Summary

MD

22 Jan. 2019

Prolog, files summary

```
list.files("../../3._Data/5b._Data_clean/")
```

```
##  [1] "1982_2017_unsuitable_pools_only_ver2.csv"
##  [2] "2009_2017-2_fish_ver2.csv"
##  [3] "2009_2017-2_holds_no_water_ver2.csv"
##  [4] "all_cov_scaled.RDS"
##  [5] "colored_for_data_archive"
##  [6] "Daphnia_dynamics_1982_2017_2.csv"
##  [7] "Data_hydroperiod_Means.csv"
##  [8] "distances_matrix.RDS"
##  [9] "dry_wet_82-17_core.RDS"
## [10] "environment_PCA.RDS"
## [11] "environment_PCA_reduced.RDS"
## [12] "Island_measures_vers4.csv"
## [13] "islands_groups100.RDS"
## [14] "islands_groups200.RDS"
## [15] "MetapopData_pH_conductivity_1998_2017.csv"
## [16] "occupancies_longispina_82-17_core.RDS"
## [17] "occupancies_magna_82-17_core.RDS"
## [18] "occupancies_pulex_82-17_core.RDS"
## [19] "plantcover_2013_2017.csv"
## [20] "Pools_coordinates_2017_vers7.csv"
## [21] "Pools_hard_data_vers12.csv"
## [22] "Pools_hard_data_vers12.xls"
## [23] "revisit.longispina.RDS"
## [24] "revisit.magna.RDS"
## [25] "revisit.pulex.RDS"
## [26] "Summary_of_data_metapopulation_ver2.docx"
## [27] "temp_rain_TZS_1970_2005.xls"
## [28] "temp_rain_TZS_2006-2017.xlsx"
## [29] "VIP_DEdata5.csv"
## [30] "WindSpeed_Russaro_2006-2018.csv"
```

This is the last files pack, all files are up-to-date. RDS files correspond to outputs from this script. Note that i changed format from .xls to .csv for some files (e.g., hard_data, because it is more easy to import into R without additional package)

I. Occupancies data

```
#### Get occupancy data ####
data <- read.csv("../../3._Data/5b._Data_clean/Daphnia_dynamics_1982_2017_2.csv", h = T)

# Compute total number of sites, and make distinction between sites sampled since 1982 and others (adde
nb.sites.total = length(unique(data$poolname))
id.sites.total = as.character(data$poolname)
visites.bySite = table(data$poolname)

# Keep only ponds with a complete history
nb.visites = (36 * 2)  # 1982 -> 2017 : 36 y * 2 samples
nb.sites.core = sum(visites.bySite == nb.visites)
nb.sites.added = sum(visites.bySite != nb.visites)
id.sites.core = names(which(visites.bySite == nb.visites))
id.sites.added = names(which(visites.bySite != nb.visites))

# Well, when looking into harddata file, N-28 is weird (because of split, right ?)
# Easier to remove it. (N-28A is already removed)

id.sites.core <- id.sites.core[id.sites.core != "N-28"]
```

Splite samples S1 & S2, create sites by years matrices by species & by samples, and save them

```
# Split samples
data.sample1 <- data[data$sample == 1 & as.character(data$poolname) %in% id.sites.core, ]
data.sample2 <- data[data$sample == 2 & as.character(data$poolname) %in% id.sites.core, ]

# Create sites by years matrix for the each species (x3) and for each visit (x2)
occupancy.magna.s1 <- acast(data.sample1[, c("year", "magna", "poolname")], poolname ~ year, value.var =
occupancy.longispina.s1 <- acast(data.sample1[, c("year", "longispina", "poolname")], poolname ~ year,
    value.var = "longispina")
occupancy.pulex.s1 <- acast(data.sample1[, c("year", "pulex", "poolname")], poolname ~ year, value.var =
occupancy.magna.s2 <- acast(data.sample2[, c("year", "magna", "poolname")], poolname ~ year, value.var =
occupancy.longispina.s2 <- acast(data.sample2[, c("year", "longispina", "poolname")], poolname ~ year,
    value.var = "longispina")
occupancy.pulex.s2 <- acast(data.sample2[, c("year", "pulex", "poolname")], poolname ~ year, value.var =

# Then create lists & save them as .RDS
occupancies.longispina.82_17.core = list(occupancy.longispina.s1, occupancy.longispina.s2)
occupancies.magna.82_17.core = list(occupancy.magna.s1, occupancy.magna.s2)
occupancies.pulex.82_17.core = list(occupancy.pulex.s1, occupancy.pulex.s2)

## Create line number for islands groups
saveRDS(list(grep("^F-|^FO-|^FS-|^FW-|^FSS-|^LA-", rownames(occupancy.magna.s1)),
             grep("^G-", rownames(occupancy.magna.s1)),
             grep("^K-|^M-|^LON-|^LONA-|^LG-", rownames(occupancy.magna.s1)),
             grep("^N-", rownames(occupancy.magna.s1)),
             grep("^SK-|^SKN-|^SKO-|^SKW-", rownames(occupancy.magna.s1))), "./data/islandsGroups.RDS")

# Let as comments, already done once, useless to do it each time
# saveRDS(occupancies.longispina.82_17.core,
# './data/occupancies_longispina_82-17_core.RDS')
```

```
# saveRDS(occupancies.magna.82_17.core, './data/occupancies_magna_82-17_core.RDS')
# saveRDS(occupancies.pulex.82_17.core, './data/occupancies_pulex_82-17_core.RDS')
```

Things that can be change / upgrade :

- Adding sites which are not in the core set (using 1982_2017_unsuitable_pools_only_ver2)

II. Take a look at sites state (w/d)

```
# Sometimes, value is 'y ' instead of 'y', i replaced the former by the later Then, change to numeric
# values : n = 0, y = 1

data$water <- as.character(data$water)
data$water[data$water == "y " & !is.na(data$water)] <- "y"
data$water[data$water == "y"] <- 1
data$water[data$water == "n"] <- 0
data$water <- as.numeric(data$water)

# First, as previously, only take core sites
dt.sample1 = data[data$sample == 1 & as.character(data$poolname) %in% id.sites.core, ]
dt.sample2 = data[data$sample == 2 & as.character(data$poolname) %in% id.sites.core, ]
```

Since dry/wet state only affects links between observations and the true state, more exactly, the detectability is the only thing which depends on those d/w states, and actually, it is estimated only in wet sites since we assume that detectability is 0 in dry site. Because of this, we can replace NA's by dry or wet (needed for the model, it cannot deal with NA here) without any effect on estimates. I choosed to put dry (0).

```
# Create both matrices

dt.sample1[dt.sample1$year == 1982, "water"] <- 0
dt.sample1[is.na(dt.sample1$water), "water"] <- 0
dt.sample2[is.na(dt.sample2$water), "water"] <- 0

dry_wet_state.sample1 <- acast(dt.sample1[, c("year", "water", "poolname")], poolname ~ year, value.var
dry_wet_state.sample2 <- acast(dt.sample2[, c("year", "water", "poolname")], poolname ~ year, value.var

# #Save d/w states
# saveRDS(list(dry_wet_state.sample1,dry_wet_state.sample2),'./data/dry_wet_82-17_core.RDS')
```

For estimations, that does not really make sense to fit an additional paramter for the persistence in dry site since all ponds can go through cycles of dry/wet states within a season.

Thus, these information should be used only in the detectability issue. Meaning, assuming that detection is zero in dry site, but species can be present (see V.2.1).

