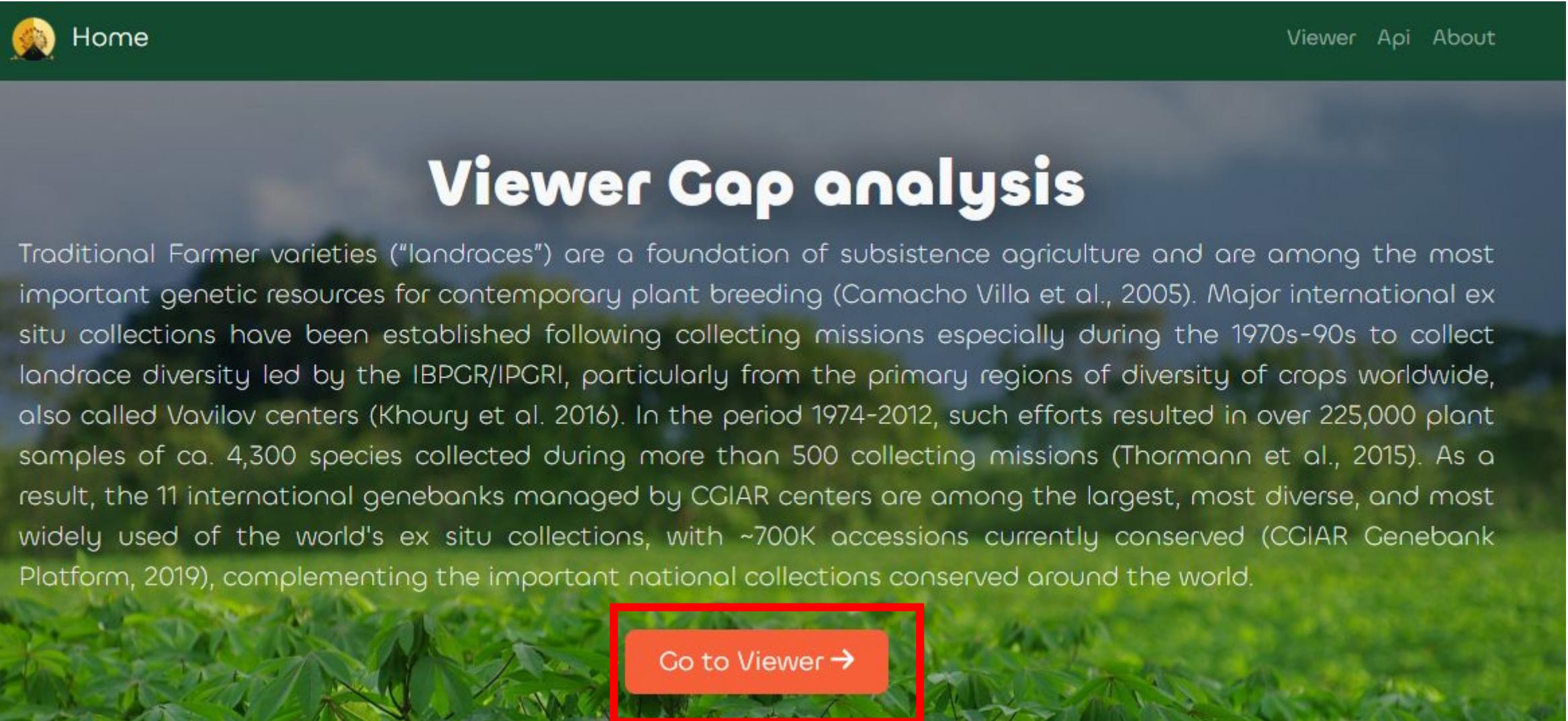


Tutorial to upload a gap map  
to Viewer Gap analysis

# 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



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
- Accesion\_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_database	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	5.55555557		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_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			USDA		24.2	5.56666667	USDA_?	

