The influence of macroclimate suitability, determined by the niche boundaries distance, on plant populations performance

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Abstract:

The relation between macroclimate suitability and species performance was studied at global scale for the first time by Csergö *et al,* based on data from 93 populations of 34 plant species worldwide. Species Distribution Models (SDMs) were used to calculate climate suitability. Populations were predicted to decline in less favourable climates and to persist in favourable climates. However no correlation between the population growth rate and climate suitability was found. We assumed here that climate suitability calculation, based on SDMs was not the best metric for this study and we proposed a novel method, relating climate suitability to the distance of populations to niche boundaries. The relation of the new measure to the population performance, represented by four demographic rates including the population growth rate, was tested, but no correlation was found. We conclude that the available data is too scarce to evidence if the lack of relationship between climate suitability and demographic parameters is due to constraints imposed by biotic interactions between species i, or if the global effect of climate suitability, constraining demographic strategies is not well represented by the climatic variables we used.

Keywords:

Climate change, species distribution models, matrix population models, population dynamics, biotic interactions, unilaterality of biotic vs. abiotic factors, population growth rate, COMPADRE Plant Matrix Database.

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Introduction:

Understanding the relation between the environmental conditions and population performance is important in order to predict their response to climate change and integrate this knowledge in conservation management (Thomson *et al,* 2001). Individuals can support a range of climate conditions which influence their performance, in isolation from interactions with other individuals from the same or different species (Vasseur *et al*, 2014). In real ecological situations, macroclimates can affect the population dynamics at different degrees, depending on their environmental situation. The performance, which is expected to be high in the most suitable climate and low in the less suitable climate, may be biased by ecological processes such as biotic interactions and apparent demographic balance (Csergö *et al*, 2017). However the predominant role of abiotic or biotic or both interactions on the occurrence, abundance and performance population has always been a debate between scientists (Soberon 2007So).

The work of Csergö *et al* has tested for the first time the unilaterality of biotic vs. abiotic factors in a global perspective by studying the impact of the climate suitability predicted from Species Distribution Models (SDMs) on the population performance (Csergö *et al*, 2017; Guisan *et al*, 2005). The performance was represented by means and temporal variations demographic rates, calculated from recent and rare data of 34 tree and herbaceous perennial plant species provided by the COMPADRE Plant Matrix Database (Csergö *et al*, 2017). Some correlations were found but no significant relation with the population growth rate and the climate suitability, which was supposed to be positive, was demonstrated.

The ability of SDMs' to predict the demographic processes that control species' persistence remains uncertain, and we hypothesized that the population suitability predicted suitability by SDMs was not necessarily the best predictor of their demographic performance (Thuiller *et al*. 2014). Therefore, we proposed a new measure of the climate suitability based on the distance to the niche boundaries inspired by the fundamental niche as defined by Hutchinston in 1957.

The fundamental niche of a species is defined as the set of conditions within which a species can live in the absence of competitors (Soberón, 2017). In a multidimensional space, the centre of the fundamental niche brings together the most suitable climate conditions for the species (Lamotte,

1979).The suitable conditions progressively decrease with the distance from the centre, until the boundaries, where the less suitable climate are found (Bohner *et al*, 2020). So the more distant from the niche boundaries towards the niche center, the more the climate suitability increases and also the demographic performance.

70 This property is valid without biotic interactions, so the correlation between the minimal distance to niche boundaries and the performance will also allow to study the congruence between the realized and the fundamental niche in a global perspective. Again, the study will only be based on climate suitability, which allows to keep the purpose of the study to test the unilaterality of the interactions.

So we supposed a positive relation between the minimal distance to niche boundaries and the
75 performance. This is similar to ask the question: **Does climate suitability at range margins constrain population growth rate in plants?**

We worked on 102 population from 37 species, including the 34 species of Csergö *et al.* To represent the performance we worked on four demographic rates representing the most the preferance for us (Bohner *et al*, 2020): the temporal variation in λ (CVλ), and the mean in population growth rate
80 (λ), time to quasi extinction and fecundity.