III. Spatialized aspects

III.1 Baseline distance matrix

```r
# Need to include {geosphere} package to compute distances among sites; igraph can be used for doing
# various things on the adjacency matrix (on the network) e.g., compute sites groups (modularity)
library(geosphere)
```

```
## The legacy packages maptools, rgdal, and rgeos, underpinning the sp package,
## which was just loaded, will retire in October 2023.
## Please refer to R-spatial evolution reports for details, especially
## https://r-spatial.org/r/2023/05/15/evolution4.html.
## It may be desirable to make the sf package available;
## package maintainers should consider adding sf to Suggests:.
## The sp package is now running under evolution status 2
##      (status 2 uses the sf package in place of rgdal)
```

```r
require(igraph)
```

```
## Le chargement a nécessité le package : igraph

## Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
## logical.return = TRUE, : aucun package nommé 'igraph' n'est trouvé
```

```r
# Get sites positions & keep only core sites
sites.position <- read.csv("../../3._Data/5b._Data_clean/Pools_coordinates_2017_vers7.csv", h = T, sep =
    dec = ",")

sites.position.core <- sites.position[sites.position$name %in% id.sites.core, ]
sites.position.added <- sites.position[sites.position$name %in% id.sites.added, ]
sites.position.total <- sites.position[sites.position$name %in% id.sites.total, ]

## Ordering site as other data...
sites.position.core = sites.position.core[order(sites.position.core$name),c(1,14,11)]

saveRDS(sites.position.core, "./data/sites.positions.RDS")

# Compute distances among sites, output a distances matrix using distVincentEllipsoid function.
# distance.euclidean=distm(sites.position.core[,c(2,3)], sites.position.core[,c(2,3)],fun=distVincentyE


# As previously, already done, unnecessary to do it again
# saveRDS(distance.euclidean,'./data/distances_matrix.RDS')

# Plot, not really readable + can be used to compute e.g., islands group

# g <- graph.adjacency(distance.euclidean, weighted = T) lo <-
# layout.norm(as.matrix(sites.position[,c(6,5)]))

## walktrap.community(g) plot(cluster_fast_greedy(as.undirected(g)),g, layout = lo, vertex.size = 1)
```

Note that for now, it is only a distance matrix. Can be used as a baseline to complexify connectivity matrix.

Possible changes :

- Separate islands groups

- Separate islands
- Include watersheet (directionnality)
- Change to resistance map

III.2. Watersheet

```
# Watersheet are included in the harddata file
sites.harddata <- read.csv("../../3._Data/5b._Data_clean/Pools_hard_data_vers12.csv", h = T, sep = ";")
sites.harddata <- sites.harddata[as.character(sites.harddata$poolname) %in% id.sites.core, ]
```

Do not use this for now. **To update.**

IV. Environmental covariates

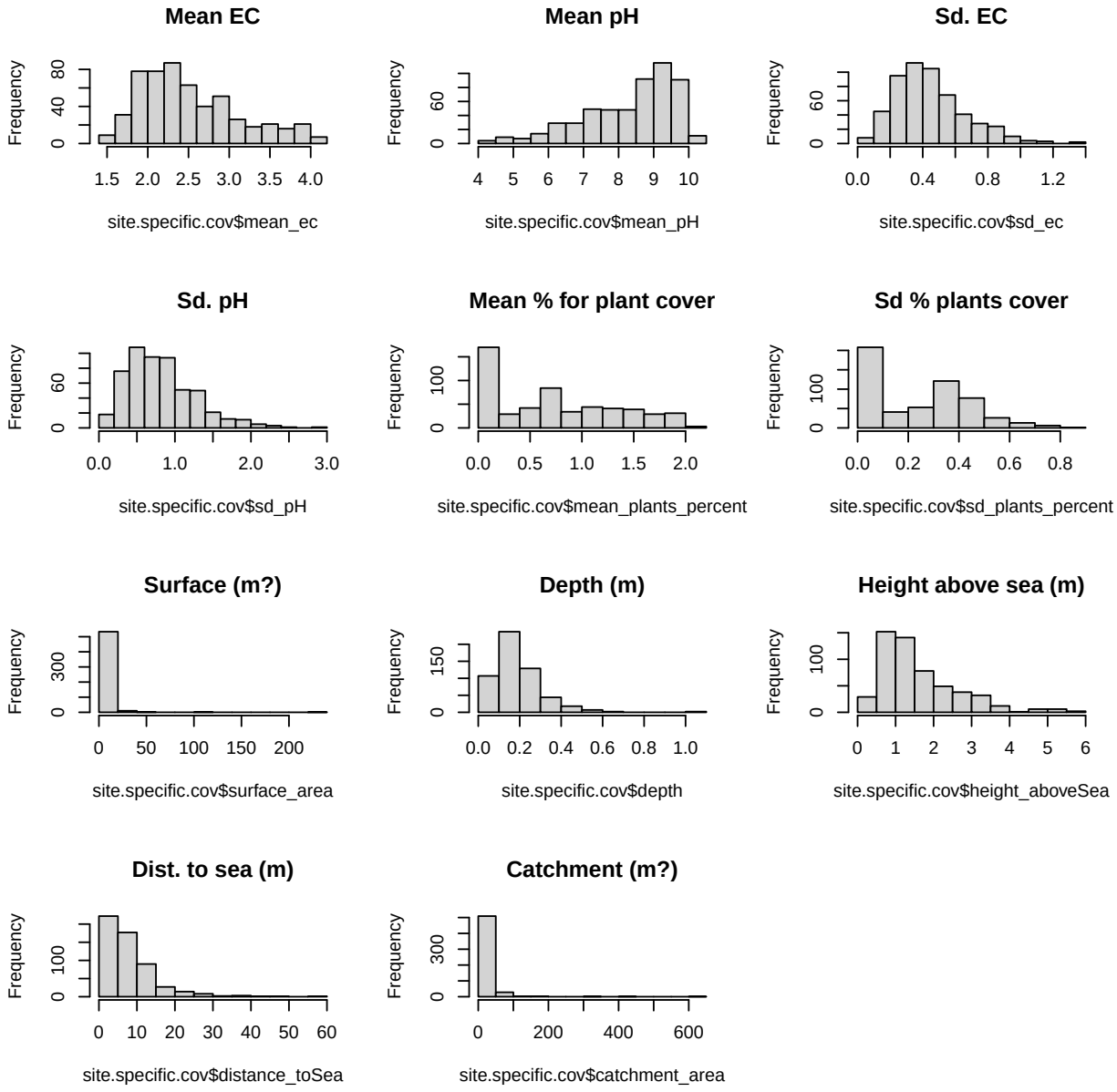
IV.1. Raw data, change scales and transform to approx. gaussian distribution.

```
# Get data & keep only core sites
sites.harddata <- read.csv("../../3._Data/5b._Data_clean/Pools_hard_data_vers12.csv",h=T,sep=';',dec=',
sites.harddata <- sites.harddata[as.character(sites.harddata$poolname) %in% id.sites.core,]

# Keep only variable of interest and convert everything in meters
sites.harddata <- sites.harddata[,c('poolname','surface_area','depth','height_aboveSea','sometimes_subm
sites.harddata[,c('height_aboveSea','depth','distance_toSea')] <- sites.harddata[,c('height_aboveSea','


# Plant cover, both variables are redondant, we can choose to use one or the other
sites.plantcover <- read.csv("../../3._Data/5b._Data_clean/plantcover_2013_2017.csv",h=T)
sites.plantcover <- sites.plantcover[as.character(sites.plantcover$poolname) %in% id.sites.core,]

sites.plantcover$plants <- log10(1+sites.plantcover$plants)
sites.plantcover$plants_rank <- log10(sites.plantcover$plants_rank)

# sites.plantcover$plants <- sqrt(sites.plantcover$plants)
# sites.plantcover$plants_rank <- sqrt(sites.plantcover$plants_rank)

# Compute mean and variance
sites.pcov <- data.frame(poolname=rep("", length(id.sites.core)))
sites.pcov[,c('poolname','mean_plants_percent','mean_plants_rank')] <- aggregate(sites.plantcover[,c('pl
sites.pcov[,c('sd_plants_percent','sd_plants_rank')] <- aggregate(sites.plantcover[,c('plants','plants_

# Keep percents
sites.pcov <- sites.pcov[,c('poolname','mean_plants_percent','sd_plants_percent')]


# Hydroperiod
# sites.hydroperiod <- read.csv("../3._Data/5b._Data_clean/Data_hydroperiod_Means.csv", h = T)
# sites.hydroperiod <- sites.hydroperiod[as.character(sites.hydroperiod$poolname) %in% id.sites.core,]
#
# # Some sites are missing  (ca. 4.5% missing), i choose to replace NA by mean value (see e.g., Dray &
```

```
# sites.hydroperiod[is.na(sites.hydroperiod$meanhydro),'meanhydro'] <- mean(sites.hydroperiod$meanhydro
# sites.hydroperiod[is.na(sites.hydroperiod$meandesi),'meandesi'] <- mean(sites.hydroperiod$meandesi, n
#
# # Also, we can compute this kind of summary stat here ; gives mean time between dessication events
# sites.hydroperiod$mean_length_water_cycle <- sites.hydroperiod$meanhydro / (1+sites.hydroperiod$meand
# # Only keep var. of interest
# sites.hydroperiod <- sites.hydroperiod[,c('poolname','mean_length_water_cycle')]


# pH/EC
sites.physicochim <- read.csv("../../3._Data/5b._Data_clean/MetapopData_pH_conductivity_1998_2017.csv",
sites.physicochim <- sites.physicochim[as.character(sites.physicochim$poolname) %in% id.sites.core,]

sites.physicochim$conduct_uS <- log10(sites.physicochim$conduct_uS)

# Compute mean & var for EC and pH
sites.pc <- data.frame(poolname=rep("", length(id.sites.core)))
sites.pc[,c('poolname','mean_ec')] <- aggregate(sites.physicochim$conduct_uS, by = list(sites.physicochi
sites.pc$mean_pH <- aggregate(sites.physicochim$pH, by = list(sites.physicochim$poolname), mean, na.rm =
sites.pc$sd_ec <- aggregate(sites.physicochim$conduct_uS, by = list(sites.physicochim$poolname), sd, na
sites.pc$sd_pH <- aggregate(sites.physicochim$pH, by = list(sites.physicochim$poolname), sd, na.rm = T)

## Read Fish Data
sites.fishes <- read.csv("../../3._Data/5b._Data_clean/2009_2017-2_fish_ver2.csv")
```

