Deep Sea GDM

Setup

Loading packages

```
library(raster)
```

```
## Loading required package: sp
```

```
library(leaflet)
library(gdm)
```

```
## Loading required package: foreach
```

```
## Loading required package: doParallel
```

```
## Loading required package: iterators
```

```
## Loading required package: parallel
```

```
library(ENMTools)
```

```
## Loading required package: dismo
```

```
library(DT)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:raster':
##
##     intersect, select, union
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.5-6
```

```
library(ggvegan)
```

```
## Loading required package: ggplot2
```

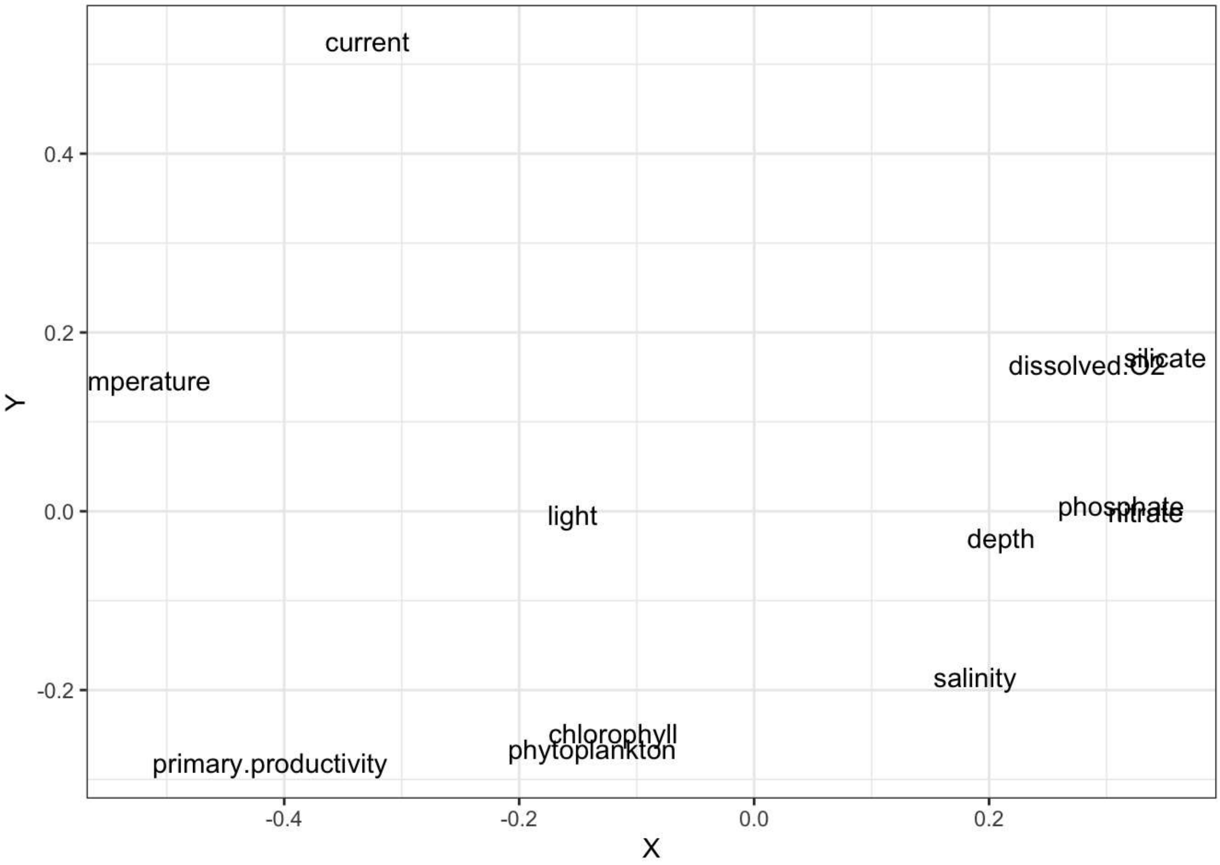
```
library(knitr)
library(ggplot2)
library(ggforce)
```

Loading data

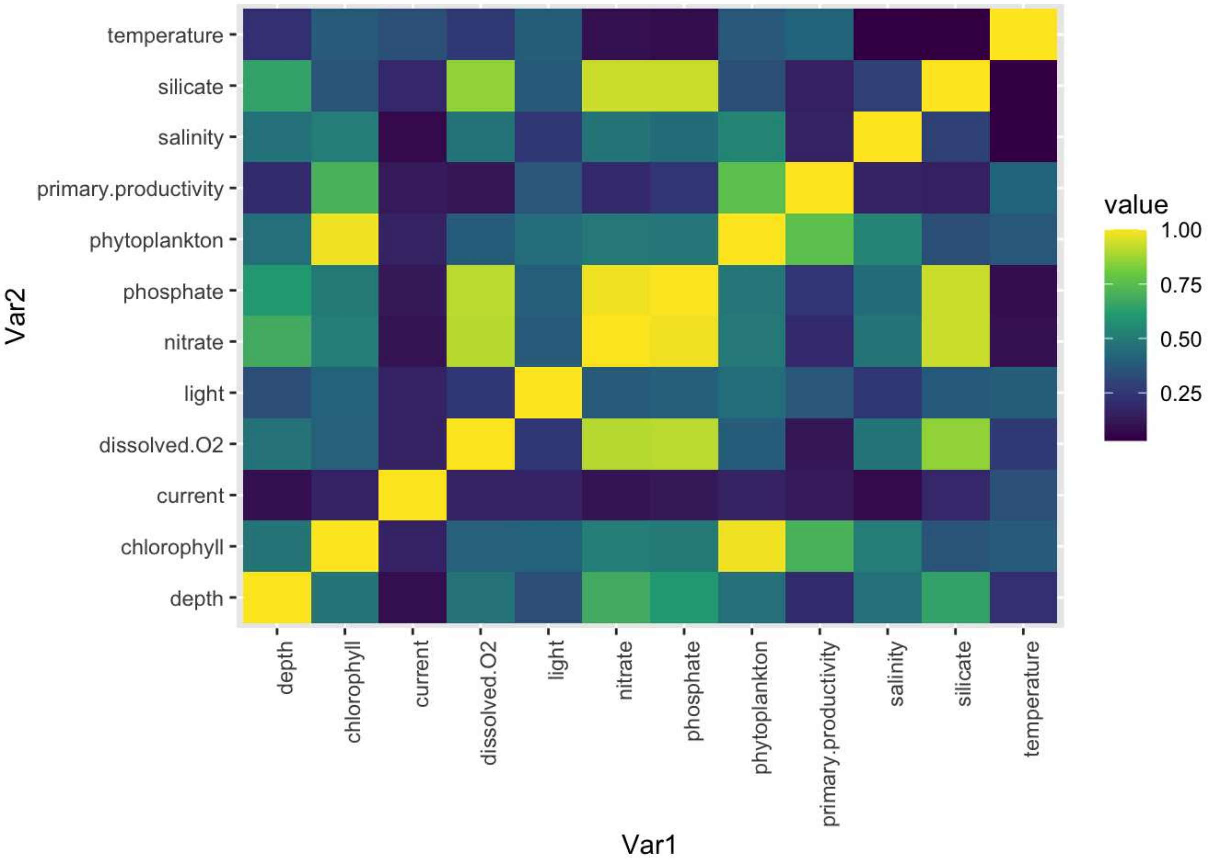
We're going to bring in our env rasters and species lat/longs for plotting purposes, but for the actual analysis we'll be using the values we extracted from these in a data frame.

```
setwd("~/Dropbox/BiK-F/Hanieh Saeedi/Deep Sea GDM/")
env.files <- list.files("./Biooracle_Present_Mean_Benthic/",
                        pattern = ".asc", full.names = TRUE)
env <- stack(env.files)
names(env) <- c("depth", "chlorophyll", "current", "dissolved.O2",
                "light", "nitrate", "phosphate", "phytoplankton",
                "primary.productivity", "salinity", "silicate",
                "temperature")

species <- read.csv("./occurrence_data_merged.csv")

env <- crop(env, c(min(species$decimalLongitude, na.rm = TRUE) + 5,
                   max(species$decimalLongitude, na.rm = TRUE) + 5,
                   min(species$decimalLatitude, na.rm = TRUE) + 5,
                   max(species$decimalLatitude, na.rm = TRUE)) + 5)

env <- setMinMax(env)

crs(env) <- "+proj=longlat +datum=WGS84 +no_defs"

raster.cor.plot(env)
```

```
## $cor.mds.plot
```


current
mperature
dissolved.O2
silicate
light
phosphate
nitrate
depth
salinity
chlorophyll
phytoplankton
primary.productivity
0.4
0.2
0.0
-0.2
-0.4
-0.2
0.0
0.2
Y
X

```
##
## $cor.heatmap
```

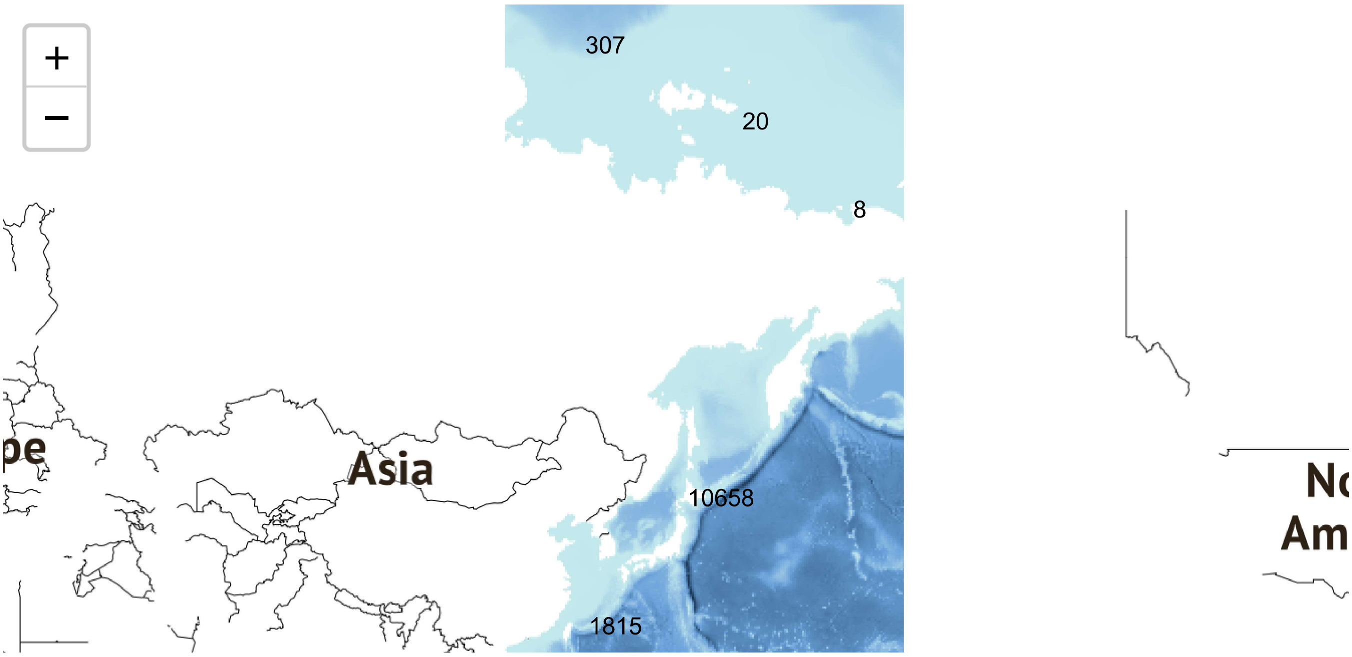

temperature
silicate
salinity
primary.productivity
phytoplankton
phosphate
nitrate
light
dissolved.O2
current
chlorophyll
depth
Var2
depth
chlorophyll
current
dissolved.O2
light
nitrate
phosphate
phytoplankton
primary.productivity
salinity
silicate
temperature
Var1
value
1.00
0.75
0.50
0.25

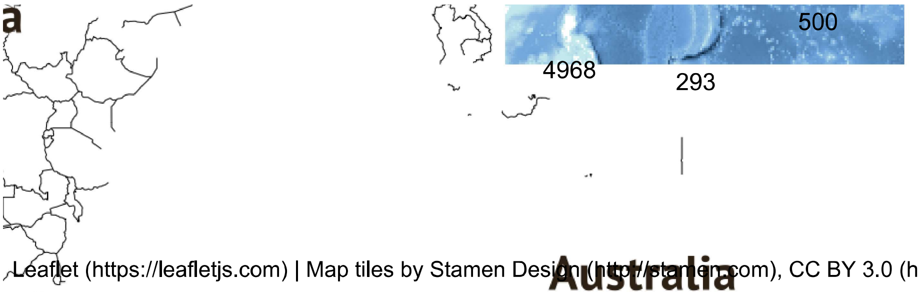
```
species.df <- read.csv("./species-site.csv")
species.df <- species.df[,which(colSums(species.df) > 0)]

latlon.df <- xyFromCell(env, species.df$cells)
species.df <- species.df %>%
  select(-cells)

env.df <- read.csv("./env.csv")

deep.df <- cbind(latlon.df, env.df, species.df)

deep.df <- deep.df[complete.cases(deep.df),]

deep.df <- deep.df[,which(colSums(deep.df) != 0)]

dim(deep.df)
```

```
## [1]  2646 10920
```

Visualization

```
pal <- colorNumeric(c("#001529", "#6BA3DB", "#DBFFF2"), values(env[["depth"]]),
                    na.color = "transparent")

m <- leaflet(species) %>%
  addProviderTiles("Stamen.TonerLines") %>%
  addRasterImage(env[["depth"]], color = pal) %>%
  addProviderTiles("Stamen.TerrainLabels") %>%
  addCircleMarkers(lng = ~decimalLongitude, lat = ~decimalLatitude,
                   clusterOptions = leaflet::markerClusterOptions(),
                   popup = ~ as.character(scientificName)) %>%
  setView(lng = (max(species$decimalLongitude) + min(species$decimalLongitude))/2,
          lat = (max(species$decimalLatitude) + min(species$decimalLatitude))/2,
          zoom = 2)

m
```





Leaflet (https://leafletjs.com) | Map tiles by Stamen Design (http://stamen.com), CC BY 3.0 (http://creativecommons.org/licenses/by/3.0) — Map data © OpenStreetMap (https://www.openstreetmap.org/copyright) contributors

Analysis

RDA prep and PCNM

We're going to do a pcnm (Principal Coordinates of Neighbourhood Matrix) on our lat/long data to transform our sptaial data into a format suitable for rda. First, now that we've gotten rid of all the rows with NAs and species with no data, we need to unpack that df we just packed.

```
latlon.df <- deep.df[,1:2]
env.df <- deep.df[,3:14]
species.df <- deep.df[,15:ncol(deep.df)]
species.df <- decostand(species.df, "hellinger")
```

```
deep.pcnm <- pcnm(dist(latlon.df))

save(deep.pcnm, file = "deep.pcnm.Rda")
```

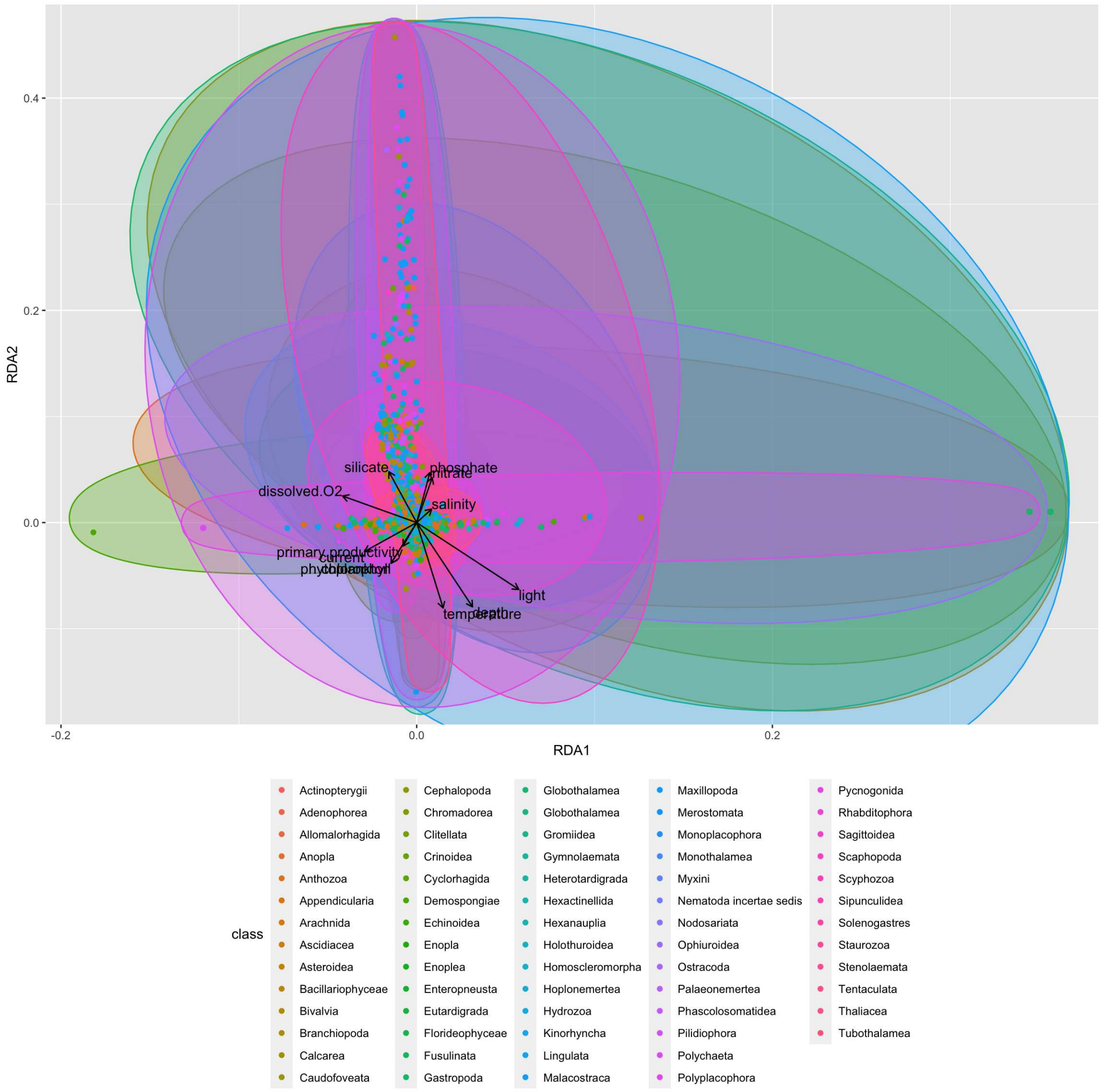
Final RDA

```
deep.rda <- rda(species.df ~ . + deep.pcnm$vectors, data = env.df, na.action = "na.
exclude", scale = TRUE)
save(deep.rda, file = "deep.rda.Rda")
deep.summary <- summary(deep.rda)
full.var.explained <- deep.summary$constr.chi/deep.summary$tot.chi
print(paste("Proportion of variance explained: ", full.var.explained))
```

```
## [1] "Proportion of variance explained:  0.435919352039385"
```

Plotting all classes together

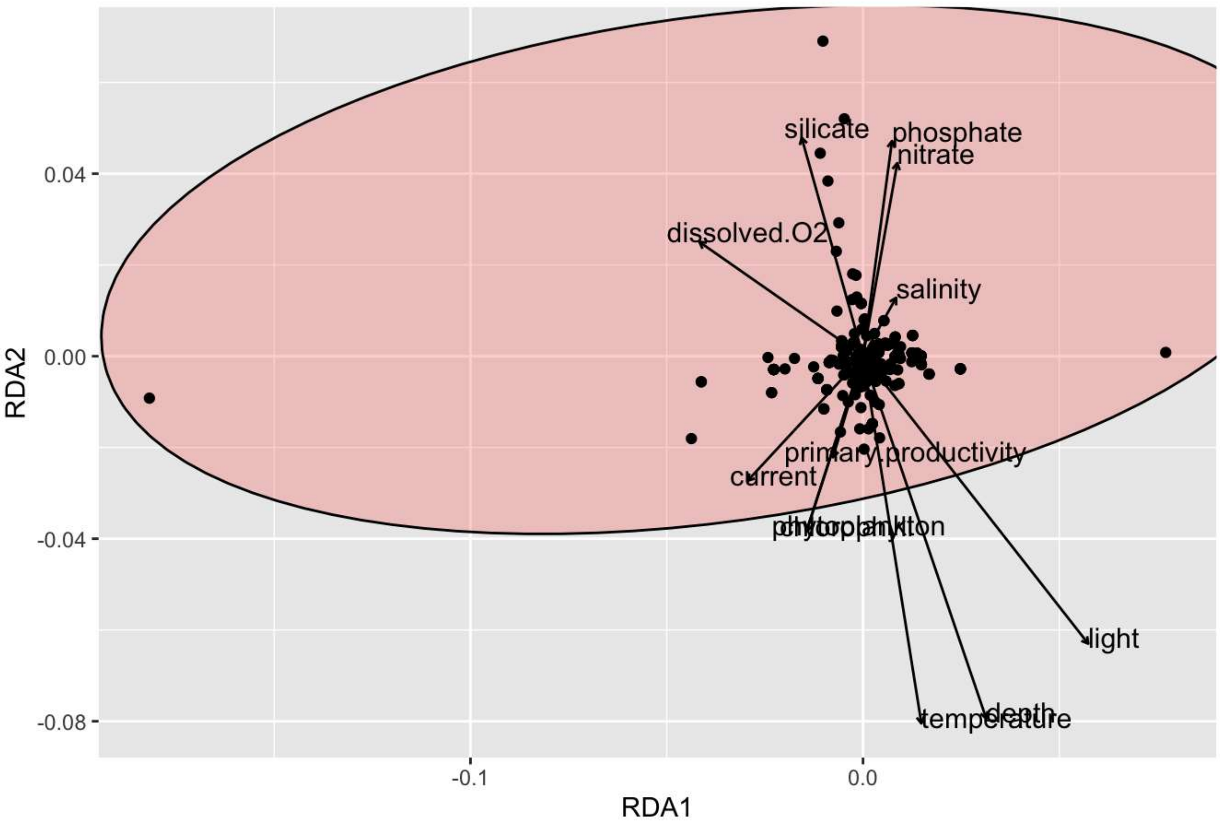
```
plot.df <- fortify(deep.rda)
species$scientificName <- gsub(" ", ".", species$scientificName)
plot.class.df <- unique(species[,c("scientificName", "class")])
plot.class.df <- plot.class.df[complete.cases(plot.class.df),]

# Removing this one since it has two classes listed
plot.class.df <- filter(plot.class.df, scientificName != "Protopelagonemertes.beebei")
plot.class.df <- filter(plot.class.df, scientificName != "")
plot.class.df <- filter(plot.class.df, class != "")

plot.df <- filter(plot.df, Label != "Protopelagonemertes.beebei")
plot.df <- filter(plot.df, Label != "")

rownames(plot.class.df) <- plot.class.df$scientificName

plot.df$class <- plot.class.df[plot.df$Label, "class"]
plot.df <- plot.df[complete.cases(plot.df),]

p <- ggplot(plot.df, aes(RDA1, RDA2, color = class)) +
  geom_mark_ellipse(aes(fill = class), show.legend = FALSE) +
  geom_point() + theme(legend.position = "bottom")

plot.env.df <- as.data.frame(deep.summary$biplot)[1:12,]

p <- p + geom_segment(data = plot.env.df, aes(x=0, xend=RDA1, y=0, yend=RDA2),
                      color="black", arrow=arrow(length=unit(0.01,"npc"))) +
  geom_text(data = plot.env.df,
            aes(x=RDA1,y=RDA2,label=rownames(plot.env.df),
                hjust=0.5*(1-sign(RDA1)),vjust=0.5*(1-sign(RDA2))),
            color="black", size=4)

p
```



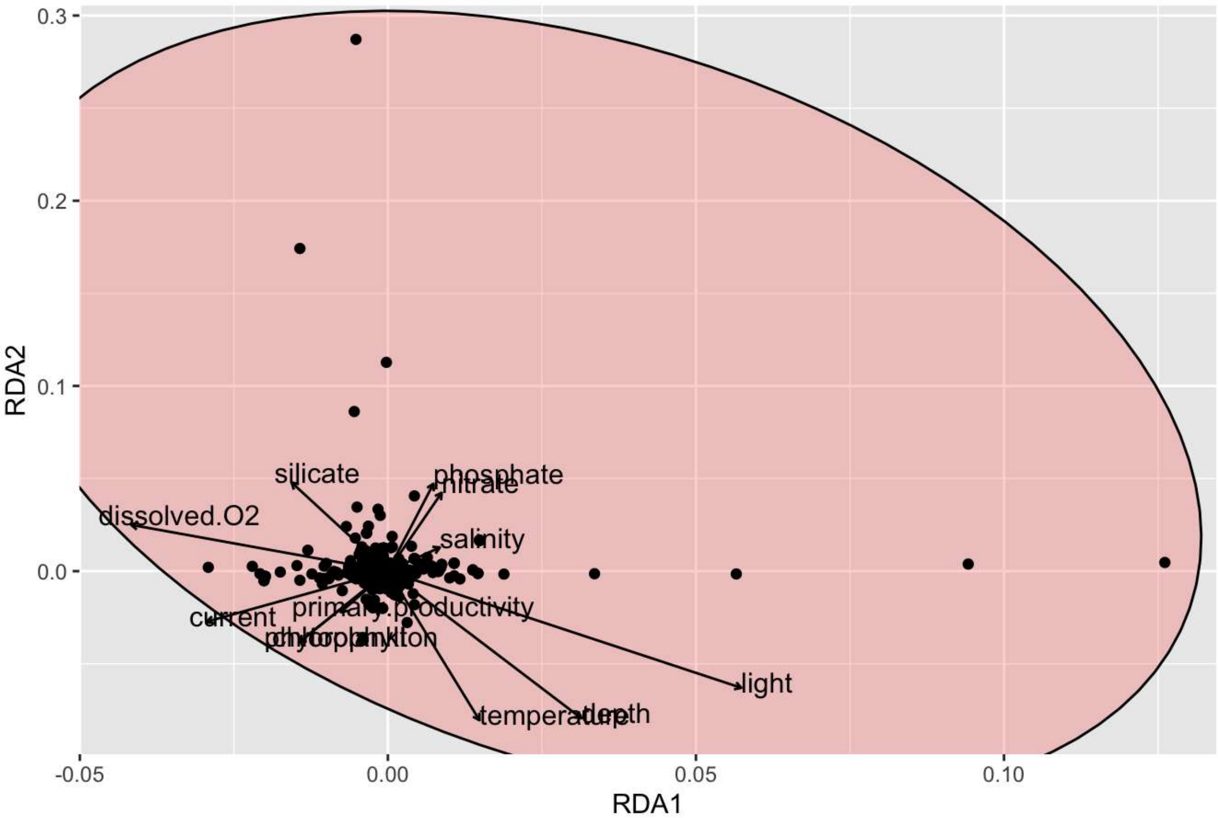
Full RDA, one plot per class

```
for(i in unique(plot.df$class)){
  this.plot.df <- plot.df[plot.df$class == i,]

  p <- ggplot(this.plot.df, aes(RDA1, RDA2)) +
    geom_mark_ellipse(aes(fill = class), show.legend = FALSE) +
    geom_point() + ggtitle(i)

  plot.env.df <- as.data.frame(deep.summary$biplot)[1:12,]

  p <- p + geom_segment(data = plot.env.df, aes(x=0, xend=RDA1, y=0, yend=RDA2),
                        color="black", arrow=arrow(length=unit(0.01,"npc"))) +
    geom_text(data = plot.env.df,
              aes(x=RDA1,y=RDA2,label=rownames(plot.env.df),
                  hjust=0.1*(1-sign(RDA1)),vjust=0.1*(1-sign(RDA2))),
              color="black", size=4)

  print(p)
}
```

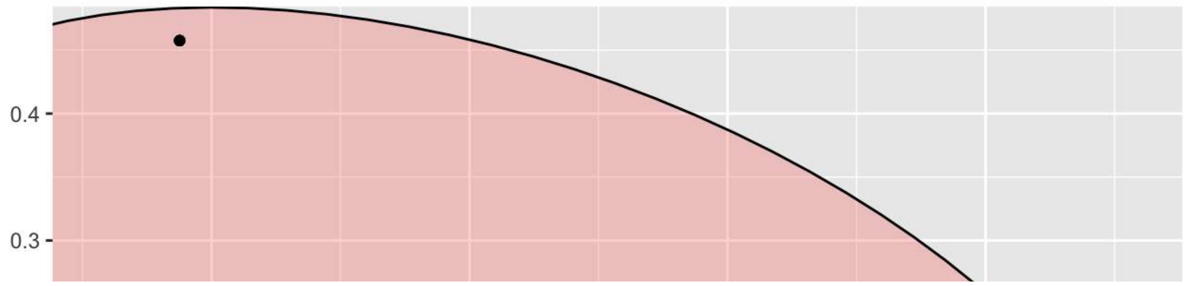
Demospongiae

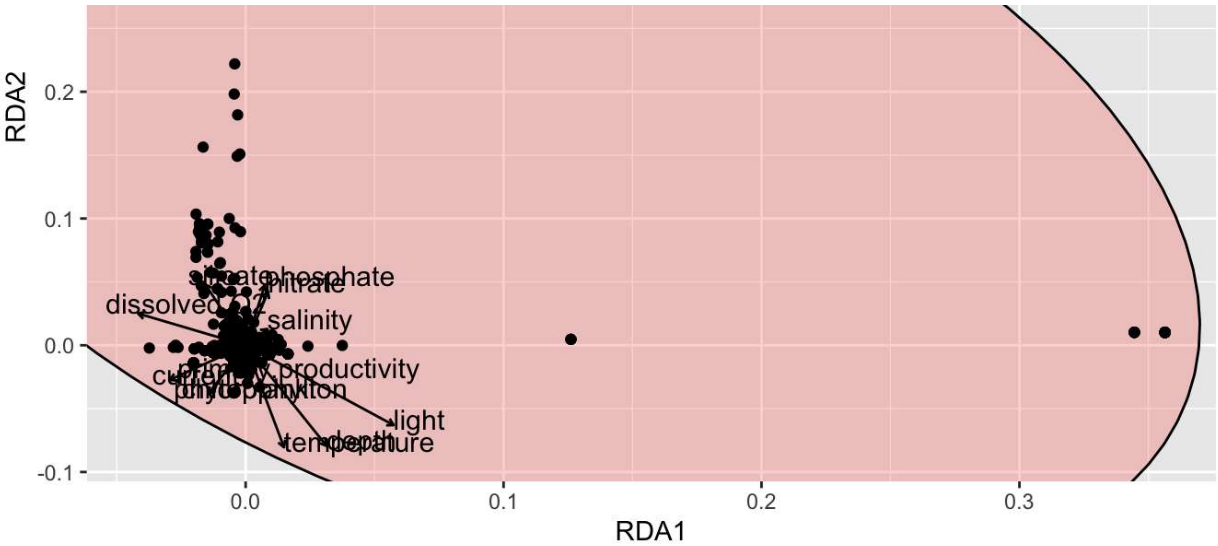


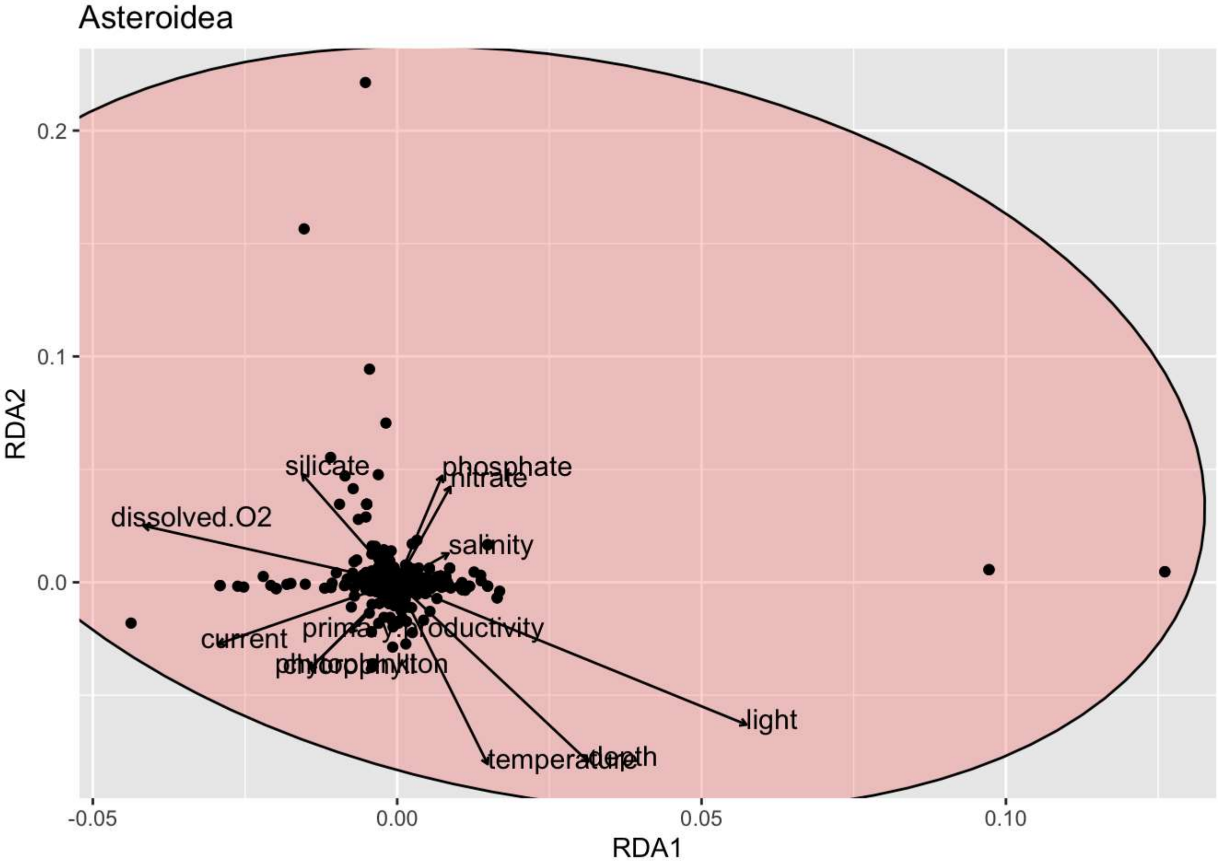
Hydrozoa

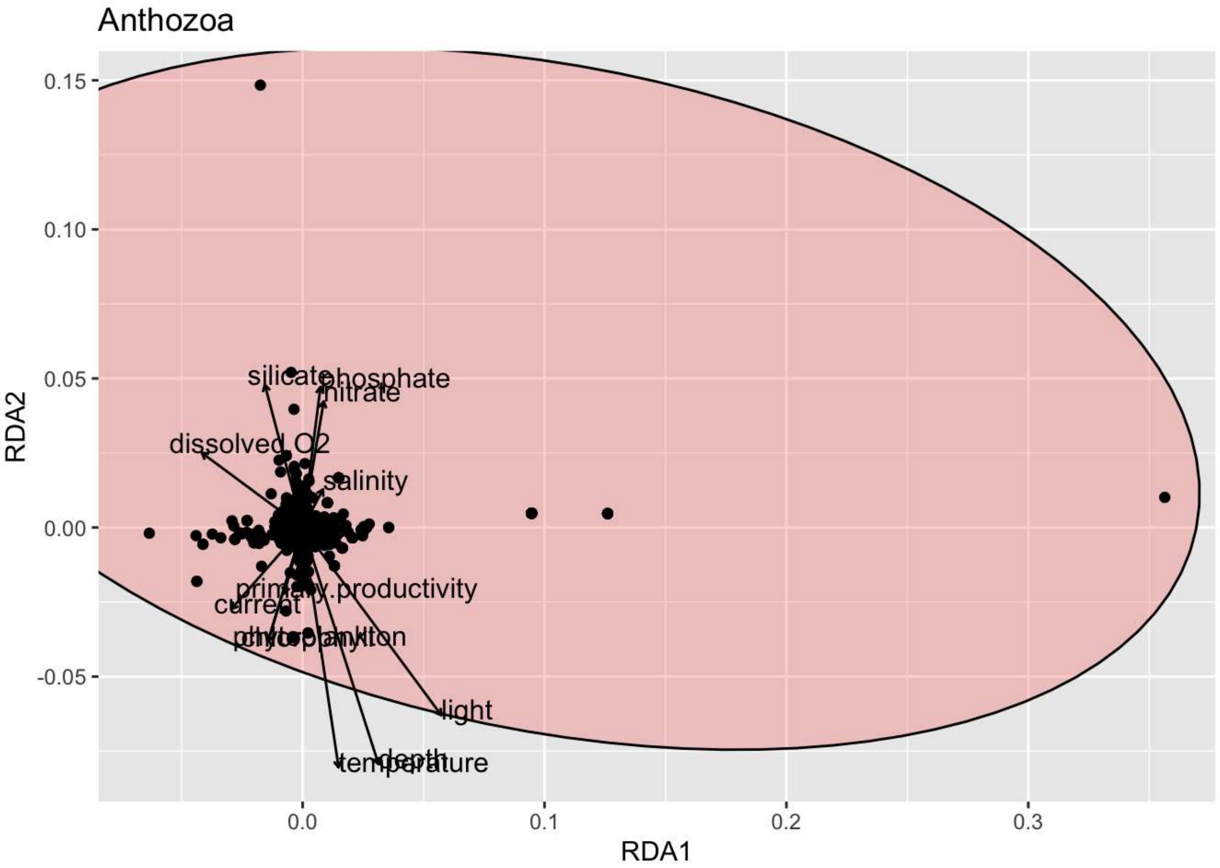


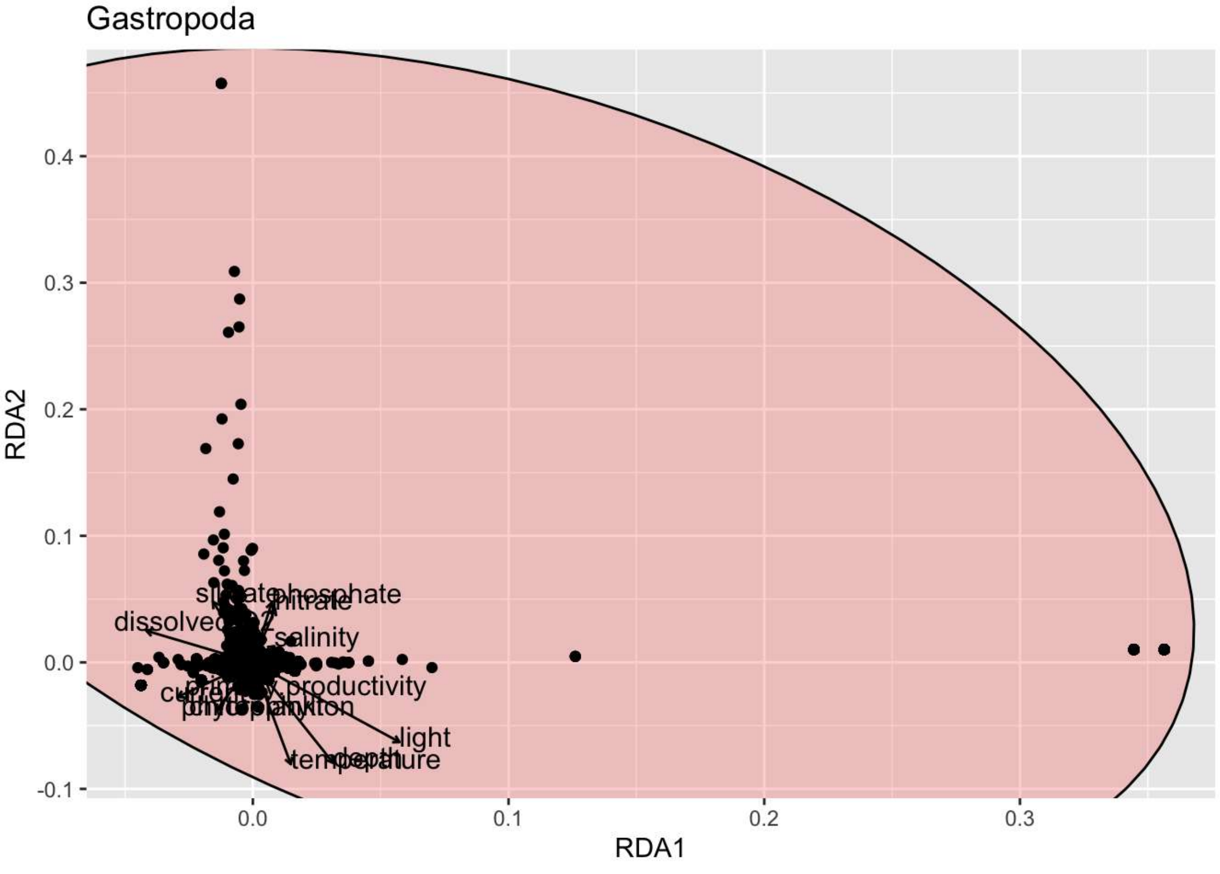
Bivalvia



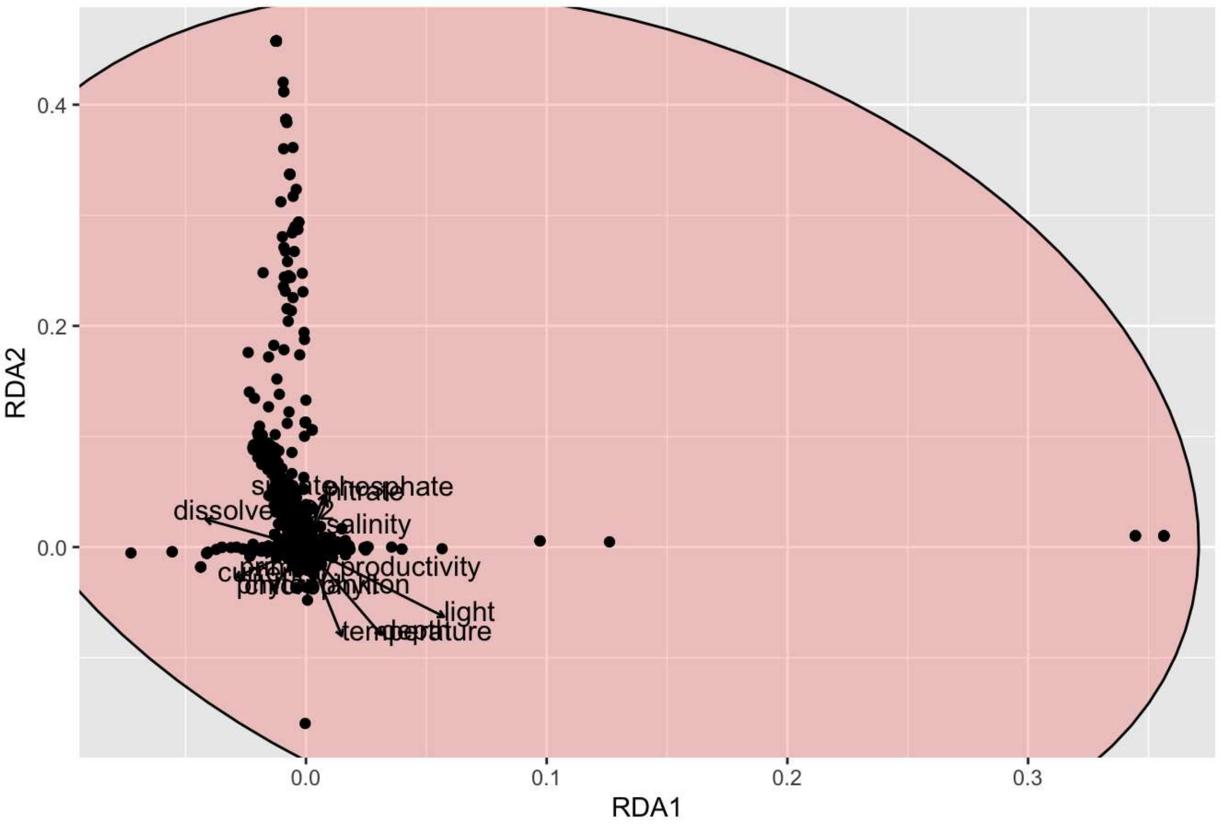

RDA2
0.2
0.1
0.0
-0.1
RDA1
0.0
0.1
0.2
0.3
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth


Asteroidea
RDA2
0.2
0.1
0.0
RDA1
-0.05
0.00
0.05
0.10
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

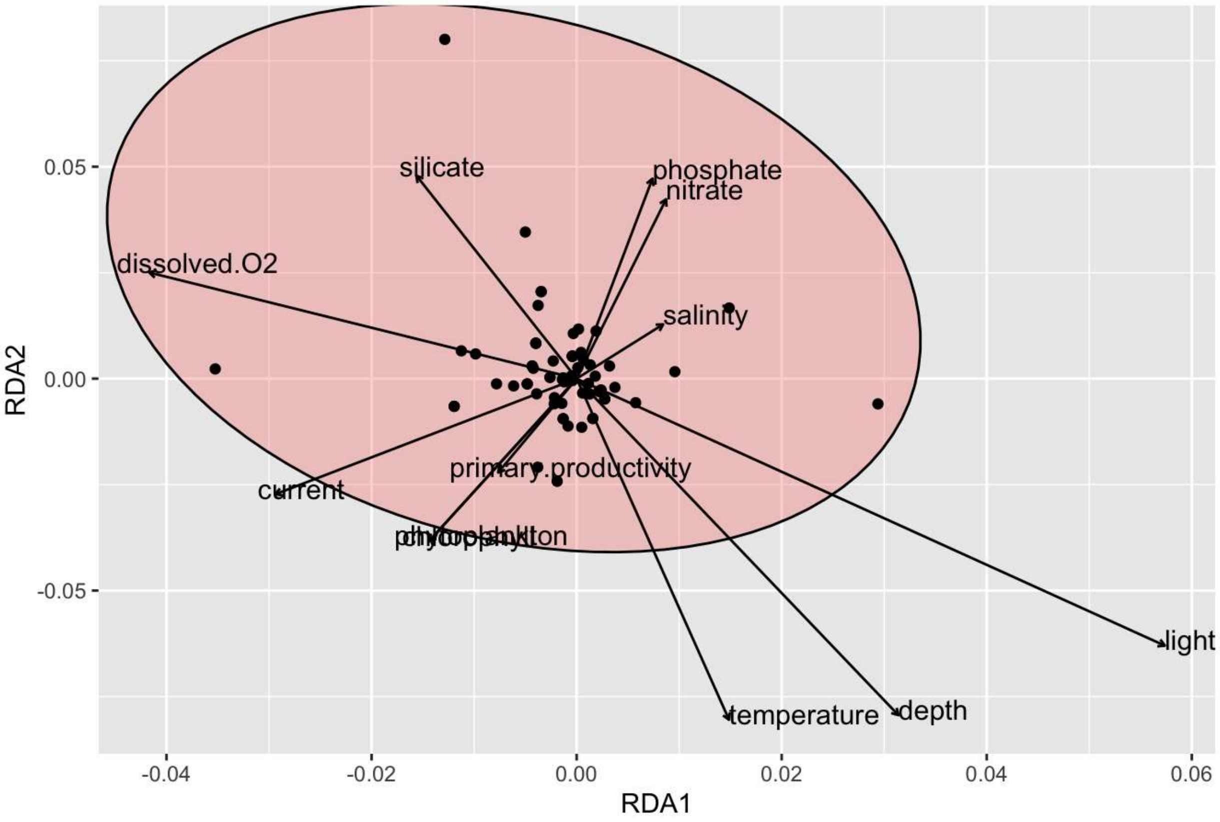

Anthozoa
RDA2
RDA1
0.15
0.10
0.05
0.00
-0.05
0.0
0.1
0.2
0.3
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
depth
temperature


Gastropoda
RDA2
RDA1
0.4
0.3
0.2
0.1
0.0
-0.1
0.0
0.1
0.2
0.3
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
phytoplankton
chlorophyll
light
depth
temperature