# Equivalences

- Y=species\_name
- Latitude=latitude
- Longitude=longitude
- source\_db=source\_database
- database\_id= accesion\_id

# Format gap analysis raster file

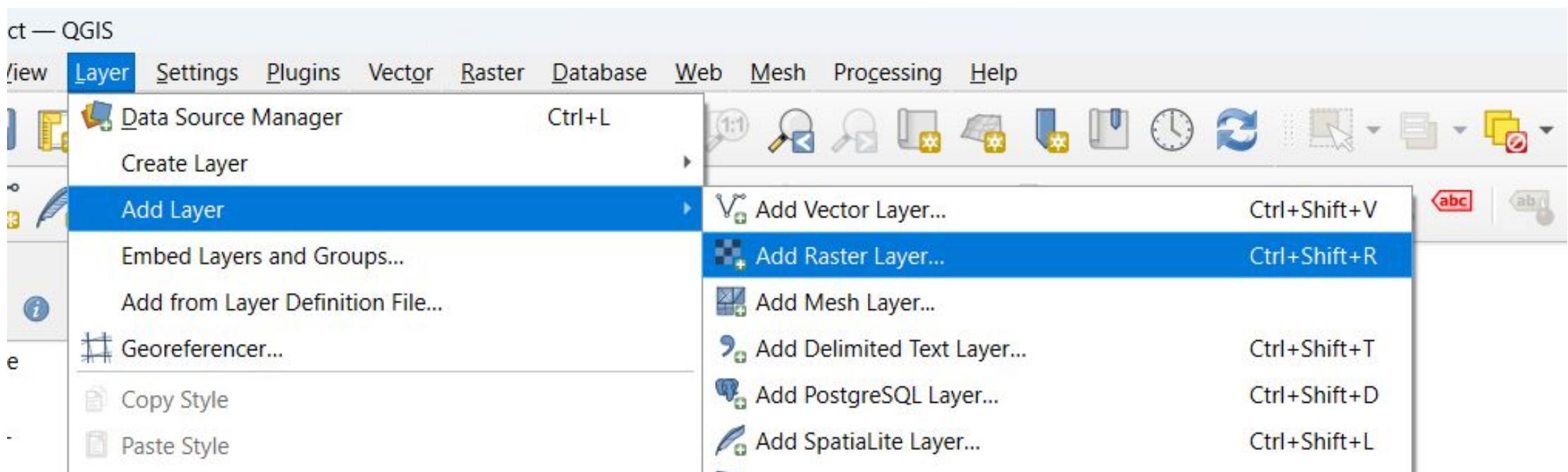