- Vegetation : **which one should we use ? -> log10(1+x) on percents**

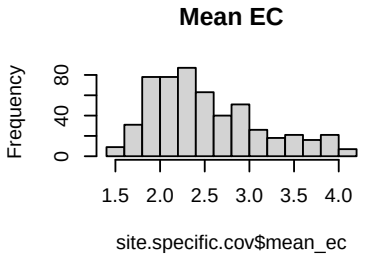
```
# Aggregate all hard data

# site.specific.cov <- merge(merge(merge(sites.pc,sites.hydroperiod),sites.pcov),sites.harddata)
site.specific.cov <- merge(merge(sites.pc,sites.pcov),sites.harddata)

 # Histogram raw data

 par(mfrow=c(4,3))
 hist(site.specific.cov$mean_ec, main = "Mean EC")
 hist(site.specific.cov$mean_pH, main = "Mean pH")
 hist(site.specific.cov$sd_ec, main = "Sd. EC")
 hist(site.specific.cov$sd_pH, main = "Sd. pH")
 hist(site.specific.cov$mean_plants_percent , main = "Mean % for plant cover")
 hist(site.specific.cov$sd_plants_percent, main = "Sd % plants cover")
 hist(site.specific.cov$surface_area, main = "Surface (m?)")
 hist(site.specific.cov$depth, main = "Depth (m)")
 hist(site.specific.cov$height_aboveSea, main = "Height above sea (m)")
 hist(site.specific.cov$distance_toSea, main = "Dist. to sea (m)")
 hist(site.specific.cov$catchment_area, main = "Catchment (m?)")
```

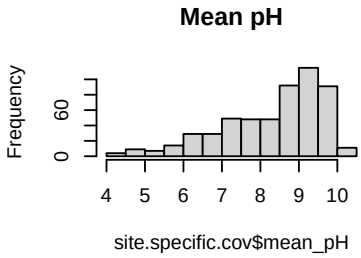


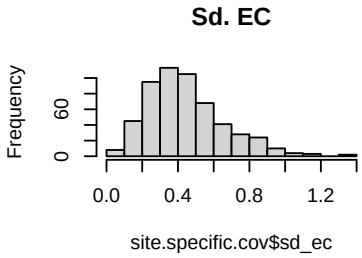
Some transformations to approximate normal distributions (transformations are performed before anything else).

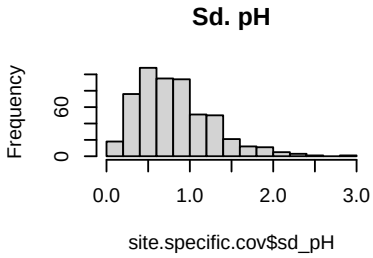
```
site.specific.cov$surface_area <- log10(site.specific.cov$surface_area)
site.specific.cov$depth <- log10(site.specific.cov$depth)
site.specific.cov$height_aboveSea <- log10(site.specific.cov$height_aboveSea)
site.specific.cov$distance_toSea <- log10(site.specific.cov$distance_toSea)
site.specific.cov$catchment_area <- log10(site.specific.cov$catchment_area)

# Histogram transformed data

par(mfrow = c(4, 3))
hist(site.specific.cov$mean_ec, main = "Mean EC")
hist(site.specific.cov$mean_pH, main = "Mean pH")
```

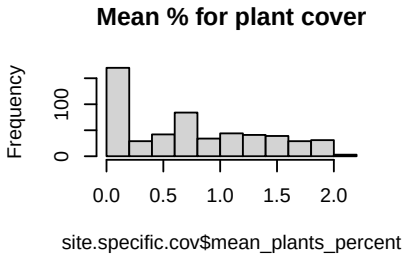
```r
hist(site.specific.cov$sd_ec, main = "Sd. EC")
hist(site.specific.cov$sd_pH, main = "Sd. pH")
hist(site.specific.cov$mean_plants_percent, main = "Mean % for plant cover")
hist(site.specific.cov$sd_plants_percent, main = "SD % plants cover")
hist(site.specific.cov$surface_area, main = "Surface (m?)")
hist(site.specific.cov$depth, main = "Depth (m)")
hist(site.specific.cov$height_aboveSea, main = "Height above sea (m)")
hist(site.specific.cov$distance_toSea, main = "Dist. to sea (m)")
hist(site.specific.cov$catchment_area, main = "Catchment (m?)")
```

