Seagrant: Understanding climate impacts on the Maine coastal fish and invertebrate community through synthesis of the Maine-New Hampshire Inshore Trawl Survey

Project Description

From the proposal:

> The overarching goal of this research is to synthesize data collected through the Maine-New Hampshire Inshore Trawl Survey to understand how climate change, fishing, and other environmental drivers are impacting key fish and invertebrate communities in coastal Maine waters.

Objective 1

- Analyze changes in biodiversity in space and time and evaluate associations with environmental factors and fishing
- To be rerun with updated Maine DMR data

Analysis

- biodiversity metrics/ maps
- GAMMs

Data

- Will double check that all necessary data is available in data folder

Scripts

- See Ashley's code folder for scripts
- pulled relevant scripts from original Seagrant directory

Objective 2

- Identify species groups and assess changes in habitat suitability if functional groups and communities in space and time

Analysis

- removed shrimp and other unimportant invertebrates from top 50 species analysis
- feeding guilds from NOAA IEA definitions (https://noaa-edab.github.io/tech-doc/aggroups.html)
- stratified mean for NMDS convergence and simplified plotting using NOAA IEA procedure (https://noaa-edab.github.io/tech-doc/inshoresurvdat.html#data-analysis-29)
- Bray-Curtis dissimilarity matrix for NMDS and anosim/adonis

Data

- raw data from Maine DMR portal (https://mainedmr.shinyapps.io/MaineDMR_Trawl_Survey_Portal/) (MaineDMR_Trawl_Survey_Catch_Data_2021-05-14.csv)
- old data (full-me-dmr-expcatch.csv)
- species with feeding guild designation (species_groups.csv)
- 4 community matrices for top 50 species and functional groups (biomass and abundance) - output from ME_trawl_NMDS_species_7.21.R and ME_trawl_NMDS_groups_7.21.R saved for future use in Rmarkdowns or NMDS so you don't have to run beginning cleaning code

Scripts

- set up with here function, so directory paths should work on any computer
- Scripts located in code subfolder of objective 2 folder
- Scripts that end in 7.21 are updated scripts from July 2021, the older versions are saved and have more versions of plots but are pretty messy
- basic plotting that is not for NMDS in ME_trawl_plots.R
- old script (ME_trawl_NMDS.R) went with the old data and trying out different NMDS plots
- Pretty self explanatory anosim_adonis_analysis_7.21.R
- NEFSC_NMDS_groups.R putting science center data into functional groups- not needed anymore
- All Rmarkdowns in subfolder

Objective 3

- Analyze joint distribution of key predator-prey species within the community, with a particular focus on lobster and cod
- contact Andrew Allyn (aallyn@gmri.org (mailto:aallyn@gmri.org)) for questions or code

Objective 4

- Evaluate how ecosystem changes align with shifts in diversity and composition of fishery landings over time in ports along Maine's coastline

Analysis

Data

- Landings data from DMR portal (https://mainedmr.shinyapps.io/Landings_Portal/)
- In data folder MaineDMR_Modern_Landings_Data_All.csv
- County and species specific landings 2008-2020
- 2006-2007 data from Rob Watts excel sheet JerelleJesse_06-07_Non-ConfidentialSpeciesByCounty_8-20-2021
- reformatted for csv MaineDMR_2006_2007_Landings.csv (rob.watts@maine.gov (mailto:rob.watts@maine.gov))

Scripts

- leverage objective 1 code to start

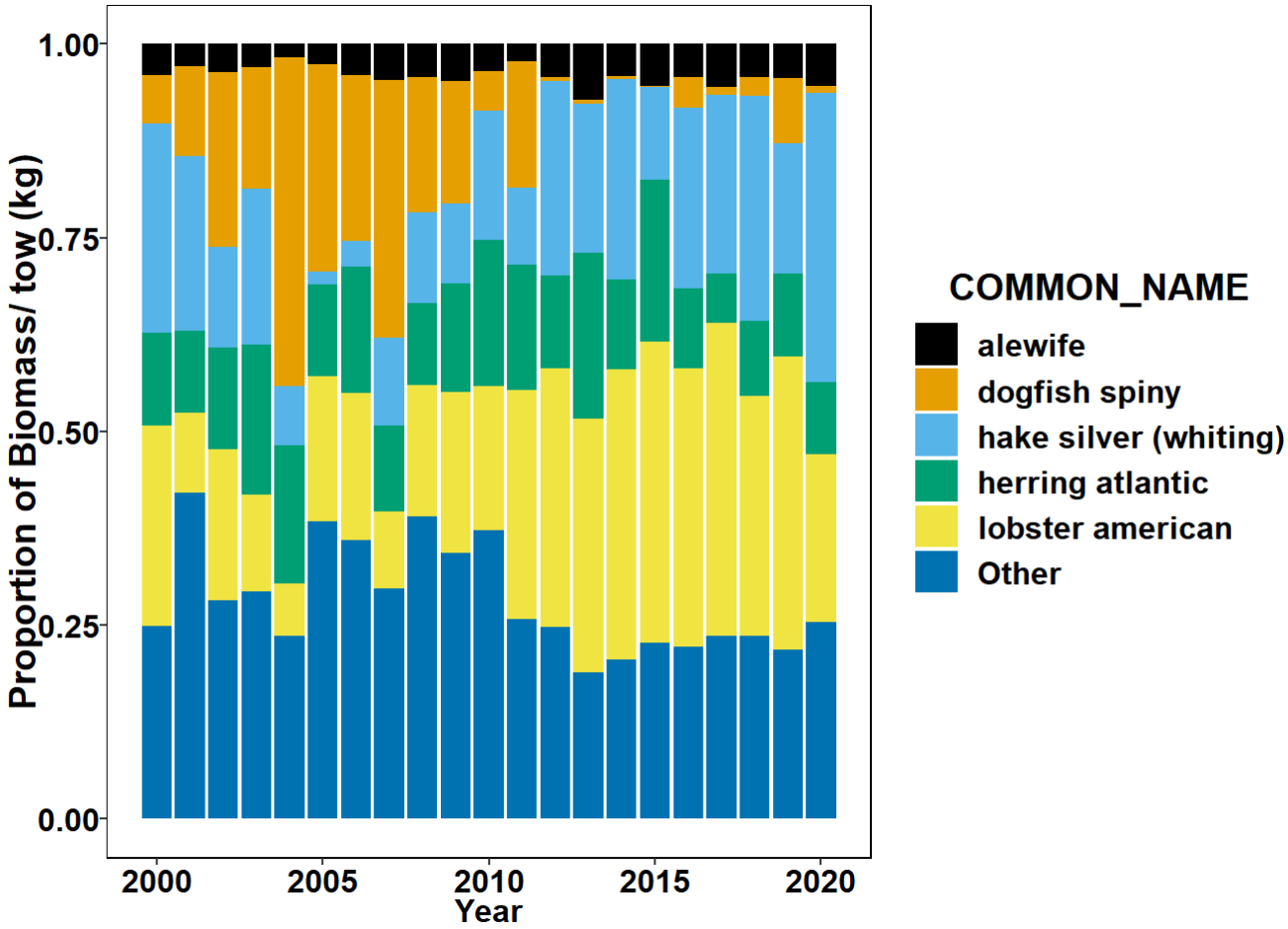
Contact

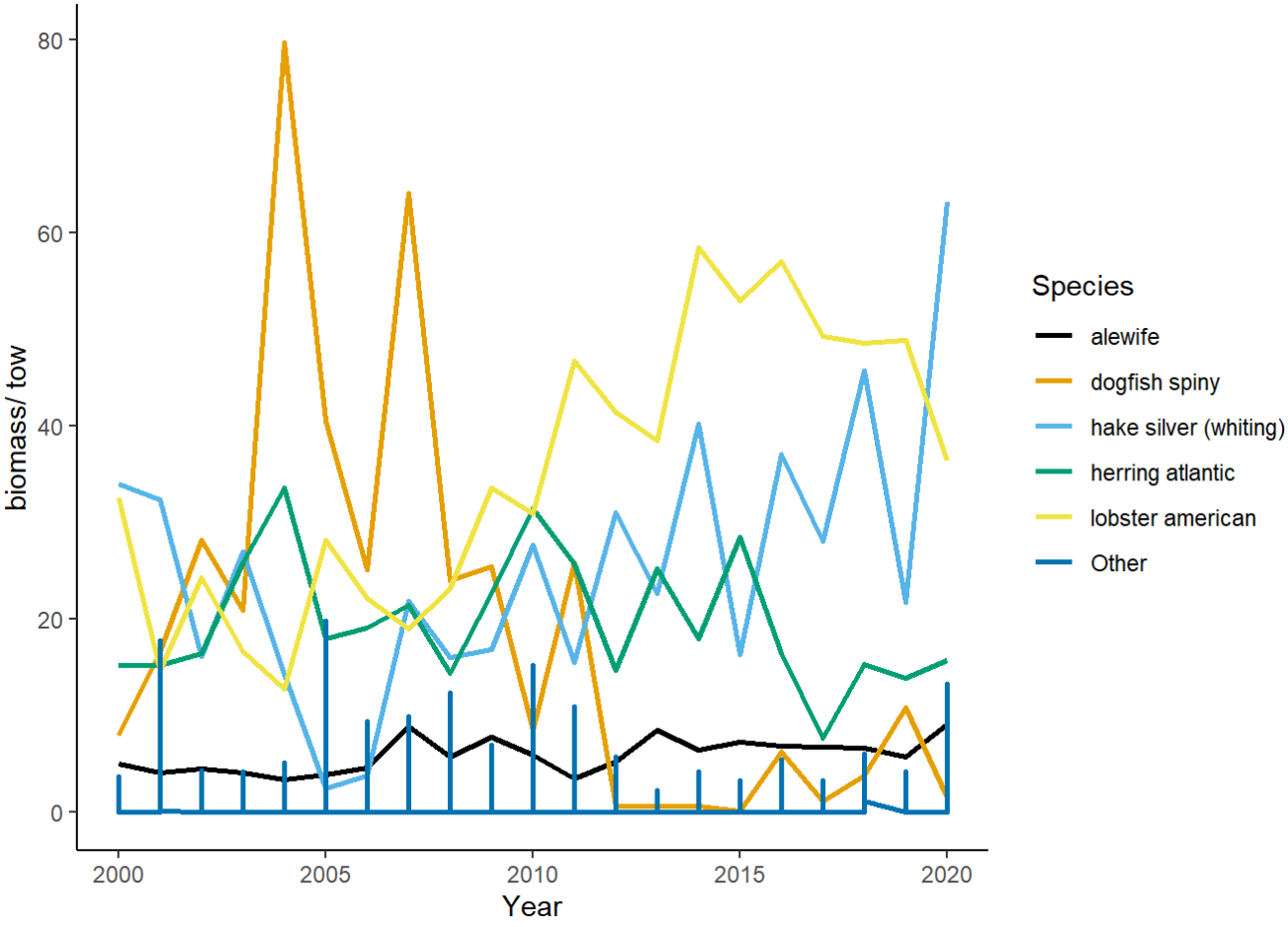
Jerelle Jesse (jjesse@gmri.org (mailto:jjesse@gmri.org))

Maine-New Hampshire Inshore Trawl

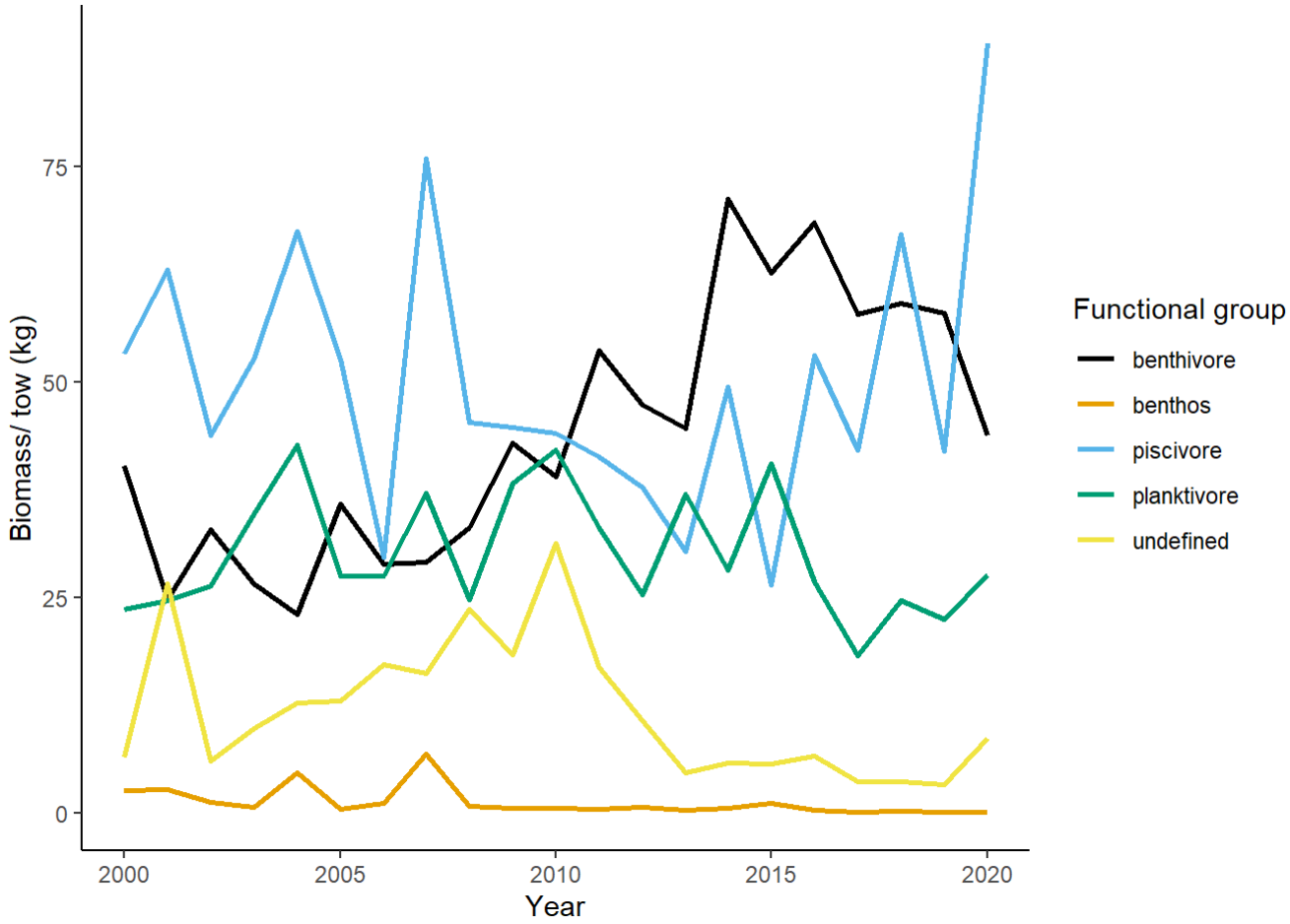
Trawl plots

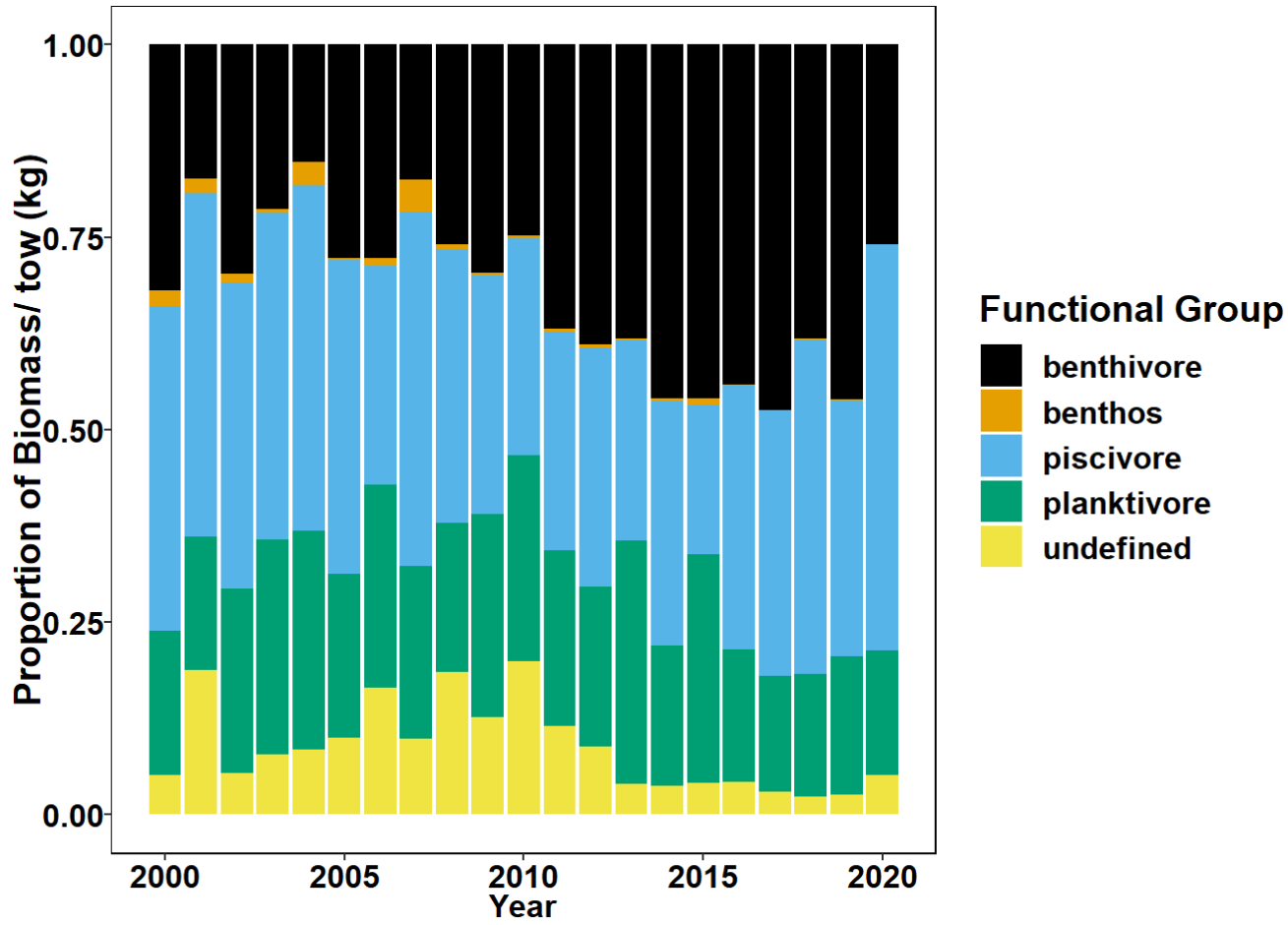
Top 5 species

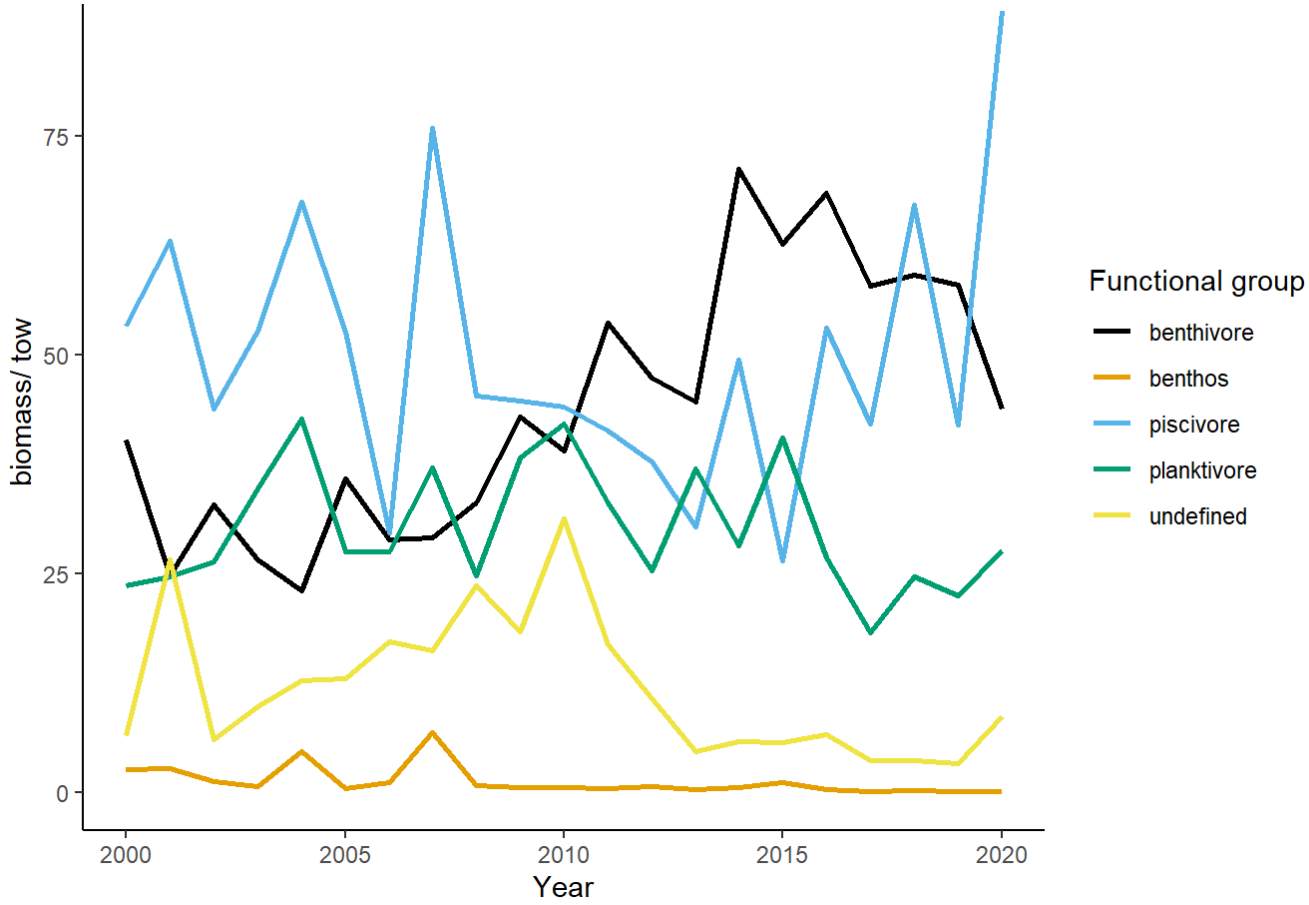

Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
alewife
dogfish spiny
hake silver (whiting)
herring atlantic
lobster american
Other


biomass/ tow
80
60
40
20
0
2000
2005
2010
2015
2020
Year
Species
alewife
dogfish spiny
hake silver (whiting)
herring atlantic
lobster american
Other

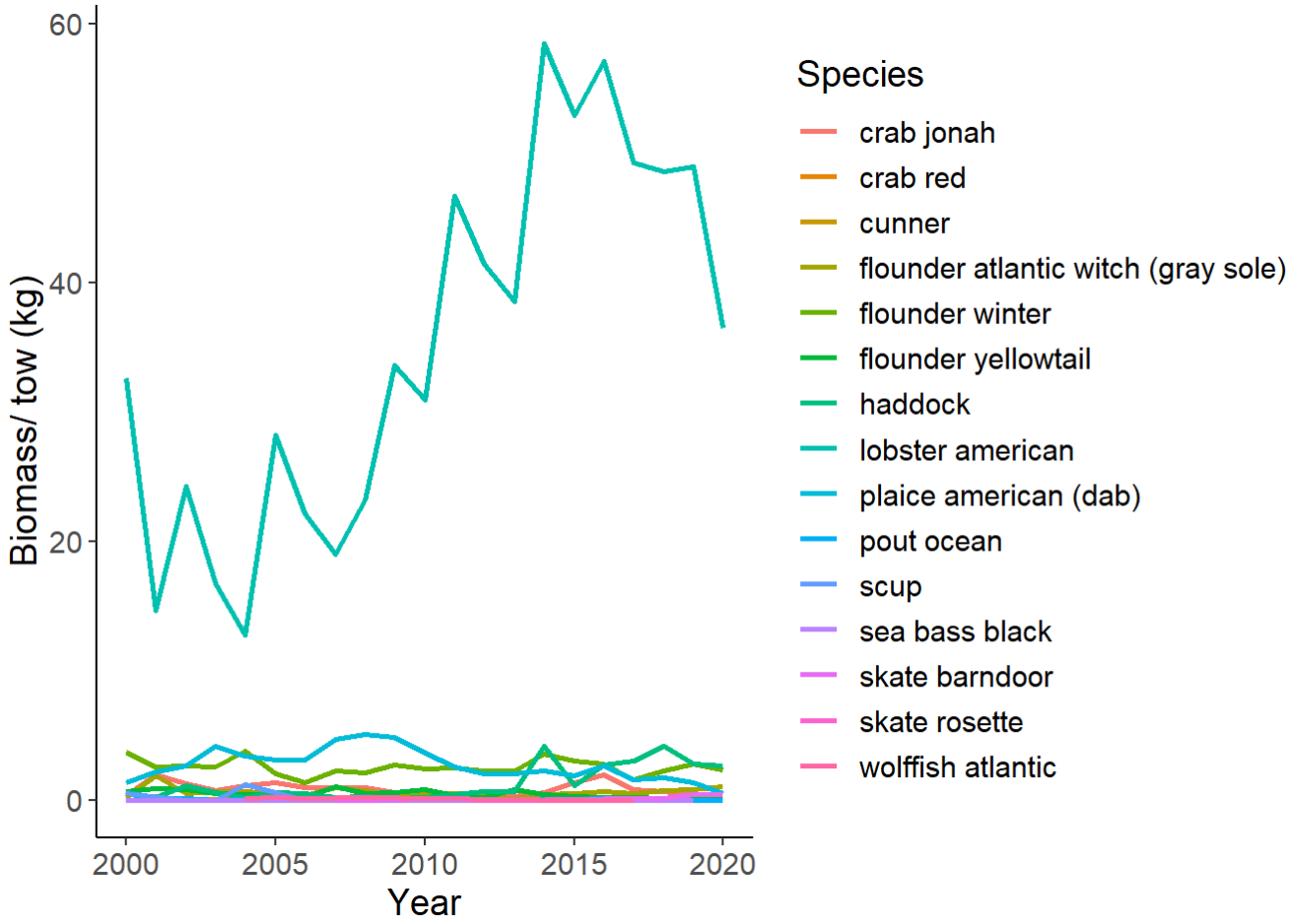
Functional Groups

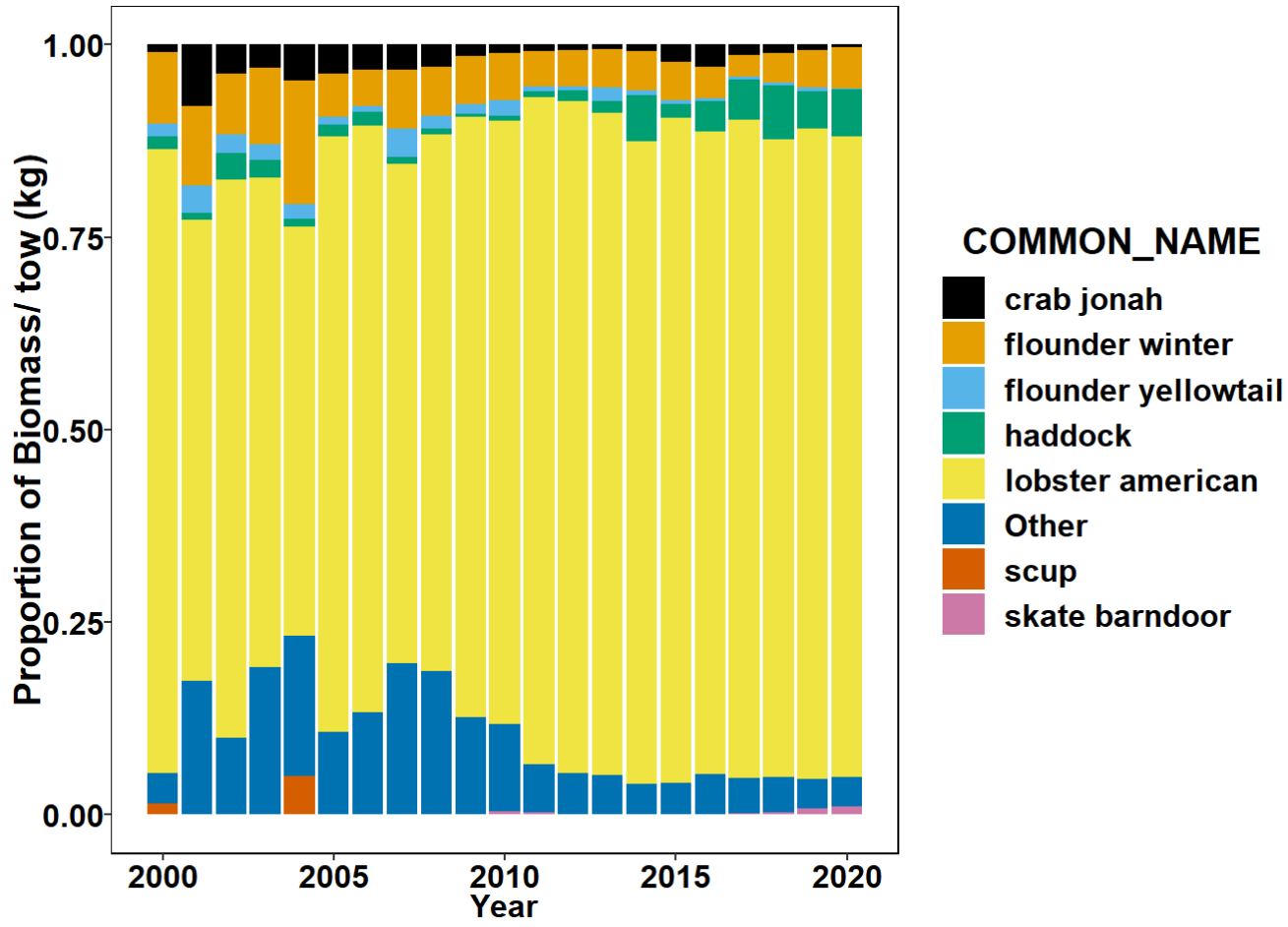

Biomass/ tow (kg)
75
50
25
0
2000
2005
2010
2015
2020
Year
Functional group
benthivore
benthos
piscivore
planktivore
undefined


Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
Functional Group
benthivore
benthos
piscivore
planktivore
undefined

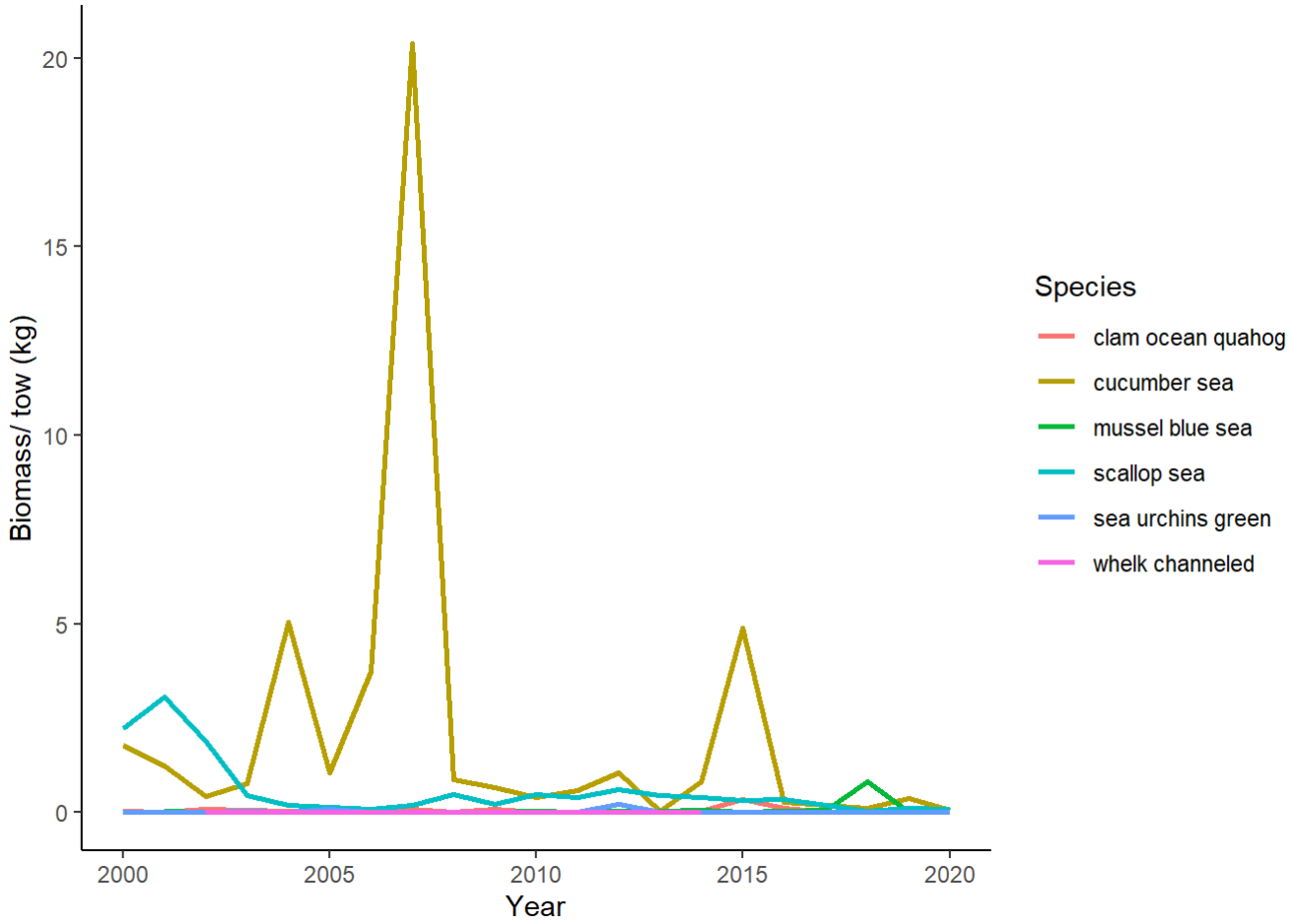

biomass/ tow
75
50
25
0
2000
2005
2010
2015
2020
Year
Functional group
benthivore
benthos
piscivore
planktivore
undefined

