

Tutorial to upload a gap map to Viewer Gap analysis

Please check your inputs

- ☐ Identify your gap map
- ☐ Format your raster file (only is accepted grids with gaps in numeric values, no gaps must be format as NA!)

Click on Go to Viewer

The image is a screenshot of a web application interface. At the top, there is a dark green header bar. On the left side of the header, there is a small circular logo with a sun and a plant, followed by the text "Home". On the right side of the header, there are three links: "Viewer", "Api", and "About". Below the header, the main content area has a background image of green foliage. In the center, the title "Viewer Gap analysis" is displayed in a large, bold, white font. Below the title, there is a paragraph of text in a light green font. At the bottom center, there is a red rectangular button with the text "Go to Viewer" and a right-pointing arrow. The button is highlighted with a red border.

Home Viewer Api About

Viewer Gap analysis

Traditional Farmer varieties ("landraces") are a foundation of subsistence agriculture and are among the most important genetic resources for contemporary plant breeding (Camacho Villa et al., 2005). Major international ex situ collections have been established following collecting missions especially during the 1970s-90s to collect landrace diversity led by the IBPGR/IPGRI, particularly from the primary regions of diversity of crops worldwide, also called Vavilov centers (Khoury et al. 2016). In the period 1974-2012, such efforts resulted in over 225,000 plant samples of ca. 4,300 species collected during more than 500 collecting missions (Thormann et al., 2015). As a result, the 11 international genebanks managed by CGIAR centers are among the largest, most diverse, and most widely used of the world's ex situ collections, with ~700K accessions currently conserved (CGIAR Genebank Platform, 2019), complementing the important national collections conserved around the world.

Go to Viewer →

Landraces Gap Analysis

Format occurrence file for LGA and CWRGA

Please format only the germplasm occurrences to the following format:

- Species_name= species name with underline
- Country = Country ISO2 CODE
- Source_database = source
- Accession_id = internal database id

A	B	C	D	E	F	G	H	I	J	K
id	species_name	ext_id	crop	landrace_groups	country	institution_name	source_data	latitude	longitude	accession_id
	triticum_turgidum		triticum_turgidum				GENESYS	34.783333	-5.6	GENESYS_948
	triticum_turgidum		triticum_turgidum				GENESYS	34.816667	-5.55	GENESYS_968
	triticum_turgidum		triticum_turgidum				GENESYS	33.916667	-5.4	GENESYS_969
	triticum_turgidum		triticum_turgidum				GENESYS	34.066667	-5.6	GENESYS_970
	triticum_turgidum		triticum_turgidum				GENESYS	34.016667	-5.15	GENESYS_971
	triticum_turgidum		triticum_turgidum				GENESYS	34.066667	-5	GENESYS_972
	triticum_turgidum		triticum_turgidum				GENESYS	33.966667	-4.933333	GENESYS_973
	triticum_turgidum		triticum_turgidum				GENESYS	19.5	-12.1333	GENESYS_5529
	triticum_turgidum		triticum_turgidum				GENESYS	19.958	-13.0273	GENESYS_5530
	triticum_turgidum		triticum_turgidum				GENESYS	20.4274	-12.4537	GENESYS_5531
	triticum_turgidum		triticum_turgidum				USDA	24.2	5.5666667	USDA_2

Take the file
triticum_turgidum_occurrences_
IDs and format to get a similar
csv file.

	A	B	C	D	E	F	G	H	I	J	K
	id	species_name	ext_id	crop	landrace_groups	country	institution_name	source_data	latitude	longitude	accession_id
		triticum_turgidum		triticum_turgidum				GENESYS	34.783333	-5.6	GENESYS_948
		triticum_turgidum		triticum_turgidum				GENESYS	34.816667	-5.55	GENESYS_968
		triticum_turgidum		triticum_turgidum				GENESYS	33.916667	-5.4	GENESYS_969
		triticum_turgidum		triticum_turgidum				GENESYS	34.066667	-5.6	GENESYS_970
		triticum_turgidum		triticum_turgidum				GENESYS	34.016667	-5.15	GENESYS_971
		triticum_turgidum		triticum_turgidum				GENESYS	34.066667	-5	GENESYS_972
		triticum_turgidum		triticum_turgidum				GENESYS	33.966667	-4.933333	GENESYS_973
		triticum_turgidum		triticum_turgidum				GENESYS	19.5	-12.1333	GENESYS_5529
0		triticum_turgidum		triticum_turgidum				GENESYS	19.958	-13.0273	GENESYS_5530
1		triticum_turgidum		triticum_turgidum				GENESYS	20.4274	-12.4537	GENESYS_5531
2		triticum_turgidum		triticum_turgidum				IISDA	24.2	5.56666667	IISDA_2

Equivalences

- Y=species_name
- Latitude=latitude
- Longitude=longitude
- source_db=source_database
- database_id= accession_id

