Modelo Pseudotsuga menziesii

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Preparar el entorno

```
library(sp)
```

```
## Warning: package 'sp' was built under R version 4.2.3
```

```
library(rgdal)
```

```
## Warning: package 'rgdal' was built under R version 4.2.3
```

```
## Please note that rgdal will be retired during 2023,
## plan transition to sf/stars/terra functions using GDAL and PROJ
## at your earliest convenience.
## See https://r-spatial.org/r/2022/04/12/evolution.html and https://github.com/r-spatial/evolution
## rgdal: version: 1.6-6, (SVN revision 1201)
## Geospatial Data Abstraction Library extensions to R successfully loaded
## Loaded GDAL runtime: GDAL 3.5.2, released 2022/09/02
## Path to GDAL shared files: C:/Users/vshal/AppData/Local/R/win-library/4.2/rgdal/gdal
## GDAL binary built with GEOS: TRUE
## Loaded PROJ runtime: Rel. 8.2.1, January 1st, 2022, [PJ_VERSION: 821]
## Path to PROJ shared files: C:/Users/vshal/AppData/Local/R/win-library/4.2/rgdal/proj
## PROJ CDN enabled: FALSE
## Linking to sp version:1.6-0
## To mute warnings of possible GDAL/OSR exportToProj4() degradation,
## use options("rgdal_show_exportToProj4_warnings"="none") before loading sp or rgdal.
```

```
library(raster)
```

```
## Warning: package 'raster' was built under R version 4.2.3
```

```
library(dismo)
library(rJava)
```

```
## Warning: package 'rJava' was built under R version 4.2.3
```

```
library(rworldmap)
```

```
## ### Welcome to rworldmap ###
```

```
## For a short introduction type :   vignette('rworldmap')
```

```
library(rworldxtra)

sessionInfo()
```

```
## R version 4.2.2 (2022-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 22621)
## 
## Matrix products: default
## 
## locale:
## [1] LC_COLLATE=Spanish_Mexico.utf8  LC_CTYPE=Spanish_Mexico.utf8   
## [3] LC_MONETARY=Spanish_Mexico.utf8 LC_NUMERIC=C                   
## [5] LC_TIME=Spanish_Mexico.utf8    
## 
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base     
## 
## other attached packages:
## [1] rworldxtra_1.01 rworldmap_1.3-6 rJava_1.0-6     dismo_1.3-9    
## [5] raster_3.6-20   rgdal_1.6-6     sp_1.6-0       
## 
## loaded via a namespace (and not attached):
##  [1] spam_2.9-1        tidyselect_1.2.0  terra_1.7-29      xfun_0.38        
##  [5] bslib_0.4.2       lattice_0.20-45   colorspace_2.0-3  vctrs_0.6.1      
##  [9] generics_0.1.3    htmltools_0.5.5   viridisLite_0.4.1 yaml_2.3.7       
## [13] utf8_1.2.3        rlang_1.1.0       jquerylib_0.1.4   pillar_1.9.0     
## [17] foreign_0.8-83    glue_1.6.2        lifecycle_1.0.3   fields_14.1      
## [21] dotCall64_1.0-2   munsell_0.5.0     gtable_0.3.1      codetools_0.2-18 
## [25] evaluate_0.20     knitr_1.42        fastmap_1.1.1     maptools_1.1-6   
## [29] fansi_1.0.4       Rcpp_1.0.10       scales_1.2.1      cachem_1.0.7     
## [33] jsonlite_1.8.4    gridExtra_2.3     ggplot2_3.4.1     digest_0.6.31    
## [37] dplyr_1.1.1       grid_4.2.2        cli_3.6.1         tools_4.2.2      
## [41] magrittr_2.0.3    maps_3.4.1        sass_0.4.5        tibble_3.2.1     
## [45] pkgconfig_2.0.3   rmarkdown_2.20    rstudioapi_0.14   viridis_0.6.2    
## [49] R6_2.5.1          compiler_4.2.2
```

Cargar puntos de presencia

```
ocurrencias <- read.delim("ocurrence/occurrence.txt")
dim(ocurrencias)
```

```
## [1] 581 257
```

```
str(ocurrencias[,c("species","decimalLongitude","decimalLatitude")])
```

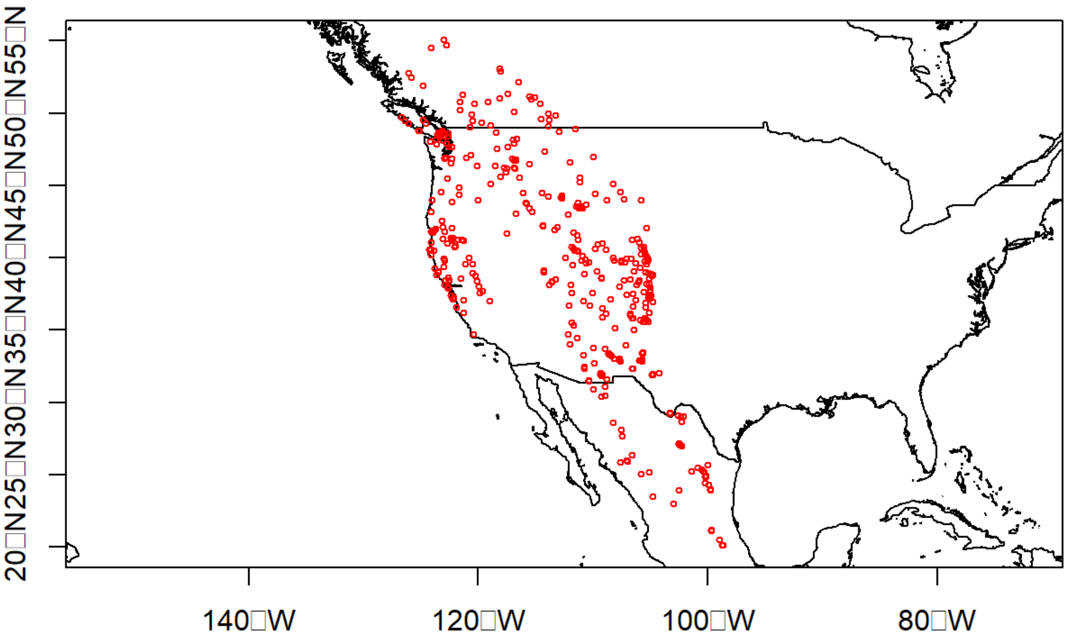
```
## 'data.frame':    581 obs. of  3 variables:
##  $ species         : chr  "Pseudotsuga menziesii" "Pseudotsuga menziesii" "Pseudotsuga menziesii" "Pseudotsuga menziesii"
...
##  $ decimalLongitude: num  -108 -107 -124 -106 -107 ...
##  $ decimalLatitude : num  33 32.4 40.6 33.4 32.3 ...
```

```
ocurrencias <- ocurrencias[,c("species","decimalLongitude","decimalLatitude")]
ocurrencias$species <- as.factor(ocurrencias$species)
head(ocurrencias)
```

```
##                 species decimalLongitude decimalLatitude
## 1 Pseudotsuga menziesii        -107.7388        32.97971
## 2 Pseudotsuga menziesii        -106.5688        32.35220
## 3 Pseudotsuga menziesii        -124.2571        40.56730
## 4 Pseudotsuga menziesii        -105.6267        33.37847
## 5 Pseudotsuga menziesii        -106.5598        32.34767
## 6 Pseudotsuga menziesii        -108.4573        33.27496
```

Visualizar Puntos de presencia

```
mundo <- getMap(resolution = "high")
plot(mundo, axes = TRUE, xlim = c(-130,-95), ylim = c(20,55))
points(ocurrencias$decimalLongitude, ocurrencias$decimalLatitude, cex = 0.5, col = "red")
```

