Run HMSC for plants with traits

2023-04-03

### Model inputs :

## Loading required package: coda

# Crozet

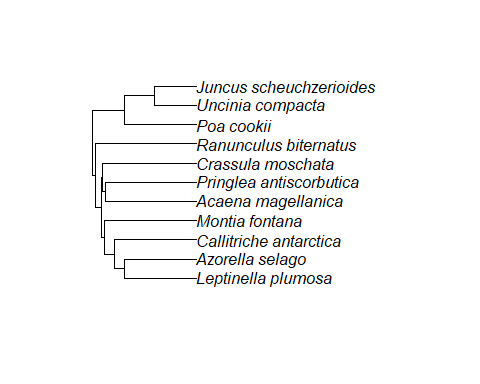
colnames(Y\_cro)

## [1] "Acaena magellanica" "Azorella selago"   
## [3] "Callitriche antarctica" "Crassula moschata"   
## [5] "Juncus scheuchzerioides" "Leptinella plumosa"   
## [7] "Montia fontana" "Poa cookii"   
## [9] "Pringlea antiscorbutica" "Ranunculus biternatus"   
## [11] "Uncinia compacta"

TrData\_cro

## taxon height\_m SLA  
## Acaena magellanica Acaena magellanica 0.09000000 11.968600  
## Azorella selago Azorella selago 0.13933333 8.714400  
## Callitriche antarctica Callitriche antarctica 0.09500000 37.899000  
## Crassula moschata Crassula moschata 0.03833333 22.334500  
## Juncus scheuchzerioides Juncus scheuchzerioides 0.03157143 14.478000  
## Leptinella plumosa Leptinella plumosa 0.06433333 18.350000  
## Montia fontana Montia fontana 0.15942105 40.043500  
## Poa cookii Poa cookii 0.33187500 10.485444  
## Pringlea antiscorbutica Pringlea antiscorbutica 0.18818182 6.759625  
## Ranunculus biternatus Ranunculus biternatus 0.02425000 15.023571  
## Uncinia compacta Uncinia compacta 0.08214286 9.940400

ape::plot.phylo(phyloTree\_cro)



# Kerguelen

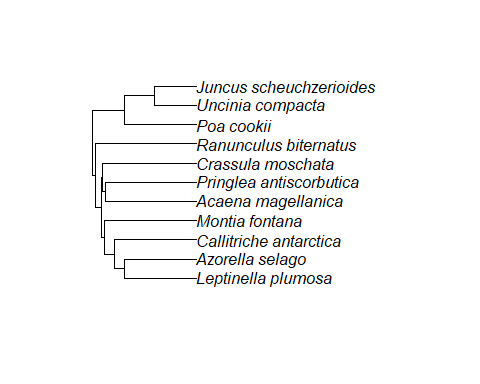
colnames(Y\_ker)

## [1] "Acaena magellanica" "Azorella selago"   
## [3] "Callitriche antarctica" "Crassula moschata"   
## [5] "Juncus scheuchzerioides" "Leptinella plumosa"   
## [7] "Montia fontana" "Poa cookii"   
## [9] "Pringlea antiscorbutica" "Ranunculus biternatus"   
## [11] "Uncinia compacta"

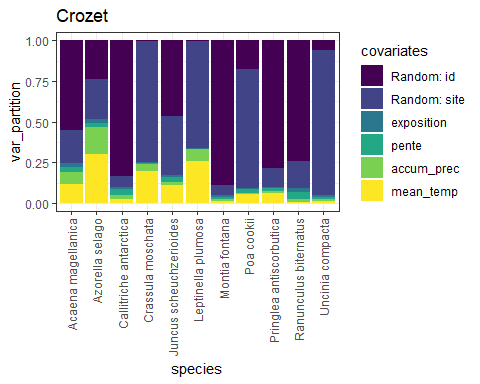
TrData\_ker

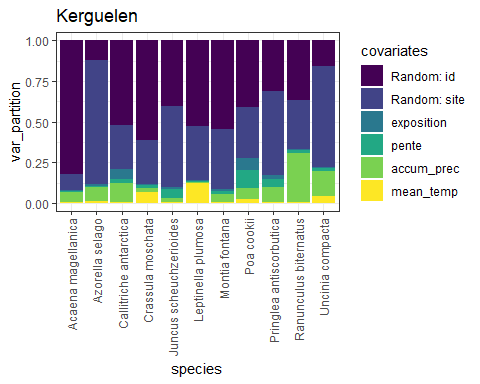
## taxon height\_m SLA  
## Acaena magellanica Acaena magellanica 0.09000000 11.968600  
## Azorella selago Azorella selago 0.13933333 8.714400  
## Callitriche antarctica Callitriche antarctica 0.09500000 37.899000  
## Crassula moschata Crassula moschata 0.03833333 22.334500  
## Juncus scheuchzerioides Juncus scheuchzerioides 0.03157143 14.478000  
## Leptinella plumosa Leptinella plumosa 0.06433333 18.350000  
## Montia fontana Montia fontana 0.15942105 40.043500  
## Poa cookii Poa cookii 0.33187500 10.485444  
## Pringlea antiscorbutica Pringlea antiscorbutica 0.18818182 6.759625  
## Ranunculus biternatus Ranunculus biternatus 0.02425000 15.023571  
## Uncinia compacta Uncinia compacta 0.08214286 9.940400

ape::plot.phylo(phyloTree\_ker)



