

Albacore Diet Synthesis C

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Trait variation in albacore diet across geographies

About

This document contains code for loading mostly manipulated data for global albacore prey communities consumed and for conducting multivariate community analyses and traitglm on albacore diets across ocean basins, using habitat association, gregariousness traits and cluster # output from cluster analyses.

Workspace

Data needs

- Species (L): alb_prob_preyPA ==> “./data/output_data/alb_prob_preyPA_use.csv”
- Env/Site (R): alb_prob_covars ==> “./data/output_data/alb_prob_covars_use.csv”
- Traits (Q): alb_prob_traits ==> “./data/output_data/alb_prob_traits_use.csv”

Load DFs for analyses

```
#L - species df
alb_prob_preyPA = read.csv(here("./data/output_data/alb_prob_preyPA_use.csv")) %>%
  dplyr::select(-X)
#Currently imported with sites as rows
#Data are integers, could be numeric if modelling issues

#Example code
#alb_adult_prey[,1:ncol(alb_adult_prey)] = lapply(alb_adult_prey[,1:ncol(alb_adult_prey)], as.numeric)

dim(alb_prob_preyPA) #225 obs, 123 species

## [1] 209 123

#R - covars df
alb_prob_covars = read.csv(here("./data/output_data/alb_prob_covars_use.csv")) %>%
  dplyr::select(-X)
#Currently imported with sites as rows
```

```

#As factors
alb_prob_covars[,1:ncol(alb_prob_covars)] = lapply(alb_prob_covars[,1:ncol(alb_prob_covars)], as.factor)

#Q - trait df
alb_prob_traits = read.csv(here("./data/output_data/alb_prob_traits_use.csv"))%>%
  dplyr::select(-X)

#Needs species as rows
#Assign species as rownames
rownames(alb_prob_traits) <- alb_prob_traits$prey_sp
#Order species list if needed
alb_prob_traits <- alb_prob_traits[ order(row.names(alb_prob_traits)), ]
#Traits as factors for analyses
alb_prob_traits[,1:ncol(alb_prob_traits)] = lapply(alb_prob_traits[,1:ncol(alb_prob_traits)], as.factor)

dim(alb_prob_traits) #123 17

## [1] 123 17

```

DF Checks

Traits

Check trait values distribution if needed.

```

summary(alb_prob_traits$life_stage)

summary(alb_prob_traits$vert_habitat) #merge bathypelagic and mesopelagic

summary(alb_prob_traits$horz_habitat) #potential merger of continental shelf/slope, and coastal/reef as

summary(alb_prob_traits$diel_migrant_cat)

summary(alb_prob_traits$season_cat)

summary(alb_prob_traits$gregarious)

summary(alb_prob_traits$prob.clust.num) #low numbers in cluster #8 = 2

```

Trait variable levels look good.

```

levels(alb_prob_traits$vert_habitat) #check

## [1] "benthic"      "demersal"      "epipelagic"    "mesopelagic"

levels(alb_prob_traits$horz_habitat) #check

## [1] "coastal"       "continental shelf" "oceanic"

```

```
levels(alb_prob_traits$gregarious) #check
```

```
## [1] "schooling" "solitary"
```

Covars

```
#Summary stats on covars
unique(alb_prob_covars$StudyID) #22 studies
unique(alb_prob_covars$OceanBasin) #6 Ocean basins
unique(alb_adult_fo$OceanBasinQ) #10 Ocean basin quarters, but data gets thin for many
unique(alb_prob_covars$YearEnd) #-27 years (or groups of years) are represented in this study
unique(alb_prob_covars$code) #10 Longhurst provinces represented, similar to Ocean Basin Q but also get
unique(alb_prob_covars$pred_life) #
```

We'll be using the best covars based on balance and replication ==> pred_life, OceanBasin, lat_cat.

```
#Check representation
#summary(alb_adult_covars)

summary(alb_prob_covars$lat_cat)
#temperate tropical
# 178      31

summary(alb_prob_covars$pred_life)
# adult juvenile mixed
# 54       62      93
#Predator life stage
alb_prob_covars$pred_life <- factor(alb_prob_covars$pred_life,
                                         levels = c("mixed", "adult", "juvenile"))

#Check
#levels(alb_prob_covars$pred_life)

summary(alb_prob_covars$OceanBasin)
#           Indian Mediterranean      N Atlantic      N Pacific      S Atlantic      S Pacific
#             15                  29                 78                 62                  8                  17

#Select some covars & traits
alb_prob_covars$OceanBasin <- factor(alb_prob_covars$OceanBasin, levels = c("Mediterranean", "N Atlantic"))
#Check
#levels(alb_prob_covars$OceanBasin)

summary(alb_prob_covars$OceanBasinQ)
#Not going to use

summary(alb_prob_covars$code)
#Not going to use
```

DF manips for multivariate analyses

```
## Make sure species names match abund matrix
rownames(alb_prob_traits) == colnames(alb_prob_preyPA) #awesome!

# Then create the mvabund matrix
alb_prob_preyPA_mv = as.mvabund(alb_prob_preyPA)

#Check again that species names match trait values
rownames(alb_prob_traits) == colnames(alb_prob_preyPA_mv) #awesome!

#Check all matrix dimensions
dim(alb_prob_traits) #123 species and 17 traits
dim(alb_prob_preyPA_mv) #209 obs, 123 species
dim(alb_prob_covars) #209 obs, 13 variables

#Species df is ready --> alb_prob_preyPA_mv

#Covars --> want to use
#alb_prob_covars$OceanBasin
#alb_prob_covars$pred_life
#alb_prob_covars$lat_cat

#Traits - select and manipulate that df - ideally we want to use the same df here
traits_use = alb_prob_traits[,c(2:6,13,17)] %>%
  dplyr::rename(cluster = prob.clust.num)
#All still factors
#Using all traits
#traits_use[,1:6]
#and just clusters
```

TRAIT GLMS

MODEL TALLY

Manyglms for model comparisons

- prob_life_spp
- prob_ocean_spp
- prob_lat_spp
- prob_life_clusters_many
- prob_ocean_clusters_many
- prob_life_trait_many
- prob_ocean_trait_many

LASSO glm1path models for significance testing

- prob_life_cluster_LASSO
- prob_ocean_cluster_LASSO
- prob_life_trait_LASSO
- prob_ocean_trait_LASSO
- prob_lat_trait_LASSO

READ MODELS BACK IN

Species and environment matrix models - manyglm.

```
#/Users/tashhardy/Documents/GitHub/albacore-diet-global/outputs_figures/traitglms/prob_models

prob_life_spp = readRDS(here("outputs_figures/traitglms/prob_models/prob_life_spp.rds"))
prob_ocean_spp = readRDS(here("outputs_figures/traitglms/prob_models/prob_ocean_spp.rds"))
prob_lat_spp = readRDS(here("outputs_figures/traitglms/prob_models/prob_lat_spp.rds"))
```

Species, cluster number and environment models - manyglms + LASSOs.

```
#Manyglms
prob_life_clusters_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_life_clusters_many.rds"))
prob_ocean_clusters_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_ocean_clusters_many.rds"))

#LASSO glms
prob_life_cluster_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_life_cluster_LASSO.rds"))
prob_ocean_cluster_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_ocean_cluster_LASSO.rds"))
```

Species, traits and environment models - manyglms + LASSOs.

```
# Manyglms
prob_life_trait_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_life_trait_many.rds"))
prob_ocean_trait_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_ocean_trait_many.rds"))
prob_lat_trait_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_lat_trait_many.rds"))

#LASSO glms
prob_life_trait_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_life_trait_LASSO.rds"))
prob_ocean_trait_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_ocean_trait_LASSO.rds"))
prob_lat_trait_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_lat_trait_LASSO.rds"))
```

Interaction models

```
#Manyglm
prob_inter_trait_many = readRDS(here("outputs_figures/traitglms/prob_models/prob_inter_trait_many.rds"))

#LASSO glms
prob_inter_trait_LASSO = readRDS(here("outputs_figures/traitglms/prob_models/prob_inter_trait_LASSO.rds"))
```

Species models

SPP Manyglm - Predator Life Stage add:, eval=FALSE

```

prob_life_spp <- traitglm(L = alb_prob_preyPA_mv,
                           R = alb_prob_covars$pred_life,
                           family=binomial(link = "logit")
                           ) #note default is "manyglm"

```

SPP Manyglm - Ocean Basin

```

prob_ocean_spp <- traitglm(L = alb_prob_preyPA_mv,
                           R = alb_prob_covars$OceanBasin,
                           family=binomial(link = "logit")
                           ) #note default is "manyglm"

#check model output if needed

```

SPP Manyglm - Latitude

```

prob_lat_spp <- traitglm(L = alb_prob_preyPA_mv,
                           R = alb_prob_covars$lat_cat,
                           family=binomial(link = "logit")
                           ) #note default is "manyglm"

#check model output if needed