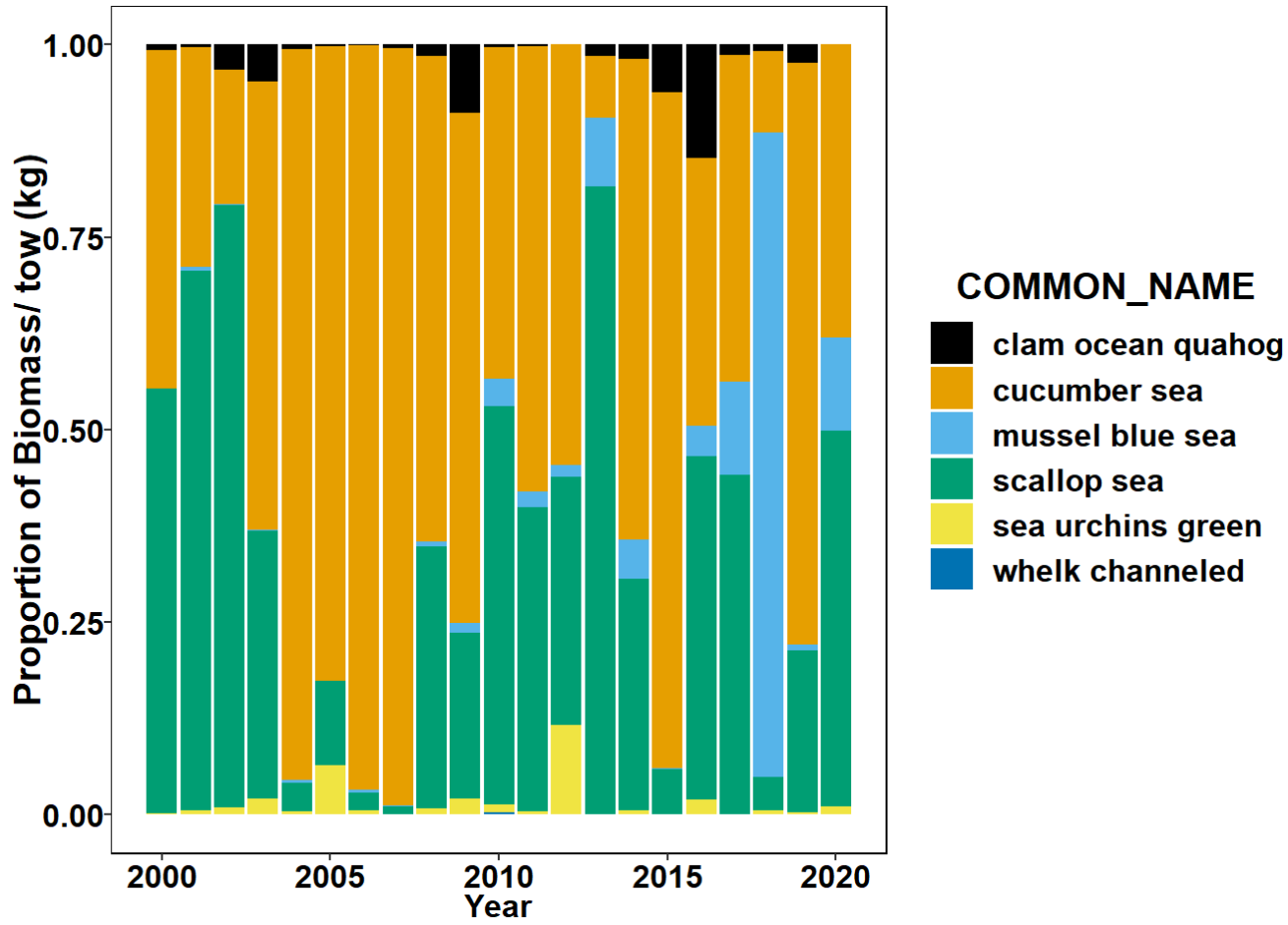
Benthivore


Biomass/ tow (kg)
60
40
20
0
2000
2005
2010
2015
2020
Year
Species
crab jonah
crab red
cunner
flounder atlantic witch (gray sole)
flounder winter
flounder yellowtail
haddock
lobster american
plaice american (dab)
pout ocean
scup
sea bass black
skate barndoor
skate rosette
wolffish atlantic

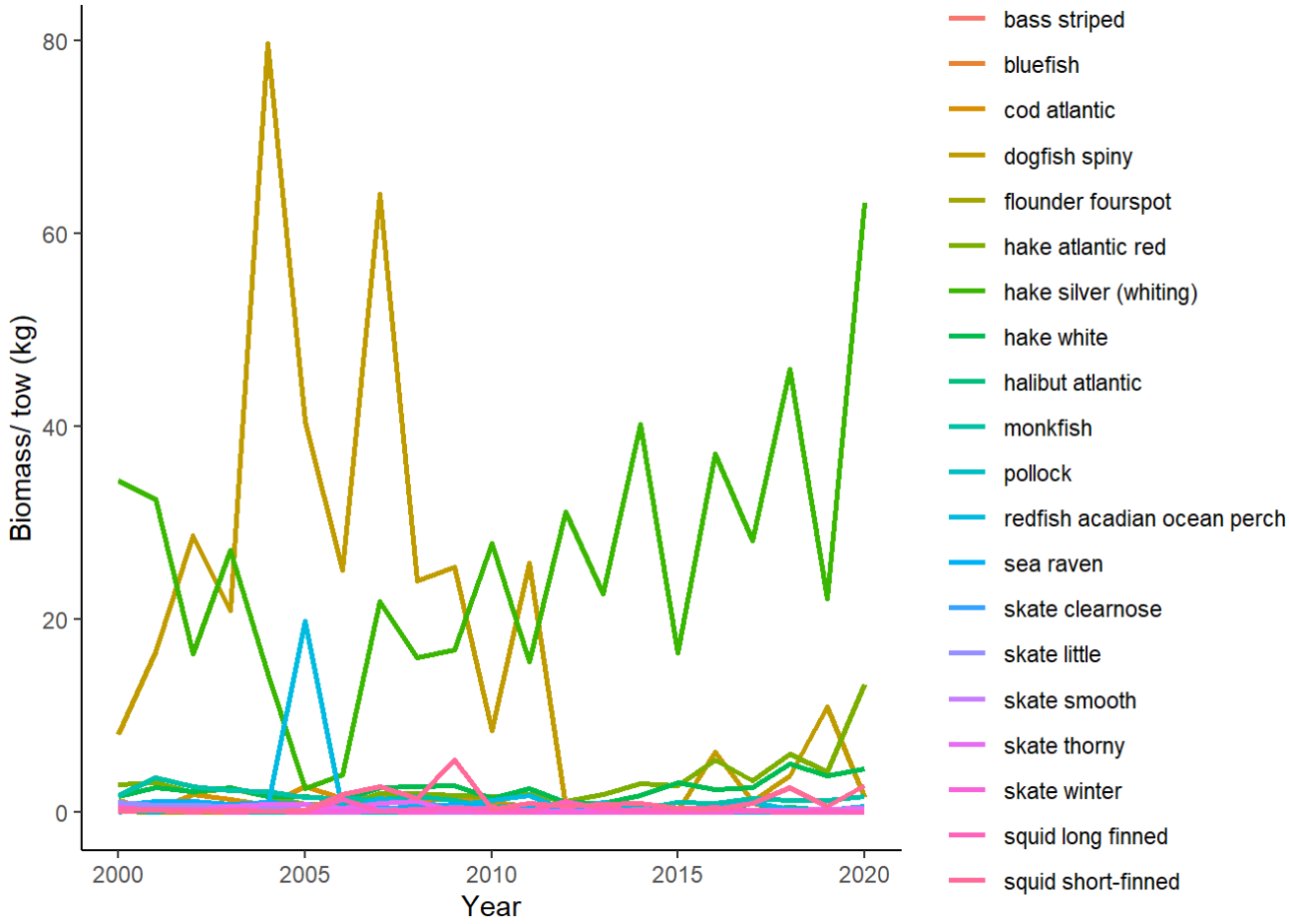

Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
crab jonah
flounder winter
flounder yellowtail
haddock
lobster american
Other
scup
skate barndoor

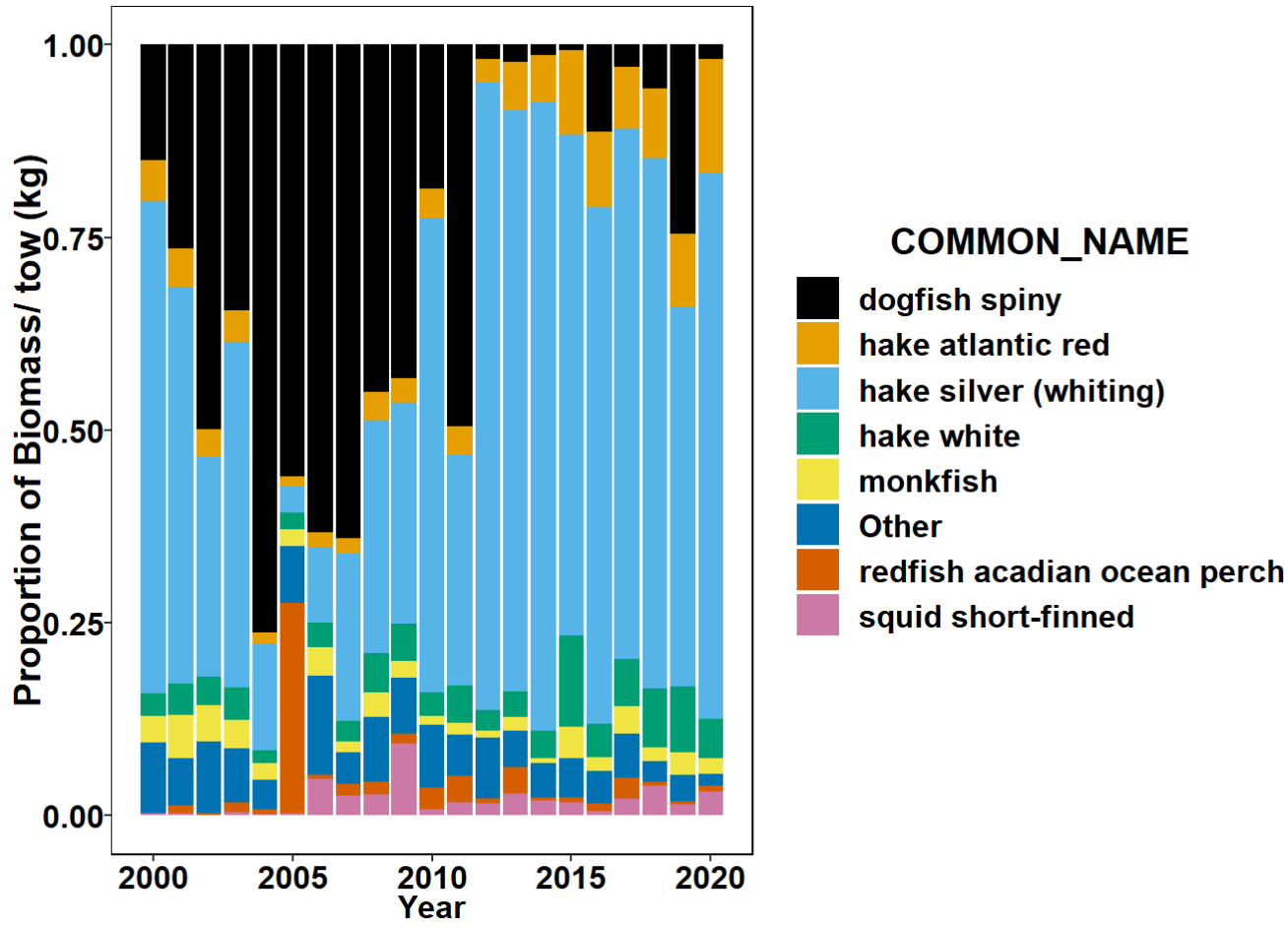
Benthos


Biomass/ tow (kg)
20
15
10
5
0
2000
2005
2010
2015
2020
Year
Species
clam ocean quahog
cucumber sea
mussel blue sea
scallop sea
sea urchins green
whelk channeled

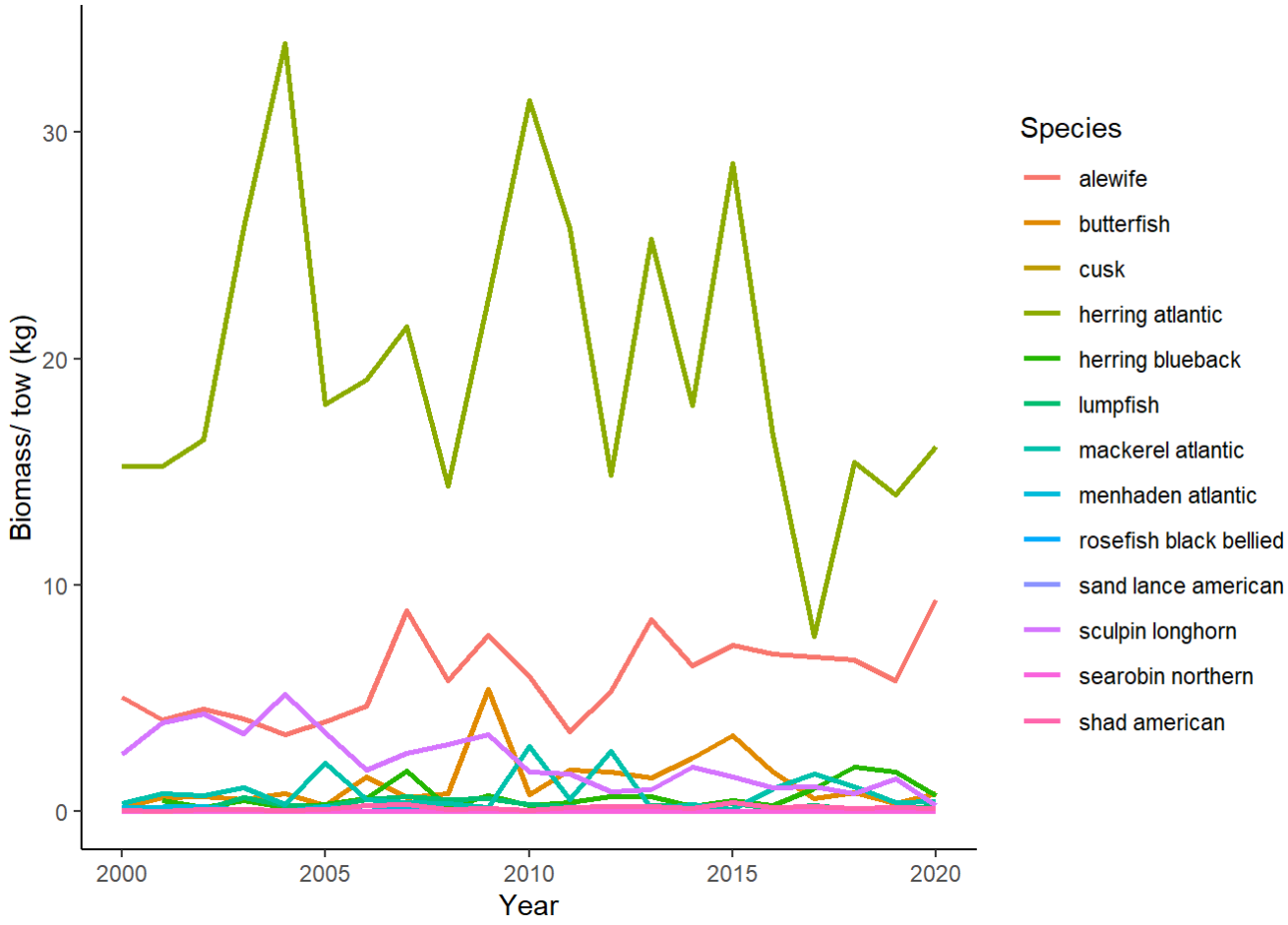

Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
clam ocean quahog
cucumber sea
mussel blue sea
scallop sea
sea urchins green
whelk channeled

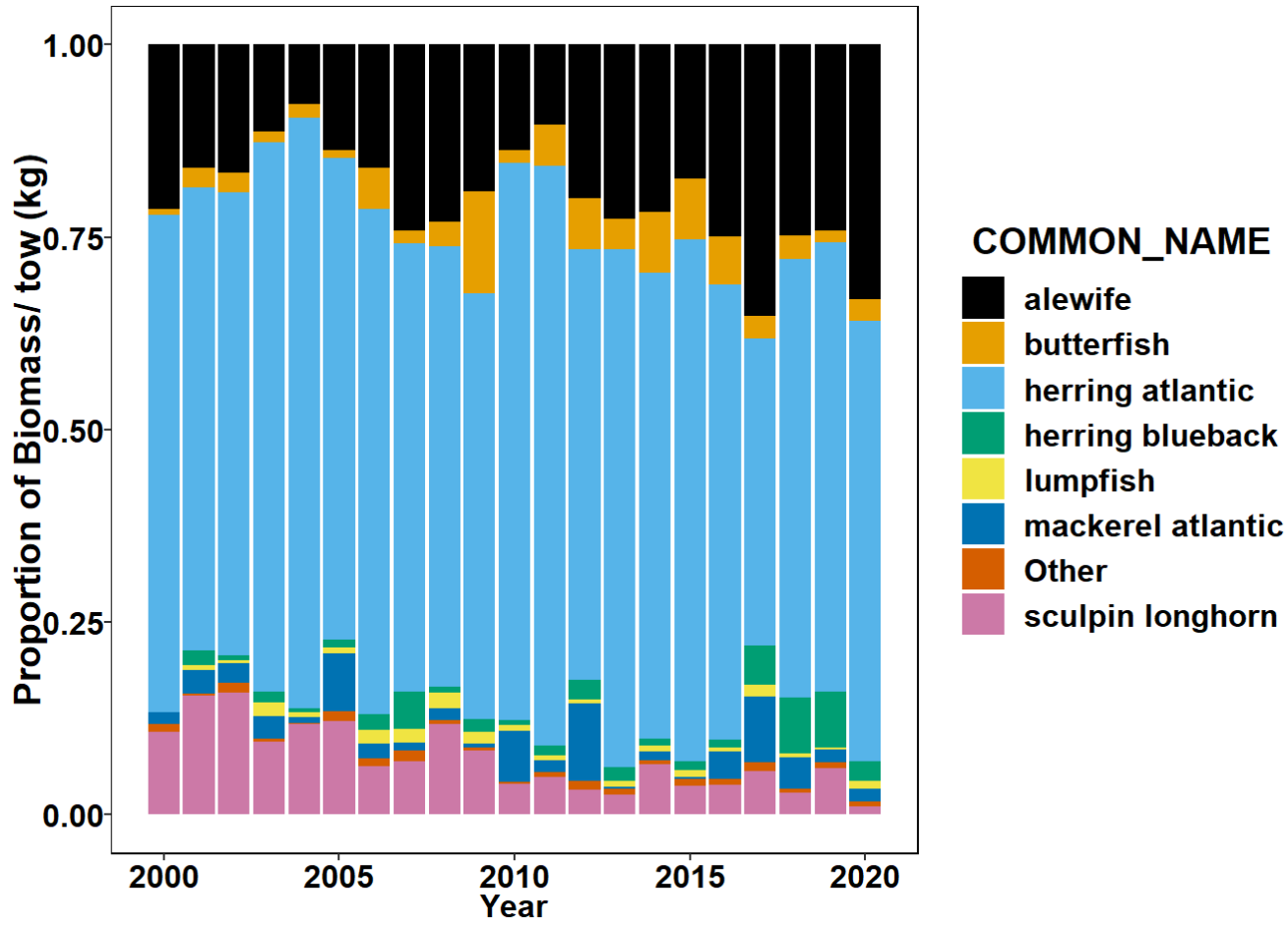
Piscivore


Biomass/ tow (kg)
80
60
40
20
0
2000
2005
2010
2015
2020
Year
bass striped
bluefish
cod atlantic
dogfish spiny
flounder fourspot
hake atlantic red
hake silver (whiting)
hake white
halibut atlantic
monkfish
pollock
redfish acadian ocean perch
sea raven
skate clearnose
skate little
skate smooth
skate thorny
skate winter
squid long finned
squid short-finned


Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
dogfish spiny
hake atlantic red
hake silver (whiting)
hake white
monkfish
Other
redfish acadian ocean perch
squid short-finned

Planktivore

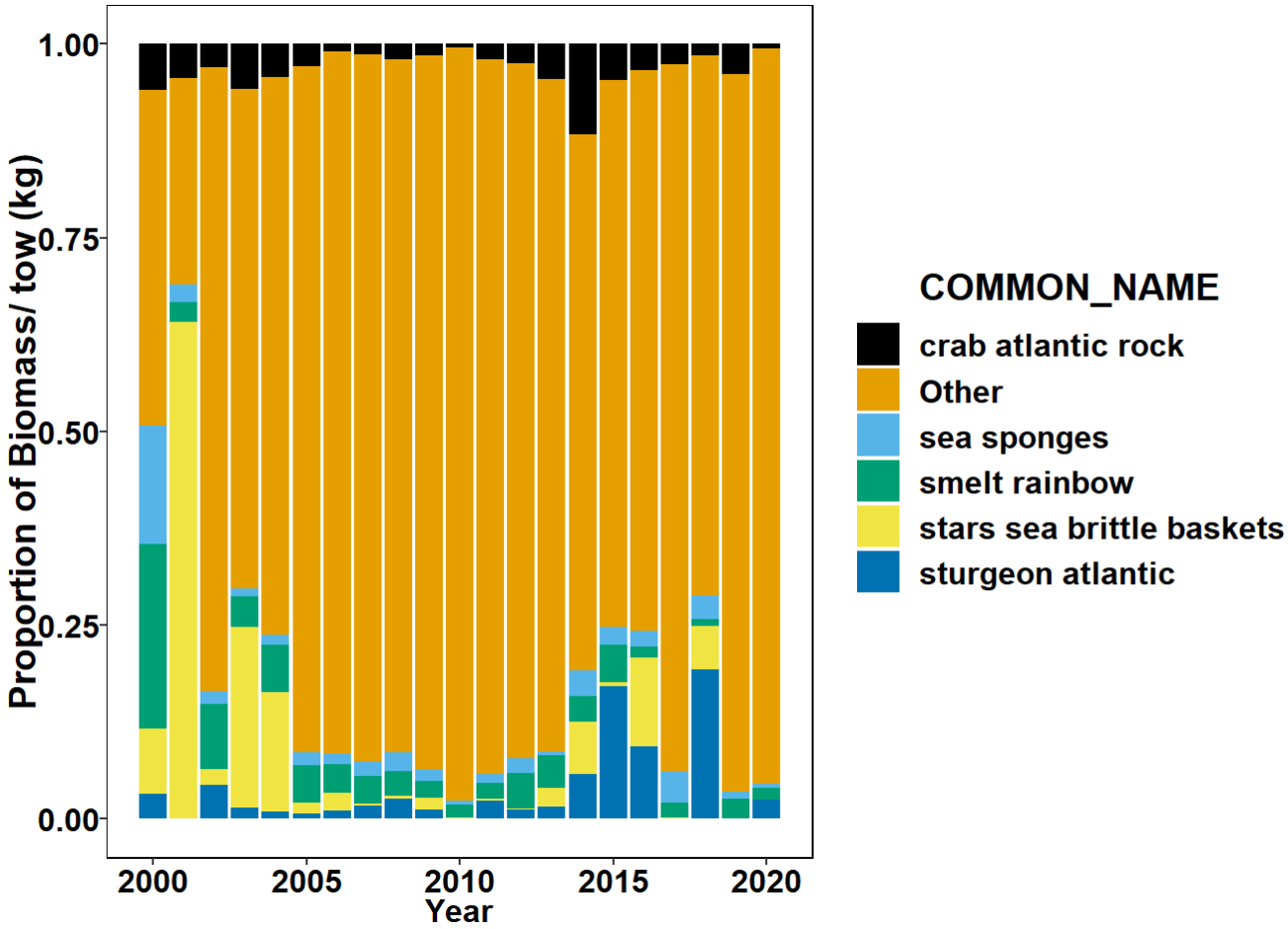

Biomass/ tow (kg)
30
20
10
0
2000
2005
2010
2015
2020
Year
Species
alewife
butterfish
cusk
herring atlantic
herring blueback
lumpfish
mackerel atlantic
menhaden atlantic
rosefish black bellied
sand lance american
sculpin longhorn
searobin northern
shad american


Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
alewife
butterfish
herring atlantic
herring blueback
lumpfish
mackerel atlantic
Other
sculpin longhorn

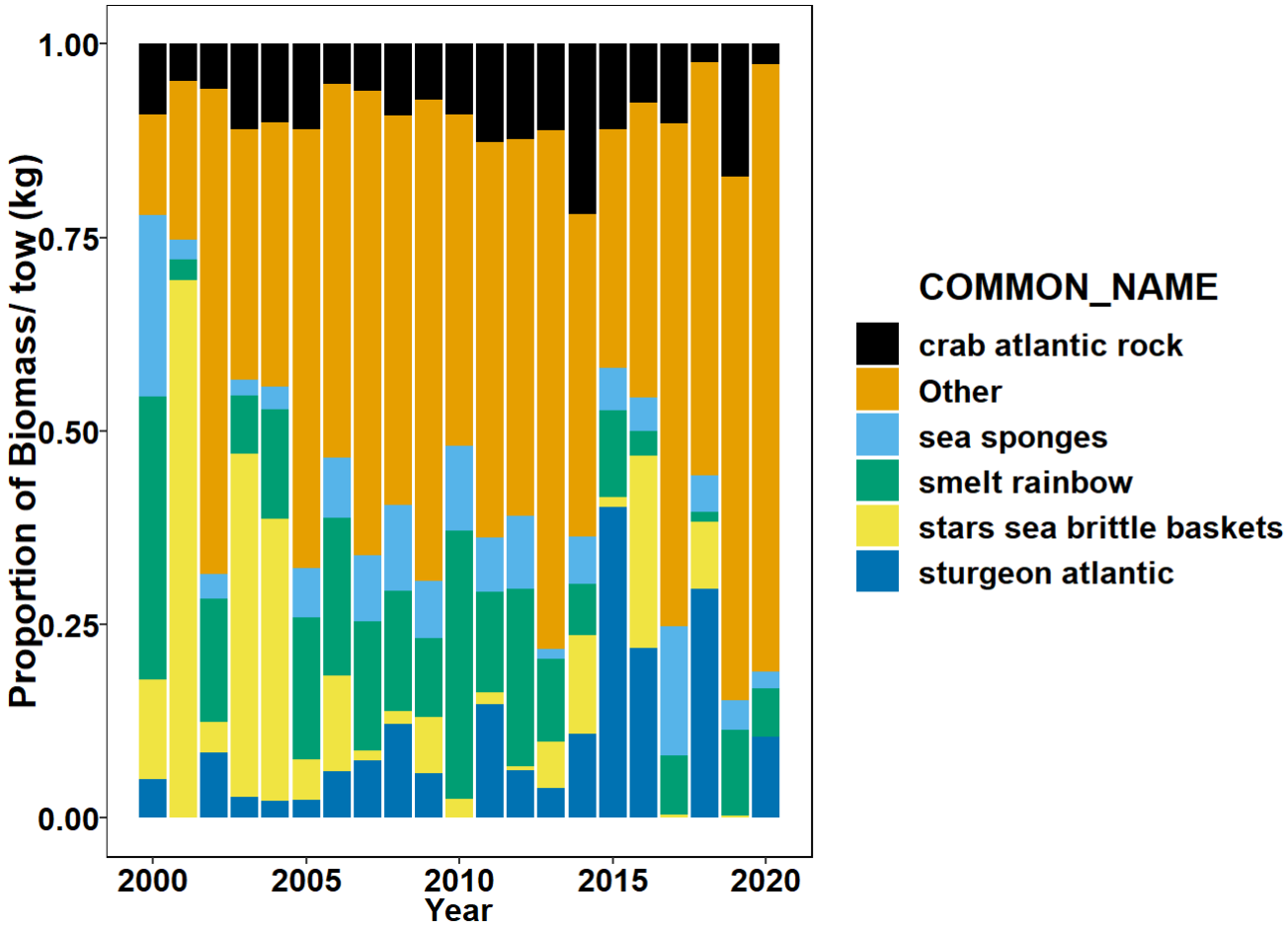
Undefined

Y… <int>	COMMON_NAME <chr>	weight_prop <dbl>	catch_prop <dbl>
2000	alligatorfish	3.258388e-03	3.395207e-01
2000	barnacle	1.396825e-02	3.809524e-02
2000	buckler dory	6.060606e-04	1.212121e-02
2000	clam ax-head	5.925926e-03	1.333333e-01
2000	clam false quahog	1.481481e-04	1.481481e-02
2000	crab atlantic rock	4.008321e-01	2.960901e+00
2000	crab green	6.666667e-04	1.333333e-02
2000	crab snow	1.031169e-02	8.259740e-02
2000	crab spider uncl	2.800000e-03	2.666667e-02
2000	crab toad	6.132718e-03	3.439509e-01

1-10 of 1,223 rows Previous **1** 2 3 4 5 6 … 123 Next


1.00
0.75
0.50
0.25
0.00
Proportion of Biomass/ tow (kg)
2000
2005
2010
2015
2020
Year
COMMON_NAME
crab atlantic rock
Other
sea sponges
smelt rainbow
stars sea brittle baskets
sturgeon atlantic

No shrimp


Proportion of Biomass/ tow (kg)
1.00
0.75
0.50
0.25
0.00
2000
2005
2010
2015
2020
Year
COMMON_NAME
crab atlantic rock
Other
sea sponges
smelt rainbow
stars sea brittle baskets
sturgeon atlantic

Nonmetric Multidimensional Scaling- Top 50 biomass species

Data

- Top 50 biomass species
- average across depth strata using the NOAA IEA technical document (https://noaa-edab.github.io/tech-doc/inshoresurvdat.html#data-analysis-29)

	Sea… <chr>	Reg… <int>	Y… <int>	alewife <dbl>	bass.striped <dbl>	butterfish <dbl>	cod.atlantic <dbl>	crab.atlantic.rock <dbl>
1	Fall	1	2000	5.380384	0	0.3518519	1.9828704	0.2225000
2	Fall	1	2001	11.422884	0	2.8428307	0.3520811	2.8416667
3	Fall	1	2002	4.145476	0	3.3043183	2.2230952	0.0600000
4	Fall	1	2003	4.924375	0	3.5231250	10.3700000	0.0000000
5	Fall	1	2004	6.528253	0	3.2305702	4.6161111	0.0000000
6	Fall	1	2005	3.781491	0	0.7742105	13.4031579	0.2315789

6 rows | 1-10 of 59 columns

Set up data for NMDS

- split community matrix into two dataframes- one for grouping variables and one for species biomass
- calculate dissimilarity matrix with Bray-Curtis distances

```
#set up final grouping data into dataframe
ME_group_data<-trawl_data_arrange[, c(1,2,3,55,56,57,58)]
ME_NMDS_data<-as.matrix(trawl_data_arrange[,4:53])

#calculate distance matrix
ME_NMDS_distance<- vegdist(ME_NMDS_data, method="bray")
```

