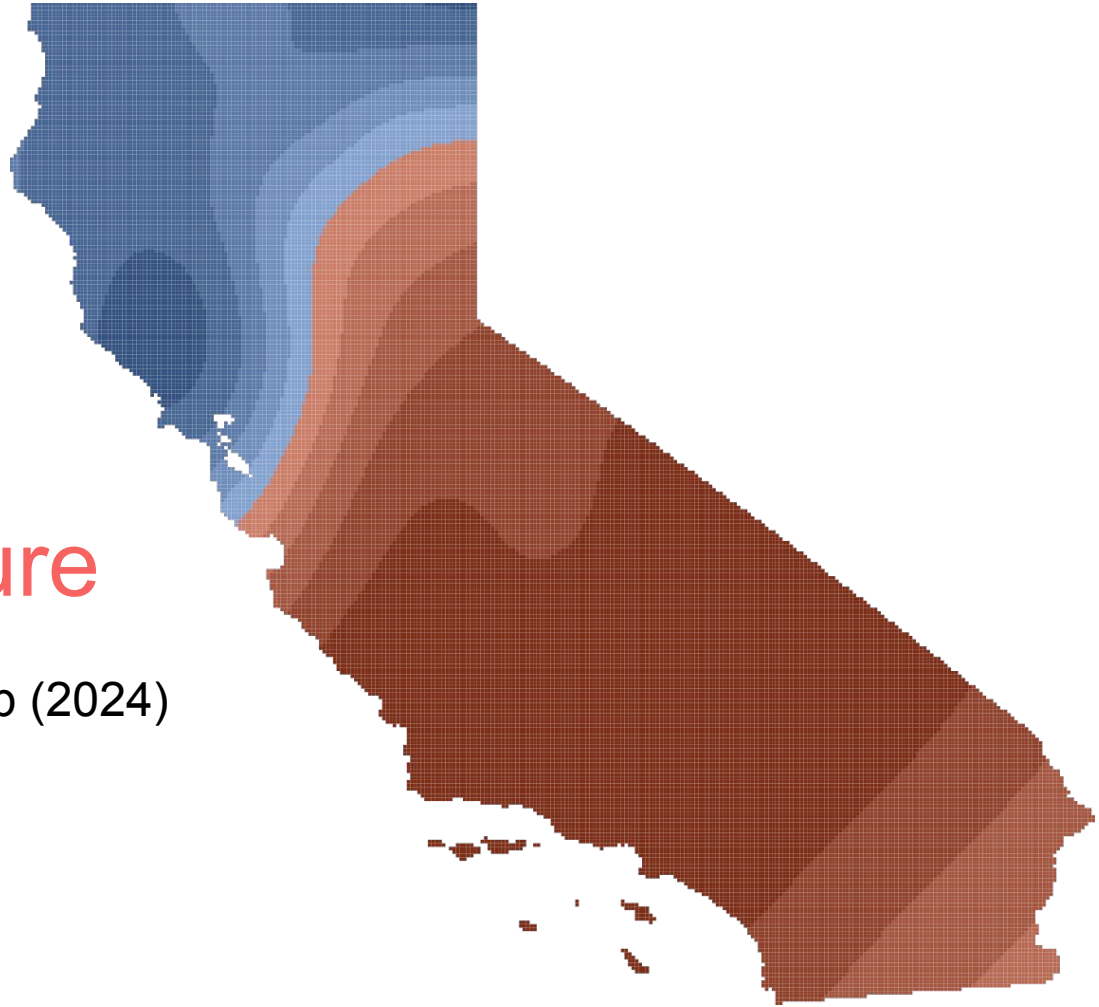
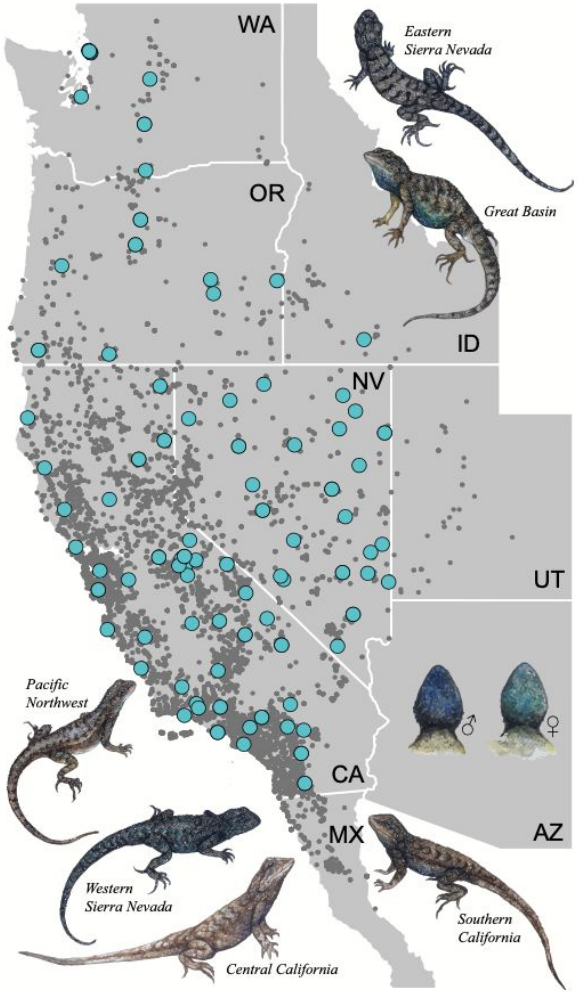
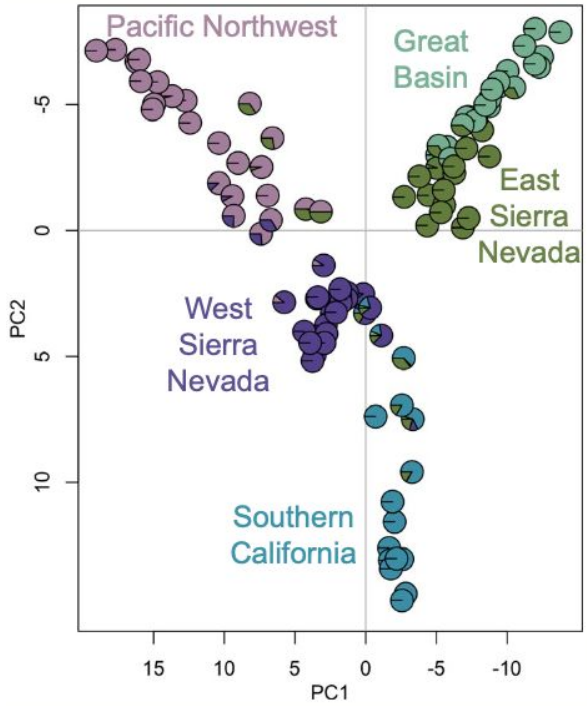
Population structure