We expected a positive relationship between the minimal distance to the niche boundaries and the population growth rate, and a negative relationship the temporal variation in the observed population growth rates. We also predicted a fecundity and a time to quasi extinction higher in more suitable climate (Fig. 1).
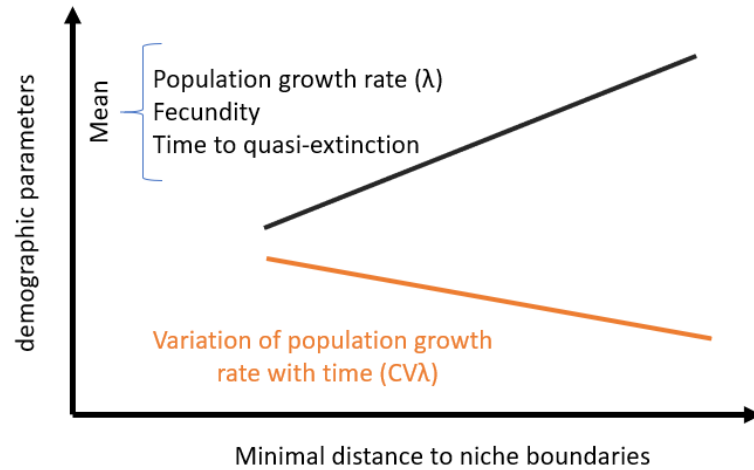
Figure 1: 2 Naive expectations of relationships between predicted the minimal distance to niche boundaries and mean and temporal variability of integrated population performance metrics. We expected a positive relationship between the minimal distance to niche boundaries and population growth rate, fecundity and Time to quasi-extinction, and negative relationships with the temporal variation (CV) in population growth rate. CV = coefficient of variation across annual censuses, i.e. temporal variability in demographic performance.

Methods:

We reanalysed the 102 populations across 37 plant species studied by Csergö et al. and we chose four of the demographic parameters they analyzed in their study: the temporal variation in growth rate (CVλ), and the mean in population growth rate (λ), time to quasi extinction and fecundity. We created a model to calculate the minimal distance to niche boundaries for each population. Then Mixed Linear Models (LMMs) were used to test the correlations between our measures and each of the demographic parameters.

Data:

-population and occurrence data

The study included 102 populations across 37 species. Three species with enough data (*Actaea elata, Cecropia obtusifolia and Digitalis purpurea*) were added to the 34 species used by Csergö et al in their article. Occurrence data were originally compiled from multiple dataset such as GBIF (Global

Biodiversity Information Facility), BIEN (Botanical Information and Ecology Network), local and regional herbaria and digitized species distribution maps from atlases. The species were previously sorted in order to have presence data adequate for fitting quality SDMs, which were obtained using four different techniques to obtain robust estimates: generalized linear models, generalized boosted regression models, random forest and maximum entropy modelling as carried out in the BIOMOD 2 library (Csergö *et al*, 2017 Appendix S1.3).

-Climatic data

The eight same climatic factors from Csergö et al were selected: annual mean temperature, temperature seasonality, mean temperature of warmest quarter, mean temperature of the coldest quarter, precipitation seasonality and precipitation of wettest quarter from WORLDCLIM dataset (worldclim.org) and annual and seasonality of global evapotranspiration from the CGIAR Consortium for Spatial Information (cgiarcsi.community). These factors were download at 5 arc-min resolution (i.e corresponds to 1/12 ° or 9.1 km at the equator).

-Demographic metrics

Matrix projection models, based on three years of field observations (two transition matrix) and representing the proportion of individuals that transition across different stage were extracted from COMPADRE 3.0.0 on 21 July 2014 (Salguero-Gómez *et al.* 2015). Individual matrices were available for each year and for each population separately and allowed the calculation of the mean population growth rate. The stochastic population growth rate (λiid), corresponding to the arithmetic mean of log[N(t+1) – N(t)] were chosen among five other measures, to represent the growth rate. Its temporal variation (CV_{det}) was calculated as the coefficient of variation from deterministic growth rate matrix projections.

The fecundity was calculated as an average of the transition matrix among stages, weighted by the stable stage distribution.

Finally, the time to quasi extinction was obtained by calculating the time to 95% probability of reaching a set threshold. It was calculated from the initial number of individuals and the growth rate, by doing simulation over 300 years.

All these demographic measures were calculated by Csergö *et al* (Appendix S1.2).

Modelling the distance to niche boundaries:

135   The minimal distances to the niche boundaries were calculated with R 3.2.4 (rproject.org). The multidimensional space of the eight climatic factors was reduced by applying a Principal Component Analysis (PCA), where the two first axes represented respectively 51.5 % and 24.9 % of the initial variance in the original factors (Fig. 2).

For each species, occurrence data were projected in the reduced climatic plane. The niches were

140   modeled in that plane as occurrence density using kernel density estimations (ks package). Niche boundaries were delimited by choosing the 99% percentile of occurrence density in order to delimit a polygon that surrounds 99% of the occurrences. Depending on the species' distribution occurrence in the climatic plane, several polygons could constitute the niche.