Run the NMDS and extract scores

- change in community composition
- uses rank order
- stress < 0.2 is good, < 0.1 is great, <0.05 is excellent representation in reduced dimensions

```
ME_NMDS=metaMDS(ME_NMDS_distance, # Our community-by-species matrix
                k=2, # The number of reduced dimensions
                method="bray",
                trymax=200) #increase iterations
```

```
## Run 0 stress 0.2121976
## Run 1 stress 0.2057908
## ... New best solution
## ... Procrustes: rmse 0.03260853  max resid 0.3907521
## Run 2 stress 0.207885
## Run 3 stress 0.2066022
## Run 4 stress 0.2126567
## Run 5 stress 0.2117096
## Run 6 stress 0.2090653
## Run 7 stress 0.2127132
## Run 8 stress 0.2061185
## ... Procrustes: rmse 0.008997804  max resid 0.07750829
## Run 9 stress 0.2120618
## Run 10 stress 0.2121856
## Run 11 stress 0.2061184
## ... Procrustes: rmse 0.008992806  max resid 0.07749652
## Run 12 stress 0.2064777
## Run 13 stress 0.2058398
## ... Procrustes: rmse 0.003094323  max resid 0.03803567
## Run 14 stress 0.2078695
## Run 15 stress 0.2135671
## Run 16 stress 0.2061183
## ... Procrustes: rmse 0.008977382  max resid 0.07733821
## Run 17 stress 0.2118637
## Run 18 stress 0.2065612
## Run 19 stress 0.2124997
## Run 20 stress 0.2065748
## Run 21 stress 0.2133277
## Run 22 stress 0.2057111
## ... New best solution
## ... Procrustes: rmse 0.00395844  max resid 0.03825867
## Run 23 stress 0.2120847
## Run 24 stress 0.2063852
## Run 25 stress 0.2061811
## ... Procrustes: rmse 0.01033487  max resid 0.08282011
## Run 26 stress 0.2129884
## Run 27 stress 0.20681
## Run 28 stress 0.2139782
## Run 29 stress 0.2057848
## ... Procrustes: rmse 0.002541256  max resid 0.0229569
## Run 30 stress 0.2123711
## Run 31 stress 0.2120959
## Run 32 stress 0.2090882
## Run 33 stress 0.2065496
## Run 34 stress 0.2314908
## Run 35 stress 0.2078696
## Run 36 stress 0.2078851
## Run 37 stress 0.2065612
## Run 38 stress 0.2064649
## Run 39 stress 0.2068109
## Run 40 stress 0.2068101
## Run 41 stress 0.2066023
## Run 42 stress 0.2228289
```

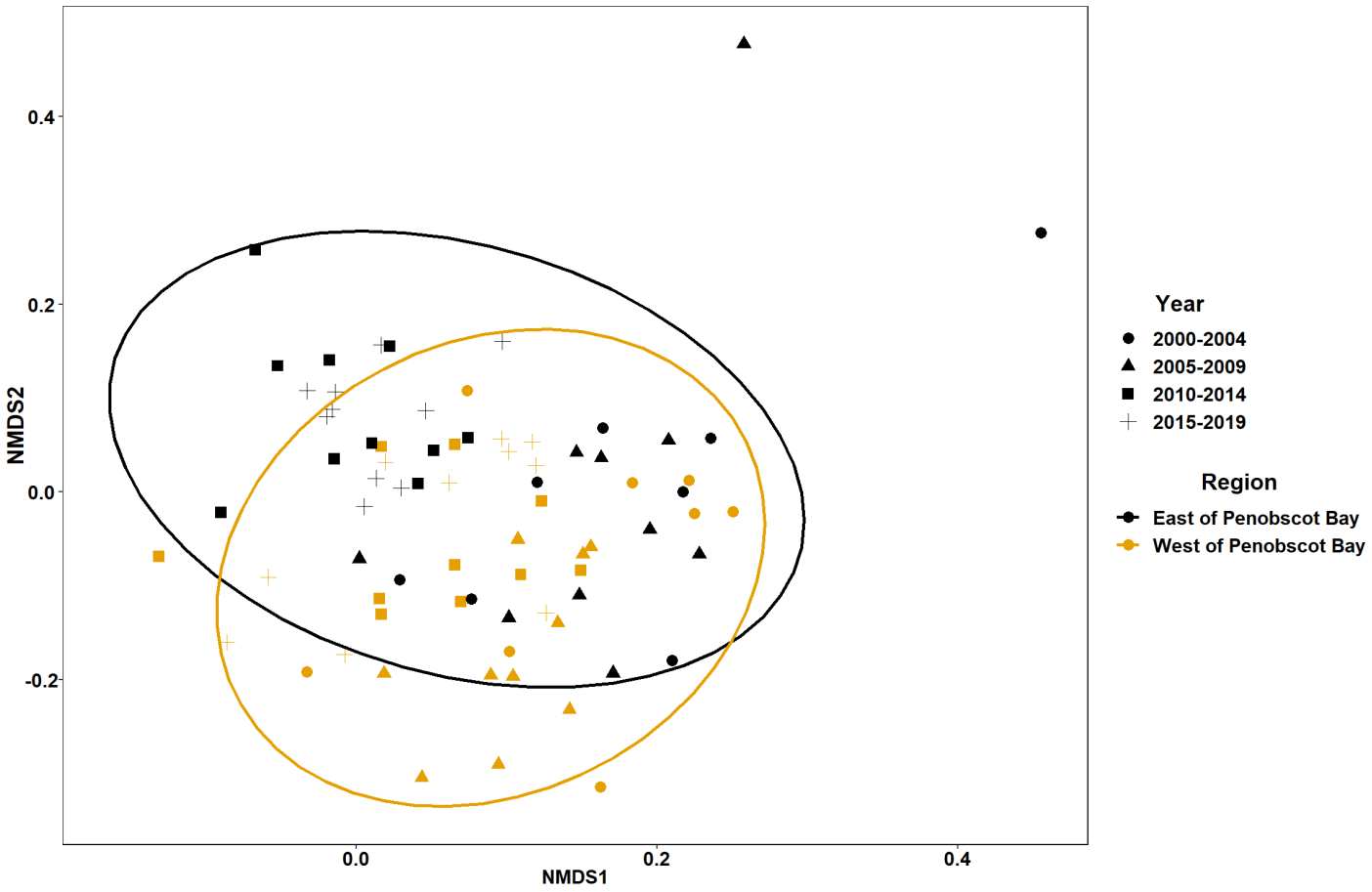
```
## Run 43 stress 0.2117409
## Run 44 stress 0.2346884
## Run 45 stress 0.2065999
## Run 46 stress 0.2065853
## Run 47 stress 0.2065871
## Run 48 stress 0.20787
## Run 49 stress 0.4165635
## Run 50 stress 0.206812
## Run 51 stress 0.2063172
## Run 52 stress 0.212956
## Run 53 stress 0.2273767
## Run 54 stress 0.2121424
## Run 55 stress 0.2131374
## Run 56 stress 0.2090879
## Run 57 stress 0.2286814
## Run 58 stress 0.2063667
## Run 59 stress 0.2220723
## Run 60 stress 0.2063955
## Run 61 stress 0.2063136
## Run 62 stress 0.229283
## Run 63 stress 0.2078751
## Run 64 stress 0.2064627
## Run 65 stress 0.2126292
## Run 66 stress 0.2061264
## ... Procrustes: rmse 0.007105145  max resid 0.07700621
## Run 67 stress 0.2120917
## Run 68 stress 0.2129648
## Run 69 stress 0.206487
## Run 70 stress 0.2061524
## ... Procrustes: rmse 0.00734878  max resid 0.07782809
## Run 71 stress 0.2060866
## ... Procrustes: rmse 0.00739737  max resid 0.0739193
## Run 72 stress 0.416565
## Run 73 stress 0.2120858
## Run 74 stress 0.2302658
## Run 75 stress 0.2065616
## Run 76 stress 0.2145424
## Run 77 stress 0.2065613
## Run 78 stress 0.2117192
## Run 79 stress 0.2065547
## Run 80 stress 0.2078697
## Run 81 stress 0.2138939
## Run 82 stress 0.2064631
## Run 83 stress 0.2068108
## Run 84 stress 0.2120437
## Run 85 stress 0.2283524
## Run 86 stress 0.2057105
## ... New best solution
## ... Procrustes: rmse 0.0002644395  max resid 0.00239894
## ... Similar to previous best
## *** Solution reached
```

```
#extract NMDS scores for ggplot
data.scores = as.data.frame(scores(ME_NMDS))
#add columns to data frame
data.scores$Stratum = trawl_data_arrange$Stratum
data.scores$Region = trawl_data_arrange$Region
data.scores$Year = trawl_data_arrange$Year
data.scores$Season= trawl_data_arrange$Season
data.scores$Year_groups= trawl_data_arrange$YEAR_GROUPS
data.scores$Year_decades= trawl_data_arrange$YEAR_DECADES
data.scores$Region_new=trawl_data_arrange$REGION_NEW
data.scores$Region_year=trawl_data_arrange$REGION_YEAR
data.scores$Season_year=trawl_data_arrange$SEASON_YEAR
```

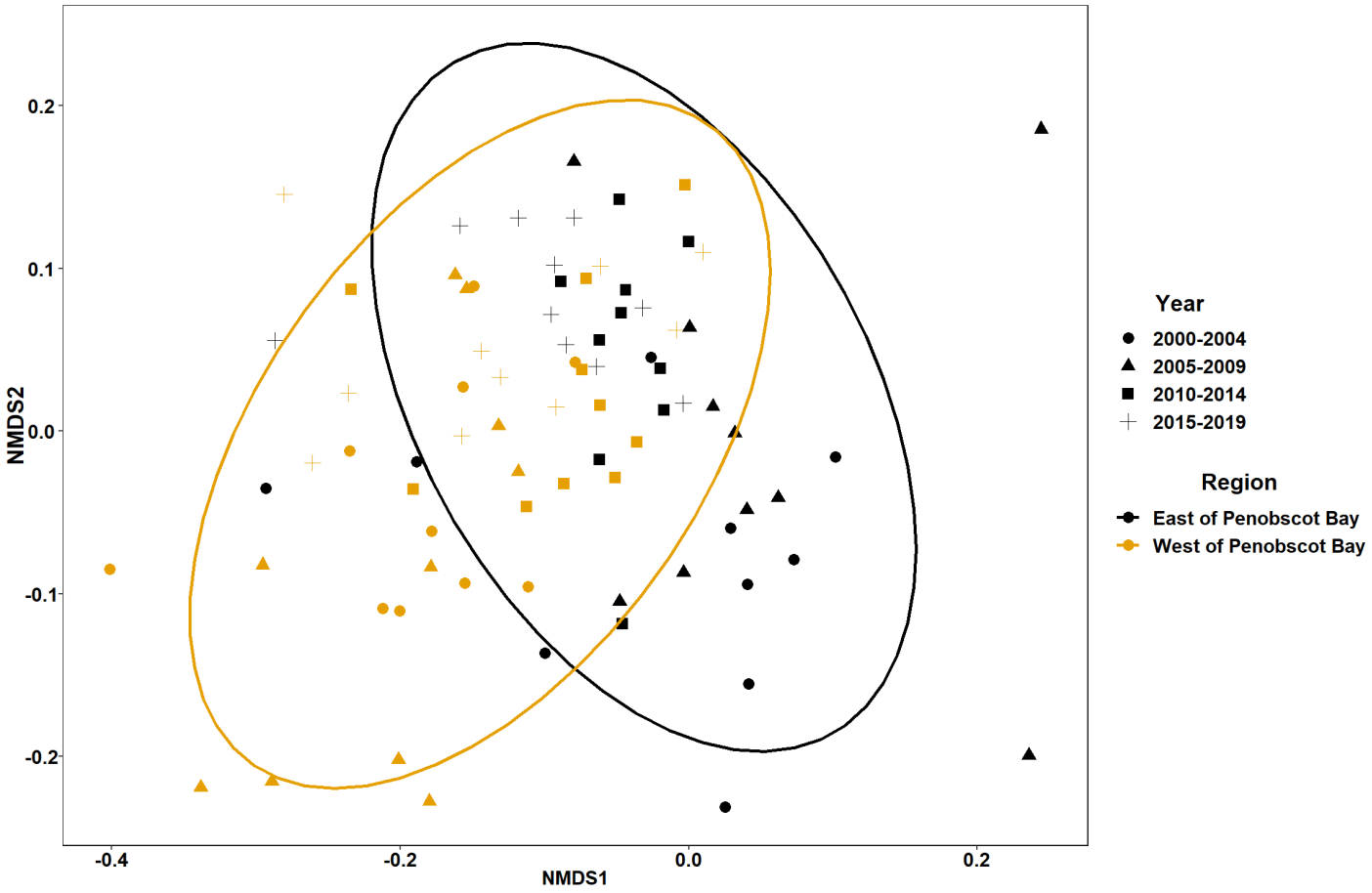
Plots

Region

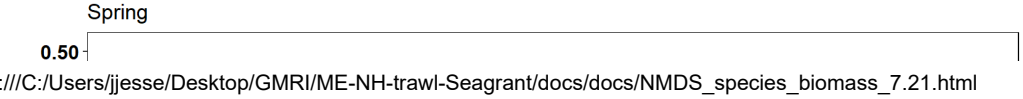
Spring

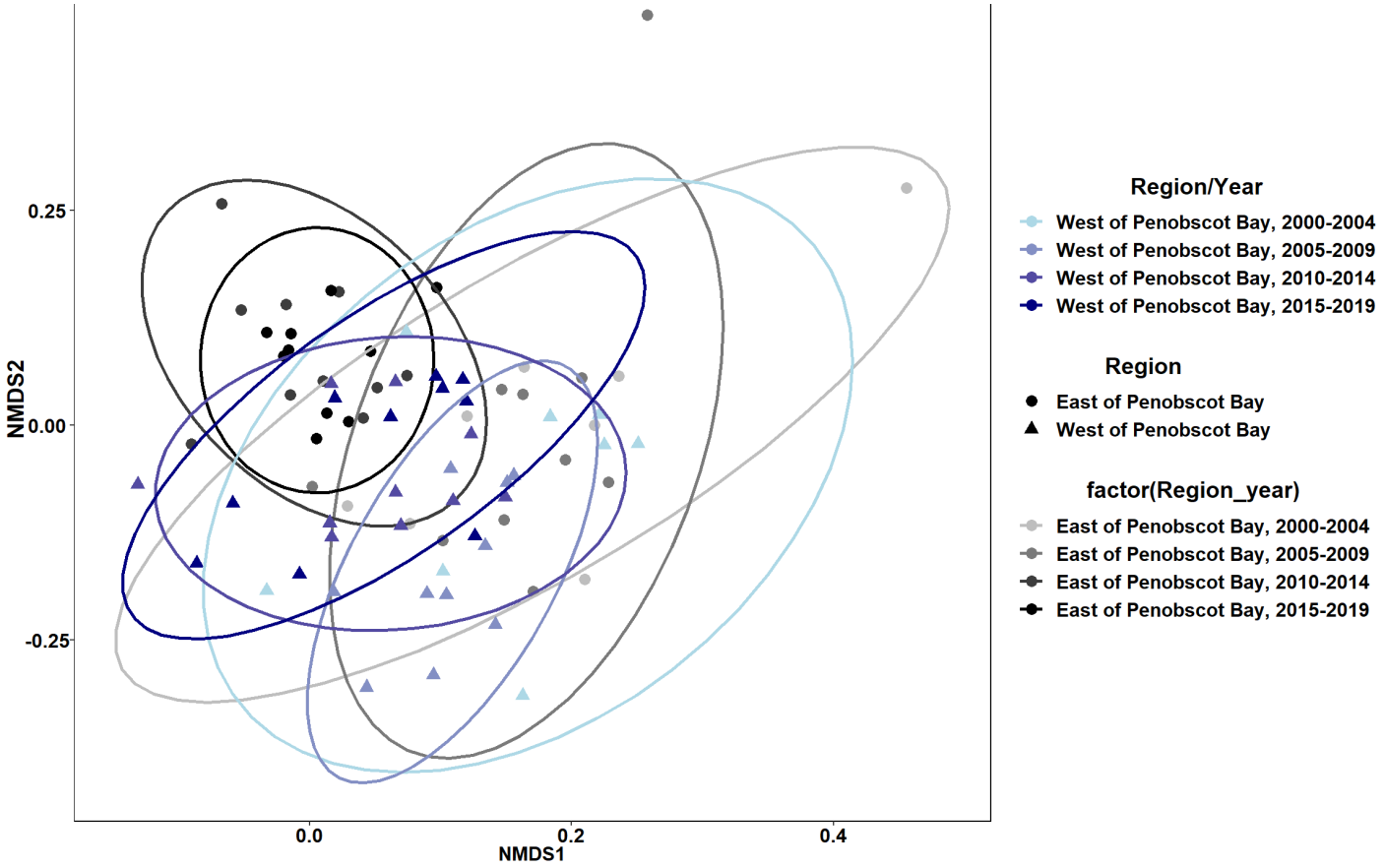


Fall

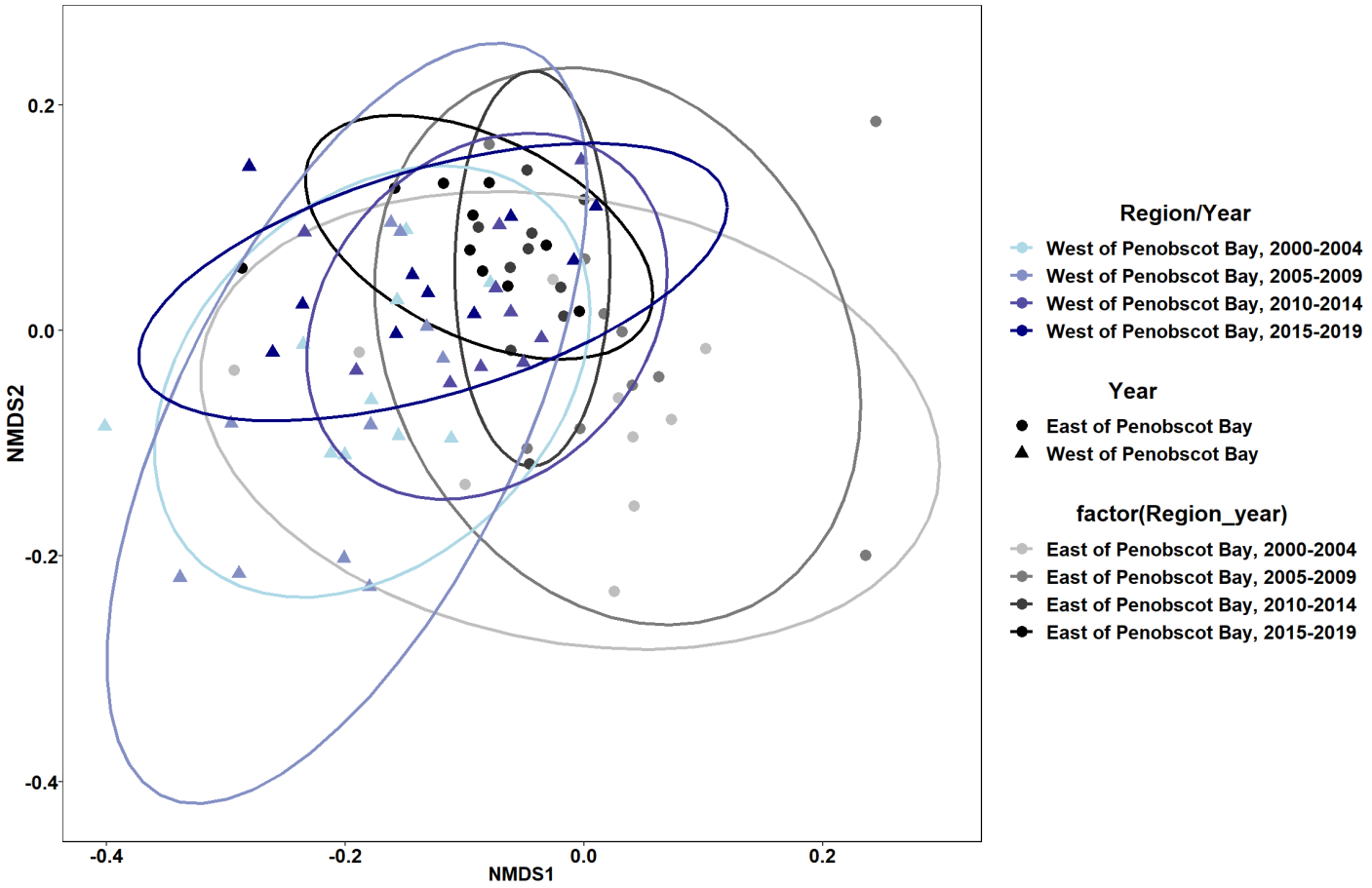


Spring



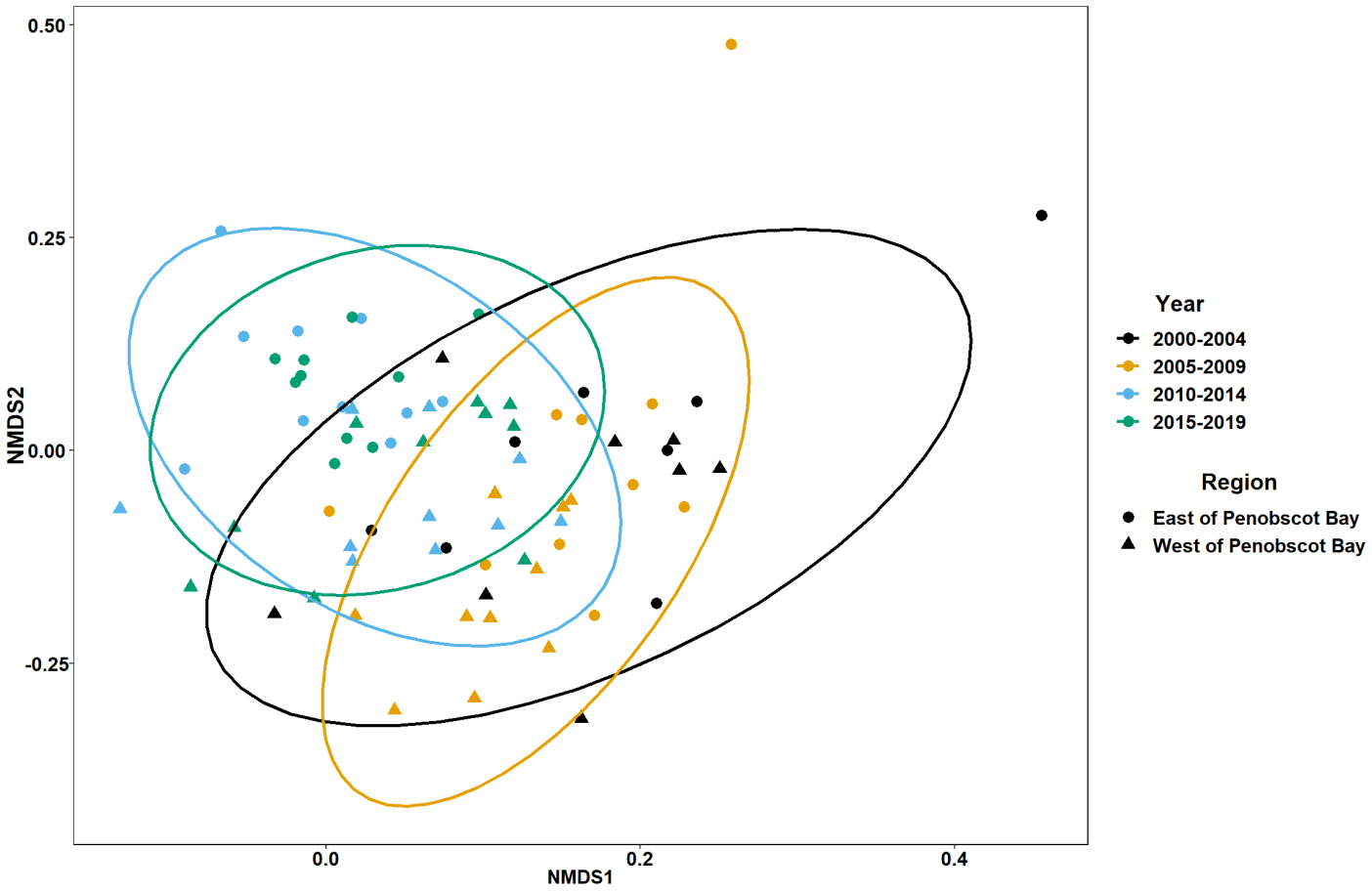

0.25
0.00
-0.25
NMDS2
0.0
0.2
0.4
NMDS1
Region/Year
West of Penobscot Bay, 2000-2004
West of Penobscot Bay, 2005-2009
West of Penobscot Bay, 2010-2014
West of Penobscot Bay, 2015-2019
Region
East of Penobscot Bay
West of Penobscot Bay
factor(Region_year)
East of Penobscot Bay, 2000-2004
East of Penobscot Bay, 2005-2009
East of Penobscot Bay, 2010-2014
East of Penobscot Bay, 2015-2019

Fall

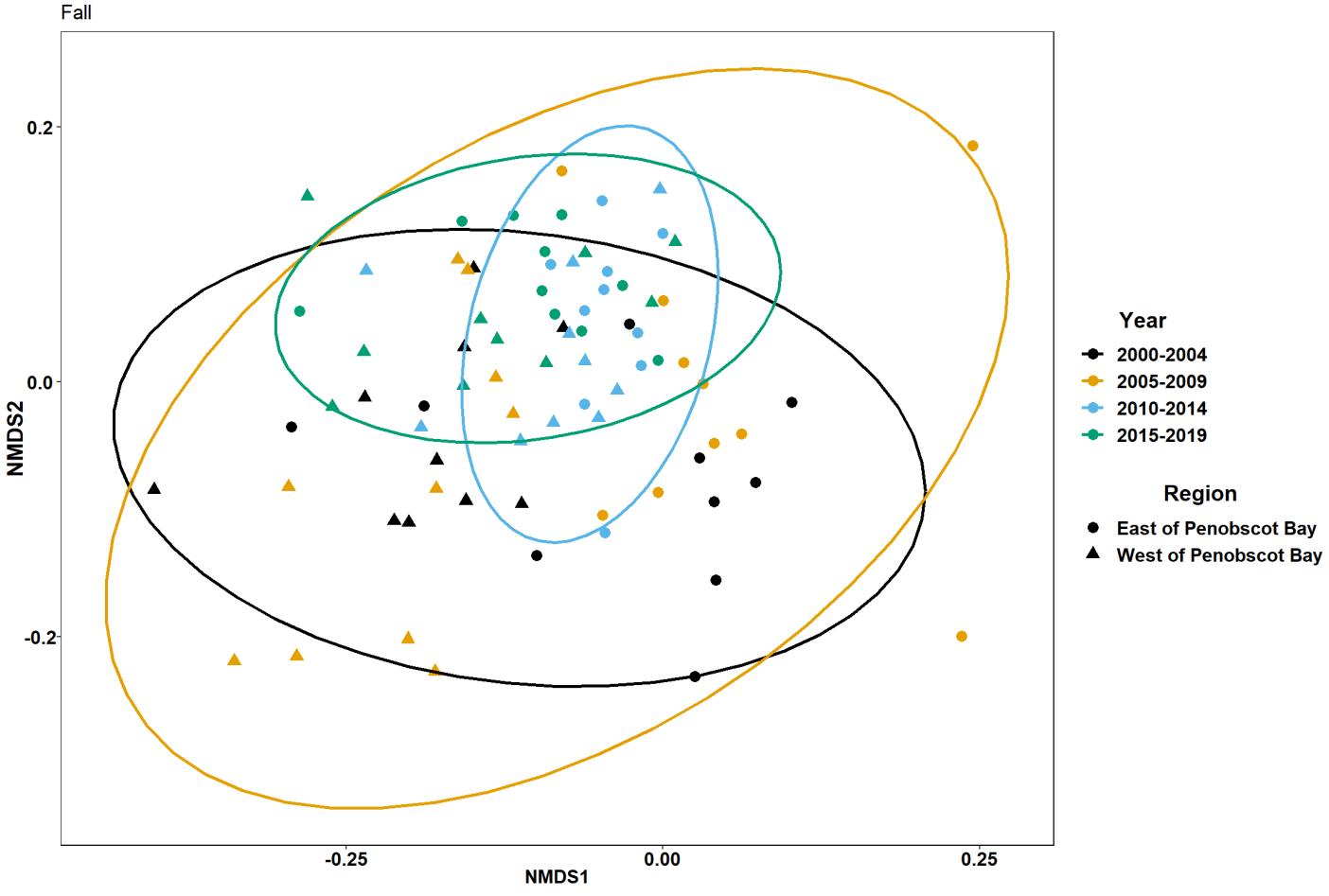

0.2
0.0
-0.2
-0.4
NMDS2
-0.4
-0.2
0.0
0.2
NMDS1
Region/Year
West of Penobscot Bay, 2000-2004
West of Penobscot Bay, 2005-2009
West of Penobscot Bay, 2010-2014
West of Penobscot Bay, 2015-2019
Year
East of Penobscot Bay
West of Penobscot Bay
factor(Region_year)
East of Penobscot Bay, 2000-2004
East of Penobscot Bay, 2005-2009
East of Penobscot Bay, 2010-2014
East of Penobscot Bay, 2015-2019

