library(googledrive)

library(vegan)

library(lmtest)

library(DHARMa)

library(lme4)

library(geoR)

library(spacetime)

library(gstat)

library(sf)

library(sp)

library(nlme)

library(MASS)

library(betapart)

library(dplyr)

library(ggplot2)

library(patchwork)

library(gdm)

library(vegan)

library(piecewiseSEM)

library(MuMIn)

library(caret)

library(tidyverse)

library(lmtest)

library(lme4)

library(AER)

library(asbio)

library(cowplot)

library(ape)

library(reshape2)

library(iNEXT)

library(vegan)

library(ggplot2)

library(grid)

library(viridis)

Datasheet1<-read.csv("Preisser\_Dataset.csv", header=TRUE)

#Jitter coordinates to remove repeats - required for autocorrelation analyses

LatJitt<-jitter(Datasheet1$Latitude, factor=0.1, amount=NULL)

LongJitt<-jitter(Datasheet1$Longitude, factor=0.1, amount=0) #having some trouble getting same number of decimal points in longitude - restricted due to being a neg high number?

#changing from amount=NULL to amount=0 seems to fix this by changing the numbers more

#bind jittered coordinates to datasheet

Datasheet<-cbind(Datasheet1, LongJitt, LatJitt)

#convert abundance to presence/absence

datasheetPA <- decostand(x=Datasheet[,9:35], method="pa")

#add PA matrix to datasheet

Datasheet2<-cbind(Datasheet, datasheetPA)

#sum PA rows to get richness for each individual and add to datasheet - not summing unknown trems, immature trems, unknown nems, cyst nems

divtest<-rowSums(Datasheet2[,38:60])

Datasheet2$SpRich<-divtest

#UW 026118\_01, UW 110086\_01, UW 155836\_01, UW 5523\_03

#UW 2269\_01

#increasing sp richness to reflect cases where unknown/immature trems represent

#the only trematode species in that host - 17077\_01, 17851\_02, 2269\_01

Datasheet2$HostID[73]

Datasheet2$HostID[77]

Datasheet2$HostID[79]

Datasheet2$SpRich[73]<-Datasheet2$SpRich[73]+1

Datasheet2$SpRich[77]<-Datasheet2$SpRich[77]+1

Datasheet2$SpRich[79]<-Datasheet2$SpRich[79]+1

#P/A only datasheet w/ richness

DatasheetRich<-Datasheet2[,c(1:7,36:65)]

DatasheetRich$SpRich

###Polynomial equation testing

ggplot(DatasheetRich, aes(Year, SpRich) ) +

 geom\_point() +

 stat\_smooth()

lm(SpRich ~ poly(Year, 6, raw = TRUE), data = DatasheetRich) %>%

 summary()

lm(SpRich~poly(Year,4)+poly(SL,4), Datasheet2) %>%

 summary()

####check for temporal autocorrelation

RichLM<-glm(SpR2 ~ Year2,

 family=poisson(link = "log"))

summary(RichLM)

time<-Year2

RichDW<-dwtest(RichLM, order.by = time, alternative = "two.sided", iterations = 1000,

 exact =FALSE, tol = 1e-10)

RichDW

####check for spatial autocorrelation

simulationoutput3<-simulateResiduals(fittedModel=RichLM)

testSpatialAutocorrelation(simulationOutput = simulationoutput3,

 x=Datasheet2$LongJitt, y=Datasheet2$LatJitt)

####################YES TEMPORAL AUTOCORRELATION in residuals (didn't test raw data)

####################NO SPATIAL AUTOCORRELATION in residuals (didn't test raw data)

##test for overdispersion

Datasheet2AB<-Datasheet2[,c(1,65)]

Datasheet2AB

rd <- glm(SpRich ~ ., data = Datasheet2AB, family = poisson)

dispersiontest(rd,trafo=1)

#data: rd

#z = -53.245, p-value = 1

#alternative hypothesis: true alpha is greater than 0

#sample estimates:

# alpha

#-0.9633028

##Accounting for temporal autocorrelation

sites1<-paste(Datasheet2$Latitude,Datasheet2$Longitude)

test.mod2<-glmmPQL(SpRich~Year+SL,random=~1+Year|sites1, data=Datasheet2,

 family=poisson(link = "log"), correlation = corAR1(), verbose=FALSE)

summary(test.mod2)

##Making partial residual plot

#to model relationship between richness and year (partial regression plot) holding all other variables constant

