

Tutorial to perform a Crop Wild Relatives ex-situ gap análisis using GapAnalysis R package.

Open the CWR_GAPANALYSIS.R file

Please check your inputs

- ☐ Occurrence data
- ☐ Species distribution model thresholded
- ☐ An ecoregion shapefile. If it is not available you can download using the package
- ☐ Species names

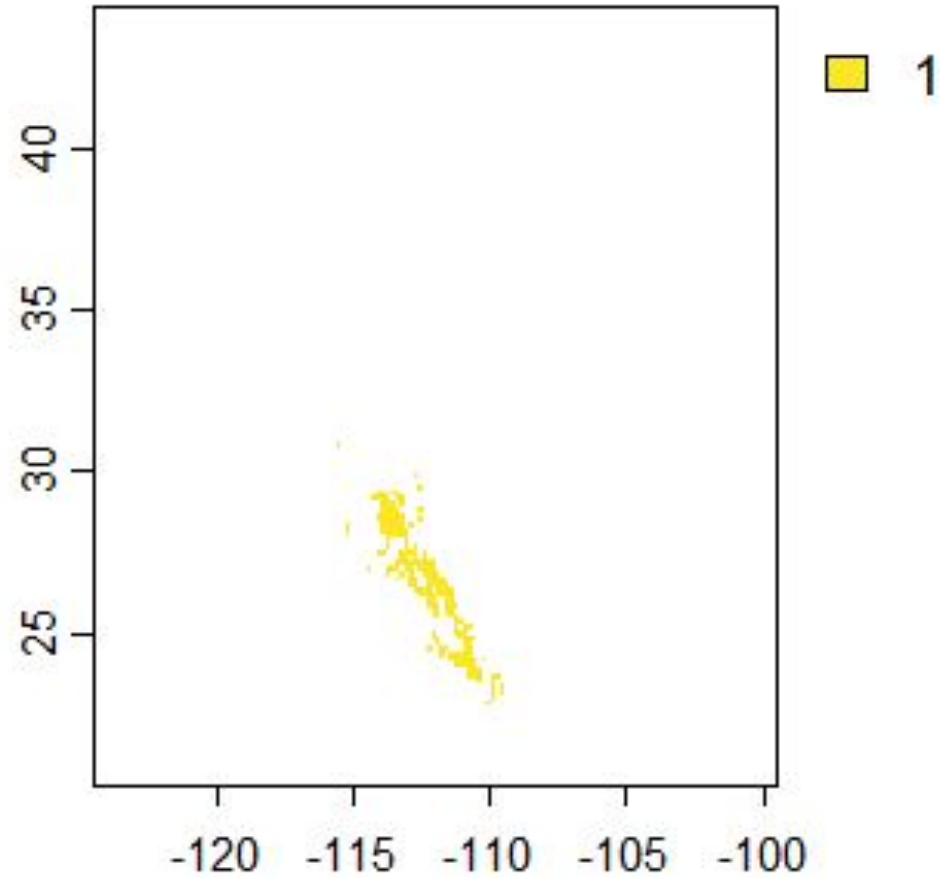
This example Will use
Cucurbita cordata

Prepare your occurrence data to fit the following table format

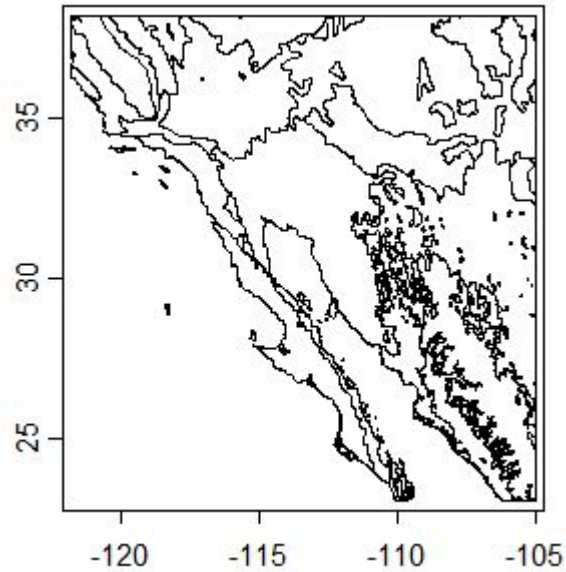
- Prepare your occurrence data to fit the following table format. You will need the column species (Species name using underline to separate Genus and species), latitude and longitude in decimal coordinate format and a column type which has the values H for occurrences not found in the germplasm collection and G to represent the germplasm occurrences