Time

Spring

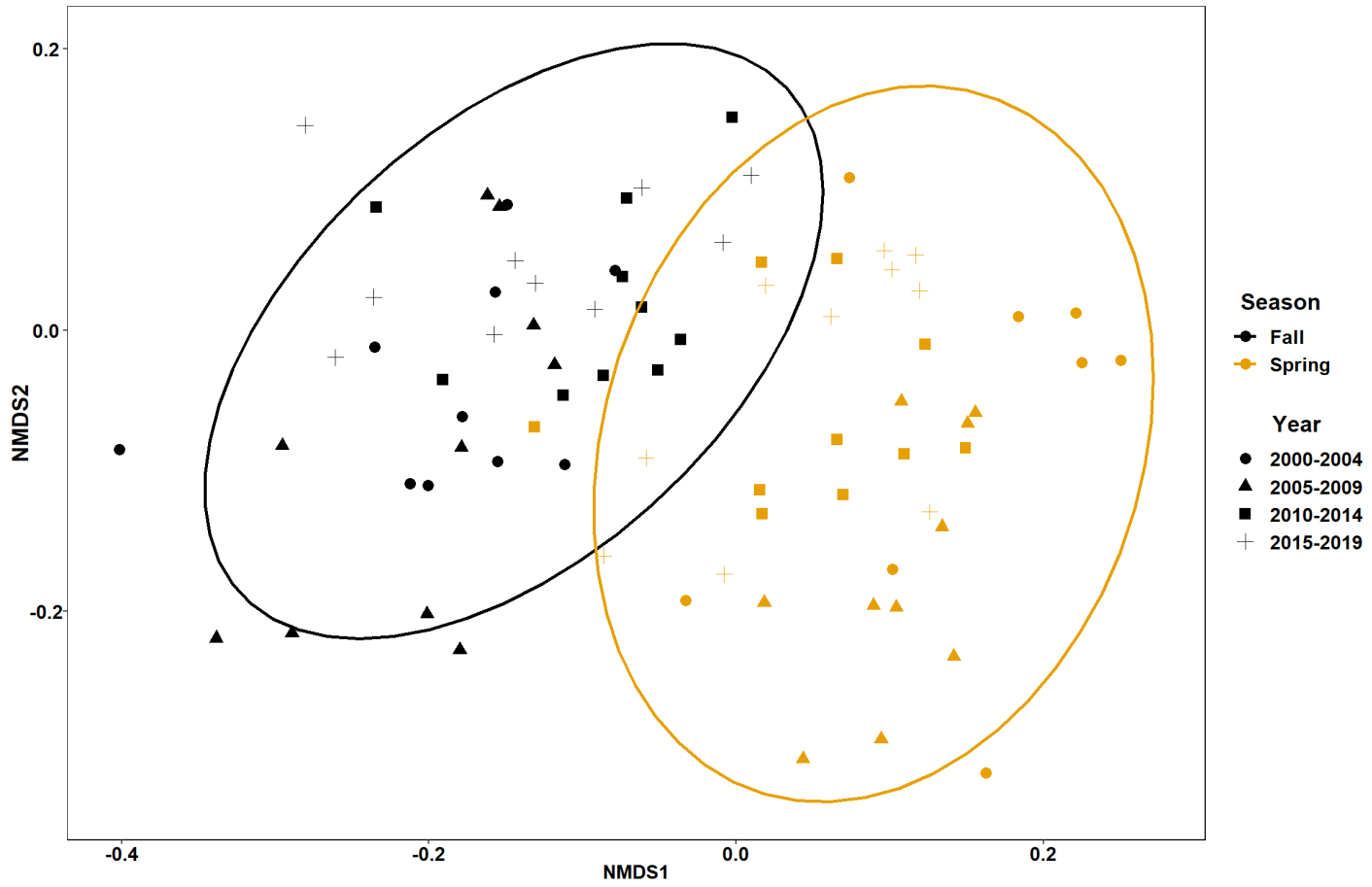


Fall

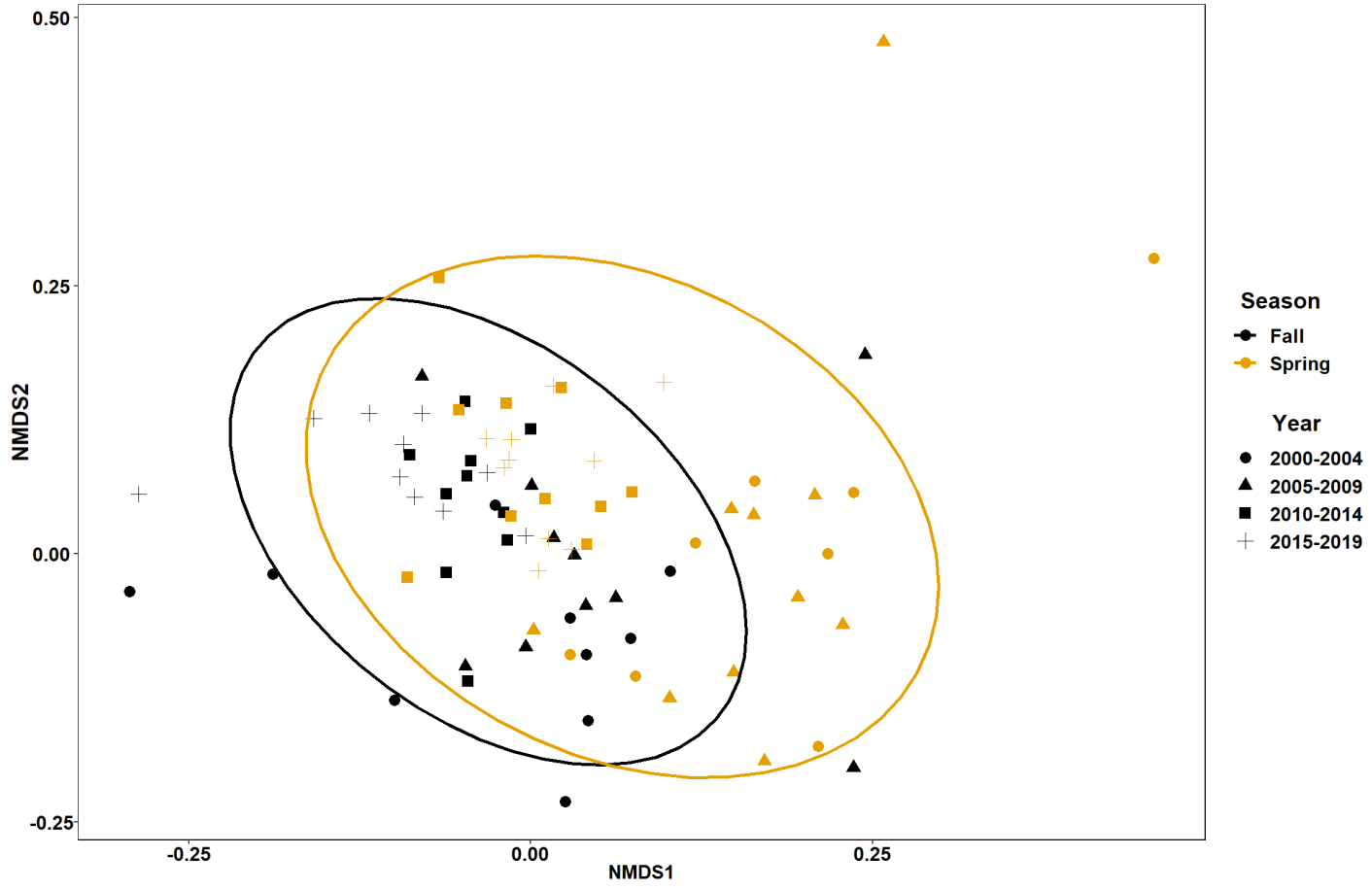


Season

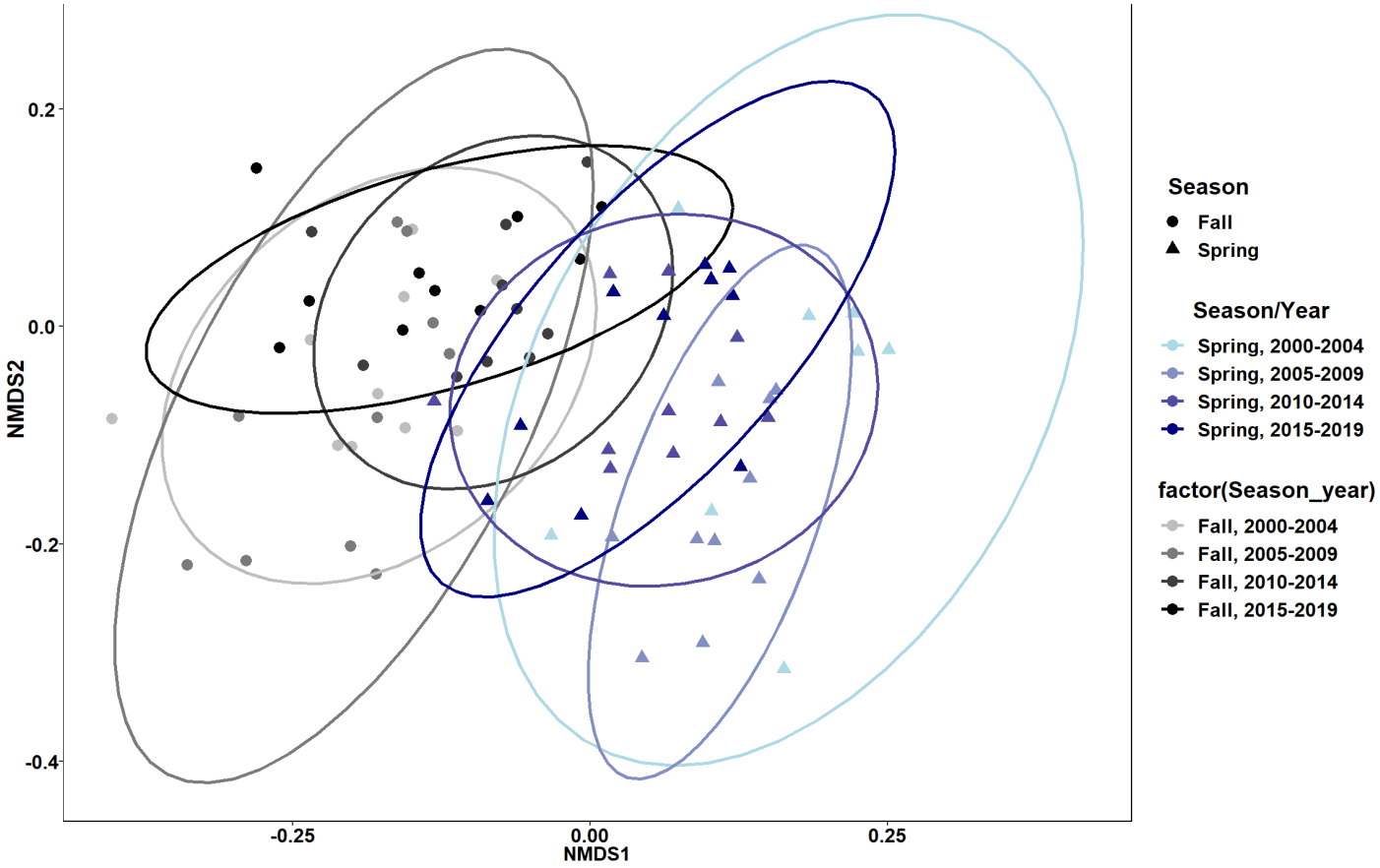
West



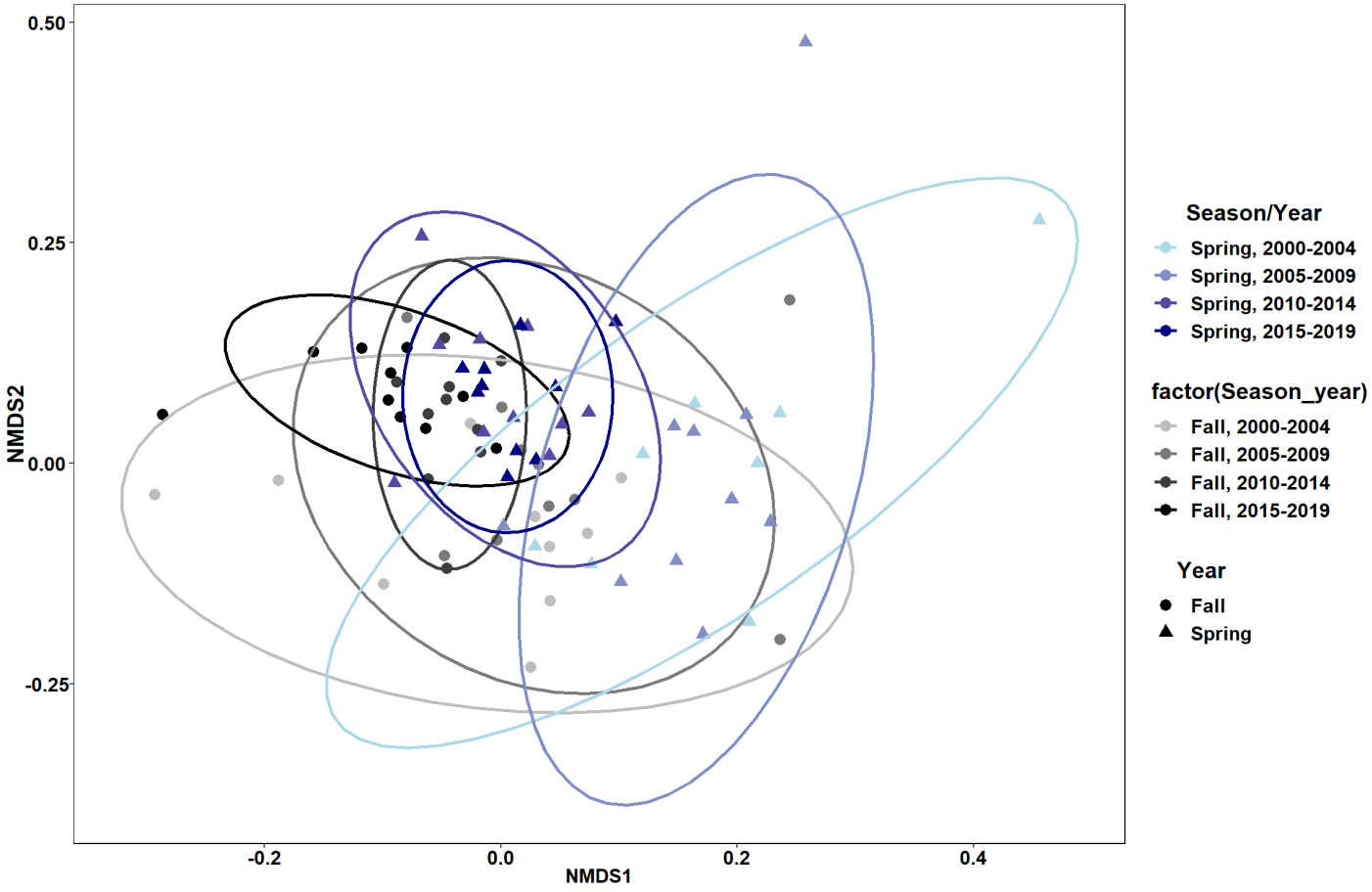
East



West


0.2
0.0
-0.2
-0.4
NMDS2
-0.25
0.00
0.25
NMDS1
Season
Fall
Spring
Season/Year
Spring, 2000-2004
Spring, 2005-2009
Spring, 2010-2014
Spring, 2015-2019
factor(Season_year)
Fall, 2000-2004
Fall, 2005-2009
Fall, 2010-2014
Fall, 2015-2019

East


0.50
0.25
0.00
-0.25
NMDS2
-0.2
0.0
0.2
0.4
NMDS1
Season/Year
Spring, 2000-2004
Spring, 2005-2009
Spring, 2010-2014
Spring, 2015-2019
factor(Season_year)
Fall, 2000-2004
Fall, 2005-2009
Fall, 2010-2014
Fall, 2015-2019
Year
Fall
Spring

Nonmetric Multidimensioanl Scaling- Functional group biomass

Data

- functional groups based on NOAA IEA feeding guilds (https://noaa-edab.github.io/tech-doc/aggroups.html)
- average across depth strata using the NOAA IEA procedure (https://noaa-edab.github.io/tech-doc/inshoresurvdat.html#data-analysis-29)

	Sea… <chr>	Reg… <int>	Y… <int>	benthivore <dbl>	benthos <dbl>	piscivore <dbl>	planktivore <dbl>	undefined <dbl>	YEAR_GR… <chr>
1	Fall	1	2000	30.60977	0.9329012	77.09522	13.07894	4.2592593	2000-2004
2	Fall	1	2001	47.61454	1.6392593	129.71385	27.03765	3.4701323	2000-2004
3	Fall	1	2002	18.78933	0.1253846	124.10729	21.38419	0.3071276	2000-2004
4	Fall	1	2003	52.99875	0.0500000	114.75687	29.33979	6.7406250	2000-2004
5	Fall	1	2004	28.93660	0.0450000	347.72374	113.07280	4.2019335	2000-2004
6	Fall	1	2005	41.88070	0.0277193	327.19086	30.81101	10.1458814	2005-2009

6 rows | 1-10 of 14 columns

Set up data for NMDS

- split community matrix into two dataframes- one for grouping variables and one for species biomass
- calculate dissimilarity matrix with Bray-Curtis distances

```
#set up final grouping data into dataframe
ME_group_data<-trawl_data_arrange[, c(1,2,3,9,10,11,12,13)]
ME_NMDS_data<-as.matrix(trawl_data_arrange[,4:8])

#calculate distance matrix
ME_NMDS_distance<- vegdist(ME_NMDS_data, method="bray")
```

Run the NMDS and extract scores

- change in community composition
- uses rank order
- stress < 0.2 is good, < 0.1 is great, <0.05 is excellent representation in reduced dimensions

```
ME_NMDS=metaMDS(ME_NMDS_distance, # Our community-by-species matrix
                k=2, # The number of reduced dimensions
                method="bray",
                trymax=200) #increase iterations
```

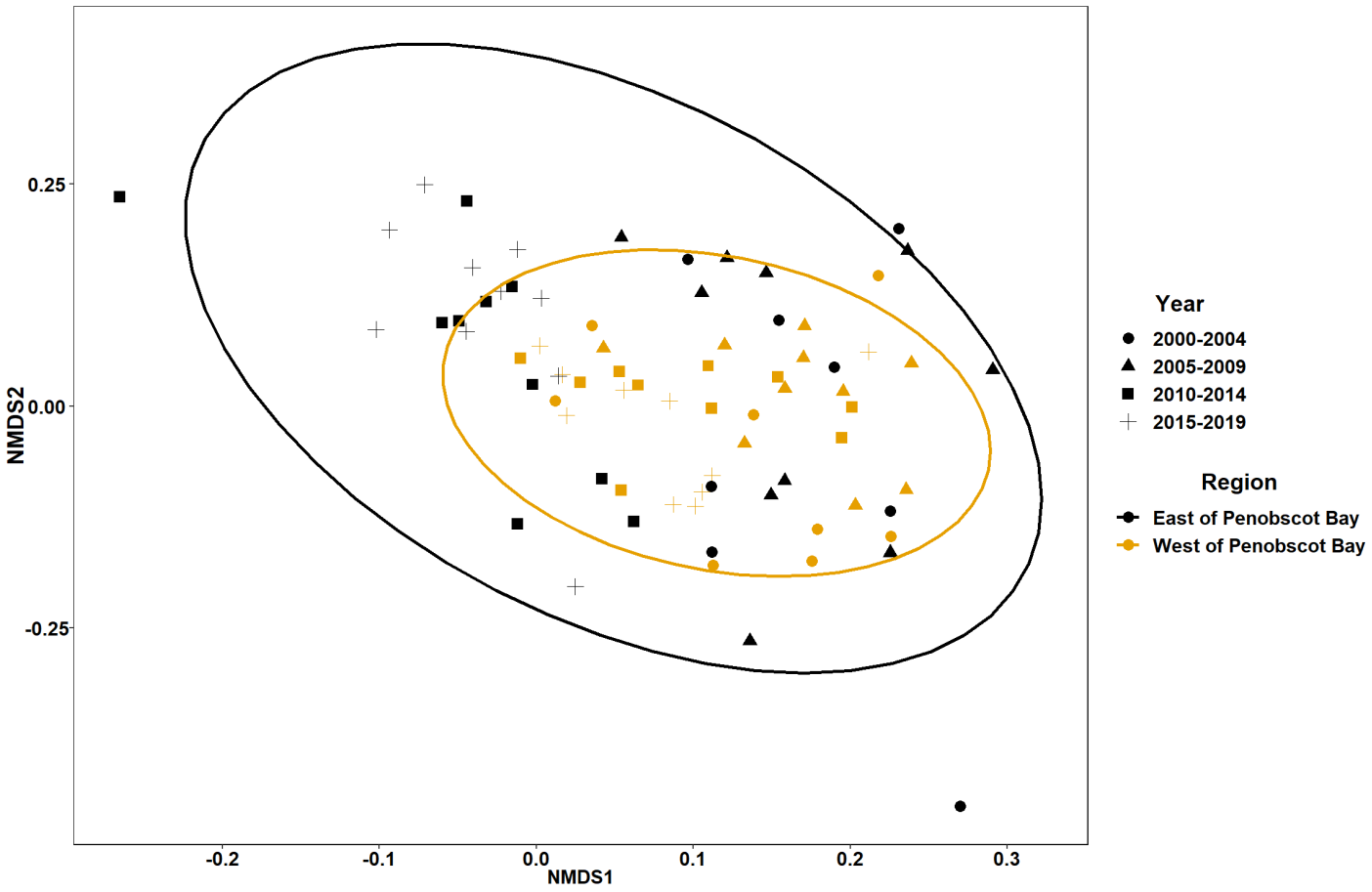
```
## Run 0 stress 0.1741426
## Run 1 stress 0.1756294
## Run 2 stress 0.1877507
## Run 3 stress 0.1746683
## Run 4 stress 0.1756323
## Run 5 stress 0.1741403
## ... New best solution
## ... Procrustes: rmse 0.0006199605  max resid 0.007893183
## ... Similar to previous best
## Run 6 stress 0.1741405
## ... Procrustes: rmse 7.09628e-05  max resid 0.0005544999
## ... Similar to previous best
## Run 7 stress 0.1773452
## Run 8 stress 0.1746632
## Run 9 stress 0.1756293
## Run 10 stress 0.1773453
## Run 11 stress 0.1773441
## Run 12 stress 0.1877506
## Run 13 stress 0.175632
## Run 14 stress 0.174663
## Run 15 stress 0.1756323
## Run 16 stress 0.1756295
## Run 17 stress 0.1756295
## Run 18 stress 0.1756293
## Run 19 stress 0.1877569
## Run 20 stress 0.1741425
## ... Procrustes: rmse 0.0006007181  max resid 0.007808326
## ... Similar to previous best
## *** Solution reached
```

```
#extract NMDS scores for ggplot
data.scores = as.data.frame(scores(ME_NMDS))
#add columns to data frame
data.scores$Stratum = trawl_data_arrange$Stratum
data.scores$Region = trawl_data_arrange$Region
data.scores$Year = trawl_data_arrange$Year
data.scores$Season= trawl_data_arrange$Season
data.scores$Year_groups= trawl_data_arrange$YEAR_GROUPS
data.scores$Year_decades= trawl_data_arrange$YEAR_DECADES
data.scores$Region_new=trawl_data_arrange$REGION_NEW
data.scores$Region_year=trawl_data_arrange$REGION_YEAR
data.scores$Season_year=trawl_data_arrange$SEASON_YEAR
```

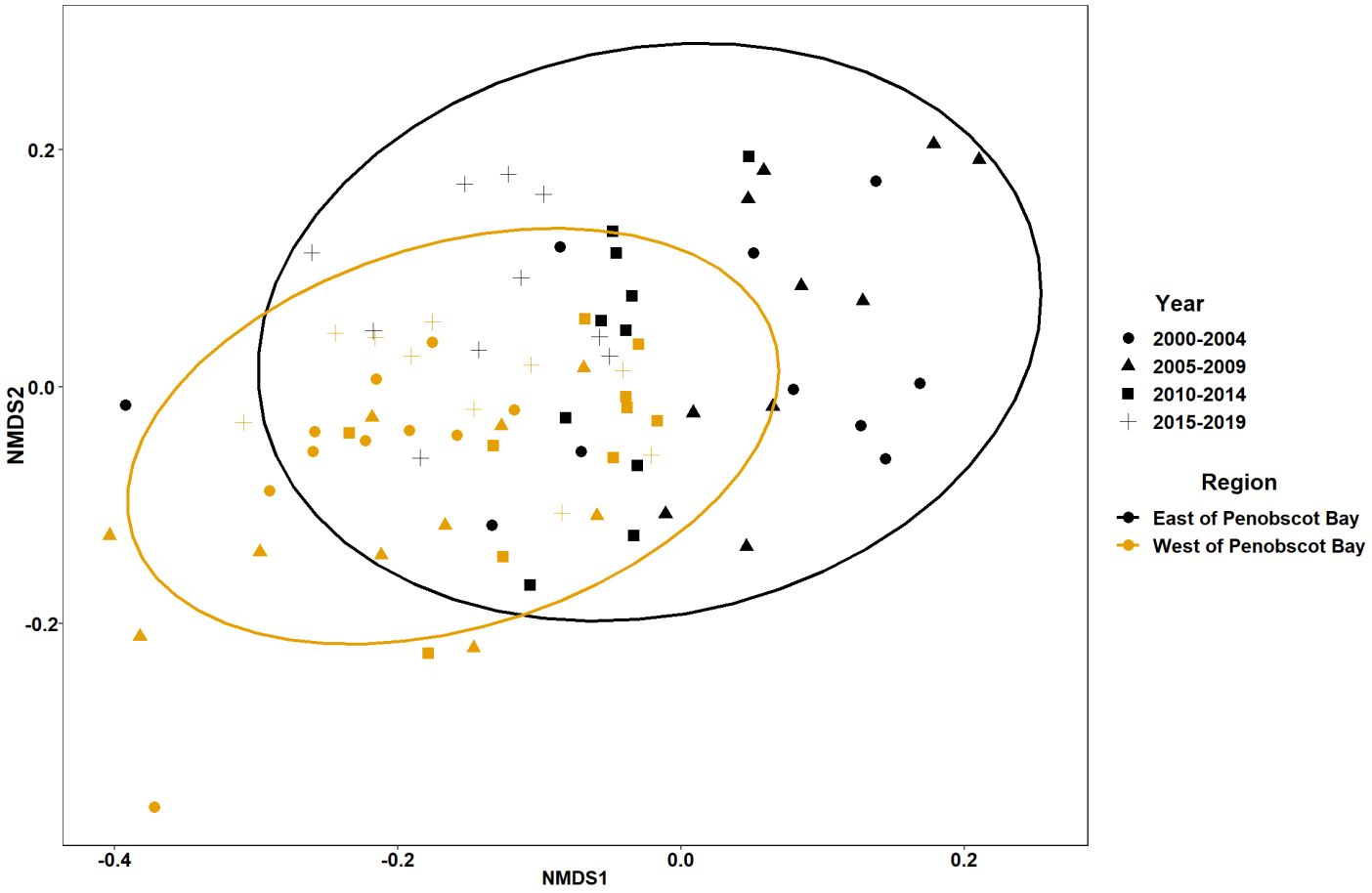
Plots

Region

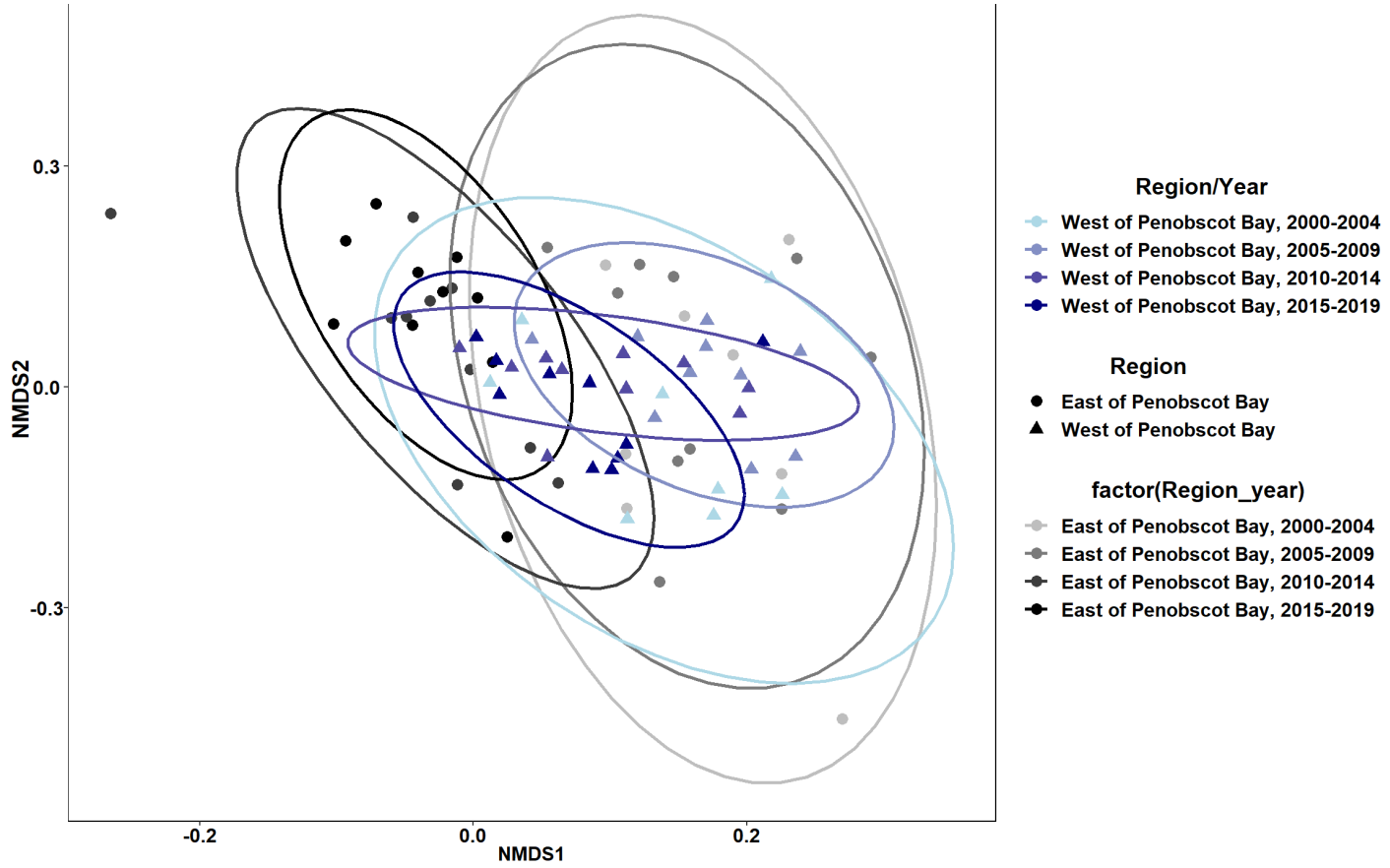
Spring



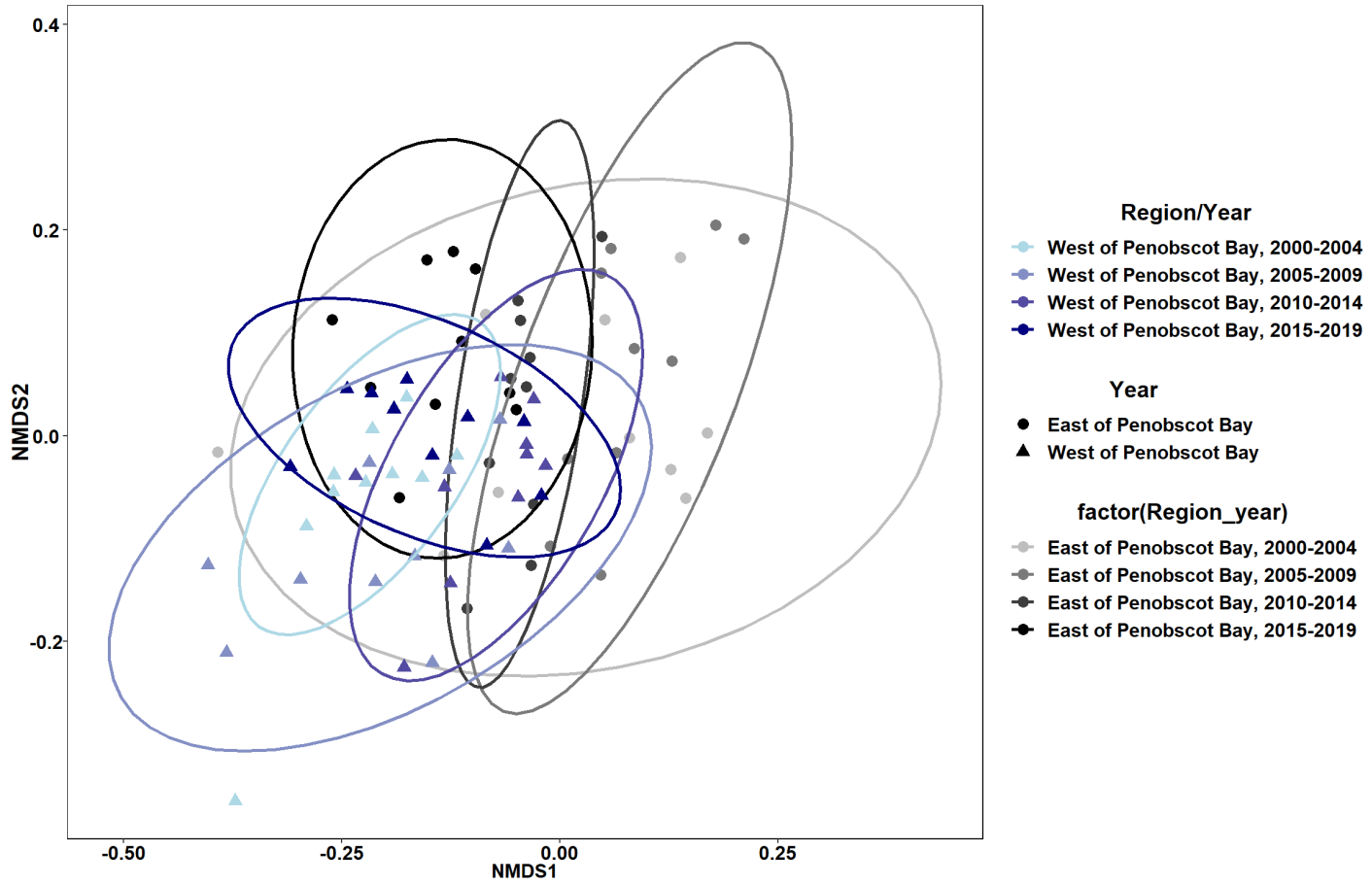
Fall



Spring

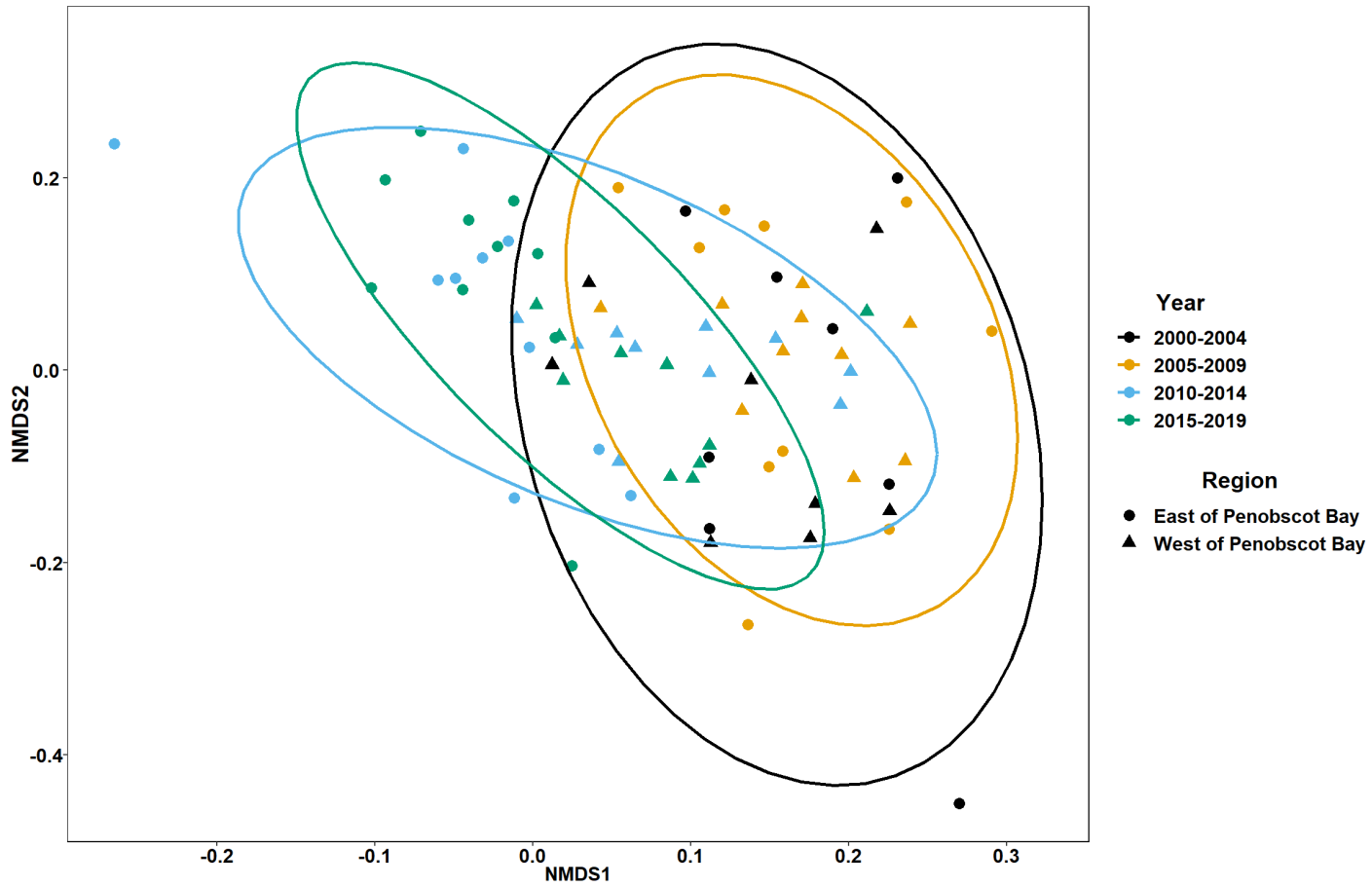

0.3
0.0
-0.3
NMDS2
-0.2
0.0
0.2
NMDS1
Region/Year
West of Penobscot Bay, 2000-2004
West of Penobscot Bay, 2005-2009
West of Penobscot Bay, 2010-2014
West of Penobscot Bay, 2015-2019
Region
East of Penobscot Bay
West of Penobscot Bay
factor(Region_year)
East of Penobscot Bay, 2000-2004
East of Penobscot Bay, 2005-2009
East of Penobscot Bay, 2010-2014
East of Penobscot Bay, 2015-2019

