Univariate plotting & summary metrics of spatial model output

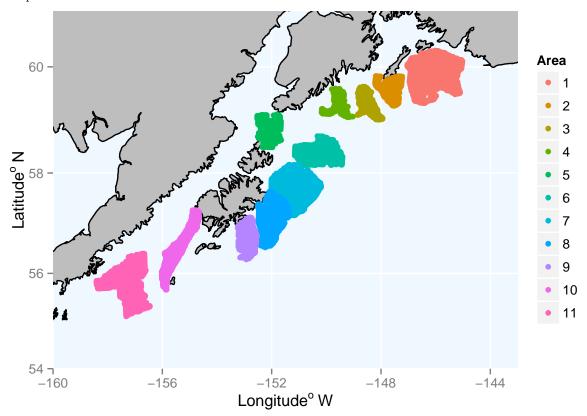
Ben Williams October 26, 2015

This is the initial examination using Ole's model output file 2015-11-12.

The *vplot* function will generate a figure for each year and area. Input a dataframe containing the species of interest, subsets of the "All_sp_index_meanCPUEByArea.csv" file. The location of this may change when the model is updated.

A seperate file can be used to house a data frame of species names and trophic guilds etc. This file can be used to inform vplot of the groups to plot (example code below). Further this will allow for relatively painless exmainations of guild variance vs the whole, etc.

Map of area locations



Function for generating figures

```
vplot <- function(x, title=""){
   require(ggplot2)
   theme_set(theme_bw(base_size=12,base_family='Times New Roman')+
   theme(panel.grid.major = element_blank(),
   panel.grid.minor = element_blank()))
a <- aggregate(vari~area+year,data=x,FUN=sum)
b <- aggregate(Mean.totalDensity~area+year,data=x,FUN=sum)</pre>
```

```
c <- merge(a, b, by=c("area", "year"))
c$se <- sqrt(c$vari)
c$uci <- c$se*2 + c$Mean.totalDensity
c$lci <- c$Mean.totalDensity - c$se*2
c$Area <- factor(c$area)

year.range <- c(1984,1987,1990,1993,1996,seq(1999,2015,by=2))
ggplot(c, aes(year, Mean.totalDensity, group=Area, color=Area))+geom_line()+
    geom_ribbon(aes(ymin=lci, ymax=uci, fill=Area), alpha=.2, linetype=0)+
    ylim(min(c$lci), max(c$uci))+ scale_x_continuous(limits=c(1984, 2015), breaks=year.range)+ggtitle(tit
    theme(text=element_text(family="Helvetica"),axis.text.x = element_text(angle = 90,hjust=1,vjust=0.5))
}</pre>
```

Subset groups based upon "trawl_species_control_file.csv"

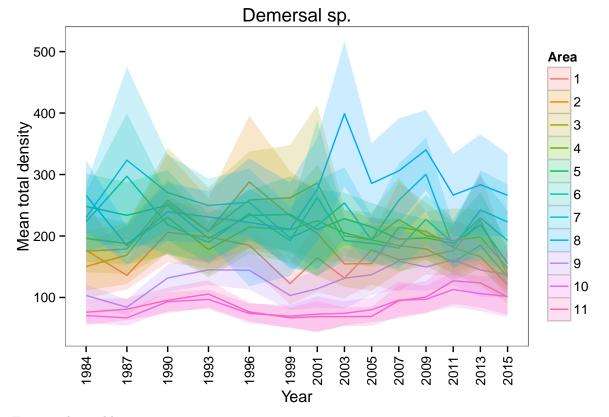
```
sp <- subset(trawl_species, pelagic.benthic!='pelagic')
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))</pre>
```

Define the group to plot based upon the species names pulled from the database

```
group <- meanCPUE[meanCPUE$Species %in% sp.names,]</pre>
```

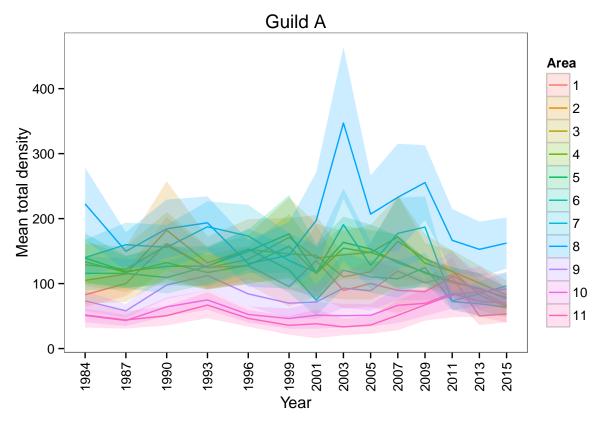
Plot the group

```
vplot(group,title="Demersal sp.")
```

