

NALgen

NALgen (Neutral and Adaptive Landscape Genetics) is a method for modeling the process of gene flow and predicting the resulting pattern of (neutral and adaptive) genetic variation across (continuous) landscapes.

NALgen: Analysis Steps

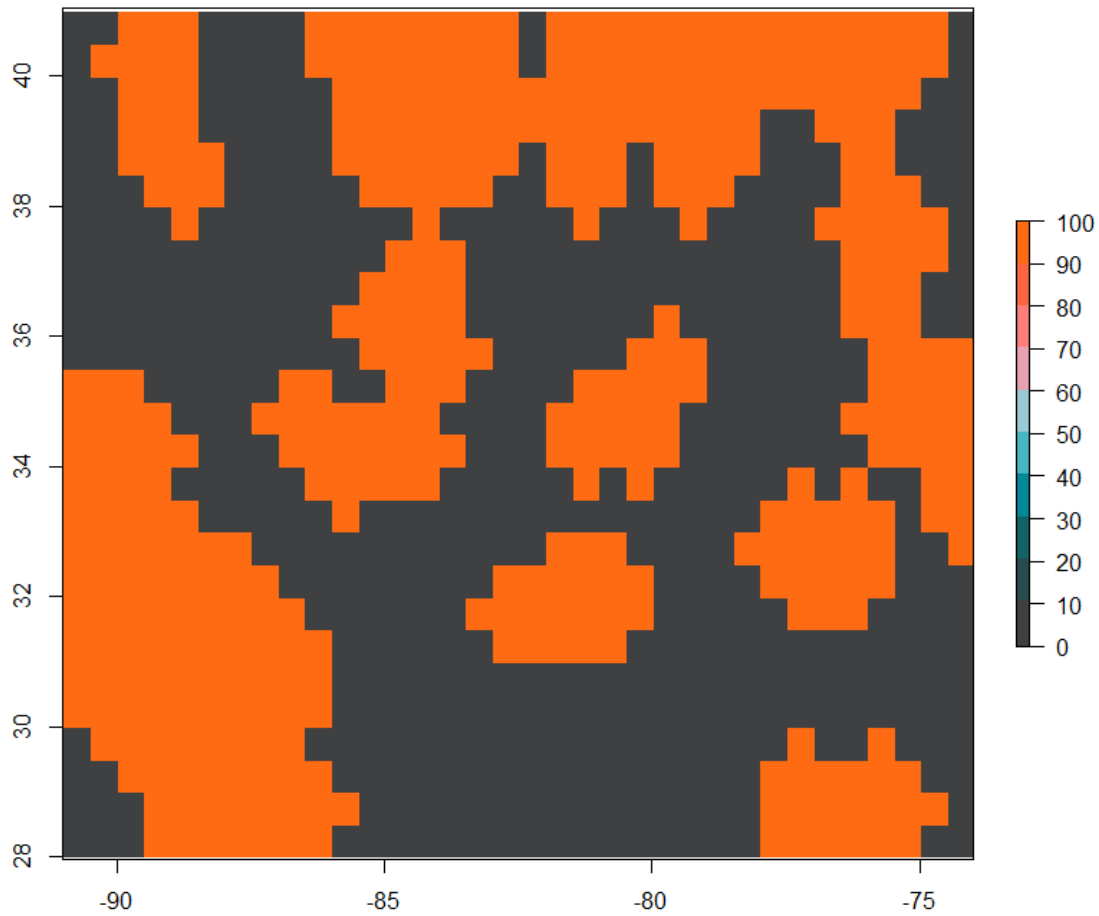
To evaluate the NALgen method of modeling neutral and adaptive genetic variation across continuous landscapes:

- *Generated several landscapes, and then simulated genotypes based on the generated landscapes*
- *Used multivariate analyses*
 - to infer population structure in the simulated data
 - to find covariance between genetic and environmental data.
- *Modeled neutral and adaptive genetic variation across continuous landscapes*
 - Information about population structure used to create response variable
 - Transformed environmental data (based on genetic-environmental covariance) used as predictors
- *Evaluated performance of model (using subsets of 20 randomly-distributed populations)*
 - Compared against original landscape used to simulate genotypes
 - Compared against inferred map of ancestry based on genotypes simulated for each cell (all 884 populations)