```

SPP Manyglm - Life Stage - Check multivariate model outputs

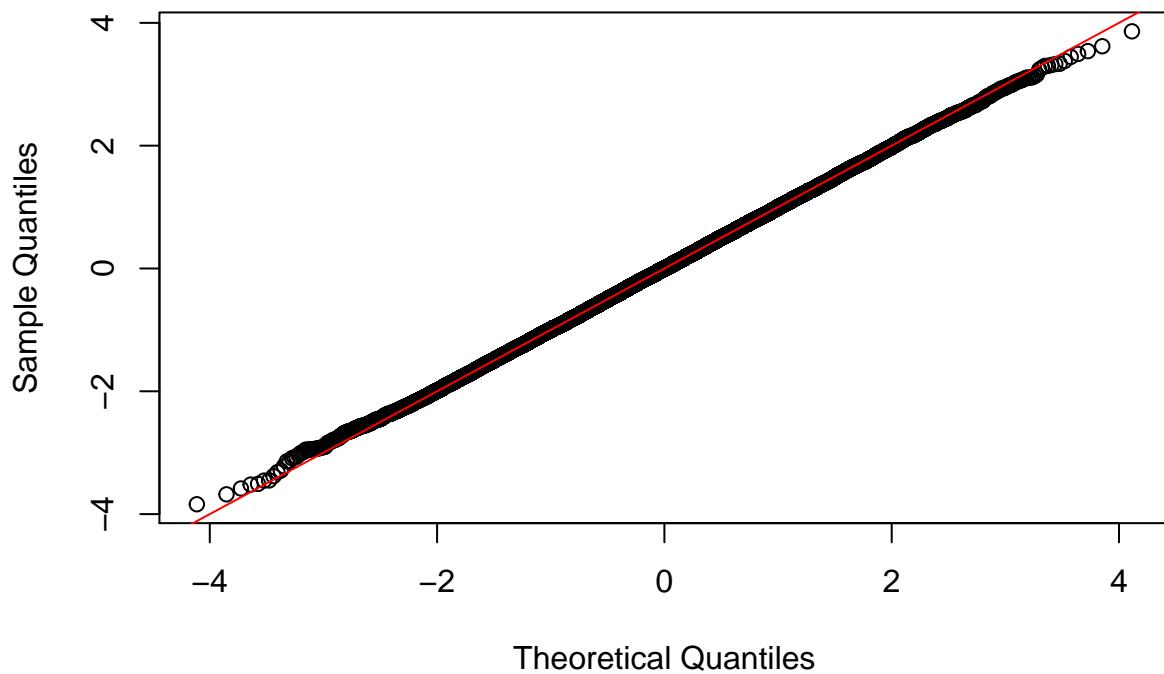
Note that multivariate residuals look good and we have a pretty good fit.

```

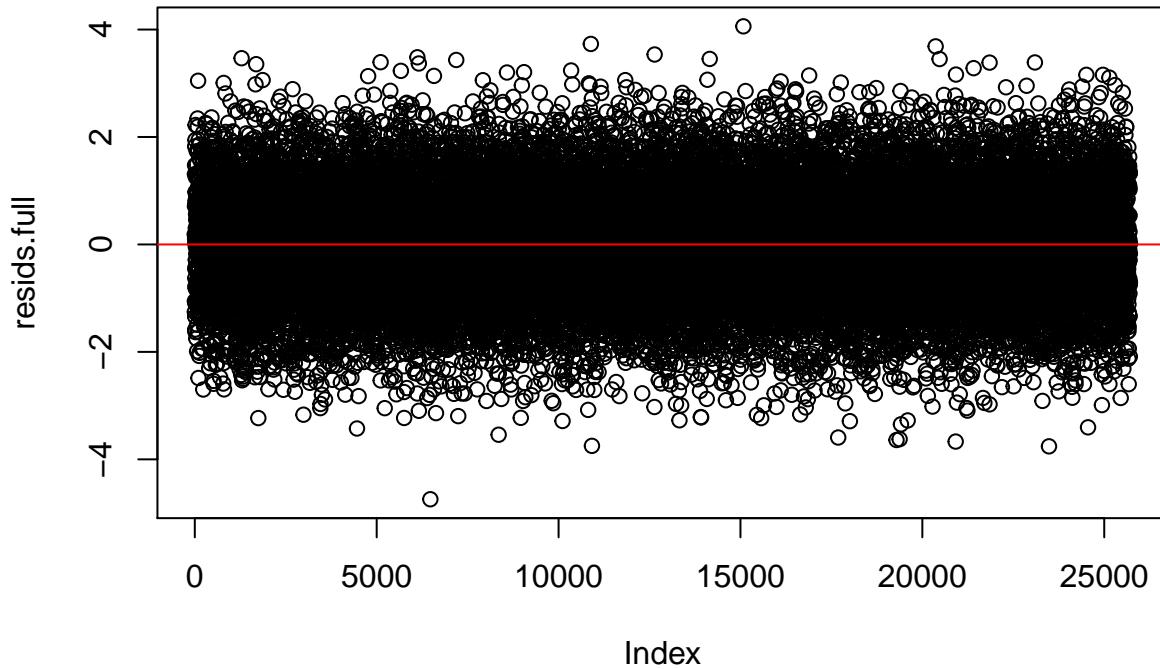
# Check model output - residuals TEST
qqnorm(residuals(prob_life_spp)[which(residuals(prob_life_spp) < 10000)])
abline(c(0, 1), col = "red")

```

Normal Q-Q Plot



```
# omit non-finite residuals FULL MODEL
resids.full = residuals(prob_life_spp)[is.finite((residuals(prob_life_spp)))]
plot(resids.full)
abline(c(0, 0), col = "red")
```



SAVE OUTPUTS SO FAR

```
#/Users/tashhardy/Documents/GitHub/albacore-diet-global/outputs_figures/traitglms/prob_models

saveRDS(prob_life_spp, file = here("outputs_figures/traitglms/prob_models/prob_life_spp.rds"))
saveRDS(prob_ocean_spp, file = here("outputs_figures/traitglms/prob_models/prob_ocean_spp.rds"))
saveRDS(prob_lat_spp, file = here("outputs_figures/traitglms/prob_models/prob_lat_spp.rds"))
```

Trait clusters models

Predator Life Stage MANYGLM Clusters - Predator Life Stage

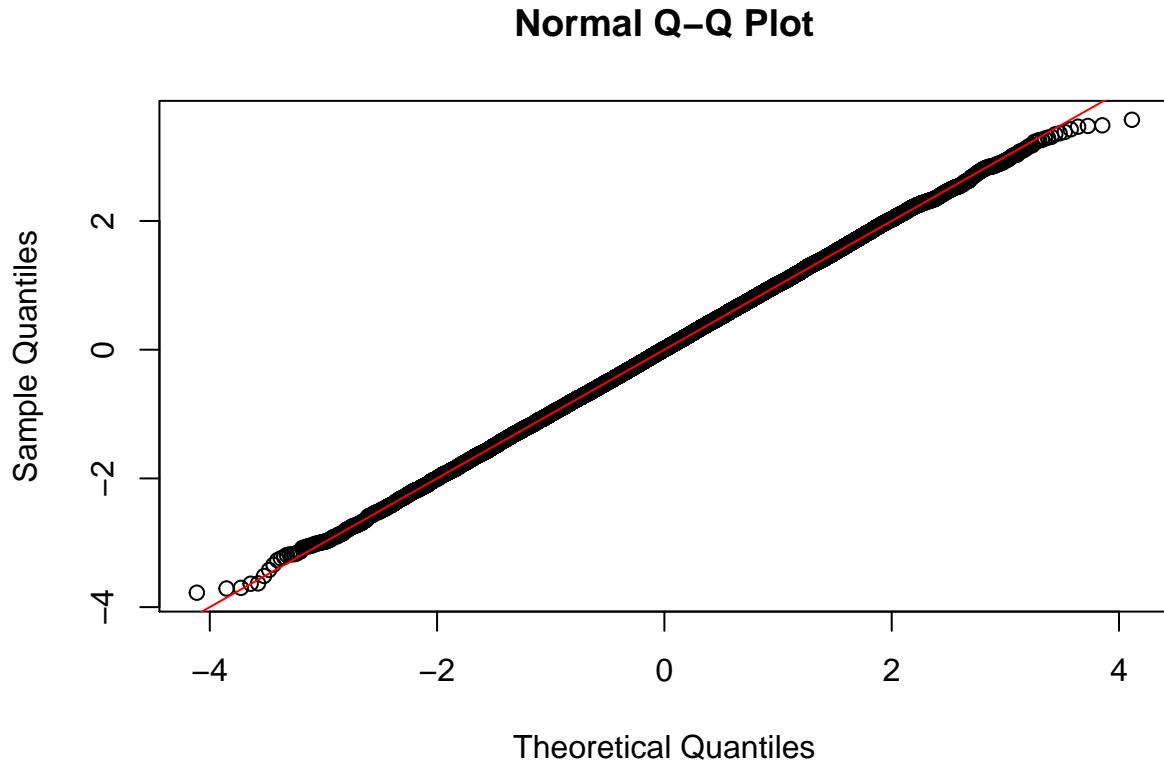
Trait (cluster)*Env (life stage) - Manyglm

```
prob_life_clusters_many <- traitglm(L = alb_prob_preyPA_mv,
                                      R = alb_prob_covars$pred_life,
                                      Q = traits_use$cluster,
                                      family=binomial(link = "logit")
                                      ) #note default is "manyglm"
```