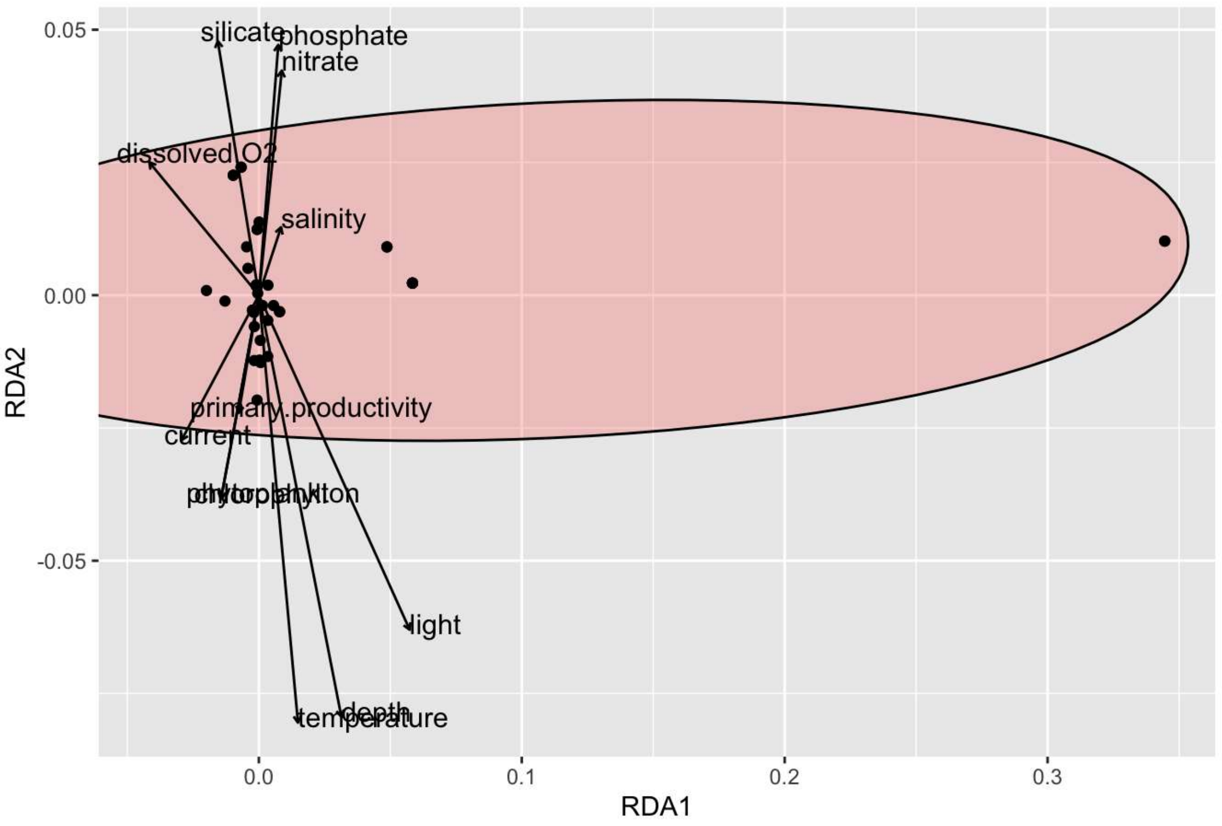
Malacostraca



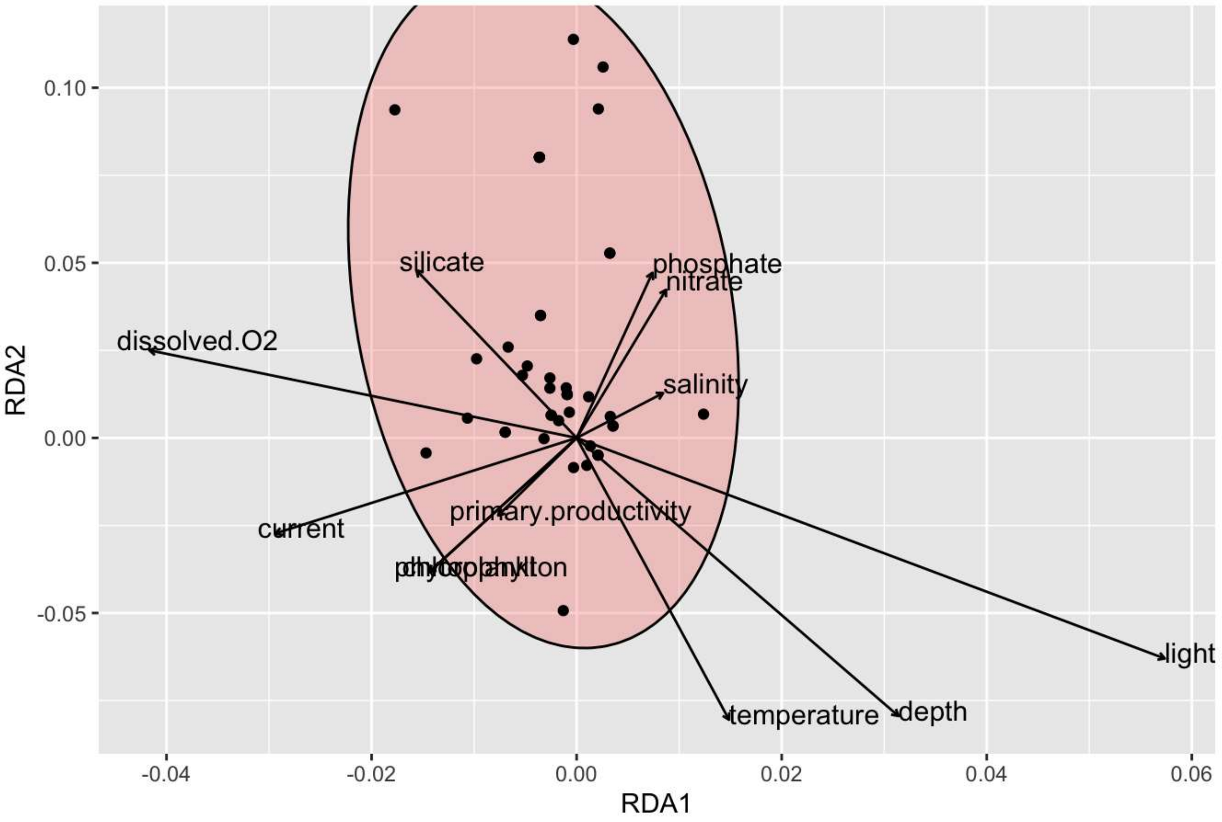
Hexactinellida

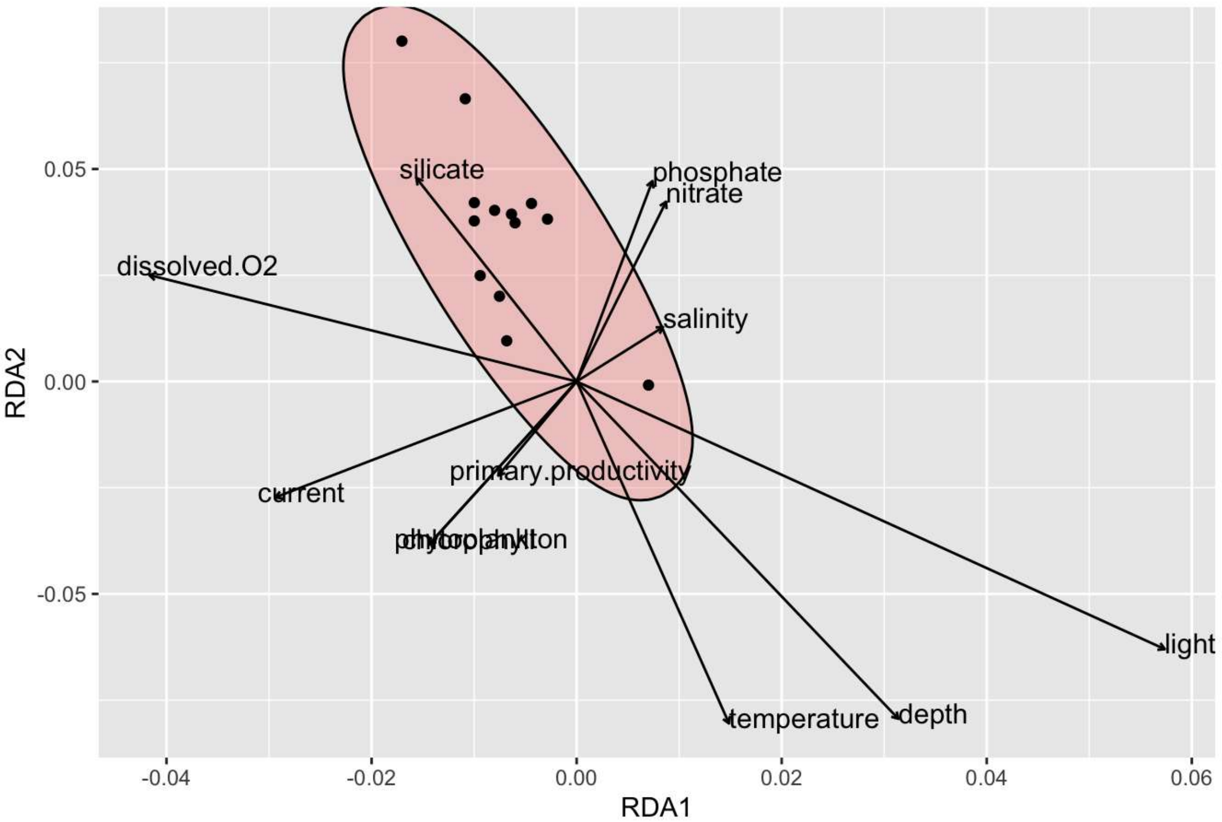


Polyplacophora

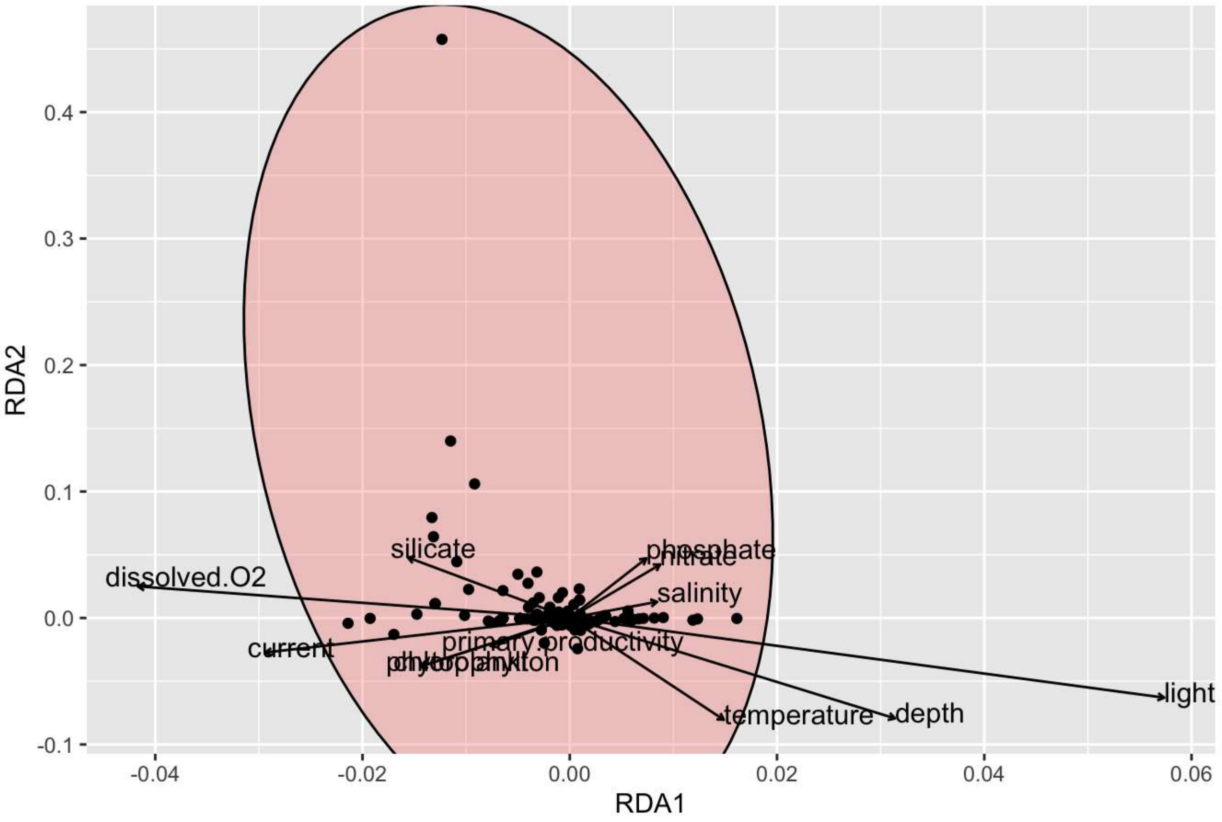


Chromadorea

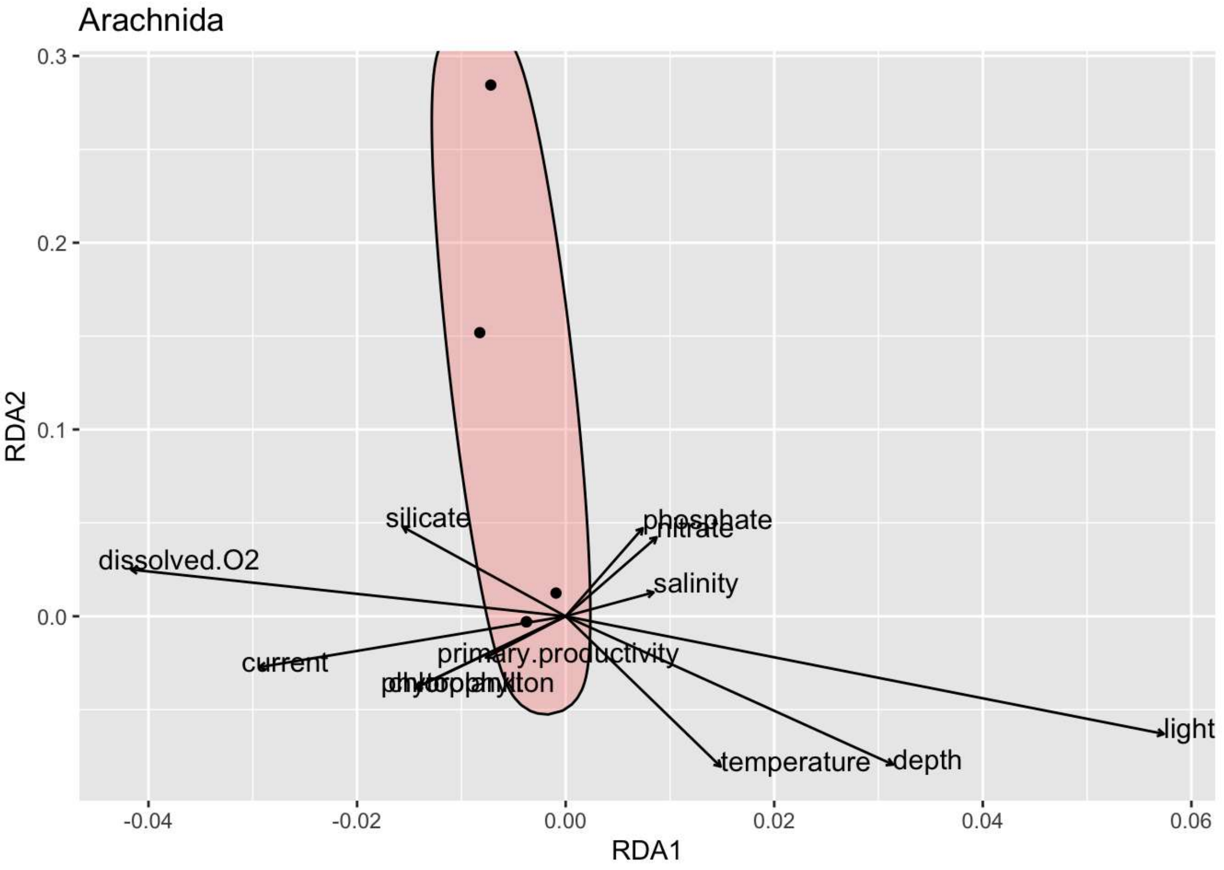


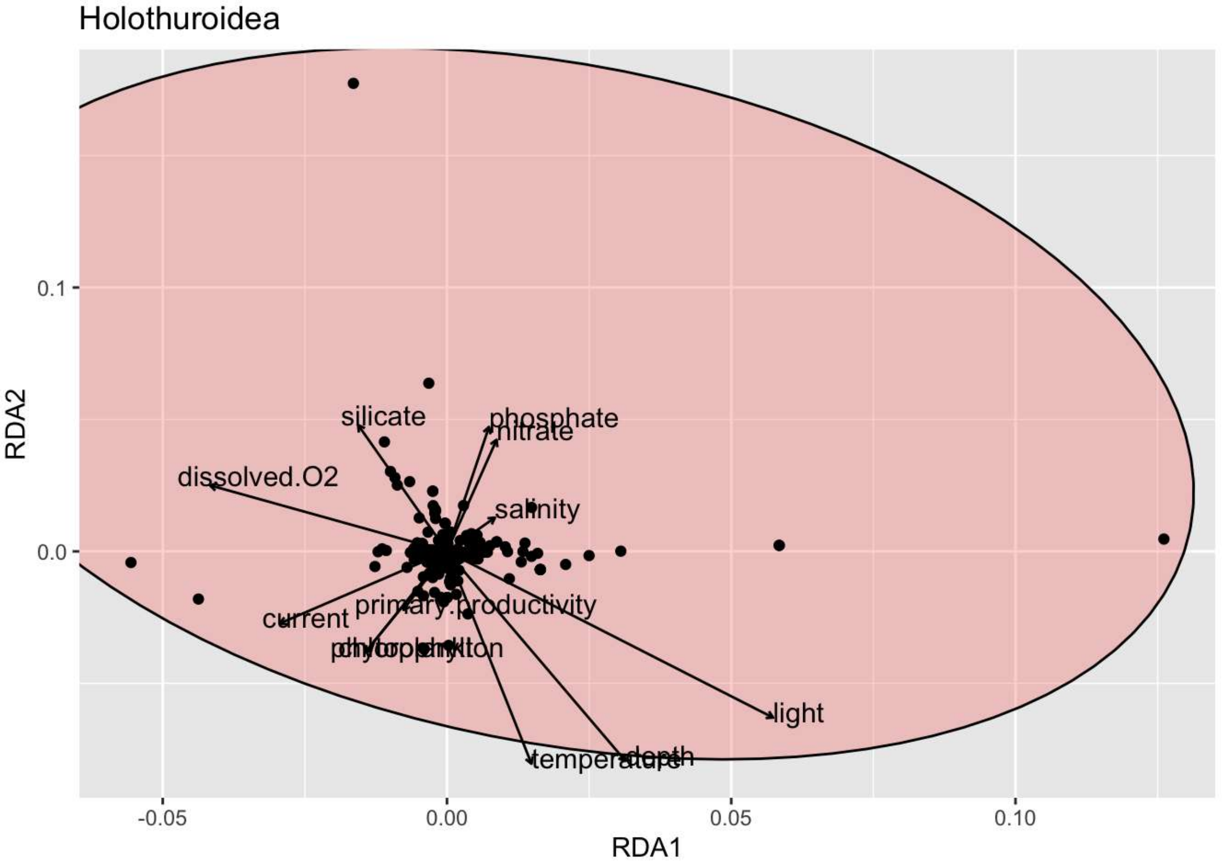


Solenogastres

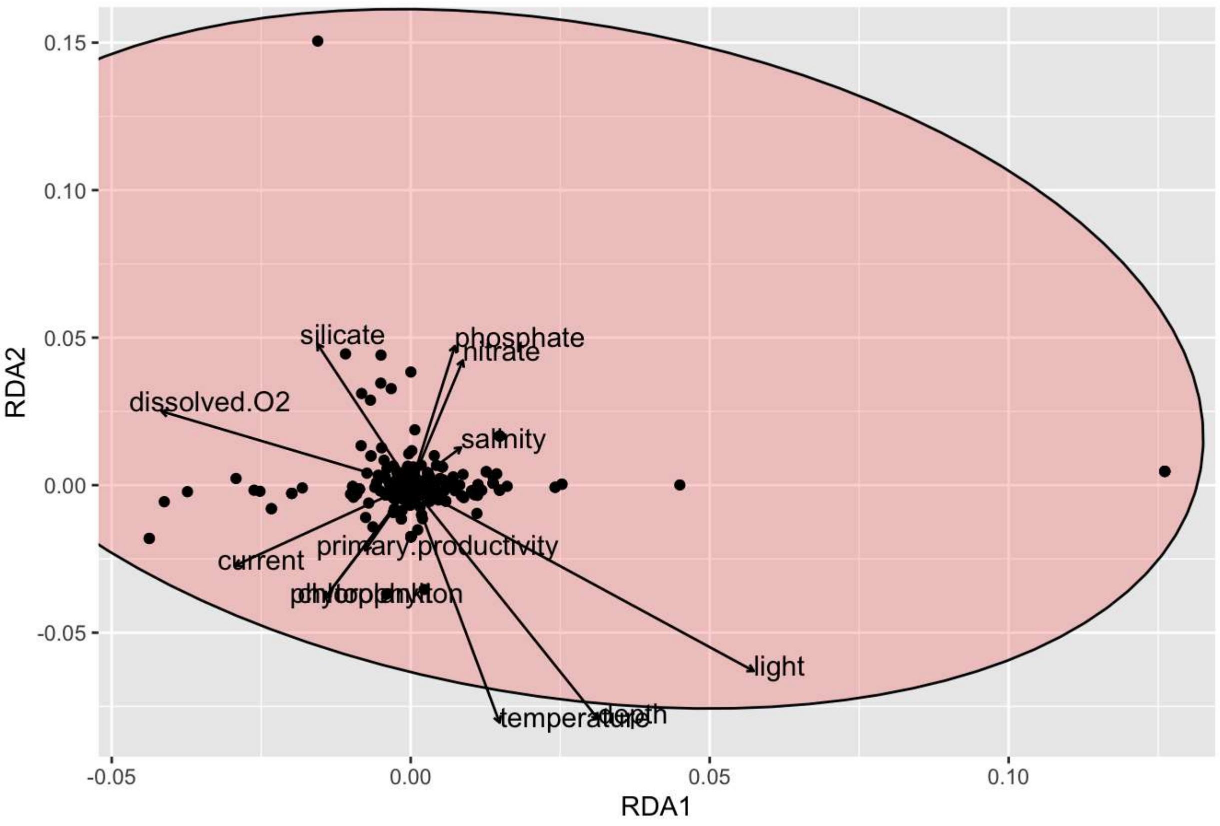


Hexanauplia

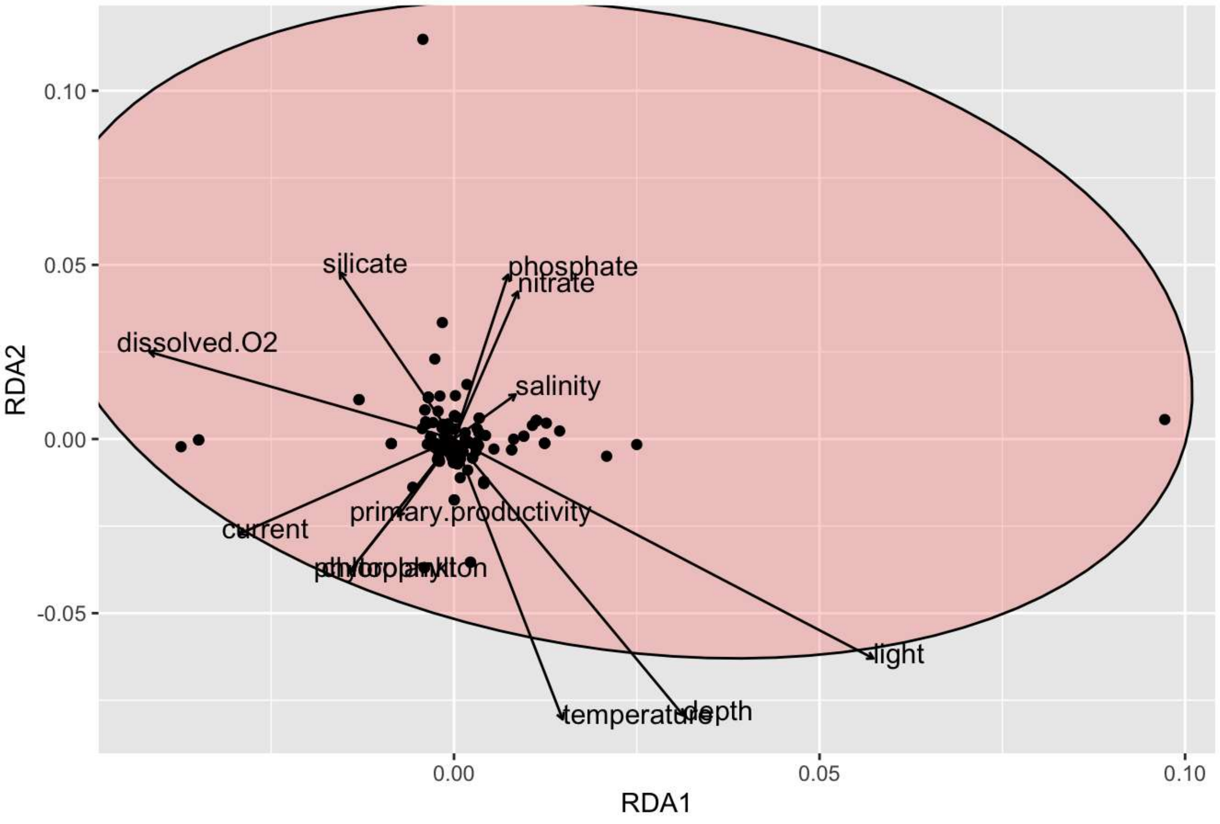

Arachnida
RDA2
RDA1
0.3
0.2
0.1
0.0
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
chlorophyll
phytoplankton
light
temperature
depth


Holothuroidea
RDA2
RDA1
0.1
0.0
-0.05
0.00
0.05
0.10
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
chlorophyll
phytoplankton
light
temperature
depth

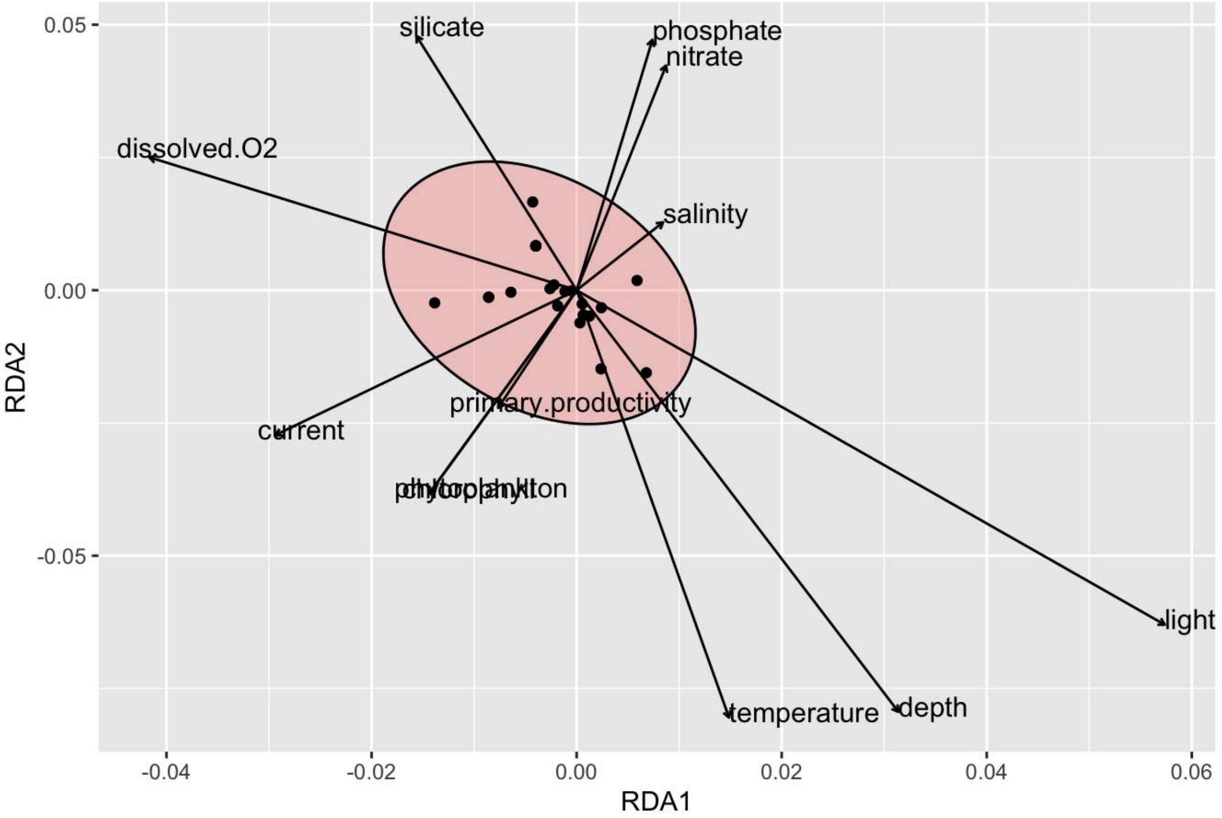
Echinoidea



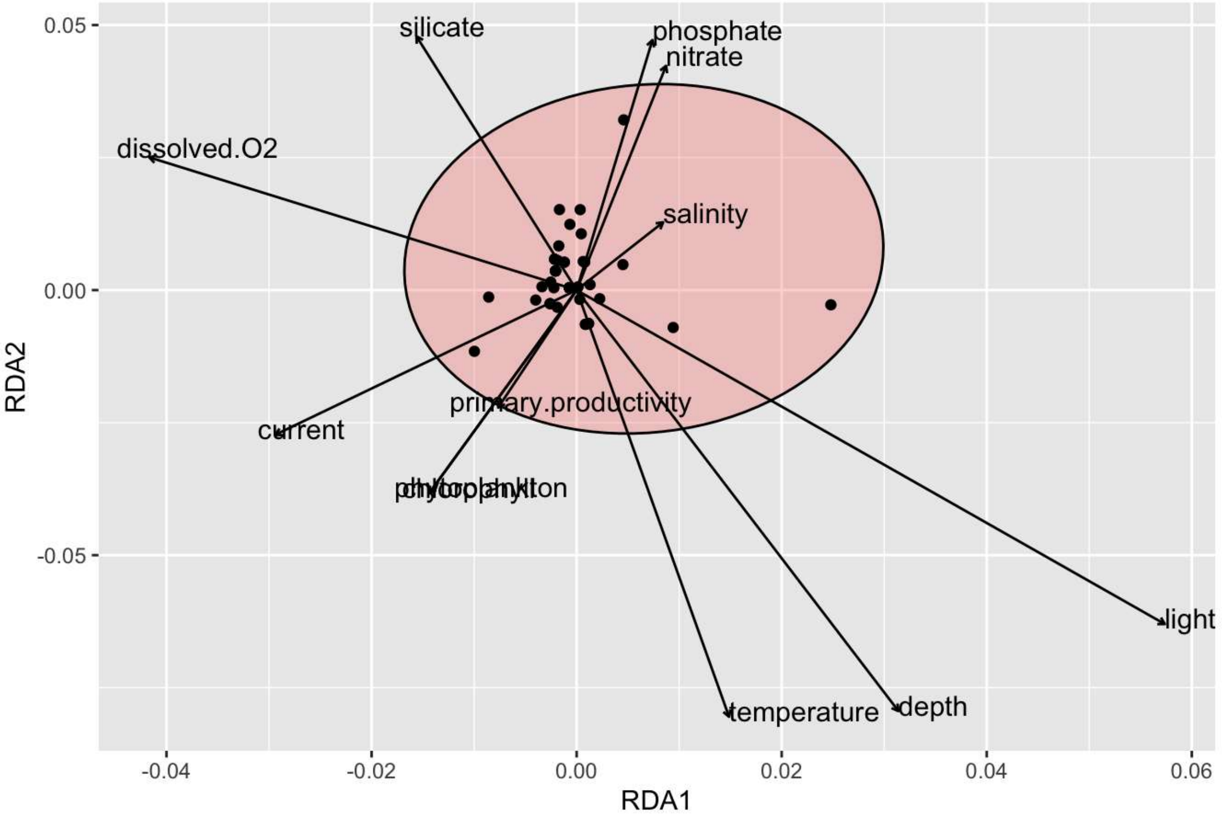
Pycnogonida

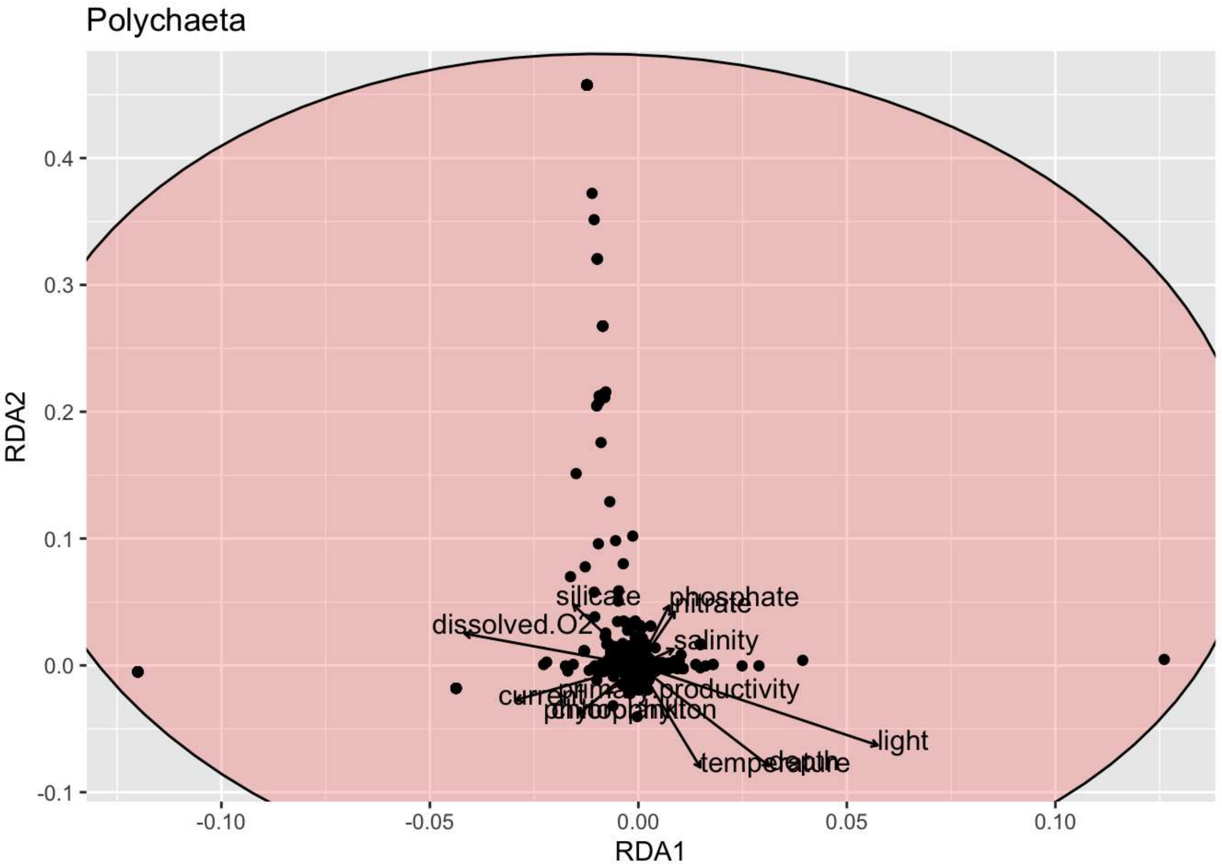


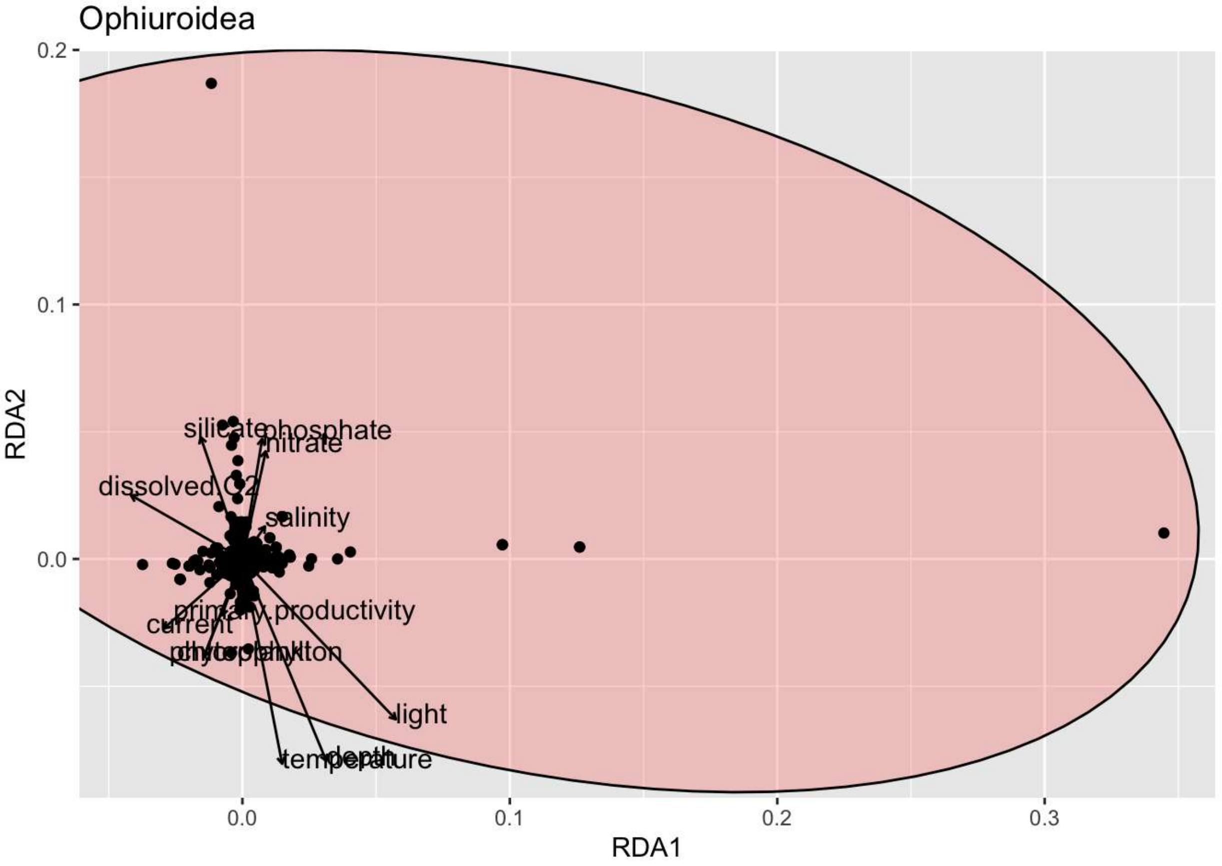
Calcarea

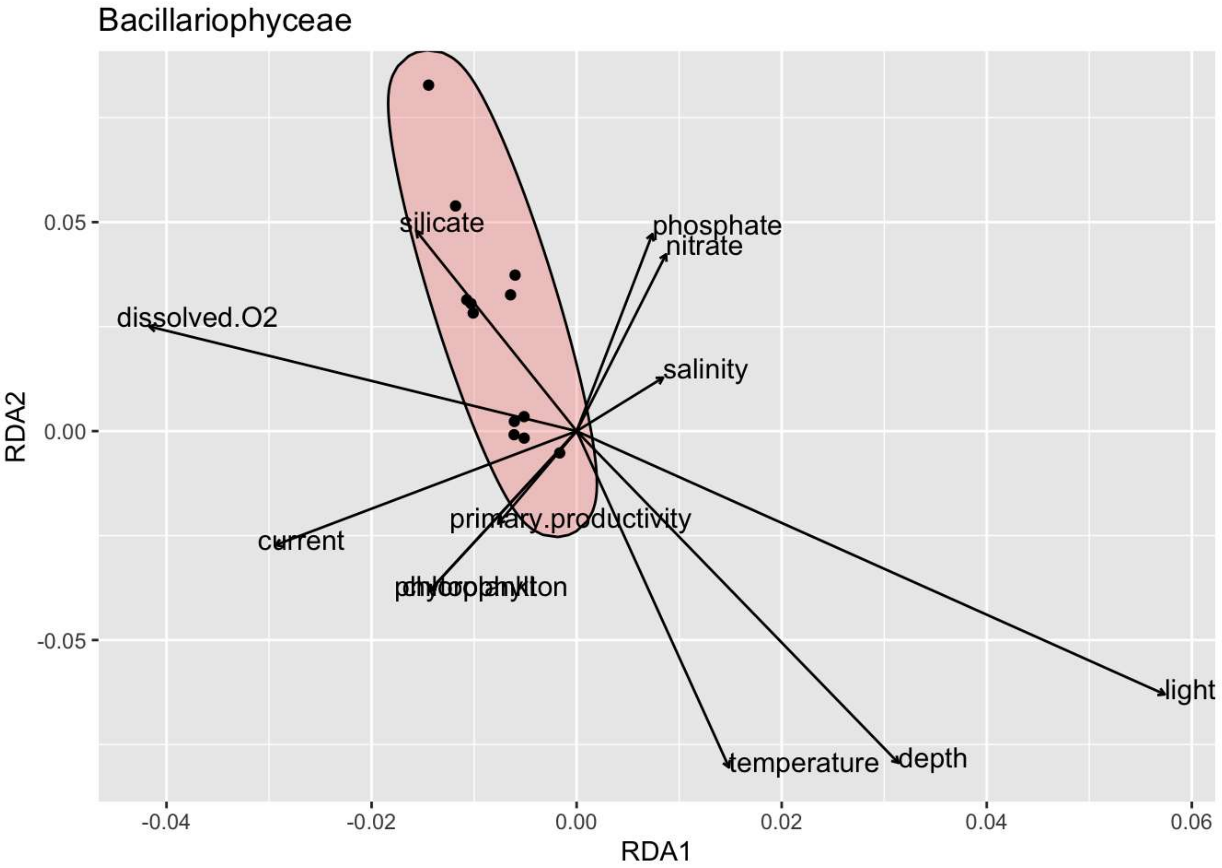


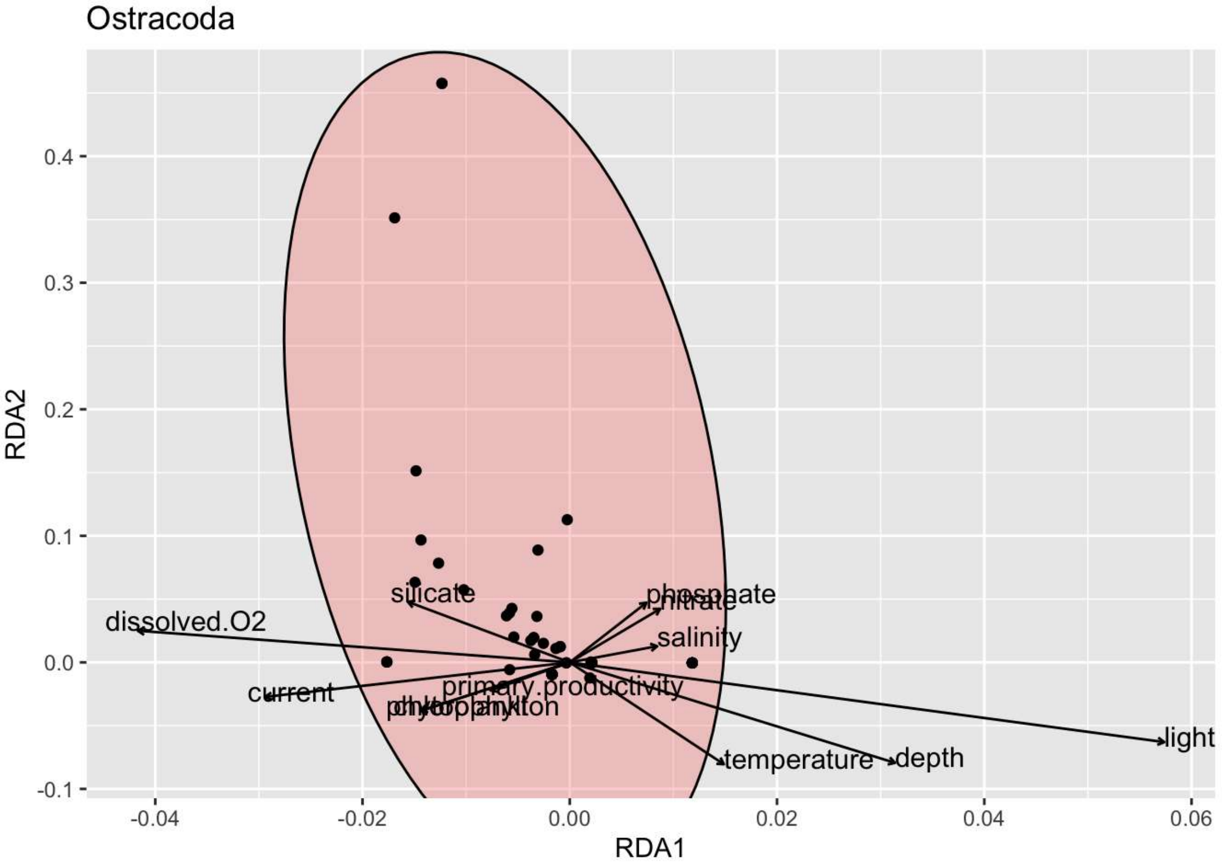
Rhabditophora

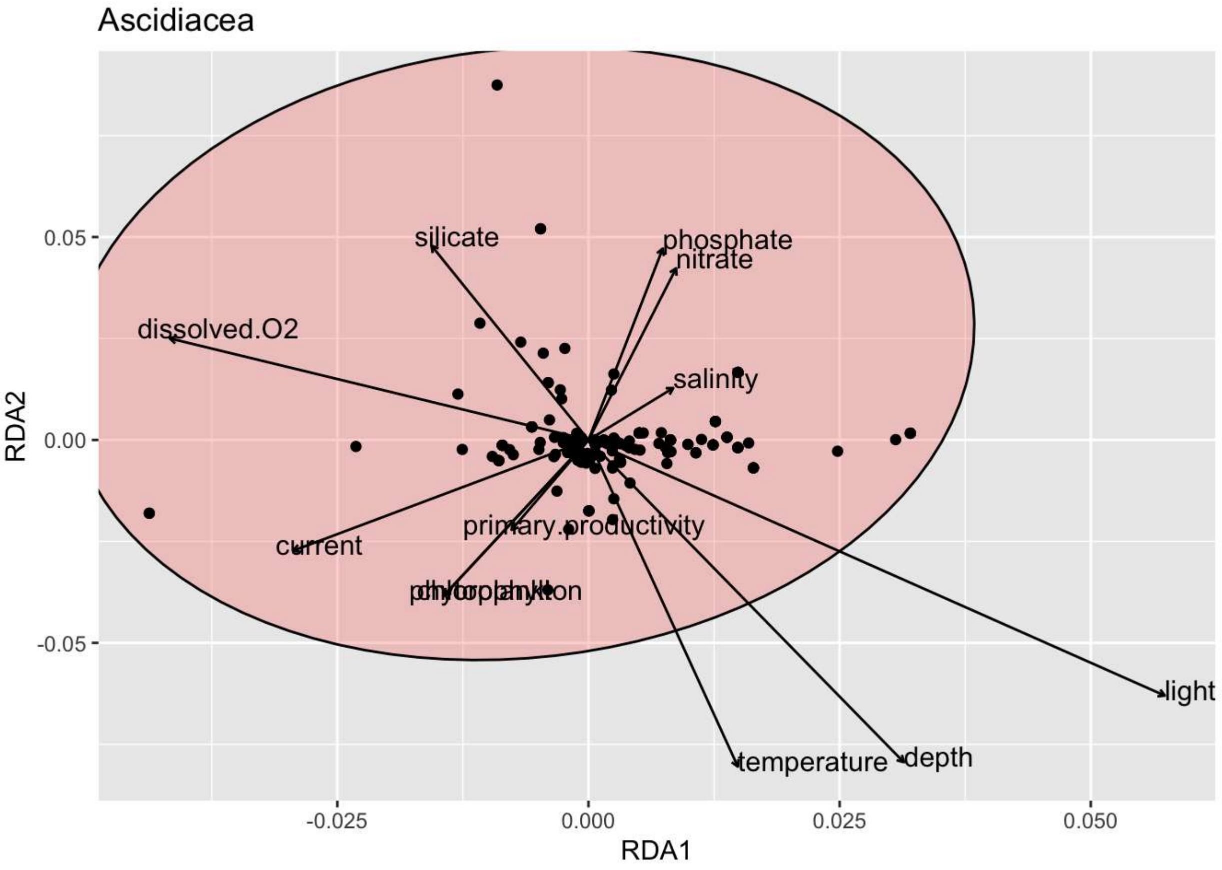



Polychaeta

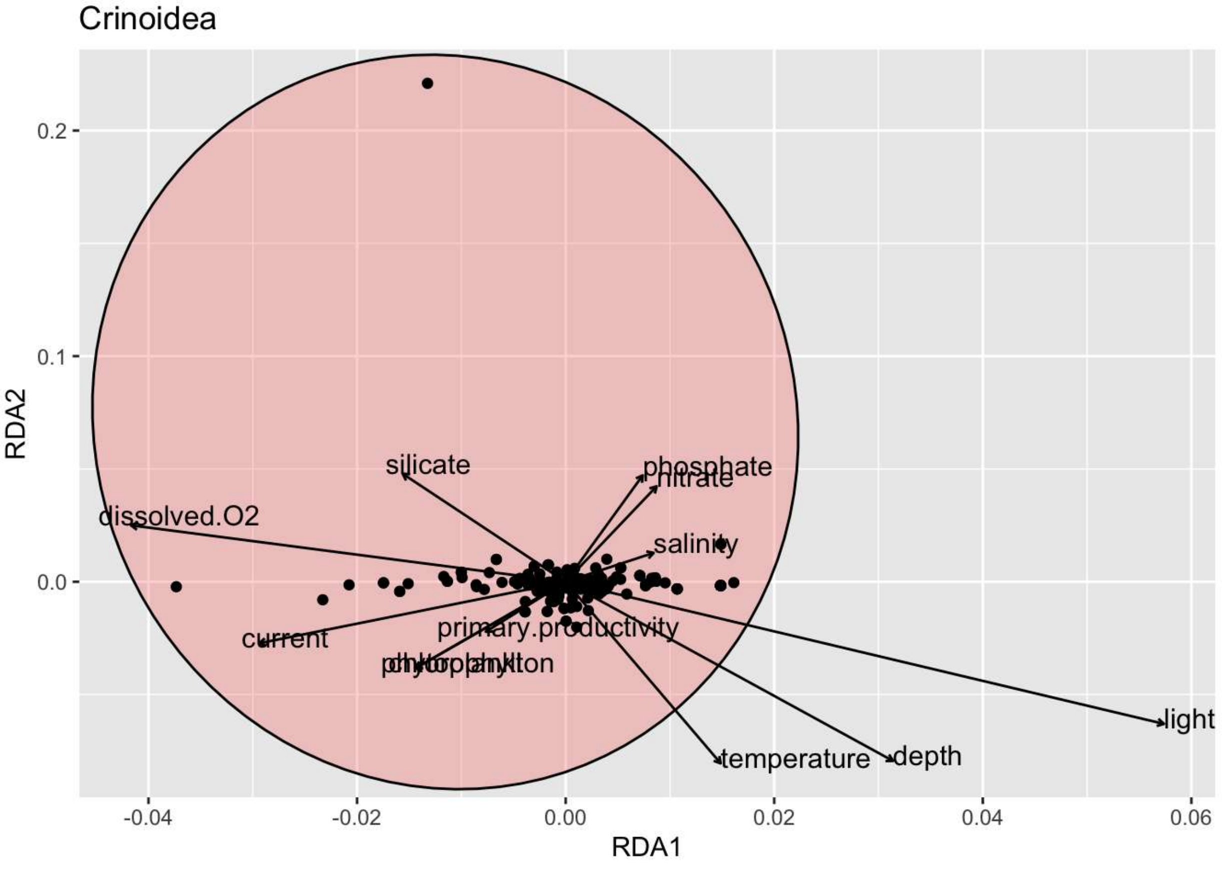

Ophiuroidea


Bacillariophyceae
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

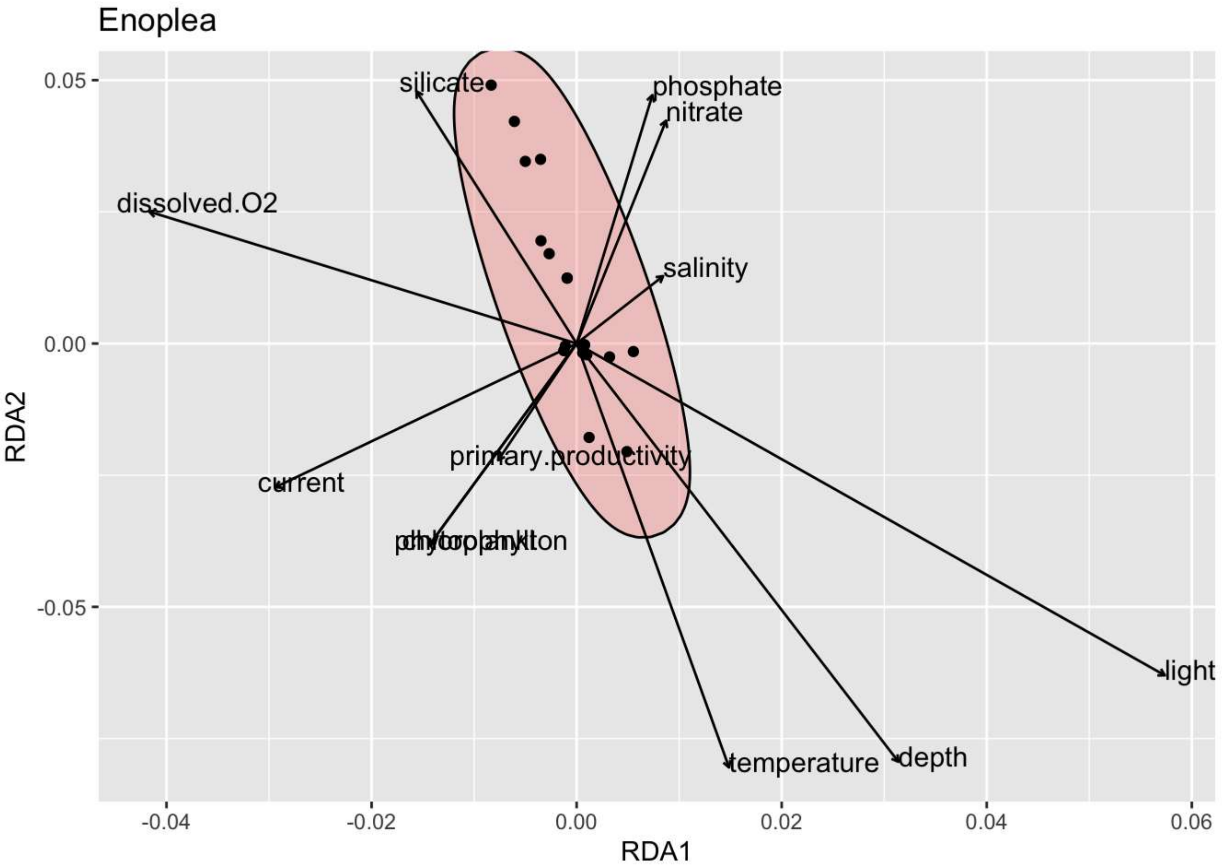

Ostracoda
RDA2
RDA1
0.4
0.3
0.2
0.1
0.0
-0.1
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
chlorophyll
phytoplankton
light
temperature
depth