Format gap analysis raster file

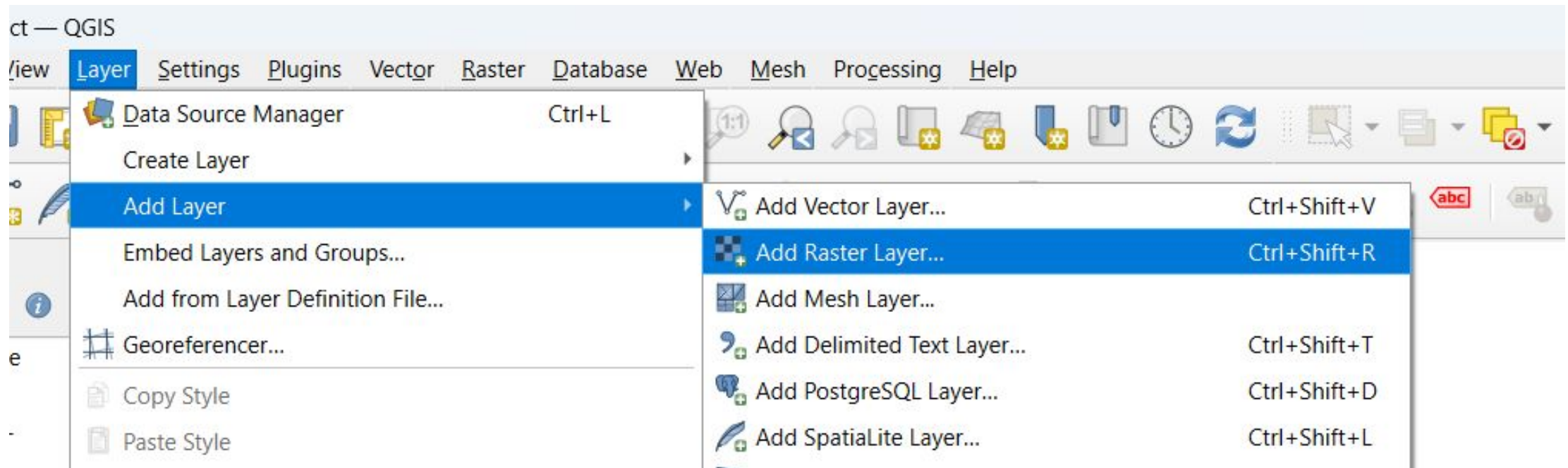
QGIS instructions

Go to your folder

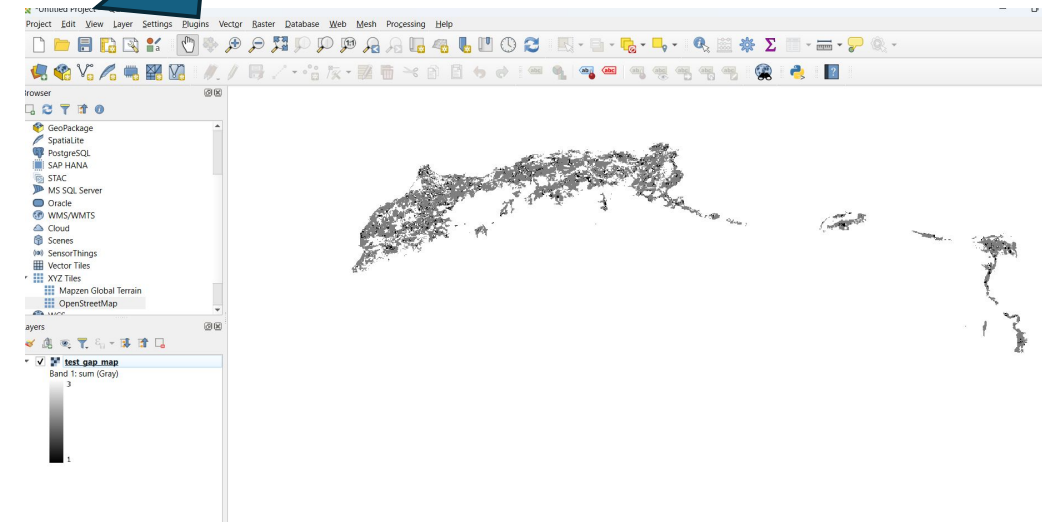
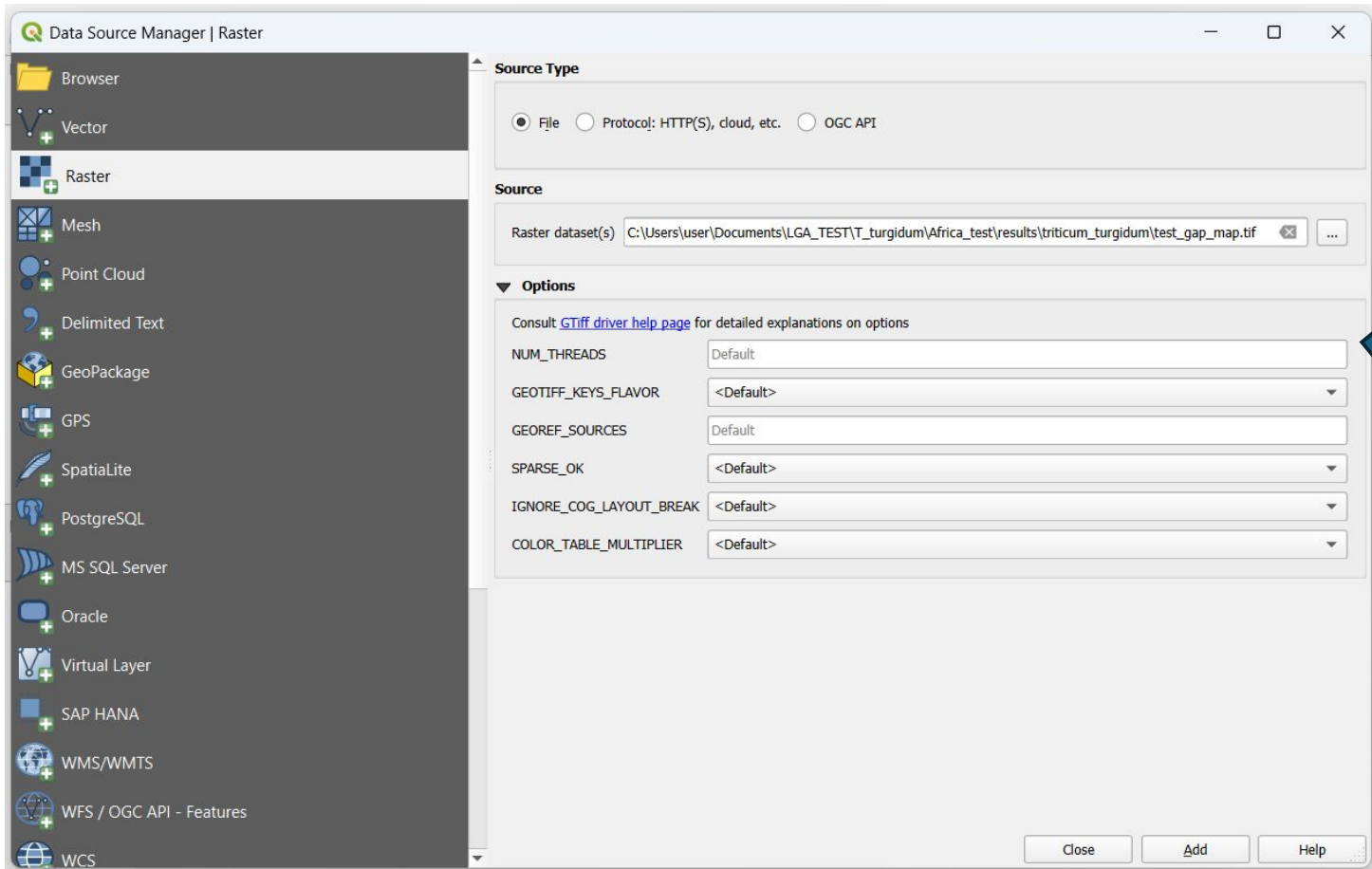
- T_turgidum\Africa_test\results\triticum_turgidum
- Your gap map is named: test_gap_map.tif
- Please remove the values in the raster as 1 to 2. They are low and medium probabilities gaps (You can use QGIS or R)

