Metodologia

DATA

We start off with three main fields of information on the individuals we’re analyzing, which would be “genotypes”, “fam” and “map”. Inside “genotypes” we can find that we have 425 individuals (number of rows) and 582892 SNPs ( number of columns). Inside “fam” we can see the information related to an individual’s family. Finally, in “map”, we find information on each SNP.

Next, we have to merge the phenotypic information on the individuals with their respective genotypic information,

QUALITY CONTROL