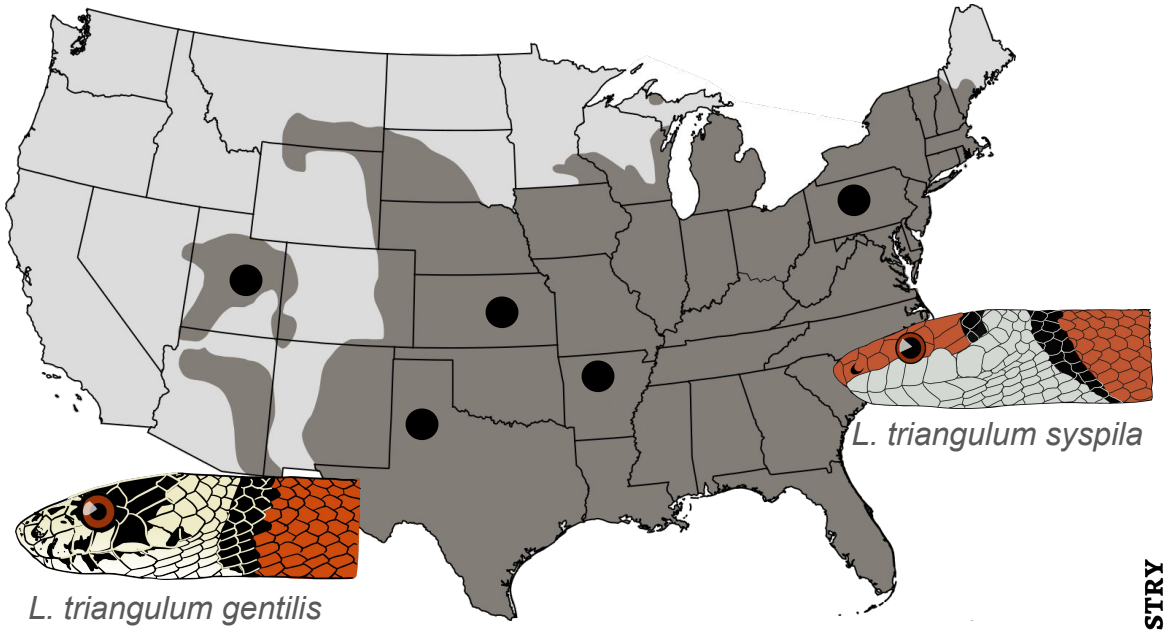
Anne Chambers & Anusha Bishop (2024)



