

Breakout room exercise Session S06 on Multidimensional scaling (10 minutes)

1. Load the R script **BreakoutS06.R** posted in the Slack channel of the course. This file contains an instruction to load a data file containing a population differentiation measure, Rst, for Y-chromosomal STR data, reported by Xu et al. (2015). We use these measures as distances, and analyse them by classical metric multidimensional scaling.
2. Load the data in the R environment.
3. Construct a neat symmetric distance matrix from the Rst measures. Keep the continental grouping of each population in a separate variable.
4. Make a map of the populations of using the first two dimensions of the MDS output.
5. Compute the goodness-of-fit of the map.
6. Take care to label or colour populations according to their continental grouping. Do populations from the same continental group cluster?
7. Save your MDS plot in PDF format and compare your results with those discussed in the online session after the breakout room closes.