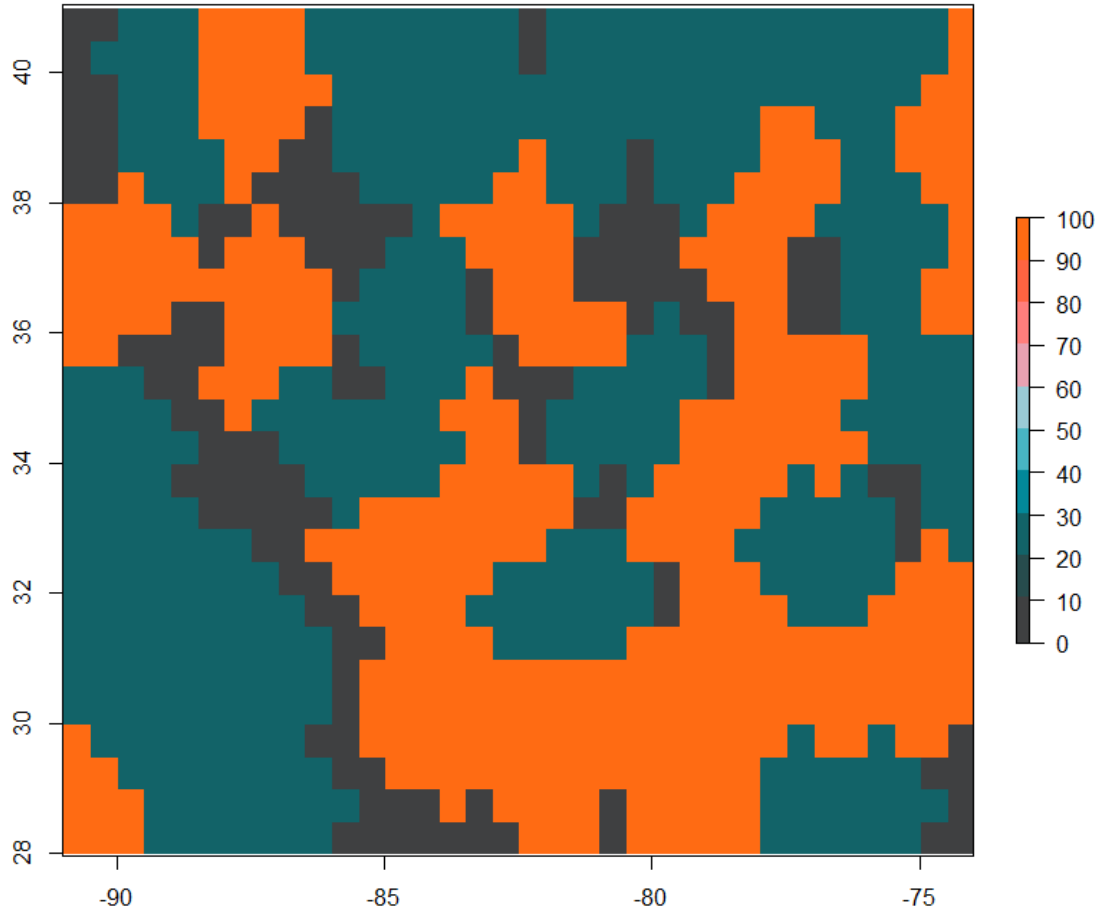
Landscape Genetic Simulations

- **Generating simple (low-complexity) landscapes and simulating genotypes**
 - *landscapeR* package: simulating simple landscapes (barrier and two different values of carrying capacity/habitat suitability): landscape 1 has low permeability cells (carrying capacity = 5) between habitable patches (carrying capacity = 100), while landscape 2 has high permeability cells (carrying capacity = 25), in addition to barriers (carrying capacity = 0)
 - *popRange* package: simulating 50 **selected** and 500 **neutral** SNPs based on the *landscapeR*-generated landscape.
- **Generating high-complexity landscapes and simulating genotypes**
 - *virtualspecies* package: landscape generation based on Bioclim data
 - Collinearity removed from climatic variables,
 - PCA of remaining variables performed,
 - Ranges of PCA values specified (for three metapopulations).
 - *popRange* package: simulating 50 *selected* and 500 **neutral** SNPs based on the *virtualspecies*-generated landscape.

