# Working example of using Convex Hull Ensembles with the che package

#### Matt Hill 2019

```
library(che)
library (raster)

#> Loading required package: sp
library (maptools)

#> Checking rgeos availability: TRUE
library (rgeos)

#> rgeos version: 0.5-2, (SVN revision 621)

#> GEOS runtime version: 3.8.0-CAPI-1.13.1

#> Linking to sp version: 1.4-1

#> Polygon checking: TRUE

# simple world outline from maptools package
data("wrld_simpl")
```

this data is the in the che package - will implement neater soon....

```
load("../data/insect_dist.Rdata")
```

## Bioclim data

```
bioclimall <- raster::getData('worldclim', var='bio', res=2.5)</pre>
```

# Background creation

This is an important part of a presence-background type modelling. While the che is presence-only, we use GAMs to rank variable pairs based on relative performance, so the backround is used. In this example, the native range for the species is South Africa

```
e <- extent (10, 40, -35, -15)
SAfrica <- crop (bioclimall, e)
#convert to a stack
SAfrica <- stack(unstack(SAfrica))</pre>
```

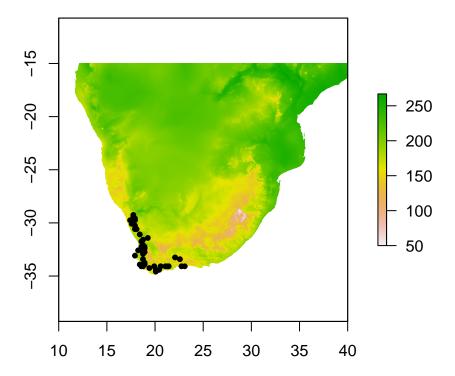
# Species data

#### Halotydeus destructor

This mite is native to South Africa

```
dist <- insect_dist[insect_dist$Species =="h_destructor" & insect_dist$Range == "Native",]

sp_df <- cbind(as.data.frame(dist[,c("Longitude", "Latitude")]),raster::extract(SAfrica, as.data.frame(plot (SAfrica[[1]]))
points(as.data.frame(dist[,c("Longitude", "Latitude")]), pch=20)</pre>
```



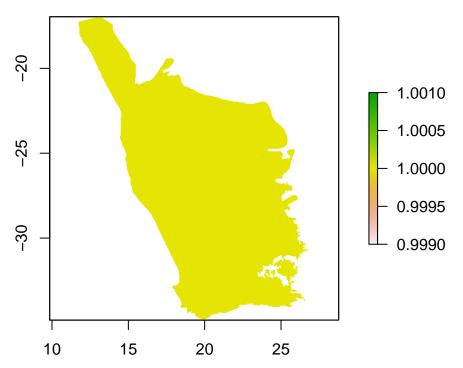
#### **Biomes**

The biomes are available as a shapefile from WWF

```
if (!file.exists("official/wwf_terr_ecos.shp")){
   temp <- tempfile()
   download.file("https://c402277.ssl.cf1.rackcdn.com/publications/15/files/original/official_teow.zip",
   unzip(temp)
   unlink(temp)
}
terres <- readShapePoly("official/wwf_terr_ecos.shp")
#> Warning: readShapePoly is deprecated; use rgdal::readOGR or sf::st_read
```

## Create a raster using biomes and native range points

Using the che::background\_builder function to set up sampling environment



Using the che::prepare\_data function to prepare the data for the modelling process

## Parallel processing of GAMs

```
model.out <- che_model(spp = "h_destuctor", parallel = TRUE, model.data=model.data)
#> Loading required package: parallel
```

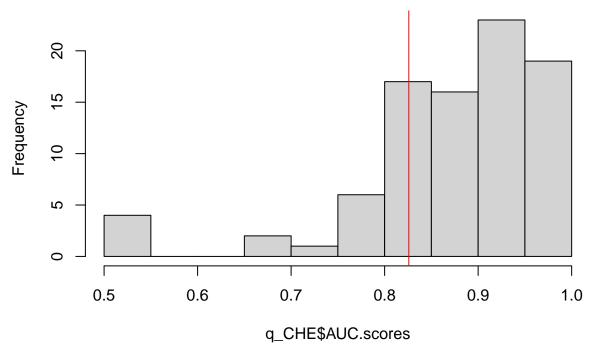
# Reconcile outputs

```
q_CHE <- che_out(model.out, 0.25)</pre>
```

The historgram shows the distribution of relative predictor pair performance, the redlie indicating where the bottom 25% would be excluded from.

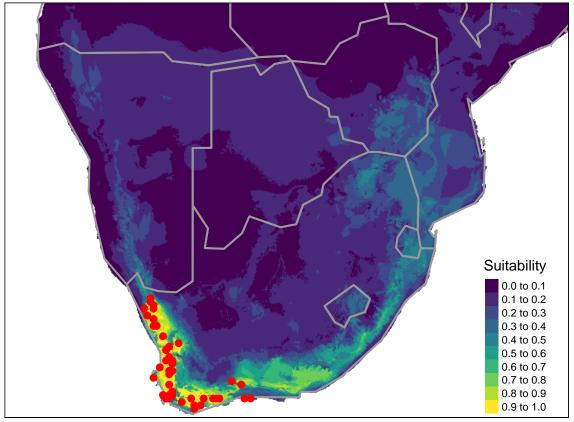
```
hist(q_CHE$AUC.scores)
abline(v=q_CHE$AUC.thresh, col="red")
```

# Histogram of q\_CHE\$AUC.scores



The resulting map can be plotted using your plotting package of choice, tmap is quite useful.

```
tm_dots(size=0.3, col="red")+
  tm_layout(legend.position=c("right", "BOTTOM"))
#> Warning: The shape wrld_simpl is invalid. See sf::st_is_valid
#> Linking to GEOS 3.8.0, GDAL 3.0.4, PROJ 6.3.1
#> Warning: Currect projection of shape c_dist unknown. Long-lat (WGS84) is
#> assumed.
```



☐ Overall resence-only

its done a reasonable job. There is now an opportunity here to test the model predictions using presence-only indices like the Boyce score etc.