender soles+North pacific hake+Sidestripe shrimp 0.8265307  
Spotted ratfish+Slender soles+North pacific hake+Sidestripe shrimp 0.8264968  
Slender soles+North pacific hake 0.8253870  
Spotted ratfish+Slender soles+North pacific hake 0.8247300  
 p.value  
Slender soles+North pacific hake+Sidestripe shrimp 0.005  
Spotted ratfish+Slender soles+North pacific hake+Sidestripe shrimp 0.005  
Slender soles+North pacific hake 0.005  
Spotted ratfish+Slender soles+North pacific hake 0.005

# A4  
   
 B=strassoc(species\_cluster\_matrix, cluster=cluster\_groups$AreaGrouping ,func="B")  
 sel=which(B[,"A4"]>0.2)  
 sel

Sablefish Arrowtooth flounder Pacific herring   
 2 3 6   
 Walleye pollock Rex sole Flathead sole   
 7 9 10   
 Spotted ratfish Shortfin eelpout Blackbelly eelpout   
 11 12 13   
 Slender soles Pacific dover sole Sidestripe shrimp   
 14 16 17   
 Northern shrimp Pink shrimp Spot prawn   
 18 19 20   
 English sole Longnose skate Pacific spiny dogfish   
 21 23 24   
 Eulachon   
 25

sc= indicators(X=species\_cluster\_matrix[,sel],   
 cluster=cluster\_groups$AreaGrouping, group="A4", verbose=TRUE,  
 At=0.5, Bt=0.2)

Target site group: A4  
Number of candidate species: 19  
Number of sites: 414   
Size of the site group: 162   
Starting species 1 ... accepted combinations: 101   
Starting species 2 ... accepted combinations: 1108   
Starting species 3 ... accepted combinations: 1364   
Starting species 4 ... accepted combinations: 1921   
Starting species 5 ... accepted combinations: 2348   
Starting species 6 ... accepted combinations: 2600   
Starting species 7 ... accepted combinations: 2814   
Starting species 8 ... accepted combinations: 2905   
Starting species 9 ... accepted combinations: 2991   
Starting species 10 ... accepted combinations: 3039   
Starting species 11 ... accepted combinations: 3040   
Starting species 12 ... accepted combinations: 3064   
Starting species 13 ... accepted combinations: 3070   
Starting species 14 ... accepted combinations: 3080   
Starting species 15 ... accepted combinations: 3082   
Starting species 16 ... accepted combinations: 3082   
Starting species 17 ... accepted combinations: 3082   
Starting species 18 ... accepted combinations: 3082   
Starting species 19 ... accepted combinations: 3083   
Number of valid combinations: 3083  
Number of remaining species: 18   
Calculating statistical significance (permutational test)...

print(sc, sqrtIVt = 0.8)

A B sqrtIV  
Pink shrimp 0.9298359 0.7407407 0.8299201  
Spotted ratfish+Pink shrimp 0.9285687 0.7345679 0.8258915  
Sidestripe shrimp+Pink shrimp 0.9517931 0.7037037 0.8184011  
Blackbelly eelpout 0.8932683 0.7469136 0.8168196  
Spotted ratfish+Sidestripe shrimp+Pink shrimp 0.9512793 0.6975309 0.8145837  
Pink shrimp+Eulachon 0.9501998 0.6975309 0.8141214  
Spotted ratfish+Blackbelly eelpout 0.8913655 0.7407407 0.8125705  
Blackbelly eelpout+Eulachon 0.9184360 0.7160494 0.8109535  
Spotted ratfish+Pink shrimp+Eulachon 0.9503368 0.6913580 0.8105695  
Spotted ratfish+Blackbelly eelpout+Eulachon 0.9180775 0.7098765 0.8072928  
Sidestripe shrimp+Pink shrimp+Eulachon 0.9620321 0.6666667 0.8008463  
 p.value  
Pink shrimp 0.005  
Spotted ratfish+Pink shrimp 0.005  
Sidestripe shrimp+Pink shrimp 0.005  
Blackbelly eelpout 0.005  
Spotted ratfish+Sidestripe shrimp+Pink shrimp 0.005  
Pink shrimp+Eulachon 0.005  
Spotted ratfish+Blackbelly eelpout 0.005  
Blackbelly eelpout+Eulachon 0.005  
Spotted ratfish+Pink shrimp+Eulachon 0.005  
Spotted ratfish+Blackbelly eelpout+Eulachon 0.005  
Sidestripe shrimp+Pink shrimp+Eulachon 0.005

