Processing Occurrence Data

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Description

This R markdown document describes cleaning of occurrence data and generation of background points for *Cuscuta* species described in Masanga *et al.* (submitted).

Load libraries

```r
library(raster)
```

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

```r
library(maps)
library(rgdal)
```

```
## rgdal: version: 1.5-12, (SVN revision 1018)
## Geospatial Data Abstraction Library extensions to R successfully loaded
## Loaded GDAL runtime: GDAL 3.1.1, released 2020/06/22
## Path to GDAL shared files: /Library/Frameworks/R.framework/Versions/4.0/Resources/library/rgdal/gdal
## GDAL binary built with GEOS: TRUE
## Loaded PROJ runtime: Rel. 6.3.1, February 10th, 2020, [PJ_VERSION: 631]
## Path to PROJ shared files: /Library/Frameworks/R.framework/Versions/4.0/Resources/library/rgdal/proj
## Linking to sp version:1.4-2
## To mute warnings of possible GDAL/OSR exportToProj4() degradation,
## use options("rgdal_show_exportToProj4_warnings"="none") before loading rgdal.
```

```r
library(rgbif)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:raster':
##
##     intersect, select, union
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
data(worldMapEnv)
```

Field data for Kenya collected by Runo lab

```
occ <- read.csv("Data/Cuscuta_georeferenced.csv")
cc <- subset(occ, Cuscuta.Species=="C. campestris")[,1:2]
nrow(cc)
```

```
## [1] 26
```

```
cr <- subset(occ, Cuscuta.Species=="C. reflexa")[,1:2]
nrow(cr)
```
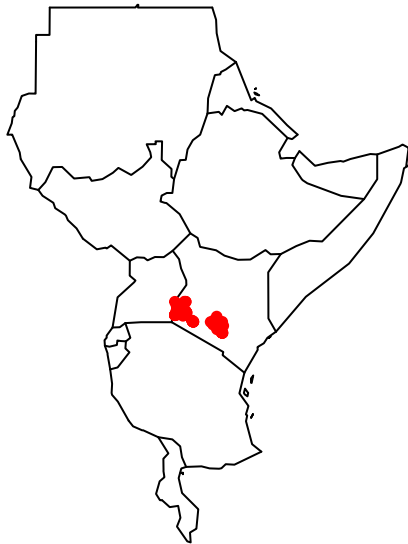
```
## [1] 67
```

```
ck <- subset(occ, Cuscuta.Species=="C. kilimanjari")[,1:2]
nrow(ck)
```

```
## [1] 3
```

C. reflexa

```
## Get all occurrences
# no African occurrences in GBIF
map(database="world", regions=c("Kenya","Tanzania","Ethiopia","Uganda","Rwanda","Burundi","Sudan","Soutl
points(cr$Long, cr$Lat, col="red", pch=20)
```
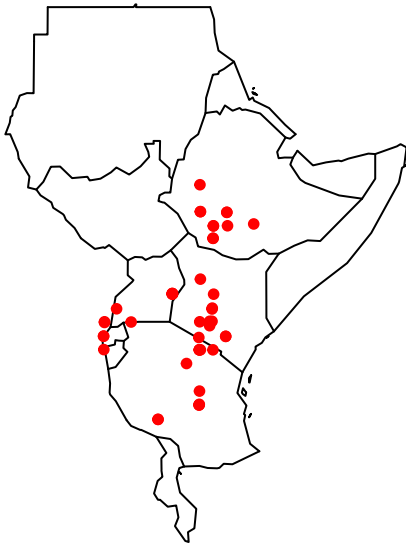

C. kilimanjari

```
# combine w/GBIF data
#citation: GBIF.org (31 August 2020) GBIF Occurrence Download https://doi.org/10.15468/dl.muwe3t
gbif.ck <- read.csv("Data/C.kilimanjari_GBIF_JM.csv", header = T)
gbif.ck <- gbif.ck %>% select(Lat, Long)

ck.all <- rbind(ck, gbif.ck)
nrow(ck.all)
```

```
## [1] 46
```

```
map(database="world", regions=c("Kenya","Tanzania","Ethiopia","Uganda","Rwanda","Burundi","Sudan","Sout
points(ck.all$Long, ck.all$Lat, col="red", pch=20)
```


C. campestris

```
# combine w/GBIF data
#citation: GBIF.org (31 August 2020) GBIF Occurrence Download https://doi.org/10.15468/dl.y8rtg4
gbif.cc <- read.csv("Data/C.campestris_GBIF_JM.csv", header = T)
gbif.cc <- gbif.cc %>% select(Lat,Long)

cc.all <- rbind(cc, gbif.cc)
nrow(cc.all)
```

```
## [1] 46
```

```
map(database="world", regions=c("Kenya","Tanzania","Ethiopia","Uganda","Rwanda","Burundi","Sudan","Sout
points(cc.all$Long, cc.all$Lat, col="red", pch=20)
```