QGIS instructions

# Go to your folder

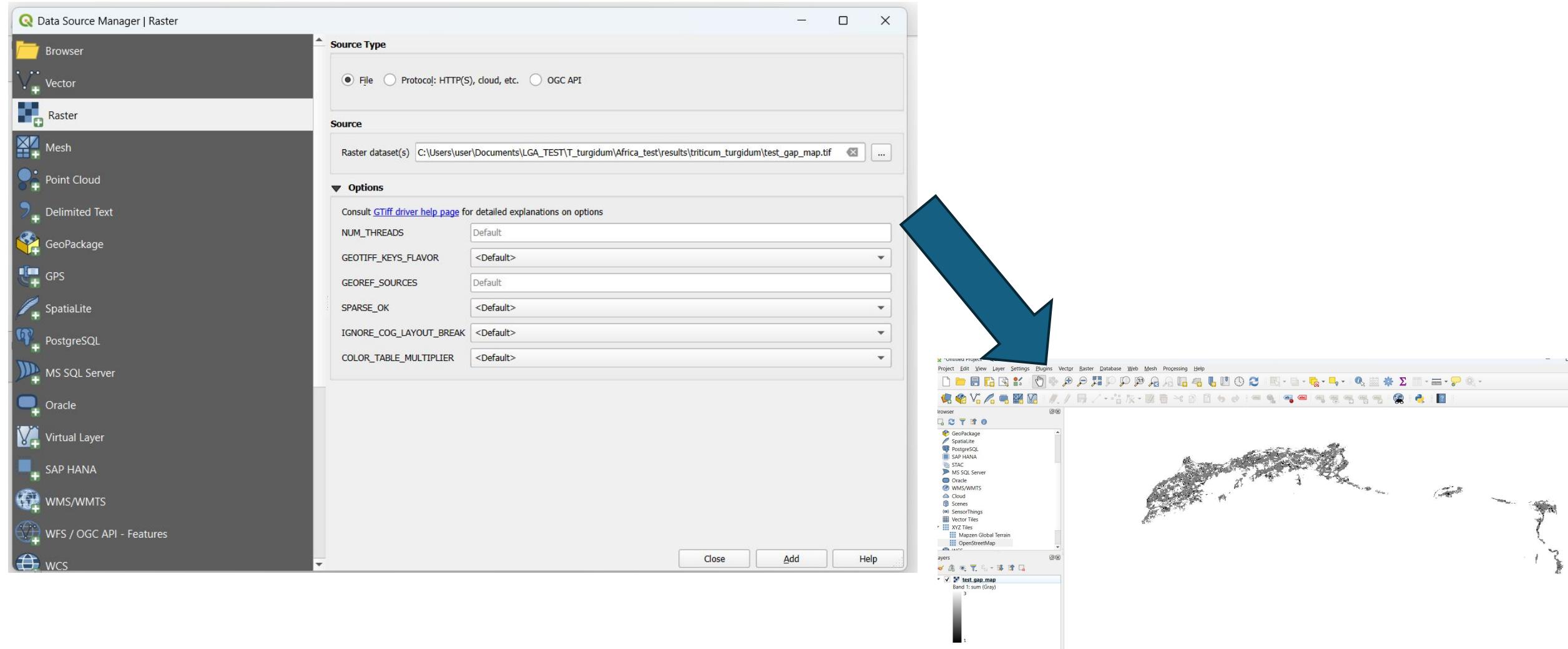
- T\_turgidum\Africa\_test\results\triticum\_turgidum
- Your gap map is named: test\_gap\_map.tif