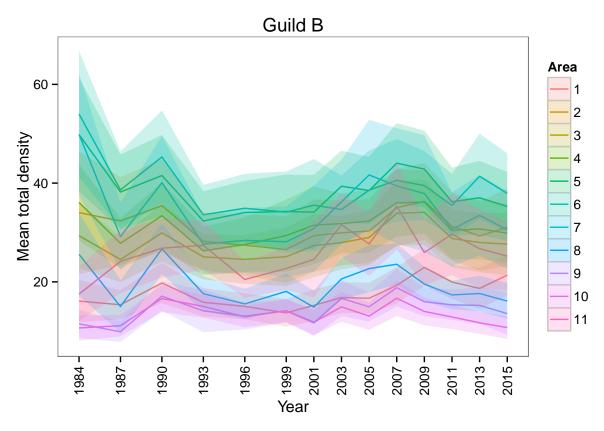


Examine by guild

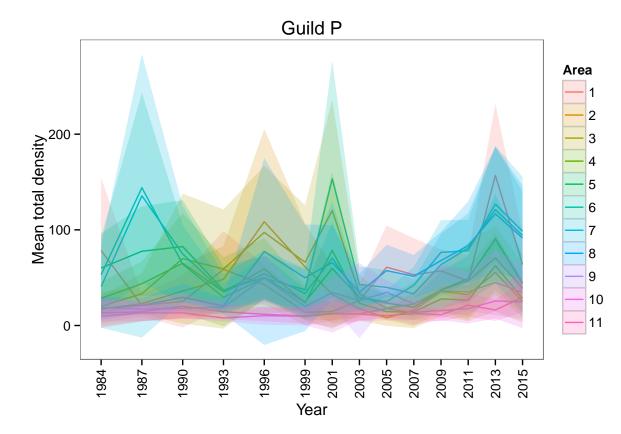
```
sp <- subset(trawl_species, guild=='A')
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))
group <- meanCPUE[meanCPUE$Species %in% sp.names,]
vplot(group, title="Guild A")</pre>
```



```
sp <- subset(trawl_species, guild=='B')
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))
group <- meanCPUE[meanCPUE$Species %in% sp.names,]
vplot(group, title="Guild B")</pre>
```

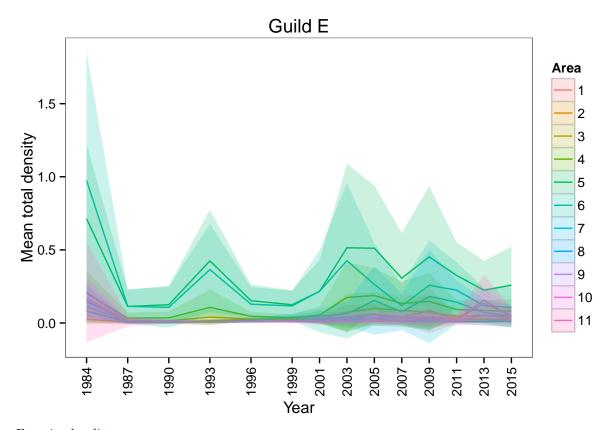


```
sp <- subset(trawl_species, guild=='P')
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))
group <- meanCPUE[meanCPUE$Species %in% sp.names,]
vplot(group, title="Guild P")</pre>
```



```
sp <- subset(trawl_species, guild=='E')
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))
group <- meanCPUE[meanCPUE$Species %in% sp.names,]

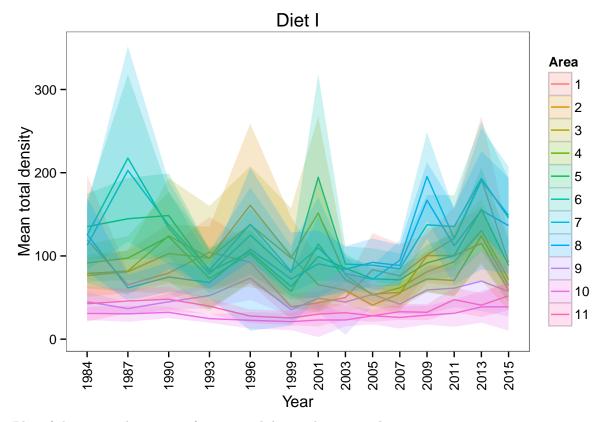
vplot(group, title="Guild E")</pre>
```



Examine by diet

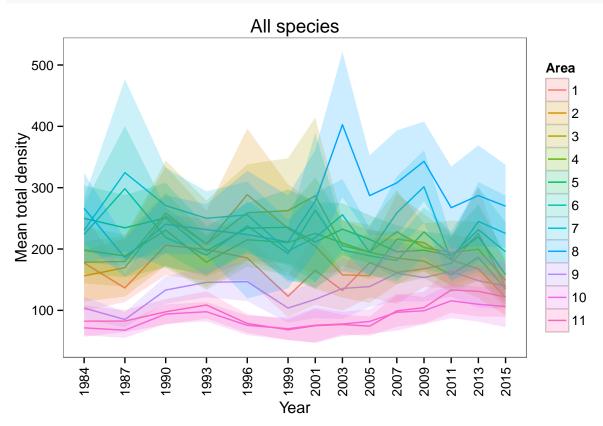
```
sp <- subset(trawl_species, diet1=='I' | diet2=="I")
sp <- droplevels(sp)
sp.names <- as.list(levels(sp$database.name))
group <- meanCPUE[meanCPUE$Species %in% sp.names,]

vplot(group, title="Diet I")</pre>
```