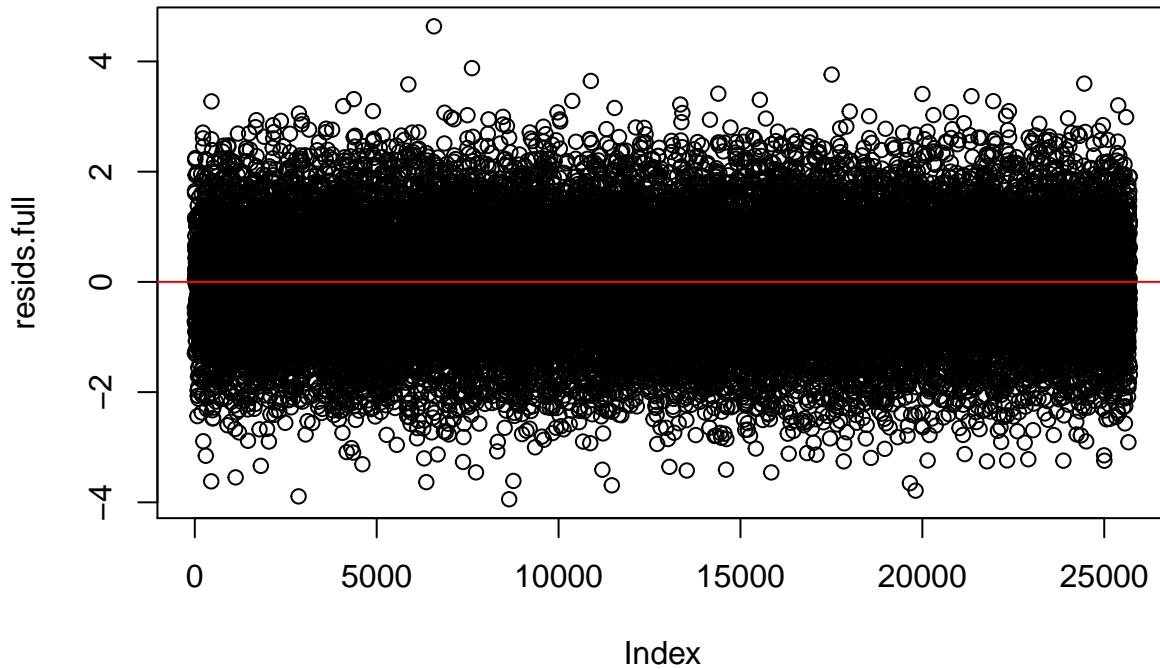
Note that outputs for all models look the same because residuals are the same, as we fit models to the same species and covariate datasets.

```
# Check model output - residuals TEST
qqnorm(residuals(prob_life_clusters_many)) [which(residuals(prob_life_clusters_many) <
```

```
 10000)])
abline(c(0, 1), col = "red")
```



```
# omit non-finite residuals FULL MODEL
resids.full = residuals(prob_life_clusters_many)[is.finite((residuals(prob_life_clusters_many)))]
plot(resids.full)
abline(c(0, 0), col = "red")
```



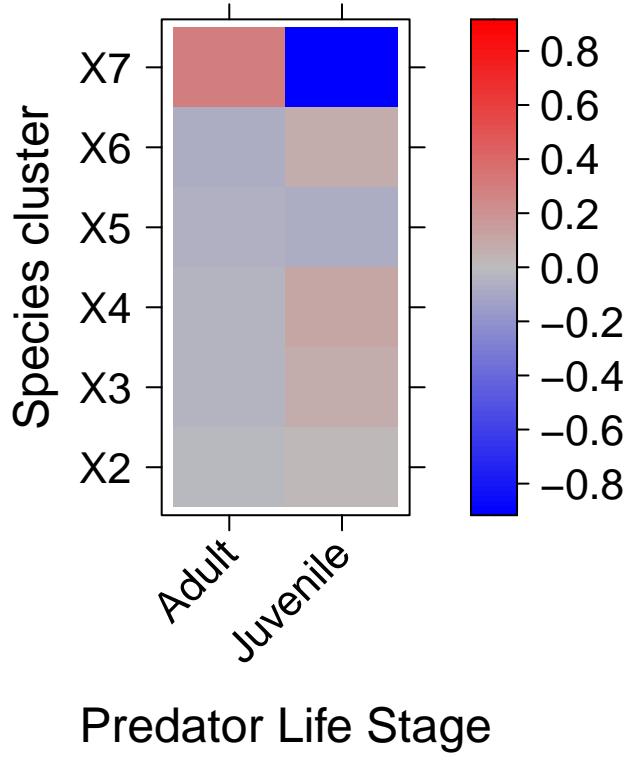
Visualise results of traitglm fit with manyglm routine, reference levels are the first cluster group and the mixed albacore life stage group.

```
a = max(abs(prob_life_clusters_many$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_life_clusters_many$fourth.corner))

rownames(temp) = c("Adult", "Juvenile")

prob_life_clusters_many_graph = levelplot(temp, xlab = list("Predator Life Stage",
  cex = 1.5), ylab = list("Species cluster", cex = 1.5), col.regions = colort(100),
  at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
  colorkey = list(labels = list(cex = 1.3)))

print(prob_life_clusters_many_graph)
```



```
ggsave(here("./outputs_figures/traitglms/prob_all_simple/prob_life_clusters_many_graph.pdf"),
       plot = as.ggplot(prob_life_clusters_many_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_clusters_many_graph.jpeg"),
       plot = as.ggplot(prob_life_clusters_many_graph), width = 12, height = 12, dpi = 300)
```

GLM1PATH Clusters - Predator Life Stage

Using method = glm1path == LASSO model.

```
prob_life_cluster_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                       R = alb_prob_covars$pred_life,
                                       Q = traits_use$cluster,
                                       family=binomial(link = "logit"),
                                       method="glm1path"
                                       ) #note default is "manyglm"
```

NOTE: We do not get a lot of significant values for the clusters as a trait.

```
a = max(abs(prob_life_cluster_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_life_cluster_LASSO$fourth.corner))

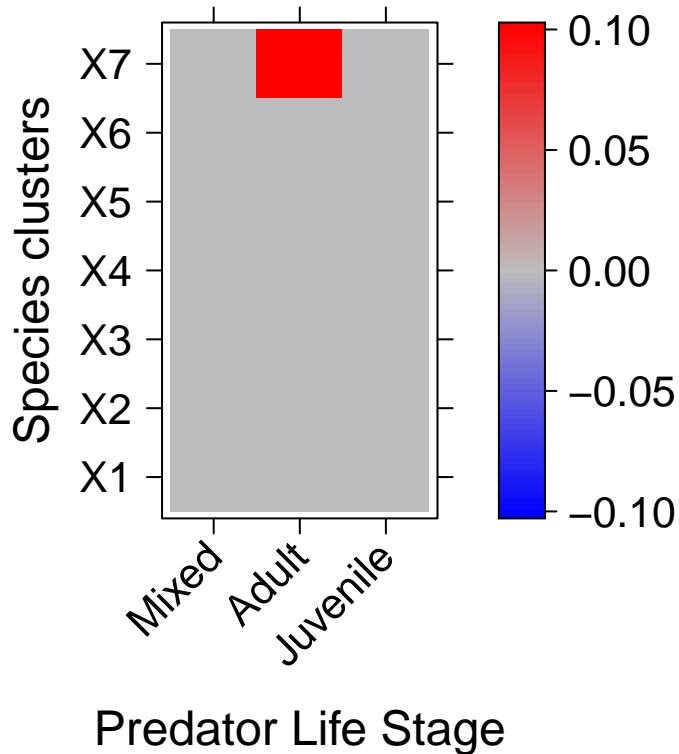
rownames(temp) = c("Mixed", "Adult", "Juvenile")
```

```

prob_life_cluster_LASSO_graph = levelplot(temp, xlab = list("Predator Life Stage",
  cex = 1.5), ylab = list("Species clusters", cex = 1.5), col.regions = colort(100),
  at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
  colorkey = list(labels = list(cex = 1.3)))

print(prob_life_cluster_LASSO_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_cluster7_LASSO_graph.pdf"),
  plot = as.ggplot(prob_life_cluster_LASSO_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_cluster7_LASSO_graph.jpeg"),
  plot = as.ggplot(prob_life_cluster_LASSO_graph), width = 12, height = 12, dpi = 300)