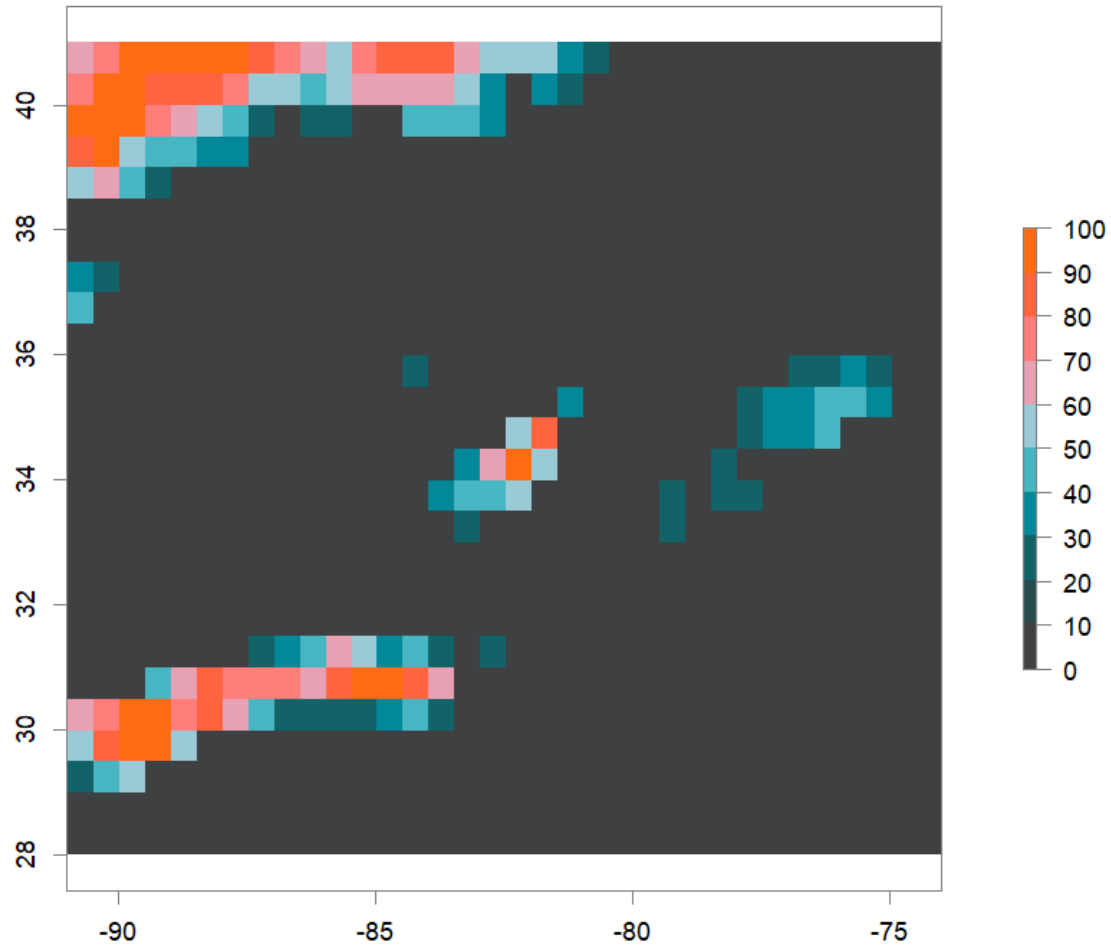
Simulated genotypes (50 selected and 500 neutral biallelic loci (SNPs), separately and combined): two migration coefficients ($m=0.1$ and 0.5) x two levels of landscape complexity (low and high) x two levels of landscape permeability (low and high)



