GenABEL tutorial

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Chapter 1

Overview

`GenABEL-package` is an R library developed to facilitate Genome-Wide Association (GWA) analysis of binary and quantitative traits. `GenABEL-package` is implemented as an R library. R is a free, open source language and environment for general-purpose statistical analysis (available at `http://www.r-project.org/`). It implements powerful data management and analysis tools. Though it is not strictly necessary to learn everything about R to run `GenABEL-package`, it is highly recommended as this knowledge will improve flexibility and quality of your analysis.

Originally `GenABEL-package` was developed to facilitate GWA analysis of quantitative traits using data coming from extended families and/or collected form genetically isolated populations. At the same time `GenABEL-package` implements a large number of procedures used in analysis of population-based data; it supports analysis of binary and quantitative tarits, and of survival (time-till-event) data. Most up-to-date information about `GenABEL-package` can be found at the web-site `http://mga.bionet.nsc.ru/nlru/GenABEL/`.

`GenABEL-package` is a part of more extensive `ABEL` collection (`http://mga.bionet.nsc.ru/~yurii/ABEL/`) of software supporting different kinds of GWA analyses.

This tutorial was originally written to serve as a set of exercises for the "Advances in population-based studies of complex genetic disorders" (GE03) course of the Netherlands Institute of Health Sciences (Nihes).

If you read this tutorial not as a part of the GE03 course, and you are eager to start with you GWA analysis without reading all the not-so-strictly-necessary staff, start directly from the section 5 ("Genome-wide association analysis").

Otherwise, you can start with R basics and simple association analyises using few SNPs in section 2, "Introduction to R". In the next section, 4 ("Introduction to `GenABEL-package`") you will learn how to work with the `gwaa.data-class`, which is used to store GWA data in `GenABEL-package` and will perform some simple large-scale analyses.

In the next section, 5 ("Genome-wide association analysis"), you will do quality control of genetic data and do association analysis under realistic conditions. This section is the core of this tutorial.

The section 7 ("GWA in presence of genetic stratification: practice") is dedicated to analysis in presence of populational stratification and analysis of family-based data.

Genetic data imputations are covered in section **??**, ”**??**”.

The last section, 10 (”Analysis of selected region”), is dedicated to analysis of haplotype association and analysis of SNP interactions.

Information on importing the data from different formats to `GenABEL-package` is given in appendix A (”Importing data to `GenABEL-package`”). Answers to exercises are provided at the end of respective chapters.

Experienced R users start directly with the section (4, ”Introduction to `GenABEL-package`”).

Chapter 2

Introduction to R

In this section we will consider base R data types and operations, and tools for analysis of qualitative and quantitative traits. Only basic R functionality – the things which are crucial to know before we can proceed to genetic association analysis – will be covered within this section. If you want to make most of your data, though, we strongly recommend that you improve your knowledge of R using books other than this. A number of excellent manuals ('An introduction to R', 'Simple R', 'Practical Regression and Anova using R', and others) is available free of charge from the R project web-site (http://www.r-project.org).

In the first part of this chapter you will learn about the most important R data types and will learn how to work with R data. Next, we will cover exploratory data analysis. The chapter will end with introduction to regression analysis.

2.1 Basic R data types and operations

On the contrast to many other statistical analysis package, analysis in R is not based on graphic user interface, but is command line-based. When you first start R, a command prompt appears. To get help and overview of R, type `help.start()` on the command line and press `enter`. This will start internet browser and open the main page of the R documentation.

Let us first use R as a powerful calculator. You can directly operate with numbers in R. Try multiplying two by three:

```
> 2*3
```

```
[1] 6
```

Other standard arithmetic operations can be performed in similar manner:

```
> 2/3
```

```
[1] 0.6666667
```

(division)

```
> 2^3
```

```
[1] 8
```

(power)

```
> 2-3
```

```
[1] -1
```

(subtraction)

```
> 2+3
```

```
[1] 5
```

(summation)[1].

Mathematical functions, such as square roots, base-10 logarithm, and exponentiation, are available in R as well:

```
> sqrt(5)
```

```
[1] 2.236068
```

```
> log10(2.24)
```

```
[1] 0.350248
```

```
> exp(0.35)
```

```
[1] 1.419068
```

Here, we have computed e to the power of base-10 logarithm of the square root of the sum of two and three. After each operation performed, we have rounded the result to the two digits after the floating point – just in order to do less typing.

The arithmetic operations and functions can be nested and therefore we can obtain the above result in one line, and without the 2nd-digit approximation:

```
> exp(log10(sqrt(2+3)))
```

```
[1] 1.418337
```

R functions include not only the standard mathematical ones, but also a wide range of statistical function, for example, probability density functions of many probability distributions. We will make extensive use of these at a later stage, when computing significance and estimating statistical power.

For any function with name say 'fun', help may be obtained by typing 'help(fun)' (or ?fun) on the command line.

R help pages have standard layout, documenting usage of the function, explaining function arguments, providing details of implementation and/or usage, explaining the value returned by the function, and giving references and examples of the function use.

---

[1]For complete list of arithmetic operations try `help("+")`

Most of the documented functions have examples of their usage at the end of the 'help' page, and these examples can be evaluated in R. E.g. try 'example(log10)'.

Exercise 1.   Explore help for Wilcoxon test

Explore the help page for the Wilcoxon test (function: `wilcox.test`) and answer the questions:

1. When exact Wilcoxon test is computed by default?
2. If the default conditions for the exact test are not satisfied, what approximation is used?

If you do not know the exact name for the function you look for, try 'help.search("query")', where `query` is the keyword.

Exercise 2.   Finding functions and help pages

Try to find out what are the functions to do

1. Fisher exact test
2. T-test

One of important R operations is *assignment*, which is done with '<-' operator. A (new) variable name should be provided on the left-hand side of this operator and on the right-hand side, there must be either name of already existing variable or an expression. For example, we if want to assign value '2' to variable 'a', and value '3' to the variable 'b' we would use the assignment operator:

```
> a <- 2
> b <- 3
```

Typing the variable name in R command line will return its' value, e.g.

```
> b

[1] 3
```

Evaluation of the expression

```
> exp(log10(sqrt(a+b)))

[1] 1.418337
```

gives the expected result we have obtained above using numerical arguments.

While the variables 'a' and 'b' contain single numeric values, variables in general can be multi-dimensional; an one-dimensional example of such is a vector (array). Let us create an example vector and experiment with it:

```
> v <- c(1,3,5,7,11)
```

Here, 'c()' is a function, which **c**ombines its arguments to make a vector. This vector is then assigned to a variable named 'v'.

Now, let us try different operations with this vector:

```
> v + 1
```

```
[1]  2  4  6  8 12
```

It is easy to see that the result is a vector, which is obtained by adding one to each element of the original vector v. Other arithmetic operations and mathematical functions behave in the same way, e.g. the operation is performed for each element of the vector, and the results are returned:

```
> 1/v
```

```
[1] 1.00000000 0.33333333 0.20000000 0.14285714 0.09090909
```

```
> log(v)
```

```
[1] 0.000000 1.098612 1.609438 1.945910 2.397895
```

What happens if two vectors are supplied as function arguments? Let us define a new vector

```
> ov <- c(1,2,3,4,5)
```

and add it to the vector v:

```
> v + ov
```

```
[1]  2  5  8 11 16
```

You can see that the summation was done element-wise, i.e. the first element of the result vector is obtained as the sum of the first elements of v and ov, the second is the sum of the second elements, and so forth.

Other arithmetic operations with two vectors are performed in the same element-wise manner:

```
> v * ov
```

```
[1]  1  6 15 28 55
```

(multiplication)

```
> v^ov
```

```
[1]      1      9    125   2401 161051
```

(power).

The vector operations considered above returned a same-length vector as output. There are others – statistical and summary – functions which evaluate a vector as a whole and return a single value as output. For example, to obtain a sum of vector's elements, use

```
> sum(v)
```

```
[1] 27
```

Other examples of such functions involve length, returning number of elements of a vector, mean, returning the mean, var, returning the variance, etc.:

```
> length(v)

[1] 5

> mean(v)

[1] 5.4

> var(v)

[1] 14.8
```

One of the basic, and probably most used, data operations in R is *sub-setting*. This refers to an operations which help you deriving a subset of the data. Let us create a short vector and play a bit with sub-setting. This vector will contain 5 simple character strings:

```
> a <- c("I am element 1","I am element 2","I am element 3","I am element 4","I am element 5")
> a

[1] "I am element 1" "I am element 2" "I am element 3" "I am element 4"
[5] "I am element 5"
```

To find out what is the value of the *i*-th element of this vector, you can sub-set it by `a[i]`. For example the 3rd elements is:

```
> a[3]

[1] "I am element 3"
```

You can also select a bigger sub-set, e.g. all elements from 2 to 4:

```
> a[c(2:4)]

[1] "I am element 2" "I am element 3" "I am element 4"
```

Here, operation `c(2:4)` stays for 'combine numbers from 2 to 4 into a vector'. An equivalent result is obtained by

```
> a[c(2,3,4)]

[1] "I am element 2" "I am element 3" "I am element 4"
```

We can also easily get disjoint elements; e.g. if you want to retrieve elements 1, 3, and 5, you can do that with

```
> dje <- c(1,3,5)
> dje

[1] 1 3 5

> a[dje]

[1] "I am element 1" "I am element 3" "I am element 5"
```

One of very attractive features of R data objects is possibility to derive a sub-set based on some condition. Let us consider two vectors, `tmphgt`, containing the height of some subjects, and `tmpids`, containing their identification codes (IDs):

```
> tmphgt <- c(150,175,182,173,192,168)
> tmphgt

[1] 150 175 182 173 192 168

> tmpids <- c("fem1","fem2","man1","fem3","man2","man3")
> tmpids

[1] "fem1" "fem2" "man1" "fem3" "man2" "man3"
```

Imagine you need to derive the IDs of the people with height over 170 cm. To do that, we need to combine several operations. First, we shoudl run the logical function `>170` on the height data:

```
> vec <- (tmphgt>170)
> vec

[1] FALSE  TRUE  TRUE  TRUE  TRUE FALSE
```

This returns a logical vector whose elements are 'TRUE', when a particular element of the `tmphgt` satisfies the condition `>170`. The returned logical vector, in turn, can be applied to sub-set any other vector of the same length[2], including itself. Thus if you need to see what are the heights in people, which are taller than 170 cm, you can use

```
> tmphgt[vec]

[1] 175 182 173 192
```

As you can see, only the elements of `tmphgt`, for which the corresponding value of `vec` was 'TRUE', are returned. In the same manner, the logical vector `vec` can be applied to select elements of the vector of IDs:

```
> tmpids[vec]

[1] "fem2" "man1" "fem3" "man2"
```

You can combine more than one logical condition to derive sub-sets. For example, to see what are the IDs of people taller than 170 but shorter than 190 cm, you can use

```
> vec <- (tmphgt>170 & tmphgt<190)
> vec

[1] FALSE  TRUE  TRUE  TRUE FALSE FALSE
```

---

[2] Actually, you can apply it to a longer vector too, and then the logical vector will be "expanded" to total length by repeating the original vector head-to-tail. However, we will not use this in our exercises.

```
> tmpids[vec]
```

```
[1] "fem2" "man1" "fem3"
```

A better[3] way to do logical sub-setting assumes use of the `which()` function on the top of the logical vector. This function reports which elements are TRUE. To obtain above results you can run:

```
> vec <- which(tmphgt>170 & tmphgt<190)
> vec
```

```
[1] 2 3 4
```

```
> tmpids[vec]
```

```
[1] "fem2" "man1" "fem3"
```

You can see that no `vec` contains a vector, whose elements are the indexes of the elements of `tmphgt` for which the logical condition satisfies.

Sub-setting for 2D objects (matrices) is done in similar manner. Let us construct a simple matrix and do several sub-setting operations on it:

```
> a <- matrix(c(        11,12,13,
+                   21,22,23,
+                   31,32,33
+                         ),nrow=3,ncol=3)
> a
```

```
     [,1] [,2] [,3]
[1,]   11   21   31
[2,]   12   22   32
[3,]   13   23   33
```

To obtain the element in the 2nd row and 2nd column, you can use

```
> a[2,2]
```

```
[1] 22
```

To access the elemnt from the second row and third column, use

```
> a[2,3]
```

```
[1] 32
```

Note that here, the row index (2) comes first, and the column index (3) comes second.

To obtain the 2x2 set of elements contained in upper left corner, you can do

```
> a[1:2,1:2]
```

```
     [,1] [,2]
[1,]   11   21
[2,]   12   22
```

---

[3] Because it treats NAs for you

	1	2	3
1	1	4	7
2	2	5	8
3	3	6	9

Table 2.1: Vector representation of a matrix. Elements in the table are the vector indices of the matrix elements.

Or you can even get the variables, which reside in corners:

```
> a[c(1,3),c(1,3)]

     [,1] [,2]
[1,]   11   31
[2,]   13   33
```

If one of the dimensions is not specified, complete vector is returned for this dimension. For example, here we retrieve the first row

```
> a[1,]

[1] 11 21 31
```

...and the third column

```
> a[,3]

[1] 31 32 33
```

...or columns 1 and 3:

```
> a[,c(1,3)]

     [,1] [,2]
[1,]   11   31
[2,]   12   32
[3,]   13   33
```

Other way to address elements of a matrix is to use one-dimensional index. For example, if you want to access element in the 2nd row and 2nd column, instead of

```
> a[2,2]

[1] 22
```

you can use

```
> a[5]

[1] 22
```

This way of accessing the elements of a matrix is based on the fact, that each matrix can be preseted as a vector, whose elements are numbered consequtively: the element in the upper-left corner has index 1, the element in the second row of the first column has index 2, and the last elemnt in the borrom-right corner has the maximal value, as shown in Table 2.1.

As well as with vectors, you can sub-set matrices using logical conditions or indexes. For example, if we want to see what elements of a are greater than 21, we can run

```
> a>21
```

```
      [,1]   [,2] [,3]
[1,] FALSE FALSE TRUE
[2,] FALSE  TRUE TRUE
[3,] FALSE  TRUE TRUE
```

or, better

```
> which(a>21)
```

```
[1] 5 6 7 8 9
```

Note that in the latter case, a vector whose elements give the 1-D indexes of the matrix, is returned. This vector indicates the elemnts of matrix a, for which the condition (a>21) is satisfied.

You can obtain the values of the matrix's elements, for which the condition isfulfilled, either by

```
> a[a>21]
```

```
[1] 22 23 31 32 33
```

or

```
> a[which(a>21)]
```

```
[1] 22 23 31 32 33
```

Once again, the latter method should be prefered. Consider an example, where some elements of the matrix are missing (NA) – a situation which is common in real data analysis. Let us replace the elemnt number 5 with NA and perform sub-setting operations on the resulting matrix:

```
> a
```

```
     [,1] [,2] [,3]
[1,]   11   21   31
[2,]   12   22   32
[3,]   13   23   33
```

```
> a[5] <- NA
> a
```

```
      [,1] [,2] [,3]
[1,]    11   21   31
[2,]    12   NA   32
[3,]    13   23   33

> a[a>21]

[1] NA 23 31 32 33

> a[which(a>21)]

[1] 23 31 32 33
```

You can see that when `a[a>21]` was used, not only the elements which are greater than 21 were returned, but also `NA` was. As a rule, this is not what you want, and `which` should be used unless you do want to make some use of the `NA` elements.

In this section, we have generated a number of R data objects. Some of these were numeric (e.g. vector of heights, `tmphgt`) and some were character, or string (e.g. vector of study IDs, `tmpids`). Some times you need to figure out what is the class of a certain object. This can be done using the `class()` function. For example,

```
> tmphgt

[1] 150 175 182 173 192 168

> class(tmphgt)

[1] "numeric"

> tmpids

[1] "fem1" "fem2" "man1" "fem3" "man2" "man3"

> class(tmpids)

[1] "character"
```

What happens if we try to find out the class of

```
> a

      [,1] [,2] [,3]
[1,]    11   21   31
[2,]    12   NA   32
[3,]    13   23   33
```

– an object, which contains a matrix?

```
> class(a)

[1] "matrix"
```

Results are expected – we find out that `a` is a matrix, which is correct. At the same time, a matrix is an upper-level class, which contains a number of elemnts, belonging to some lower-level (e.g. character/numeric) class. To see what is the class of the matrix's elements, try

```
> a[1,]
```

```
[1] 11 21 31
```

```
> class(a[1,])
```

```
[1] "numeric"
```

which says that elemnts (at least of the first row) are numeric. Because all elements of a matrix should have the same class, we can conclude that `a` is a matrix containing numeric values.

At this point, it is worthwile inspecting what data objects were created during our work. This can be done with the `ls()` command:

```
> ls()
```

```
[1] "a"      "b"      "dje"   "ov"     "tmphgt" "tmpids" "v"      "vec"
```

Obviously, this "list" command is very useful – you will soon find that it is just too easy to forget the name of a variable which it took long time to create. Some times you may wish to remove some of the data objects because you do not need then anymore. You can remove an object using the `rm()` command, where the names of objects to be deleted are listed as arguments. For example, to remove `tmphgt` and `tmpids` variable you can use

```
> rm(tmphgt,tmpids)
```

If you now look up what data obejcts are still left in you workspace with the `ls()` command

```
> ls()
```

```
[1] "a"   "b"   "dje" "ov"  "v"   "vec"
```

you find that you have successfully deleted `tmphgt` and `tmpids`.

At this point, you can exit R by typing `q()` on the command line and pressing `Enter`.

Summary:

- You can get access to the top-level R documentation by `help.start()` command. To search help for some keyword `keywrd`, you can use `help.search(keywrd)` command. To get description of some function `fun`, use `help(fun)`.

- You can use R as a powerful calculator

- It is possible to get sub-sets of vectors and matrices by specifying index value or a logical condition (of the same length as the vector / matrix) between square brackets (`[`, `]`)

- When you obtain an element of a matrix with `[i,j]`, i is the row and j is the column of the matrix.

- Function `which(A)` returns index of the elements of A which are `TRUE`

- You can see objects available in your workspace by using the `ls()` command

- Unnecessary object (say, `tmphgt`) can be deleted from the workspace using `rm` command, e.g. `rm(tmphgt)`

- You can leave R using the `q()` command

Exercise 3.   Exploring srdta

In this exercise, you will explore few vectors representing different data on study subjects described in `srdta` example data set supplied together with `GenABEL-package`. First, you need to load `GenABEL-package` by typing

```
> library(GenABEL)
```

and load the data by

```
> data(srdta)
```

The vector containing study subjects sex can be accessed through `male(srdta)`; this vector's value is one when the corresponding person is male and zero otherwise. The vector containing SNP names can be accessed via `snpnames(srdta)`, chromosome ID – through `chromosome(srdta)` and map – through `map(srdta)`. Explore these vectors and answer the questions.

1. What is the ID and sex of the first person in the data set?
2. Of the 22nd person?
3. How many males are observed among first hundred subjects?
4. How many FEMALES are among 4th hundred?
5. What is the male proportion in first 1000 people?
6. What is the FEMALE proportion in second 1000 (1001:2000) people?
7. What is name, chromosome and map position of 33rd maker?
8. What is distance between markers 25 and 26?

2.2   Data frames

A *data frame* is a class of R data, which, basically, is a data table. In such tables, it is usually assumed that rows correspond to subjects (observations) and

columns correspond to variables (characteristics) measured on these subjects. A nice feature of data frames is that columns (variables) have names, and the data can be addressed by referencing to these names[4].

We will explore R data frames using example data set `assoc`. Start R with double-click on the file named `assocbase.RData`. You can see the names of the loaded objects by using the "list" command:

```
> ls()
```

```
[1] "assoc"
```

Thus, only one object is loaded. The class of this object is:

```
> class(assoc)
```

```
[1] "data.frame"
```

– a data frame.

The dimensionality of a data frame (or a matrix) can be determined by using the `dim()` command:

```
> dim(assoc)
```

```
[1] 250    7
```

Here, the first number corresponds to the number of rows (subjects) and the second to the number of columns (variables). Thus, the data frame `assoc` contains the data on 250 subjects, who are characterised by 7 variables each.

Let us now figure out what are the names of the 7 variables present in the data frame. To see what are the variable names, use the command `names()`:

```
> names(assoc)
```

```
[1] "subj" "sex"  "aff"  "qt"    "snp4" "snp5" "snp6"
```

These variables correspond to the personal identifier (ID, variable `subj`), sex, affection status, quantitative trait `qt` and several SNPs. Each variable can have its own type (numeric, character, logic), but all variables must have the same length – thus forming a matrix-like data structure.

A variable from a data frame (say, `fram`), which has some name (say, `nam`) can be accessed through `fram$nam`. This will return a conventional vector, containing the values of the variable. For example to see the affection status (`aff`) in the data frame `assoc`, use

```
> assoc$aff
```

```
 [1]  0  1  1  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  1  0  0  1  0
[26]  0  1  0  0  1  1  0  0  0  0  0  0  0  0  1  0  0  1 NA  0  0  0  0  0  0
[51]  1  1  0  1  0  0  0  0  0  1  0  1  0  0  0  0  0  0  0  1  0  0  0  0  0
[76]  0  0  1  1  1  0  0  0  0  0  0  0  0  1  1  0  0  0  0  1 NA  0  0  0  0
```

---

[4]This may also be true for matrices; more fundamental difference is though that a matrix *always* contains variables of the same data type, e.g. character or numeric, while a data frame may contain variables of different types

```
[101]  1 0 0 1 1 0 1 0 0 0 0 0 0 1 1 0 0 0 0 0 0 0 1 0
[126]  1 0 0 0 1 0 0 0 1 0 1 NA 1 0 0 0 0 0 0 0 0 0 1 0 0
[151]  0 0 0 0 0 0 0 1 1 1 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
[176]  0 0 1 1 NA 0 0 0 0 1 1 1 1 0 NA 1 0 0 0 0 0 0 1 1 0
[201]  0 0 0 0 0 0 0 0 0 0 1 0 0 0 1 0 0 0 0 1 0 0 0 0 0
[226]  0 0 0 1 1 0 0 0 0 0 1 0 0 0 0 1 0 0 0 1 0 0 0 0 0
```

The `aff` (affected) variable here codes for a case/control status, conventinally, the cases are coded as "1" and controls as "0". You can also see several "NA"s, which stays for missing observation.

Exercise 4.   Exploring `assoc`

1. Investigate types of the variables presented in data frame `assoc`. For each variable, write down the class.

Data frame may be thought of as a matrix which is a collection of (potentily different-type) vectors. All sub-setting operations discussed before for matrices are applicable to a data frame, while all operations dicussed for vectors are applicable to data frame's variables.

Thus, as any particular variable present in a data frame is a conventional vector, its elements can be accessed using the vector's indices. For example, if you would like to know what are the ID, sex and affection status for the person with index 75, you can request

```
> assoc$subj[75]
```

```
[1] 1409
```

```
> assoc$sex[75]
```

```
[1] 1
```

```
> assoc$aff[75]
```

```
[1] 0
```

Alternatively, using the matrix-style of sub-setting, you can see all the data for person 75:

```
> assoc[75,]
```

```
   subj sex aff        qt snp4 snp5 snp6
75 1409   1   0 1.014664  A/B  B/A  B/B
```

In the same manner as with matrices, you can get data for e.g. subjects 5 to 15 by

```
> assoc[5:15,]
```

```
   subj sex aff        qt snp4 snp5 snp6
5  1533   0   0  0.1009220  A/B  B/A  B/A
6  2466   1   0 -0.1724321  A/B  A/A  A/A
7  2425   0   0 -0.3378473  B/B  A/A  A/A
8  1068   0   0 -1.7112925  A/A  B/B  <NA>
9   198   1   0 -0.4815822  A/B  B/A  B/A
10 1496   1   0  1.2281232  A/A  B/B  B/B
11  909   0   0  0.5993945  A/B  B/A  B/A
12 1213   0   0  1.9792190  A/A  B/B  B/B
13  181   1   0  1.5435921  A/A  B/B  B/B
14 1783   0   0 -1.6242738  A/B  B/A  B/A
15 1914   0   0 -0.5160331  A/A  B/B  B/B
```

The result is actually a new data frame containing data only on people with index from 5 to 15:

```
> x<-assoc[5:15,]
> class(x)

[1] "data.frame"

> dim(x)

[1] 11  7
```

As well as with matrices and vectors, it is possible to sub-set elements of a data frame based on (a combination of) logical conditions. For example, if you are interested in people who have the qt values over 1.4, you can find out what are the indices of these people

```
> vec <- which(assoc$qt>1.4)
> vec

 [1]  12  13  33  41  54  68  72  76  89 106 118 142 156 161 175 181 193 219 241
```

and then show the compelte data with

```
> assoc$subj[vec]

 [1] 1213  181 1737 1319  516 1355  186 1426 1284  822 2129  212 1443  704 1648
[16] 1628  562  858  698
```

At the same time, if you only want to check what are the IDs of these people, try

```
> assoc$subj[vec]

 [1] 1213  181 1737 1319  516 1355  186 1426 1284  822 2129  212 1443  704 1648
[16] 1628  562  858  698
```

Or, if we are interested to find what are the IDs and what are the SNP genotypes of these people, we can try

```
> assoc[vec,c(1,5,6,7)]
```

```
    subj snp4 snp5 snp6
12   1213  A/A  B/B  B/B
13    181  A/A  B/B  B/B
33   1737  A/A  B/B  B/B
41   1319  A/A  B/A  B/A
54    516  A/B  B/A  B/A
68   1355  A/A  B/B  B/B
72    186  A/A  B/A  B/A
76   1426  A/B  B/A  B/A
89   1284  A/A  B/B  B/B
106   822  A/B  B/A  B/A
118  2129  A/B  B/A  B/A
142   212  A/B  B/A  B/A
156  1443  A/A  B/B  B/B
161   704  A/B  B/A  B/A
175  1648  A/B  B/A  B/A
181  1628  A/B  B/A  B/A
193   562  A/A  B/B  B/B
219   858  A/B  B/A  B/A
241   698  B/B  A/A  A/A
```

here, we select people identified by `vec` in the first dimension (subjects), and by `c(1,5,6,7)` we select first, fifth, sixth and seventh column (variable).

The same result can be obtained using variables' names insted of the variables' indices. To remind you the variables' names:

```
> names(assoc)

[1] "subj" "sex"  "aff"  "qt"   "snp4" "snp5" "snp6"
```

And now make a vector of the variables' names of interest and filter the data based on it:

```
> namstoshow <- c("subj","snp4","snp5","snp6")
> assoc[vec,namstoshow]

    subj snp4 snp5 snp6
12   1213  A/A  B/B  B/B
13    181  A/A  B/B  B/B
33   1737  A/A  B/B  B/B
41   1319  A/A  B/A  B/A
54    516  A/B  B/A  B/A
68   1355  A/A  B/B  B/B
72    186  A/A  B/A  B/A
76   1426  A/B  B/A  B/A
89   1284  A/A  B/B  B/B
106   822  A/B  B/A  B/A
118  2129  A/B  B/A  B/A
142   212  A/B  B/A  B/A
156  1443  A/A  B/B  B/B
161   704  A/B  B/A  B/A
```

```
175 1648  A/B  B/A  B/A
181 1628  A/B  B/A  B/A
193  562  A/A  B/B  B/B
219  858  A/B  B/A  B/A
241  698  B/B  A/A  A/A
```

A more convenient way to access data presented in a data frame is through "attaching" it to the R search path by

```
> attach(assoc)
```

After that, the variables can be accessed directly, e.g.

```
> subj[75]
```

```
[1] 1409
```

instead of `assoc$subj[75]`.

While it is possible to explore the data presented in a data frame using the sub-setting operations and screen output, and modify certain data elements using the assignment ("<-") operation, you can also explore and modify the data contained in a data frame[5] by using `fix()` command (e.g. try `fix(assoc)`). However, normally this is not necessary.

With attached data frames, a possible complication is that later on you may have several data frames which contain the variables with the same names. The variable which will be used when you directly use the name would be the one from the data frame attached last. You can use `detach()` function to remove a certain data frame from the search path, e.g. after

```
> detach(assoc)
```

we can not use direct reference to the name (try `subj[75]`) anymore, but have to use the full path instead:

```
> assoc$subj[75]
```

```
[1] 1409
```

> **Summary:**
>
> - The list of available objects can be viewed with `ls()`; a class of some object `obj` can be interrogated with `class(obj)`.
>
> - Simple summary statistics for numeric variables can be generated by using `summary` function
>
> - Histogram for some variable `var` can be generated by `hist(var)`
>
> - A variable with name `name` from a data frame `frame`, can be accessed through `frame$name`.

---

[5]and also a matrix

- You can attach the data frame to the search path by `attach(frame)`. Then the variables contained in this data frame may be accessed directly. To detach the data frame (because, e.g., you are now interested in other data frame), use `detach(frame)`.

Exercise 5.   Explore phenotypic part of `srdta`

Load the `srdta` data object supplied with GenABEL by loading the package with `library(GenABEL)` and then loading the data with `data(srdta)`. The `srdta` object contains a data frame with phenotypes. This data frame may be accessed through `phdata(srdta)`. Explore this data frame and answer the questions

1. What is the value of the 4th variable for the subject number 75?
2. What is the value of variable 1 for person 75? Check what is the value of this variable for the first ten people. Can you guess what first variable is?
3. What is the sum of variable 2? Can you guess what data variable 2 contains?

2.3   Exploratory analysis of qualitative and quantitative traits

Let us now attach the data frame `asscoc`

```
> attach(assoc)
```

and explore it.

Let us first check how many of the subjects are males. In the `sex` variable, males are coded with "1" and females with "0". Therefore to see the numer of males, you can use

```
> sum(sex==1)

[1] 129
```

and to determine what is male sex proportion you can use

```
> sum(sex==1)/length(sex)

[1] 0.516
```

This way to compute the proportion would only work correctly if there are no missing observations (`lenght()` returns the total length of a variable, including `NA`s).

Because of the way the males are coded, the same answer is reached by

```
> mean(sex)
```

```
[1] 0.516
```

However, that would not have worked if the sex was coded differently, e.g. with "1" for males and "2" for females.

Let us now try to find out the mean of the quantitative trait `qt`. By definition, the mean of a variable, say x (with i-th element denoted as x_i) is

$$\bar{x} = \frac{\Sigma_{i=1}^{N} x_i}{N}$$

where N is the number of measurements.

If we try to find out the mean of `qt` by direct use of this formula, we first need to find out the sum of the `qt`'s elements. The `sum()` function of R precisely does the operation we need. However, if we try it

```
> sum(qt)
```

```
[1] NA
```

this returns "NA". The problem is that the `qt` variable contains "NA"s (try `qt` to see these) and by default the "NA" is returned. We can, however, instruct the `sum()` function to remove "NA"s from consideration:

```
> sum(qt,na.rm=T)
```

```
[1] -26.4733
```

where `na.rm=T` tells R that missing variables should be be removed (NonAvailable.ReMove=True)[6].

We can now try to compute the mean with

```
> sum(qt,na.rm=T)/length(qt)
```

```
[1] -0.1058932
```

This result, however, is not correct. The `length()` function returns the total length of a vector, which includes "NA"s as well. Thus we need to compute the number of the `qt`'s elements, which are not missing.

For this, we can use R function `is.na()`. This function returns `TRUE` if supplied argument is missing (`NA`) and `FALSE` otherwise. Let us apply this function to the vector `assoc$qt`:

```
> is.na(qt)
```

```
  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 [13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE
 [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 [37]  TRUE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE
 [49] FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 [61] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 [73] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

---

[6]The same argument works for a number of R statistical functions such as `mean`, `median`, `var`, etc

```
 [85] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
 [97] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[109] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[121] FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE
[133] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[145] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[157] FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE
[169] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[181] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[193] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE
[205] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[217] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[229] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[241] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

Indeed, the 7 missing elements are correctly identified. However, we are interested in elements which are **not** missing. To get these, we can use the logical function NOT (!), which changes all `FALSE` to `TRUE` and visa versa:

```
> !is.na(qt)
```

```
  [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [13]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE
 [25]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [37] FALSE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
 [49]  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [61]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [73]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [85]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
 [97]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[109]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[121]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE
[133]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[145]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[157]  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[169]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[181]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[193]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE  TRUE  TRUE
[205]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[217]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[229]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
[241]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Thus the number of elements which are not missing[7] is

```
> sum(!is.na(qt))
```

```
[1] 243
```

Finally, we can compute the mean of the `qt` with

---

[7]A hidden trick here is that arithmetic operations treat `TRUE` as one and `FALSE` as zero

```
> sum(qt,na.rm=T)/sum(!is.na(qt))
```

```
[1] -0.1089436
```

While this way of computing the mean is enlightening in the sense of how to treat the missing values, the same correct result should be normally achieved by supplying the `na.rm=T` argument to the `mean()` function:

```
> mean(qt,na.rm=T)
```

```
[1] -0.1089436
```

The function `table(x)` produces a frequency table for the variable `x`. Thus, we can use

```
> table(sex)
```

```
sex
  0   1
121 129
```

which, again, tells us that there are 129 males and 121 females in this data set. This function excludes missing observations form consideration.

Tables of other qualitative variables, such as affection and SNPs, can be generated in the same manner.

As with arithmetic operations and mathematical functions, most of the R operations can be combined within a single line. Let us try to combine logical conditions and the `table()` command to check the distribution of number of affected in men and women separately:

```
> table(aff[which(sex==1)])
```

```
 0  1
95 31
```

```
> table(aff[which(sex==0)])
```

```
 0  1
95 24
```

On R command line pressing the "up-arrow" button makes the last typed command re-appear (pressing it one more time will bring you to the one before the last, so on). This is very handy when you have to repeat the same analysis of different variables

---

Exercise 6.   Explore `assoc`

Explore phenotypic variables presented in `assoc`

  1. How many affected and unaffected are present in the data set?

2. What is the proportion of affected?

3. What is the distribution of snp4 (how many different genotype classes are present and what are the counts)?

Contingency tables for pairs of variables (cross-tables) can be generated in R using the `table` command we have used in previous section to explore frequency distributions. For example, if you want cross-tabulate sex and affection status in the data frame `assoc`, you can use

```
> table(sex,aff)

   aff
sex  0  1
  0 95 24
  1 95 31
```

Here, the first variable (sex) is presented in rows and the second (affection status) in columns.

As is usually the case with R, the output may be saved as a new object (of class 'table', which is a variety of a matrix):

```
> a<-table(sex,aff)
> class(a)

[1] "table"

> a

   aff
sex  0  1
  0 95 24
  1 95 31
```

and this object may be analysed further.

For example, we can easily get the number of affected male with

```
> a[2,2]

[1] 31
```

Alternatively, we can analyse the resulting contingency table `a` with more complex functions. If we want to see proportions in this table, we can use

```
> prop.table(a)

   aff
sex          0          1
  0 0.38775510 0.09795918
  1 0.38775510 0.12653061
```

Needless to say, this is equivalent to

```
> prop.table(table(assoc$sex,assoc$aff))
```

```
            0          1
  0 0.38775510 0.09795918
  1 0.38775510 0.12653061
```

In the above table, we see what proportion of people belong to four different classes (affected male, affected female, unaffected male and unaffected female). We may be though interested in the proportion of males in affected and unaffected. This may be achieved by

```
> prop.table(a,2)

   aff
sex         0          1
  0 0.5000000 0.4363636
  1 0.5000000 0.5636364
```

saying us that 56.4% of affected are male.

Alternatively, we may be interested in proportion of affected among males/females. To answer this question, run

```
> prop.table(a,1)

   aff
sex         0          1
  0 0.7983193 0.2016807
  1 0.7539683 0.2460317
```

saying us that 56.4% of male are affected.

Other useful contingency table analysis function is `fisher.test`, which implements the Fisher Exact Test of independence:

```
> fisher.test(a)

        Fisher's Exact Test for Count Data

data:  a
p-value = 0.4457
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.676759 2.482869
sample estimates:
odds ratio
  1.290313
```

Exploration of genetic data within base R, though possible, may be a bit of a pain. For example, we can easily generate contingency table of SNP5 vs affected status:

```
> a <- table(aff,snp5)
> a

   snp5
aff A/A B/A B/B
  0  31  88  68
  1   8  26  17
```

We can also look up what is the proportion of affected among different genotypic
groups

```
> prop.table(a,2)

   snp5
aff        A/A        B/A        B/B
  0 0.7948718 0.7719298 0.8000000
  1 0.2051282 0.2280702 0.2000000
```

showing that proportion of cases is similar in 'A/A' and 'A/B' genotypic groups
and somewhat decreased in 'B/B'. It is easy to test if this affection is statistically
independent of genotype by

```
> chisq.test(a)

        Pearson's Chi-squared test

data:  a
X-squared = 0.2511, df = 2, p-value = 0.882
```

which gives (insignificant) genotypic association test on two degrees of freedom.

However, testing Hardy-Weinberg equilibrium, testing allelic effects, and
even computation of allelic frequency is not so straightforward. Such spe-
cific genetic tests are implemented in special R libraries, such as `genetics` and
`GenABEL-package` and will be covered in later sections of this document.

At this moment we will switch to exploratory analysis of quantitative traits.
We will make use of the `srdta` data supplied with `GenABEL-package`. As you
can remember from an exercise, the library is loaded with `library(GenABEL)`
and the data are loaded with `data(srdta)`: Then the phenotypic data frame
may be accessed through `phdata(srdta)`.

Exercise 7.   Explore phenotypes in `srdta`

Explore phenotypic data content of `srdta` object (`phdata(srdta)`).

1. How many observations and variables are presented in the data frame?

2. What are the classes of these variables?

As it was mentioned before, the function `summary()` generates a summary
statistics for an object. For example, to see summary for trait `qt1`, we can use

```
> summary(phdata(srdta)$qt1)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
-4.6000 -0.9500 -0.3100 -0.2981  0.3800  3.2000  3.0000
```

> **summary is quite useful function which may operate in different ways for
> objects of different classes. Try `summary(phdata(srdta))`.**

With R, it is also easy to explore the data graphically. For example, the
histogram for `qt1` may be generated by

Histogram of phdata(srdta)$qt1
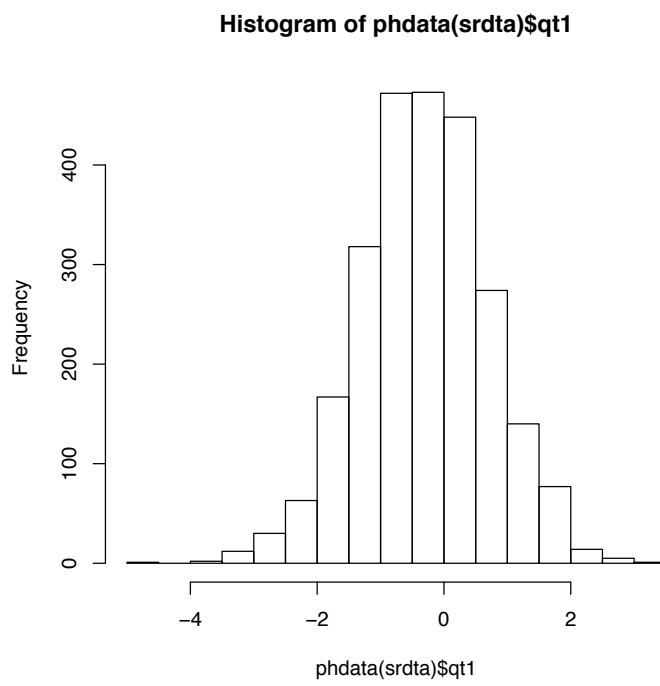
Figure 2.1: Histogram of qt1
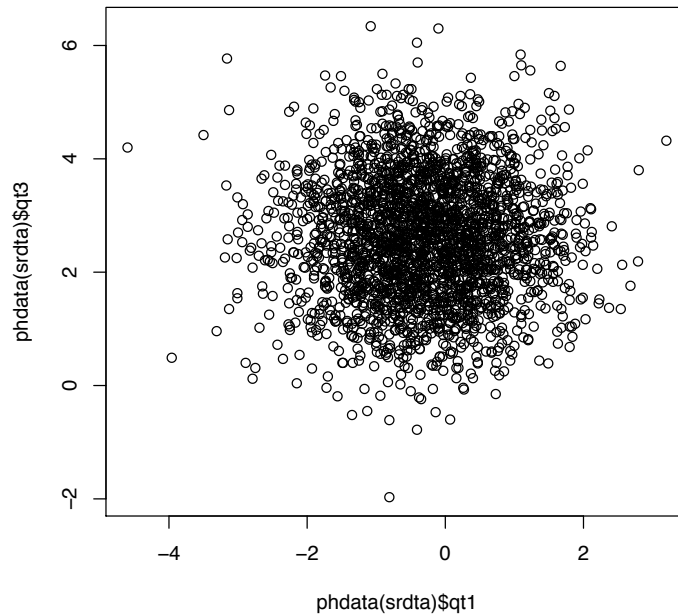
Figure 2.2: Scatter-plot of qt1 against qt3

```
> hist(phdata(srdta)$qt1)
```

(resulting histogram is shown at figure 2.1)

In similar manner, scatter-plots may be generated. To see relation between qt1 and qt3, you can run

```
> plot(phdata(srdta)$qt1,phdata(srdta)$qt3)
```

(resulting plot is shown at figure 2.2)

The mean, median, minimum and maximum of the distribution of the trait may be found out using functions mean, median, min and max, respectively. The variance and standard deviation can be computed with var and sd.

To compute correlation between two variables (or all variables in a matrix/data frame), use cor.

In GenABEL-package, there is a special function designed to facilitate phenotypic quality control. This function takes names of variables and a data frame as an input, and returns summary statistics, list of outliers (using False Discovery Rate) and graphs.

For example, to do QC of sex, age and qt3, try

```
> check.trait(c("sex","age","qt3"),phdata(srdta))

--------------------------------
Trait sex has 2500 measurements
Missing: 0 ( 0 %)
```
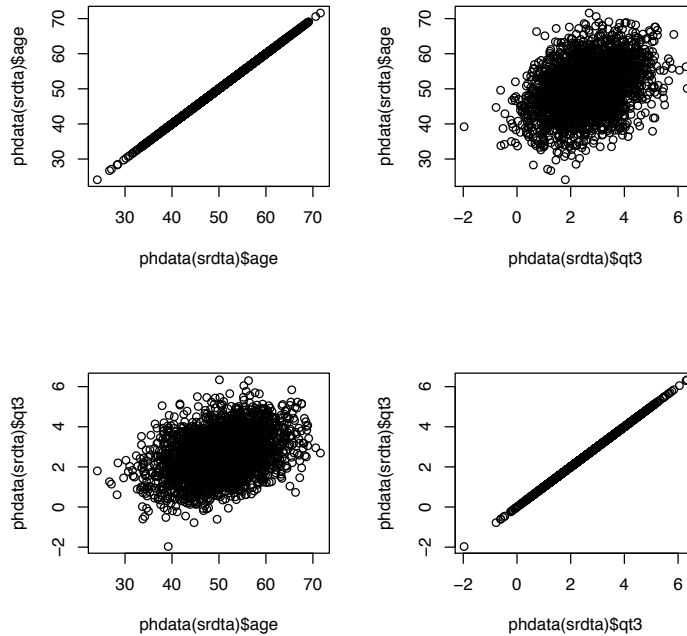
Figure 2.3: Quality control graph for `sex, age, qt3`

```
Mean = 0.51 ; s.d. = 0.5
NO outliers discovered for trait sex
--------------------------------
Trait age has 2500 measurements
Missing: 0 ( 0 %)
Mean = 50.0378 ; s.d. = 7.060125
NO outliers discovered for trait age
--------------------------------
Trait qt3 has 2489 measurements
Missing: 11 ( 0.44 %)
Mean = 2.60859 ; s.d. = 1.101154
NO outliers discovered for trait qt3
```

The corresponding graph is depicted at figure **??**.

 Before you start with the exercise: if a function returns unexpected results, and you are confident that syntax was right, checking help page is always a good idea!

Exercise 8.   **Exploring phenotypic part of `srdta`**

Explore `phdata` part of `srdta` object

1. How many people has age over 65 years?

2. What is the sex distribution (proportion of males) in the people over 65 years old?

3. What is the mean, median, minimum and maximum age in the sample?

4. Compare the distribution of qt3 in people younger and older than 65 years. Use function `sd(A)` to get standard deviation of A

5. Produce distributions of different traits. Do you see something special?

6. What is correlation between qt3 and age?

2.4   Regression analysis

While contingency tables, bi-plots and correlation are powerful tools to analyse relations between pairs of variable, a more general framework allowing investigation of relation of an outcome to multiple predictors is regression. In R, function `lm` implements linear regression modelling, and function `glm` implements generalised linear regression. In this section, we will use these two functions to analyse quantitative an binary outcomes.

You can do linear regression to check if trait `qt2` has relation with sex and age by

```
> a <- lm(phdata(srdta)$qt2 ~ phdata(srdta)$age + phdata(srdta)$sex)
```

The results of analysis are stored in object 'a', which has class 'lm' and contains may sub-objects:

```
> class(a)

[1] "lm"

> names(a)

 [1] "coefficients"  "residuals"     "effects"       "rank"
 [5] "fitted.values" "assign"        "qr"            "df.residual"
 [9] "xlevels"       "call"          "terms"         "model"
```

At this moment you do not need to understand all these sub-objects; the meaningful summary of analysis is produced with

```
> summary(a)

Call:
lm(formula = phdata(srdta)$qt2 ~ phdata(srdta)$age + phdata(srdta)$sex)

Residuals:
   Min     1Q Median     3Q    Max
 -5.65  -1.80  -1.03  -0.31 883.08

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)        -1.55892    4.41667   -0.353    0.724
phdata(srdta)$age   0.14022    0.08668    1.618    0.106
phdata(srdta)$sex   1.30377    1.22393    1.065    0.287


Residual standard error: 30.59 on 2497 degrees of freedom
Multiple R-squared: 0.001518,       Adjusted R-squared: 0.0007181
F-statistic: 1.898 on 2 and 2497 DF,  p-value: 0.1501
```

You can see that qt2 is not associated with age or sex.

As before, to make easy access to your data (basically, to avoid typing ph-data(srdta) before every trait name, you may attach the data to the search path:

```
> attach(phdata(srdta))
```

Then,the above expression to run linear regression analysis simplifies to:

```
> summary(lm(qt2 ~ age + sex))

Call:
lm(formula = qt2 ~ age + sex)

Residuals:
   Min    1Q Median    3Q    Max
 -5.65  -1.80  -1.03  -0.31 883.08


Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.55892    4.41667   -0.353    0.724
age          0.14022    0.08668    1.618    0.106
sex          1.30377    1.22393    1.065    0.287


Residual standard error: 30.59 on 2497 degrees of freedom
Multiple R-squared: 0.001518,       Adjusted R-squared: 0.0007181
F-statistic: 1.898 on 2 and 2497 DF,  p-value: 0.1501
```

with the same results.

Analysis of binary outcomes may be performed using glm function, using *binomial family* for the error distribution and the link function. For example, to figure out if your binary trait (bt) is associated with sex and age, you need to tell that this is binary trait:

```
> a <- glm(bt ~ age + sex, family="binomial")
> summary(a)

Call:
glm(formula = bt ~ age + sex, family = "binomial")

Deviance Residuals:
   Min      1Q  Median     3Q     Max
-1.992  -1.091  -0.444   1.094   1.917
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.639958   0.330519 -14.038  < 2e-16 ***
age          0.088860   0.006463  13.749  < 2e-16 ***
sex          0.379593   0.084138   4.512 6.44e-06 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 3450.5  on 2488  degrees of freedom
Residual deviance: 3216.5  on 2486  degrees of freedom
  (11 observations deleted due to missingness)
AIC: 3222.5

Number of Fisher Scoring iterations: 4
```

There is strong association between `bt` and sex and age. If you want to characterise the strength of association to a binary trait with Odds Ratios, take the exponents of the regression coefficient. For example, the odds ratio associated with male is

```
> exp(0.3796)
```

```
[1] 1.4617
```

2.5   Answers to exercises

Вырезано цензурой

Chapter 3

Introduction to genetic association analysis in R

When analyzing several (dozens of) SNPs, facilities of base R are sufficient and efficient for data storage and analysis. Few specific test, such as these of Hardy-Weinberg Equilibrium (HWE) and Linkage Disequilibrium (LD), are implemented in different libraries, e.g. `genetics` and `GenABEL-package`.

In this section, we will describe library `genetics` and will make use of it to guide you through simple genetic analysis exercise using a small example data set. In the last part, you will investigate a bigger data set as based on the knowledge obtained in the first part, and will answer the questions.

3.1 Characterisation of genetic data

3.2 Exploring genetic data with library `genetics`

Library `genetics` was written by Gregory R. Warnes to facilitate analysis of genetic data in R. This library

- Implements genetic analysis tests, such as test for Hardy-Weinberg equilibrium and Linkage disequilibrium.

- Implements new data classes, such as `genotype`, `haplotype` and `LD.data.frame`.

- Modifies default R functions, such as `summary` and `plot` to correctly analyse and present these new classes.

- Facilitates export of the data from R to the formats supported by such genetic analysis packages as GenePop and QTDT.

Start `R` by double-click on the file `ge03d1p1.RData`. Load library `genetics`, which we will need for testing HWE and computations of LD by

> `library(genetics)`

NOTE: THIS PACKAGE IS NOW OBSOLETE.

```
The R-Genetics project has developed an set of enhanced genetics
packages to replace 'genetics'. Please visit the project homepage
at http://rgenetics.org for informtion.
```

The file you have loaded contains single data frame `assocg`. Let us briefly explore it:

```
> class(assocg)
```

```
[1] "data.frame"
```

```
> names(assocg)
```

```
[1] "subj" "sex"  "aff"  "qt"   "snp4" "snp5" "snp6"
```

```
> dim(assocg)
```

```
[1] 250    7
```

You can see that `assocg` looks remarkably similar to the previously explored data frame `assoc` (section 2.2, page 20). Indeed, they are almost equivalent. Let us present the data for the subjects 5 to 15 and compare this output to that presented on page 23:

```
> assocg[5:15,]
```

```
      subj sex aff        qt snp4 snp5 snp6
1533 1533   0   0  0.1009220  A/B  B/A  B/A
2466 2466   1   0 -0.1724321  A/B  A/A  A/A
2425 2425   0   0 -0.3378473  B/B  A/A  A/A
1068 1068   0   0 -1.7112925  A/A  B/B <NA>
198   198   1   0 -0.4815822  A/B  B/A  B/A
1496 1496   1   0  1.2281232  A/A  B/B  B/B
909   909   0   0  0.5993945  A/B  B/A  B/A
1213 1213   0   0  1.9792190  A/A  B/B  B/B
181   181   1   0  1.5435921  A/A  B/B  B/B
1783 1783   0   0 -1.6242738  A/B  B/A  B/A
1914 1914   0   0 -0.5160331  A/A  B/B  B/B
```

The data are identical. However, the SNP data presented in the new data frame have special class `genotype`, as implemented in `genetics` library:

```
> class(assocg$snp4)
```

```
[1] "genotype" "factor"
```

Previously, the SNP genotypes were coded as characters. This new way of presentation allows library `genetics` to recognise the SNP data as genetic and analyse them accordingly.

Let us attach the `assocg` data frame and explore what data analysis advantages are achieved by application of library `genetics`.