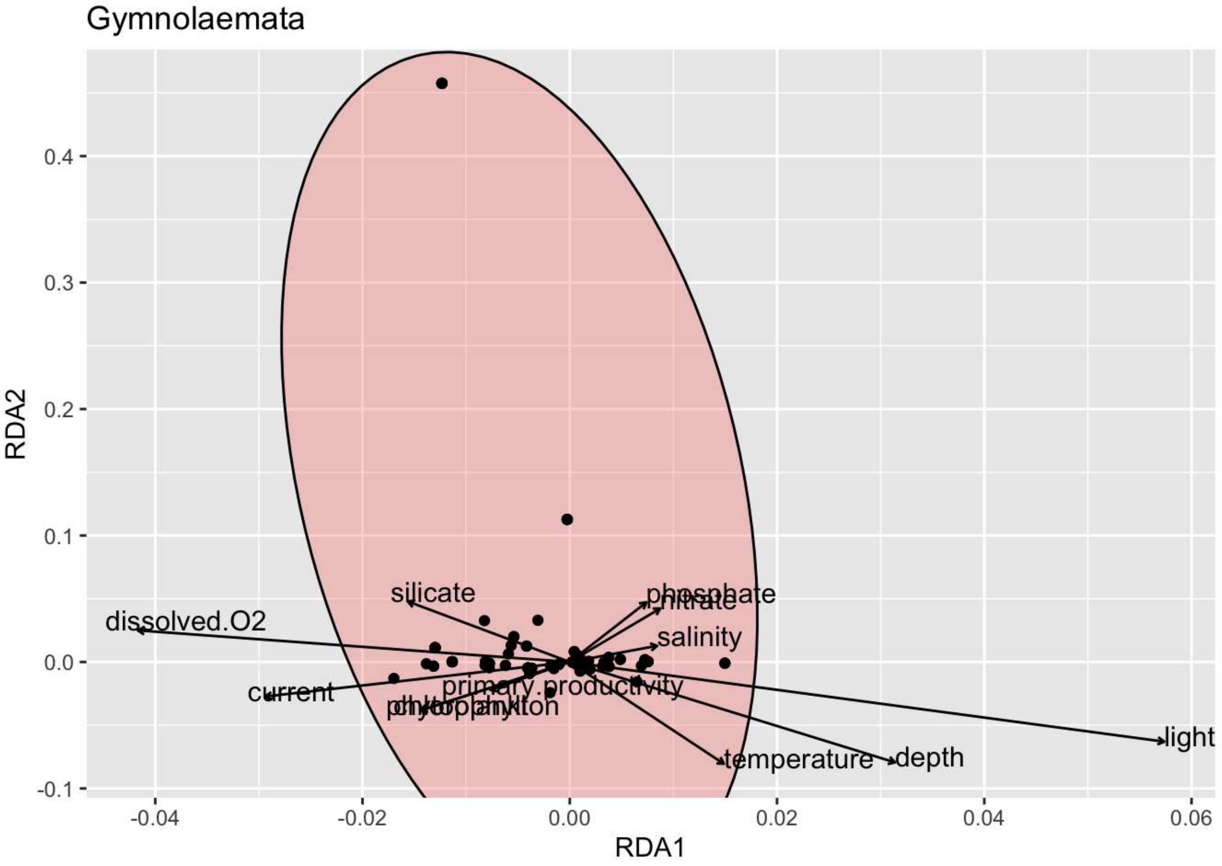


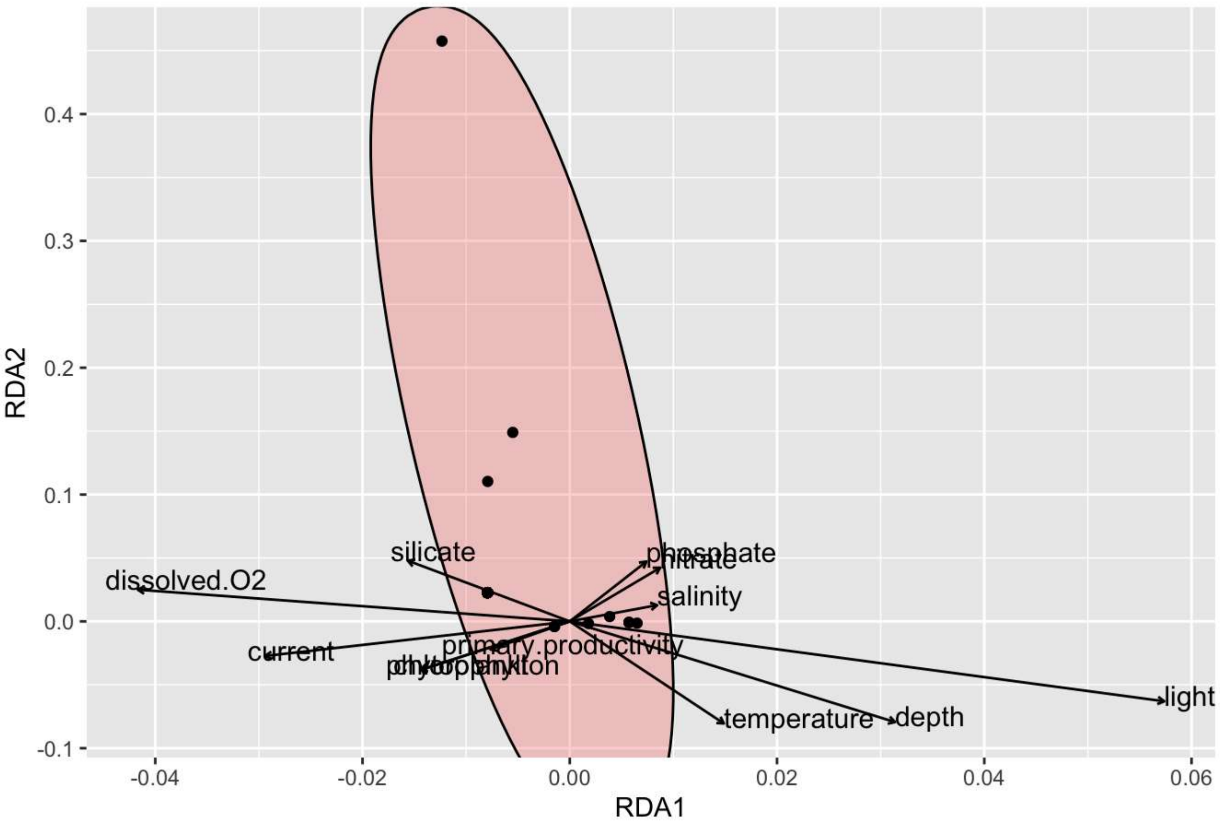
Ascidiacea



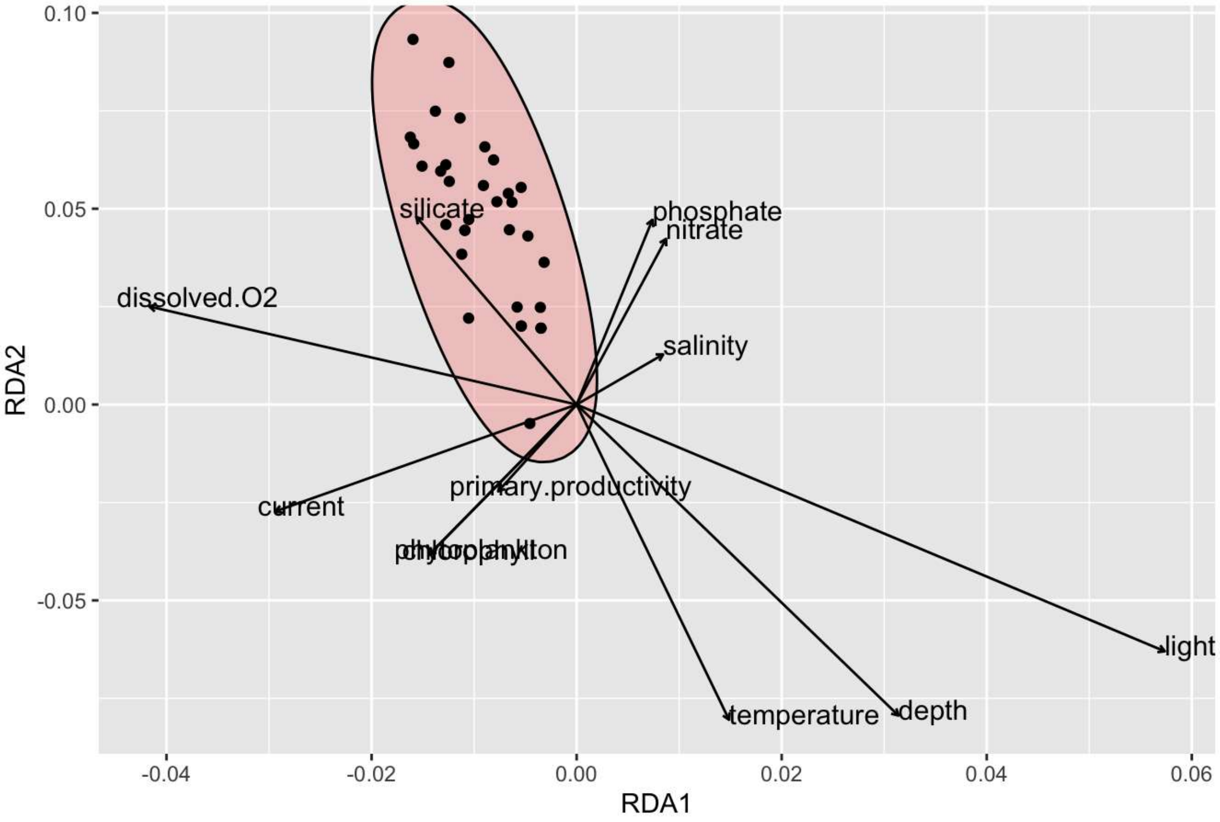
Crinoidea


Enoplea
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

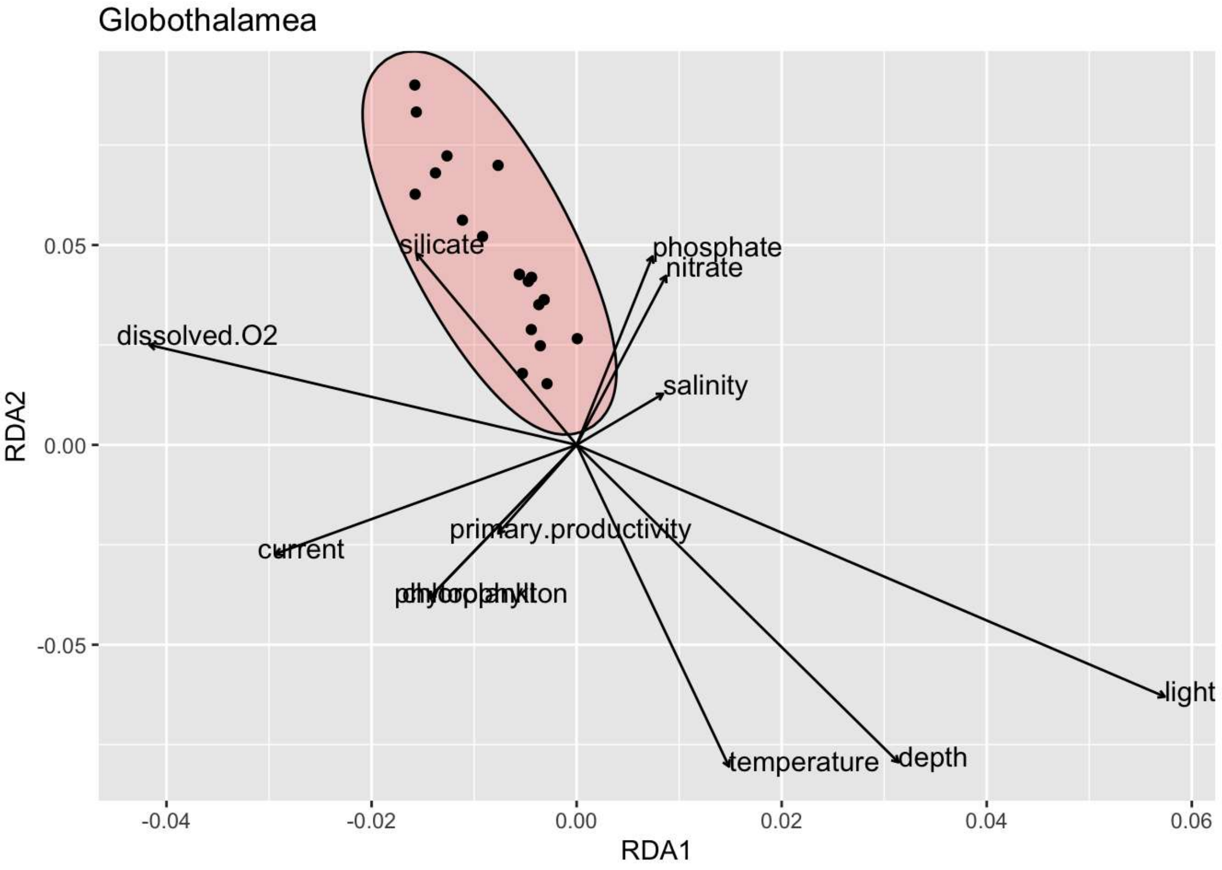

Gymnolaemata
RDA2
RDA1
0.4
0.3
0.2
0.1
0.0
-0.1
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
chlorophyll
phytoplankton
light
temperature
depth

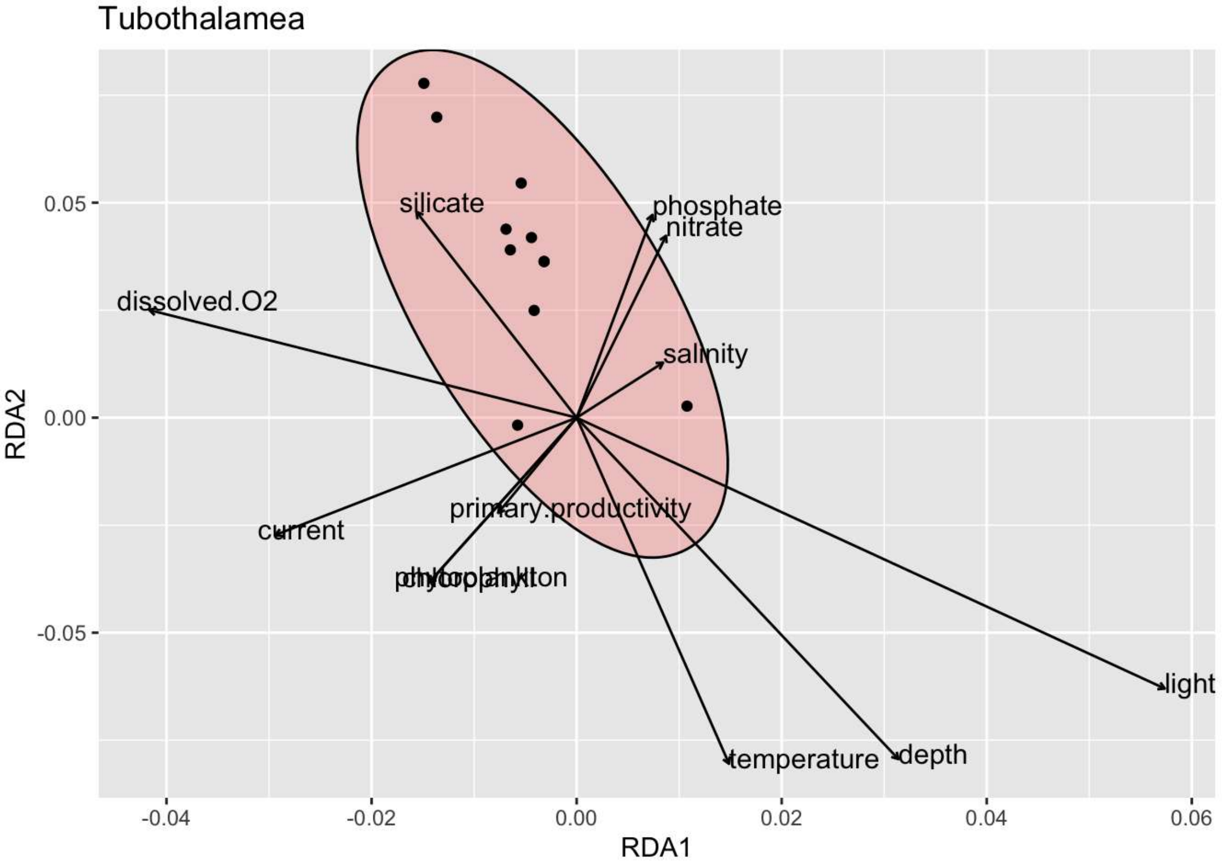


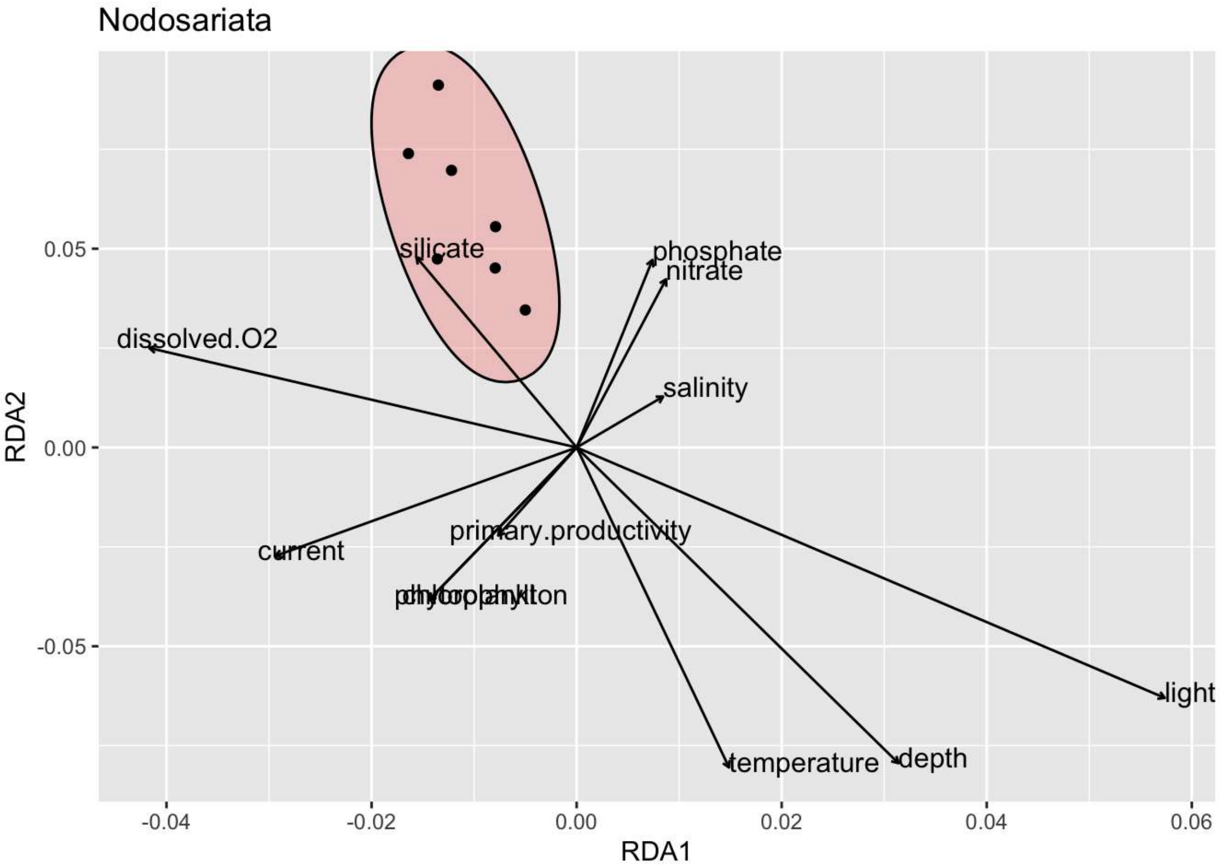
Clitellata

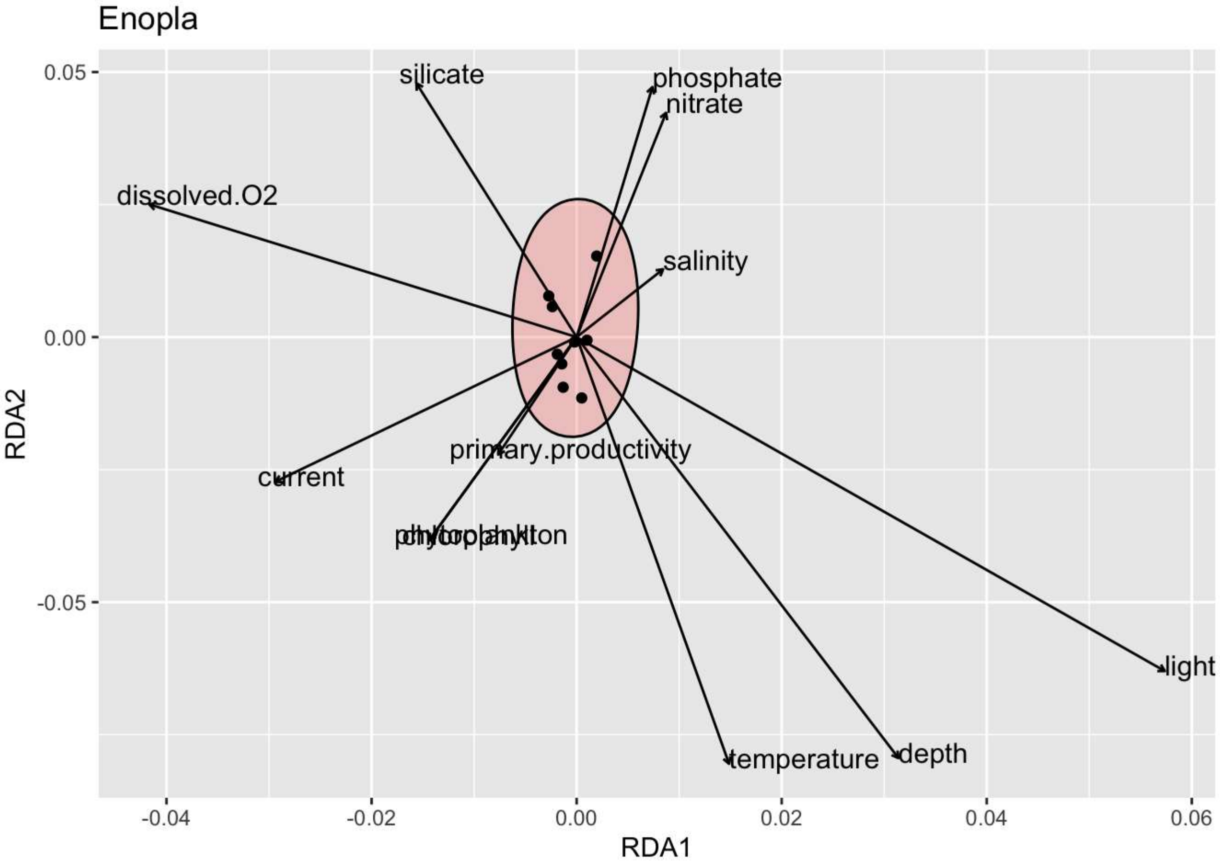


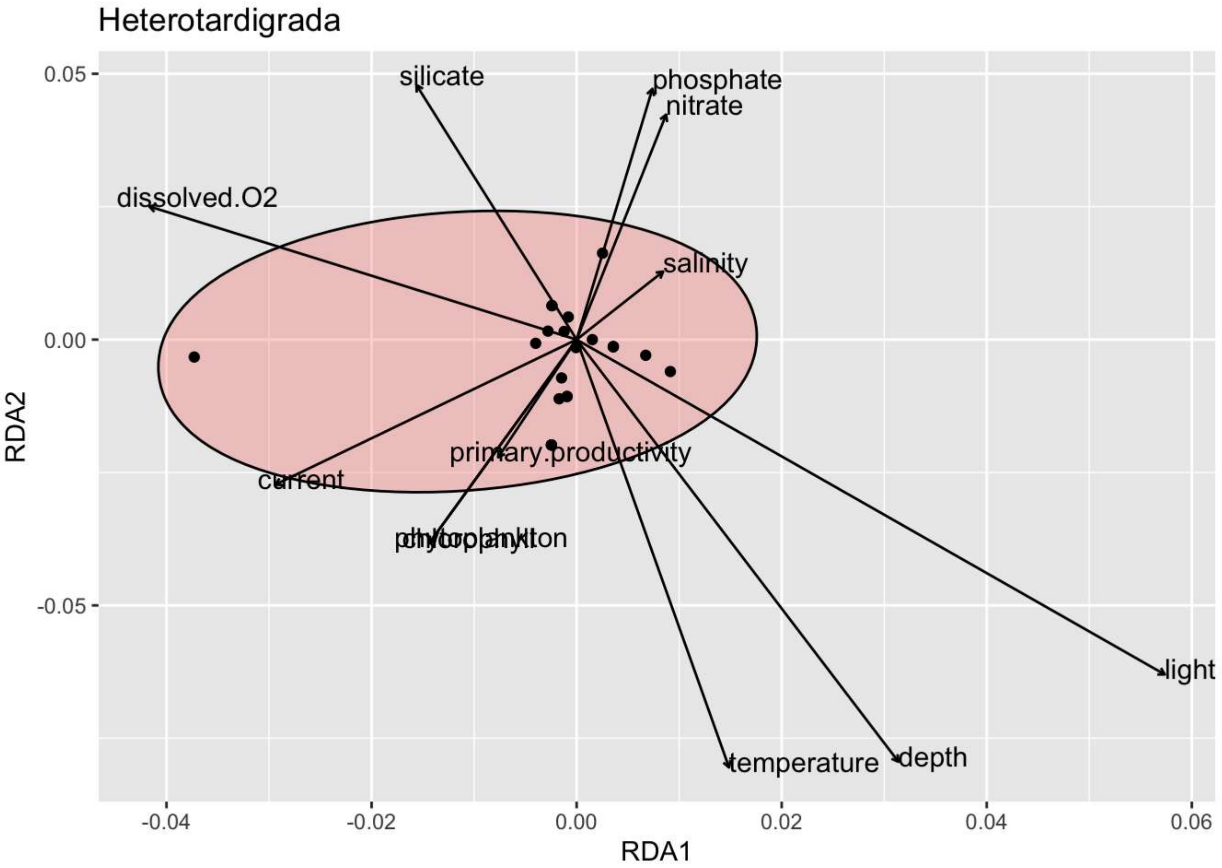
Monothalamea

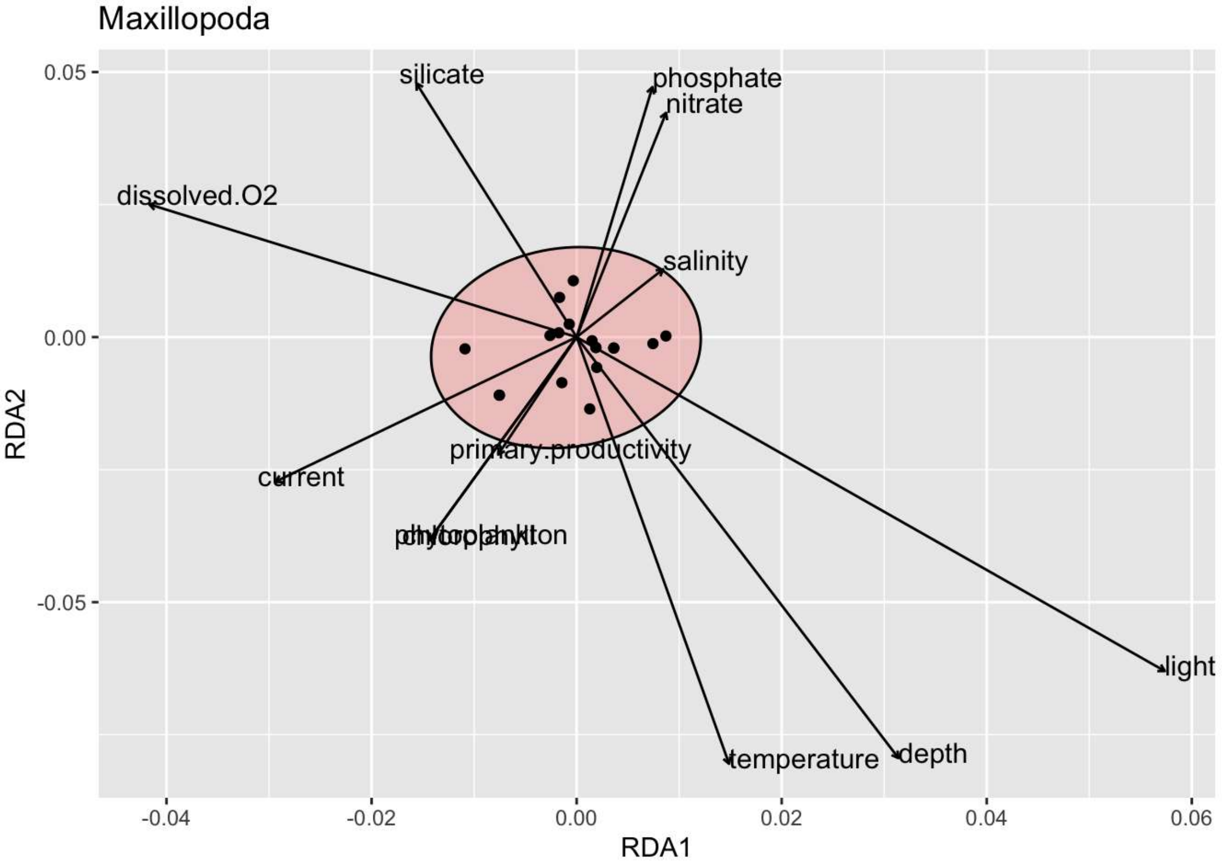

Globothalamea
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

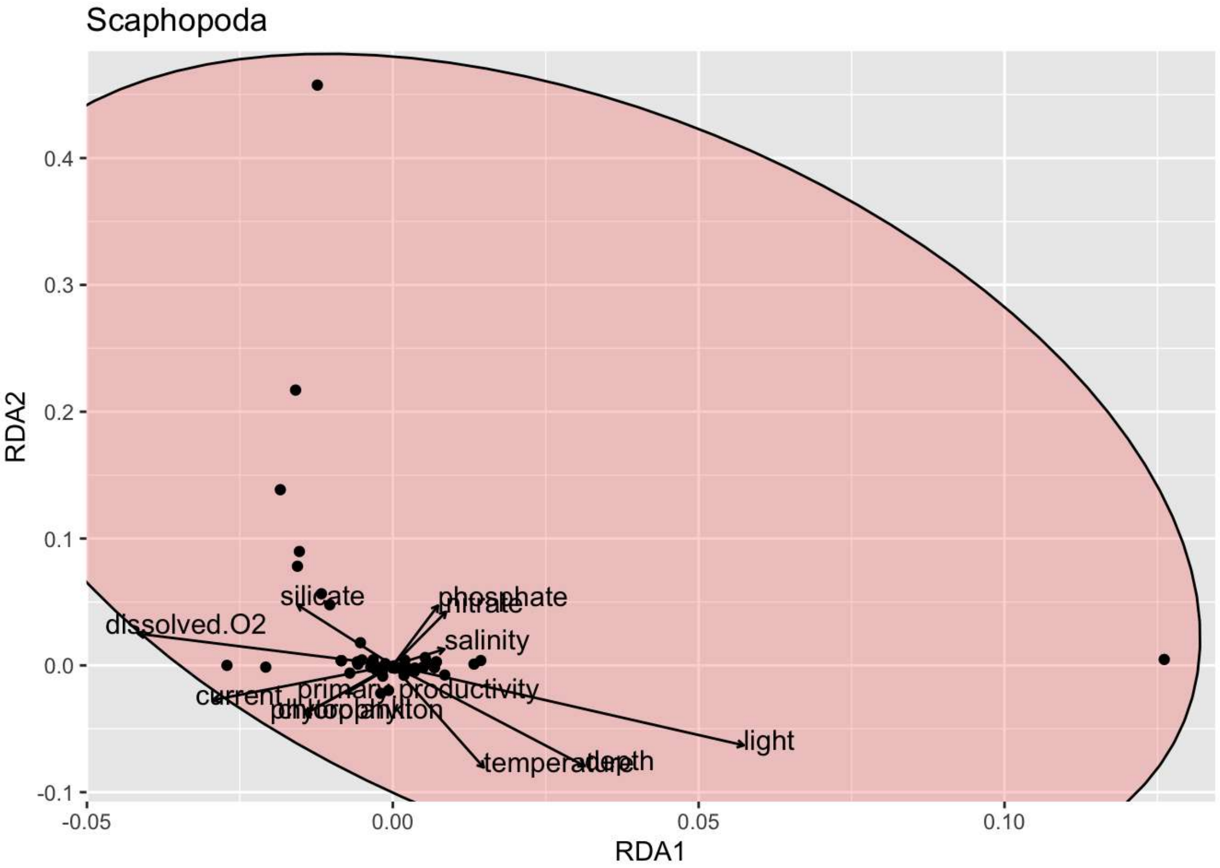

Tubothalamea
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

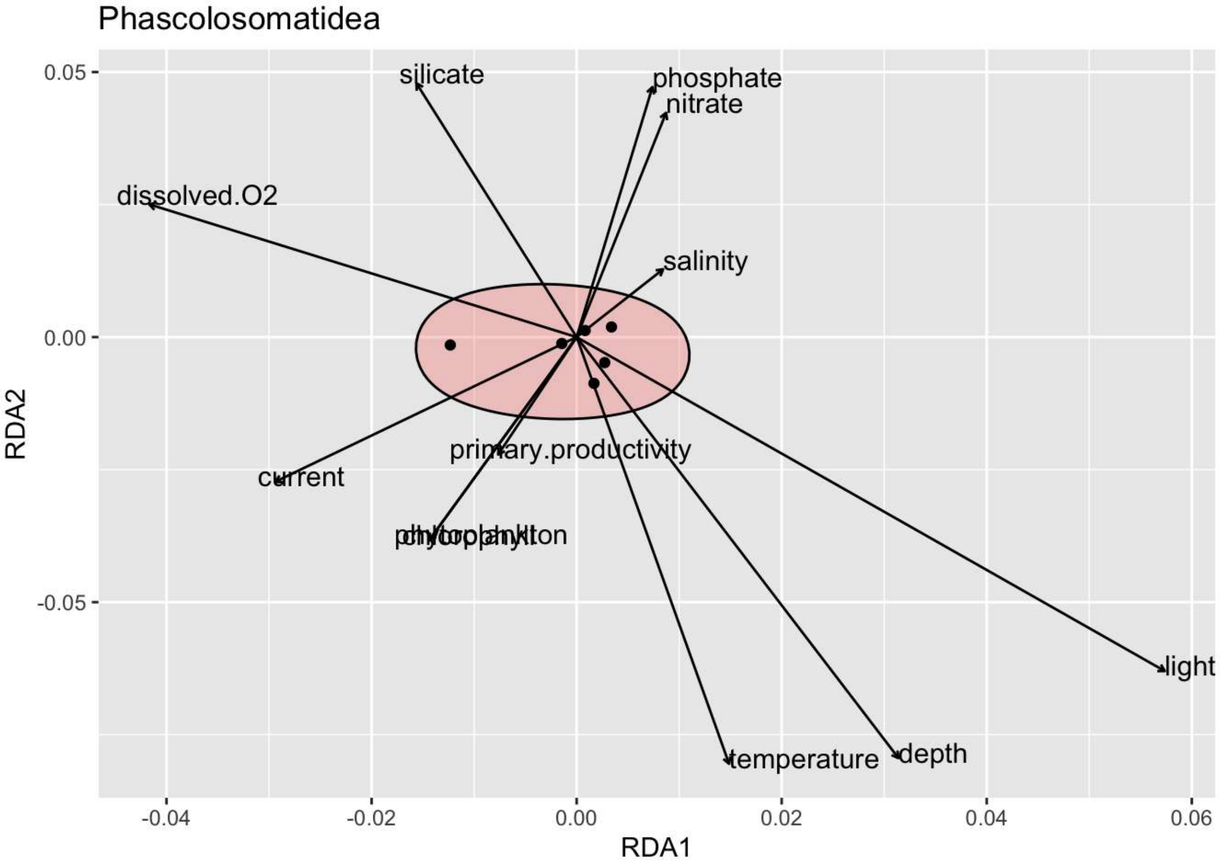

Nodosariata
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth

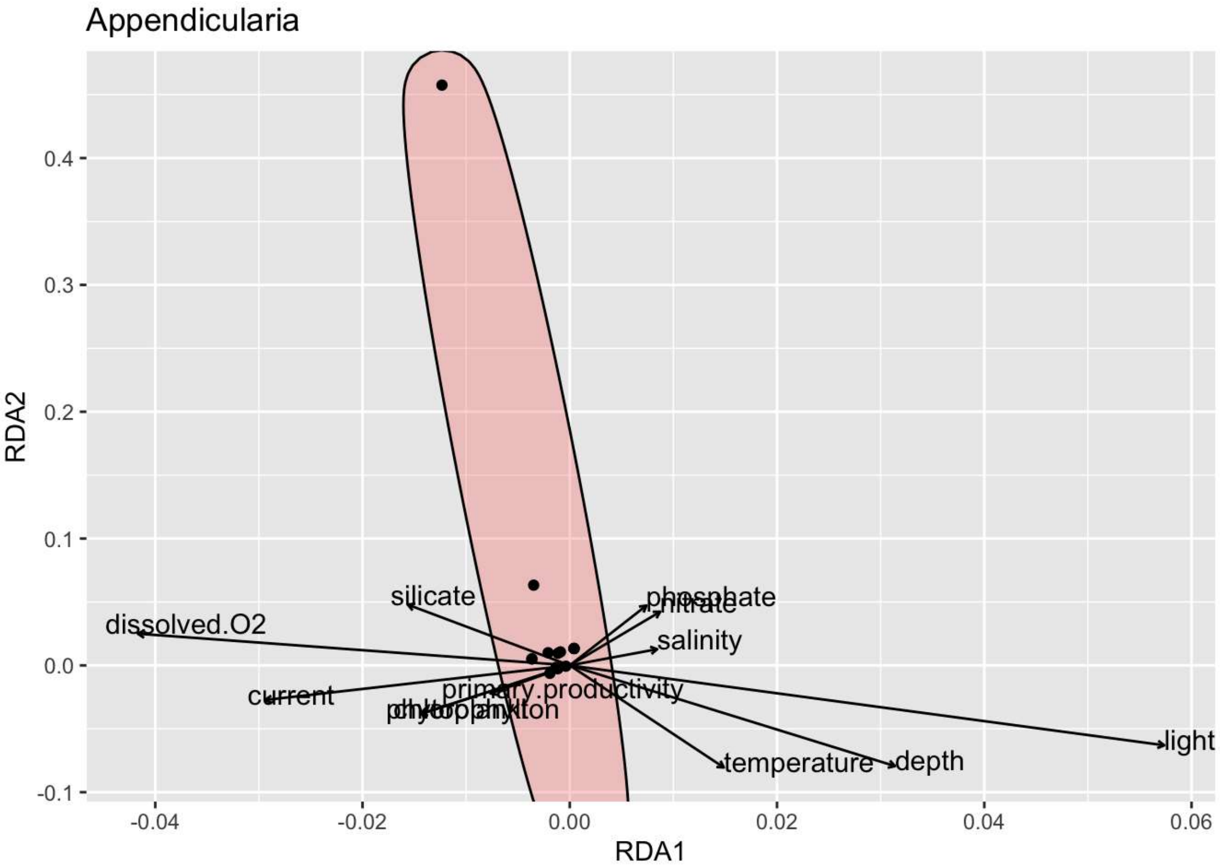

Enopla
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth


Heterotardigrada
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1
RDA2

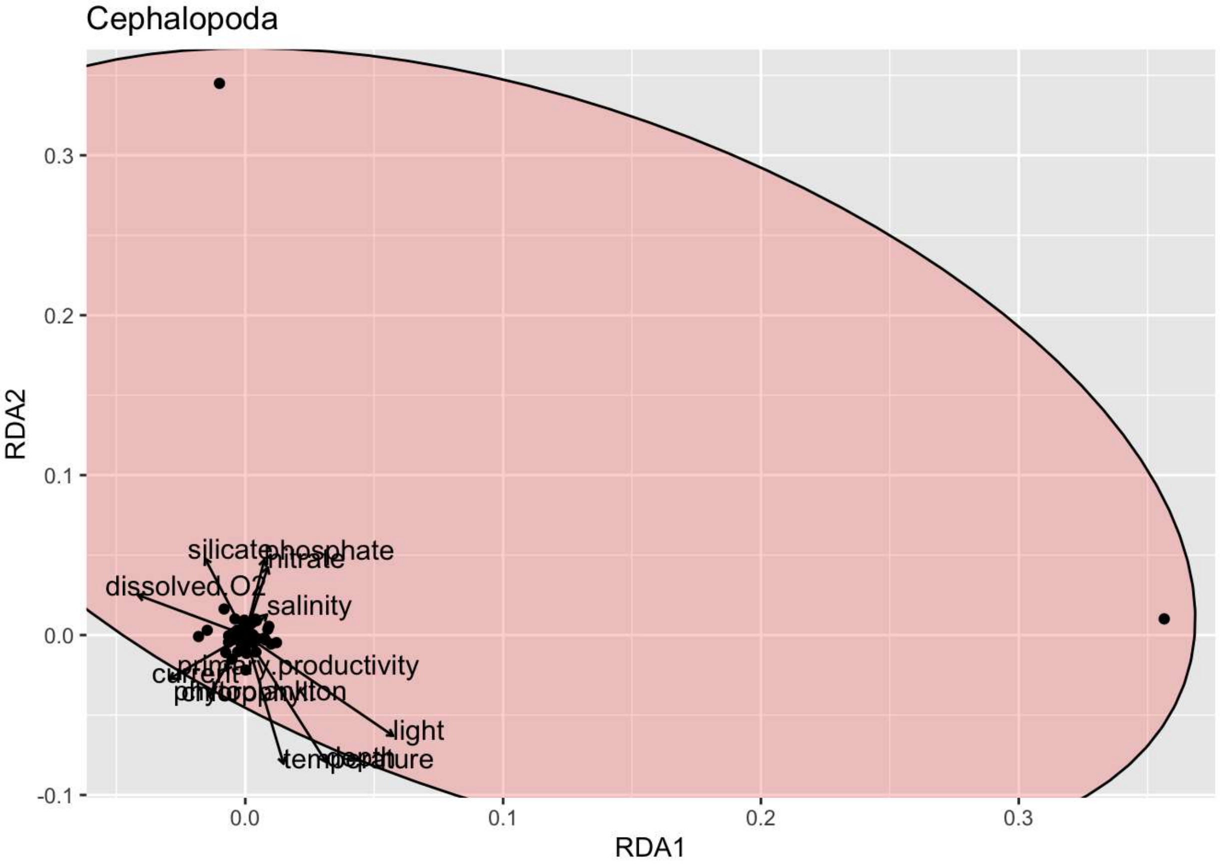

Maxillopoda
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1
RDA2


Scaphopoda
RDA2
RDA1
0.4
0.3
0.2
0.1
0.0
-0.1
-0.05
0.00
0.05
0.10
silicate
phosphate
nitrate
dissolved.O2
salinity
current
primary.productivity
phytoplankton
chlorophyll
light
temperature
depth