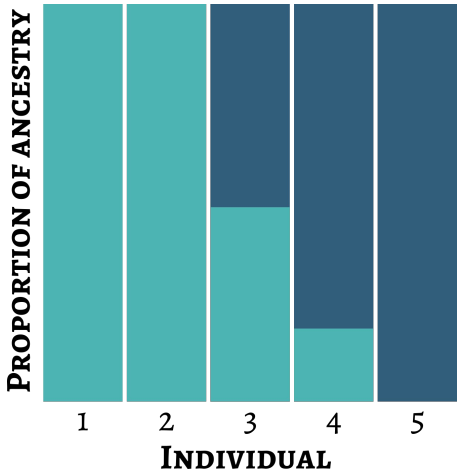


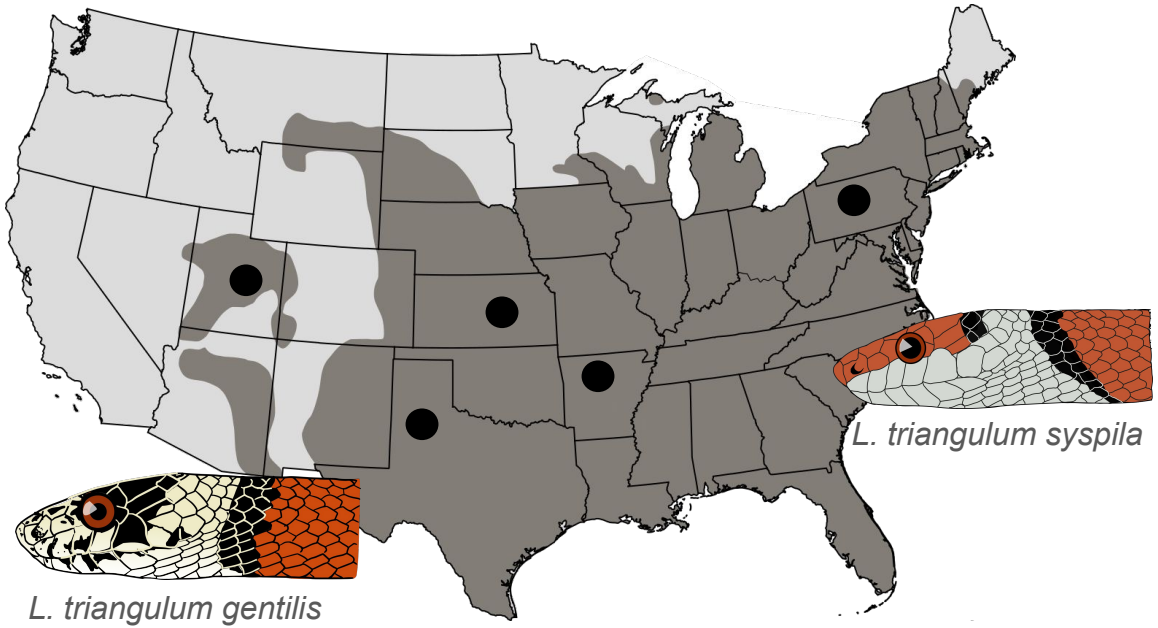


Bouzid et al. (2022)

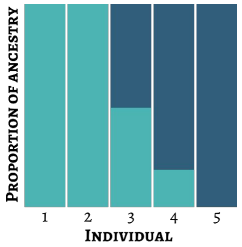


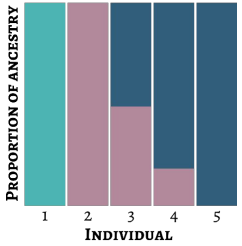
Two clusters
(K = 2)

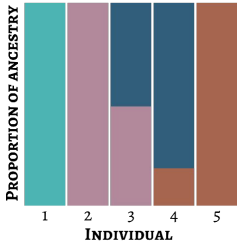


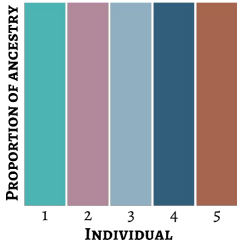


Range of clusters (K = 2–5)