Once the niche was determined, the climatic values of the populations were extracted (i.e. using their

145   geographic coordinates) and projected them in the PCA plane.

The function ecospat.NicheInnerness was then used to calculate the minimal distance to the niche boundaries for each population (provided by Olivier Broennimann; soon to be found in the ecospat package v3.1,). This function takes a set of target points and a niche represented by a spatial polygon as input and creates a sample of 100 000 points which covers uniformly all the niche space and calculates

150   all the distances between these points and the limit line (with the function gDistance, rgeos package v0.5-2). The maximum distance is retained. Then, all the possible distances between the target populations and the margins are calculated with the function gDistance. The minimum one is retained. If the population do not belong to the niche, its distance is set as negative. Finally, the ratio of the minimal distance of the target point to the maximum distance possible in the niche space is calculated

155   and returned by the function.
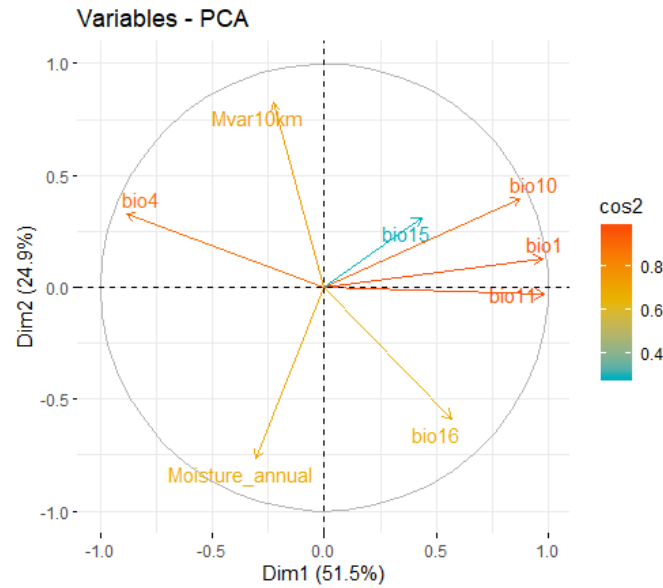
Figure 2: Correlation circle with the quality of variables representation (cos^2): bio1 - Annual mean temperature, bio4 - Mean temperature of warmest quarter, bio10 - Mean temperature of coldest quarter, bio11 - Precipitation seasonality, bio15 - Precipitation of wettest quarter, bio16 - Annual and seasonality of global potential evapotranspiration, Moisture_annual - annual of global evapotranspiration, Mvar10km – seasonality of global evapotranspiration. bio1, bio4, bio10,bio11 are the most representative variables.

Statistical analysis:

Several Linear Mixed Models (LMMs) were fitted to examine the impact of the minimal distance to niche boundaries on temporal variation, and mean in population growth rates, population extinction risk and fecundity. The final model we retained used a random intercept by species to reflect the diverse population within a species. The minimal distance to niche boundaries and the growth type (herbaceous perennial or tree) were modelled as fixed effects. The matrix dimension (number of stages in life cycle) and study duration (number of projection matrices over the course of the study) was not the variables of interest and were put in offset. Alternative models were discarded after comparison within an analysis of variance (ANOVA) of the Bayesian Index Criterion (BIC).

Then, the marginal and conditional 'variance explained' R2 values were calculated to describe the proportion of variance explained respectively by only the fixed factors and both factors (Nakagawa, 2013). Moreover, the confidence intervals representing the correlation of the response variable with the fixed effects were obtained.

The same models but using climate suitability measured by Csergö et al. instead of the minimal distance to niche boundaries were also tested to compare the effects of the two metrics on the demographic parameters.

The package used to fit the models was the *lme4* package. The one which allowed plotting them was the *sjPlot* package.

Results:

The populations studied occurred principally at niche margins (minimal distance: [0.00-0.50]). Only one population was found outside the niche (minimal distance = -1.85).

A negative non-significant correlation, nearly flat between the mean population growth rate and the minimal distance was observed (λiid=0.0303±0.0937 SD; Fig. 3a). A lot of populations with a λ=1 were observed all along the niche and several with a λ>1 were especially near the niche extremities. None of them at a null distance had a λ≈0. No evidence that λ was related to the distance in either trees or herbaceous perennials was showed.

The temporal variation population growth rate increased with the distance. The model fitted relatively well with data (Rc^2=0.4436; Table 1) but the confidence intervals encompassed zero ($CV\lambda_{det}$= 0.0325±0.0635 SD; Fig. 3b). However, there was a significant variation between Trees (GT_{Tree}= -0.0685±0.0835 SD; Table 1).