#run original model with everything except the variable of interest

test.mod2a<-test.mod<-glmmPQL(SpRich~SL,random=~1|sites1, data=Datasheet2,

 family=poisson(link = "log"), correlation=corCAR1(), verbose=FALSE)

#run new model with variable of interest against everything else

test.mod2b<-test.mod<-glmmPQL(Year~SL,random=~1|sites1, data=Datasheet2,

 family=poisson(link = "log"), correlation=corCAR1(), verbose=FALSE)

#get residuals of each model

resid.2a<-residuals(test.mod2a)

resid.2b<-residuals(test.mod2b)

x <- resid.2b

y <- resid.2a

jpeg(file="PartialRegressionPlot.jpeg",

 width=8, height=6, units="in", res=300)

plot(x,y,type="n",

 xlab="Residuals from Model 2", ylab="Residuals from Model 1")

part <- lm(y~x)

wx = par("usr")[1:2]

new.x = seq(wx[1],wx[2],len=100)

pred = predict(part, new=data.frame(x=new.x), interval="conf")

lines(new.x,pred[,"fit"],lwd=2)

lines(new.x,pred[,"lwr"],lty=3)

lines(new.x,pred[,"upr"],lty=3)

points(x,y,pch=16,col="black")

dev.off()

#####checking for relationship between host body size and time

hist((Datasheet2$SL))

Size<-log10(Datasheet2$SL)

Size2<-Datasheet2$SL

Year2<-Datasheet2$Year

HostSLMod<-glm(Size ~ Year2)

summary(HostSLMod)

plot(Size2, Year2)

colnames(Datasheet2)

DatasheetSize<-Datasheet2[,c(5,7)]

DatasheetSize

ggplot(DatasheetSize, aes(Year, SL) ) +

 geom\_point() +

 stat\_smooth()

#########Splitting up dataset into decades for beta diversity analyses

#all decades except two (60s and 70s) reach or are close to the asymptote

#and are within 2 species of the total estimated diversity for each decade (via iNext)

Datasheet2\_1930<-Datasheet2[Datasheet2$Year < 1940,] #14 #14

Datasheet2\_1940<-Datasheet2[Datasheet2$Year < 1950 & Datasheet2$Year > 1939,] #14 #14

Datasheet2\_1950<-Datasheet2[Datasheet2$Year < 1960 & Datasheet2$Year > 1949,] #6 #6

Datasheet2\_1960<-Datasheet2[Datasheet2$Year < 1970 & Datasheet2$Year > 1959,] #8 #8

Datasheet2\_1970<-Datasheet2[Datasheet2$Year < 1980 & Datasheet2$Year > 1969,] #11 #11

Datasheet2\_1980<-Datasheet2[Datasheet2$Year < 1990 & Datasheet2$Year > 1979,] #13 #13

Datasheet2\_1990<-Datasheet2[Datasheet2$Year < 2000 & Datasheet2$Year > 1989,] #13 #13

Datasheet2\_2000<-Datasheet2[Datasheet2$Year < 2010 & Datasheet2$Year > 1999,] #16 #16

Datasheet2\_2010<-Datasheet2[Datasheet2$Year > 2009,] #14 #14

Datasheet2\_1930$Decade.1=1930

Datasheet2\_1940$Decade.1=1940

Datasheet2\_1950$Decade.1=1950

Datasheet2\_1960$Decade.1=1960

Datasheet2\_1970$Decade.1=1970

Datasheet2\_1980$Decade.1=1980

Datasheet2\_1990$Decade.1=1990

Datasheet2\_2000$Decade.1=2000

Datasheet2\_2010$Decade.1=2010

Datasheet3D<-rbind(Datasheet2\_1930,Datasheet2\_1940,Datasheet2\_1950,Datasheet2\_1960,

 Datasheet2\_1970, Datasheet2\_1980, Datasheet2\_1990, Datasheet2\_2000,

 Datasheet2\_2010)

###Rarefaction

#removing all columns except break and species abundance (removed unknowns and metacercaria\_sp2)

Datasheet3.2D<-Datasheet3D[,c(66,9:14,16:31)]

##aggregate based on decade

Datasheet3.2D\_agg<-aggregate(. ~ Decade.1, Datasheet3.2D, sum)

rownames(Datasheet3.2D\_agg)<-Datasheet3.2D\_agg[,1]

Datasheet3.2D\_agg[,1]<-NULL

testinext3D<-iNEXT((t(Datasheet3.2D\_agg)), q = 0, datatype = "abundance", size = NULL, endpoint = NULL,

 knots = 40, se = TRUE, nboot = 50)

ggiNEXT(testinext3D, type = 1, se = TRUE, facet.var = "none",

 color.var = "none", grey = FALSE)