Data collection and survey design The surveys were conducted in the four areas (Chatham Sound, Strait of Juan de Fuca, Haro Strait and Strait of Georgia) using the same survey design. Each study area was divided into 2 km by 2 km grid cells at depths of 80 to 300 m. A random sample of grid cells (80 in Chatham Sound, 40 in the Strait of Juan de Fuca, 40 in Haro Strait, and 40 in the Strait of Georgia) was chosen prior to each survey. A subset of these randomly stations was chosen haphazardly to be sampled each day based on the trawlability of the seafloor at the location, the weather conditions and the end location of the previous days fishing (to maximize efficiency and the number of samples collected). At each of the selected blocks a bottom trawl survey tow was conducted. Fishing was only conducted during daylight hours. The bottom trawl fishing was conducted using the CCGS research vessel Neocaligus, using an American shrimp trawl. The shrimp trawl had a net width of 10 to 11 m and the net opening height was 2 to 3 m off the seafloor. The net utilized roller gear and 1.8 m trawl doors. Net mensuration (measuring the mouth opening) was used to determine the time when the trawl doors reached the seafloor and was in fishing configuration. Each bottom trawl tow targeted five minutes of on bottom time in the Chatham Strait area (due to high catch rates of eulachon) and 20 minutes of on bottom time in the other study areas. The beginning and end positions were recorded using an on board GPS unit and these positions and the average net width (10.5 m) were used to estimate the area swept. Auxiliary information on the bottom depth, vessel speed and warp length were collected for each set. Depth and temperature were also collected on 10 second intervals throughout the bottom trawl tow using a Star-Oddi DST centi-TD temperature-depth logger mounted on the headrope of the net. Each bottom trawl catch was sorted by species, or in the case of some larger catches, a random subsample of the catch was taken and the resulting data expanded to account for the total catch. The total weight of each species captured in a bottom trawl tow was measured using a motion-compensated scale. The catch weight was then divided by the area swept in each tow to calculate a catch-per-unit-of-effort (CPUE) for each species collected in the bottom trawl. Statistical analysis Comparisons of diversity were made between areas and seasons within study areas. Four diversity measures were examined using the full data set (including all species); species richness (the total number of species captured), the Shannon-Weiner diversity index, the Simpson index and Pielou’s species evenness (using CPUE for each species). Comparisons were made using analysis of variance (ANOVA), where area, season and an interaction term between area and season were the independent factors. Pairwise comparisons were made for significant terms in the ANOVA using Tukey’s post-hoc test. Significance was judged at a p < 0.05. To identify community similarity among months and areas a series of correlation analyses that compared catch composition and multivariate analyses of catch data were used. These analyses were conducted on the 25 most abundant species and taxonomic groupings in the catch (measured by total CPUE across all study areas and months). Pairwise correlations among species CPUE were computed and compared to identify potential patterns in co-occurrence of species in the catches. There were highly skewed distributions in these catch data sets, so a log transformation was used to best meet normality assumptions. Because of the presence of zero catches for some species in some trawl hauls we added a small constant value (1/2 of the smallest positive catch for the species) to the CPUE data prior to transformation. Other constants were tested in exploratory analyses, such as adding 1 or 10% of the mean value, but ½ of the minimum positive catch produced the most normal distribution across the wide variety of species. Cluster analysis based on Bray-Curtis dissimilarity matrices were used to compare month and area combinations of catches. Two clustering methods, hierarchical cluster analysis with Ward’s minimum variance method (Murtagh and Legendre 2014) and a non-hierarchical method, k-means clustering (Borcard et al. 2018) were used. In the k-means optimization of the Ward’s classification, the mean taxa values for each of the clusters from the Ward’s classification were used as a starting point for the k-means optimization and the sum of the squared Euclidean distances within the groups was minimized. Dendrograms based on the Bray-Curtis dissimilarity were used to identify similar patterns in catch composition among areas and months. In the hierarchical cluster analysis, we determined the number of clusters based on silhouette width (a measure of how well a site is clustered) and species fidelity analysis (a measure of how well a cluster is characterized by a set of indicator species) (Borcard et al. 2018). The silhouette width is based on the average dissimilarity between a site and all sites of the cluster to which it belongs, compared to the same measure computed for the next closest cluster; silhouette widths range from -1 to 1 (Borcard et al. 2018). The optimal number of clusters is the number which maximizes the average silhouette width. Species fidelity analysis is based on the concepts of specificity (highest when the species is present in the target group but not elsewhere) and fidelity (highest when the species is present in all sites of the target group). We applied the Dufrêne and Legendre (1997) IndVal index available in the R package ‘labdsv’, which is a function of specificity and fidelity. The optimal number of clusters is the number which maximizes the IndVal index. Non-metric dimensional scaling was also applied to the data. For NMDS, we tested second and fourth root transformations (Clarke 1993) and chose fourth root based on the stress value, NMDS convergence and NMDS axes plot. Cluster membership was tested using analysis of similarity (ANOSIM) and discriminant function analysis (DFA). For ANOSIM and DFA, the catch data were log (+ constant) transformed prior to analysis. The constant used for each species was one-half of the minimum positive catch (CPUE > 0) for that species. All analyses were conducted using R software (R Core Team 2019) and significance for all tests was judged at p < 0.05. We used canonical correspondence analysis (CCA) (ter Braak 1986) to identify the primary environmental variables structuring deep-sea coral and sponge assemblages in Alaska (Table 2). Our CCA compared the deep-sea coral and sponge data (12 taxa, Table 1) to the nine environmental variables. In this sense, the deep-sea coral and sponge data set is the response matrix and the environmental data set is the explanatory matrix. The CCA was conducted using the ‘vegan’ package in R. The use of CCA should be limited to situations where rare species are well sampled and are seen as potential indicators of particular characteristics of an ecosystem (Borcard et al. 2018). In our data set, only one taxon was rare (FO < 0.01, Table 1) and taxa were well sampled with the data set consisting of over 850 transect locations. The taxa data are the raw, untransformed abundances in CCA. CCA results were tested by permutation, which combined with a variable selection process (the ‘ordistep’ function in the ‘vegan’ package), was used to find the most parsimonious relationships between the environmental and deep-sea coral and sponge data sets. We displayed the relationships in a biplot. In the biplot, arrows for related environmental variables point in the same general direction, representing a gradient from low values (arrow base) to high values (arrow point). Taxa are located in the biplot along the environmental gradient at their mean position weighted by abundance, so taxa occurring near the point of a variable arrow are positively influenced (more abundant) by that environmental variable.