Instructions for qgis

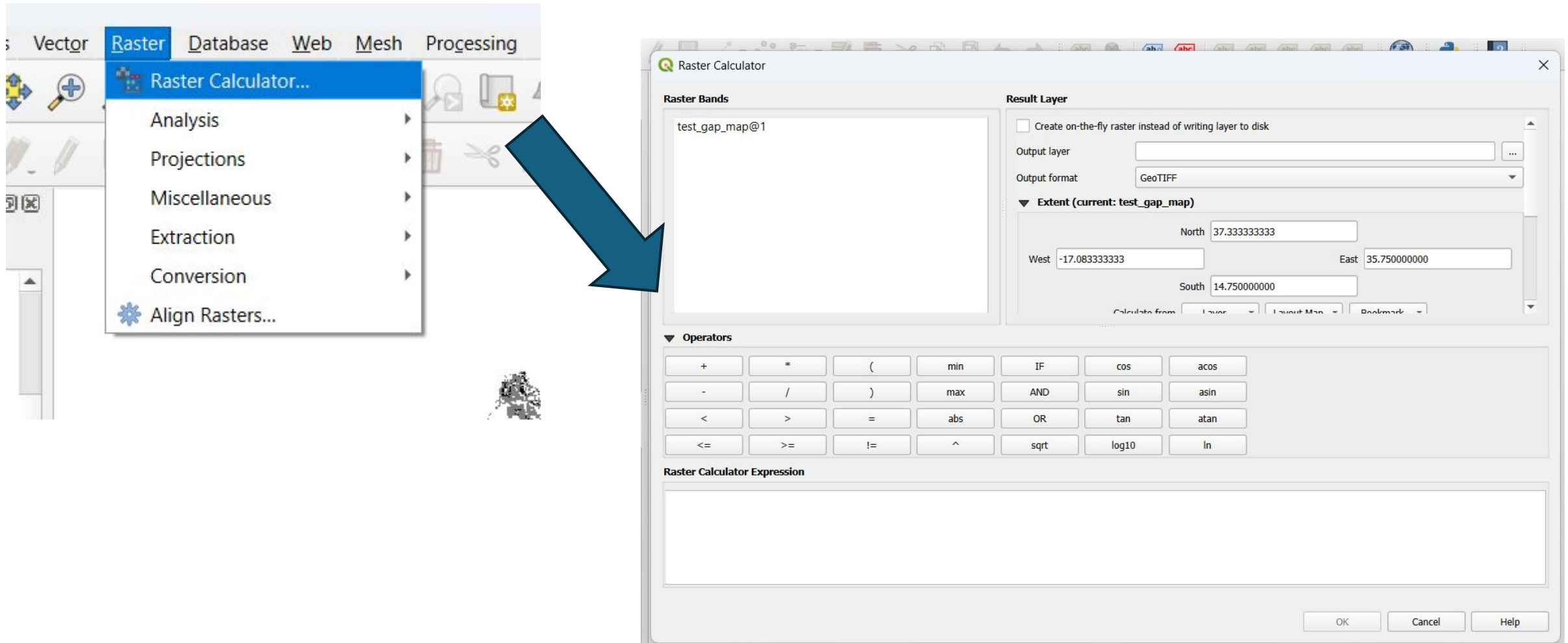
- Step 1) Click in Add Layer > Add Raster Layer