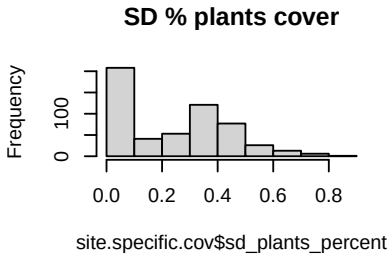


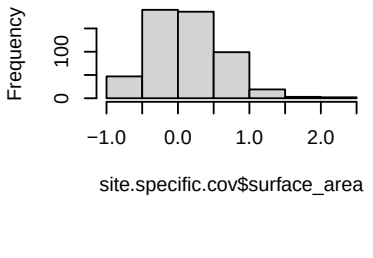


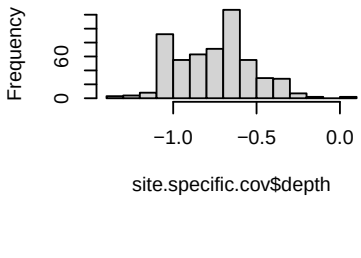


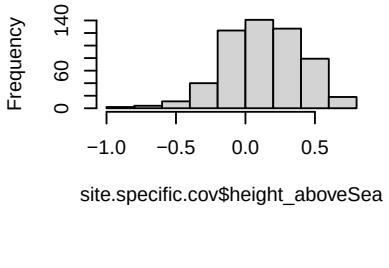


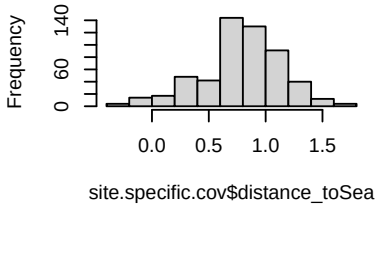


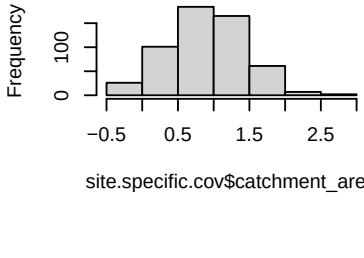






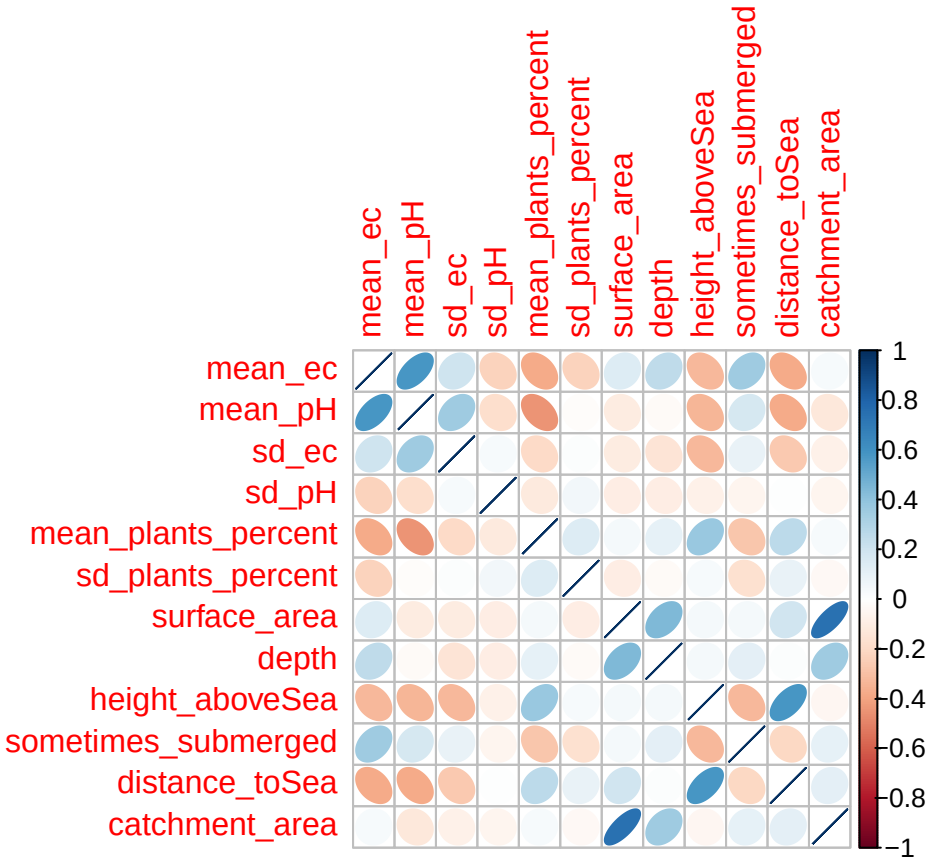




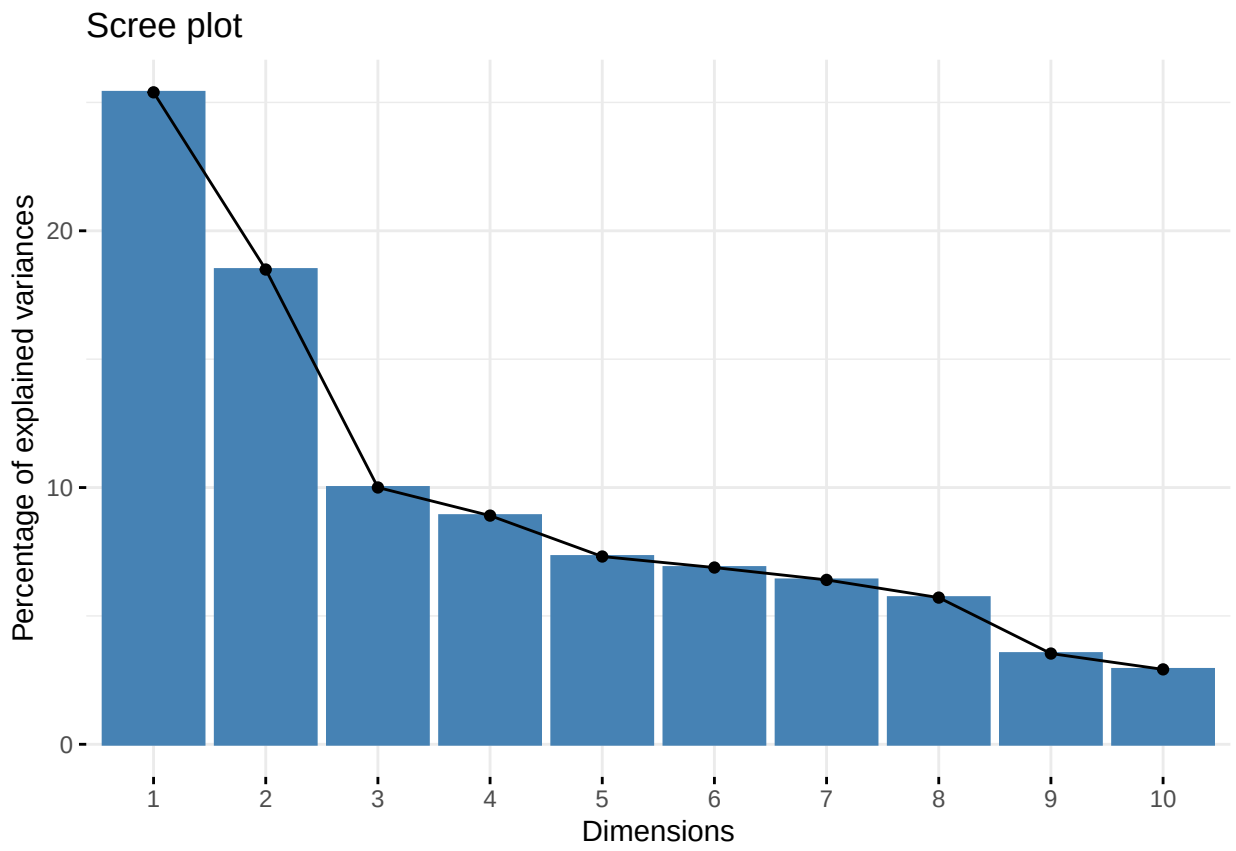


IV.2. Look at collinearity & try to reduce dimensionality

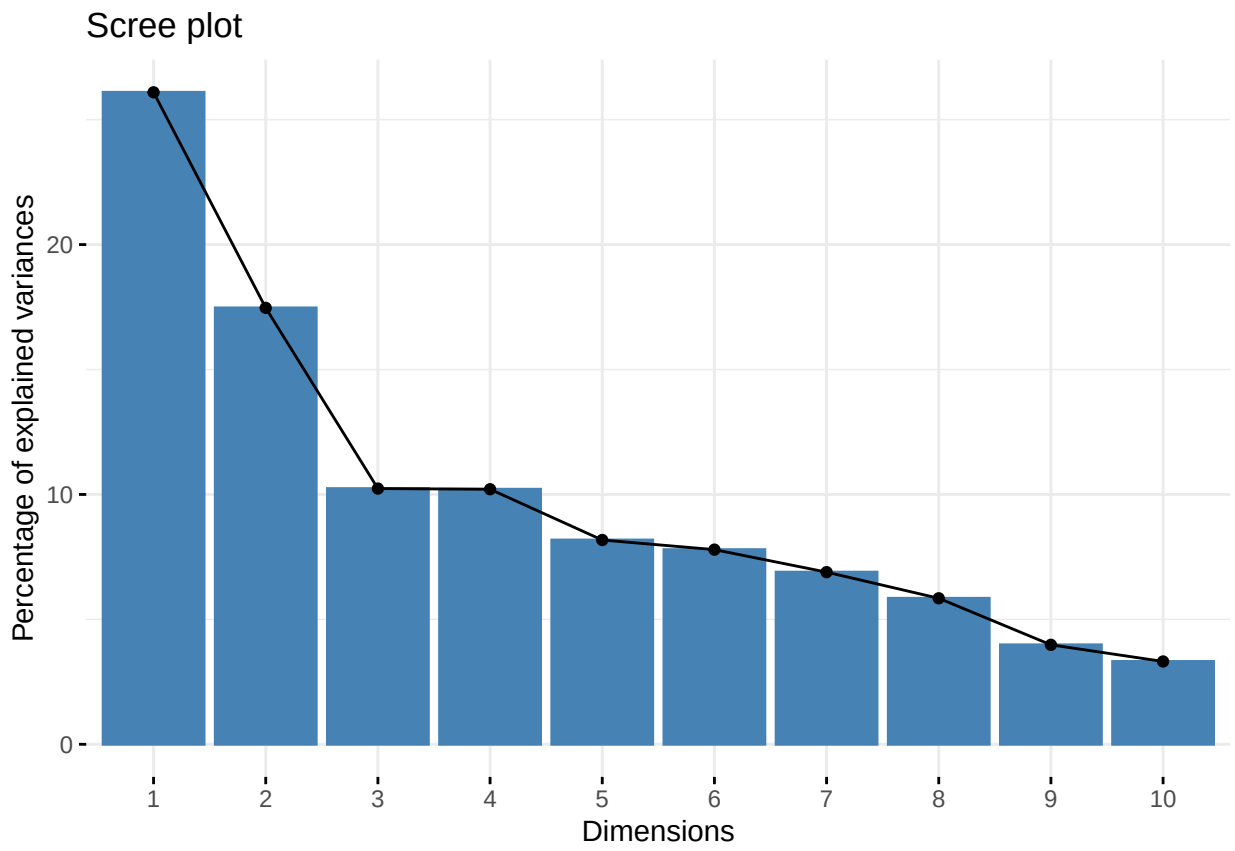
```
corrplot(cor(site.specific.cov[, -1], use = "na.or.complete"), method = "ellipse")
```




```
# Standardizing ([,c(-1)], because site names are removed)
site.specific.cov.scaled <- scale(site.specific.cov[, c(-1)])

# PCA (on all variable)
pca = prcomp(site.specific.cov.scaled)

# PCA (and kick out pH, catchment area)
pca_someOut = prcomp(site.specific.cov.scaled[,c(-2,-12)])


# Visualized eigenvalues & var contrib to axes
fviz_eig(pca)
```




```
fviz_eig(pca_someOut)
```




```
# Explained variance :
kable(get_eigenvalue(pca))
```