```
> attach(assocg)
```

As we noted in section 2.2, testing Hardy-Weinberg equilibrium, testing allelic effects, and even computation of allelic frequency is not so straightforward in base R. These tests, are, however, easy with library `genetics`. To see the allelic frequencies and other summary statistics for a SNP, you can use

```
> summary(snp4)

Number of samples typed: 243 (97.2%)

Allele Frequency: (2 alleles)
   Count Proportion
A    323        0.66
B    163        0.34
NA    14          NA


Genotype Frequency:
     Count Proportion
B/B    29       0.12
A/B   105       0.43
A/A   109       0.45
NA      7         NA

Heterozygosity (Hu)  = 0.4467269
Poly. Inf. Content   = 0.3464355
```

To check these characteristics in controls and cases separately, you can use

```
> summary(snp4[aff==0])

Number of samples typed: 190 (97.9%)

Allele Frequency: (2 alleles)
   Count Proportion
A    255        0.67
B    125        0.33
NA     8          NA


Genotype Frequency:
     Count Proportion
B/B    22       0.12
A/B    81       0.43
A/A    87       0.46
NA      4         NA

Heterozygosity (Hu)  = 0.4426469
Poly. Inf. Content   = 0.3440288

> summary(snp4[aff==1])
```

```
Number of samples typed: 53 (94.6%)

Allele Frequency: (2 alleles)
    Count Proportion
A     68        0.64
B     38        0.36
NA     6          NA


Genotype Frequency:
     Count Proportion
B/B     7        0.13
A/B    24        0.45
A/A    22        0.42
NA      3          NA

Heterozygosity (Hu)  = 0.4643306
Poly. Inf. Content   = 0.3541731
```

Let us check if HWE holds for the SNPs described in this data frame. We can do exact test for HWE by

> *HWE.exact(snp4)*

```
        Exact Test for Hardy-Weinberg Equilibrium

data:  snp4
N11 = 109, N12 = 105, N22 = 29, N1 = 323, N2 = 163, p-value = 0.666
```

If you want to check HWE using controls only, you can do it by

> *HWE.exact(snp4[aff==0])*

```
        Exact Test for Hardy-Weinberg Equilibrium

data:  snp4[aff == 0]
N11 = 87, N12 = 81, N22 = 22, N1 = 255, N2 = 125, p-value = 0.6244
```

Let us check if the there is LD between snp4 and snp5:

> *LD(snp4,snp5)*

```
Pairwise LD
-----------
                  D         D'       Corr
Estimates: 0.2009042 0.9997352 0.8683117

            X^2 P-value   N
LD Test: 354.3636       0 235
```

The output shows results of the test for significance of LD, and estimates of the magnitude of LD (D' and correlation, r). To obtain r^2, you can either square the correlation manually

```
> 0.8683117*0.8683117
```

```
[1] 0.7539652
```

or simply ask LD() to report it by

```
> LD(snp4,snp5)$"R^2"
```

```
[1] 0.7539652
```

> The latter command is possible because the LD() function actually computes more things than it reports. This is quite common for R functions. You can apply names() function to the analysis objects to see (at least part of) what was actually computed. Try
>
> ```
> > ld45 <- LD(snp4,snp5)
> ```
>
> and check what are the sub-objects contained in this analysis object
>
> ```
> > names(ld45)
> ```
>
> ```
> [1] "call"    "D"       "D'"      "r"       "R^2"     "n"       "X^2"
> [8] "P-value"
> ```
>
> Any of these variables can be accessed through object$var syntax, e.g. to check D' we can use
>
> ```
> > ld45$"D'"
> ```
>
> ```
> [1] 0.9997352
> ```

To check LD for more that two SNPs, we can compute an LD analysis object by

```
> ldall <- LD(data.frame(snp4,snp5,snp6))
```

and later check

```
> ldall$"P-value"
```

```
     snp4 snp5 snp6
snp4   NA    0    0
snp5   NA   NA    0
snp6   NA   NA   NA
```

to see significance,

```
> ldall$"D'"
```

```
     snp4      snp5      snp6
snp4   NA 0.9997352 0.8039577
snp5   NA        NA 0.9997231
snp6   NA        NA        NA
```

for D' and

```
> ldall$"R^2"
```
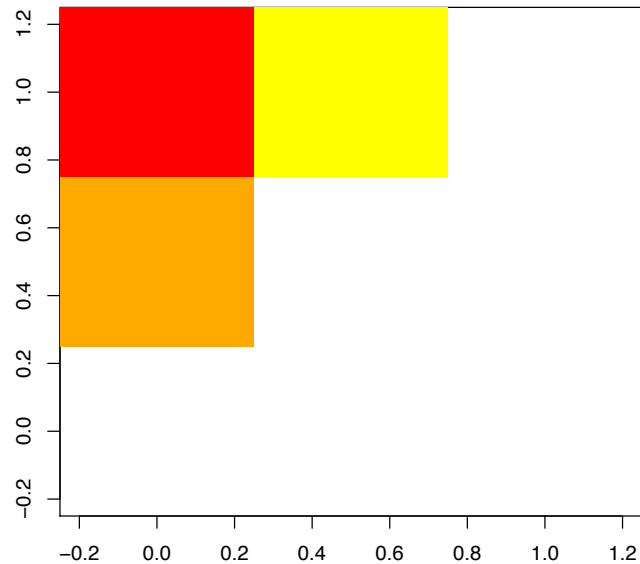
Figure 3.1: r^2 plot for snp4, snp5 and snp6

```
      snp4       snp5       snp6
snp4    NA 0.7539652 0.5886602
snp5    NA        NA 0.8278328
snp6    NA        NA        NA
```

for r^2.

You can also present e.g. r^2 matrix as a plot by

```
> image(ldall$"R^2")
```

A more neat way to present it requires specification of the set of threshold (break points) and colors to be used (you do not need to try this example if you do not want):

```
> image(ldall$"R^2",breaks=c(0.5,0.6,0.7,0.8,0.9,1),col=heat.colors(5))
```

Resulting plot is shown at figure 3.1.

For any R command, you can get help by typing help(command). Try help(image) if you are interested to understand what are "breaks" and "col"; or try help(heat.colors) to figure this color schema out.

Similar to our HWE checks, we may want to compute (and compare) LD in cases and controls separately:
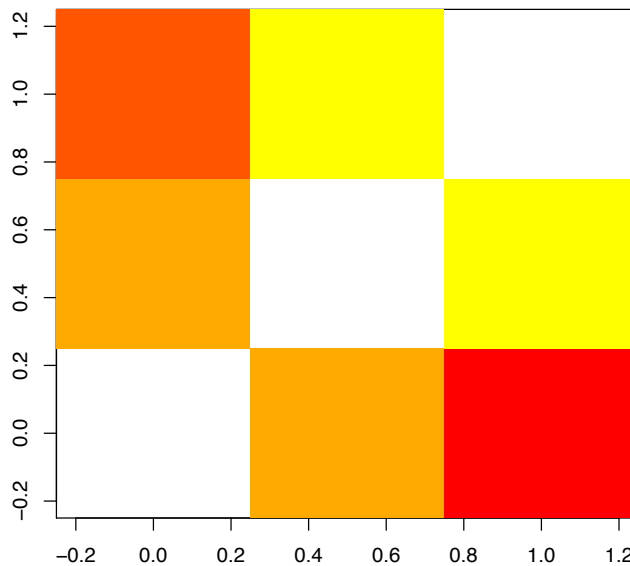
Figure 3.2: r^2 plot for snp4, snp5 and snp6. Above diagonal: LD in cases; below: controls

```
> ldcases <- LD(data.frame(snp4,snp5,snp6)[aff==1,])
> ldcases$"R^2"


     snp4      snp5      snp6
snp4   NA 0.7615923 0.6891558
snp5   NA        NA 0.8943495
snp6   NA        NA        NA

> ldcontr <- LD(data.frame(snp4,snp5,snp6)[aff==0,])
> ldcontr$"R^2"


     snp4      snp5      snp6
snp4   NA 0.7512458 0.5616395
snp5   NA        NA 0.8075894
snp6   NA        NA        NA
```

and even present it results for cases and controls on the same graph (you do not need to produce this graph, which is presented at the figure 3.2):

```
> image(ldcases$"R^2",breaks=c(0.5,0.6,0.7,0.8,0.9,1),col=heat.colors(5))
> image(t(ldcontr$"R^2"),breaks=c(0.5,0.6,0.7,0.8,0.9,1),col=heat.colors(5),add=T)
```

3.3 Genetic association analysis

3.4 Example association analysis

Now, after we have described genetic and phenotypic data separately, we are ready to test association between these two. In previous sections, we showed that association between a binary trait and genotype may be analysed using contingency tables (functions `table`, `prop.table`, `fisher.test`, etc.). The association between a quantitative trait and genotype may be done using correlations, T-test, etc.

However, a more flexible analysis is possible when using regression modelling. First, we will investigate relation between the quantitative trait `qt` and the SNPs by using linear regression

```
> mg <- lm(qt~snp4)
```

The `lm` command fits linear regression model to the data and returns an analysis object. The summary of analysis may be generated with

```
> summary(mg)

Call:
lm(formula = qt ~ snp4)

Residuals:
     Min      1Q  Median      3Q     Max
-2.63700 -0.62291 -0.01225  0.58922  3.05561

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.081114   0.092517  -0.877    0.382
snp4A/B     -0.108366   0.132079  -0.820    0.413
snp4B/B     -0.006041   0.201820  -0.030    0.976

Residual standard error: 0.9659 on 240 degrees of freedom
  (7 observations deleted due to missingness)
Multiple R-squared: 0.003049,       Adjusted R-squared: -0.005259
F-statistic: 0.367 on 2 and 240 DF,  p-value: 0.6932
```

From the summary output, it is clear that the model assumes arbitrary (estimated) effects of the genotypes AA, AB and BB. Neither effect of AB nor BB is significant in this case. The global test on two degrees of freedom (bottom of the output) is also not significant.

If you want to include some covariate into your model, e.g. sex, you can easily do that by adding the term to the formula:

```
> summary(lm(qt~sex+snp4))

Call:
lm(formula = qt ~ sex + snp4)

Residuals:
```

```
      Min       1Q   Median       3Q      Max
-2.66442 -0.62417 -0.00875  0.59705  3.08086
```

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.110298   0.115260  -0.957    0.340
sex          0.053018   0.124493   0.426    0.671
snp4A/B     -0.104429   0.132628  -0.787    0.432
snp4B/B     -0.002452   0.202340  -0.012    0.990
```

```
Residual standard error: 0.9676 on 239 degrees of freedom
  (7 observations deleted due to missingness)
Multiple R-squared: 0.003805,      Adjusted R-squared: -0.0087
F-statistic: 0.3043 on 3 and 239 DF,  p-value: 0.8223
```

You can also allow for interaction by using the "*" operator

```
> summary(lm(qt~sex*snp4))
```

```
Call:
lm(formula = qt ~ sex * snp4)
```

```
Residuals:
     Min       1Q   Median       3Q      Max
-2.57049 -0.64596 -0.00264  0.61094  3.01970
```

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.20579    0.13834  -1.487    0.138
sex          0.22649    0.18647   1.215    0.226
snp4A/B      0.05222    0.19024   0.274    0.784
snp4B/B      0.18071    0.28576   0.632    0.528
sex:snp4A/B -0.30191    0.26566  -1.136    0.257
sex:snp4B/B -0.35508    0.40531  -0.876    0.382
```

```
Residual standard error: 0.9684 on 237 degrees of freedom
  (7 observations deleted due to missingness)
Multiple R-squared: 0.01041,      Adjusted R-squared: -0.01047
F-statistic: 0.4984 on 5 and 237 DF,  p-value: 0.7773
```

Note that both main effects of sex and snp4, and also effects of interaction are estimated in this model.

Of interest in genetic studies may be three other models: additive, dominant and recessive.

The additive model assumes that the difference between mean trait's values between 'AA' and 'BB' is twice the difference between 'AA' and 'BB', that is the mean value of the trait for heterozygous genotypes is right in between the two homozygotes. To test additive model, we first need to recode the predictor (genotype) as a numeric factor to be used as covariate. This can be easy done with function `as.numeric`:

```
> add4 <- as.numeric(snp4)-1
```

We can check if recoding was done correctly by producing the table

```
> table(snp4,add4)

     add4
snp4   0   1   2
  A/A 109   0   0
  A/B   0 105   0
  B/B   0   0  29
```

Now to test the additive model run

```
> summary(lm(qt~add4))

Call:
lm(formula = qt ~ add4)

Residuals:
    Min      1Q   Median      3Q     Max
-2.54813 -0.62104 -0.02754  0.60584  3.00652

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.10476    0.08710  -1.203    0.230
add4        -0.03563    0.09133  -0.390    0.697

Residual standard error: 0.9651 on 241 degrees of freedom
  (7 observations deleted due to missingness)
Multiple R-squared: 0.0006313,      Adjusted R-squared: -0.003516
F-statistic: 0.1522 on 1 and 241 DF,  p-value: 0.6968
```

The model assuming dominant action of the 'A' allele means that the means of genotypes 'AA' and 'AB' are the same. This is equivalent to the model of recessive action of 'B' allele. To code SNP4 according to this model, we can use function replace:

```
> dom4 <- add4
> dom4[dom4==2] <- 1
> table(snp4,dom4)

     dom4
snp4   0   1
  A/A 109   0
  A/B   0 105
  B/B   0  29
```

To test association with a binary outcome, we will use function glm with binomial family:

```
> summary(glm(aff~snp4,family="binomial"))
```

```
Call:
glm(formula = aff ~ snp4, family = "binomial")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7433  -0.7204  -0.6715  -0.6715   1.7890

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.3749     0.2386  -5.761 8.35e-09 ***
snp4A/B       0.1585     0.3331   0.476    0.634
snp4B/B       0.2297     0.4952   0.464    0.643
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 254.91  on 242  degrees of freedom
Residual deviance: 254.58  on 240  degrees of freedom
  (7 observations deleted due to missingness)
AIC: 260.58

Number of Fisher Scoring iterations: 4
```

To make a test of global significance of the SNP effect, you can use

```
> anova(glm(aff~snp4,family="binomial"),test="Chisq")

Analysis of Deviance Table

Model: binomial, link: logit

Response: aff

Terms added sequentially (first to last)


     Df Deviance Resid. Df Resid. Dev Pr(>Chi)
NULL                   242     254.91
snp4  2  0.32894        240     254.58   0.8483
```

In the manner similar to that described for quantitative traits, additive and dominance/recessive models can be tested by proper coding of the genotypic variable, e.g. to test the additive model, use

```
> summary(glm(aff~as.numeric(snp4),family="binomial"))

Call:
glm(formula = aff ~ as.numeric(snp4), family = "binomial")

Deviance Residuals:
```

```
    Min       1Q   Median       3Q      Max
-0.7549  -0.7139  -0.6747  -0.6747   1.7842


Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)     -1.4913     0.4164  -3.581 0.000342 ***
as.numeric(snp4)  0.1272     0.2268   0.561 0.574994
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 254.91  on 242  degrees of freedom
Residual deviance: 254.60  on 241  degrees of freedom
  (7 observations deleted due to missingness)
AIC: 258.6


Number of Fisher Scoring iterations: 4
```

Now you have learned all commands necessary to answer the questions of the next section.

Exit R by typing `q()` command (do not save image) and and proceed to the self exercise.

3.5 Exercise: Exploring genetic data using library genetics

Start R by double-click over the file `ge03d1p2.RData` (Windows) or by changing to the directory containing the data, starting R and loading the data set with `load("ge03d1p2.RData")` (Linux). Explore the data frame present and answer the questions.

Ex. 1 — How many SNPs are described in this data frame?

Ex. 2 — What is the frequency (proportion) of snp1 allele 'A'?

Ex. 3 — What is its frequency of 'A' in affected (aff==1)?

Ex. 4 — How many cases and controls are present in the data set?

Ex. 5 — If all subjects are used to test HWE, are there any SNPs out of HWE at nominal $P \leq 0.05$? Which ones?

Ex. 6 — If only controls are used to test the SNPs which are out of HWE in total sample, are these still out of HWE?

Ex. 7 — Which SNP pairs are in strong LD ($r^2 \geq 0.8$)?

Ex. 8 — For SNPs in strong LD, what is r^2 for separate samples of cases and controls?

Ex. 9 — Is there significant association between affection status and sex? What is P-value for association?

Ex. 10 — Is association between the disease and `qt` significant?

Ex. 11 — Which SNPs are significantly associated with affection status at nominal p-value ≤ 0.05? Use general genotypic (2 d.f.) model.

Ex. 12 — Test association between `aff` and snp5 and snp10, allowing for the SNPs interaction effect. Use arbitrary (not an additive) model. Do you observe significant interaction? How can you describe the model of concert action of snp5 and snp10?

Ex. 13 — Test for association between the quantitative trait `qt` and SNPs 1-10 using additive model. Which SNPs are associated at nominal $P \leq 0.05$?

Ex. 14 — **OPTIONAL, difficulty is medium, but may be time-consuming.** If you adjust the analysis under additive model for sex, how do the findings change? Before doing the exercise, please check the answer to **previous** exercise – it shows a quick way to do testing for all 10 SNPs.

Ex. 15 — Which SNPs are associated with the quantitative trait `qt` at nominal $P \leq 0.05$ when general genotypic (2 d.f. test) model is used?

Ex. 16 — **ADVANCED:** How can you describe the model of action of the significant SNPs? Test if the data are compatible with additive/dominant/recessive model.

3.6 Answers to exercises

Chapter 4

Introduction to
`GenABEL-package`

In this section, you will become familiar with the `GenABEL-package` library, designed for GWA analysis. Compared to `genetics` package, it provides specific facilities for storage and manipulation of large amounts of data, very fast tests for GWA analysis, and special functions to analyse and graphically present the results of GWA analysis (thus "analysis of analysis").

Start R and load `GenABEL-package` library using command

```
> library(GenABEL)
```

After that, load example data set using the command

```
> data(srdta)
```

4.1 General description of `gwaa.data-class`

The object you have loaded, `srdta`, belongs to the `gwaa.data` class. This is a special class developed to facilitate GWA analysis.

In GWA analysis, different types of data are used. These include the phenotypic and genotypic data on the study participants and chromosome and location of every SNP. For every SNP, it is desirable to know the details of coding (what are alleles? – A, T, G, C? – and what is the strand – '+' or '-', 'top' or 'bot'? – this coding is for).

One could attempt to store all phenotypes and genotypes together in a single table, using, e.g. one row per study subject; than the columns will correspond to study phenotypes and SNPs. For a typical GWA data set, this would lead to a table of few thousands rows and few hundreds of thousands to millions of columns. Such a format is generated when one downloads HapMap data for a region. To store GWA data in such tables internally, within R, proves to be inefficient. In `GenABEL-package`, special data class, `gwaa.data-class` is used to store GWA data.

You may consider an object of `gwaa.data-class` as a 'black box' from which you can get specific data using specific functions. If you are interested in internal

structure of the `gwaa.data-class`, you can find the description in section B.1
(Internal structure of `gwaa.data-class`).

   The data frame, which contains all phenotypic data in the study may be
accessed using the `phdata` function. Let us have a look at few first rows of the
phenotypic data frame of `srdta`:

```
> phdata(srdta)[1:5,]
```

```
  id sex  age   qt1     qt2  qt3 bt
1 p1   1 43.4 -0.58    4.46 1.43  0
2 p2   1 48.2  0.80    6.32 3.90  1
3 p3   0 37.9 -0.52    3.26 5.05  1
4 p4   1 53.8 -1.55 888.00 3.76  1
5 p5   1 47.5  0.25    5.70 2.89  1
```

   The rows of this data frame correspond to study subjects, and the columns
correspond to the variables. There are two default variables, which are always
present in `phdata`. The first of these is "id", which contains study subject
identification code. This identification code can be arbitrary character, numer,
or alphanumeric combination, but every person must be coded with an unique
ID. The second default variable is "sex", where males are coded with ones ("1")
and females are coded with zero ("0").

   It is important to understand that this data frame is not supposed to be
directly modified by the user, as its structure is coupled to the structure of
genotypic data. If at some point you need to manipulate (add/delete) the phe-
notypes included in `phdata`, you need to use such `GenABEL-package` functions
as `add.phdata` and `del.phdata` (see section 4.2).

   The other part of an object of `gwaa.data-class` is `gtdata`, which contains
all GWA genetic information in an object of class `snp.data` class. It is not
supposed to be modified directly by user. The genotypic data can be accessed
through `gtdata` function, e.g.

```
> gtdata(srdta[1:10,1:10])
```

```
@nids = 10
@nsnps = 10
@nbytes = 3
@idnames = p1 p2 p3 p4 p5 p6 p7 p8 p9 p10
@snpnames = rs10 rs18 rs29 rs65 rs73 rs114 rs128 rs130 rs143 rs150
@chromosome = 1 1 1 1 1 1 1 1 1 1
@coding =  08 0b 0c 03 04 03 0c 04 08 0f
@strand =  01 01 02 01 01 01 02 01 01 01
@map = 2500 3500 5750 13500 14250 24500 27000 27250 31000 33250
@male = 1 1 0 1 1 0 0 1 0 0
@gtps =
40 40 40 80 40 40 40 40 c0 c0
40 40 00 00 40 40 40 c0 40 40
40 40 00 80 40 40 40 40 c0 c0
```

As you can see, these data are of little direct use as these are stored in an internal
format – you need to coerce that to other data type if you want to manipulate
/ analyse these data using non-`GenABEL-package` functions (see section **??**).

The number of individuals described in an object of `gwaa.data-class` can be accessed through `nids` function, e.g.

```
> nids(srdta)
```

```
[1] 2500
```

and the number of SNPs using the `nsnps` function:

```
> nsnps(srdta)
```

```
[1] 833
```

The IDs of individuals included in the study can be accessd via `idnames` function, for example IDs of the first 7 individuals in the study are

```
> idnames(srdta)[1:7]
```

```
[1] "p1" "p2" "p3" "p4" "p5" "p6" "p7"
```

The sex of the individuals can be accessed using the `male` function:

```
> male(srdta)[1:7]
```

```
p1 p2 p3 p4 p5 p6 p7
 1  1  0  1  1  0  0
```

where males (heterogametic sex) are assigned with '1' and a homogametic sex (females) are assigned value '0'.

Names of SNPs can be accessed using `snpnames` function; for example the names of the first 10 SNPs in the `srdta` are

```
> snpnames(srdta)[1:10]
```

```
 [1] "rs10"  "rs18"  "rs29"  "rs65"  "rs73"  "rs114" "rs128" "rs130" "rs143"
[10] "rs150"
```

SNP annotation include (presented for the first 10 SNPs only):

- Chromosome:

  ```
  > chromosome(srdta)[1:10]
  ```

  ```
   rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
    "1"    "1"    "1"    "1"    "1"   "1"   "1"   "1"   "1"   "1"
  ```

- Map position

  ```
  > map(srdta)[1:10]
  ```

  ```
   rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
   2500   3500   5750  13500  14250 24500 27000 27250 31000 33250
  ```

- Coding (where the second allele is the "effect" or "coded" one):

  ```
  > coding(srdta)[1:10]
  ```

```
 rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
 "TG"   "GA"   "GT"   "AT"   "AG"  "AT"  "GT"  "AG"  "TG"  "CA"
```

For every SNP, coding is presented with a pair of characters, for example ”AG”. For ’AG’ polymorphism, you may expect ”AA”, ”AG” and ”GG” genotypes to be found in population. The order (that is ”AG” vs ”GA”) is important – the first allele reported is the one which will be used as a reference in association analysis, and thus the effects are reported for the second allele. You can also access the reference allele with the method `refallele`

```
> refallele(srdta)[1:10]
```

```
 rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
  "T"    "G"    "G"    "A"    "A"   "A"   "G"   "A"   "T"   "C"
```

and the effective (or ’coded’) allelel with

```
> effallele(srdta)[1:10]
```

```
 rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
  "G"    "A"    "T"    "T"    "G"   "T"   "T"   "G"   "G"   "A"
```

- Strand on which the coding is reported (’+’, ’-’ or missing, ’u’):

```
> strand(srdta)[1:10]
```

```
 rs10   rs18   rs29   rs65   rs73 rs114 rs128 rs130 rs143 rs150
  "+"    "+"    "-"    "+"    "+"   "+"   "-"   "+"   "+"   "+"
```

Summary:

- `GenABEL-package` uses special data class, `gwaa.data-class`, to store GWA data.

- To access the content of an object of `gwaa.data-class`, a number of functions is used

---

Exercise 1.   Exploring IDs in `srdta`

Explore `srdta`.

   1. How many people are included in the study?

   2. How many of these are males?

   3. How many are females?

   4. What is male proportion?

Exercise 2.   Exploring SNPs in `srdta`

 Explore SNPs contained in `srdta` using functions to access SNP names (`snpnames`) and map (`map`) location

1. What are names of markers located after 2,490,000 b.p.?
2. Between 1,100,000 and 1,105,000 b.p.?

4.2   Accessing and modifying phenotypic data

As it was already mentioned, the object returned by `phdata` contains phenotypic data and is an conventional data frame, wich obligatory includes 'id' and 'sex' variables, and ordered an a way that it couples to the genotypic data.

Being a data frame, `phdata` may be accessed using corresponding methods:

```
> phdata(srdta)[1:5,]

  id sex  age   qt1    qt2  qt3 bt
1 p1   1 43.4 -0.58   4.46 1.43  0
2 p2   1 48.2  0.80   6.32 3.90  1
3 p3   0 37.9 -0.52   3.26 5.05  1
4 p4   1 53.8 -1.55 888.00 3.76  1
5 p5   1 47.5  0.25   5.70 2.89  1

> class(phdata(srdta))

[1] "data.frame"

> phdata(srdta)[1:5,2]

[1] 1 1 0 1 1

> phdata(srdta)[1:5,"sex"]

[1] 1 1 0 1 1

> phdata(srdta)$sex[1:5]

[1] 1 1 0 1 1
```

The modification of the phenotypic data is performed using special methods, because of specific restrictions on phenotypic data frames. There are two main functions which allow you to add (`add.phdata`) and delete (`del.phdata`) phenotypes from `phdata` part of an object of `gwaa.data-class`.

For example, if you want to add a variable (say, square of age) computed from the 'age' variable of `srdta`

```
> phdata(srdta)[1:5,]

  id sex  age   qt1    qt2  qt3 bt
1 p1   1 43.4 -0.58   4.46 1.43  0
2 p2   1 48.2  0.80   6.32 3.90  1
3 p3   0 37.9 -0.52   3.26 5.05  1
4 p4   1 53.8 -1.55 888.00 3.76  1
5 p5   1 47.5  0.25   5.70 2.89  1
```

```
> age2 <- phdata(srdta)$age^2
```

you need to use **add.phdata** function:

```
> srdta <- add.phdata(srdta,newph=age2,name="age_squared")
> phdata(srdta)[1:5,]
```

```
   id sex  age   qt1    qt2  qt3 bt age_squared
p1 p1   1 43.4 -0.58   4.46 1.43  0     1883.56
p2 p2   1 48.2  0.80   6.32 3.90  1     2323.24
p3 p3   0 37.9 -0.52   3.26 5.05  1     1436.41
p4 p4   1 53.8 -1.55 888.00 3.76  1     2894.44
p5 p5   1 47.5  0.25   5.70 2.89  1     2256.25
```

You can add more then one variable at once using the same function, however, in this case the second ('newph') argument of the function should be a data frame, which contains 'id' variable specifing the IDs of individuals. Imagine we have the data for individuals 'p1', 'p2' and 'p7' (we will generate random data for them; pay attention only to the result):

```
> newvalues <- matrix(rnorm(3*5),3,5)
> newdata <- data.frame(id=c("p1","p2","p7"),ph1=1,ph2=1,ph3=1,ph4=1,ph5=1)
> newdata[,c(2:6)] <- newvalues
> newdata
```

```
  id         ph1          ph2         ph3        ph4          ph5
1 p1  1.2069910  0.322405804   0.8903404  1.932106  0.17681061
2 p2  0.5066433  0.006376763  -0.2554177  1.107408  0.06014109
3 p7 -1.3744746 -2.002762635  -0.4972180 -1.117053 -0.37109845
```

These data can be added to phenotypic data with

```
> srdta <- add.phdata(srdta,newdata)
> phdata(srdta)[1:10,]
```

```
      id sex  age   qt1    qt2  qt3 bt age_squared         ph1          ph2
p1    p1   1 43.4 -0.58   4.46 1.43  0     1883.56   1.2069910  0.322405804
p2    p2   1 48.2  0.80   6.32 3.90  1     2323.24   0.5066433  0.006376763
p3    p3   0 37.9 -0.52   3.26 5.05  1     1436.41          NA           NA
p4    p4   1 53.8 -1.55 888.00 3.76  1     2894.44          NA           NA
p5    p5   1 47.5  0.25   5.70 2.89  1     2256.25          NA           NA
p6    p6   0 45.0  0.15   4.65 1.87  0     2025.00          NA           NA
p7    p7   0 52.0 -0.56   4.64 2.49  0     2704.00  -1.3744746 -2.002762635
p8    p8   1 42.5    NA   5.77 2.68  1     1806.25          NA           NA
p9    p9   0 29.7 -2.26   0.71 1.45  0      882.09          NA           NA
p10  p10   0 45.8 -1.32   3.26 0.85  0     2097.64          NA           NA
            ph3        ph4          ph5
p1    0.8903404  1.932106  0.17681061
p2   -0.2554177  1.107408  0.06014109
p3           NA        NA          NA
p4           NA        NA          NA
p5           NA        NA          NA
```

```
p6          NA        NA         NA
p7  -0.4972180 -1.117053 -0.37109845
p8          NA        NA         NA
p9          NA        NA         NA
p10         NA        NA         NA
```

Finally, if you need, you can delete some phenotypes from the `phdata` using `del.phdata` function. Let us delete the phenotypes we have just added:

```
> srdta <- del.phdata(srdta,c("age_squared","ph1","ph2","ph3","ph4","ph5"))
> phdata(srdta)[1:10,]

     id sex  age   qt1    qt2  qt3 bt
p1   p1   1 43.4 -0.58   4.46 1.43  0
p2   p2   1 48.2  0.80   6.32 3.90  1
p3   p3   0 37.9 -0.52   3.26 5.05  1
p4   p4   1 53.8 -1.55 888.00 3.76  1
p5   p5   1 47.5  0.25   5.70 2.89  1
p6   p6   0 45.0  0.15   4.65 1.87  0
p7   p7   0 52.0 -0.56   4.64 2.49  0
p8   p8   1 42.5    NA   5.77 2.68  1
p9   p9   0 29.7 -2.26   0.71 1.45  0
p10 p10   0 45.8 -1.32   3.26 0.85  0
```

Summary:

- Phenotypic data contained in an object of `gwaa.data-class` can be accessed using `phdata` functions

- You can add phenotypes using `add.phdata` function

- You can delete phenotypes using `del.phdata` function

4.3   Sub-setting and coercing gwaa.data

It is possible to sub-set the object, which stores the GWA data in the manner similar to that used for conventional `R` matrices and data frames. Very primitively, you may think of an object of class `gwaa.data` as a matrix whose rows correspond to study subjects and columns correspond to SNPs studied (though the actual object is a way more complicated). For example, if we would like to investigate what is the content of `srdta` for the first 5 people and 3 SNPs, we can run

```
> ssubs <- srdta[1:5,1:3]
> class(ssubs)

[1] "gwaa.data"
attr(,"package")
[1] "GenABEL"
```

As you can see, by sub-setting we obtained a smaller object of `gwaa.data`-`class`. The two major parts it contains are phenotypic data, which can be accessed through `phdata` (discussed in section 4.2):

```
> phdata(ssubs)

   id sex  age   qt1     qt2  qt3 bt
p1 p1   1 43.4 -0.58    4.46 1.43  0
p2 p2   1 48.2  0.80    6.32 3.90  1
p3 p3   0 37.9 -0.52    3.26 5.05  1
p4 p4   1 53.8 -1.55  888.00 3.76  1
p5 p5   1 47.5  0.25    5.70 2.89  1
```

and genotypc data, whcih can be accessed via `gtdata` function:

```
> gtdata(ssubs)

@nids = 5
@nsnps = 3
@nbytes = 2
@idnames = p1 p2 p3 p4 p5
@snpnames = rs10 rs18 rs29
@chromosome = 1 1 1
@coding =  08 0b 0c
@strand =  01 01 02
@map = 2500 3500 5750
@male = 1 1 0 1 1
@gtps =
40 40 40
40 40 00
```

whose content is not quite straightforward to read.

To get human-readable information, genotypic object should be coerced to a regular `R` data type, e.g. character, using `as.character()` function:

```
> as.character(gtdata(ssubs))

   rs10  rs18  rs29
p1 "T/T" "G/G" "G/G"
p2 "T/T" "G/G" NA
p3 "T/T" "G/G" NA
p4 "T/T" "G/G" NA
p5 "T/T" "G/A" "G/G"
```

Other useful coercion is to "numeric":

```
> as.numeric(gtdata(ssubs))

   rs10 rs18 rs29
p1    0    0    0
p2    0    0   NA
p3    0    0   NA
p4    0    0   NA
p5    0    1    0
```

Note that conversion to numeric happened according to the underlying genotype and the rules specified by SNP coding:

```
> coding(ssubs)
```

```
rs10 rs18 rs29
"TG" "GA" "GT"
```

– the genotype, which is made of the 'first' allele of the 'code' is converted to 0, the heterozygote to '1' and a himozygote for the second allele is converted to '2'.

For example, when coding is "GA", as is for the **rs18** (the second SNP), homozygotes for the first allele, as specified by coding ("G") are converted to zeros ("0"), heterozygotes are converted to ones ("1"), and homozygotes for the second allele ("A") are converted to twos ("2"). Clearly, when numerically converted data are used for association analysis, the effects will be estimated for the second allele, while first will be used as a reference.

Genotypic data converted to standard **R** format can be used in any further analysis.

Several useful genetic analysis libraries were developed for R. These include **genetics** (analysis of linkage disequilibrium and many other useful functions) and **haplo.stats** (analysis of association between traits and haplotypes). These use there own genetic data formats.

One can translate **GenABEL-package** genetic data to the format used by "genetics" library by **as.genotype()**:

```
> as.genotype(gtdata(ssubs))
```

```
NOTE: THIS PACKAGE IS NOW OBSOLETE.

  The R-Genetics project has developed an set of enhanced genetics
  packages to replace 'genetics'. Please visit the project homepage
  at http://rgenetics.org for informtion.


    rs10 rs18 rs29
p1  T/T  G/G  G/G
p2  T/T  G/G  <NA>
p3  T/T  G/G  <NA>
p4  T/T  G/G  <NA>
p5  T/T  G/A  G/G
```

To translate **GenABEL-package** data to the format used by "haplo.stats" you can use function **as.hsgeno()**

```
> as.hsgeno(gtdata(ssubs))
```

```
   rs10.a1 rs10.a2 rs18.a1 rs18.a2 rs29.a1 rs29.a2
p1       1       1       1       1       1       1
p2       1       1       1       1      NA      NA
p3       1       1       1       1      NA      NA
p4       1       1       1       1      NA      NA
p5       1       1       1       2       1       1
```

Actually, most users will not need the latter function, as `GenABEL-package` provides a functional interface to "haplo.stats" (such `GenABEL-package` functions as `scan.haplo()` and `scan.haplo.2D()`).

It is possible to select sub-sets of `gwaa.data-class` based not only on index (e.g. first 10 people and SNP number 33), but also based on names.

For example, if we would like to retrieve phenotypic data on people with IDs "p141", "p147" and "p2000", we can use

```
> phdata(srdta[c("p141","p147","p2000"),])

        id sex  age    qt1  qt2  qt3 bt
p141   p141   0 47.2  0.51 5.23 2.17  0
p147   p147   0 43.2  0.14 4.47 1.73  0
p2000 p2000   0 43.1 -1.53 2.78 2.70  1
```

here, the first part of expression sub-sets `srdta` on selected IDs, and the second tells which part of the retrieved sub-set we want to see. You can try `srdta[c("p141","p147","p2000"),]`, but be prepared to see long output, as all information will be reported.

In similar manner, we can also select on SNP name. For example, if we are interested to see information on SNPs "rs10" and "rs29" for above people, we can run

```
> phdata(srdta[c("p141","p147","p2000"),c("rs10","rs29")])

        id sex  age    qt1  qt2  qt3 bt
p141   p141   0 47.2  0.51 5.23 2.17  0
p147   p147   0 43.2  0.14 4.47 1.73  0
p2000 p2000   0 43.1 -1.53 2.78 2.70  1

> gtdata(srdta[c("p141","p147","p2000"),c("rs10","rs29")])

@nids = 3
@nsnps = 2
@nbytes = 1
@idnames = p141 p147 p2000
@snpnames = rs10 rs29
@chromosome = 1 1
@coding =  08 0c
@strand =  01 02
@map = 2500 5750
@male = 0 0 0
@gtps =
40 40
```

To see the actual genotypes for the above three people and two SNPs, use

```
> as.character(srdta[c("p141","p147","p2000"),c("rs10","rs29")])

      rs10  rs29
p141  "T/T" "G/G"
p147  "T/T" "G/G"
p2000 "T/G" "G/T"
```

or

```
> as.numeric(srdta[c("p141","p147","p2000"),c("rs10","rs29")])
```

```
      rs10 rs29
p141     0    0
p147     0    0
p2000    1    1
```

Exercise 3.   Exploring rs114

Explore genotypes for SNP "rs114"

1. What is the coding and which allele is the reference one?
2. What is the frequency of **non-reference** ("effective") allele in total sample?
3. What is the frequency of effective allele in male?
4. What is the frequency of effective allele in female?
5. What is the frequency of the **reference** allele in total sample, males and females?

Summary:

- It is possible to obtain subsets of objects of `gwaa.data-class` and `snp.data-class` using standard 2D sub-setting model `[i,j]`, where `i` corresponds to study subjects and `j` corresponds to SNPs.

- It is possible to provide ID and SNP names instead of indexes when sub-setting an object of class `gwaa.data-class`.

- Function `as.numeric()` converts genotypic data from `snp.data-class` to regular integer numbers, which can be used in analysis with R.

- Function `as.character()` converts genotypic data from `snp.data-class` to character format.

- Function `as.genotype()` converts genotypic data from `snp.data-class` to the format used by library `genetics`.

- Function `as.hsgeno()` converts genotypic data from `snp.data-class` to the format used by library `haplo.stats`.

4.4 Exploring genetic data

Implementation of function `summary()` to summarize genotypic part of `gwaa.data-class` is very useful in genetic data exploration and quality control (QC). Let us try application of this function to the `ssubs`:

```
> a <- summary(ssubs)
> a

     Chromosome Position Strand A1 A2 NoMeasured CallRate Q.2 P.11 P.12 P.22
rs10          1     2500      + T  G           5      1.0 0.0    5    0    0
rs18          1     3500      + G  A           5      1.0 0.1    4    1    0
rs29          1     5750      - G  T           2      0.4 0.0    2    0    0
     Pexact        Fmax       Plrt
rs10      1  0.0000000 1.0000000
rs18      1 -0.1111111 0.7386227
rs29      1  0.0000000 1.0000000
```

In the first section, the summary is generated for phenotypic data. In the second section, summary is generated for genotypic data. In this section, `NoMeasured` refers to the number of genotypes scores, `CallRate` to the proportion of these, `Q.2` is the frequency of the 'B' allele. The counts in three genotypic classes are provided next. `Pexact` refers to exact P-value for the test of Hardy-Weinberg equilibrium.

As you've seen above, an object of the class `gwaa.data-class` is sub-settable in standard manner: `[i,j]`, where `i` is an index of a study subject and `j` is an index of a SNP. Importantly, `i` could be a list of indexes:

```
> vec <- which(phdata(srdta)$age>=65)
> vec

 [1]   64  122  186  206  207  286  385  386  492  514  525  536  545  565  613
[16]  632  649  673  701  779  799  981 1008 1131 1186 1223 1281 1383 1471 1489
[31] 1501 1565 1584 1673 1679 1782 1821 1832 1866 1891 1953 2081 2085 2140 2224
[46] 2268 2291 2384 2420 2453

> summary(gtdata(srdta[vec,1:3]))

     Chromosome Position Strand A1 A2 NoMeasured CallRate       Q.2 P.11 P.12
rs10          1     2500      + T  G          48     0.96 0.1354167   36   11
rs18          1     3500      + G  A          47     0.94 0.2765957   25   18
rs29          1     5750      - G  T          45     0.90 0.1555556   32   12
     P.22    Pexact        Fmax      Plrt
rs10    1 1.0000000  0.02131603 0.8843626
rs18    4 0.7245853  0.04298643 0.7697067
rs29    1 1.0000000 -0.01503759 0.9188943
```

This shows summary of first three genotypes for people with age greater then or equal to 65 y.o. The same result may be achieved by sub-setting using a vector of logical values:

```
> vec <- (phdata(srdta)$age>=65)
> table(vec)

vec
FALSE   TRUE
 2450     50

> summary(gtdata(srdta[vec,1:3]))
```

```
      Chromosome Position Strand A1 A2 NoMeasured CallRate       Q.2 P.11 P.12
rs10           1     2500      + T  G          48     0.96 0.1354167   36   11
rs18           1     3500      + G  A          47     0.94 0.2765957   25   18
rs29           1     5750      - G  T          45     0.90 0.1555556   32   12
      P.22    Pexact        Fmax      Plrt
rs10     1 1.0000000  0.02131603 0.8843626
rs18     4 0.7245853  0.04298643 0.7697067
rs29     1 1.0000000 -0.01503759 0.9188943
```

or a list with IDs of study subjects:

```
> vec1 <- idnames(srdta)[vec]
> vec1
```

```
 [1] "p64"   "p122"  "p186"  "p206"  "p207"  "p286"  "p385"  "p386"  "p492"
[10] "p514"  "p525"  "p536"  "p545"  "p565"  "p613"  "p632"  "p649"  "p673"
[19] "p701"  "p779"  "p799"  "p981"  "p1008" "p1131" "p1186" "p1223" "p1281"
[28] "p1383" "p1471" "p1489" "p1501" "p1565" "p1584" "p1673" "p1679" "p1782"
[37] "p1821" "p1832" "p1866" "p1891" "p1953" "p2081" "p2085" "p2140" "p2224"
[46] "p2268" "p2291" "p2384" "p2420" "p2453"
```

```
> summary(gtdata(srdta[vec1,1:3]))
```

```
      Chromosome Position Strand A1 A2 NoMeasured CallRate       Q.2 P.11 P.12
rs10           1     2500      + T  G          48     0.96 0.1354167   36   11
rs18           1     3500      + G  A          47     0.94 0.2765957   25   18
rs29           1     5750      - G  T          45     0.90 0.1555556   32   12
      P.22    Pexact        Fmax      Plrt
rs10     1 1.0000000  0.02131603 0.8843626
rs18     4 0.7245853  0.04298643 0.7697067
rs29     1 1.0000000 -0.01503759 0.9188943
```

Let us explore the object returned by summary function when applied to
snp.data class in more details:

```
> a <- summary(gtdata(srdta[vec1,1:3]))
> class(a)
```

```
[1] "data.frame"
```

Thus, the object returned is a data.frame. Therefore it should have dimensions
and names:

```
> dim(a)
```

```
[1]  3 14
```

```
> names(a)
```

```
 [1] "Chromosome" "Position"   "Strand"     "A1"         "A2"
 [6] "NoMeasured" "CallRate"   "Q.2"        "P.11"       "P.12"
[11] "P.22"       "Pexact"     "Fmax"       "Plrt"
```
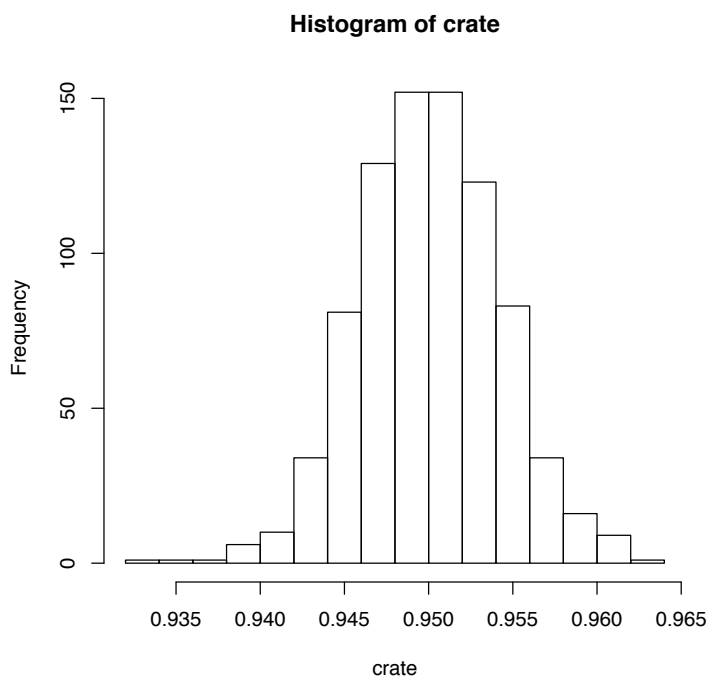
Histogram of crate

Figure 4.1: Histogram of the call rate

Indeed, we derived 8 characteristics ("NoMeasured", "CallRate", "Q.2", "P.11", "P.12", "P.22", "Pexact", "Chromosome") for the first 3 SNPs.

Exercise 4.   Testing HWE for 10 SNPs

Test if Hardy-Weinberg equilibrium holds for the first 10 SNPs

1. Total sample
2. In cases (`bt` is 1)
3. In controls (`bt` is 0)

Let us analyse the distribution of call rate in the whole study. For this, we first need to obtain the vector of call rates:

```
> sumgt <- summary(gtdata(srdta))
> crate <- sumgt[,"CallRate"]
```

This vector may be presented by a histogram

```
> hist(crate)
```

which shows that most SNPs have call rate between 93 and 97% (figure 4.1).

As next step, you would like to produce a summary table, showing how many markers had call rate lower than, say, 93%, between 93 and 95%, between 95 and 99% and more than 99%. You can use `catable()` command for that:

```
> catable(crate,c(.93,.95,.99))
```

```
     X<=0.93 0.93<X<=0.95 0.95<X<=0.99 X>0.99
No         0     415.000     418.000      0
Prop       0       0.498       0.502      0
```

Similar procedure may be applied to see deviation from HWE:

```
> hwp <- sumgt[,"Pexact"]
> catable(hwp,c(0.05/nsnps(srdta),0.01,0.05,0.1))
```

```
     X<=6.00240096038415e-05 6.00240096038415e-05<X<=0.01 0.01<X<=0.05
No                    2.000                        7.000      23.000
Prop                  0.002                        0.008       0.028
     0.05<X<=0.1   X>0.1
No        31.000 770.000
Prop       0.037   0.924
```

The first cut-off category will detect SNPs which are deviating from HWE at the Bonferroni-corrected P-level.

However, for these data it will make more sense to table cumulative distribution:

```
> catable(hwp,c(0.05/nsnps(srdta),0.01,0.05,0.1),cum=T)
```

```
     X<=6.00240096038415e-05 X<=0.01 X<=0.05 X<=0.1 all X
No                     2.000   9.000  32.000 63.000    833
Prop                   0.002   0.011   0.038  0.076      1
```

If you would like to investigate the minor allele frequency (MAF) distribution, the same logic would apply. First, derive MAF with

```
> afr <- sumgt[,"Q.2"]
> maf <- pmin(afr,(1.-afr))
```

Next, generate histograms for frequency and MAF:

```
> par(mfcol=c(2,1))
> hist(afr)
> hist(maf)
```

(shown at the figure 4.2) and then generate table describing frequency distribution:

```
> catable(afr,c(0.01,0.05,0.1,0.2,0.5,0.8,0.9,0.95,0.99))
```

```
     X<=0.01 0.01<X<=0.05 0.05<X<=0.1 0.1<X<=0.2 0.2<X<=0.5 0.5<X<=0.8
No    22.000       53.000      99.000    132.000    313.000    187.000
Prop   0.026        0.064       0.119      0.158      0.376      0.224
     0.8<X<=0.9 0.9<X<=0.95 0.95<X<=0.99 X>0.99
No       18.000        8.00        1.000      0
Prop      0.022        0.01        0.001      0
```

```
> catable(maf,c(0,0.01,0.05,0.1,0.2),cum=T)
```
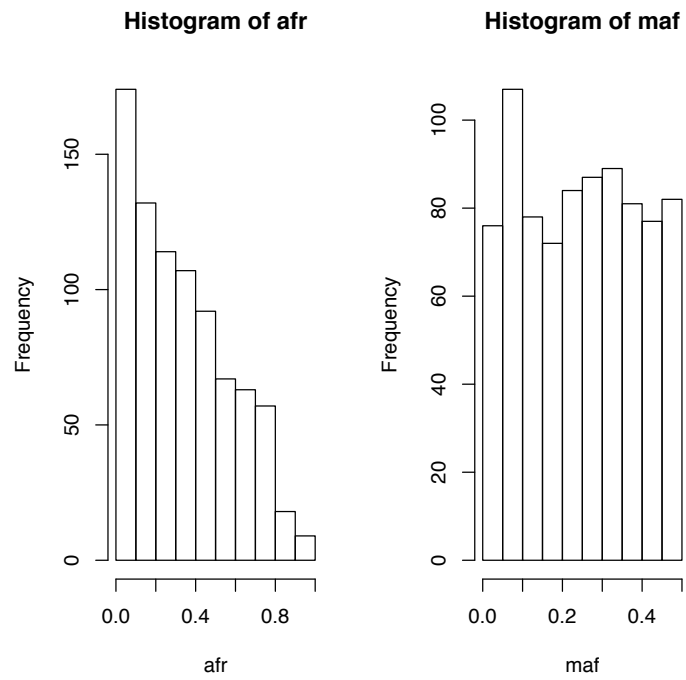
Figure 4.2: Histogram of the call rate

```
      X<=0 X<=0.01 X<=0.05 X<=0.1 X<=0.2 all X
No       0  22.000  76.000 183.00  333.0   833
Prop     0   0.026   0.091   0.22    0.4     1
```

Note that we used "0" as the first category – this will give you the number of monomorhic SNPs which we recommend to exclude from analysis.

Other function, `perid.summary`, produces summary SNP statistics per person. Let us try producing this summary for the first 10 people:

```
> perid.summary(srdta[1:10,])
```

```
    NoMeasured NoPoly       Hom     E(Hom)       Var            F    CallPP
p1         790    707 0.7987342 0.6600319 0.4048662  0.407986159 0.9483794
p2         792    714 0.7474747 0.6585152 0.5090002  0.260508049 0.9507803
p3         783    700 0.6206897 0.6618209 0.4332890 -0.121625581 0.9399760
p4         789    705 0.6070976 0.6601276 0.5251900 -0.156029161 0.9471789
p5         790    707 0.6658228 0.6619821 0.5288936  0.011362319 0.9483794
p6         787    703 0.7662008 0.6622227 0.3770418  0.307830275 0.9447779
p7         794    709 0.6309824 0.6587669 0.4527349 -0.081423884 0.9531813
p8         793    711 0.7023960 0.6587232 0.5163296  0.127968868 0.9519808
p9         788    711 0.6675127 0.6573272 0.5599395  0.029723748 0.9459784
p10        797    713 0.6587202 0.6614644 0.4889042 -0.008105999 0.9567827
          Het
p1  0.2012658
p2  0.2525253
p3  0.3793103
p4  0.3929024
p5  0.3341772
p6  0.2337992
p7  0.3690176
p8  0.2976040
p9  0.3324873
p10 0.3412798
```

This table lists the number of genotypes scored for the person, call rate, and heterozygosity. The outliers who have increased average heterozygosity may be suggestive of contaminated DNA samples.

Let us analyse the distribution of heterozygosity:

```
> het <- perid.summary(srdta)$Het
> mean(het)
```

```
[1] 0.3309457
```

```
> catable(het,c(0.1,0.25,0.3,0.35,0.5))
```

```
      X<=0.1 0.1<X<=0.25 0.25<X<=0.3 0.3<X<=0.35 0.35<X<=0.5 X>0.5
No     7.000      73.000     339.000    1281.000      800.00     0
Prop   0.003       0.029       0.136       0.512        0.32     0
```

```
> hist(het)
```
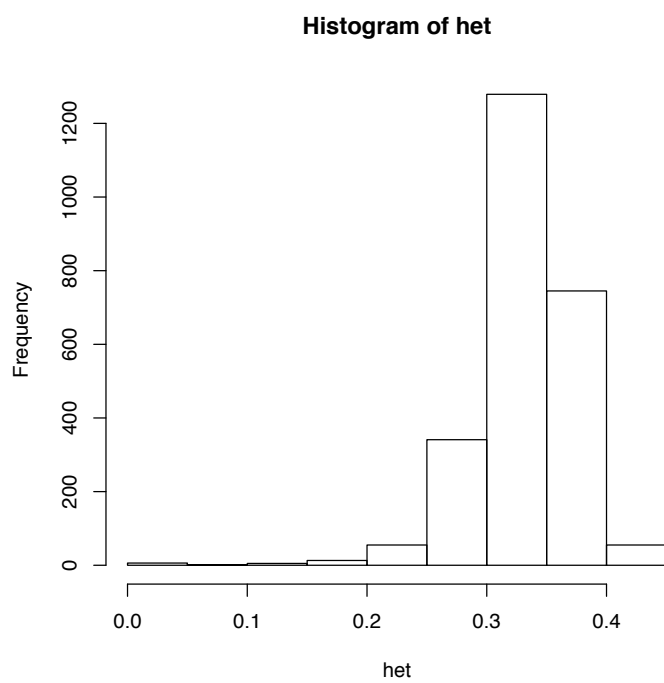
Histogram of het

Figure 4.3: Histogram of heterozygosity

The resulting histogram is presented in figure 4.3. It is easy to see that few people have very low heterozygosity, but there are no outliers with extremely high values.

In this section, we covered low-level functions `summary` and `perid.summary`. Based on these, an upper-level genetic data quality control function, `check.marker`, is based. That function will be covered in the next section.

Summary:

- When `summary()` function is applied to an `gtdata` subset of `gwaa.data-class`, it return summary statistics for SNPs, including exact test for Hardy-Weinberg equilibrium.

- When `perid.summary()` function is applied to an object of `gwaa.data-class` (or `gtdata` part of it), it return per-person summary statistics, including the call rate within this person and its' heterozygosity.

Exercise 5.   Characterizing call rate

Characterise the distribution of call rates within study subjects and produce a histogram. How many people have call rate below 93%?

4.5   Answers to exercises

Answer (Ex. 1) — Load the data with

```
> data(srdta)
```

Number of people:

```
> nids(srdta)
```

```
[1] 2500
```

Number of males:

```
> sum(male(srdta))
```

```
[1] 1275
```

Number of females:

```
> nids(srdta) - sum(male(srdta))
```

```
[1] 1225
```

... or you could get the same answer like this[1]:

```
> sum(male(srdta)==0)
```

```
[1] 1225
```

The proportion of males can be computed using above results

---

[1] This is something covered later in the section 4.3 ("Sub-setting and coercing gwaa.data")

```
> sum(male(srdta))/nids(srdta)
```

```
[1] 0.51
```

or by using `mean()` function:

```
> mean(male(srdta))
```

```
[1] 0.51
```

Answer (Ex. 2) — The names of markers located after 2,490,000 b.p. are

```
> vec <- (map(srdta)>2490000)
> snpnames(srdta)[vec]
```

```
[1] "rs9273" "rs9277" "rs9279" "rs9283"
```

The names of markers located between 1,100,000 and 1,105,000 b.p. are:

```
> vec <- (map(srdta)>1100000 & map(srdta)<1105000)
> snpnames(srdta)[vec]
```

```
[1] "rs4180" "rs4186" "rs4187"
```

Answer (Ex. 3) — To learn what allele of "rs114" is the reference you need to run

```
> coding(srdta)["rs114"]
```

```
rs114
 "AT"
```

Here, the first ("A") allele is the reference and thus the second ("T") is the effective one. Remember that when using `as.numeric` function to convert the genotypes to human-readable and `R`-operatable format, the homozygotes for reference will be coded as "0", heterozygotes as "1" and the non-reference ("effective") homozygotes will be coded as "2":

```
> table(as.character(gtdata(srdta[,"rs114"])),as.numeric(gtdata(srdta[,"rs114"])))
```

```
        0    1    2
  A/A 1868    0    0
  A/T    0  491    0
  T/T    0    0   34
```

To compute frequency of the effective allele of SNP "rs114" in total sample, you can go two ways. First, we can try to take a sum of all "rs114" genotypes and divide it by twice the number of people:

```
> a <- as.numeric(gtdata(srdta[,"rs114"]))
> sum(a)
```

```
[1] NA
```

This, however, returns NA, because some of the genotypes are missing. We can deal with this problem by running `sum()` with the option `na.rm=TRUE`:

```
> sum(a,na.rm=T)
```

```
[1] 559
```

so the number of 'effect' alleles is 559.

However, now we do not know what was the number of people for whom the genotype was measured! – `nids` would return the *total* number of people, but not the number of ones measured for "rs114".

This problem can be dealt with through using `is.na(A)` function which returns true when some element of `A` is not measured. Thus, the number of people with measured genotype for "rs114" is