# model structure:  
m = Hmsc(Y=Y, XData = XData, XFormula = XFormula,  
 TrData = TrData, TrFormula = TrFormula,  
 phyloTree = phylo\_cro,  
 distr="probit",  
 studyDesign = studyDesign, ranLevels=list(site=rL.site, id=rL.id))

Variance partition for Crozet 

Variance partition for Kerguelen 

Make map of Crozet based on beta predicted values

crozet = TRUE  
cro <- sf::st\_read("../data/SIG/Contours/CRO\_contours.shp")

## Reading layer `CRO\_contours' from data source   
## `C:\Users\Camille\Documents\ASICS\data\SIG\Contours\CRO\_contours.shp'   
## using driver `ESRI Shapefile'  
## Simple feature collection with 1 feature and 3 fields  
## Geometry type: MULTIPOLYGON  
## Dimension: XY  
## Bounding box: xmin: 51.64115 ymin: -46.4747 xmax: 51.87478 ymax: -46.34136  
## Geodetic CRS: WGS 84

source("../ASICS\_code/process\_occurrences.R")

## ── Attaching packages ─────────────────────────────────────── tidyverse 1.3.2 ──  
## ✔ tibble 3.1.8 ✔ dplyr 1.1.0  
## ✔ tidyr 1.3.0 ✔ stringr 1.5.0  
## ✔ readr 2.1.3 ✔ forcats 1.0.0  
## ✔ purrr 1.0.1   
## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ tidyr::extract() masks magrittr::extract()  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()  
## ✖ purrr::set\_names() masks magrittr::set\_names()  
## Linking to GEOS 3.9.3, GDAL 3.5.2, PROJ 8.2.1; sf\_use\_s2() is TRUE  
##   
## Loading required package: sp  
##   
##   
## Attaching package: 'raster'  
##   
##   
## The following object is masked from 'package:dplyr':  
##   
## select  
##   
##   
## Loading required package: abind

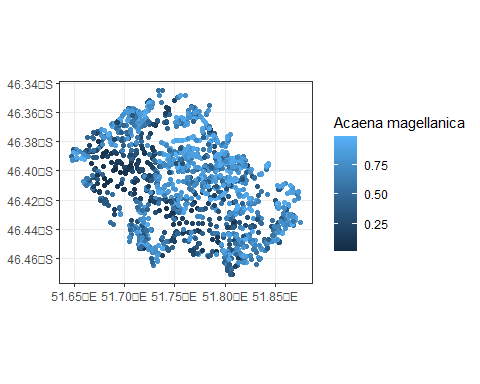
pred\_cro <- predict(m\_cro)  
map\_cro <- cbind(env\_vars[models\_cro[[1]]$XData$id, ], pred\_cro)  
  
  
  
  
Epred\_cro <- Reduce("+",pred\_cro)/length(pred\_cro)  
dim(Epred\_cro)

## [1] 1940 11

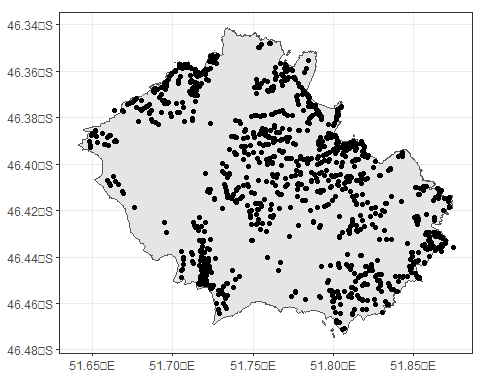
head(Epred\_cro, 10)

## Acaena magellanica Azorella selago Callitriche antarctica Crassula moschata  
## 1 0.953 0.842 0.025 0.001  
## 2 0.875 0.863 0.009 0.001  
## 3 0.496 0.900 0.002 0.009  
## 4 0.609 0.835 0.004 0.006  
## 5 0.408 0.804 0.004 0.024  
## 6 0.344 0.860 0.003 0.010  
## 8 0.501 0.811 0.016 0.025  
## 9 0.397 0.818 0.012 0.279  
## 10 0.612 0.760 0.009 0.023  
## 11 0.395 0.756 0.003 0.036  
## Juncus scheuchzerioides Leptinella plumosa Montia fontana Poa cookii  
## 1 0.129 0.000 0.107 0.165  
## 2 0.230 0.002 0.028 0.078  
## 3 0.223 0.012 0.004 0.069  
## 4 0.095 0.003 0.005 0.177  
## 5 0.594 0.038 0.007 0.083  
## 6 0.135 0.015 0.003 0.199  
## 8 0.609 0.041 0.056 0.098  
## 9 0.206 0.315 0.031 0.279  
## 10 0.175 0.035 0.017 0.133  
## 11 0.142 0.063 0.001 0.112  
## Pringlea antiscorbutica Ranunculus biternatus Uncinia compacta  
## 1 0.514 0.853 0.747  
## 2 0.191 0.697 0.736  
## 3 0.021 0.347 0.468  
## 4 0.091 0.369 0.362  
## 5 0.015 0.244 0.460  
## 6 0.026 0.241 0.227  
## 8 0.029 0.515 0.508  
## 9 0.043 0.365 0.193  
## 10 0.046 0.474 0.358  
## 11 0.021 0.231 0.231