- Please remove the values in the raster as 1 to 2. They are low and medium probabilities gaps (You can use QGIS or R)

# Instructions for qgis

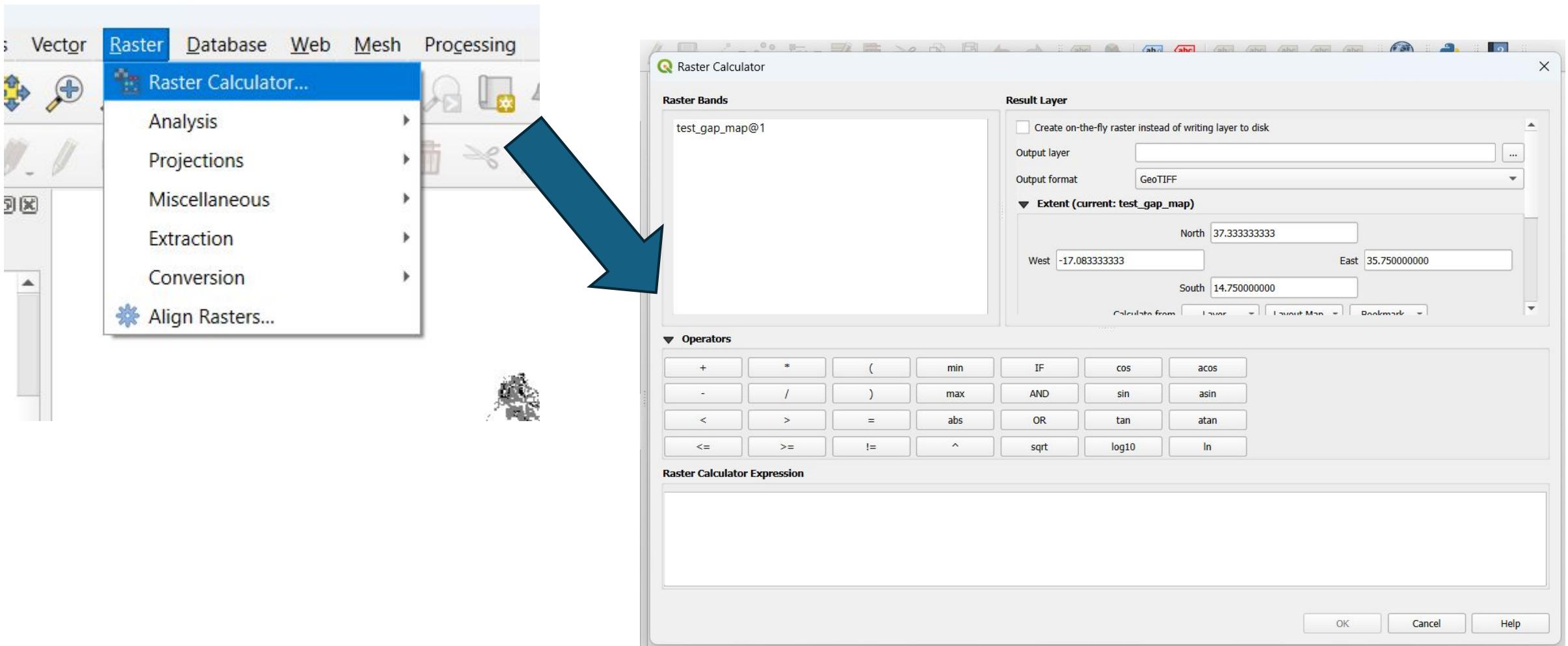
- Step 1 ) Click in Add Layer > Add Raster Layer