####Remove 60s and 70s from datasheet as they didn't reach their asymptote

Datasheet3E<-rbind(Datasheet2\_1930,Datasheet2\_1940,Datasheet2\_1950,Datasheet2\_1980,

 Datasheet2\_1990, Datasheet2\_2000,Datasheet2\_2010)

Datasheet3.2E<-Datasheet3E[,c(66,9:14,16:31)]

Datasheet3.2E\_agg<-aggregate(. ~ Decade.1, Datasheet3.2E, sum)

rownames(Datasheet3.2E\_agg)<-Datasheet3.2E\_agg[,1]

Datasheet3.2E\_agg[,1]<-NULL

####Beta Diversity Analyses - Between time periods

BetaDiv\_Btwn<-beta.pair.abund(Datasheet3.2E\_agg, index.family = "bray")

Bray\_Btwn\_3040<-BetaDiv\_Btwn$beta.bray[1]

Bray\_Btwn\_4050<-BetaDiv\_Btwn$beta.bray[7]

Bray\_Btwn\_5080<-BetaDiv\_Btwn$beta.bray[12]

Bray\_Btwn\_8090<-BetaDiv\_Btwn$beta.bray[16]

Bray\_Btwn\_9000<-BetaDiv\_Btwn$beta.bray[19]

Bray\_Btwn\_0010<-BetaDiv\_Btwn$beta.bray[21]

Bray\_Btwn<-c(Bray\_Btwn\_3040,Bray\_Btwn\_4050,Bray\_Btwn\_5080,

 Bray\_Btwn\_8090,Bray\_Btwn\_9000,Bray\_Btwn\_0010)

Uni\_Btwn\_3040<-BetaDiv\_Btwn$beta.bray.gra[1]

Uni\_Btwn\_4050<-BetaDiv\_Btwn$beta.bray.gra[7]

Uni\_Btwn\_5080<-BetaDiv\_Btwn$beta.bray.gra[12]

Uni\_Btwn\_8090<-BetaDiv\_Btwn$beta.bray.gra[16]

Uni\_Btwn\_9000<-BetaDiv\_Btwn$beta.bray.gra[19]

Uni\_Btwn\_0010<-BetaDiv\_Btwn$beta.bray.gra[21]

Uni\_Btwn<-c(Uni\_Btwn\_3040,Uni\_Btwn\_4050,Uni\_Btwn\_5080,

 Uni\_Btwn\_8090,Uni\_Btwn\_9000,Uni\_Btwn\_0010)

Bal\_Btwn\_3040<-BetaDiv\_Btwn$beta.bray.bal[1]

Bal\_Btwn\_4050<-BetaDiv\_Btwn$beta.bray.bal[7]

Bal\_Btwn\_5080<-BetaDiv\_Btwn$beta.bray.bal[12]

Bal\_Btwn\_8090<-BetaDiv\_Btwn$beta.bray.bal[16]

Bal\_Btwn\_9000<-BetaDiv\_Btwn$beta.bray.bal[19]

Bal\_Btwn\_0010<-BetaDiv\_Btwn$beta.bray.bal[21]

Bal\_Btwn<-c(Bal\_Btwn\_3040,Bal\_Btwn\_4050,Bal\_Btwn\_5080,

 Bal\_Btwn\_8090,Bal\_Btwn\_9000,Bal\_Btwn\_0010)

Decade\_Comparison<-c(1:6)

BetaDiv\_Btwn\_Bray<-as.data.frame(cbind(Decade\_Comparison,Bray\_Btwn,Uni\_Btwn,Bal\_Btwn))

BetaDiv\_Btwn\_Bray\_melt<-melt(BetaDiv\_Btwn\_Bray, id.vars="Decade\_Comparison")

color=c("black", "#009E73", "#0072B2")

jpeg(file="DissimilarityAbundBtwnDecades\_Apr28.jpeg",

 width=8, height=6, units="in", res=300)