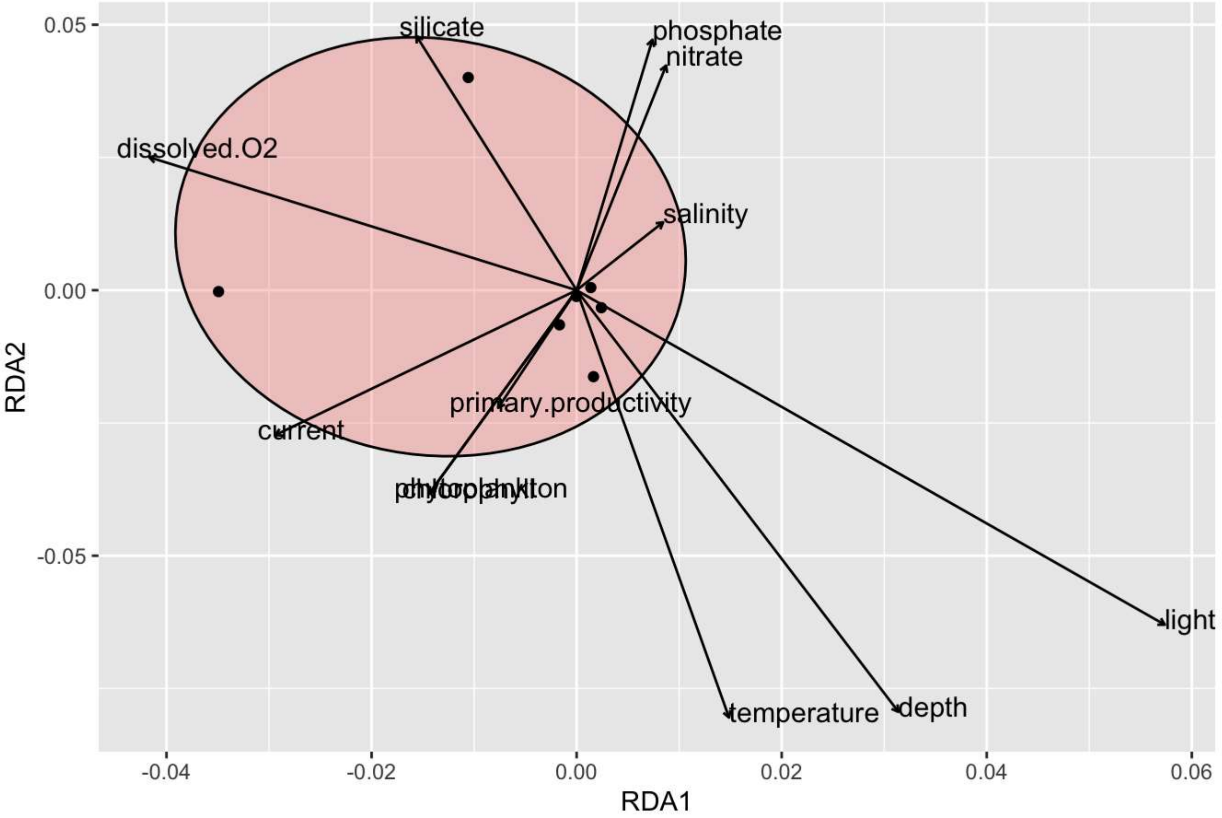

Phascolosomatidea
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth

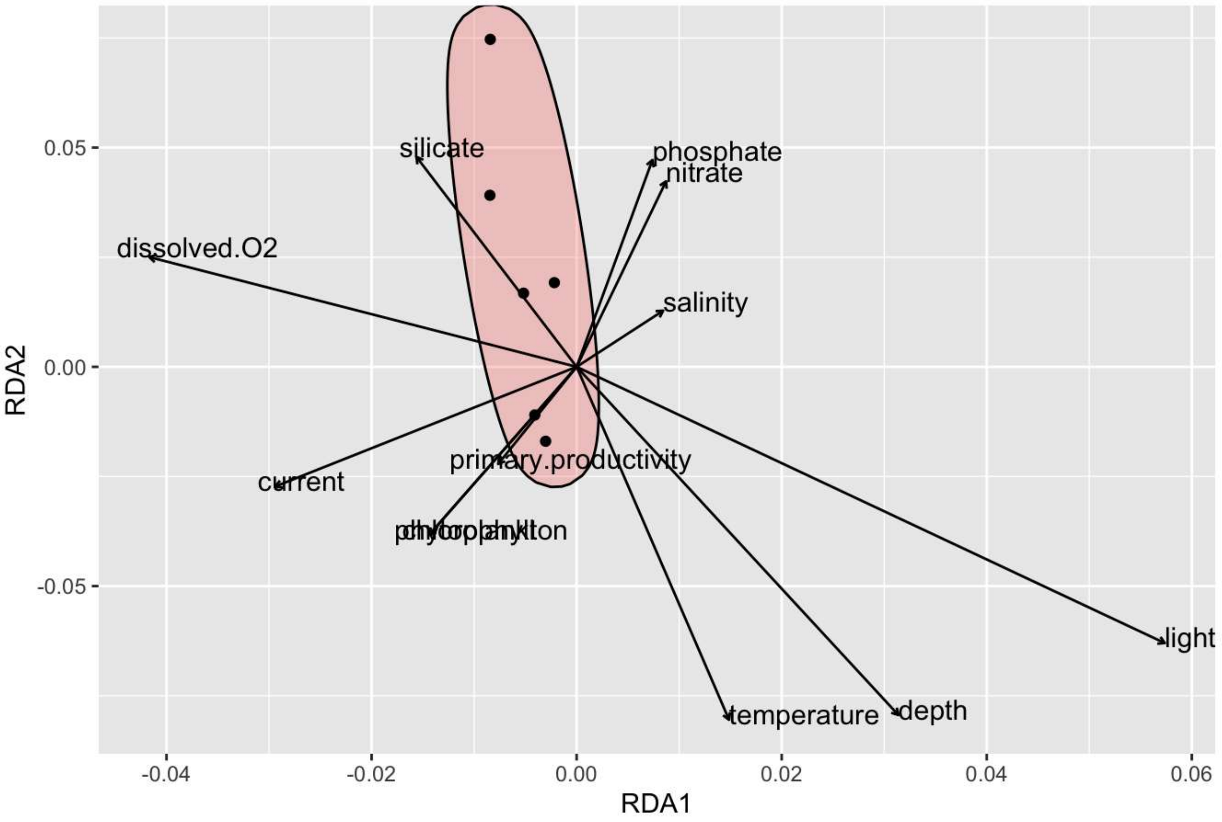


Appendicularia

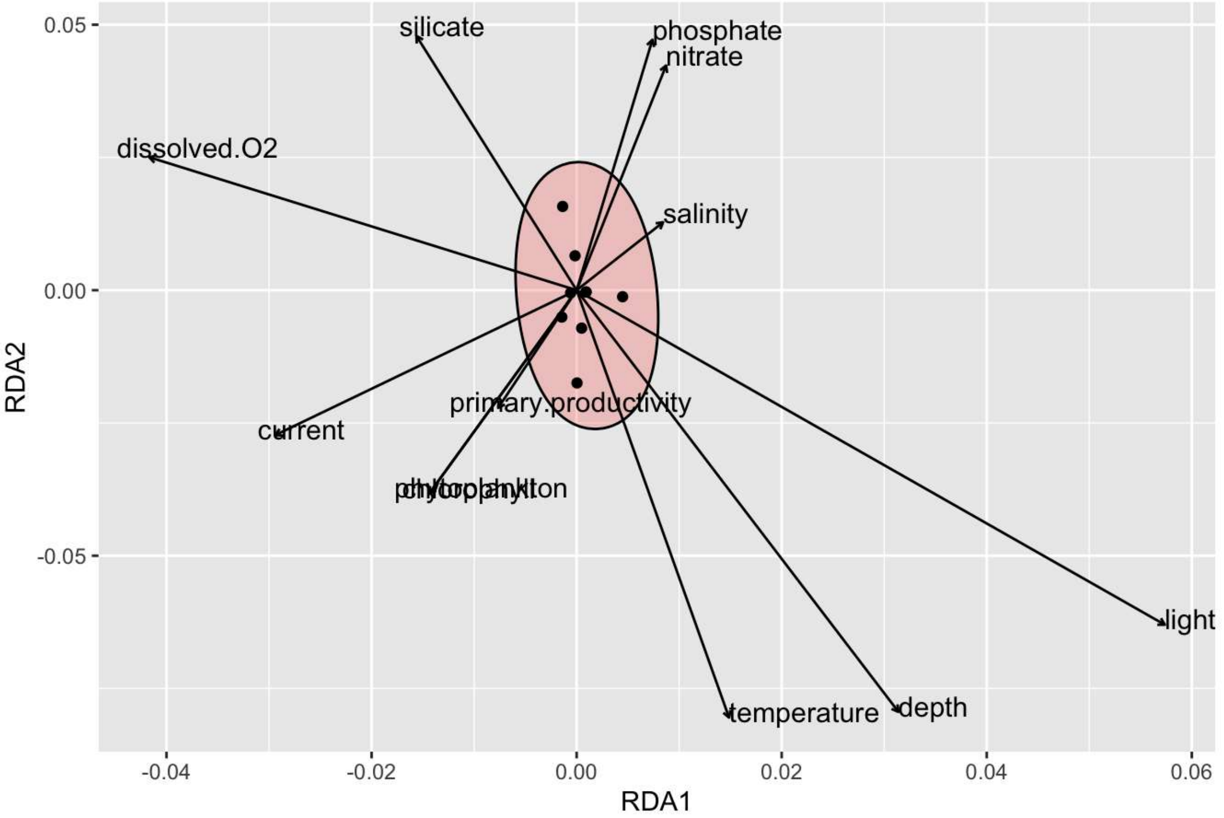


Cephalopoda

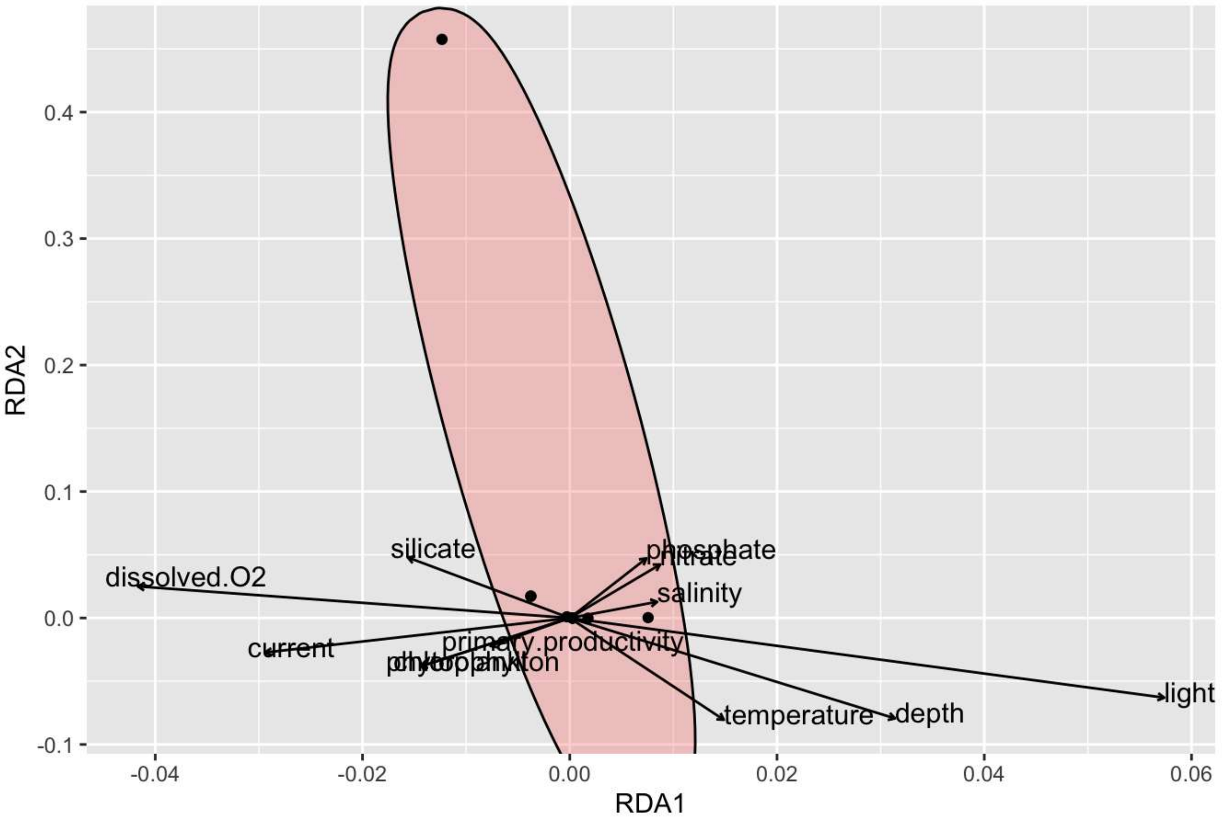

Enteropneusta

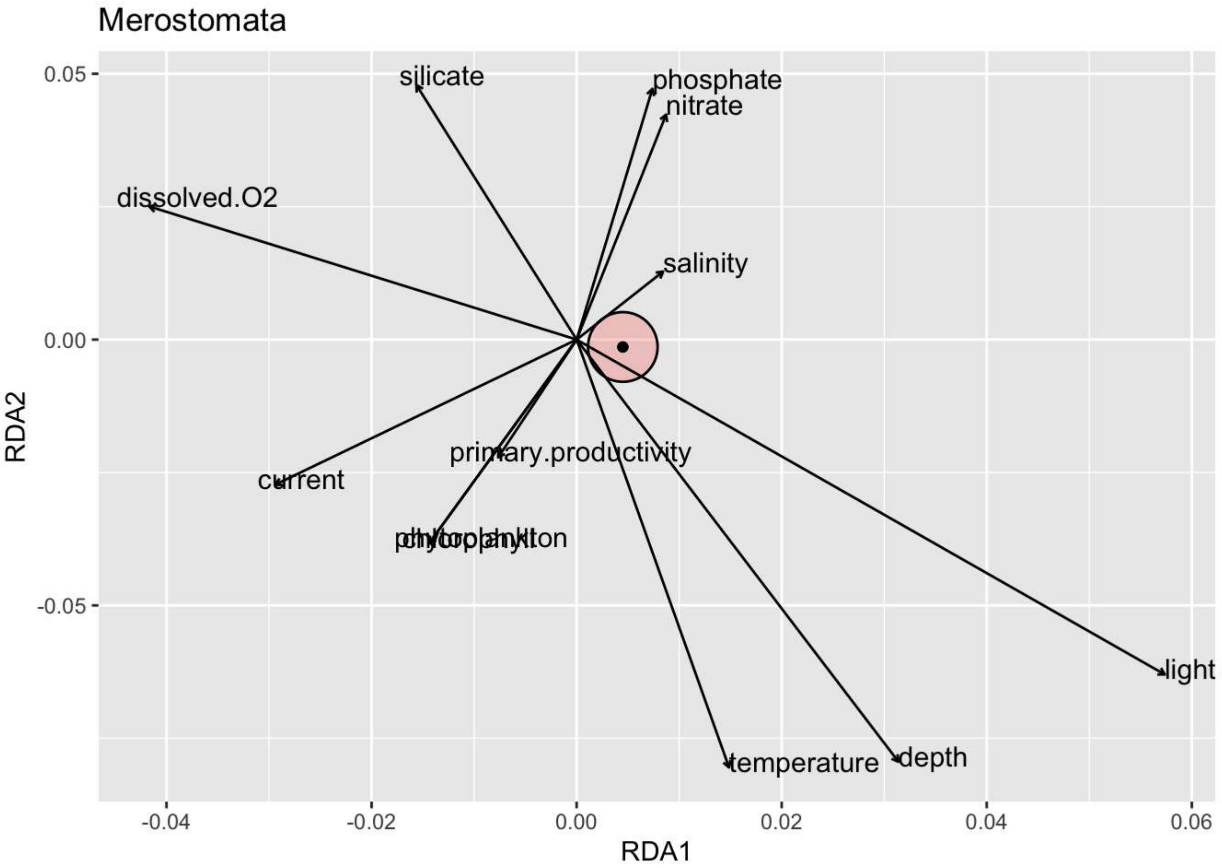

Pilidiophora

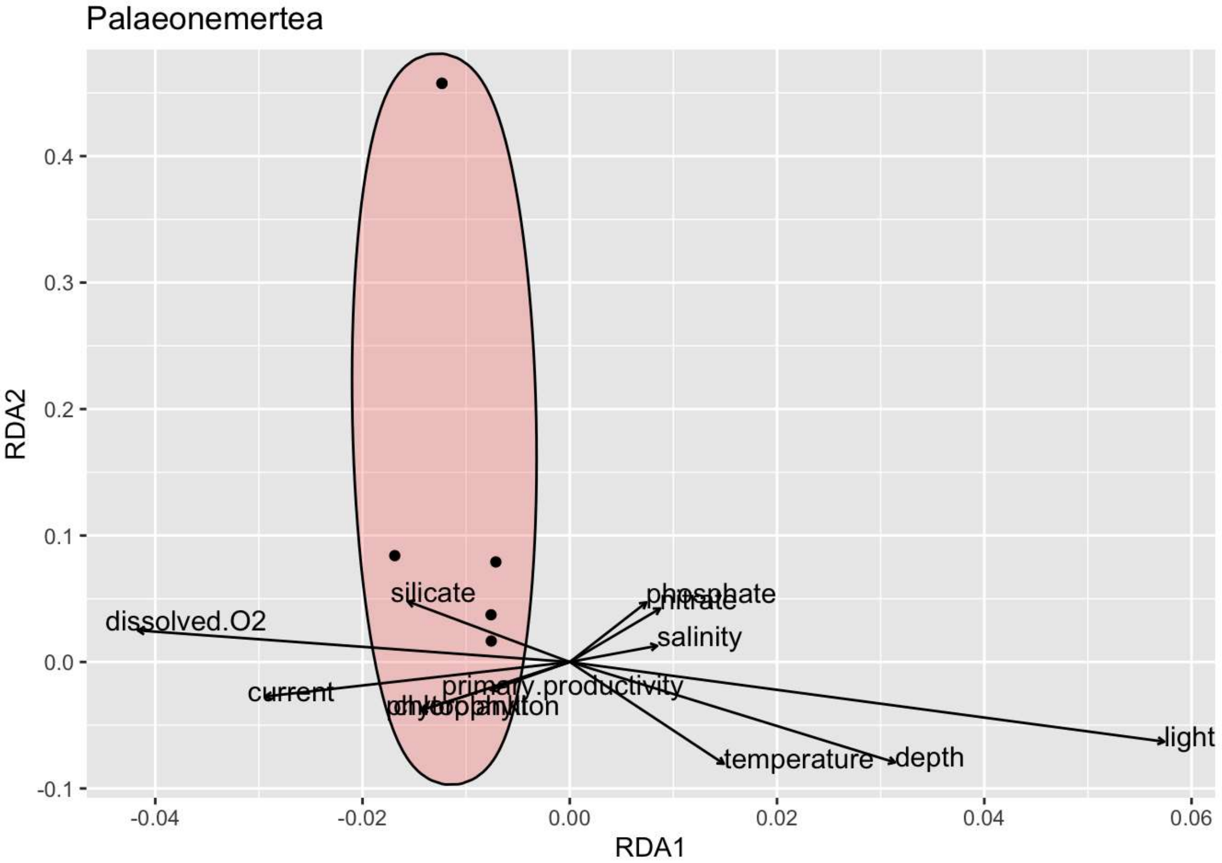
Anopla



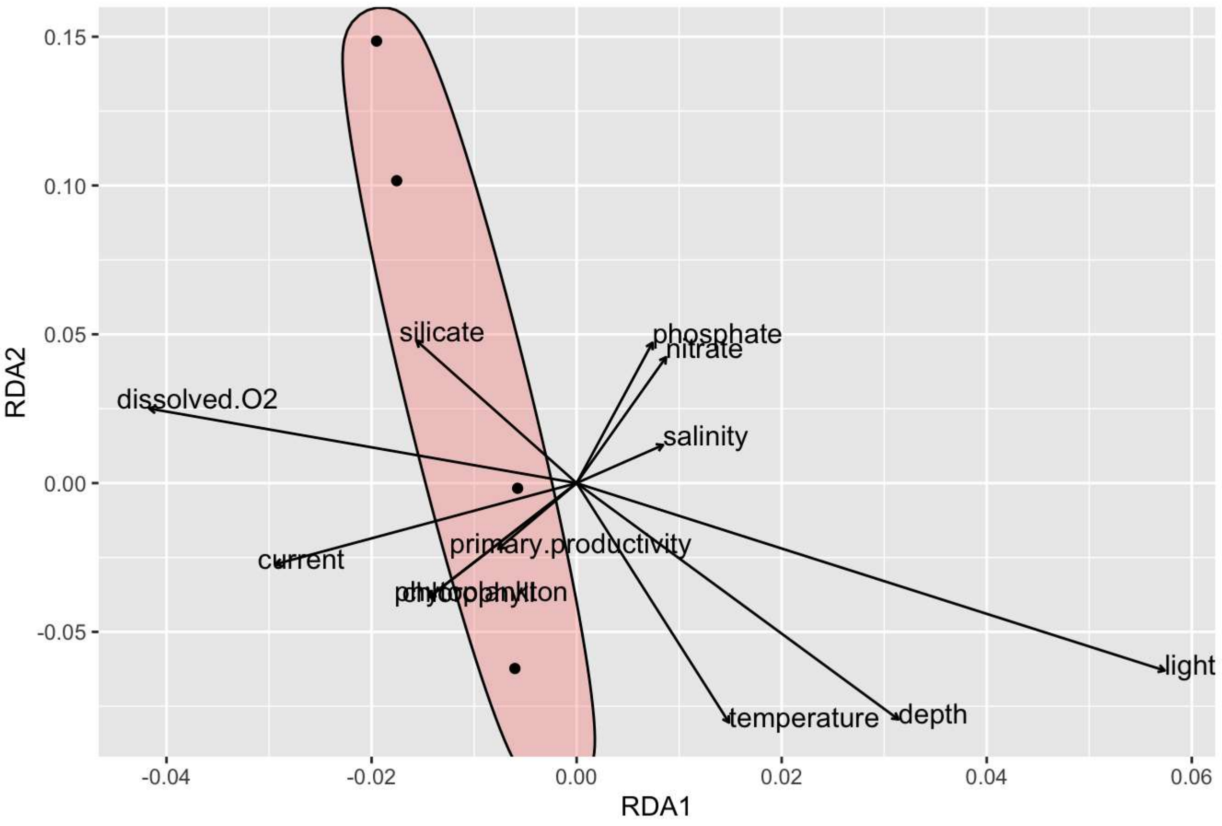
Stenolaemata



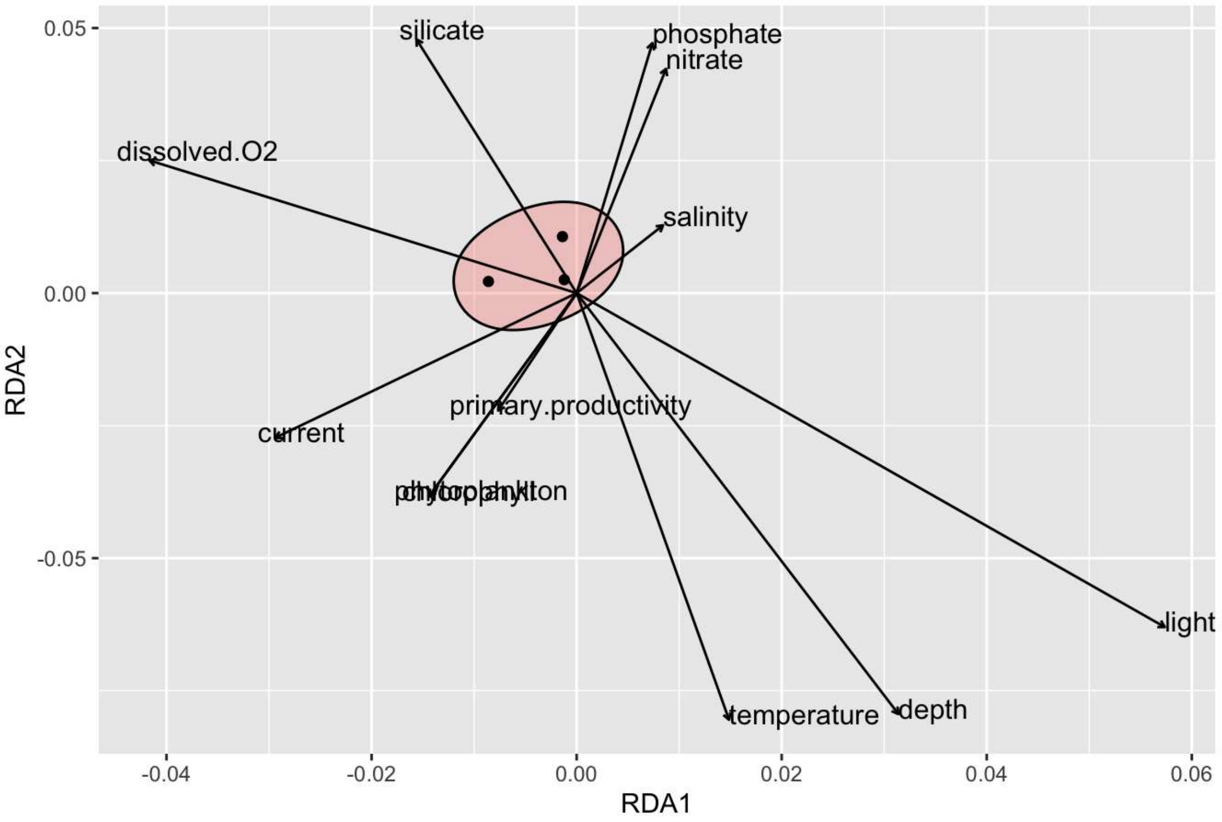

Merostomata
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06


Palaeonemertea
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
RDA2
RDA1
0.4
0.3
0.2
0.1
0.0
-0.1
-0.04
-0.02
0.00
0.02
0.04
0.06

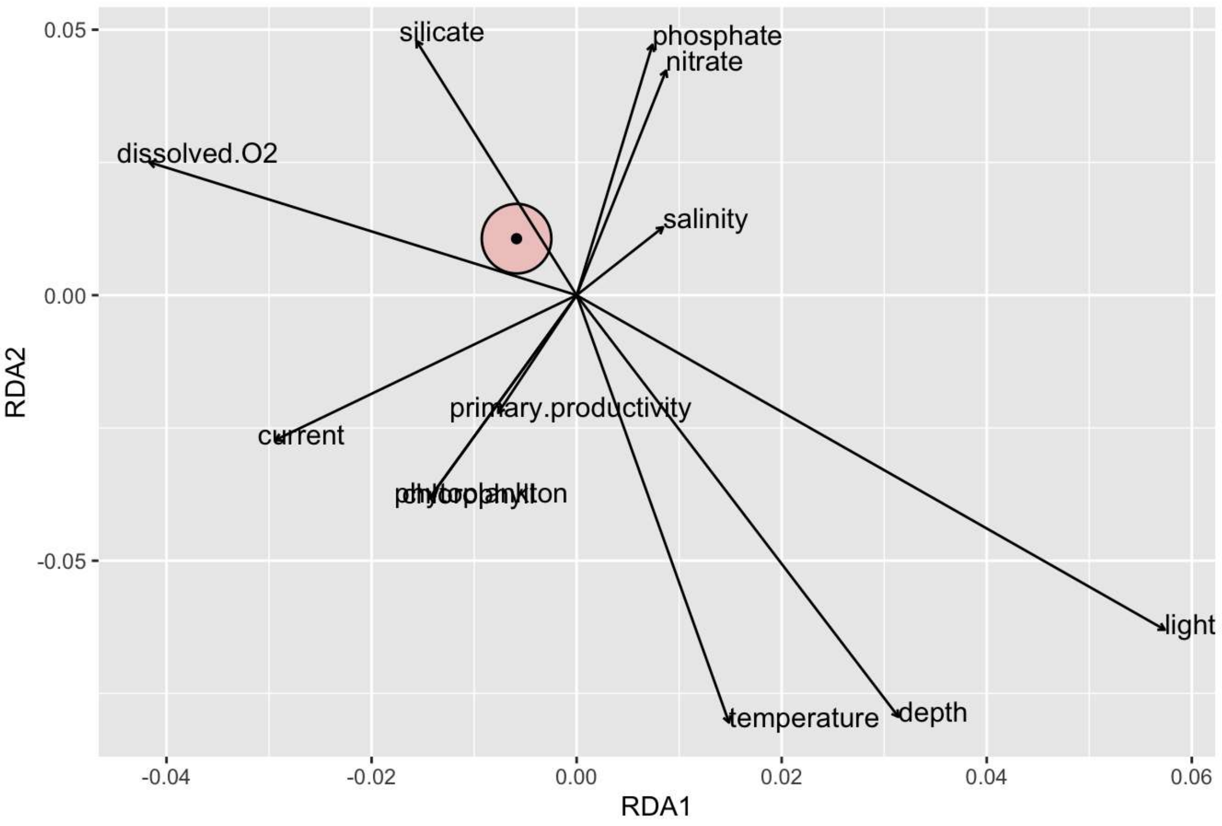
Caudofoveata



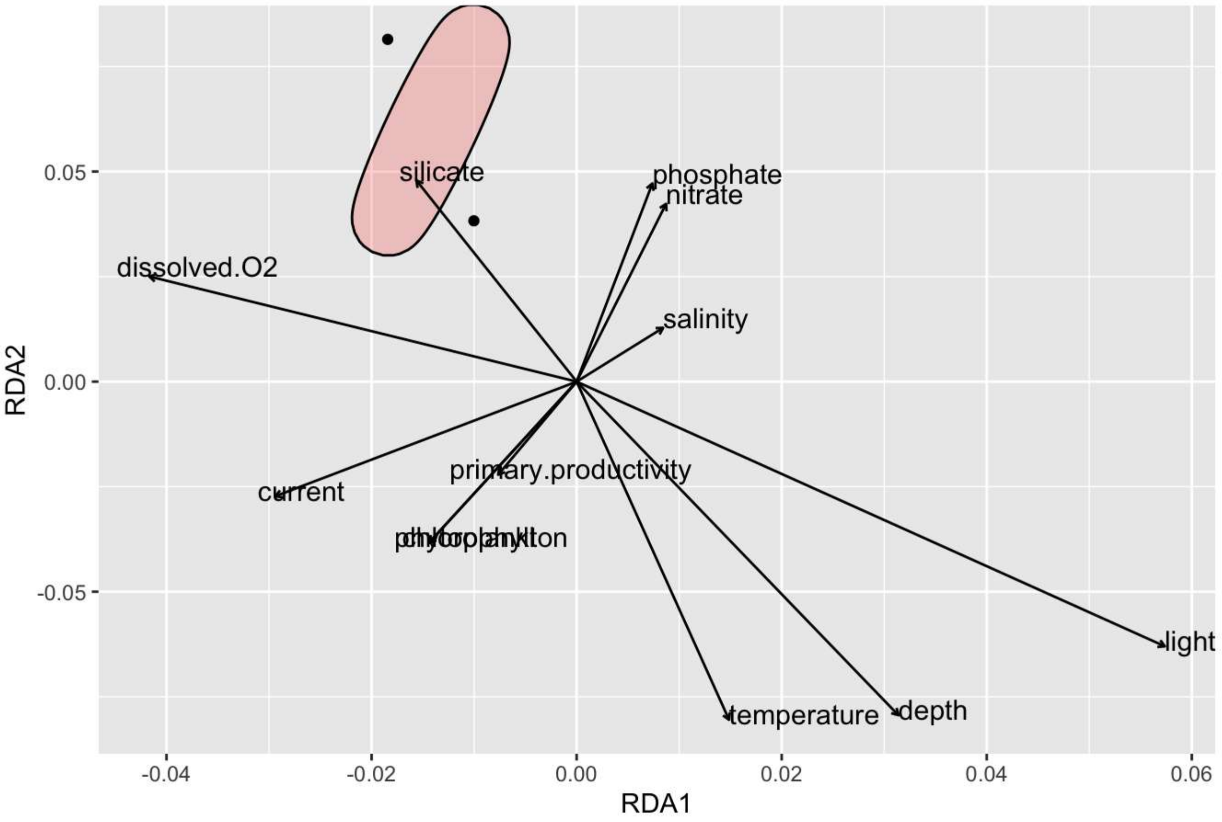
Adenophorea

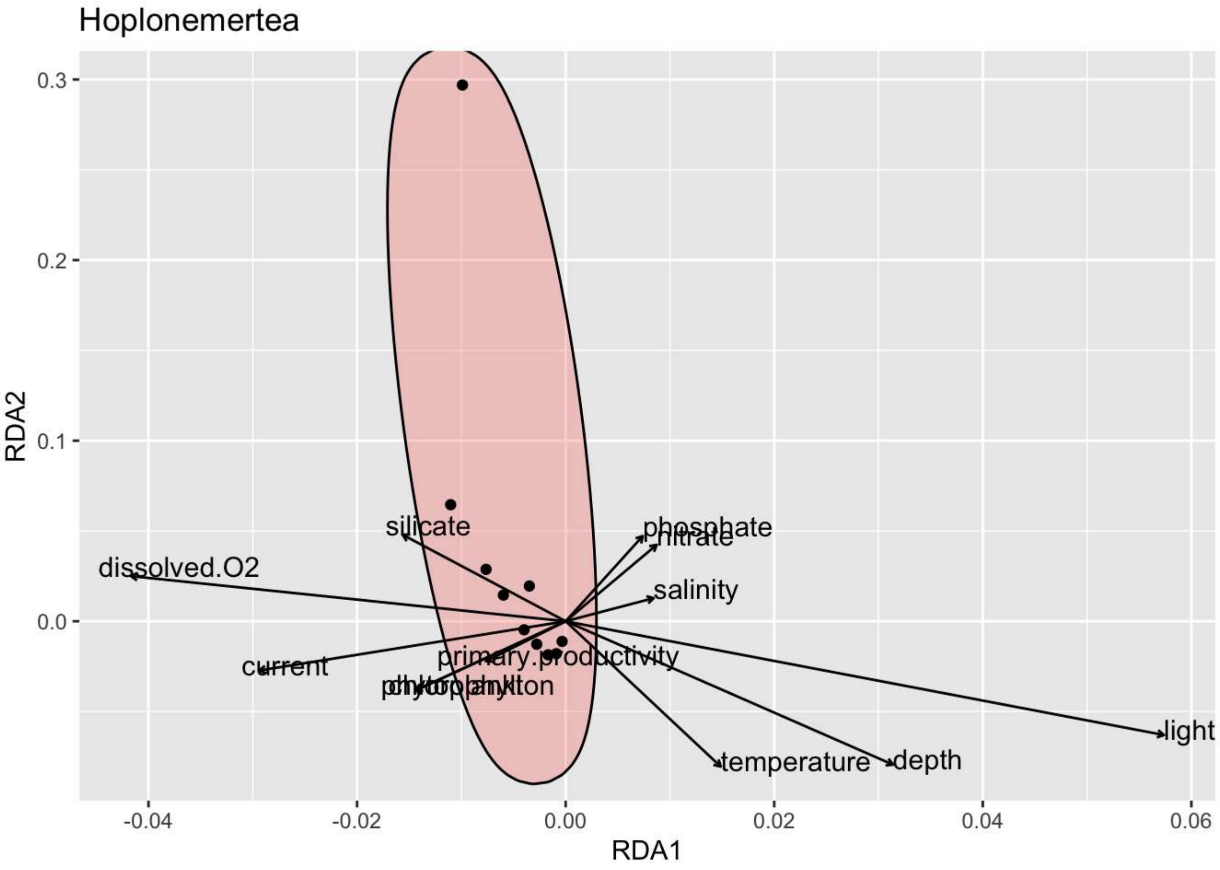


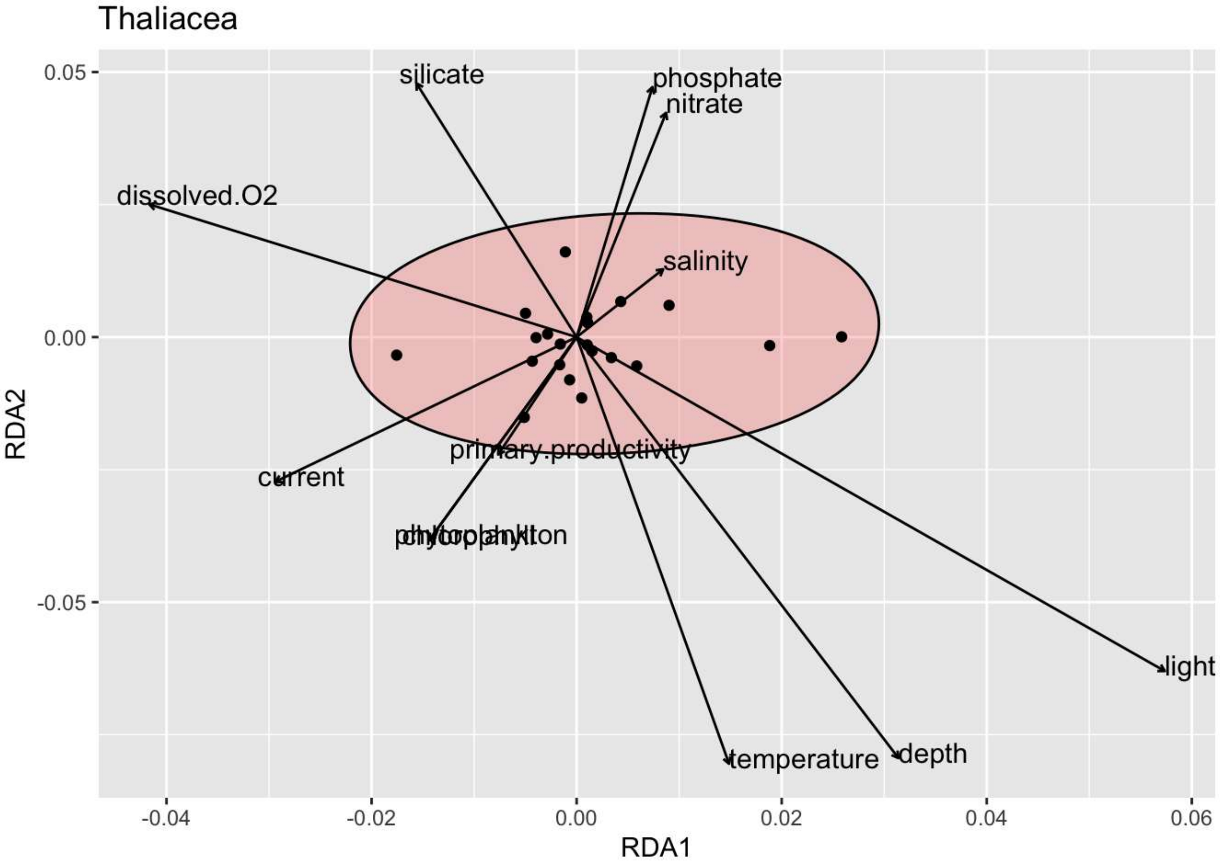
Cyclorhagida

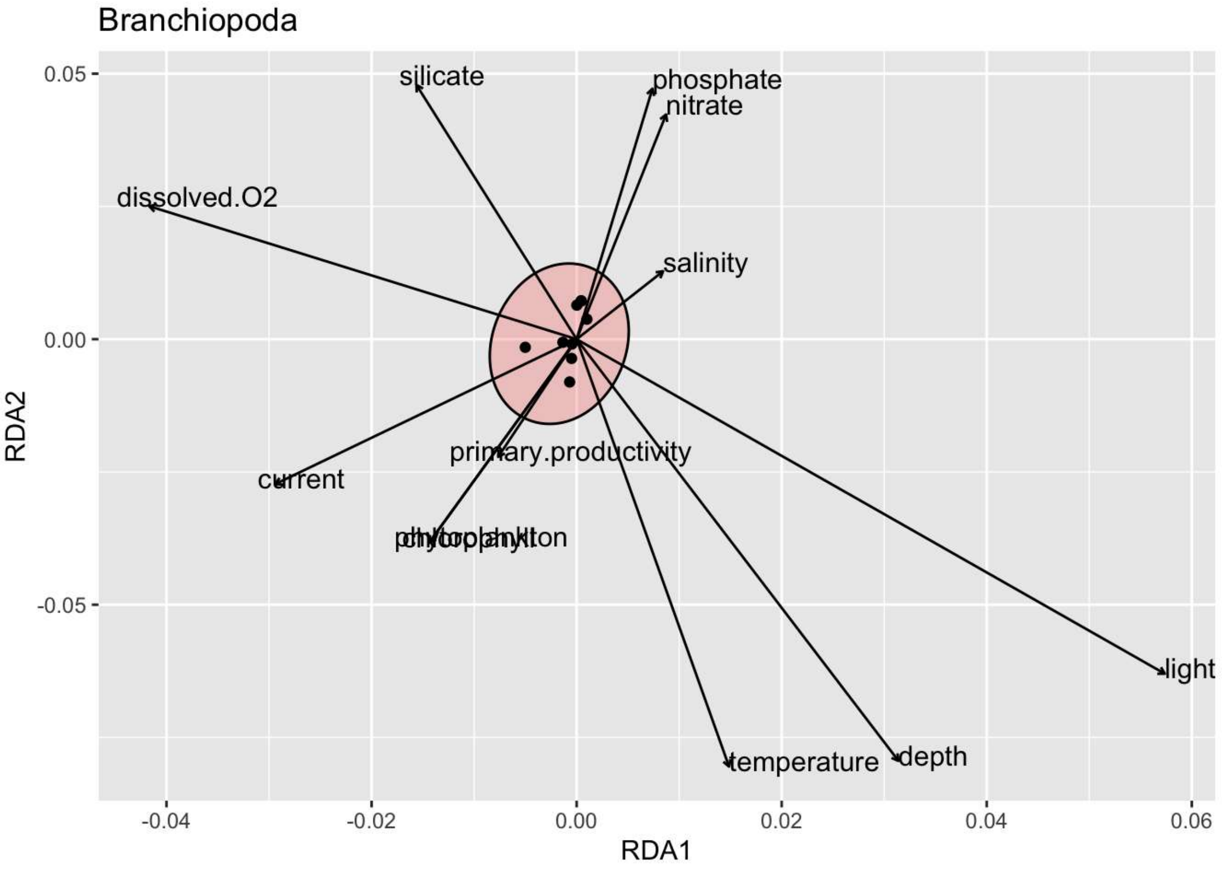


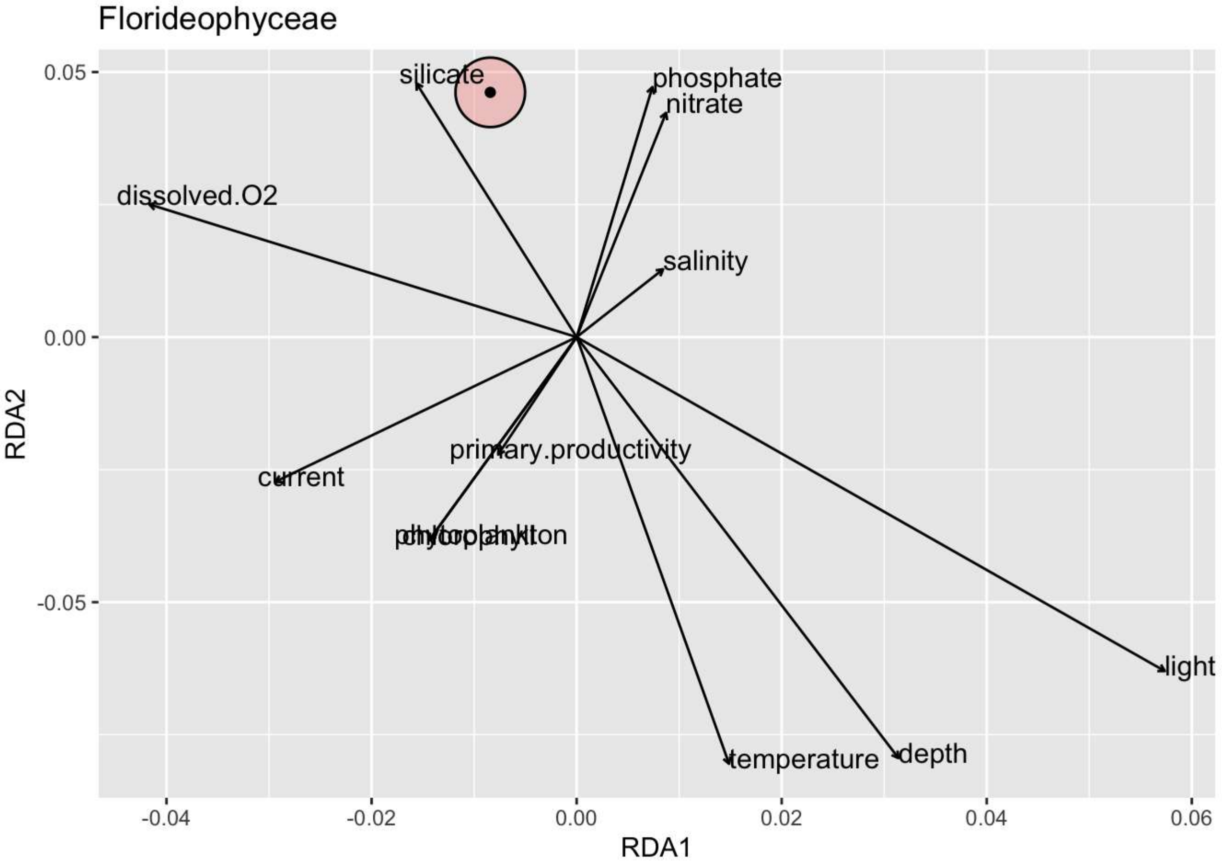
Scyphozoa

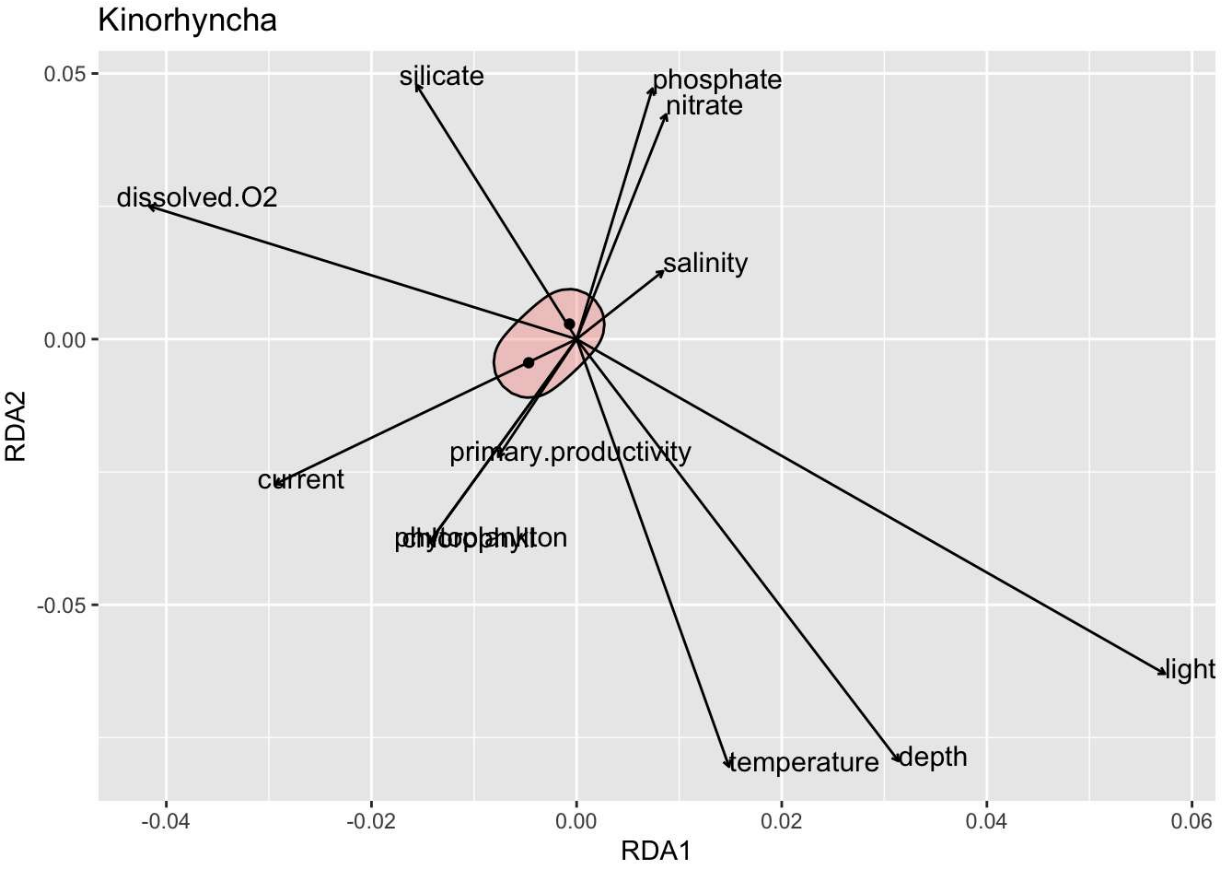


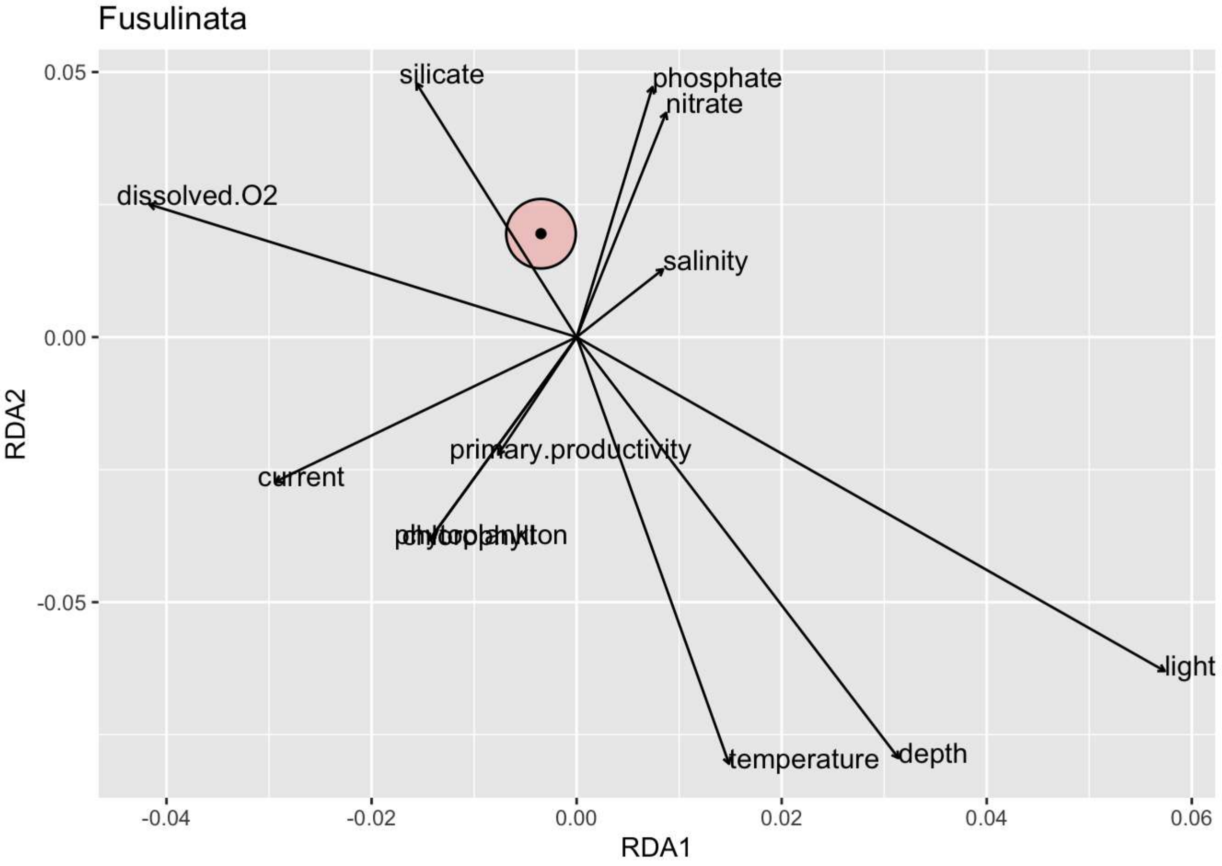

Hoplonemertea
RDA2
RDA1
0.3
0.2
0.1
0.0
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth


Thaliacea
RDA2
RDA1
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth

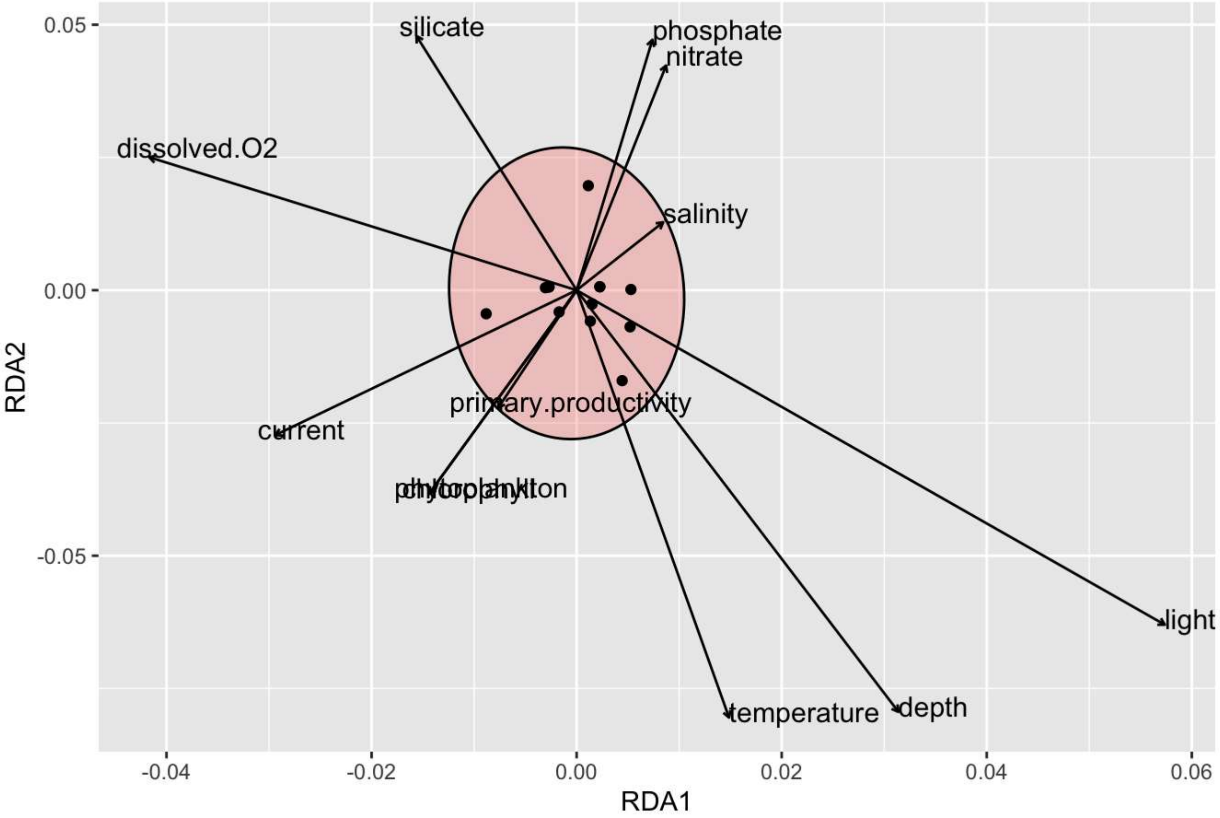

Branchiopoda
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1


Florideophyceae
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
phytoplankton
chlorophyll
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1