Fall

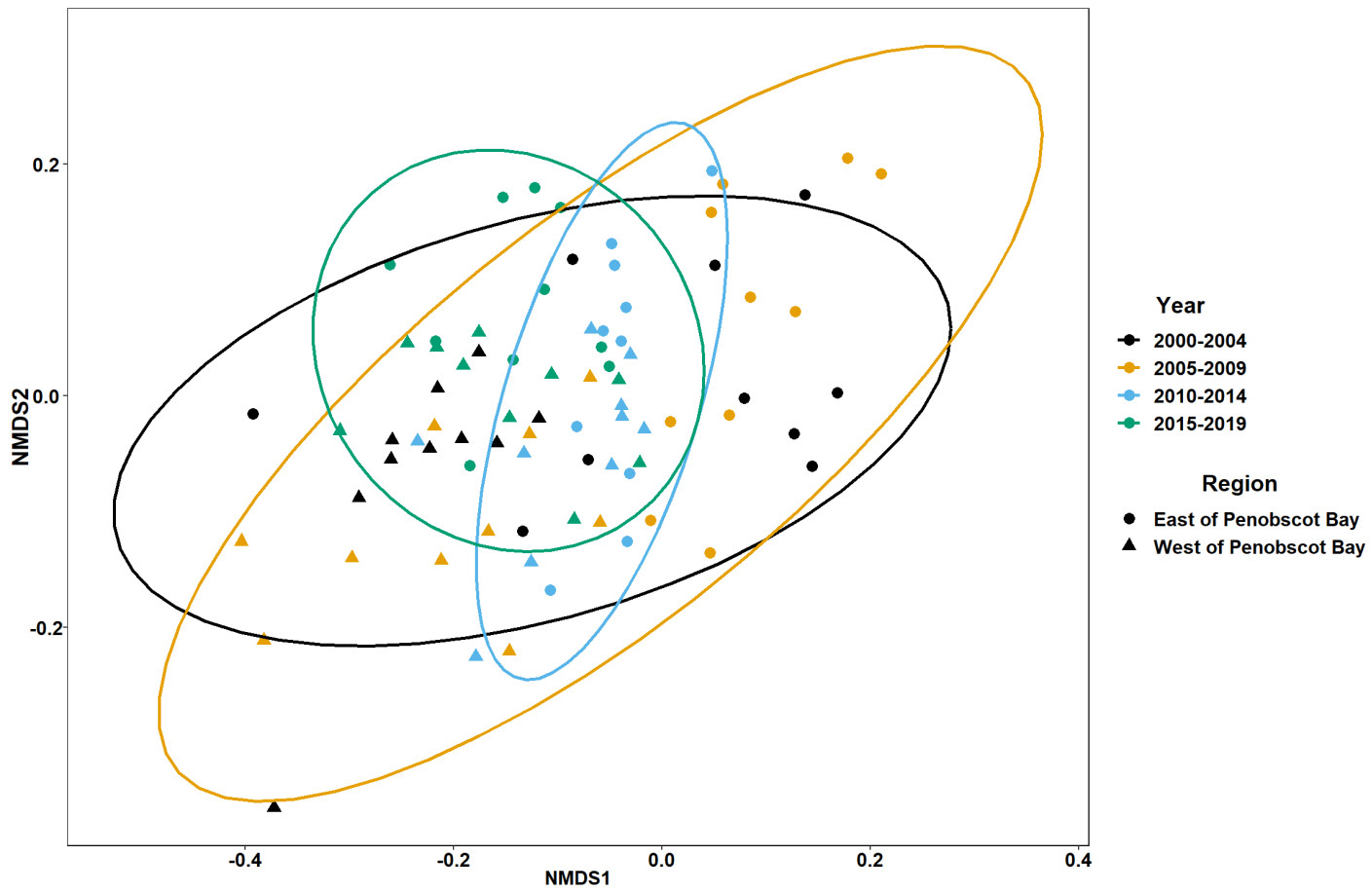

0.4
0.2
0.0
-0.2
NMDS2
-0.50
-0.25
0.00
0.25
NMDS1
Region/Year
West of Penobscot Bay, 2000-2004
West of Penobscot Bay, 2005-2009
West of Penobscot Bay, 2010-2014
West of Penobscot Bay, 2015-2019
Year
East of Penobscot Bay
West of Penobscot Bay
factor(Region_year)
East of Penobscot Bay, 2000-2004
East of Penobscot Bay, 2005-2009
East of Penobscot Bay, 2010-2014
East of Penobscot Bay, 2015-2019

Time

Spring

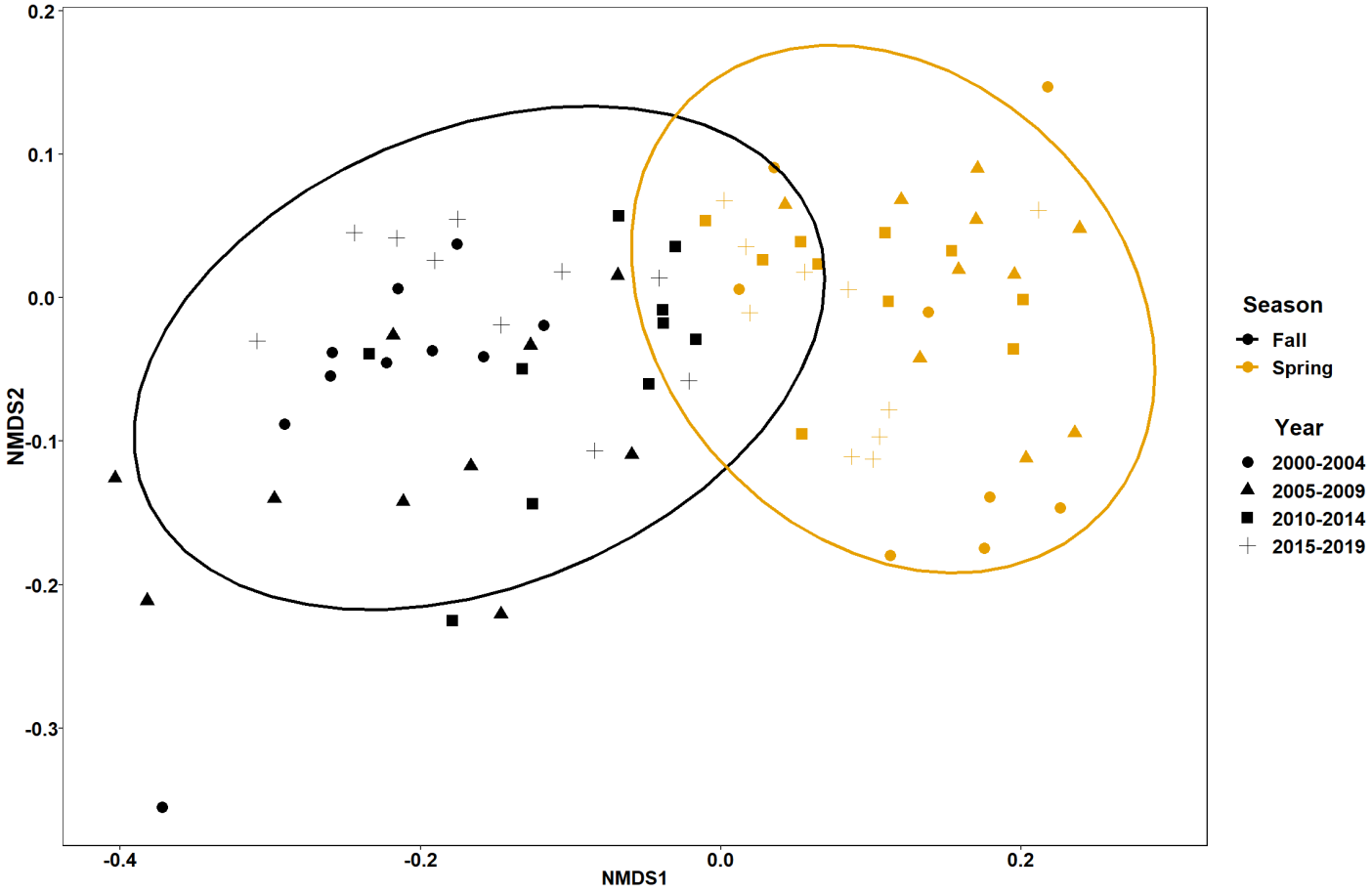


Fall

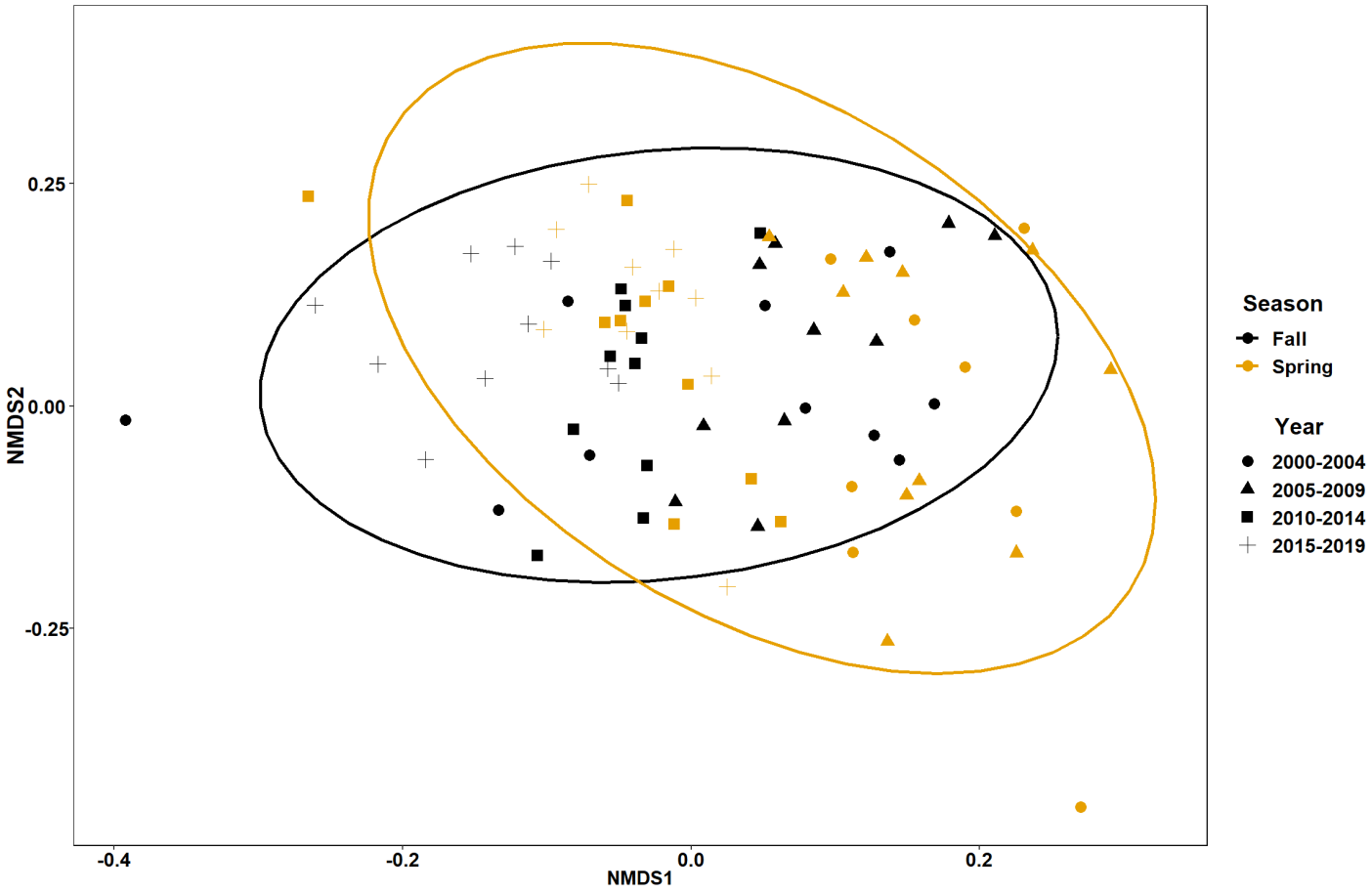


Season

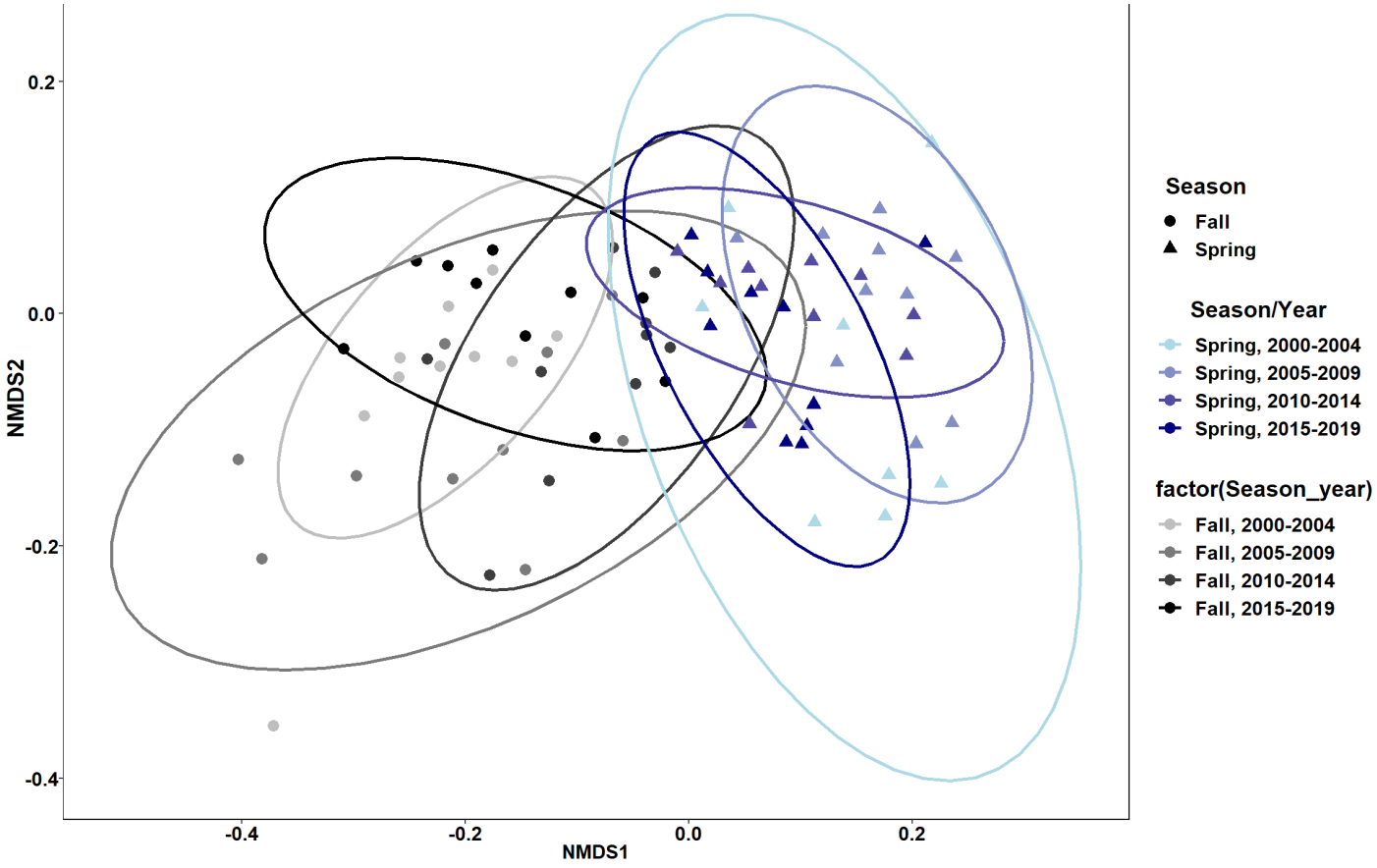
West



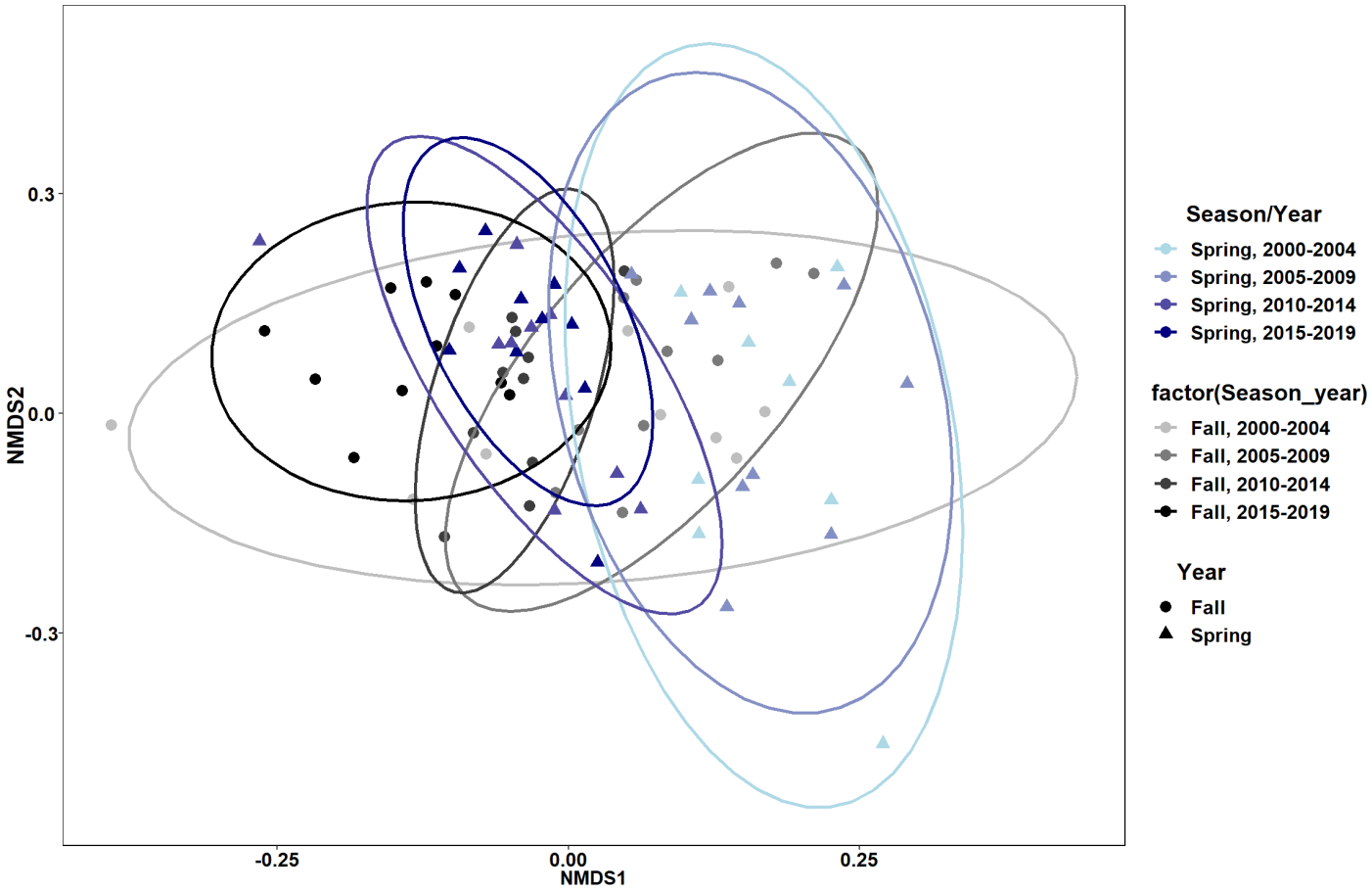
East



West


0.2
0.0
-0.2
-0.4
NMDS2
-0.4
-0.2
0.0
0.2
NMDS1
Season
Fall
Spring
Season/Year
Spring, 2000-2004
Spring, 2005-2009
Spring, 2010-2014
Spring, 2015-2019
factor(Season_year)
Fall, 2000-2004
Fall, 2005-2009
Fall, 2010-2014
Fall, 2015-2019

East


0.3
0.0
-0.3
NMDS2
-0.25
0.00
0.25
NMDS1
Season/Year
Spring, 2000-2004
Spring, 2005-2009
Spring, 2010-2014
Spring, 2015-2019
factor(Season_year)
Fall, 2000-2004
Fall, 2005-2009
Fall, 2010-2014
Fall, 2015-2019
Year
Fall
Spring

Analysis of Similarity and Analysis of Variance

Analysis of Similarity and Analysis of Variance

Data

- Biomass of top 50 species
- average across depth strata using the NOAA IEA technical document (https://noaa-edab.github.io/tech-doc/inshoresurvdat.html#data-analysis-29)
- calculate dissimilarity matrix with Bray-Curtis distances

	Sea… <chr>	Reg… <int>	Y… <int>	alewife <dbl>	bass.striped <dbl>	butterfish <dbl>	cod.atlantic <dbl>	crab.atlantic
1	Fall	1	2000	5.380384	0	0.3518519	1.9828704	0.22
2	Fall	1	2001	11.422884	0	2.8428307	0.3520811	2.84
3	Fall	1	2002	4.145476	0	3.3043183	2.2230952	0.06
4	Fall	1	2003	4.924375	0	3.5231250	10.3700000	0.00
5	Fall	1	2004	6.528253	0	3.2305702	4.6161111	0.00
6	Fall	1	2005	3.781491	0	0.7742105	13.4031579	0.23

6 rows | 1-9 of 59 columns

Analysis of similarity (Anosim)

- tests statistically whether there is a significant difference between two or more groups
- works by testing if distances between groups are greater than within groups
- significant values mean that there is a statistically significant difference in the communities between the groups
- R statistic closer to 1 is more dissimilar

Region

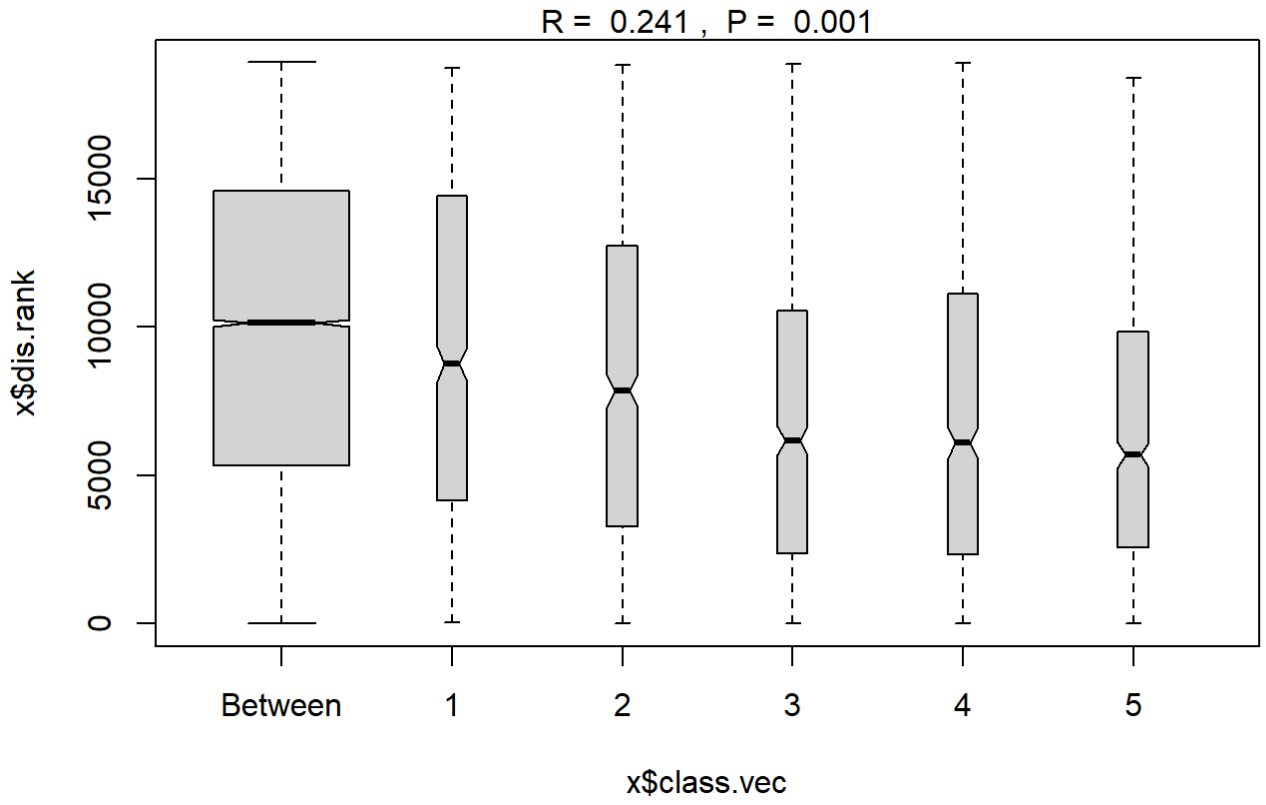
```
#region
ano_region<- anosim(trawl_dist, trawl_data_arrange$Region, permutations = 999)
ano_region #regions are statistically different communities
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$Region,      permutations = 999)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.2409
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
```

```
summary(ano_region)
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$Region,      permutations = 999)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.2409
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##     90%     95%   97.5%     99%
## 0.00992 0.01280 0.01757 0.02199
##
## Dissimilarity ranks between and within classes:
##         0%     25%     50%      75%  100%     N
## Between  4 5339.25 10126.5 14569.75 18915 15210
## 1       47 4152.00  8749.0 14402.00 18739   741
## 2        9 3263.00  7841.0 12723.00 18816   741
## 3        2 2364.00  6163.0 10546.00 18845   741
## 4        1 2319.00  6086.0 11106.00 18907   741
## 5       11 2575.00  5686.0  9835.00 18380   741
```

```
plot(ano_region) #regions don't look very different in plot though...confidence bands all
 overlap
```



Region grouped

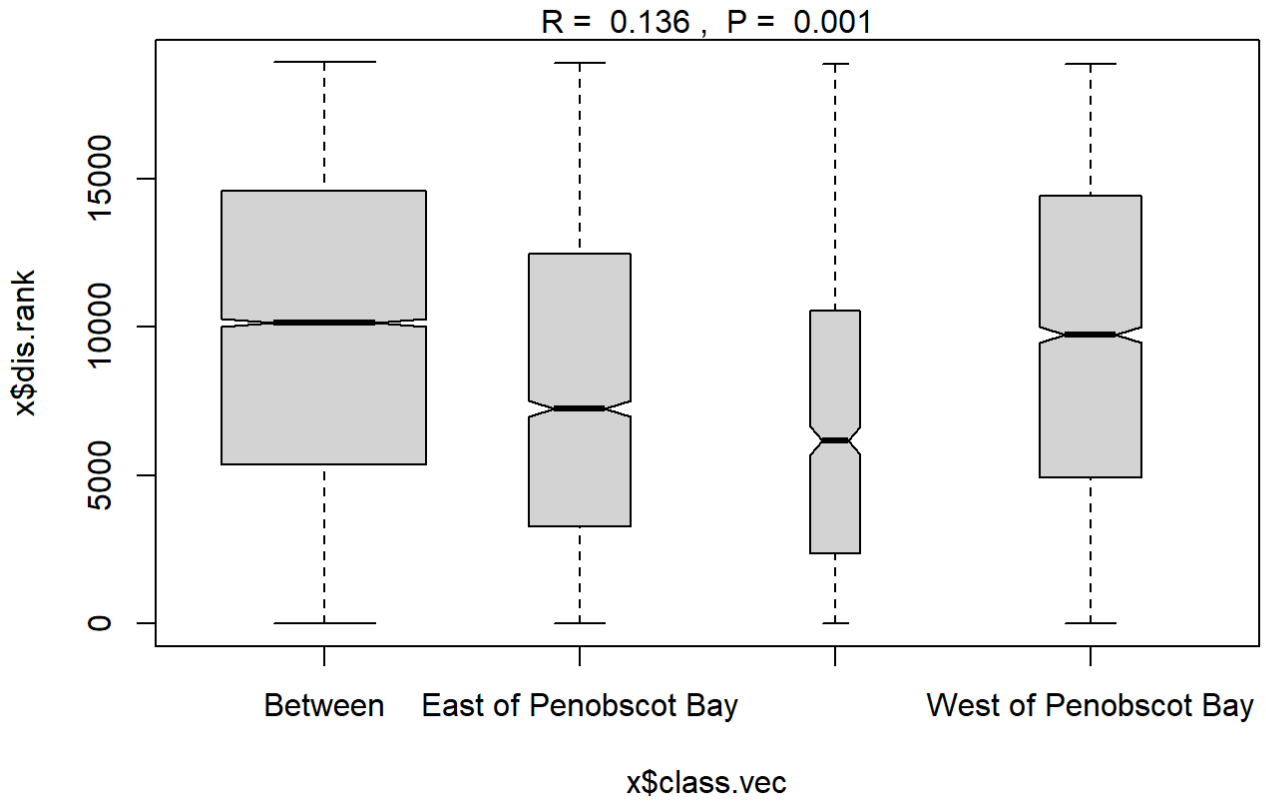
```
#region
ano_region_groups<- anosim(trawl_dist, trawl_data_arrange$REGION_NEW, permutations = 999)
ano_region_groups #regions are statistically different communities
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$REGION_NEW,      permutations = 99
9)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1356
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
```

```
summary(ano_region_groups)
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$REGION_NEW,      permutations = 99
9)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1356
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##    90%    95%  97.5%    99%
## 0.0206 0.0265 0.0324 0.0378
##
## Dissimilarity ranks between and within classes:
##                        0%    25%     50%     75%  100%     N
## Between                 4 5348.0 10153.5 14585.5 18915 12168
## East of Penobscot Bay   1 3285.5  7245.0 12459.5 18907  3003
## Penobscot Bay           2 2364.0  6163.0 10546.0 18845   741
## West of Penobscot Bay   9 4921.0  9748.0 14430.0 18860  3003
```

```
plot(ano_region_groups) #
```



Year

```
#Time
ano_year<- anosim(trawl_dist, trawl_data_arrange$Year, permutations = 999)
ano_year #years are statistically different communities
```