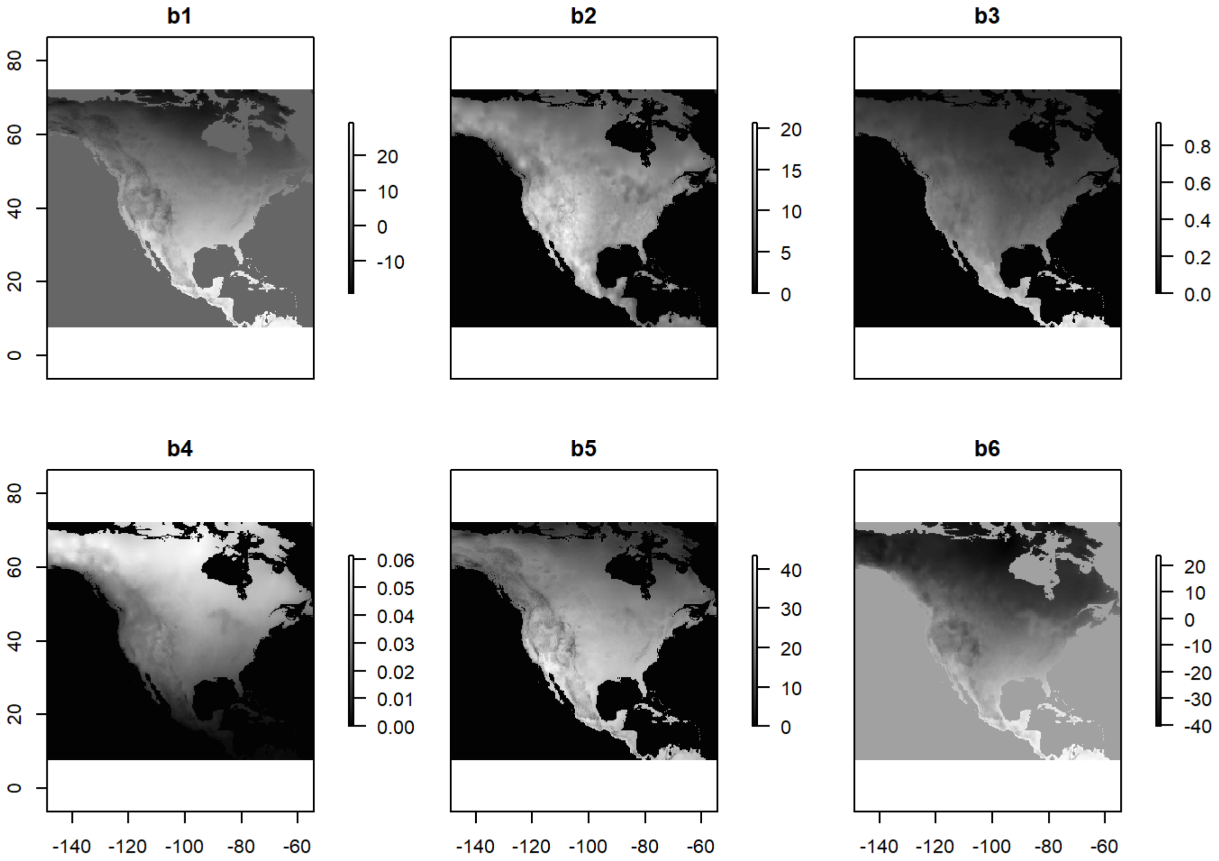


Cargar datos ambientales

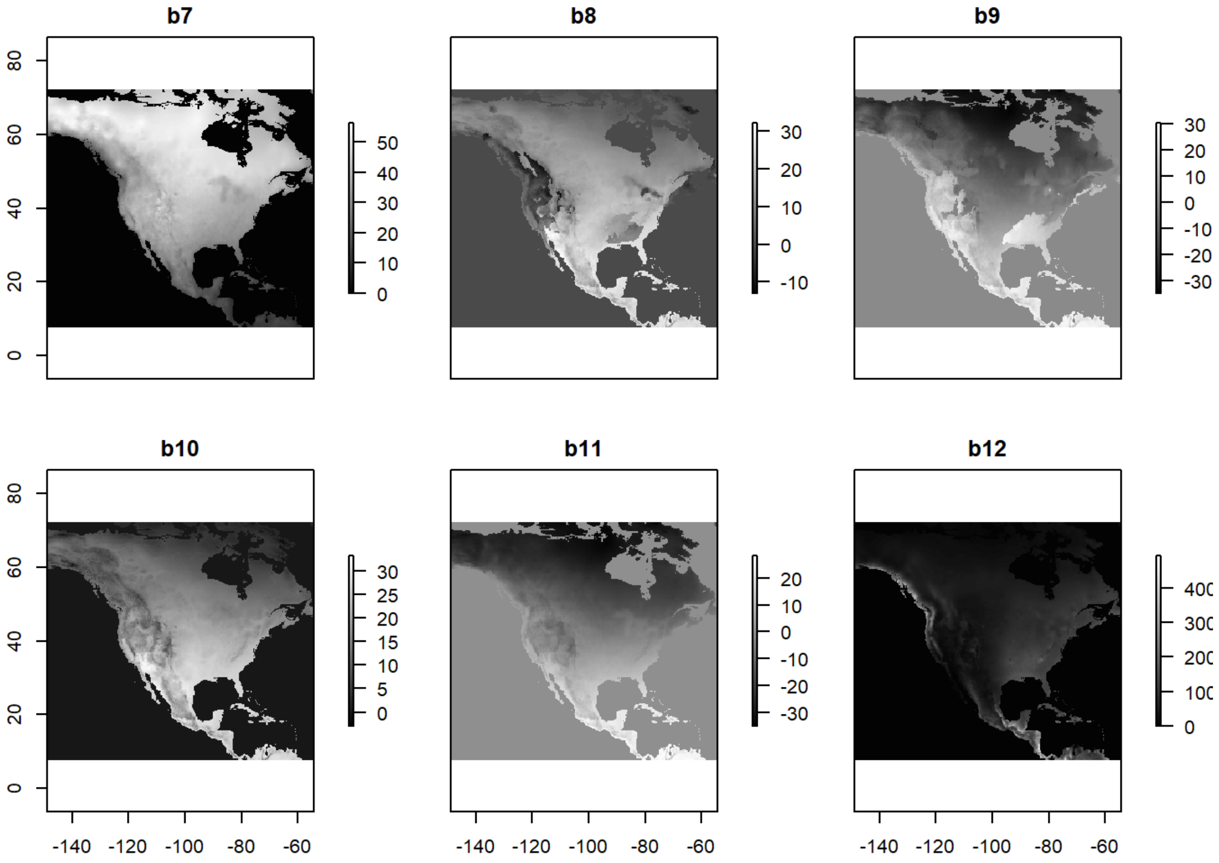
```
bio_vars <- stack("Bioclim/bioclim_40var_ok_recorte.tif")
names(bio_vars) <- paste('b',1:40,sep='')
bio_vars
```

```
## class      : RasterStack
## dimensions : 388, 567, 219996, 40  (nrow, ncol, ncell, nlayers)
## resolution : 0.1666667, 0.1666656  (x, y)
## extent     : -148.8117, -54.31171, 7.687657, 72.3539  (xmin, xmax, ymin, ymax)
## crs        : +proj=longlat +datum=WGS84 +no_defs
## names      : b1, b2, b3, b4, b5, b6, b7, b8, b9, b10, b11, b12, b13, b14, b15, ...
```

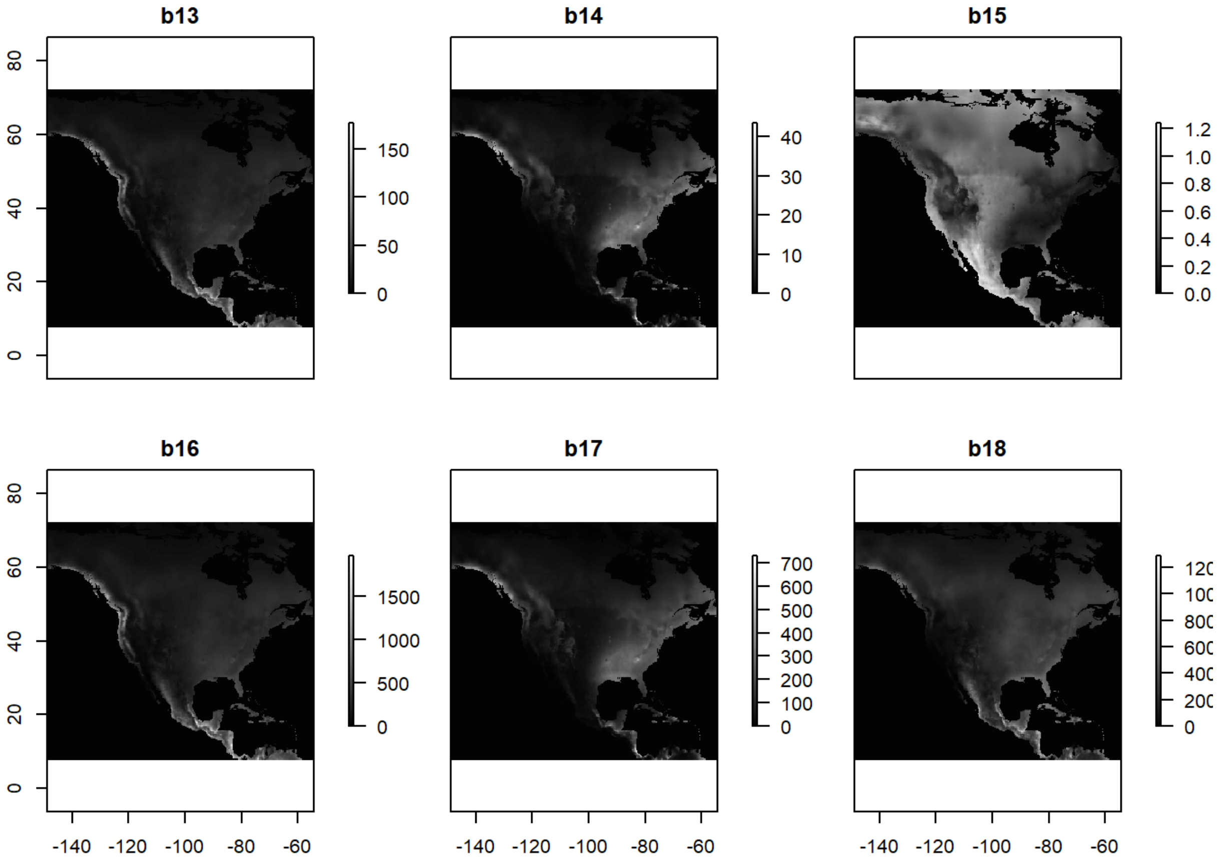
```
plot(bio_vars, c(1:6), col = grey(1:100/100), nc=3)
```



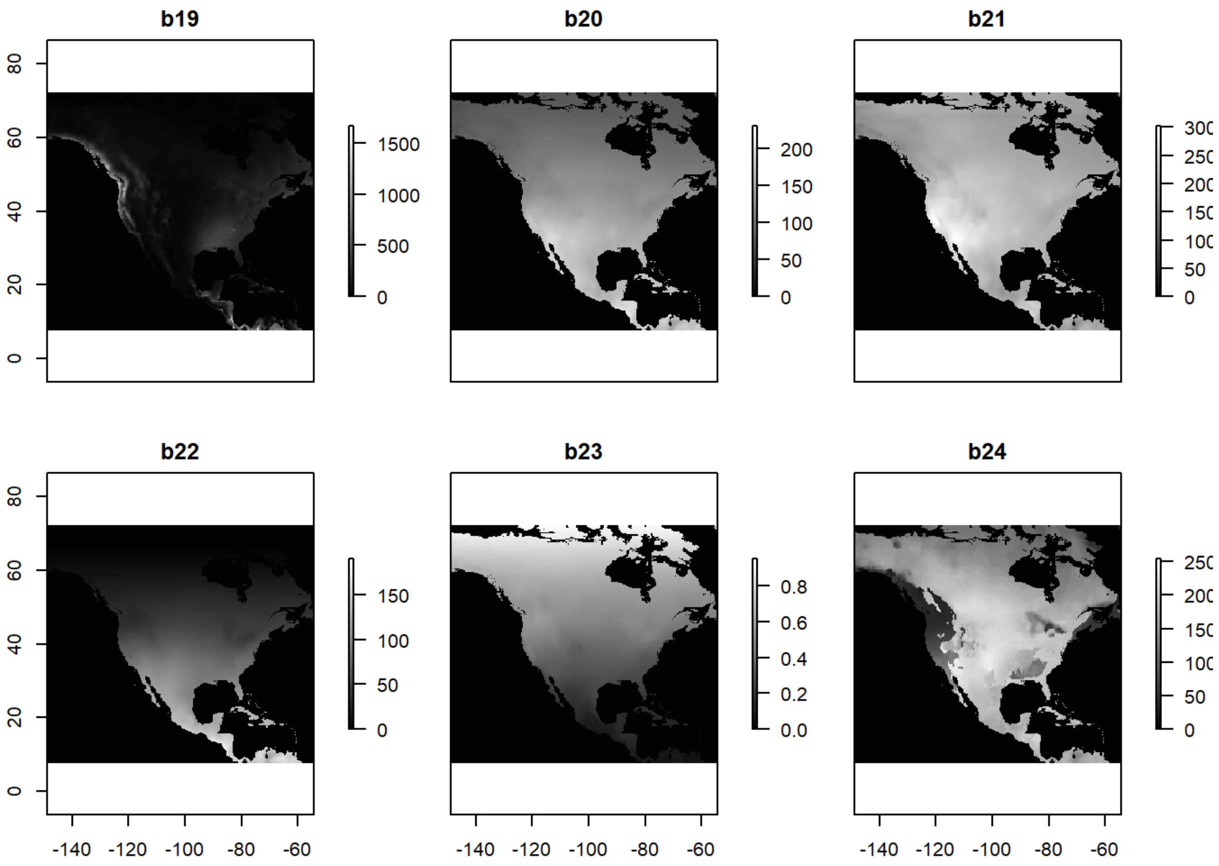
```
plot(bio_vars, c(7:12), col = grey(1:100/100), nc=3)
```



