**Exercise 7 – Outgroup f3-statistics**

1. Read the first part of SI 7 from Haak et al. (2015), p. 61-67. Write 1-2 sentences on what you learned.
2. Meet with your group and do some research to figure out what you are interested in doing for the mini-project. Explore whether datasets are available, and **be prepared to talk collectively with your instructor on Tuesday** about you would like to do.
3. Take your individual and run the outgroup f3 test. With whom are your individuals most closely related?
4. Try using different outgroups, such as another African population (Yoruba, Khomani), a present-day East Asian (Han, Dai), the Ust’-Ishim individual, the Altai Neanderthal and Denisovan, and the chimp. For whom do you get similar patterns? For whom does this not work?
5. In class, you will be assigned one of the sets with more than one individual. Determine whether the individuals within the set are most genetically similar to each other, justifying their being grouped into a clade. Use outgroup f3-statistics and the tools you learned from the lecture to come to a conclusion. Keep in mind that you will need to change the population ID names – please make these edits in the “**data.eigen.altered.ind**” file and use that to calculate the f3-statistic. Write a short paragraph explaining whether the decision to put the individuals in one group seems justified to you, using your outgroup f3 values.