```
> nids(srdta)
```

```
[1] 2500
```

```
> nmeasured <- sum(!is.na(a))
> nmeasured
```

```
[1] 2393
```

(note the "!" before `is.na`, which means NOT, so we get these elements which are not NA). The frequency of the 'effect' allele thus is

```
> sum(a,na.rm=T)/(2*nmeasured)
```

```
[1] 0.116799
```

An easier way would be to compute mean value of "rs114" with the `mean( ... ,na.rm=TRUE)` function and divide it by 2:

```
> mean(a,na.rm=T)/2
```

```
[1] 0.116799
```

To compute frequency of the effective allele of "rs114" in males, you can use

```
> amale <- as.numeric(gtdata(srdta[male(srdta)==1,"rs114"]))
> mean(amale,na.rm=T)/2
```

```
[1] 0.1164216
```

To compute frequency of the effective allele in females, you can use

```
> afemale <- as.numeric(gtdata(srdta[male(srdta)==0,"rs114"]))
> mean(afemale,na.rm=T)/2
```

```
[1] 0.1171942
```

The frequencies of the reference allele are computed very simply as one minus the frequency of the effective allele:

```
> 1 - mean(a,na.rm=T)/2
```

```
[1] 0.883201
```

```
> 1 - mean(amale,na.rm=T)/2
```

```
[1] 0.8835784
```

```
> 1 - mean(afemale,na.rm=T)/2
```

```
[1] 0.8828058
```

Answer (Ex. 4) — To test for HWE in first 10 SNPs in total sample

```
> summary(gtdata(srdta[,1:10]))
```

```
      Chromosome Position Strand A1 A2 NoMeasured CallRate        Q.2 P.11 P.12
rs10           1     2500      +  T  G       2384   0.9536 0.13255034 1792  552
rs18           1     3500      +  G  A       2385   0.9540 0.28029350 1232  969
rs29           1     5750      -  G  T       2374   0.9496 0.13774221 1763  568
rs65           1    13500      +  A  T       2378   0.9512 0.71972246  182  969
rs73           1    14250      +  A  G       2385   0.9540 0.01341719 2331   44
rs114          1    24500      +  A  T       2393   0.9572 0.11679900 1868  491
rs128          1    27000      -  G  T       2391   0.9564 0.02488499 2281  101
rs130          1    27250      +  A  G       2379   0.9516 0.69377890  222 1013
rs143          1    31000      +  T  G       2377   0.9508 0.47728229  655 1175
rs150          1    33250      +  C  A       2369   0.9476 0.65998312  267 1077
      P.22        Pexact          Fmax         Plrt
rs10    40 7.897327e-01 -0.006880004 7.355343e-01
rs18   184 7.608230e-01 -0.007017332 7.315304e-01
rs29    43 7.955141e-01 -0.007241148 7.227853e-01
rs65  1227 6.475412e-01 -0.010016746 6.246577e-01
rs73    10 1.792470e-12  0.303150234 1.281239e-12
rs114   34 7.663683e-01  0.005487764 7.894076e-01
rs128    9 9.408599e-06  0.129600629 1.000431e-05
rs130 1144 9.615127e-01 -0.002140946 9.168114e-01
rs143  547 6.512540e-01  0.009313705 6.497695e-01
rs150 1025 5.518478e-01 -0.012948436 5.281254e-01
```

To test it in cases

```
> summary(gtdata(srdta[phdata(srdta)$bt==1,1:10]))
      Chromosome Position Strand A1 A2 NoMeasured  CallRate        Q.2 P.11
rs10           1     2500      +  T  G       1197 0.9622186 0.13700919  888
rs18           1     3500      +  G  A       1189 0.9557878 0.28511354  605
rs29           1     5750      -  G  T       1176 0.9453376 0.14285714  859
rs65           1    13500      +  A  T       1185 0.9525723 0.72700422   83
rs73           1    14250      +  A  G       1187 0.9541801 0.01053075 1167
rs114          1    24500      +  A  T       1190 0.9565916 0.12184874  918
rs128          1    27000      -  G  T       1183 0.9509646 0.02409129 1129
rs130          1    27250      +  A  G       1188 0.9549839 0.68392256  117
rs143          1    31000      +  T  G       1192 0.9581994 0.48489933  320
rs150          1    33250      +  C  A       1182 0.9501608 0.66624365  127
      P.12 P.22        Pexact          Fmax         Plrt
rs10   290   19 4.635677e-01 -0.024514202 3.871421e-01
rs18   490   94 7.759191e-01 -0.010949158 7.052930e-01
rs29   298   19 2.832575e-01 -0.034722222 2.214580e-01
rs65   481  621 4.647357e-01 -0.022595469 4.348023e-01
rs73    15    5 3.988770e-08  0.393614304 2.423624e-08
rs114  254   18 8.924018e-01  0.002606831 9.285104e-01
rs128   51    3 2.747904e-02  0.083175674 3.157174e-02
rs130  517  554 8.407527e-01 -0.006569292 8.207476e-01
rs143  588  284 6.848365e-01  0.012522119 6.654994e-01
rs150  535  520 5.568363e-01 -0.017756050 5.409408e-01
```

in controls

```
> summary(gtdata(srdta[phdata(srdta)$bt==0,1:10]))
```

```
      Chromosome Position Strand A1 A2 NoMeasured  CallRate        Q.2 P.11
rs10           1     2500      +  T  G        1177 0.9453815 0.12744265  897
rs18           1     3500      +  G  A        1185 0.9518072 0.27426160  623
rs29           1     5750      -  G  T        1188 0.9542169 0.13215488  897
rs65           1    13500      +  A  T        1183 0.9502008 0.71344041   98
rs73           1    14250      +  A  G        1188 0.9542169 0.01641414 1154
rs114          1    24500      +  A  T        1192 0.9574297 0.11157718  941
rs128          1    27000      -  G  T        1197 0.9614458 0.02589808 1141
rs130          1    27250      +  A  G        1181 0.9485944 0.70491109  104
rs143          1    31000      +  T  G        1174 0.9429719 0.46805792  334
rs150          1    33250      +  C  A        1176 0.9445783 0.65306122  139
     P.12 P.22        Pexact           Fmax        Plrt
rs10  260   20 7.933317e-01  0.006751055 8.178295e-01
rs18  474   88 9.418133e-01 -0.004812165 8.683219e-01
rs29  268   23 5.288436e-01  0.016525913 5.737373e-01
rs65  482  603 8.871139e-01  0.003540522 9.031273e-01
rs73   29    5 6.941219e-06  0.244001185 5.537568e-06
rs114 236   15 8.846527e-01  0.001356081 9.627084e-01
rs128  50    6 7.745807e-05  0.172107564 7.552399e-05
rs130 489  588 8.887439e-01  0.004728114 8.710047e-01
rs143 581  259 8.604122e-01  0.006165442 8.326938e-01
rs150 538  499 7.968462e-01 -0.009574142 7.424986e-01
```

SNPs 'rs73' and 'rs128' are out of HWE (at $p \leq 0.05$) in total sample, and also in cases and controls.

Answer (Ex. 5) — To characterize ID call rate, you can run the following commands:

```
>   idsummary <- perid.summary(srdta)
>   idsummary[1:5,]
   NoMeasured NoPoly       Hom     E(Hom)       Var          F    CallPP
p1        790    790 0.7987342 0.6696986 0.5448255  0.3906601 0.9483794
p2        792    792 0.7474747 0.6685502 0.5390602  0.2381191 0.9507803
p3        783    783 0.6206897 0.6712102 0.4888671 -0.1536561 0.9399760
p4        789    789 0.6070976 0.6700900 0.4077382 -0.1909382 0.9471789
p5        790    790 0.6658228 0.6710232 0.4340010 -0.0158077 0.9483794
        Het
p1 0.2012658
p2 0.2525253
p3 0.3793103
p4 0.3929024
p5 0.3341772

>   idcall <- idsummary$Call
>   idcall[1:5]
[1] 0.9483794 0.9507803 0.9399760 0.9471789 0.9483794

>   catable(idcall,c(0.9,0.93,0.95,0.98,0.99))
     X<=0.9 0.9<X<=0.93 0.93<X<=0.95 0.95<X<=0.98 0.98<X<=0.99 X>0.99
No        0      13.000     1186.000      1301.00            0      0
Prop      0       0.005        0.474         0.52            0      0
```

```
>    table(idcall<0.93)
```

```
FALSE   TRUE
 2487     13
```

To produce a histogram of call rates, use `hist(idcall)`

Chapter 5

Genome-wide association analysis

In the first parts of this section you will be guided through a GWA analysis of a small data set. In the last part you will investigate a larger data set by yourself, do a verification study and will answer the questions. All data sets used assume a study in a relatively homogeneous population. Try to finish the first part in the morning and the second part in the afternoon.

Though only few thousands of markers located at four small chromosomes are used in the scan, we still going to call it Genome-Wide (GW), as the amount of data we will use is approaches the amount to be expected in a real experiment. However, because the regions are small, and the LD between SNPs is high, some specific features (e.g. relatively high residual inflation, which occurs because large proportion of SNPs are in LD with the reuly associated ones) are specific features of this data set, which are not observed in true GWA studies.

Start R and load **GenABEL-package** library by typing

```
> library(GenABEL)
```

and load the data which we will use in this section by

```
> data(ge03d2ex)
```

Investigate the objects loaded by command

```
> ls()
```

```
[1] "ge03d2ex"
```

The **ge03d2ex** is an object of the class **gwaa.data**:

```
> class(ge03d2ex)
```

```
[1] "gwaa.data"
attr(,"package")
[1] "GenABEL"
```

To check what are the names of variables in the phenotypic data frame, use

```
> names(phdata(ge03d2ex))
```

```
[1] "id"     "sex"    "age"    "dm2"    "height" "weight" "diet"   "bmi"
```

We can attach this data frame to the R search path by

```
> attach(phdata(ge03d2ex))
```

5.1   Data descriptives and first round of GWA analysis

Let us investigate what are the traits presented in the data frame loaded and what are the characteristics of the distribution by using specific GenABEL-package function descriptive.trait:

```
> descriptives.trait(ge03d2ex)
```

```
        No    Mean     SD
id      136      NA     NA
sex     136   0.529  0.501
age     136  49.069 12.926
dm2     136   0.632  0.484
height  135 169.440  9.814
weight  135  87.397 25.510
diet    136   0.059  0.236
bmi     135  30.301  8.082
```

You can see that phenotypic frame contains the data on 136 people; the data on sex, age, height, weight, diet and body mass index (BMI) are available. Our trait of interest is dm2 (type 2 diabetes). Note that every single piece of information in this data set is simulated; however, we tried to keep our simulations in a way we think the control of T2D may work.

You can produce a summary for cases and controls separately and compare distributions of the traits by

```
> descriptives.trait(ge03d2ex,by=dm2)
```

	No(by.var=0)	Mean	SD	No(by.var=1)	Mean	SD	Ptt	Pkw
id	50	NA	NA	86	NA	NA	NA	NA
sex	50	0.420	0.499	86	0.593	0.494	0.053	0.052
age	50	47.038	13.971	86	50.250	12.206	0.179	0.205
dm2	50	NA	NA	86	NA	NA	NA	NA
height	49	167.671	8.586	86	170.448	10.362	0.097	0.141
weight	49	76.534	17.441	86	93.587	27.337	0.000	0.000
diet	50	0.060	0.240	86	0.058	0.235	0.965	0.965
bmi	49	27.304	6.463	86	32.008	8.441	0.000	0.001

	Pexact
id	NA
sex	0.074
age	NA
dm2	NA

```
height     NA
weight     NA
diet    1.000
bmi        NA
```

Here, the `by` argument specifies the grouping variable. You can see that cases and controls are different in weight, which is expected, as T2D is associated with obesity.

Similarly, you can produce grand GW descriptives of the marker data by using

```
> descriptives.marker(ge03d2ex)

$`Minor allele frequency distribution`
      X<=0.01 0.01<X<=0.05 0.05<X<=0.1 0.1<X<=0.2     X>0.2
No   146.000      684.000     711.000     904.000  1555.000
Prop   0.036        0.171       0.178       0.226     0.389


$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
      X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No      46.000   71.000 125.000 275.000  4000
Prop     0.012    0.018   0.031   0.069     1


$`Distribution of proportion of successful genotypes (per person)`
      X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99 X>0.99
No    1.000           0            0      135.000      0
Prop  0.007           0            0        0.993      0


$`Distribution of proportion of successful genotypes (per SNP)`
      X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99    X>0.99
No   37.000       6.000      996.000     1177.000  1784.000
Prop  0.009       0.002        0.249        0.294     0.446


$`Mean heterozygosity for a SNP`
[1] 0.2582298

$`Standard deviation of the mean heterozygosity for a SNP`
[1] 0.1592255

$`Mean heterozygosity for a person`
[1] 0.2476507

$`Standard deviation of mean heterozygosity for a person`
[1] 0.04291038
```

It is of note that we can see inflation of the proportion of the tests for HWE at particular threshold, as compared to the expected. This may indicate poor genotyping quality and/or genetic stratification.

We can test the GW marker characteristics in controls by

```
> descriptives.marker(ge03d2ex,ids=(dm2==0))
```

```
$`Minor allele frequency distribution`
     X<=0.01 0.01<X<=0.05 0.05<X<=0.1 0.1<X<=0.2   X>0.2
No   233.000      676.000     671.000     898.000 1522.00
Prop   0.058        0.169       0.168       0.224    0.38


$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No          0    3.000  14.000  98.000  4000
Prop        0    0.001   0.003   0.024     1


$`Distribution of proportion of successful genotypes (per person)`
     X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99 X>0.99
No        0           0            0           50      0
Prop      0           0            0            1      0


$`Distribution of proportion of successful genotypes (per SNP)`
     X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99   X>0.99
No   37.000      49.000    1523.000             0 2391.000
Prop  0.009       0.012       0.381             0    0.598


$`Mean heterozygosity for a SNP`
[1] 0.2555009


$`Standard deviation of the mean heterozygosity for a SNP`
[1] 0.1618707


$`Mean heterozygosity for a person`
[1] 0.252572


$`Standard deviation of mean heterozygosity for a person`
[1] 0.04714886
```

Apparently, HWE distribution holds better in controls than in the total sample.

Let us check whether there are indications that deviation from HWE is due to cases. At this stage we are only interested in HWE distribution table, and therefore will ask to report the distrbution for cases (`dm2==1`) and report only the table two:

```
> descriptives.marker(ge03d2ex,ids=(dm2==1))[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No     45.000    79.00 136.000 268.000  4000
Prop    0.011     0.02   0.034   0.067     1
```

and for the controls

```
> descriptives.marker(ge03d2ex,ids=(dm2==0))[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No          0    3.000  14.000  98.000  4000
Prop        0    0.001   0.003   0.024     1
```

It seems that indeed excessive number of markers are out of HWE in cases. If no laboratory procedure (e.g. DNA extraction, genotyping, calling) were done for cases and controls separately, this may indicate possible genetic heterogeneity specific for cases.

In essence, 'descriptives.marker' function uses 'summary' function to generate HW P-values distribution. It may be interesting to generate this distribution using the 'summary' function You do not need to do so, but this example shows how you can generate summaries from underlying SNP-tables. First, we need to compute summary SNP statistics by

```
> s <- summary(gtdata(ge03d2ex[(dm2==1),]))
```

Note the you have produced the summary for the gtdata slot of ge03d2ex; this is the slot which actually contain all genetic data in special compressed format.

You can see first 5 rows of this very long summary table by

```
> s[1:5,]
```

```
          Chromosome Position Strand A1 A2 NoMeasured  CallRate        Q.2 P.11
rs1646456          1      653      +  C  G         85 0.9883721 0.32941176   34
rs4435802          1     5291      +  C  A         86 1.0000000 0.09302326   70
rs946364           1     8533      -  T  C         84 0.9767442 0.24404762   46
rs299251           1    10737      +  A  G         85 0.9883721 0.03529412   79
rs2456488          1    11779      +  G  C         85 0.9883721 0.33529412   38
          P.12 P.22     Pexact        Fmax       Plrt
rs1646456   46    5 0.05089075 -0.22493734 0.03233812
rs4435802   16    0 1.00000000 -0.10256410 0.19978917
rs946364    35    3 0.37413083 -0.12924909 0.21777250
rs299251     6    0 1.00000000 -0.03658537 0.63937447
rs2456488   37   10 0.81059718  0.02344356 0.82918345
```

Note that the column 'Pexact' provides exact HWE test *P*-values we need. We can extract these to a separate vector by

```
> pexcas <- s[,"Pexact"]
```

and do characterization of the cummulative distribution by

```
> catable(pexcas,c(0.001,0.01,0.05,0.1,0.5),cumulative=TRUE)
```

```
     X<=0.001 X<=0.01 X<=0.05  X<=0.1  X<=0.5 all X
No      79.00 136.000 268.000 390.000 1359.00  4000
Prop     0.02   0.034   0.067   0.098    0.34     1
```

You can generate the distribution for controls in similar manner.

Let us first try do GWA scan using the raw (before quality control) data. We will use the score test, as implemented in the qtscore()[1] function of GenABEL-package for testing:

```
> an0 <- qtscore(dm2,ge03d2ex,trait="binomial")
```

_____

[1] consider 'mlreg' function if you want to run true linear regression

The first argument used describes the model; here it is rather simple — the affection status, `dm2`, is supposed to depend on SNP genotype only.

You can see what information is computed by this function by using

```
> an0
```

```
***** 'scan.gwaa' object *****
*** Produced with:
qtscore(formula = dm2, data = ge03d2ex, trait.type = "binomial")
*** Test used: binomial
*** no. IDs used: 136 ( id199 id287 id300 , ... )
*** Lambda: 1.033102
*** Results table contains 4000 rows and 9 columns
*** Output for 10 first rows is:
            N      effB    se_effB      chi2.1df       P1df      effAB     effBB
rs1646456 135 0.9487666  5.0501959 0.0352941176 0.8509807 1.5558824 0.4831933
rs4435802 134 2.6822601  1.6765631 2.5595403237 0.1096305 2.5142857        NA
rs946364  134 0.6376645  0.4012104 2.5260391714 0.1119810 0.7277883 0.2869565
rs299251  135 0.5592122  0.5740215 0.9490674319 0.3299568 0.5569620        NA
rs2456488 135 0.8669860  1.5393112 0.3172278551 0.5732784 0.9736842 0.6907895
rs3712159 133 0.8282737  2.4803134 0.1115153279 0.7384255 0.5641026       Inf
rs4602970 136 1.5227297  2.2683336 0.4506421219 0.5020302 1.5131579        NA
rs175910  134 0.9949826 57.3970087 0.0003005055 0.9861693 0.5600000 4.0727273
rs1919938 136 0.9303079  3.5515057 0.0686164762 0.7933619 0.1160000 0.1958333
rs8892781 133 1.0953022 14.9055712 0.0053997133 0.9414220 1.0952381        NA
            chi2.2df       P2df
rs1646456 3.885667042 0.14329734
rs4435802 2.559540324 0.10963046
rs946364  3.020970009 0.22080286
rs299251  0.949067432 0.32995679
rs2456488 0.493411146 0.78137072
rs3712159 1.358996877 0.50687116
rs4602970 0.450642122 0.50203018
rs175910  5.012993241 0.08155345
rs1919938 6.001763944 0.04974318
rs8892781 0.005399713 0.94142198
    ...
___ Use 'results(object)' to get complete results table ___
```

Here, let us look at the 'Results table'. `P1df`, `P2df` and `Pc1df` are most interesting; the first two are vectors of 1 and 2 d.f. *P*-values obtained in the GWA analysis, the last one is 1 d.f. P-value corrected for inflation factor λ (which is presented in `lambda` object). `effB` corresponds to (approximate) Odds Ratios estimate for the SNP.

Let us see if there is evidence for the inflation of the test statistics; for that let us obtain λ with

```
> lambda(an0)
```

```
$estimate
[1] 1.033102
```

```
$se
[1] 0.0005639231

$iz0
[1] 1

$iz2
[1] 1
```

The estimate of λ is 1.03, suggesting inflation of the test and some degree of stratification. Though the value abtained seems to be small, it should be noted that λ grows linearly with smaple size, so for this small number of cases and controls the value is worrisome.

The λ is computed by regression in a Q-Q plot. Both estimation of λ and production of the $\chi^2 - \chi^2$ plot can be done using the `estlambda` function; this was already done automatically when running `qtscore` function, but let us repeat this manually:

```
> estlambda(an0[,"P1df"],plot=TRUE)

$estimate
[1] 1.033102

$se
[1] 0.0005639231
```

The corresponding $\chi^2 - \chi^2$ plot is presented in Figure 5.1.

> The 'se' produced by `estlambda` *can not* be used to test if inflation is significant and make conclusions about presence of significant or insignificant stratification.

We can also present the obtained results using the "Manhatten plot", where a SNP genomic position is on the X-axes and $-log_{10}$ of the P-value is shown on Y-axes:

```
> plot(an0)
```

The resulting plot is presented in the figure 5.2. By default, $-log_{10}(P-value)$ of not corrected 1 d.f. test are presented; see help to figure out how this behaviour can be changed.

We can also add the corrected P-values to the plot with

```
> add.plot(an0,df="Pc1df",col=c("lightblue","lightgreen"))
```

You can see that P-values corrected by genoic control are uniformly lower than the P-values from 'raw' analysis. This is to be expected as genomic control simply divides the 'raw' χ^2 statistics by a constant λ for all SNPs.

You can also generate a descriptive table for the "top" (as ranked by P-value) results by
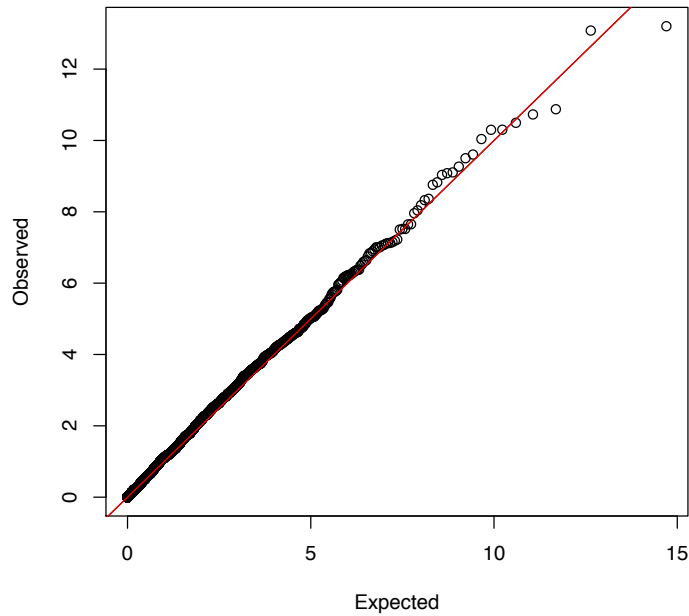
Figure 5.1: $\chi^2 - \chi^2$ plot for a GWA scan. Black line of slope 1: expected under no inflation; Red line: fitted slope.

```
> descriptives.scan(an0)
```

```
Summary for top 10 results, sorted by P1df
          Chromosome Position Strand A1 A2   N        effB     se_effB   chi2.1df
rs1719133           1  4495479      +  T  A 136 0.33729339  0.09282784  13.202591
rs2975760           3 10518480      +  A  T 134 3.80380024  1.05172986  13.080580
rs7418878           1  2808520      +  A  T 136 3.08123060  0.93431795  10.875745
rs5308595           3 10543128      -  C  G 133 3.98254950  1.21582875  10.729452
rs4804634           1  2807417      +  C  G 132 0.43411456  0.13400290  10.494949
rs3224311           2  6009769      +  G  C 135 3.15831710  0.98401491  10.301681
rs26325             3 10617781      +  A  C 135 0.09742793  0.03035964  10.298495
rs8835506           2  6010852      +  A  T 132 3.17720829  1.00274087  10.039543
rs3925525           2  6008501      +  C  G 135 2.98416931  0.96286458   9.605423
rs2521089           3 10487652      -  T  C 135 2.50239493  0.81179595   9.502064
                 P1df      effAB       effBB   chi2.2df          P2df         Pc1df
rs1719133 0.0002795623 0.4004237    0.000000 14.729116 0.0006333052 0.0003504258
rs2975760 0.0002983731 3.4545455   10.000000 13.547345 0.0011434877 0.0003732694
rs7418878 0.0009743183 3.6051282    4.871795 12.181064 0.0022642036 0.0011762545
rs5308595 0.0010544366 3.3171429         Inf 10.766439 0.0045930101 0.0012699705
rs4804634 0.0011970132 0.5240642    0.173913 11.200767 0.0036964462 0.0014362332
rs3224311 0.0013290907 3.4151786    4.250000 11.658283 0.0029405999 0.0015897278
rs26325   0.0013313876 0.1097724          NA 10.298495 0.0013313876 0.0015923930
```

qtscore(dm2, ge03d2ex, binomial)
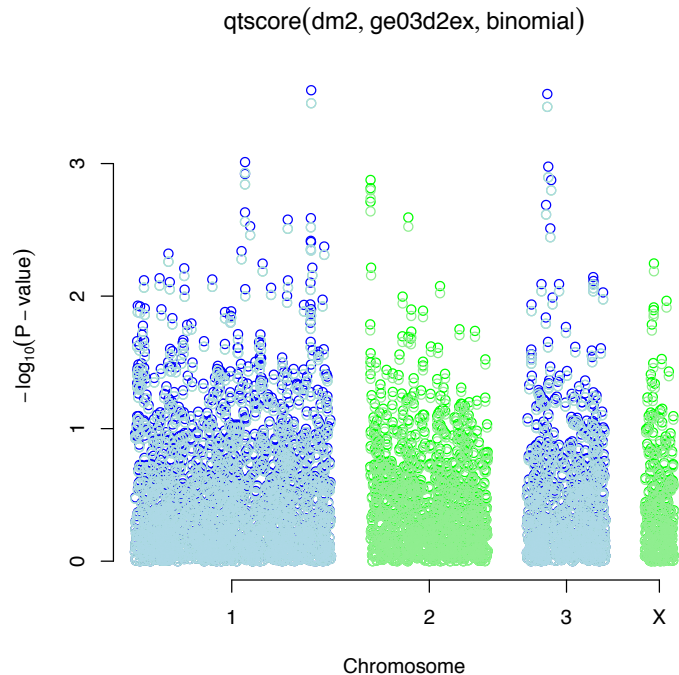
Figure 5.2: $-log_{10}(P-value)$ from the genome scan before QC procedure. Raw analysis: darker circles; corrected analysis: lighter circles

```
rs8835506 0.0015321522 3.4903846  4.125000 11.513206 0.0031618340 0.0018248521
rs3925525 0.0019400358 3.2380952  4.121212 10.782867 0.0045554384 0.0022944719
rs2521089 0.0020524092 2.5717703  4.772727  9.933387 0.0069661425 0.0024233145
```

or, equivalently, by 'summary(an0)'

Here you see top 10 results, sorted by P-value with 1 d.f. If you want to sort by the corrected P-value, you can use descriptives.scan(an0,sort="Pc1df"); to see more then 10 (e.g. 25) top results, use descriptives.scan(an0,top=25). You can combine all these options. Large part of results reports NA as effect estimates and 9.99 as *P-value* for 2 d.f. test – for these markers only two out of three possible genotypes were observed, and consequently 2 d.f. test could not be performed.

Now let us apply qtscore() function with times argument, which tells it to compute empirical GW (or experiment-wise) significance

```
> an0.e <- qtscore(dm2,ge03d2ex,times=200,quiet=TRUE)

  |
  |                                                                    |   0%
  |
  |===================================================================| 100%
```

(you may skip the 'quiet=TRUE' argument, then you will see progress)

Now let us generate the summary of the results

```
> descriptives.scan(an0.e,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome Position Strand A1 A2   N       effB    se_effB
rs1719133          1  4495479      +  T  A 136 -0.26520640 0.07298850
rs2975760          3 10518480      +  A  T 134  0.23406549 0.06471782
rs7418878          1  2808520      +  A  T 136  0.20890976 0.06334746
rs5308595          3 10543128      -  C  G 133  0.24455163 0.07465893
rs4804634          1  2807417      +  C  G 132 -0.20504486 0.06329344
rs3224311          2  6009769      +  G  C 135  0.21336328 0.06647611
rs26325            3 10617781      +  A  C 135 -0.48753666 0.15192190
rs1646456          1      653      +  C  G 135 -0.01234568 0.06571489
rs4435802          1     5291      +  C  A 134  0.18596491 0.11623851
rs946364           1     8533      -  T  C 134 -0.10965978 0.06899654
             chi2.1df P1df  Pc1df      effAB      effBB  chi2.2df P2df
rs1719133 13.20259149 0.415 0.525 -0.20808824 -0.7375000 14.729116   NA
rs2975760 13.08057990 0.450 0.555  0.27551020  0.4090909 13.547345   NA
rs7418878 10.87574494 0.900 0.935  0.28074054  0.3268398 12.181064   NA
rs5308595 10.72945213 0.915 0.950  0.25648324  0.4623656 10.766439   NA
rs4804634 10.49494904 0.940 0.970 -0.11938296 -0.3845238 11.200767   NA
rs3224311 10.30168114 0.955 0.985  0.27786338  0.3151515 11.658283   NA
rs26325   10.29849491 0.955 0.985 -0.48753666         NA 10.298495   NA
rs1646456  0.03529412 1.000 1.000  0.10047847 -0.1798246  3.885667   NA
rs4435802  2.55954032 1.000 1.000  0.18596491         NA  2.559540   NA
rs946364   2.52603917 1.000 1.000 -0.07302231 -0.3014706  3.020970   NA
```

Experimental-wise significance is computed by the empirical procedure, thus we consider P-values ≤ 0.05 to be GW-significant. However, none of the SNPs hits GW significance. If, actually, any did pass the threshold, we could not trust the results, because the distribution of the HWE test and presence of inflation factor for the association test statistics suggest that the data may contain multiple errors (indeed they do). Therefore before association analysis we need to do rigorous Quality Control (QC).

Note that at certain SNP, corrected *P-values* become equal to 1 – at this point order is arbitrary because sorting could not be done.

Summary:

- The `descriptives` family of functions was developed to facilitate production of tables which can be directly used in a manuscript — it is possible to save the output as a file, which can be open by Excel or Word. See e.g. `help(descriptives.trait)` for details.

- The inflation of test statistics compared to null (1 d.f.) may be estimated with `estlambda` function.

5.2 Genetic data QC

The major genetic data QC function of `GenABEL-package` is `check.marker()`.
We will now use that to perform our data QC; the output is rather self-explaining.
Because of possible genetic heterogeneity of the study data it is good idea to
skip Hardy-Weinberg checks in the first round of QC. This can be achieved by
setting HWE P-value selection threshold to zero (`p.level=0`):

```
> qc1 <- check.marker(ge03d2ex,p.level=0)

Excluding people/markers with extremely low call rate...
4000 markers and 136 people in total
0 people excluded because of call rate < 0.1
6 markers excluded because of call rate < 0.1
Passed: 3994 markers and 136 people

Running sex chromosome checks...
197 heterozygous X-linked male genotypes found
1 X-linked markers are likely to be autosomal (odds > 1000 )
2 male are likely to be female (odds > 1000 )
0 female are likely to be male (odds > 1000 )
0 people have intermediate X-chromosome inbreeding (0.5 > F > 0.5)
If these people/markers are removed, 0 heterozygous male genotypes are left
Passed: 3993 markers and 134 people


no X/Y/mtDNA-errors to fix



RUN 1
3993 markers and 134 people in total
304 (7.613323%) markers excluded as having low (<1.865672%) minor allele frequency
36 (0.9015778%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
1 (0.7462687%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2747262 (s.e. 0.03721277)
3 (2.238806%) people excluded because too high autosomal heterozygosity (FDR <1%)
Excluded people had HET >= 0.4856887
Mean IBS is 0.7721942 (s.e. 0.02066635), as based on 2000 autosomal markers
2 (1.492537%) people excluded because of too high IBS (>=0.95)
In total, 3653 (91.4851%) markers passed all criteria
In total, 128 (95.52239%) people passed all criteria

RUN 2
3653 markers and 128 people in total
80 (2.189981%) markers excluded as having low (<1.953125%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2748341 (s.e. 0.01695461)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7674474 (s.e. 0.01813738), as based on 2000 autosomal markers
```

```
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 3573 (97.81002%) markers passed all criteria
In total, 128 (100%) people passed all criteria


RUN 3
3573 markers and 128 people in total
0 (0%) markers excluded as having low (<1.953125%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2748341 (s.e. 0.01695461)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7730395 (s.e. 0.01805395), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 3573 (100%) markers passed all criteria
In total, 128 (100%) people passed all criteria
```

Note that normally you will *NEVER* run this simple form of the QC function
– you should always provide a number of thresholds specific to the platform
you used for genotyping. See help to `check.marker()` for detailed list of argu-
ments. Default values used by the function are rather relaxed compared to the
thresholds routinely used nowadays with most of the platforms.

> **The computation of all pairwise proportion of alleles identical-by-state (IBS)
> by `ibs()` function, which is also called by `check.marker()` may take quite some
> time, which is proportional to the square of the number of subjects. This
> is not a problem with the small number of people we use for this example
> or when modern computers are used. However, the computers in the Nihes
> computer room are very old. Therefore be prepared to wait for long time
> when you will do a self-exercise with 1,000 people.**

From the output you can see that QC starts with checking the data for SNPs
and people with extremely low call rate. Six markers are excluded from further
analysis due to very low call rate. Next, X-chromosomal errors are identified.
The function finds out that all errors (heterozygous male X-genotypes) are due
to two people with wrong sex assigned and one marker, which looks like an
autosomal one. This actually could be a marker from pseudoautosomal region,
which should have been arranged as a separate "autosome". Nine people are
found to have intermediate inbreeding at the X-chromosome and also excluded
from analysis.

Then, the procedure finds the markers with low call rate (≤ 0.95 by default)
across people, markers with low MAF (by default, low MAF is defined as less
than few copies of the rare allele, see help for details); people with low call rate
(default value: ≤ 0.95) across SNPs, people with extreme heterozygosity (at
FDR 0.01) and these who have GW IBS ≥ 0.95. These default parameters may
be changed if you wish (consult help).

Because some of the people fail to pass the tests, the data set is not guar-
anteed to be really "clean" after single iteration, e.g. some marker may not

pass the call threshold after we exclude few informative (but apparently having low quality) samples. Therefore the QC is repeated iteratively until no further errors are found.

You can generate short summary of QC by marker and by person through

```
> summary(qc1)
```

```
$`Per-SNP fails statistics`
          NoCall NoMAF NoHWE Redundant Xsnpfail
NoCall        42     0     0         0        0
NoMAF         NA   384     0         0        0
NoHWE         NA    NA     0         0        0
Redundant     NA    NA    NA         0        0
Xsnpfail      NA    NA    NA        NA        1
```

```
$`Per-person fails statistics`
           IDnoCall HetFail IBSFail isfemale ismale isXXY otherSexErr
IDnoCall          1       0       0        0      0     0           0
HetFail          NA       3       0        0      0     0           0
IBSFail          NA      NA       2        0      0     0           0
isfemale         NA      NA      NA        2      0     0           0
ismale           NA      NA      NA       NA      0     0           0
isXXY            NA      NA      NA       NA     NA     0           0
otherSexErr      NA      NA      NA       NA     NA    NA           0
```

Note that the original data, ge03d2ex, are not modified during the procedure; rather, check.markers() generate a list of markers and people which pass or do not pass certain QC criteria. The objects returned by check.markers() are:

```
> names(qc1)
```

```
 [1] "nofreq"    "nocall"    "nohwe"     "Xmrkfail"  "hetfail"
 [6] "idnocall"  "ibsfail"   "isfemale"  "ismale"    "otherSexErr"
[11] "snpok"     "idok"      "call"
```

The element idok provides the list of people who passed all QC criteria, and snpok provides the list of SNPs which passed all criteria. You can easily generate a new data set, which will consist only of these people and markers by

```
> data1 <- ge03d2ex[qc1$idok,qc1$snpok]
```

If there are any residual sporadic X-errors (male heterozygosity), these can (and should!) be fixed (set to NA) by

```
> data1 <- Xfix(data1)
```

```
no X/Y/mtDNA-errors to fix
```

Applying this function does not make any difference for the example data set, but you will need to use it for the bigger data set.

At this point, we are ready to work with the new, cleaned, data set data1. However, if we try

```
> length(dm2)
```

```
[1] 136
```

we can see that the original phenotypic data are attached to the search path (there are only 128 people left in the 'clean' data set). Therefore we need to detach the data by

```
> detach(phdata(ge03d2ex))
```

and attach new data by

```
> attach(phdata(data1))
```

At this stage, let us check if the first round of QC improves the fit of genetic data to HWE, which may have been violated due to by genotyping errors which we hopefully (at least partly!) eliminated:

```
> descriptives.marker(data1)[2]
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
      X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No      44.000   66.000 117.000 239.000  3573
Prop     0.012    0.018   0.033   0.067     1
```

```
> descriptives.marker(data1[dm2==1,])[2]
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
      X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No      46.000    70.00 127.000 228.000  3573
Prop     0.013     0.02   0.036   0.064     1
```

```
> descriptives.marker(data1[dm2==0,])[2]
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
      X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No           0        0   7.000  91.000  3573
Prop         0        0   0.002   0.025     1
```

You can see that the fit to HWE improved, but cases are still have excess number of markers out of HWE. This may be due to genetic sub-structure.

5.3 Finding genetic sub-structure

Now, we are ready for the second round of QC – detection of genetic outliers which may contaminate our results. We will detect genetic outliers using a technique, which resembles the one suggested by Price at al.

As the first step, we will compute a matrix of genomic kinship between all pairs of people, using only autosomal[2] markers by

```
> data1.gkin <- ibs(data1[,autosomal(data1)],weight="freq")
```

---

[2]the list of autosomal markers contained in `data` is returned by `autosomla(data)` function

> This step may take few minutes on large data sets or when using old computers!

You can see the 5x5 upper left sub-matrix by

```
> data1.gkin[1:5,1:5]
```

```
               id199         id300         id403         id415         id666
id199   0.494427766 3255.00000000 3253.00000000 3241.00000000 3257.0000000
id300  -0.011754266    0.49360296 3261.00000000 3250.00000000 3264.0000000
id403  -0.012253378   -0.01262949    0.50541775 3247.00000000 3262.0000000
id415  -0.001812109    0.01388179   -0.02515438    0.53008236 3251.0000000
id666  -0.018745051   -0.02127344    0.02083723   -0.02014175    0.5306584
```

The numbers below the diagonal show the genomic estimate of kinship (aka 'genomic kinship' or 'genome-wide IBD'), the numbers on the diagonal correspond to 0.5 plus the genomic homozigosity, and the numbers above the diagonal tell how many SNPs were typed successfully for both subjects (thus the IBD estimate is derived using this number of SNPs).

Second, we transform this matrix to a distance matrix using standard `R` command

```
> data1.dist <- as.dist(0.5-data1.gkin)
```

Finally, we perform Classical Multidimensional Scaling by

```
> data1.mds <- cmdscale(data1.dist)
```

by default, the first two principal components are computed and returned.

> This may take few minutes on large data sets or when using old computers!

We can present the results graphically by

```
> plot(data1.mds)
```

The resulting plot is presented in figure 5.3. Each point on the plot corresponds to a person, and the 2D distances between points were fitted to be as close as possible to these presented in the original IBS matrix. You can see that study subjects clearly cluster in two groups.

You can identify the points belonging to clusters by

```
> km <- kmeans(data1.mds,centers=2,nstart=1000)
> cl1 <- names(which(km$cluster==1))
> cl2 <- names(which(km$cluster==2))
> if (length(cl1)>length(cl2)) {x<-cl2;cl2<-cl1;cl1<-x}
> cl1

[1] "id2097" "id6954" "id2136" "id858"
```
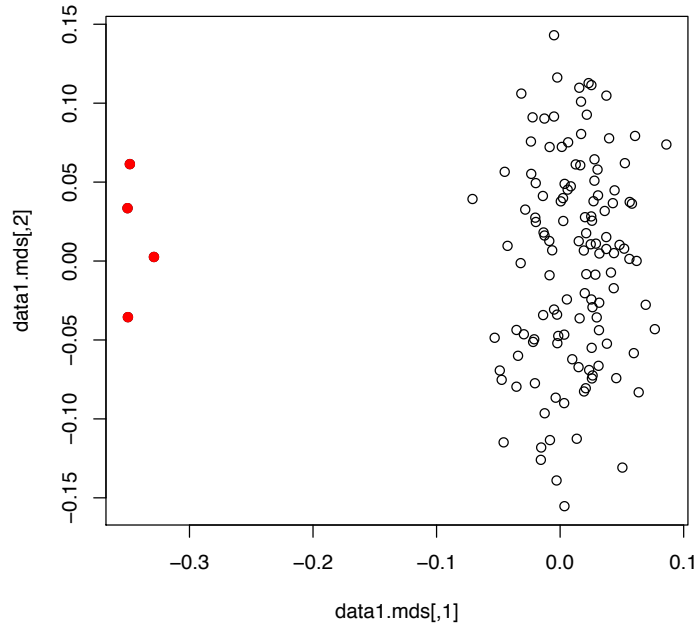
Figure 5.3: Mapping samples on the space of the first two Principle Components resulting from analysis of genomic kinship. Red dots identify genetic outliers

```
> cl2

  [1] "id199"  "id300"  "id403"  "id415"  "id666"  "id689"  "id765"  "id830"
  [9] "id908"  "id980"  "id994"  "id1193" "id1423" "id1505" "id1737" "id1827"
 [17] "id1841" "id2068" "id2094" "id2151" "id2317" "id2618" "id2842" "id2894"
 [25] "id2985" "id3354" "id3368" "id3641" "id3831" "id3983" "id4097" "id4328"
 [33] "id4380" "id4395" "id4512" "id4552" "id4710" "id4717" "id4883" "id4904"
 [41] "id4934" "id4961" "id5014" "id5078" "id5274" "id5275" "id5454" "id5853"
 [49] "id5926" "id5969" "id6237" "id6278" "id6352" "id6501" "id6554" "id6663"
 [57] "id6723" "id7499" "id7514" "id7541" "id7598" "id7623" "id7949" "id8059"
 [65] "id8128" "id8281" "id8370" "id8400" "id8433" "id8772" "id8880" "id8890"
 [73] "id8957" "id8996" "id9082" "id9901" "id9930" "id1857" "id2528" "id4862"
 [81] "id9184" "id5677" "id6407" "id5472" "id2135" "id8545" "id4333" "id1670"
 [89] "id1536" "id6917" "id6424" "id3917" "id9628" "id9635" "id4729" "id5190"
 [97] "id6399" "id6062" "id620"  "id1116" "id6486" "id41"   "id677"  "id4947"
[105] "id9749" "id6428" "id7488" "id5949" "id2924" "id5783" "id4096" "id903"
[113] "id9049" "id185"  "id1002" "id362"  "id9014" "id5044" "id2749" "id2286"
[121] "id4743" "id4185" "id8330" "id6934"
```

Four outliers are presented in the smaller cluster.

> **Now you will need to use the BIGGER cluster for to select study subjects.**
> **Whether this will be `cl1` or `cl2` in you case, is totally random.**

We can form a data set which is free from outliers by using only people from the bigger cluster:

```
> data2 <- data1[cl2,]
```

After we dropped the outliers, we need to repeat QC using `check.markers()`. At this stage, we want to allow for HWE checks (we will use only controls and exclude markers with FDR ≤ 0.2):

```
> qc2 <- check.marker(data2,hweids=(phdata(data2)$dm2==0),fdr=0.2)
```

```
Excluding people/markers with extremely low call rate...
3573 markers and 124 people in total
0 people excluded because of call rate < 0.1
0 markers excluded because of call rate < 0.1
Passed: 3573 markers and 124 people

Running sex chromosome checks...
0 heterozygous X-linked male genotypes found
0 X-linked markers are likely to be autosomal (odds > 1000 )
0 male are likely to be female (odds > 1000 )
0 female are likely to be male (odds > 1000 )
0 people have intermediate X-chromosome inbreeding (0.5 > F > 0.5)
If these people/markers are removed, 0 heterozygous male genotypes are left
Passed: 3573 markers and 124 people

no X/Y/mtDNA-errors to fix


RUN 1
3573 markers and 124 people in total
40 (1.119507%) markers excluded as having low (<2.016129%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (FDR <0.2)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2780246 (s.e. 0.01642372)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7712231 (s.e. 0.01238305), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 3533 (98.88049%) markers passed all criteria
In total, 124 (100%) people passed all criteria

RUN 2
3533 markers and 124 people in total
0 (0%) markers excluded as having low (<2.016129%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
```

```
0 (0%) markers excluded because they are out of HWE (FDR <0.2)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2780246 (s.e. 0.01642372)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7716007 (s.e. 0.01237596), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 3533 (100%) markers passed all criteria
In total, 124 (100%) people passed all criteria

> summary(qc2)

$`Per-SNP fails statistics`
         NoCall NoMAF NoHWE Redundant Xsnpfail
NoCall        0     0     0         0        0
NoMAF        NA    40     0         0        0
NoHWE        NA    NA     0         0        0
Redundant    NA    NA    NA         0        0
Xsnpfail     NA    NA    NA        NA        0

$`Per-person fails statistics`
          IDnoCall HetFail IBSFail isfemale ismale isXXY otherSexErr
IDnoCall         0       0       0        0      0     0           0
HetFail         NA       0       0        0      0     0           0
IBSFail         NA      NA       0        0      0     0           0
isfemale        NA      NA      NA        0      0     0           0
ismale          NA      NA      NA       NA      0     0           0
isXXY           NA      NA      NA       NA     NA     0           0
otherSexErr     NA      NA      NA       NA     NA    NA           0
```

> **If the procedure did not run, check previous Note.**

Indeed, in the updated data set few markers do not pass our QC criteria and we need to drop a few markers. This is done by

```
> data2 <- data2[qc2$idok,qc2$snpok]
```

This is going to be our final analysis data set, therefore let us attach the phenotypic data to the search path, then we do not need to type `phdata(data2)$...` to access `dm2` status or other variables:

```
> detach(phdata(data1))
> attach(phdata(data2))
> ####
> #ge03d2ex.clean <- data2
> #save(ge03d2ex.clean,file="ge03d2ex.clean.RData")
> ####
```

Before proceeding to GWA, let us check if complete QC improved the fit of genetic data to HWE:

```
> descriptives.marker(data2)[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No           1    2.000   2e+01 101.000  3533
Prop         0    0.001   6e-03   0.029     1

> descriptives.marker(data2[phdata(data2)$dm2==1,])[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No           0        1  17.000  79.000  3533
Prop         0        0   0.005   0.022     1

> descriptives.marker(data2[phdata(data2)$dm2==0,])[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No           0        0   7.000  91.000  3533
Prop         0        0   0.002   0.026     1
```

You can see that now there is no excessive number of SNPs out of HWE in the sample (total, or cases, or controls)

5.4 GWA association analysis

Let us start again with descriptives of the phenotypic and marker data

```
> descriptives.trait(data2,by=dm2)
```

	No(by.var=0)	Mean	SD	No(by.var=1)	Mean	SD	Ptt	Pkw
id	47	NA	NA	77	NA	NA	NA	NA
sex	47	0.426	0.500	77	0.597	0.494	0.065	0.064
age	47	45.752	13.313	77	50.593	12.465	0.047	0.062
dm2	47	NA	NA	77	NA	NA	NA	NA
height	46	167.911	8.689	77	170.423	10.646	0.157	0.213
weight	46	77.015	17.528	77	94.160	26.963	0.000	0.000
diet	47	0.064	0.247	77	0.065	0.248	0.981	0.981
bmi	46	27.424	6.598	77	32.235	8.335	0.001	0.001

	Pexact
id	NA
sex	0.067
age	NA
dm2	NA
height	NA
weight	NA
diet	1.000
bmi	NA

You can see that relation to weight is maintained in this smaller, but hopefully cleaner, data set; moreover, relation to age becomes boundary significant.

If you check descriptives of markers (only HWE part shown)

```
> descriptives.marker(data2)[2]
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No          1    2.000    2e+01 101.000  3533
Prop        0    0.001    6e-03   0.029     1
```

you can see that the problems with HWE are apparently fixed; we may guess
that these were caused by the Wahlund's effect.

Run the score test on the cleaned data by

```
> data2.qt <- qtscore(dm2,data2,trait="binomial")
```

and check lambda

```
> lambda(data2.qt)
```

```
$estimate
[1] 1.036958
```

```
$se
[1] 0.0007178
```

```
$iz0
[1] 1.009061
```

```
$iz2
[1] 1
```

there is still some inflation, which is explained by the fact that we investigate
only few short chromosomes with high LD and few causative variants.

Produce the association analysis plot by

```
> plot(data2.qt,df="Pc1df")
```

(figure 5.4).

Produce the scan summary by

```
> descriptives.scan(data2.qt,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome Position Strand A1 A2   N      effB   se_effB   chi2.1df
rs1719133          1  4495479      +  T   A 124 0.3167801 0.08614528 13.522368
rs4804634          1  2807417      +  C   G 121 0.4119844 0.12480696 10.896423
rs8835506          2  6010852      +  A   T 121 3.5378209 1.08954331 10.543448
rs4534929          1  4474374      +  C   G 123 0.4547151 0.14160410 10.311626
rs1013473          1  4487262      +  A   T 124 2.7839368 0.86860745 10.272393
rs3925525          2  6008501      +  C   G 124 3.2807631 1.03380675 10.070964
rs3224311          2  6009769      +  G   C 124 3.2807631 1.03380675 10.070964
rs2975760          3 10518480      +  A   T 123 3.1802120 1.00916993  9.930784
rs2521089          3 10487652      -  T   C 123 2.7298775 0.87761175  9.675679
rs1048031          1  4485591      +  G   T 122 0.4510793 0.14548378  9.613391
                P1df     effAB     effBB   chi2.2df        P2df       Pc1df
```

qtscore(dm2, data2, binomial)
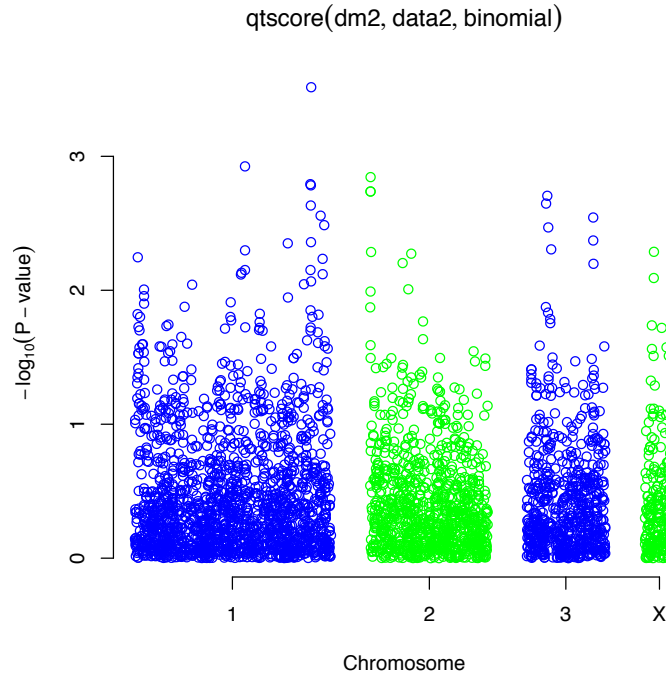
Figure 5.4: $-log_{10}(CorrectedP-value)$ from the genome scan after the QC procedure

```
rs1719133 0.0002357368 0.3740771 0.0000000 14.677906 0.0006497303 0.0003048399
rs4804634 0.0009635013 0.6315789 0.1739130 12.375590 0.0020543516 0.0011885463
rs8835506 0.0011660066 4.0185185 4.0185185 12.605556 0.0018312105 0.0014292471
rs4534929 0.0013219476 0.4830918 0.1739130 10.510272 0.0052206352 0.0016136479
rs1013473 0.0013503553 3.0495868 5.8441558 10.926296 0.0042401869 0.0016471605
rs3925525 0.0015062424 3.6923077 4.0000000 11.765985 0.0027864347 0.0018306610
rs3224311 0.0015062424 3.6923077 4.0000000 11.765985 0.0027864347 0.0018306610
rs2975760 0.0016253728 3.0000000 8.0000000 10.172522 0.0061810866 0.0019704699
rs2521089 0.0018672326 3.0147059 5.0000000 10.543296 0.0051351403 0.0022533033
rs1048031 0.0019316360 0.4844720 0.1714286  9.965696 0.0068545128 0.0023284084
```

Comparison with the top 10 from the scan before QC shows that results changed substantially with only few markers overlapping.

You can see similar results when accessing empirical GW significance:

```
> data2.qte <- qtscore(dm2,data2,times=200,quiet=TRUE,trait="binomial")

  |
  |                                                                     |   0%
  |
  |=====================================================================| 100%

> descriptives.scan(data2.qte,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome Position Strand A1 A2   N      effB   se_effB  chi2.1df
rs1719133          1  4495479      +  T  A 124 0.3167801 0.08614528 13.522368
rs4804634          1  2807417      +  C  G 121 0.4119844 0.12480696 10.896423
rs8835506          2  6010852      +  A  T 121 3.5378209 1.08954331 10.543448
rs4534929          1  4474374      +  C  G 123 0.4547151 0.14160410 10.311626
rs1013473          1  4487262      +  A  T 124 2.7839368 0.86860745 10.272393
rs1048031          1  4485591      +  G  T 122 0.4510793 0.14548378  9.613391
rs3925525          2  6008501      +  C  G 124 3.2807631 1.03380675 10.070964
rs3224311          2  6009769      +  G  C 124 3.2807631 1.03380675 10.070964
rs2521089          3 10487652      -  T  C 123 2.7298775 0.87761175  9.675679
rs2975760          3 10518480      +  A  T 123 3.1802120 1.00916993  9.930784
          P1df Pc1df     effAB     effBB  chi2.2df P2df
rs1719133 0.340 0.405 0.3740771 0.0000000 14.677906 0.545
rs4804634 0.865 0.925 0.6315789 0.1739130 12.375590 0.950
rs8835506 0.920 0.965 4.0185185 4.0185185 12.605556 0.925
rs4534929 0.965 0.970 0.4830918 0.1739130 10.510272 1.000
rs1013473 0.965 0.970 3.0495868 5.8441558 10.926296 1.000
rs1048031 0.985 0.985 0.4844720 0.1714286  9.965696 1.000
rs3925525 0.965 0.985 3.6923077 4.0000000 11.765985 0.990
rs3224311 0.965 0.985 3.6923077 4.0000000 11.765985 0.990
rs2521089 0.985 0.985 3.0147059 5.0000000 10.543296 1.000
rs2975760 0.970 0.985 3.0000000 8.0000000 10.172522 1.000
```

Again, none of the SNPs hits GW 5% significance. Still, you can see that after QC top markers achieve somewhat "better" significance.

In the last part, we will do several adjusted and stratified analyses. Only empirical P-values will be estimated to make the story shorter. To adjust for sex and age, we can

```
> data2.qtae <- qtscore(dm2~sex+age,data2,times=200,quiet=T,trait="binomial")

  |
  |                                                                    |   0%
  |
  |====================================================================| 100%

> descriptives.scan(data2.qtae)

Summary for top 10 results, sorted by P1df
          Chromosome Position Strand A1 A2   N      effB   se_effB  chi2.1df
rs1719133          1  4495479      +  T  A 124 0.5057834 0.1386464 13.307976
rs2398949          1  4828375      -  A  C 122 0.4163599 0.1253217 11.037861
rs4804634          1  2807417      +  C  G 121 0.5811444 0.1769232 10.789433
rs7522488          3 11689797      -  G  A 123 1.8718644 0.5707656 10.755565
rs8835506          2  6010852      +  A  T 121 2.0575431 0.6501899 10.014228
rs1037237          3 11690145      +  C  G 124 1.8144282 0.5735660 10.007206
rs3925525          2  6008501      +  C  G 124 2.0202686 0.6406356  9.944799
rs3224311          2  6009769      +  G  C 124 2.0202686 0.6406356  9.944799
rs1013473          1  4487262      +  A  T 124 1.8148181 0.5864622  9.576043
rs4534929          1  4474374      +  C  G 123 0.6262025 0.2045254  9.374220
```

```
          P1df Pc1df     effAB      effBB   chi2.2df  P2df
rs1719133 0.440 0.600 0.4853657 0.2242383 13.367455 0.860
rs2398949 0.820 0.910 0.3110042 2.8197228 16.111010 0.430
rs4804634 0.855 0.925 0.7420448 0.3389525 12.112794 0.980
rs7522488 0.855 0.925 1.3995557 3.1160361 11.256933 1.000
rs8835506 0.945 0.970 2.3758119 2.2365358 12.302956 0.960
rs1037237 0.950 0.970 1.3400938 2.9836475 10.674189 1.000
rs3925525 0.955 0.970 2.3028971 2.2451502 11.988964 0.985
rs3224311 0.955 0.970 2.3028971 2.2451502 11.988964 0.985
rs1013473 0.965 0.990 1.8390955 2.8613308  9.893424 1.000
rs4534929 0.970 0.990 0.6022249 0.3747712  9.381086 1.000
```

You can see that there is little difference between adjusted and unadjusted analysis, but this is not always the case; adjustment may make your study much more powerful when covariates explain a large proportion of environmental trait variation.

Finally, let us do stratified (by BMI) analysis. We will contracts obese ($BMI \geq 30$) cases to all controls.