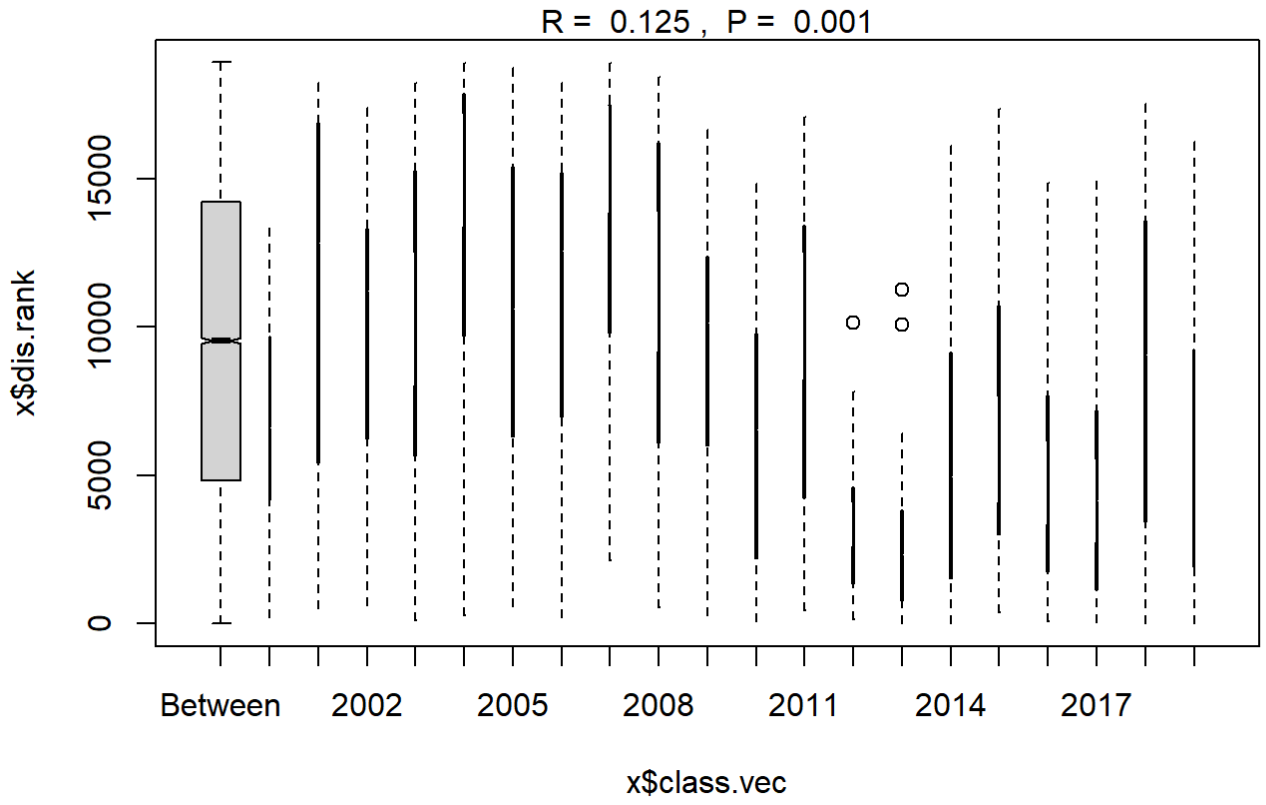
```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$Year, permutations = 999)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1252
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
```

```
summary(ano_year)
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$Year, permutations = 999)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1252
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##    90%    95%  97.5%    99%
## 0.0191 0.0271 0.0307 0.0348
##
## Dissimilarity ranks between and within classes:
##           0%     25%     50%      75%  100%     N
## Between    1 4812.25  9534.5 14222.75 18915 18050
## 2000     217 4819.50  6612.5  9320.00 13344    10
## 2001     525 5418.00 12824.0 16868.00 18217    45
## 2002     619 6225.00 11209.0 13296.00 17389    45
## 2003      99 5655.00 10274.0 15244.00 18230    45
## 2004     260 9688.00 15280.0 17844.00 18887    45
## 2005     567 6315.00 10597.0 15396.00 18738    45
## 2006     198 6976.00 12562.0 15194.00 18221    45
## 2007    2131 9788.00 15651.0 17493.00 18900    45
## 2008     559 6095.00 11538.0 16202.00 18430    45
## 2009     266 5985.00 10139.0 12380.00 16642    45
## 2010      58 2203.00  6548.0  9759.00 14837    45
## 2011     457 4235.00 10369.0 13419.00 17082    45
## 2012     133 1364.00  3343.0  4590.00 10153    45
## 2013      18  795.00  2333.0  3796.00 11260    45
## 2014       6 1516.00  4963.0  9125.00 16084    45
## 2015     380 3017.00  5877.0 10700.00 17347    45
## 2016      70 1749.00  4757.0  7694.00 14871    45
## 2017      35 1168.00  4137.0  7191.00 14935    45
## 2018      12 3428.00  9051.0 13573.00 17500    45
## 2019      16 1930.00  4588.0  9241.00 16238    45
```

```
plot(ano_year)
```

```
## Warning in (function (z, notch = FALSE, width = NULL, varwidth = FALSE, : some
## notches went outside hinges ('box'): maybe set notch=FALSE
```



Year blocks

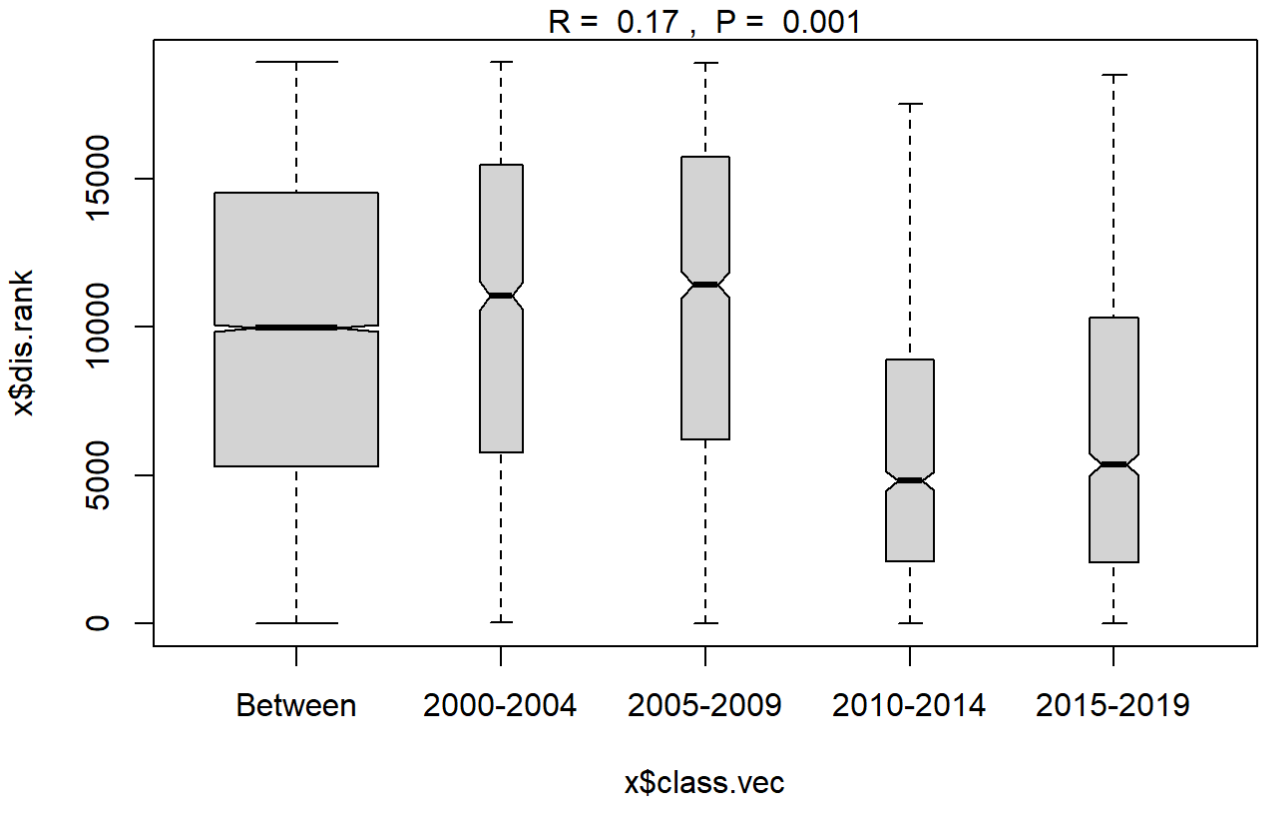
```
#Year blocks
ano_year_blocks<- anosim(trawl_dist, trawl_data_arrange$YEAR_GROUPS, permutations = 999)
ano_year_blocks #years are statistically different communities
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$YEAR_GROUPS,      permutations = 9
99)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1698
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
```

```
summary(ano_year_blocks)
```

```
##
## Call:
## anosim(x = trawl_dist, grouping = trawl_data_arrange$YEAR_GROUPS,      permutations = 9
99)
## Dissimilarity: bray
##
## ANOSIM statistic R: 0.1698
##       Significance: 0.001
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##     90%     95%   97.5%     99%
## 0.00942 0.01280 0.01632 0.01865
##
## Dissimilarity ranks between and within classes:
##           0%     25%   50%      75%  100%     N
## Between    1 5308.25  9966 14517.50 18915 14250
## 2000-2004 54 5768.50 11052 15452.75 18913   990
## 2005-2009 15 6208.00 11413 15720.00 18909  1225
## 2010-2014  6 2086.00  4807  8907.00 17501  1225
## 2015-2019  3 2053.00  5370 10302.00 18480  1225
```

```
plot(ano_year_blocks)
```



Analysis of variance (Adonis)

- Permanova
- tests whether there is a difference between means of groups
- works by calculating the sum of squares from the centroid of the group

Region and Year

```
adonis<-adonis2(trawl_dist~Region*Year, data=ME_group_data, by="terms", permutations = 999
9)
adonis
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 9999
##
## adonis2(formula = trawl_dist ~ Region * Year, data = ME_group_data, permutations = 999
9, by = "terms")
##              Df SumOfSqs      R2       F Pr(>F)
## Region        1   2.4733 0.08292 19.3464  1e-04 ***
## Year          1   2.3702 0.07947 18.5400  1e-04 ***
## Region:Year   1   0.5655 0.01896  4.4233  2e-04 ***
## Residual    191  24.4176 0.81865
## Total       194  29.8265 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(adonis)
```

```
##        Df           SumOfSqs             R2                F
##  Min.   :  1.0   Min.   : 0.5655   Min.   :0.01896   Min.   : 4.423
##  1st Qu.:  1.0   1st Qu.: 2.3702   1st Qu.:0.07947   1st Qu.:11.482
##  Median :  1.0   Median : 2.4733   Median :0.08292   Median :18.540
##  Mean   : 77.6   Mean   :11.9306   Mean   :0.40000   Mean   :14.103
##  3rd Qu.:191.0   3rd Qu.:24.4176   3rd Qu.:0.81865   3rd Qu.:18.943
##  Max.   :194.0   Max.   :29.8265   Max.   :1.00000   Max.   :19.346
##                                                      NA's   :2
##      Pr(>F)
##  Min.   :0.0001000
##  1st Qu.:0.0001000
##  Median :0.0001000
##  Mean   :0.0001333
##  3rd Qu.:0.0001500
##  Max.   :0.0002000
##  NA's   :2
```

Region and year block

```
#with year blocks
adonis<-adonis2(trawl_dist~Region*YEAR_GROUPS, data=ME_group_data, by="terms", permutation
s = 9999)
adonis
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 9999
##
## adonis2(formula = trawl_dist ~ Region * YEAR_GROUPS, data = ME_group_data, permutations
= 9999, by = "terms")
##                      Df SumOfSqs      R2       F Pr(>F)
## Region                1   2.4733 0.08292 20.0943  1e-04 ***
## YEAR_GROUPS           3   3.3389 0.11194  9.0424  1e-04 ***
## Region:YEAR_GROUPS    3   0.9979 0.03346  2.7024  1e-04 ***
## Residual            187  23.0164 0.77168
## Total               194  29.8265 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(adonis)
```

```
##        Df           SumOfSqs             R2                F
##  Min.   :  1.0   Min.   : 0.9979   Min.   :0.03346   Min.   : 2.702
##  1st Qu.:  3.0   1st Qu.: 2.4733   1st Qu.:0.08292   1st Qu.: 5.872
##  Median :  3.0   Median : 3.3389   Median :0.11194   Median : 9.042
##  Mean   : 77.6   Mean   :11.9306   Mean   :0.40000   Mean   :10.613
##  3rd Qu.:187.0   3rd Qu.:23.0164   3rd Qu.:0.77168   3rd Qu.:14.568
##  Max.   :194.0   Max.   :29.8265   Max.   :1.00000   Max.   :20.094
##                                                      NA's   :2
##      Pr(>F)
##  Min.   :1e-04
##  1st Qu.:1e-04
##  Median :1e-04
##  Mean   :1e-04
##  3rd Qu.:1e-04
##  Max.   :1e-04
##  NA's   :2
```

Region groups and year block

```
#with year blocks
adonis<-adonis2(trawl_dist~REGION_NEW*YEAR_GROUPS, data=ME_group_data, by="terms", permuta
tions = 9999)
adonis
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 9999
##
## adonis2(formula = trawl_dist ~ REGION_NEW * YEAR_GROUPS, data = ME_group_data, permutat
ions = 9999, by = "terms")
##                          Df SumOfSqs      R2       F Pr(>F)
## REGION_NEW                2   2.8660 0.09609 11.7024 0.0001 ***
## YEAR_GROUPS               3   3.3389 0.11194  9.0888 0.0001 ***
## REGION_NEW:YEAR_GROUPS    6   1.2124 0.04065  1.6502 0.0044 **
## Residual                183  22.4091 0.75132
## Total                   194  29.8265 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(adonis)
```

```
##        Df           SumOfSqs            R2                F
##  Min.   :  2.0   Min.   : 1.212   Min.   :0.04065   Min.   : 1.650
##  1st Qu.:  3.0   1st Qu.: 2.866   1st Qu.:0.09609   1st Qu.: 5.370
##  Median :  6.0   Median : 3.339   Median :0.11194   Median : 9.089
##  Mean   : 77.6   Mean   :11.931   Mean   :0.40000   Mean   : 7.480
##  3rd Qu.:183.0   3rd Qu.:22.409   3rd Qu.:0.75132   3rd Qu.:10.396
##  Max.   :194.0   Max.   :29.826   Max.   :1.00000   Max.   :11.702
##                                                     NA's   :2
##      Pr(>F)
##  Min.   :0.000100
##  1st Qu.:0.000100
##  Median :0.000100
##  Mean   :0.001533
##  3rd Qu.:0.002250
##  Max.   :0.004400
##  NA's   :2
```

Pairwise

- Vegan does not have a function for this, but I found a wrapper that seems frequently used on github
- select groups to test, one pair at a time
- Adjust p-values for multiple tests

Region

```
#pair-wise test to see what is different
pair<-pairwise.adonis2(trawl_dist~Region, data=ME_group_data, by="terms", permutations = 9
999)
summary(pair)
```

```
##             Length Class  Mode
## parent_call 1      -none- character
## 1_vs_2      6      anova  list
## 1_vs_3      6      anova  list
## 1_vs_4      6      anova  list
## 1_vs_5      6      anova  list
## 2_vs_3      6      anova  list
## 2_vs_4      6      anova  list
## 2_vs_5      6      anova  list
## 3_vs_4      6      anova  list
## 3_vs_5      6      anova  list
## 4_vs_5      6      anova  list
```

```
pair #shows all the regions are significantly different except 3 and 4
```

```
## $parent_call
## [1] "trawl_dist ~ Region , strata = Null"
##
## $`1_vs_2`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    1.1374 1.13737  7.9949 0.09518  1e-04 ***
## Residuals 76   10.8119 0.14226         0.90482
## Total     77   11.9492                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`1_vs_3`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    1.8898 1.88977  14.078 0.15629  1e-04 ***
## Residuals 76   10.2019 0.13424         0.84371
## Total     77   12.0917                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`1_vs_4`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    2.2077 2.20767  15.829 0.17237  1e-04 ***
## Residuals 76   10.5999 0.13947         0.82763
## Total     77   12.8076                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`1_vs_5`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    2.1038  2.1037   15.89 0.17292  1e-04 ***
## Residuals 76   10.0621  0.1324         0.82708
## Total     77   12.1658                 1.00000
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2_vs_3`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model     R2 Pr(>F)
## Region     1    0.5465 0.54645  4.3301 0.0539 0.0016 **
## Residuals 76    9.5910 0.12620         0.9461
## Total     77   10.1374                1.0000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2_vs_4`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    0.8377 0.83772  6.3737 0.07738  1e-04 ***
## Residuals 76    9.9890 0.13143         0.92262
## Total     77   10.8267                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2_vs_5`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    1.7680 1.76803  14.217 0.15759  1e-04 ***
## Residuals 76    9.4512 0.12436         0.84241
## Total     77   11.2192                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`3_vs_4`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    0.2281 0.22808  1.8482 0.02374 0.0794 .
## Residuals 76    9.3790 0.12341         0.97626
## Total     77    9.6071                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## $`3_vs_5`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    1.2119 1.21194  10.418 0.12055  1e-04 ***
## Residuals 76    8.8412 0.11633         0.87945
## Total     77   10.0531                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`4_vs_5`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Region     1    1.2815 1.28154  10.542 0.12181  1e-04 ***
## Residuals 76    9.2392 0.12157         0.87819
## Total     77   10.5207                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## attr(,"class")
## [1] "pwadstrata" "list"
```

Region groups

```
#pair-wise test to see what is different
pair<-pairwise.adonis2(trawl_dist~REGION_NEW, data=ME_group_data, by="terms", permutations
= 9999)
summary(pair)
```

```
##                                              Length Class  Mode
## parent_call                                  1      -none- character
## West of Penobscot Bay_vs_Penobscot Bay       6      anova  list
## West of Penobscot Bay_vs_East of Penobscot Bay 6      anova  list
## Penobscot Bay_vs_East of Penobscot Bay       6      anova  list
```

```
pair #shows all the regions are significantly different except 3 and 4
```

```
## $parent_call
## [1] "trawl_dist ~ REGION_NEW , strata = Null"
##
## $`West of Penobscot Bay_vs_Penobscot Bay`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model     R2 Pr(>F)
## REGION_NEW   1     1.245 1.24503  8.7093 0.0704  1e-04 ***
## Residuals  115    16.440 0.14295         0.9296
## Total      116    17.685                1.0000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`West of Penobscot Bay_vs_East of Penobscot Bay`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## REGION_NEW   1    2.2491 2.24913  15.415 0.09099  1e-04 ***
## Residuals  154   22.4700 0.14591         0.90901
## Total      155   24.7191                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`Penobscot Bay_vs_East of Penobscot Bay`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## REGION_NEW   1    0.5328 0.53284   4.082 0.03428  6e-04 ***
## Residuals  115   15.0112 0.13053         0.96572
## Total      116   15.5440                1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## attr(,"class")
## [1] "pwadstrata" "list"
```

Year blocks

```
#pair-wise test to see what is different for year blocks
pair<-pairwise.adonis2(trawl_dist~YEAR_GROUPS, data=ME_group_data, by="terms", permutation
s = 9999)
summary(pair)
```

```
##                         Length Class  Mode
## parent_call             1      -none- character
## 2000-2004_vs_2005-2009 6      anova  list
## 2000-2004_vs_2010-2014 6      anova  list
## 2000-2004_vs_2015-2019 6      anova  list
## 2005-2009_vs_2010-2014 6      anova  list
## 2005-2009_vs_2015-2019 6      anova  list
## 2010-2014_vs_2015-2019 6      anova  list
```

```
pair
```

```
## $parent_call
## [1] "trawl_dist ~ YEAR_GROUPS , strata = Null"
##
## $`2000-2004_vs_2005-2009`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    0.5499 0.54989  3.1888 0.03315 0.0026 **
## Residuals   93   16.0372 0.17244         0.96685
## Total       94   16.5871                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2000-2004_vs_2010-2014`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    1.1475 1.14748  8.5301 0.08402  1e-04 ***
## Residuals   93   12.5104 0.13452         0.91598
## Total       94   13.6579                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2000-2004_vs_2015-2019`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    1.7906 1.79056  12.878 0.12163  1e-04 ***
## Residuals   93   12.9309 0.13904         0.87837
## Total       94   14.7215                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2005-2009_vs_2010-2014`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    1.2072 1.20723   8.727 0.08177  1e-04 ***
## Residuals   98   13.5566 0.13833         0.91823
## Total       99   14.7639                 1.00000
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2005-2009_vs_2015-2019`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    1.6775 1.67753  11.762 0.10716  1e-04 ***
## Residuals   98   13.9772 0.14262         0.89284
## Total       99   15.6547                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $`2010-2014_vs_2015-2019`
## Permutation: free
## Number of permutations: 9999
##
## Terms added sequentially (first to last)
##
##             Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## YEAR_GROUPS  1    0.3126 0.31256  2.9311 0.02904 0.0052 **
## Residuals   98   10.4504 0.10664         0.97096
## Total       99   10.7629                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## attr(,"class")
## [1] "pwadstrata" "list"
```

Dispersion

- anosim very sensitive to heterogeneity (Anderson and Walsh 2013)
- Could get false significant results from differences in variance instead of mean
- adonis is less affected by heterogeneity for *balanced designs*
- PRIMER can deal with dispersion issues, but vegan does not yet
- tests null hypothesis that there is no difference in dispersion between groups
- p-value <0.05 means difference is significant

Region

```
#betadisper test homogeneity of dispersion among groups
#Region
bd<-betadisper(trawl_dist,ME_group_data$Region)
bd
```

```
##
##  Homogeneity of multivariate dispersions
##
## Call: betadisper(d = trawl_dist, group = ME_group_data$Region)
##
## No. of Positive Eigenvalues: 83
## No. of Negative Eigenvalues: 111
##
## Average distance to median:
##      1      2      3      4      5
## 0.3754 0.3522 0.3255 0.3354 0.3214
##
## Eigenvalues for PCoA axes:
## (Showing 8 of 194 eigenvalues)
## PCoA1 PCoA2 PCoA3 PCoA4 PCoA5 PCoA6 PCoA7 PCoA8
## 7.177 4.988 3.828 2.354 1.707 1.515 1.353 1.176
```

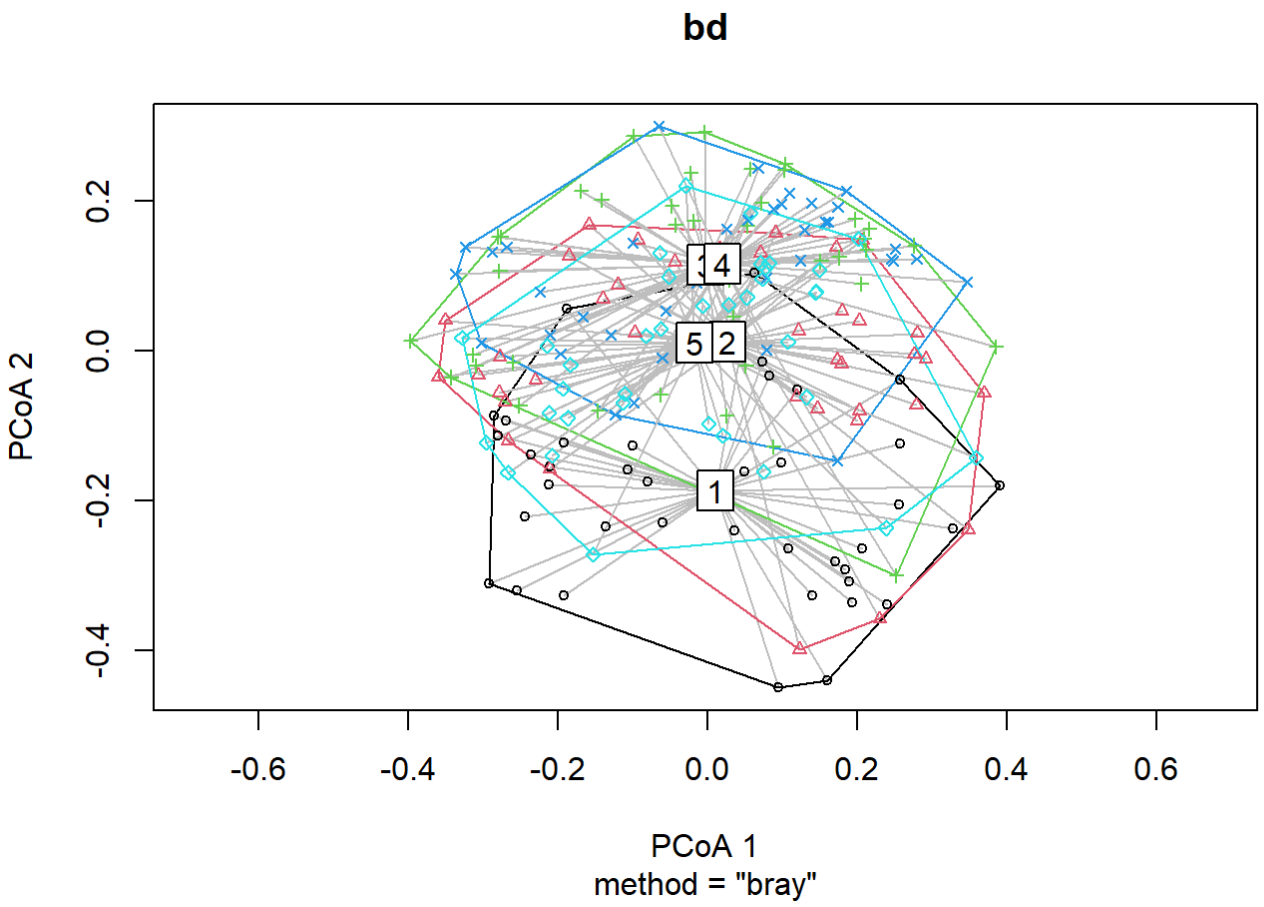
```
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df  Sum Sq   Mean Sq F value  Pr(>F)
## Groups      4 0.07648 0.0191204  2.0314 0.09165 .
## Residuals 190 1.78838 0.0094125
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#test based on permutations
permutest(bd)
```

```
##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 999
##
## Response: Distances
##            Df  Sum Sq   Mean Sq      F N.Perm Pr(>F)
## Groups      4 0.07648 0.0191204 2.0314    999  0.096 .
## Residuals 190 1.78838 0.0094125
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(bd)
```



Year

```
#Year
bd<-betadisper(trawl_dist,ME_group_data$Year)
bd
```

```
##
##  Homogeneity of multivariate dispersions
##
## Call: betadisper(d = trawl_dist, group = ME_group_data$Year)
##
## No. of Positive Eigenvalues: 83
## No. of Negative Eigenvalues: 111
##
## Average distance to median:
##   2000   2001   2002   2003   2004   2005   2006   2007   2008   2009   2010
## 0.2937 0.3911 0.3688 0.3792 0.4275 0.3783 0.3880 0.4373 0.3760 0.3541 0.3072
##   2011   2012   2013   2014   2015   2016   2017   2018   2019
## 0.3562 0.2519 0.2343 0.2767 0.3180 0.2854 0.2742 0.3512 0.2904
##
## Eigenvalues for PCoA axes:
## (Showing 8 of 194 eigenvalues)
## PCoA1 PCoA2 PCoA3 PCoA4 PCoA5 PCoA6 PCoA7 PCoA8
## 7.177 4.988 3.828 2.354 1.707 1.515 1.353 1.176
```

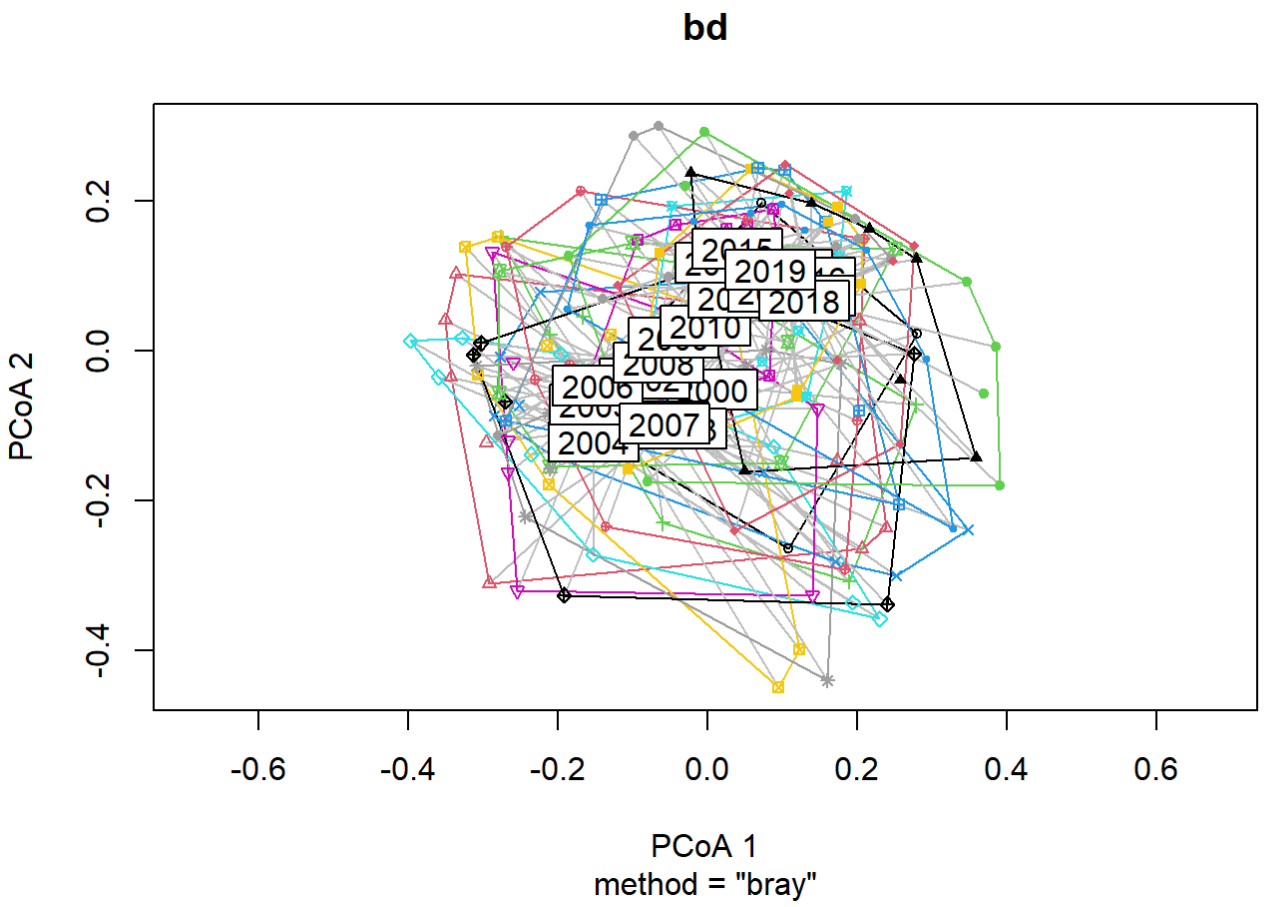
```
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df  Sum Sq  Mean Sq F value    Pr(>F)
## Groups     19 0.63018 0.033167  3.6271 2.865e-06 ***
## Residuals 175 1.60025 0.009144
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#test based on permutations
permutest(bd)
```

```
##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 999
##
## Response: Distances
##            Df  Sum Sq  Mean Sq      F N.Perm Pr(>F)
## Groups     19 0.63018 0.033167 3.6271    999  0.001 ***
## Residuals 175 1.60025 0.009144
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(bd)
```



Year block

```
#Year blocks
bd<-betadisper(trawl_dist,ME_group_data$YEAR_GROUPS)
bd
```

```
##
##  Homogeneity of multivariate dispersions
##
## Call: betadisper(d = trawl_dist, group = ME_group_data$YEAR_GROUPS)
##
## No. of Positive Eigenvalues: 83
## No. of Negative Eigenvalues: 111
##
## Average distance to median:
## 2000-2004 2005-2009 2010-2014 2015-2019
##    0.3991    0.4011    0.3045    0.3175
##
## Eigenvalues for PCoA axes:
## (Showing 8 of 194 eigenvalues)
## PCoA1 PCoA2 PCoA3 PCoA4 PCoA5 PCoA6 PCoA7 PCoA8
## 7.177 4.988 3.828 2.354 1.707 1.515 1.353 1.176
```

