

Environmental Layers

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Check for Correlation

This is based on background points from C. kilimanjari

```
library(Hmisc)
```

```
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
## Loading required package: ggplot2
##
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
library(raster)
```

```
## Loading required package: sp
##
## Attaching package: 'raster'
## The following objects are masked from 'package:Hmisc':
##
##     mask, zoom
```

```
e <- extent(25,45,-10,15)
```

```
env1 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_01.tif', header=T)
env1 <- crop(env1, e)
```

```
env3 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_03.tif', header=T)
env3 <- crop(env3, e)
```

```
env5 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_05.tif', header=T)
env5 <- crop(env5, e)
```

```
env15 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_15.tif', header=T)
env15 <- crop(env15, e)
```

```
env17 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_17.tif', header=T)
env17 <- crop(env17, e)
```

```

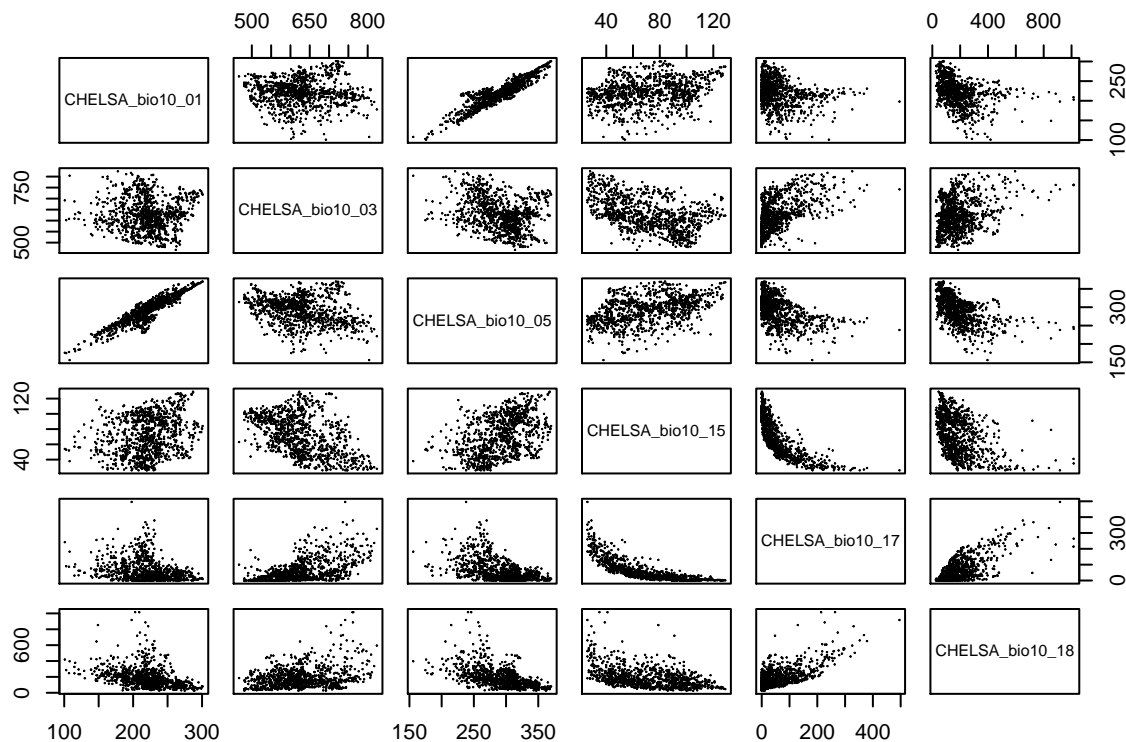
env18 <- raster('~/.scratch/data/env/CHELSA/CHELSA_bio10_18.tif', header=T)
env18 <- crop(env18, e)

env <- stack(env1, env3, env5, env15, env17, env18)

randoz <- read.table('Ckilimanjari.bg.txt', header=T)
bioclims <- extract(env, randoz)
write.table(bioclims, file='bioclims.txt', row.names=F, quote=F)

# correlations
tmp <- read.table("Data/bioclims.txt", header=T)
pairs(tmp[,1:6], cex=0.05)

```



```

rcorr(as.matrix(tmp))

```

```

##          CHELSA_bio10_01 CHELSA_bio10_03 CHELSA_bio10_05 CHELSA_bio10_15
## CHELSA_bio10_01          1.00          -0.03           0.92           0.25
## CHELSA_bio10_03          -0.03           1.00          -0.28          -0.50
## CHELSA_bio10_05           0.92          -0.28           1.00           0.44
## CHELSA_bio10_15           0.25          -0.50           0.44           1.00
## CHELSA_bio10_17          -0.28           0.52          -0.50          -0.78
## CHELSA_bio10_18          -0.37           0.30          -0.54          -0.44
##          CHELSA_bio10_17 CHELSA_bio10_18
## CHELSA_bio10_01          -0.28          -0.37
## CHELSA_bio10_03           0.52           0.30
## CHELSA_bio10_05          -0.50          -0.54
## CHELSA_bio10_15          -0.78          -0.44
## CHELSA_bio10_17           1.00           0.70
## CHELSA_bio10_18           0.70           1.00
##

```

```

## n= 989
##
##
## P
##          CHELSA_bio10_01 CHELSA_bio10_03 CHELSA_bio10_05 CHELSA_bio10_15
## CHELSA_bio10_01          0.3232          0.0000          0.0000
## CHELSA_bio10_03 0.3232          0.0000          0.0000
## CHELSA_bio10_05 0.0000          0.0000          0.0000
## CHELSA_bio10_15 0.0000          0.0000          0.0000
## CHELSA_bio10_17 0.0000          0.0000          0.0000          0.0000
## CHELSA_bio10_18 0.0000          0.0000          0.0000          0.0000
##          CHELSA_bio10_17 CHELSA_bio10_18
## CHELSA_bio10_01 0.0000          0.0000
## CHELSA_bio10_03 0.0000          0.0000
## CHELSA_bio10_05 0.0000          0.0000
## CHELSA_bio10_15 0.0000          0.0000
## CHELSA_bio10_17          0.0000
## CHELSA_bio10_18 0.0000

```

Methods Summary

Species distribution models were based on five bioclimatic variables: annual mean temperature (bio1), isothermality (bio3), precipitation seasonality (bio15), precipitation of the driest quarter (bio17), and precipitation of the warmest quarter (bio18). Four of the variables (bio1, bio3, bio15, and bio18) were previously reported as important variables for species distribution models for [*C. chinensis*] (<https://bmcecol.biomedcentral.com/track/pdf/10.1186/s12898-020-00295-6>) and the fifth (bio17) had high feature importance in preliminary analyses. Bioclimatic data were obtained from the CHELSA dataset. All variables had Pearson's correlation coefficients less than 0.8 when assessed across the background extent of the study.