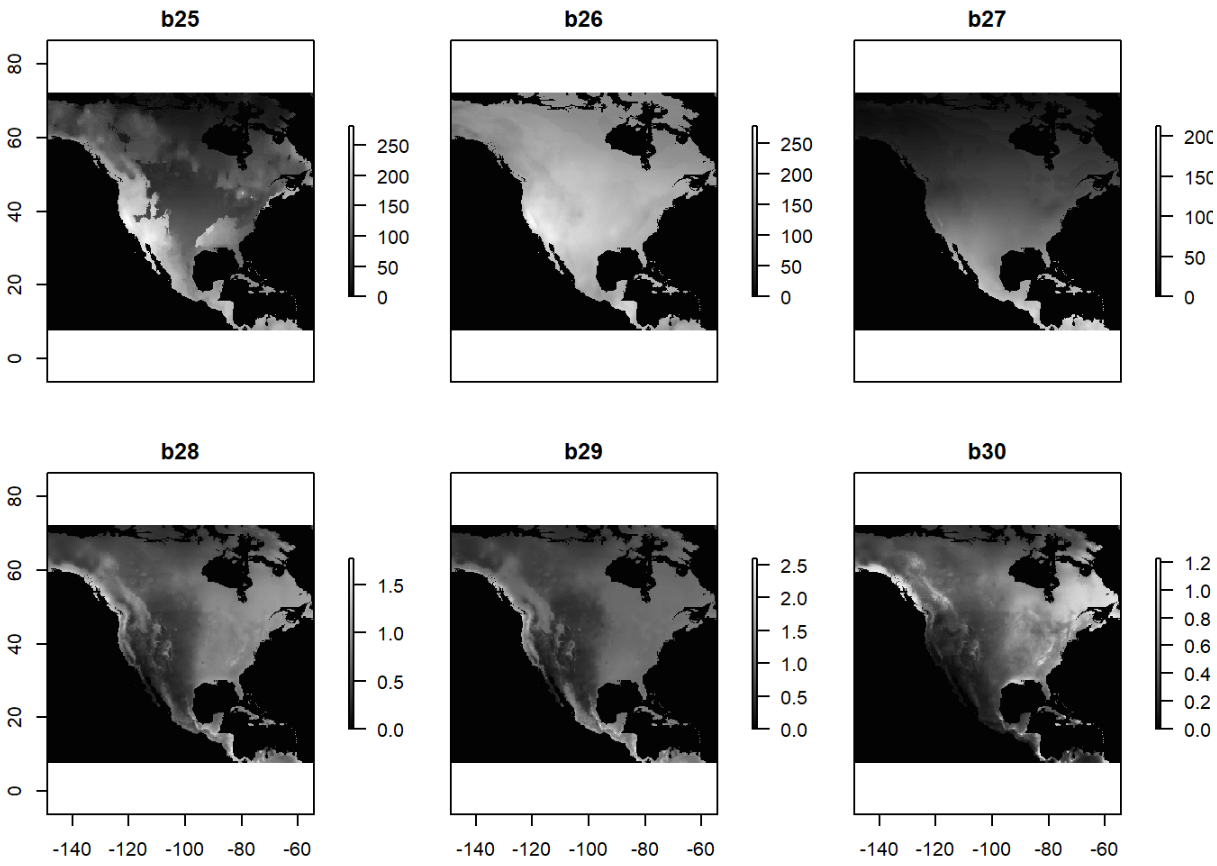
```
plot(bio_vars, c(13:18), col = grey(1:100/100), nc=3)
```



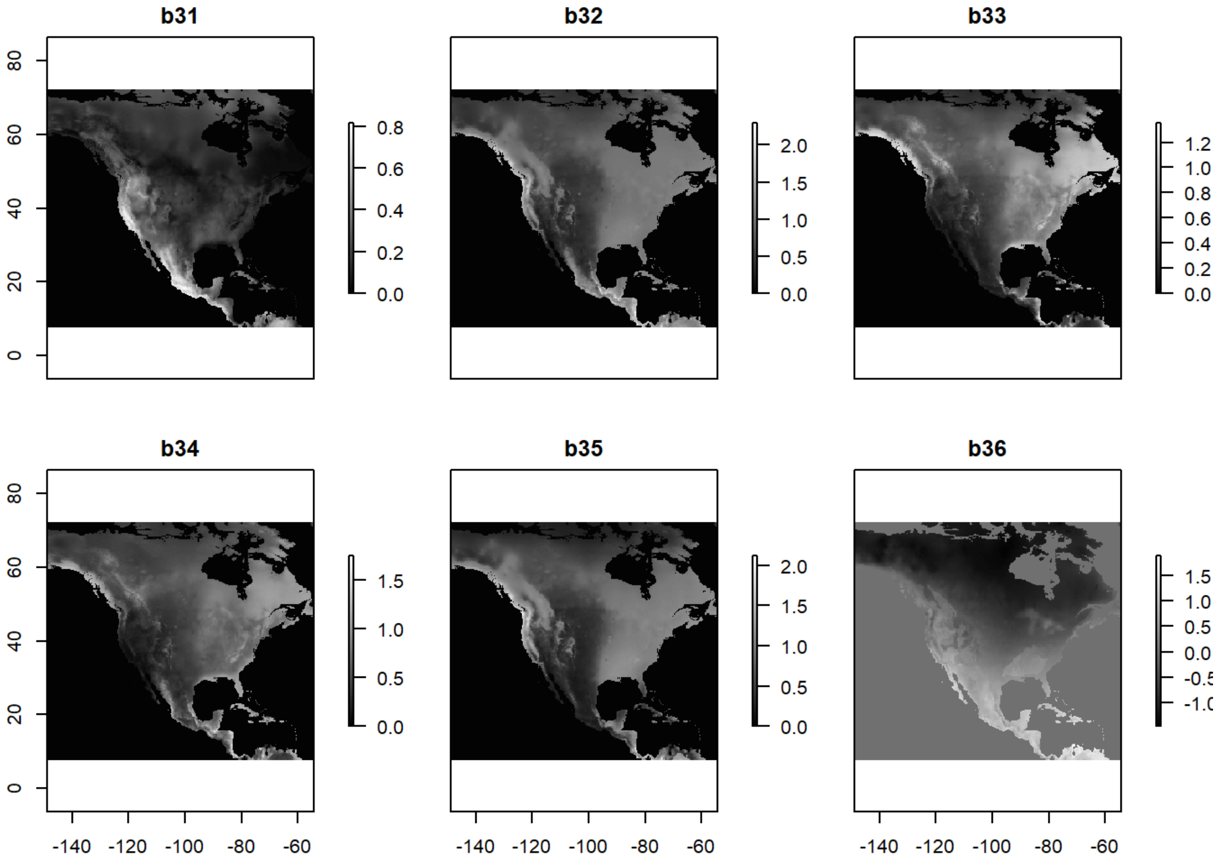
```
plot(bio_vars, c(19:24), col = grey(1:100/100), nc=3)
```