The time to quasi-extinction was high (300) for most of the populations regardless of their minimal distance. A non-significant positive relationship of the distance with the time to quasi-extinction was observed (-8.8865±66.6582 SD, Fig. 3d). Moreover this model did not fit well with data (Rc^2=0.1756; Table 1).

The correlation with the fecundity and the minimal distance to niche boundaries was the only fitted with the data but was not significant (0.0102±0.0112 SD; Rc^2=0.6378; Fig 3b; Table 1).

The comparison between models containing the minimal distance to niche boundaries and the ones with the climate suitability calculated from SDMs showed more fitted models for the current study, except for the growth rate with a Rc^2 pratically similar (Rc^2= 0.222 / 0.225). However no big differences were noted.

Table 1: Effects of climate suitability on demographic processes

Model structure and predicted variable	Selected variable	Var	SD	R_m^2	R_c^2
λ_{iid}~SMDN+(1|SP)+GT+offset(MD)+offset(SL)				0.0066	0.2225
Stochastic population growth rate	Intercept	0.0086	0.0930		
$CV\lambda_{det}$~SMDN+(1|SP)+GT+offset(MD)+offset(SL)				0.1165	0.4436
Temporal variation of deterministic population growth	Intercept	0.0032	0.0565		
rates	GT_{Tree}	-0.0685	0.0835		
TExt~SMDN+(1|SP)+GT+offset(MD)+offset(SL)				0.0675	0.1757
Time to 95% probability of quasi-extinction	Intercept	1172	34.23		
Fe~SMDN+(1|SP)+GT+offset(MD)+offset(SL)				0.1527	0.6379
Fecundity	Intercept	0.0001	0.0125		

The first column shows the fixed effects in the full models and the abbreviated and full name of predicted variables. The next columns show the variance and standard deviation for significant slopes and the intercept. The marginal and conditional R^2 values ere also calculated. SP – Species, MD - matrix dimension, SL - study length, GT - growth type, SMDN – standardized minimal distance to niche boundaries, CV - coefficient of variation. Effect sizes for models of transient dynamics and underlying demographic processes are comparatively presented in Fig. 3.
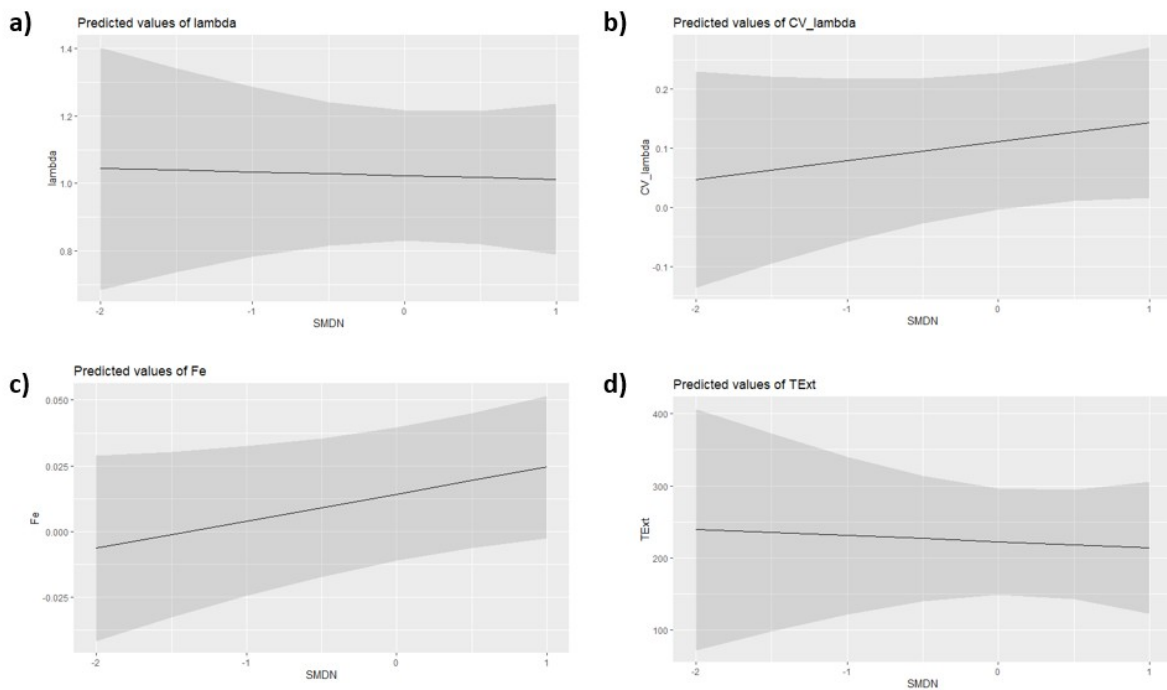
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Figure 3: The relation-ship between the minimal distance to niche boundaries and the population performance: a) lambda - stochastic population growth rates, b) CV_lambda - temporal variation of deterministic population growth rates , c) Fe - fecundity, and d) TExt - time to quasi-extinction. SMDN- Scaled Minimum Distance to Niche boundaries. Dotted lines represent 95% confidence intervals around the mean

