

The SNP association analysis

Genome-wide association studies (GWAS) is a method of identifying susceptibility loci for complex diseases. It is based on the technique of scanning genomes of many subjects in order to identify the genetic variation possibly responsible for a disease through statistical tests. In this lab, we use a R package called SNPassoc to perform the SNP association analysis

Step

1. Start with the installation of the SNPassoc package typing the following commands:

```
> install.packages("SNPassoc") # A package for association studies
> library(SNPassoc)
```

2. Use the built-in data for this package, which can be loaded with the data function, as follows:

```
> data(SNPs)
```

3. The previous step loads two data objects in the workspace. Take a look at the data objects that were just loaded:

```
> head(SNPs)
> head(SNPs.info.pos)
```

Q1: What is the total number of SNPs? What are the column names of the first five columns?

4. Now, create an SNP object using the following setupSNP function with the SNP information in columns 6 to 40

```
> mySNP <- setupSNP(SNPs, 6:40, sep=" ")
```

5. With this data object, carry out an association test for the trait and variables of your interest with the following association function:

```
> myres <- association(casco~sex+snp10001+blood.pre, data = mySNP, model.interaction = c("dominant", "codominant"))
```

6. Take a look at the results by issuing the following command:

```
> myres
```

Q2: Is there any significant SNP? Run SNP associate analysis for fifth SNP and show your result.