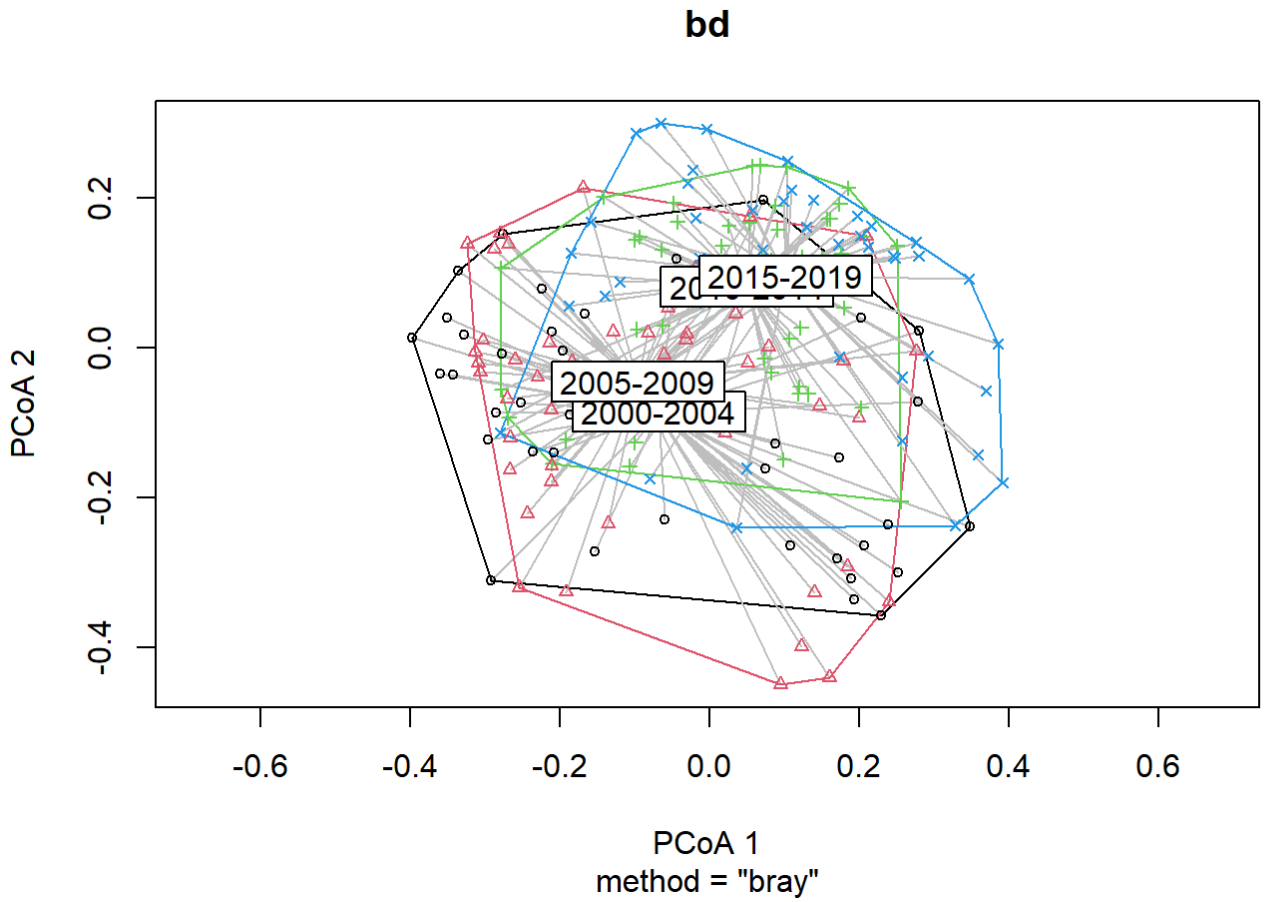
```
anova(bd)
```

```
## Analysis of Variance Table
##
## Response: Distances
##            Df  Sum Sq  Mean Sq F value    Pr(>F)
## Groups      3 0.39156 0.130521  14.687 1.205e-08 ***
## Residuals 191 1.69735 0.008887
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#test based on permutations
permutest(bd)
```

```
##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 999
##
## Response: Distances
##            Df  Sum Sq  Mean Sq      F N.Perm Pr(>F)
## Groups      3 0.39156 0.130521 14.687    999  0.001 ***
## Residuals 191 1.69735 0.008887
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(bd)
```



Indicator species analysis

- test if a species if found significantly more in one group compared to another
- all combinations of groups

Region

```
#see which species are found significantly more in each Region
inv_region<-multipatt(ME_NMDS_data, ME_group_data$Region, func = "r.g", control = how(nper
m=999))
summary(inv_region)
```

```
##
##  Multilevel pattern analysis
##  ---------------------------
##
##  Association function: r.g
##  Significance level (alpha): 0.05
##
##  Total number of species: 50
##  Selected number of species: 37
##  Number of species associated to 1 group: 17
##  Number of species associated to 2 groups: 15
##  Number of species associated to 3 groups: 3
##  Number of species associated to 4 groups: 2
##
##  List of species associated to each combination:
##
##  Group 1  #sps.  9
##                               stat p.value
## flounder.yellowtail         0.789   0.001 ***
## cod.atlantic                0.517   0.001 ***
## haddock                     0.412   0.001 ***
## dogfish.spiny               0.379   0.001 ***
## hake.atlantic.red           0.280   0.003 **
## mackerel.atlantic           0.219   0.031 *
## squid.long.finned           0.211   0.042 *
## butterfish                  0.210   0.046 *
## redfish.acadian.ocean.perch 0.205   0.001 ***
##
##  Group 2  #sps.  4
##                       stat p.value
## alewife             0.455   0.001 ***
## crab.northern.stone 0.354   0.001 ***
## smelt.rainbow       0.340   0.001 ***
## sturgeon.atlantic   0.256   0.004 **
##
##  Group 4  #sps.  3
##               stat p.value
## cucumber.sea 0.224   0.002 **
## scallop.sea  0.205   0.048 *
## crab.green   0.172   0.008 **
##
##  Group 5  #sps.  1
##                  stat p.value
## flounder.winter 0.646   0.001 ***
##
##  Group 1+2  #sps.  7
##                         stat p.value
## plaice.american..dab. 0.676   0.001 ***
## shad.american         0.401   0.001 ***
## cunner                0.380   0.001 ***
## sculpin.longhorn      0.334   0.002 **
## herring.blueback      0.305   0.002 **
## monkfish              0.291   0.002 **
```

```
## crab.red              0.219   0.002 **
##
##  Group 1+5  #sps.  6
##                                     stat p.value
## sea.raven                          0.533   0.001 ***
## skate.little                       0.477   0.001 ***
## pout.ocean                         0.460   0.001 ***
## skate.smooth                       0.299   0.003 **
## skate.winter                       0.229   0.019 *
## flounder.atlantic.witch..gray.sole. 0.215   0.038 *
##
##  Group 3+4  #sps.  1
##                      stat p.value
## crab.atlantic.rock 0.347   0.001 ***
##
##  Group 4+5  #sps.  1
##             stat p.value
## crab.jonah 0.339   0.001 ***
##
##  Group 1+2+5  #sps.  1
##               stat p.value
## skate.thorny 0.297   0.001 ***
##
##  Group 2+3+4  #sps.  1
##                    stat p.value
## herring.atlantic 0.319   0.001 ***
##
##  Group 3+4+5  #sps.  1
##                   stat p.value
## halibut.atlantic 0.26   0.002 **
##
##  Group 1+2+3+4  #sps.  1
##                         stat p.value
## hake.silver..whiting. 0.209   0.034 *
##
##  Group 2+3+4+5  #sps.  1
##                    stat p.value
## lobster.american 0.329   0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Year block

```
#see which species are found significantly more in each Region
inv_year<-multipatt(ME_NMDS_data, ME_group_data$YEAR_GROUPS, func = "r.g", control = how(n
perm=999))
summary(inv_year)
```

```
##
##  Multilevel pattern analysis
##  ---------------------------
##
##  Association function: r.g
##  Significance level (alpha): 0.05
##
##  Total number of species: 50
##  Selected number of species: 24
##  Number of species associated to 1 group: 14
##  Number of species associated to 2 groups: 8
##  Number of species associated to 3 groups: 2
##
##  List of species associated to each combination:
##
##  Group 2000-2004  #sps.  6
##               stat p.value
## scallop.sea  0.374   0.001 ***
## skate.little 0.321   0.001 ***
## sea.raven    0.318   0.001 ***
## monkfish     0.281   0.001 ***
## skate.winter 0.236   0.005 **
## scup         0.202   0.001 ***
##
##  Group 2005-2009  #sps.  4
##                         stat p.value
## plaice.american..dab. 0.269   0.002 **
## wolffish.atlantic     0.207   0.022 *
## cod.atlantic          0.188   0.043 *
## squid.short.finned    0.184   0.021 *
##
##  Group 2010-2014  #sps.  1
##             stat p.value
## crab.green 0.152   0.003 **
##
##  Group 2015-2019  #sps.  3
##                    stat p.value
## hake.atlantic.red 0.337   0.001 ***
## haddock           0.305   0.001 ***
## hake.white        0.303   0.001 ***
##
##  Group 2000-2004+2005-2009  #sps.  5
##                    stat p.value
## sculpin.longhorn  0.436   0.001 ***
## menhaden.atlantic 0.233   0.007 **
## smelt.rainbow     0.213   0.014 *
## skate.thorny      0.206   0.026 *
## lumpfish          0.171   0.025 *
##
##  Group 2010-2014+2015-2019  #sps.  3
##                   stat p.value
## lobster.american 0.499   0.001 ***
## skate.barndoor   0.231   0.011 *
```

```
## halibut.atlantic 0.230   0.010 **
##
##  Group 2000-2004+2005-2009+2015-2019  #sps.  1
##             stat p.value
## crab.jonah 0.286   0.001 ***
##
##  Group 2000-2004+2010-2014+2015-2019  #sps.  1
##                        stat p.value
## hake.silver..whiting. 0.279   0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Objective 4: Fishery Landings

Objective 4: Fishery Landings

Data

- Maine DMR landings data
- 2006-2020

y…	county	species	weight	value
<int>	<chr>	<chr>	<dbl>	<dbl>
2006	Cumberland	Cod Atlantic	1205523.00	2.062011e+06
2006	Cumberland	Crab Atlantic Rock	24586.00	9.410000e+03
2006	Cumberland	Crab Jonah	4473.00	2.091000e+03
2006	Cumberland	Cusk	46317.00	3.879400e+04
2006	Cumberland	Eel American	124.00	8.595000e+03
2006	Cumberland	Flounder Atlantic Witch (Gray Sole)	921410.00	1.767704e+06
2006	Cumberland	Flounder Winter	72189.00	1.279800e+05
2006	Cumberland	Haddock	1020195.00	1.599995e+06
2006	Cumberland	Hake White	1587602.00	1.752227e+06
2006	Cumberland	Halibut Atlantic	6472.00	2.424400e+04

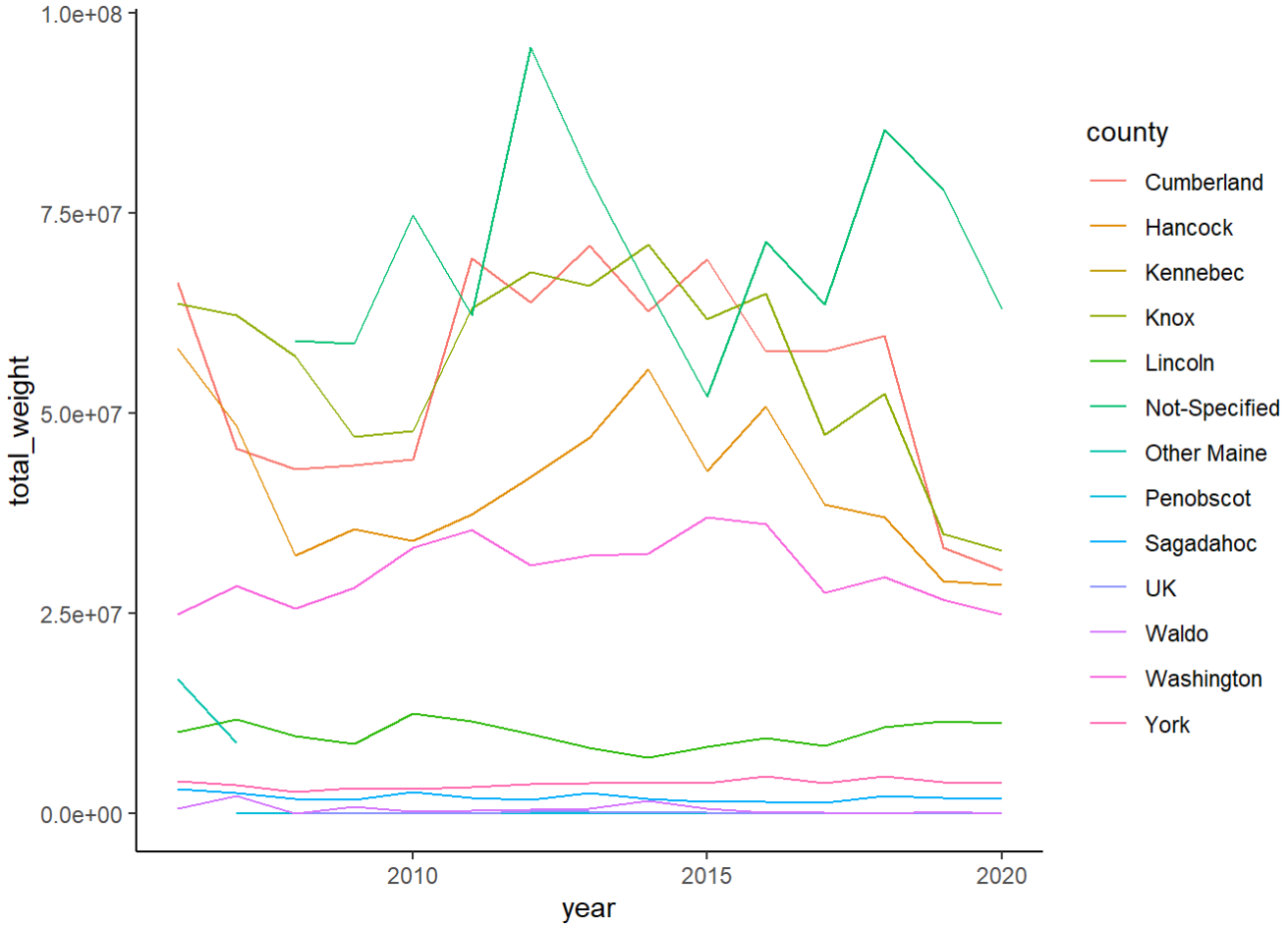
1-10 of 1,574 rows Previous **1** 2 3 4 5 6 … 158 Next

County

county	year	total_weight
<chr>	<int>	<dbl>
Cumberland	2006	66344010.00
Cumberland	2007	45679970.00
Cumberland	2008	43060400.56
Cumberland	2009	43547619.72
Cumberland	2010	44260999.99

county <chr>	year <int>	total_weight <dbl>
Cumberland	2011	69354737.57
Cumberland	2012	63936155.41
Cumberland	2013	71021905.65
Cumberland	2014	62833800.31
Cumberland	2015	69278555.28

1-10 of 161 rows Previous **1** 2 3 4 5 6 ... 17 Next



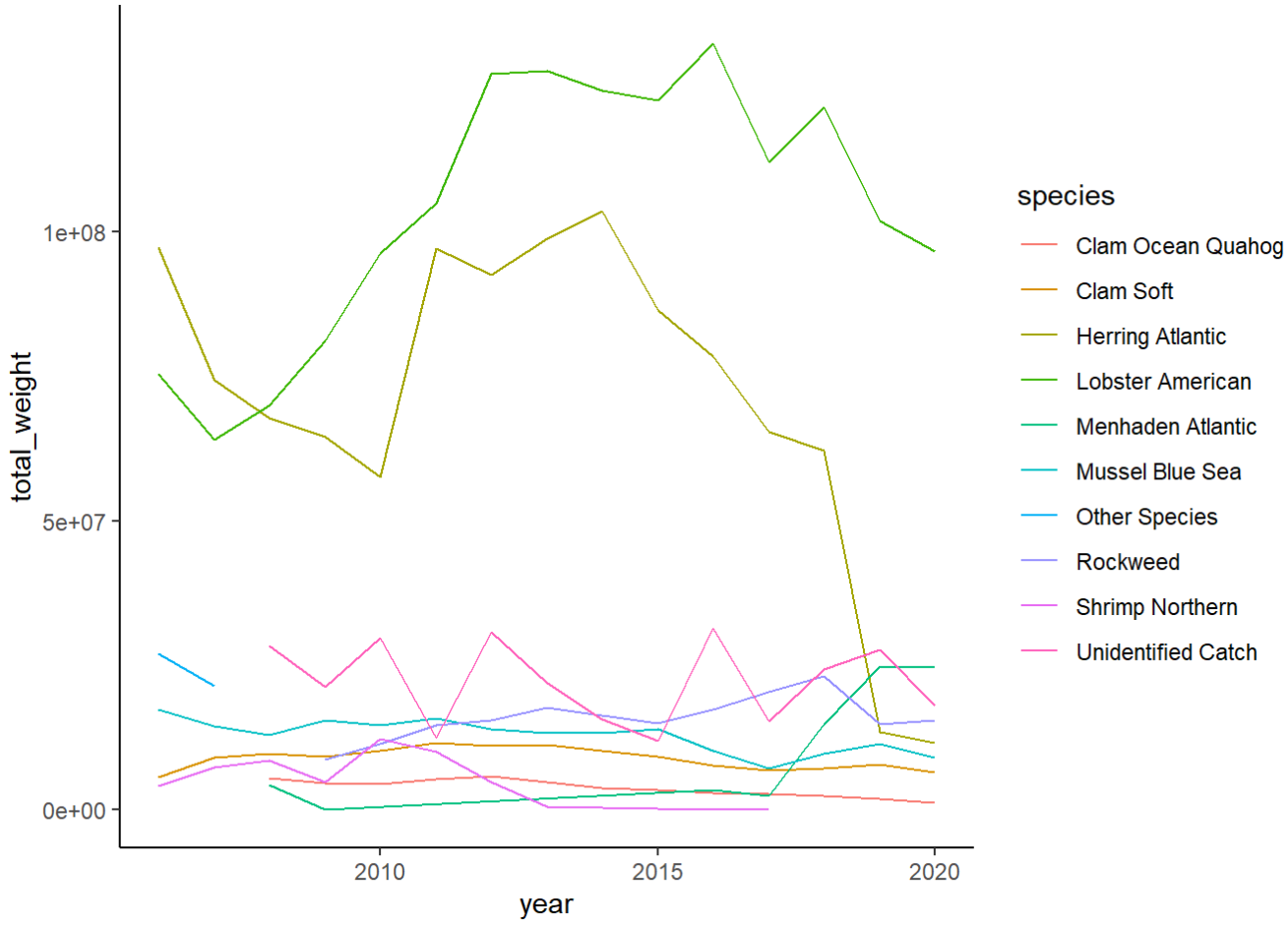
Species

species <chr>	year <int>	total_weight <dbl>
	2019	21.00
Bloodworms	2006	160651.00
Bloodworms	2007	411067.00
Bloodworms	2008	537010.65

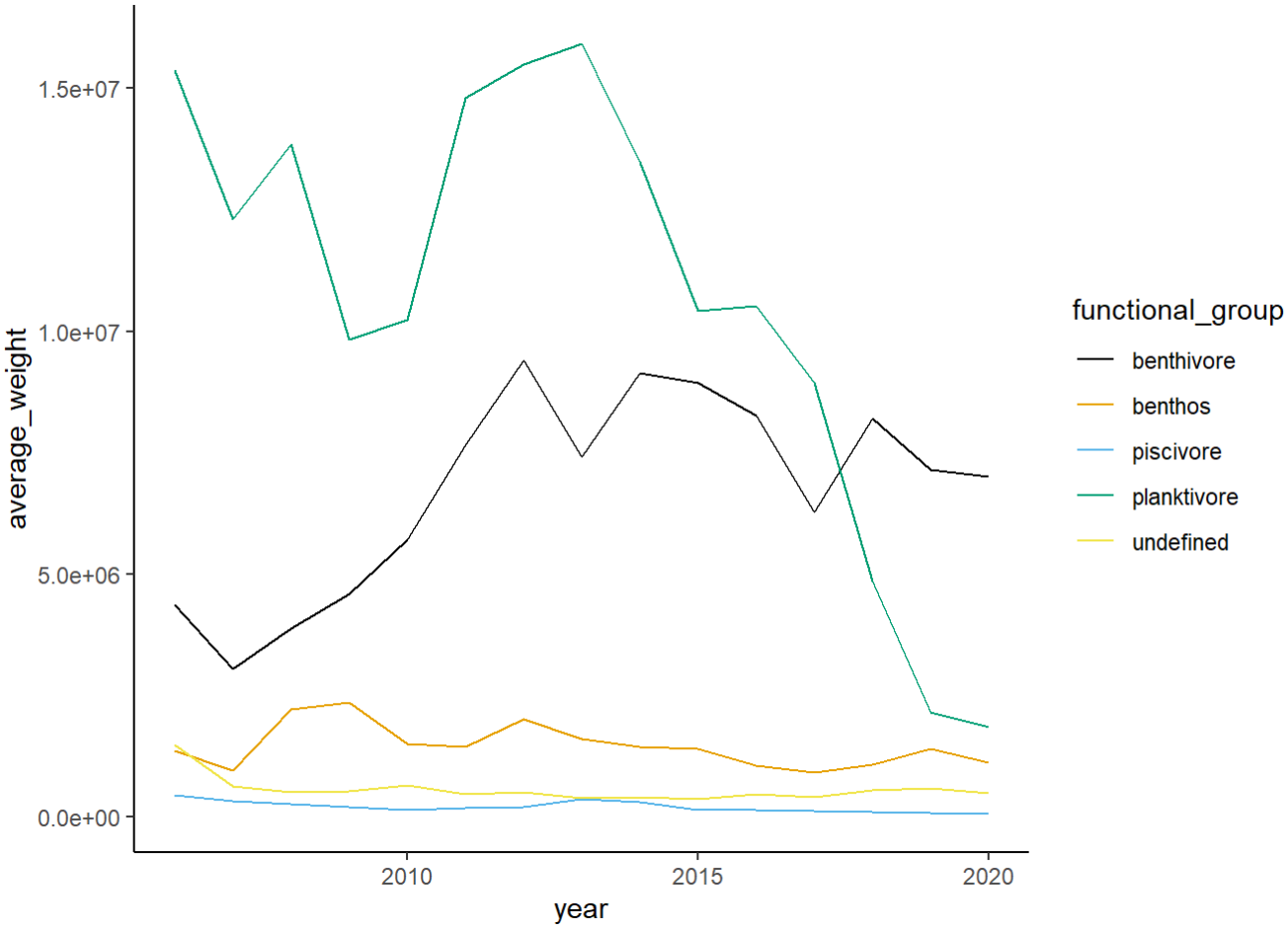
species <chr>	year <int>	total_weight <dbl>
Bloodworms	2009	574299.67
Bloodworms	2010	534228.21
Bloodworms	2011	525827.03
Bloodworms	2012	457037.39
Bloodworms	2013	470242.76
Bloodworms	2014	447767.48

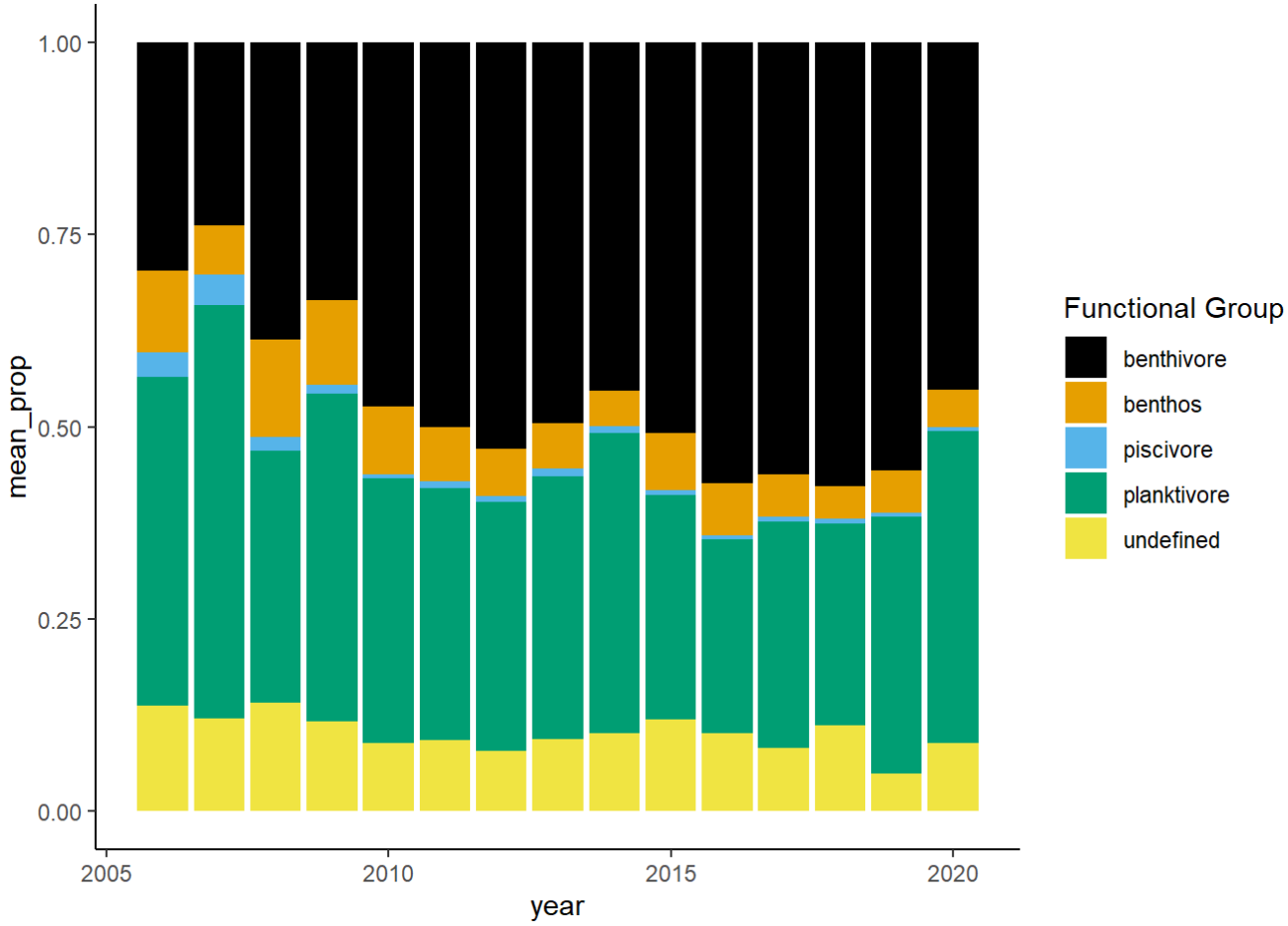
1-10 of 524 rows Previous **1** 2 3 4 5 6 ... 53 Next

Top 10 species

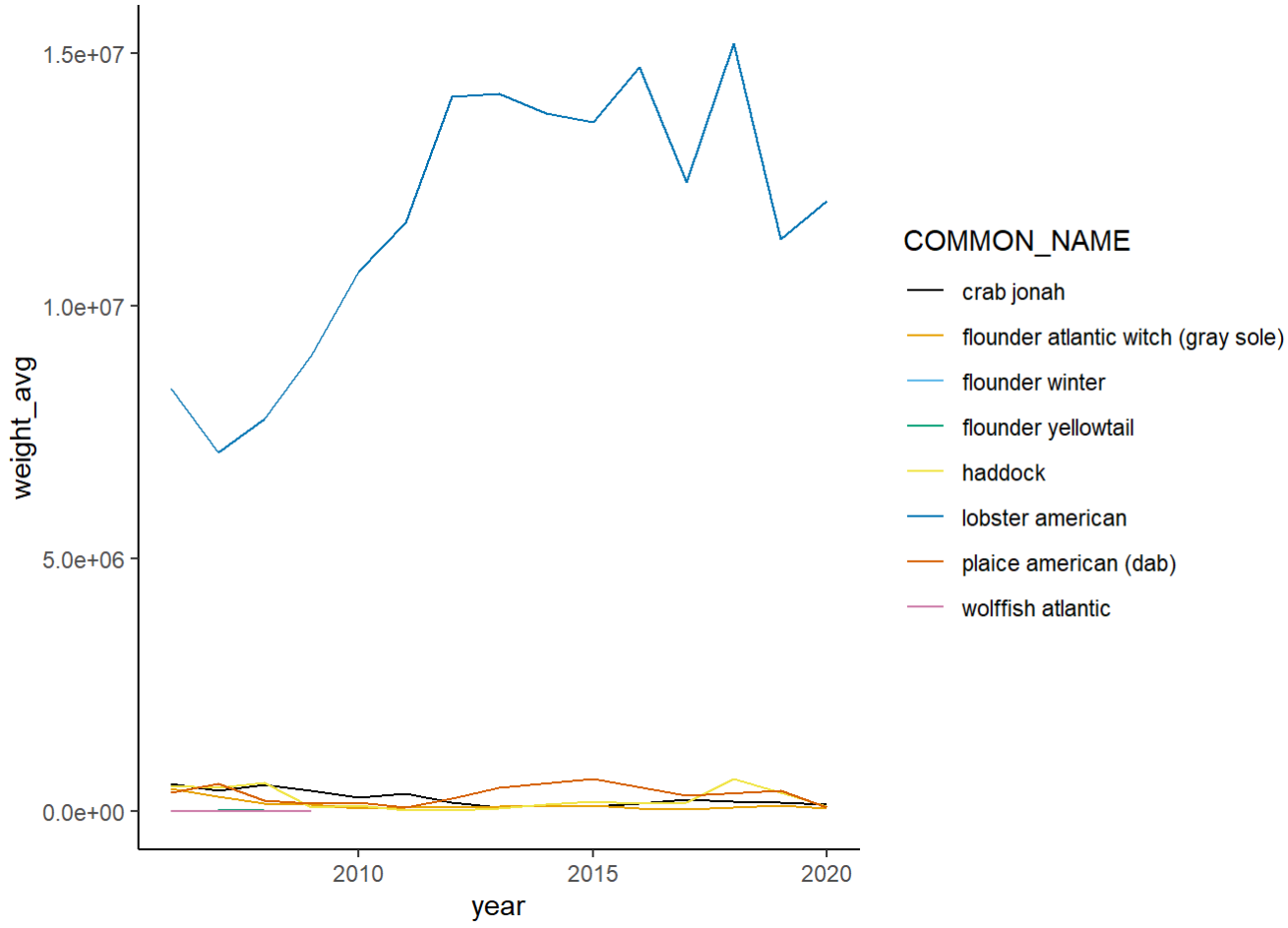


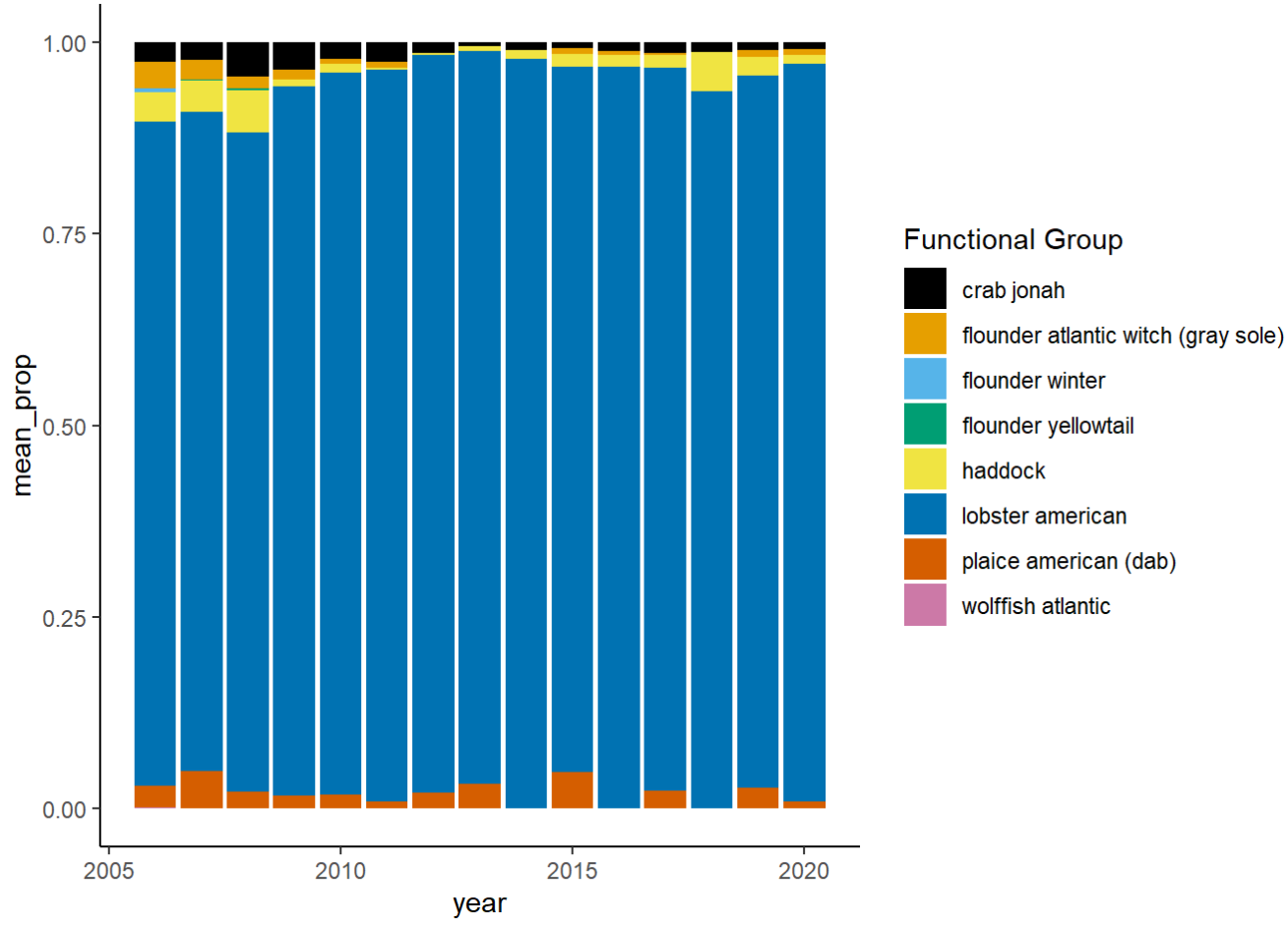
Functional Groups


average_weight
1.5e+07
1.0e+07
5.0e+06
0.0e+00
2010
2015
2020
year
functional_group
benthivore
benthos
piscivore
planktivore
undefined