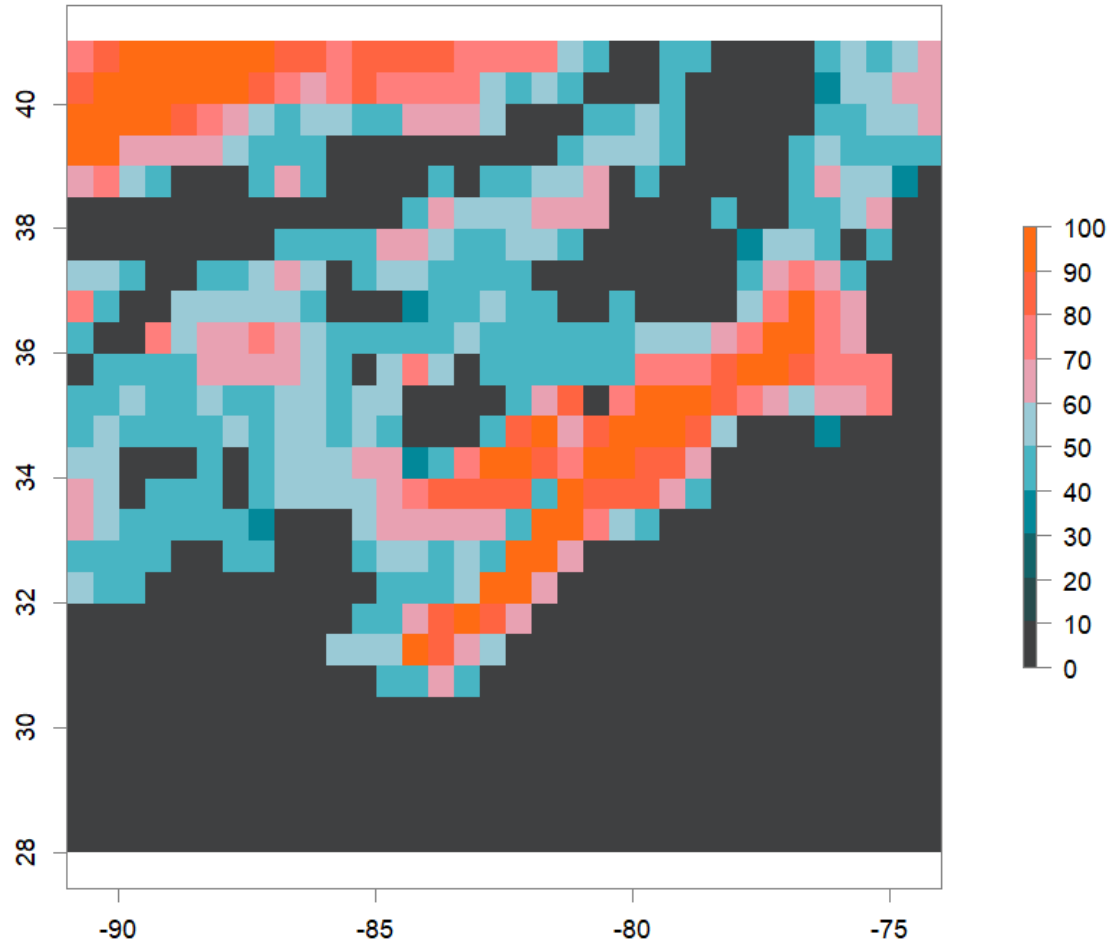
Low-Complexity
Low-Permeability
(LCLP) landscape



Low-Complexity
High-Permeability
(LCHP) landscape



High-Complexity
Low-Permeability
(HCLP) landscape



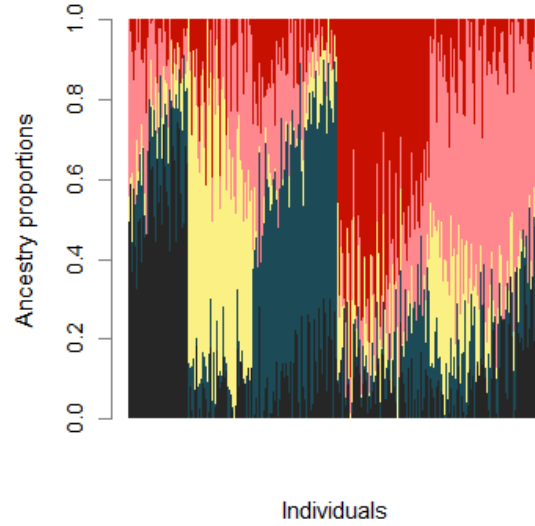
High-Complexity
High-Permeability
(HCHP) landscape

Setup of Evaluation Step: *884-population reference*

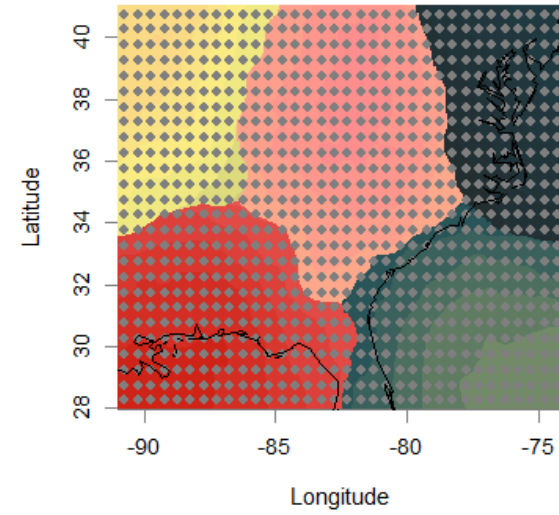
The original landscapes used to simulate the genetic data, as well as population structure results obtained from these complete genetic datasets, will be used in evaluating the NALgen method.