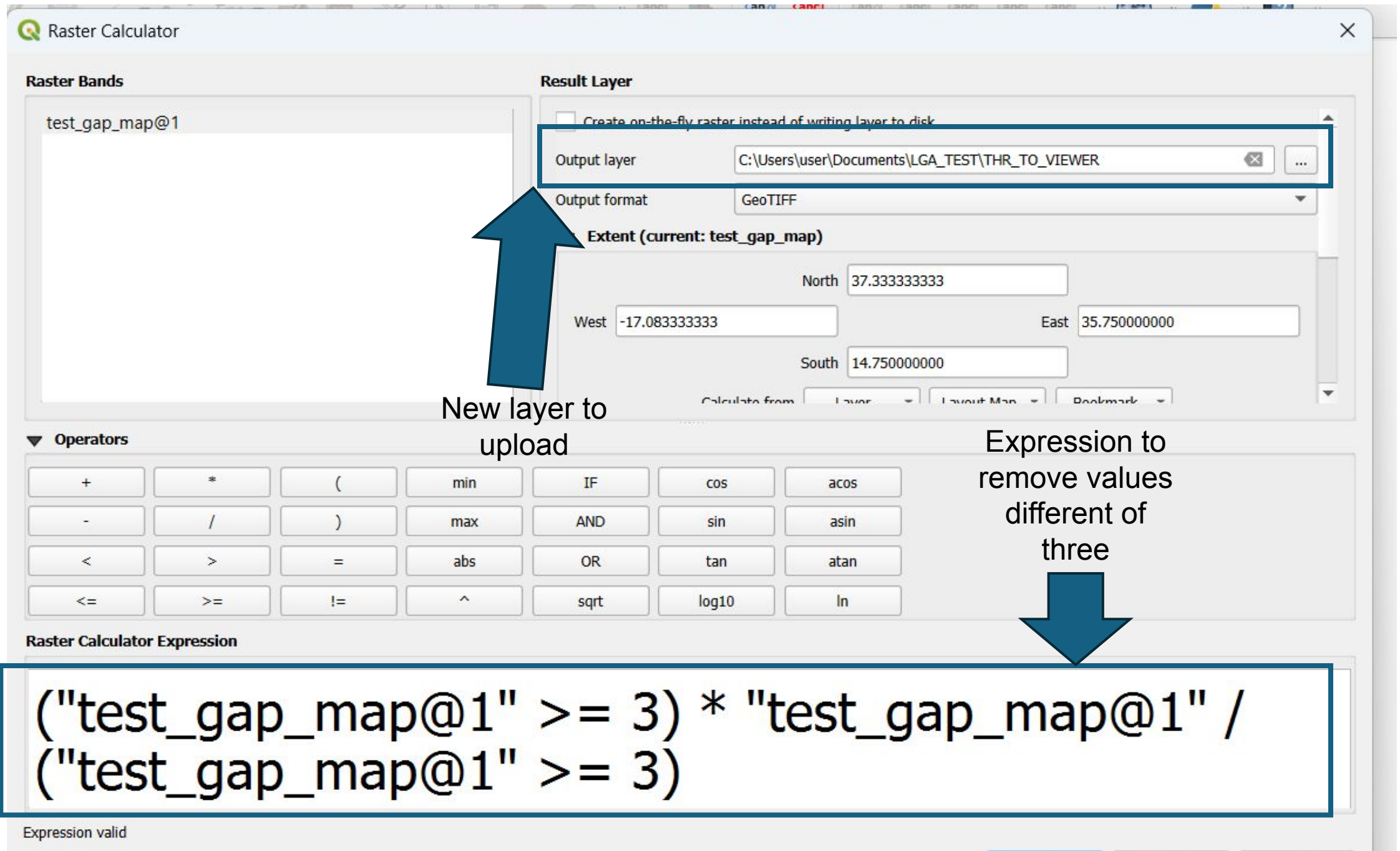


Step 2) Load your gap map file test_gap_map.tif and click on Add



Step 3. Remove values different of three





Expression to remove values different to three

```
("test_gap_map@1" >= 3) *  
"test_gap_map@1" / ("test_gap_map@1"  
>= 3)
```

Format raster for CWRGA

In your R write the following lines

```
#Call terra librarylibrary(terra)
#Change the value of the gap map from 1 to 3
grs_exsitu$gGaps[grs_exsitu$gGaps==1] <- 3
#save raster
filewriteRaster(grs_exsitu$gGaps,"C_cordata_gap.tif",overwrite=
T)
```

Instructions to use Gap Analysis Viewer



Home

Viewer Api About

Step 1 Project

Step 2 Country

Step 3 Major Crops

Search by name...