# merge with coordinates from the sites that we kept in the analysis:  
  
Epred\_cro <- cbind(Epred\_cro, cro\_sites\_xy[rownames(Epred\_cro), c("latitude", "longitude")])  
  
Epred\_cro %<>% st\_as\_sf(coords = c("longitude", "latitude" ), crs = 4326)  
  
Epred\_cro %>%  
 ggplot() +  
 geom\_sf( aes(color = `Acaena magellanica`))



# merge with coords:  
cro\_com\_mat <- cbind(cro\_com\_mat, cro\_sites\_xy[rownames(cro\_com\_mat) %in% cro\_sites\_xy$numero\_observation, c("latitude", "longitude")]) %>%  
 st\_as\_sf(coords = c("longitude", "latitude" ), crs = 4326)  
  
# extract plants of interest:  
A\_magellanica <- cro\_com\_mat %>%  
 dplyr::filter(`Acaena magellanica` >0) %>%  
 dplyr::select(`Acaena magellanica`, geometry)  
  
# plot presences:  
A\_magellanica %>%  
 ggplot() +  
 geom\_sf(data=cro) +  
 geom\_sf( )



Same for Kerguelen

crozet = FALSE  
source("../ASICS\_code/process\_occurrences.R")  
ker <- sf::st\_read("../data/SIG/Contours/KER\_contours.shp")

## Reading layer `KER\_contours' from data source   
## `C:\Users\Camille\Documents\ASICS\data\SIG\Contours\KER\_contours.shp'   
## using driver `ESRI Shapefile'  
## Simple feature collection with 10 features and 4 fields  
## Geometry type: MULTIPOLYGON  
## Dimension: XY  
## Bounding box: xmin: 68.41941 ymin: -50.01868 xmax: 70.55675 ymax: -48.45173  
## Geodetic CRS: WGS 84

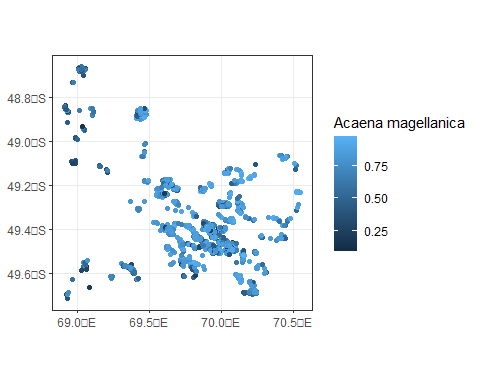
m\_ker <- models\_ker[[1]]  
# get predicted values :   
pred\_ker <- predict(m\_ker)  
# this is a list of length = 1000 ( 4 chains of 250 samples)   
dim(pred\_ker[[1]])

## [1] 2425 11

# To simplify, we take the means --> posterior mean predictions  
  
Epred\_ker <- Reduce("+",pred\_ker)/length(pred\_ker)  
dim(Epred\_ker)

## [1] 2425 11

# merge with coordinates from the sites that we kept in the analysis:  
  
Epred\_ker <- cbind(Epred\_ker, ker\_sites\_xy[rownames(Epred\_ker), c("latitude", "longitude")]) %>%  
 as.data.frame  
#Epred\_ker <- Epred\_ker[-which(is.na(Epred\_ker$longitude)), ]  
Epred\_ker %<>% st\_as\_sf(coords = c("longitude", "latitude" ), crs = 4326)  
Epred\_ker %>%  
 ggplot() +  
 geom\_sf( aes(color = `Acaena magellanica`))



# compare with the presence only:  
# merge with coords:  
ker\_com\_mat <- cbind(ker\_com\_mat, ker\_sites\_xy[rownames(ker\_com\_mat) %in% ker\_sites\_xy$numero\_observation, c("latitude", "longitude")]) %>%  
 st\_as\_sf(coords = c("longitude", "latitude" ), crs = 4326)  
  
# extract plants of interest:  
A\_magellanica <- ker\_com\_mat %>%  
 dplyr::filter(`Acaena magellanica` >0) %>%  
 dplyr::select(`Acaena magellanica`, geometry)  
  
# plot presences:  
A\_magellanica %>%  
 ggplot() +  
 geom\_sf(data=ker) +  
 geom\_sf( )