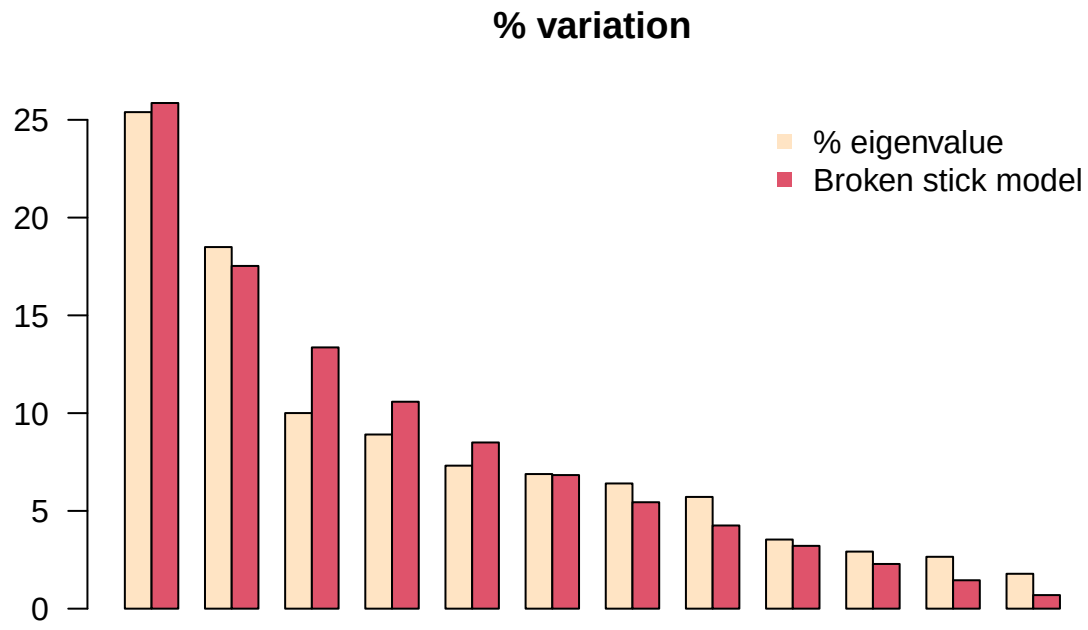
	eigenvalue	variance.percent	cumulative.variance.percent
Dim.1	3.0471951	25.393292	25.39329
Dim.2	2.2190511	18.492093	43.88538
Dim.3	1.2003611	10.003009	53.88839
Dim.4	1.0688200	8.906833	62.79523
Dim.5	0.8776671	7.313892	70.10912
Dim.6	0.8261584	6.884653	76.99377
Dim.7	0.7684117	6.403431	83.39720
Dim.8	0.6856742	5.713952	89.11116
Dim.9	0.4241440	3.534533	92.64569
Dim.10	0.3501614	2.918011	95.56370
Dim.11	0.3182634	2.652195	98.21590
Dim.12	0.2140925	1.784104	100.00000

```
kable(get_eigenvalue(pca_someOut))
```

	eigenvalue	variance.percent	cumulative.variance.percent
Dim.1	2.6093541	26.093541	26.09354
Dim.2	1.7465482	17.465482	43.55902

	eigenvalue	variance.percent	cumulative.variance.percent
Dim.3	1.0234382	10.234382	53.79341
Dim.4	1.0208412	10.208412	64.00182
Dim.5	0.8176208	8.176208	72.17803
Dim.6	0.7791388	7.791388	79.96941
Dim.7	0.6890718	6.890718	86.86013
Dim.8	0.5843473	5.843473	92.70360
Dim.9	0.3981060	3.981060	96.68466
Dim.10	0.3315337	3.315337	100.00000

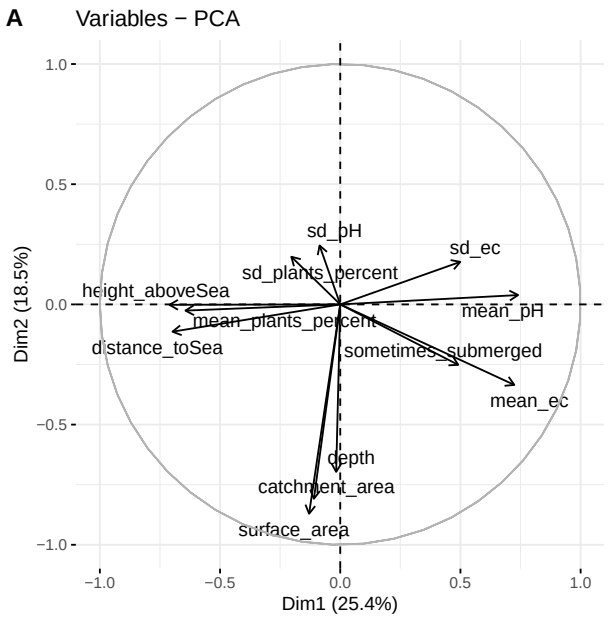
```
# Broken-sticks (coming with the book of Borcard et al. 2011
# http://www.davidzeleny.net/anadat-r/doku.php/en:start)
evplot(pca$sdev^2)
```

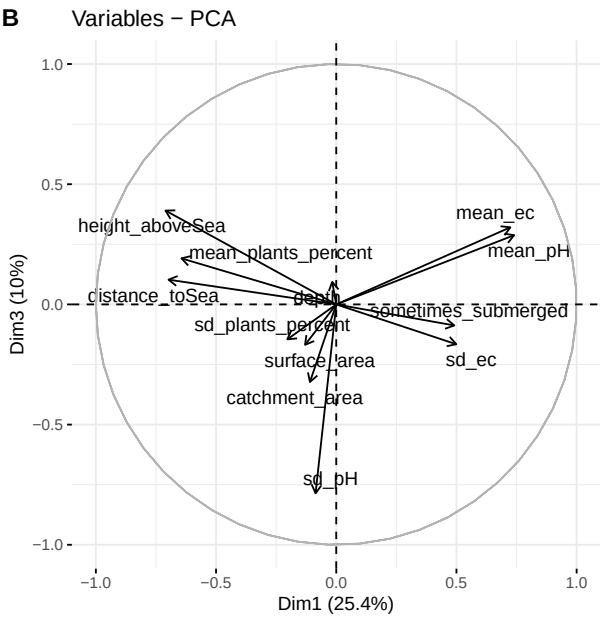


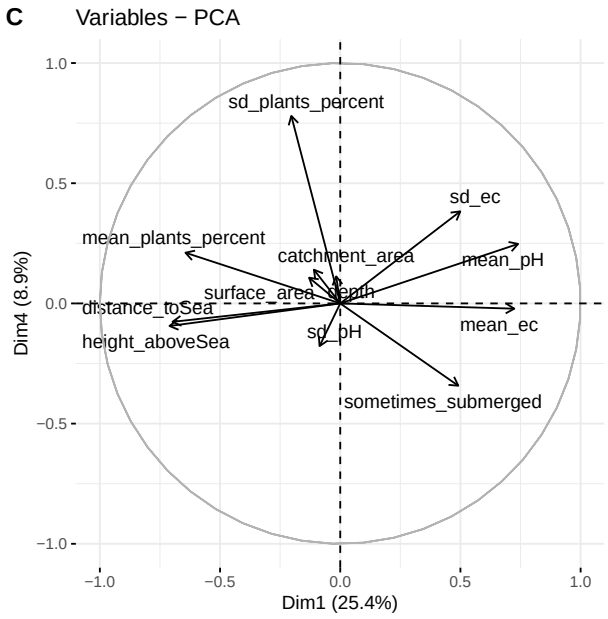
Well, two first PC axes explain ca. 44% of the total variance.