```

Ocean Basin MANYGLM Clusters - Ocean Basin

Trait (cluster)*Env (ocean basin) - Manyglm

```

prob_ocean_clusters_many <- traitglm(L = alb_prob_preyPA_mv,
  R = alb_prob_covars$OceanBasin,
  Q = traits_use$cluster,
  family=binomial(link = "logit")
) #note default is "manyglm"

```

```

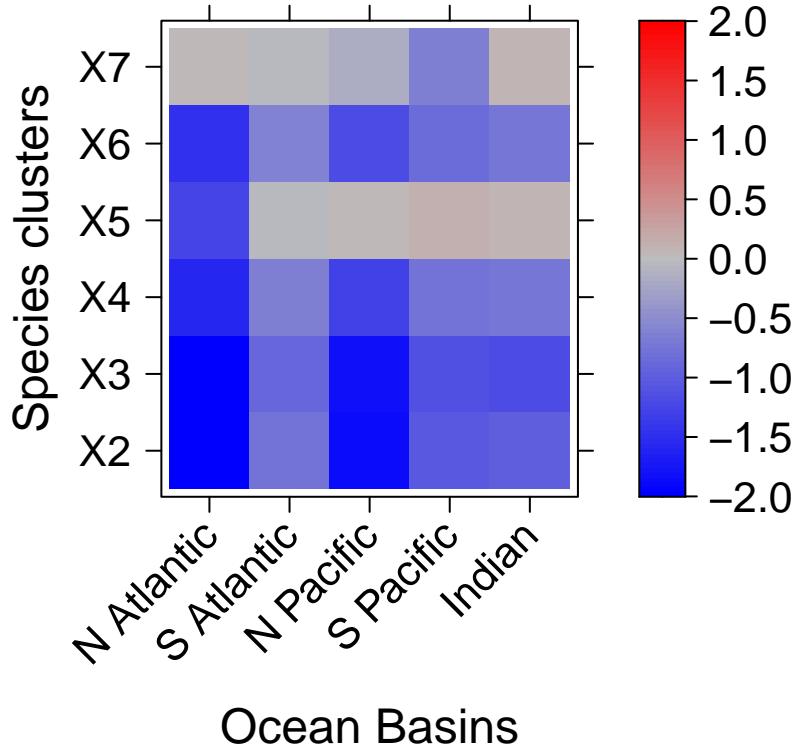
a      = max( abs(prob_ocean_clusters_many$fourth.corner) )
colort = colorRampPalette(c("blue","grey","red")) #can replace "grey" with "white"
temp = t(as.matrix(prob_ocean_clusters_many$fourth.corner))

rownames(temp) = c("#Mediterranean",
                   "N Atlantic",
                   "S Atlantic",
                   "N Pacific",
                   "S Pacific",
                   "Indian")

prob_ocean_clusters_many_graph = levelplot(temp,
                                             xlab=list("Ocean Basins", cex=1.5),
                                             ylab=list("Species clusters", cex=1.5),
                                             col.regions=colort(100),
                                             at=seq(-a, a,length=100),
                                             scales = list(x=list(rot = 45, cex=1.3), y=list(cex=1.3)),
                                             colorkey=list(labels=list(cex=1.3)))

print(prob_ocean_clusters_many_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_clusters_many_graph.pdf"),
       plot = as.ggpplot(prob_ocean_clusters_many_graph), width=12, height=12, dpi=300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_clusters_many_graph.jpeg"),

```

```
plot = as.ggplot(prob_ocean_clusters_many_graph), width=12, height=12, dpi=300)
```

GLM1PATH Clusters - Ocean Basin

Using method = glm1path == LASSO model.

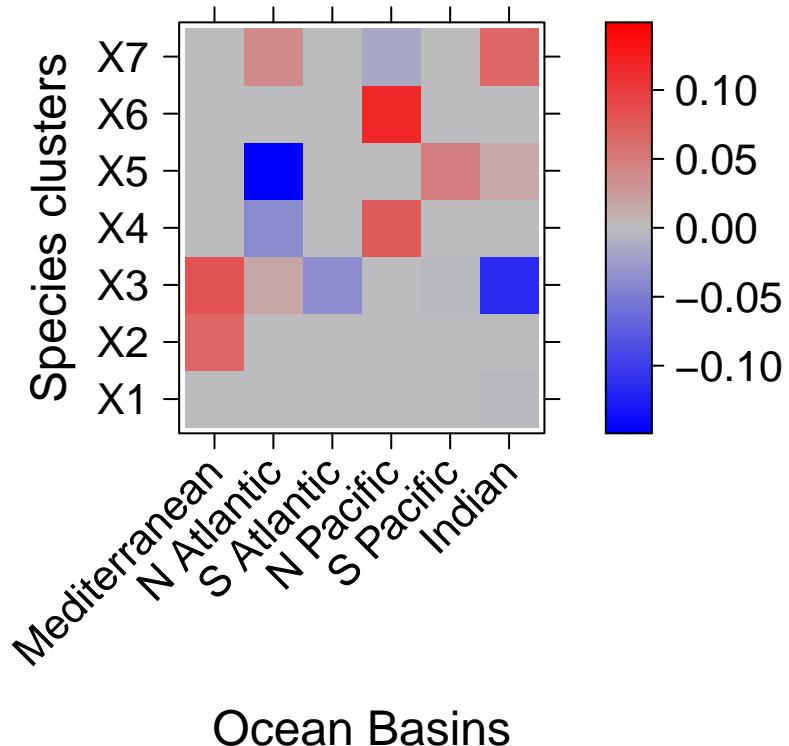
```
prob_ocean_cluster_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                         R = alb_prob_covars$OceanBasin,
                                         Q = traits_use$cluster,
                                         family=binomial(link = "logit"),
                                         method="glm1path"
                                         ) #note default is "manyglm"

a = max(abs(prob_ocean_cluster_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_ocean_cluster_LASSO$fourth.corner))

rownames(temp) = c("Mediterranean", "N Atlantic", "S Atlantic", "N Pacific", "S Pacific",
                  "Indian")

prob_ocean_cluster_LASSO_graph = levelplot(temp, xlab = list("Ocean Basins", cex = 1.5),
                                             ylab = list("Species clusters", cex = 1.5), col.regions = colort(100), at = seq(-a,
                                                                                           a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
                                             colorkey = list(labels = list(cex = 1.3)))

print(prob_ocean_cluster_LASSO_graph)
```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_cluster_LASSO_graph.pdf"),
       plot = as.ggplot(prob_ocean_cluster_LASSO_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_cluster_LASSO_graph.jpeg"),
       plot = as.ggplot(prob_ocean_cluster_LASSO_graph), width = 12, height = 12, dpi = 300)

```

Latitude Not done yet. Latitude models had lower explanatory power than ocean basin or predator life stage.

```

#/Users/tashhardy/Documents/GitHub/albacore-diet-global/outputs_figures/traitglms/prob_models

#Manyglm
saveRDS(prob_life_clusters_many, file = here("outputs_figures/traitglms/prob_models/prob_life_clusters"))
saveRDS(prob_ocean_clusters_many, file = here("outputs_figures/traitglms/prob_models/prob_ocean_clusters"))

#LASSO glms
saveRDS(prob_life_cluster_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_life_cluster_LASSO"))
saveRDS(prob_ocean_cluster_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_ocean_cluster_LASSO"))

```

SAVE CLUSTER OUTPUTS

Trait models

Predator Life Stage MANYGLM Trait values - Predator Life Stage

Trait (trait matrix)*Env (life stage) - Manyglm

```

prob_life_trait_many <- traitglm(L = alb_prob_preyPA_mv,
                                    R = alb_prob_covars$pred_life,
                                    Q = traits_use[,1:6],
                                    #traits_use_try,
                                    family=binomial(link = "logit")
                                    ) #note default is "manyglm"