Indicator species for each of the resolved clusters was also determined using multilevel pattern analysis (REFERENCE).

# Results

Two hundred and four individual taxonomic groups were identified from survey catches across the four areas and 16 months of surveys (Supplemental Material 1). These included 89 species, 8 families and 2 genus of fishes and 69 species, 12 genus and 10 families, 1 superfamily, 2 orders, 1 suborder, 5 classes, 1 subphylum, and 4 phyla of invertebrates. Fishes were dominant by biomass, comprising 90% of the total CPUE. However, the top 25 species captured across regions included 6 invertebrate groups (Table 1). The top 25 species comprised 97.4% of the mean CPUE across the regions and were dominated throughout all months by spotted ratfish (Hydrolagus colliei) and walleye pollock (Gadus chalcogrammus) which together comprised greater than 50% of the CPUE in most month-area combinations (Figure 2). In general, the species were not strongly correlated to each other (Figure 3). The strongest positive correlations were among the shrimp species, eelpout species and a few other fishes (slender sole, flathead sole and eulachon). Negative correlations tended to be strongest between the larger bodied fish species (e.g. hake, the skate species, Pacific cod and spiny dogfish) and shrimp species (Figure 3). The most abundant species, spotted ratfish had low correlations with all species, perhaps reflecting the ubiquitous nature of the species throughout the study area.