```
> data2.qtse <- qtscore(dm2~sex+age,data2,ids=((bmi>30 & dm2==1) | dm2==0),times=200,quiet=TRUE

  |
  |                                                                      |   0%
  |
  |======================================================================| 100%

> descriptives.scan(data2.qtse,sort="Pc1df")

Summary for top 10 results, sorted by Pc1df
          Chromosome Position Strand A1 A2  N      effB   se_effB  chi2.1df
rs7522488          3 11689797      -  G  A 88 1.7561171 0.5560485 9.9742822
rs1037237          3 11690145      +  C  G 88 1.7561171 0.5560485 9.9742822
rs9630764          1  3897972      +  T  A 88 1.7595598 0.5615384 9.8185891
rs1891586          1  2297398      -  C  T 88 0.5340528 0.1733886 9.4869655
rs3215698          X 13559835      -  T  A 88 0.4806715 0.1571512 9.3553776
rs794264           1  2534738      -  C  A 87 1.7252112 0.5832358 8.7497608
rs2884479          X 13618173      +  A  C 86 0.5896309 0.1990222 8.7772281
rs1646456          1      653      +  C  G 87 0.8853536 1.3981894 0.4009605
rs4435802          1     5291      +  C  A 86 1.7961795 1.1926370 2.2682082
rs946364           1     8533      -  T  C 86 0.7682453 0.5994013 1.6427231
          P1df Pc1df     effAB     effBB   chi2.2df  P2df
rs7522488 0.895 0.920 1.3215457 3.1245402 11.299048 0.990
rs1037237 0.895 0.920 1.3215457 3.1245402 11.299048 0.990
rs9630764 0.925 0.940 1.9346110 3.3161548  9.831616 1.000
rs1891586 0.960 0.965 0.5836292 0.3065275  9.518213 1.000
rs3215698 0.965 0.980 0.3406693 0.2701336  9.941713 1.000
rs794264  0.995 0.995 2.2543966 3.5369544  8.965654 1.000
rs2884479 0.995 0.995 0.2872964 0.4639136 14.266996 0.625
rs1646456 1.000 1.000 1.1455730 0.6013127  2.201546 1.000
rs4435802 1.000 1.000 1.7919867        NA  2.268208 1.000
rs946364  1.000 1.000 0.8791195 0.4696496  2.188118 1.000
```

Again, noting interesting at GW significance level. If we would have had found something, naturally, we would not known if we mapped a T2D or obesity gene (or a gene for obesity in presence of T2D, or the one for T2D in presence of obesity).

Let us save 'data1', 'data1.gkin', 'data2.qt' and 'cl1' objects now

```
> save(data1,cl1,data1.gkin,data2.qt,file="data1.RData")
```

These data will be used later in section 7, "GWA in presence of genetic stratification: practice", in which we will perform GWA using different methods to account for strtatification, and will compare the results with these obtaining by removing outliers ('data2.qt').

Let us also save the cleaned 'data2' object, which will be later used in section 9 ("Meta-analysis of GWA scans"):

```
> save(data2,file="data2.RData")
```

At this point, you acquired the knowledge necessary for the self-exercise. Please close R by q() command and proceed to the next section.

5.5   Genome-wide association analysis exercise

During the exercise, you will work with a larger data set (approximately 1,000 people and 7,000+ SNPs). You are to do complete three-round QC; perform GWA analysis with `dm2` as the outcome of interest and identify 10 SNPs which you would like to take to the stage 2 (replication) scan. You will do replication analysis using a confirmatory data set. If you did everything right, the SNPs which you identified as significant or replicated will be located in know T2D genes.

Please keep in mind that the data are simulated, and do not take your findings too seriously!

Start R by going to "Start -> Programs -> R -> R-?.?.?". Load `GenABEL-package` library by

```
> library(GenABEL)
```

The two data sets we will use in this exercise are part of the `GenABEL-package` distribution. The first one ("discovery" set) can be loaded by

```
> data(ge03d2)
```

Please move along the lines detailed in the guided exercise and try to answer following questions:

Ex. 1 — How many cases and controls are presented in the original data set?

Ex. 2 — How many markers are presented in the original data set?

Ex. 3 — Is there evidence for inflation of the HWE test staistics?

Ex. 4 — Analyse empirical GW significance. How many SNPs pass genome-wide significance threshold, after correction for the inflation factor? Write down the names of these SNPs for further comparison.

Ex. 5 — Perform first steps of the genetic data QC.

Ex. 6 — How many males are 'genetically' females?

Ex. 7 — How many females are 'genetically' males?

Ex. 8 — How many people are quessed to have 'XXY' genotype?

Ex. 9 — How many sporadic X errors do you still observe even when the female male and non-X X-markers are removed? (do not forget to `Xfix()` these

Ex. 10 — How many "twin" DNAs did you discover?

Ex. 11 — Perform second step of QC.

Ex. 12 — How many genetic outliers did you discover?

Ex. 13 — How many cases and controls are presented in the data after QC?

Ex. 14 — How many markers are presented in the data after QC?

Ex. 15 — Is there evidence for inflation of the HWE test staistics?

Ex. 16 — Perform GWA analysis of the cleaned data, using asimptotic test and plot the results. What is the estimate of λ for the 1 d.f. test?

Ex. 17 — Analyse empirical GW significance. How many SNPs pass genome-wide significance threshold, after correction for the inflation factor?

Ex. 18 — Do these SNPs overlap much with the ones ranked at the top before the QC? If not, what could be the reason?

Ex. 19 — Select 10 SNPs which you would like to follow-up. Say, you've selected rs1646456, rs7950586, rs4785242, rs4435802, rs2847446, rs946364, rs299251, rs2456488, rs1292700, and rs8183220. Make a vector of these SNPs with

```
> vec12<-c("rs1646456","rs7950586","rs4785242","rs4435802","rs2847446","rs946364","rs299251","r
```

Load the stage 2 (replicaton) data set by

```
> data(ge03d2c)
```

and select the subset of SNPs you need by

```
> confdat <- ge03d2c[,vec12]
```

Analyse the `confdat` for association with `dm2`.

Ex. 20 — Given the two-stage design, and applying the puristic criteria specified in the lecture, for how many SNPs you can claim a significant finding?

Ex. 21 — Using the same criteria, for how many SNPs you can claim a replicated finding?

Ex. 22 — If time permits, characterise the mode of inheritance of the significant SNPs. You can convert data from `GenABEL-package` format to the format used by `dgc.genetics` and `genetics` libraries by using `as.genotype()` function. Consult help for details. Please do not attempt to convert more then few

dozens SNPs: the format of `genetics` is not compressed, which means conversion may take long and your low-memory computer may even crash if you attempt to convert the whole data set.

Ex. 23 — If time permits, do analysis with adjustment for covariates and stratified analysis.

Ex. 24 — If time permits, try to do first round of QC allowing for HWE checks (assume FDR of 0.1 for total sample). In this case, can you still detect stratification in the "cleaned" data?

5.6   Answers to exercises

Answer (Ex. 1) — :
```
> table(phdata(ge03d2)$dm2)

  0   1
487 463
```

Answer (Ex. 2) — :
```
> nsnps(ge03d2)

[1] 7589
```

Answer (Ex. 3) — Yes:
```
> descriptives.marker(ge03d2)[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No    331.000  367.000 479.000 807.000  7589
Prop    0.044    0.048   0.063   0.106     1
```

Answer (Ex. 4) — :
```
> res0 <- qtscore(dm2,data=ge03d2,times=200,quiet=TRUE,trait="binomial")
  |
  |                                                                    |   0%
  |
  |====================================================================| 100%
> lambda(res0)

$estimate
[1] 2.036652

$se
[1] 0.006781986
```

```
$iz0
[1] 1.665047

$iz2
[1] 2.569015

> ds <- descriptives.scan(res0)

Summary for top 10 results, sorted by P1df

> ds
```

	Chromosome	Position	Strand	A1	A2	N	effB	se_effB	chi2.1df
rs3845221	1	1874765	+	G	T	942	3.249560	0.59849064	29.48047
rs4266194	1	2250206	+	C	A	942	3.103768	0.55951975	30.77142
rs8284432	1	2300686	+	C	T	939	2.558543	0.45843497	31.14799
rs2784788	1	3030569	+	G	A	943	3.107857	0.57169496	29.55243
rs3632063	2	8572345	+	T	A	937	3.167618	0.58260243	29.56113
rs6934167	3	11813645	−	G	C	942	2.778040	0.50014205	30.85250
rs6386070	1	583935	+	G	C	942	2.976929	0.57274468	27.01561
rs7903146	1	1047389	+	A	T	940	0.482230	0.09228697	27.30409
rs9350372	1	1191492	−	C	G	937	2.267829	0.44434642	26.04818
rs4015712	1	2137388	−	C	A	944	2.965481	0.55264526	28.79370

	P1df	Pc1df	effAB	effBB	chi2.2df	P2df
rs3845221	0.004975124	0.440	4.543326	Inf	29.56317	NA
rs4266194	0.004975124	0.355	2.620075	Inf	30.87429	NA
rs8284432	0.004975124	0.325	2.233559	23.7765957	31.62387	NA
rs2784788	0.004975124	0.440	2.262911	Inf	29.70503	NA
rs3632063	0.004975124	0.440	2.973396	Inf	29.56443	NA
rs6934167	0.004975124	0.350	2.060807	Inf	31.94561	NA
rs6386070	0.005000000	0.650	1.121212	Inf	28.27535	NA
rs7903146	0.005000000	0.620	0.514963	0.1466667	27.54275	NA
rs9350372	0.005000000	0.725	1.536020	Inf	31.03145	NA
rs4015712	0.005000000	0.515	2.080526	Inf	29.28263	NA

Thus, there are no genome-wide empirically significant results. The 'top' 10
SNPs are

```
> snps0 <- rownames(ds)
> snps0
 [1] "rs3845221" "rs4266194" "rs8284432" "rs2784788" "rs3632063" "rs6934167"
 [7] "rs6386070" "rs7903146" "rs9350372" "rs4015712"
```

(note that if empirical P is 1, the rank is assigned quite arbitrarily)

Answer (Ex. 5) — First step of QC

```
> qc1 <- check.marker(ge03d2,call=0.95,perid.call=0.95,p.level=0,ibs.exclude="both")

Excluding people/markers with extremely low call rate...
7589 markers and 950 people in total
0 people excluded because of call rate < 0.1
7 markers excluded because of call rate < 0.1
Passed: 7582 markers and 950 people
```

Running sex chromosome checks...
1934 heterozygous X-linked male genotypes found
2 X-linked markers are likely to be autosomal (odds > 1000)
10 male are likely to be female (odds > 1000)
6 female are likely to be male (odds > 1000)
0 people have intermediate X-chromosome inbreeding (0.5 > F > 0.5)
If these people/markers are removed, 8 heterozygous male genotypes are left
... these will be considered missing in analysis.
... Use Xfix() to fix these problems.
Passed: 7580 markers and 934 people

... 8 X/Y/mtDNA (8 0 0) impossible heterozygotes and female Ys set as missing

RUN 1
7580 markers and 934 people in total
73 (0.9630607%) markers excluded as having low (<0.267666%) minor allele frequency
75 (0.9894459%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
4 (0.4282655%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2558271 (s.e. 0.02102863)
4 (0.4282655%) people excluded because too high autosomal heterozygosity (FDR <1%)
Excluded people had HET >= 0.4702949
Mean IBS is 0.7863841 (s.e. 0.01660607), as based on 2000 autosomal markers
8 (0.856531%) people excluded because of too high IBS (>=0.95)
In total, 7432 (98.04749%) markers passed all criteria
In total, 918 (98.28694%) people passed all criteria

RUN 2
7432 markers and 918 people in total
42 (0.5651238%) markers excluded as having low (<0.2723312%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2562716 (s.e. 0.0151377)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7878353 (s.e. 0.01591243), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 7390 (99.43488%) markers passed all criteria
In total, 918 (100%) people passed all criteria

RUN 3
7390 markers and 918 people in total
0 (0%) markers excluded as having low (<0.2723312%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2562716 (s.e. 0.0151377)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7903234 (s.e. 0.01555294), as based on 2000 autosomal markers

```
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 7390 (100%) markers passed all criteria
In total, 918 (100%) people passed all criteria
> summary(qc1)

$`Per-SNP fails statistics`
          NoCall NoMAF NoHWE Redundant Xsnpfail
NoCall        82     0     0         0        0
NoMAF         NA   115     0         0        0
NoHWE         NA    NA     0         0        0
Redundant     NA    NA    NA         0        0
Xsnpfail      NA    NA    NA        NA        2


$`Per-person fails statistics`
          IDnoCall HetFail IBSFail isfemale ismale isXXY otherSexErr
IDnoCall         4       0       0        0      0     0           0
HetFail         NA       4       0        0      0     0           0
IBSFail         NA      NA       8        0      0     0           0
isfemale        NA      NA      NA       10      0     0           0
ismale          NA      NA      NA       NA      6     0           0
isXXY           NA      NA      NA       NA     NA     0           0
otherSexErr     NA      NA      NA       NA     NA    NA           0
> data1 <- ge03d2[qc1$idok,qc1$snpok]
> data1 <- Xfix(data1)

... 7 X/Y/mtDNA ( 7 0 0 ) impossible heterozygotes and female Ys set as missing

> qc2 <- check.marker(data1,call=0.95,perid.call=0.95,p.level=0)

Excluding people/markers with extremely low call rate...
7390 markers and 918 people in total
0 people excluded because of call rate < 0.1
0 markers excluded because of call rate < 0.1
Passed: 7390 markers and 918 people

Running sex chromosome checks...
0 heterozygous X-linked male genotypes found
0 X-linked markers are likely to be autosomal (odds > 1000 )
0 male are likely to be female (odds > 1000 )
0 female are likely to be male (odds > 1000 )
0 people have intermediate X-chromosome inbreeding (0.5 > F > 0.5)
If these people/markers are removed, 0 heterozygous male genotypes are left
Passed: 7390 markers and 918 people

no X/Y/mtDNA-errors to fix


RUN 1
7390 markers and 918 people in total
0 (0%) markers excluded as having low (<0.2723312%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
```

```
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2562716 (s.e. 0.0151377)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7850858 (s.e. 0.01660697), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 7390 (100%) markers passed all criteria
In total, 918 (100%) people passed all criteria

> summary(qc2)

$`Per-SNP fails statistics`
```

	NoCall	NoMAF	NoHWE	Redundant	Xsnpfail
NoCall	0	0	0	0	0
NoMAF	NA	0	0	0	0
NoHWE	NA	NA	0	0	0
Redundant	NA	NA	NA	0	0
Xsnpfail	NA	NA	NA	NA	0

```
$`Per-person fails statistics`
```

	IDnoCall	HetFail	IBSFail	isfemale	ismale	isXXY	otherSexErr
IDnoCall	0	0	0	0	0	0	0
HetFail	NA	0	0	0	0	0	0
IBSFail	NA	NA	0	0	0	0	0
isfemale	NA	NA	NA	0	0	0	0
ismale	NA	NA	NA	NA	0	0	0
isXXY	NA	NA	NA	NA	NA	0	0
otherSexErr	NA	NA	NA	NA	NA	NA	0

Answer (Ex. 6) — The list of genetic females who are coded as males is

```
> qc1$isfemale
 [1] "id3374" "id6263" "id6835" "id8410" "id8509" "id8519" "id8542" "id2701"
 [9] "id6494" "id3100"
```

Answer (Ex. 7) — The list of genetic males who are coded as females is

```
> qc1$ismale
[1] "id193"  "id8475" "id2461" "id5669" "id7245" "id8301"
```

Answer (Ex. 8) — The number of 'XXY' people is 0

Answer (Ex. 9) — Eight 'sporadic' X-errors are left after removing people with likely sex code errors (seven in the data set after first step of QC)

Answer (Ex. 10) — The list of IDs failing IBS checks ('twin' DNAs) is

```
> qc1$ibsfail
```

```
[1] "id3368" "id9668" "id5437" "id956"  "id386"  "id660"  "id2115" "id8370"
```

Answer (Ex. 11) — The second step of QC:

```
> data1.gkin <- ibs(data1[,autosomal(data1)],weight="freq")
> data1.dist <- as.dist(0.5-data1.gkin)
> data1.mds <- cmdscale(data1.dist)
> km <- kmeans(data1.mds,centers=2,nstart=1000)
> cl1 <- names(which(km$cluster==1))
> cl2 <- names(which(km$cluster==2))
> if (length(cl1)>length(cl2)) {x<-cl2;cl2<-cl1;cl1<-x}
> cl1

 [1] "id2097" "id2126" "id2878" "id3021" "id3176" "id4554" "id4756" "id7436"
 [9] "id7533" "id9396" "id9546" "id4021" "id2171" "id6954" "id2136" "id5056"
[17] "id1751" "id6626" "id2970" "id1300" "id8639" "id1729" "id9398" "id9904"
[25] "id858"

> data2 <- data1[cl2,]
> qc2 <- check.marker(data2,hweids=(phdata(data2)$dm2==0),fdr=0.2)

Excluding people/markers with extremely low call rate...
7390 markers and 893 people in total
0 people excluded because of call rate < 0.1
0 markers excluded because of call rate < 0.1
Passed: 7390 markers and 893 people

Running sex chromosome checks...
0 heterozygous X-linked male genotypes found
0 X-linked markers are likely to be autosomal (odds > 1000 )
0 male are likely to be female (odds > 1000 )
0 female are likely to be male (odds > 1000 )
0 people have intermediate X-chromosome inbreeding (0.5 > F > 0.5)
If these people/markers are removed, 0 heterozygous male genotypes are left
Passed: 7390 markers and 893 people

no X/Y/mtDNA-errors to fix


RUN 1
7390 markers and 893 people in total
5 (0.067659%) markers excluded as having low (<0.2799552%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (FDR <0.2)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2565083 (s.e. 0.01505982)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7954663 (s.e. 0.01129292), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 7385 (99.93234%) markers passed all criteria
In total, 893 (100%) people passed all criteria
```

```
RUN 2
7385 markers and 893 people in total
0 (0%) markers excluded as having low (<0.2799552%) minor allele frequency
0 (0%) markers excluded because of low (<95%) call rate
0 (0%) markers excluded because they are out of HWE (FDR <0.2)
0 (0%) people excluded because of low (<95%) call rate
Mean autosomal HET is 0.2565083 (s.e. 0.01505982)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.7916793 (s.e. 0.01169976), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 7385 (100%) markers passed all criteria
In total, 893 (100%) people passed all criteria
```

> *summary(qc2)*

```
$`Per-SNP fails statistics`
          NoCall NoMAF NoHWE Redundant Xsnpfail
NoCall         0     0     0         0        0
NoMAF         NA     5     0         0        0
NoHWE         NA    NA     0         0        0
Redundant     NA    NA    NA         0        0
Xsnpfail      NA    NA    NA        NA        0


$`Per-person fails statistics`
          IDnoCall HetFail IBSFail isfemale ismale isXXY otherSexErr
IDnoCall         0       0       0        0      0     0           0
HetFail         NA       0       0        0      0     0           0
IBSFail         NA      NA       0        0      0     0           0
isfemale        NA      NA      NA        0      0     0           0
ismale          NA      NA      NA       NA      0     0           0
isXXY           NA      NA      NA       NA     NA     0           0
otherSexErr     NA      NA      NA       NA     NA    NA           0
```

> *data2 <- data2[qc2$idok,qc2$snpok]*
> *data2 <- Xfix(data2)*

```
no X/Y/mtDNA-errors to fix
```

> *####*
> *#ge03d2.clean <- data2*
> *#save(ge03d2.clean,file="ge03d2.clean.RData")*
> *####*

Answer (Ex. 12) — The list of genetic outliers is

> *cl1*

```
 [1] "id2097" "id2126" "id2878" "id3021" "id3176" "id4554" "id4756" "id7436"
 [9] "id7533" "id9396" "id9546" "id4021" "id2171" "id6954" "id2136" "id5056"
[17] "id1751" "id6626" "id2970" "id1300" "id8639" "id1729" "id9398" "id9904"
[25] "id858"
```

Answer (Ex. 13) — :

```
> table(phdata(data2)$dm2)

  0   1
472 421
```

Answer (Ex. 14) — :

```
> nsnps(data2)

[1] 7385
```

Answer (Ex. 15) — No:

```
> descriptives.marker(data2)[2]

$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No          1    4.000  44.000 258.000  7385
Prop        0    0.001   0.006   0.035     1
```

Answer (Ex. 16) — :

```
> qts <- qtscore(dm2,data2,trait="binomial")
> lambda(qts)

$estimate
[1] 1.137922

$se
[1] 0.001087627

$iz0
[1] 1.131274

$iz2
[1] 1
```

Answer (Ex. 17) — :

```
> res1 <- qtscore(dm2,data=data2,times=200,quiet=TRUE,trait="binomial")
  |
  |                                                                  |   0%
  |
  |==================================================================| 100%
> ds1 <- descriptives.scan(res1)
Summary for top 10 results, sorted by P1df
> ds1
```

	Chromosome	Position	Strand	A1	A2	N	effB	se_effB	chi2.1df
rs7903146	1	1047389	+	A	T	887	0.4732487	0.09237813	26.24463
rs289981	1	1043860	−	T	G	882	1.6084203	0.35859445	20.11833
rs70099	2	8857747	+	C	A	883	2.3164180	0.52491058	19.47436
rs3436694	2	8921418	−	C	G	885	2.0983499	0.47455324	19.55176
rs7064741	1	1044233	−	C	G	885	0.6175678	0.14988526	16.97663
rs2975760	3	10518480	+	A	T	888	1.4799188	0.38810107	14.54073
rs3074653	2	8915495	−	G	C	885	1.6536317	0.44797502	13.62605
rs5243830	1	1371499	+	A	G	888	16.2973905	4.53947050	12.88919
rs5743183	1	648911	+	C	T	882	0.5025524	0.14066512	12.76409
rs9386314	1	756075	−	C	A	889	0.6716160	0.19058053	12.41895

	P1df	Pc1df	effAB	effBB	chi2.2df	P2df
rs7903146	0.004975124	0.004975124	0.5218925	0.1037251	26.80404	0.005
rs289981	0.025000000	0.125000000	1.3125000	2.3066907	21.00192	0.075
rs70099	0.035000000	0.150000000	2.1524086	Inf	20.04047	0.115
rs3436694	0.035000000	0.150000000	1.9610224	Inf	20.49069	0.080
rs7064741	0.150000000	0.390000000	0.5769088	0.4686275	17.83121	0.355
rs2975760	0.430000000	0.795000000	1.1013919	3.3706932	22.84103	0.020
rs3074653	0.635000000	0.910000000	1.5340654	4.0687285	14.31287	0.935
rs5243830	0.765000000	0.945000000	Inf	Inf	13.73963	0.970
rs5743183	0.800000000	0.950000000	0.4646406	0.6684303	13.97357	0.955
rs9386314	0.855000000	0.975000000	0.5847590	0.6154026	14.99598	0.850

There are SNPs which are empirically genome-wide significant in the data. To
get the list of 'top' 10 SNPs:

```
> snps1 <- rownames(ds1)
> snps1
```

```
 [1] "rs7903146" "rs289981"  "rs70099"   "rs3436694" "rs7064741" "rs2975760"
 [7] "rs3074653" "rs5243830" "rs5743183" "rs9386314"
```

Answer (Ex. 18) — There is little overlap between SNPs before and after
QC:

```
> snps0
```

```
 [1] "rs3845221" "rs4266194" "rs8284432" "rs2784788" "rs3632063" "rs6934167"
 [7] "rs6386070" "rs7903146" "rs9350372" "rs4015712"
```

```
> snps1
```

```
 [1] "rs7903146" "rs289981"  "rs70099"   "rs3436694" "rs7064741" "rs2975760"
 [7] "rs3074653" "rs5243830" "rs5743183" "rs9386314"
```

Answer (Ex. 19) — :

```
> data(ge03d2c)
> snps1
```

```
 [1] "rs7903146" "rs289981"  "rs70099"   "rs3436694" "rs7064741" "rs2975760"
 [7] "rs3074653" "rs5243830" "rs5743183" "rs9386314"
```

```
> confdat <- ge03d2c[,snps1]
> rep <- qtscore(dm2,confdat,times=10000,quiet=TRUE)
```

```
  |
  |                                                                      |  0%
  |
  |======================================================================| 100%
> descriptives.scan(rep)
```

Summary for top 10 results, sorted by P1df

	Chromosome	Position	Strand	A1	A2	N	effB	se_effB
rs2975760	3	10518480	+	A	T	192	0.16759919	0.05487999
rs7903146	1	1047389	+	A	T	191	-0.20235475	0.07195827
rs289981	1	1043860	-	T	G	193	0.13512064	0.05646226
rs7064741	1	1044233	-	C	G	193	-0.13146201	0.05935313
rs3436694	2	8921418	-	C	G	193	0.17717855	0.08512525
rs3074653	2	8915495	-	G	C	190	0.15567151	0.07620495
rs5743183	1	648911	+	C	T	191	-0.09809264	0.08440061
rs9386314	1	756075	-	C	A	193	-0.05607552	0.06194938
rs70099	2	8857747	+	C	A	192	0.04474665	0.10180430
rs5243830	1	1371499	+	A	G	195	0.04527559	0.17760398

	chi2.1df	P1df	Pc1df	effAB	effBB	chi2.2df	P2df
rs2975760	9.32643863	0.0166	0.6114	0.2363080345	0.24878575	10.905443	0.0202
rs7903146	7.90797784	0.0413	0.6973	-0.2327637890	-0.25359712	8.443328	0.0786
rs289981	5.72699574	0.1479	0.8269	0.0166666667	0.19727891	6.586622	0.2101
rs7064741	4.90583841	0.2050	0.8872	-0.2232316677	-0.06719368	8.569669	0.0746
rs3436694	4.33216994	0.2759	0.9322	0.1221340388	0.58641975	5.316940	0.4207
rs3074653	4.17303421	0.3034	0.9357	0.1088501292	0.59722222	5.524265	0.3821
rs5743183	1.35077106	0.9190	0.9988	-0.1142919106	-0.12578616	1.440586	0.9981
rs9386314	0.81935620	0.9823	0.9997	-0.0948499882	0.01960784	1.790760	0.9928
rs70099	0.19319191	0.9998	1.0000	0.0002587992	0.56547619	1.292451	0.9998
rs5243830	0.06498646	1.0000	1.0000	-0.1921052632	0.55789474	1.860430	0.9889

Answer (Ex. 20) — Two-stage P-value is

```
>    snps1
 [1] "rs7903146" "rs289981"  "rs70099"    "rs3436694" "rs7064741" "rs2975760"
 [7] "rs3074653" "rs5243830" "rs5743183" "rs9386314"

>    finres <- matrix(NA,10,3)
>    colnames(finres) <- c("Stage 1","Replication","Combined")
>    rownames(finres) <- snps1
>    for (i in 1:10) {
+        finres[i,1] <- res1[which(snpnames(data2)==snps1[i]),"Pc1df"]
+        finres[i,2] <- rep[which(snpnames(confdat)==snps1[i]),"P1df"]
+        finres[i,3] <- finres[i,1]*finres[i,2]
+    }
>    finres
```

	Stage 1	Replication	Combined
rs7903146	0.004975124	0.0413	0.0002054726
rs289981	0.125000000	0.1479	0.0184875000
rs70099	0.150000000	0.9998	0.1499700000
rs3436694	0.150000000	0.2759	0.0413850000

```
rs7064741 0.390000000      0.2050 0.0799500000
rs2975760 0.795000000      0.0166 0.0131970000
rs3074653 0.910000000      0.3034 0.2760940000
rs5243830 0.945000000      1.0000 0.9450000000
rs5743183 0.950000000      0.9190 0.8730500000
rs9386314 0.975000000      0.9823 0.9577425000
>     for (i in 1:10) {
+        if (finres[i,3] <= 0.05) {
+            print(c("---------",rownames(finres)[i],"-------"))
+
+            print(c(rownames(finres)[i],"stage 1:"))
+            ph <- phdata(data2)$dm2
+            gt <- as.numeric(data2[,rownames(finres)[i]])
+            print(summary(glm(ph~gt,family=binomial))$coef)
+
+            print(c(rownames(finres)[i],"stage 2:"))
+            ph <- phdata(confdat)$dm2
+            gt <- as.numeric(confdat[,rownames(finres)[i]])
+            print(summary(glm(ph~gt,family=binomial))$coef)
+
+            print(c(rownames(finres)[i],"Joint:"))
+            ph <- c(phdata(data2)$dm2,phdata(confdat)$dm2)
+            gt <- c(as.numeric(data2[,rownames(finres)[i]]),as.numeric(confdat[,row
+            print(summary(glm(ph~gt,family=binomial))$coef)
+        }
+     }

[1] "---------" "rs7903146" "-------"
[1] "rs7903146" "stage 1:"
              Estimate Std. Error    z value      Pr(>|z|)
(Intercept)  0.08024472 0.07682467  1.044518 2.962460e-01
gt          -0.74685964 0.14906771 -5.010204 5.437238e-07
[1] "rs7903146" "stage 2:"
               Estimate Std. Error     z value     Pr(>|z|)
(Intercept)  0.001895645  0.1686559  0.01123972 0.991032189
gt          -0.902521348  0.3296467 -2.73784449 0.006184331
[1] "rs7903146" "Joint:"
              Estimate Std. Error    z value      Pr(>|z|)
(Intercept)  0.06652706 0.06990581  0.9516671 3.412659e-01
gt          -0.77557677 0.13580221 -5.7110762 1.122640e-08
[1] "---------" "rs289981"  "-------"
[1] "rs289981" "stage 1:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.7895683  0.1686946 -4.680461 2.862312e-06
gt           0.4836336  0.1088004  4.445145 8.783281e-06
[1] "rs289981" "stage 2:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -1.0644645    0.383275 -2.777287 0.005481483
gt           0.5699411    0.241041  2.364499 0.018054487
[1] "rs289981" "Joint:"
```

```
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.8342403  0.1542809 -5.407281 6.398868e-08
gt           0.4963232  0.0990676  5.009944 5.444577e-07
[1] "---------" "rs3436694" "-------"
[1] "rs3436694" "stage 1:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.2592162 0.07519988 -3.447029 5.667876e-04
gt           0.7385083 0.16987721  4.347307 1.378194e-05
[1] "rs3436694" "stage 2:"
              Estimate Std. Error   z value    Pr(>|z|)
(Intercept) -0.3683936  0.1589513 -2.317651 0.02046831
gt           0.7304292  0.3606365  2.025389 0.04282744
[1] "rs3436694" "Joint:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.2790299 0.06795526 -4.106083 4.024252e-05
gt           0.7391791 0.15373558  4.808120 1.523565e-06
[1] "---------" "rs2975760" "-------"
[1] "rs2975760" "stage 1:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.3171429 0.08729818 -3.632870 0.0002802862
gt           0.3944701 0.10419297  3.785957 0.0001531181
[1] "rs2975760" "stage 2:"
              Estimate Std. Error   z value    Pr(>|z|)
(Intercept) -0.5969939  0.1928321 -3.095926 0.001961992
gt           0.6942268  0.2323045  2.988435 0.002804103
[1] "rs2975760" "Joint:"
              Estimate Std. Error   z value      Pr(>|z|)
(Intercept) -0.3659711 0.07942275 -4.607888 4.067798e-06
gt           0.4463331 0.09495765  4.700338 2.597310e-06
> replicatedsnps <- rownames(finres)[finres[,"Stage 1"]<=0.05 &
+                           finres[,"Replication"]<=0.05 & finres[,"Combined"]<=0.05]
> replicatedsnps

[1] "rs7903146"

