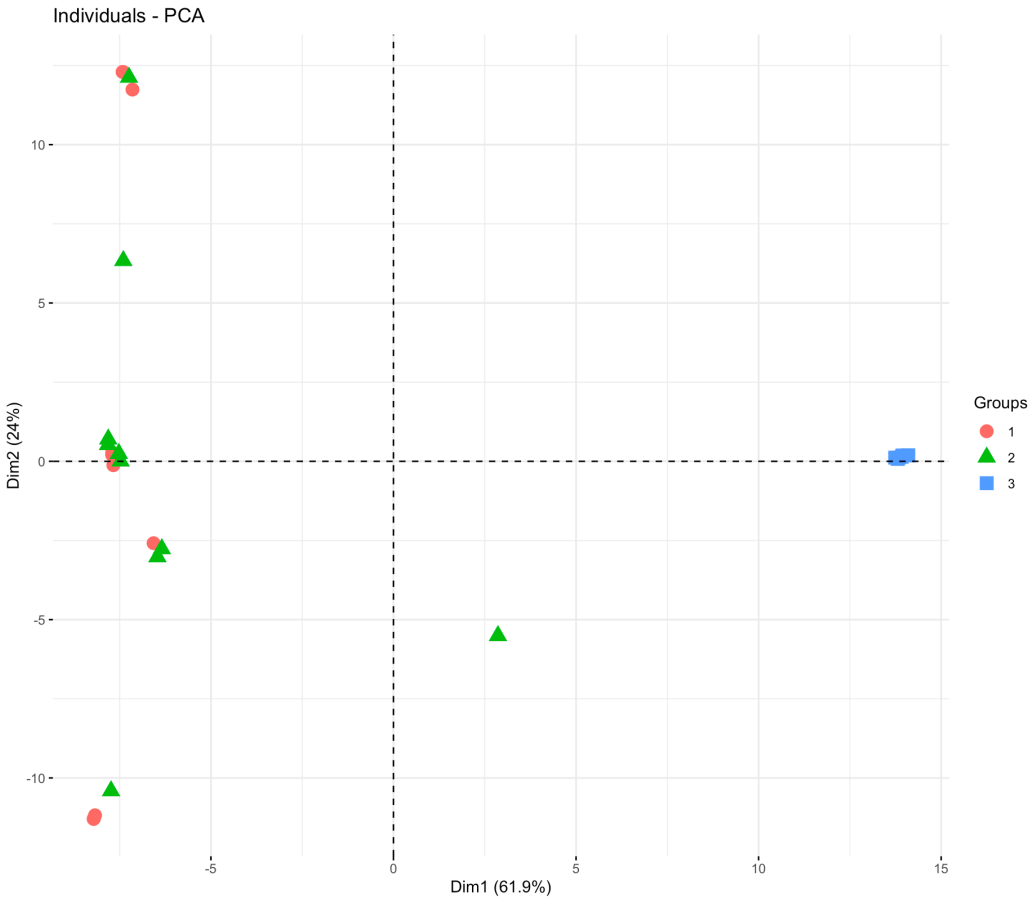
Heinrich: Migration with Structure and R

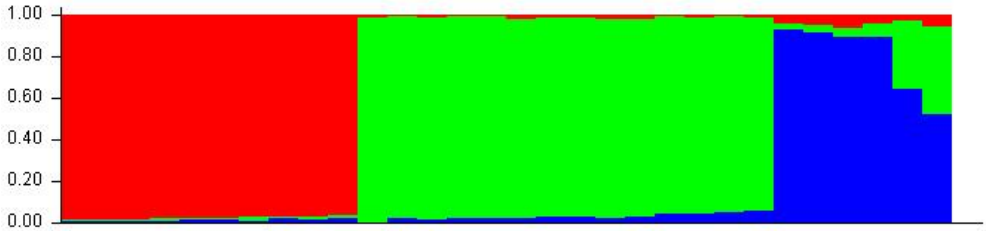
6.1 Three populations with migration

PCA plot:



Here, it is relatively easy to see the different groups that were simulated using slim. However, the two populations that had migration between them are often overlapping with significantly less differentiation as compared to the third group. This makes sense as the blue population was left alone during the simulation where as the other two had some exchange of their mutations which would make them more similar genetically.