Between1<-ggplot(BetaDiv\_Btwn\_Bray\_melt, aes(x=Decade\_Comparison))+

 geom\_point(aes(y = value, color = variable), shape=15, size=3) +

 geom\_line(aes(y = value, color = variable)) +

 labs(y="Dissimilarity", x="", col="Beta Diversity Measure")+

 ggtitle("Balanced Variation, Unidirectional Gradients, and

 Total Dissimilarity Between Time Periods")+

 labs(x="Decade Comparison", y="Dissimilarity",

 col="Beta Diversity Measure")+

 theme(plot.title = element\_text(hjust = 0.5),

 panel.background = element\_blank(),axis.text.x=element\_blank(),

 axis.ticks.x = element\_blank(),legend.position = "none") + labs(tag = "A") +

 scale\_color\_manual(values = c("black","#009E73", "#0072B2"))

dev.off()

#"#009E73", "#0072B2"

####Beta Diversity Analyses - Within time periods

colnames(Datasheet2\_1930)

Datasheet2\_1930.1<-Datasheet2\_1930[,c(1,9:14,16:31)]

Datasheet2\_1940.1<-Datasheet2\_1940[,c(1,9:14,16:31)]

Datasheet2\_1950.1<-Datasheet2\_1950[,c(1,9:14,16:31)]

Datasheet2\_1980.1<-Datasheet2\_1980[,c(1,9:14,16:31)]

Datasheet2\_1990.1<-Datasheet2\_1990[,c(1,9:14,16:31)]

Datasheet2\_2000.1<-Datasheet2\_2000[,c(1,9:14,16:31)]

Datasheet2\_2010.1<-Datasheet2\_2010[,c(1,9:14,16:31)]

rownames(Datasheet2\_1930.1) <- Datasheet2\_1930.1[,1]

Datasheet2\_1930.1[,1] <- NULL

rownames(Datasheet2\_1940.1) <- Datasheet2\_1940.1[,1]

Datasheet2\_1940.1[,1] <- NULL

rownames(Datasheet2\_1950.1) <- Datasheet2\_1950.1[,1]

Datasheet2\_1950.1[,1] <- NULL

rownames(Datasheet2\_1980.1) <- Datasheet2\_1980.1[,1]

Datasheet2\_1980.1[,1] <- NULL

rownames(Datasheet2\_1990.1) <- Datasheet2\_1990.1[,1]

Datasheet2\_1990.1[,1] <- NULL

rownames(Datasheet2\_2000.1) <- Datasheet2\_2000.1[,1]

Datasheet2\_2000.1[,1] <- NULL

rownames(Datasheet2\_2010.1) <- Datasheet2\_2010.1[,1]

Datasheet2\_2010.1[,1] <- NULL

Bray\_TP30<-beta.multi.abund(Datasheet2\_1930.1, index.family="bray")

Bray\_TP40<-beta.multi.abund(Datasheet2\_1940.1, index.family="bray")

Bray\_TP50<-beta.multi.abund(Datasheet2\_1950.1, index.family="bray")

Bray\_TP80<-beta.multi.abund(Datasheet2\_1980.1, index.family="bray")

Bray\_TP90<-beta.multi.abund(Datasheet2\_1990.1, index.family="bray")

Bray\_TP00<-beta.multi.abund(Datasheet2\_2000.1, index.family="bray")

Bray\_TP10<-beta.multi.abund(Datasheet2\_2010.1, index.family="bray")

Decade\_W<-as.vector(c(1930, 1940, 1950, 1980, 1990, 2000, 2010))

Bray\_Within30<-Bray\_TP30$beta.BRAY

Bray\_Within40<-Bray\_TP40$beta.BRAY

Bray\_Within50<-Bray\_TP50$beta.BRAY

Bray\_Within80<-Bray\_TP80$beta.BRAY

Bray\_Within90<-Bray\_TP90$beta.BRAY

Bray\_Within00<-Bray\_TP00$beta.BRAY

Bray\_Within10<-Bray\_TP10$beta.BRAY

Uni\_Within30<-Bray\_TP30$beta.BRAY.GRA

Uni\_Within40<-Bray\_TP40$beta.BRAY.GRA

Uni\_Within50<-Bray\_TP50$beta.BRAY.GRA

Uni\_Within80<-Bray\_TP80$beta.BRAY.GRA

Uni\_Within90<-Bray\_TP90$beta.BRAY.GRA

Uni\_Within00<-Bray\_TP00$beta.BRAY.GRA

Uni\_Within10<-Bray\_TP10$beta.BRAY.GRA

Bal\_Within30<-Bray\_TP30$beta.BRAY.BAL

Bal\_Within40<-Bray\_TP40$beta.BRAY.BAL

Bal\_Within50<-Bray\_TP50$beta.BRAY.BAL

Bal\_Within80<-Bray\_TP80$beta.BRAY.BAL

Bal\_Within90<-Bray\_TP90$beta.BRAY.BAL

Bal\_Within00<-Bray\_TP00$beta.BRAY.BAL

Bal\_Within10<-Bray\_TP10$beta.BRAY.BAL

Total\_Bray<-as.vector(c(Bray\_Within30,Bray\_Within40,Bray\_Within50,Bray\_Within80,