species	latitude	longitude	type
Cucurbita_cordata	23.37500	-109.7750	H
Cucurbita_cordata	23.45138	-109.9279	H
Cucurbita_cordata	23.22694	-109.9625	H
Cucurbita_cordata	23.05833	-110.0250	H
Cucurbita_cordata	23.50039	-110.0837	H

Load your SDM thresholded



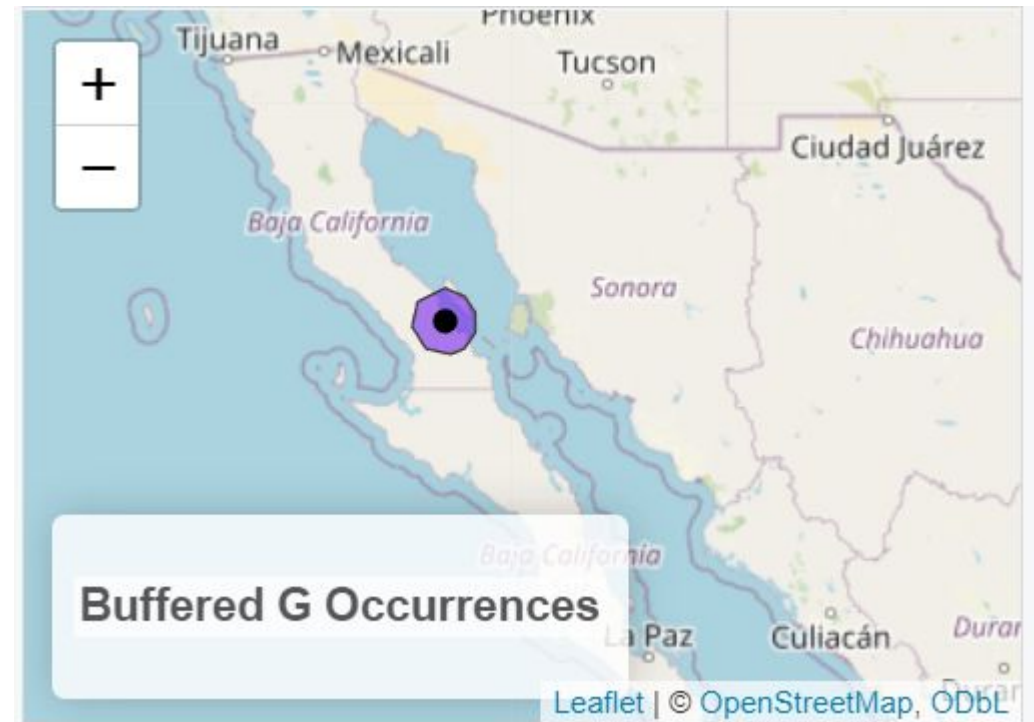
Load your ecosystems shapefile



Step 1: Prepare buffers (50 Km around germplasm accessions)

```
#Running generateGBuffers
```

```
gBuffer <- generateGBuffers(taxon = taxon,  
                           occurrenceData = CucurbitaData,  
                           bufferDistM = 50000  
)
```



Step 2: Calculate sample representativeness score (SRS)