Third and fourth one explain resp. ca. 10% and 9% ; compared to the % of variance brought by each variable (~ 100/12 var = 8.3%), not sure whether it is interesting to keep them or not. We can go into more details. Moreover, using the "broken sticks" criterion, we should not.

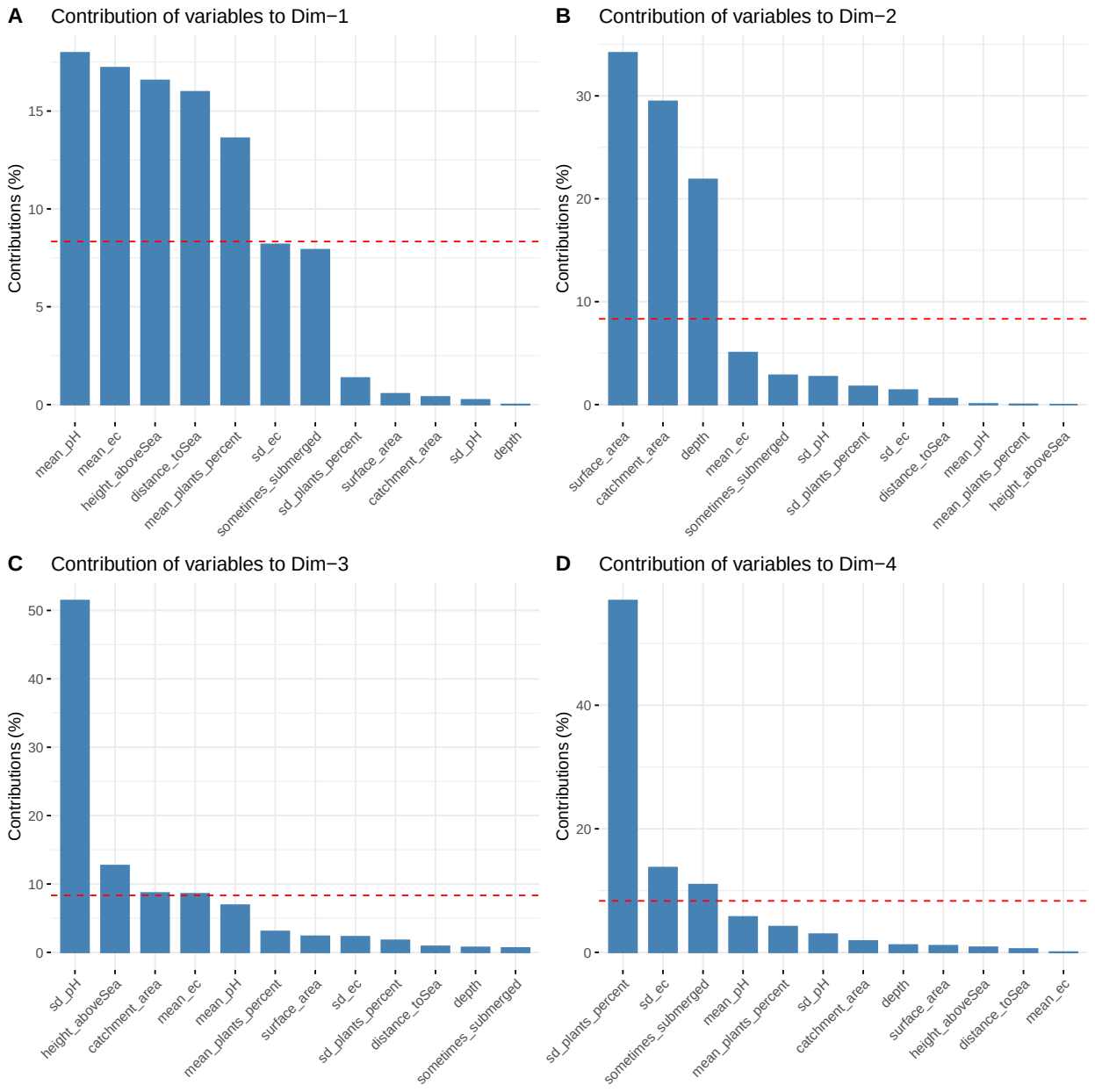
```
# With all cov.
# Correlation circle
plot_grid(fviz(pca, "var", axes = c(1, 2), repel = T),
          fviz(pca, "var", axes = c(1, 3), repel = T),
          fviz(pca, "var", axes = c(1, 4), repel = T), labels = c("A", "B", "C"))
```