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Discussion:

Populations at the niche centre, in high range of climate suitability are supposed to have an important population growth rate and time to quasi-extinction, which traduces a linear positive relationship between these demographic parameters and the minimal distance to niche boundaries. However, at the spatial and temporal resolution of this study, no significant correlation is observed, with even a reverse trend (negative relationship). Only the fecundity factor reflects hypotheses and increases with the distance but it slope is not significant. These results suggest different properties between the realised and the fundamental niche. Models would not fit with this theoretical representation and the positive correlation between performance and climate suitability does not seem to exist.

Conceptual issues:

According to the results, no relationship between predicted climate suitability and the performance is demonstrated in species ecological niche in a global dimension. It would mean that either climate suitability have no impact on population performances and would be determined by biotic interactions, or that the multiple demographic strategies decouple most of the time and in an important way population dynamics from macroclimate suitability (Pearson & Dawson 2003).

However, the first proposition is not possible. The effect of climate factors situated at the limit of the ecological niches is well illustrated by the climate change and leads to a diminution of population performance (Hoegh-Guldberg, 1999).

The second is more plausible but most of the time local studies on microclimate traduces an important role of climate in demographic constrains. Moreover, some studies showed that the climate had a greater influence than species composition on historical population dynamics (Adler *et al*, 2008). A methodological issue is then not to be excluded.

Methodological limits:

Two techniques to determine the climate suitability range of species were tried. Once based on observed distribution data but it capacity to reflect the population dynamic was questioned (Marcelo *et al*, 2016) and the other based on the distance to niche boundaries. This latter can also be called into

question, based on the fundamental niche theory, which represents an ideal to determined. Biotic interactions are not represented, preventing the realized niche to approach the fundamental niche.

Actually, the climate suitability of a species is really hard to determine. Population can occur in different micro climates and be well-adapted to them. From one population to another the niche boundaries could be different and these different populations could then have a different performance value under similar climate conditions.

Finding a way to determine the climate suitability, could be the most important challenge for this study.

Moreover, the study may not represent well a global representative range of all the environmental conditions due to the poor spatial replication. Only one to five populations per species were available and did not covered all the representative distances to niche boundaries. However more valid data take time to be obtained.

Finding models being able to represent species performance remains a real challenge, which would facilitate conservation management.

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```
#bil direct relie à hdr
setwd("Z:/projects-ext/GEODEM/Zoe")

#import libraries
library(corrplot)
library(sp)
library(dplyr)
library(raster)
library(rgeos)
library(ks)
library(raptr)
library(ggplot2)
library(geosphere)
library(PBSmapping)
library(rgdal)
library(sf)
library(stringr)
library(ade4)
library(plyr)
library(FactoMineR)
library(factoextra)
library(xlsx)
source("functions_innerness_OB_22.05.2019.r")

#Import data from WORLDCLIM and CGIAR
ameanT <- raster("ClimateVariables/Bioclim/wc5/bio1.bil")
seasonT <- raster("ClimateVariables/Bioclim/wc5/bio4.bil")
meanTwq <- raster("ClimateVariables/Bioclim/wc5/bio10.bil")
meanTcq <- raster("ClimateVariables/Bioclim/wc5/bio11.bil")
seasonP <- raster("ClimateVariables/Bioclim/wc5/bio15.bil")
wqP <- raster("ClimateVariables/Bioclim/wc5/bio16.bil")
Aevap <- raster("ClimateVariables/Moisture/Moisture_annual.asc")
Sevap <- raster("ClimateVariables/Moisture/Mvar10km.asc")

#verification
plot(ameanT, main="Annual mean temperature")

#stack the factors together in a multidimensional plane
clim<-stack(ameanT,seasonT,meanTwq,meanTcq,seasonP,wqP,Aevap,Sevap)
clim