Presented hereinafter are the reference results (mapped ancestry coefficients) that NALgen modeling based on 20 randomly-distributed populations will be compared against.

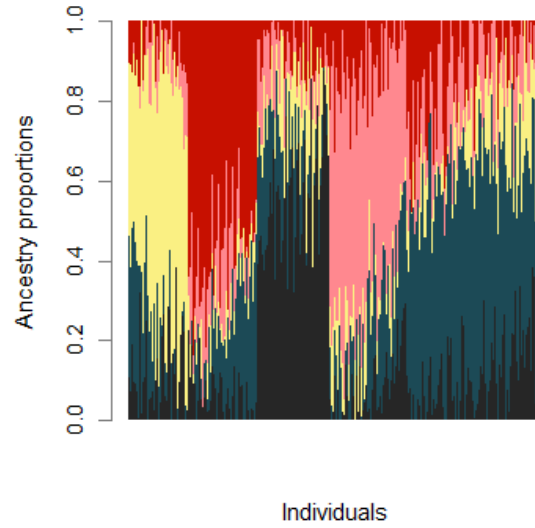
Ancestry: LCLP landscape ($m = 0.1$)



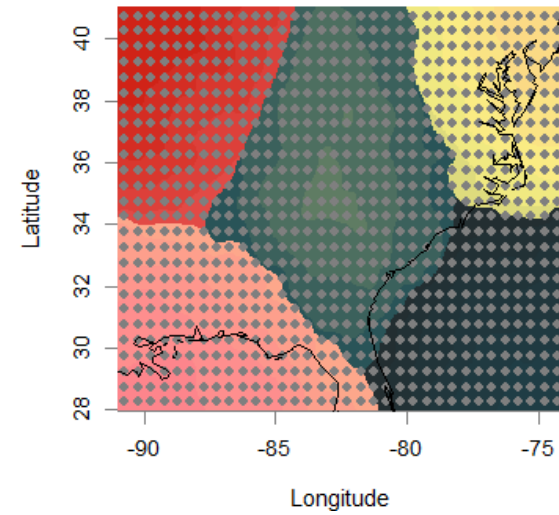
Mapped ancestry: LCLP landscape ($m = 0.1$)



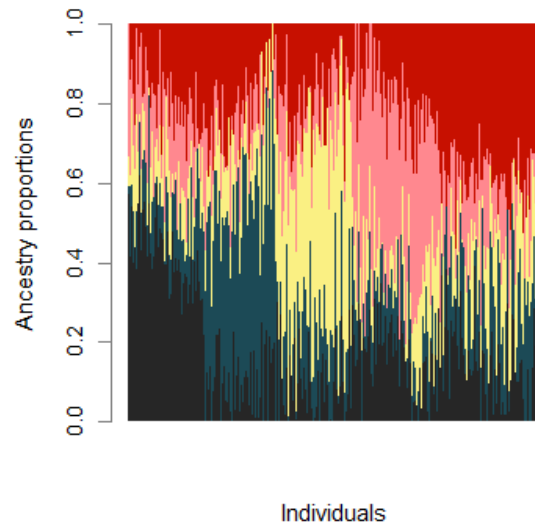
Ancestry: LCHP landscape ($m = 0.1$)



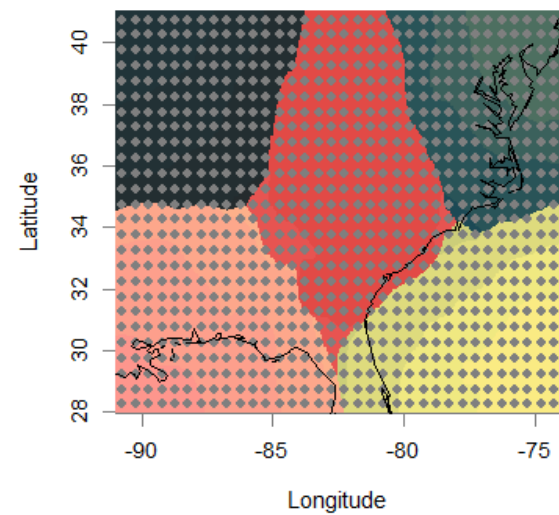
Mapped ancestry: LCHP landscape ($m = 0.1$)