> sigsnps <- rownames(finres)[finres[,"Combined"]<=0.05]
> sigsnps

[1] "rs7903146" "rs289981"  "rs3436694" "rs2975760"
```

At the first glance, 1 SNPs may be claimed as replicated because both first stage and replication P-values are ≤ 0.05 and effects are consistent, and additionally 3 may be claimed as 'significant' because joint p-values are ≤ 0.05 and the effects are consistent. Generally, a more thorough simulation experiment should be performed.

Answer (Ex. 21) — SNP "rs7903146" had empirical p-value ≤ 0.05 at both stages, and very strong joint significance. It can be claimed as replicated.
You can check if any of the SNPs you have identified as significant or replicated are the ones which were simulated to be associated with dm2 by using the command show.ncbi(c("snpname1","snpname2","snpname3")) where snpnameX

stands for the name of your identified SNP. The "true" SNPs can be found on NCBI and some are located in known T2D genes (just because we used these names to name the "significant" ones).

Chapter 6

GWA analysis in presence of stratification: theory

In genetic association studies, we look for association between a genetic polymorphism and the value of a trait of interest. The best scenario – the one we always hope for – is that the observed association results from causation, that is the polymorphism studied is functionally involved in the control of the trait. However, association has no direction, and making causal inference in epidemiology in general and in genetic epidemiology in particular is usually not possible based on statistical analysis only.

In fact, most associations observed in genetic studies are due to a confounder – an (unobserved) factor which is associated with both the genetic polymorphism and the trait analysed. Presence of such factor leads to induced, "secondary" correlation between the trait and the polymorphism; if we would have controlled for that factor in the association model, the relation between the polymorphism and the trait would have gone.

There are two major types of confounders leading to induced correlation in genetic association studies. One type is "good" confounding of association by the real, unobserved functional variant, which is, as a rule, not present on the SNP array, but is in linkage disequilibrium (LD) with typed SNP. Under this scenario, the functional variant is associated with the trait because of causative relation; at the same time it is associated with a typed polymorphism located nearby because of LD. This confounding induces secondary correlation between the typed polymorphism and the trait, making localistion of the true functional polymorphism (LD mapping) possible.

Other major type of confounding observed in genetic association studies is confounding by population (sub)structure. Let us consider a study in which subjects come from two distantly related populations, say Chinese and European. Due to genetic drift, these two populations will have very different frequencies at many loci throughout the genome. At the same time, these two populations are different phenotypically (prevalence of different disease, mean value of quantitative traita) due to accumulated genetic and cultural differences. Therefore any of these traits will show association with multiple genomic loci. While some of these associations may be genuine genetic associations in a sense that either the polymorphisms themselves, or the polymorphisms close by are causally

involved, most of these associations will be genetically false positives – noise associations generated by strong genetic and phenotypic divergence between the two populations.

The scenario described above is extreme and indeed it is hard to imagine a genetic asociation study in which two very distinct populations are so blintly mixed and analysed not taking this mixture into account. However, a more subtle scenario where several slightly genetically different populations are mixed in the same study is frequently the case and a matter of concern in GWA studies.

In this chapter, we will define what is genetic structure, and how it can be quantified (section 6.1); what are the effects of genetic structure on the standard association tests (section 6.2) and specific association tests which take possible genetic structure into account (section 6.3).

6.1 Genetic structure of populations

A major unit of genetic structure is a genetic population. Different definitions of genetic population are available, for example Wikipedia defines population (biol.) as "the collection of inter-breeding organisms of a particular species". The genetics of populations is "the study of the allele frequency distribution and change under the influence of . . . evolutionary processes". In the framework of population genetics, the main characteristics of interest of a group of individuals are their genotypes, frequencies of alleles in this group, and the dynamics of these distributions in time. While the units of interest of population genetics are alleles, the units of evolutionary processes are acting upon are organisms. Therefore a definition of a genetic population should be based on the chance that different alleles, present in the individuals in question can mix together; if such chance is zero, we may consider such groups as different populations, each described by its own genotypic and allelic frequencies and their dynamic. Based on these considerations, a genetic population may be defined a in the following way:

Two individuals, I_1 and I_2, belong to the same population if (a) the probability that they would have an offspring in common is greater then zero and (b) this probability is much higher than the probability of I_1 and I_2 having an offspring in common with some individual I_3, which is said to belong to other genetic population.

Here, to have an offspring in common does not imply having a direct offspring, but rather a common descendant in a number of generations.

However, in gene discovery in general and GWA studies in particular we are usually not interested in future dinamics of alleles and genotypes distributions. What is the matter of concern in genetic association studies is potential common ancestry – that is that individuals may share common ancestors and thus share in common the alleles, which are exact copies of the same ancestral allele. Such alleles are called "identical-by-descent", or IBD for short. If the chance of IBD is high, this reflects high degree of genetic relationship. As a rule, relatives share many features, both environmental and genetic, which may lead to confounding.

Genetic relationship between a pair of individuals is quantified using the "coefficient of kinship", which measures that chance that gametes, sampled at random from these individuals, are IBD.

Thus for the purposes of gene-discovery we can define genetic population use retrospective terms and based on the concept of IBD:

Two individuals, I_1 and I_2, belong to the same genetic population if (a) their genetic relationship, measured with the coefficient of kinship, is greater then zero and (b) their kinship is much higher than kinship between them and some individual I_3, which is said to belong to other genetic population.

One can see that this definition is quantitative and rather flexible (if not to say arbitrary): what we call a "population" depends on the choice of the threshold for the "much-higher" probability. Actually, what you define as "the same" genetic population depends in large part on the scope aims of your study. In human genetics literature you may find references to a particular genetically isolated population, population of some country (e.g. "German population", "population of United Kingdom"), European, Caucasoid or even general human population. Defining a population is about deciding on some probability threshold.

In genetic association studies, it is frequently assumed that study participants are "unrelated" and "come from the same genetic population". Here, "unrelated" means, that while study participants come from the same population (so, there is non-zero kinship between them!), this kinship is so low that it has very little effect on the statistical testing procedures used to study association between genes and phenotypes.

In the following sections we will consider the effects of population structure on the istribution of genotypes in a study population. We will start with assumption of zero kinship between study participants, which would allow us to formulate Hary-Weinberg principle (section 6.1.1). In effect, there is no such thing as zero kinship between any two organisms, however, when kinship is very low, the effects of kinship on genotypic distribution are minimal, as we will see in section 6.1.2. The effects of substructure – that is when study sample consist of several genetic populations – onto genotypic distribution will be considered in section 6.1.3. Finally, we will generalize the obtained results for the case of arbitrary structures and will see what are the effects of kinship onto joint distribution of genotypes and phenotypes in section **??**.

6.1.1 Hardy-Weinberg equilibrium

To describe genetic structure of populations we will use rather simplistic model approximating genetic processes in natural populations. Firstly, we will assume that the population under consideration has infinitely large size, which implies that we can work in terms of probabilities, and no random process take place. Secondly, we accept non-overlapping

$$\text{generation} \Rightarrow \text{gametic pool} \Rightarrow \text{generation}$$

model. This model assumes that a set of individuals contributes gametes to genetic pool, and dies out. The gametes are sampled randomly from this pool in pairs to form individuals of the second generation. The selection acts on individuals, while mutation occurs when the gametic pool is formed. The key point of this model is the abstract of gametic pool: if you use that, you do not need to consider all pair-wise mating between male and female individuals; you rather

consider some abstract infinitely large pool, where gametes are contributed to with the frequency proportional to that in previous generation. Interestingly, this rather artificial construct has a great potential to describe the phenomena we indeed observe in nature.

In this section, we will derive Hardy-Weinberg low (this analog of the Mendel's low for populations). The question to be answered is, if some alleles at some locus segregate according to Mendel's lows and aggregate totally at random, what would be genotypic distribution in a population?

Let us consider two alleles, wild type normal allele (N) and a mutant (D), segregating at some locus in the population and apply the "generation $\Rightarrow$ gametic pool $\Rightarrow$ generation" model. Let us denote the ferquency of the D allele in the gametic pool as q, and the frequency of the other allele, N, as $p = 1 - q$. Gametes containing alleles N and D are sampled at random to form diploid individuals of the next generation. The probability to sample a "N" gamete is p, and the probability that the second sampled gamete is also "N" is also p. According to the rule, which states that joint probability of two independent events is a product of their probabilities, the probability to sample "N" and "N" is $p \cdot p = p^2$. In the same manner, the probability to sample "D" and then "D" is $q \cdot q = q^2$. The probability to sample first the mutant and then normal allele is $q \cdot p$, the same is the probability to sample "D" first and "N" second. In most situations, we do not (and can not) distinguish heterozygous genotypes DN and ND and refer to both of them as "ND". In this notation, frequency of ND will be $q \cdot p + p \cdot q = 2 \cdot p \cdot q$. Thus, we have computed the genotypic distribution for a population formed from a gametic pool in which the frequency of D allele was q.

To obtain the next generation, the next gametic pool is generated. The frequency of D in the nect gametic pool is $q^2 + \frac{1}{2} \cdot 2 \cdot p \cdot q$. Here, q^2 is the probability that a gamete-contributing individual has genotype DD; $2 \cdot p \cdot q$ is the probability that a gamete-contributing individual is ND, and $\frac{1}{2}$ is the probability that ND individual contributes D allele (only half of the gametes contributed by individuals with ND genotype are D); see Figure 6.1. Thus the freqeuncy of D in the gametic pool is $q^2 + \frac{1}{2} \cdot 2 \cdot p \cdot q = q \cdot (q + p) = q$ – exactly the same as it was in previous gametic pool.

Thus, if assumptions of random segregation and aggregation hold, the expected frequency of NN, ND and DD genotypes are stable over generations and can be related to the allelic frequencies using the follwoing relation

$$
\begin{aligned}
P(NN) &= (1 - q) \cdot (1 - q) & = p^2, \\
P(ND) &= q \cdot (1 - q) + (1 - q) \cdot q & = 2 \cdot p \cdot q, \\
P(DD) &= q \cdot q & = q^2
\end{aligned}
\tag{6.1}
$$

which is known as Hardy-Weinberg equlibrium (HWE) point.

There are many reasons, in which random segregation and aggregation, and, consequently, Hardy-Weinberg equilibrium, are violated. It is very important to realize that, especially if the study participants are believed to come from the same genetic population, most of the times when deviation from HWE is detected, this deviation is due to technical reasons, i.e. genotyping error. Therefore testing for HWE is a part of the genotypic quality control procedure in most studies. Only when the possibility of technical errors is eliminated, other possible explanations may be considered. In a case when deviation from HWE can
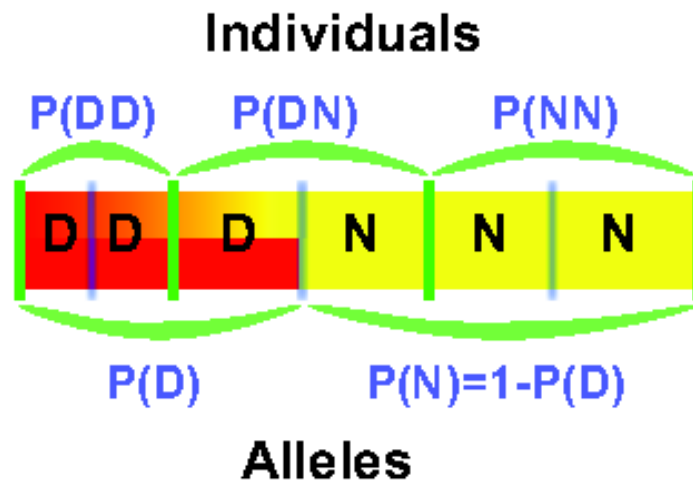
Figure 6.1: Genotypic and allelic frequency distribution in a population; $q = P(D) = P(DD) + \frac{1}{2} \cdot P(DN)$.

not be explained by technical reasons, the most frequent explanation would be that the sample tested is composed of representatives of different genetic populations, or more subtle genetic structure. However, unless study participants represent a mixture of very distinct genetic populations – the chances of which coming unnoticed are low – the efffects of genetic structure on HWE are difficult to detect, at least for any single marker, as you will see in the next sections.

6.1.2 Inbreeding

Inbreeding is preferential breeding between (close) relatives. An extreme example of inbreeding is a selfing, a breeding system, observed in some plants. The inbreeding is not uncommon in animal and human populations. Here, the main reason for inbreeding are usually geographical (e.g. mice live in very small interbred colonies – dems – which are usually established by few mice and are quite separated from other dems) or cultural (e.g. noble families of Europe).

Clearly, such preferential breeding between relatives violates the assumption of random aggregation, underling Hardy-Weinberg principle. Relatives are likely to share the same alleles, inherited from common ancestors. Therefore their progeny has an increased chance of being *autozygous* – that is to inherit a copy of exactly the same ancestral allele from both parents. An autozygous genotype is always homozygous, therefore inbreeding should increase the frequency of homozygous, and decrease the frequency of heterozygous, genotypes.

Inbreeding is quantified by the *coefficient of inbreeding*, which is defined as the probability of autozygosity. This coefficient may characterize an individual, or a population in general, in which case this is expectation that a random individual from the population is autozygous at a random locus. The coefficient of inbreeding is closely related to the coefficient of kinship, defined earlier for a pair of individuals as the probability that two alleles sampled at random from these individuals, are IBD. It is easy to see that the coefficient of inbreeding for
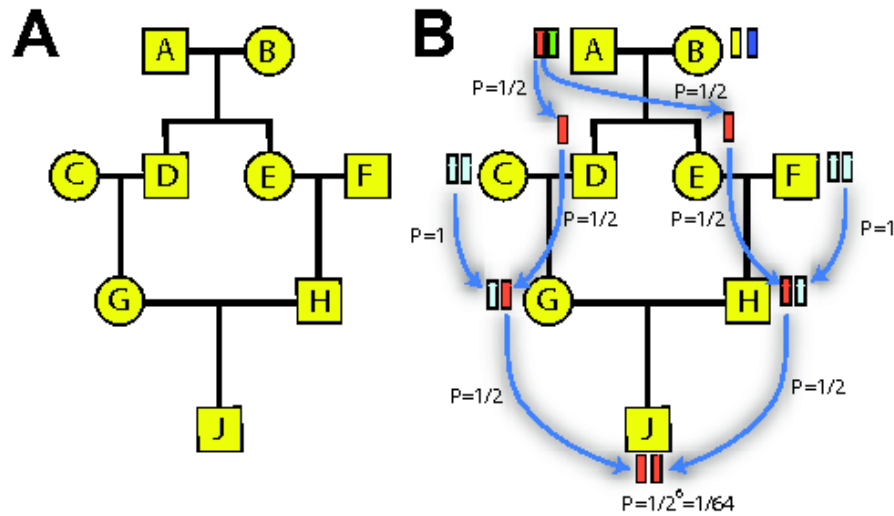
Figure 6.2: Inbred family structure (A) and probability of individual "G" being autozygous for the "Red" ancestral allele

a person is the same as the kinship between its parents.

Let us compute the inbreeding coefficient for the person **J** depicted at figure 6.2. **J** is a child of **G** and **H**, who are cousins. **J** could be autozygous at for example "red" allele of founder grand-grand-parent **A**, which could have been transmitted through the meioses $\mathbf{A} \Rightarrow \mathbf{D}$, $\mathbf{D} \Rightarrow \mathbf{G}$, and $\mathbf{G} \Rightarrow \mathbf{J}$, and also through the path $\mathbf{A} \Rightarrow \mathbf{E}$, $\mathbf{E} \Rightarrow \mathbf{H}$, and $\mathbf{H} \Rightarrow \mathbf{J}$ (Figure 6.2 **B**). What is the chance for **J** to be autozygous for the "red" allele? The probability that this particular founder allele is transmitted to **D** is $1/2$, the same is the probability that the allele is transmitted from **D** to **G**, and the probability that the allele is transmitted from **G** to **J**. Thus the probability that the "red" allele is transmitted from **A** to **J** is $1/2 \cdot 1/2 \cdot 1/2 = 1/2^3 = 1/8$. The same is the chance that that allele is transmitted from **A** to **E** to **H** to **J**, therefore the probability that **J** would be autozygous for the red allele is $1/2^3 \cdot 1/2^3 = 1/2^6 = 1/64$. However, we are interested in autozygosity for any founder allele; and there are four such alleles ("red", "green", "yellow" and "blue", figure 6.2 **B**). For any of these the probability of autozygosity is the same, thus the total probability of autozygosity for **J** is $4 \cdot 1/64 = 1/2^4 = 1/16$.

Now we shall estimate the expected genotypic probability distribution for a person characterized with some arbitrary coefficient of inbreeding, F – or for a population in which average inbreeding is F. Consider a locus with two alleles, A and B, with frequency of B denoted as q, and frequency of A as $p = 1 - q$. If the person is autozygous for some founder allele, the founder allele may be either A, leading to autozygous genotype AA, or the founder allele may be B, leading to genotype BB. The chance that the founder allele is A is p, and the chance that the founder allele is B is q. If the person is not autozygous, then the expected genotypic frequencies follow HWE. Thus, the probability of genotype AA is $(1 - F) \cdot p^2 + F \cdot p$, where the first term corresponds to probability that the person is AA given it is not inbred (p^2), multiplied by the probability that
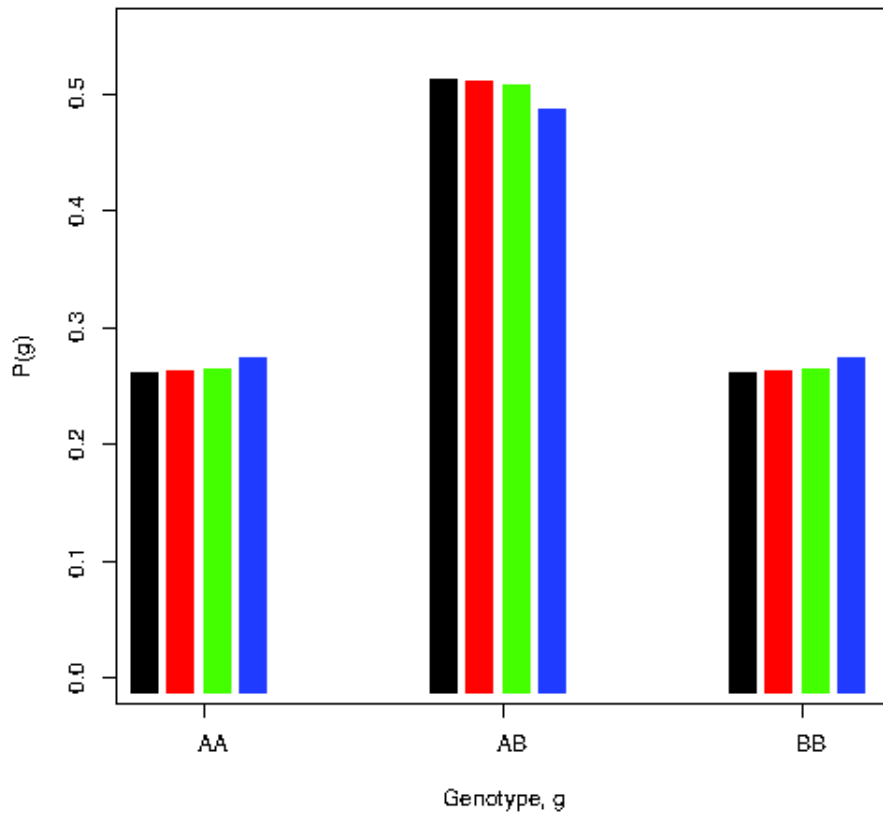
Figure 6.3: Genotypic probability distribution for a locus with 50% frequency of the B allele; black bar, no inbreeding; red, $F = 0.001$; green, $F = 0.01$; blue, $F = 0.05$

it is not inbred $(1 - F)$, and the second term corresponds to probability that a person is AA given it is inbred (p), multiplied by the probability that the person is inbred (F). This computations can be easily done for all genotypic classes leading to the expression for HWE under inbreeding.

$$\begin{aligned} P(AA) &= (1 - F) \cdot p^2 + F \cdot p &= p^2 + p \cdot q \cdot F \\ P(AB) &= (1 - F) \cdot 2 \cdot p \cdot q + F \cdot 0 &= 2 \cdot p \cdot q \cdot (1 - F) \\ P(BB) &= (1 - f) \cdot q^2 + F \cdot q &= q^2 + p \cdot q \cdot F \end{aligned} \quad (6.2)$$

How much is inbreeding expected to modify genotypic distribution in human populations? The levels of inbreeding observed in human genetically isolated populations typically vary between 0.001 (low inbreeding) to 0.05 (relatively high), see PARDO *et al.* (2005); RUDAN *et al.* (2003). The genotypic distribution for $q = 0.5$ and different values of the inbreeding coefficient is shown at the figure 6.3.

What is the power to detect deviation from HWE due to inbreeding? For that, we need to estimate the expectation of the χ^2 statistics (the non-centrality parameter, NCP) used to test for HWE. The test for HWE is performed using

standard formula

$$T^2 = \sum_i \frac{(O_i - E_i)^2}{E_i} \tag{6.3}$$

where summation is performed over all classes (genotypes); O_i is the count observed in i-th class, and E_i is the count expected under the null hypothesis (HWE). Under the null hypothesis, this test statistic is distributed as χ^2 with number of degrees of freedom equal to the number of genotypes minus the number of alleles.

Thus the expectation of this test statistic for some q, F, and N (sample size) is

$$
\begin{aligned}
E[T^2] &= \frac{(N(q^2+pqF)-Nq^2)^2}{Nq^2} + \frac{(N2pq(1-F)-N2pq)^2}{N2pq} + \frac{(N(p^2+pqF)-Np^2)^2}{Np^2} \\
&= \frac{(NpqF)^2}{Nq^2} + \frac{(-2NpqF)^2}{N2pq} + \frac{(NpqF)^2}{Np^2} \\
&= Np^2F^2 + 2NpqF^2 + Nq^2F^2 \\
&= NF^2(p^2 + 2pq + q^2) \\
&= N \cdot F^2
\end{aligned}
\tag{6.4}
$$

Interestingly, the non-centrality parameter does not depend on the allelic frequency. Given the non-centrality parameter, it is easy to compute the power to detect deviation from HWE for any given F. For example, to achieve the power of > 0.8 at $\alpha = 0.05$, for a test with one degree of freedom the non-centrality parameter should be > 7.85. Thus, if $F = 0.05$, to have 80% power, $N \cdot F^2 > 7.85$, that is the required sample size should be $N > \frac{7.85}{F^2} = \frac{7.85}{0.0025} = 3140$ people.

Thus, even in populations with strong inbreeding, rather large sample sizes are required to detect the effects of inbreeding on HWE at a particular locus, even at relatively weak significance level of 5%.

While the chance that deviation from HWE due to inbreeding will be statistically significant is relatively small, inbreeding may have clear effects on the results of HWE testing in GWA study. Basically, if testing is performed at a threshold corresponding to nominal significance α, a proportion of markers which show significant deviation will be larger than α. Clearly, how large this proportion will be depends on the inbreeding and on size of the study – expectation of T^2 is a function of both N an F. A proportion of markers showing significant deviation form HWE at different values of inbreeding, sample size, and nominal significance threshold, is shown in table 6.1. While deviation of this proportion from nominal one is minimal at large α's and small sample sizes and coefficients of inbreeding, it may be 10-fold and even 100-fold higher than the nominal level at reasonable values of N and F for smaller thresholds.

6.1.3   Mixture of genetic populations: Wahlund's effect

Consider the following artificial example. Imagine that recruitment of study participants occurs at a hospital, which serves two equally size villagec(V_1 and (V_2); however, the villages are very distinct because of cultural reasons, and most marriages occur within a village. Thus these two villages represent two genetically distinct populations. Let us consider a locus with two alleles, A and

Table 6.1: Expected proportion of markers deviating from HWE in a sample of N people coming from a population with average inbreeding F. Proportion of markers is shown for particular test statistic threshold, corresponding to nominal significance α.

		α		
N	F	0.05	10^{-4}	$5 \cdot 10^{-8}$
	0.001	0.0501	$1.008 \cdot 10^{-4}$	$5.077 \cdot 10^{-8}$
1,000	0.005	0.0529	$1.205 \cdot 10^{-4}$	$7.025 \cdot 10^{-8}$
	0.010	0.0615	$1.885 \cdot 10^{-4}$	$14.503 \cdot 10^{-8}$
	0.001	0.0511	$1.081 \cdot 10^{-4}$	$5.784 \cdot 10^{-8}$
10,000	0.005	0.0790	$3.544 \cdot 10^{-4}$	$36.991 \cdot 10^{-8}$
	0.010	0.1701	$19.231 \cdot 10^{-4}$	$426.745 \cdot 10^{-8}$

Table 6.2: Genotypic proportions in a mixed population

Village	%Sample	$p(A)$	$P(AA)$	$P(AB)$	$P(BB)$
V_1	50	0.9	0.81	0.18	0.01
V_2	50	0.2	0.04	0.32	0.64
				Observed	
Pooled	100	0.55	0.425	0.25	0.325
				Expected	
			0.30	0.50	0.20
				Difference	
			0.125	-0.250	0.125

B. The frequency of A is 0.9 in V_1 and it is 0.2 in V_2. In each population, marriages occur at random, and HWE holds for the locus. What genotypic distribution is expected in a sample ascertained in the hospital, which represents a 1 : 1 mixture of the two populations?

The expected gentypic proportions are presented in table 6.2. First, assuming that HWE holds for each of the populations, we can compute genotypic proportions within these (rows 1 and 2 of table 6.2). If our sample represents a 1 : 1 mixture of these populations, then the frequency of some genotype is also 1 : 1 mixture of the respective frequencies. For example, frequency of AA genotype would be $\frac{0.81}{2} + \frac{0.04}{2} = 0.425$, and so on. The frequency of the A allele in pooled sample will be $0.425 + \frac{0.25}{2} = 0.55$. Based on this frequency we would expect genotypic frequency distribution of 0.3, 0.5 and 0.2, for AA, AB, and BB, respectively. As you can see the observed distribution has much higher frequencies of homozygous genotypes – excess of homozygotes.

It is notable, that the differences between the observed homozygotes frequencies and these expected under HWE are both 0.125, and, consequently, the observed heterozygosity is less than that expected by $0.125 \cdot 2 = 0.25$.

The phenomenon of deviation from HWE due to the fact that considered population consist of two sub-populations, is known as "Wahlund's effect", after the scientist who has first considered and quantified genotypic distribution under such modelWAHLUND (1928).

Such marked differences between observed and expected under HWE are very easily detected; for the above example, a sample of ≈ 35 people is enough

Table 6.3: Genotypic proportions of $PPAR$GenABEL-packagemma $Pro12Ala$ genotype in a mixed population

Ethnics	%Sample	$p(Pro)$	$P(Pro/Pro)$	$P(Pro/Ala)$	$P(Ala/Ala)$
Caucasian	50	0.85	0.7225	0.2550	0.0225
Afro-American	50	0.99	0.9801	0.0198	0.0.001
				Observed	
Pooled	100	0.92	0.8513	0.1374	0.0113
				Expected	
			0.8464	0.1472	0.0064
				Difference	
			0.0049	-0.0098	0.0049

to reject the hypothesis of HWE (power $> 80\%$ at $\alpha = 0.05$).

However, the differences we can see in real life are not so marked. For example, the common Pro allele at position 12 of the peroxisome proliferator-activated receptor gamma is associated with increased risk for type 2 diabetes. The frequency of the Pro allele is about 85% in European populations and Caucasian-Americans, about 97% in Japan and 99% in African-American (see table 1 from Ruiz-NarvÃ_ąez (2005)). Table 6.3 shows hypothetical observed and expected genotypic proportions in a sample composed of 50% Caucasians and 50% African-American.

You can see that observed distribution and the one expected under HWE are very similar; only a sample as large as 1,800 people would allow detection of the deviation from HWE (power $> 80\%$ at $\alpha = 0.05$). The situation is similar for most genes observed in real life – while the frequencies may be (or may be not) very different for populations, which diverged long time ago, for relatively close populations expected frequency differences are small and large sample sizes are required to detect deviation from HWE due to Wahlund's effect at a particular fixed locus.

Let us summarize, what genotypic proportions are expected in a sample, which is a mixture of two populations. Let each population is in HWE, and the frequency of the B allele is q_1 in population one and q_2 in population two. Let the proportion of individuals coming from population one is m in the mixed population, and consequently the proportion of individuals from population two is $(1 - m)$. The allelic frequencies, and genotypic distributions in the original and mixed populations are presented in tale 6.4.

The frequency of the B allele in the mixed population is just the weighted average of the allelic frequencies in the two populations, $\bar{q} = m \cdot q_1 + (1 - m) \cdot q_2$. Let us denote the frequency of the A allele as $\bar{p} = 1 - \bar{q}$. It can be demonstrated that the genotypic frequency distribution in the mixed sample is the function of the frequency of allele B in the sample, $\bar{q}$, and "disequilibrium" parameter D:

$$\begin{aligned}
P(AA) &= \bar{p}^2 + \bar{p} \cdot \bar{q} \cdot F_{st} \\
P(AB) &= 2 \cdot \bar{p} \cdot \bar{q} \cdot (1 - F_{st}) \\
P(BB) &= \bar{q}^2 + \bar{p} \cdot \bar{q} \cdot F_{st}
\end{aligned} \tag{6.5}$$

where

$$F_{st} = \frac{m \cdot (1 - m) \cdot (q_1 - q_2)^2}{\bar{p} \cdot \bar{q}} \tag{6.6}$$

Table 6.4: Expected genotypic proportions in a mixed population; F_{st} is defined by equation 6.6

Population	Prop.	$p(B)$	$P(AA)$	$P(AB)$	$P(BB)$
P_1	m	q_1	p_1^2	$2p_1q_1$	q_1^2
P_2	$(1-m)$	q_2	p_2^2	$2p_2q_2$	q_2^2
				Observed	
Pooled	1.0	$\bar{q} = mq_1$ $+(1-m)q_2;$	mp_1^2 $+(1-m)p_2^2;$	$2mp_1q_1$ $+2(1-m)p_2q_2;$	mq_1^2 $+(1-m)q_2^2$
				Expected	
			$\overline{p}^2$	$2\overline{pq}$	$\overline{q}^2$
				Difference	
			$\overline{pq}F_{st}$	$-2\overline{pq}F_{st}$	$\overline{pq}F_{st}$

You can see that equation 6.5, expressing the genotypic frequencies distribution under Wahlund's effect, is remarkably similar (actually, is specifically re-written in a form similar) to the equation 6.2, expressing the genotypic proportions under the effects of inbreeding. Again, the reason is that F_{st} (as well as F of equation 6.2) is easily estimated from the data as the ratio between the observed and expected variances of the genotypic distributions. Then the expected non-centrality parameter for the test of HWE is simply $N \cdot F_{st}^2$, where N is the sample size. Therefore our results concerning the proportion of tests expected to pass a particular significance threshold when genome-wide data are analyzed (table 6.1) hold, with replacement of F with F_{st}.

We can compute that the values of F_{st}, corresponding to the population mixtures presented in tables 6.2 and 6.3 are 0.49 and 0.067, respectively, which gives us a shortcut to estimate the sample size required to detect deviation from HWE due to Wahlund's effect (at $\alpha = 0.05$ and power 80%): $N > 7.85/0.49^2 \approx 32$ and $N > 7.85/0.067^2 \approx 1771$.

A typical value of F_{st} for European populations is about 0.002 (up to 0.023 NELIS *et al.* (2009)); very large sample sizes are required to detect deviation from HWE at any given locus at such small F_{st}'s. However, the effects onto the proportion of markers failing to pass HWE test in GWA may be visibly inflated (table 6.1).

6.2 Effects of population structure on standard tests for association

6.2.1 Standard tests for genetic association

Standard tests for association between genes and a binary trait are the test for allele frequency difference between cases and controls, and the Armitage's trend test for proportions (that the proportion of cases changes across genotypic groups). For quantitative traits, one of the standard tests is the score test for association, which is closely related – even equivalent – to the Armitage's trend test.

We will start with presenting the study data as 2x3 table, where the rows correspond to the case/control status and columns correspond to genotypic groups, and the cells contain counts of events (table 6.5). For example, r_0 is the number

Table 6.5: Counts of cases and controls with different genotypes

Status	Genotype			Total
	AA	AB	BB	
Case	r_0	r_1	r_2	R
Control	s_0	s_1	s_2	S
Total	n_0	n_1	n_2	N

Table 6.6: Counts of alleles in cases and controls

Status	A	B	Total
Case	$2 \cdot r_0 + r_1$	$r_1 + 2 \cdot r_2$	$2 \cdot R$
Control	$2 \cdot s_0 + s_1$	$s_1 + 2 \cdot s_2$	$2 \cdot S$
Total	$2 \cdot n_0 + n_1$	$n_1 + 2 \cdot n_2$	$2 \cdot N$

of cases with genotype AA, s_0 is the number of controls with genotype AA and so on.

This table can be re-arranged in a 2x2 allelic table, presented in table 6.6. Each cell of this table contains the counts of alleles present in cases and controls, e.g. total number of A alleles in cases is $2 \cdot r_0$ (twice the number of cases who are homozygous for the A allele) plus the number of A alleles present in heterozygous cases (r_1).

Based on these tables, we can test if the allelic frequency is different between the cases and controls, using standard χ^2 test, formulated as

$$T^2 = \sum_i \frac{(O_i - E_i)^2}{E_i} \tag{6.7}$$

where summation is performed over all cells (defined by combination of genotype/allele and phenotype); O_i is the count observed in i-th class, and E_i is the count expected under the null hypothesis (equal frequencies in cases and controls). Under the null hypothesis, this test statistic is distributed as χ^2 with number of degrees of freedom equal to the number of independent classes.

The null hypothesis assumes that the frequency of the A allele is the same in both cases and controls, and is equal to the frequency for A in the total sample: $\bar{p} = \frac{2 \cdot n_0 + n_1}{2 \cdot N}$. Thus the expected count of A in cases is $2 \cdot R \cdot \bar{p}$, and the expected count of B alleles is $2 \cdot R \cdot (1 - \bar{p})$. Similarly, for cases, the expected count of A is $2 \cdot S \cdot \bar{p}$, and the expected count of B is $2 \cdot S \cdot (1 - \bar{p})$.

Now, for the table 6.6 we can re-write the allelic test as

$$T_A^2 = \frac{((2r_0+r_1)-2R\bar{p})^2}{2R\bar{p}} + \frac{((r_1+2r_2)-2R(1-\bar{p}))^2}{2R(1-\bar{p})}$$
$$+ \frac{((2s_0+s_1)-2S\bar{p})^2}{2S\bar{p}} + \frac{((s_1+2s_2)-2S(1-\bar{p}))^2}{2S(1-\bar{p})}$$

With some algebra, it can be demonstarted that this expression simplifies to

$$T_a^2 = \frac{2N\{2N(r_1 + 2r_2) - 2R(n_1 + 2n_2)\}^2}{(2R)2(N - R)\{2N(n_1 + 2n_2) - (n_1 + 2n_2)^2\}} \tag{6.8}$$

Under the null hypothesis that the frequency of alleles is the same in cases and controls (and, as you will see later, that HWE halds in total sample) the test statistic is distributed as χ^2 with one degree of freedom.

An alternative, Armitage's trend test for proportions, can be used to test the null hypothesis. This test is performed using the 2x3 genotypic table (6.5). The null hypothesis assumes that the frequency of cases is the same in all genotypic groups; alternative is that the frequency is not the same, but are, however, not totally arbitrary. As it follows from the name of the test, a trend in proportions is assumed, that is the frequency of cases among people with heterozygous genotypes AB should be exactly between the frequencies of cases in two homozygous classes. This hypothesis may be formalized using parameters $beta_0$, the expected frequency of cases in the AA group, and β_1, the increase in frequency of cases in the AB group. The expected frequency of cases in the AB group is then $(\beta_0 + \beta_1)$; the frequency of cases in the BB group is assumed to be $(\beta_0 + 2 \cdot \beta_1)$. Parameters p_0 and p_1 can be estimated using the maximum likelihood; $\hat{\beta}_1 = \frac{(r_1 + 2r_2) - \overline{p}R}{(n_1 + 4n_2) - \overline{p}N}$, where $\overline{p} = \frac{2n_2 + n_1}{2N}$ is the frequency of the B allele in the total sample. Then, β_0 is estimated as $\hat{\beta}_0 = \frac{R}{N} - \hat{\beta}_1 \overline{p}$. Is can be shown that the chi-square test 6.7 based on these expectations takes the form

$$T_t^2 = \frac{N\{N(r_1 + 2r_2) - R(n_1 + 2n_2)\}^2}{R(N-R)\{N(n_1 + 4n_2) - (n_1 + 2n_2)^2\}} \qquad (6.9)$$

It can be shown that $T_t^2 = T_a^2$ if $n_1 = 2\sqrt{n_0 \cdot n_2}$, which is equivalent to the condition that HWE halds exactly, in which case the counts of heterozygotes should be $2Npq$, with $p = \sqrt{n_0/N}$ and $q = \sqrt{n_2/N}$. When HWE holds for the total sample, the two tests are (at least assymptotically) equivalent. Thus the test T_a^2 is the test for association in presence of HWE; when HWE does not hold, even in absence of association, the values of T_a^2 are greater then the values of T_t^2 test, possibly leading to false positive conclusions about association in presence of deviations from HWE. Therefore the trend test T_t^2 is to be prefered when testing for genetic association SASIENI (1997).

For study of association between genotype and a quantitative traits, linear regression analysis is performed. Let us denote the vector of phenotypes as y, with particular values y_i $(i = 1, \ldots, N)$. Let code the genotypes with a quantitative variable, which reflects the number of B allels. Thus, we will code AA as 0, AB as 1, and BB as 2. Let us denote the vector of genotypes as g, with particular values g_i $(i = 1, \ldots, N)$ taking the value of 0, 1 or 2. The linear regression model assumes that the expectation of the trait is

$$E[y_i] = \mu + \beta_g \cdot g_i$$

where μ is intercept and β_g is the coefficient of regression of the genotype on the phenotype.

The estimate of β_g is provided by a well-known expresion

$$\hat{\beta} = \frac{Cov(y, g)}{Var(g)} = \frac{\sum x_i g_i / N - \sum x_i \sum g_i / N^2}{\sum g_i^2 / N - (\sum g_i)^2 / N^2} = \frac{N \sum x_i g_i - \sum x_i \sum g_i}{N \sum g_i^2 - (\sum g_i)^2} \quad (6.10)$$

Under the null hypothesis, the variance of $\hat{\beta}$ is $Var_0(\hat{\beta}_g) = \frac{Var(y)}{N \cdot Var(g)}$, and the score test statistic

$$T_q^2 = \frac{\hat{\beta}_g^2}{Var_0(\hat{\beta}_g)} = \frac{Cov(y, g)^2}{Var(g)^2} \cdot \frac{N \cdot Var(g)}{Var(y)} = N \frac{Cov(y, g)^2}{Var(y) \cdot Var(g)} \qquad (6.11)$$

is distributed as χ^2 with one degree of freedom. Here, $Var_0\hat{\beta}_g$ denotes the variance under the null hypothesis. Denote the correlation between y and g, $\frac{Cov(y,g)}{\sqrt{Var(y) \cdot Var(g)}}$, as r. Then $T_q^2 = N \cdot r^2$.

It is worth to note that Armitage's trend test can be expressed as a linear regression test. In the table 6.5 Let us code the genotypic groups based on the number of B allels. Thus, we will code AA as 0, AB as 1, and BB as 2. Let us also code the cases with "1" and controls with "0". Let y denote the vector of phenotypes and g the vector of genotypes coded in this way. Then, if we perform linear regression of the case-control status onto the number of B allels in the genotype, the estimate of the regression coefficient is (following 6.10)

$$\hat{\beta} = \frac{\sum x_i g_i - \sum x_i \sum g_i / N}{\sum g_i^2 - (\sum g_i)^2 / N} = \frac{(r_1 + 2r_2) - \overline{p}R}{(n_1 + 4n_2) - \overline{p}N}$$

Thus, the expected proportions in the Armitage's trend test are provided by solution of linear regression equation, in which regression of case-control status, coded as "0" and "1" is performed onto the number of B allels. It can be further demonstrated that the trend test statistics 6.9 can be expressed as $T_t^2 = N \cdot r^2$, where r^2 is squared coefficient of correlation between y and g.

In the next two sections we will consider the effects of genetic structure on the standard tests for association described above. The extensive treatment of the problem is mainly due to the seminal works of Devlin, Roeder, Bacanu, and colleaguesBACANU *et al.* (2000, 2002); DEVLIN and ROEDER (1999); DEVLIN *et al.* (2001); here, some of their results are repeated.

The genetic structure of the sudy population will be characterized by the kinship matrix – a square matrix, which, for all pairs of individuals in question, provides their pair-wise kinship coefficients (defined at page 140). The kinship coefficient between persons i and j will be defined as f_{ij}.

6.2.2 Effects of genetic structure on standard tests

As it was demonstrated above, the Armitage's trend test for association can be expressed as $T_a^2 = \frac{\hat{\beta}^2}{Var(\hat{\beta})}$. Genetic structure affects both numerator and denominator of this expression. Indeed, if measurments are dependent, the varaiance of the estimate is likely to be under-estimated if such dependence is not accounted for, leading to the inflation of the tests statistic. Secondly, even in absence of association, the estimate of the effect may be biased, again, leading to increased value of the test statistic.

Let us consider following artificial example. Let study cases are closely related individuals – sibs[1] – coming from one family, and study contols are sibs from other family. In essence, we compare the squared frequency difference between the two groups to the variance of this difference. If groups are formed by independent individuals, we can detect arbitrary small frequency differences by increasing the sample size, and consequently, decreasing the variance of the frequency estimate. This definitely is not the case when our study sample consist of a large sibship – whatever is the sibship size, only four alleles may be present in the parents, and the precision of the estimate of the allele frequency in the general population is limited – as if we had two people at maximum. If we do not

---

[1] brothers and sisters

take this consideration into account, we are likely to over-estimate the precision of the frequency estimate; the denominator of the test statistic becomes small, and the statistic becomes large. Secondly, the parents of the "case" and "control" sibships have a high chance to be genotypically different, just by chance; and any genotypic configuration leading to the different number of B alleles will be reflected in diffence in frequencies between sibships, given the sibships are large. Assuming HWE, the chance that two parental couples will have different number of B alleles is one minus the chance that they will have the same number of B alleles:

$$
\begin{aligned}
P(\#B_1 \neq \#B_2) \quad &= 1 - (P(\#B_1 = \#B_2 = 0) + P(\#B_1 = \#B_2 = 1) + \ldots + P(\#B_1 = \#B_2 = 4)) \\
&= 1 - (P(\#B_1 = 0)P(\#B_2 = 0) + \ldots + P(\#B_1 = 4)P(\#B_2 = 4)) \\
&= 1 - (q^8 + 16p^2q^6 + 36p^4q^4 + 16p^6q^2 + p^8)
\end{aligned}
$$

which, for a common allele with frequency of 0.2 translates to the probability 0.64.

Let us quantify these two sources of bias. Following DEVLIN *et al.* (2001) let us assume that the number of cases and the number of controls is the same, N. Let us denote the vector of genotypes, coded as 0, 1, and 2 of cases as X, with X_i $(i = 1, \ldots, N)$ being the genotype of the i-th case, and the vector of genotypes of controls as Y (with Y_j, $j = 1, \ldots, N$ being the genotype of j-th control). The trend and the allelic tests statistic are proportional to the square of $T = \sum X_i - \sum Y_j$. The variance of this statistic, in general form, is

$$
\begin{aligned}
Var(T) = \quad &\sum_{i=1}^{N} Var(X_i) + \sum_{i=1}^{N} Var(Y_i) \\
&+ 2\sum_{i<j} Cov(X_i, X_j) + 2\sum_{i<j} Cov(Y_i, Y_j) \\
&- 2\sum_i \sum_j Cov(X_i, Y_j)
\end{aligned} \tag{6.12}
$$

Let us consider a sitatuation in which cases come from one popualtion, and controls from the other population; each of the populations is in HWE and the difference between the populations is characterized with F_{st} (see equation 6.6). Under this model, $Var(X_i) = Var(Y_i) = 2pq(1 + F_{st})$, and the covariance between any pair of genotypes from the same population is $4pqF_{st}$. Then

$$
\begin{aligned}
Var(T) \quad &= \quad 2pq(1 + F_{st}) \cdot N + 2pq(1 + F_{st}) \cdot N \\
&\quad\quad + 2 \cdot 2pqF_{st} \cdot N(N-1)/2 + 2 \cdot 2pqF_{st} \cdot N(N-1)/2 + 0 \\
&= \quad 4pqN \cdot (1 + F_{st} + 2F_{st}(N-1)) \approx 4pqN(1 + 2NF_{st})
\end{aligned} \tag{6.13}
$$

here, $4pqN$ corresponds to the binomial variance of T in absence of genetic structure, while $F_{st} + 2 \cdot F_{st} \cdot (N-1)$ reflects the inflation of the variance. As the second term is the function of the sample size, large inflation may be achieved even with small vaules of F_{st}. Note that here the sample size is $2N$, as we assumed N cases and N controls.

Above we have considered an example in which we know the F_{st} between the population of cases and the population of controls. In a practical study, a number of cases and controls is usually sampled from each genetically different population. Let the proportion of individuals sampled from population c among cases is a_c and the proportion of individuals coming from that population among controls is u_c. Then, it can be shown that

$$
Var(T) \approx 4pqN(1 + 2 \cdot N \cdot F_{st} \cdot \sum_c (a_c - u_c)^2) \tag{6.14}
$$

As it follows from this equation, the variance of the estimated frequency difference depends on the composition of the sample. Maximal inflation is achieved when the cases and controls are sampled from different populations, while if $\sum_c (a_c - u_c)^2 = 0$ – which is achieved by sampling equal number of cases and controls from each sub-population – the variance inflation is minimal.

These results canbe generalized to arbitrary relations between cases and controls. Let us denote kinship between cases i and j as f_{ij}^X, kinship between controls as f_{ij}^Y, and the kinship between a case and a control as f_{ij}^{XY}. ThenDEVLIN *et al.* (2001)

$$Var(T) = 4pqN \cdot (1 \quad + F_{st} + \tfrac{2}{N}\sum_{i<j} f_{ij}^X \\ + \tfrac{2}{N}\sum_{i<j} f_{ij}^Y - \tfrac{2}{N}\sum_i \sum_j f_{ij}^{XY}) \tag{6.15}$$

This equation demonstrates that the variance is inflated not only in a case when cases and controls come from genetically distinct populations, but that also "criptic relations" among either cases (some $f_{ij}^X > 0$) or controls (some $f_{ij}^Y > 0$) may lead to increased variance of the test. Because summation (e.g. $\sum_{i<j} f_{ij}^X$) is performed overl all pairs of cases/controls, cryptic relations may have a strong impact onto inflation of the variance.

Generally, the variance of the T can be expressed as $Var(T) = 4Npq(1+F_{st}+ D(f^X, f^Y, f^{XY}))$. Here, $4Npq$ corresponds to the binomial variance assuming HWE and independence between cases and controls, the second term – F_{st} – accounts for increase in variance due to deviation from HWE, and the last, which is a function of kinship – $D(f^X, f^Y, f^{XY})$ – accounts for dependencies bewteen cases and controls. The test $\frac{T^2}{4Npq(1+F_{st}+D(f^X,f^Y,f^{XY}))}$ is distributed as χ^2 with one degree fo freedom.

The allelic and Armitage's trend statistics can be expressed as $T_a^2 = \frac{T^2}{4Npq}$ and $T_t^2 = \frac{T^2}{4Npq \cdot (1+F_{st})}$. What is their distribution when there is relatedness / stratification bewteen cases and controls? Clearly, both of them are distributed as $\tau^2 \cdot \chi^2$, where $\tau^2 > 1$ is the variance inflatiopn factor. It easy to show that it is equal to $\tau^2 = 1 + F_{st} + D(f^X, f^Y, f^{XY})$ for the allelic and $\tau^2 = \frac{1+F_{st}+D(f^X,f^Y,f^{XY})}{1+F_{st}}$ for the trend test.

In above, we have accounted for the over-dispersion of the test statistic due to possible relatedness between the cases and controls, and demonstrated that the allelic and the trend test are inflated by some constant τ^2, which reflects the inflation of the variance, $Var(T) = \sigma^2 \cdot \tau^2$, where σ^2 is the variance estimated under the assumption of independence. However, in the beginning of this section we have discussed another source of the infaltion of the test statistic – the bias in frequencies between cases and controls due to confounding. Let cases and controls are sampled from different populations, whose difference is characterized by F_{st}, and let for some marker the allele frequency difference – which occures entirely due to genetic structure of the sampels – between casese and controls is d. The test statistic T is then distributed as Normal with mean Nd and variance computed in previous section, $\sigma^2 \cdot \tau^2$, $N(Nd, \sigma^2\tau^2)$. To address the issue of bias, we need to figure out the distribution of the mean – $2Nd$. In general, the expected frequency difference is zero – indeed, if we consider a large number of subpopulations, or a large number of markers, if allelic frequencies are determined by random effects, the deviation is likely to occure in any direction, resultin in zero on average. The variance of the d is

$2pqF_{st}$, thus the variance of $2Nd$ is $(2N)^2 2pqF_{st}$.[2] Thus finally, T is expected to be distributed as $N(0, \sigma^2 \cdot \tau^2 + 8pqF_{st}N^2)$. If we consider the variance of allelic test, $\sigma^2 = 4pqN$, then $T \sim N(0, \sigma^2(\tau^2 + 2F_{st}N))$, and, denoting $2F_{st}N$ as ν^2, $T \sim N(0, \sigma^2(\tau^2 + \nu^2))$. Similar expression may be obtained for the Armitage's trend test.

Thus, in presence of genetic structure both allelic and the trend test are distributed as $(\tau^2 + \nu^2) \cdot \chi^2$. Note that while σ^2 is a function of allelic frequency, the inflation factors τ^2 and ν^2 depend on the differentiation between the populations in question, as measured by F_{st}, sample size, N, and the composition of the case-control sample (a_c, u_c), but does not depend on the allele frequency.

As it was mentioned earlier, the Armitage's trend test can be re-formulated as a regression-based score test, in which genotypes are coded as 0, 1, and 2, and phenotypes as 0 and 1. Therefore all above arguments apply to the analysis of quantitative traits as well. The test statistic $T_q^2 = \frac{\hat{\beta}_g^2}{Var(\hat{\beta}_g)}$ in which $\hat{\beta}$ and $Var(\hat{\beta})$ are estimated using independence assumption is inflated because of over-dispersion ($Var(\hat{\beta})$ is under-estimated if the relatedness is not accounted for), and also $\hat{\beta}_g$ may be biased, because different genetic populations may well be characterized by different mean value of the trait (e.g. because of environmental influences). It can be shown that also for quantitative traits T_q^2 is distributed as $(\tau^2 + \nu^2) \cdot \chi^2$, where τ^2 is inflation due to over-dispersion, and ν^2 is the inflation because of bias.

6.2.3 Genomic control

From previous section it follows that in presence of genetic structure the standard association statistics may be inflated and the distribution is described as $(\tau^2 + \nu^2) \cdot \chi^2$. Let us denote $(\tau^2 + \nu^2)$ as λ for short. λ depends on the genetic structure of the sample, as characterized by pairwise kinship, and sample size, N. For binary trait analysis, it also depends on the composition of the case-control sample, as expressed by the proportio of cases/conrols coming from particular population, c (a_c, u_c). For quantitative trait, it depends of neritability of the trait, and environmentally detemined differences co-occuring with the difference in kinship. However, λ does not depend on the allele frequency. Therefore, for any particular study sample, if F_{st} is constant over the genome, λ is also a constant.

Therefore λ can be estimated from the genomic data, using "null" loci – a set of random markers, which are believed not to be associated with the trait. This estimate can then be used to correct the values of the test statistic at the tested loci – a procedure, known as "genomic control". The test statistics computed from these loci thus estimates the distrbution of the test statistic under the null hypothesis of no association. Let us consider M "null" markers, and denote the test statistic obtained from i-th marker as T_i^2. Given genetic structure determines inflation λ, $T^2 \sim \lambda \cdot \chi_1^2$. The mean of a random variable coming from χ_1^2 is equal to 1; if a random variable comes from $\lambda \cdot \chi_1^2$, the mean would be λ. Thus we can estimate λ as the mean of the obtained "null" tests. In practice, it is recommended to use the ratio between the observed median

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[2] For the case when some proportion, a_c, among cases comes from population c, and some proportion of controls, u_c, comes from population c $Var(d) = 2pqF_{st} \sum_c (a_c - u_c)^2$

and the one expected for χ_1^2:

$$\hat{\lambda} = \frac{Median(T_i^2)}{0.4549} \tag{6.16}$$

For the tested markers, the corrected value of the test statistic is obtained by simple division of the original test statistic value on $\hat{\lambda}$, $T_{corrected}^2 = T_{original}^2/\lambda$. Note that this procedure is correct only if the same number of study participants was typed for any marker, as you will see later.

As you can see, the genomic control procedure is computationally extremely simple – one needs to compute the test statistic using a simple test (e.g. score test), compute the median to estimate λ, and divide the original test statistics values onto $\hat{\lambda}$.

How to choose "null loci" is a GWA study? In a genome, we expect that a small proportion of markers is truly associated with the trait. Therefore in practice, all loci are used to estimate λ. Of cause, if very strong (or multiple weak) true associations are present, true association will increase the average value of the test, and genomic control correction will be conservative. To relax this, it has been suggestedSLADEK *et al.* (2007) to use, say, 95% of the least significant associations for estimation of the inflation factor; however, the question of selection of cut-off is not obvious, and all markers are used in practice in most studies.

We have observed that the inflation factor λ is a function of sample size, N – the bigger is the sample size, the larger is inflation. If this is the case, how can we compare inflations between different GWA studies? A good idea is to use a standardized inflation, say, inflation per 1,000 subjects. For a quantitative trait analysis, inflation factor can be expressed as $\lambda \approx (1 + N * D(sample))$, where $N * D(sample)$ is a term, which grows linear with sample size, at some rate determined by sample characteristics.

Therefore a standarsized inflation factor can be etimated as

$$\hat{\lambda}_{1000} = 1 + \frac{\hat{\lambda} - 1}{N} \cdot 1000,$$

where N is the sample size and $\hat{\lambda}$ is the estimate from the total sample.

What about a case-control sample? For such samples, a standardized λ is computed for a fixed number of cases and controls, say 1000; we will denote such standardized inflation as $\lambda_{1000,1000}$ to distinguish it from the one computed for a quantitative traits. If we denote the number of cases as N_a and the number of controls as N_u, then

$$\hat{\lambda}_{1000,1000} = 1 + \frac{500 \cdot (\hat{\lambda} - 1) \cdot (N_a + N_u)}{N_a \cdot N_u}$$

Clearly, we have assumed that in our GWA study the sample size was equal for all studied markers; this fact allows for very simple estimation of $\hat{\lambda}$ (equation 6.16) and correction of the test statistic. It may happen, however, that the number of participants typed for different marker loci is different; for example, this may happen when all study participans were typed for SNP panel one, and then a part of the study was additionally typed at a different panel. In such

situation, expectation of a T_q^2 test for a quantitative trait can be expressed as

$$E[T_q^2] = 1 + (\lambda_{1000} - 1) \cdot \frac{N}{1000}$$

It is straightforward to obtain an estimate of λ_{1000} by performing linear regression of the observed test statistic values onto the sample size used; note that the intercept should be fixed to 1 in this procedure. Other, more effective procedures may be thought of.

For binary traits, if sample is composed from N_a cases and N_u controls, the expression for the expected value of the test statistic is similar to that obtained for quantitative traits, however, geometric mean of the number of cases and controls are usedFREEDMAN *et al.* (2004):

$$E[T_t^2] = 1 + (\lambda_{1000,1000} - 1) \cdot \frac{\frac{1}{1000} + \frac{1}{1000}}{\frac{1}{N_a} + \frac{1}{N_u}}$$

This relation can be used to estimate $\lambda_{1000,1000}$.

We have considered the genomic control procedure for the tests assuming additive effects of the locus onto phenotype. Under this model, inflation of the tests (λ) does not depend on allelic frequency, which allows a straightforward estimation of λ and further correction of the tests. Does the same apply to other genetic models?

In figure 6.4 the results for additive, dominant, recessive, and over-dominant model tests are presented. Simulated study consisted of 1000 cases and 1000 controls; the differentiation between the case and control populations was assumed $F_{st} = 0.002$. Armitage's trend test was used in analysis. One can see that when a common polymorphism is studies ($0.05 < q < 0.95$), the additive model test (green line) does not depend on the frequency of the B. The range of allele frequencies in which the additive model does not depend on these depends of the values of F_{st} and the sample size: the larger differentiation, and the smaller the sample size, the narrower is the range.

However, other one degree of freedom tests (recessive, red; dominant, blue; over-dominant, cyan) do depend on the allele frequency very much across all the range of allelic frequencies (figure 6.4, see ZHENG *et al.* (2005) for details).

Thus, it is important to remember that the genomic control was developed for, and works with additive genetic models; even in this framework, behaviour of λ depends on allelic frequencies when theses are too low or too high – thus application of genome-wide derived inflation factor to such marker loci may be incorrect for loci with low minor allele frequency. What is somewaht sustaining statistically is the fact that such correction will be conservative, and not liberal – but the same may be worrysome biologically (e.g. missed true positives). For other types of model, lambda can, at least in theory, be estimated taking into account the allelic frequency of the locus in question. However, these methods are not implemented yet in packages for genome-wide association analyses.

Other important thing to remember about genomic control is that it assumes uniorm F_{st} across the genome. This may not be the case for some (e.g. selected) genomic regions. Such regions may still generate very high test statistic, even after appropriate genomic control correctionCAMPBELL *et al.* (2005); basically, the frequency distribution at such loci may vary from population to population much more then the average across the genome. A number of methods
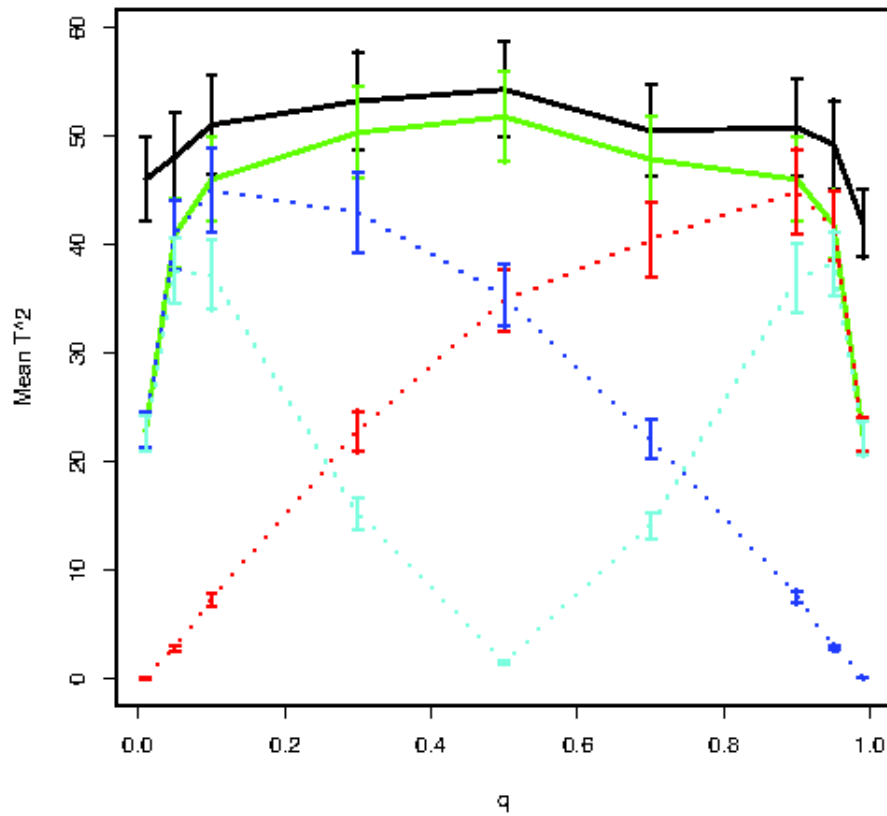
Figure 6.4:   Mean T_t^2 test statistic as frequency of the B allele, q. Models considered: additive, green; recessive, red; dominant, blue; over-dominant, cyan.

taking genetic structure of study population into account directly (structured association, EIGENSTRAT, reviewed later), can deal with such situations.

Finally, what levels of genomic control inflation parameter are acceptable in GWA studies? As the question is of how much the total test statistic is affected, non-standardized inflation may be used to address the question. Despite of lack of clear guidance, the general practice in the field is to consider the values of $\hat{\lambda} < 1.01$ as small, $\hat{\lambda} < 1.05$ as moderate and still acceptable. If $\hat{\lambda} > 1.1$, this suggest strong influence of genetic structure or other design factors on the test statistic. While GC statistically correct method, such analysis lacks power; good practice is to consider use of other methods, which take the structure of the sample into account in diect manner.

6.3   Analysis of structured populations

A study populaion may be structured in at least two ways. Firstly, while study participants may be "independent" in that kinship between them is expected to be very low (e.g. random sample from a large outbred population), they may belong to rather different genetic populations. An extreme example of such study is a study aiming to combine the data from a sample obtained by random ascertainment from the population of Bejing and a sample from Amsterdam. While in any of the samples people are only remotedly related ("independent"), the two samples in question are characterized by high genetic differences; also the environmental influences may be very different for the two populations. The distribution of the trait under the study may be essentially different between the two populations: not only the mean values, but also variances.

On the other hand, consider a family-based sample from genetically isolated population. Here, environmental influences are more or less uniform for all study participants; the distribution of the trait may be assumed to be governed by the same set of rules for all study participants. However, they are characterized by high and variable kinship between each other.

These two flavours of stratification may be expressed in terms of kinship. When we talk about different "populations", we assume very low kinship and high genetic differentiation between the members of these; when we talk about "relatedness", we assume high kinship and small degree of differentiation. This is illustrated at figure 6.5. Roughly speaking, when we expect that study participants share common ancestors few (1-4) generation ago, the kinship between study participants is high, and the study can be classified as a family-based one (Study 1 of figure 6.5). When common ancestors between study participants is expected say >5 generations ago, the kinship between study participants is low, and such study may be classified as a population-based sample of "independent" people (Studies 2 and 3 of figure 6.5). Now consider two groups of study participants (samples 2 and 3). Any person from group 2 is expected to share a common ancestor with a person from the same study group with much higher probability than with a person form group 3; thus these represent two genetic population (see page 141 for the retrospective definition of genetic population). It shouldbe kept in mind that if kinship is very low (expected common ancestors dozns of generations ago), this would translate in high degree of genetic differentiation. Moreover, this reflects a long history of isolation, which usually means geographic sepration, and accumulation of cultural and other environ-
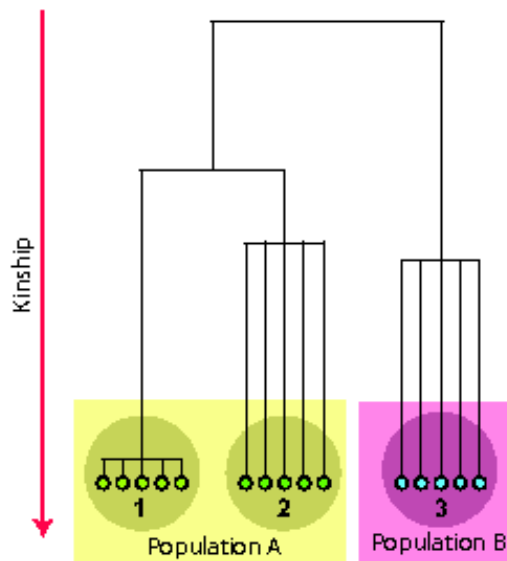
Figure 6.5: Three samples from two populations. 1: Family-based sample; 2,3: random sample of "independent" people

mentsl differences between the populations, which may be crucial in association studies.

Of cause, a particular study is usually characterized by some mixture of populations and some relatednes between study participants. We will, however, first consider the two extreme scenarios – analysis of samples of "independent" subjects from different populations, and analysis of a family-based study.

6.3.1 Structured association

If study populayion consist of a mixture of several distinct genetic populayions, and, within each sub-population, the study participants are remotedly related, structured asoiation analysis may be the method of choice. In such analysis, effect and its variance are estimated within each strata separately, and then these estimates are pooled to generate global statistics. The strata can be known from design (e.g. place of birth or ethnicity of parents) or estimated from GWA data. By doing this, we allow for arbitrary trait distribution, characterized by stratum-specific mean and variance, in each stratum. Clearly, this may be crucial when different populations characterized by different environments are included in analysis.

Combining the evidence across strata may be done using a number of methods, e.g. Cochran-Mantel-Haenszel test for binary outcomes. One of the most simple ways to combine the evidences coming from multiple strata – or studies – is to use fixed effects inverse variance meta-analysis.

In essence, this method is equivalent to combining likelihoods coming from separate studies, using quadratic approximation. Denote coefficients of regression estimated in N studies/strata as β_i, and associated squared standard errors

of the estimates as s_i^2 where $i \in 1, 2, ..., N$. Note that the regression coefficient should be reported on the same scale, e.g. centimeters, meters, or using observations reported on the standard normal scale. Define weights for individual studies as

$$w_i = \frac{1}{s_i^2}$$

Then the pooled estimate of the regression coefficient is

$$\beta = \frac{\sum_{i=1}^{N} w_i \beta_i}{\sum_{i=1}^{N} w_i}$$

As you can see, the weights have straightforward interpretation: the bigger the weight of the study (meaning the small is the standard error in the study), the larger is the contribution from this study onto the pooled estimate.

The standard error of the pooled estimate is computed as

$$s^2 = \frac{1}{\sum_{i=1}^{N} w_i}$$

and the χ^2-test for association is computed in standard manner as

$$T^2 = \frac{\beta^2}{s^2} = \frac{\left(\sum_{i=1}^{N} w_i \beta_i\right)^2}{\sum_{i=1}^{N} w_i}$$

or, alternatively, the Z-test is

$$Z = \frac{\beta}{s} = \frac{\sum_{i=1}^{N} w_i \beta_i}{\sqrt{\sum_{i=1}^{N} w_i}}$$

When binary traits are studied, and results are expressed as Odds Ratios with $P - values$, it is also possible to apply inverse variance method. For this, you need to transform your Odds Ratios using natural logarithm, and, on this scale, estimate the standard error. Generic inverse variance pooling may be applied to the data transformed this way; the final results are back-transformed onto Odds Ratio scale using exponentiation.

In meta-analysis procedure, it is assumed that study populations are composed of genetically homogenous "unrelated" individuals. Each study is first analysed seprately, and genomic control should either show no inflation of the test statistic, or a small one, which should be corrected with GC prior to combinaning of strata/studies. If some of the stata demonstrate large residual inflation, this may suggest further sub-structure present in that strata – it should be dealt with using further sub-division and structure association, or methods described further in this chapter, prior to attempting the pooling of results.

The meta-analytic methodology to perform structured association analysis outlined above has advantage of simplicity. However, it assumes goodness of quadratic approximation of the likelihood function, which is achieved if numbers are large. If numbers are not large (e.g. rare polymorphisms), a more complicated strategy can be used. A regression model, allowing for study-specific mean, effects of nuisance parameters, and residual variances, but unique (across the studies) effect of interest may be formulated. Analysis of such model is equivalent to the above-described meta-analysis procedure, under large numbers assumption.

6.3.2 Mixed models based approach

In this section we will consider the methods used to analyse samples in which close family relations may be persent; theses may be family-based samples from outbred populations, or random samples from genetically siaolted populations, where, due to limited population size, relatives are likely to be present by chance.

The mixed model based ideology stems from the classical animal breeding and human heritability analysis methodology, dating back to works of FisherFISHER (1918). He proposed a model in which a very large number of Mendeian genes contribute small effects to the phenotype (infenitisimal model). We may express this model as

$$y_i = \mu + G_i + e_i \tag{6.17}$$

– the value of the trait of i-th person is sum of grand population mean, contribution from multiple additively acting genes of small effect (G_i), and residual error (e_i).

Under this assumption, the distribution of the trait in a pedigree is described by a multivariate normal distribution with number of dimensions equal to the number of phenotyped people, with the expectation of the trait value for some individual i equal to

$$E[y_i] = \mu$$

where μ is grand population mean (intercept). The variance-covariance matrix is defined through its elements V_{ij} – covariance between the phenotypes of person i and person j:

$$V_{ij} = \begin{cases} \sigma_e^2 + \sigma_G^2 & \text{if } i = j \\ 2 \cdot f_{ij} \cdot \sigma_G^2 & \text{if } i \neq j \end{cases} \tag{6.18}$$

where σ_G^2 is variance due genes, f_{ij} is kinship between persons i and j, and σ_e^2 is the residual variance. The proportion of variance explainable by the additive genetic effects,

$$h^2 = \frac{\sigma_G^2}{\sigma_G^2 + \sigma_e^2}$$

is termed (narrow-sense) "heritability".

Fixed effects of some factor, e.g. SNP, may be included into the model by modifying the expression for the expectation, e.g.

$$E[y_i] = \mu + \beta_g \cdot g$$

leading to so-called "measured genotypes" modelBOERWINKLE *et al.* (1986).

In essence, this is a linear mixed effects model – the one containing both fixed (e.g. SNP) and random (polygenic) effects. A large body of literature is dedicated to this class of models, and finding the solution for such regression represents no great methodological challenge. Applicability of this model to GWA analysis was first proposed by Yu and colleaguesYU *et al.* (2006). Two problems occure with application of this model to GWA analysis: firstly, if standard Maximum Likelihood (or Restricted Maximum Lileihood) approach is used to estimate this model, the computational time is excessiveAULCHENKO *et al.* (2007a); secondly, the pedigree – and thus the kinship matrix – may be not known for study participant.

Let us first consider exisiting solutions to the first problem. High computational complexity occures if both random and fixed effects part of the model

are estimated simulatneously, and this procedure is repeated for every SNP analysed. However, we may assume that the effects of SNP are liklely to be small. Thus, inclusion of the SNP into the model is not likely to change the estimates of the components of variance. Therefore a two-step procedure was suggestedAULCHENKO and STRUCHALIN (submitted); CHEN and ABECASIS (2007): firstly, the mixed model containing all terms but these involving SNPs, is estimated (this includes estimation of the components of variance, and possibly the nuisance fixed effects); secondly, these estimates are then used to compute a test for association for every SNP in analysis. For details on this test, see CHEN and ABECASIS (2007) for original formulation, and AULCHENKO and STRUCHALIN (submitted) for extension to multiple variables and interaction effects tested in step two. The model is implemented in MACH and ProbABEL software packages.

Another method, bearing close resemblance to the method described above, is GRAMMAR – Genome-wide Rapid Analysis using Mixed Models and RegressionAULCHENKO *et al.* (2007a). Here, in step one, not only the mixed model is estimated, but also the environmental residuals,

$$\hat{e}_i = y_i - (\hat{\mu} + \hat{G}_i)$$

are estimated. These are free of correlations, and can be used as the new "trait" in further analysis. This procedue allows for very fast GWA analysis in step 2 (for large sample sizes, much faster then above-described two-step approach), also it has a great flexibility as the environmental residuals can be analysed using a large variaty of methods. At the same time, the GRAMMAR test for association is conservative, and the estimates of the effects obtained in step 2 are downward biasedAULCHENKO *et al.* (2007a). While conservativity of the test may be dealt with using "reverse genomic control"AMIN *et al.* (2007), the issue of bias in effect estimates has no solution yet. The GRAMMAR model is implemented in GenABEL software packageAULCHENKO *et al.* (2007b).

Strictly speaking, above described two-step tests are correct if the distributions of covariates in the first and the second parts of the model are independent conditional on the estimated phenotypic variance-covariance matrix. This assumption is most likely to be true when the covariates included in the base model are environmental ones, and thus are not expected to exhibit conditional correlation with SNPs. However, when endogenous risk factors, such as e.g. body mass index, are included as the covariates in the base model, some SNPs are expected to exhibit covariance with this covariate. In such situation the two-step test is not strictly correct, but given relatively weak SNP-phenotype correlations normally observed in GWAS should normally keep good statistical properties in most situations. The properties of the test under such conditions are still awaiting their description.

The methodology described here applies to study of association of quantitative traits. For binary traits, no formal practical GWA solution is available yet. The best current strategy to analyze binary traits in samples of relatives may be to treat the binary outcome as if it was quantitative. As you have seen with Armitage's trend test, which is equaivalent to the score test for a quantitative variable when oucome is coded with "0" and "1" (page 152), this approach leads to correct inferences about significance.

6.3.3 Estimation of kinship matrix from genomic data

Another problem with application of mixed models to analysis of GWA data is that pedigree is required to estimate the kinship matrix. The expectation of kinship can be estimated from pedigree data using standard methods, for example the kinship for two outbred sibs is 1/4, for grandchild-grandparent is 1/8, etc. For an outbred person, the kinship coefficient is 1/2 – that is two gametes sampled from this person at random are IBD only if the same gamete is sampled. However, in many situations, pedigree information may be absent, incomplete, or not reliable. Moreover, the estimates obtained using pedigree data reflect the expectation of kinship, while the true realization of kinship may vary around this expectation. In presence of genomic data it may therefore be desirable to estimate the kinship coefficient from these, and not from pedigree. It can be demonstrated that unbiased and positive semi-definite estimator of the kinship matrixAstle and Balding ((in press) can be obtained by computing the kinship coefficients between individuals i and j with

$$\hat{f}_{ij} = \frac{1}{L} \sum_{l=1}^{L} \frac{(g_{l,i} - p_l)(g_{l,j} - p_l)}{p_l(1 - p_l)} \tag{6.19}$$

where L is the number of loci, p_l is the allelic frequency at l-th locus and $g_{l,j}$ is the genotype of j-th person at the l-th locus, coded as 0, 1/2, and 1, corresponding to the homozygous, heterozygous, and other type of homozygous genotype.Amin *et al.* (2007); Astle and Balding ((in press); Price *et al.* (2006) The frequency is computed for the allele which, when homozygous, corresponds to the genotype coded as "1'.

Inetrestingly, use of the kinship matrix instead of pedigree kinship (when available) may lead to higher power, especially when "dense" pedigres and traits with high heritability are considered (YSA, unpublished data). This is likely to happen because genomic-based kinship is likely to reflect true genetic relations better than (possibly not completely correct) pedigree expectations.

6.3.4 EIGENSTRAT and related methods

EIGENSTRATPrice *et al.* (2006) method combines the ideas underlying structured association and the genomic kinship matrix. Basically, it allows for structured association, with strata and more subtle structure identified through the use of genomic data.

The genomic kinship matrix is computed as described earlier (equation 6.19). This matrix reflects genetic similarities between study participants. A reverse metric, distance matrix, is computed as $0.5 - f$. Classical multi-dimensional scaling (CMDS) is applied to identify a number (say, k) of first principal components (PCs) of variation of the distance matrix. The idea behind CMDS is mapping of the all pair-wise distances defined by the original matrix to some k-dimentional space. Each study participant is presented as a dot in this space, and these dots are constructed in such way, that the distance between these is maximally close to the distances observed in the original distance matrix. Thus, if two genetically distinct populations are present in a sample, the first principal axe of variation ($k = 1$) will identify these. Generally, of n distinct populations are present, these can be identified by $k = n - 1$ first axes.
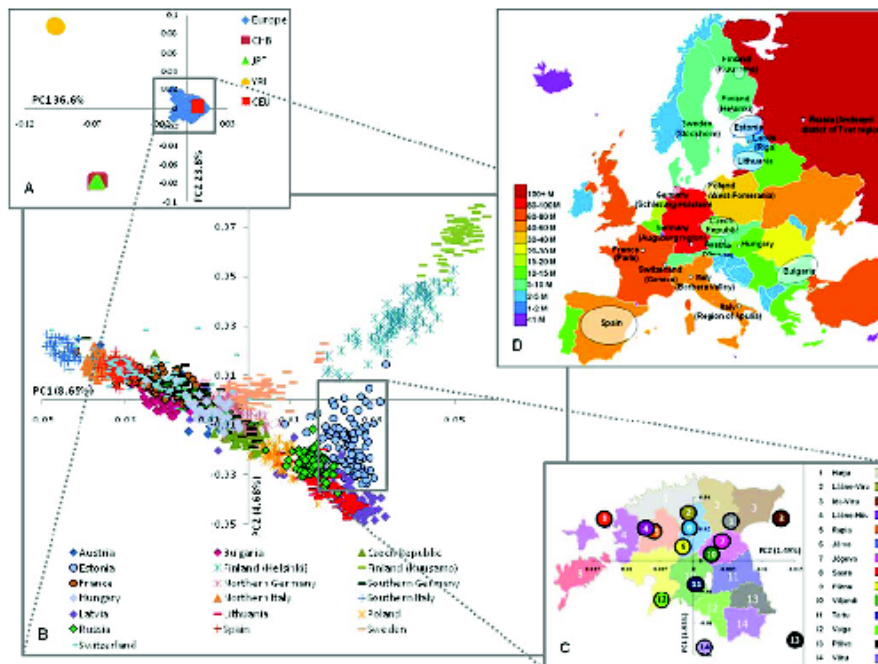
Figure 6.6: The European genetic structure (based on 273,464 SNPs). Three levels of structure as revealed by PC analysis are shown: A) inter-continental; B) intra-continental; and C) inside a single country (Estonia), where median values of the PC1&2 are shown. D) European map illustrating the origin of sample and population size. CEU – Utah residents with ancestry from Northern and Western Europe, CHB – Han Chinese from Beijing, JPT - Japanese from Tokyo, and YRI – Yoruba from Ibadan, Nigeria. (reproduced from NELIS *et al.* (2009)) NEED PERMISSION FROM PLoS ONE!

To demonstrate this principle, results of CMDS of the genomic distance matrix for the HapMap participants, and a number of people from Europe, are presented at figure 6.6. On panel **A**, the results of CMDS of the distance matrix to to the space of the first two PCs are present. Inter-continental differences are obvious – there are three distinct clusters, corresponding to Yoruba (yellow-brown), Asian (green and dark brown), and European (blue and red) study participant. You can see that mapping to the first two principal components perfectly distinguishes these three populations. The same methodology can be used to distinguish between more subtly divided populations – at panel **B** of figure 6.6 the mapping of European populations is present. The panel **C** presents even further detalisation of genetic distances – to the level of single country.

Note that configuration of European cluster in panel **A** is not exactly the same as in panel **B**. This happens because the distance matrix, computed based on formula 6.19, depends on allelic frequencies, as estimated in the total sample. Clearly, these are different, when all continents or Europeans only are used. Consecutive analysis of sub-samples allows distinguishing more and more subtle differences between populations.

Interestingly, the genetic distances co-incide very well with geographic distances, i.e. the populations close geographically are also close genetically. Thus, most isolation between human populations is explained by geographic distance.

How these principal components may be incorporated in association analysis? Different populations may have diferent mean values (or prevalences) of the trait under the study, which, coupled with genetic differences, leads to confounding and false positives in association study. A simple method would be to try to account for these differences in the means by incorporating the principal components as covariates into association analysisSLADEK *et al.* (2007). Another, related method would be to perform linear adjustment of both the phenotype and the genotype onto PCs (i.e. compute the residuals from linear regression of genotypes/phenotypes onto PCs). Then simple score test for association (T_q^2, equation 6.11) can be used to analyze association. This comprises the original EIGENSTRAT methodology suggested by Price and colleaguesPRICE *et al.* (2006).

A practically interesting question is how many PCs to include into analysis? By default, EIGENSTRAT uses 10 PCs, but this is rather arbitrary number. In general, "significant" PCs should be included into analysis. Patterson and colleaguesPATTERSON *et al.* (2006) suggested including the leading PCs, which significantly explain progressively more genetic variation. Alternatively, it was argued that PCs significantly associated with the phenotype should be includedNOVEMBRE and STEPHENS (2008), as inclusion of other PCs is not only unnecessary, but may also reduce power.

Note that methods described here allow for differences in means between the populations, but not for the difference in variances. It would be interesting to address the question what effects violation of this assumption may have on association studies, and develop extended methods allowing for difference in variances. This would first probably require a study of inter-populatinal variances.

6.3.5 Summary: what method to use?

What methods should be used for analysis of particular study? An simplified overview is provided at figure 6.7.

Basically, if study participants come from the same genetic population, are characterozed by low degree of kinship, and confounding, as measured with genomic control (GC) inflation parameter λ is small, GC is enough to correct for residual bias.

If study participants come from substantially different populations, and, for each population, above conditions hold, structured association may be used.

If study participants are characterized by high degree of kinship, mixed-model based methods should be used.

EIGENSTRAT and PC-based adjustment methods should be used in somewhat intermediate situation when differentiation between the populations and kinship between study participants is not too high: while substantial population differentiation may mean differences in variances, which EIGENSTRAT/PCBA does not account for, it is also known that these methods do not perform very well in pedigrees (YSA, Najaf Amin, unpublished data).

Clearly, a particular study may have its own specifics and should be considered separately. As difference between outlined scenarios is quantitative rather
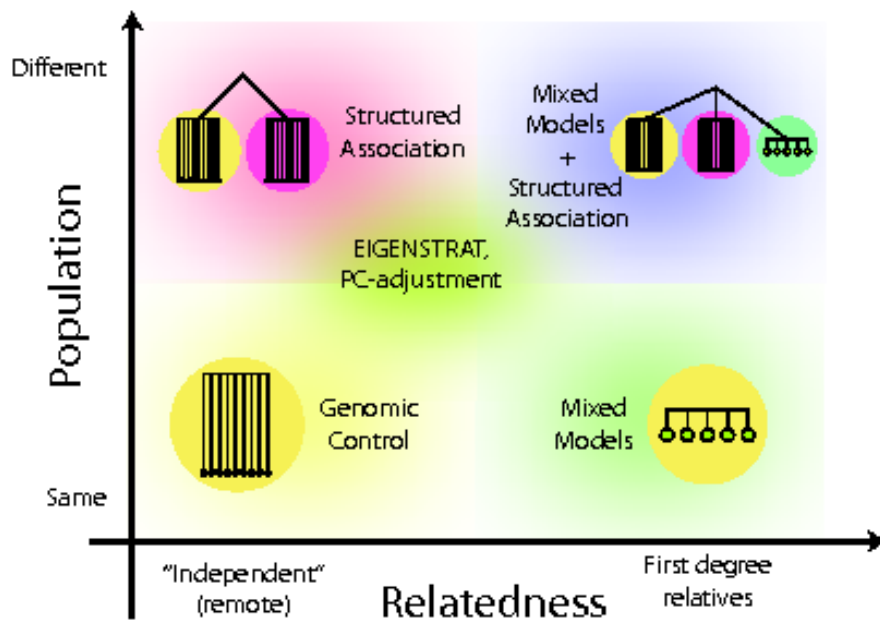
Figure 6.7: Applicability of different methods for association analysis.

than qualitative, there is no single recipe for analysis when genetic structure is present in a study sample.

6.4 Links

Here are some useful links to software which can be used for analysis in structured populations:

EIGENSTRAT: `http://genepath.med.harvard.edu/~reich/EIGENSTRAT.htm`

GenABEL: `http://mga.bionet.nsc.ru/~yurii/ABEL/`

MACH: `http://www.sph.umich.edu/csg/abecasis/mach/`

PLINK: `http://pngu.mgh.harvard.edu/~purcell/plink/`

Chapter 7

GWA in presence of genetic stratification: practice

Both ethnic admixture and presence of close relationships represents examples of confounding in association analysis. However, the methods to correct for stratification as resulting from mixture of subjects coming from different genetic populations, and methods to correct for family relations may be slightly different, and will be described separately in the next sections.

7.1 Analysis with ethnic admixture

In previous section we detected genetic stratification by analysis of genomic kinship matrix and excluded genetic outliers from our further analysis. When there are only a few such outliers, exclusion them from analysis is a good option. However, in large studies cases and controls are usually selected across a number of locations and genetic populations, and stratification is expected by design. In such case, analysis of association should account for this stratification.

Let us do structured association analysis using the `data1` data derived in previous section.

If you are not running R yet, start R and load `GenABEL-package` library by typing