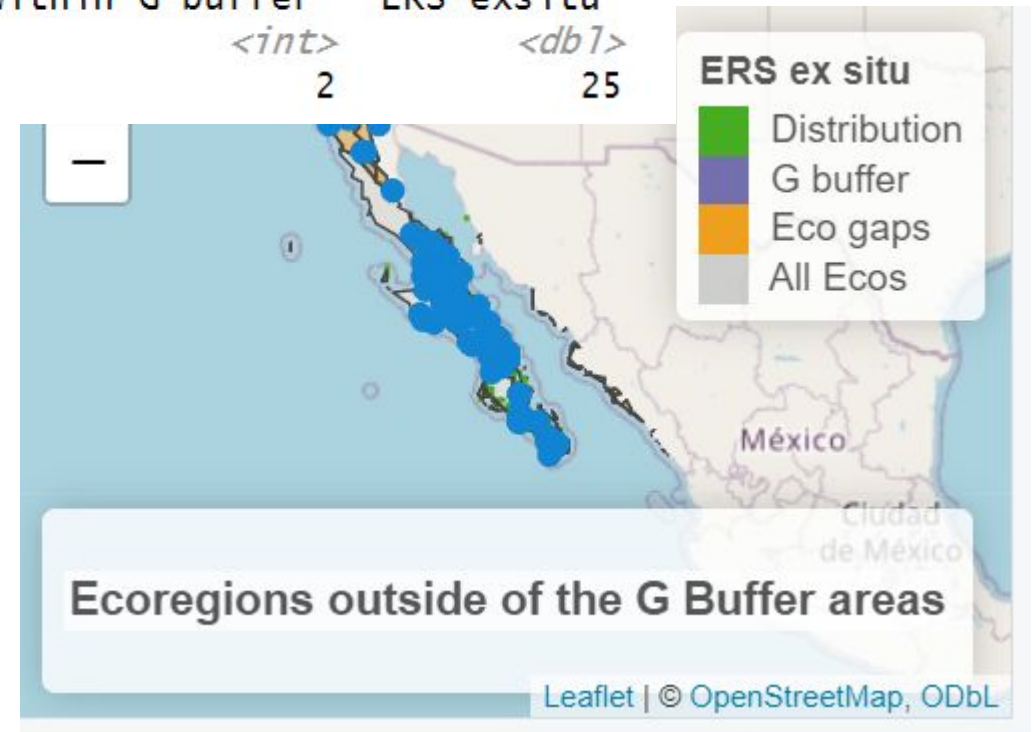
- SRS shows that *C. cordata* only has one germplasm accession (poorly collected)

```
> srs_exsitu <- SRSex(taxon = taxon,
+                      occurrence_Data = CucurbitaData
+ )
> srs_exsitu
# A tibble: 1 x 8
  Taxon                `Total records` `Total with coordinat...` `Total G records` G records with coord...` `Total H records`
  <chr>                <int>          <int>          <int>          <int>          <int>
1 Cucurbita_cordata      139            139            1              1             138
# i abbreviated names: 1`Total with coordinates`, 2`G records with coordinates`
# i 2 more variables: `H records with coordinates` <int>, `SRS exsitu` <dbl>
> |
```


Step 3: Calculate Ecological representativeness score (ERS)