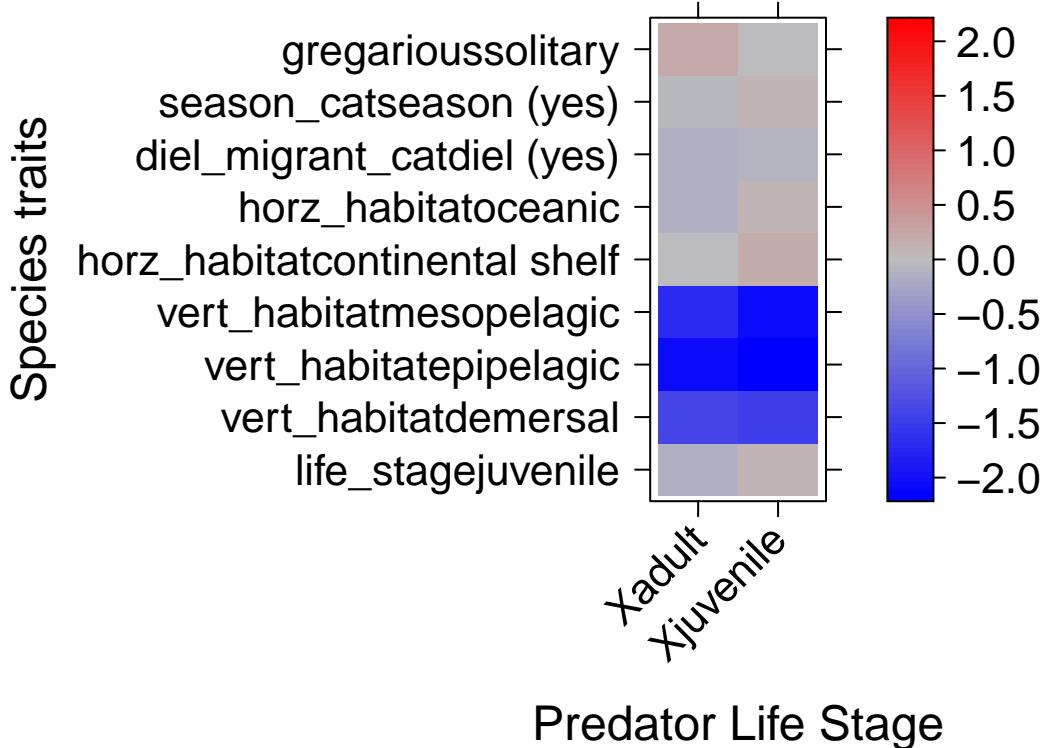
a = max(abs(prob_life_trait_many$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_life_trait_many$fourth.corner))

# rownames(temp) = c('Adult', 'Juvenile', 'Mixed') colnames(temp) = c('Vert.
# habitat - benthic', 'Vert. habitat - demersal', 'Vert. habitat - epipelagic',
# 'Vert. habitat - mesopelagic', 'Vert. habitat - bathypelagic', 'Horz. habitat
# - reef-associated', 'Horz. habitat - coastal', 'Horz. habitat - continental
# shelf', 'Horz. habitat - continental slope', 'Horz. habitat - oceanic', 'Diel
# migrant (yes)', 'Seasonal migrant (yes)', 'Gregarious - schooling')

prob_life_many_4th = levelplot(temp, xlab = list("Predator Life Stage", cex = 1.5),
                               ylab = list("Species traits", cex = 1.5), col.regions = colort(100), at = seq(-a,
                               a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
                               colorkey = list(labels = list(cex = 1.3)))

```

```
print(prob_life_many_4th)
```



```
ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_many_4th.pdf"),
       plot = as.ggplot(prob_life_many_4th), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_many_4th_graph.jpeg"),
       plot = as.ggplot(prob_ocean_cluster_LASSO_graph), width = 12, height = 12, dpi = 300)

# dev.copy2pdf(file=here('./outputs_figures/traitglms/fourth_lifestage.png'),
# width=12, height=5)
```

GLM1PATH Trait values - Predator Life Stage

Using method = glm1path == LASSO model.

```
prob_life_trait_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                      R = alb_prob_covars$pred_life,
                                      Q = traits_use[,1:6],
                                      family=binomial(link = "logit"),
                                      method="glm1path"
) #note default is "manyglm"
```

```
a = max(abs(prob_life_trait_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
```

```

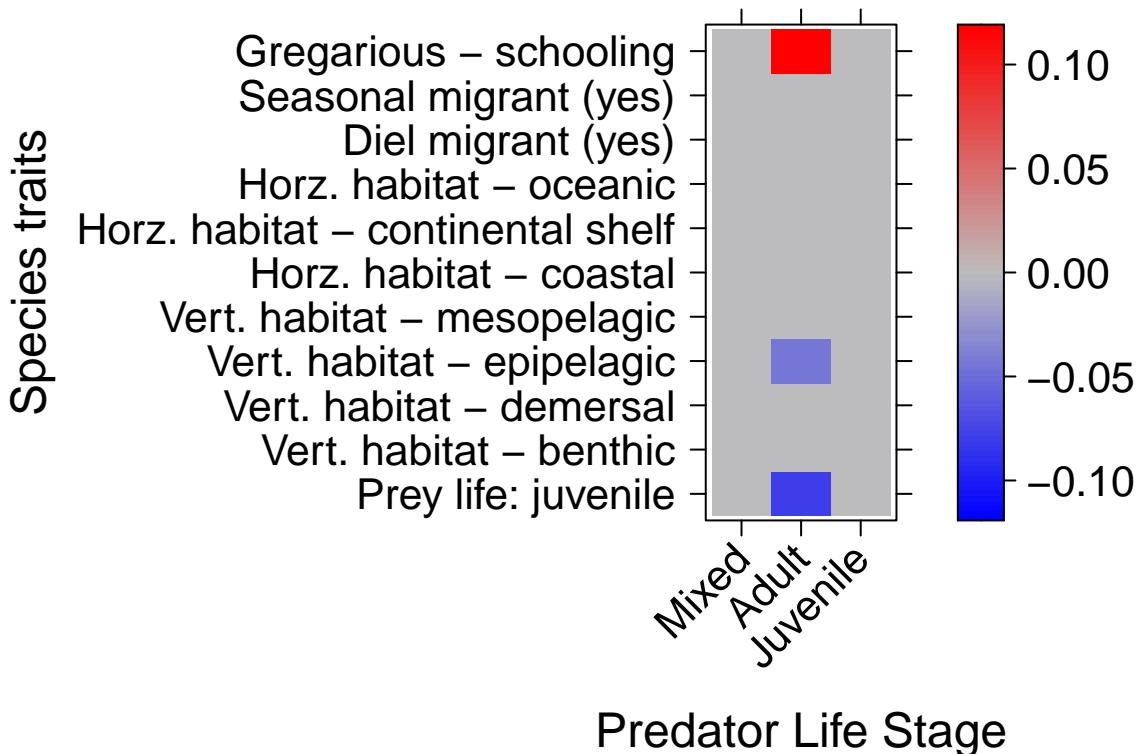
temp = t(as.matrix(prob_life_trait_LASSO$fourth.corner))

rownames(temp) = c("Mixed", "Adult", "Juvenile")
colnames(temp) = c("Prey life: juvenile", "Vert. habitat - benthic", "Vert. habitat - demersal",
  "Vert. habitat - epipelagic", "Vert. habitat - mesopelagic", "Horz. habitat - coastal",
  "Horz. habitat - continental shelf", "Horz. habitat - oceanic", "Diel migrant (yes)",
  "Seasonal migrant (yes)", "Gregarious - schooling")

prob_life_LASSO_graph = levelplot(temp, xlab = list("Predator Life Stage", cex = 1.5),
  ylab = list("Species traits", cex = 1.5), col.regions = colort(100), at = seq(-a,
  a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
  colorkey = list(labels = list(cex = 1.3)))

print(prob_life_LASSO_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_LASSO_graph.pdf"),
  plot = as.ggplot(prob_life_LASSO_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_life_LASSO_graph.jpeg"),
  plot = as.ggplot(prob_life_LASSO_graph), width = 12, height = 12, dpi = 300)

```

Ocean Basin MANYGLM Trait values - Ocean Basin

Trait (trait matrix)*Env (ocean basin) - Manyglm

```

prob_ocean_trait_many <- traitglm(L = alb_prob_preyPA_mv,
                                    R = alb_prob_covars$OceanBasin,
                                    Q = traits_use[,1:6],
                                    family=binomial(link = "logit")
                                    ) #note default is "manyglm"

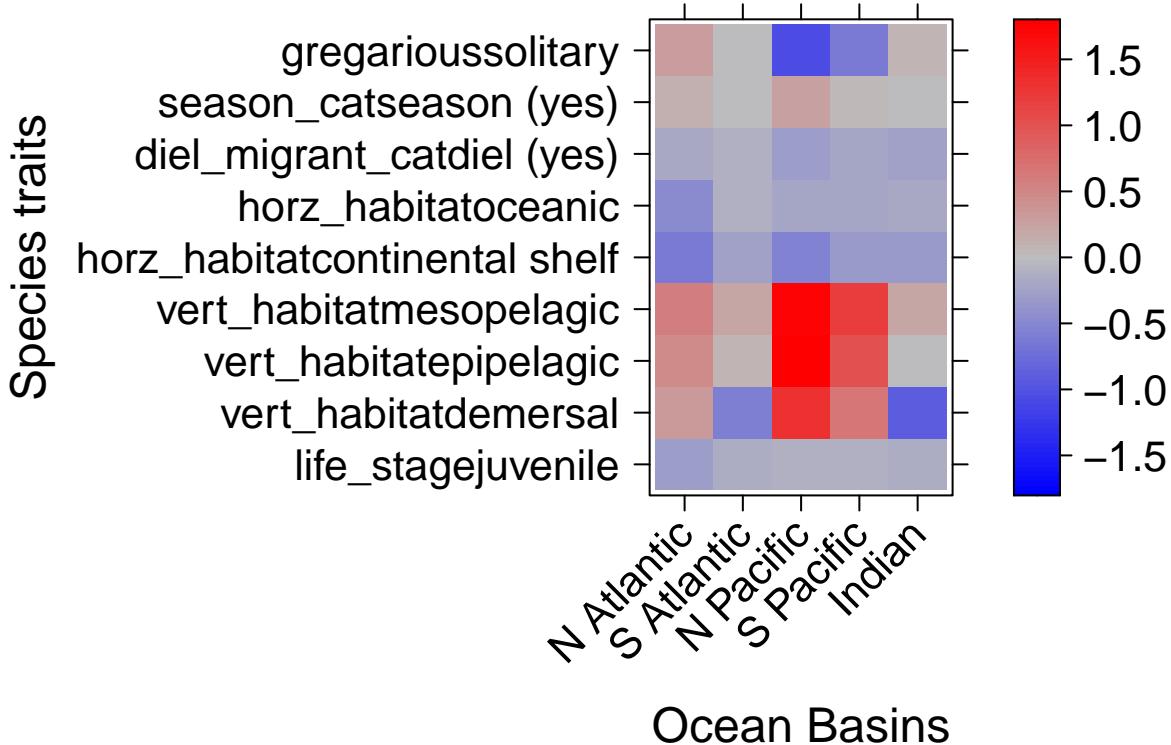
a      = max( abs(prob_ocean_trait_many$fourth.corner) )
colort = colorRampPalette(c("blue","grey","red")) #can replace "grey" with "white"
temp = t(as.matrix(prob_ocean_trait_many$fourth.corner))