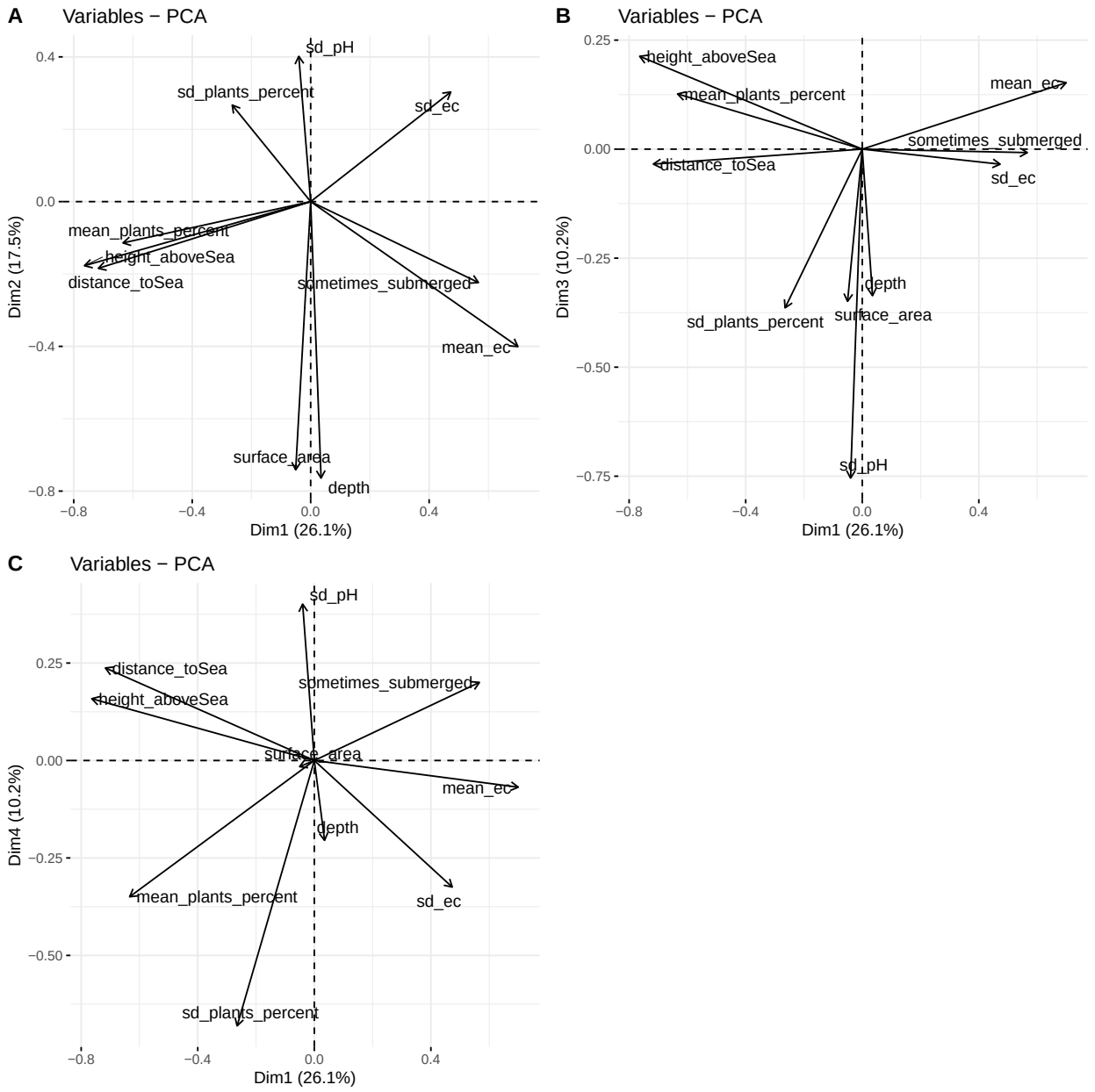




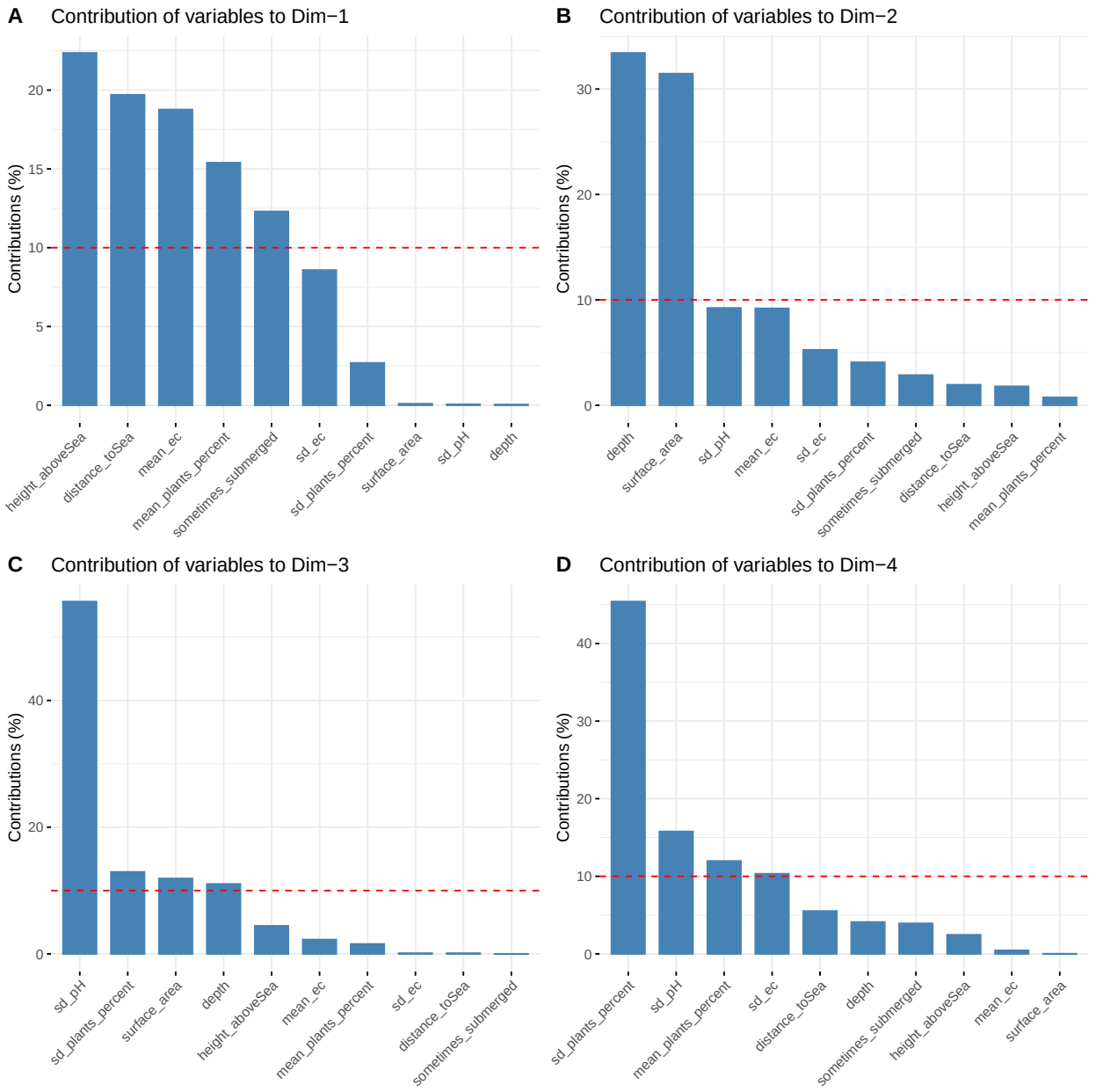

```
# Then four firsts axes
plot_grid(fviz_contrib(pca, axes = 1, "var"),
          fviz_contrib(pca, axes = 2, "var"),
          fviz_contrib(pca, axes = 3, "var"),
          fviz_contrib(pca, axes = 4, "var"), labels = c("A", "B", "C", "D"))
```




```
# Without pH, catchmentArea
plot_grid(fviz(pca_someOut, "var", axes = c(1, 2), repel = T),
          fviz(pca_someOut, "var", axes = c(1, 3), repel = T),
          fviz(pca_someOut, "var", axes = c(1, 4), repel = T), labels = c("A", "B", "C"))
```




```
# Then four firsts axes
plot_grid(fviz_contrib(pca_someOut, axes = 1, "var"),
          fviz_contrib(pca_someOut, axes = 2, "var"),
          fviz_contrib(pca_someOut, axes = 3, "var"),
          fviz_contrib(pca_someOut, axes = 4, "var"), labels = c("A", "B", "C", "D"))
```



From here, we have to choose how many axes to use, to sum up :

1. PC I : Reflect terrestrial vs. marine influence
2. PC II : Reflect site geometry
3. PC III / IV : Not clear, PC III is mainly drived by pH variance. PC IV, mainly drived by variation in plant cover

DE : This pH variance thing is interesting, but I do not really know what it means. Maybe we play around with this in the hope to get some feeling for what it may tell us.

```
# Compute coordinates in PC plan
site.specific.cov.PCAaxes <- site.specific.cov.scaled %*% pca$rotation
```

```r
# Compute coordinate in PC plan (without pH, catchmentArea)
site.specific.cov_withoutpHCatchment.PCAaxes <- site.specific.cov.scaled[,c(-2,-12)] %*% pca_someOut$ro

# Save all scaled cov
# saveRDS(as.data.frame(site.specific.cov.scaled), "../3._Data/5b._Data_clean/all_cov_scaled.RDS")

# Save them (all, can select PC axes later)
# saveRDS(site.specific.cov.PCAaxes, "./data/environment_PCA.RDS")
# saveRDS(site.specific.cov_withoutpHCatchment.PCAaxes, "../3._Data/5b._Data_clean/environment_PCA_redu
```

V. Preliminary analysis

V.1.Detectability

V.2.1. Computing Likelihood function Let's say, ψ stand for the probability that a site is occupied, d_w the probability of detecting species knowing presence. One assumption here, is that the occupancy status of a site do not change between repeats.

Here, we have two visits for a given number of sites (say N, same site can be consider several times if it has been doubly-sampled more than once). Note that, I consider that overall metapopulation occupancy (ψ) does not change among years.

Therefore, there are 4 possible outcomes :

1. two non detection or absence (00): or species is not here, and therefore not detected, or present and not detected 2 times. So that $P(X = 00) = (1 - \psi) + \psi(1 - d_w)^2$
2. (also .3, it is symmetric) one absence and one presence (01 or 10) : species is present, and detected one time only : $P(X = 01) = P(X = 10) = \psi d_w(1 - d_w)$
3. two detection (11) : species is present, and detected two times : $P(X = 11) = \psi d_w^2$

If there is **a** (11), **b** (01), **c** (10), **d** (00), $\mathbf{X} = x_1, ..., x_n$ is the vector of observed values. Then the likelihood function reads :

$$\mathcal{L}(\psi, d_w|x_1, ..., x_n) = \prod_{i=1}^{N} P(X = x_i)$$

$$\mathcal{L}(\psi, d_w|x_1, ..., x_n) = P(X = 11)^a P(X = 01)^b P(X = 10)^c P(X = 00)^d$$

Take the log :

$$log\ \mathcal{L}(\psi, d_w|\ x_1, ..., x_n) = a.Log[P(X = 11)] + (b + c).Log[P(X = 01)] + d.Log[P(X = 00)]$$