- ERS shows that only two regions are within Germplasm buffer of 50 km

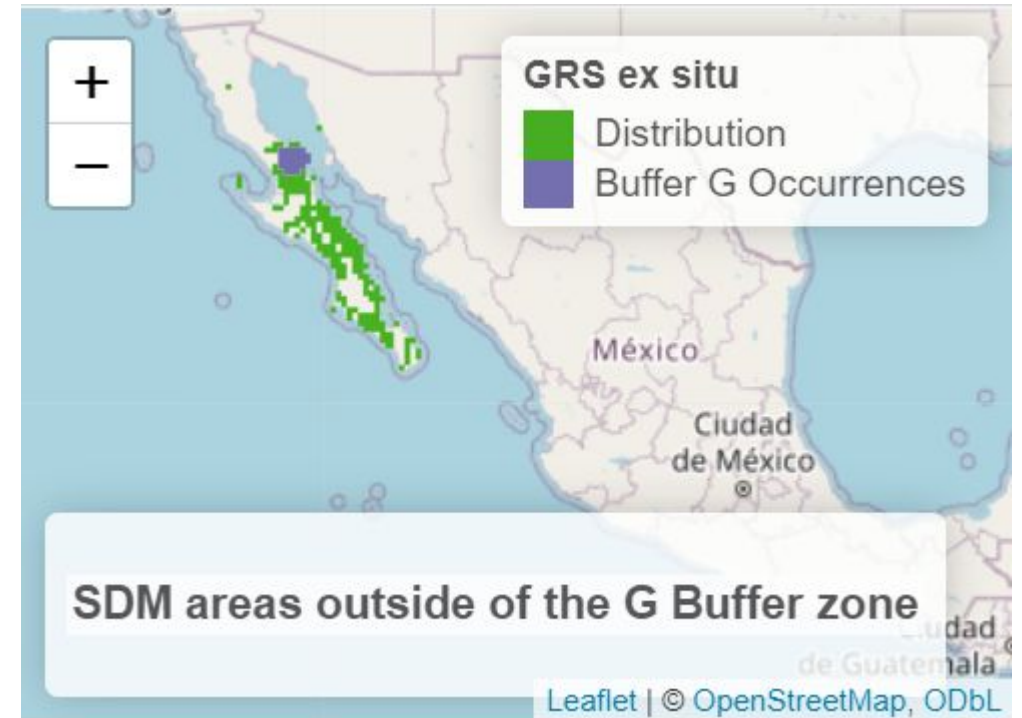
```
> ers_exsitu$results
# A tibble: 1 x 4
  Taxon                `Ecoregions with records` `Ecoregions within G buffer` `ERS exsitu`
  <chr>                <int>                <int>          <dbl>
1 Cucurbita_cordata      8                  2             25
```



Step 4: Calculate Geographical Representativeness score (GRS)

```
> grs_exsitu$results
# A tibble: 1 × 4
  Taxon                `Area of model km2` `G buffer areas in model km2` `GRS exsitu`
  <chr>                <dbl>          <dbl>          <dbl>
1 Cucurbita_cordata    61585.         6004.          9.75
```

- GRS shows that only 10% of the SDM is represented in germplasm accessions
- Areas in green represent the geographical áreas within the species distribution model to be collected!



Before the step 5

- FCS is the average of SRS,ERS, and GRS
- The values taken are:
- URGENT PRIORITY
- HIGH PRIORITY
- MEDIUM PRIORITY
- LOW PRIORITY

```
if (sp_fcs < 25) {  
  score <- "UP"  
}  
else if (sp_fcs >= 25 & sp_fcs < 50) {  
  score <- "HP"  
}  
else if (sp_fcs >= 50 & sp_fcs < 75) {  
  score <- "MP"  
}  
else {  
  score <- "LP"  
}
```

Step 5: Calculate the Final Conservation Score (FCS)

- FCS is the average of the SRS, GRS, and ERS
- FCS shows that *C. cordata* is a urgent priority for conservation

```
> fcs_exsitu <- FCSEX(taxon = taxon,  
+                     srsex = srs_exsitu,  
+                     grsex = grs_exsitu,  
+                     ersex = ers_exsitu)  
> fcs_exsitu  
# A tibble: 1 × 6  
  Taxon          `SRS exsitu` `GRS exsitu` `ERS exsitu` `FCS exsitu` `FCS existu score`  
  <chr>          <dbl>      <dbl>      <dbl>      <dbl> <chr>  
1 Cucurbita_cordata 0.725      9.75      25      11.8 UP
```

Step 6: Prepare your collects!

- Use leaflets or a visualization GIS tool to go for potential material