rownames(temp) = c("#Mediterranean",
                  "N Atlantic",
                  "S Atlantic",
                  "N Pacific",
                  "S Pacific",
                  "Indian")

prob_ocean_trait_many_graph = levelplot(temp,
                                         xlab=list("Ocean Basins", cex=1.5),
                                         ylab=list("Species traits", cex=1.5),
                                         col.regions=colort(100),
                                         at=seq(-a, a,length=100),
                                         scales = list(x=list(rot = 45, cex=1.3), y=list(cex=1.3)),
                                         colorkey=list(labels=list(cex=1.3)))

print(prob_ocean_trait_many_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_trait_many_graph.pdf"),
       plot = as.ggplot(prob_ocean_trait_many_graph), width=12, height=12, dpi=300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_trait_many_graph.jpeg"),
       plot = as.ggplot(prob_ocean_trait_many_graph), width=12, height=12, dpi=300)

```

*GLM1PATH Trait values - Ocean Basin**

Using method = glm1path == LASSO model.

```

prob_ocean_trait_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                      R = alb_prob_covars$OceanBasin,
                                      Q = traits_use[,1:6],
                                      family=binomial(link = "logit"),
                                      method="glm1path"
                                      ) #note default is "manyglm"

```

```

a = max(abs(prob_ocean_trait_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_ocean_trait_LASSO$fourth.corner))

rownames(temp) = c("Mediterranean", "N Atlantic", "S Atlantic", "N Pacific", "S Pacific",
                  "Indian")

colnames(temp) = c("Prey life: juvenile", "Vert. habitat - benthic", "Vert. habitat - demersal",

```

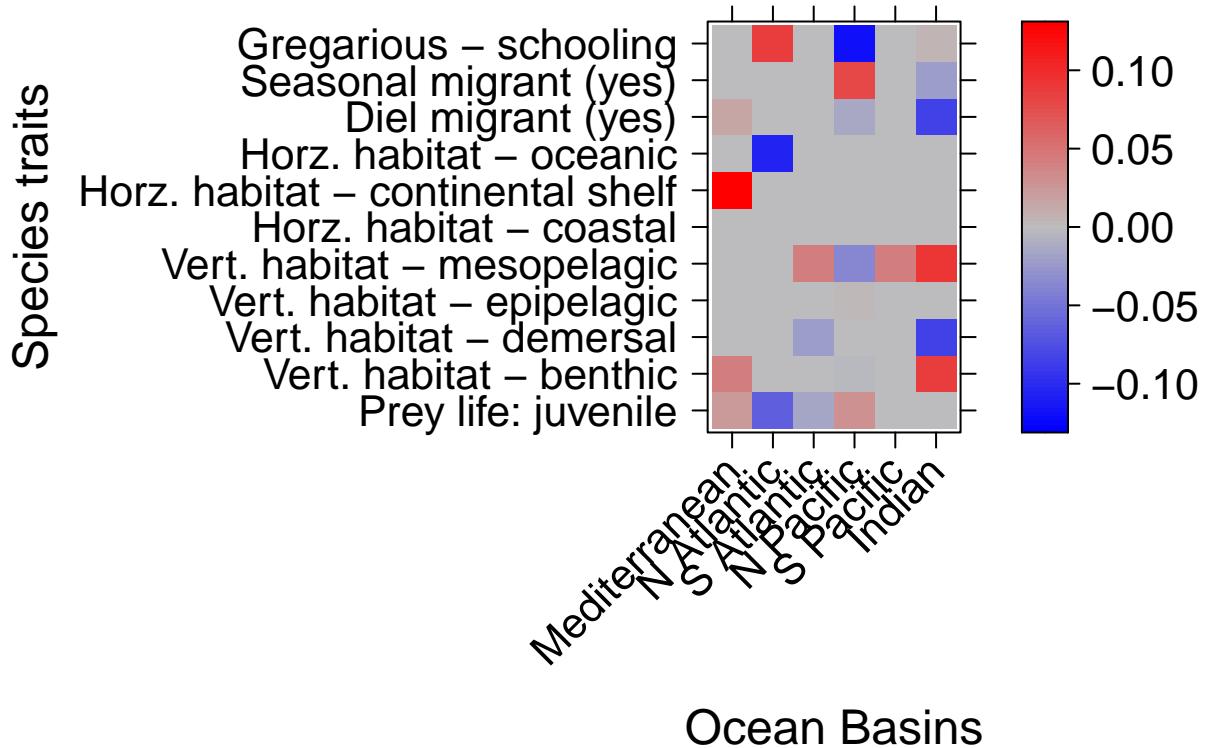
```

"Vert. habitat - epipelagic", "Vert. habitat - mesopelagic", "Horz. habitat - coastal",
"Horz. habitat - continental shelf", "Horz. habitat - oceanic", "Diel migrant (yes)",
"Seasonal migrant (yes)", "Gregarious - schooling")

prob_ocean_LASSO_graph = levelplot(temp, xlab = list("Ocean Basins", cex = 1.5),
    ylab = list("Species traits", cex = 1.5), col.regions = colort(100), at = seq(-a,
        a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
    colorkey = list(labels = list(cex = 1.3)))

print(prob_ocean_LASSO_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_LASSO_graph.pdf"),
    plot = as.ggplot(prob_ocean_LASSO_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_ocean_LASSO_graph.jpeg"),
    plot = as.ggplot(prob_ocean_LASSO_graph), width = 12, height = 12, dpi = 300)

```

Temperate / Tropical MANYGLM Trait values - Latitude

Trait (trait matrix)*Env (latitude) - Manyglm

```

prob_lat_trait_many <- traitglm(L = alb_prob_preyPA_mv,
    R = alb_prob_covars$lat_cat,
    Q = traits_use[,1:6],

```

```

family=binomial(link = "logit")
) #note default is "manyglm"

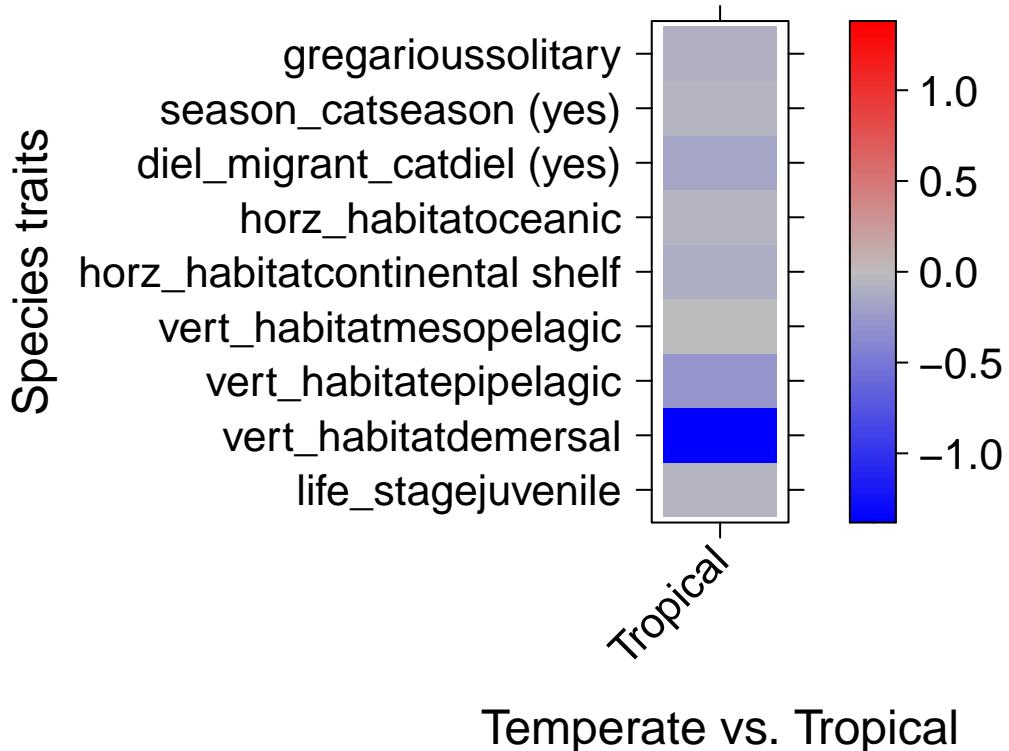
a = max(abs(prob_lat_trait_many$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_lat_trait_many$fourth.corner))

rownames(temp) = c("Tropical")

prob_lat_trait_many_graph = levelplot(temp, xlab = list("Temperate vs. Tropical",
  cex = 1.5), ylab = list("Species traits", cex = 1.5), col.regions = colort(100),
  at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
  colorkey = list(labels = list(cex = 1.3)))

print(prob_lat_trait_many_graph)

```



```

# ggsave(here('outputs_figures/traitglms/prob_all_simple/prob_lat_trait_many_graph.pdf'),
# plot = as.ggplot(prob_lat_trait_many_graph), width=12, height=12, dpi=300)

