

Advanced R Programming for Bioinformatics

Exercises for Session 10: Large data

1. The file `sisg.nc` is a netCDF file with a subset of SNP data from the HapMap project.
 - (a) Read in the first ten SNPs for each person
 - (b) For each person, compute the proportion of SNPs at which they are heterozygous (i.e. have `genotype==1`)
2. The file `SEAFlights.db` is a SQLite database with the same data as `SEAFlights.csv`. Read in the arrival and departure delays for all flights from SFO.
3. Create a SQLite database with the data from `sisg.nc` and compare the speed of reading and writing in the two formats.
4. Design an R class as a front-end to netCDF files as follows;
 - (a) the object will store the connection to the netCDF file
 - (b) a method for `['` stores which rows/columns are selected, but does not read or modify the file
 - (c) a method for `as.matrix()` (1 or 2 dimensional) returns the object converted to a matrix, i.e. reads in the data
 - (d) for enthusiastic people: the object optionally stores a function as a transformation for each variable, which is applied when the data are read in