#remove the no avalaible coordinates
climdf.all<-na.omit(getValues(clim))

#Creation of a sample of 20 000/2 millions pixels
#On crée un echantillon de 20 000 sur les 2 millions, à enlever après !!
Comment sait si espèces à ces endroits??
climdf<-climdf.all[sample(1:nrow(climdf.all),20000),]

##ACP##
#We reduce the dimension in two axes
pca=PCA(climdf, scale.unit = TRUE, ncp = 2, graph = TRUE)
plot(pca)

#Contribution coeficient of each factors for each dimension
pca$var$cor

#Representation of the factors' contributions
fviz_pca_var(pca, col.var = "cos2",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE)

##ACP end##

#list creation
dist= c() #no standardized distance
distStand=c() #standardized distance
#initilisation of population's number
ini=1

#Importation of population's demographic data
```

```
dem<-read.csv(file="dem/Final_Dataset_final.csv")


##DISTANCE CALCLUATION##

#Species name importation
species<-read.csv(file="species_name.csv")

#Loop for the 37 species
for (i in 1:37){

    #we are gradually importing the names of the species on the list
    namesp<-species[i,1]
    namesp
    #Species distribution data importation
    sp<-read.csv(paste0("occ/",namesp,".csv"))
    #visualization
    plot(ameanT, main=paste0("Annual mean temperature ",namesp))
    points(sp)

    #prend la valeur des couches au point donné, extrait la vleur des
facteurs au point
    spdf<-extract(clim,sp)

    #We take the species coordinates in the space of the PCA
    sp.scores<-predict(pca, newdata=spdf)$coord

    #function to define the niche by its density
    niche <- kde(x=na.omit(sp.scores),compute.cont=TRUE)
    #visualization
    plot(niche, main=paste0(namesp))

    #define the limits of the niche
    #level=niche1$cont[length(niche1$cont)] : we take the last element of
cont(=its length)that takes into account 99% of the points of the species
in the niche
    #the niche can contain several polygons
    env <-
contourLines(niche$eval.point[[1]],niche$eval.points[[2]],niche$estimate,le
vel=niche$cont[length(niche$cont)])

     #list creation
    liste=list()
    length=1:length(env)
    length
    #we stock the number of polygons of the niche in the liste
    #we remove the first element of the of each polygon:"level"
    for (k in 1:length(env))
      liste[[k]]=Polygons(list(Polygon(env[[k]][-1])),ID=length[k])

    #we create a class with the polygons
    poly=SpatialPolygons(liste)
    plot(poly, axes=TRUE,main=paste0(namesp))

    #coordinates are extracted for the species' populations (LON, LAT)
    pop<-dem[dem$SpeciesAccepted==paste0(namesp),59:58]
    pop
    #we take the number of populations in the species
    nbpop<-nrow(pop)
    nbpop

    #climatic factors are extracted at the points of presence of the species
    climpop<-extract(clim,pop)
    climpop
    #coordinates are imported into the PCA space
    scorespop<-predict(pca, newdata=as.data.frame(climpop))$coord
    #We don't want a matrix but coordinates to use it in the fontion
    scorespopSP<-SpatialPoints(scorespop)
    plot(scorespopSP,add=T, main=paste0(namesp) )

    ##distance calculation##
```

```
  NI<-ecospat.NicheInnerness(foc.pop=scorespopSP,niche=poly,bck=NA,
test=NA, bck2=NA)
  NI
  distanceMin<-NI$NI.abs#we get the "raw" minimal distance
  distanceMinStand<-NI$NI#we get the standardized minimal distance
  distanceMin

  for (n in 1:nbpop){
    dist[ini]<-distanceMin[n]
    dist[ini]
    distStand[ini]<-distanceMinStand[n]
    ini=ini+1}
}

dist
distStand

##CORRELATION LAMBDA AND DIST##
#file creation
SMDN<-distStand
MDN<-dist
SP<-dem$SpeciesAccepted
CS<-dem$HabSuit
Fe<-dem$Fecundity
TExt<-dem$timeto95ext_200
lambda<-dem$lambdaiid
CV_lambda<-dem$CV_lambdas
GT<-dem$GrowthType
MD<-dem$MatrixDimension
SL<-dem$StudyLength


myDat <- data.frame(SP, lambda, CV_lambda, SMDN, MDN, CS, Fe, TExt, GT, MD,
SL)
corrDat <- myDat
names(myDat) <- c("species","growth rate","CV growth rate","Minimal
distance boundaries","standardized Minimal distance boundaries", "Habitat
suitability", "Fecundity", "Time to quasi-extinction", "Growth rate",
"Matrix dimension", "Study length")
myDat