```
> library(GenABEL)
```

and load the 'data1' workspace generated in section 5 ("Genome-wide association analysis").

```
> load("data1.RData")
> ls()
```

```
[1] "cl1"       "data1"      "data1.gkin" "data2.qt"
```

First, let us check how much test statistic inflation is there if we ignore stratification.

```
> data1.qt <- qtscore(dm2,data1)
> lambda(data1.qt)
```

```
$estimate
[1] 1.051744

$se
[1] 0.000756613

$iz0
[1] 1.015643

$iz2
[1] 1
```

We now will consider several ways to account for stratification, namely, strucutured association analysis, method of Price et al. (EIGENSTRAT), a similar method based on adjusting for the principal components of variation of genomic kinship matrix, and use of a mixed model.

One of the ways to do that is to perform *structured association* analysis. In such analysis, effect and its variance are estimated within each strata separately, and then these estimates are pooled to generate global statistics. The strata can be known from design (e.g. place of birth or ethnicity of parents) or estimated from GWA data.

To do structured association analysis we need to define a variable which will tell what population the study subjects belong to. In previous section, we stored the names of 'outlier' subjects in variable cl1:

```
> cl1
```

```
[1] "id2097" "id6954" "id2136" "id858"
```

We can use function %in% to find out what names of subjects are in cl1:

```
> pop <- as.numeric(idnames(data1) %in% cl1)
```

Let us check how the 'population' is distributed among the cases and controls:

```
> table(pop,phdata(data1)$dm2)
```

```
pop  0  1
  0 47 77
  1  0  4
```

As we have seen before, one of the clusters contains only the cases.

Now, structured association may be done with qtscore function by specifying strata argument:

```
> data1.sa <- qtscore(dm2,data=data1,strata=pop)
> lambda(data1.sa)
```

```
$estimate
[1] 1.03431

$se
```
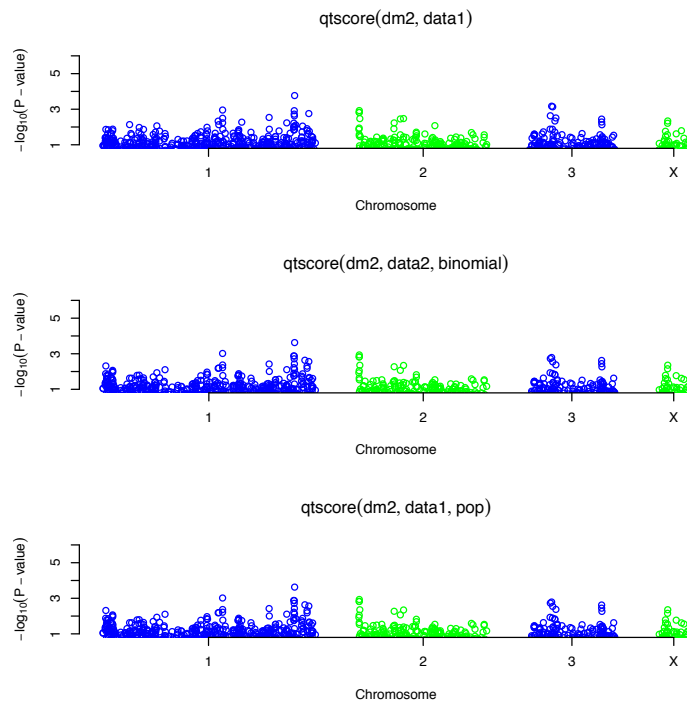
Figure 7.1:   Comparison of the original results, results of analysis excluding outliers, and structured association analysis.

```
[1] 0.0007059588

$iz0
[1] 1.006671

$iz2
[1] 1
```

We can compare the original results, results of analysis excluding outliers, and structured association analysis by

```
> par(mfcol=c(3,1))
> plot(data1.qt,ylim=c(1,6))
> plot(data2.qt,ylim=c(1,6))
> plot(data1.sa,ylim=c(1,6))
> par(mfcol=c(1,1))
```

The resulting plot is presented at figure 7.1. In this case, there is little difference, because all people belonging to the smaller sub-population are cases.

Other way to adjust for genetic (sub)structure is to apply the method of Price et al. (*EIGENSTRAT*), which make use of principal components of the genomic kinship matrix to adjust both phenotypes and genotypes for possible stratification. In `GenABEL-package`, such analysis is done using `egscore` function.

```
> data1.eg <- egscore(dm2,data=data1,kin=data1.gkin)
> lambda(data1.eg)

$estimate
[1] 1.102747

$se
[1] 0.001043038
```

The analysis plot may be added to the previous one by

```
> par(mfcol=c(3,1))
> plot(data1.eg,ylim=c(1,6))
```

Now let us apply *adjustment for the stratification by use of the principal components of genetic variation.* For that we first need to extract the principal components of genetic variation by constructing the distance matrix

```
> dst <- as.dist(0.5-data1.gkin)
```

and performing the classical multidimensional scaling

```
> pcs <- cmdscale(dst,k=10)
> pcs[1:5,]

                [,1]         [,2]        [,3]         [,4]         [,5]
id199  0.030289769  0.057952824  0.10342206 -0.020496319 -0.02678162
id300  0.031798583  0.004789923  0.02947431  0.033227508  0.05977593
id403  0.060654557  0.079249013 -0.06111279 -0.081417523  0.03294180
id415 -0.004913697 -0.030714900  0.07807686  0.017468144  0.03078079
id666 -0.012639670  0.016176179 -0.08784632 -0.002322116  0.02957059
              [,6]        [,7]         [,8]          [,9]        [,10]
id199  0.08021104  0.01144582 -0.020228061 -0.001507913 -0.060483058
id300  0.03702791  0.02887831  0.005142389 -0.005340720  0.094991803
id403 -0.01481834 -0.01259170  0.040037267 -0.048689378  0.007304146
id415 -0.02472941  0.07900292  0.075300986  0.028609310  0.021747288
id666 -0.04742543 -0.11594090  0.106539735  0.026380262 -0.022472669
```

Now we can use these PCs for adjustment:

```
> data1.pca <- qtscore(dm2~pcs[,1]+pcs[,2]+pcs[,3],data1)
> lambda(data1.pca)

$estimate
[1] 1.004946

$se
[1] 0.0007356663

$iz0
[1] 1

$iz2
[1] 1
```

```
> plot(data1.pca,ylim=c(1,6))
```

Finally, let us use the full genomic kinship matrix for the adjustemnt for pupulational structure. First, let us estimate the polygenic model with

```
> h2a <- polygenic(dm2,data1,kin=data1.gkin)
```

The resulting 'heritability' estimate is

```
> h2a$esth2
```

```
[1] 0.3840789
```

Now we can perform mixed model approximation analysis using `mmscore` function

```
> data1.mm <- mmscore(h2a,data1)
> lambda(data1.mm)
```

```
$estimate
[1] 1
```

```
$se
[1] NA
```

```
> plot(data1.mm,ylim=c(1,6))
> par(mfcol=c(1,1))
```

The resulting plot is presented at figure 7.2.

Again, the difference between three analysis methods is marginal because there are no highly differentiated SNPs in the data set, and one sub-population is presented by cases only. Still, the signals at chromosome one and three slightly improved, while these at two and X went down.

Load and analyse the data set presented in file `stratified.RData`. GWA data presented in this file concern a study containing data from several populations. All these populations originate from the same base population some generations ago. Some of these populations mantained large size and some were small. There was little (2.5%) migration between populations.

Two traits ('quat' and 'bint') ara available for analysis. Investigate relations between phenotypes and covariates. Perform association analysis. Answer the questions

Ex. 1 — What covariates are significantly associated with the traits?

Ex. 2 — How many SNPs and IDs are presented in the data set?

Ex. 3 — How many SNPs and IDs pass the quality control (use SNP and ID call rate of 0.98)?

Ex. 4 — Is there evidence for stratification coming from the distribution of GW test for HWE (what is λ?)

Ex. 5 — Is there evidence that the test statistics for trait `quat` is inflated (what is λ?)
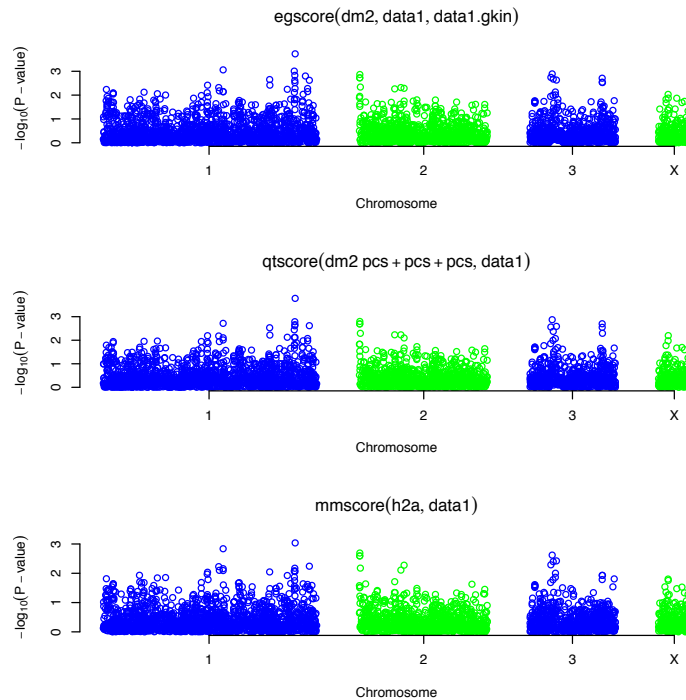
Figure 7.2: Comparison of method of Price et al., principal components adjustment and mixed modelling.

Ex. 6 — Is there evidence that the test statistics for trait `bint` is inflated (what is λ?)

Ex. 7 — How many genetically distinct populations are present in the data set? How many people belong to each population?

Ex. 8 — Is the case/control and quantitative trait disbalance between populations?

Ex. 9 — For the quantitative trait, what method corrects best for stratification (in terms of minimal residual inflation)?

Ex. 10 — What is the strongest SNP associated with trait `quat`? What model (method and covariates used) gives best results? Is the finding GW-significant?

Ex. 11 — What is the strongest SNP associated with trait `bint`? What model (method and covariates used) gives best results? Is the finding GW-significant?

7.2 Analysis of family data

In this section we will consider analysis of quantitative traits in a family-based cohort, where participants were not selected for the value of the trait under analysis. Such data may be generated in any study selecting participants based

on kinship (e.g. collections of sibships, nuclear or extended families); also any study in a genetically isolated population is likely to end up with a large proportion of relatively closely related individuals, even if ascertainment was random with the respect to kinship.

In pedigree-based association analysis the pedigree works as a confounder – exactly in the same manner as ethnic origin may work in a population-based study. Any genetic polymorphism is inherited through genealogy, and therefore genotypes are more similar between close relatives. In the same manner, any other heritable trait will be also more similar between relatives, and therefore certain degree of association is expected between *any* genetic marker and *any* heritable trait in a family-based sample. If additive 1 d.f. test for association is considered, the effect of confounding by pedigree can be shown to inflate the resulting null distribution of presumably χ_1^2 test statistics by a certain constant λ.

As you remember, this is exactly what happens when simple test for association is applied to a population-based data with ethnic admixture. In a population-based study with strong admixture (both in terms of the proportion and ethnic "distance"), some genomic regions may have been differentially selected in different populations. In such situation, use of genomic control does not prevent false-positive association between a trait and these regions, and other methods, such as EIGENSTRAT or Structured Association, are to be used.

For pedigree-based data coming from (relatively) genetically homogeneous population it can be shown that λ is a function of trait's heritability and pedigree structure, expressed as kinship matrix. Thus, genomic control is a simple and valid method to study association in genetically homogeneous families. However, this method reduces (or summarises if you prefer) all the abundant information about heritability and relationship into a single parameter λ, therefore it is not the most powerful method.

In quantitative genetics, a mixed polygenic model of inheritance may be considered as "industrial standard" – this model has sound theoretical bases and is proven by time to describe well inheritance of complex quantitative traits. This model describes the vector of observed quantitative traits as

$$Y = \mu + G + e \tag{7.1}$$

where μ is the intercept, G is contribution from polygene, and e is random residual.

It is assumed that for each individual its "personal" random residual e_i is distributed as Normal with mean zero and variance σ_e^2. As these residuals are independent between pedigree members, the joint distribution of residuals in the pedigree can be modelled using multivariate normal distribution with variance-covariance matrix proportional to the identity matrix I (this is a matrix with diagonal elements equal to 1, and off-diagonal elements equal to zero): $e \sim MVN(0, I\sigma_e^2)$.

The polygenic component G describes the contribution from multiple independently segregating genes all having a small additive effect onto the trait (infinitesimal model). For a person for whom parents are not known, it is assumed that G_i is distributed as Normal with mean zero and variance σ_G^2. Assuming model of infinitely large number of genes, it can be shown that given polygenic values for parents, the distribution of polygene in offspring follows Normal distribution with mean $(G_m + G_f)/2$ and variance $\sigma_G^2/2$, where G_m is maternal

and G_f is paternal polygenic values. From this, it can be shown that jointly the distribution of polygenic component in a pedigree can be described as multivariate normal with variance-covariance matrix proportional to the relationship matrix Φ: $G \sim MVN(0, \Phi\sigma_G^2)$.

Thus the log-likelihood for this model can be written as a function of three parameters:

$$L(\mu, \sigma_G^2, \sigma_e^2) = -\frac{1}{2} \cdot log_e \left|(\Phi \cdot \sigma_G^2 + I \cdot \sigma_e^2)\right|$$
$$+ (Y - \mu)^T \cdot (\Phi \cdot \sigma_G^2 + I \cdot \sigma_e^2)^{-1} \cdot (Y - \mu) \qquad (7.2)$$

where μ is intercept, σ_G^2 is the proportion of variance explained by the polygenic component, and σ_e^2 is the residual variance.

Covariates such as sex, age, or a genetic marker studied for association can be easily included into the model:

$$Y = \mu + \sum_j \beta_j \cdot C_j + G + e$$

Here, C_j is the vector containing j-th covariate and $beta_j$ is the coefficient of regression of Y onto that covariate.

This mixed morel leads to likleihood

$$L(\mu, \sigma_G^2, \sigma_e^2, \beta_1, \beta_2, ...) = -\frac{1}{2} \cdot log_e \left|(\Phi \cdot \sigma_G^2 + I \cdot \sigma_e^2)\right|$$
$$+ \left(Y - (\mu + \sum_j \beta_j \cdot C_j)\right)^T \cdot \left(\Phi \cdot \sigma_G^2 + I \cdot \sigma_e^2\right)^{-1}$$
$$\cdot \left(Y - (\mu + \sum_j \beta_j \cdot C_j)\right) \qquad (7.3)$$

This general formulation can be easily adopted to test genetic association; for example, an effect of a SNP can be incorporated into regression model

$$Y = \mu + \beta_g \cdot g + G + e$$

where g is the vector containing genotypic values. In this mode, you can specify a variety of 1 d.f. models by different coding of the vector g. For example, if you consider an "AG" polymorphism and want to estimate and test additive effect of the allele "G", you should code "AA" as 0 (zero), "AG" as 1 and "GG" as 2. Under this coding, the β_g will estimate additive contribution from the "G" allele. If you are willing to consider dominant model for G, you should code "AA" and "AG" as 0 and "GG" as 1. Recessive and over-dominant models can be specified in a similar manner. If, however, you want to estimate general 2 d.f. model, the specification should be different:

$$Y = \mu + \beta_a \cdot g + \beta_d \cdot I_{g=2} + G + e$$

where g is coded as 0, 1 or 2, exactly the same as in the additive model, and $I_{g=2}$ is the binary indicator which takes value of one when g is equal to 2 and zero otherwise. In this model, β_a will estimate the additive and β_d – the dominance

effect. There may be other, alternative coding(s) allowing for essentially the same model, for example

$$Y = \mu + \beta_1 \cdot I_{g=1} + \beta_2 \cdot I_{g=2} + G + e$$

would estimate trait's deviation in these with $g = 1$ (β_1) and these with $g = 2$ (β_2) from the reference ($g = 0$).

The classical way to estimate mixed polygenic model and test for significance is Maximum Likelihood (ML) or Restricted ML (REML) using equation (7.3). However, when large pedigrees are analysed, ML/REML solution may take prohibitively long time, i.e. from minutes to hours for single SNP analysis, making study of hundreds of thousand of SNPs impossible. Therefore fast approximate tests were developed for the purposes of GWA association analysis in samples of relatives.

Here we will cover two of fast approximations available, FAmily-based Score Test for Association (FASTA, Chen & Abecasis, 2007) and Genome-wide Rapid Analysis using Mixed Models And Score test (GRAMMAS, Amin et al, 2007). Both tests are based on the classical polygenic mixed model and are performed in two steps.

First, polygenic model as specified by equation (7.1) and likelihood (7.2) is estimated using available data.

Secondly, the maximum likelihood estimates (MLEs) of the intercept, $\hat{\mu}$, proportion of variance explained by the polygenic component, $\hat{\sigma}_G^2$, and residual variance, $\hat{\sigma}_e^2$, are used to compute the FASTA test statistics

$$T_F^2 = \frac{\left((g - E[g])^T \cdot (\Phi \cdot \hat{\sigma}_G^2 + I \cdot \hat{\sigma}_e^2)^{-1} \cdot (Y - \hat{\mu})\right)^2}{(g - E[g])^T \cdot (\Phi \cdot \hat{\sigma}_G^2 + I \cdot \hat{\sigma}_e^2)^{-1} \cdot (g - E[g])}$$

It can be shown that T_F^2 follows χ_1^2 when pedigree structure is 100% complete and 100% correct. As this is never actually the case, application of GC to correct for residual inflation is recommended.

FASTA test results in unbiased estimates of the SNP effect and correct $P - values$. Please keep in mind that this is correct – as for any score test – only when alternative is reasonably close to the null, i.e. when the SNP explains small proportion of trait's variance. Disadvantages of this test are that is can be relatively slow when thousands of study subjects are analysed, and that permutation procedures can not be applied to estimate genome-wide significance, because the data structure is not exchangeable.

Other test, GRAMMAS, also exploits MLEs from the polygenic model (7.1). However, these are used to first compute the vector of environmental residuals $\hat{e}$, using standard equation

$$\hat{e} = \hat{\sigma}_e^2 \cdot (\Phi \cdot \hat{\sigma}_G^2 + I \cdot \hat{\sigma}_e^2)^{-1} \cdot (Y - \hat{\mu})$$

These residuals, in turn, are used to run simple score test:

$$T_G^2 = \frac{\left((g - E[g])^T \cdot \hat{e}\right)^2}{(g - E[g])^T \cdot (g - E[g])}$$

This test is conservative, but GC can be used to correct for the deflation of the test statistics.

The fact that environmental residuals $\hat{e}$ are not dependent on pedigree structure leads to a nice property of the GRAMMAS test: the data structure becomes exchangeable and permutations may be used to estimate genome-wide significance. When used in combination with GC, $P - values$ derived from GRAMMAS test are correct; however, there is a downward bias in estimates of SNP effects.

When using FASTA or GRAMMAS test, it is recommended to estimate genomic kinship matrix from available genome-wide data, and use it in analysis instead of pedigree kinship. This solution firstly does not rely on the completeness and quality of pedigree; secondly, genomic kinship is more likely to give a better estimate of a *true* covariance between individual genomes, while pedigree kinship provides one with expectation. Therefore use of genomic kinship is expected to lead to better estimates of polygenic model, and thus better power to detect association in GWA analysis. This being said, we generally advocate use of genomic, and not pedigree kinship. Of cause, you can only implement this solution when you have GWA data; in a candidate gene study you will have to rely on the pedigree structure to estimate kinship matrix.

7.3 Example GWA analysis using family-based data

In this section, we will explore small data set (150 people, 5827 SNPs). Let us load and explore it:

```
> load("RData/erfsmall.RData")
> ls()

[1] "erfs"  "pkins"

> class(erfs)

[1] "gwaa.data"
attr(,"package")
[1] "GenABEL"

> class(pkins)

[1] "matrix"
```

You can see that there a two objects, **erfs** and **pkins**, presented in the data. The class of the first object is standard **GenABEL-package**'s **gwaa.data-class**; this is the object containing GWA data. The other object contains kinship matrix, as estimated from pedigree data.

You can check the number of people and SNPs in the data set with

```
> nids(erfs)

[1] 150

> nsnps(erfs)

[1] 5827
```

As usual, it is advisable to check the distribution of SNPs by chromosome:

```
> table(chromosome(erfs))
```

```
  1  10  11  12  13  14  15  16  17  18  19   2  20  21  22  23   3   4   5   6
484 251 224 285 188 210 206 189 159 170 149 481 130 100 132  26 403 300 320 397
  7   8   9   X
286 253 206 278
```

(here, 23 stays for pseudo-autosomal region of the X chromosome); you can see that markers are evenly spread over the chromosomes.

Summary marker statistics can be generated by

```
> descriptives.marker(gtdata(erfs))
```

```
$`Minor allele frequency distribution`
     X<=0.01 0.01<X<=0.05 0.05<X<=0.1 0.1<X<=0.2    X>0.2
No    17.000      26.000      75.000    437.000 5272.000
Prop   0.003       0.004       0.013      0.075    0.905
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No          2   14.000  83.000 319.000  5827
Prop        0    0.002   0.014   0.055     1
```

```
$`Distribution of proportion of successful genotypes (per person)`
     X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99 X>0.99
No        0       1.000        2.000       12.00  135.0
Prop      0       0.007        0.013        0.08    0.9
```

```
$`Distribution of proportion of successful genotypes (per SNP)`
     X<=0.9 0.9<X<=0.95 0.95<X<=0.98 0.98<X<=0.99   X>0.99
No   77.000      33.000      214.000     208.000 5295.000
Prop  0.013       0.006        0.037       0.036    0.909
```

```
$`Mean heterozygosity for a SNP`
[1] 0.4402752
```

```
$`Standard deviation of the mean heterozygosity for a SNP`
[1] 0.08287253
```

```
$`Mean heterozygosity for a person`
[1] 0.4354001
```

```
$`Standard deviation of mean heterozygosity for a person`
[1] 0.01305448
```

You can see that the quality of genotypic data is quite reasonable: call rate is generally high, both per-person and per SNP, and there is little deviation from Hardy-Weinberg equilibrium.

Let us explore pedigree kinship matrix. First, let us just look how this matrix looks like by displaying few elements from the upper-left corner:

```
> pkins[1:5,1:5]
```

```
            id1         id2         id3         id4         id5
id1 5.00000e-01 8.56146e-05 1.01984e-04 2.33397e-04 8.56146e-05
id2 8.56146e-05 5.00000e-01 3.96513e-03 2.56896e-05 2.51269e-01
id3 1.01984e-04 3.96513e-03 5.00000e-01 1.21593e-05 3.96513e-03
id4 2.33397e-04 2.56896e-05 1.21593e-05 5.00000e-01 2.56896e-05
id5 8.56146e-05 2.51269e-01 3.96513e-03 2.56896e-05 5.00000e-01
```

By definition, pedigree kinship should take values between 0 and 0.5 (plus some small amount from inbreeding); kinship between (non-inbred) sibs or an offspring and the parent is 1/4. You can see that in the upper-left corner there is one inbred sib-pair (or parent-offspring pair; "id2" and "id5"). You can also see that this matrix is symmetric around the diagonal.

Let us summarise the distribution of kinship coefficients; in doing this we want to generate the summary for every off-diagonal element only once. Function `lower.tri` can be used to get the "lower triangle" sub-matrix elements:

```
> summary(pkins[lower.tri(pkins)])
```

```
    Min.   1st Qu.   Median      Mean   3rd Qu.      Max.
0.0000000 0.0004999 0.0028500 0.0062810 0.0053780 0.2633000
```

As you can see, average relationship corresponds to that expected between second cousins ($1/64 = 0.015625$) and third cousins ($1/256 = 0.00390625$).

We can also draw a histogram of the distribution of the kinship coefficients (shown at figure 7.4A):

```
> hist(pkins[lower.tri(pkins)])
```

and see that most elations are indeed remote.

Let us estimate genomic kinship matrix using autosomal data with the command `ibs`, and look up the elements in the upper-left corner:

```
> gkins <- ibs(erfs[,autosomal(erfs)],weight="freq")
> gkins[1:5,1:5]
```

```
              id1          id2          id3         id4         id5
id1  0.513083834  5.439000e+03  5.446000e+03 5441.00000000 5440.0000000
id2 -0.012569446  4.931959e-01  5.524000e+03 5524.00000000 5521.0000000
id3  0.001516184 -8.551323e-03  5.044065e-01 5529.00000000 5528.0000000
id4  0.010459422 -1.471218e-02 -3.467894e-03    0.50739823 5523.0000000
id5 -0.007957596  2.561484e-01 -8.925127e-03   -0.02205665    0.4943105
```

Here, the estimated kinship is shown below the diagonal, and the number of informative SNP pairs used for estimation is shown above the diagonal.

You can see that "genomic kinship" coefficients may take values lower than zero, which is consequence of the fact that in effect "genomic kinship" is simply covariance between the vectors of individual genotypes. This quantity, though it provides an unbiased estimate of kinship, can be lower than zero.

```
> summary(gkins[lower.tri(gkins)])
```
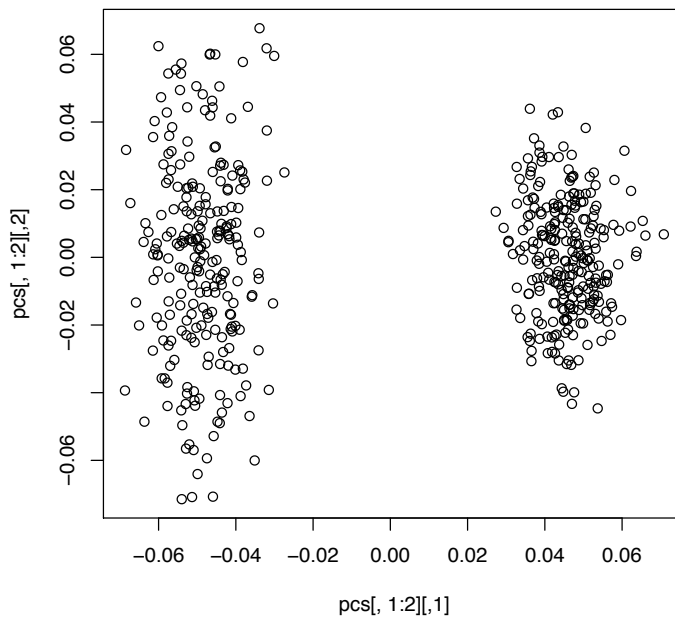
Figure 7.3: Population structure of 'strdat1' data

```
     Min.    1st Qu.    Median      Mean   3rd Qu.      Max.
-0.038980 -0.011930 -0.005826 -0.003362  0.000481  0.268000
```

here, the average is quite close to that obtained with pedigree kinship.

We can also draw a histogram of the distribution of "genomic kinship" coefficients (shown at figure 7.4B):

```
> hist(gkins[lower.tri(gkins)])
```

and can easily graphically present relations between genomic and pedigree kinship with

```
> plot(pkins[lower.tri(pkins)],gkins[lower.tri(gkins)])
```

(shown at figure 7.5), and estimate correlation between the two with

```
> cor(pkins[lower.tri(pkins)],gkins[lower.tri(gkins)])
```

```
[1] 0.9161499
```

From the graph, you can clearly see that, though there is a very strong correlation between genomic and pedigree kinships, these are not identical.

In real data, you may find that there are some points where pedigree data clearly suggest relation different from that suggested by genomic data. Which one to believe? Generally, pedigrees are more prone to errors than genotypic

Histogram of pkins[lower.tri(pkins)]

Histogram of gkins[lower.tri(gkins)]
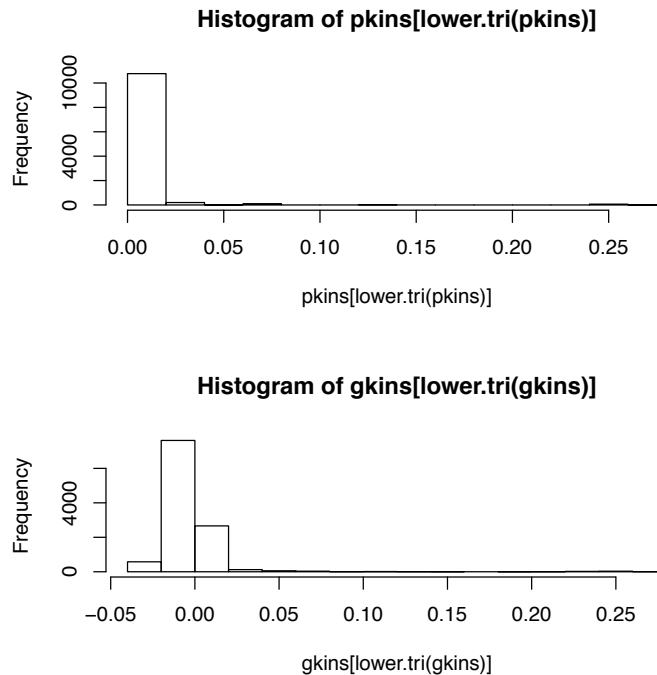
Figure 7.4: Distribution of the pedigree (upper histogram) and genomic (lower histogram) kinship coefficients for `erfs` data set.

data. In the data containing close relatives it is better to rely on "genomic kinship".

Let us first analyse the data using plain GC method:

```
> qts <- qtscore(qtbas,data=erfs)
```

You can check the estimate of the inflation factor λ with

```
> lambda(qts)$est
```

```
[1] 1.125012
```

This is relatively high value, suggesting presence of close relatives in data and high heritability of the trait.

The top 10 hits from GWA analysis can be displayed with

```
> descriptives.scan(qts,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome   Position Strand A1 A2   N      effB   se_effB chi2.1df
rs1781670         13 2694164735      u  1  2 150  0.5236543 0.1348423 15.08125
rs1872087         17 3329938025      u  1  2 150 -0.4958918 0.1329806 13.90584
rs1043883          8 1745120471      u  1  2 128  0.5132294 0.1403802 13.36630
rs377859          10 2173644540      u  1  2 150 -0.5901680 0.1625124 13.18797
```

```
rs1861659        16 3171591122     u  1  2 150  0.5270266 0.1478622 12.70430
rs1672299        12 2602365489     u  1  2 150 -0.5149239 0.1469410 12.28006
rs11062          17 3262519467     u  1  2 150  0.5321081 0.1580270 11.33801
rs2141693        12 2590653716     u  1  2 150  1.3143719 0.3986408 10.87109
rs716623         13 2749359437     u  1  2 150  0.4724783 0.1458132 10.49953
rs774033         12 2531521679     u  1  2 150 -0.4601787 0.1435537 10.27601
                    P1df      effAB      effBB chi2.2df       P2df        Pc1df
rs1781670 0.0001029814  0.6906708  1.0317669 15.84361 0.0003627468 0.0002508996
rs1872087 0.0001921999 -0.5500476 -0.9839850 13.98868 0.0009170561 0.0004384850
rs1043883 0.0002561863  0.3204631  1.1004272 14.19845 0.0008257431 0.0005670857
rs377859  0.0002817517 -0.5794118 -1.1877540 13.19253 0.0013654589 0.0006174836
rs1861659 0.0003648165  0.3450954  1.1140306 13.79358 0.0010110248 0.0007781712
rs1672299 0.0004578242 -0.6530651 -0.9961549 12.87154 0.0016031702 0.0009536341
rs11062   0.0007593646  0.4922344  1.1305957 11.42110 0.0033108545 0.0015003962
rs2141693 0.0009767716  1.3143719         NA 10.87109 0.0009767716 0.0018800745
rs716623  0.0011940492  0.1922801  0.9718987 12.66176 0.0017804639 0.0022508609
rs774033  0.0013477134 -0.5442070 -0.9178935 10.45943 0.0053550526 0.0025088454
```

here, nominal $P-values$ after genomic control are given in column named
"Pc1df".

We can estimate genome-wide empirical significance by using the same function with `times` argument, which tells the number of permutations:

```
> qts.e <- qtscore(qtbas,data=erfs,times=200,quiet=TRUE)

  |
  |                                                                    |   0%
  |
  |====================================================================| 100%
```

```
> descriptives.scan(qts.e,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome   Position Strand A1 A2   N        effB   se_effB
rs1781670         13 2694164735      u  1  2 150  0.52365430 0.1348423
rs1872087         17 3329938025      u  1  2 150 -0.49589178 0.1329806
rs1043883          8 1745120471      u  1  2 128  0.51322939 0.1403802
rs377859          10 2173644540      u  1  2 150 -0.59016796 0.1625124
rs1861659         16 3171591122      u  1  2 150  0.52702662 0.1478622
rs1672299         12 2602365489      u  1  2 150 -0.51492394 0.1469410
rs11062           17 3262519467      u  1  2 150  0.53210805 0.1580270
rs2017143          1    2252811      u  1  2 150  0.04200869 0.1338613
rs2840531          1    2318570      u  1  2 150 -0.35176535 0.2002343
rs2477703          1    2458154      u  1  2 150 -0.14676181 0.1519094
             chi2.1df  P1df  Pc1df      effAB       effBB   chi2.2df  P2df
rs1781670 15.08124536 0.360  0.705  0.6906708  1.03176686 15.8436112 0.750
rs1872087 13.90584450 0.575  0.855 -0.5500476 -0.98398504 13.9886838 0.975
rs1043883 13.36630002 0.715  0.920  0.3204631  1.10042723 14.1984536 0.970
rs377859  13.18797157 0.735  0.930 -0.5794118 -1.18775397 13.1925294 0.995
rs1861659 12.70429594 0.810  0.975  0.3450954  1.11403056 13.7935817 0.980
rs1672299 12.28005767 0.870  0.990 -0.6530651 -0.99615492 12.8715445 1.000
```

```
rs11062   11.33801475 0.975 0.995  0.4922344  1.13059573 11.4210979 1.000
rs2017143  0.09848463 1.000 1.000  0.2555726  0.01458913  1.5429109 1.000
rs2840531  3.08623677 1.000 1.000 -0.3889020 -0.36730336  3.2760351 1.000
rs2477703  0.93337596 1.000 1.000 -0.1681636 -0.27086570  0.9548231 1.000
```

(argument "quiet" supress warning messages; this is used for the purposes of this tutorial, normally you do not need to specify this option)

As you can see, in this analysis nothing comes even close to genome-wide significance, as indicated by genome-wide corrected $P-values$ (column "Pc1df") all $>> 0.05$.

Let us estimate polygenic model with

```
> h2 <- polygenic(qtbas,kin=gkins,data=erfs)
```

The results of estimation are contained in "h2an" element of the resulting analysis object:

```
> h2$h2an

$minimum
[1] 200.9972


$estimate
[1] 0.03850405 0.77968841 1.54153952


$gradient
[1] -1.136868e-07 -5.684342e-08  1.101186e-07


$code
[1] 1


$iterations
[1] 12
```

In the "estimate" list, the MLEs shown correspond to intercept $\hat{\mu}$, heritability $\hat{h}^2 = \hat{\sigma}_G^2/(\hat{\sigma}_G^2 + \hat{\sigma}_e^2)$, and total variance $\hat{\sigma}_T^2 = \hat{\sigma}_G^2 + \hat{\sigma}_e^2$. You can see that heritability of the trait is indeed high – almost 80%.

Under these conditions (hight heritability, presence of close relatives) we may expect that FASTA and GRAMMAS analysis exploiting heritability model and relationship matrix in exact manner may have better power compared to simple GC.

Let us run FASTA test using estimated polygenic model, as specified by `h2` object:

```
> mms <- mmscore(h2,data=erfs)
```

There is little residual inflation left when we use "genomic kinship" matrix:

```
> lambda(mms)$est

[1] 1
```

And the significance of "top" hit becomes an order of magnitude better compared to plain GC:

```
> descriptives.scan(mms,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome   Position Strand A1 A2   N       effB   se_effB  chi2.1df
rs1781670         13 2694164735      u  1  2 150  0.5280481 0.1444019 13.372139
rs1953817          6 1403824983      u  1  2 150 -0.5141566 0.1543596 11.094902
rs11062           17 3262519467      u  1  2 150  0.5409064 0.1624135 11.091753
rs774033          12 2531521679      u  1  2 150 -0.4852698 0.1457531 11.084874
rs1043883          8 1745120471      u  1  2 128  0.4873708 0.1515702 10.339302
rs1672299         12 2602365489      u  1  2 150 -0.4829157 0.1519733 10.097360
rs2384933         16 3139192007      u  1  2 150 -0.5466347 0.1723503 10.059355
rs1370139          6 1381958118      u  1  2 149  0.6704706 0.2116017 10.039709
rs1054889          2  324154337      u  1  2 150  0.4765958 0.1509593  9.967379
rs896986           2  336951524      u  1  2 150 -0.4735895 0.1513640  9.789461
                     P1df        Pc1df effAB effBB chi2.2df P2df
rs1781670 0.0002553899 0.0002553899    NA    NA        0   NA
rs1953817 0.0008656536 0.0008656536    NA    NA        0   NA
rs11062   0.0008671249 0.0008671249    NA    NA        0   NA
rs774033  0.0008703475 0.0008703475    NA    NA        0   NA
rs1043883 0.0013022725 0.0013022725    NA    NA        0   NA
rs1672299 0.0014848188 0.0014848188    NA    NA        0   NA
rs2384933 0.0015157632 0.0015157632    NA    NA        0   NA
rs1370139 0.0015320140 0.0015320140    NA    NA        0   NA
rs1054889 0.0015933812 0.0015933812    NA    NA        0   NA
rs896986  0.0017551492 0.0017551492    NA    NA        0   NA
```

If you compare these results to that obtained with simple GC, you can also
see that the ranks of top hits have changed quite a bit; unbiased estimated of
genetic effects were obtained.

However, we can not estimate genome-wide significance with FASTA, because
the data structure is not exchangeble.

Using GRAMMAS method, you can estimate nominal $P - values$ by

```
> grs <- qtscore(h2$pgres,data=erfs,clam=FALSE)
> lambda(grs)$est
```

```
[1] 0.7864778
```

In the above analysis, note that the estimated "inflation" factor λ is less
than one, i.e. now it is the GRAMMAS *deflation* factor. In order to obtain
non-concervative test statistics, we had to say to qtscore that deflation is OK
(parameter `clam=FALSE`).

We can see "top" nominal corrected $P - values$ with

```
> descriptives.scan(grs,sort="Pc1df")
```

```
Summary for top 10 results, sorted by Pc1df
          Chromosome   Position Strand A1 A2   N        effB    se_effB
rs1781670         13 2694164735      u  1  2 150  0.10543625 0.03316109
rs1953817          6 1403824983      u  1  2 150 -0.11570443 0.03763454
rs774033          12 2531521679      u  1  2 150 -0.10777281 0.03530344
rs11062           17 3262519467      u  1  2 150  0.11723796 0.03886279
```

```
rs988457              X 4318354390      u  1  2 150   0.08596545 0.02973400
rs1672299            12 2602365489      u  1  2 150  -0.10338769 0.03613646
rs1054889             2  324154337      u  1  2 150   0.10060789 0.03564684
rs1043883             8 1745120471      u  1  2 128   0.09719095 0.03495001
rs2384933            16 3139192007      u  1  2 150  -0.10913661 0.03958013
rs7141672            14 2851979738      u  1  2 150   0.10188182 0.03716035
            chi2.1df        P1df      effAB       effBB  chi2.2df        P2df
rs1781670 10.109331 0.001475205  0.10640049   0.2107828 10.109751 0.006378160
rs1953817  9.452063 0.002109117 -0.12909511  -0.2188059  9.586110 0.008287102
rs774033   9.319322 0.002267499 -0.12787712  -0.2149561  9.492933 0.008682320
rs11062    9.100568 0.002555302  0.08864787   0.2820712  9.806829 0.007421199
rs988457   8.358747 0.003838352  0.01088472   0.1705728  8.902349 0.011664860
rs1672299  8.185525 0.004222595 -0.12352309  -0.2018643  8.393310 0.015045819
rs1054889  7.965666 0.004767296  0.05921009   0.2144888  8.894878 0.011708513
rs1043883  7.733159 0.005421582  0.04374657   0.2148896  8.765118 0.012493348
rs2384933  7.603028 0.005827035 -0.11565587  -0.2057438  7.643917 0.021884901
rs7141672  7.516813 0.006112573  0.07576841   0.2356800  8.024857 0.018089412
              Pc1df
rs1781670 0.0003367712
rs1953817 0.0005268300
rs774033  0.0005767867
rs11062   0.0006697772
rs988457  0.0011138349
rs1672299 0.0012548232
rs1054889 0.0014601180
rs1043883 0.0017144147
rs2384933 0.0018758833
rs7141672 0.0019912707
```

By comparing this output to that from FASTA test, you can see that $P-values$ are quite close, but the effects are underestimated with GRAMMAS, as expected.

However, the streangths of GRAMMAS test is not only its speed, but also possiblity to estimate genome-wide significance. This can be done by

```
> grs.e <- qtscore(h2$pgres,data=erfs,times=200,clam=FALSE,quiet=TRUE)

  |
  |                                                                      |   0%
  |
  |======================================================================| 100%

> descriptives.scan(grs.e,sort="Pc1df")

Summary for top 10 results, sorted by Pc1df
          Chromosome    Position Strand A1 A2   N        effB    se_effB
rs1781670         13 2694164735      u  1  2 150  0.10543625 0.03316109
rs1953817          6 1403824983      u  1  2 150 -0.11570443 0.03763454
rs774033          12 2531521679      u  1  2 150 -0.10777281 0.03530344
rs11062           17 3262519467      u  1  2 150  0.11723796 0.03886279
rs988457           X 4318354390      u  1  2 150  0.08596545 0.02973400
```

```
rs1672299          12 2602365489    u  1  2 150 -0.10338769 0.03613646
rs1054889           2  324154337    u  1  2 150  0.10060789 0.03564684
rs2017143           1    2252811    u  1  2 150  0.02121630 0.03291983
rs2840531           1    2318570    u  1  2 150 -0.06596747 0.04924262
rs2477703           1    2458154    u  1  2 150 -0.02346832 0.03735833
```

	chi2.1df	P1df	Pc1df	effAB	effBB	chi2.2df	P2df
rs1781670	10.1093309	0.995	0.755	0.10640049	0.21078277	10.1097511	1
rs1953817	9.4520634	1.000	0.900	-0.12909511	-0.21880586	9.5861099	1
rs774033	9.3193222	1.000	0.915	-0.12787712	-0.21495609	9.4929330	1
rs11062	9.1005678	1.000	0.945	0.08864787	0.28207116	9.8068293	1
rs988457	8.3587468	1.000	0.985	0.01088472	0.17057284	8.9023487	1
rs1672299	8.1855251	1.000	0.990	-0.12352309	-0.20186430	8.3933102	1
rs1054889	7.9656656	1.000	0.995	0.05921009	0.21448884	8.8948782	1
rs2017143	0.4153596	1.000	1.000	0.04950544	0.03323599	0.8344174	1
rs2840531	1.7946401	1.000	1.000	-0.07118474	-0.08469889	1.8565797	1
rs2477703	0.3946292	1.000	1.000	-0.03408208	-0.03569994	0.4818462	1

As you can see, now the "top" hit starts approaching genome-wide significance (genome-wide $P - value \sim 10\%$), showing the power of kinship-based methods under high heritability model.

Finally, let us plot $-log_{10}$ nominal $P - values$ from different methods across the genome. Let black dots correspond to GC, green to GRAMMAS and red to FASTA (figure 7.6):

```
> plot(mms,df="Pc1df")
> add.plot(grs,df="Pc1df",col=c("lightgreen","lightblue"),cex=1.2)
> add.plot(qts)
```

You can see that there is a great degree of correlation between the FASTA and GRAMMAS $P - values$, while plain GC really stands apart.

7.4 Exercise: analysis of family data

Exercise 1 *Repeat heritability estimation, FASTA and GRAMMAS analysis of previous section using pediree kinship (`pkins` object). Discuss the results.*

In the next section, you will explore a small (695 people) subset of people from ERF, a family-based study with participants coming from a genetically isolated population and sampled based on kinship (all living descendants of 22 couples living in the area in mid-XIXth century). The study participants were genotyped using Illumina 6K "linkage" array. QC was already performed. Your trait of interest is "qtbas".

Explore the data set and answer the questions:

Exercise 2 *Describe the trait "qt". Can you detect significant outliers at visual inspection? Is trait distributed normally? What are significant covariates?*

Exercise 3 *Explore relations between genomic and pedigree kinship (these are provided in data as `gkin` and `pkin` data objects, respectively). What are your conclusions? Which matrix would you use later on?*
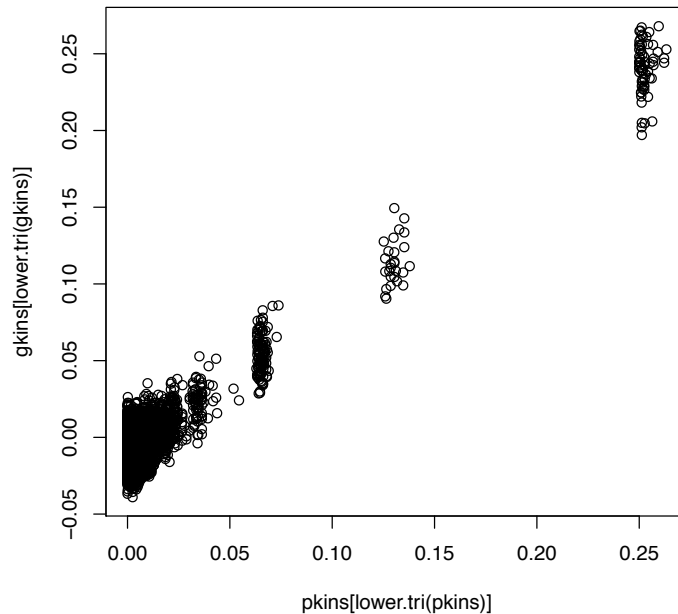
Figure 7.5: Scatter-plot relating pedigree and genomic kinships for `erfs` data set.

Exercise 4 *What is the heritability of the trait (take care: polygenic analysis may rung for a long while)? Based on heritability analysis, how would you rank different methods of GWA analysis for this trait (and why)?*

Exercise 5 *Do GWA analysis using simple score test with genomic control. Estimate genome-wide significance. What are your conclusions?*

Run GWA analysis using the "best" method and model as you have decided in previous exercises. Estimate genome-wide significance. What are your conclusions? Did they change compared to simple analysis?

Exercise 6 *Repeat the last "best" analysis using pedigree kinship. How your results change?*

Exercise 7 *If you have any time left – repeat analysis using "qt" trait. This one is much more fun, but also more laborous to analyse.*

7.5 Answers to exercises

Answer (Ex. 1) — Basically, all covariates are significantly associated with the traits:

```
> summary(lm(quat~sex+age+age2,data=phdata(strdat)))
```

```
Call:
lm(formula = quat ~ sex + age + age2, data = phdata(strdat))

Residuals:
    Min      1Q  Median      3Q     Max
-5.1188 -1.0260 -0.0389  1.0221  5.5506

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.3312562  1.4595518   0.227    0.821
sex          0.9190870  0.1399336   6.568 1.29e-10 ***
age          0.1465840  0.0588066   2.493    0.013 *
age2        -0.0024764  0.0005839  -4.241 2.65e-05 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 1.559 on 496 degrees of freedom
Multiple R-squared:  0.33,        Adjusted R-squared: 0.326
F-statistic: 81.44 on 3 and 496 DF,  p-value: < 2.2e-16

> summary(glm(bint~sex+age+age2,data=phdata(strdat),family=binomial))

Call:
glm(formula = bint ~ sex + age + age2, family = binomial, data = phdata(strdat))

Deviance Residuals:
    Min      1Q   Median      3Q     Max
-1.4500 -1.0139  -0.5967  1.1013  2.2229

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -6.280565   2.361455  -2.660 0.007823 **
sex          0.809689   0.198527   4.078 4.53e-05 ***
age          0.305322   0.099277   3.075 0.002102 **
age2        -0.003825   0.001033  -3.702 0.000214 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 673.01  on 499  degrees of freedom
Residual deviance: 605.06  on 496  degrees of freedom
AIC: 613.06

Number of Fisher Scoring iterations: 4
```

Answer (Ex. 2) — How many SNPs and IDs are presented in the data set?