Solving $\frac{d\ log\mathcal{L}(\psi,d_w|\mathbf{X})}{d\psi} = 0$ for ψ leads to :

$$\hat{\psi} = -\frac{a + b + c}{(a + b + c + d)(d_w - 2)d_w}$$

Then, we can replace ψ by $\hat{\psi}$ in $log\mathcal{L}(\psi, d_w|\mathbf{X})$, and solving $\frac{d\ log\mathcal{L}(\psi,d_w|\mathbf{X})}{d\ d_w} = 0$ for d_w, which leads to :

$$\hat{d_w} = \frac{2a}{2a + b + c}$$

This formula corresponds to the max. likelihood estimate of detectability. (Similar to MacKenzie et al., 2003)

Interestingly, d and ψ do not enter in the last formula.

```r
# Read repeated visits
detectability <- read.table("../../3._Data/5b._Data_clean/VIP_DEdata5.csv",header=T,sep=';')

# Remove lines with NA (cannot be used, reduce dataset from 3690 lines to 3458)
detectability <- na.omit(detectability)

# In all case, we have to compute a, b (, c) and d for each species
# Actually, distinguish between b & c is useless. So I consider only 3 category : say a, b (=b+c), and
# Note that, the 'd' category is also useless (disapear when computing max. likelihood estimate)

# Construct function
category <- function(x){if(x[1]==0 & x[2]==0){return('d')}else if(x[1]==1 & x[2]==1){return('a')} else

# Apply to data
detectability$M_categories <- apply(detectability[,c('magna_VIP','magna_DE')], 1, FUN = category)
detectability$P_categories <- apply(detectability[,c('pulex_VIP','pulex_DE')], 1, FUN = category)
detectability$L_categories <- apply(detectability[,c('longispina_VIP','longispina_DE')], 1, FUN = categ

# Over all years, detectability are :
magna_detectability <- table(detectability$M_categories)
pulex_detectability <- table(detectability$P_categories)
longispina_detectability <- table(detectability$L_categories)

# Compute dw
p.loglik <- function(x){(2*x[['a']])/(2*x[['a']]+x[['b']])}

# Could also compute expected occupancy, don't use it here
# psi.loglik <- function(x){((2*x[['a']]+x[['b']])^2)/(4*x[['a']]*(x[['a']]+x[['b']]+x[['d']]))}

kable(data.frame("D.magna" = p.loglik(magna_detectability),
           "D.pulex" = p.loglik(pulex_detectability),
           "D.longispina" = p.loglik(longispina_detectability), row.names = "Detectability"))
```

V.1.1. Applying the likelihood function to data

	D.magna	D.pulex	D.longispina
Detectability	0.8538283	0.8009479	0.8357222

```r
## For profile likelihood estimations
# e.g. longi when magna is here (indp. of pulex)
table(detectability %>% as_tibble() %>% filter(M_categories %in% c('a', 'b')) %>% pull(L_categories))
```

```
##
##   a   b   d
## 113  56 572
```

```r
# e.g., longi when magna and pulex are there
table(detectability %>% as_tibble() %>% filter(P_categories %in% c('a', 'b') & M_categories %in% c('a',
```

```
##
##  a  b  d
##  4  7 26
```

```
# e.g., longi when magna and pulex are NOT there
table(detectability %>% as_tibble() %>% filter(P_categories %in% c('d') & M_categories %in% c('d')) %>%
```

```
##
##    a    b    d
##  248   79 2174
```

Next, we could compare that with estimates from the Bayesian model.

V.2. Bayesian model

I just present a few general concepts of the bayesian model

V.2.1 Model

Transitions rates The idea here is to change from discrete time model (the one we use with snails) to a continuous time version here. That does not change lot a things, but at the end, we get rates that are the same than in the levins metapopulation model.

Globally, we consider demographics rates : colonization : $\gamma = c.p$, where p is the metapopulation occupancy and c, the per-capita colonization rate. Extinction is simply e, which do not depends on p (meaning, we do not consider rescue effect).

Note that here, p, is simply overall metapopulation occupancy (i.e. proportion of occupied sites, no spatial aspect)

Thus, the model reads :

- For a **occupied** site at t_1 transitionning to **empty** at t_2 : $P(1 \rightarrow 0) = (1 - e^{-(\gamma+e)})(\frac{e}{\gamma+e})$
- For a **occupied** site at t_1 transitionning to **occupied** at t_2 : $P(1 \rightarrow 1) = 1 - (1 - e^{-(\gamma+e)})(\frac{e}{\gamma+e})$
- For a **empty** site at t_1 transitionning to **occupied** at t_2 : $P(0 \rightarrow 1) = (1 - e^{-(\gamma+e)})(\frac{\gamma}{\gamma+e})$
- For a **empty** site at t_1 transitionning to **empty** at t_2 : $P(0 \rightarrow 0) = 1 - (1 - e^{-(\gamma+e)})(\frac{\gamma}{\gamma+e})$

Actually, we split this into two component, we fit separate (c, e) for the summer and (c, e) winter period.

Detectability Idea behind the detectability layer is that observations are not perfects, we can miss a species when present. If we do not consider this biais in the model, we will overestimate the number of transitions and therefore demographic rates. So, we link the true occupancies ($x_{i,t}$ a "latent" variable in the model, which are not observed) to the observations ($y_{i,t}$).

Transitions in the previous section refer to transitions among "true" states ($x_{i,t}$), and the detectability layer link those true states ($x_{i,t}$) to observed ones ($y_{i,t}$).

Then, the detectability (d) is the probability of detecting a species knowing it is present.

We split this into two detectabilities : d_w in wet site, and d_d in dry site, and assume that $d_d = 0$. (Hereafter, $d = d_w$)

- Thus, in wet sites : $P(y_{i,t} = 1|x_{i,t} = 1) = d$, whereas $P(y_{i,t} = 0|x_{i,t} = 1) = 1 - d$. And, $P(y_{i,t} = 0|x_{i,t} = 0) = 1$ and $P(y_{i,t} = 1|x_{i,t} = 0) = 0$
- And, in dry sites : $P(y_{i,t} = 1) = 0$ and $P(y_{i,t} = 0) = 1$

Spatialization aspects Without going into details, we include space here using the Euclidean Distance Matrix (say **D**, where $D_{ij} = D_{ji}$ is the distance between i and j).

As describe in III., **D** is compute from GPS positions and using DistVincentEllipsoid function from distm() function ({geosphere} package).

Now, in $\gamma = c.p$, we cannot consider p as being the same for everyone, and then, we need a site-specific p_i.

Classic way for that (with n the number of site, $\frac{1}{\alpha}$ the mean colonization distance, and x_j the 'true' occupancy status of site j) :

$$p_i = \sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}$$

Using this definition, c has not anymore the same meaning that in Levins metapopulation model, so we scale p_i such that c becomes the same c than in Levins. (I will write a small document on this). Under some assumptions, p_i now reads:

$$p_i = \frac{\sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}}{\frac{1}{n}(\sum_i \sum_j e^{-\alpha \; D_{ij}})}$$

Explanation for this last forumla. We want to have a c which is the same as in the Levins model. But in our case, $p_i = \sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}$. Then we search equivalence between cp and $c' \sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}$

$$E[cp] = E[c' \sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}]$$

For the left part :

$$E[c \sum^{n} \frac{x_i}{n}] = c \; \frac{1}{n} \sum^{n} E[x_i]$$

For the right part :

$$E[c' \sum_{j \neq i}^{n} x_j \; e^{-\alpha \; D_{ij}}] = c' \sum^{n} E[x_j] E[e^{-\alpha \; D_{ij}}] = c' \sum^{n} E[x_j] \; (\frac{1}{n^2} \; \sum_i \sum_j e^{-\alpha \; D_{ij}})$$

Well, equivalence between :

$$c \; \frac{1}{n} \sum^{n} E[x_i] \; and \; c' \sum^{n} E[x_j] \; (\frac{1}{n^2} \; \sum_i \sum_j e^{-\alpha \; D_{ij}})$$

Then

$$\frac{1}{n} \; c = \frac{c'}{(\frac{1}{n^2} \; \sum_i \sum_j e^{-\alpha \; D_{ij}})}$$

And lastly

$$c = \frac{c'}{(\frac{1}{n^2} \; \sum_i \sum_j e^{-\alpha \; D_{ij}}) * n} = \frac{c'}{(\frac{1}{n} \; \sum_i \sum_j e^{-\alpha \; D_{ij}})}$$