There were significant differences among seasons and areas in terms of diversity of the catch. Species evenness measured by the Pielou’s evenness index showed lower diversity in the winter compared to other seasons (Figure 4), but the difference was only significant between fall and winter. The only significant difference among areas was the higher evenness at Chatham Sound sites compared to Haro Strait sites (Figure 4). Chatham sound also had higher evenness than the other two areas, although not significant. For Simpsons diversity index both area and season were significant, but not the interaction term. The Strait of Georgia had a higher diversity than the other areas, but not significantly higher than any of the other areas (Figure 4). The post-hoc tests revealed a significant difference between Chatham Sound and the Strait of Georgia, but no significant differences in the individual seasons were detected. Species richness was the only diversity measure where a significant area and season interaction term was found to be significant (Figure 4). Species richness in the spring was lower than the other seasons, while fall richness was the highest. Species richness was lower in the Strait of Juan de Fuca than in all other areas (Figure 4). There were some significant differences detected by the post-hoc tests among season and area combinations, but there were no consistent patterns, except that the number of species captured in the winter in Haro Strait and the Strait of Georgia were the highest and the Strait of Juan de Fuca the lowest in winter, spring and summer (Figure 4). Cluster analysis clearly showed that the regional differences in community assemblages were stronger than seasonal differences (Figure 6). With the exception of October 2017 in the Haro Strait area which was similar to the same time period in the Strait of Georgia, each of the months of sampling were more similar to other months in the same area, than the same month in different areas.

# Discussion

# Acknowledgments

# References

# Tables

ft <- flextable(samples\_wide)  
ft <- set\_caption(ft, "Number of bottom trawl hauls conducted by season, area and year using the small mesh bottom trawl in 2017-2019.",   
 autonum = run\_autonum(seq\_id = "tab", bkm = "Table1"))  
ft

**Table** **:** Number of bottom trawl hauls conducted by season, area and year using the small mesh bottom trawl in 2017-2019.

| Month | Year | Chatham Sound | Haro Strait | Strait of Georgia | Strait of Juan de Fuca |
| --- | --- | --- | --- | --- | --- |
| Oct | 2,017 |  | 4 | 3 | 11 |
| Nov | 2,017 |  | 5 |  | 5 |
| Dec | 2,017 |  | 8 | 7 | 5 |
| Jul | 2,018 | 31 |  |  |  |
| Sep | 2,018 | 33 |  |  |  |
| Oct | 2,018 | 23 |  |  |  |
| Nov | 2,018 | 28 |  |  |  |
| Jan | 2,018 |  | 9 | 6 | 3 |
| Feb | 2,018 |  | 12 | 13 | 11 |
| Mar | 2,018 |  | 12 | 11 | 9 |
| Apr | 2,018 |  | 10 |  | 18 |
| May | 2,018 |  | 9 | 9 | 18 |
| Jun | 2,018 |  | 8 | 9 | 9 |
| Feb | 2,019 | 18 |  |  |  |
| Mar | 2,019 | 29 |  |  |  |
| Jan | 2,019 |  | 10 | 11 | 7 |
| Total |  | 162 | 87 | 69 | 96 |

#kableExtra::kable\_styling(font\_size = 8) %>%  
# add\_header\_above(c(" "=3,"Region"=6), bold=TRUE)# %>%  
   
#kableExtra::footnote(alphabet =   
#c("16 quadrats also identified in the data", "24 quadrats also identified in the data", "Quadrat counts in the data were all $\\\\geq$ 32", "32 quadrats also identified in the data", "8 quadrats also identified in the data", "Survey plan consisted of priority levels assigned to sites (if no Northern Abalone were found in the first 8 quadrats, surveying was stopped in low priority sites but continued in high priority sites)"), threeparttable = TRUE, general\_title = "",escape = FALSE)  
   
 #Note: do not break footnote over more than one line or returns "makecell[l]" at start of footnote

# Figures

|  |
| --- |
| Locations of bottom trawls carried out in each of the four study regions during 2017-2018. |