```
> nsnps(strdat)
```

```
[1] 10000
```

```
> nids(strdat)
[1] 500
```

Answer (Ex. 3) — Let us perform the QC:

```
> qc <- check.marker(strdat,call=0.98,perid.call=0.98,p.level=0)
Excluding people/markers with extremely low call rate...
10000 markers and 500 people in total
0 people excluded because of call rate < 0.1
0 markers excluded because of call rate < 0.1
Passed: 10000 markers and 500 people

RUN 1
10000 markers and 500 people in total
30 (0.3%) markers excluded as having low (<0.5%) minor allele frequency
0 (0%) markers excluded because of low (<98%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<98%) call rate
Mean autosomal HET is 0.2035464 (s.e. 0.004215707)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.8330758 (s.e. 0.00554754), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 9970 (99.7%) markers passed all criteria
In total, 500 (100%) people passed all criteria

RUN 2
9970 markers and 500 people in total
0 (0%) markers excluded as having low (<0.5%) minor allele frequency
0 (0%) markers excluded because of low (<98%) call rate
0 (0%) markers excluded because they are out of HWE (P <0)
0 (0%) people excluded because of low (<98%) call rate
Mean autosomal HET is 0.2035464 (s.e. 0.004215707)
0 people excluded because too high autosomal heterozygosity (FDR <1%)
Mean IBS is 0.8270014 (s.e. 0.005755664), as based on 2000 autosomal markers
0 (0%) people excluded because of too high IBS (>=0.95)
In total, 9970 (100%) markers passed all criteria
In total, 500 (100%) people passed all criteria
> strdat1 <- strdat[qc$idok,qc$snpok]
```

The number of IDs and SNPs passing are

```
> nsnps(strdat1)
[1] 9970
> nids(strdat1)
[1] 500
```

Answer (Ex. 4) — Not really:

```
> descriptives.marker(strdat1)[2]
```

```
$`Cumulative distr. of number of SNPs out of HWE, at different alpha`
     X<=1e-04 X<=0.001 X<=0.01 X<=0.05 all X
No           1   6.000  73.000 378.000  9970
Prop         0   0.001   0.007   0.038     1
```

Answer (Ex. 5) — Yes:

```
> qts.q <- qtscore(quat~sex+age+age2,strdat1)
> lambda(qts.q)

$estimate
[1] 1.633427

$se
[1] 0.0003823764

$iz0
[1] 1.557426

$iz2
[1] 1.282158
```

Answer (Ex. 6) — Yes:

```
> qts.b <- qtscore(bint~sex+age+age2,strdat1)
> lambda(qts.b)

$estimate
[1] 2.093596

$se
[1] 0.000838563

$iz0
[1] 1.947389

$iz2
[1] 1.448017
```

Answer (Ex. 7) — Two genetically distinct populations are present in the data set. These can be visualised with

```
> gkin <- ibs(strdat1,w="freq")
> dst <- as.dist(0.5-gkin)
> pcs <- cmdscale(dst,k=10)
> plot(pcs[,1:2])
```

(graph presented in figure 7.3)
The populations can be dustinguished with

```
> pop <- 1*(pcs[,1]>0)
```

mmscore(h2, erfs)
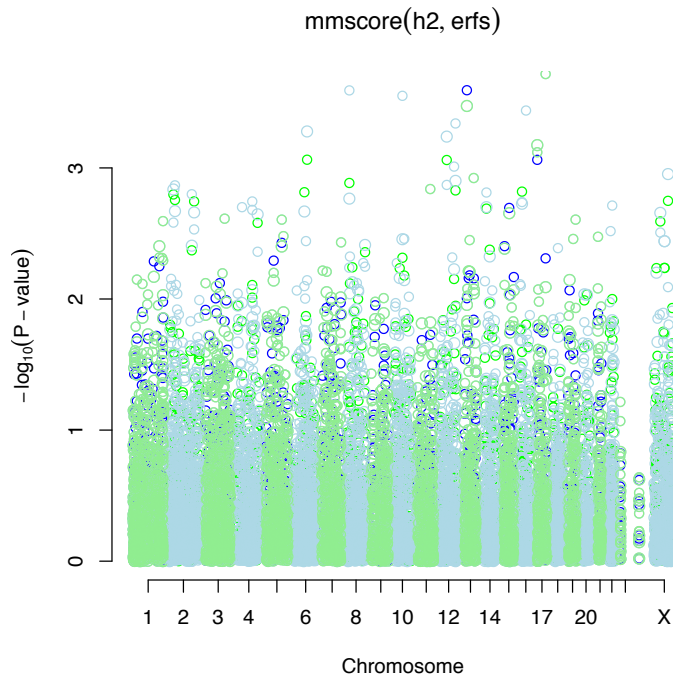
Figure 7.6:   Comparison of FASTA (red), GRAMMAS (green), and plain GC (black).

and the number of people belonging to each can be computed with

```
> table(pop)

pop
  0   1
242 258
```

Answer (Ex. 8) — Yes, there is significant case/control disbalance:

```
> descriptives.trait(strdat1,by=pop)
```

	No(by.var=0)	Mean	SD	No(by.var=1)	Mean	SD	Ptt	Pkw
id	242	NA	NA	258	NA	NA	NA	NA
sex	242	0.537	0.500	258	0.527	0.500	0.822	0.822
age	242	50.946	9.042	258	49.762	9.897	0.163	0.138
age2	242	2676.962	917.847	258	2573.786	991.693	0.228	0.138
quat	242	2.321	1.751	258	1.119	1.851	0.000	0.000
bint	242	0.657	0.476	258	0.159	0.366	0.000	0.000

	Pexact
id	NA
sex	0.858
age	NA
age2	NA

```
quat    NA
bint  0.000
```

Answer (Ex. 9) — MMSCORE corrects best for stratification in terms of minimal residual inflation:

```
> sa <- qtscore(quat~sex+age+age2,strdat1,strat=pop)
> lambda(sa)$est

[1] 1.019565

> es <- egscore(quat~sex+age+age2,strdat1,kin=gkin)
> lambda(es)$est

[1] 1.043936

> pcs <- cmdscale(as.dist(0.5-gkin),k=10)
> pc <- qtscore(quat~sex+age+age2+pcs[,1]+pcs[,2]+pcs[,3],strdat1,strat=pop)
> lambda(pc)$est

[1] 1.025369

> h2an <- polygenic(quat~sex+age+age2,data=strdat1,kin=gkin)
> h2an$h2an

$minimum
[1] 932.8796


$estimate
[1]  1.705618046  0.002208056  0.111974053 -0.002151578  0.802834082
[6]  2.188456701


$gradient
[1]    0.480568  -211.194297    11.611393 29349.669469    13.261603
[6]   -88.132314


$code
[1] 4


$iterations
[1] 100

> mm <- mmscore(h2an,strdat1)
> lambda(mm)$est

[1] 1.115282
```

Answer (Ex. 10) — The best results are achieved with `mmscore`:

```
> summary(mm)

Summary for top 10 results, sorted by P1df
          Chromosome  Position Strand A1 A2   N       effB   se_effB chi2.1df
snp13598           1   8326962      +  1  2 500 -0.7531795 0.1581588 22.67830
snp358367         19 263284193      +  1  2 500  1.1021752 0.2387578 21.31014
```

```
snp314412          17 231431537     +  1  2 500 -0.9551964 0.2396511 15.88643
snp162350           9 118783325     +  1  2 500  1.6538365 0.4348730 14.46306
snp155145           8 111959587     +  1  2 500 -1.4398365 0.3905136 13.59421
snp293669          16 216390949     +  1  2 500  2.0797905 0.5647042 13.56429
snp102095           6  74672442     +  1  2 500  0.5992210 0.1683224 12.67331
snp123032           7  89813084     +  1  2 500  0.4761745 0.1341130 12.60639
snp289207          15 211238602     +  1  2 500 -1.0830521 0.3110327 12.12514
snp340440          18 249874969     +  1  2 500 -0.3672634 0.1061263 11.97593
                 P1df           Pc1df effAB effBB chi2.2df P2df
snp13598  1.915187e-06 6.503015e-06    NA    NA        0   NA
snp358367 3.906599e-06 1.235653e-05    NA    NA        0   NA
snp314412 6.725913e-05 1.605450e-04    NA    NA        0   NA
snp162350 1.429351e-04 3.168480e-04    NA    NA        0   NA
snp155145 2.268843e-04 4.807139e-04    NA    NA        0   NA
snp293669 2.305294e-04 4.876772e-04    NA    NA        0   NA
snp102095 3.709122e-04 7.490880e-04    NA    NA        0   NA
snp123032 3.844300e-04 7.736871e-04    NA    NA        0   NA
snp289207 4.974671e-04 9.763916e-04    NA    NA        0   NA
snp340440 5.389222e-04 1.049564e-03    NA    NA        0   NA
```

Chapter 8

Imperfect knowledge about genotypes

This chapter is mostly copy-pasted from `ProbABEL-package` manual – user is encouraged to check it directly for the latest version.

8.1 Motivation

Many statistical and experimental techniques, such as imputations and high-throughput sequencing, generate data which are informative for genome-wide association analysis and are probabilistic in the nature.

When we work with directly genotyped markers using such techniques as SNP or microsatellite typing, we would normally know the genotype of a particular person at a particular locus with very high degree of confidence, and, in case of biallelic marker, can state whether genotype is AA, AB or BB.

On the contrary, when dealing with imputed or high-throughput sequencing data, for many of the genomic loci we are quite uncertain about the genotypic status of the person. Instead of dealing with known genotypes we work with a probability distribution that is based on observed information, and we have estimates that true underlying genotype is either AA, AB or BB. The degree of confidence about the real status is measured with the probability distribution $\{P(AA), P(AB), P(BB)\}$.

Several techniques may be applied to analyse such data. The most simplistic approach would be to pick up the genotype with highest probability, i.e. $\max_g[P(g = AA), P(g = AB), P(g = BB)]$ and then analyse the data as if directly typed markers were used. The disadvantage of this approach is that it does not take into account the probability distribution – i.e. the uncertainty about the true genotypic status. Such analysis is statistically wrong: the estimates of association parameters (regression coefficients, odds or hazard ratios, etc.) are biased, and the bias becomes more pronounced with greater probability distribution uncertainty (entropy).

One of the solutions that generate unbiased estimates of association parameters and takes the probability distribution into account is achieved by performing association analysis by means of regression of the outcome of interest onto estimated genotypic probabilities.

The `ProbABEL-package` package was designed to perform such regression in a fast, memory-efficient and consequently genome-wide feasible manner. Currently, `ProbABEL-package` implements linear, logistic regression, and Cox proportional hazards models. The corresponding analysis programs are called `palinear`, `palogist`, and `pacoxph`.

8.2   Input files

`ProbABEL-package` takes three files as input: a file containing SNP information (e.g. the MLINFO file of MACH), a file with genome- or chromosome-wide predictor information (e.g. the MLDOSE or MLPROB file of MACH), and a file containing the phenotype of interest and covariates.

Optionally, the map information can be supplied (e.g. the "legend" files of HapMap).

The dose/probability file may be supplied in filevector format in which case `ProbABEL-package` will operate much faster, and in low-RAM mode (approx. $\approx$ 128 MB). See the R libraries `GenABEL-package` and `DatABEL-package` on how to convert MACH and IMPUTE files to filevector format (functions: `mach2databel()` and `impute2databel()`, respectively).

8.2.1   SNP information file

In the simplest scenario, the SNP information file is an MLINFO file generated by MACH. This must be a space or tab-delimited file containing SNP name, coding for allele 1 and 2 (e.g. A, T, G or C), frequency of allele 1, minor allele frequency and two quality metrics ("Quality", the average maximum posterior probability and "Rsq", the proportion of variance decrease after imputations).

Actually, for `ProbABEL-package`, it does not matter what is written in this file – this information is just brought forward to the output. However, **it is critical** that the number of columns is seven and the number of lines in the file is equal to the number of SNPs in the corresponding DOSE file (plus one for the header line).

The example of SNP information file content follows here (also to be found in `ProbABEL/examples/test.mlinfo`)

```
SNP Al1 Al2 Freq1 MAF Quality Rsq
rs7247199 G A 0.5847 0.4150 0.9299 0.8666
rs8102643 C T 0.5847 0.4150 0.9308 0.8685
rs8102615 T A 0.5006 0.4702 0.9375 0.8932
rs8105536 G A 0.5783 0.4213 0.9353 0.8832
rs2312724 T C 0.9122 0.0877 0.9841 0.9232
```

Note that header line is present in the file. The file describes five SNPs.

8.2.2   Genomic predictor file

Again, in the simplest scenario this is an MLDOSE or MLPROB file generated by MACH. Such file starts with two special columns plus, for each of the SNPs under consideration, a column containing the estimated allele 1 dose (ML-DOSE). In an MLPROB file, two columns for each SNP correspond to posterior

probability that person has two ($P_{A_1 A_1}$) or one ($P_{A_1 A_2}$) copies of allele 1. The first "special" column is made of the sequential id, followed by an arrow followed by study ID (the one specified in the MACH input files). The second column contains the method keyword (e.g. "MLDOSE").

An example of the few first lines of an MLDOSE file for five SNPs described in SNP information file follows here (also to be found in the file `ProbABEL/examples/test.mldose`)

```
1->id636728 MLDOSE 0.974 0.974 0.968 0.971 2
2->id890314 MLDOSE 0.947 0.947 0.113 0.944 1.094
3->id102874 MLDOSE 1.005 1.004 NaN 1.002 2
4->id200949 MLDOSE 1.968 1.969 1.973 1.977 2
5->id336491 MLDOSE 1.007 1.006 1.001 1.004 2
6->id988766 MLDOSE 1.006 1.006 1 1.003 2
7->id21999 MLDOSE 1.968 1.969 1.973 1.977 2
8->id433893 MLDOSE 1.006 1.006 1.001 1.004 2
9->id688932 MLDOSE 1.006 1.006 1.001 1.004 2
10->id394203 MLDOSE 1.967 1.968 1.972 1.976 1.999
11->id995678 MLDOSE 1.014 1.014 1.006 1.009 2
```

The order of SNPs in the SNP information file and DOSE-file must be the same. This should be the case if you just used MACH outputs.

Therefore, by all means, the number of columns in the genomic predictor file must be the same as the number of lines in the SNP information file plus one.

The dose/probability file may be supplied in filevector format (`.fvi` and `.fvd` files) in which case `ProbABEL` will operate much faster, and in low-RAM mode (approx. 128 MB). On the command line simply specify the `.fvi` file as argument for the `-dose` option (cf. section 8.3 for more information on the options accepted by `ProbABEL`). See the R libraries GenABEL and DatABEL on how to convert MACH and IMPUTE files to filevector format (functions: `mach2databel()` and `impute2databel()`, respectively).

8.2.3 Phenotypic file

The phenotypic data file contains phenotypic data, but also specifies the analysis model. There is a header line, specifying the variable names. The first column should contain personal study IDs. It is assumed that **both the total number and the order of these IDs are exactly the same as in the genomic predictor (MLDOSE) file described in previous section**. This is not difficult to arrange using e.g. R; an example is given in the `ProbABEL/examples` directory.

Missing data should be coded with 'NA', 'N' or 'NaN' codes. Any other coding will be converted to some number which will be used in analysis! E.g. coding missing as '-999.9' will result in an analysis which will consider -999.9 as indeed a true measurements of the trait/covariates.

In the case of linear or logistic regression (programs `palinear` and `palogist`, respectively), the second column specifies the trait under analysis, while the third, fourth, etc. provide information on covariates to be included into analysis. An example few lines of phenotypic information file designed for linear regression analysis follow here (also to be found in `ProbABEL/examples/height.txt`)

```
id height sex age
```

```
id636728 174.429795159687 0 56.5664877162697
id890314 168.176943059097 0 74.8311971509938
id102874 178.612190619767 1 45.2478051768211
id200949 171.770230117638 0 46.7362651142108
id336491 185.941629656499 1 61.2743318817997
id988766 173.159286450017 1 43.9794924518567
id21999 167.478282481124 0 64.842094190157
id433893 168.33178468379 1 49.2526444099125
id688932 171.691587811178 0 50.3954417563357
id394203 173.491495887183 1 71.6498502881161
```

Note again that the order of IDs is the same between the MLDOSE file and the phenotypic data file. The model specified by this file is $height \sim \mu + \text{sex} + \text{age}$, where μ is the intercept.

Clearly, you can for example include `sex × age` interaction terms by specifying another column having a product of sex and age here.

For logistic regression, it is assumed that in the second column cases are coded as "1" and controls as "0". An couple of example lines of a phenotypic information file designed for logistic regression analysis follow here (also to be found in `ProbABEL/examples/logist_data.txt`)

```
id chd sex age othercov
id636728 0 0 56.5664877162697 -0.616649220436139
id890314 0 0 74.8311971509938 0.695315865158652
id102874 1 1 45.2478051768211 -0.919192364890525
id200949 0 0 46.7362651142108 -0.623212536893650
id336491 0 1 61.2743318817997 -0.0835744351009496
id988766 0 1 43.9794924518567 -0.360419162609288
id21999 1 0 64.842094190157 -0.180940346913155
id433893 0 1 49.2526444099125 0.126374731789777
id688932 0 0 50.3954417563357 1.06437576032067
id394203 1 1 71.6498502881161 -1.18226498491599
```

You can see that in the first 10 people, there are three cases, as indicated by "chd" equal to one. The model specified by this file is $chd \sim \mu + \text{sex} + \text{age} + \text{othercov}$.

In case of the Cox proportional hazards model, the composition of the phenotypic input file is a bit different. In the second column and third column, you need to specify the outcome in terms of follow-up time (column two) and event (column three, "1" if an event occurred and zero if censored). Columns starting from four (inclusive) specify covariates to be included into the analysis. An example few lines of a phenotypic information file designed for the Cox proportional hazards model analysis follow here (also to be found in `ProbABEL/examples/coxph_data.txt`)

```
id fupt_chd chd sex age othercov
id636728 3.187930645 0 0 56.56648772 -0.61664922
id890314 2.099691952 0 0 74.83119715 0.695315865
id102874 9.133488079 1 1 45.24780518 -0.919192365
id200949 7.525406804 0 0 46.73626511 -0.623212537
id336491 6.798229522 0 1 61.27433188 -0.083574435
```

```
id988766 6.149545358 0 1 43.97949245 -0.360419163
id21999 1.013546103 1 0 64.84209419 -0.180940347
id433893 1.282853098 0 1 49.25264441 0.126374732
id688932 8.340206657 0 0 50.39544176 1.06437576
id394203 3.392345681 1 1 71.64985029 -1.182264985
```

You can see that for the first ten people, the event occurs for three of them, while for the other seven there is no event during the follow-up time, as indicated by the "chd" column. Follow-up time is specified in the preceding column. The covariates included into the model are age (presumably at baseline), sex and "othercov"; thus the model, in terms of `R/survival` is
Surv(fuptime_chd, chd) $\sim$ sex + age + othercov.

8.2.4 Optional map file

If you would like map information (e.g. base pair position) to be included in your outputs, you can supply a map file. These follow HapMap "legend" file format. For example, for the five SNPs we considered the map-file may look like (example can be found in `ProbABEL/examples/test.map`)

```
rs position 0 1
rs7247199 204938 A G
rs8102643 207859 C T
rs8102615 211970 A T
rs8105536 212033 A G
rs2312724 217034 C T
```

The order of the SNPs in the map file should follow that in the SNP information file. Only information from the second column – the SNP location – is actually used to generate the output.

8.3 Running an analysis

To run linear regression, you should use the program called `palinear`; for logistic analysis use `palogist`, and for the Cox proportional hazards model use `pacoxph` (all are found in the `ProbABEL/bin/` directory after you have compiled the program).

There are in total 11 command line options you can specify to the `ProbABEL-package` analysis functions `palinear` or `palogist`. If you run either program without any argument, you will get a short explanation to command line options:

```
user@server:~$ palogist

Usage: ../bin/palogist options

Options:
--pheno       : phenotype file name
--info        : information (e.g. MLINFO) file name
--dose        : predictor (e.g. MLDOSE/MLPROB) file name
--map         : [optional] map file name
```

```
--nids        : [optional] number of people to analyse
--chrom       : [optional] chromosome (to be passed to output)
--out         : [optional] output file name (default is regression.out.txt)
--skipd       : [optional] how many columns to skip in predictor
    (dose/prob) file (default 2)
--ntraits     : [optional] how many traits are analysed (default 1)
--ngpreds     : [optional] how many predictor columns per marker
    (default 1 = MLDOSE; else use 2 for MLPROB)
--separat     : [optional] character to separate fields (default is space)
--score       : use score test
--no-head     : do not report header line
--allcov      : report estimates for all covariates (large outputs!)
--interaction : which covariate to use for interaction with SNP
  (default is no ineraction, 0)
--mmscore     : score test for association between a trait and genetic
    polymorphism, in samples of related individuals
--robust      : report robust (aka sandwich, aka Hubert-White) standard
    errors
--help        : print help
```

8.3.1   Basic analysis options

However, for a simple run only three options are mandatory, which specify the necessary files needed to run the regression analysis.

These options are **-dose** (or **-d**), specifying the genomic predictor/MLDOSE file described in sub-section 8.2.2; **-pheno** (or **-p**), specifying the phenotypic data file described in sub-section 8.2.3; and **-info** (or **-i**), specifying the SNP information file described in sub-section 8.2.1.

If you change to the `ProbABEL/examples` directory you can run an analysis of height by running

```
user@server:~/ProbABEL/examples/$ ../bin/palinear -p height.txt
-d test.mldose -i test.mlinfo
```

Output from the analysis will be directed to the `regression.out.csv` file.

The analysis of a binary trait (e.g. chd) can be run with

```
user@server:~/ProbABEL/examples/$ ../bin/palogist -p logist_data.txt
 -d test.mldose -i test.mlinfo
```

To run a Cox proportional hazards model, try

```
user@server:~/ProbABEL/examples/$ ../bin/pacoxph -p coxph_data.txt
 -d test.mldose -i test.mlinfo
```

Please have a look at the shell script files `example_qt.sh`, `example_bt.sh` and `example_all.sh` to have a better overview of the analysis options.

To run an analysis with MLPROB files, you need specify the MLPROB file with the `-d` option and also specify that there are two genetic predictors per SNP, e.g. you can run linear model with

```
user@server:~/ProbABEL/examples/$ ../bin/palinear -p height.txt
 -d test.mlprob -i test.mlinfo
 --ngpreds=2
```

8.3.2 Advanced analysis options

The option `-interaction` allows you to include interaction between SNPs and any covariate. If for example your model is

$$\text{trait} \sim \text{sex} + \text{age} + \text{SNP},$$

running the program with the option `-interaction=2` will model

$$\text{trait} \sim \text{sex} + \text{age} + \text{SNP} + \text{age} \times \text{SNP}.$$

The option `-robust` allows you to compute so-called "robust" (a.k.a. "sandwich", a.k.a. Hubert-White) standard errors (cf. section 8.7 "Methodology" for details).

With the option `-mmscore` a score test for association between a trait and genetic polymorphisms in samples of related individuals is performed. A file with the inverse of the variance-covarince matrix goes as input parameter with that option, e.g. `-mmscore <filename>`. The file has to contain the first column with id names exactly like in phenotype file, BUT OMITTING people with no measured phenotype. The rest is a matrix. The phenotype file in case of using the `-mmscore` argument may contain any amount of covariates (this is different from previous versions). The first column contains id names, the second the trait. The others are covariates.

An example of how a polygenic object estimated by `GenABEL-package` can be used with ProbABEL is provided in `ProbABEL/examples/mmscore.R`

Though technically `-mmscore` allows for inclusion of multiple covariates, these should be kept to minimum as this is a score test. We suggest that any covariates explaining an essential proportion of variance should be fit as part of `GenABEL-package`'s `polygenic` procedure.

8.3.3 Running multiple analyses at once: `probabel.pl`

The Perl script `bin/probabel.pl_example` represents a handy wraper for `ProbABEL-package` functions. To start using it the configuration file `bin/probabel_config.cfg_example` needs to be edited. The configuration file consists of five columns. Each column except the first is a pattern for files produced by `MACH` (imputation software). The column named "cohort" is an identifying name of a population ("ERGO" in this example), the column "mlinfo_path" is the full path to mlinfo files, including a pattern where the chromosome number has been replaced by `_._chr_._`. The columns "mldose_path", "mlprobe_path" and "legend_path" are paths and patterns for "mldose", "mlprob" and "legend" files, respectively. These also need to include the pattern for the chromosome as used in the column for the "mlinfo" files. Probably you also have to change the variable `$config` in the script to point to the full path of the configuration file and the variable `@anprog` to point full path to the `ProbABEL-package` scripts.

8.4 Output file format

Let us consider what comes out of the linear regression analysis described in the previous section. After the analysis has run, in the output file you will find something like

```
name A1 A2 Freq1 MAF Quality Rsq n Mean_predictor_allele chrom
+>  position beta_SNP_add sebeta_SNP_add chi2_SNP
rs7247199 G A 0.5847 0.415 0.9299 0.8666 182 0.564439 19
+>  204938 -0.218693 0.734966 0.0905063
rs8102643 C T 0.5847 0.415 0.9308 0.8685 182 0.564412 19
+>  207859 -0.218352 0.734214 0.0904094
```

Here, only the first three lines of output have been shown. Note that lines starting with `+>` are actually the ones continuing the previous line – they have just been wrapped so we can see these long lines.

The header provides a short description of what can be found in a specific column. The first column provides the SNP name and next six are descriptions which were taken directly from the SNP information file. Therefore, these describe allele frequencies and the quality in your total imputations, not necessarily in the data under analysis.

In contrast, starting with the next column, named **n**, the output concerns the data analysed. Column 8 (**n**) tells the number of subjects for whom complete phenotypic information was available. At this point, unless you have complete measurements on all subjects, you should feel alarmed if the number here is exactly the number of people in the file – this may indicate you did not code missing values according to **ProbABEL-package** format ('NA', 'NaN', or 'N').

The next column, nine ("Mean_predictor_allele"), gives the estimated frequency of the predictor allele (**A1**) in subjects with complete phenotypic data.

If the **-chrom** option was used, in the next column you will find the value specified by this option. If **-map** option was used, in the subsequent column you will find map location taken from the map-file. The subsequent columns provide coefficients of regression of the phenotype onto genotype, corresponding standard errors, and Wald χ^2 test value.

8.5   Preparing input files

In the **ProbABEL/bin** directory you can find the **prepare_data.R** file – an R script that arranges phenotypic data in right format. Please read this script for details.

8.6   Memory use and performance

Maximum likelihood regression is implemented in **ProbABEL-package**. With 6,000 people and 2.5 millions SNPs, a genome-wide scan is completed in less that an hour for a linear model with 1-2 covariates and overnight for logistic regression or the Cox proportional hazards model (figures for a PC bought back in 2007).

Memory may be an issue with **ProbABEL-package** if you use MACH text dose/probability files, e.g. for large chromosomes, such as chromosome one consumed up to 5 GB of RAM with 6,000 people.

We suggest that dose/probability file is to be supplied in filevector format in which case **ProbABEL-package** will operate about 2-3 times faster, and in low-RAM mode (approx. 128 MB). See the R libraries **GenABEL-package** and

`DatABEL-package` on how to convert MACH and IMPUTE files to filevector format (functions: `mach2databel()` and `impute2databel()`, respectively).

When '–mmscore' option is used, the analysis may take quite some time.

8.7 Methodology

8.7.1 Analysis of population-based data

Linear regression assuming normal distribution

Standard linear regression theory is used to estimate coefficients of regression and their standard errors. We assume a linear model with expectation

$$E[\mathbf{Y}] = \mathbf{X}\,\boldsymbol{\beta} \tag{8.1}$$

and variance-covariance matrix

$$\mathbf{V} = \sigma^2 \mathbf{I},$$

where $\mathbf{Y}$ is the vector of phenotypes of interest, $\mathbf{X}$ is the design matrix, $\boldsymbol{\beta}$ is the vector of regression parameters, σ^2 is the variance and $\mathbf{I}$ is the identity matrix.

The maximum likelihood estimates (MLEs) for the regression parameters are given by

$$\hat{\beta} = (\mathbf{X}^T\mathbf{X})^{-1}\mathbf{X}^T\mathbf{Y} \tag{8.2}$$

and the MLE of the residual variance is

$$\hat{\sigma}^2 = \frac{(\mathbf{Y} - \mathbf{X}\hat{\beta})^T(\mathbf{Y} - \mathbf{X}\hat{\beta})}{N - r_X}, \tag{8.3}$$

where N is the number of observations and r_X is the rank of $\mathbf{X}$ (i.e. the number of columns of the design matrix).

The variance-covariance matrix for the parameter estimates under alternative hypothesis can be computed as

$$\mathbf{var}_{\hat{\beta}} = \hat{\sigma}^2(\mathbf{X}^T\mathbf{X})^{-1}. \tag{8.4}$$

For the j-the element $\hat{\beta}(j)$ of the vector of estimates the standard error under the alternative hypothesis is given by the square root of the corresponding diagonal element of the above matrix, $\mathbf{var}_{\hat{\beta}}(jj)$, and the Wald test can be computed with

$$T^2(j) = \frac{\hat{\beta}(j)^2}{\mathbf{var}_{\hat{\beta}}(jj)},$$

which asymptotically follows the χ^2 distribution with one degree of freedom under the null hypothesis.

When testing significance for more than one parameter simultaneously, several alternatives are available. Let us first partition the vector of parameters into two components, $\beta = (\beta_g, \beta_x)$, and our interest is testing the parameters contained in β_g (SNP effects), while β_x (e.g. effects of sex, age, etc.) are considered nuisance parameters. Let us define the vector of the parameters of interest which are fixed to certain values under the null hypothesis as $\beta_{g,0}$.

Firstly, the likelihood ratio test can be obtained with

$$LRT = 2\left(\text{logLik}(\hat{\beta}_g, \hat{\beta}_x) - \text{logLik}(\beta_{g,0}, \hat{\beta}_x)\right),$$

which under the null hypothesis is asymptotically distributed as χ^2 with the number of degrees of freedom equal to the number of parameters specified by β_g. Assuming the normal distribution, the log-likelihood of a model specified by the vector of parameters β and residual variance σ^2 can be computed as

$$\text{logLik}(\beta, \sigma^2) = -\frac{1}{2}\left(N \cdot \log_e \sigma^2 + (\mathbf{Y} - \beta\mathbf{X})^T(\mathbf{I}/\sigma^2)(\mathbf{Y} - \beta\mathbf{X})\right).$$

Secondly, the Wald test can be used; for that the inverse variance-covariance matrix of $\hat{\beta}_g$ should be computed as

$$\mathbf{var}_{\hat{\beta}_g}^{-1} = \mathbf{var}_{\hat{\beta}}^{-1}(g,g) - \mathbf{var}_{\hat{\beta}}^{-1}(g,x)\left(\mathbf{var}_{\hat{\beta}}^{-1}(x,x)\right)^{-1}\mathbf{var}_{\hat{\beta}}^{-1}(x,g),$$

where $\mathbf{var}_{\hat{\beta}}^{-1}(a,b)$ correspond to sub-matrices of the inverse of the variance-covariance matrix of $\hat{\beta}$, involving either only parameters of interest (g,g), nuisance parameters (x,x) or combination of these (x,g), (g,x).

The Wald test statistics is then computed as

$$W^2 = (\hat{\beta}_g - \beta_{g,0})^T \, \mathbf{var}_{\hat{\beta}_g}^{-1}(\hat{\beta}_g - \beta_{g,0}),$$

which asymptotically follows the χ^2 distribution with the number of degrees of freedom equal to the number of parameters specified by β_g. The Wald test generally is computationally easier than the LRT, because it avoids estimation of the model specified by the parameter's vector $(\beta_{g,0}, \hat{\beta}_x)$.

Lastly, similar to the Wald test, the score test can be performed by use of $\mathbf{var}_{(\beta_{g,0}, \hat{\beta}_x)}$ instead of $\mathbf{var}_{\hat{\beta}}$.

Logistic regression

For logistic regression, the procedure to obtain parameters estimates, their variance-covariance matrix, and tests are similar to these outlined above with several modifications.

The expectation of the binary trait is defined as the expected probability of the event as defined by the logistic function

$$E[\mathbf{Y}] = \pi = \frac{1}{1 + e^{-(\mathbf{X}\beta)}}.$$

The estimates of the parameters are obtained not in one step, as is the case of the linear model, but using an iterative procedure (iteratively re-weighted least squares). This procedure is not described here for the sake of brevity.

The log-likelihood of the data is computed using the binomial probability formula:

$$\text{logLik}(\beta) = \mathbf{Y}^T \log_e \pi + (\mathbf{1} - \mathbf{Y})^T \log_e(\mathbf{1} - \pi),$$

where $\log_e \pi$ is a vector obtained by taking the natural logarithm of every value contained in the vector π.

Robust variance-covariance matrix of parameter estimates

For a linear model, these are computed using formula

$$\mathbf{var}_r = (\mathbf{X}^T\mathbf{X})^{-1}(\mathbf{X}^T\mathbf{R}\mathbf{X})(\mathbf{X}^T\mathbf{X})^{-1},$$

where $\mathbf{R}$ is a diagonal matrix containing squares of residuals of $\mathbf{Y}$. The same formula may be used for "standard" analysis, in which case the elements of the $\mathbf{R}$ matrix are constant, namely mean residual sum of squares (the estimate of σ^2).

Similar to that, the robust matrix is computed for logistic regression with

$$\mathbf{var}_r = (\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}(\mathbf{X}^T\mathbf{R}\mathbf{X})(\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1},$$

where $\mathbf{1}$ is the vector of ones and $\mathbf{W}$ is the diagonal matrix of "weights" used in logistic regression.

Cox proportional hazards model

The implementation of the Cox proportional hazard model used in `ProbABEL-package` is entirely based on the code of R library `survival` developed by Thomas Lumley (function `coxfit2`), and is therefore not described here.

Many thanks to Thomas for making his code available under GNU GPL!

8.7.2 Analysis of pedigree data

The framework for analysis of pedigree data follows the two-step logic developed in the works of Aulchenko *et al.* (2007) and Chen and Abecasis (2007). General analysis model is a linear mixed model which defines the expectation of the trait as

$$E[\mathbf{Y}] = \mathbf{X}\beta,$$

identical to that defined for linear model (cf. section 8.1). To account for correlations between the phenotypes of relatives which may be induced by family relations the variance-covariance matrix is defined to be proportional to the linear combination of the identity matrix $\mathbf{I}$ and the relationship matrix $\boldsymbol{\Phi}$:

$$\mathbf{V}_{\sigma^2,h^2} = \sigma^2\left(2h^2\boldsymbol{\Phi} + (1-h^2)\mathbf{I}\right),$$

where h^2 is the heritability of the trait. The relationship matrix $\boldsymbol{\Phi}$ is twice the matrix containing the coefficients of kinship between all pairs of individuals under consideration; its estimation is discussed in a separate section "8.7.2" (8.7.2).

Estimation of a model defined in such a way is possible by numerical maximization of the likelihood function, however, the estimation of this model for large pedigrees is laborious, and is not computationally feasible for hundreds of thousands to millions of SNPs to be tested in the context of GWAS, as we have demonstrated previously (Aulchenko *et al.*, 2007).

Two-step score test for association

A two-step score test approach is therefore used to decrease the computational burden. Let us first re-define the expectation of the trait by splitting the design matrix in two parts, the "base" part $\mathbf{X}_x$, which includes all terms not changing across all SNP models fit in GWAS (e.g. effects of sex, age, etc.), and the part including SNP information, $\mathbf{X_g}$:

$$E[\mathbf{Y}] = \mathbf{X}_x \beta_x + \mathbf{X}_g \beta_g.$$

Note that the latter design matrix may include not only the main SNP effect, but e.g. SNP by environment interaction terms.

At the first step, a linear mixed model not including SNP effects

$$E[\mathbf{Y}] = \mathbf{X}_x \beta_x$$

is fitted. The maximum likelihood estimates (MLEs) of the model parameters (regression coefficients for the fixed effects $\hat{\beta}_x$, the residual variance $\hat{\sigma}_x^2$ and the heritability $\hat{h}_x^2$) can be obtained by numerical maximization of the likelihood function

$$\text{logLik}(\beta_x, h^2, \sigma^2) = -\frac{1}{2} \left(\log_e |\mathbf{V}_{\sigma^2, h^2}| + (\mathbf{Y} - \beta_x \mathbf{X}_x)^T \mathbf{V}_{\sigma^2, h^2}^{-1} (\mathbf{Y} - \beta_x \mathbf{X}_x) \right),$$

where $\mathbf{V}_{\sigma^2, h^2}^{-1}$ is the inverse and $|\mathbf{V}_{\sigma^2, h^2}|$ is the determinant of the variance-covariance matrix.

At the second step, the unbiased estimates of the fixed effects of the terms involving SNP are obtained with

$$\hat{\beta}_g = (\mathbf{X}_g^T \mathbf{V}_{\hat{\sigma}^2, \hat{h}^2}^{-1} \mathbf{X}_g)^{-1} \mathbf{X}_g^T \mathbf{V}_{\hat{\sigma}^2, \hat{h}^2}^{-1} \mathbf{R}_{\hat{\beta}_x},$$

where $\mathbf{V}_{\hat{\sigma}^2, \hat{h}^2}^{-1}$ is the variance-covariance matrix at the point of the MLE estimates of $\hat{h}_x^2$ and $\hat{\sigma}_x^2$ and $\mathbf{R}_{\hat{\beta}_x} = \mathbf{Y} - \hat{\beta}_x \mathbf{X}_x$ is the vector of residuals obtained from the base regression model. Under the null model, the inverse variance-covariance matrix of the parameter's estimates is defined as

$$\mathbf{var}_{\hat{\beta}_g} = \hat{\sigma}_x^2 (\mathbf{X}_g^T \mathbf{V}_{\hat{\sigma}^2, \hat{h}^2}^{-1} \mathbf{X}_g)^{-1}.$$

Thus the score test for joint significance of the terms involving SNP can be obtained with

$$T^2 = (\hat{\beta}_g - \beta_{g,0})^T \mathbf{var}_{\hat{\beta}_g}^{-1} (\hat{\beta}_g - \beta_{g,0}),$$

where $\beta_{g,0}$ are the values of parameters fixed under the null model. This test statistics under the null hypothesis asymptotically follows the χ^2 distribution with the number of degrees of freedom equal to the number of parameters tested. The significance of an individual j-the elements of the vector $\hat{\beta}_g$ can be tested with

$$T_j^2 = \hat{\beta}_g^2(j) \mathbf{var}_{\hat{\beta}_g}^{-1}(jj),$$

where $\hat{\beta}_g^2(j)$ is the square of the j-th element of the vector of estimates $\hat{\beta}_g$, and $\mathbf{var}_{\hat{\beta}_g}^{-1}(jj)$ corresponds to the j-th diagonal element of $\mathbf{var}_{\hat{\beta}_g}^{-1}$. The latter statistics asymptotically follows χ_1^2.

Estimation of the kinship matrix

The relationship matrix $\boldsymbol{\Phi}$ used in estimation of the linear mixed model for pedigree data is twice the matrix containing the coefficients of kinship between all pairs of individuals under consideration. This coefficient is defined as the probability that two gametes randomly sampled from each member of the pair are identical-by-descent (IBD), that is they are copies of exactly the same ancestral allele. The expectation of kinship can be estimated from pedigree data using standard methods, for example the kinship for two outbred sibs is 1/4, for grandchild-grandparent is 1/8, etc. For an outbred person, the kinship coefficient is 1/2 – that is two gametes sampled from this person at random are IBD only if the same gamete is sampled. However, if the person is inbred, there is a chance that a maternal and paternal chromosomes are also IBD. The probability of this is characterized by kinship between individual's parents, which is defined as the individual's inbreeding coefficient, F. In this case, the kinship coefficient for the individual is $F + 1/2$. Similar logic applies to computation of the kinship coefficient for other types of pairs in inbred pedigrees.

The kinship matrix can be computed using the pedigree data using standard methods. However, in many cases, pedigree information may be absent, incomplete, or not reliable. Moreover, the estimates obtained using pedigree data reflect the expectation of the kinship, while the true realization of kinship may vary around this expectation. In presence of genomic data it may therefore be desirable to estimate the kinship coefficient from these, and not from pedigree. It can be demonstrated that unbiased and positive semi-definite estimator of the kinship matrix can be obtained (Astle and Balding, 2010; Amin *et al.*, 2007) by computing the kinship coefficients between individuals i and j with

$$\hat{K}_{ij} = \frac{1}{L} \sum_{l=1}^{L} \frac{(g_{l,i} - p_l)(g_{l,j} - p_l)}{p_l(1 - p_l)}$$

where L is the number of loci, p_l is the allelic frequency at l-th locus and $g_{l,j}$ is the genotype of j-th person at the l-th locus, coded as 0, 1/2, and 1, corresponding to the homozygous, heterozygous, and other type of homozygous genotype. The frequency is computed for the allele which, when homozygous, corresponds to the genotype coded as "1".

8.8 How to cite

If you used `ProbABEL-package` for your analysis please give a link to the `GenABEL project` home page

> `http://www.genabel.org/`

and cite the `ProbABEL-package` paper to give us some credit:

> Aulchenko YS, Struchalin MV, van Duijn CM.
> *ProbABEL package for genome-wide association analysis of imputed data.*
> BMC Bioinformatics. 2010, 11:134.

A proper reference may look like

For the analysis of imputed data, we used the `ProbABEL-package` from the `GenABEL` suite of programs (Aulchenko *et al.*, 2010).

If you have used the Cox proportional hazard model, please mention the `R` package `survival` by Thomas Lumley. Additionally to the above citation, please tell that

The Cox proportional hazards model implemented in `ProbABEL-package` makes use of the source code of the `R` package "`survival`" as implemented by T. Lumley.

Chapter 9

Meta-analysis of GWA scans

9.1 Standard meta-analysis methods

Imagine you are interested in the effect of a certain polymorphism onto a particular disease. After scanning literature, you find some studies that implicate certain allele as significantly increasing the risk of the disease, but you will typically find also that other studies were inconclusive (no significant association), and that even some of the studies implicated the same allele as "protective". Your gut feeling may be that the allele is indeed the risk one, because you feel that the studies contradicting to this hypothesis were based on small number of subjects; however, how do you quantify this feeling? In this situation you need to perform meta-analysis of available data to come up with the joint effect size estimate and P-value, as based on all available data.

Let us first consider a situation when you are interested in the effect of the allele on a quantitative phenotype, expressed as a coefficient of regression of the trait onto the number of this allele in the genotype. Under a favorable scenario, from every individual study you would know the estimate of this regression coefficient, and the standard error of the estimate (or, equivalently, the $P-value$ or the test statistics value for association).

One of approaches frequently used in meta-analysis of the data coming from a number of independent studies is the inverse variance method. In essence, this method is equivalent to combining likelihoods coming from separate studies, using quadratic approximation. Denote coefficients of regression estimated in N studies as β_i, and associated squared standard errors of the estimates as s_i^2 where $i \in 1, 2, ..., N$. Note that the regression coefficient should be reported on the same scale, e.g. centimeters, meters, or using observations reported on the standard normal scale. Define weights for individual studies as

$$w_i = \frac{1}{s_i^2}$$

Then the pooled estimate of the regression coefficient is

$$\beta = \frac{\sum_{i=1}^{N} w_i \beta_i}{\sum_{i=1}^{N} w_i}$$

As you can see, the weights have straightforward interpretation: the bigger the weight of the study (meaning the small is the standard error in the study), the larger is the contribution from this study onto the pooled estimate.

The standard error of the pooled estimate is computed as

$$s^2 = \frac{1}{\sum_{i=1}^{N} w_i}$$

and the χ^2-test for association is computed in standard manner as

$$T^2 = \frac{\beta^2}{s^2} = \frac{\left(\sum_{i=1}^{N} w_i \beta_i\right)^2}{\sum_{i=1}^{N} w_i}$$

or, alternatively, the Z-test is

$$Z = \frac{\beta}{s} = \frac{\sum_{i=1}^{N} w_i \beta_i}{\sqrt{\sum_{i=1}^{N} w_i}}$$

Let us try to do meta-analysis using the inverse variance pooling method. Imagine we have information from four different studies reporting effect and the standard error of the same allele:

Table 9.1: Estimated regression coefficients from four studies

Study	n	β	s_β	χ^2
1	225	0.16	0.07	5.224
2	560	0.091	0.042	4.694
3	437	0.072	0.048	2.25
4	89	-0.03	0.12	0.062
Total	1311	?	?	?

Let us try to access the joint significance of the association using these data. First, let us define a vector of regression coefficients and squared standard errors:

```
> beta <- c(0.16,0.091,0.072,-0.03)
> s <- c(0.07,0.042,0.048,0.12)
> s2 <- s*s
> s2

[1] 0.004900 0.001764 0.002304 0.014400
```

Compute the weight for individual studies as

```
> w <- 1/s2
> w

[1] 204.08163 566.89342 434.02778  69.44444
```

Estimate pooled regression coefficient as

```
> pbeta <- sum(w*beta)/sum(w)
> pbeta
```

```
[1] 0.08898527
```

and pooled squared standard error as

```
> ps2 <- 1/sum(w)
> ps2
```

```
[1] 0.0007846539
```

To access significance of association in meta-analysis, let us compute χ^2 test statistics and the $P - value$ with

```
> pchi2 <- pbeta*pbeta/ps2
> pchi2
```

```
[1] 10.09155
```

```
> ppvalue <- 1. - pchisq(pchi2,1)
> ppvalue
```

```
[1] 0.001489504
```

We conclude that there is a significant association in meta-analysis.

There is an important effect which should be considered when doing meta-analysis of published data. Given numerous polymorphisms available in human genome, a particular polymorphism usually becomes a focus of interest only when it was shown to be significantly associated in some study which reports it. Put it other way around: only when a significant association was detected and reported, more studies are likely to be performed on the same polymorphism. This first report, however, is not guaranteed to demonstrate a true association: it may well report a false-positive, or, even in presence of association, it is likely to over-estimate the effect of the polymorphism. Thus there is a positive bias in literature reports, and this bias is particularly strong for the first report, a phenomenon frequently referenced to as "champion's" or "winner's curse".

The observations we have just considered are quite typical in that the first study, where the association was originally discovered, reports the biggest effect and most significant effect, while the follow-up studies suggest smaller effect.

Therefore, when you meta-analyse data from publications it is always good idea to exclude the first report (in case it is positive – and it is always positive!) and check if significant association is still observed. Let us try to do that:

```
> beta <- beta[2:4]
> s2 <- s2[2:4]
> w <- w[2:4]
> pbeta <- sum(w*beta)/sum(w)
> pbeta
```

```
[1] 0.07544522
```

```
> ps2 <- 1/sum(w)
> ps2
```

```
[1] 0.0009342602
```

```
> pchi2 <- pbeta*pbeta/ps2
> pchi2
```

```
[1] 6.092501
```

```
> ppvalue <- 1. - pchisq(pchi2,1)
> ppvalue
```

```
[1] 0.01357568
```

Indeed, when the first "champion" report is excluded, the overall evidence is decreased and results become less significant, though still pointing to the same direction.

When binary traits are studied, and results are reported as Odds Ratios with $P - values$, it is also possible to apply inverse variance method. For this, you need to transform your Odds Ratios using natural logarithm, and, on this scale, estimate the standard error. Generic inverse variance pooling may be applied to the data transformed this way; the final results are back-transformed onto Odds Ratio scale using exponentiation.

Let us consider a simple example. Let Odds Ratios and χ^2 test statistics values coming from four studies of a binary phenotype are as following: $\theta_1 = 1.5$ ($\chi^2 = 5.1$), $\theta_2 = 1.3$ ($\chi^2 = 2.2$), $\theta_3 = 0.9$ ($\chi^2 = 0.5$), $\theta_4 = 1.2$ ($\chi^2 = 3.1$).

Let us first transform the Odds Ratio to the logarithmic scale with

```
> or <- c(1.5,1.3,0.9,1.2)
> lnor <- log(or)
> lnor
```

```
[1]  0.4054651  0.2623643 -0.1053605  0.1823216
```

To compute standard errors from known χ^2 values, one can use simple relation

$$\chi^2 = \frac{\beta^2}{s^2}$$

and thus

$$s^2 = \frac{\beta^2}{\chi^2}$$

Thus to compute the square standard errors corresponding to the log-Odds Ratio, we can use

```
> chi2or <- c(5.1,2.2,0.5,3.1)
> s2lnor <- lnor*lnor/chi2or
> s2lnor
```

```
[1] 0.03223568 0.03128864 0.02220168 0.01072295
```

Now we can combine log-Odds Ratios and corresponding standard errors using inverse variance method:

