Bioinformatics practice

1. Generate a work folder under your personal folder

2. Determine your phenotype for the next monogenic traits with one of your classmate:

Facial dimples (dominant) or not

Freckle (dominant) or not

Roman nose (dominant) or not

Unattached earlobe (dominant) or attached earlobe

Widow’s peak (dominant) or not

Wooly hair (dominant) or not

3. Generate an input file from the data of chosen father, mother and child with gedit text editor which is highly similar to this:



The name of the file is”fam.inp”. We assume that heterozygous genotype is linked to all dominant phenotypes.

4. Save the fam.inp file with ANSI character set.

5. Type the next command to use Phase software:

./PHASE –P fam.inp fam.out

6. Check the output files.

7.Check the pop.inp and pop.known file.

8. Run the following command:

./PHASE pop.inp pop.out

9. Check the output files.

10. Run the following command:

./PHASE –kpop.known pop.inp popknown.out

9. Compare the output file of the two previous running.