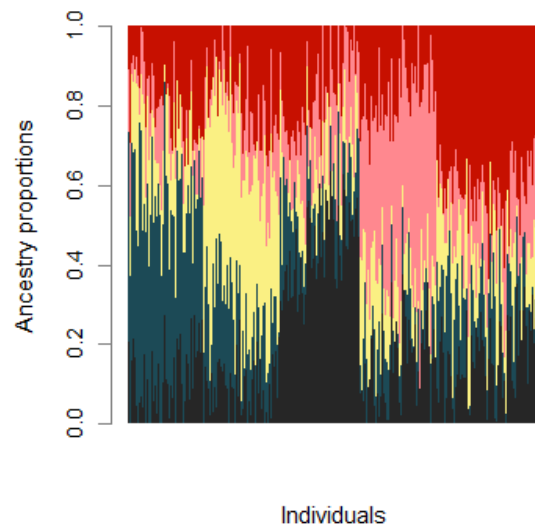
Ancestry: LCLP landscape ($m = 0.5$)



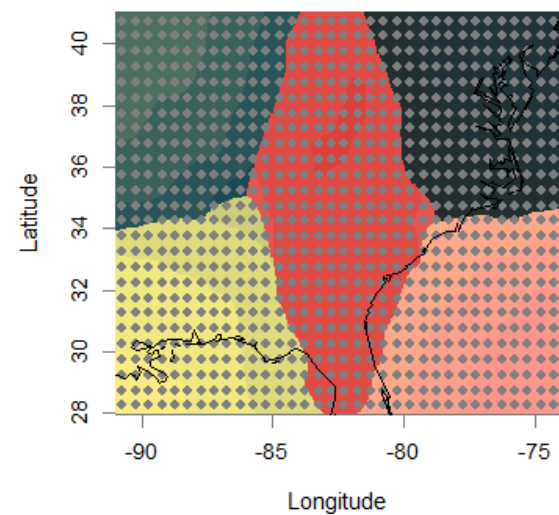
Mapped ancestry: LCLP landscape ($m = 0.5$)



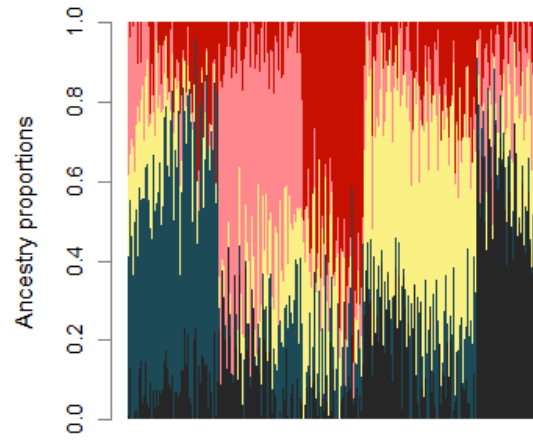
Ancestry: LCHP landscape ($m = 0.5$)



Mapped ancestry: LCHP landscape ($m = 0.5$)

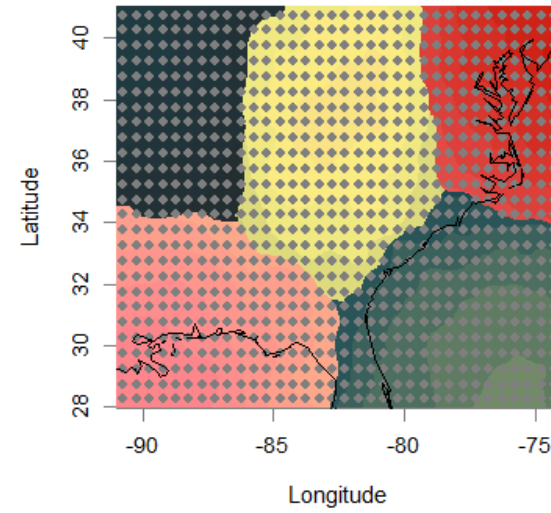


Ancestry: HCLP landscape (m = 0.1)