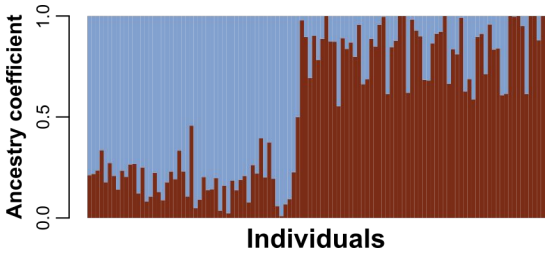




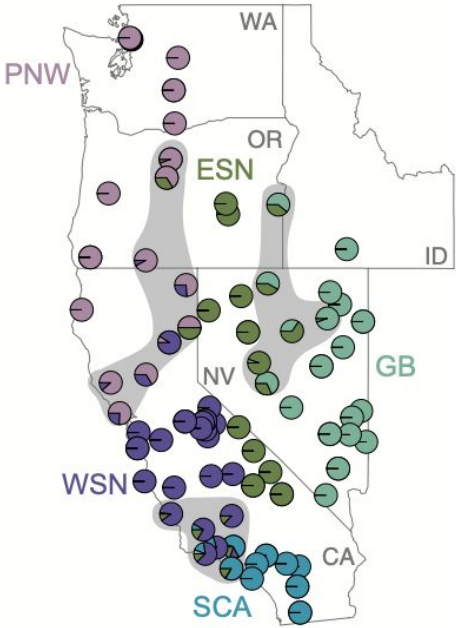


Visualizing population structure results

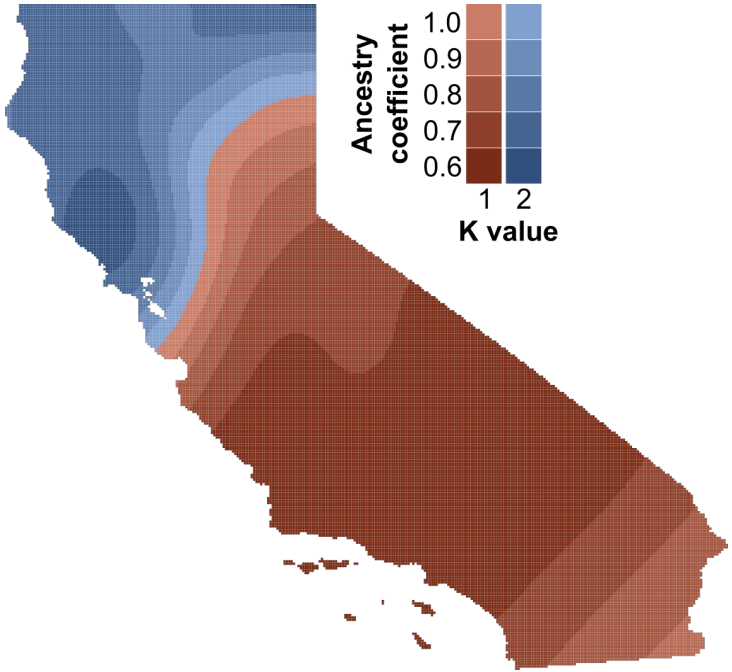
Structure plot



Pie charts



Map of kriged ancestry coefficients



Bouzid et al. (2022)

Methods to infer population structure

STRUCTURE (Pritchard et al. 2000, *Genetics*)
fastSTRUCTURE, CLUMPP, FRAPPE, GENELAND
ADMIXTURE, TESS, Ohana

All of these methods estimate allele frequencies, are sensitive to sampling (individuals and loci), and based on genetic assumptions of HWE and LE between loci

Ensure your sampling is thorough and even, sites are unlinked, test a range of cluster numbers, and have a good knowledge of your study system!

EXERCISE

https://thewanglab.github.io/algatr/articles/TESS_vignette.html

Process input data files

```
# Load example dataset
load_algatr_example()

# Convert vcf to genotype matrix
liz_dosage <- vcf_to_dosage(liz_vcf)
```

VCF (object or file path)

See what **`liz_dosage`** looks like using **`head(liz_dosage)`**

Process input data files

```
# First, create a grid for kriging
krig_raster <- raster::aggregate(CA_env[[1]],
                                 fact = 6)
```

Raster layer

`fact` = factor to aggregate cells

See what happens when you change **`fact`** and replot

```
terra::plot(CA_env[[1]],
            col = mako(100),
            axes = FALSE)
```