#exporter les données dans un fichier csv vide
write.csv(corrDat,file="Z:/projects-ext/GEODEM/Zoe/dem/clean data.csv")
write.csv(corrDat,file="Z:/projects-ext/GEODEM/Zoe/dem/Correlation
file.csv")
```

```
library(Rcpp)
library (rstanarm)
library(Matrix)
library(lme4)
library(shiny)
library(shinystan)
library(nlme)
library(sjPlot)
library(car)


corrDat <- read.csv(file="C:/Users/Zoe/Desktop/First step
project/correlation/correlation file.csv")

hist(corrDat$MDN)
hist(corrDat$SMDN)
hist(corrDat$lambda)
hist(corrDat$CV_lambda)
hist(corrDat$TExt)
hist(corrDat$Fe)
hist(corrDat$GT)
hist(corrDat$MD)
hist(corrDat$SL)


#offset preparation
b<- offset(MD)
c<- offset(SL)

lm<-lm(CS~SMDN)
plot(x = SMDN, y = CS, main="Relationship between the climate suitability
and\n the minimal distances to the niche boundaries for populations",
xlab="Minimal distances to the niche boundaries", ylab="Climate
suitability")
abline(lm)

#1)Stochastic population growth rate

lm1<-lm(lambda~SMDN)
plot(x = SMDN, y = lambda, main="Relationship between the population growth
rate and\n the minimal distances to the niche boundaries for populations",
xlab="Minimal distances to the niche boundaries", ylab="Growth rate")
abline(lm1, conf.int=T)

lambda1<-lmer(lambda~SMDN+(1|SP)+GT+b+c,data=corrDat)
lambda3<-lmer(lambda~SMDN+(1|SP)+(1|GT)+b+c,data=corrDat)
lambda4<-lmer(lambda~SMDN+(1|SP)+(SMDN|GT)+GT+b+c,data=corrDat)
lambda5<-lmer(lambda~SMDN+(1+SMDN|SP)+GT+b+c,data=corrDat)
lambda6<-lmer(lambda~SMDN+(1+SMDN|SP)+(1|GT)+b+c,data=corrDat)
lambda7<-lmer(lambda~SMDN+(1+SMDN|SP)+(SMDN|GT)+b+c,data=corrDat)

anova(lambda1,lambda3,lambda4,lambda5,lambda6,lambda7)
summary(lambda1)
confint(lambda1)
r.squaredGLMM(lambda1)
Anova(lambda1)


plot_model (lambda1,type="pred",pred.type="re",terms="SMDN")
plot_model (lambda1,type="slope",pred.type="re")
plot_model (lambda1,type="std",pred.type="re")


#Temporal variation of deterministic population growth rates

lm2<-lm(CV_lambda~SMDN)
plot(x = SMDN, y = CV_lambda, main="Relationship between the temporal
variation growth rate and\n the minimal distances to the niche boundaries
for populations", xlab="Minimal distances to the niche boundaries",
ylab="Temporal variation growth rate")
abline(lm2)
```

```
CV_lambda1<-lmer(CV_lambda~SMDN+(1|SP)+GT+b+c,data=corrDat)
CV_lambda3<-lmer(CV_lambda~SMDN+(1|SP)+(1|GT)+b+c,data=corrDat)
CV_lambda4<-lmer(CV_lambda~SMDN+(1|SP)+(SMDN|GT)+GT+b+c,data=corrDat)
CV_lambda5<-lmer(CV_lambda~SMDN+(1+SMDN|SP)+GT+b+c,data=corrDat)
CV_lambda6<-lmer(CV_lambda~SMDN+(1+SMDN|SP)+(1|GT)+b+c,data=corrDat)
CV_lambda7<-lmer(CV_lambda~SMDN+(1+SMDN|SP)+(SMDN|GT)+b+c,data=corrDat)

anova(CV_lambda1,CV_lambda3,CV_lambda4,CV_lambda5,CV_lambda6,CV_lambda7)
summary(CV_lambda1)
confint(CV_lambda1)
r.squaredGLMM(CV_lambda1)
Anova(CV_lambda1)

plot_model(CV_lambda1,type="pred",pred.type="re",terms="SMDN")
plot_model(CV_lambda1,type="slope",pred.type="re")
plot_model(CV_lambda1,type="std",pred.type="re")