Structure plot:

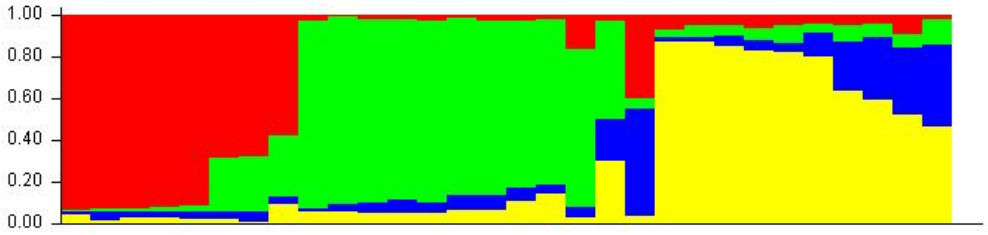


Similarly, the structure plot also very clearly shows the three separate populations so it should be fairly certain that this result is correct.

6.2 Write your own simulation

For my own SLiM script I added four populations that all merged off of the fist one. The migration happened from the first to the second, the second to the third, and so on.

Structure plot:



After checking k values two through seven I found that the correct k value of four did in fact also have the most negative Ln P(D) value. However, this structure plot was significantly more convoluted than the first one, presumably as I had more migration between the populations and all populations were effected not just two of them.

6.3 Some mysteries

Mystery file One

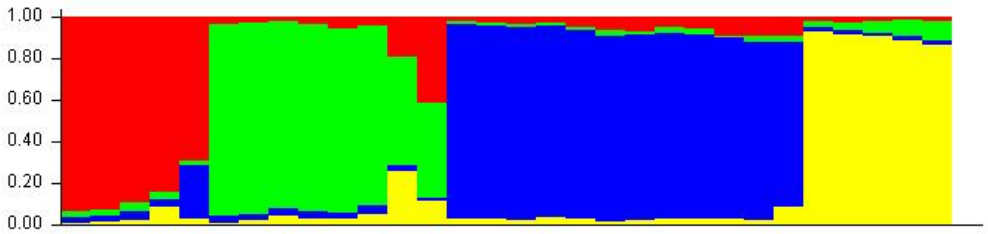
Structure plot:

For the first mystery file the best fit was a k value of 6. Looking at the graph, this one also showed the clearest differences between the population so it made sense in that regard as well.

It seems like there was one population that merged with all others in this simulation and that the remaining 5 were all fairly separated from each other with minimal migration. However, they do seem to be different sizes when looking at the plot since some regions such as the pink are significantly longer than others, like the light blue.

Mystery file Two

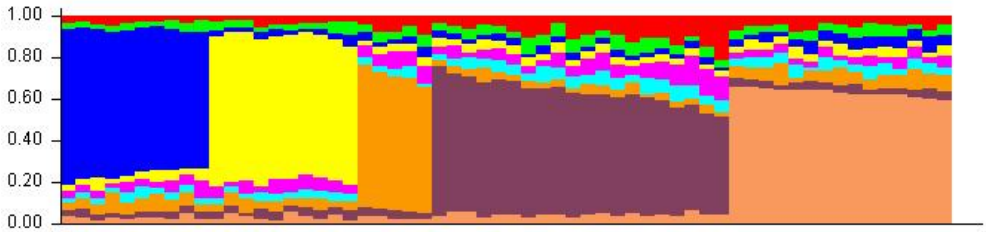
Structure plot:



For this data I got a population count of four using Structure. The populations are all fairly easy to tell apart so this would seem to make sense. The migration seems to be happening primarily form the red and the green populations into the others. (From left to right) All of the populations appear to have a similar size to each other, with perhaps the red or yellow being somewhat smaller.

Mystery file Three

Structure plot:



For the final data file Structures lowest value was for a k of 9. This was significantly higher than the other data sets so the slightly decreased clarity would make sense. However, it still seems like the separate populations can be visually told apart. The migration seems to be happening form the light brown to the rest of the population primarily, but also between all other populations to a lesser extent. It isn't very easy to determine the population sizes but if I would make a guess I would say that the yellow and blue are both slightly smaller.