Building replicate models

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```
library(ENMTools)
```

```
## Loading required package: raster
```

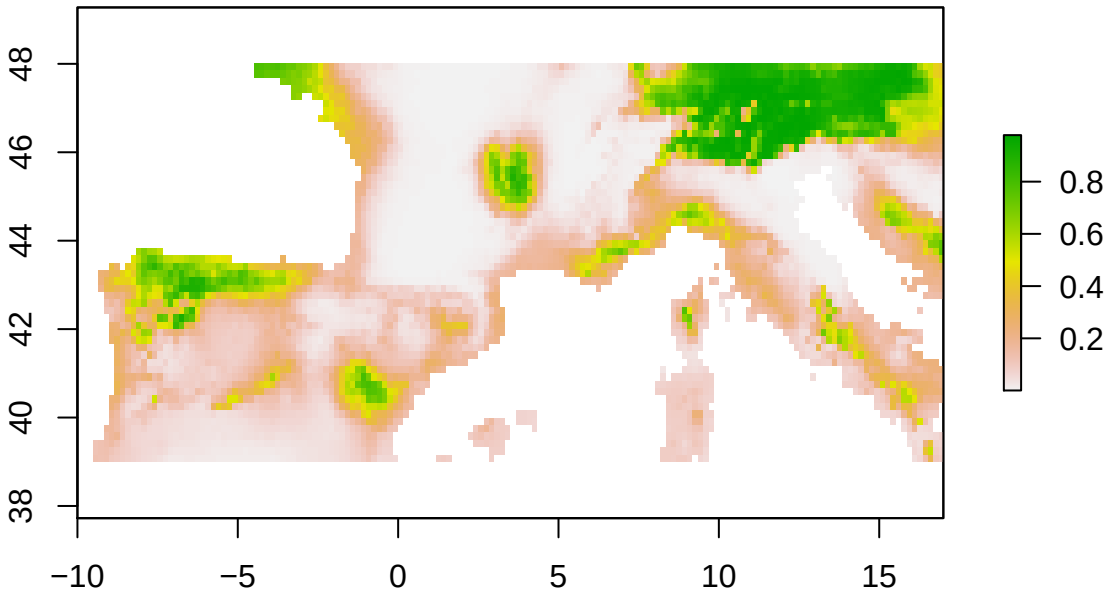
```
## Loading required package: sp
```

```
## Loading required package: dismo
```

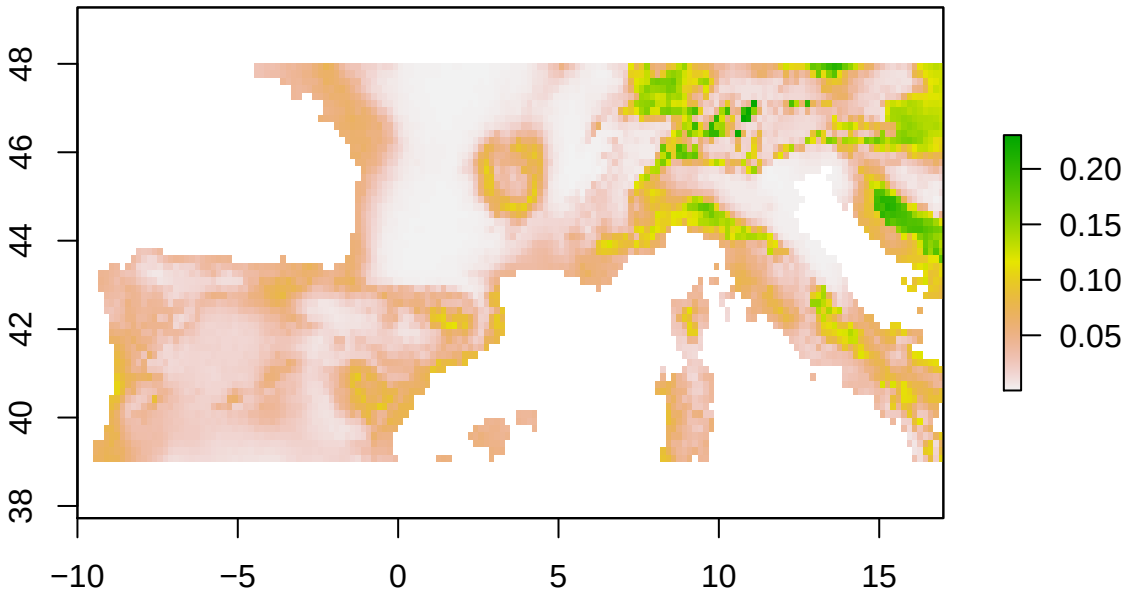
```
monticola <- iberolacerta.clade$species$monticola
```

Here's a quick and dirty way to do a bunch of replicate models where we repeat the random sampling of our training and test data.