Raster layer

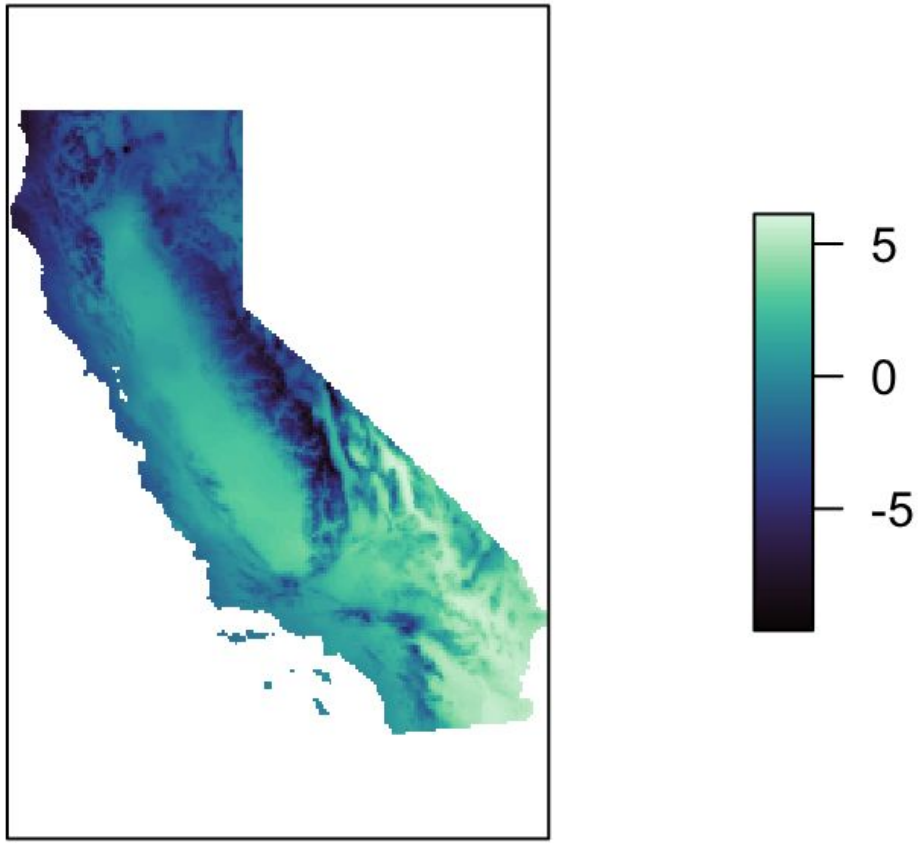
`col` = color palette

`axes` = whether to display axes

Process input data files

```
terra::plot(CA_env[[1]],
            col = mako(100),
            axes = FALSE)
```

See how this plot compares to one made using **`CA_env[[1]]`**



Run TESS with *K* selection

```
tess3_result <- tess_ktest(liz_dosage,
                           liz_coords,
                           Kvals = 1:10,
                           ploidy = 2,
                           K_selection = "auto")
```

Dosage matrix

Sampling coordinates

`Kvals` = range of *K* values to test

`ploidy` = ploidy of genetic data

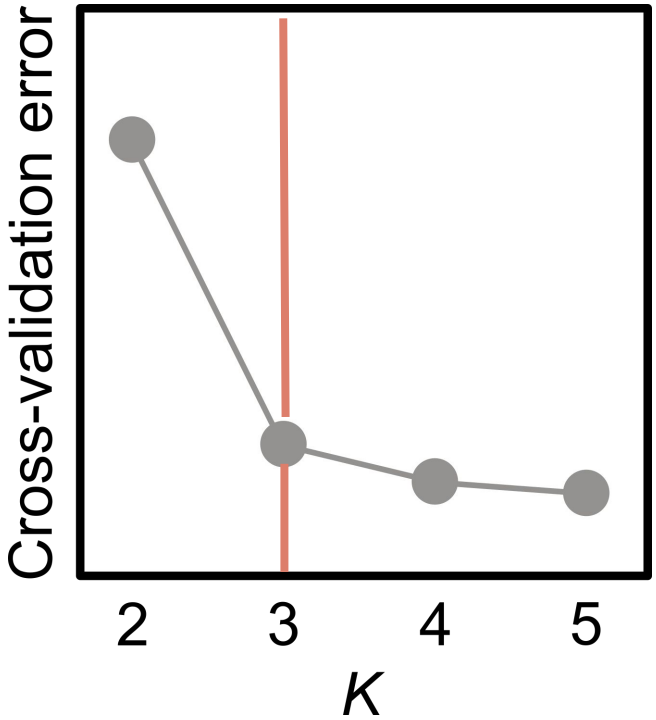
`K_selection` = type of *K* selection

*You can provide a single value to the **`Kvals`** argument and it won't perform K-selection but will run TESS*

