# A genetic atlas of human admixture history

Companion website for "*A genetic atlas of human admixture history*"

Hellenthal et al, Science (2014)

## INSTRUCTIONS

This interactive map summarizes the results described in the paper "*A genetic atlas of human admixture history*", Hellenthal et al, Science (2014). This help page gives a brief summary of the content and structure of the page. (We also suggest reading the FAQ and the tutorial accessible under the 'Historical event' menu.) To begin, click on a labelled population on the map (or select one from the "Target" drop-down menu at top). You will see displayed details of past admixture events which we infer to have occurred in forming that population.

For simple admixture events (two source populations admixing at a single point in time) or in "mixing coefficients" view, coloured circles or pie charts on the map depict the inferred genetic make-up of the two (blue and orange) admixing sources involved in the event for the selected population. The real admixing sources will not usually have been sampled, but we infer details of their DNA make-up. To do this, the DNA of each of the two source populations is represented in terms of a mixture of segments of DNA shared with sampled "donor" populations displayed on the map, with the area of each circle (or slice of a pie) proportional to the mixing coefficients for that donor.

For complex admixture events (involving admixture between more than two sources, possibly at different times), in "contrasts" view squares depict the differences in inferred genetic make-up between the two sources, with the area of each square proportional to the amount by which the given "donor" population more greatly represents (shares DNA segments with) one source over the other. (These differences tend to be more stably estimated than the mixing coefficients that we present as circles in these more complex cases.).

The box on the right provides more details about the event depicted, including the estimated date of the admixture event, the total estimated proportion of admixture from the first (orange) source, and our conclusion ("no admixture", "one date", "one date, multiway", or "multiple dates"). In the box, "side 1" depicts donor populations involved in the mixture describing the orange source and "side 2" depicts donor populations involved in the mixture describing the blue source. Coancestry curves are shown for all pairs of donor populations whose tick-boxes are selected (unless "no curves" is indicated next to the donor population), with black lines the raw data and green lines the fit under the given date(s) and proportion(s) of admixture.

For some populations, we conducted multiple analyses and/or inferred multiple events in a single analysis. For such populations, our results for each analysis and each event are given, and you can toggle between these results using the drop-down menu under "Analysis". The analysis selected by default is the "full" analysis that uses all populations as potential donors.

In the "Historical event" drop-down menu, we also provide a tutorial on how to use the site, followed by a selection of historical interpretations of admixture signals we see - many of which are shared among several groups. Each event provides text describing our genetic inference and how it might relate to historically attested events, as well as allowing users to click individually on all groups related to the described signal. (These events are also presented in the Supplementary Information.).

Tratto da:    http://admixturemap.paintmychromosomes.com/