Plot of the sum and variance of mean total density by year and area

vplot(meanCPUE, title="All species")

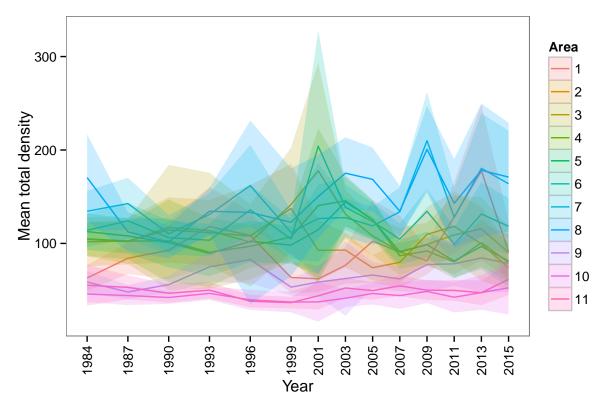


Area 8 jumps out as higher than the other areas

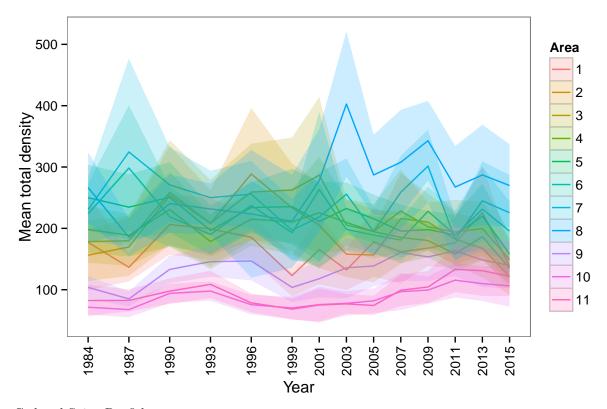
Examine all species minus Walleye Pollock, Arrowtooth Flounder and Pacific Halibut

```
#subset by area
smean <- subset(meanCPUE, Species!="Gadus.chalcogrammus" & Species!="Atheresthes.stomias"& Species!="Hissmean <- droplevels(smean)

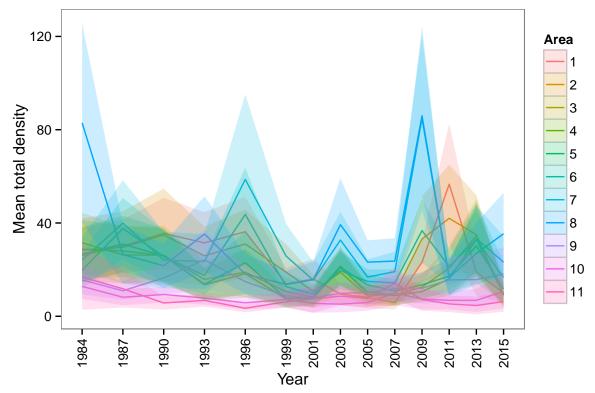
vplot(smean)</pre>
```



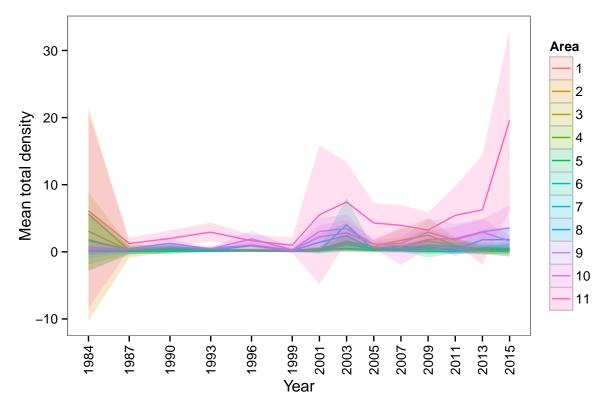
Walleye Pollock, Arrowtooth Flounder and Pacific Halibut



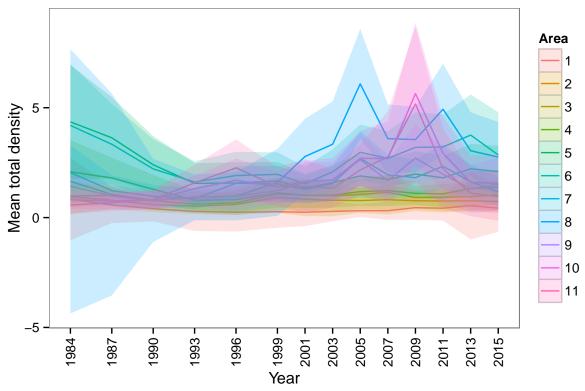
Cod and Spiny Dogfish



Capelin, Herring, and Eulachon



Rock Sole, Yellowfin Sole, Bigmouth Sculpin, Ling Cod



Bairdi Crab