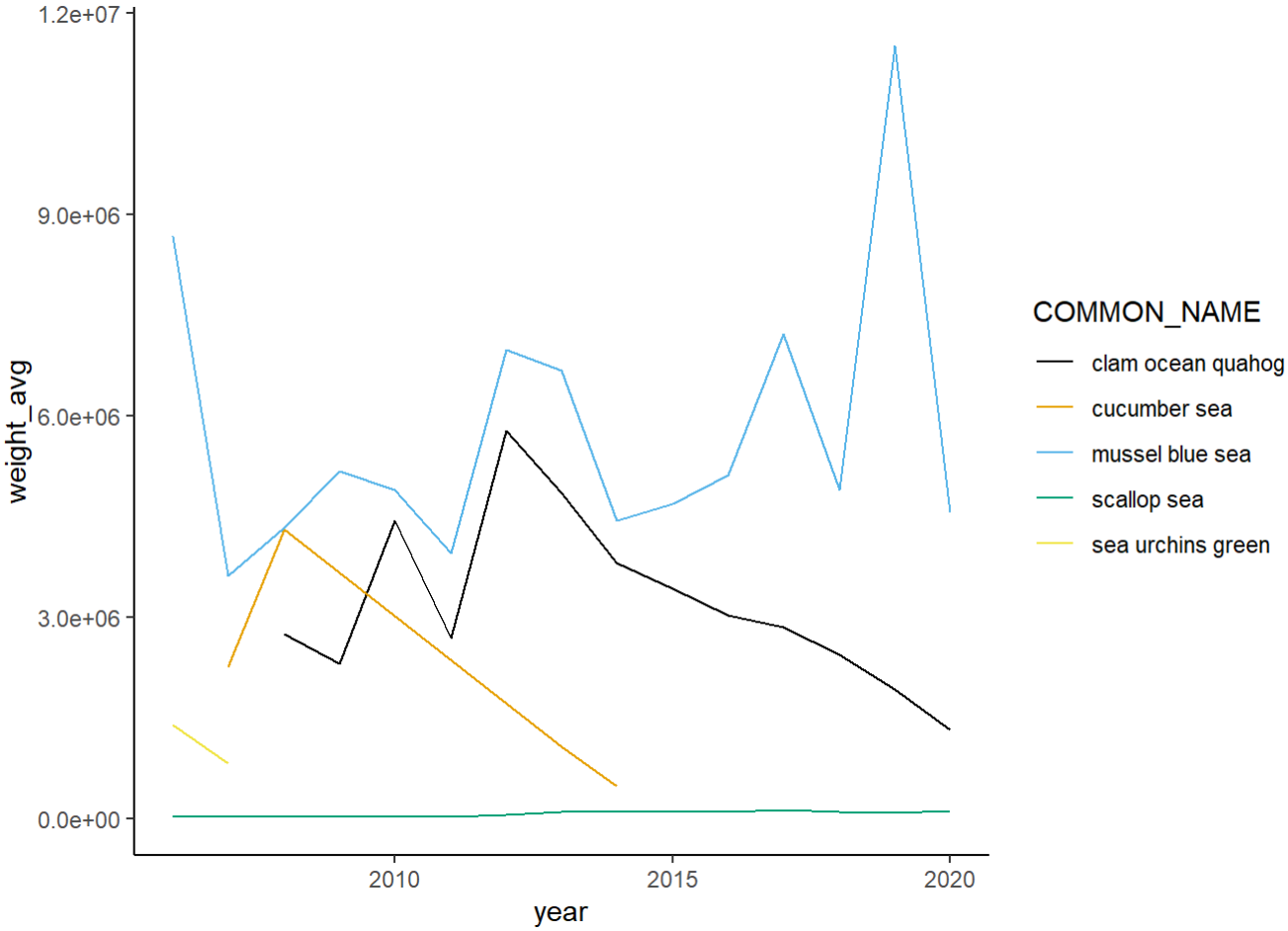

mean_prop
1.00
0.75
0.50
0.25
0.00
2005
2010
2015
2020
year
Functional Group
benthivore
benthos
piscivore
planktivore
undefined

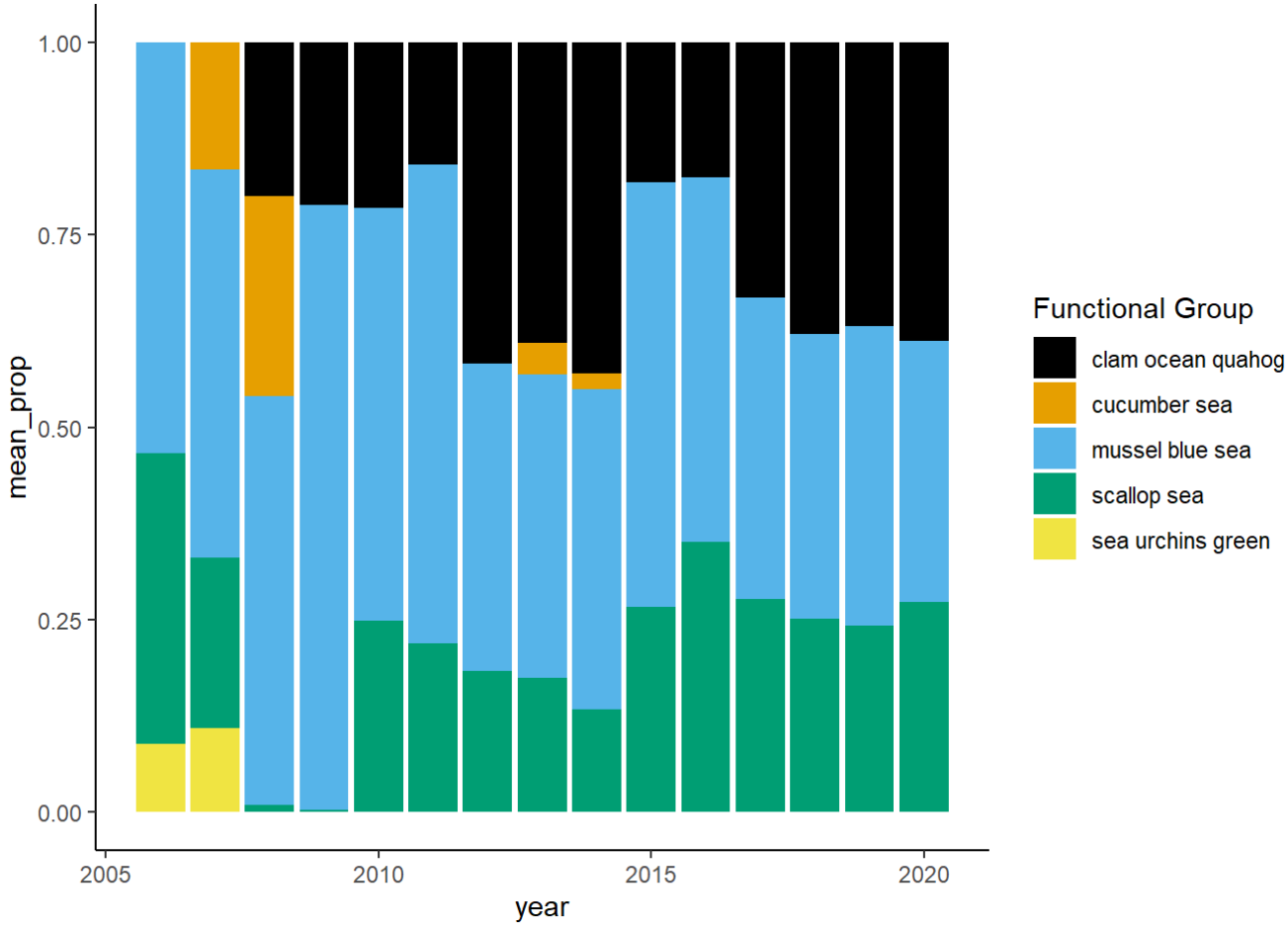
Benthivore


1.5e+07
1.0e+07
5.0e+06
0.0e+00
weight_avg
2010
2015
2020
year
COMMON_NAME
crab jonah
flounder atlantic witch (gray sole)
flounder winter
flounder yellowtail
haddock
lobster american
plaice american (dab)
wolffish atlantic

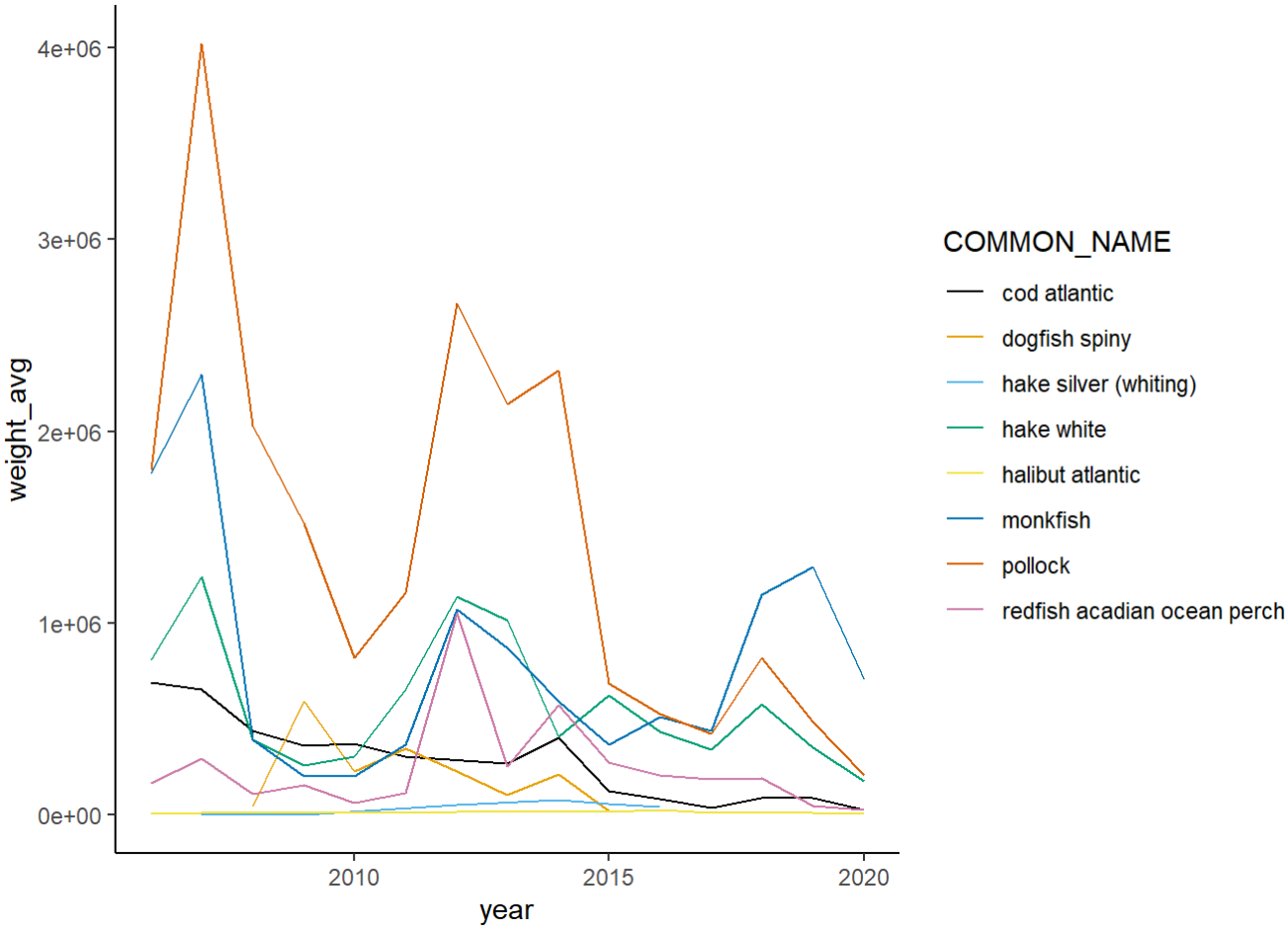

1.00
0.75
0.50
0.25
0.00
mean_prop
2005
2010
2015
2020
year
Functional Group
crab jonah
flounder atlantic witch (gray sole)
flounder winter
flounder yellowtail
haddock
lobster american
plaice american (dab)
wolffish atlantic

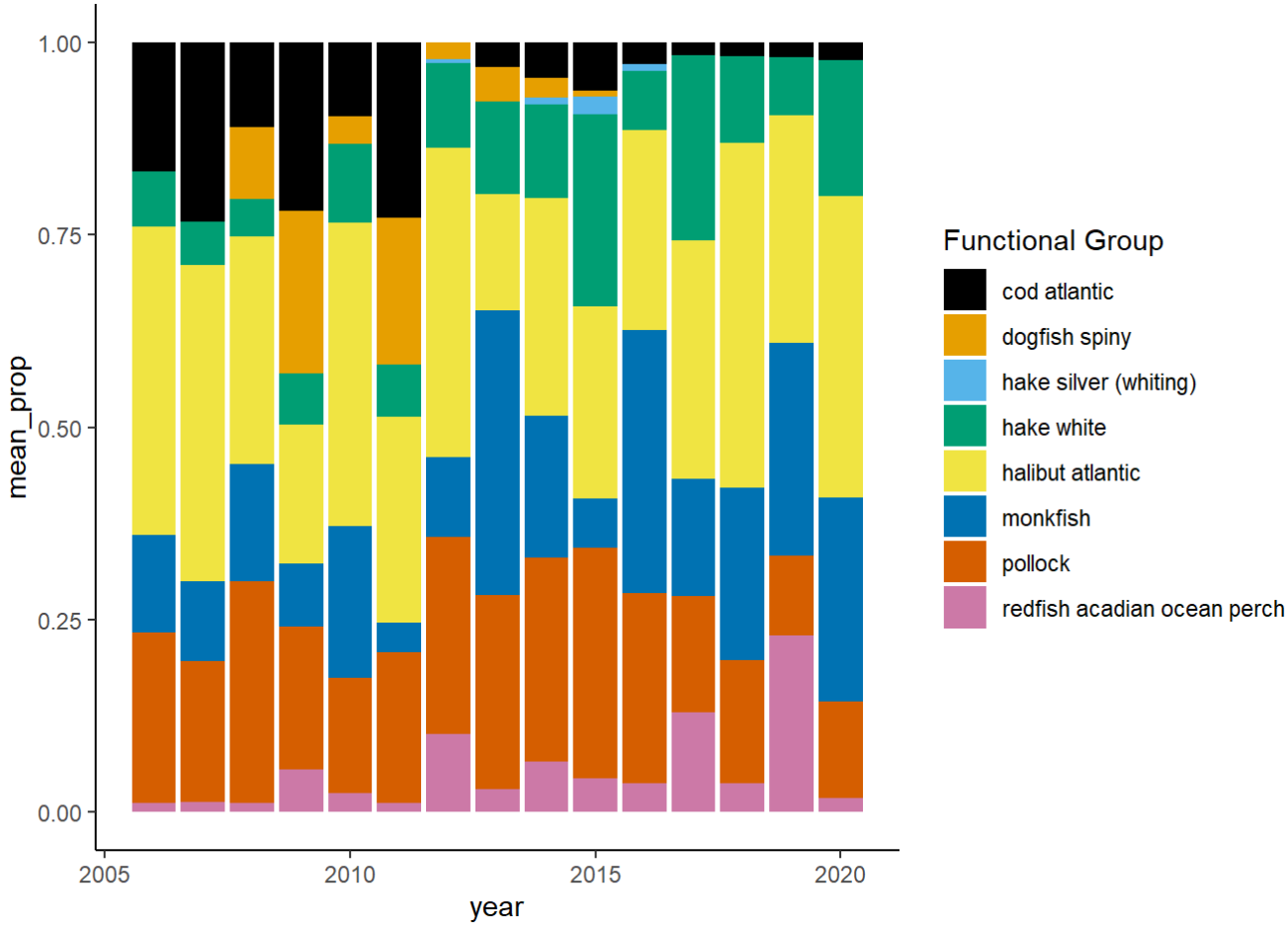
Benthos


1.2e+07
9.0e+06
6.0e+06
3.0e+06
0.0e+00
weight_avg
2010
2015
2020
year
COMMON_NAME
clam ocean quahog
cucumber sea
mussel blue sea
scallop sea
sea urchins green

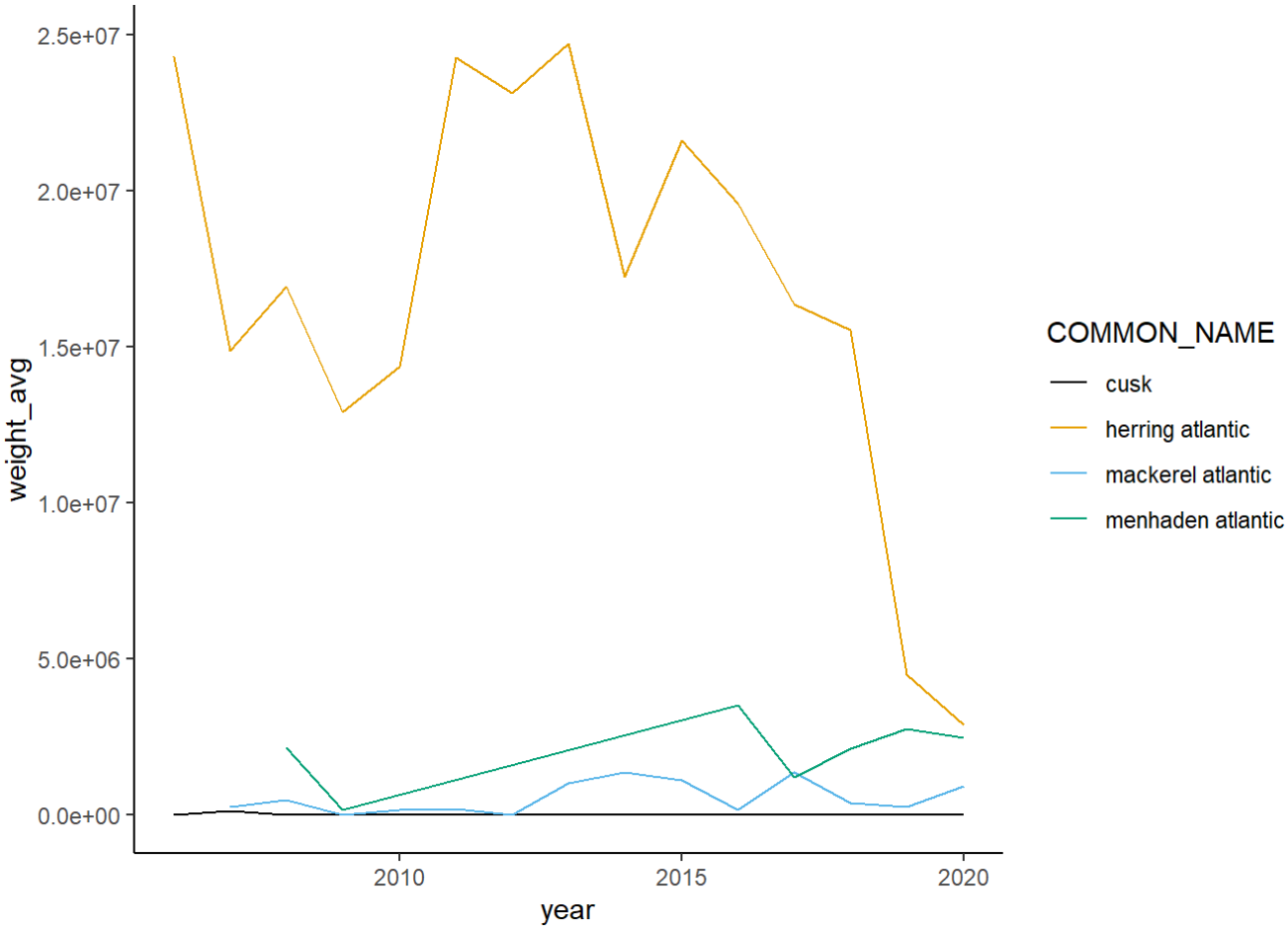

1.00
0.75
0.50
0.25
0.00
mean_prop
2005
2010
2015
2020
year
Functional Group
clam ocean quahog
cucumber sea
mussel blue sea
scallop sea
sea urchins green

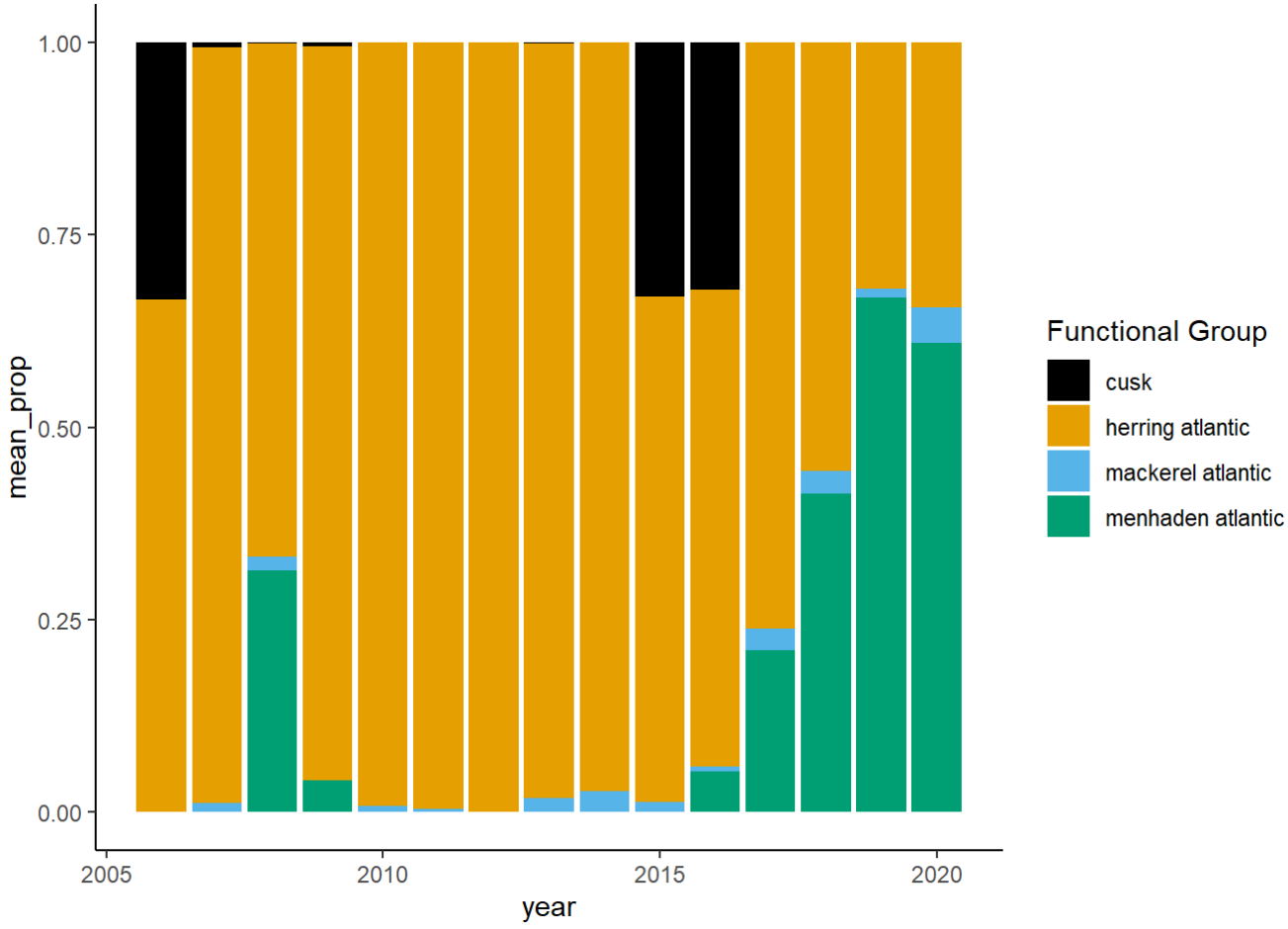
Piscivore


4e+06
3e+06
2e+06
1e+06
0e+00
weight_avg
2010
2015
2020
year
COMMON_NAME
cod atlantic
dogfish spiny
hake silver (whiting)
hake white
halibut atlantic
monkfish
pollock
redfish acadian ocean perch

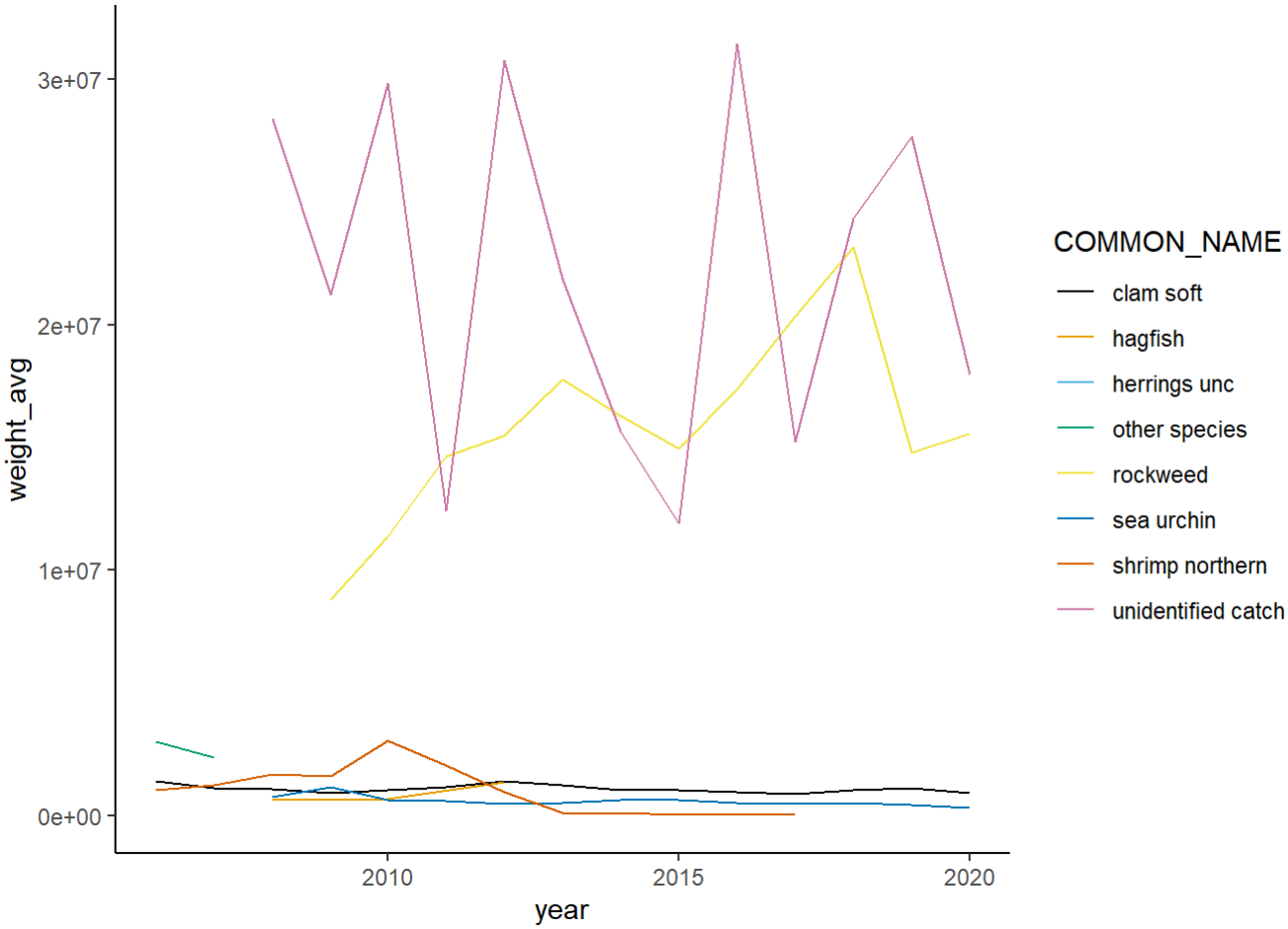

1.00
0.75
0.50
0.25
0.00
mean_prop
2005
2010
2015
2020
year
Functional Group
cod atlantic
dogfish spiny
hake silver (whiting)
hake white
halibut atlantic
monkfish
pollock
redfish acadian ocean perch

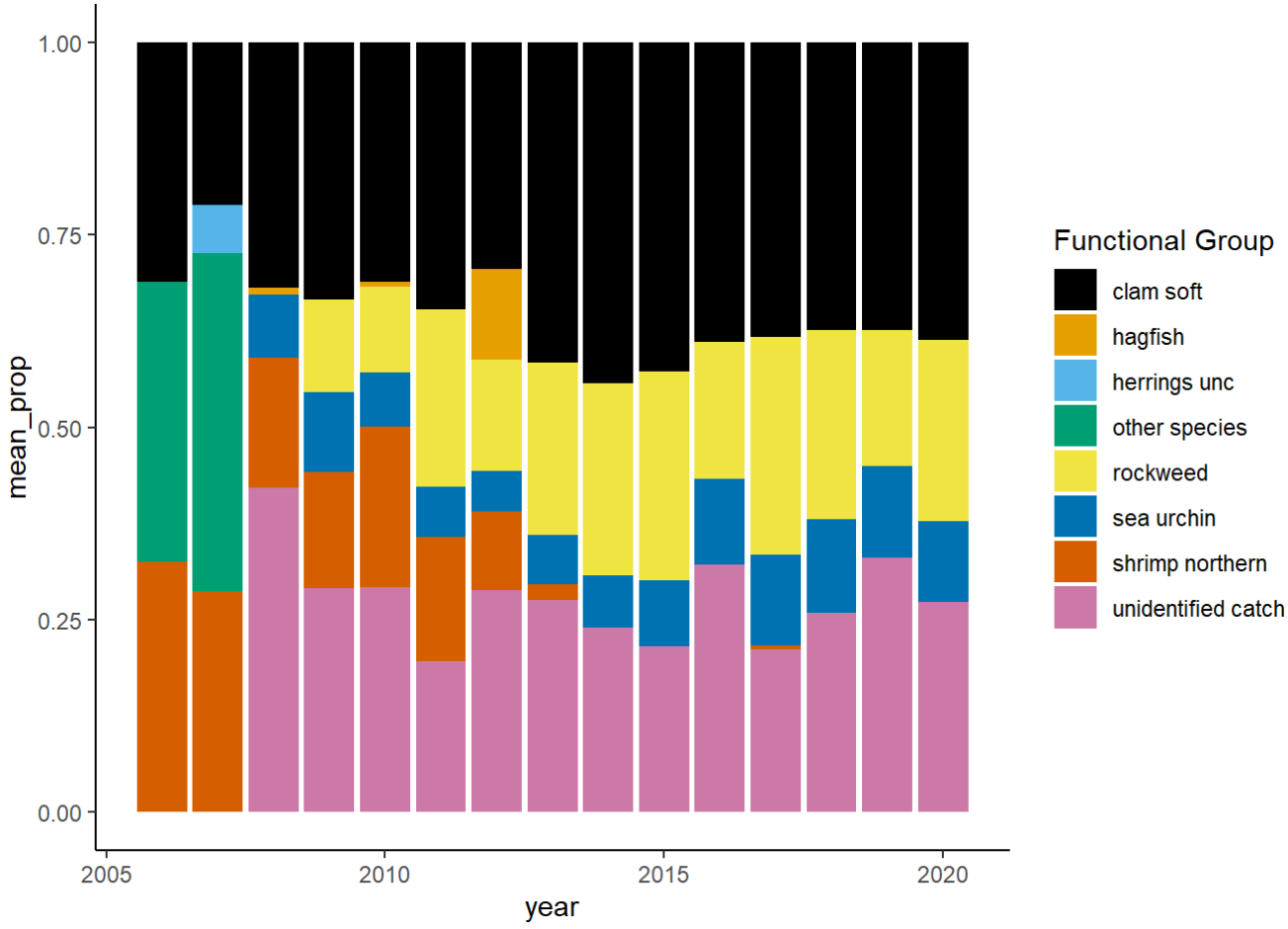
Planktivore


2.5e+07
2.0e+07
1.5e+07
1.0e+07
5.0e+06
0.0e+00
weight_avg
2010
2015
2020
year
COMMON_NAME
cusk
herring atlantic
mackerel atlantic
menhaden atlantic


1.00
0.75
0.50
0.25
0.00
mean_prop
2005
2010
2015
2020
year
Functional Group
cusk
herring atlantic
mackerel atlantic
menhaden atlantic

Undefined


3e+07
2e+07
1e+07
0e+00
weight_avg
2010
2015
2020
year
COMMON_NAME
clam soft
hagfish
herrings unc
other species
rockweed
sea urchin
shrimp northern
unidentified catch


1.00
0.75
0.50
0.25
0.00
mean_prop
2005
2010
2015
2020
year
Functional Group
clam soft
hagfish
herrings unc
other species
rockweed
sea urchin
shrimp northern
unidentified catch