Historical biogeography traditionally deals with relationships among species, genera, and higher taxonomic groups and the areas they occupy.

John Avise, animal geneticist at University of Georgia, coined the term "phylogeography" to describe "the history and formation of species" from a geographical perspective.

The classic phylogeographic analysis by Avise and his students involved the identification of a strong geographical signal within species separating populations from the Atlantic seacoast from the Gulf of Mexico seacoast. The presence of two quite distinct genotypes within all these unrelated species has been explained by Pleistocene glacial and inter-glacial events.

Due to advances in DNA sequencing and fingerprinting methods, historical biogeography has recently begun to integrate relationships of populations within species and the areas they occupy.
One of the most debated, and still unresolved, issues in phylogeography is the geographical origin of *Homo sapiens* - the “Eve hypothesis” as maternally inherited mitochondrial DNA (mtDNA) is often used.

The “out-of-Africa” scenario is often supported - as shown here - and is consistent with the fossil record. However, different ways of analyzing DNA support an “out-of-Asia” scenario as well.

Steps in a phylogeographic study:
1. Sample populations widely across geographical range of species
2. Sample multiple individuals from each population to access levels of variation in cpDNA, mtDNA, or nuclear genes
3. Identify and quantify genotypes for each population [haplotypes if cpDNA or mtDNA]
4. Construct minimum spanning tree for the haplotypes
5. Overlay geographical distributions onto the tree (or use Nested Clade Analysis in complicated studies)
Phylogeography — Historical Biogeography of the Species

Example 1: Cryptic invasion of a non-native genotype of *Phragmites australis* (common reed) into North America (Saltonstall 2002)

Native population in Great Lakes  Invasive population in Great Lakes

Phylogeography — Historical Biogeography of the Species

Genotyping of common reed from herbarium specimens prior to 1910 indicates the widespread presence of 11 native genotypes and 1 southern genotype also seen in South America and Asia

Minimum spanning tree for all genotypes

North American genotypes

Invasive form

Europe, Australasia, Africa, South America

Note that the native North American genotypes are closely related and they are unrelated to the invasive form from the Old World

Phylogeography — Historical Biogeography of the Species

Genotyping of common reed from herbarium specimens prior to 1910 indicates the widespread presence of 11 native genotypes and 1 southern genotype also seen in South America and Asia

A few populations scattered from Connecticut to Maryland prior to 1910 also exhibited the invasive genotype
Genotyping of common reed from modern populations (both herbarium specimens after 1960 and extant populations) indicates the same distributions of genotypes. However, the invasive genotype has dramatically spread across North America since 1910.

The “invasive” nature of the introduced common reed is more dramatically seen in the time sequence of genotyping of pre-1900 to modern populations. The native North American genotypes are systematically replaced by the invasive form along the eastern seaboard of Connecticut, Rhode Island, and Massachusetts.

Example 2: History of the North Atlantic during the Pleistocene - differentiation in refugia (nunataks) or recent (Holocene) migration? (Brochmann et al. 2003)
Example 2: History of the North Atlantic during the Pleistocene - differentiation in refugia (nunataks) or recent (Holocene) migration? (Brochmann et al. 2003)

Nodding saxifrage, Saxifraga cernua

1. North Atlantic populations do not show endemic genotypes
2. Migration of several genotypes into (mixed) populations of North Atlantic regions

3. Lack of endemic genotypes is supported by the general lack of endemic species in the glaciated North Atlantic region. Genotype and species endemism, however, is high in “refugia” south of glaciated regions.

Levels of species endemism in the North Atlantic - black pie sections indicate proportion of endemism