 Bray\_Within90,Bray\_Within00,Bray\_Within10))

Unidirectional\_Gradients<-as.vector(c(Uni\_Within30,Uni\_Within40,Uni\_Within50,Uni\_Within80,

 Uni\_Within90,Uni\_Within00,Uni\_Within10))

Balanced\_Variation<-as.vector(c(Bal\_Within30,Bal\_Within40,Bal\_Within50,Bal\_Within80,

 Bal\_Within90,Bal\_Within00,Bal\_Within10))

BetaDiv\_Within\_Bray<-as.data.frame(cbind(Decade\_W, Total\_Bray, Unidirectional\_Gradients, Balanced\_Variation))

BetaDiv\_Within\_Bray\_Melt<-melt(BetaDiv\_Within\_Bray, id.vars="Decade\_W")

jpeg(file="DissimilarityAbundWithinDecades\_Apr28.jpeg",

 width=8, height=6, units="in", res=300)

Within1<-ggplot(BetaDiv\_Within\_Bray\_Melt, aes(x=Decade\_W))+

 geom\_point(aes(y = value, color = variable), shape=15, size=3) +

 geom\_line(aes(y = value, color = variable)) +

 labs(y="Dissimilarity", x="", col="Beta Diversity Measure")+

 ggtitle("Balanced Variation, Unidirectional Gradients, and

 Total Dissimilarity Between Time Periods")+

 labs(x="Decade", y="Dissimilarity",

 col="Beta Diversity Measure")+

 theme(plot.title = element\_text(hjust = 0.5),

 panel.background = element\_blank(),axis.text.x=element\_blank(),

 axis.ticks.x = element\_blank(),

 legend.position = "none")+

 labs(tag = "B") +

 scale\_color\_manual(values = c("black","#009E73", "#0072B2"))

dev.off()

# extract the legend from one of the plots

legend <- get\_legend(

 # create some space to the left of the legend

 Within + theme(legend.box.margin = margin(0, 0, 0, 2)) #get within legend by removing "legend=none" argument

)

plots<-plot\_grid(Between1/Within1)

# add the legend to the row we made earlier. Give it one-third of

# the width of one plot (via rel\_widths).

plot\_grid(plots, legend, rel\_widths = c(3,.8))

jpeg(file="DissimilarityAbund\_BW\_Decades\_Apr28.jpeg",

 width=9, height=6, units="in", res=300)

plot\_grid(plots, legend, rel\_widths = c(3,.8))

dev.off()

###########Make proportion bar plot

meltDatasheet3.2D<-melt(Datasheet3.2D, id.vars="Decade.1")

jpeg(file="ProportionalAbund\_Apr28.jpeg",

 width=8, height=6, units="in", res=300)

ggplot(meltDatasheet3.2D, aes(fill=variable, y=value, x=Decade.1))+geom\_bar(position="fill", stat="identity")+

scale\_fill\_manual(values=c("#000000","#050E69",

 "#1525CA","#5E6BF4","#959DF9","#BEC3FB","#E0E2FB","#C2F3F7","#93EDF4",

 "#5AC9D2","#31B8C2","#11949E","#08646B","#4E4F0C","#84861D","#B7BA1A",

 "#D7DA10","#F6FA0E","#F7F992","#EAEAC4","#CACAC8","#90908F"))+

 labs(x="Decade", y="Proportional Abundance",

 col="Parasite Species")+

 ggtitle("Proportion of Parasite Species Abundances Across Nine Decades")+

 theme(plot.title = element\_text(hjust = 0), panel.background = element\_blank(), axis.text.x = element\_blank(),

 axis.ticks.x = element\_blank())

dev.off()

############Betadisper & Adonis

#remove hosts with Metacercaria sp2 (P/A only, and this analysis uses abundances) - UW 151702\_08

#remove hosts where the only parasite is unknown trem (can't analyze) - UW 2269\_01

#Remove fish with no parasites (UW 026118\_01, UW 110086\_01, UW 155836\_01, UW 5523\_03)

Datasheet3E\_Zero<-Datasheet3E[-c(5,75,35,42,86,27),]

rownames(Datasheet3E\_Zero)<-Datasheet3E\_Zero[,1]