#Time to 95% probability of quasi-extinction

lm3<-lm(TExt~SMDN)
plot(x = SMDN, y = TExt, main="Relationship between the time to quasi
extinction and\n the minimal distances to the niche boundaries for
populations", xlab="Minimal distances to the niche boundaries", ylab="Time
to quasi-extinction")
abline(lm3)

Time1<-lmer(TExt~SMDN+(1|SP)+GT+b+c,data=corrDat)
Time3<-lmer(TExt~SMDN+(1|SP)+(1|GT)+b+c,data=corrDat)
Time4<-lmer(TExt~SMDN+(1|SP)+(SMDN|GT)+GT+b+c,data=corrDat)
Time5<-lmer(TExt~SMDN+(1+SMDN|SP)+GT+b+c,data=corrDat)
Time6<-lmer(TExt~SMDN+(1+SMDN|SP)+(1|GT)+b+c,data=corrDat)
Time7<-lmer(TExt~SMDN+(1+SMDN|SP)+(SMDN|GT)+b+c,data=corrDat)

anova(Time1,Time3,Time4,Time5,Time6,Time7)
summary(Time1)
r.squaredGLMM(Time1)
confint(Time1)
Anova(Time1)


plot_model(Time1,type="pred",pred.type="re",terms="SMDN")
plot_model(Time1,type="slope",pred.type="re")
plot_model(Time1,type="std",pred.type="re")


#Fecundity

lm4<-lm(Fe~SMDN)
plot(x = SMDN, y = Fe,  main="Relationship between the fecundity and\n the
minimal distances to the niche boundaries for populations", xlab="Minimal
distances to the niche boundaries", ylab="Fecundity")
abline(lm4)

Fe1<-lmer(Fe~SMDN+(1|SP)+GT+b+c,data=corrDat)
Fe3<-lmer(Fe~SMDN+(1|SP)+(1|GT)+b+c,data=corrDat)
Fe4<-lmer(Fe~SMDN+(1|SP)+(SMDN|GT)+GT+b+c,data=corrDat)
Fe5<-lmer(Fe~SMDN+(1+SMDN|SP)+GT+b+c,data=corrDat)
Fe6<-lmer(Fe~SMDN+(1+SMDN|SP)+(1|GT)+b+c,data=corrDat)
Fe7<-lmer(Fe~SMDN+(1+SMDN|SP)+(SMDN|GT)+b+c,data=corrDat)

anova(Fe1,Fe3,Fe4,Fe5,Fe6,Fe7)
summary(Fe1)
confint(Fe1)
r.squaredGLMM(Fe1)
Anova(Fe1)

plot_model(Fe1,type="pred",pred.type="re",terms="SMDN")
plot_model(Fe1,type="slope",pred.type="re")
```

```
plot_model(Fe1,type="std",pred.type="re")
```

```
##ANNA Article##

hist(corrDat$CS)

#2)Stochastic population growth rate


lambda2<-lmer(lambda~CS+(1|SP)+GT+b+c,data=corrDat)

summary(lambda2)
confint(lambda2)
r.squaredGLMM(lambda2)


plot_model(lambda2,type="pred",pred.type="re",terms=c("CS"))
plot_model(lambda2,type="std",pred.type="re")


#Temporal variation of deterministic population growth rates

CV_lambda2<-lmer(CV_lambda~CS+(1|SP)+GT+b+c,data=corrDat)

summary(CV_lambda2)
confint(CV_lambda2)
r.squaredGLMM(CV_lambda2)
anova(CV_lambda2)

plot_model(CV_lambda2,type="pred",pred.type="re",terms="CS")
plot_model(CV_lambda2,type="std",pred.type="re")

#Time to 95% probability of quasi-extinction

Time2<-lmer(TExt~CS+(1|SP)+GT+b+c,data=corrDat)

summary(Time2)
r.squaredGLMM(Time2)
confint(Time2)
anova(Time2)

plot_model(Time2,type="pred",pred.type="re",terms="CS")
plot_model(Time2,type="std",pred.type="re")

#Fecundity
lm5<-lm(Fe~CS)
plot(x = CS, y = Fe, main="Relationship between the fecundity and\n climate
suitability for populations", xlab="Climate suitabiliy", ylab="Fecundity")
abline(lm5)

Fe2<-lmer(Fe~CS+(1|SP)+GT+b+c,data=corrDat)

summary(Fe2)
confint(Fe2)
anova(Fe2)
r.squaredGLMM(Fe2)

plot_model(Fe2,type="pred",pred.type="re",terms="CS")
plot_model(Fe2,type="std",pred.type="re")
```