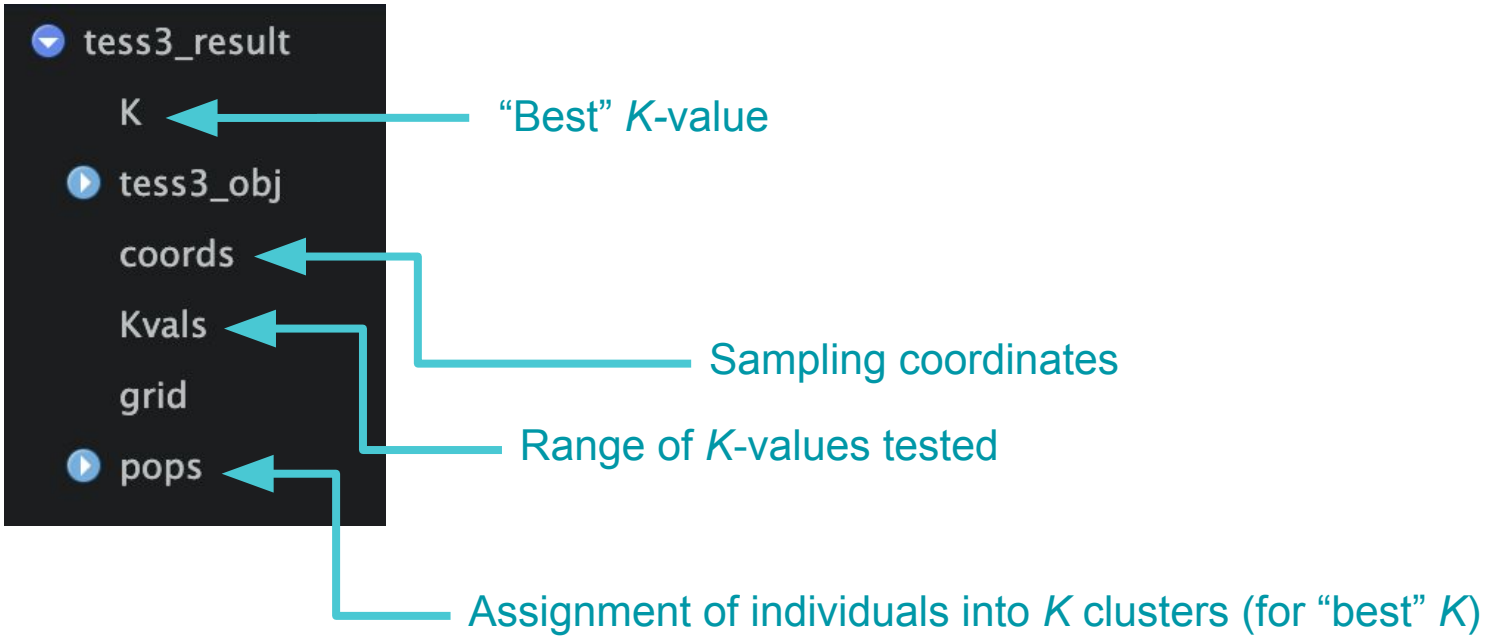
Run TESS with *K* selection

```
tess3_result <- tess_ktest(liz_dosage,
                           liz_coords,
                           Kvals = 1:10,
                           ploidy = 2,
                           K_selection = "auto")
```

See what happens when you set
K_selection = “manual”



Interpret TESS results



What is in the **`tess3_obj`** element of this list?

Interpret TESS results

```
# Get TESS object and best K from results
tess3_obj <- tess3_result$tess3_obj
bestK <- tess3_result[["K"]]
```

Extract TESS object and best *K* value from TESS results

```
# Get Qmatrix with ancestry coefficients
qmat <- tess3r::qmatrix(tess3 = tess3_obj,
                        K = bestK)
```