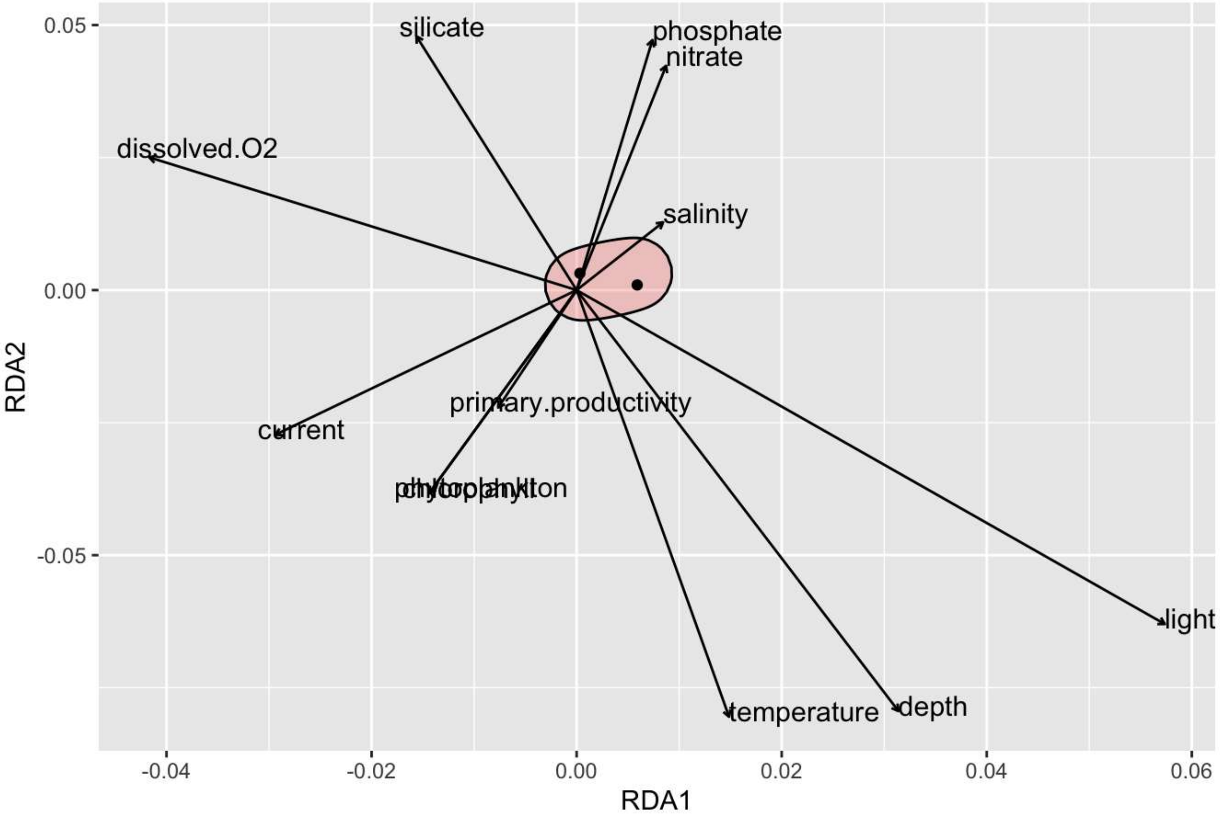

Kinorhyncha
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1

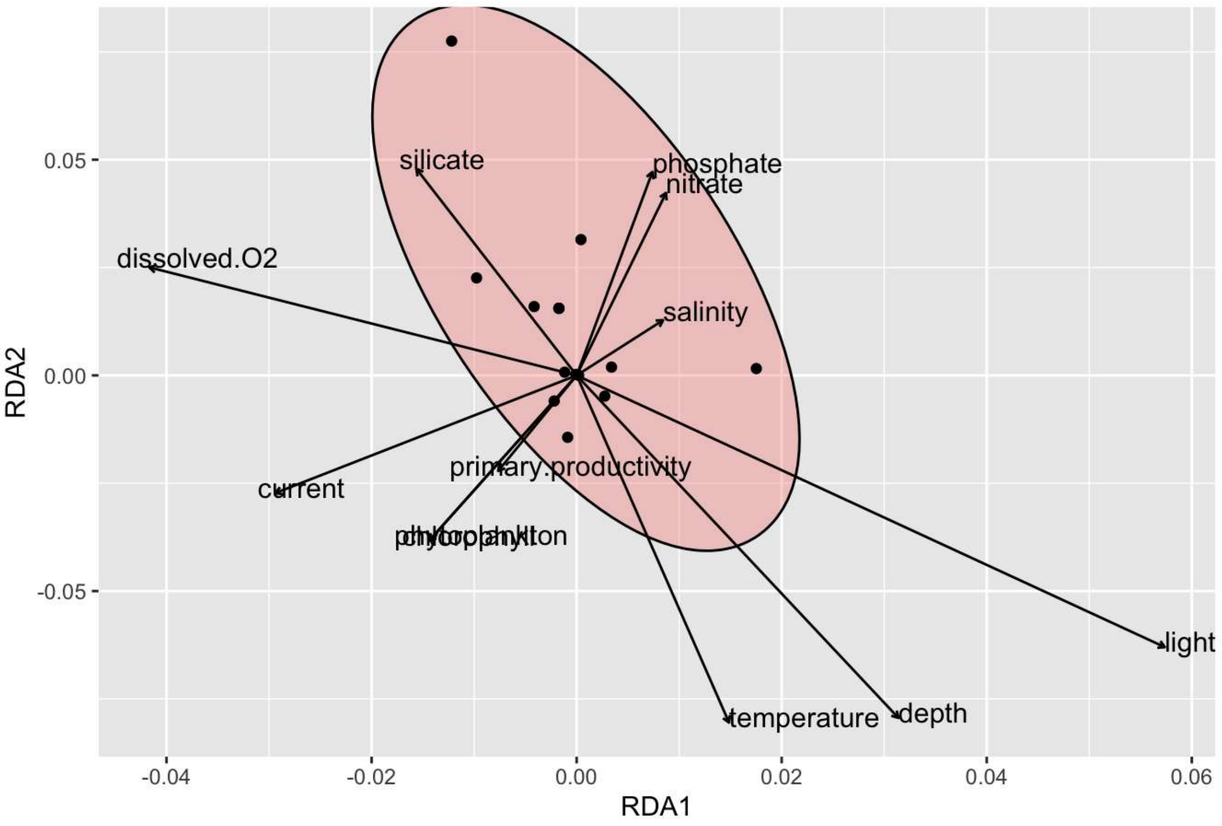

Fusulinata
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1

Myxini

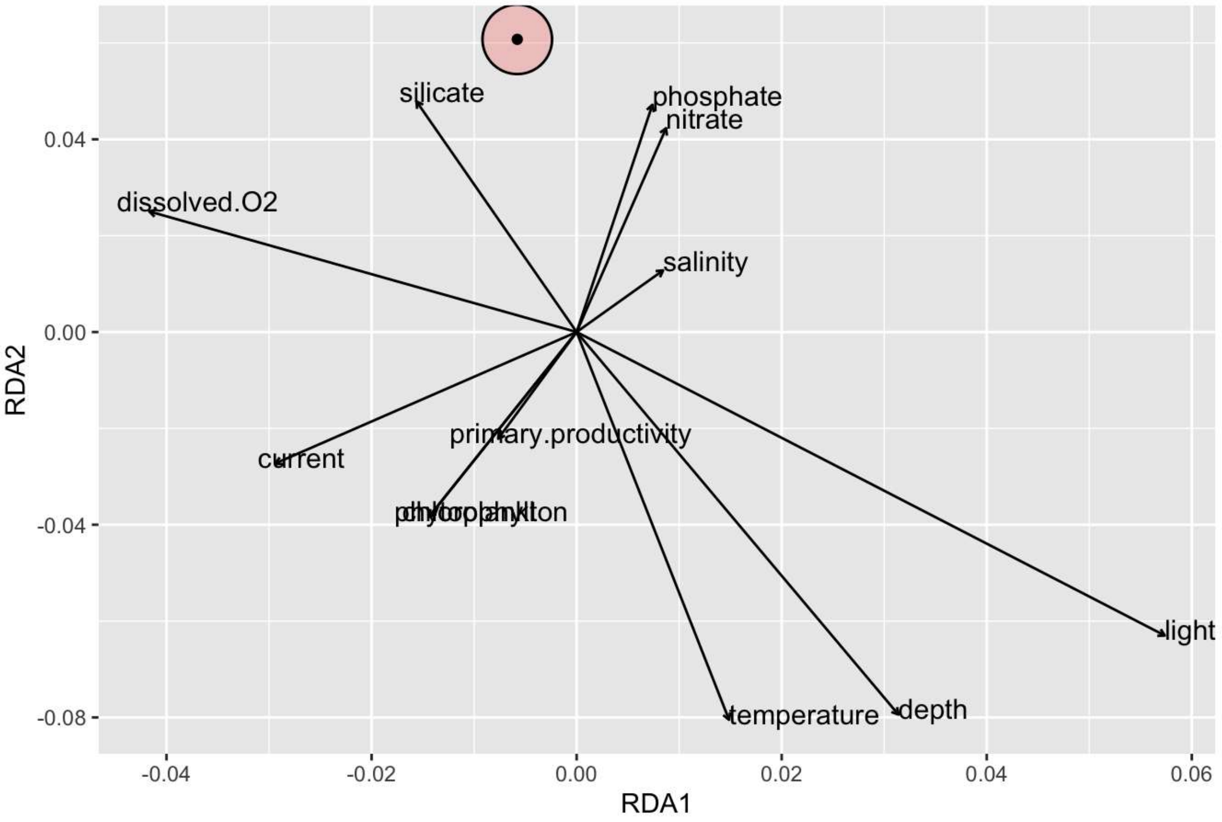


Globothalamea



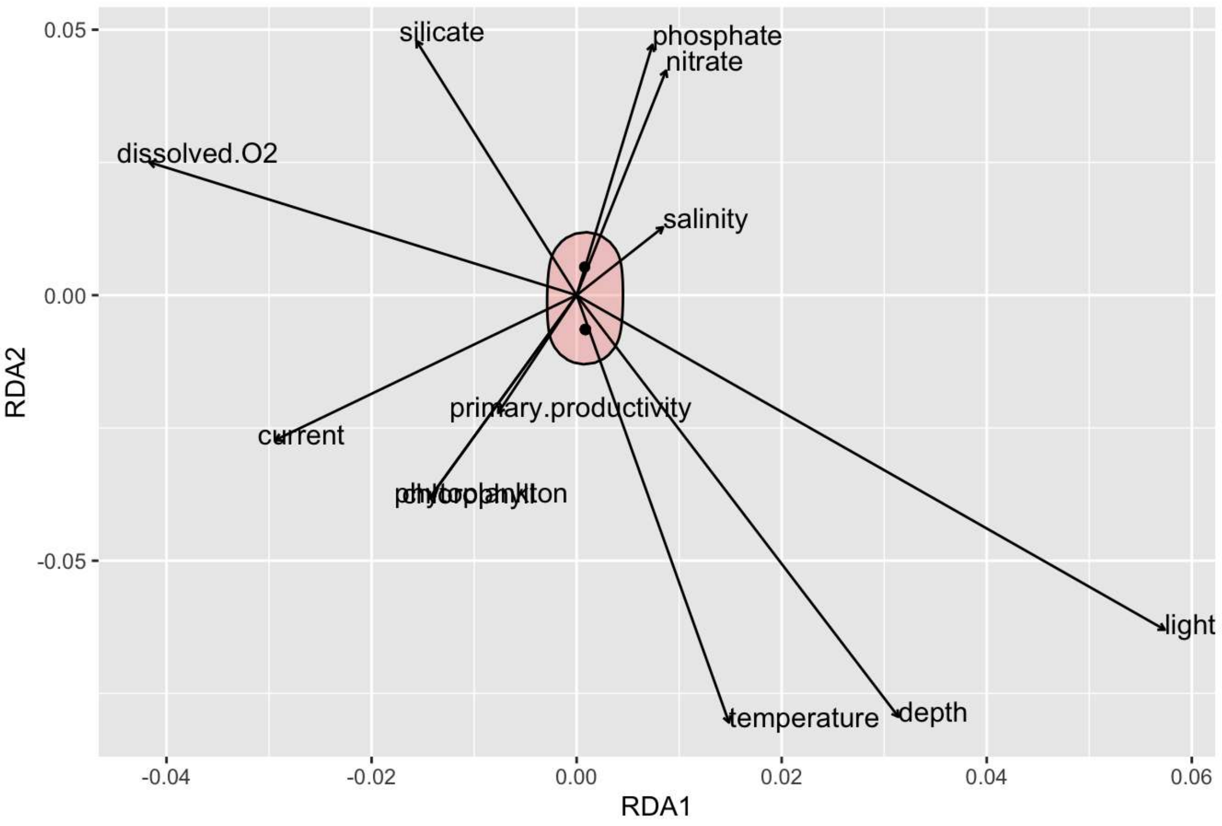


Sipunculidea

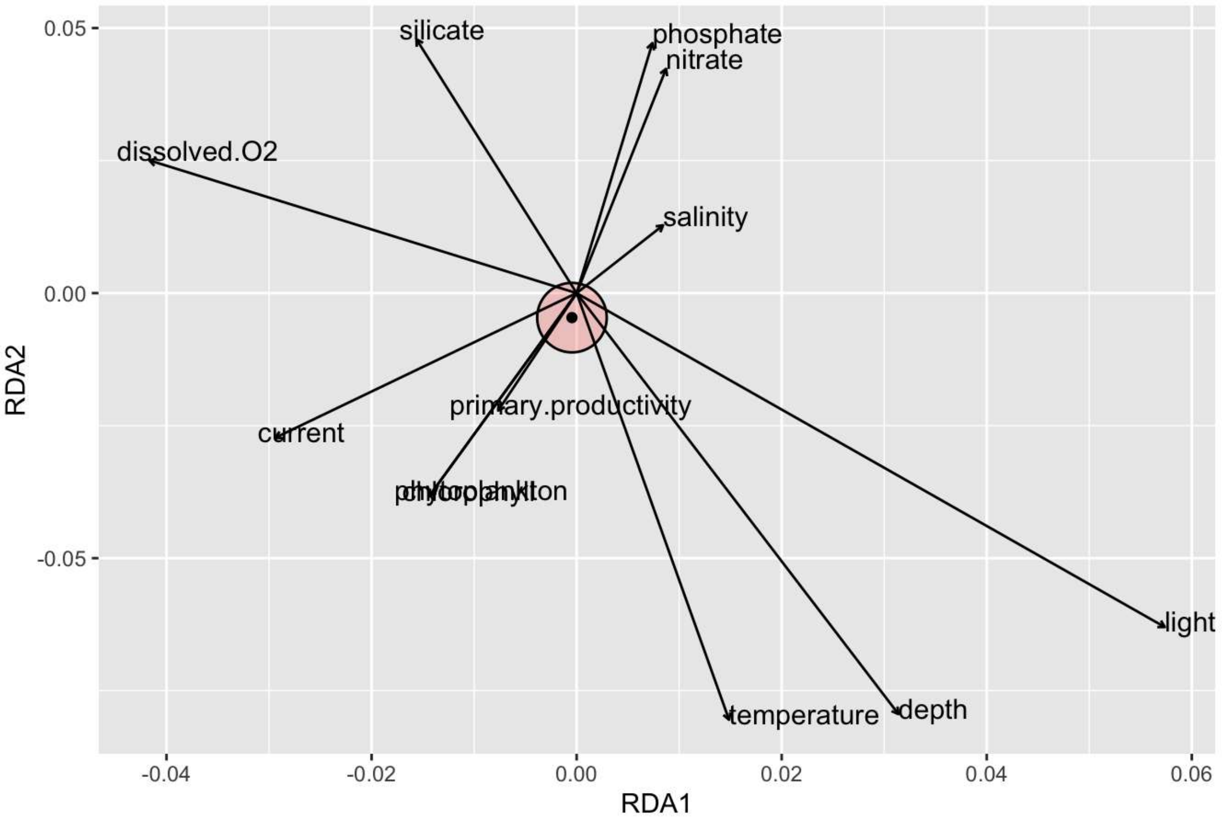


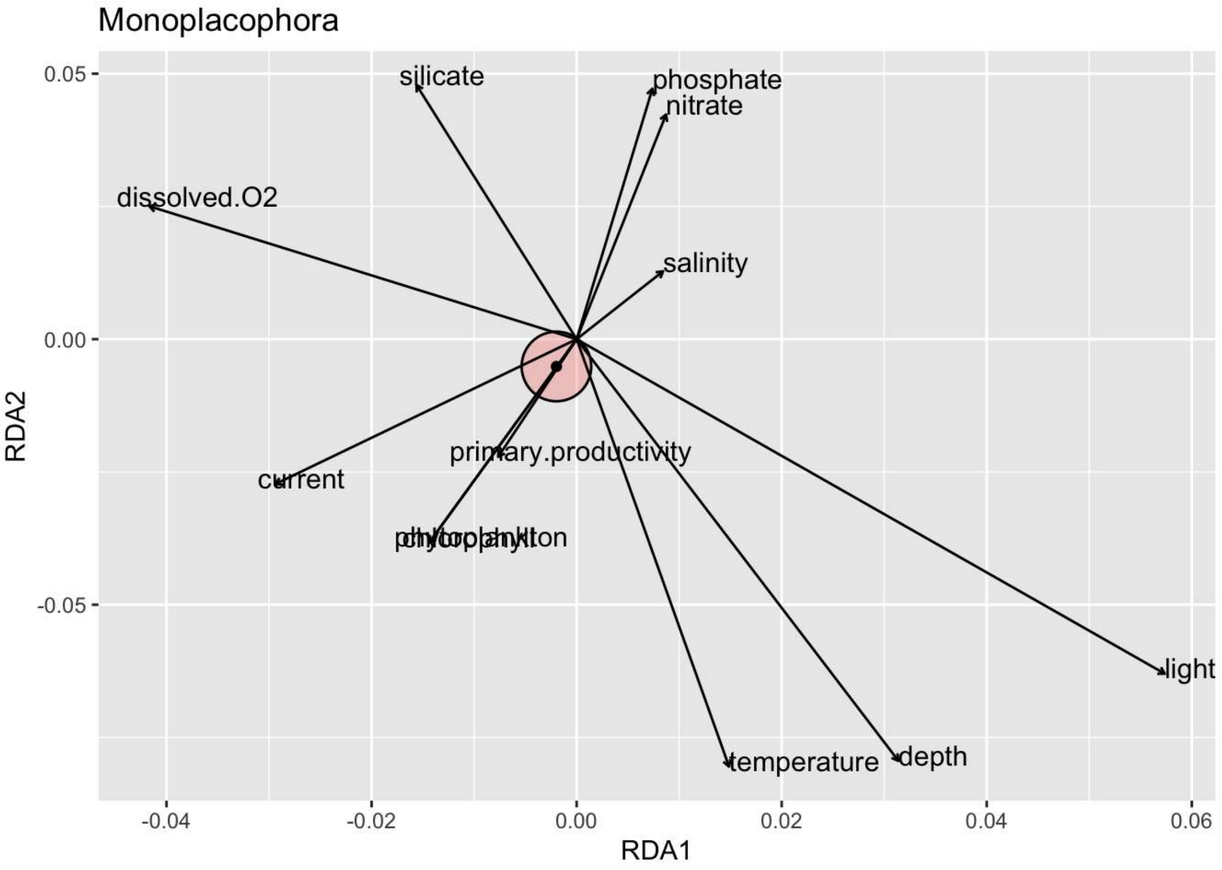
Gromiidea

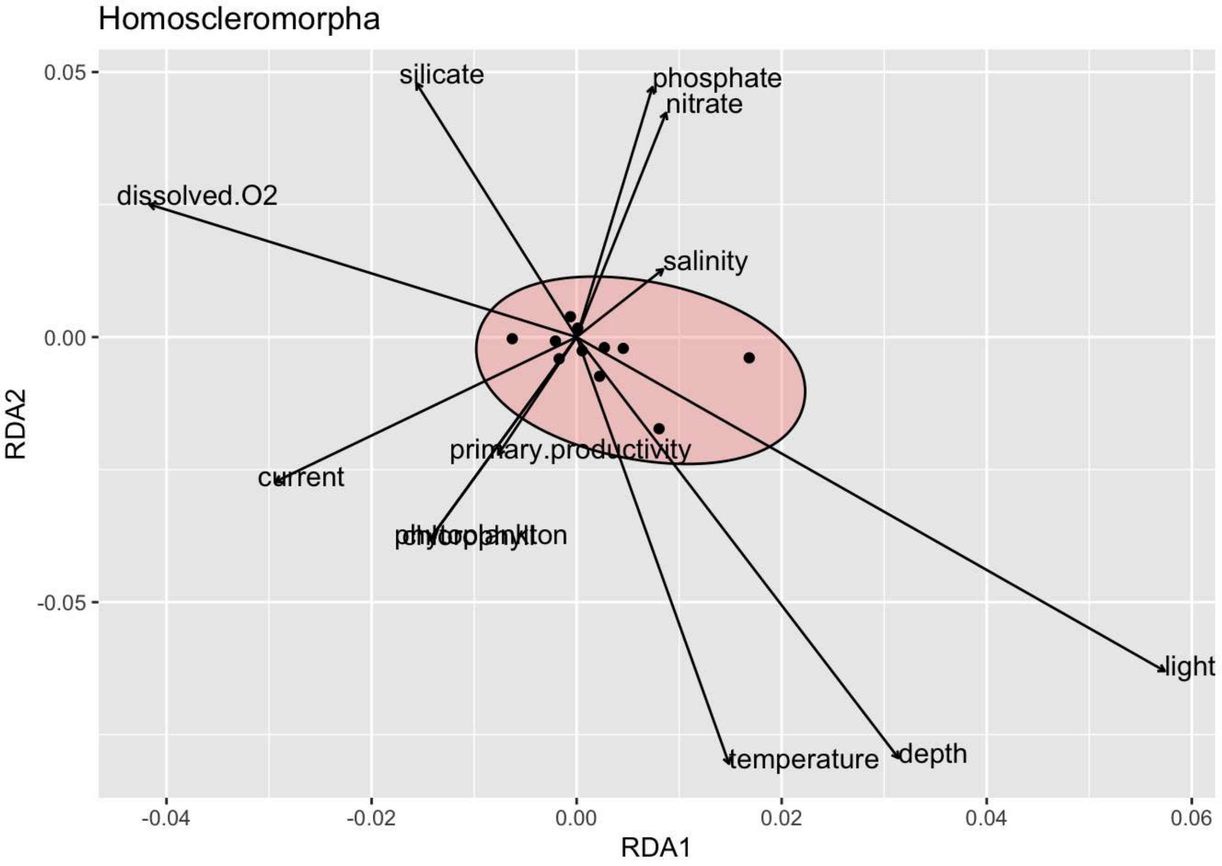
Staurozoa



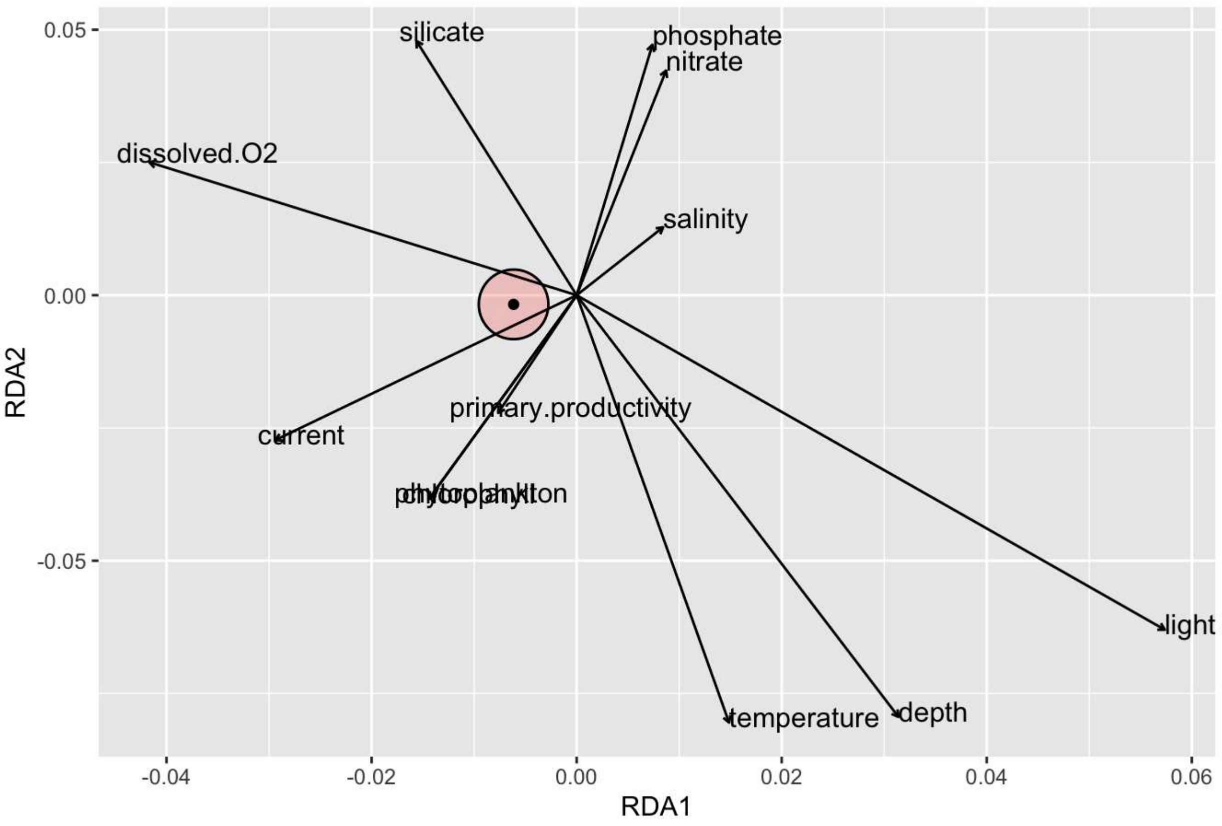
Tentaculata



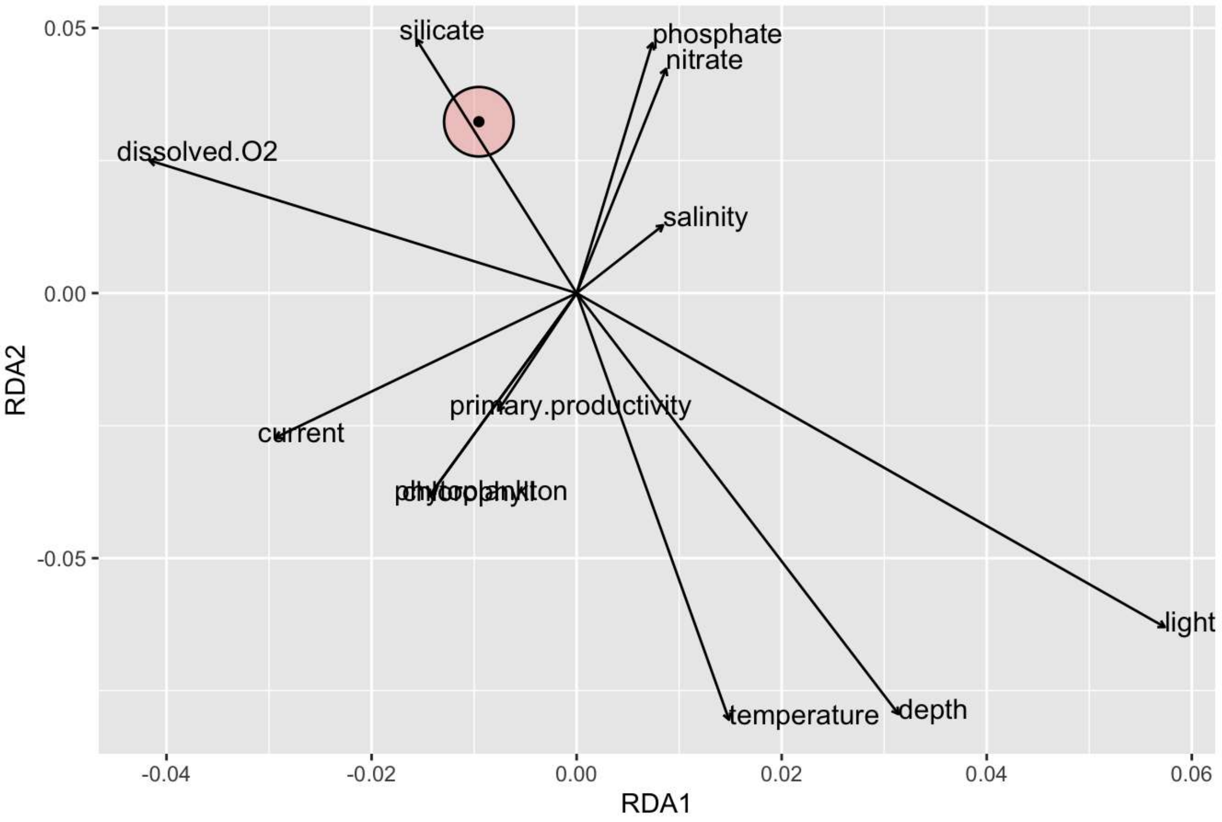

Monoplacophora
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1

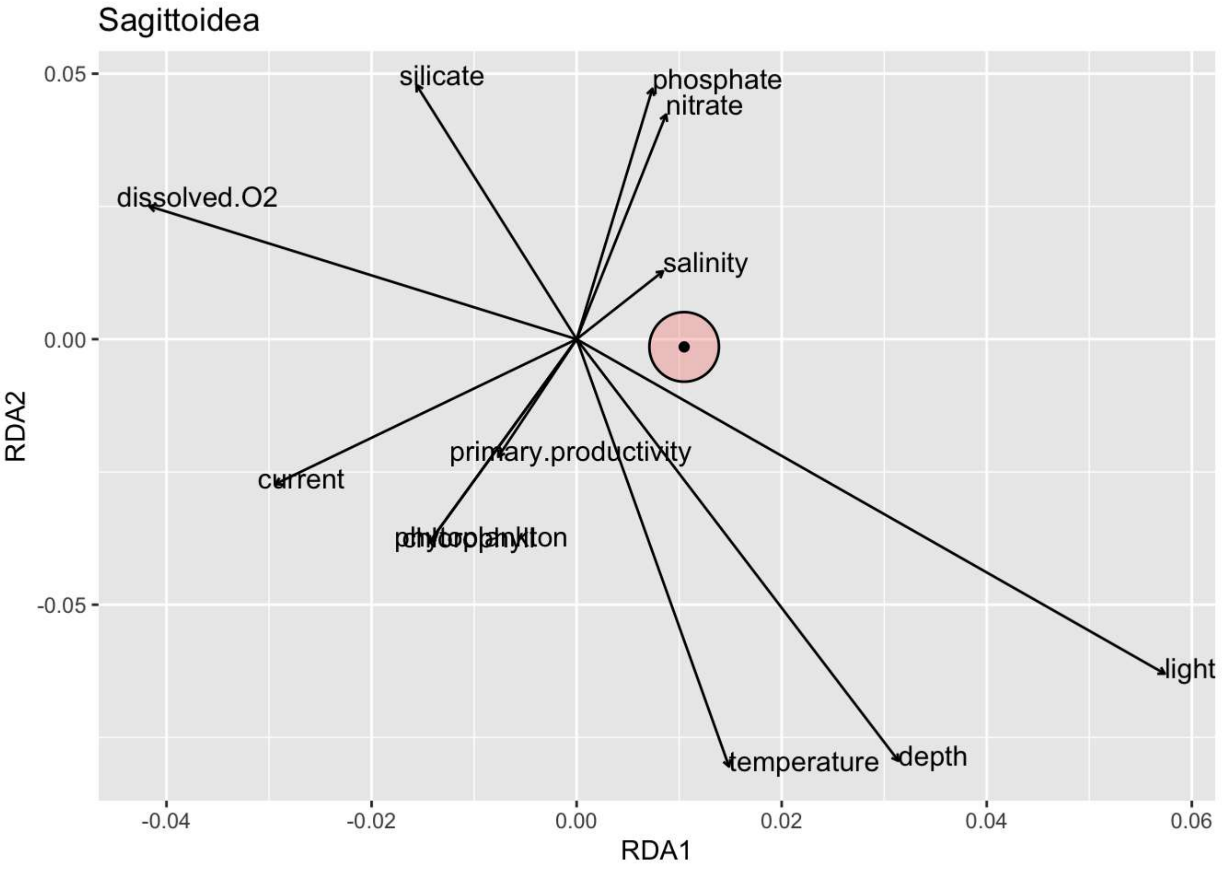

Homoscleromorpha
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
RDA2
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1

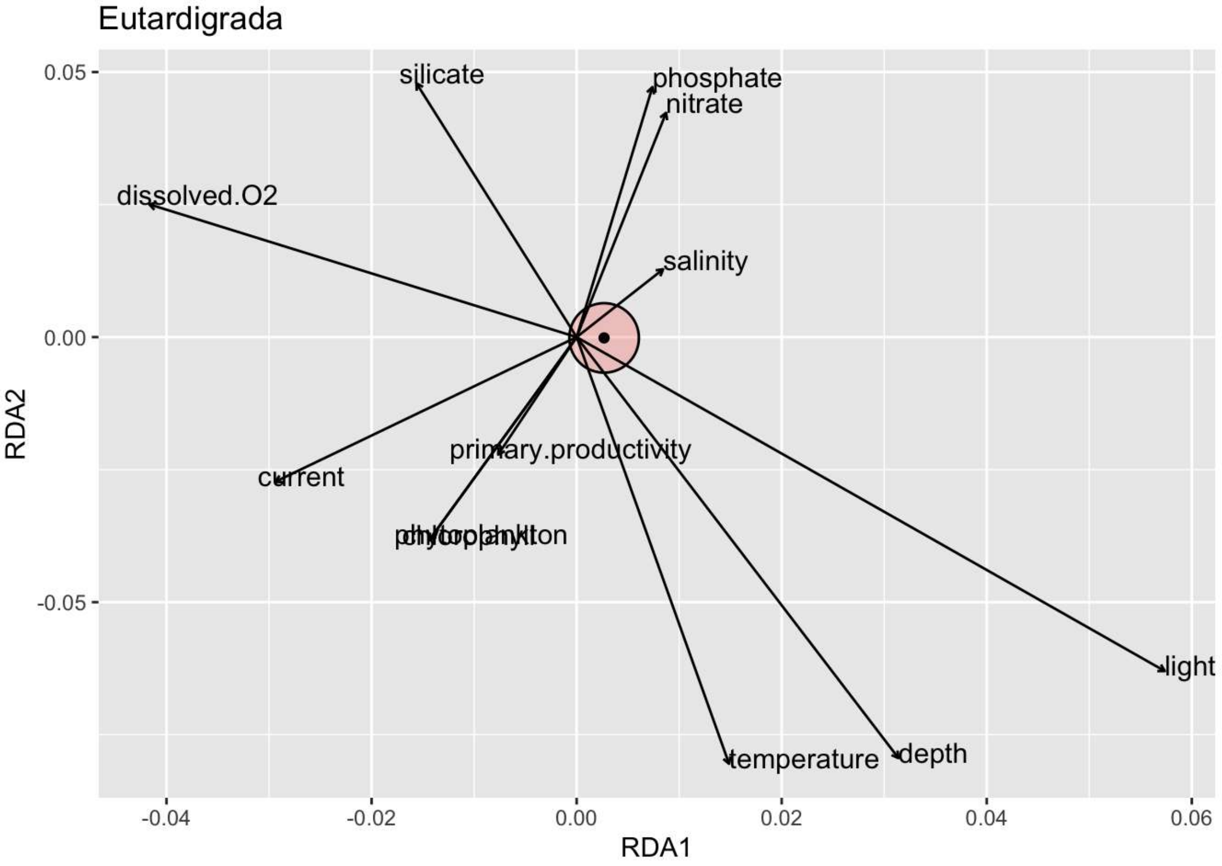
Lingulata

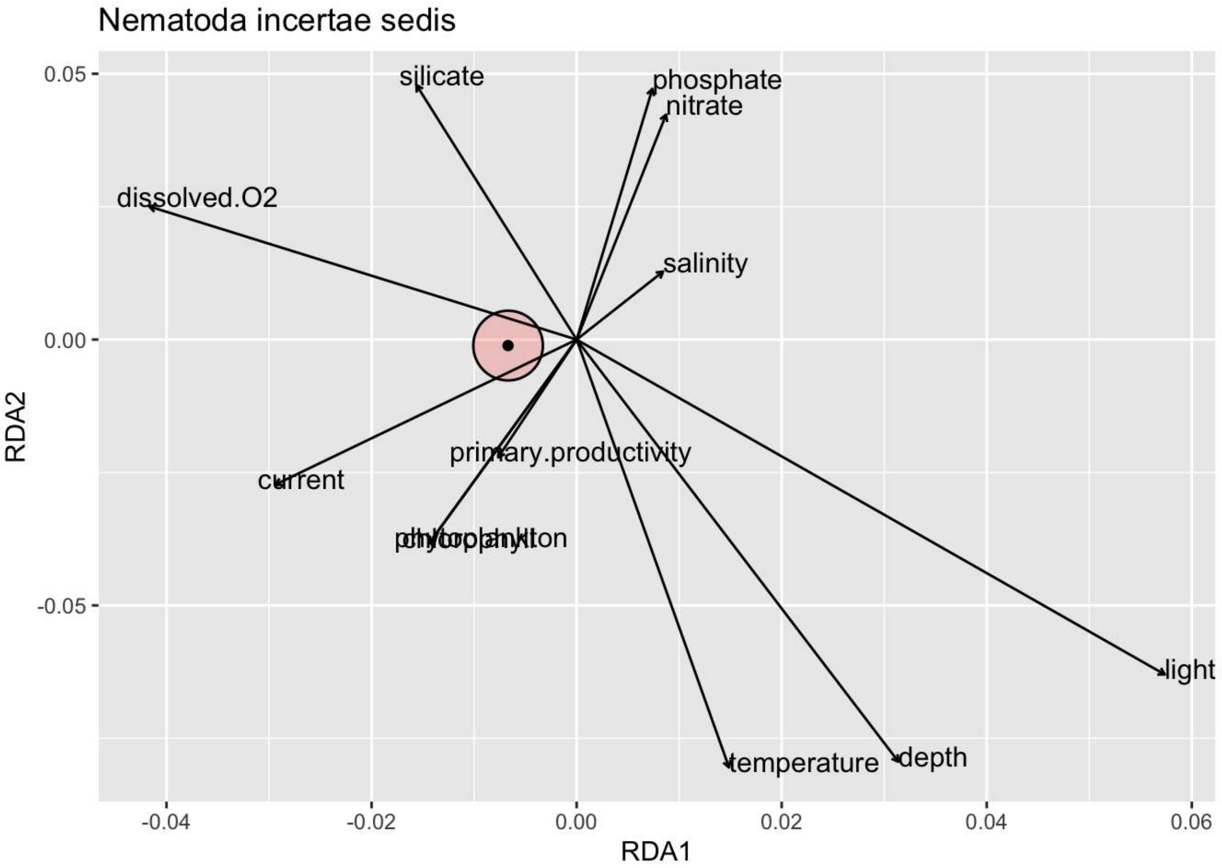


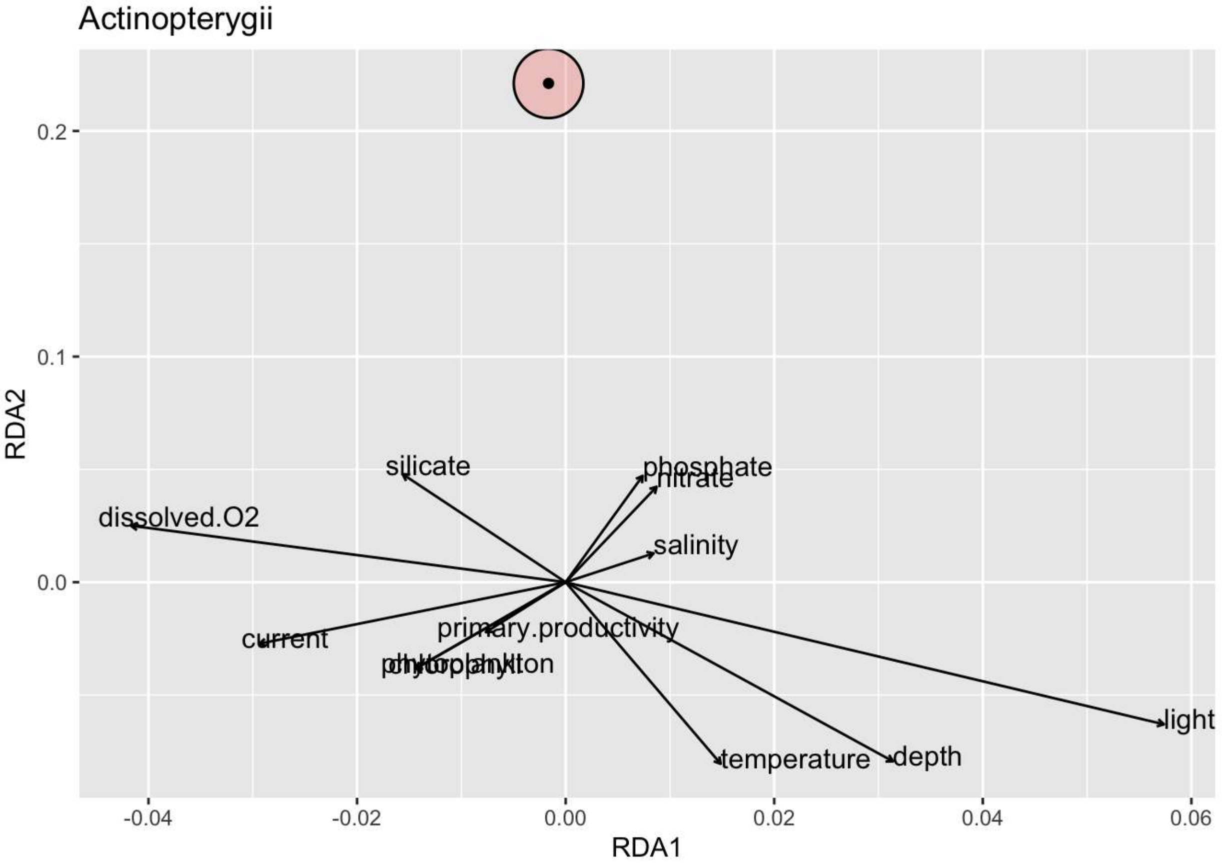
Allomalorhagida




Sagittoidea
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1
RDA2


Eutardigrada
silicate
phosphate
nitrate
dissolved.O2
salinity
primary.productivity
current
chlorophyll
phytoplankton
light
temperature
depth
0.05
0.00
-0.05
-0.04
-0.02
0.00
0.02
0.04
0.06
RDA1
RDA2





ANOVA

Now we’re going to do an ANOVA on the rda object with “by = terms” to measure the importance of each term in the env data frame.

```
deep.aov <- anova(deep.rda, by = "terms")
deep.aov
save(deep.aov, file = "deep.aov.Rda")
```

RDA By Class

```
full.class.df <- read.csv("./occurrence_data_merged.csv")

class.df <- full.class.df %>%
  group_by(class) %>%
  summarise(n.species = n_distinct(scientificName))

class.df <- class.df %>%
  arrange(desc(n.species)) %>%
  filter(class != "NA") %>%
  filter(class != "")

kable(class.df)
```

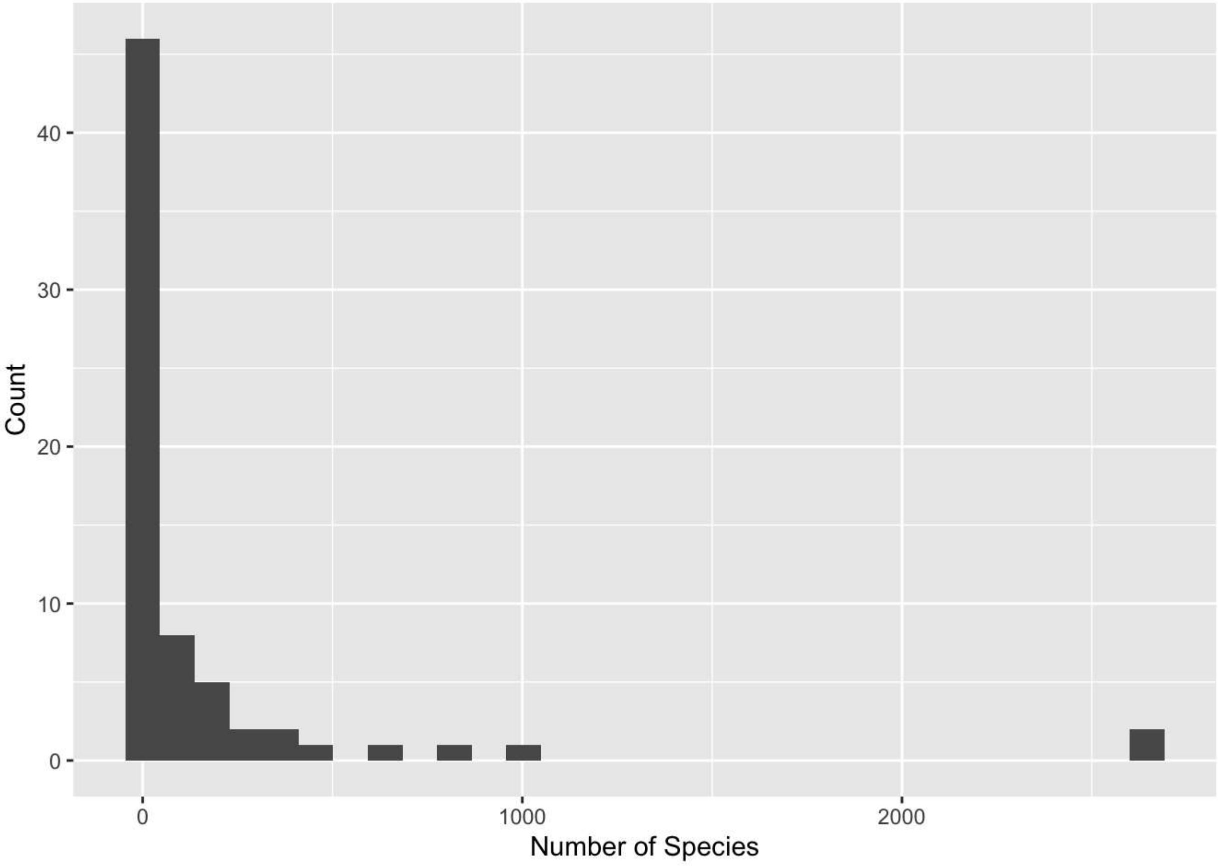
class	n.species
Malacostraca	2647
Gastropoda	2614
Anthozoa	1001
Polychaeta	809
Bivalvia	638
Ophiuroidea	448
Asteroidea	392
Hydrozoa	392
Demospongiae	295
Echinoidea	268
Holothuroidea	220
Crinoidea	213
Ascidiacea	203
Hexanauplia	188
Pycnogonida	156
Gymnolaemata	129
Ostracoda	116
Hexactinellida	80
Cephalopoda	66
Scaphopoda	64

class	n.species
Rhabditophora	56
Chromadorea	54
Clitellata	50
Polyplacophora	42
Monothalamea	33
Calcarea	25
Sipunculidea	23
Thaliacea	23
Heterotardigrada	22
Appendicularia	21
Enoplea	21
Globothalamea	21
Maxillopoda	20
Myxini	14
Solenogastres	14
Bacillariophyceae	12
Enopla	11
Homoscleromorpha	11
Hoplonemertea	11
Stenolaemata	11
Tubothalamea	11
Anopla	9
Branchiopoda	9
Enteropneusta	7
Nodosariata	7
Arachnida	6
Palaeonemertea	6
Phascolosomatidea	6
Pilidiophora	6
Staurozoa	5
Caudofoveata	4
Adenophorea	3

class	n.species
Globothalamea	2
Kinorhyncha	2
Merostomata	2
Scyphozoa	2
Actinopterygii	1
Allomalorhagida	1
Cyclorhagida	1
Eutardigrada	1
Florideophyceae	1
Fusulinata	1
Gromiidea	1
Lingulata	1
Monoplacophora	1
Nematoda incertae sedis	1
Sagittoidea	1
Tentaculata	1
Turbellaria	1

```
qplot(class.df$n.species, xlab = "Number of Species", ylab = "Count")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

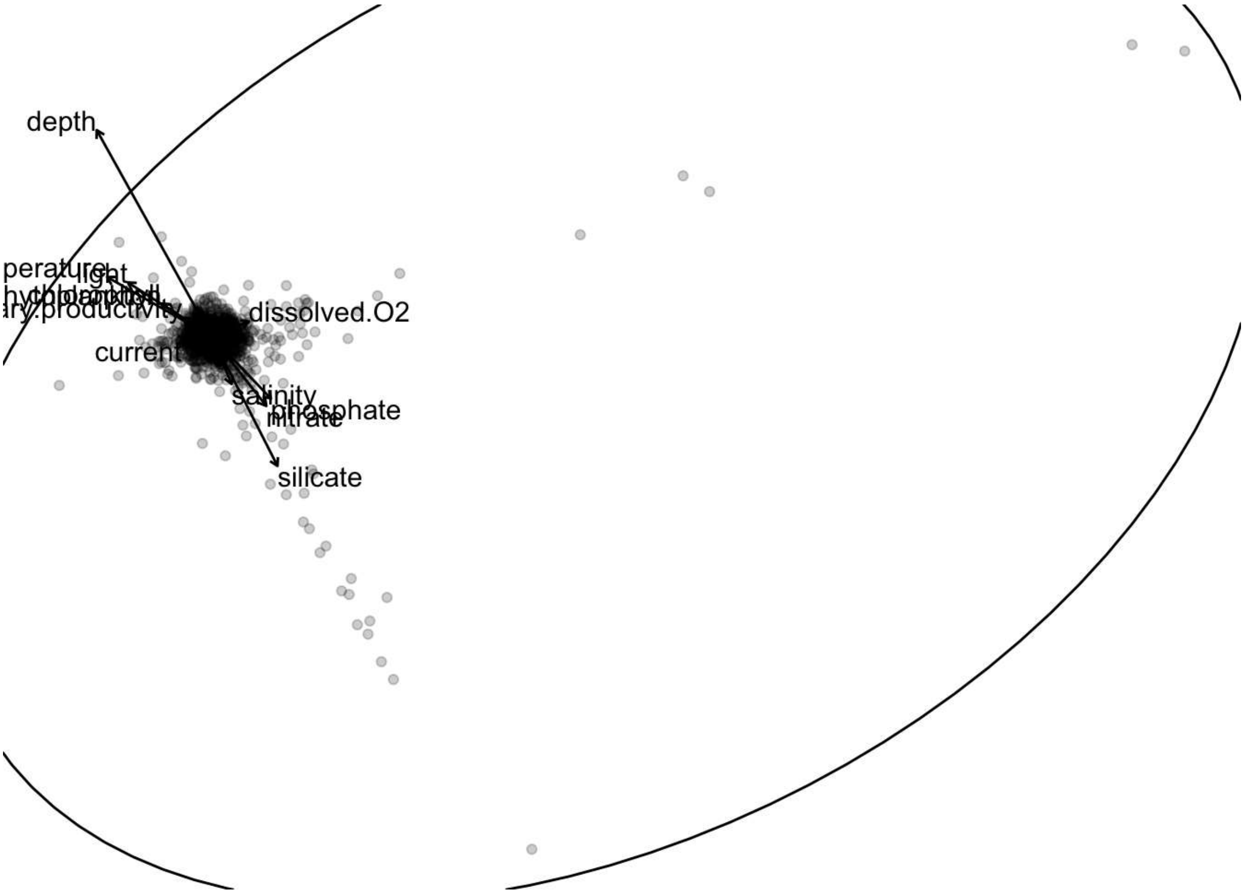


Plots of individual class RDAs

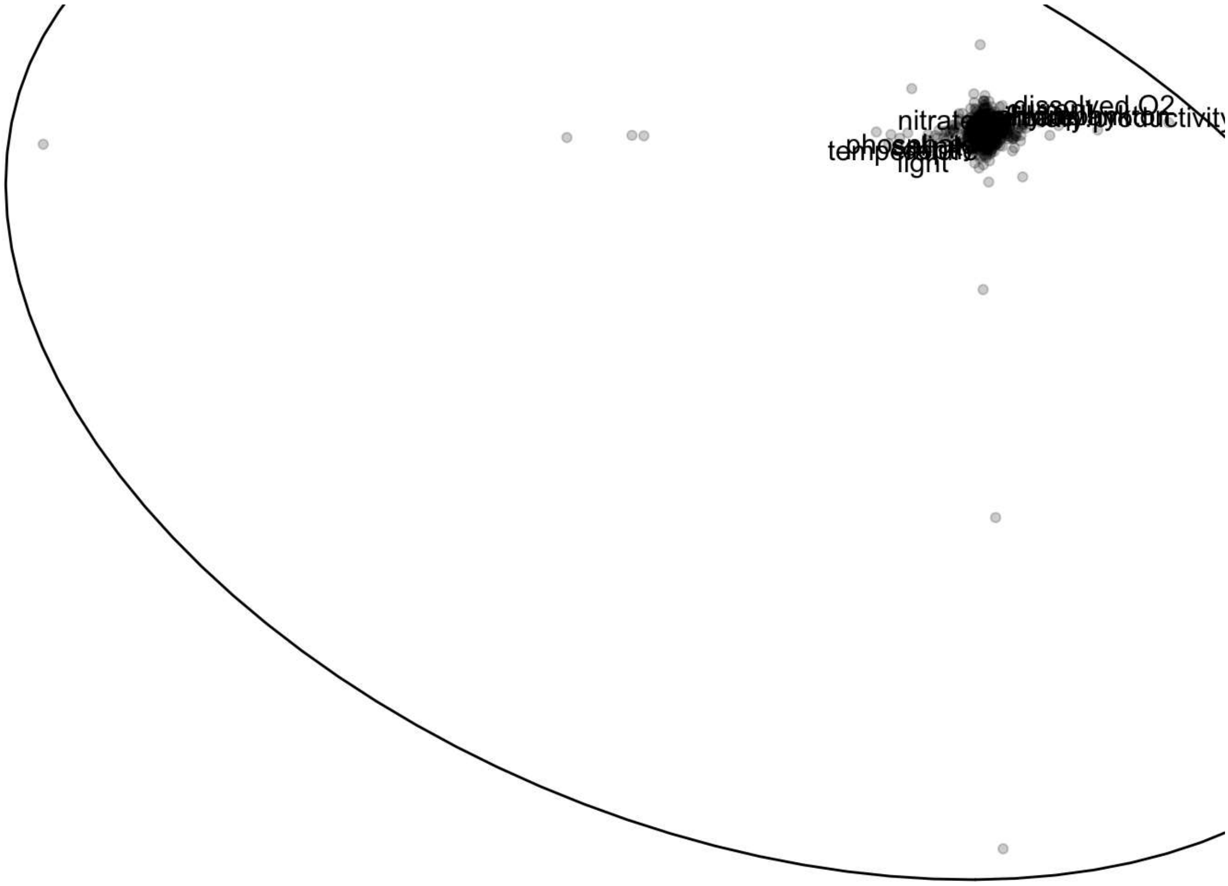
```
min.species <- 10

rda.and.anova <- function(this.species.df, this.class){

  rdafile <- paste0(this.class, ".rda.Rda")
  summaryfile <- paste0(this.class, ".summary.Rda")
  aovfile <- paste0(this.class, ".aov.Rda")

  if(file.exists(rdafile)){
    load(rdafile)
    load(summaryfile)
    load(aovfile)
  } else {
    this.rda <- rda(this.species.df ~ . + deep.pcnm$vectors, data = env.df, na.acti
on = "na.exclude", scale = TRUE)
    this.summary <- summary(this.rda)
    this.anova <- anova(this.rda, by = "terms")
  }

  full.var.explained <- this.summary$constr.chi/this.summary$tot.chi
  print(paste("Proportion of variance explained: ", full.var.explained))

  print(this.anova)
  plot.df <- fortify(this.rda)

  p <- ggplot(plot.df, aes(RDA1, RDA2)) +
    geom_mark_ellipse(show.legend = FALSE) +
    geom_point(alpha = 0.2) + theme_void()

  plot.env.df <- as.data.frame(this.summary$biplot)[1:12,]

  p <- p + geom_segment(data = plot.env.df,
                        aes(x=0, xend=RDA1 * 50, y=0, yend=RDA2 * 50),
                        color="black", arrow=arrow(length=unit(0.01,"npc"))) +
    geom_text(data = plot.env.df,
              aes(x=RDA1 * 50,y=RDA2 * 50,label=rownames(plot.env.df),
                  hjust=0.5*(1-sign(RDA1)),vjust=0.5*(1-sign(RDA2))),
              color="black", size=4)

  print(p)

  save(this.rda, file = rdafile)
  save(this.summary, file = summaryfile)
  save(this.anova, file = aovfile)

}

for(i in 1:nrow(class.df)){
  this.class <- as.character(class.df[i,1])

  species.list <- full.class.df %>%
    filter(class == this.class) %>%
    distinct(scientificName)

  species.list$scientificName <- gsub(" ", ".", species.list$scientificName)

  this.species.df <- species.df[,colnames(species.df) %in% species.list$scientificN
```

```
ame]

  if(class.df[i,2] >= min.species){
    cat(paste("Doing RDA for", this.class, "...\n"))
    try(rda.and.anova(this.species.df, this.class))

    cat("\n\n\n")
  }
}
```

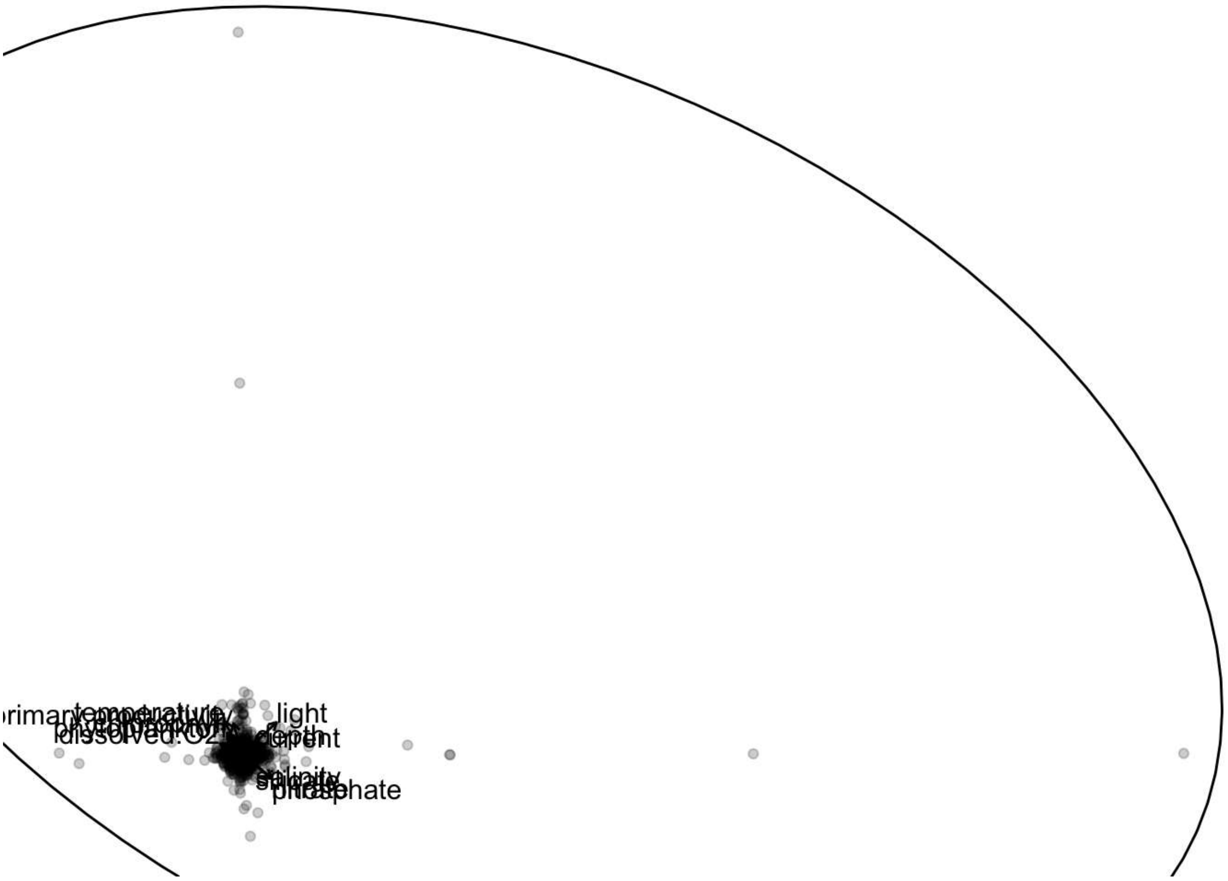
```
## Doing RDA for Malacostraca ...
## [1] "Proportion of variance explained:  0.451510111415947"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1     2.52 2.6415  0.001 ***
## chlorophyll             1     0.68 0.7185  0.928
## current                 1     1.18 1.2436  0.079 .
## dissolved.O2            1     0.87 0.9151  0.787
## light                   1     1.03 1.0851  0.066 .
## nitrate                 1     0.93 0.9717  0.506
## phosphate               1     0.89 0.9292  0.392
## phytoplankton           1     0.70 0.7344  0.974
## primary.productivity    1     0.64 0.6684  0.915
## salinity                1     0.53 0.5522  0.889
## silicate                1     1.15 1.2111  0.014 *
## temperature             1     0.70 0.7309  0.999
## deep.pcnm$vectors    1204  1108.83 0.9667  0.957
## Residual             1429  1361.35
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