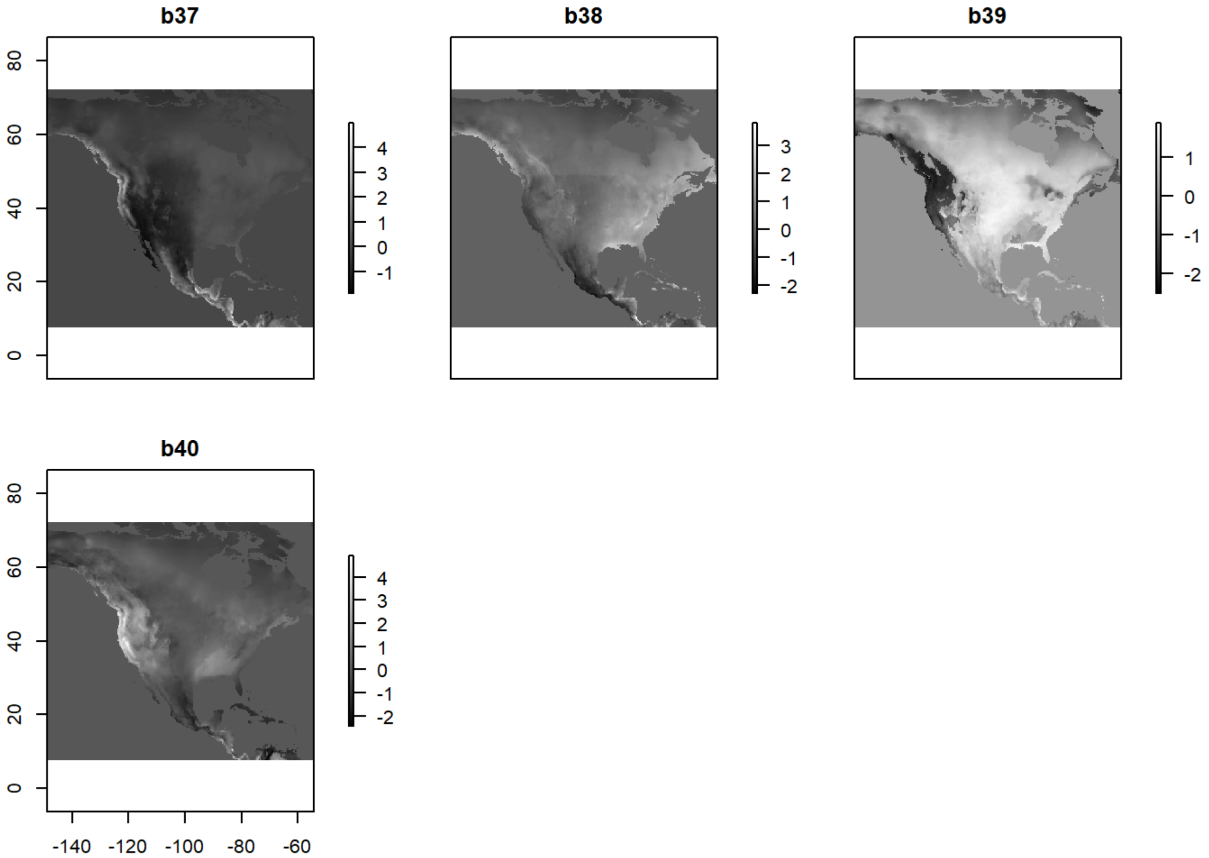
```
plot(bio_vars, c(25:30), col = grey(1:100/100), nc=3)
```



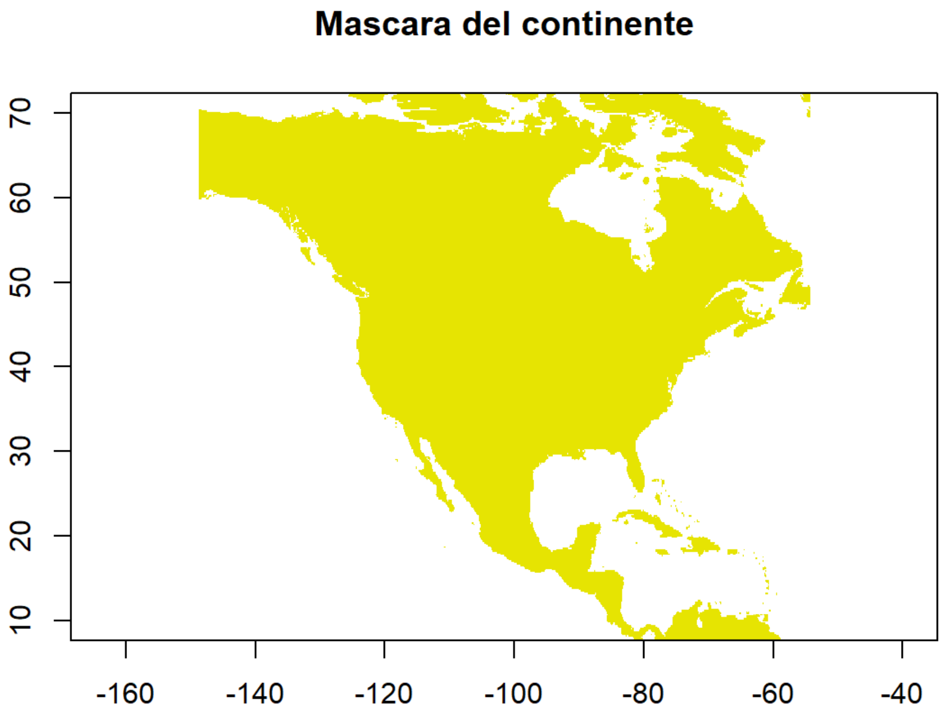
```
plot(bio_vars, c(31:36), col = grey(1:100/100), nc=3)
```



```
plot(bio_vars, c(37:40), col = grey(1:100/100), nc=3)
```



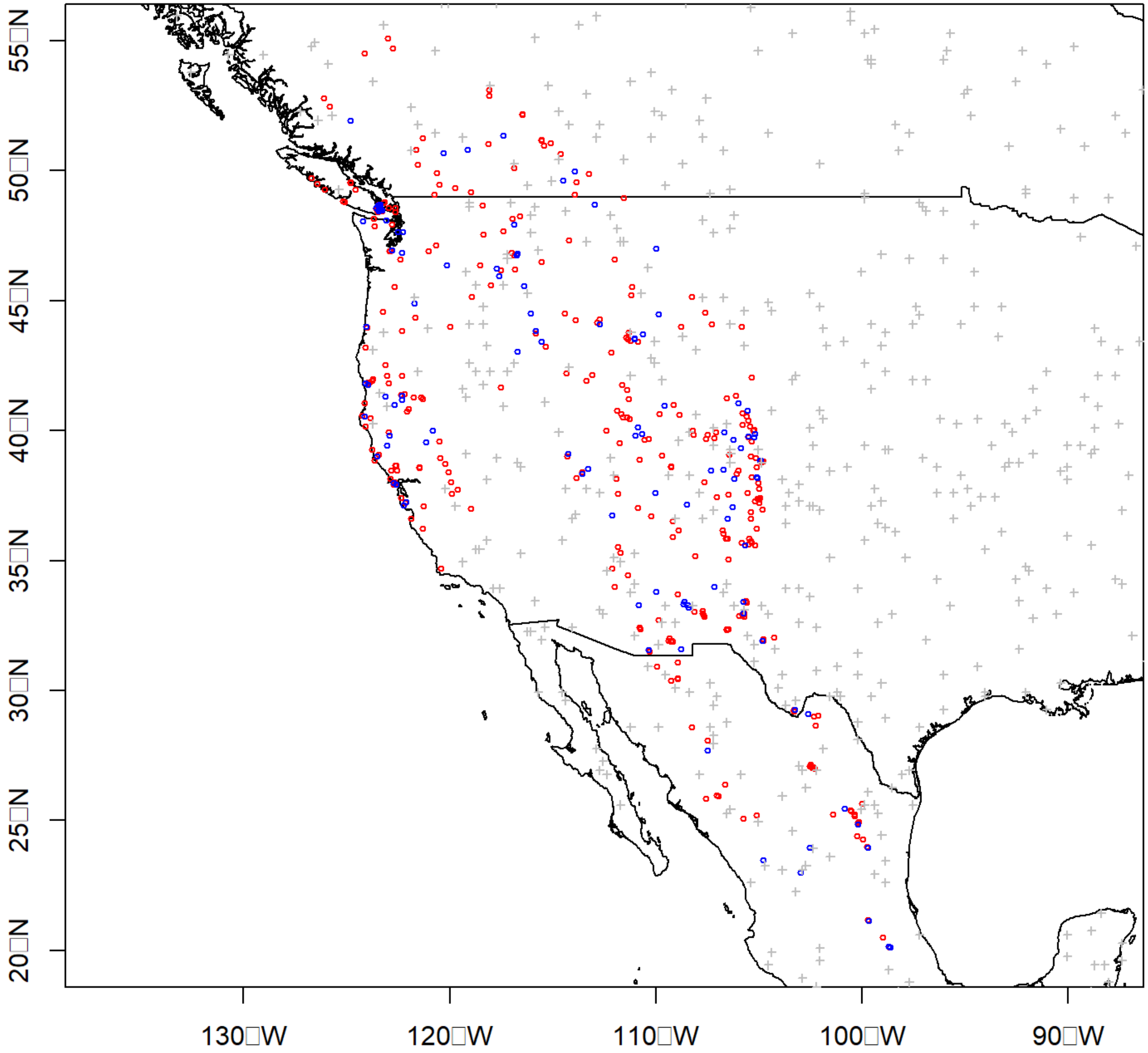
```
mask_reclass_table <- matrix(c(-Inf, 0, NA, 0, Inf, 1), ncol=3, byrow=TRUE)
bio_vars_mask <- reclassify(subset(bio_vars, 12), mask_reclass_table)
plot(bio_vars_mask, legend = FALSE, main = "Mascara del continente")
```


Mascara del continente
70
60
50
40
30
20
10
-160
-140
-120
-100
-80
-60
-40

Definir conjuntos de puntos de entrenamiento y de control

```
set.seed(1)

fold <- kfold(ocurrencias, k = 5)
ocurrencias_entrenamiento <- ocurrencias[ fold != 1, ]
ocurrencias_control <- ocurrencias[ fold == 1, ]

plot(mundo, axes = TRUE, xlim = c(-130,-95), ylim = c(20,55),
     main = "Puntos de entrenamiento y de control de Pseudotsuga menziesii")
points(ocurrencias_entrenamiento$decimalLongitude, ocurrencias_entrenamiento$decimalLatitude,
       cex = 0.5, col = "red")
points(ocurrencias_control$decimalLongitude, ocurrencias_control$decimalLatitude,
       cex = 0.5, col = "blue")

puntos_aleatorios_fondo <- randomPoints(bio_vars_mask, 1000)
points(puntos_aleatorios_fondo, col = "gray", cex = 0.5, pch = 3)
```