# Step 2) Load your gap map file test\_gap\_map.tif and click on Add



# Step 3. Remove values different of three



Raster Calculator

Raster Bands

Result Layer

Create on-the-fly raster instead of writing layer to disk

Output layer: C:\Users\user\Documents\LGA\_TEST\THR\_TO\_VIEWER

Output format: GeoTIFF

Extent (current: test\_gap\_map)

North: 37.3333333333

West: -17.0833333333

East: 35.7500000000

South: 14.7500000000

Calculate from: Layer

Layout Map

Bookmark

New layer to upload

Operators

+	*	(	min	IF	cos	acos
-	/	)	max	AND	sin	asin
<	>	=	abs	OR	tan	atan
<=	>=	!=	^	sqrt	log10	ln

Expression to remove values different of three

Raster Calculator Expression

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

Expression valid

# 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 library
library(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

Select Project ▾

Step 2 Country

Select Country ▾

Step 3 Major Crops

Search by name...



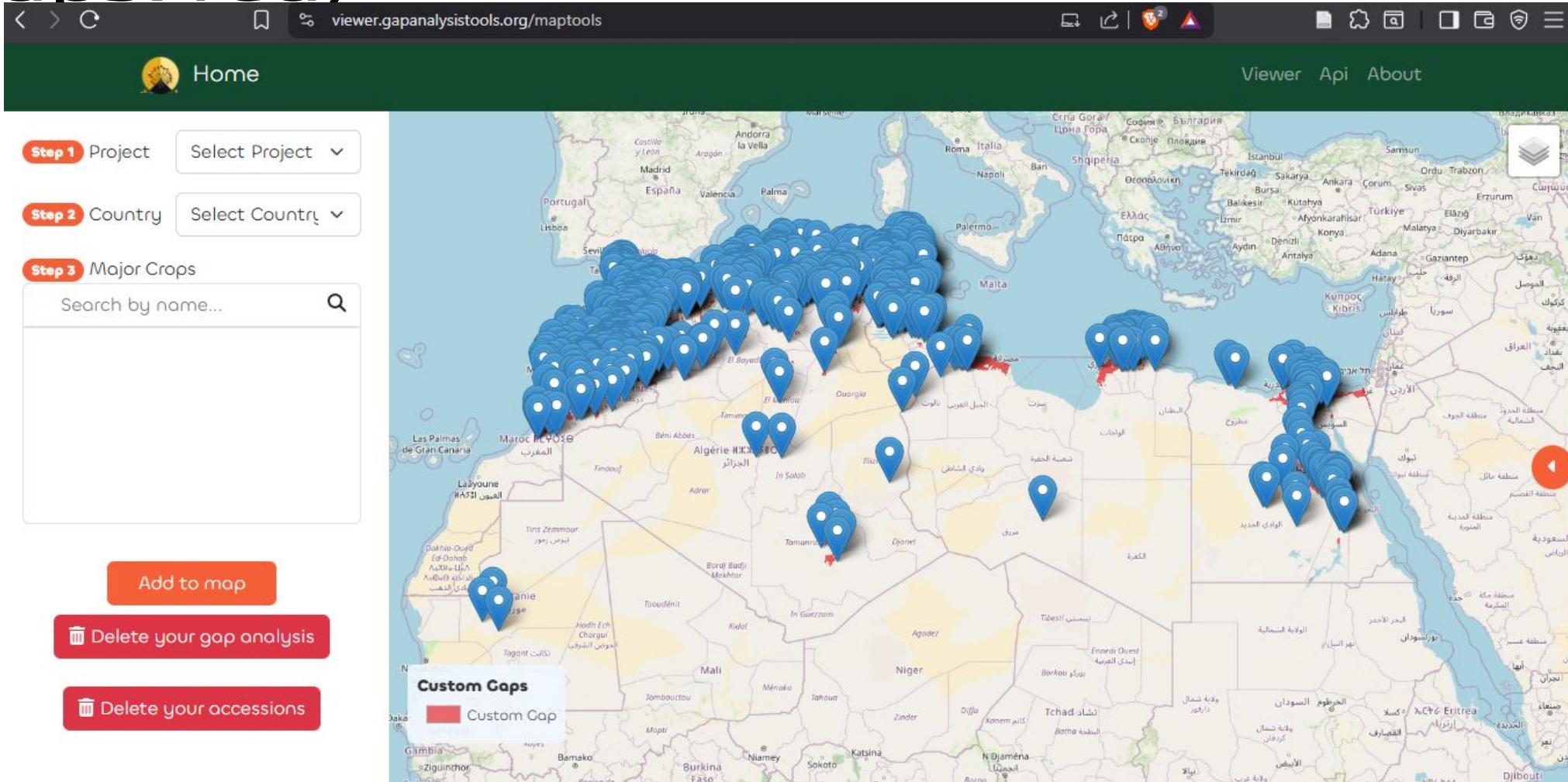
Add to map

Upload your gap analysis

Upload your accessions

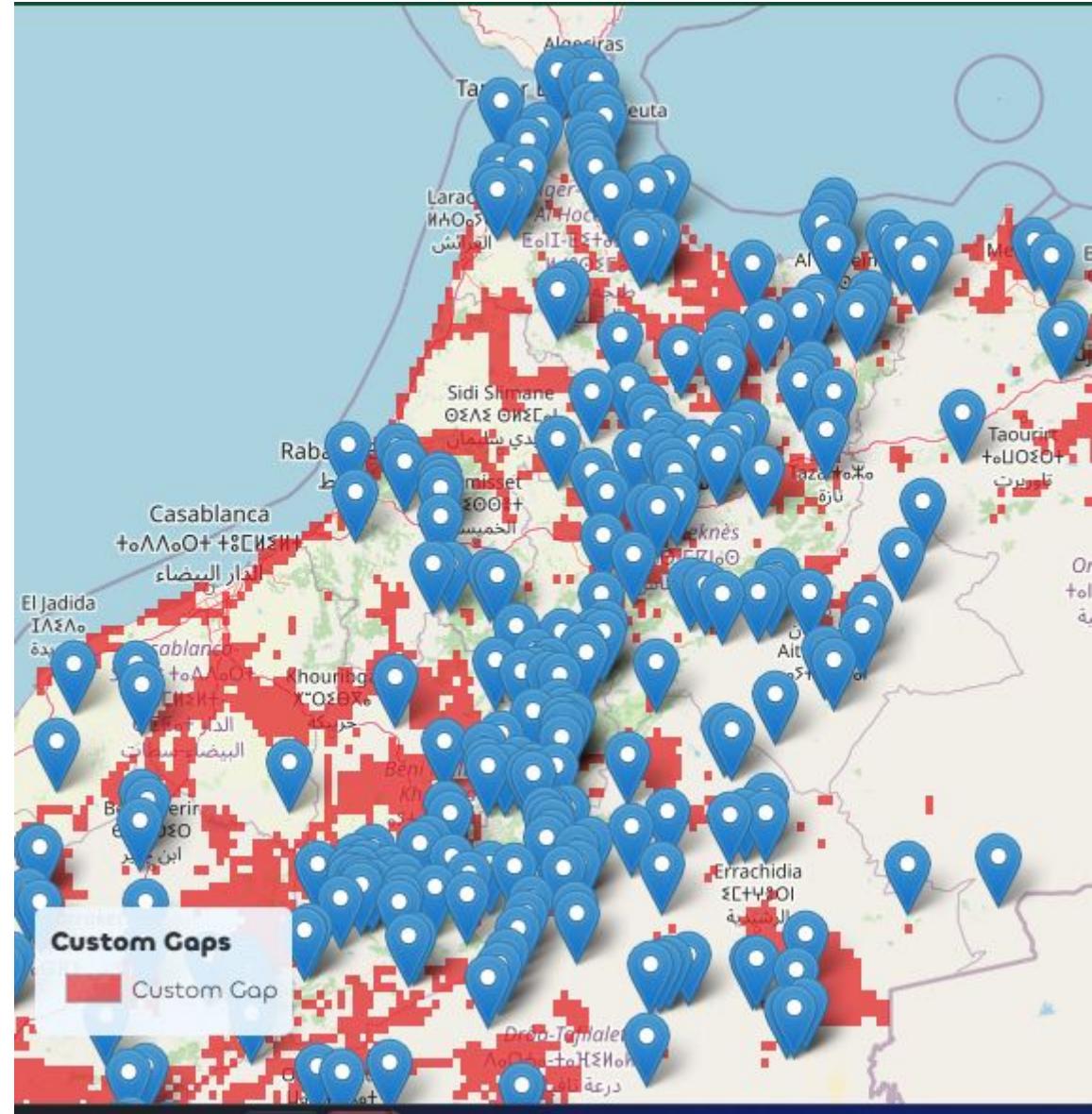


# Your germplasm data and gap map are ready to be visualized! (Accessions: Blue, gaps: red)



# 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)



Home

Viewer API About

Step 1 Project

Select Project ▾

Step 2 Country

Select Country ▾

Step 3 Major Crops

Search by name...