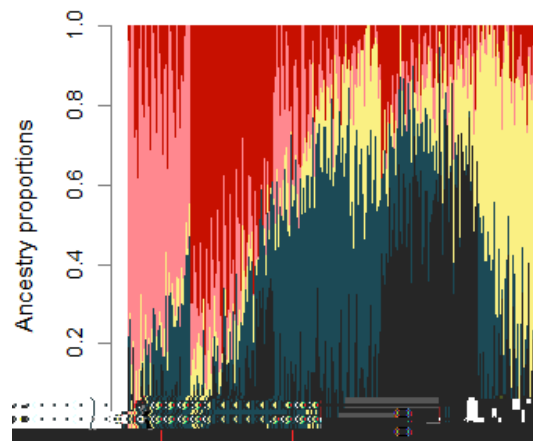


Individuals

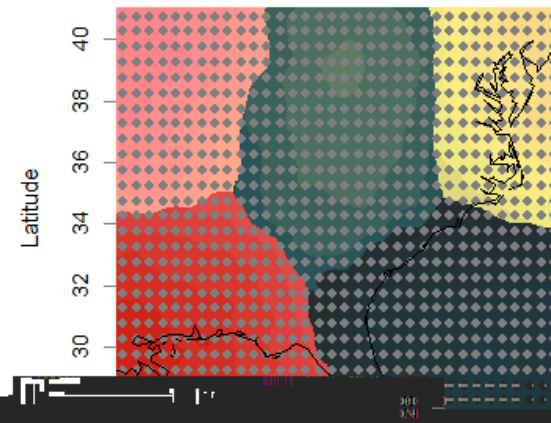
Mapped ancestry: HCLP landscape (m = 0.1)



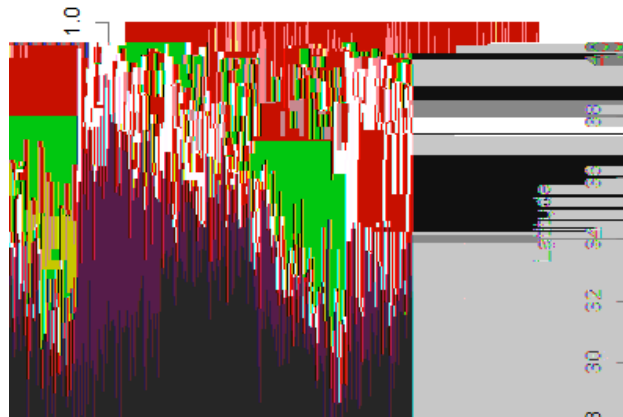
Ancestry: HCHP landscape (m = 0.1)



Mapped ancestry: HCHP landscape (m = 0.1)

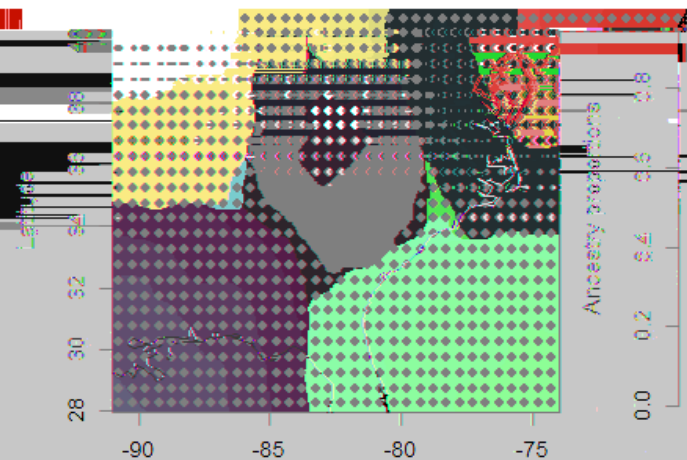


Ancestry: HCLP landscape (m = 0.5)



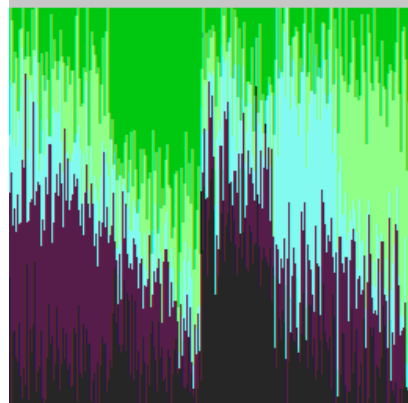
Individuals

Mapped ancestry: HCLP landscape (m = 0.5)