Add to map

Upload your gap analysis

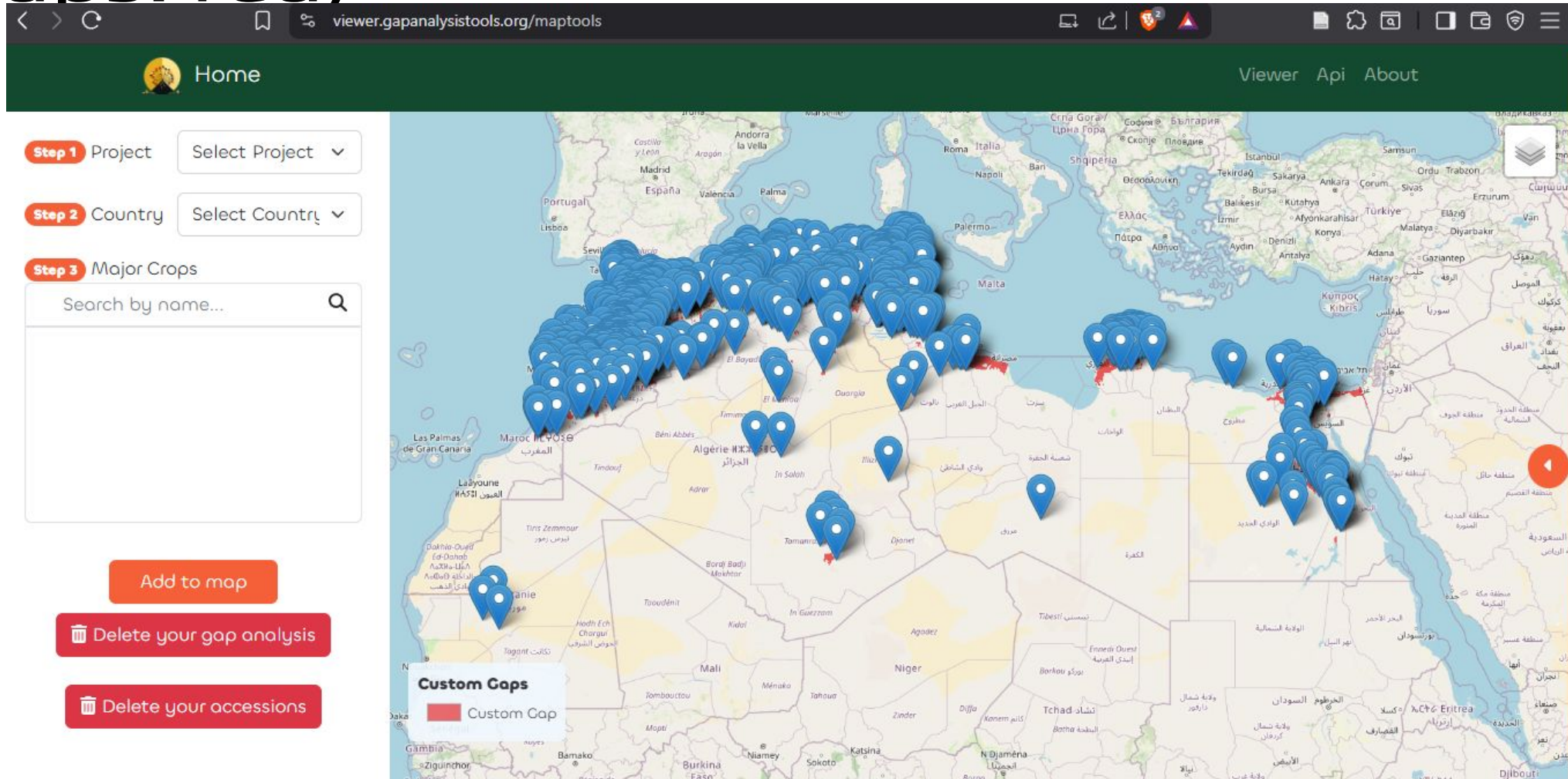
Upload your accessions



Upload gap
map in tif format

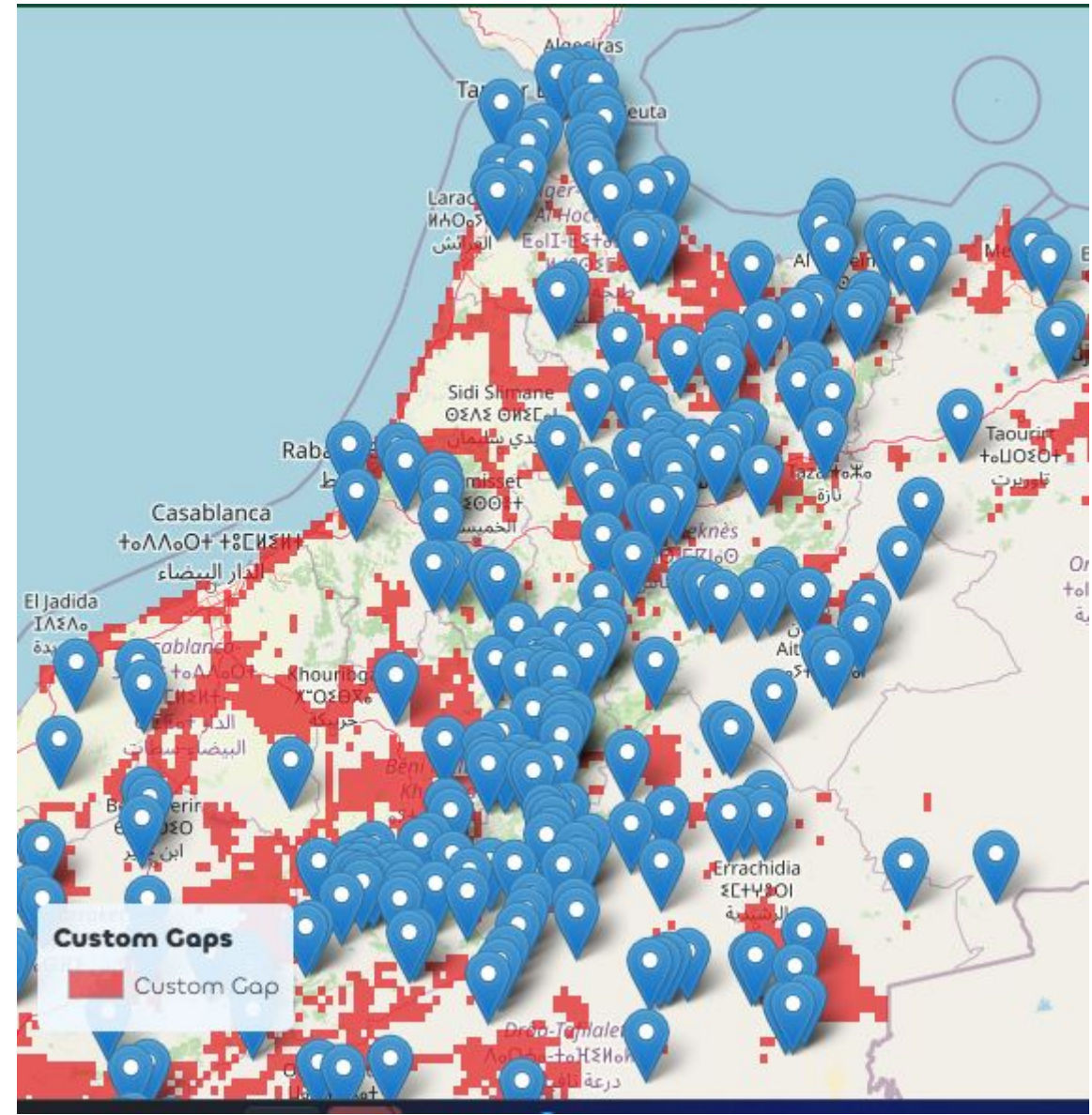
Upload Accessions used for
modeling in your research
areas

Your germplasm data and gap map are ready to be visualized! (Accessions: Blue, gaps: red)



Zoom in

- In this case the coastal areas are potential gaps in the germplasm collection!
- Let's try a collecting plan!