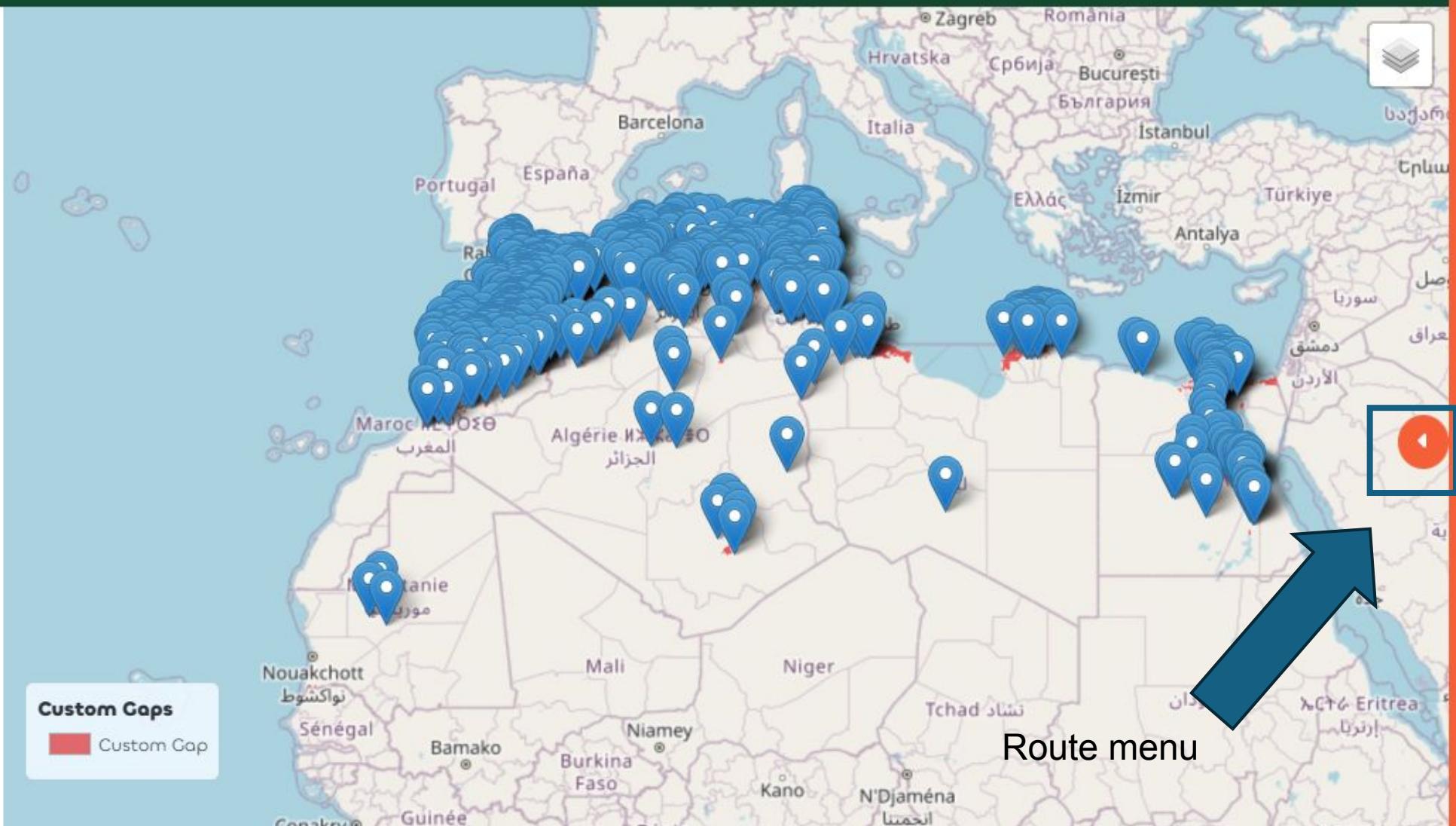
Add to map

Delete your gap analysis

Delete your accessions

Custom Gaps

Custom Gap



# Route 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



Zagreb  
Hrvatska  
Italia  
Barcelona  
España  
Portugal  
Rai  
Maroc  
المغرب  
Algérie  
الجزائر  
Nouakchott  
نواكشوط  
Sénégal  
Bamako  
Niamey  
Burkina Faso  
Tchad  
Mali  
Niger  
Niortanie  
موريتانيا  
Mauritanie