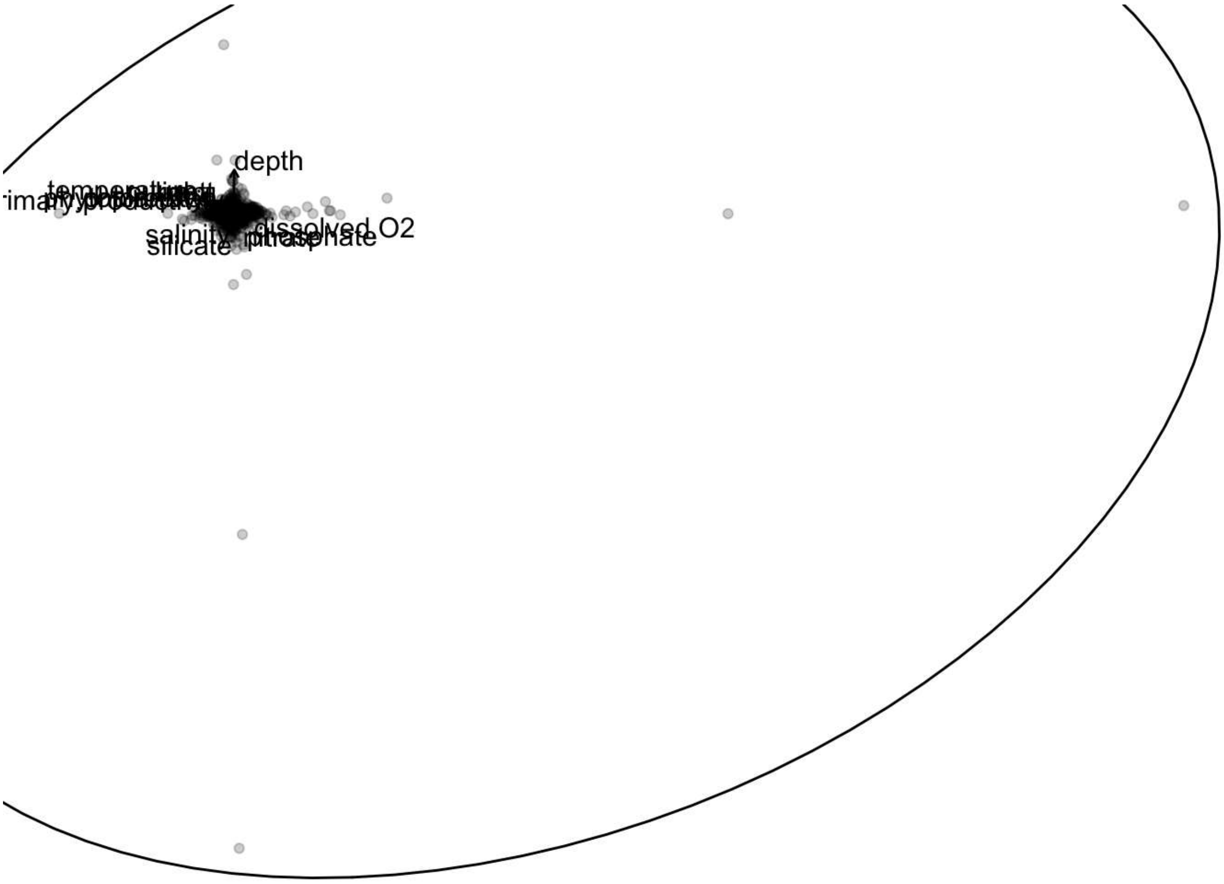
```
##
##
##
## Doing RDA for Gastropoda ...
## [1] "Proportion of variance explained:  0.404776269218991"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1     0.76 0.7361  0.790
## chlorophyll             1     0.45 0.4398  1.000
## current                 1     0.80 0.7717  0.686
## dissolved.O2            1     0.70 0.6820  0.969
## light                   1     1.45 1.4094  0.002 **
## nitrate                 1     0.66 0.6371  0.989
## phosphate               1     0.70 0.6787  0.601
## phytoplankton           1     0.43 0.4210  1.000
## primary.productivity    1     0.37 0.3578  0.998
## salinity                1     0.34 0.3292  0.984
## silicate                1     0.85 0.8227  0.827
## temperature             1     0.62 0.6006  0.989
## deep.pcnm$vectors    1204   994.09 0.8006  1.000
## Residual             1429  1473.77
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



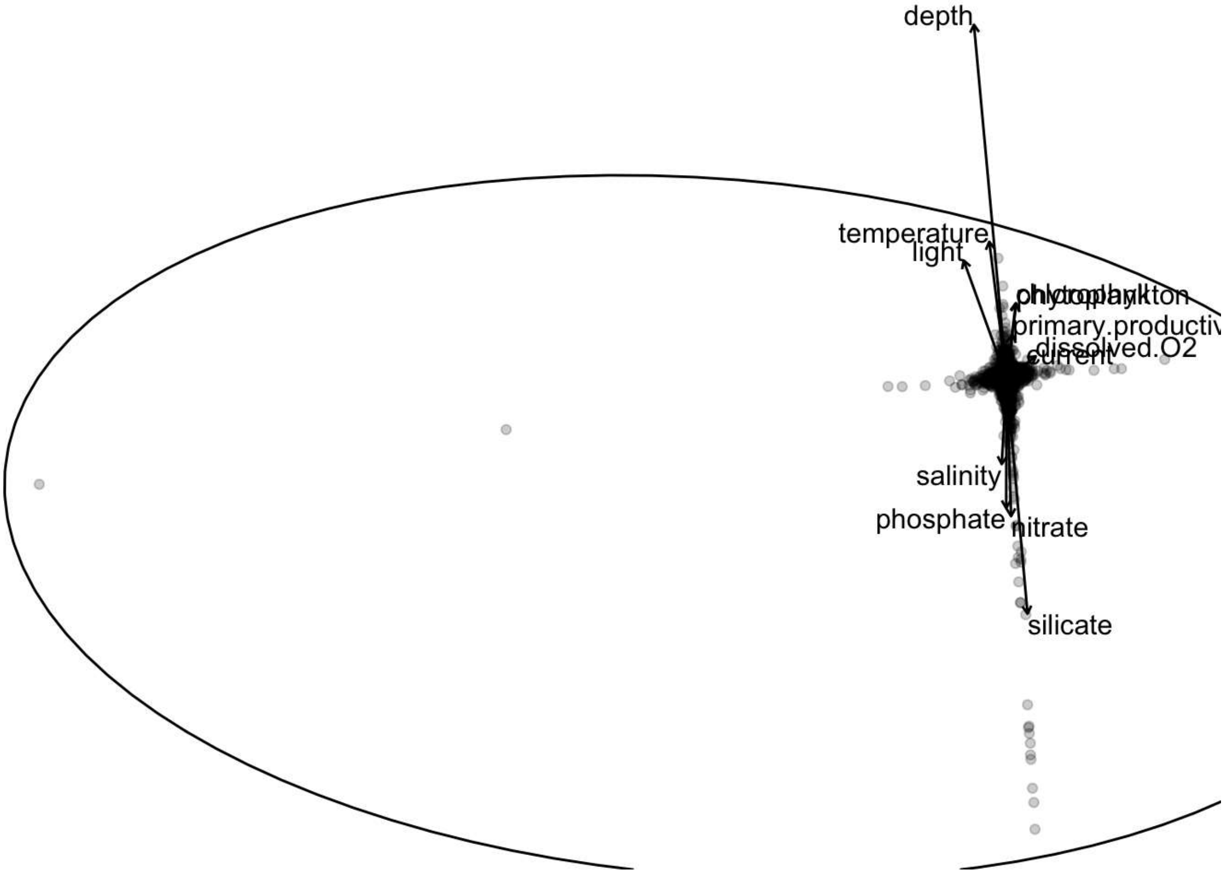
```
##
##
##
## Doing RDA for Anthozoa ...
## [1] "Proportion of variance explained:  0.44082397105085"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1     0.23 0.6355  0.995
## chlorophyll             1     0.13 0.3731  1.000
## current                 1     0.36 1.0131  0.377
## dissolved.O2            1     0.18 0.5077  1.000
## light                   1     0.54 1.5194  0.001 ***
## nitrate                 1     0.45 1.2692  0.067 .
## phosphate               1     0.20 0.5626  0.925
## phytoplankton           1     0.15 0.4303  1.000
## primary.productivity    1     0.12 0.3402  1.000
## salinity                1     0.12 0.3495  0.986
## silicate                1     0.49 1.3870  0.010 **
## temperature             1     0.17 0.4815  1.000
## deep.pcnm$vectors    1204   396.24 0.9283  0.992
## Residual             1429   506.61
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
##
##
## Doing RDA for Polychaeta ...
## [1] "Proportion of variance explained:  0.432516310286428"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)  
## depth                   1     0.48 1.6981  0.020 *
## chlorophyll             1     0.26 0.9173  0.427  
## current                 1     0.39 1.3766  0.095 .
## dissolved.O2            1     0.30 1.0757  0.277  
## light                   1     0.27 0.9440  0.735  
## nitrate                 1     0.20 0.7132  0.986  
## phosphate               1     0.18 0.6557  0.694  
## phytoplankton           1     0.35 1.2325  0.147  
## primary.productivity    1     0.41 1.4712  0.123  
## salinity                1     0.34 1.2055  0.210  
## silicate                1     0.28 0.9817  0.493  
## temperature             1     0.26 0.9156  0.606  
## deep.pcnm$vectors    1204   302.09 0.8936  0.989  
## Residual             1429   401.21                
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

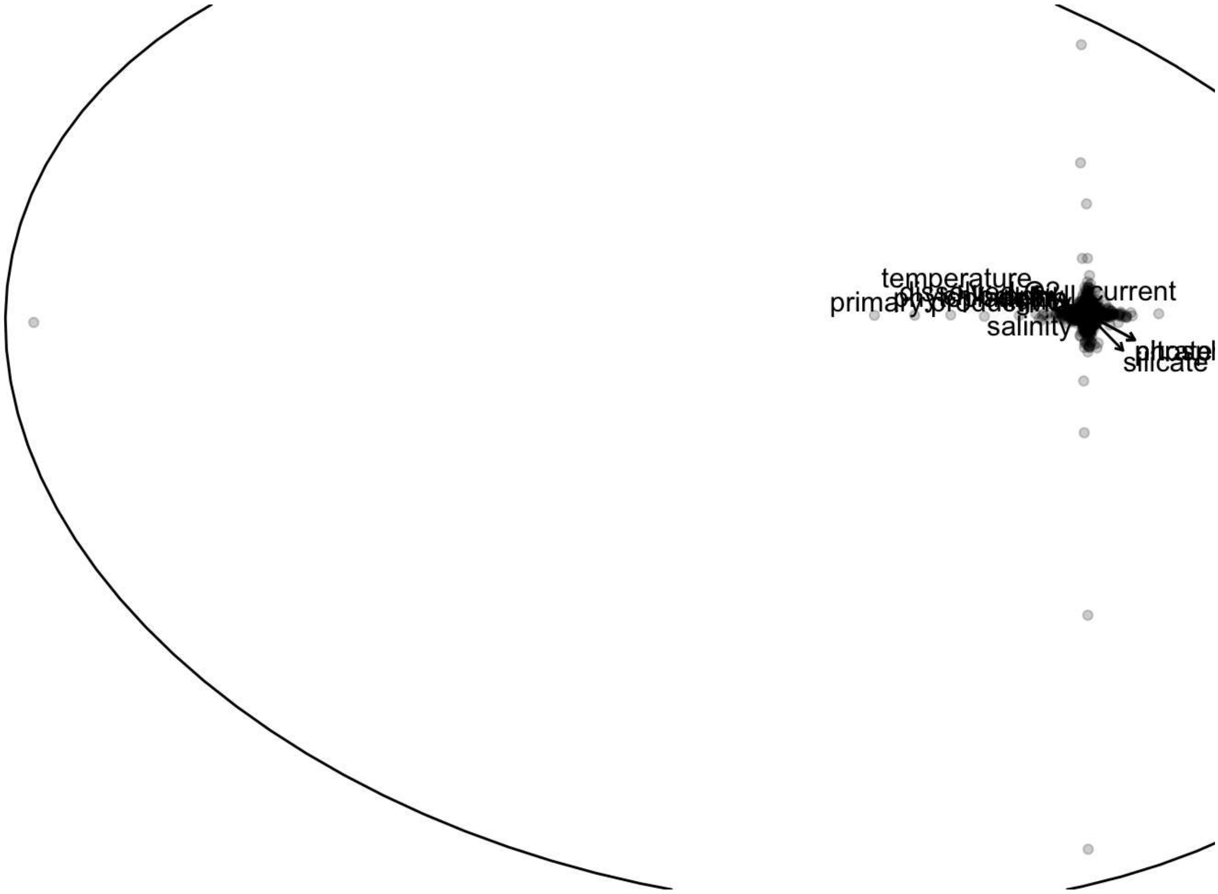


```
##
##
##
## Doing RDA for Bivalvia ...
## [1] "Proportion of variance explained:  0.432623031471425"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)    
## depth                   1     0.83 3.7343  0.001 ***
## chlorophyll             1     0.23 1.0332  0.299    
## current                 1     0.20 0.9060  0.522    
## dissolved.O2            1     0.23 1.0108  0.379    
## light                   1     0.23 1.0288  0.349    
## nitrate                 1     0.16 0.7066  0.990    
## phosphate               1     0.15 0.6843  0.594    
## phytoplankton           1     0.20 0.9096  0.535    
## primary.productivity    1     0.16 0.7294  0.579    
## salinity                1     0.24 1.0989  0.267    
## silicate                1     0.32 1.4340  0.009 ** 
## temperature             1     0.17 0.7832  0.852    
## deep.pcnm$vectors    1204   239.57 0.8933  0.999    
## Residual             1429   318.30                  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

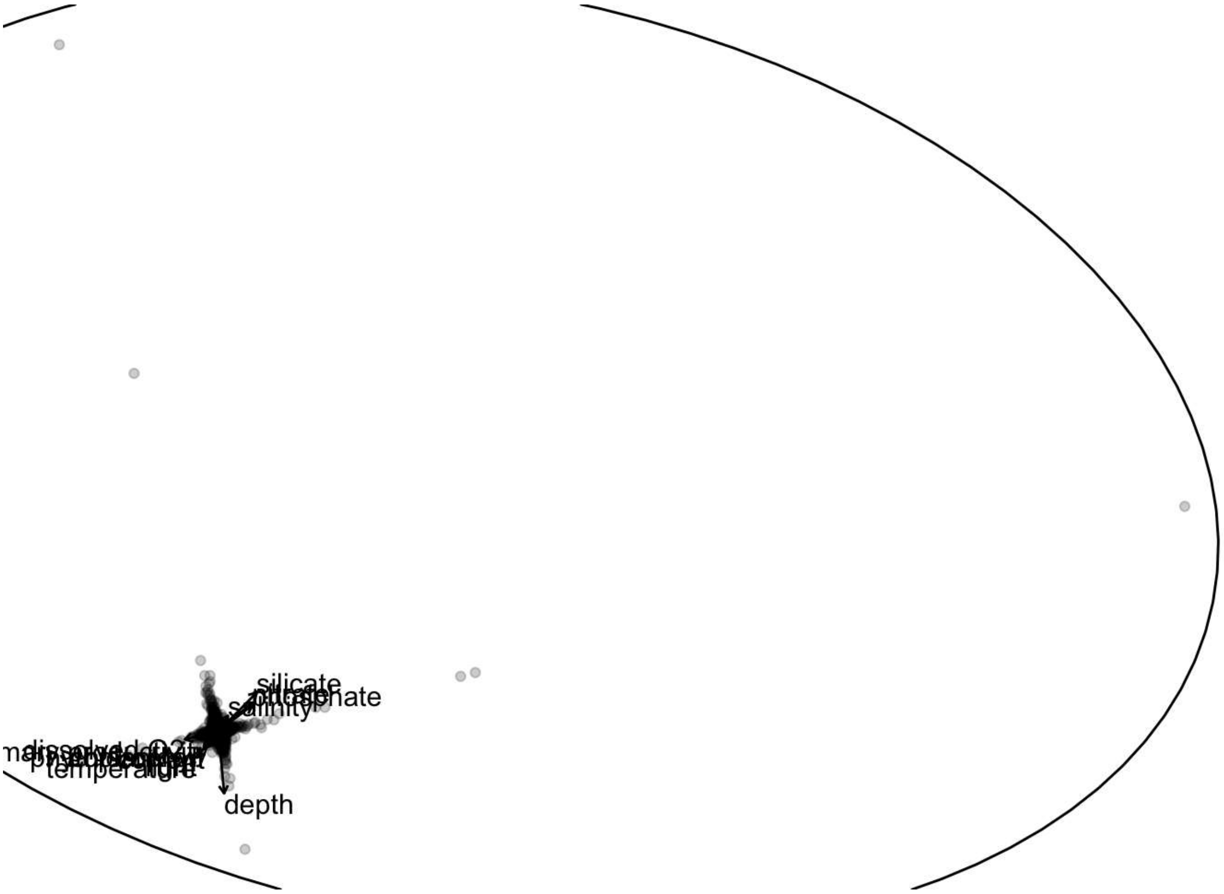


```
##
##
##
## Doing RDA for Ophiuroidea ...
## [1] "Proportion of variance explained:  0.4430351483678"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                         Df Variance      F Pr(>F)
## depth                    1    0.115 0.6862  0.959
## chlorophyll              1    0.052 0.3088  1.000
## current                  1    0.129 0.7714  0.754
## dissolved.O2             1    0.133 0.7962  0.893
## light                    1    0.164 0.9797  0.579
## nitrate                  1    0.121 0.7195  0.981
## phosphate                1    0.134 0.8013  0.360
## phytoplankton            1    0.065 0.3897  1.000
## primary.productivity     1    0.055 0.3271  1.000
## salinity                 1    0.077 0.4608  0.749
## silicate                 1    0.232 1.3835  0.022 *
## temperature              1    0.101 0.6043  0.997
## deep.pcnm$vectors     1204  189.126 0.9373  0.930
## Residual              1429  239.495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

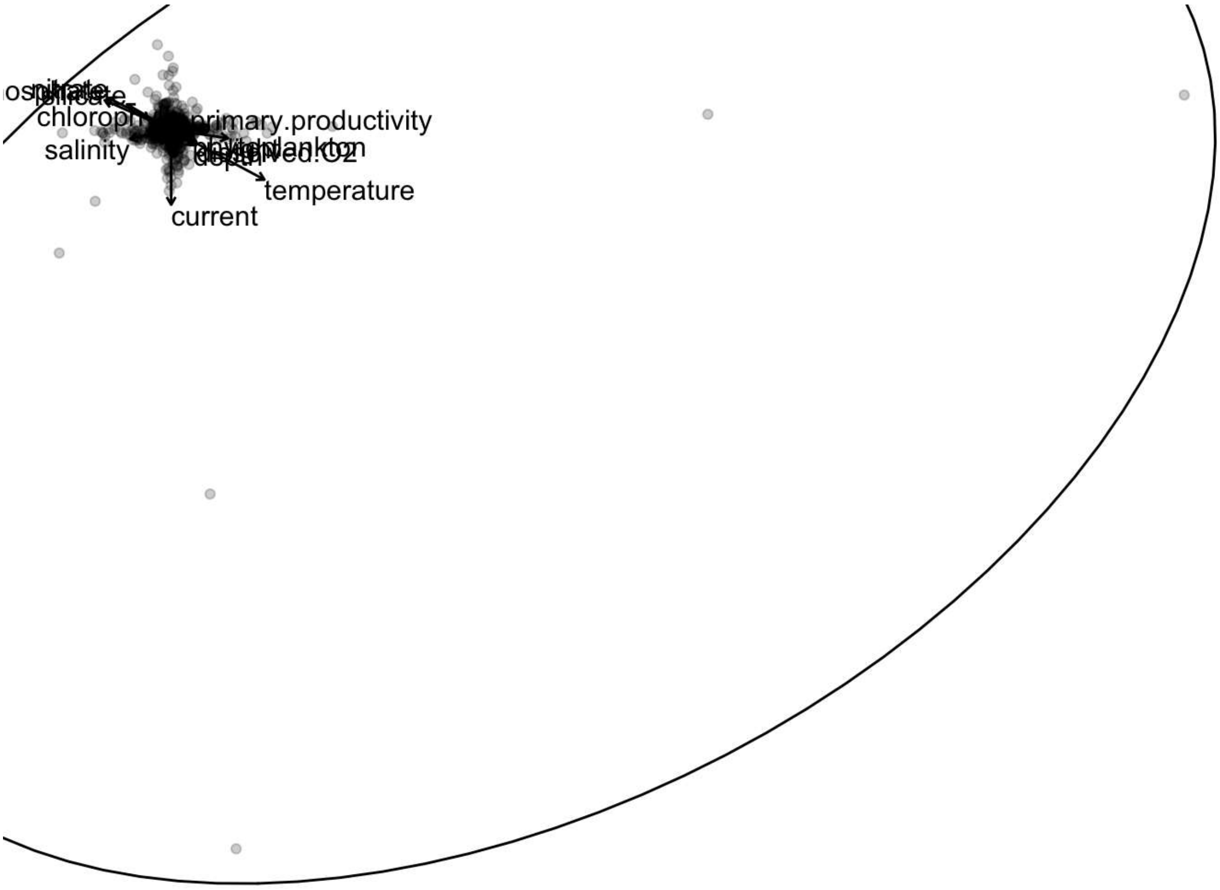
```
##
##
##
## Doing RDA for Asteroidea ...
## [1] "Proportion of variance explained:  0.433246253206663"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.215 1.4350  0.053 .
## chlorophyll             1    0.059 0.3952  1.000
## current                 1    0.095 0.6368  0.954
## dissolved.O2            1    0.118 0.7888  0.925
## light                   1    0.156 1.0408  0.307
## nitrate                 1    0.123 0.8195  0.849
## phosphate               1    0.086 0.5715  0.859
## phytoplankton           1    0.059 0.3943  1.000
## primary.productivity    1    0.064 0.4260  0.987
## salinity                1    0.066 0.4370  0.812
## silicate                1    0.174 1.1632  0.097 .
## temperature             1    0.125 0.8326  0.785
## deep.pcnm$vectors    1204  162.427 0.8999  0.989
## Residual             1429  214.233
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



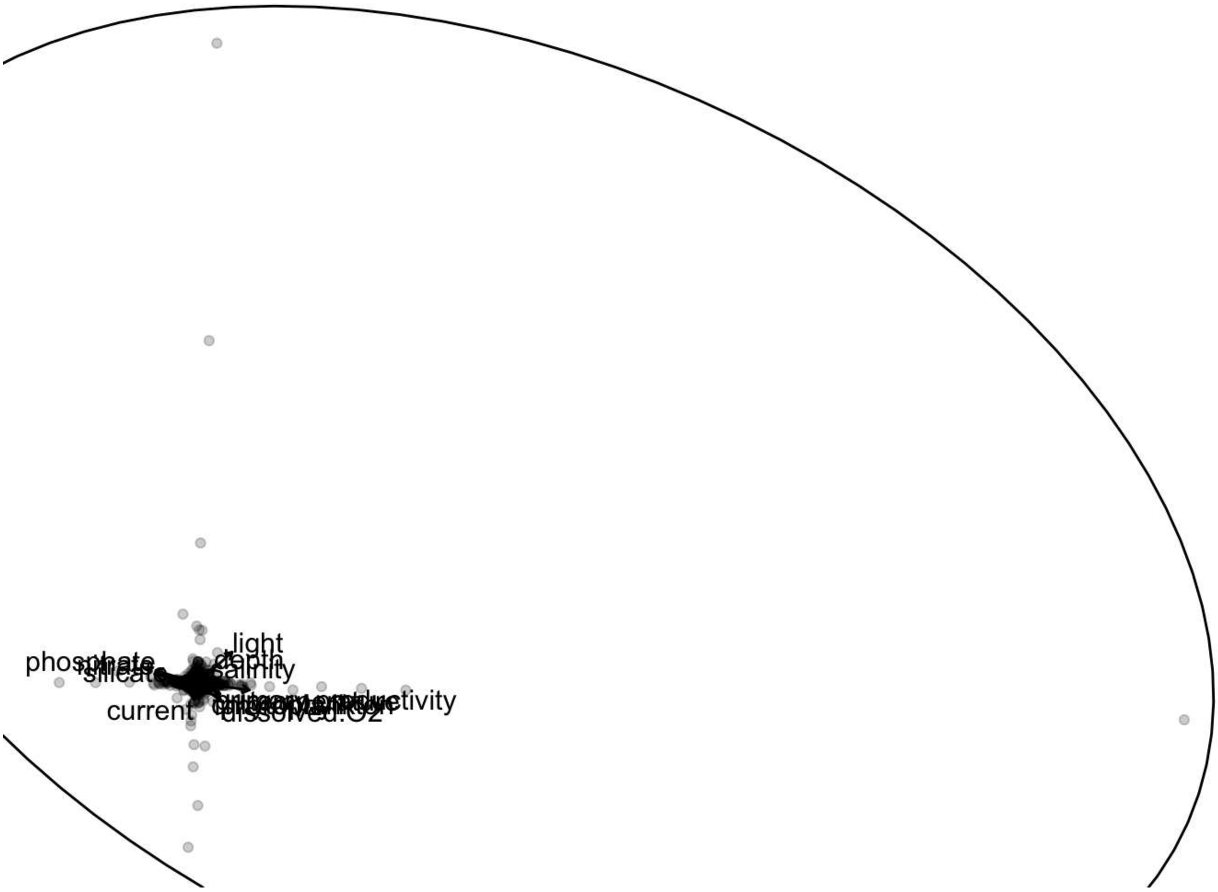
```
##
##
##
## Doing RDA for Hydrozoa ...
## [1] "Proportion of variance explained:  0.455784677373504"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.185 1.3073  0.141
## chlorophyll             1    0.068 0.4803  0.966
## current                 1    0.172 1.2196  0.187
## dissolved.O2            1    0.139 0.9814  0.448
## light                   1    0.109 0.7746  0.989
## nitrate                 1    0.100 0.7048  0.952
## phosphate               1    0.078 0.5499  0.816
## phytoplankton           1    0.069 0.4877  0.993
## primary.productivity    1    0.081 0.5730  0.755
## salinity                1    0.140 0.9912  0.299
## silicate                1    0.171 1.2068  0.105
## temperature             1    0.094 0.6685  0.919
## deep.pcnm$vectors    1204  167.691 0.9858  0.650
## Residual             1429  201.904
```



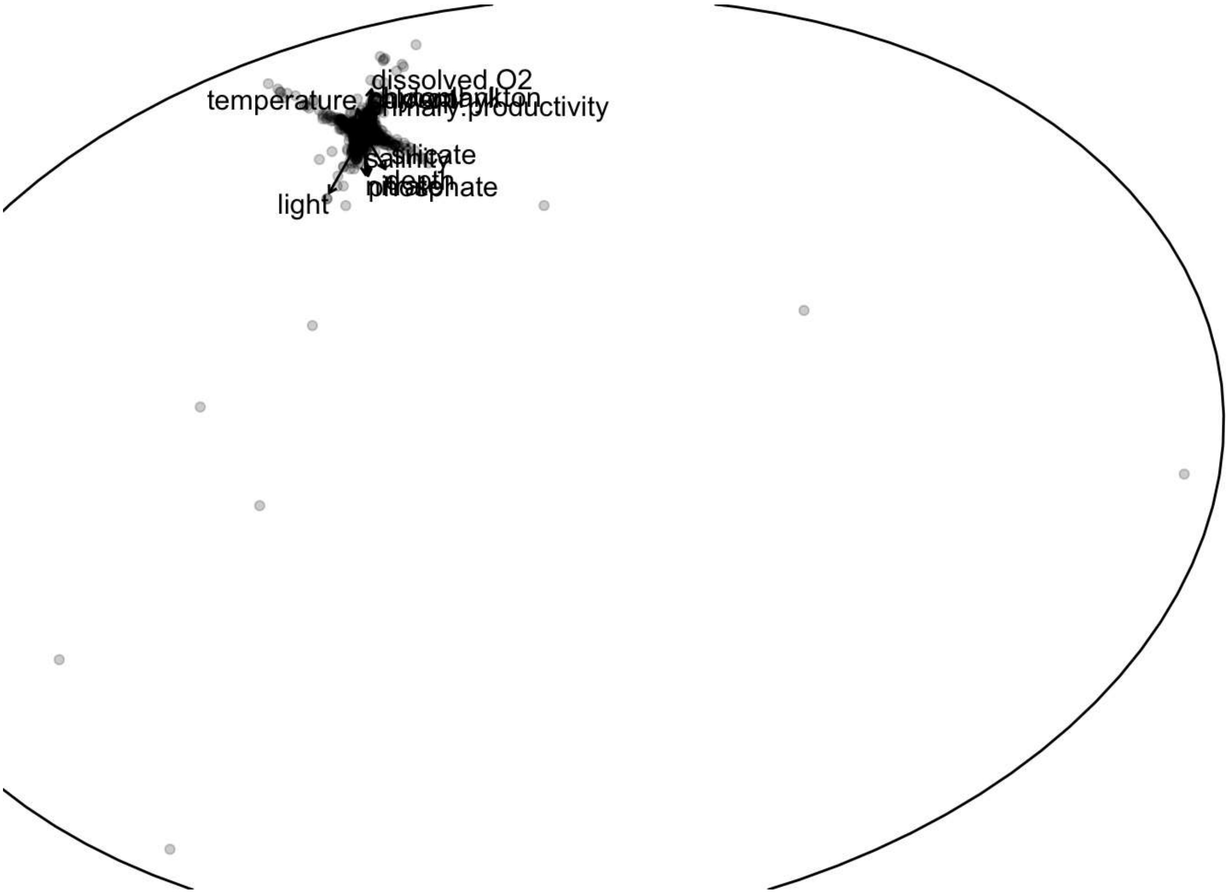
```
##
##
##
## Doing RDA for Demospongiae ...
## [1] "Proportion of variance explained:  0.459937672976656"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)    
## depth                   1    0.074 0.7412  0.840    
## chlorophyll             1    0.038 0.3817  0.993    
## current                 1    0.100 1.0089  0.383    
## dissolved.O2            1    0.101 1.0194  0.381    
## light                   1    0.149 1.5040  0.001 ***
## nitrate                 1    0.120 1.2120  0.093 .  
## phosphate               1    0.078 0.7839  0.372    
## phytoplankton           1    0.098 0.9855  0.401    
## primary.productivity    1    0.048 0.4803  0.905    
## salinity                1    0.030 0.3015  0.954    
## silicate                1    0.140 1.4086  0.016 *  
## temperature             1    0.090 0.9073  0.574    
## deep.pcnm$vectors    1204  119.897 1.0019  0.478    
## Residual             1429  142.036                  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



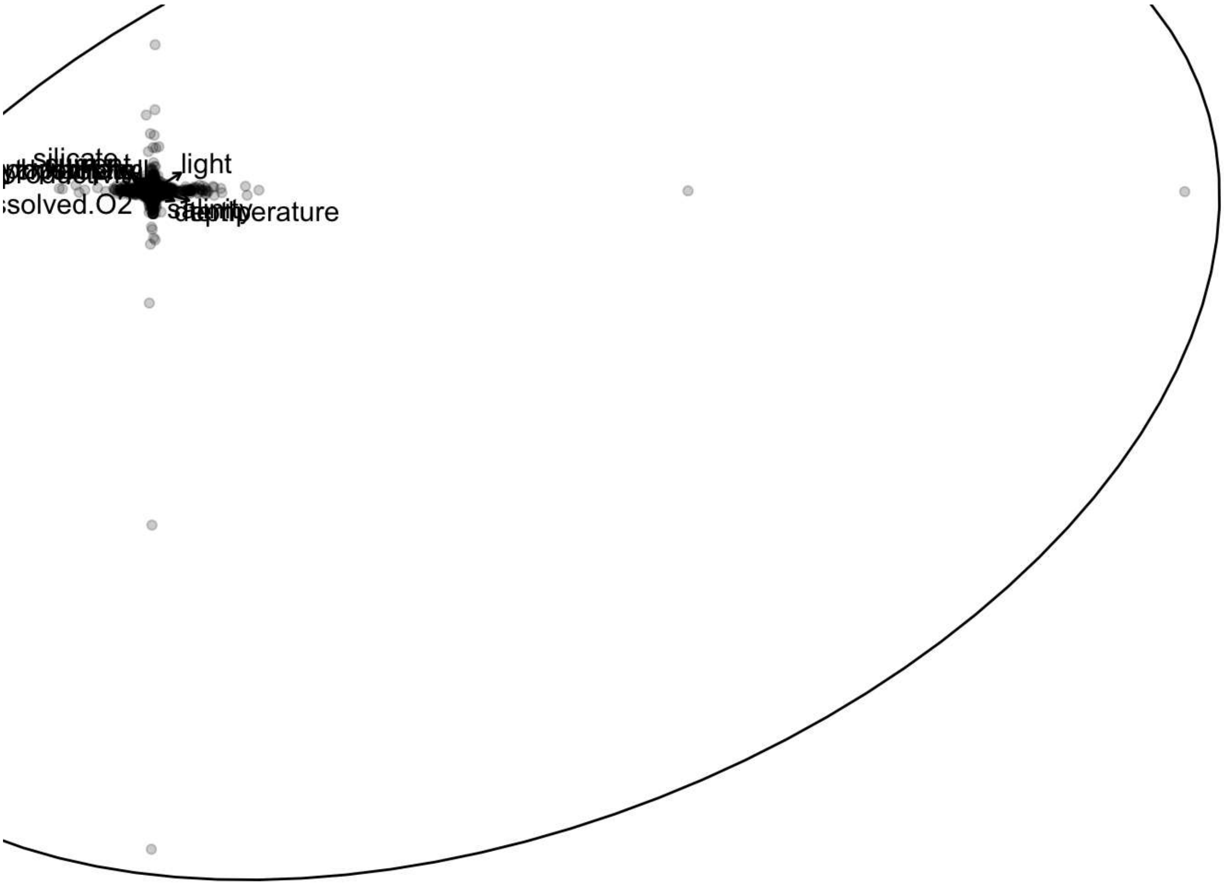
```
##
##
##
## Doing RDA for Echinoidea ...
## [1] "Proportion of variance explained:  0.424914332287771"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.168 1.6210  0.022 *
## chlorophyll             1    0.028 0.2697  1.000
## current                 1    0.067 0.6405  0.886
## dissolved.O2            1    0.064 0.6139  0.997
## light                   1    0.116 1.1212  0.083 .
## nitrate                 1    0.096 0.9254  0.548
## phosphate               1    0.073 0.7046  0.543
## phytoplankton           1    0.037 0.3544  1.000
## primary.productivity    1    0.022 0.2125  1.000
## salinity                1    0.037 0.3528  0.918
## silicate                1    0.114 1.1025  0.202
## temperature             1    0.073 0.7025  0.928
## deep.pcnm$vectors    1204  108.733 0.8698  0.999
## Residual             1429  148.372
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



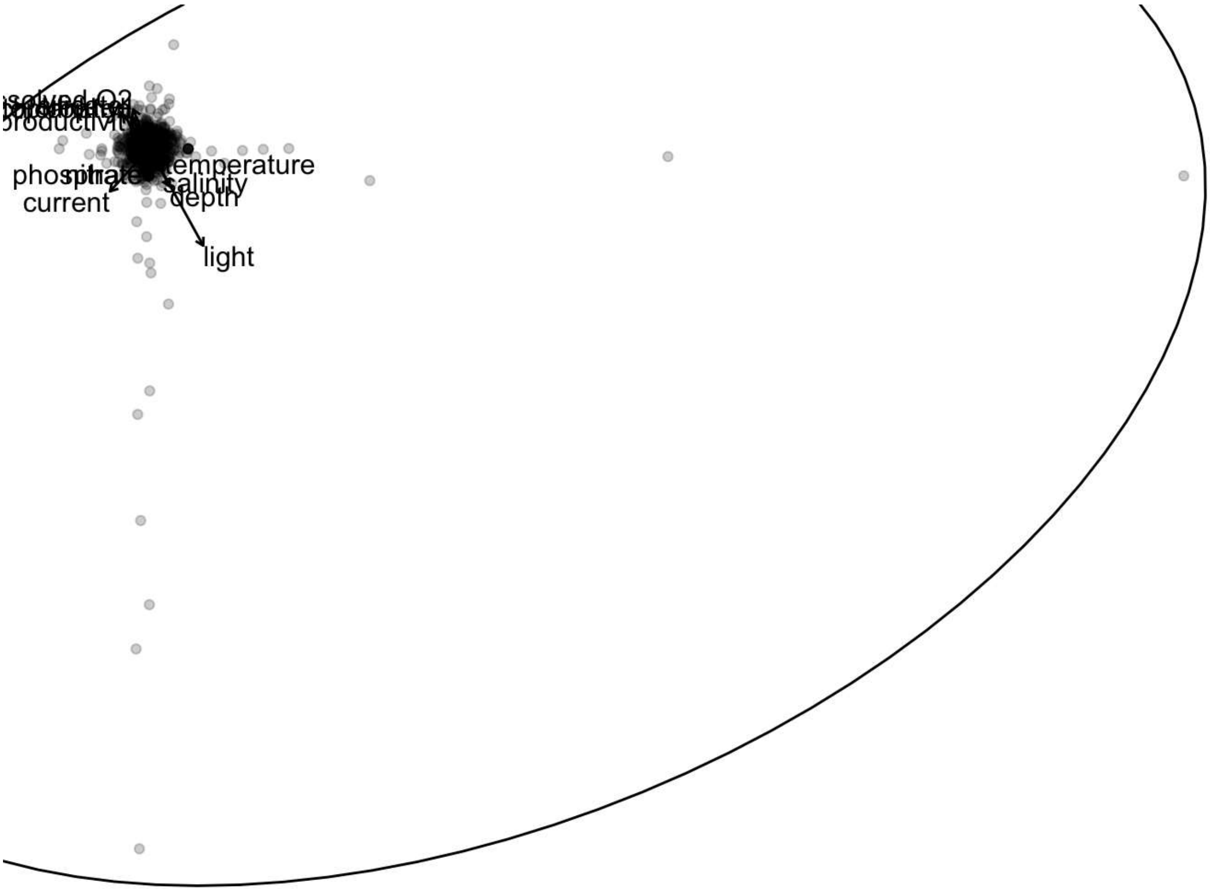
```
##
##
##
## Doing RDA for Holothuroidea ...
## [1] "Proportion of variance explained:  0.444306755606141"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.125 1.6395  0.008 **
## chlorophyll             1    0.081 1.0580  0.254
## current                 1    0.160 2.1037  0.012 *
## dissolved.O2            1    0.090 1.1776  0.130
## light                   1    0.091 1.1975  0.012 *
## nitrate                 1    0.090 1.1813  0.102
## phosphate               1    0.068 0.8928  0.289
## phytoplankton           1    0.091 1.1913  0.234
## primary.productivity    1    0.055 0.7163  0.547
## salinity                1    0.030 0.3940  0.815
## silicate                1    0.173 2.2719  0.001 ***
## temperature             1    0.082 1.0821  0.305
## deep.pcnm$vectors    1204   85.948 0.9366  0.956
## Residual             1429  108.916
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



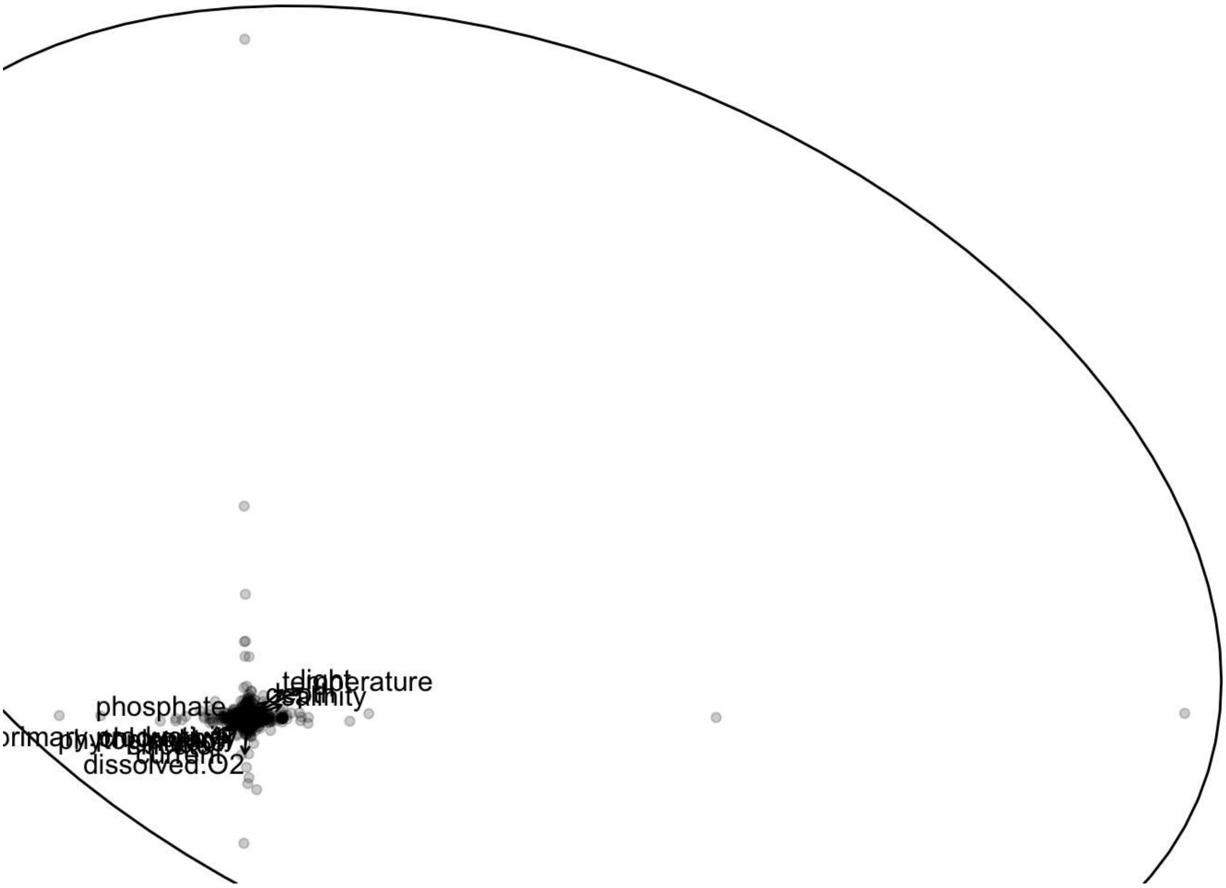
```
##
##
##
## Doing RDA for Crinoidea ...
## [1] "Proportion of variance explained:  0.446736284603058"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.038 0.4707  0.993
## chlorophyll             1    0.024 0.3060  0.999
## current                 1    0.062 0.7829  0.660
## dissolved.O2            1    0.038 0.4743  1.000
## light                   1    0.087 1.0945  0.185
## nitrate                 1    0.070 0.8796  0.637
## phosphate               1    0.054 0.6824  0.547
## phytoplankton           1    0.030 0.3758  1.000
## primary.productivity    1    0.019 0.2410  1.000
## salinity                1    0.020 0.2517  0.995
## silicate                1    0.067 0.8344  0.832
## temperature             1    0.030 0.3730  1.000
## deep.pcnm$vectors    1204   91.488 0.9527  0.812
## Residual             1429  113.972
```



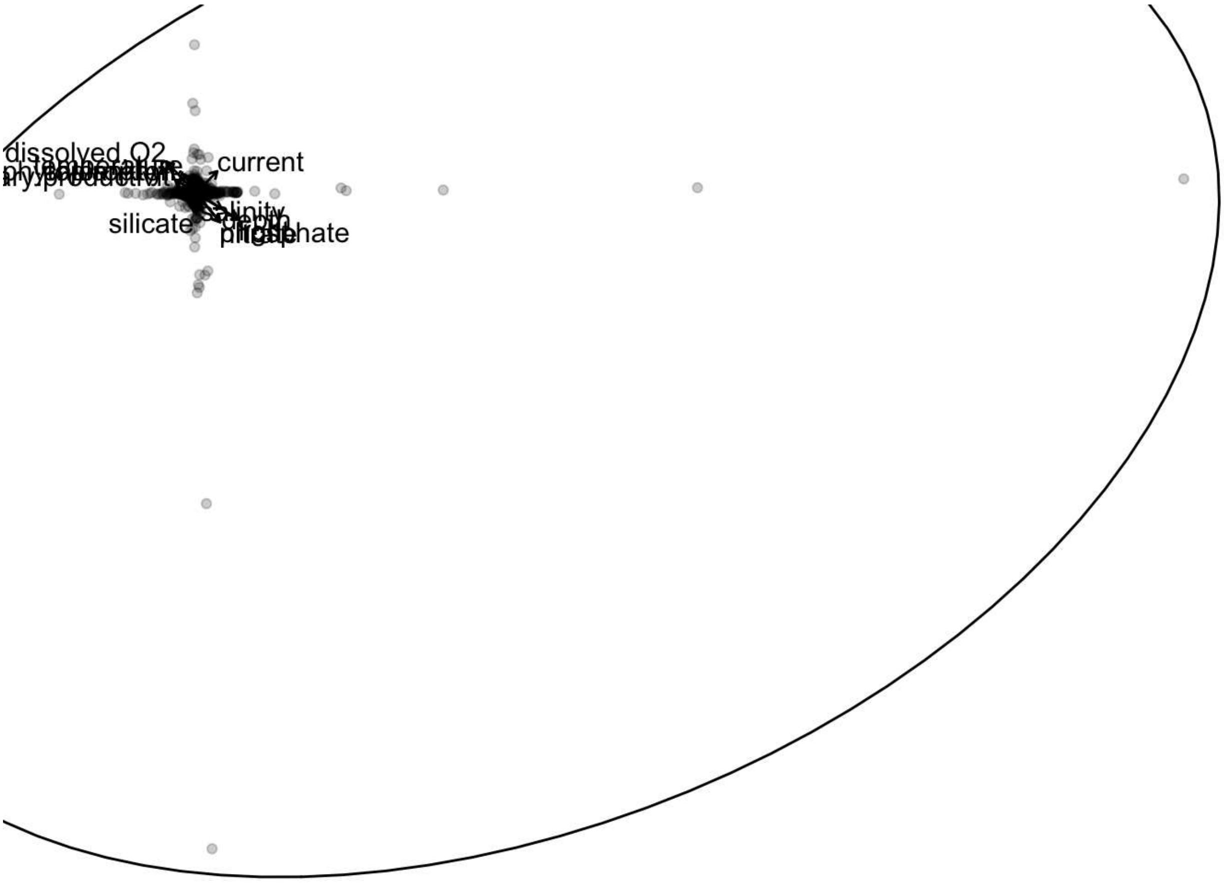
```
##
##
##
## Doing RDA for Ascidiacea ...
## [1] "Proportion of variance explained:  0.428482548380265"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)    
## depth                   1    0.043 0.6009  0.924    
## chlorophyll             1    0.070 0.9765  0.304    
## current                 1    0.145 2.0205  0.038 *  
## dissolved.O2            1    0.049 0.6815  0.953    
## light                   1    0.110 1.5323  0.001 ***
## nitrate                 1    0.058 0.8124  0.761    
## phosphate               1    0.039 0.5421  0.751    
## phytoplankton           1    0.052 0.7234  0.710    
## primary.productivity    1    0.026 0.3655  0.968    
## salinity                1    0.015 0.2151  0.998    
## silicate                1    0.058 0.8084  0.820    
## temperature             1    0.068 0.9439  0.523    
## deep.pcnm$vectors    1204   75.967 0.8813  0.982    
## Residual             1429  102.302                  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



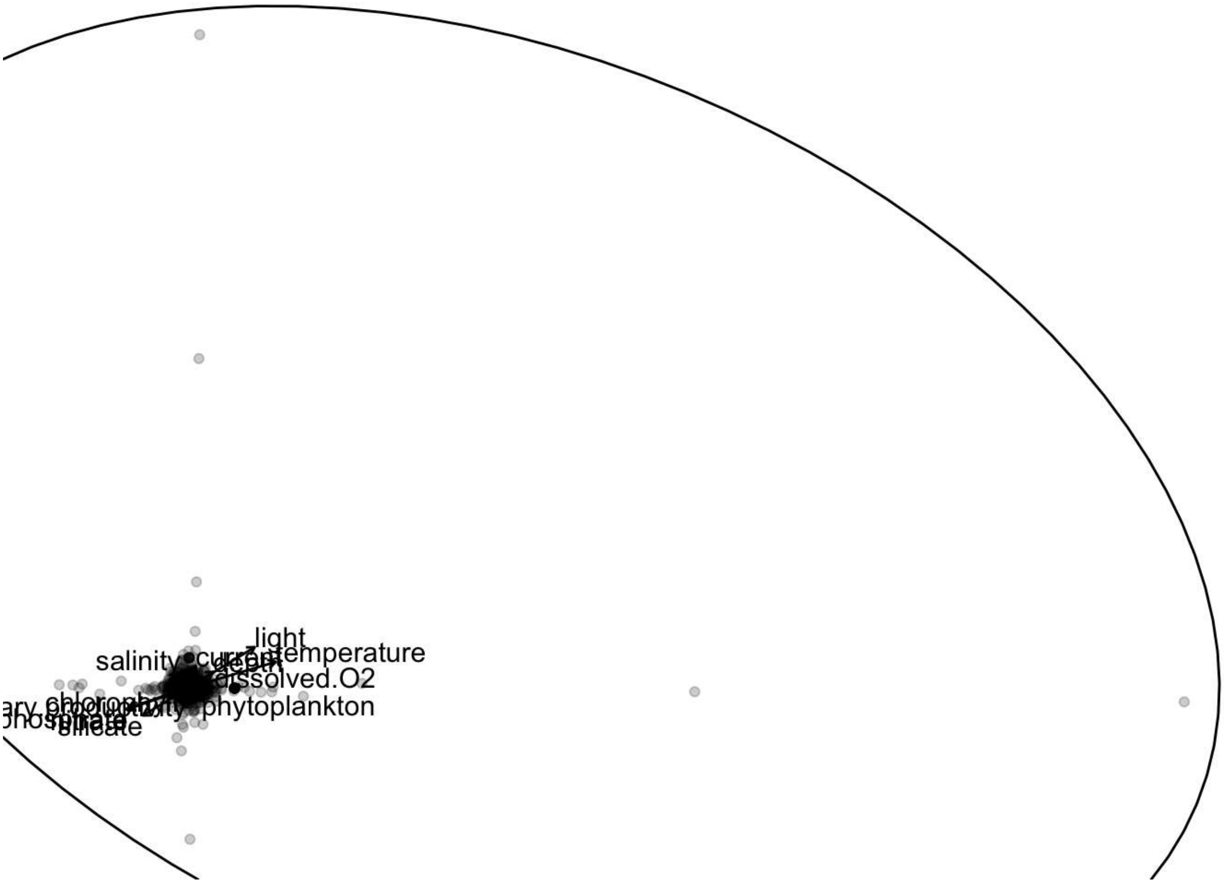
```
##
##
##
## Doing RDA for Hexanauplia ...
## [1] "Proportion of variance explained:  0.448123120446279"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.177 2.5533  0.047 *
## chlorophyll             1    0.053 0.7666  0.377
## current                 1    0.041 0.5887  0.763
## dissolved.O2            1    0.047 0.6845  0.765
## light                   1    0.093 1.3452  0.124
## nitrate                 1    0.059 0.8603  0.474
## phosphate               1    0.130 1.8804  0.066 .
## phytoplankton           1    0.066 0.9507  0.340
## primary.productivity    1    0.058 0.8371  0.290
## salinity                1    0.044 0.6305  0.331
## silicate                1    0.046 0.6629  0.874
## temperature             1    0.038 0.5427  0.873
## deep.pcnm$vectors    1204   79.364 0.9535  0.781
## Residual             1429   98.786
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



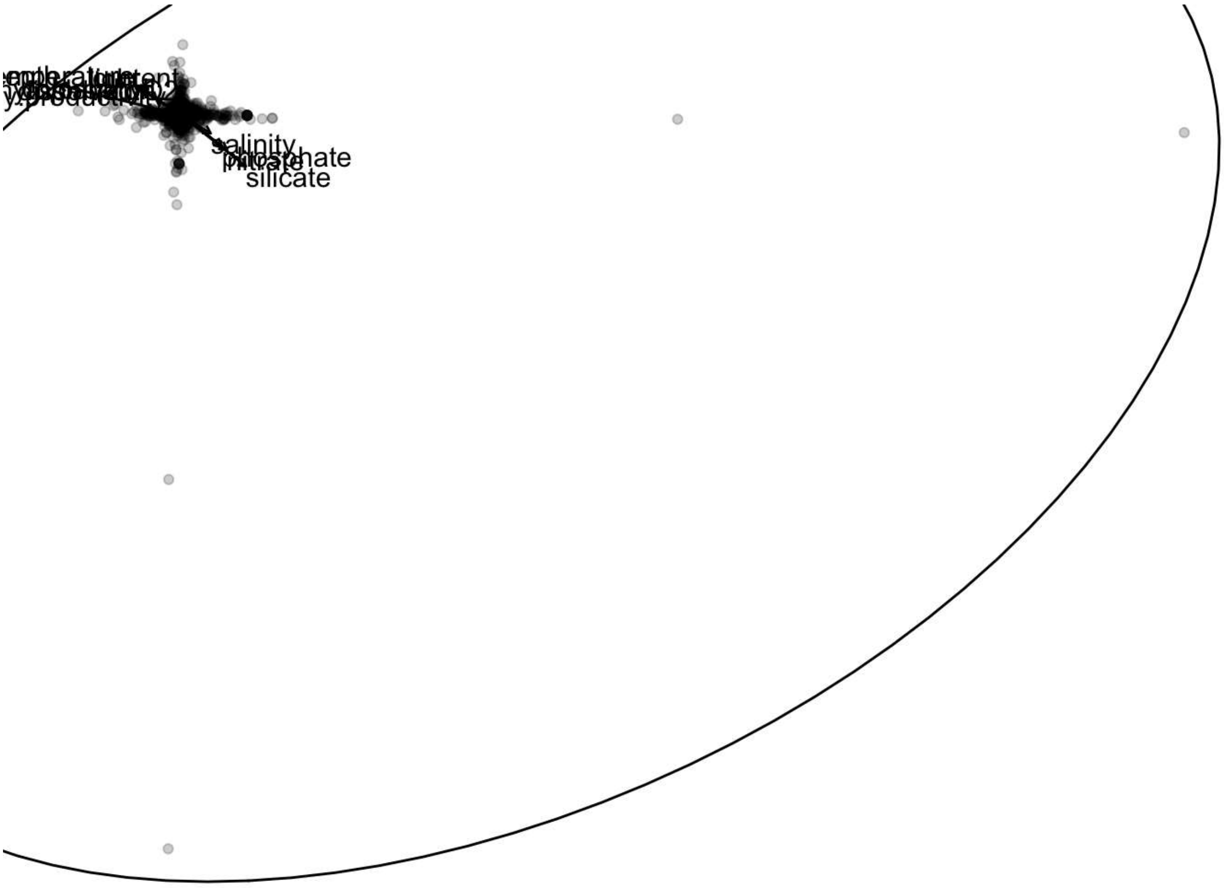
```
##
##
##
## Doing RDA for Pycnogonida ...
## [1] "Proportion of variance explained:  0.407724032174356"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.023 0.3668  0.997
## chlorophyll             1    0.028 0.4396  0.942
## current                 1    0.068 1.0906  0.328
## dissolved.O2            1    0.052 0.8273  0.734
## light                   1    0.069 1.1061  0.170
## nitrate                 1    0.049 0.7758  0.831
## phosphate               1    0.026 0.4102  0.961
## phytoplankton           1    0.016 0.2532  1.000
## primary.productivity    1    0.018 0.2862  0.990
## salinity                1    0.015 0.2364  0.994
## silicate                1    0.069 1.1048  0.289
## temperature             1    0.035 0.5593  0.975
## deep.pcnm$vectors    1204   61.100 0.8109  1.000
## Residual             1429   89.434
```