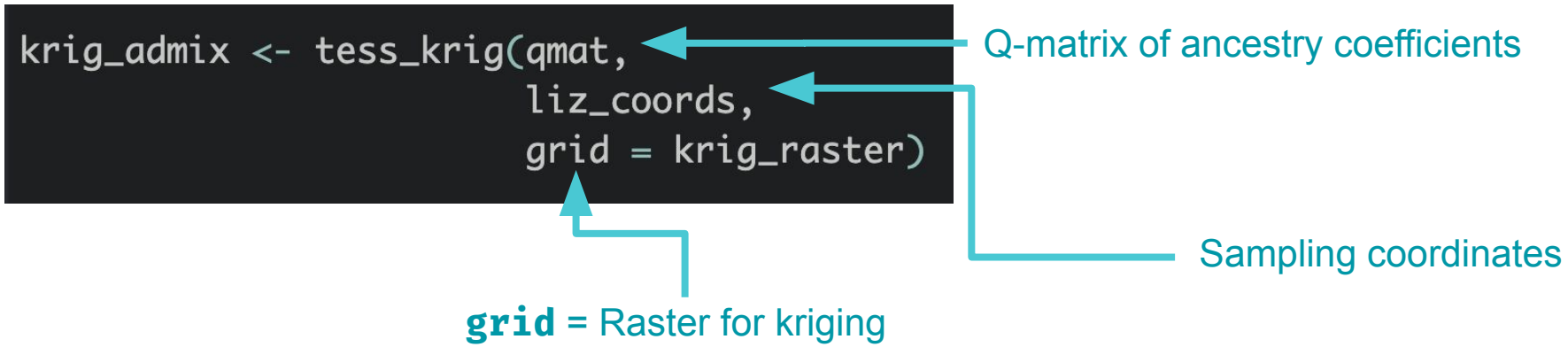
`tess3` = TESS object

`K` = *K* value to extract ancestry coefficients for

Take a look at the Q-matrix by doing **`head(qmat)`**

Krige ancestry coefficients using your raster

```
krig_admix <- tess_krig(qmat,
                        liz_coords,
                        grid = krig_raster)
```

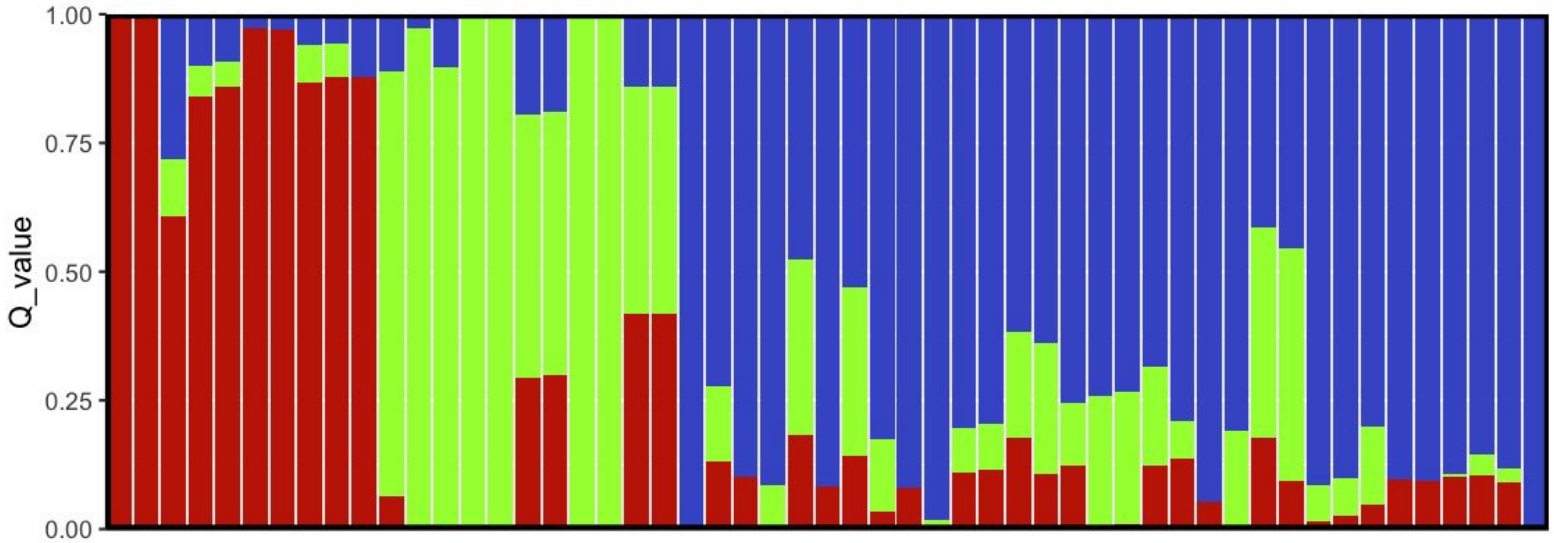


See what happens when you plot **krig_admix** (using **terra::plot**) compared to your earlier plot of **krig_raster**

Plot TESS results

```
tess_ggbarplot(qmat,
               legend = FALSE,
               sort_by_Q = TRUE)
```