```
reps <- list()

for(i in 1:10){
  thisname <- paste0("rep", i)
  reps[[thisname]] <- enmtools.gam(monticola, euro.worldclim, test.prop = 0.3)
}

repstack <- reps[[1]]$suitability

for(i in 2:10){
  repstack <- addLayer(repstack, reps[[i]]$suitability)
}

names(repstack) <- names(reps)

meanreps <- raster::calc(repstack, fun = mean, na.rm = T)
plot(meanreps)
```

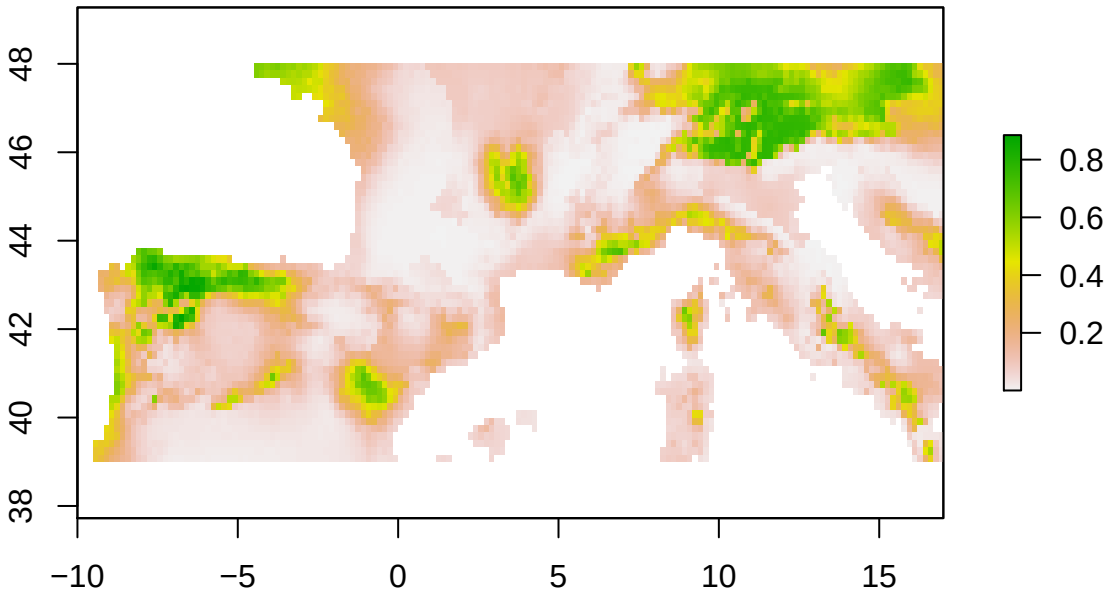



```
sdreps <- raster::calc(repstack, fun = sd, na.rm = T)
plot(sdreps)
```

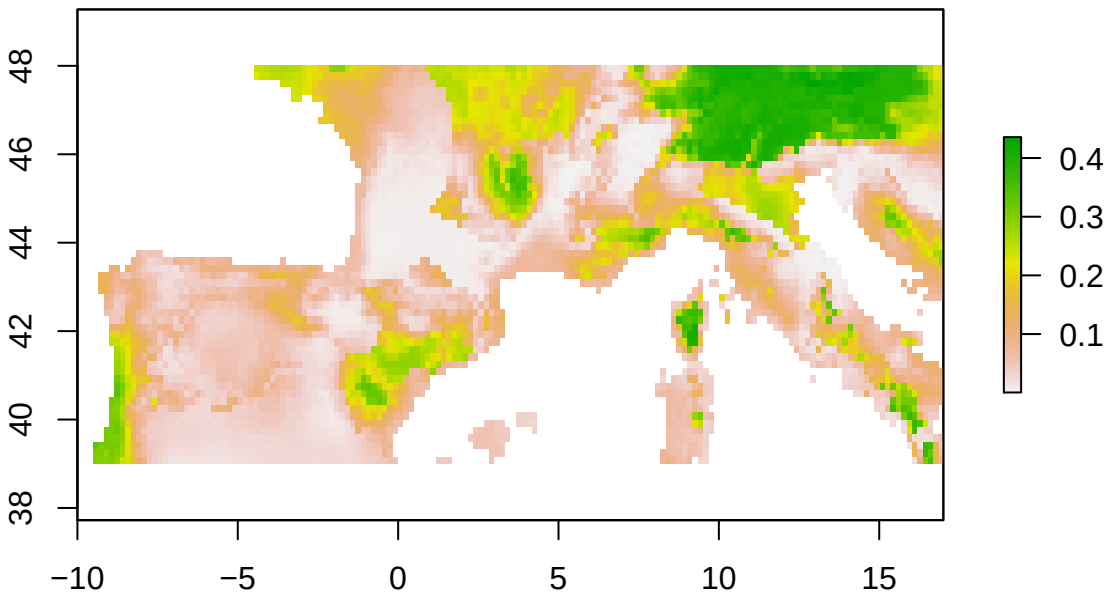


Or perhaps you want to do a bootstrap instead? That's a bit more work, but still not too bad; all we need to do is add some code to resample our presence data with replacement before the train/test split.

```
reps <- list()

for(i in 1:10){
  thisrep <- monticola
  npres <- nrow(thisrep$presence.points)
  bootrows <- sample(1:npres, npres, replace = TRUE)
  thisrep$presence.points <- thisrep$presence.points[bootrows,]
  thisname <- paste0("rep", i)
  reps[[thisname]] <- enmtools.gam(thisrep, euro.worldclim, test.prop = 0.3)
}

bootstack <- reps[[1]]$suitability

for(i in 2:10){
  bootstack <- addLayer(bootstack, reps[[i]]$suitability)
}

names(bootstack) <- names(reps)

meanboot <- calc(bootstack, fun = mean, na.rm = T)
plot(meanboot)
```




```
sdboot <- raster::calc(bootstack, fun = sd, na.rm = T)
plot(sdboot)
```


48
46
44
42
40
38
−10
−5
0
5
10
15
0.4
0.3
0.2
0.1