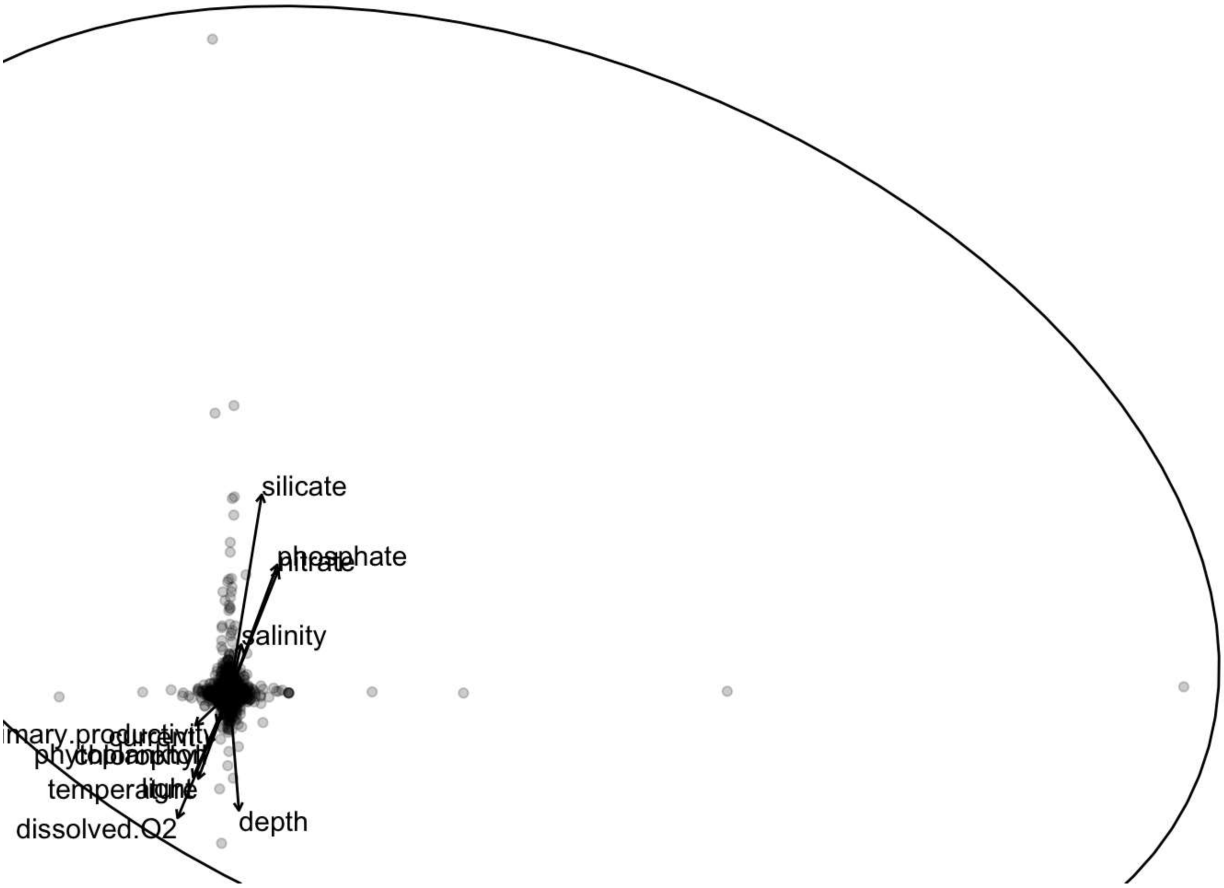
```
##
##
##
## Doing RDA for Gymnolaemata ...
## [1] "Proportion of variance explained:  0.446609945611729"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.038 0.8107  0.541
## chlorophyll             1    0.012 0.2564  0.990
## current                 1    0.017 0.3628  0.966
## dissolved.O2            1    0.038 0.8096  0.638
## light                   1    0.068 1.4598  0.019 *
## nitrate                 1    0.039 0.8491  0.582
## phosphate               1    0.013 0.2775  0.967
## phytoplankton           1    0.038 0.8148  0.465
## primary.productivity    1    0.013 0.2846  0.925
## salinity                1    0.015 0.3204  0.747
## silicate                1    0.053 1.1492  0.290
## temperature             1    0.030 0.6508  0.766
## deep.pcnm$vectors    1204   53.219 0.9512  0.746
## Residual             1429   66.407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



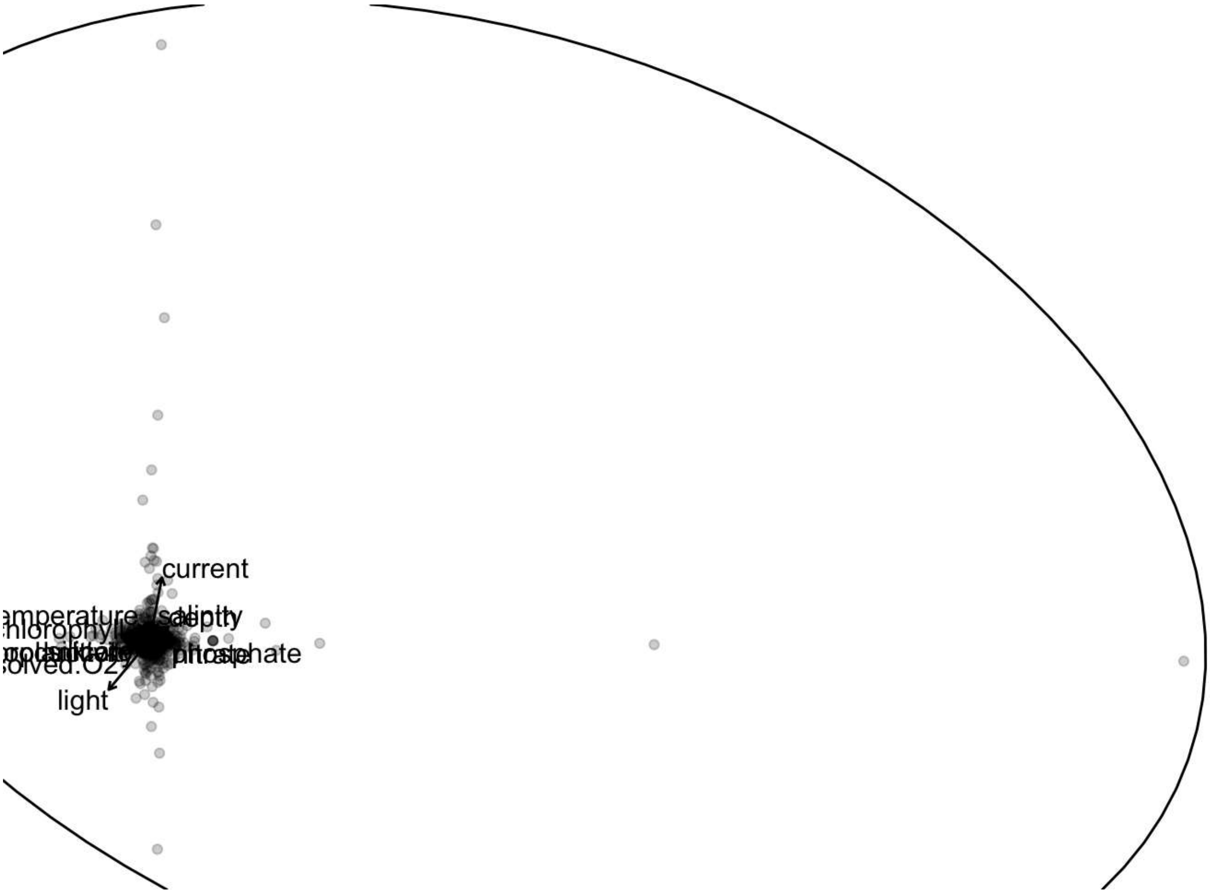
```
##
##
##
## Doing RDA for Ostracoda ...
## [1] "Proportion of variance explained:  0.461258029701185"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.1765 8.3606  0.001 ***
## chlorophyll             1   0.0020 0.0964  1.000
## current                 1   0.0062 0.2960  0.969
## dissolved.O2            1   0.0504 2.3872  0.026 *
## light                   1   0.0082 0.3862  0.999
## nitrate                 1   0.0069 0.3249  0.989
## phosphate               1   0.0174 0.8243  0.290
## phytoplankton           1   0.0056 0.2629  0.930
## primary.productivity    1   0.0117 0.5543  0.499
## salinity                1   0.0168 0.7952  0.162
## silicate                1   0.0447 2.1188  0.029 *
## temperature             1   0.0150 0.7094  0.594
## deep.pcnm$vectors    1204  25.4691 1.0020  0.597
## Residual             1429  30.1696
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



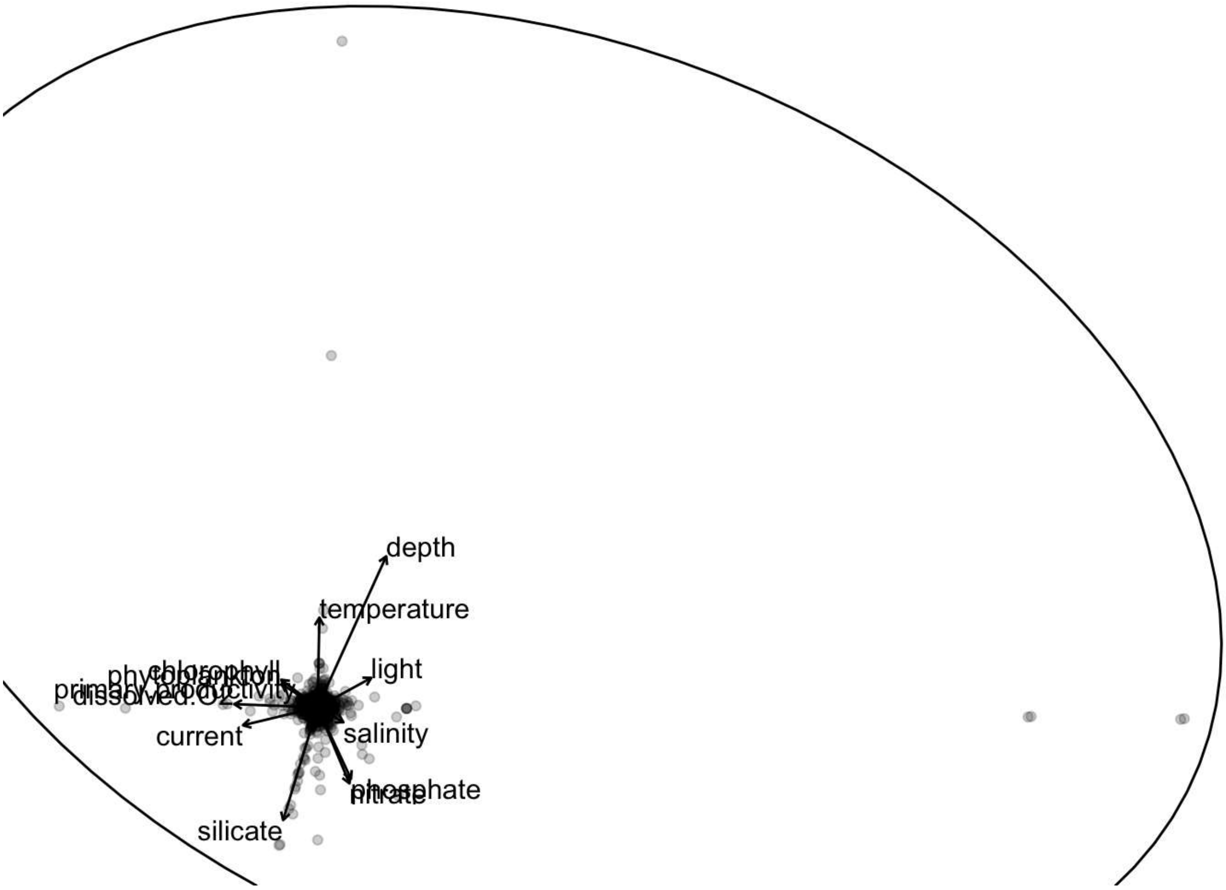
```
##
##
##
## Doing RDA for Hexactinellida ...
## [1] "Proportion of variance explained:  0.448575944043995"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.049 1.8025  0.047 *
## chlorophyll             1    0.006 0.2183  1.000
## current                 1    0.010 0.3744  0.989
## dissolved.O2            1    0.037 1.3406  0.116
## light                   1    0.016 0.5851  1.000
## nitrate                 1    0.012 0.4412  0.998
## phosphate               1    0.014 0.5250  0.720
## phytoplankton           1    0.004 0.1380  1.000
## primary.productivity    1    0.003 0.1177  1.000
## salinity                1    0.011 0.3880  0.657
## silicate                1    0.090 3.2792  0.001 ***
## temperature             1    0.010 0.3817  0.993
## deep.pcnm$vectors    1204   31.586 0.9575  0.759
## Residual             1429   39.151
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



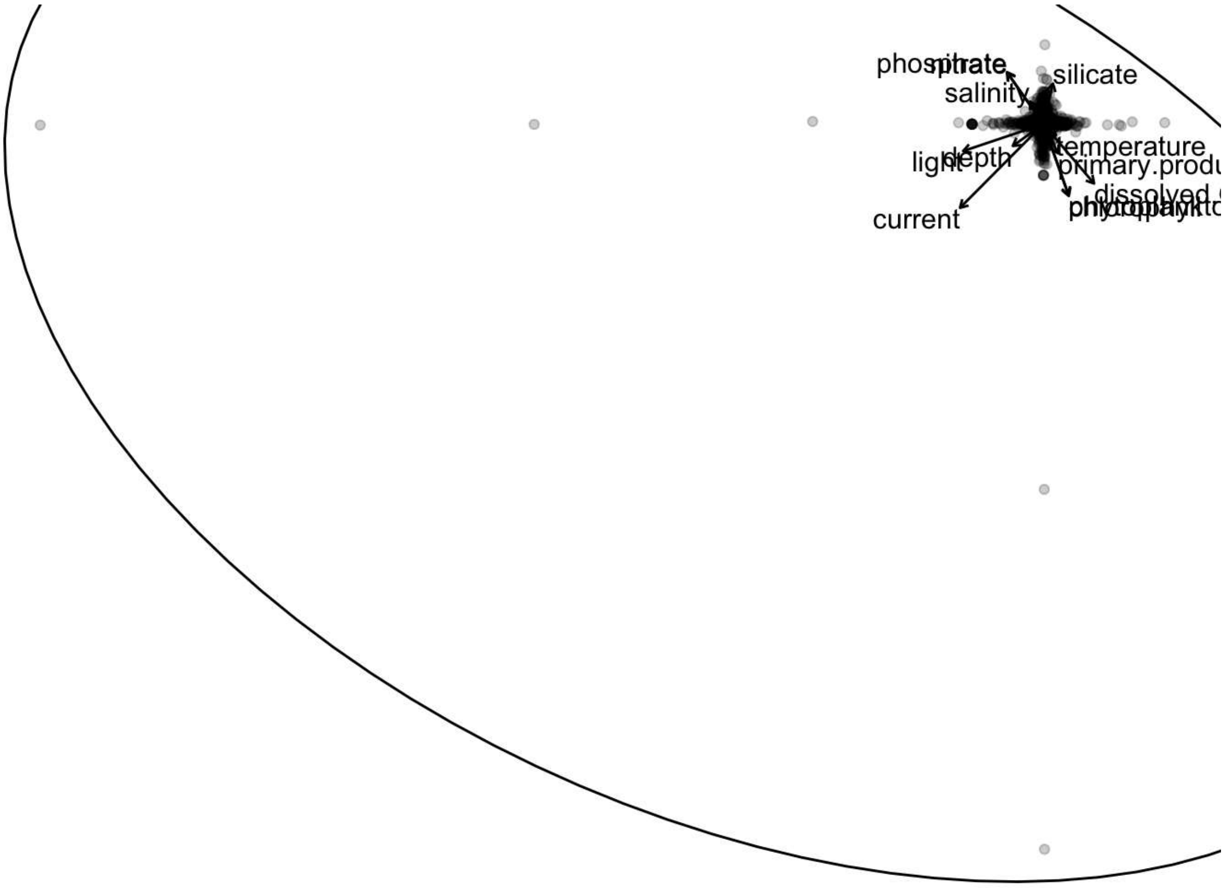
```
##
##
##
## Doing RDA for Cephalopoda ...
## [1] "Proportion of variance explained:  0.455600127670652"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.009 0.3774  0.982
## chlorophyll             1    0.008 0.3224  0.979
## current                 1    0.020 0.8209  0.553
## dissolved.O2            1    0.013 0.5337  0.982
## light                   1    0.029 1.2086  0.081 .
## nitrate                 1    0.017 0.7130  0.879
## phosphate               1    0.010 0.4006  0.902
## phytoplankton           1    0.011 0.4582  0.924
## primary.productivity    1    0.005 0.2002  0.996
## salinity                1    0.006 0.2545  0.955
## silicate                1    0.020 0.8138  0.774
## temperature             1    0.012 0.5052  0.941
## deep.pcnm$vectors    1204   28.997 0.9878  0.625
## Residual             1429   34.842
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



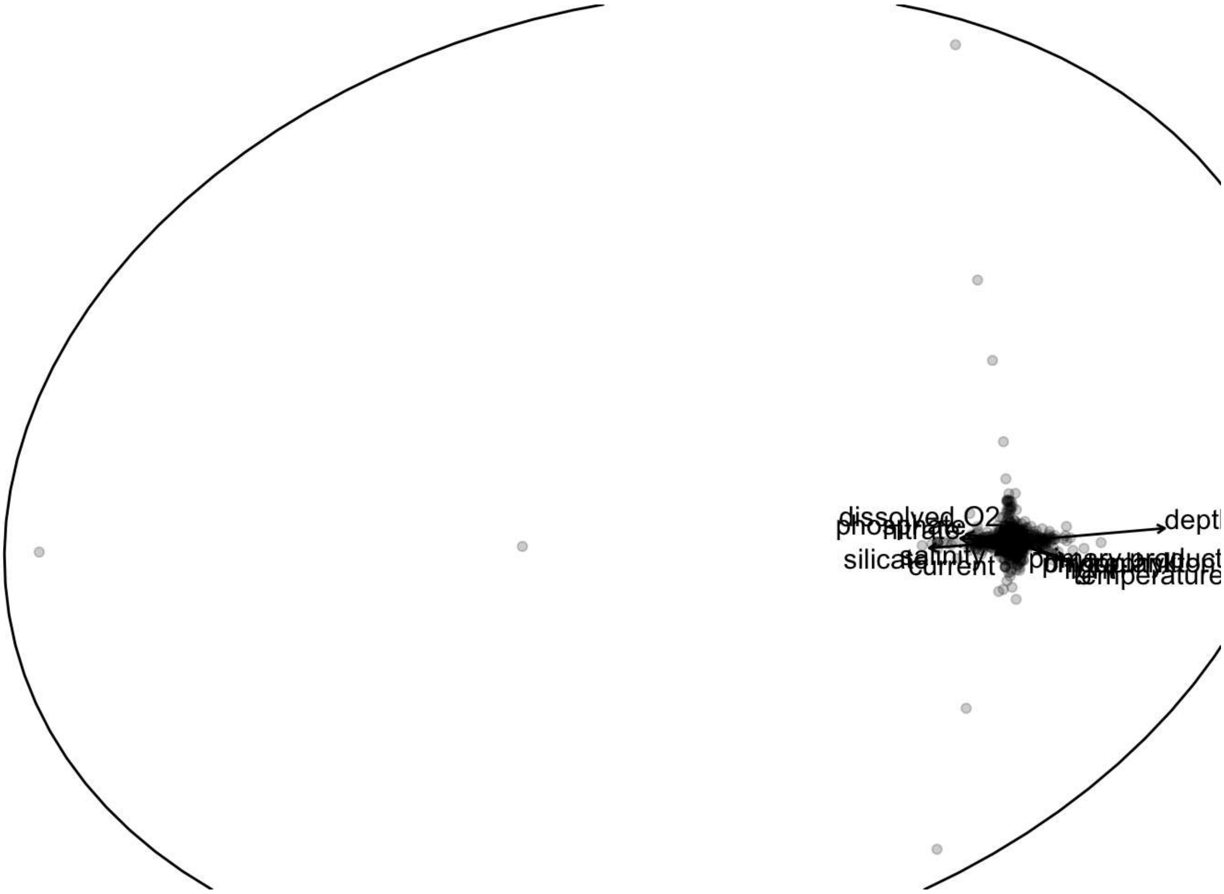
```
##
##
##
## Doing RDA for Scaphopoda ...
## [1] "Proportion of variance explained:  0.44572043981389"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1    0.115 4.6520  0.001 ***
## chlorophyll             1    0.016 0.6454  0.600
## current                 1    0.018 0.7363  0.584
## dissolved.O2            1    0.016 0.6405  0.905
## light                   1    0.021 0.8609  0.805
## nitrate                 1    0.015 0.6190  0.935
## phosphate               1    0.013 0.5122  0.736
## phytoplankton           1    0.008 0.3261  0.982
## primary.productivity    1    0.015 0.5969  0.592
## salinity                1    0.004 0.1665  0.996
## silicate                1    0.027 1.0869  0.325
## temperature             1    0.011 0.4449  0.972
## deep.pcnm$vectors    1204   28.246 0.9450  0.808
## Residual             1429   35.474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



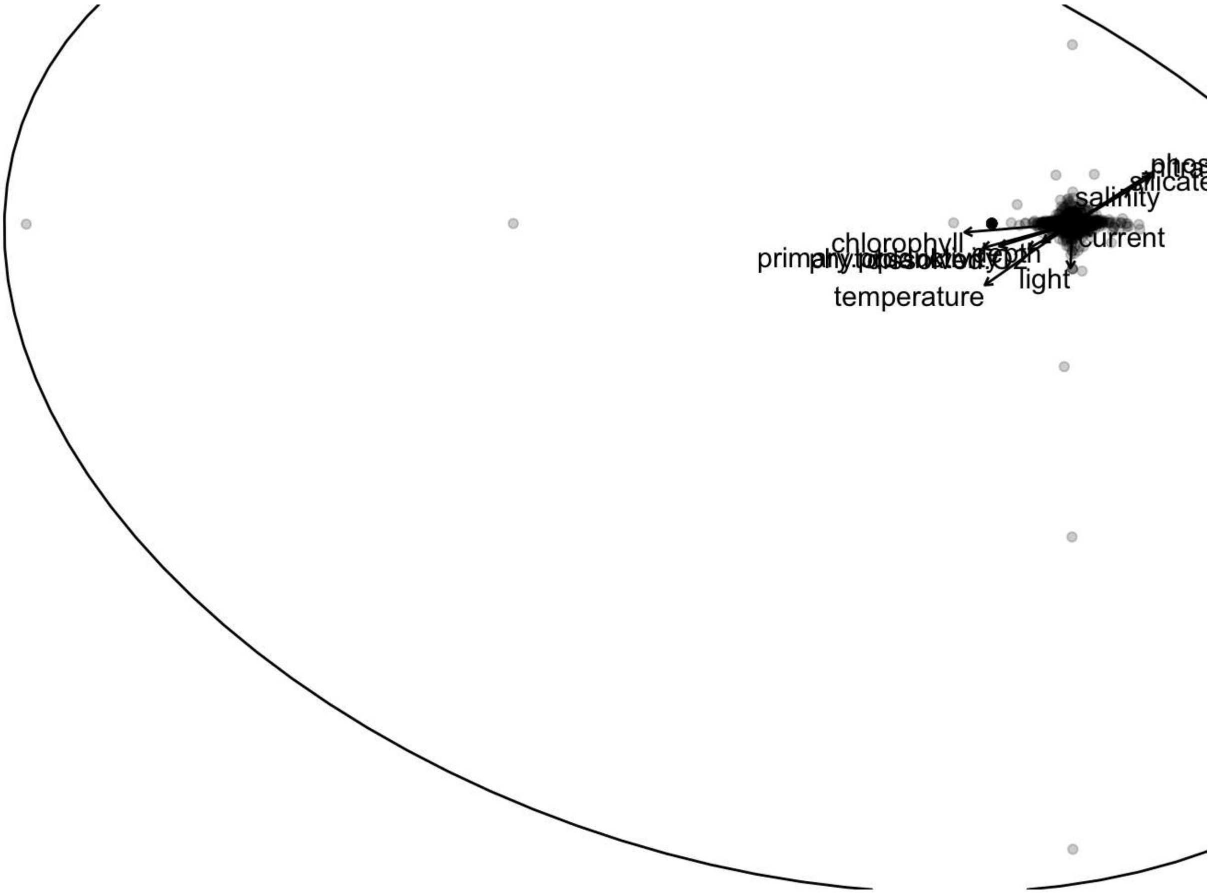
```
##
##
##
## Doing RDA for Rhabditophora ...
## [1] "Proportion of variance explained:  0.487103843347279"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)  
## depth                   1   0.0074 0.4026  0.911  
## chlorophyll             1   0.0237 1.2974  0.149  
## current                 1   0.0415 2.2684  0.056 .
## dissolved.O2            1   0.0249 1.3596  0.144  
## light                   1   0.0220 1.1997  0.176  
## nitrate                 1   0.0222 1.2145  0.210  
## phosphate               1   0.0108 0.5927  0.497  
## phytoplankton           1   0.0226 1.2361  0.207  
## primary.productivity    1   0.0189 1.0306  0.175  
## salinity                1   0.0119 0.6510  0.238  
## silicate                1   0.0199 1.0872  0.298  
## temperature             1   0.0320 1.7474  0.086 .
## deep.pcnm$vectors    1204  24.5844 1.1155  0.105  
## Residual             1429  26.1577                
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



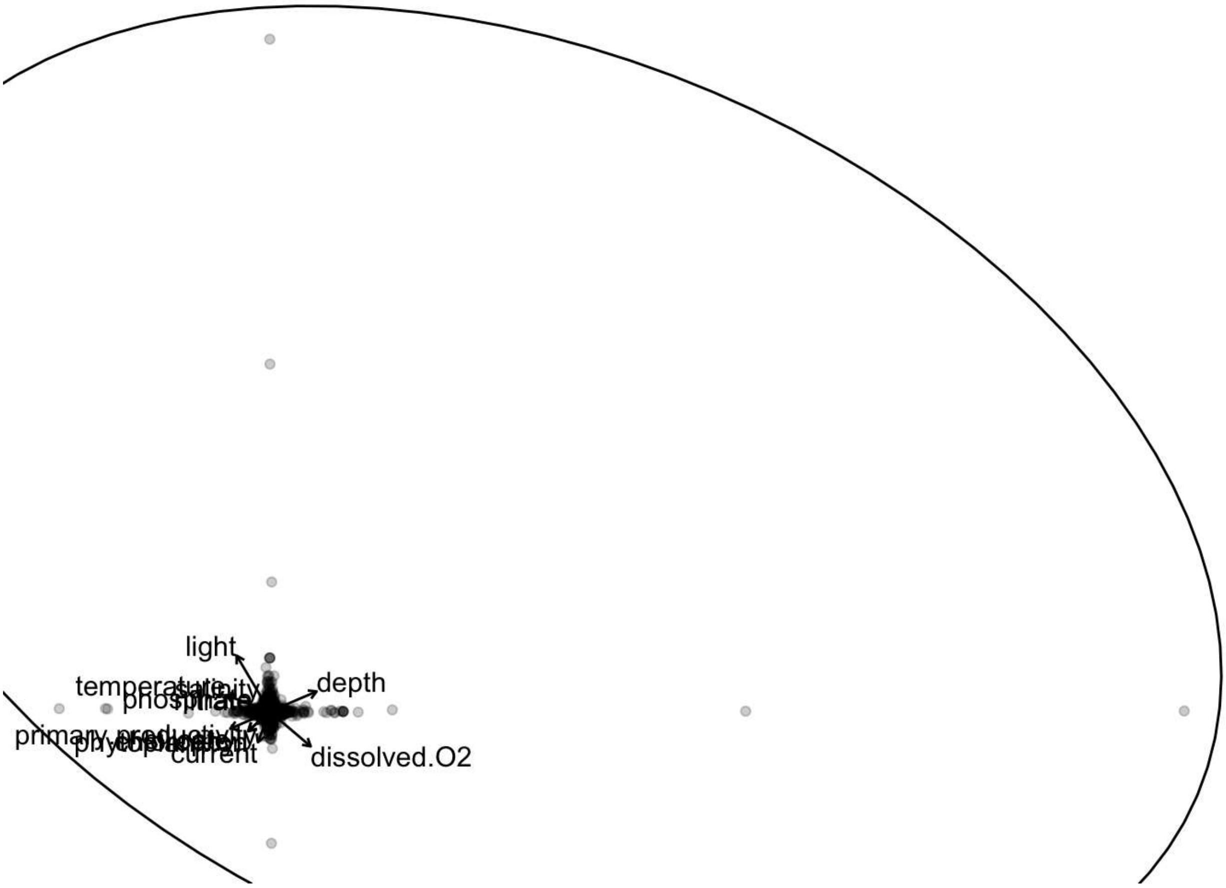
```
##
##
##
## Doing RDA for Chromadorea ...
## [1] "Proportion of variance explained:  0.505040392777934"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)   
## depth                   1   0.0667 4.4752  0.003 **
## chlorophyll             1   0.0286 1.9234  0.073 . 
## current                 1   0.0095 0.6403  0.564   
## dissolved.O2            1   0.0262 1.7591  0.057 . 
## light                   1   0.0126 0.8435  0.753   
## nitrate                 1   0.0159 1.0658  0.279   
## phosphate               1   0.0911 6.1197  0.010 **
## phytoplankton           1   0.0297 1.9926  0.073 . 
## primary.productivity    1   0.1078 7.2406  0.018 * 
## salinity                1   0.0113 0.7604  0.205   
## silicate                1   0.0094 0.6286  0.873   
## temperature             1   0.0333 2.2330  0.037 * 
## deep.pcnm$vectors    1204  21.2747 1.1864  0.011 * 
## Residual             1429  21.2833                 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



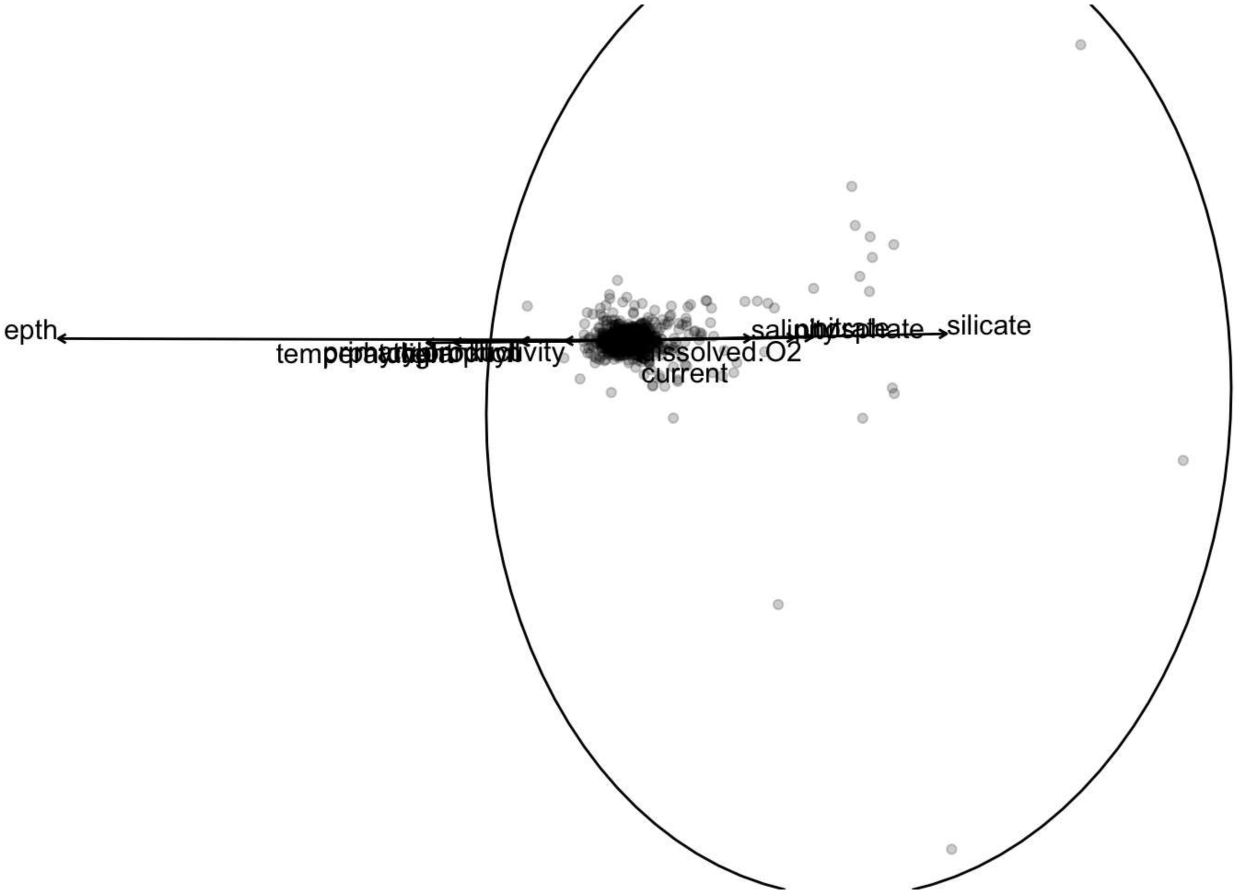
```
##
##
##
## Doing RDA for Clitellata ...
## [1] "Proportion of variance explained:  0.529454112185089"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0163 1.0326  0.152
## chlorophyll             1   0.0526 3.3305  0.045 *
## current                 1   0.0093 0.5910  0.409
## dissolved.O2            1   0.0072 0.4550  0.607
## light                   1   0.0064 0.4034  0.799
## nitrate                 1   0.0272 1.7219  0.154
## phosphate               1   0.0059 0.3734  0.472
## phytoplankton           1   0.0267 1.6883  0.142
## primary.productivity    1   0.0046 0.2891  0.445
## salinity                1   0.0009 0.0577  0.935
## silicate                1   0.0056 0.3555  0.739
## temperature             1   0.0159 1.0035  0.250
## deep.pcnm$vectors    1204  25.2352 1.3261  0.014 *
## Residual             1429  22.5862
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



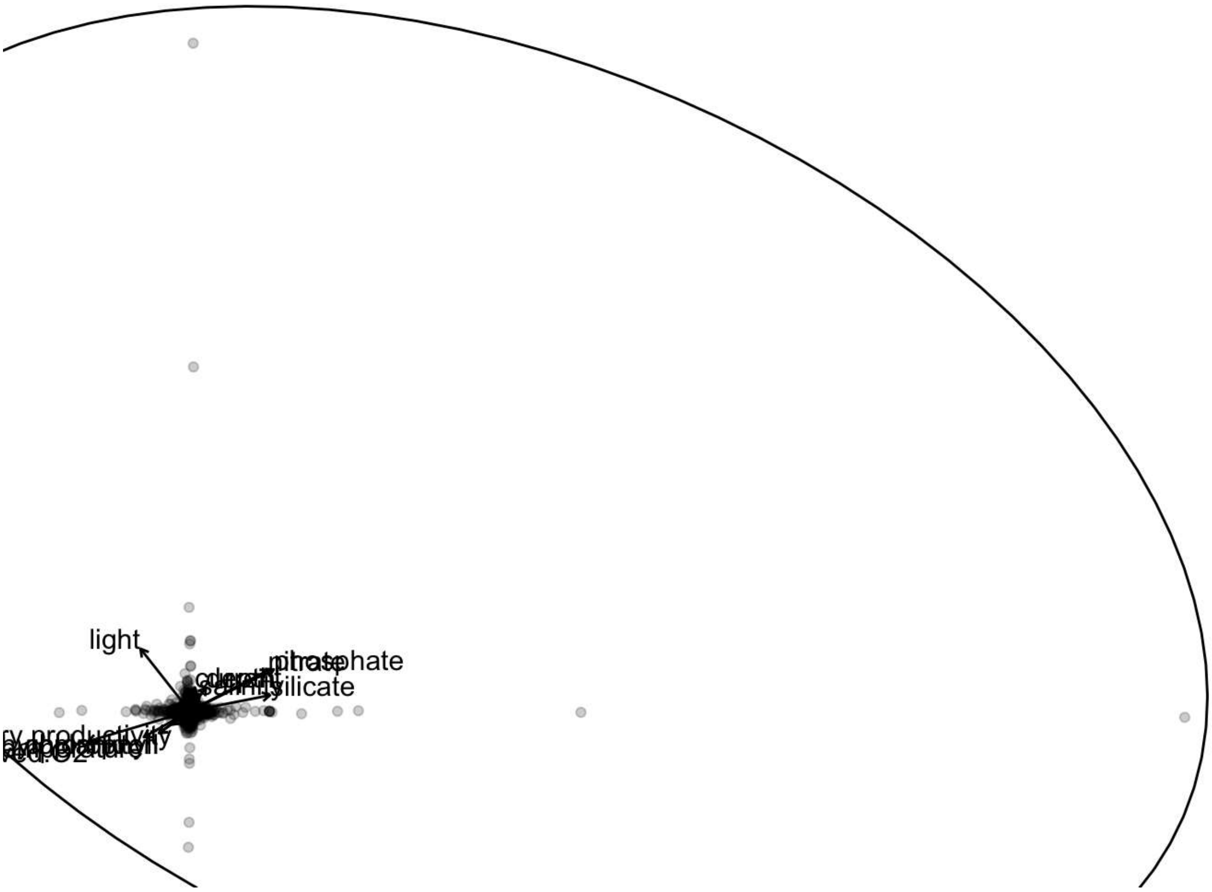
```
##
##
##
## Doing RDA for Polyplacophora ...
## [1] "Proportion of variance explained:  0.48333127421843"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0092 0.6086  0.727
## chlorophyll             1   0.0124 0.8180  0.358
## current                 1   0.0681 4.4839  0.013 *
## dissolved.O2            1   0.0143 0.9416  0.452
## light                   1   0.0217 1.4316  0.022 *
## nitrate                 1   0.0061 0.3998  0.994
## phosphate               1   0.0054 0.3537  0.862
## phytoplankton           1   0.0153 1.0062  0.311
## primary.productivity    1   0.0121 0.7940  0.319
## salinity                1   0.0068 0.4488  0.419
## silicate                1   0.0116 0.7633  0.739
## temperature             1   0.0247 1.6278  0.113
## deep.pcnm$vectors    1204  20.0922 1.0989  0.164
## Residual             1429  21.7001
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



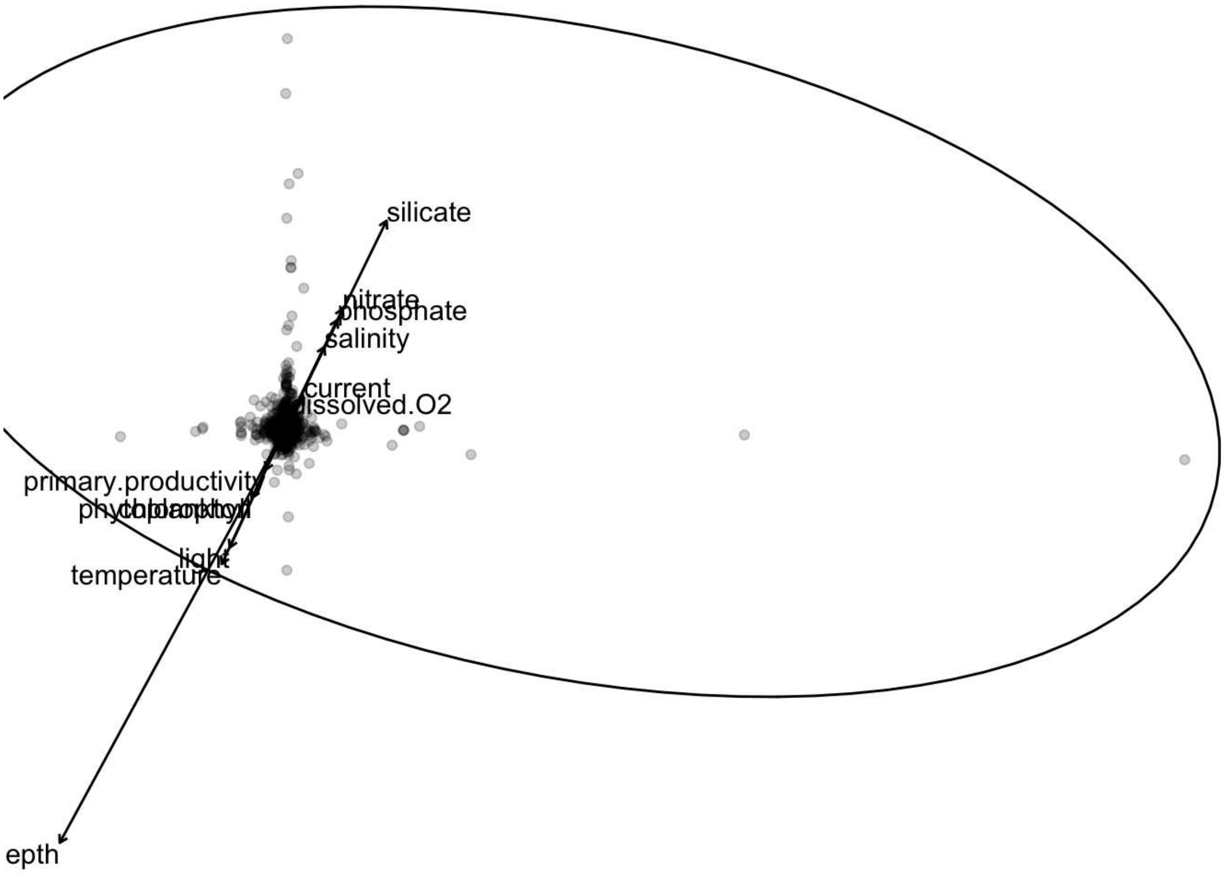
```
##
##
##
## Doing RDA for Monothalamea ...
## [1] "Proportion of variance explained:  0.455620109279718"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)    
## depth                   1   0.3550 28.2350  0.001 ***
## chlorophyll             1   0.0038  0.3031  0.893    
## current                 1   0.0155  1.2360  0.176    
## dissolved.O2            1   0.0086  0.6839  0.635    
## light                   1   0.0038  0.2997  1.000    
## nitrate                 1   0.0006  0.0496  1.000    
## phosphate               1   0.0017  0.1355  0.984    
## phytoplankton           1   0.0005  0.0402  1.000    
## primary.productivity    1   0.0004  0.0312  1.000    
## salinity                1   0.0007  0.0562  0.999    
## silicate                1   0.0113  0.9025  0.457    
## temperature             1   0.0014  0.1101  0.999    
## deep.pcnm$vectors    1204  14.6321  0.9667  0.634    
## Residual             1429  17.9645                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



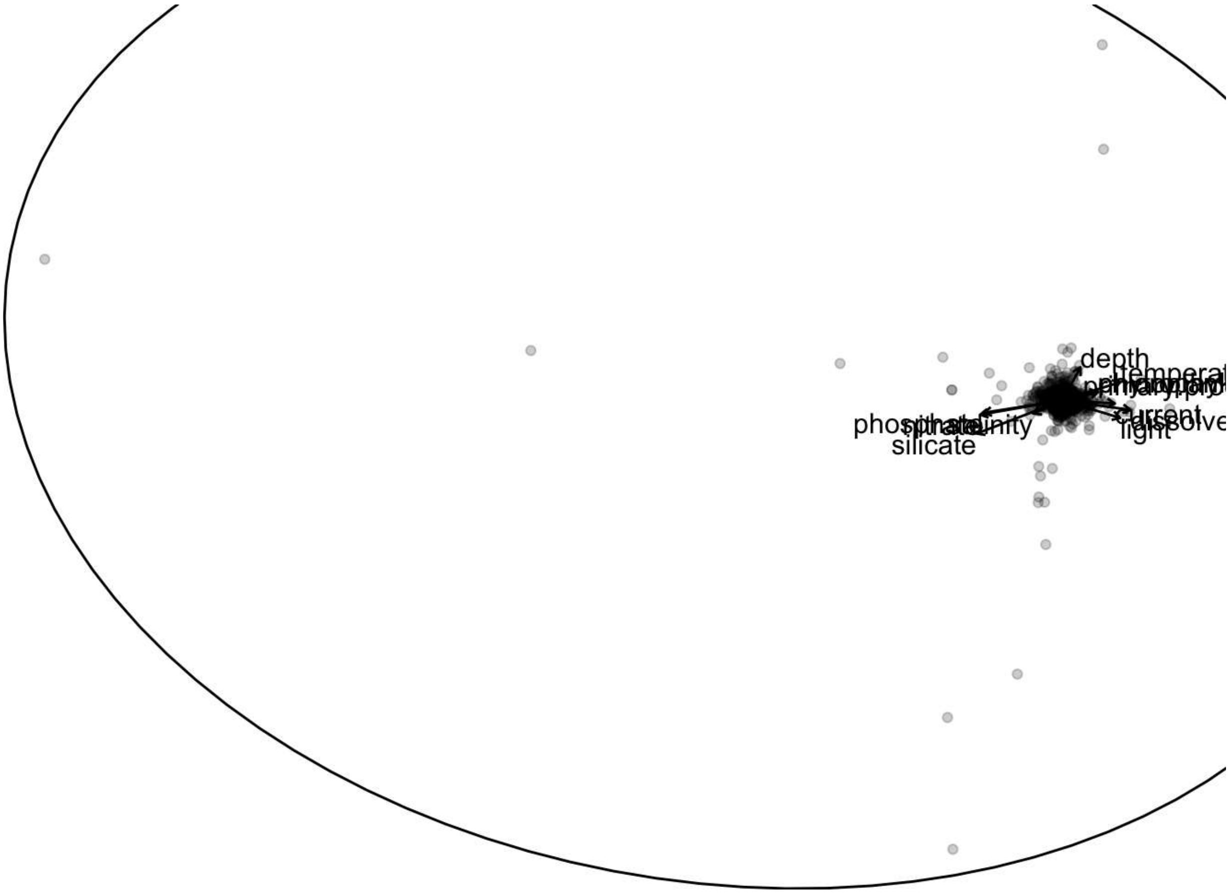
```
##
##
##
## Doing RDA for Calcarea ...
## [1] "Proportion of variance explained:  0.411898203369862"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0021 0.2148  0.975
## chlorophyll             1   0.0030 0.3002  0.854
## current                 1   0.0026 0.2650  0.972
## dissolved.O2            1   0.0106 1.0694  0.304
## light                   1   0.0122 1.2355  0.163
## nitrate                 1   0.0088 0.8924  0.522
## phosphate               1   0.0022 0.2240  0.946
## phytoplankton           1   0.0016 0.1586  0.982
## primary.productivity    1   0.0034 0.3397  0.755
## salinity                1   0.0029 0.2934  0.679
## silicate                1   0.0094 0.9501  0.429
## temperature             1   0.0024 0.2449  0.982
## deep.pcnm$vectors    1204   9.8244 0.8261  0.929
## Residual             1429  14.1144
```