# ggsave(here('outputs_figures/traitglms/prob_all_simple/prob_lat_trait_many_graph.jpeg'),
# plot = as.ggplot(prob_lat_trait_many_graph), width=12, height=12, dpi=300)

```

GLM1PATH Trait values - Latitude

Using method = glm1path == LASSO model.

```

#levels(alb_prob_covars$lat_cat)

#alb_prob_covars$lat_cat <- factor(alb_prob_covars$lat_cat, levels = c("tropical", "temperate"))

prob_lat_trait_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                    R = alb_prob_covars$lat_cat,
                                    Q = traits_use[,1:6],
                                    family=binomial(link = "logit"),
                                    method="glm1path"
                                    ) #note default is "manyglm"

a = max(abs(prob_lat_trait_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_lat_trait_LASSO$fourth.corner))

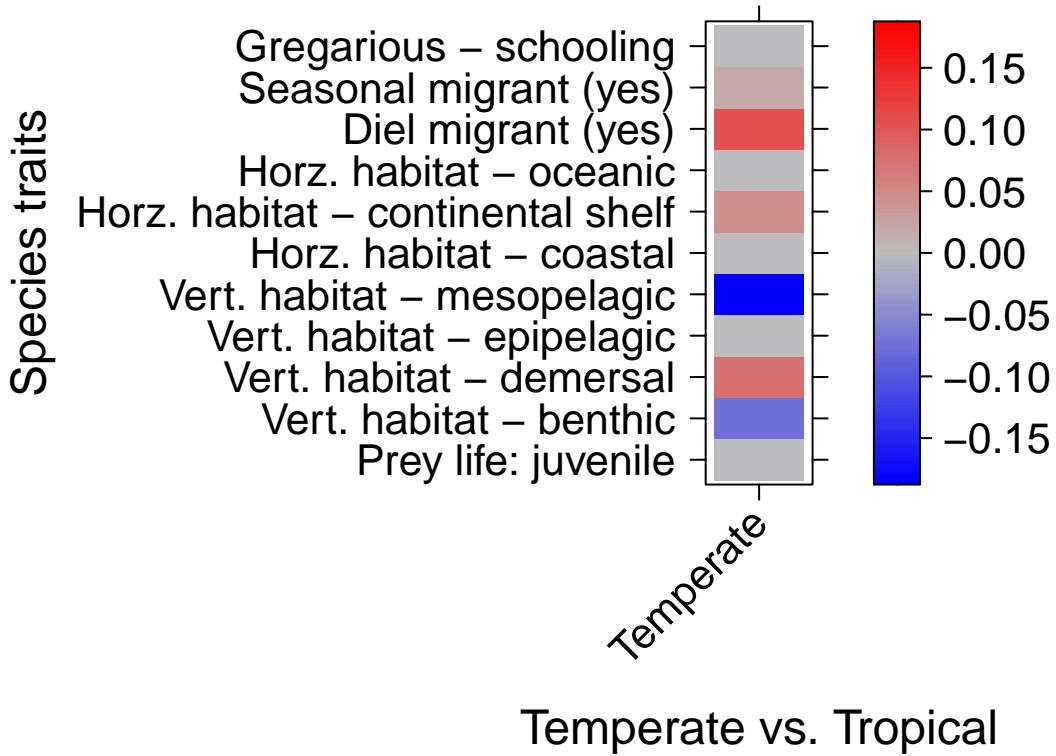
rownames(temp) = c("Temperate")

colnames(temp) = c("Prey life: juvenile", "Vert. habitat - benthic", "Vert. habitat - demersal",
                  "Vert. habitat - epipelagic", "Vert. habitat - mesopelagic", "Horz. habitat - coastal",
                  "Horz. habitat - continental shelf", "Horz. habitat - oceanic", "Diel migrant (yes)",
                  "Seasonal migrant (yes)", "Gregarious - schooling")

prob_lat_trait_LASSO_graph = levelplot(temp, xlab = list("Temperate vs. Tropical",
                                                       cex = 1.5), ylab = list("Species traits", cex = 1.5), col.regions = colort(100),
                                         at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
                                         colorkey = list(labels = list(cex = 1.3)))

print(prob_lat_trait_LASSO_graph)

```



```
# ggsave(here('outputs_figures/traitglms/prob_all_simple/prob_lat_trait_LASSO_temp_graph.pdf'),
# plot = as.ggplot(prob_lat_trait_LASSO_graph), width=12, height=12, dpi=300)

# ggsave(here('outputs_figures/traitglms/prob_all_simple/prob_lat_trait_LASSO_emp_graph.jpeg'),
# plot = as.ggplot(prob_lat_trait_LASSO_graph), width=12, height=12, dpi=300)
```

```
# Manyglm
saveRDS(prob_life_trait_many, file = here("outputs_figures/traitglms/prob_models/prob_life_trait_many.rds"))
saveRDS(prob_ocean_trait_many, file = here("outputs_figures/traitglms/prob_models/prob_ocean_trait_many.rds"))
saveRDS(prob_lat_trait_many, file = here("outputs_figures/traitglms/prob_models/prob_lat_trait_many.rds"))

#LASSO glms
saveRDS(prob_life_trait_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_life_trait_LASSO.rds"))
saveRDS(prob_ocean_trait_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_ocean_trait_LASSO.rds"))
saveRDS(prob_lat_trait_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_lat_trait_LASSO.rds"))
```

SAVE TRAITS OUTPUTS

Interactions

MANYGLM Interaction Model

```

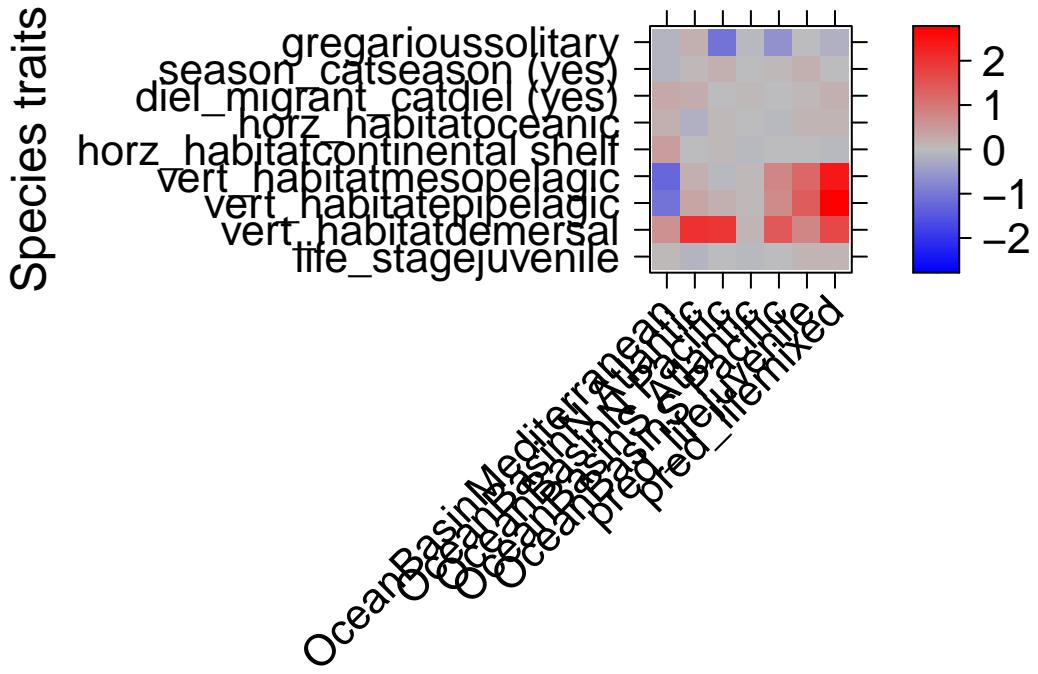
prob_inter_trait_many <- traitglm(L = alb_prob_preyPA_mv,
                                    R = alb_prob_covars[,c(4,12)],
                                    Q = traits_use[,1:6],
                                    family=binomial(link = "logit")
                                    ) #note default is "manyglm"

a = max(abs(prob_inter_trait_many$fourth.corner))
colort = colorRampPalette(c("blue", "grey", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_inter_trait_many$fourth.corner))

prob_inter_trait_many_graph = levelplot(temp, xlab = list("Predator Life Stage + Ocean Basins",
                                                       cex = 1.5), ylab = list("Species traits", cex = 1.5), col.regions = colort(100),
                                         at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
                                         colorkey = list(labels = list(cex = 1.3)))

print(prob_inter_trait_many_graph)

```



Predator Life Stage + Ocean Basins

```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_inter_trait_many_graph.pdf"),
       plot = as.ggplot(prob_inter_trait_many_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_inter_trait_many_graph.jpeg"),
       plot = as.ggplot(prob_inter_trait_many_graph), width = 12, height = 12, dpi = 300)

```

GLM1PATH Interaction Model