Puntos de entrenamiento y de control de Pseudotsuga menziesii



Realizar muestreo de valores ambientales

```
x_presencia <- extract(subset(bio_vars, 1:35), ocurrencias_entrenamiento[,2:3])
x_control <- extract(subset(bio_vars, 1:35), ocurrencias_control[,2:3])
x_fondo <- extract(subset(bio_vars, 1:35), puntos_aleatorios_fondo)

# generar vector de presincias (1) y valores del fondo (0)
y <- c(rep(1, dim(ocurrencias_entrenamiento)[1]),
       rep(0, dim(puntos_aleatorios_fondo)[1]))
x <- rbind(x_presencia, x_fondo)

specie_entrenamiento <- as.data.frame(cbind(x,y))
dim(specie_entrenamiento)
```

```
## [1] 1465   36
```

```
#str(specie_entrenamiento)
head(specie_entrenamiento)
```

```
##          b1       b2        b3          b4      b5       b6       b7        b8
## 1  9.493113 17.57683 0.5020993 0.022678930 27.5600 -7.44667 35.00667 17.362181
## 2 14.580640 16.90603 0.4689173 0.024646200 32.6800 -3.37333 36.05333 23.088070
## 3 11.342480  8.07449 0.5507676 0.008065776 18.9871  4.32667 14.66043  8.874005
## 4 10.440200 15.89849 0.4733104 0.022967471 27.4700 -6.12000 33.59000 18.321030
## 5 14.580640 16.90603 0.4689173 0.024646200 32.6800 -3.37333 36.05333 23.088070
## 6 13.854520 16.09004 0.4620034 0.024033669 31.3800 -3.44667 34.82667 22.054529
##          b9      b10      b11       b12     b13     b14       b15      b16
## 1  9.062980 17.84807 1.554323  468.9998 22.5160 2.38946 0.7022920 247.4439
## 2 12.690760 23.67258 5.622020  293.0000 14.0862 1.46639 0.7014532 153.8621
## 3 14.205380 14.37337 8.661698 1447.0000 60.4494 1.20713 0.7757894 730.8978
## 4  7.572446 18.83243 2.264138  426.0001 20.8721 2.75627 0.7148855 227.7247
## 5 12.690760 23.67258 5.622020  293.0000 14.0862 1.46639 0.7014532 153.8621
## 6 12.045030 22.67207 5.127740  352.0000 15.4698 2.22127 0.6119072 172.8021
##        b17       b18       b19      b20     b21      b22       b23       b24
## 1 45.12693 221.94791  80.18539 180.1977 270.841 100.3830 0.2983824 217.79880
## 2 26.08244 139.76450  45.53280 184.0221 273.314 103.8580 0.2917426 221.10310
## 3 38.56227  57.96872 714.88000 135.4905 219.320  57.0180 0.4175186  64.13944
## 4 52.74678 216.56461  58.93639 177.0775 261.608  99.2535 0.2963731 215.73830
## 5 26.08244 139.76450  45.53280 184.0221 273.314 103.8580 0.2917426 221.10310
## 6 40.02862 158.74860  58.29061 179.5582 264.855 101.2660 0.2925339 217.18370
##        b25      b26       b27       b28      b29      b30       b31       b32
## 1 215.1306 234.0828 113.15160 0.4115424 0.607546 0.221662 0.2691783 0.5494443
## 2 202.9901 237.6931 116.98480 0.2870778 0.392857 0.159496 0.2450126 0.3671726
## 3 199.7792 185.6432  70.07321 0.9549514 1.503062 0.280562 0.4689641 1.4582940
## 4 186.1920 231.5430 111.77560 0.3842115 0.565269 0.257073 0.2249405 0.5118567
## 5 202.9901 237.6931 116.98480 0.2870778 0.392857 0.159496 0.2450126 0.3671726
## 6 197.8496 233.1818 114.07550 0.3291340 0.426847 0.200007 0.2102104 0.4037451
##         b33       b34       b35 y
## 1 0.2555285 0.4615018 0.4419149 1
## 2 0.1831211 0.3126832 0.3123895 1
## 3 0.3352059 0.3365532 1.4436181 1
## 4 0.2858154 0.4620836 0.3686208 1
## 5 0.1831211 0.3126832 0.3123895 1
## 6 0.2239663 0.3491877 0.3588941 1
```

```
y_c <- c(rep(1, dim(ocurrencias_control)[1]),
       rep(0, dim(puntos_aleatorios_fondo)[1]))
x_c <- rbind(x_control, x_fondo)

specie_control <- as.data.frame(cbind(x_c,y_c))
```

Construir el modelo MAXENT

```
jar <- paste(system.file(package='dismo'), '/java/maxent.jar', sep='')

if (file.exists(jar)) {
  # modelo_maxent <- maxent(
  #                       x = bio_vars,
  #                       p = ocurrencias_entrenamiento[,2:3],
  #                       a = puntos_aleatorios_fondo,
  #                       silent = FALSE,
  #                       args=c(
  #                         'removeDuplicates=TRUE',
  #                         'jackknife=TRUE',
  #                         'responsecurves=TRUE',
  #                         'threads=2',
  #                         'linear=TRUE',
  #                         'quadratic=TRUE',
  #                         'hinge=FALSE',
  #                         'product=FALSE'
  #                       ))
  modelo_maxent <- maxent(
                        x = specie_entrenamiento[1:35],
                        p = specie_entrenamiento[36],
                        silent = FALSE,
                        args=c(
                          'removeDuplicates=TRUE',
                          'jackknife=TRUE',
                          'responsecurves=TRUE',
                          'threads=2',
                          'linear=TRUE',
                          'threshold=FALSE',
                          'quadratic=TRUE',
                          'hinge=FALSE',
                          'product=FALSE'
                        ))
    summary(modelo_maxent)
    saveRDS(modelo_maxent, "modelo_maxent_Pseudotsuga_menziesii.rds")

} else {
  print('maxent.jar no disponible')
}
```

Realizar evaluación del modelo

```
# evaluacion_e <- evaluate(p = ocurrencias_entrenamiento[,2:3],
#               a = puntos_aleatorios_fondo,
#               x = bio_vars,
#               model = modelo_maxent)
# evaluacion_e

evaluacion_e <- evaluate(model = modelo_maxent,
              p = specie_entrenamiento[specie_entrenamiento$y == 1,1:35],
              a = specie_entrenamiento[specie_entrenamiento$y == 0,1:35])
evaluacion_e
```

```
## class          : ModelEvaluation
## n presences    : 465
## n absences     : 1000
## AUC            : 0.9500968
## cor            : 0.7859653
## max TPR+TNR at : 0.3309454
```

```
# evaluacion_c <- evaluate(p = ocurrencias_control[,2:3],
#               a = puntos_aleatorios_fondo,
#               x = bio_vars,
#               model = modelo_maxent)
# evaluacion_c

evaluacion_c <- evaluate(model = modelo_maxent,
              p = specie_control[specie_control$y == 1,1:35],
              a = specie_control[specie_control$y == 0,1:35]
              )
evaluacion_c
```

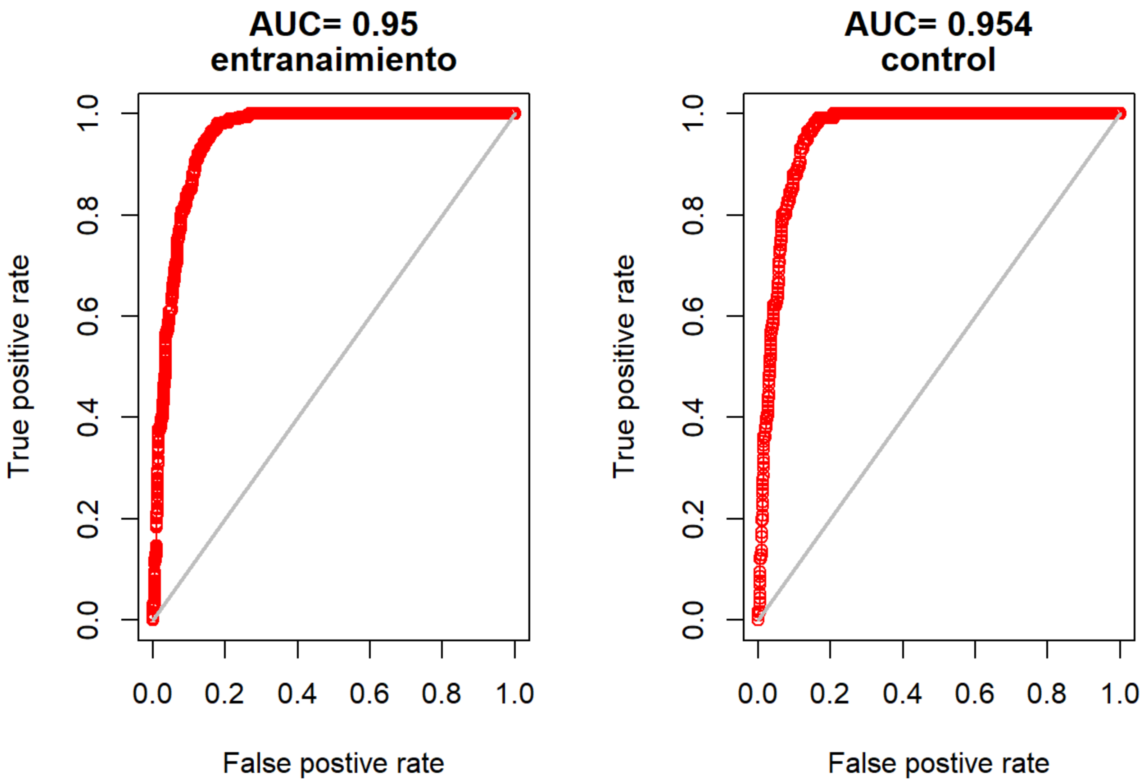
```
## class          : ModelEvaluation
## n presences    : 116
## n absences     : 1000
## AUC            : 0.9541422
## cor            : 0.6336264
## max TPR+TNR at : 0.3859974
```

```
threshold(evaluacion_c)
```