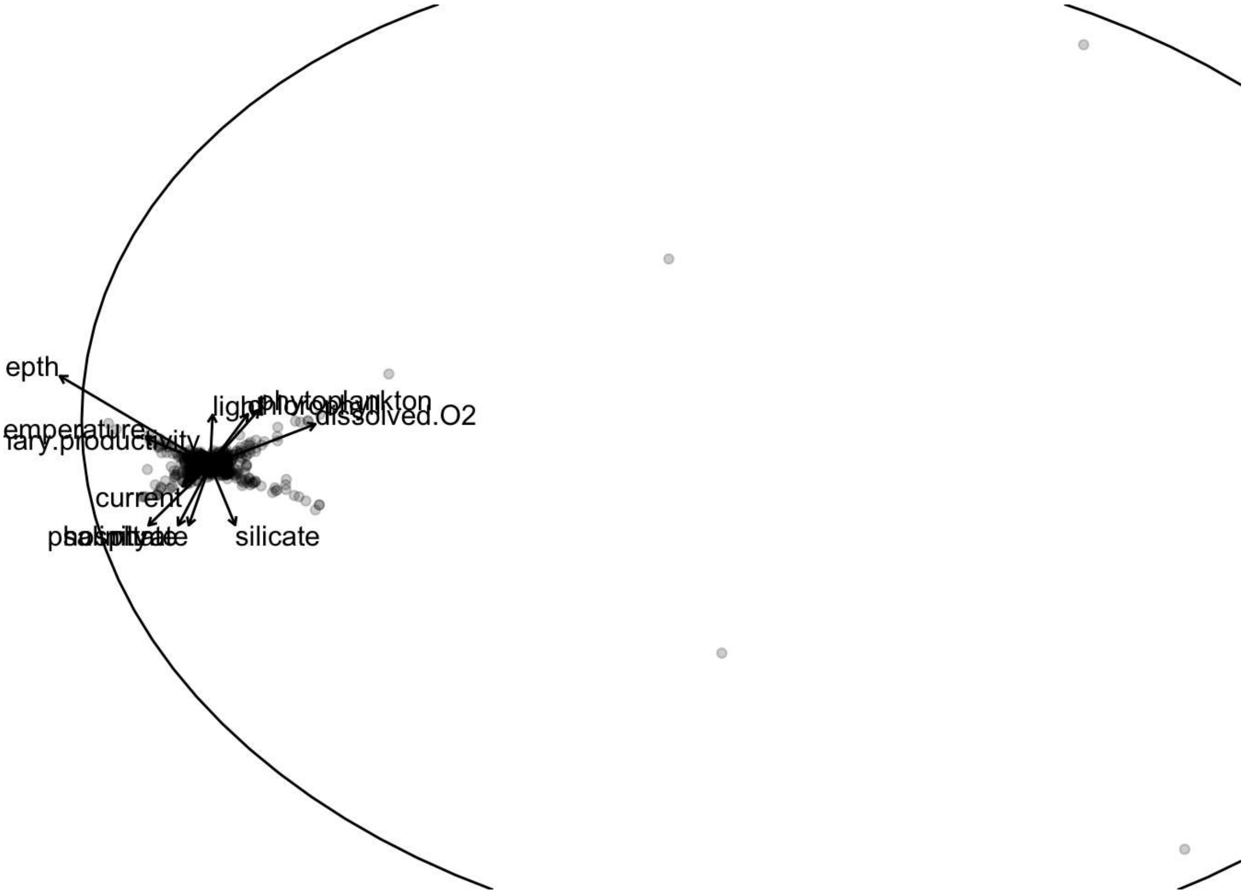
```
##
##
##
## Doing RDA for Sipunculidea ...
## [1] "Proportion of variance explained:  0.48978894055452"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)    
## depth                   1   0.0610 11.3834  0.001 ***
## chlorophyll             1   0.0011  0.2110  0.960    
## current                 1   0.0042  0.7763  0.421    
## dissolved.O2            1   0.0045  0.8493  0.495    
## light                   1   0.0030  0.5561  0.970    
## nitrate                 1   0.0050  0.9305  0.443    
## phosphate               1   0.0011  0.2062  0.935    
## phytoplankton           1   0.0010  0.1782  0.953    
## primary.productivity    1   0.0008  0.1534  0.939    
## salinity                1   0.0018  0.3281  0.581    
## silicate                1   0.0066  1.2320  0.275    
## temperature             1   0.0051  0.9455  0.400    
## deep.pcnm$vectors    1204   7.2518  1.1246  0.166    
## Residual             1429   7.6532                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



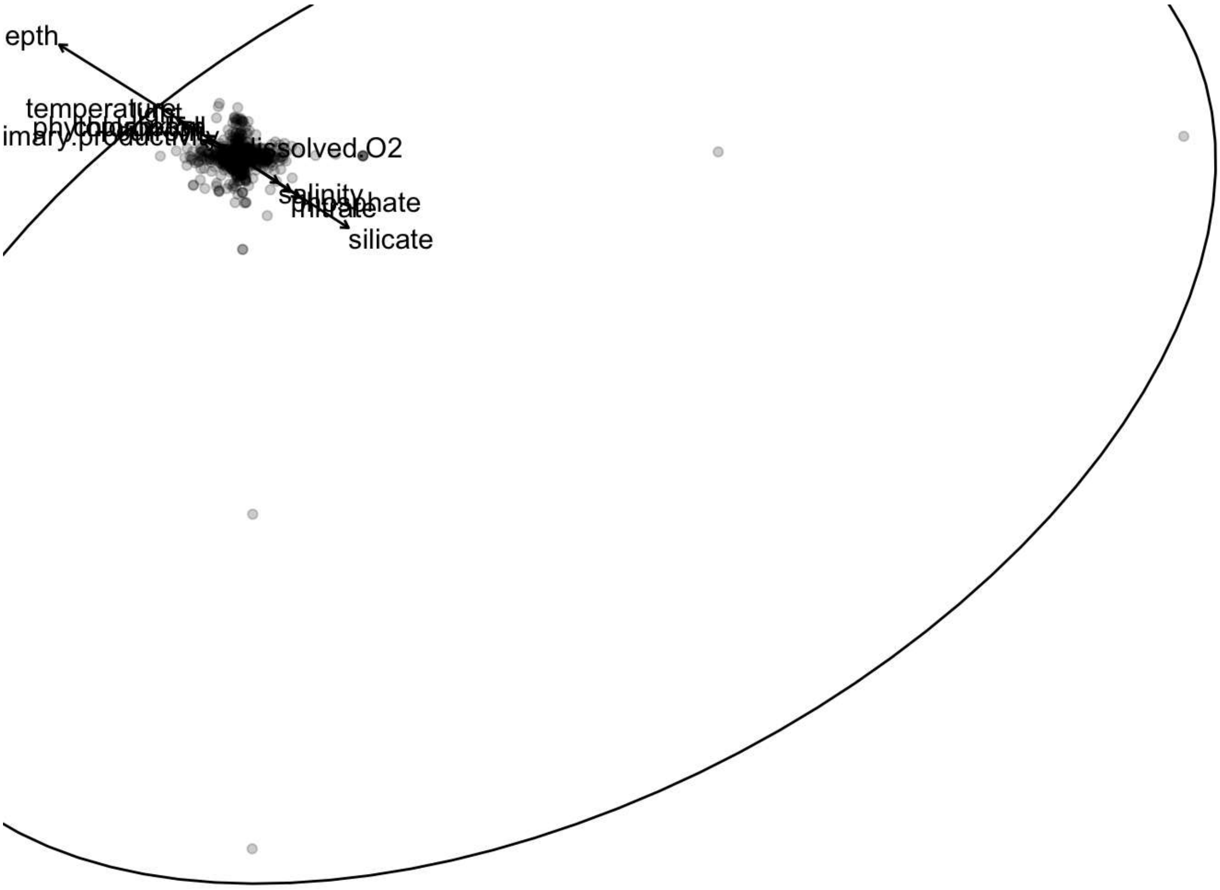
```
##
##
##
## Doing RDA for Thaliacea ...
## [1] "Proportion of variance explained:  0.458793077857427"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                         Df Variance      F Pr(>F)
## depth                    1   0.0073 0.8364  0.511
## chlorophyll              1   0.0021 0.2418  0.968
## current                  1   0.0031 0.3546  0.934
## dissolved.O2             1   0.0053 0.6057  0.853
## light                    1   0.0057 0.6488  0.963
## nitrate                  1   0.0035 0.4018  0.985
## phosphate                1   0.0027 0.3149  0.890
## phytoplankton            1   0.0004 0.0411  1.000
## primary.productivity    1   0.0016 0.1835  0.958
## salinity                 1   0.0006 0.0705  1.000
## silicate                 1   0.0103 1.1779  0.259
## temperature              1   0.0009 0.1026  1.000
## deep.pcnm$vectors    1204  10.5089 1.0020  0.516
## Residual             1429  12.4478
```



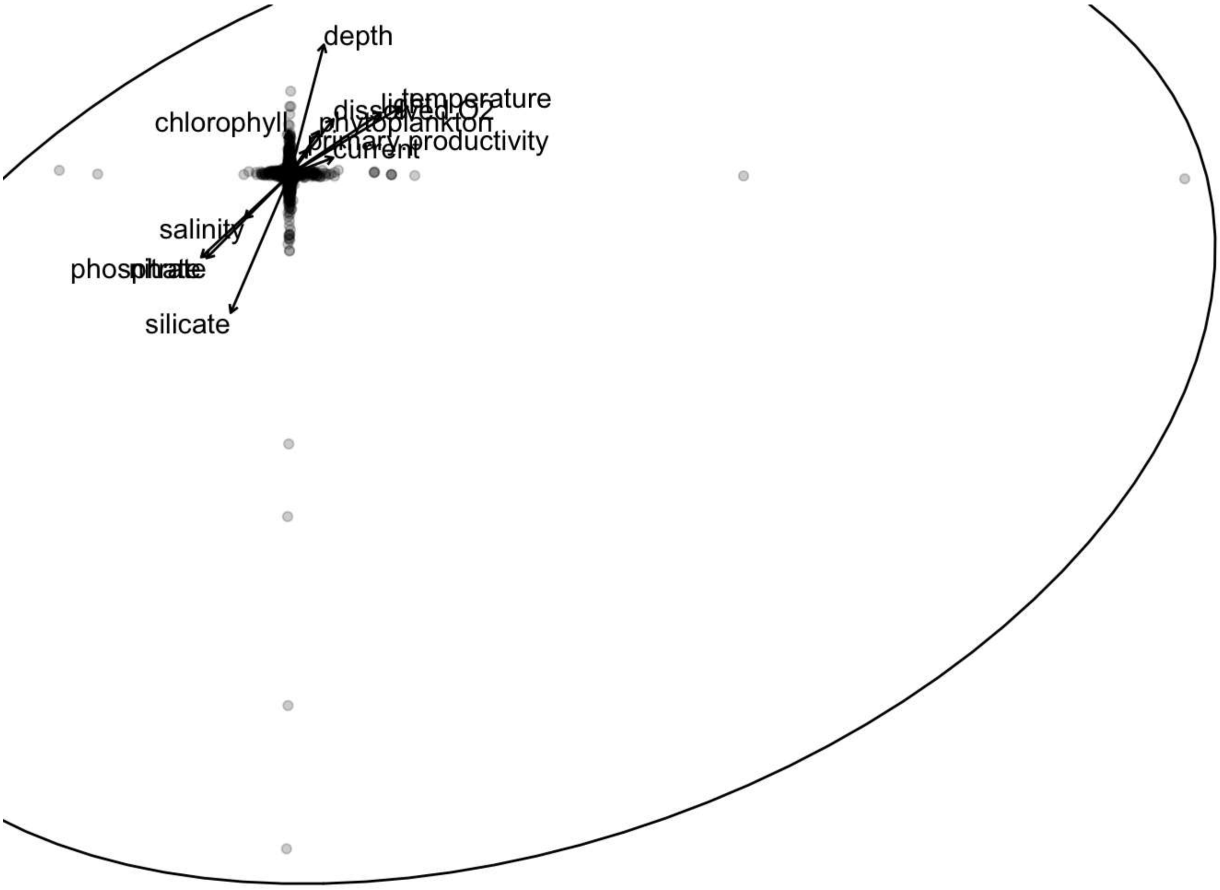
```
##
##
##
## Doing RDA for Heterotardigrada ...
## [1] "Proportion of variance explained:  0.425043125420224"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0152 1.7116  0.112
## chlorophyll             1   0.0068 0.7629  0.395
## current                 1   0.0126 1.4195  0.179
## dissolved.O2            1   0.0059 0.6701  0.731
## light                   1   0.0052 0.5825  0.975
## nitrate                 1   0.0043 0.4910  0.927
## phosphate               1   0.0028 0.3130  0.809
## phytoplankton           1   0.0106 1.1975  0.231
## primary.productivity    1   0.0052 0.5822  0.499
## salinity                1   0.0017 0.1875  0.897
## silicate                1   0.0027 0.3052  0.995
## temperature             1   0.0133 1.5002  0.190
## deep.pcnm$vectors    1204   9.2649 0.8693  0.872
## Residual             1429  12.6491
```



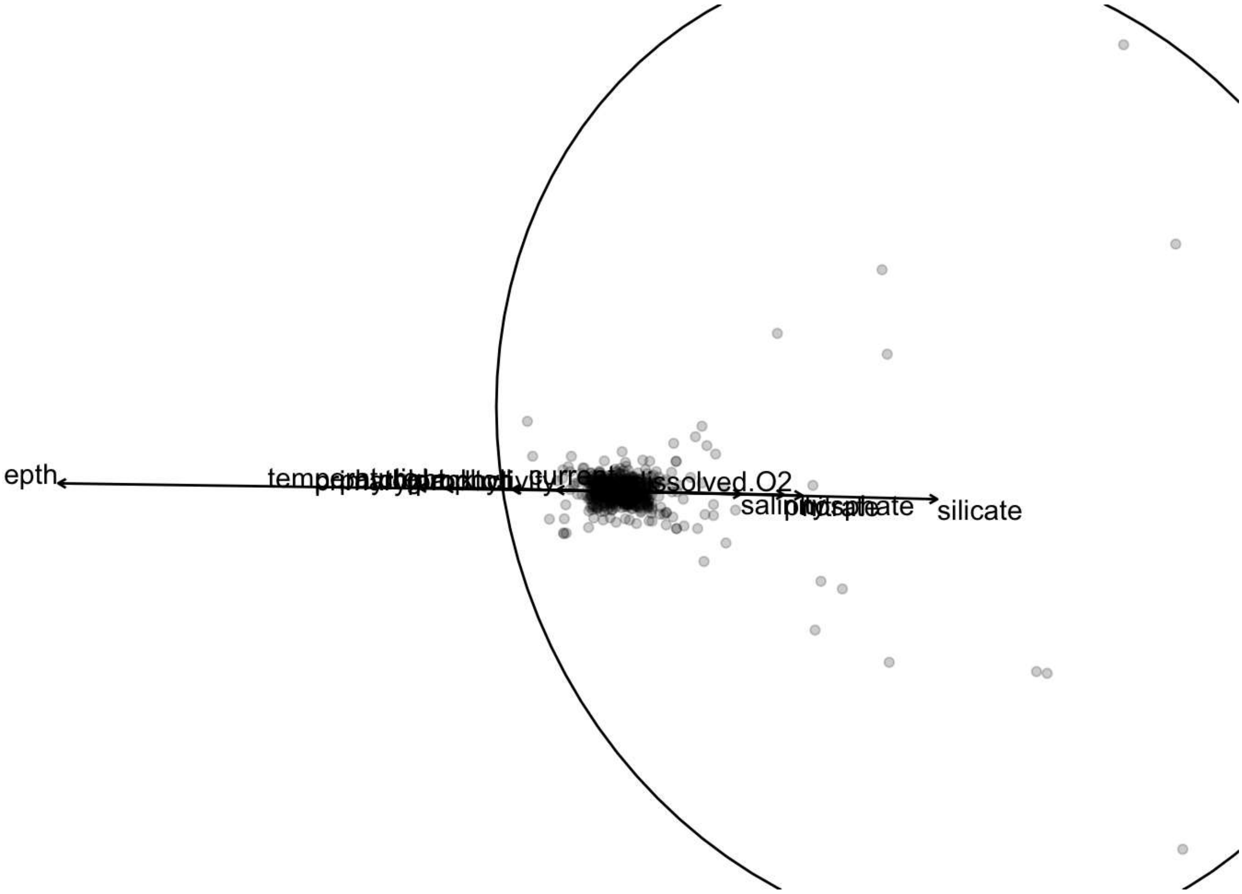
```
##
##
##
## Doing RDA for Appendicularia ...
## [1] "Proportion of variance explained:  0.509290878059112"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                         Df Variance      F Pr(>F)
## depth                   1   0.0305 5.9292  0.005 **
## chlorophyll             1   0.0032 0.6202  0.447
## current                 1   0.0007 0.1443  0.995
## dissolved.O2            1   0.0027 0.5305  0.777
## light                   1   0.0020 0.3950  0.992
## nitrate                 1   0.0016 0.3062  0.975
## phosphate               1   0.0009 0.1726  0.924
## phytoplankton           1   0.0014 0.2767  0.850
## primary.productivity    1   0.0012 0.2366  0.776
## salinity                1   0.0015 0.2991  0.571
## silicate                1   0.0008 0.1529  1.000
## temperature             1   0.0012 0.2416  0.936
## deep.pcnm$vectors    1204   7.5914 1.2241  0.023 *
## Residual             1429   7.3606
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



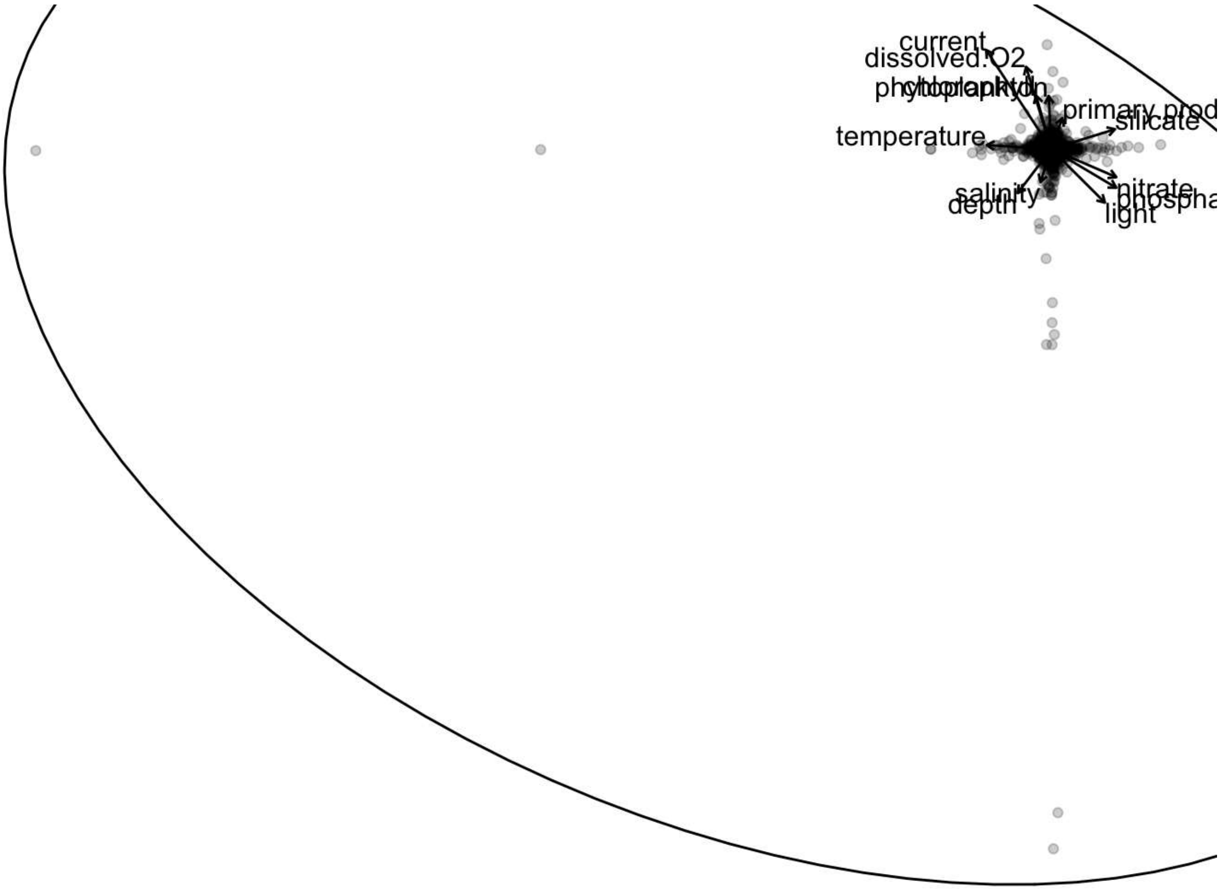
```
##
##
##
## Doing RDA for Enoplea ...
## [1] "Proportion of variance explained:  0.497235060280873"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0250 3.5494  0.009 **
## chlorophyll             1   0.0164 2.3292  0.071 .
## current                 1   0.0038 0.5384  0.641
## dissolved.O2            1   0.0078 1.1035  0.273
## light                   1   0.0060 0.8483  0.686
## nitrate                 1   0.0088 1.2576  0.191
## phosphate               1   0.0075 1.0601  0.178
## phytoplankton           1   0.0137 1.9539  0.103
## primary.productivity    1   0.0206 2.9333  0.046 *
## salinity                1   0.0032 0.4565  0.362
## silicate                1   0.0091 1.2878  0.217
## temperature             1   0.0099 1.4070  0.199
## deep.pcnm$vectors    1204   9.8129 1.1583  0.069 .
## Residual             1429  10.0553
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



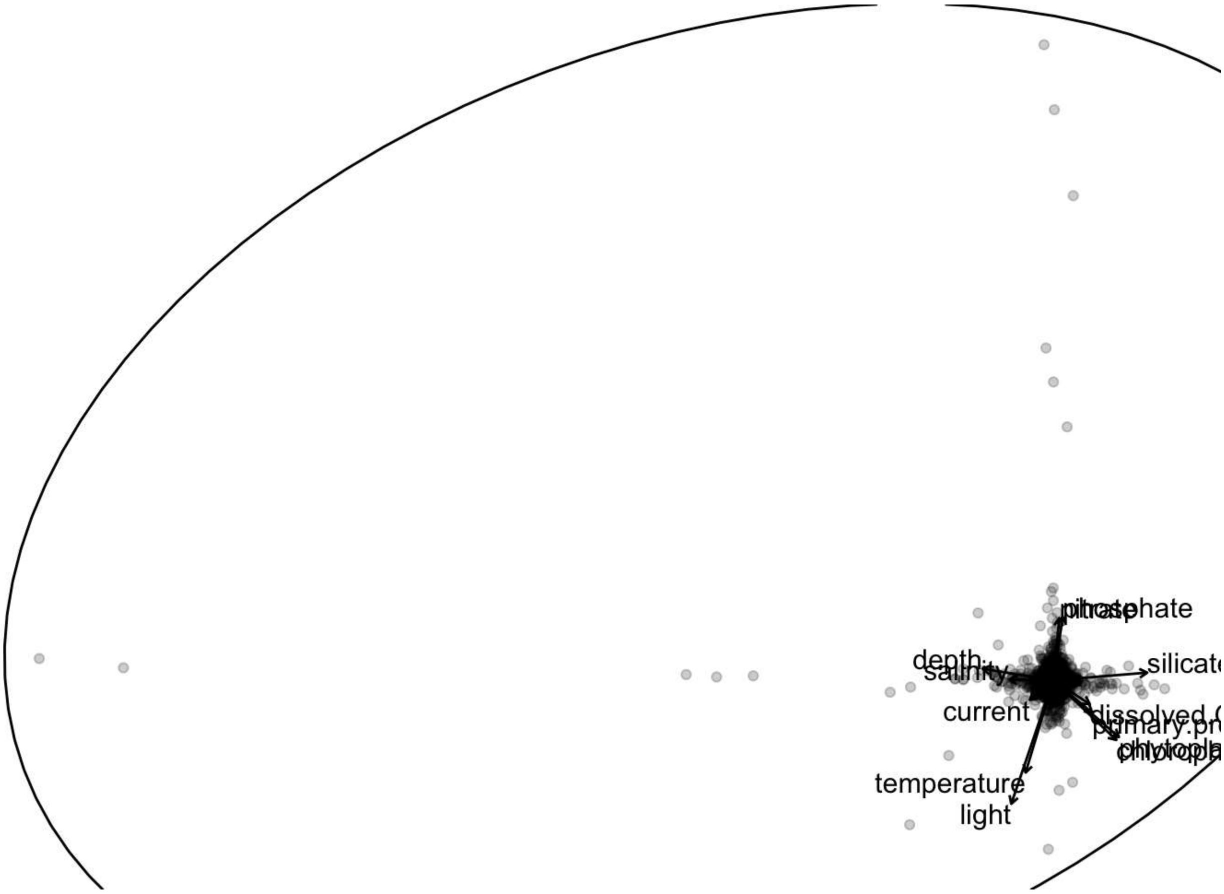
```
##
##
##
## Doing RDA for Globothalamea ...
## [1] "Proportion of variance explained:  0.491415423568282"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)
## depth                   1   0.1592 21.2943  0.001 ***
## chlorophyll             1   0.0017  0.2334  0.918
## current                 1   0.0062  0.8317  0.324
## dissolved.O2            1   0.0037  0.4890  0.788
## light                   1   0.0018  0.2466  0.999
## nitrate                 1   0.0004  0.0496  1.000
## phosphate               1   0.0002  0.0323  1.000
## phytoplankton           1   0.0001  0.0193  1.000
## primary.productivity    1   0.0007  0.0886  0.958
## salinity                1   0.0002  0.0265  1.000
## silicate                1   0.0010  0.1308  0.999
## temperature             1   0.0001  0.0140  1.000
## deep.pcnm$vectors    1204  10.1444  1.1273  0.237
## Residual             1429  10.6803
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



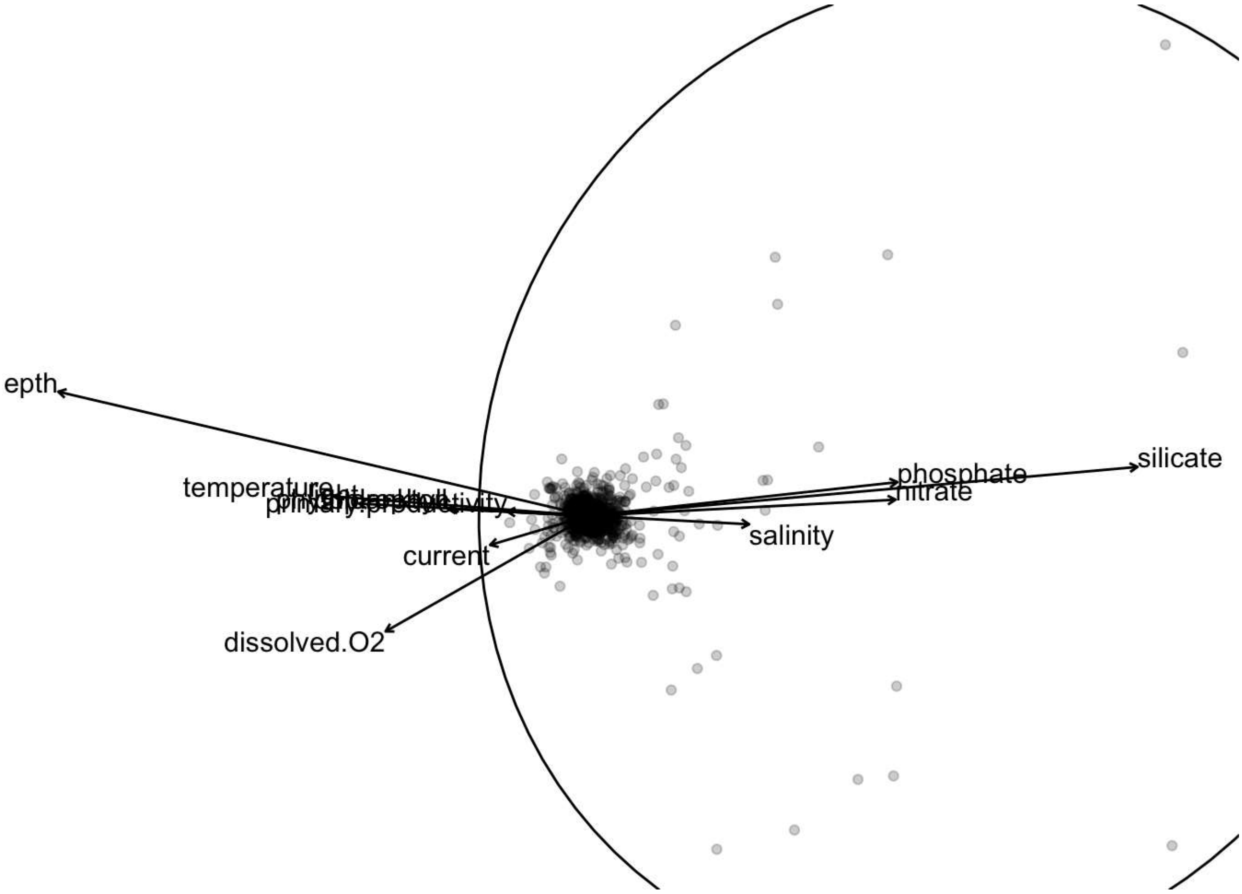
```
##
##
##
## Doing RDA for Maxillopoda ...
## [1] "Proportion of variance explained:  0.406745130388984"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0015 0.1951  0.974
## chlorophyll             1   0.0021 0.2872  0.850
## current                 1   0.0040 0.5365  0.622
## dissolved.O2            1   0.0017 0.2308  0.999
## light                   1   0.0094 1.2592  0.163
## nitrate                 1   0.0049 0.6555  0.768
## phosphate               1   0.0021 0.2819  0.861
## phytoplankton           1   0.0013 0.1734  0.968
## primary.productivity    1   0.0005 0.0638  1.000
## salinity                1   0.0012 0.1595  0.953
## silicate                1   0.0070 0.9324  0.501
## temperature             1   0.0017 0.2294  0.978
## deep.pcnm$vectors    1204   7.2840 0.8096  0.953
## Residual             1429  10.6786
```



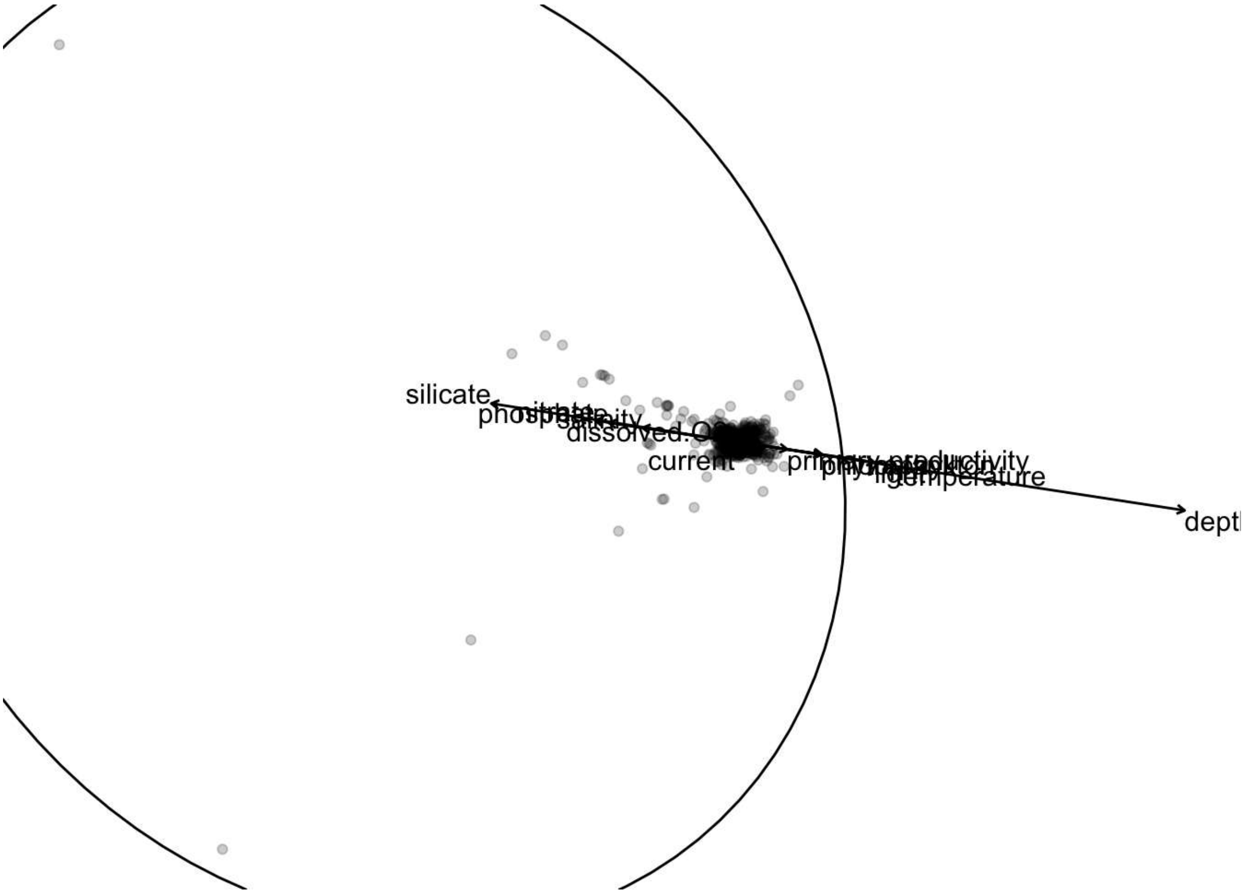
```
##
##
##
## Doing RDA for Myxini ...
## [1] "Proportion of variance explained:  0.335609338192593"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0010 0.1566  0.995
## chlorophyll             1   0.0020 0.3006  0.765
## current                 1   0.0029 0.4407  0.677
## dissolved.O2            1   0.0022 0.3424  0.957
## light                   1   0.0052 0.7925  0.747
## nitrate                 1   0.0036 0.5579  0.790
## phosphate               1   0.0009 0.1377  0.968
## phytoplankton           1   0.0009 0.1346  0.959
## primary.productivity    1   0.0009 0.1332  0.926
## salinity                1   0.0006 0.0975  0.985
## silicate                1   0.0071 1.0980  0.325
## temperature             1   0.0010 0.1570  0.982
## deep.pcnm$vectors    1204   4.6702 0.5959  0.998
## Residual             1429   9.3015
```



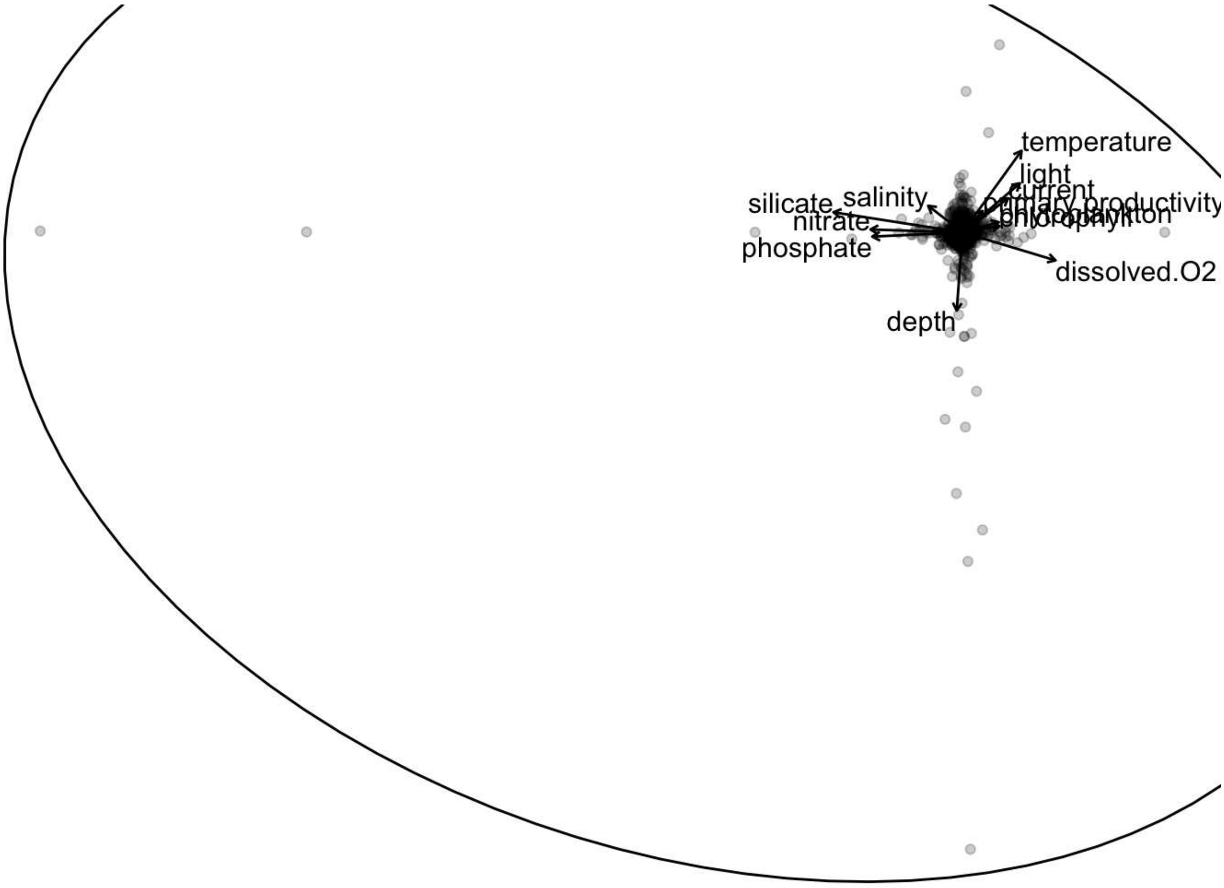
```
##
##
##
## Doing RDA for Solenogastres ...
## [1] "Proportion of variance explained:  0.4506232614491"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)
## depth                   1   0.0714 14.2832  0.001 ***
## chlorophyll             1   0.0002  0.0440  1.000
## current                 1   0.0007  0.1301  0.997
## dissolved.O2            1   0.0096  1.9253  0.082 .
## light                   1   0.0009  0.1760  1.000
## nitrate                 1   0.0016  0.3279  0.944
## phosphate               1   0.0076  1.5115  0.100 .
## phytoplankton           1   0.0015  0.2974  0.829
## primary.productivity    1   0.0001  0.0279  1.000
## salinity                1   0.0026  0.5122  0.330
## silicate                1   0.0502 10.0513  0.001 ***
## temperature             1   0.0069  1.3822  0.218
## deep.pcnm$vectors    1204   5.7048  0.9481  0.693
## Residual             1429   7.1419
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



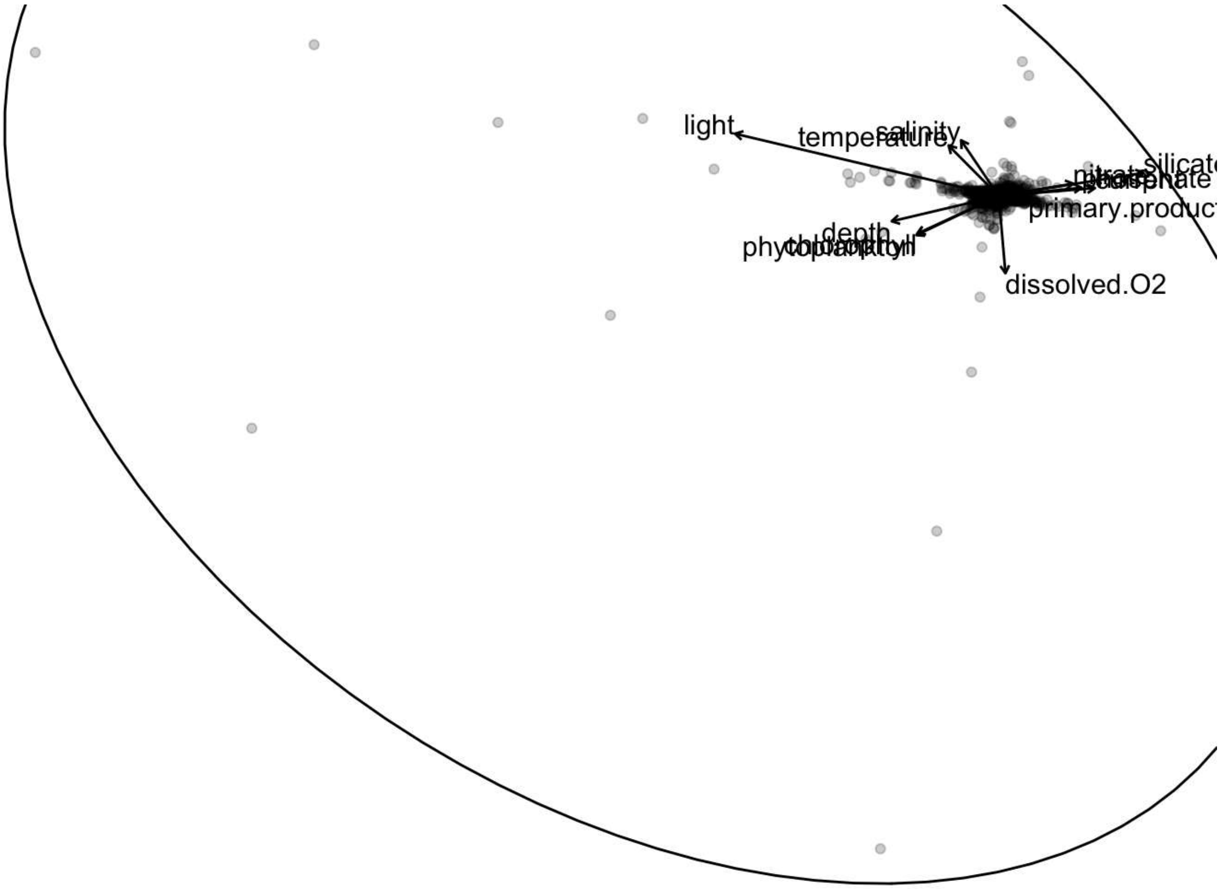
```
##
##
##
## Doing RDA for Bacillariophyceae ...
## [1] "Proportion of variance explained:  0.394768323907214"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)
## depth                   1   0.0911 17.9294  0.001 ***
## chlorophyll             1   0.0010  0.1910  0.880
## current                 1   0.0028  0.5495  0.480
## dissolved.O2            1   0.0018  0.3549  0.803
## light                   1   0.0010  0.1956  0.985
## nitrate                 1   0.0001  0.0216  0.999
## phosphate               1   0.0000  0.0033  1.000
## phytoplankton           1   0.0001  0.0137  1.000
## primary.productivity    1   0.0001  0.0184  0.996
## salinity                1   0.0000  0.0037  1.000
## silicate                1   0.0002  0.0323  1.000
## temperature             1   0.0000  0.0091  1.000
## deep.pcnm$vectors    1204   4.6390  0.7581  0.873
## Residual             1429   7.2628
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



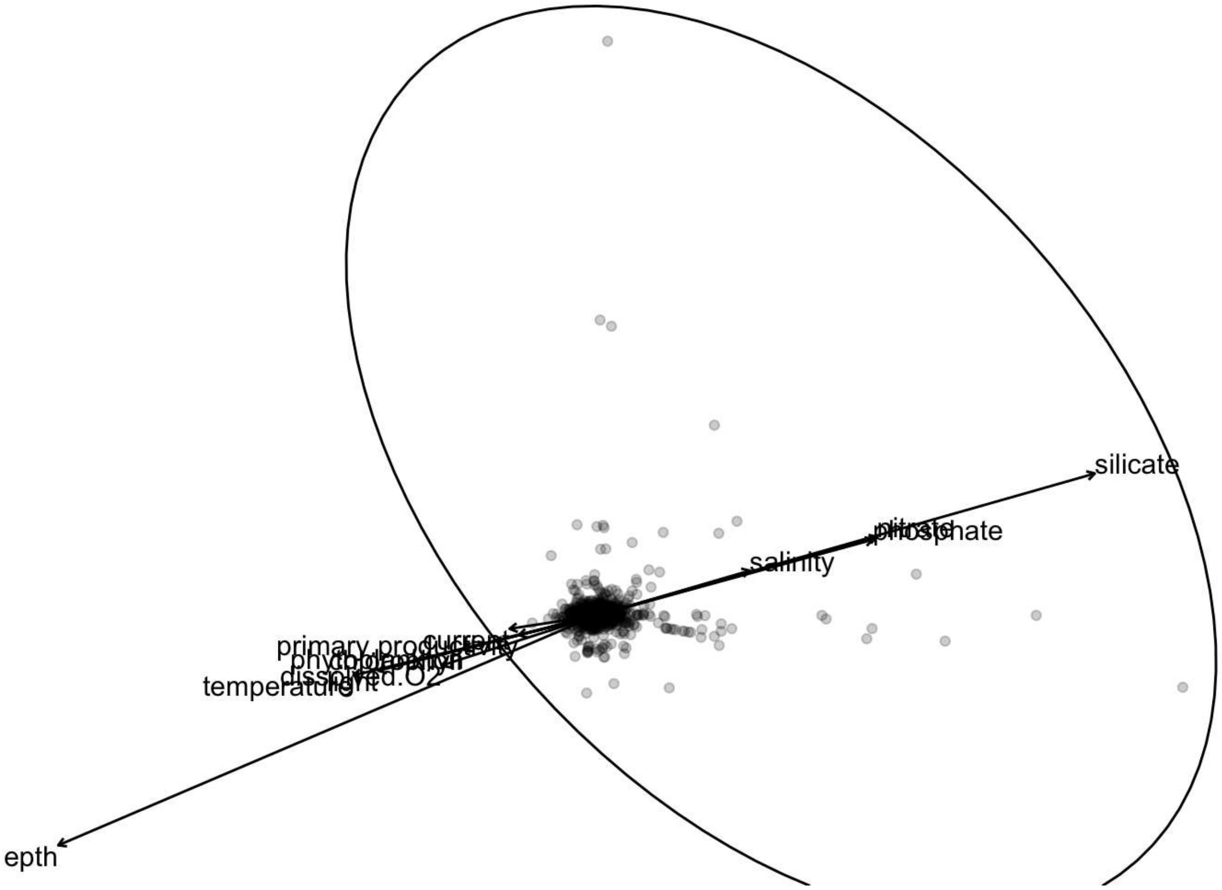
```
##
##
##
## Doing RDA for Enopla ...
## [1] "Proportion of variance explained:  0.475585787732099"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0073 1.9807  0.102
## chlorophyll             1   0.0015 0.4092  0.601
## current                 1   0.0009 0.2568  0.924
## dissolved.O2            1   0.0054 1.4634  0.158
## light                   1   0.0027 0.7428  0.821
## nitrate                 1   0.0032 0.8588  0.511
## phosphate               1   0.0014 0.3937  0.640
## phytoplankton           1   0.0003 0.0742  0.988
## primary.productivity    1   0.0009 0.2542  0.774
## salinity                1   0.0008 0.2075  0.795
## silicate                1   0.0039 1.0623  0.358
## temperature             1   0.0056 1.5352  0.200
## deep.pcnm$vectors    1204   4.7220 1.0687  0.354
## Residual             1429   5.2441
```



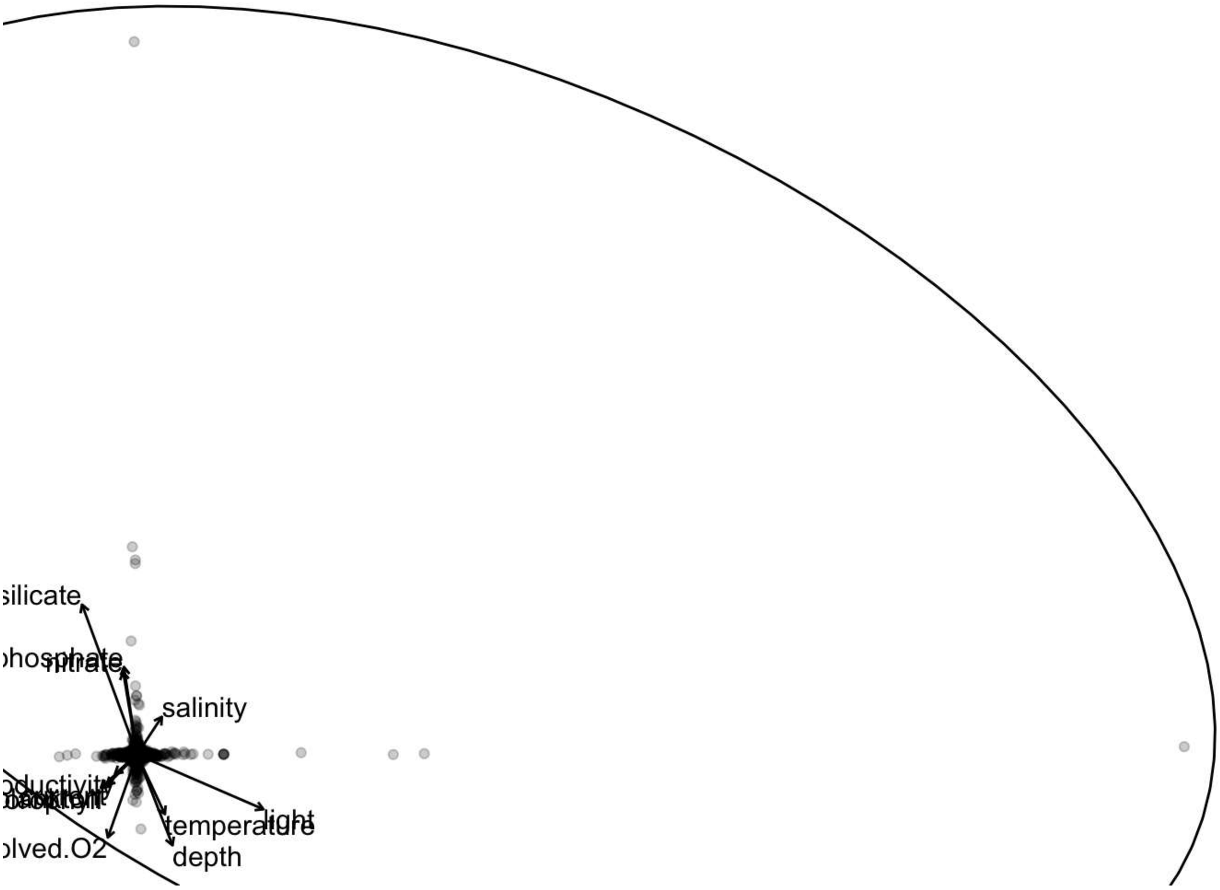
```
##
##
##
## Doing RDA for Homoscleromorpha ...
## [1] "Proportion of variance explained:  0.361927542261536"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0011 0.2235  0.919
## chlorophyll             1   0.0030 0.6083  0.428
## current                 1   0.0025 0.5009  0.622
## dissolved.O2            1   0.0043 0.8765  0.482
## light                   1   0.0062 1.2587  0.169
## nitrate                 1   0.0066 1.3356  0.161
## phosphate               1   0.0019 0.3813  0.669
## phytoplankton           1   0.0031 0.6364  0.534
## primary.productivity    1   0.0063 1.2866  0.130
## salinity                1   0.0033 0.6649  0.184
## silicate                1   0.0037 0.7485  0.654
## temperature             1   0.0052 1.0499  0.337
## deep.pcnm$vectors    1204   3.9342 0.6653  0.999
## Residual             1429   7.0188
```



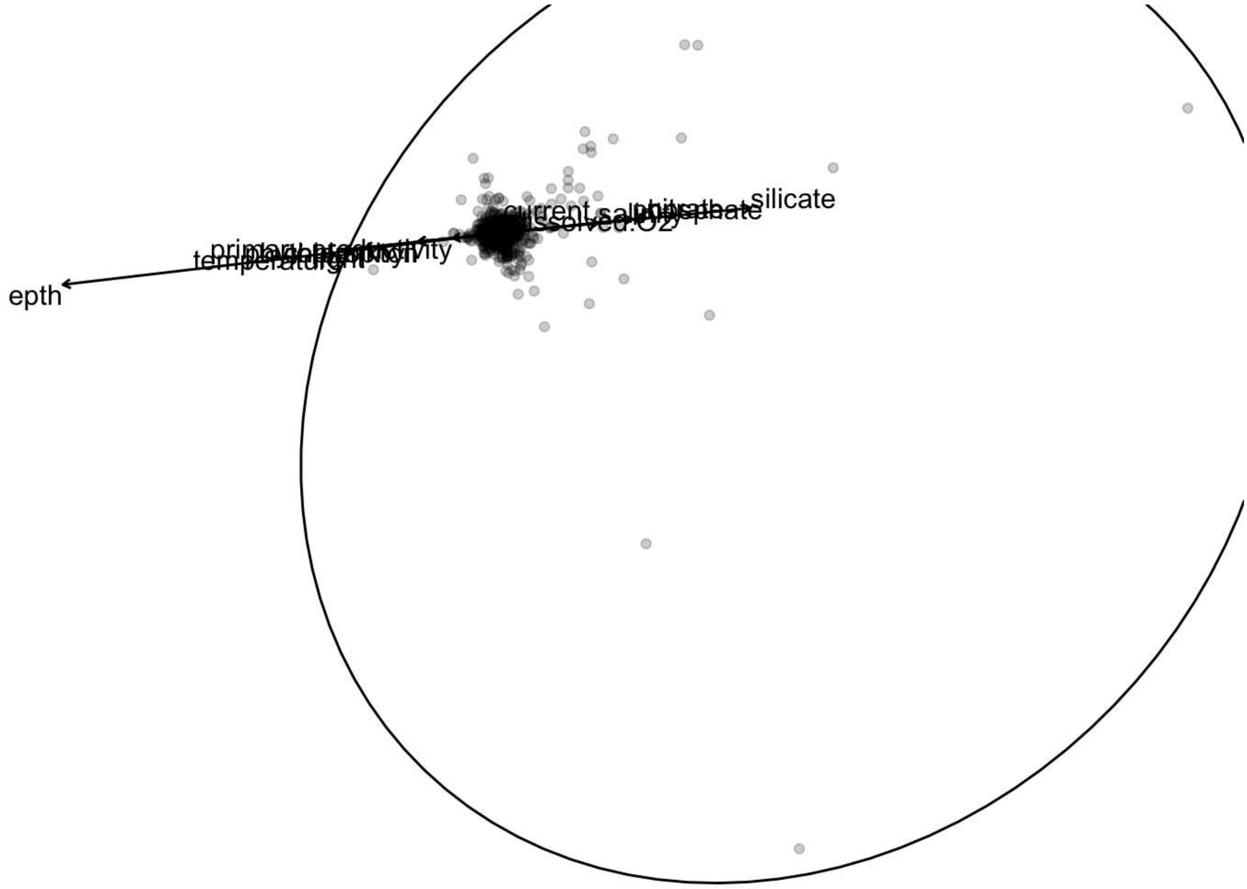
```
##
##
##
## Doing RDA for Hoplonemertea ...
## [1] "Proportion of variance explained:  0.414453787638238"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)    
## depth                   1   0.0554 12.2904  0.001 ***
## chlorophyll             1   0.0010  0.2123  0.978    
## current                 1   0.0025  0.5567  0.610    
## dissolved.O2            1   0.0073  1.6249  0.106    
## light                   1   0.0017  0.3794  0.996    
## nitrate                 1   0.0020  0.4532  0.893    
## phosphate               1   0.0042  0.9224  0.238    
## phytoplankton           1   0.0006  0.1255  0.992    
## primary.productivity    1   0.0026  0.5724  0.471    
## salinity                1   0.0019  0.4228  0.464    
## silicate                1   0.0241  5.3559  0.001 ***
## temperature             1   0.0026  0.5844  0.679    
## deep.pcnm$vectors    1204   4.4531  0.8206  0.965    
## Residual             1429   6.4410                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
##
##
## Doing RDA for Stenolaemata ...
## [1] "Proportion of variance explained:  0.335033450026453"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance      F Pr(>F)
## depth                   1   0.0023 0.4566  0.536
## chlorophyll             1   0.0011 0.2200  0.810
## current                 1   0.0011 0.2100  0.884
## dissolved.O2            1   0.0025 0.4964  0.709
## light                   1   0.0061 1.2012  0.298
## nitrate                 1   0.0008 0.1597  0.970
## phosphate               1   0.0023 0.4444  0.440
## phytoplankton           1   0.0009 0.1844  0.802
## primary.productivity    1   0.0011 0.2093  0.669
## salinity                1   0.0008 0.1580  0.788
## silicate                1   0.0094 1.8436  0.112
## temperature             1   0.0023 0.4575  0.621
## deep.pcnm$vectors    1204   3.6544 0.5930  0.971
## Residual             1429   7.3146
```



```
##
##
##
## Doing RDA for Tubothalamea ...
## [1] "Proportion of variance explained:  0.472016532418596"
## Permutation test for rda under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## Model: rda(formula = this.species.df ~ depth + chlorophyll + current + dissolve
d.O2 + light + nitrate + phosphate + phytoplankton + primary.productivity + salinit
y + silicate + temperature + deep.pcnm$vectors, data = env.df, scale = TRUE, na.act
ion = "na.exclude")
##                        Df Variance       F Pr(>F)
## depth                   1   0.0902 22.2029  0.001 ***
## chlorophyll             1   0.0010  0.2351  0.904
## current                 1   0.0040  0.9906  0.261
## dissolved.O2            1   0.0017  0.4284  0.829
## light                   1   0.0009  0.2270  0.997
## nitrate                 1   0.0001  0.0214  1.000
## phosphate               1   0.0000  0.0099  1.000
## phytoplankton           1   0.0001  0.0154  0.999
## primary.productivity    1   0.0001  0.0249  1.000
## salinity                1   0.0001  0.0166  1.000
## silicate                1   0.0005  0.1239  0.999
## temperature             1   0.0001  0.0157  1.000
## deep.pcnm$vectors    1204   5.0934  1.0409  0.468
## Residual             1429   5.8078
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


current
salinity
phosphate
silicate
dissolved.O2
primary productivity
temperature
light
epth