```

prob_inter_trait_LASSO <- traitglm(L = alb_prob_preyPA_mv,
                                    R = alb_prob_covars[,c(4,12)],
                                    Q = traits_use[,1:6],
                                    family=binomial(link = "logit"),
                                    method="glm1path"
                                    ) #note default is "manyglm"

```

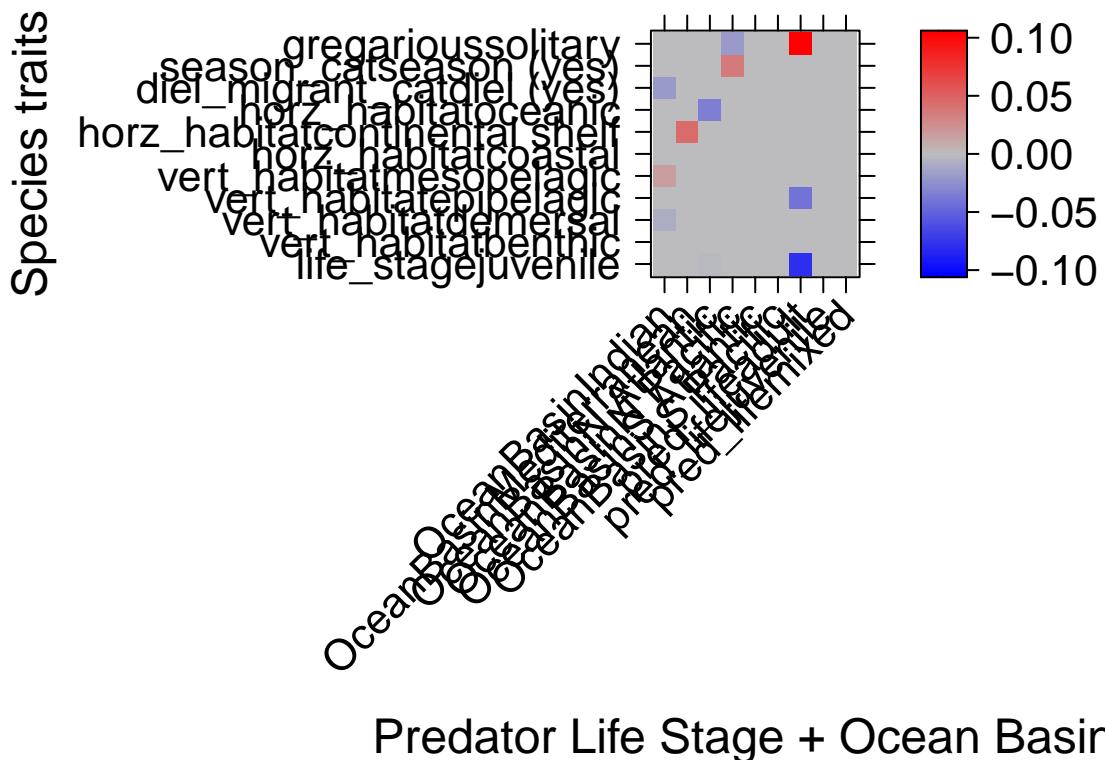
```

a = max(abs(prob_inter_trait_LASSO$fourth.corner))
colort = colorRampPalette(c("blue", "green", "red")) #can replace 'grey' with 'white'
temp = t(as.matrix(prob_inter_trait_LASSO$fourth.corner))

prob_inter_trait_LASSO_graph = levelplot(temp, xlab = list("Predator Life Stage + Ocean Basins",
    cex = 1.5), ylab = list("Species traits", cex = 1.5), col.regions = colort(100),
    at = seq(-a, a, length = 100), scales = list(x = list(rot = 45, cex = 1.3), y = list(cex = 1.3)),
    colorkey = list(labels = list(cex = 1.3)))

print(prob_inter_trait_LASSO_graph)

```



```

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_inter_trait_LASSO_graph.pdf"),
       plot = as.ggplot(prob_inter_trait_LASSO_graph), width = 12, height = 12, dpi = 300)

ggsave(here("outputs_figures/traitglms/prob_all_simple/prob_inter_trait_many_graph.jpeg"),
       plot = as.ggplot(prob_inter_trait_LASSO_graph), width = 12, height = 12, dpi = 300)

```

SAVE THESE

```
#Manyglm  
saveRDS(prob_inter_trait_many, file = here("outputs_figures/traitglms/prob_models/prob_inter_trait_many.RDS"))  
  
#LASSO glms  
saveRDS(prob_inter_trait_LASSO, file = here("outputs_figures/traitglms/prob_models/prob_inter_trait_LASSO.RDS"))
```

MODEL COMPARISON

Model Outputs Cluster, trait, spp models each for (i) predator life stage and (ii) ocean basins

```
prob_life_spp
```

Model: prob_life_spp

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$pred_life, family = binomial(link = "logit"))  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25338 Residual  
##  
##              1  
## 2*log-likelihood: -3329  
## Residual Deviance: 3329  
## AIC:             4067
```

```
prob_ocean_spp
```

Model: prob_ocean_spp

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$OceanBasin, family = binomial(link = "logit"))  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 24969 Residual  
##  
##              1  
## 2*log-likelihood: -2978  
## Residual Deviance: 2978  
## AIC:             4454
```

```
prob_lat_spp
```

Model: prob_lat_spp

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$lat_cat, family = binomial(link = "  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25461 Residual  
##  
##  
##  
## 2*log-likelihood: -3656  
## Residual Deviance: 3656  
## AIC: 4148
```

```
prob_life_clusters_many
```

Model: prob_life_clusters_many

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$pred_life, Q = traits_prob$cluster,  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25570 Residual  
##  
##  
## 2*log-likelihood: -3806  
## Residual Deviance: 3806  
## AIC: 4080
```

```
prob_ocean_clusters_many
```

Model: prob_ocean_clusters_many

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$OceanBasin, Q = traits_prob$cluster,  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25549 Residual  
##  
##  
## 2*log-likelihood: -3776  
## Residual Deviance: 3776  
## AIC: 4092
```

```
prob_life_trait_many
```

Model: prob_life_trait_many

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$pred_life, Q = traits_use[, 1:6], f  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25564 Residual  
##  
##  
##  
## 2*log-likelihood: -3764  
## Residual Deviance: 3764  
## AIC: 4050
```

```
prob_ocean_trait_many
```

Model: prob_ocean_trait_many

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$OceanBasin, Q = traits_use[, 1:6], :  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25534 Residual  
##  
##  
## 2*log-likelihood: -3746  
## Residual Deviance: 3746  
## AIC: 4092
```

```
prob_lat_trait_many
```

Model: prob_lat_trait_many

```
##  
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars$lat_cat, Q = traits_use[, 1:6], fam:  
## [1] "binomial(link=logit)"  
##  
## Degrees of Freedom: 25706 Total (i.e. Null); 25574 Residual  
##  
##  
## 2*log-likelihood: -3875  
## Residual Deviance: 3875  
## AIC: 4141
```

```
prob_inter_trait_many
```

Model: prob_inter_trait_many

```

## 
## Call: traitglm(L = alb_prob_preyPA_mv, R = alb_prob_covars[, c(4, 12)],      Q = traits_use[, 1:6],
## [1] "binomial(link=logit)"
## 
## Degrees of Freedom: 25706 Total (i.e. Null); 25514 Residual
## 
##               1
## 2*log-likelihood: -3634
## Residual Deviance: 3634
## AIC:              4020

```

Conclusions

The species models had the lowest residual deviance explained, and typically higher AIC values./ Cluster models performed slightly better than traits models, but not massive difference. Both cluster and trait sets of models outperformed species models.

The best model in terms of residual deviance explained was the latitude + traits model, however, did have higher AIC scores. The interaction model that included ocean basin + life stage had the lowest AIC but low deviance explained.