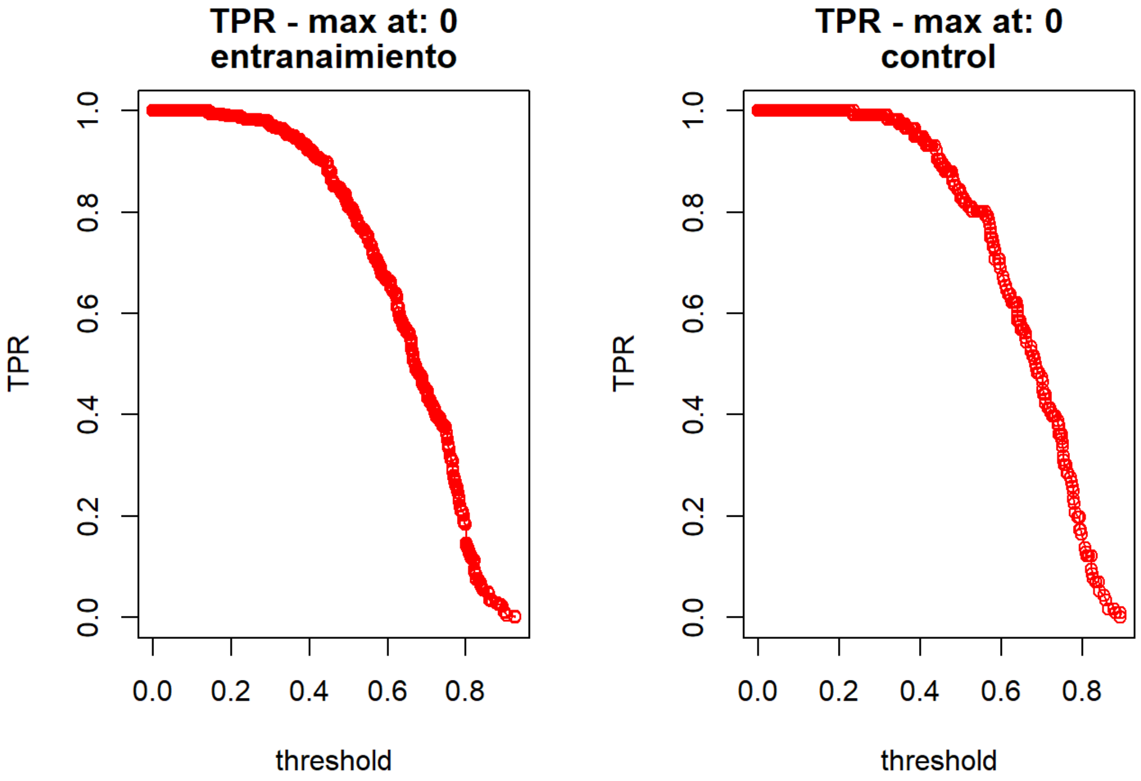
```
##                 kappa spec_sens no_omission prevalence equal_sens_spec
## thresholds 0.5599784 0.3859974   0.2347014  0.1040226       0.4568729
##             sensitivity
## thresholds   0.4492796
```

Presentar graficas de evaluación del modelo

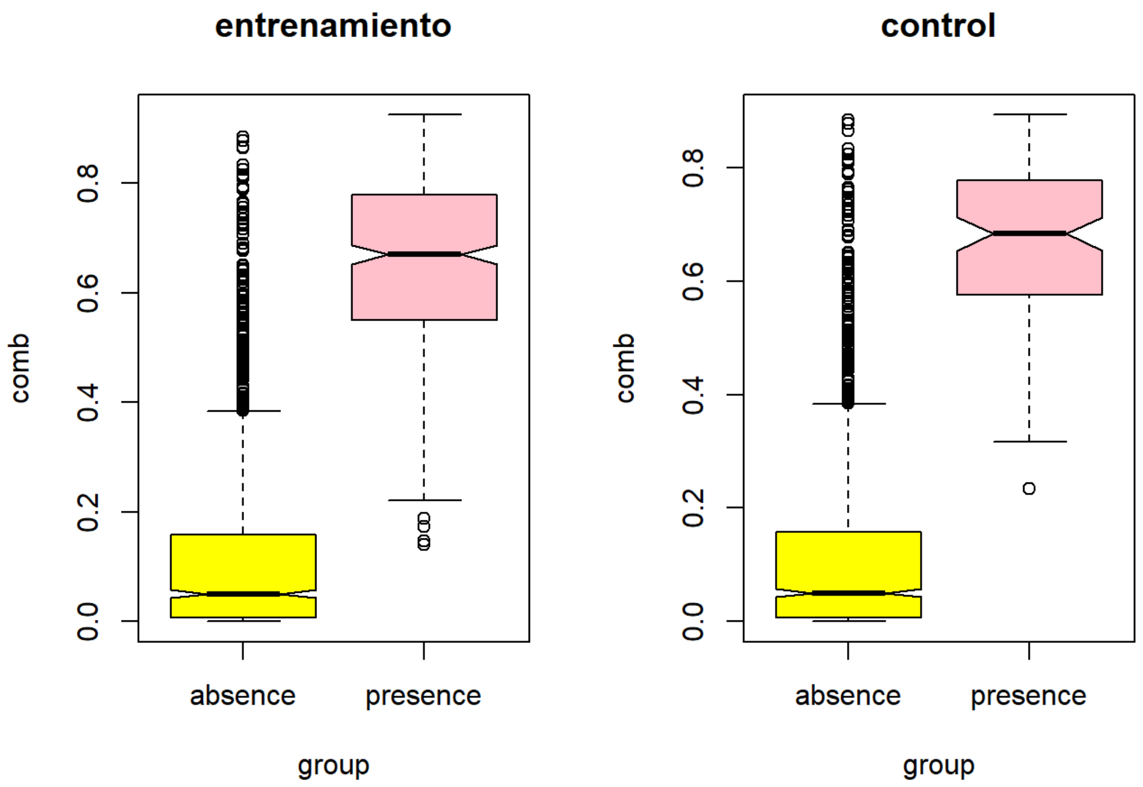
```
par(mfcol = c(1,2))

plot(evaluacion_e, 'ROC')
title(c(" "," ","entranaimiento"))
plot(evaluacion_c, 'ROC')
title(c(" "," ","control"))
```



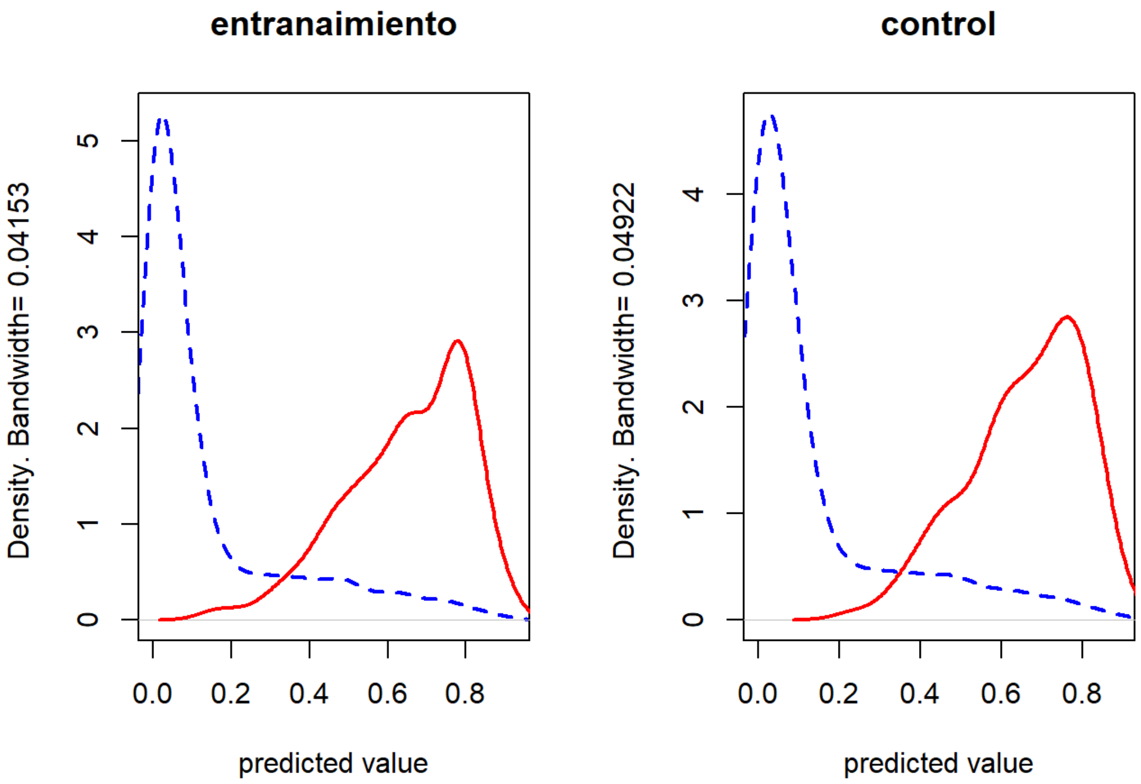
```
plot(evaluacion_e, 'TPR')
title(c(" "," ","entranaimiento"))
plot(evaluacion_c, 'TPR')
title(c(" "," ","control"))
```



```
boxplot(evaluacion_e, col=c('yellow','pink'), notch=TRUE,
        main = "entrenamiento")
boxplot(evaluacion_c, col=c('yellow','pink'), notch=TRUE,
        main = "control")
```