See what happens when you set **`sort_by_Q()`** to FALSE



Plot TESS results

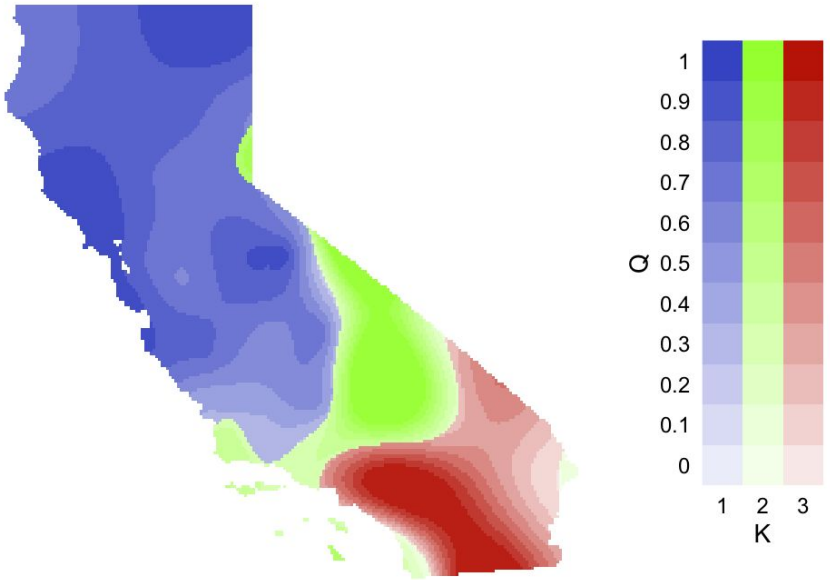
```
tess_ggplot(krig_admix,
            plot_method = "maxQ")
```

Raster with kriged ancestry coefficients

plot_method = which ancestry coefficients to colorize map using

Plot TESS results

```
tess_ggplot(krig_admix,
            plot_method = "maxQ")
```

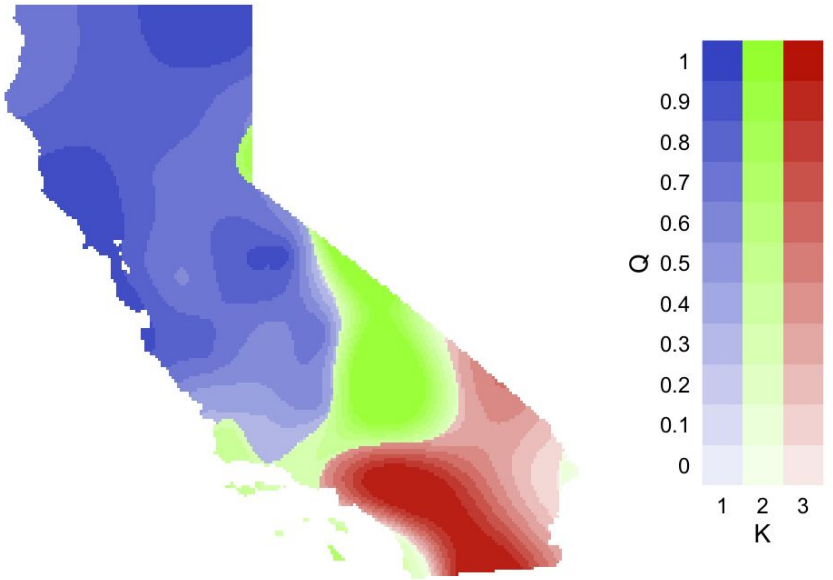


See what happens when you change the **`plot_method`** argument in the **`tess_ggplot()`** function

See what happens when you specify **`liz_coords`** using the **`coords`** argument in the **`tess_ggplot()`** function

Plot TESS results

```
tess_ggplot(krig_admix,
            plot_method = "maxQ")
```




```
Warning messages:
1: In crs_check(coords, grid) :
  No CRS found for the provided coordinates. Make sure the coordinates and the raster have the
same projection (see function details or vignette)
2: [mask] CRS do not match
```

https://thewanglab.github.io/algatr/articles/TESS_vignette.html

Exercise

1. Load the example dataset
2. Process genetic data:
   a. Convert vcf to dosage using `vcf_to_dosage()`
3. Process environmental data:
   a. Create a raster for mapping (kriging) using `raster::aggregate()`
4. Select the “best” number of *K* clusters and run TESS using `tess_ktest()`
5. Visualize results with a barplot using `tess_ggbarplot()`
6. Visualize results with a kriged map using `tess_krig()` and `tess_ggplot()`