Datasheet3E\_Zero[,1]<-NULL

Datasheet3E\_meta<-Datasheet3E\_Zero[,c(64,65)]

Datasheet3E\_multi<-Datasheet3E\_Zero[,c(8:13,15:30)]

######Betadisper

Bray\_3E<-vegdist(Datasheet3E\_multi, method="bray", binary=FALSE)

Bray\_3E.bd <- betadisper(d=Bray\_3E,

 group=Datasheet3E\_meta$Decade.1,

 type="centroid", bias.adjust=TRUE)

Bray\_3E.bd.anova<-anova(Bray\_3E.bd)

Bray\_3E.bd.anova

########Adonis

set.seed(2020)

ado.3E<-adonis(Bray\_3E ~ Decade.1, data=Datasheet3E\_meta)

ado.3E

sitecols3E<-c("midnightblue","blue","darkcyan","springgreen4","springgreen1",

 "greenyellow","yellow")

jpeg(filename="PCoA\_3E\_Apr28",

 width = 6, height = 4, units="in",res = 300)

plot(Bray\_3E.bd, hull=F, label=F,

 main=expression(""), col=sitecols3E, #was sitecols

 xlab="", ylab="", pch=c(20,20,20,20,20,20,20),cex=2, sub="",

 xaxt='n',yaxt='n',cex.main=2)

ordihull(Bray\_3E.bd, Datasheet3E\_meta$Decade.1,

 draw = c("polygon"), col = sitecols3E, alpha=0.2, lwd=0.05) #was sitecols

legend("topright",title="Decade",legend=c("1930s","1940s", "1950s", "1980s",

 "1990s", "2000s", "2010s"),

 col=sitecols3E,pch=c(20,20,20,20,20,20,20),bg="white",ncol = 1, cex = 1, pt.cex=1.5)

mtext("betadisper = not significant", side=1, line=0.25)

mtext("adonis = significant", side=1, line=1.25)

dev.off()

###################

nrow(Datasheet2)

colnames(Datasheet2)

#Remove fish with no parasites (UW 026118\_01, UW 110086\_01, UW 155836\_01, UW 5523\_03)

#Remove fish with only unknown parasites or metacercaria sp2 (UW 2269\_01, UW 151702\_08)

Datasheet2.D<-Datasheet2[-c(9,30,63,103,79,56),]

Comm<-Datasheet2.D[,c(1,9:14,16:31)]

rownames(Comm)<-Comm[,1]

Comm[,1]<-NULL

Env<-Datasheet2.D[,c(1,3:5)]

rownames(Env)<-Env[,1]

Env[,1]<-NULL

Env\_30<-Env[Env$Year < 1940,] #14 #14

Env\_40<-Env[Env$Year < 1950 & Env$Year > 1939,] #14

Env\_50<-Env[Env$Year < 1960 & Env$Year > 1949,] #6

Env\_60<-Env[Env$Year < 1970 & Env$Year > 1959,] #8

Env\_70<-Env[Env$Year < 1980 & Env$Year > 1969,] #11

Env\_80<-Env[Env$Year < 1990 & Env$Year > 1979,] #13

Env\_90<-Env[Env$Year < 2000 & Env$Year > 1989,] #13

Env\_00<-Env[Env$Year < 2010 & Env$Year > 1999,] #16

Env\_10<-Env[Env$Year > 2009,] #14

Env\_30$Decade<-1930

Env\_40$Decade<-1940

Env\_50$Decade<-1950

Env\_60$Decade<-1960

Env\_70$Decade<-1970

Env\_80$Decade<-1980

Env\_90$Decade<-1990

Env\_00$Decade<-2000

Env\_10$Decade<-2010

Env2<-as.data.frame(rbind(Env\_30,Env\_40,Env\_50,Env\_60,Env\_70,Env\_80,

 Env\_90,Env\_00,Env\_10))

Bray\_Cent<-vegdist(Comm, method="bray", binary=FALSE)

Bray\_Cent.bd <- betadisper(d=Bray\_Cent,

 group=Env2$Decade,

 type="centroid")

color<-c("midnightblue","blue","darkcyan","springgreen4","springgreen1","chartreuse3",

 "greenyellow","darkolivegreen1","yellow")

jpeg(filename="PCoA\_Centroids\_6.4.jpg",

 width = 6, height = 4, units="in",res = 300)

plot(Bray\_Cent.bd, hull=FALSE, segments=FALSE, label=F, ellipse=TRUE, conf=0.5, pch=26, col=color)

dev.off()