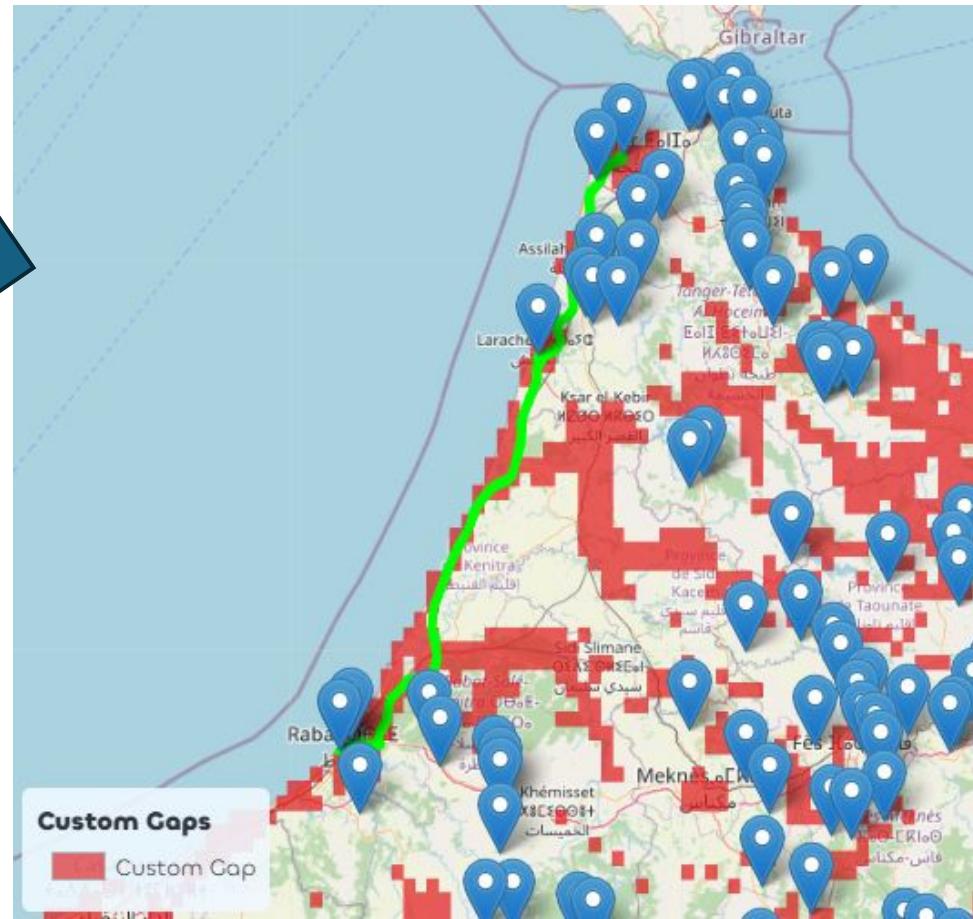
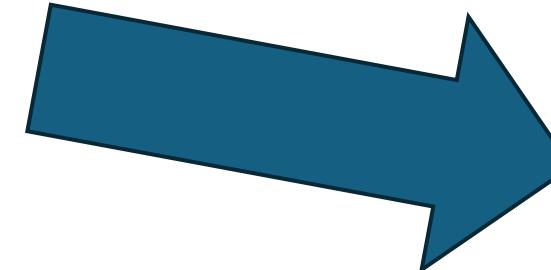
Route

Destination #1 

|| +

Get route 

# Lets imagine the following route to collect

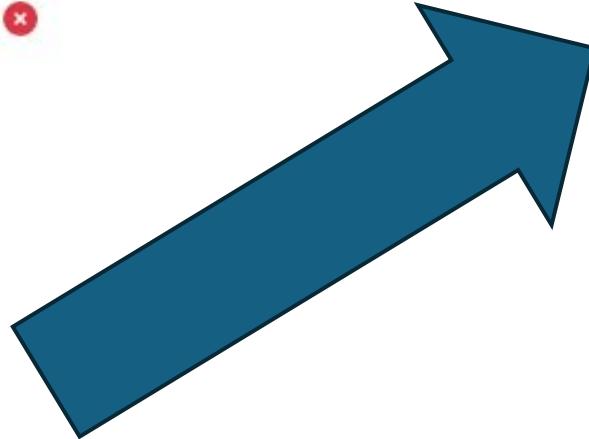


your route is likely to pass through areas with a high probability of encountering the target species



# Obtain instructions for Google maps

- Google Map navigation



## Route summary



Home

Step 1 Project

Select Project

Step 2 Country

Select

Step 3 Major Crops

Search by name...

### Route Summary

Average distance 499.757 kms

Estimated travel time 5 hours and 53 minutes

Average travel altitude 45.24 mts

#### Elevation graph



Route



Marruecos



Marruecos



Marruecos



Marruecos



Get route



Plan Route



to destination