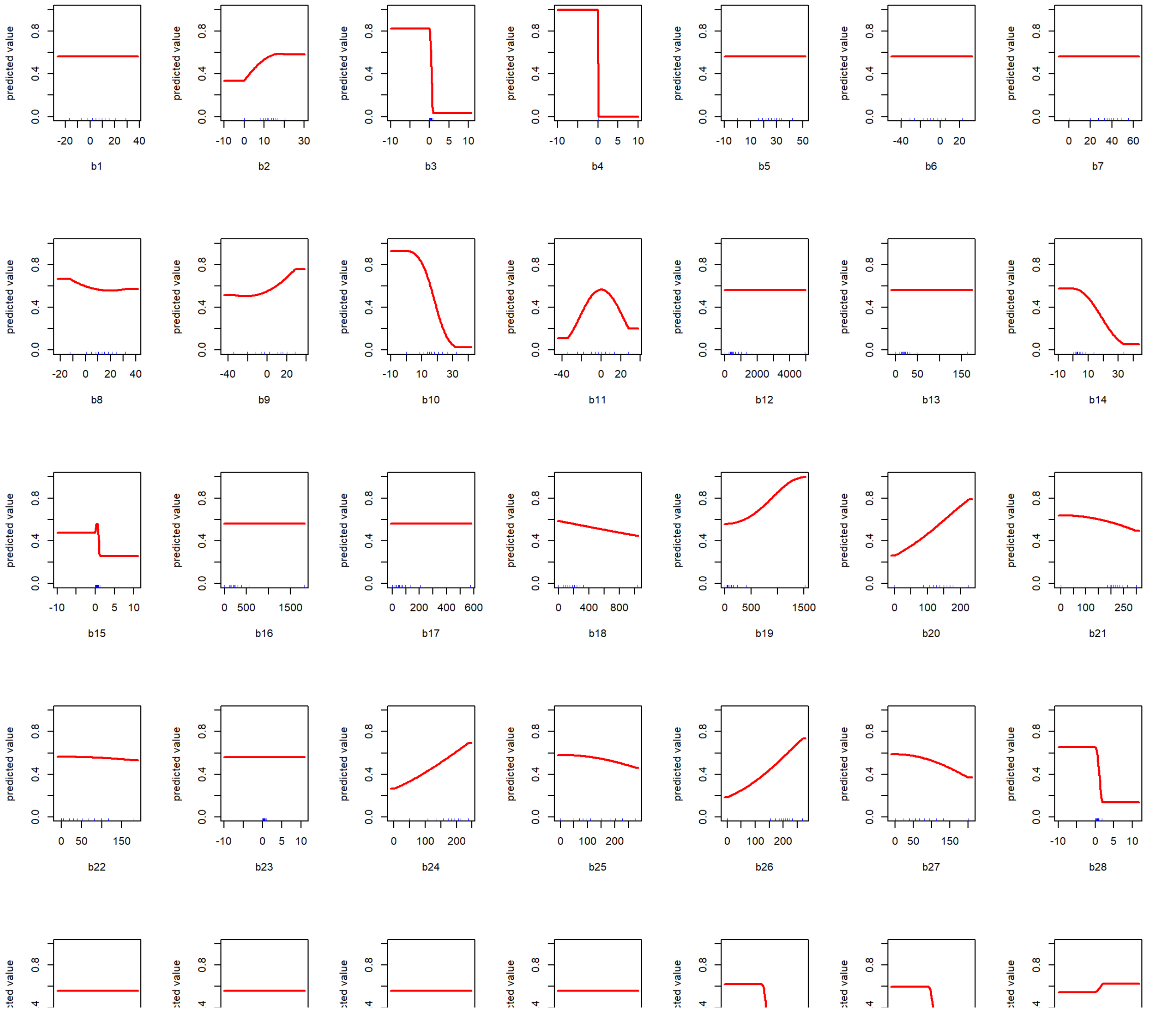


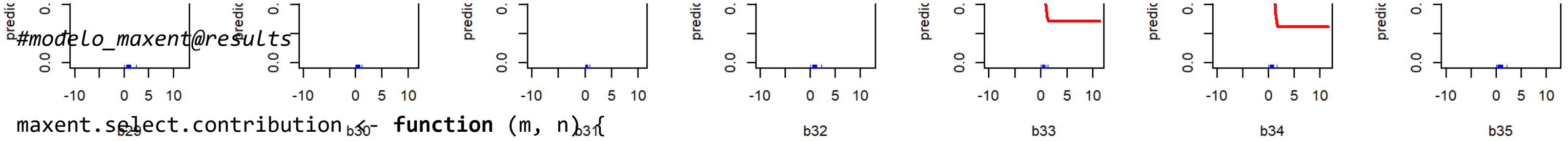
```
density(evaluacion_e)
title("entranaimiento")
density(evaluacion_c)
title("control")
```



Presentar graficas de contribución de variables

```
response(modelo_maxent)
```

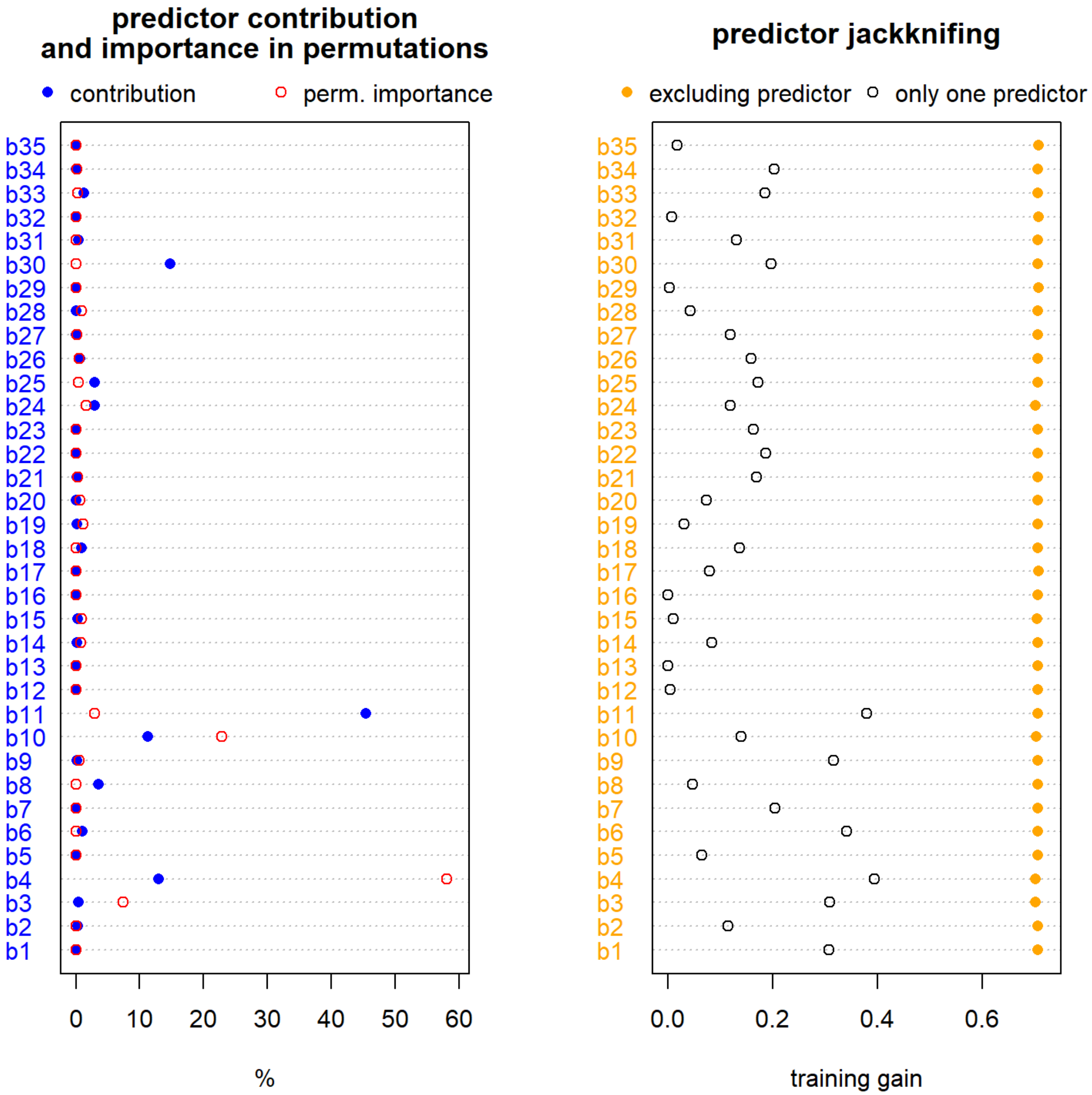

predicted value
0.0
0.4
0.8
-20 0 20 40
b1
-10 0 10 30
b2
-10 0 5 10
b3
-10 0 5 10
b4
-10 10 30 50
b5
-40 0 20
b6
0 20 40 60
b7
-20 0 20 40
b8
-40 0 20
b9
-10 10 30
b10
-40 0 20
b11
0 2000 4000
b12
0 50 150
b13
-10 10 30
b14
-10 0 5 10
b15
0 500 1500
b16
0 200 400 600
b17
0 400 800
b18
0 500 1500
b19
0 100 200
b20
0 100 250
b21
0 50 150
b22
-10 0 5 10
b23
0 100 200
b24
0 100 200
b25
0 100 200
b26
0 50 150
b27
-10 0 5 10
b28



```
#modelo_maxent@results
```

```
maxent.select.contribution <- function (m, n) {
  ## parametros: m - objeto del model maxent, n - vector de nombres de variables raster
  ## Note: with jackknifing - in order to get variables 3 and 4
  resultados <- m@results
  tabla_resultados <- data.frame(t(rep(NA,5)))
  names(tabla_resultados) <- c('variable','contribution','permutation.importance',
                               'gain.without','gain.only')
  for (i in 1:length(n)) {
    var1_name <- paste0(n[i],'.contribution')
    var1_value <- resultados[var1_name,1]
    var2_name <- paste0(n[i],'.permutation.importance')
    var2_value <- resultados[var2_name,1]
    var3_name <- paste0('Training.gain.without.',n[i])
    var3_value <- resultados[var3_name,1]
    var4_name <- paste0('Training.gain.with.only.',n[i])
    var4_value <- resultados[var4_name,1]
    tabla_resultados <- rbind(tabla_resultados,
        c(n[i],var1_value,var2_value,var3_value,var4_value))
  }
  tabla_resultados <- tabla_resultados[-1,]
  return(tabla_resultados)
}
```

```
nombres_variables <- names(subset(bio_vars, 1:35))
contribuciones_variables <- maxent.select.contribution(modelo_maxent,
                                                      nombres_variables)
contr_max <- max(as.numeric(c(contribuciones_variables[,2],
                              contribuciones_variables[,3])))
gain_max <- max(as.numeric(c(contribuciones_variables[,4],
                              contribuciones_variables[,5])))

par(mfcol = c(1,2), mar = c(5.1, 4.1, 6.1, 2.1))

dotchart(as.numeric(contribuciones_variables[,2]),
          col='blue', pch=16,
          labels=contribuciones_variables[,1],
          xlim=c(0, 1.02 * contr_max),
          main=c('predictor contribution','and importance in permutations'),
          xlab = "%"
         )

points(as.numeric(contribuciones_variables[,3]),
       seq(1:35),
       col='red', pch=1)

legend("top", inset=c(0,-0.07), xpd = TRUE,
       ncol = 2, bty = "n",
       legend = c("contribution","perm. importance"),
       pch = c(16,1), col = c("blue","red"))

dotchart(as.numeric(contribuciones_variables[,4]),
          col = 'orange', pch=16,
          labels = contribuciones_variables[,1],
          xlim = c(0, 1.02 * gain_max),
          main = 'predictor jackknifing',
          xlab = 'training gain')

points(as.numeric(contribuciones_variables[,5]),
       seq(1:35),
       col='black', pch=1)

legend("top", inset=c(0,-0.07), xpd = TRUE,
       ncol = 2, bty = "n",
       legend = c("excluding predictor","only one predictor"),
       pch = c(16,1), col = c("orange","black"))
```