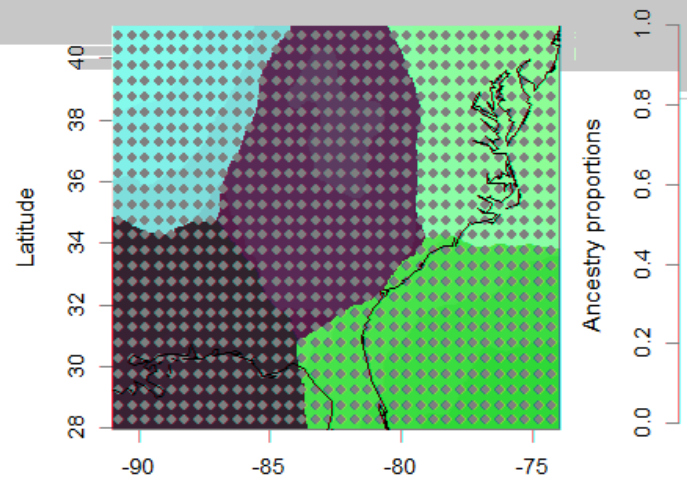
Longitude

Ancestry: HCHP landscape (m = 0.5)



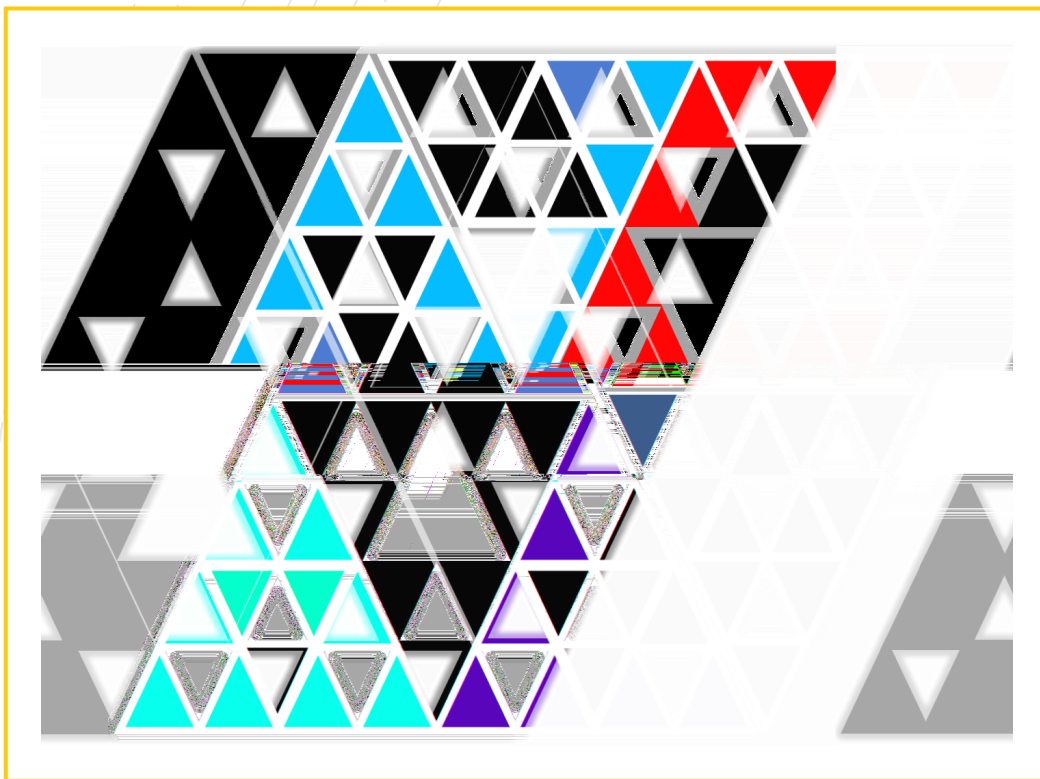
Individuals

Mapped ancestry: HCHP landscape (m = 0.5)



Longitude

NALgen Method



To determine the maximum genetic-environmental covariance, the raw data is first transformed: these transformed environmental scores form the predictors in NALgen modeling

The response variables are measures of genetic variation (neutral and adaptive): these are newly-developed metrics