Before continue go for the following questions:

- **Are the potential areas coherent with the previous knowledge of the species?**
- **Are previous collecting areas represented as red in the map?**
- **Are there missing areas where you know the species is present?**

Problems with gap analysis outputs

- **Are the potential areas coherent with the previous knowledge of the species? -> (Coherence)**
- **Are previous collecting areas represented as red in the map? -> (Omission errors)**
- **Are there missing areas where you know the species is present? - > (Commission errors)**



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Step 1 Project

Step 2 Country

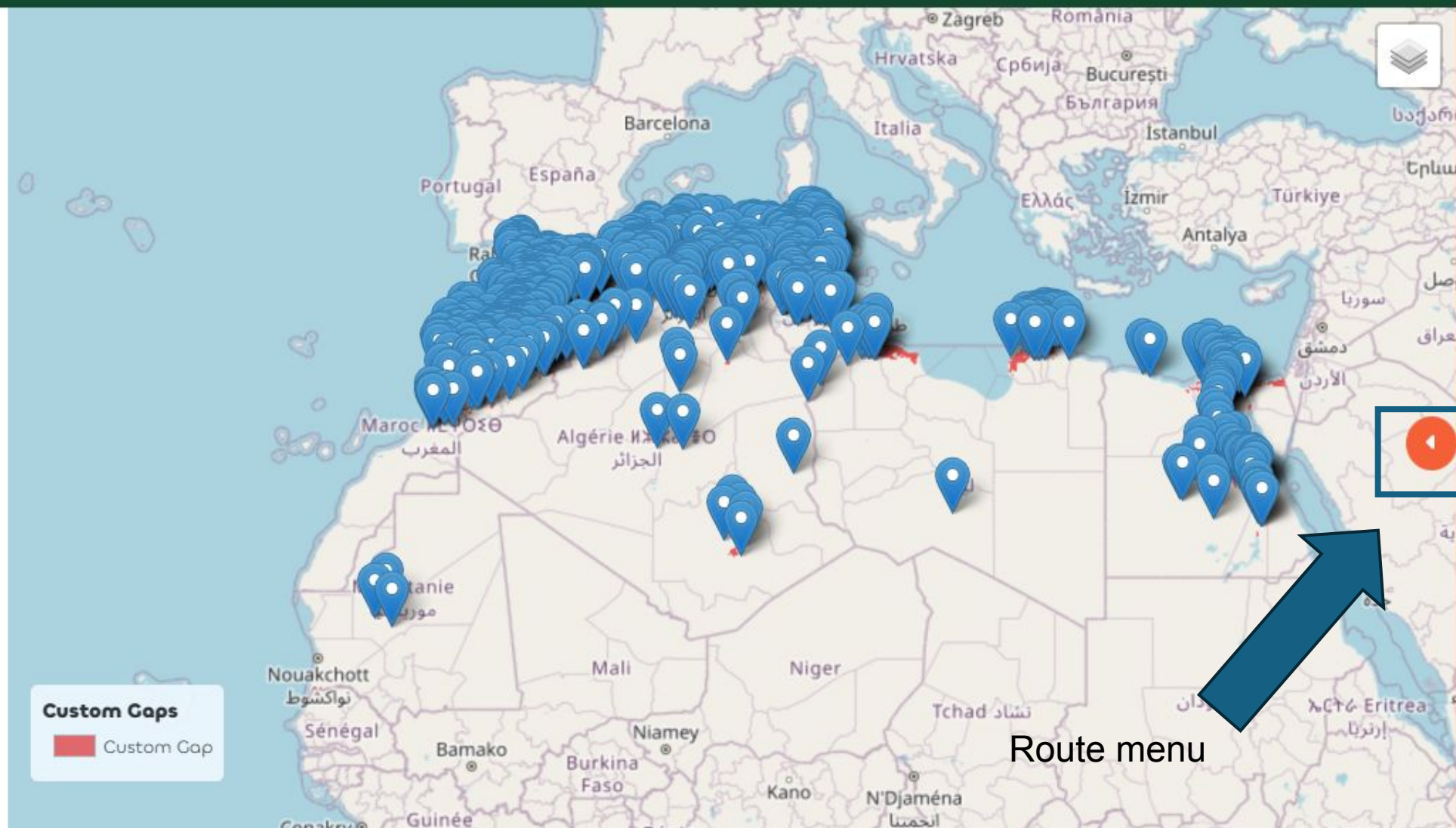
Step 3 Major Crops



Add to map

 Delete your gap analysis

 Delete your accessions



Route menu view

 Home

Viewer Api About

Step 1 Project

Select Project ▼

Step 2 Country

Select Country ▼

Step 3 Major Crops

Search by name... 