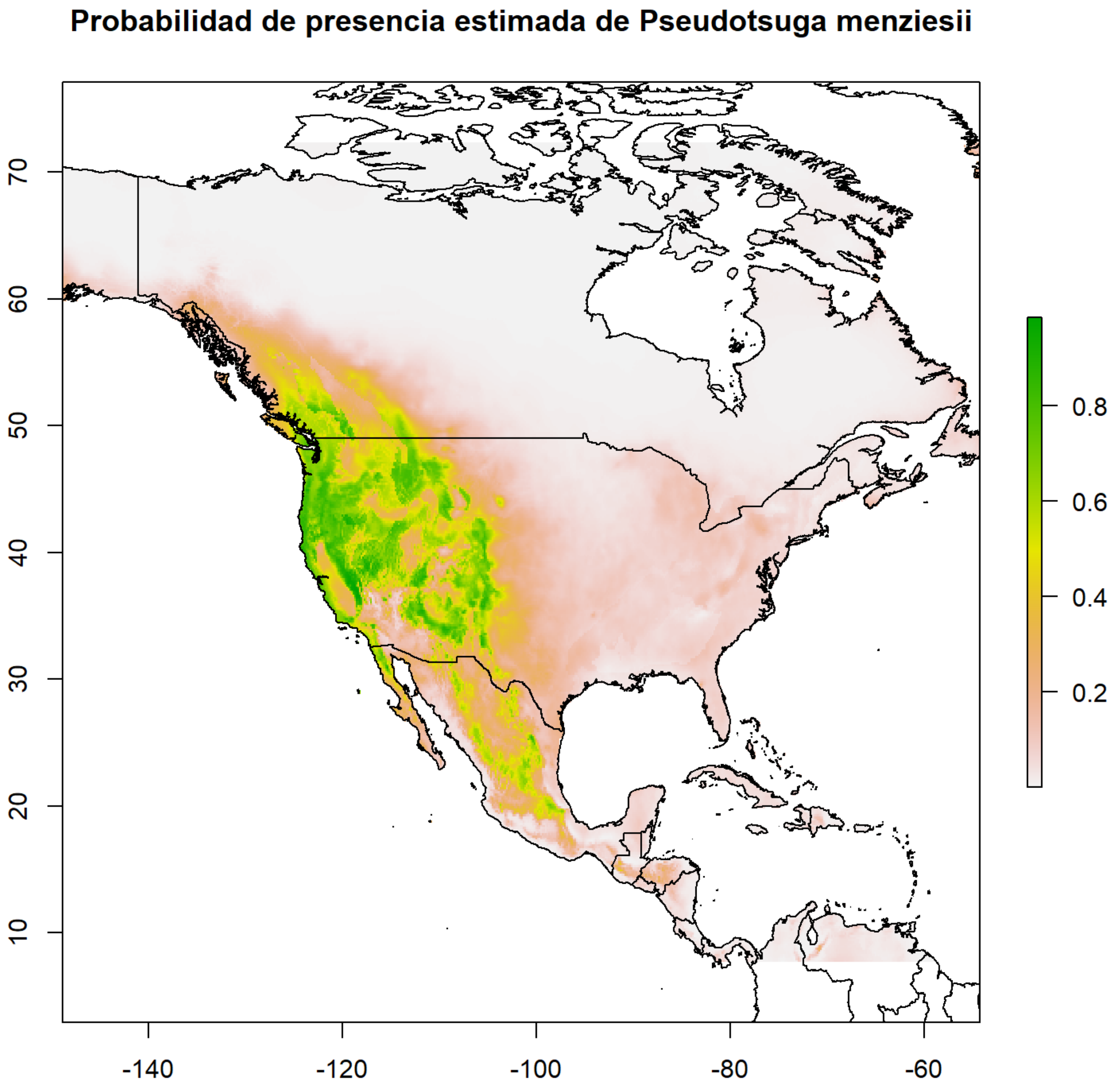

predictor contribution
and importance in permutations
● contribution
○ perm. importance
b35
b34
b33
b32
b31
b30
b29
b28
b27
b26
b25
b24
b23
b22
b21
b20
b19
b18
b17
b16
b15
b14
b13
b12
b11
b10
b9
b8
b7
b6
b5
b4
b3
b2
b1
0
10
20
30
40
50
60
%
predictor jackknifing
● excluding predictor
○ only one predictor
0.0
0.2
0.4
0.6
training gain

Realizar prediccion de idoneidad de habitat y clasificación binaria

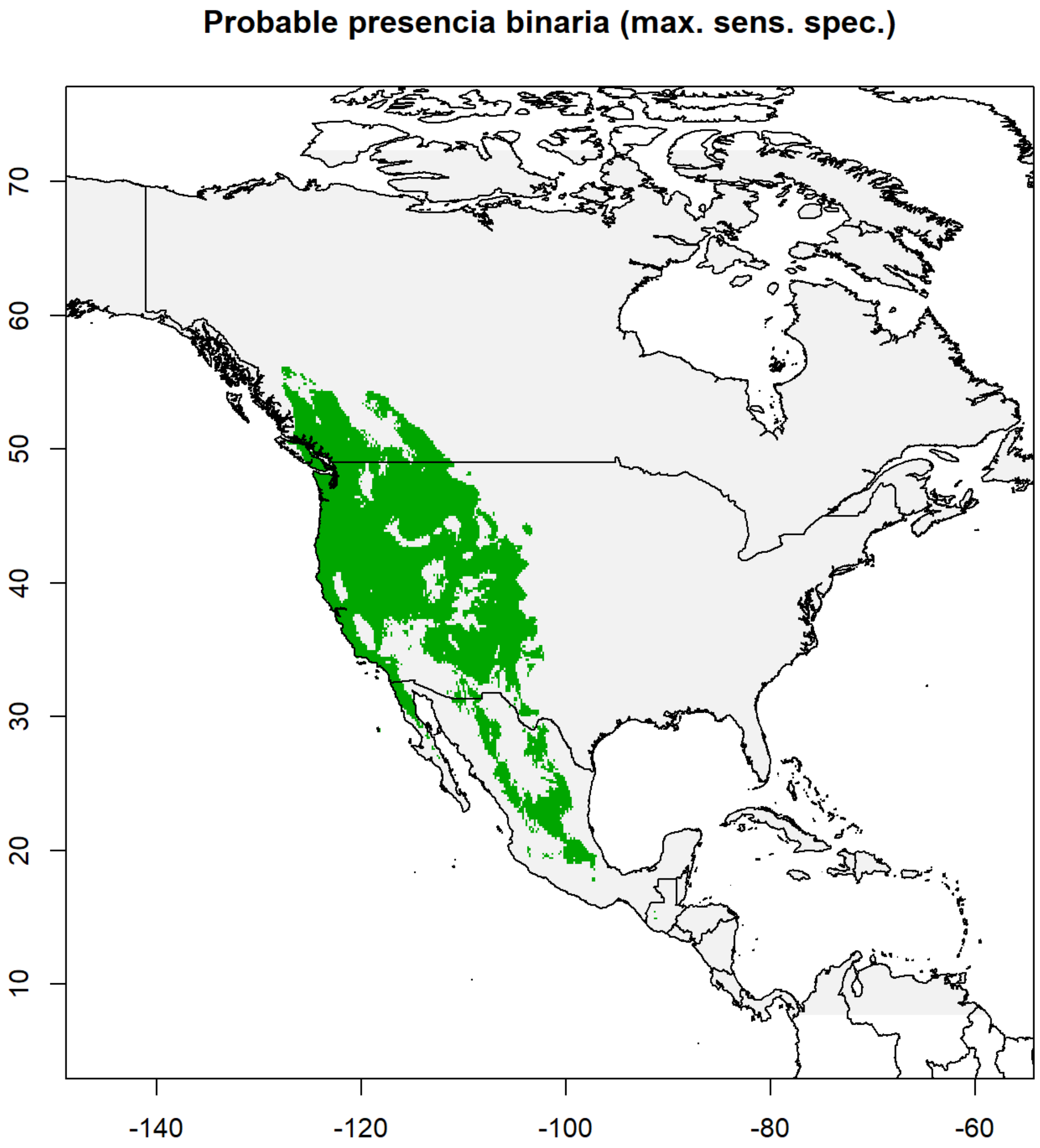
```
prediccion <- predict(subset(bio_vars, 1:35), modelo_maxent, progress='window')
```

```
## Loading required namespace: tcltk
```

```
prediccion <- prediccion * bio_vars_mask
plot(prediccion, main = "Probabilidad de presencia estimada de Pseudotsuga menziesii")
plot(mundo, add = TRUE)
```


Probabilidad de presencia estimada de Pseudotsuga menziesii
70
60
50
40
30
20
10
-140
-120
-100
-80
-60
0.8
0.6
0.4
0.2

```
especie_reclass_table <- matrix(c(-Inf, threshold(evaluacion_c)$spec_sens, 0,
                                 threshold(evaluacion_c)$spec_sens, Inf, 1),
                               ncol=3, byrow=TRUE)
prediccion_presencia <- reclassify(prediccion, especie_reclass_table)
plot(prediccion_presencia, legend = FALSE,
     main = "Probable presencia binaria (max. sens. spec.)")
plot(mundo, add = TRUE)
```


Probable presencia binaria (max. sens. spec.)
70
60
50
40
30
20
10
-140
-120
-100
-80
-60

Guadrar rasters

```
writeRaster(prediccion,
              filename = "probabilidad_presencia_Pseudotsuga_menziesii.tif",
             format="GTiff", datatype = "FLT4S", overwrite = TRUE)

writeRaster(prediccion_presencia,
              filename = "clasificacion_binaria_Pseudotsuga_menziesii.tif",
             format="GTiff", datatype = "INT2S", overwrite = TRUE)
```