Add to map

 Delete your gap analysis

 Delete your accessions



Custom Gaps
 Custom Gap


Route 



Destination #1





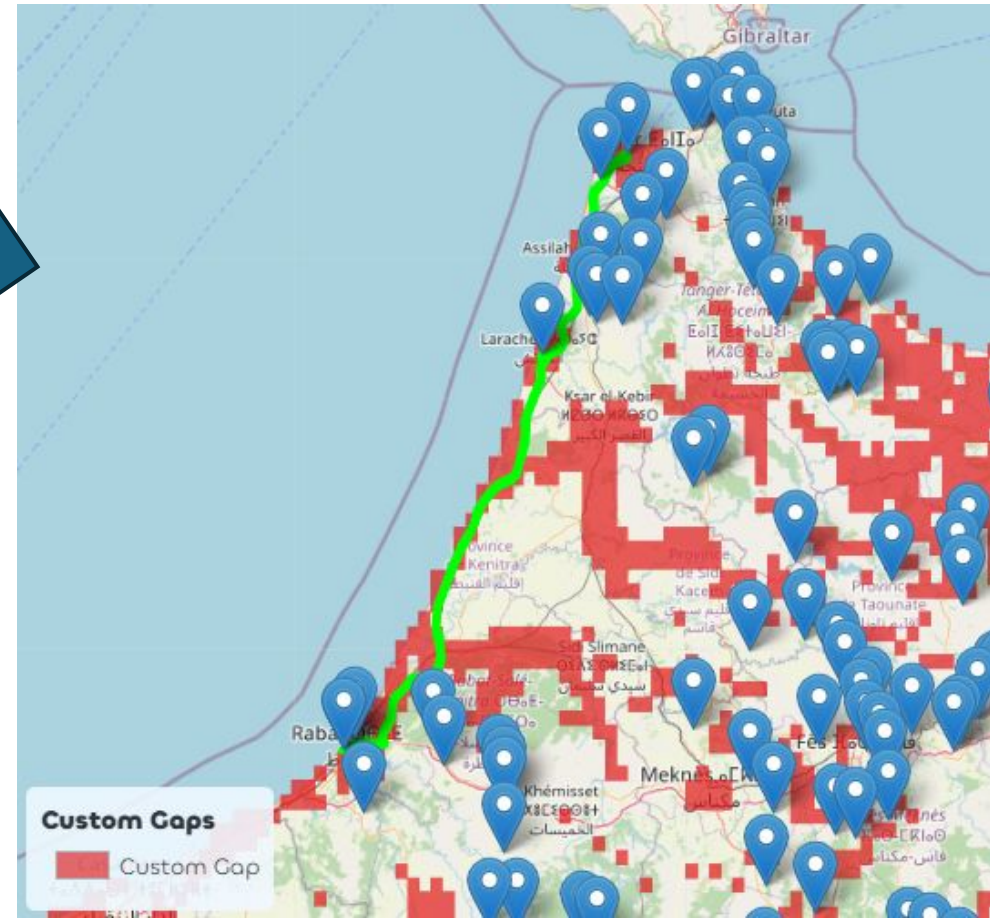
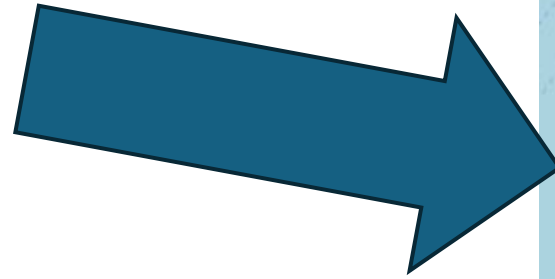
Get route 

Lets imagine the following route to collect

Route

- Rabat, Marruecos
- ||
- Larache, Marruecos
- ||
- Tánger, Marruecos
- ||
- Rabat, Marruecos

Get route



your route is likely to pass through areas with a high probability of encountering the target species

Route i

● Rabat, Marruecos ×

||

● Larache, Marruecos ×

||

● Tánger, Marruecos ×

||

● Rabat, Marruecos ×

||

+

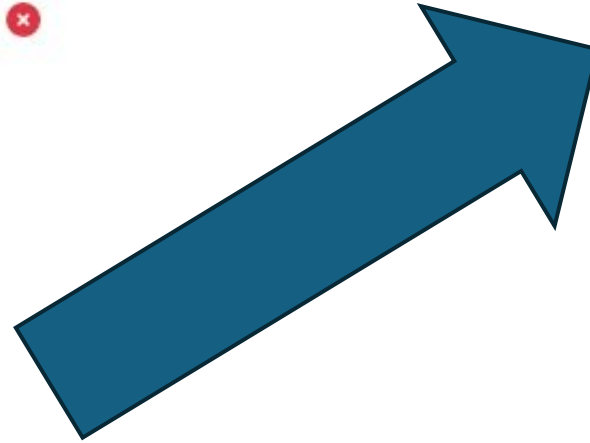
Get route 🔍

Clean Route 🗑️

Navigate to destination 🚗

Obtain instructions for Google maps

- [Google Map navigation](#)



Route summary