```
> w <- 1/s2lnor
> plnor <- sum(w*lnor)/sum(w)
> plnor
```

```
[1] 0.1650462

> ps2 <- 1/sum(w)
> ps2

[1] 0.004968165

> pchi2 <- plnor*plnor/ps2
> pchi2

[1] 5.482958

> ppval <- 1.-pchisq(pchi2,1)
> ppval

[1] 0.01920274
```

And the corresponding estimate of pooled Odds Ratio is

```
> exp(plnor)
```

```
[1] 1.179448
```

and 95% confidence interval is

```
> exp(plnor-1.96*sqrt(ps2))
```

```
[1] 1.02726
```

```
> exp(plnor+1.96*sqrt(ps2))
```

```
[1] 1.354181
```

Some times, effects are reported on different scales, and/or there may be suspect that these effects are not translatable across studies because of the differences in experimental design or for some other reasons. In this case, it may be better to poll the data without use of the effect estimate in exact manner, based only on the sign of association and its significance. This can be done by pooling Z-score values. Z-score refers to the test statistics, which has standard normal distribution under the null and can be derived e.g. by dividing estimate of the regression coefficient onto its standard error:

$$Z_i = \frac{\beta_i}{s_i}$$

The Z-score pooling methods can be derived from the inverse variance pooling by exploiting the fact that generally standard error of the estimate is proportional to $1/\sqrt{n}$, where n is the number of observations used for estimation. Therefore individual scores are assigned weights which are proportional to the square root of number of independent observations used in individual study, $w_i = \sqrt{n_i}$. The pooled Z-score statistics is computed as

$$Z = \frac{\sum_{i=0}^{N} w_i Z_i}{\sqrt{\sum_{i=0}^{N} w_i^2}}$$

We can now repeat the analysis of our first data set using Z-score pooling method. First, our data from table 9.1 are

```
> n <- c(225,560,437,89)
> beta <- c(0.16,0.091,0.072,-0.03)
> s <- c(0.07,0.042,0.048,0.12)
```

The Z-scores and weights are are:

```
> z <- beta/s
> z
```

```
[1]  2.285714  2.166667  1.500000 -0.250000
```

```
> w <- sqrt(n)
> w
```

```
[1] 15.000000 23.664319 20.904545  9.433981
```

The pooled estimate of Z-score is

```
> pz <- sum(w*z)/sqrt(sum(w^2))
> pz
```

```
[1] 3.163875
```

and corresponding $P - value$ is

```
> 1.-pchisq(pz*pz,1)
```

```
[1] 0.001556839
```

which is almost the same $P - value$ we have obtained previously using the inverse variance method. Note, however, that now we do not know the "pooled" estimate of the regression coefficient.

Other important aspects of meta-analysis, such as heterogeneity, and a wide range of methods different from the inverse variance and Z-score based methods are not covered here, and we refer the reader to more epidemiologically-oriented literature for a better review.

9.2   Exercise: meta-analysis of literature data

In this exercise, you will perform meta-analysis of results collected from literature. These results resemble these obtained for association analysis between Pro12Ala polymorphism of the PPAR-GenABEL-packagemma gene and type 2 diabetes. The data collected from literature are presented in the table 9.2.

As you can see, only the original study report significant association, while other four are insignificant and one point in opposite direction.

Answer the following questions:

Exercise 8 *Perform meta-analysis of the data presented in table 9.2. Which allele is the risk one? Is this risk significant? What is pooled Odds Ratio and 95% confidence interval? Do analysis using at least two methods. Which method is better (best) in this situation? Why?*

Exercise 9 *Perform meta-analsys excluding the original report (study 1). Is there still significant association between Pro12Ala and diabetes?*

Table 9.2: Summary of six studies of association between T2D and Pro12Ala polymorphism of the PPAR-`GenABEL-package`*mma* gene. n: number of subjects; effective allele: the allele for which the OR was estimated.

Study	Effective allele	n	OR_E	$P - value$
1	Ala	221	0.67	0.013
2	Pro	306	0.93	0.60
3	Pro	71	1.08	0.84
4	Ala	164	0.83	0.40
5	Pro	242	1.22	0.25
6	Pro	471	1.23	0.07

9.3 Reporting GWA results for future meta-analysis

In this section, we will discuss specifics of GWA analysis when meta-analysis is aimed at later stage. In order to perform meta-analysis at later stage, using either inverse variance or Z-score based method, you generally need to report only effect estimates, standard errors of The estimates (or, equivalently, $P - values$ or test statistics values), and number of observations used for estimation.

It is also clear that it is crucial to know for which allele the effect is reported, and this is the point where meta-analysis of genetic data may be very confusing. Generally, one may think that reporting what couple of nucleotide bases correspond to the polymorphism under the study and defining what allele was used as reference in the regression model may be enough. This, however, is not true for certain class of polymorphisms and may be a source of great confusion.

Consider a DNA molecule; as you know it is made of two complementary strands (forward or "+" and reverse or "-"). As you may guess, depending on the strand, what is an "A/G" polymorphism when reported on "+" strand becomes "T/C" polymorphism on the "-" strand (using complementarity rule A<->T and G<->C). This is not a big problem for most of the polymorphism classes, because if say you know that for a first study β_1 is reported for the "G" allele of the "A/G" polymorphism and in the second study β_2 is the estimate of the effect "C" allele of the same polymorphism, but coded as "T/C" (thus other strand), you can easily spot that and say the "C" is the same as "G" in this situation, and pool the two betas straightforwardly.

However, for two types of polymorphisms, "A/T" and "G/C", where you can not get away without knowing what the strand was: what is reported as the effect of "T" in "A/T" polymorphism in study one; and seemingly corresponding effect of "T" in "A/T" polymorphism in study two may be apparently reports for two opposite alleles, if strands used for reporting in two studies were different.

The story may become even more complex, because the forward/reverse orientation depends on the genomic build[1].

Thus if you want to pool your results with the results of others, there are quite a few SNP characteristics which are absolutely crucial to report, namely, the nucleotide bases describing the polymorphism, with indication which one was used as reference, and which one as "effective", strand, genomic build, and only than the effect estimate, standard error of the effect, and number of observations

---

[1] There is alternative, top/bottom, strand designation, which does not depend on genomic build. However, it is not always used.

used to do estimation.

Other characteristics which are also recommended for reporting because they describe the quality characteristics of the sample and/or provide redundant information, which is good for double checks. Such characteristics include: frequency of the effective or reference allele, call rate, P-value for Hardy-Weinberg equilibrium and may be some parameter describing what is the direction of deviation from HWE (e.g. F_{max}). When reporting results for imputed SNPs, more quality control characteristics should be included, suh as average maximal posterior probability, R^2, etc.

Let us start with arranging two data sets which could then be used for meta-analysis. Basically, we will use cleaned data from the GWA exercise you did in section 5 ("Genome-wide association analysis", page 101), and split that is two parts.

If you did not do this yet, start R and load `GenABEL-package` library, which you will need it to work with GWA-data

```
> library(GenABEL)
```

```
GenABEL v. 1.7-0 (October 05, 2011) loaded
```

```
Installed GenABEL version (1.7-0) is not the same as stable
version available from CRAN (1.6-7). Unless used intentionally,
consider updating to the latest CRAN version. For that, use
'install.packages("GenABEL")', or ask your system administrator
to update the package.
```

Load the data with

```
> load("data2.RData")
```

and then split it in two parts:

```
> nids(data2)
```

```
[1] 124
```

```
> mdta1 <- data2[1:40,]
> mdta2 <- data2[41:nids(data2),]
```

We will analyse body mass index. If you pooling results of analysis of studies which are designed in approximately the same manner, you may think of reporting the effect estimates on the same scale and use of the inverse variance method for meta-analysis.

However, in meta-analysis of multiple data sets different individual studies are likely to assess different population, will use different designs, measure different covariates, and so on. Therefore you should think of some standardisation of the outcome variable (or apply Z-score method).

Therefore for the purpose of future meta-analysis, it becomes conventional to analyse pre-adjusted data which are scaled to Standard Normal (mean of zero and variance of unity). Note that this argument applies only to meta-analysis – you may and should report effects on the original scale (e.g. in centimeters and grams) in analysis of individual studies, in order to have better interpretability.

Moreover, in meta-analysis you heavily rely on the large numbers approximation when estimating $P-values$; while for individual study you can always apply empirical, e.g. permutation-based, procedures to derive the correct $P-value$ whatever is the distribution of the trait, in meta-analysis the Normality assumption becomes crucial, and you do not want few outliers spoiling your results by screwing up $P-values$. Therefore some transformation improving normality is desirable. Note that transformation to Standard Normal does not improve the fit to normality; to do that other transformation should be applied. Probably the most famous transformations are log- and square root ones, then one may think of Box-Cox transformation. At the same time there is a transformation, called a Rank Transformation ro Normality which guarantees perfect fit to Normal in absence of heavy ties[2]. We advocate the use of Rank Transformation to Normal for meta-analysis purposes.

`GenABEL-package` implements the `ztransform` function for the purposes of Z-transformation. This function takes two (actually three – see help for details) arguments: formula (or just the variable name) and data. `ztransform` function will perform (generalised) linear regression using the specified formula, and will transform the residuals from analysis onto Z-scale by subtracting the mean and division by the standard deviation.

Let us consider what this function does practically. Let us first transform BMI from the first set without using covariates:

```
> zbmi0 <- ztransform(bmi,mdta1)
```

The histogram of the transformed variable and scatter-plot of raw against transformed BMI is given at figure 9.1, column 1. Note that the fit to Normality is not improved by this transformation; with the original BMI, the Shapiro test for deviation from normality gives

```
> shapiro.test(phdata(mdta1)$bmi)

        Shapiro-Wilk normality test

data:  phdata(mdta1)$bmi
W = 0.9328, p-value = 0.0199
```

with identical results from the transformed variable:

```
> shapiro.test(zbmi0)

        Shapiro-Wilk normality test

data:  zbmi0
W = 0.9328, p-value = 0.0199
```

This is quite natural: as you can note from scatter-plot in column 1 of figure 9.1, only the centering and the spread of the scales are different for X (original BMI) and Y (x0), otherwise there is an exact linear correspondence between the two.

We can also do transformation using sex and age-adjusted residuals with

---

[2] Ties are generated by the subjects with exactly the same trait values

```
> zbmi1 <- ztransform(bmi~sex+age,mdta1)
```

The scatter-plot of raw against transformed BMI is given at figure 9.1, column
2. Note that this transformation may slightly change the fit to Normal, which
happens because we factor out the effects of sex and age:

```
> shapiro.test(zbmi1)

        Shapiro-Wilk normality test

data:  zbmi1
W = 0.9263, p-value = 0.01224
```

From the scatter-plot in column 2 of figure 9.1, it is quite clear what happens:
the residuals from linear regression are not corresponding to the original BMI
in exact linear manner.

A similar function, which performs rank-transformation to normality, is
named **rntransform**. For example if we want to adjust BMI for sex and age
and rank-transform the residuals to Normal, we can use

```
> rnbmi1 <- rntransform(bmi~sex+age,mdta1)
```

This transformation, however, indeed improves the fit to Normal:

```
> shapiro.test(rnbmi1)

        Shapiro-Wilk normality test

data:  rnbmi1
W = 0.999, p-value = 1
```

In essence, the $P - value$ of 1 means perfect fit to Normal – and this is what
should have occurred when this transformation is used on the data without ties.
Perfectly Normal distribution of the transformed trait may be enjoyed at the
histogram presented at column 3 of figure 9.1.

Let us analyse Rank-Normal-transformed, sex and age-adjusted BMI in the
two data sets, using **qtscore** function. Analysis of the first study is done with

```
> qts1 <- qtscore(rnbmi1,mdta1)
```

and analysis of the second study is done with

```
> zbmi2 <- ztransform(bmi~sex+age,mdta2)
> qts2 <- qtscore(zbmi2,mdta2)
```

The analysis looks very simple – is not it? However, the real difficulty did
not start yet: now we need to extract coding, reference allele, strand, etc. –
otherwise we can not do right meta-analysis later on!

Let us assume that you want to summarise the GW results from additive 1
d.f. test using following variables (as, e.g., requested by consortium):

- **name: SNP name**

- **chromosome: chromosome number**
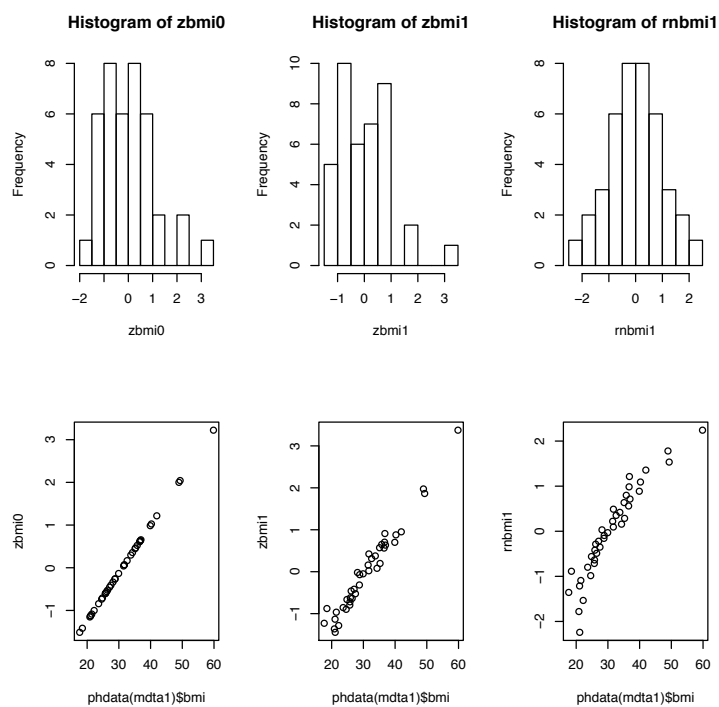
Figure 9.1: Histogram of transformed BMI and scatter-plots of the raw BMI against transformed BMI. Column 1: Z-transformation without covariates. Column 2: Z-transformation with adjustment for age and sex. Column 3: Rank-transformation to normality, after adjustment for sex and age.

- **position: physical position of the SNP**

- **refallele: reference allele**

- **codedallele: coded (effect) allele**

- **strand: strand**

- **refallfreq: frequency of the reference allele**

- **n: number of people with data available for this SNP test**

- **beta: estimate of the effect of the allele**

- **se_beta: standard error of the effect estimate**

- **p: P-value for the test**

- **p_corr: corrected P-value (we will use Genomic Control)**

- **call: SNP call rate**

- **phwe: *P*-value from the exact test for HWE**

Let us look what we get as an output from `qtscore` analysis:

```
> results(qts1)[1:2,]

          Chromosome Position Strand A1 A2  N      effB    se_effB  chi2.1df
rs1646456          1      653      +  C  G 40  0.1768955 0.2560635 0.4772414
rs4435802          1     5291      +  C  A 40 -0.4064900 0.4095768 0.9849838
              P1df       effAB      effBB  chi2.2df      P2df      Pc1df
rs1646456 0.4896745  0.09703712 0.4909062 0.6323627 0.7289272 0.4896745
rs4435802 0.3209715 -0.40649004        NA 0.9849838 0.3209715 0.3209715
```

You can see that most infromation is already present in the output, though
called using names which are different from these requested. However, we miss
reference allele frequency, SNP call rate and *P*-value from the Hardy-Weinberg
equilibrium test. These however can be computed using the `summary` function:

```
> # for data part 1:
> sum1 <- summary(gtdata(mdta1))
> sum1[1:2,]

          Chromosome Position Strand A1 A2 NoMeasured CallRate    Q.2 P.11 P.12
rs1646456          1      653      +  C  G         40        1 0.3375   16   21
rs4435802          1     5291      +  C  A         40        1 0.0875   33    7
          P.22    Pexact        Fmax      Plrt
rs1646456    3 0.4775382 -0.17400419 0.2616425
rs4435802    0 1.0000000 -0.09589041 0.4122629

> # ... and for data part 2:
> sum2 <- summary(gtdata(mdta2))
> sum2[1:2,]

          Chromosome Position Strand A1 A2 NoMeasured  CallRate        Q.2 P.11
rs1646456          1      653      +  C  G         83 0.9880952 0.33734940   36
rs4435802          1     5291      +  C  A         82 0.9761905 0.07926829   69
          P.12 P.22 Pexact        Fmax      Plrt
rs1646456   38    9      1 -0.02402597 0.826397
rs4435802   13    0      1 -0.08609272 0.289791
```

Note, however, that we now got frequency of the *effective* (or coded) allele,
not the frequency of the reference allele! The quantity we need can be easily
computed, though:

```
> # for data part 1
> refallfreq1 <- 1 - sum1[,"Q.2"]
> # ... and for data part 2
> refallfreq2 <- 1 - sum2[,"Q.2"]
```

At this moment we can arrange the required data frame:

```
> mdf1 <- data.frame(name=snpnames(qts1),chromosome=chromosome(qts1),
+        position=map(qts1),refallele=refallele(qts1),
+        codedallele=effallele(qts1),strand = strand(qts1),
+        refallelefreq = refallfreq1,n=qts1[,"N"],
```

```
+          beta=qts1[,"effB"],
+          se_beta=qts1[,"se_effB"],p=qts1[,"P1df"],
+          p_corr=qts1[,"Pc1df"],call = sum1[,"CallRate"],
+          phwe = sum1[,"Pexact"], stringsAsFactors = FALSE)
```

note the last argument – `stringsAsFactors = FALSE`. I suggest you use that
by default when constructing a new data frame – unless you are sure that you
can work out your way later on with strings saved as factors.

Let us inspect the first 5 raws of the resulting output:

```
> mdf1[1:5,]
```

```
              name chromosome position refallele codedallele strand
rs1646456 rs1646456          1      653         C           G      +
rs4435802 rs4435802          1     5291         C           A      +
rs946364   rs946364          1     8533         T           C      -
rs299251   rs299251          1    10737         A           G      +
rs2456488 rs2456488          1    11779         G           C      +
          refallelefreq  n       beta    se_beta         p    p_corr  call
rs1646456     0.6625000 40  0.1768955 0.2560635 0.4896745 0.4896745 1.000
rs4435802     0.9125000 40 -0.4064900 0.4095768 0.3209715 0.3209715 1.000
rs946364      0.7236842 38  0.2944870 0.2752734 0.2847102 0.2847102 0.950
rs299251      0.9615385 39  0.4958353 0.5989959 0.4077965 0.4077965 0.975
rs2456488     0.6625000 40  0.1145684 0.2271545 0.6140062 0.6140062 1.000
               phwe
rs1646456 0.4775382
rs4435802 1.0000000
rs946364  0.6911168
rs299251  1.0000000
rs2456488 0.7320709
```

However, it is not recommended that you perform above-described report-
ing actions unless you develop your own format. In case if you plan to use
`MetABEL-package` for meta-analysis, you best use `formetascore` function, which
basically performs operations similar to described, and reports results in format
compatible with `MetABEL-package`.

Thus, if you plan to use `MetABEL-package` for meta-analysis, required tables
can be generated with single command:

```
> mdf1 <- formetascore(bmi~sex+age,mdta1,transform=rntransform, verbosity = 2 )
```

You can see that results are the same as previously:

```
> mdf1[1:5,]
```

```
              name chromosome position strand allele1 allele2    build
rs1646456 rs1646456          1      653      +       C       G unknown
rs4435802 rs4435802          1     5291      +       C       A unknown
rs946364   rs946364          1     8533      -       T       C unknown
rs299251   rs299251          1    10737      +       A       G unknown
rs2456488 rs2456488          1    11779      +       G       C unknown
          effallele effallelefreq  n       beta    sebeta         p      pgc
```

```
rs1646456         G     0.33750000 40   0.1768955 0.2560635 0.4896745 0.4896745
rs4435802         A     0.08750000 40  -0.4064900 0.4095768 0.3209715 0.3209715
rs946364          C     0.27631579 38   0.2944870 0.2752734 0.2847102 0.2847102
rs299251          G     0.03846154 39   0.4958353 0.5989959 0.4077965 0.4077965
rs2456488         C     0.33750000 40   0.1145684 0.2271545 0.6140062 0.6140062
           lambda.estimate lambda.se lambda.iz0 lambda.iz2      pexhwe   call
rs1646456                1        NA   1.006539          1 0.4775382 1.000
rs4435802                1        NA   1.006539          1 1.0000000 1.000
rs946364                 1        NA   1.006539          1 0.6911168 0.950
rs299251                 1        NA   1.006539          1 1.0000000 0.975
rs2456488                1        NA   1.006539          1 0.7320709 1.000
```

To write all the data to a file, we can use standard R `write.csv` function:

```
> write.csv(mdf1,file="RData/part1.rnbmisexage.csv",row.names=F)
```

Similar analysis is applied to the second data set:

```
> mdf2 <- formetascore(bmi~sex+age,mdta2,transform=rntransform, verbosity = 2 )
```

We can inspect the first five lines of the output with

```
> mdf2[1:5,]
```

```
               name chromosome  position strand allele1 allele2     build
rs1646456 rs1646456          1       653      +       C       G unknown
rs4435802 rs4435802          1      5291      +       C       A unknown
rs946364   rs946364          1      8533      -       T       C unknown
rs299251   rs299251          1     10737      +       A       G unknown
rs2456488 rs2456488          1     11779      +       G       C unknown
          effallele effallelefreq  n        beta    sebeta          p
rs1646456         G    0.32926829 82 -0.04879397 0.1663650 0.76929696
rs4435802         A    0.08024691 81  0.37724197 0.2984226 0.20618701
rs946364          C    0.25903614 83 -0.14414880 0.1790329 0.42073156
rs299251          G    0.04216867 83 -0.69920378 0.3919648 0.07444912
rs2456488         C    0.34146341 82 -0.23105805 0.1520352 0.12856957
               pgc lambda.estimate    lambda.se lambda.iz0 lambda.iz2
rs1646456 0.77676571        1.070017 0.0009650323   1.036357   1.027149
rs4435802 0.22168453        1.070017 0.0009650323   1.036357   1.027149
rs946364  0.43635427        1.070017 0.0009650323   1.036357   1.027149
rs299251  0.08461892        1.070017 0.0009650323   1.036357   1.027149
rs2456488 0.14177789        1.070017 0.0009650323   1.036357   1.027149
             pexhwe      call
rs1646456 0.8038996 0.9879518
rs4435802 1.0000000 0.9759036
rs946364  1.0000000 1.0000000
rs299251  1.0000000 1.0000000
rs2456488 0.4685397 0.9879518
```

Let us write the data to a file:

```
> write.csv(mdf2,file="RData/part2.rnbmisexage.csv",row.names=F)
```

Finally let us analyse and save results for another data set, `ge03d2c`:

```
> data(ge03d2c)
> mdf3 <- formetascore(bmi~sex+age,ge03d2c,transform=rntransform, verbosity = 2 )
> write.csv(mdf3,file="RData/part3.rnbmisexage.csv",row.names=F)
```

9.4 Meta-analysis with `MetABEL`-package

Now we are ready to meta-analyse GWA data coming from three studies. For this we will need to use `MetABEL-package` package, implementing simple meta-analysis functions for GWA data. Start with loading the package:

```
> library(MetABEL)
```

We will first meta-analyse the three studies using the data frames generated in previous section, `mdf1`, `mdf2` and `mdf3`. For this we will use the core function of `MetABEL-package`, `metagwa.tables`. This function takes four arguments: two data frames with results from individual studies, and two arguments supplying the study names. Pooling of multiple studies is possible by sequential application of this function.

Let us pool two first data frames:

```
> pooled <- metagwa.tables(mdf1,mdf2,name.x="Part1",name.y="Part2")

analysing ...
Lambda Part1 = 0.9499903
Lambda Part2 = 1.098705
Corrected Lambda Part1 = 0.9499903
Corrected Lambda Part2 = 1
Lambda POOLED data = 1.023276
... DONE
```

The `pooled` data frame contains results of meta-analysis and essential details of the original studies:

```
> pooled[1:5,]
```

```
      name strand allele1 allele2 effallele chromosome position    n npops
1  rs100616      -       G       C         C          1  1911712  122     2
2 rs1006497      +       T       G         G          1  2658810  122     2
3 rs1011580      +       A       G         G          3 10048771  121     2
4 rs1011953      +       A       G         G          2  6464510  123     2
5 rs1013473      +       A       T         T          1  4487262  123     2
        beta    sebeta effallelefreq      call    pexhwe  obetaPart1
1  0.11443814 0.1850338     0.1270492 0.9919020 4.64447636  0.08819818
2 -0.07946221 0.1954998     0.1434426 0.9920082 0.16813927 -0.25425751
3 -0.06801448 0.1397522     0.5041322 0.9837773 3.15056880 -0.06755996
4  0.07539928 0.1372443     0.3292683 1.0000000 0.10373542  0.18982068
5  0.30393338 0.1334451     0.5121951 1.0000000 0.04821391  0.31522388
     obetaPart2 osePart1  osePart2      chi2         p
1  0.1230224623 0.3726827 0.2131624 0.3825070 0.5362646
2 -0.0001117686 0.3498751 0.2357343 0.1652071 0.6844070
```

```
3 -0.0683575796 0.2130800 0.1851327 0.2368565 0.6264858
4  0.0055254619 0.2228918 0.1741797 0.3018185 0.5827446
5  0.2978861467 0.2259542 0.1653644 5.1874252 0.0227509
```

If one needs to pool more studies, this data frame should be used as the first argument of the `metagwa.tables`, and `name.x` argument should take special value "POOLED":

```
> pooled <- metagwa.tables(pooled,mdf3,name.x="POOLED",name.y="mdf3")

NA for betas in both populaions
18 SNPs removed
analysing ...
Lambda mdf3 = 1.128096
Corrected Lambda mdf3 = 1
Lambda POOLED data = 1.340905
... DONE

> pooled[1:5,]
```

```
     name strand allele1 allele2 effallele chromosome position   n npops
1 rs1000475      +       T       C         C          X 13721802  91     1
2 rs1000909      -       A       G         G          2  8531681 190     1
3 rs1006092      -       T       G         G          X 13527448 190     1
4  rs100616      -       G       C         C          1  1911712 310     3
5 rs1006497      +       T       G         G          1  2658810 315     3
        beta     sebeta effallelefreq      call    pexhwe    obetaPart1
1 -0.05521349 0.11185255    0.5824176 0.4690722 5.9671619            NA
2 -0.08504871 0.13218866    0.8157895 0.9793814 2.8521518            NA
3 -0.03712065 0.08523891    0.5078947 0.9793814 6.8378385            NA
4  0.11824774 0.12085884    0.1241935 0.9780568 6.5922479    0.08819818
5 -0.02366946 0.11439872    0.1603175 0.9937465 0.2313494   -0.25425751
     obetaPart2    obetamdf3  osePart1  osePart2    osemdf3        chi2
1           NA -0.055213494        NA        NA 0.11185255 0.24366808
2           NA -0.085048708        NA        NA 0.13218866 0.41394922
3           NA -0.037120652        NA        NA 0.08523891 0.18965112
4  0.1230224623  0.121082405 0.3726827 0.2131624 0.15961076 0.95725763
5 -0.0001117686  0.005382408 0.3498751 0.2357343 0.14107317 0.04280893
         p
1 0.6215693
2 0.5199718
3 0.6632071
4 0.3278788
5 0.8360855
```

This procedure may become quite laborious if multiple studies are to be pooled. In this case, it is possible to run meta-analysis using data provided in files, by applying function `metagwa.files`. As the first argument, this function takes the path to the directory where the files with results of individual studies are stored. It is assumed that the file names are made of two parts: population/study name and an extension. Thus the second argument of the

`metagwa.files` function is the vector with names of studies, and the third
one provides extension. Other arguments, "maf", "call" and "phwe" provide the
threshold for QC filtering of SNPs in individual studies.

The function does not return any value, but rather creates a new file named
`POOLEDextens`, where "extens" is the argument supplied to the function, in the
source directory. To run analysis on the three files in the directory "RData" we
can use

```
> metagwa.files(dir="RData",pops=c("part1","part2","part3"),extens=".rnbmisexage.csv",maf=0.005

Population part1 , reading RData/part1.rnbmisexage.csv done
Dimesions after filters are 3482 20
population part2, reading RData/part2.rnbmisexage.csv done
Dimesions after filters are 3530 20
analysing ...
Lambda part1 = 0.9493588
Lambda part2 = 1.095788
Corrected Lambda part1 = 0.9493588
Corrected Lambda part2 = 1
Lambda POOLED data = 1.024196
... DONE
Dimesions after pooling are 3533 20
population part3, reading RData/part3.rnbmisexage.csv done
Dimesions after filters are 7444 20
analysing ...
Lambda part3 = 1.12461
Corrected Lambda part3 = 1
Lambda POOLED data = 1.345936
... DONE
Dimesions after pooling are 7444 22
$analysed.pops
[1] "part1" "part2" "part3"
```

extra arguments regulate the SNP exclusion criteria: `maf=0.01` tells to exclude
SNPs with minor allele frequency less then 0.5%, `call=0.95` tells to drop SNPs
with call rate less than 95%, and `phwe=1.e-8` instructs to exclude SNPs with
HWE P-value $\leq 10^{-8}$.

Now we can read and inspect the results of meta-analysis with:

```
> poolf <- read.csv("RData/POOLED.rnbmisexage.csv",strings=F)
> poolf[1:5,]

      name strand allele1 allele2 effallele chromosome position   n npops
1 rs1000909      -       A       G         G          2  8531681 190     1
2 rs1006092      -       T       G         G          X 13527448 190     1
3  rs100616      -       G       C         C          1  1911712 310     3
4 rs1006497      +       T       G         G          1  2658810 315     3
5 rs1010481      +       A       C         C          2  8409087 190     1
        beta     sebeta effallelefreq      call    pexhwe obetapart1
1 -0.08504871 0.13198426     0.8157895 0.9793814 2.8521518         NA
2 -0.03712065 0.08510711     0.5078947 0.9793814 6.8378385         NA
```

```
3  0.11825684 0.12070003     0.1241935 0.9780568 6.5922479  0.08819818
4 -0.02359567 0.11424656     0.1603175 0.9937465 0.2313494 -0.25425751
5 -0.03241475 0.12358721     0.2657895 0.9793814 0.0000000         NA
    obetapart2   obetapart3 osepart1  osepart2   osepart3       chi2
1          NA -0.085048708       NA        NA 0.13198426 0.41523235
2          NA -0.037120652       NA        NA 0.08510711 0.19023899
3  0.1230224623  0.121082405 0.3726827 0.2128792 0.15936396 0.95992605
4 -0.0001117686  0.005382408 0.3498751 0.2354211 0.14085503 0.04265582
5          NA -0.032414750       NA        NA 0.12358721 0.06879205
        p
1 0.5193256
2 0.6627178
3 0.3272055
4 0.8363747
5 0.7931037
```

9.5   Answers to the exercise

Perform meta-analysis of the data presented in table 9.2. Which allele is the risk
one? Is this risk significant? What is pooled Odds Ratio and 95% confidence
interval? Do analysis using at least two methods. Which method is better (best)
in this situation? Why?

  We first need to unify Odds Ratios by using the same effective allele. Let that
be the "risk" allele, as may be guessed from a glance to the data, namely "Pro".
When the effects are reported for the other, "Ala" allele, the corresponding ORs
for the "Pro" allele can be found using simple relation $OR_{Pro} = 1/OR_{Ala}$.

  Thus, the vector of Odds Ratios for "Pro" allele is

```
> or.pro <- c(1./.67,0.93,1.08,1./.83,1.22,1.23)
> or.pro

[1] 1.492537 0.930000 1.080000 1.204819 1.220000 1.230000
```

  The corresponding $P - values$ are

```
> p <- c(0.013,0.6,0.84,0.40,0.25,0.07)
```

  Let us find log-ORs

```
> logor.pro <- log(or.pro)
> logor.pro

[1]  0.40047757 -0.07257069  0.07696104  0.18632958  0.19885086  0.20701417
```

  Corresponding squared standard errors are

```
> s2 <- logor.pro*logor.pro/qchisq(1-p,1)
> s2

[1] 0.02599764 0.01915121 0.14531060 0.04901514 0.02988102 0.01305349
```

and weights are

```
> w <- 1/s2
> w
```

```
[1] 38.465034 52.216009  6.881811 20.401860 33.466060 76.607876
```

Thus the pooled estimate of log-OR is

```
> p.logor.pro <- sum(w*logor.pro)/sum(w)
> p.logor.pro
```

```
[1] 0.1686548
```

and the standard error is

```
> p.s <- 1/sqrt(sum(w))
> p.s
```

```
[1] 0.06622101
```

Thus the pooled estimate of Odds Ratio from association between type 2 diabetes and "Ala" allele is

```
> exp(p.logor.pro)
```

```
[1] 1.183711
```

and the 95% confidence interval is

```
> exp(p.logor.pro-1.96*p.s)
```

```
[1] 1.039627
```

```
> exp(p.logor.pro+1.96*p.s)
```

```
[1] 1.347765
```

The χ^2 test for association and corresponding $P - value$ are

```
> p.chi2 <- (p.logor.pro/p.s)^2
> p.chi2
```

```
[1] 6.486429
```

```
> p.pval <- 1-pchisq(p.chi2,1)
> p.pval
```

```
[1] 0.01087011
```

Z-score pooling though may be more appropriate method for such differentially designed studies (e.g. control groups are very different). To get Z-score pooling working, we need first find Z-scores from P-values

```
> p <- c(0.013,0.6,0.84,0.40,0.25,0.07)
> z <- sqrt(qchisq(1-p,1))
> z
```

```
[1] 2.4837693 0.5244005 0.2018935 0.8416212 1.1503494 1.8119107
```

and assign the right sign (let "+" is for the risk effect of "Pro").

```
> effsig <- c(1,-1,1,1,1,1)
> z <- z*effsig
> z
```

```
[1]  2.4837693 -0.5244005  0.2018935  0.8416212  1.1503494  1.8119107
```

Now, we need to assign weights to the studies as

```
> n <- c(221,306,71,164,242,471)
> w <- sqrt(n)
```

ane the pooled estimate of Z and corresponding $P-value$ are

```
> zpoo <- sum(w*z)/sqrt(sum(w^2))
> zpoo
```

```
[1] 2.537333
```

```
> 1-pchisq(zpoo*zpoo,1)
```

```
[1] 0.01117008
```

As you can see the results are almost identical to the previous obtained with inverse variance pooling.

9.5.1   Exercise 9:

Perform meta-analsys excluding the original report (study 1). Is there still significant association between Pro12Ala and diabetes?

The answer to this exercise can be obtained in exactly the same manner, as for the previous one, limiting our consideration to the last five studies.

Thus, the vector of Odds Ratios for "Pro" allele is

```
> or.pro <- c(0.93,1.08,1./.83,1.22,1.23)
> or.pro
```

```
[1] 0.930000 1.080000 1.204819 1.220000 1.230000
```

The corresponding $P-values$ are

```
> p <- c(0.6,0.84,0.40,0.25,0.07)
```

Let us find log-ORs

```
> logor.pro <- log(or.pro)
> logor.pro
```

```
[1] -0.07257069  0.07696104  0.18632958  0.19885086  0.20701417
```

Corresponding squared standard errors are

```
> s2 <- logor.pro*logor.pro/qchisq(1-p,1)
> s2
```

```
[1] 0.01915121 0.14531060 0.04901514 0.02988102 0.01305349
```

and weights are

```
> w <- 1/s2
> w
```

```
[1] 52.216009  6.881811 20.401860 33.466060 76.607876
```

Thus the pooled estimate of log-OR is

```
> p.logor.pro <- sum(w*logor.pro)/sum(w)
> p.logor.pro
```

```
[1] 0.1216172
```

and the standard error is

```
> p.s <- 1/sqrt(sum(w))
> p.s
```

```
[1] 0.07262917
```

Thus the pooled estimate of Odds Ratio from association between type 2 diabetes and "Ala" allele is

```
> exp(p.logor.pro)
```

```
[1] 1.129322
```

and the 95% confidence interval is

```
> exp(p.logor.pro-1.96*p.s)
```

```
[1] 0.9794776
```

```
> exp(p.logor.pro+1.96*p.s)
```

```
[1] 1.30209
```

The χ^2 test for association and corresponding $P - value$ are

```
> p.chi2 <- (p.logor.pro/p.s)^2
> p.chi2
```

```
[1] 2.803937
```

```
> p.pval <- 1-pchisq(p.chi2,1)
> p.pval
```

```
[1] 0.09403318
```

Z-score pooling though may be more appropriate method for such differentially designed studies (e.g. control groups are very different). To get Z-score pooling working, we need first find Z-scores from P-values

```
> p <- c(0.6,0.84,0.40,0.25,0.07)
> z <- sqrt(qchisq(1-p,1))
> z
```

```
[1] 0.5244005 0.2018935 0.8416212 1.1503494 1.8119107
```

and assign the right sign (let "+" is for the risk effect of "Pro").

```
> effsig <- c(-1,1,1,1,1)
> z <- z*effsig
> z
```

```
[1] -0.5244005  0.2018935  0.8416212  1.1503494  1.8119107
```

Now, we need to assign weights to the studies as

```
> n <- c(306,71,164,242,471)
> w <- sqrt(n)
```

ane the pooled estimate of Z and corresponding $P-value$ are

```
> zpoo <- sum(w*z)/sqrt(sum(w^2))
> zpoo
```

```
[1] 1.709151
```

```
> 1-pchisq(zpoo*zpoo,1)
```

```
[1] 0.08742297
```

As you can see the results are almost identical to the previous obtained with inverse variance pooling.

Chapter 10

Analysis of selected region

Small data set 'srdta', which is part of the **GenABEL-package** library, will be used in this section. Start R and load the **GenABEL-package** and the data with

```
> library(GenABEL)
> data(srdta)
```

10.1 Exploring linkage disequilibrium

See help for **r2fast**.

10.2 Haplotype analysis

Use

```
> gtforld <- as.hsgeno(srdta[,1:5])
```

to convert part of your SNPs to **haplo.stats** format.

You can also use interface function to do sliding widow analysis

```
> h2 <- scan.haplo("qt1~CRSNP",srdta,snps=c(1:5))
```

10.3 Analysis of interactions

See help for **scan.haplo.2D** and **scan.glm.2D**

Appendix A

Importing data to GenABEL-package

As described in section 4.1, **GenABEL-package** gwaa.data-class consist of phenotypic data frame and an object of snp.data-class, which contains all genetic data. To import data to **GenABEL-package**, you need to prepare two files: one containing the phenotypic, and the other containing genotypic data.

The phenotype file relates study subject IDs with values of covariates and outcomes. In the phenotypic data file, the first line gives a description (variable name) of the data contained in a particular column; the names should better be unique, otherwise R will change them.

The first column of the phenotype file **must** contain the subjects' unique ID, named "id". The IDs listed here, and in the genotypic data file, must be the same. It is recommended that the id names are given in quotation marks (see example below), which will save you a possible troubles with e.g. leading zeros.

There also should also be a column named "sex" and giving sex information (0 = female, 1 = male). Other columns in the file should contain phenotypic information.

Missing values should be coded with "NA"; binary traits should have values 0 or 1.

All subjects present in the genotypic files **must** be listed in the phenotypic file as well, because sex information provided by the phenotypic file is an essential part of the genotypic QC procedure.

An example of few first lines of a phenotype file is as follows:

```
id           sex age     bt1 qt   qt1
"cd289982"   0   30.33   NA  NA   3.93
"cd325285"   0   36.514  1   0.49 3.61
"cd357273"   1   37.811  0   1.65 5.30
"cd872422"   1   20.393  0   1.95 4.07
"cd1005389"  1   28.21   1   0.35 3.90
```

This file tells us that, for example, person 325286 is female (0 in second column), and she has "1" (usually this means a "case") value for the trait "bt1", so on. Person 289982 has measurements only for sex, age and qt1, while other measurements are missing (NA, Not Available).

If you need to add pehnotypes to a `gwaa.data-class` object already created, you can use function `add.phdata`. This function allows you to add variables contained in some data frame to the existing `data@phdata` object. The data frame to be added should contain "id" variable, identical to that existing in the object, and **should not** contain any othe variables with names identical to these already existing.

The second file you need should contains genotypic data. As described in section 4.1 ("General description of `gwaa.data-class`", page 77), `GenABEL-package` snp.data-class contains different types of information. For every SNP, information on map position, chromosome, and strand should be provided. For every person, every SNP genotype should be provided. `GenABEL-package` provides a number of function to convert these data from different formats to the internal `GenABEL-package` raw format. We will first consider our preferred format, which we informally call "Illumina"-like.

A.1   Converting from preferred format

We will consider use of `convert.snp.illumina` procedure; details of other procedures are given later. Note that what we call "illumina" format is not really a proprietary format from that company, it is just one of the possible text output format from the Illumina BeadStudio; similar formats are accepted/generated by HapMap and Affymetrix.

The file of the "Illumina" format contains SNPs in rows and IDs in columns. The first line is a "header", containing column names. The first three columns should contain information on SNP name, chromosome, and position. There is an optional (though highly recommended!) fourth column, containing strand information (acceptable codes: "+", "-", "u", the last stands for "unknown"). After that column, each of the residual ones corresponds to an individual, with ID as the column name. Genotypes should be presented by two consecutive characters (no separator).

An example of few first lines of the "illumina" genotypic file is as follows:

```
name    chr    pos strand "cd289982" "cd325285" "cd357273" "cd872422" "cd1005389"
rs1001   1    1235      +         AA         AG         AG         AA         GG
rs6679   9    2344      +         GT         GG         GG         TG         GG
rs2401  22    3455      +         AA         CC         CC         CC         AC
rs123    X   32535      -         TT         GT         TT         TT         TT
rs6679  XY    2344      -         GT         GG         GG         TG         GG
rs876    Y   23556      +         00         00         TT         GG         TT
mitoA1  mt   24245      -         AA         CC         00         00         00
```

It is clear that is not quite conventional Illumina file – because in BeadStudio the alleles are reported using the "top" strand; rather, this is an Affymetrix or HapMap-type of a file. Anyways, this file contains all required genotypic information, and this file format is the preferred one for import. Assume that the file with the genotypic data is called "gen0.illu", and is stored in the directory "RData".

First, start R and load `GenABEL-package`:

> *library(GenABEL)*

```
GenABEL v. 1.7-0 (October 05, 2011) loaded

Installed GenABEL version (1.7-0) is not the same as stable
version available from CRAN (1.6-7). Unless used intentionally,
consider updating to the latest CRAN version. For that, use
'install.packages("GenABEL")', or ask your system administrator
to update the package.
```

You can convert the data to `GenABEL-package` raw format by

```
> convert.snp.illumina(inf="RData/gen0.illu",out="RData/gen0i.raw",strand="file")
```

```
Reading genotypes from file 'RData/gen0.illu' ...
Writing to file 'RData/gen0i.raw' ...
... done.
```

Here is the content of the converted file "gen0i.raw" – internal raw data representation:

```
#GenABEL raw data version 0.1
"cd289982" "cd325285" "cd357273" "cd872422" "cd1005389"
rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
1 9 22 X XY Y mt
1235 2344 3455 32535 2344 23556 24245
04 0c 0f 08 0c 08 0f
01 01 01 02 02 01 02
69 c0
96 40
d5 80
65 40
96 40
07 40
d0 00
```

Note the option `strand="file"` – it is telling `GenABEL-package` that strand information is provided in the file.

At this moment, you can load the data into `GenABEL-package`. Assume that the phenotypic file described above is called "phe0.dat" and the converted genotypic file in the raw `GenABEL-package` format is called "gen0i.raw". You can load the data using the command

```
> df <- load.gwaa.data(phe="RData/phe0.dat",gen="RData/gen0i.raw",force=T)
```

```
ids loaded...
marker names loaded...
chromosome data loaded...
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

The option "force=TRUE" tells that `GenABEL-package` should load the data
even if it fins sex errors.

You can inspect the loaded data; let us first look into phenotypic data by by

```
> df@phdata
```

```
                 id sex    age bt1   qt  qt1
cd289982    cd289982   0 30.330  NA   NA 3.93
cd325285    cd325285   0 36.514   1 0.49 3.61
cd357273    cd357273   1 37.811   0 1.65 5.30
cd872422    cd872422   1 20.393   0 1.95 4.07
cd1005389 cd1005389   1 28.210   1 0.35 3.90
```

... and than check that the genotypes have imported right:

```
> g0 <- as.character(df@gtdata)
> g0
```

```
          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982  "A/A"  "G/T"  "A/A"  "T/T" "G/T"  NA    "A/A"
cd325285  "A/G"  "G/G"  "C/C"  "T/G" "G/G"  NA    "C/C"
cd357273  "A/G"  "G/G"  "C/C"  "T/T" "G/G"  "T/T" NA
cd872422  "A/A"  "G/T"  "C/C"  "T/T" "G/T"  "G/G" NA
cd1005389 "G/G"  "G/G"  "C/A"  "T/T" "G/G"  "T/T" NA
```

```
> as.character(df@gtdata@strand)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
  "+"    "+"    "+"    "-"    "-"    "+"    "-"
```

```
> as.character(df@gtdata@coding)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
 "AG"   "GT"   "CA"   "TG"   "GT"   "TG"   "CA"
```

In a real Illumina file, a coding on the TOP strand is supplied. Then, the
file will normally look like

```
name    chr   pos "cd289982" "cd325285" "cd357273" "cd872422" "cd1005389"
rs1001   1   1235        AA         AG         AG         AA          GG
rs6679   9   2344        GT         GG         GG         TG          GG
rs2401  22   3455        AA         CC         CC         CC          AC
rs123    X   32535       TT         GT         TT         TT          TT
rs6679  XY   2344        GT         GG         GG         TG          GG
rs876    Y   23556       00         00         TT         GG          TT
mitoA1  mt   24245       AA         CC         00         00          00
```

and the conversion command will be

```
> convert.snp.illumina(inf="RData/gen0.illuwos",out="RData/gen0iwos.raw",strand="+")
```

```
Reading genotypes from file 'RData/gen0.illuwos' ...
Writing to file 'RData/gen0iwos.raw' ...
... done.
```

In this particular data set, after conversion, the "+" strand will actually mean
not "forward", but TOP – something you should remember for this particular
data. The resulting file will look like this:

You can load the data with

```
> df <- load.gwaa.data(phe="RData/phe0.dat",gen="RData/gen0iwos.raw",force=T)
```

```
ids loaded...
marker names loaded...
chromosome data loaded...
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

Obviously, the "strand" is always "+" (here it means TOP):

```
> g1 <- as.character(df@gtdata)
> g1
```

```
         rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982  "A/A"  "G/T"  "A/A" "T/T" "G/T"  NA    "A/A"
cd325285  "A/G"  "G/G"  "C/C" "T/G" "G/G"  NA    "C/C"
cd357273  "A/G"  "G/G"  "C/C" "T/T" "G/G"  "T/T" NA
cd872422  "A/A"  "G/T"  "C/C" "T/T" "G/T"  "G/G" NA
cd1005389 "G/G"  "G/G"  "C/A" "T/T" "G/G"  "T/T" NA
```

```
> as.character(df@gtdata@strand)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
   "+"    "+"    "+"    "+"    "+"    "+"    "+"
```

```
> as.character(df@gtdata@coding)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
  "AG"   "GT"   "CA"   "TG"   "GT"   "TG"   "CA"
```

We can see that the genotypes are identical to ones we imported previously,
as should be the case:

```
> g0 == g1
```

```
          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982    TRUE   TRUE   TRUE  TRUE   TRUE    NA   TRUE
cd325285    TRUE   TRUE   TRUE  TRUE   TRUE    NA   TRUE
cd357273    TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
cd872422    TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
cd1005389   TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
```

A.2   Converting PLINK tped files

PLINK TPED (transposed-pedigree) format bears notable similarity to what
we call "Illumina" format, with few exceptions: (1) there is no header line giving
field names (and therefore IDs are stored in a separate file) (2) the first column
gives chromosome, second – SNP name, third *genetic* map (usually kept as
zeroes), the fourth – physical position, and, starting with the fifth column,
genotypic data are listed, (3) finally, within a genotypes, alleles are separated
with a space. In TPED format, the data we already worked with would look
like

```
 1    rs1001   0     1235    A A    A G    A G    A A    G G
 9    rs6679   0     2344    G T    G G    G G    T G    G G
22    rs2401   0     3455    A A    C C    C C    C C    A C
 X     rs123   0    32535    T T    G T    T T    T T    T T
XY    rs6679   0     2344    G T    G G    G G    T G    G G
 Y     rs876   0    23556    0 0    0 0    T T    G G    T T
mt    mitoA1   0    24245    A A    C C    0 0    0 0    0 0
```

Obviously, a separate file is needed to keep correspondence between geno-
types and IDs. This file emulated standard pedigree file without a header line.
The file, conventionally called a TFAM-file, should contain six columns, cor-
responding to pedigree ID, ID, father, mother, sex, and affection. Only the
second column is used by `GenABEL-package` – please make sure you use unique
IDs. Consequently, it does not matter what pedigree ID, father/mother, sex, or
affection status you assign in the file – the real information is coming from the
phenotypic data file. The TFAM file for our data will look like this:

```
1  cd289982 0 0 1 0
1  cd325285 0 0 1 0
1  cd357273 0 0 1 0
1  cd872422 0 0 1 0
1 cd1005389 0 0 1 0
```

You can convert the data from PLINK TPED format to the `GenABEL-package`
format using command `convert.snp.tped`:

```
> convert.snp.tped(tped="RData/gen0.tped",tfam="RData/gen0.tfam",out="RData/gen0tped.

Reading individual ids from file 'RData/gen0.tfam' ...
... done.  Read 5 individual ids from file 'RData/gen0.tfam'
Reading genotypes from file 'RData/gen0.tped' ...
...done.  Read 7 SNPs from file 'RData/gen0.tped'
Writing to file 'RData/gen0tped.raw' ...
... done.
```

and load the data with

```
> df <- load.gwaa.data(phe="RData/phe0.dat",gen="RData/gen0tped.raw",force=T)

ids loaded...
marker names loaded...
chromosome data loaded...
```

```
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

Obviously, the "strand" is always "+" (meaning TOP):

```
> g1 <- as.character(df@gtdata)
> g1

          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982  "A/A"  "G/T"  "A/A"  "T/T" "G/T"  NA    "A/A"
cd325285  "A/G"  "G/G"  "C/C"  "T/G" "G/G"  NA    "C/C"
cd357273  "A/G"  "G/G"  "C/C"  "T/T" "G/G"  "T/T" NA
cd872422  "A/A"  "G/T"  "C/C"  "T/T" "G/T"  "G/G" NA
cd1005389 "G/G"  "G/G"  "C/A"  "T/T" "G/G"  "T/T" NA

> as.character(df@gtdata@strand)

rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
   "+"    "+"    "+"    "+"    "+"    "+"    "+"

> as.character(df@gtdata@coding)

rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
  "AG"   "GT"   "CA"   "TG"   "GT"   "TG"   "CA"
```

We can see that the genotypes are identical to ones we imported previously, as should be the case:

```
> g0 == g1

          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982   TRUE   TRUE   TRUE   TRUE   TRUE    NA   TRUE
cd325285   TRUE   TRUE   TRUE   TRUE   TRUE    NA   TRUE
cd357273   TRUE   TRUE   TRUE   TRUE   TRUE  TRUE    NA
cd872422   TRUE   TRUE   TRUE   TRUE   TRUE  TRUE    NA
cd1005389  TRUE   TRUE   TRUE   TRUE   TRUE  TRUE    NA
```

A.3 Converting linkage-like files

Linkage-like files, also known as pre-makeped files, or pedigree files, represent a historic format which dates back to the time when only few markers could be typed – thus the number of subjects was usually greater than the number of markers. In that situation, it was natural and obvious to keep IDs in rows and markers in columns. In the first six columns, standard linkage-like file would contain pedigree ID, ID, father's ID, mother's ID, sex (coded as $1 =$ male and $2 =$ female), and affection status ($0 =$ unknown, $1 =$ unaffected, $2 =$ affected). In the following columns, genotypic information is provided. Alleles of the same genotype could be separated by a space, or by a slash ("/"). Thus the data we are working with could be presented as

```
1  cd289982 0 0 1 0   A A   G T   A A   T T   G T   0 0   A A
1  cd325285 0 0 1 0   A G   G G   C C   G T   G G   0 0   C C
1  cd357273 0 0 1 0   A G   G G   C C   T T   G G   T T   0 0
1  cd872422 0 0 1 0   A A   T G   C C   T T   T G   G G   0 0
1 cd1005389 0 0 1 0   G G   G G   A C   T T   G G   T T   0 0
```

As you can see, this file misses header line, and information what are the SNP names, position, etc. should be provided in a separate MAP-file. `GenABEL-package` accepts map in Merlin format, and an extended format. A map in Merlin format consist of header line, giving column names, and three columns with chromosome, name and position information, for example:

```
chr   name     pos
1     rs1001   1235
9     rs6679   2344
22    rs2401   3455
X     rs123    32535
XY    rs6679   2344
Y     rs876    23556
mt    mitoA1   24245
```

The data can be converted to the internal `GenABEL-package` format with

```
> convert.snp.ped(pedfile="RData/gen0.ped",mapfile="RData/map0.dat",out="RData/gen0pe
```

```
Reading map from file 'RData/map0.dat' ...
... done.  Read positions of 7 markers from file 'RData/map0.dat'
Reading genotypes from file 'RData/gen0.ped' ...
...done.  Read information for 5 people from file 'RData/gen0.ped'
Analysing marker information ...
Writing to file 'RData/gen0pedwos.raw' ...
... done.
```

and loaded with

```
> df <- load.gwaa.data(phe="RData/phe0.dat",gen="RData/gen0pedwos.raw",force=T)
```

```
ids loaded...
marker names loaded...
chromosome data loaded...
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

We can inspect the genotypic data and check that conversion results are identical to previous runs with

```
> g1 <- as.character(df@gtdata)
> g1
```

```
          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982  "A/A"  "G/T"  "A/A"  "T/T" "G/T"  NA    "A/A"
cd325285  "A/G"  "G/G"  "C/C"  "T/G" "G/G"  NA    "C/C"
cd357273  "A/G"  "G/G"  "C/C"  "T/T" "G/G"  "T/T" NA
cd872422  "A/A"  "G/T"  "C/C"  "T/T" "G/T"  "G/G" NA
cd1005389 "G/G"  "G/G"  "C/A"  "T/T" "G/G"  "T/T" NA
```

```
> as.character(df@gtdata@strand)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
   "+"    "+"    "+"    "+"    "+"    "+"    "+"
```

```
> as.character(df@gtdata@coding)
```

```
rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
  "AG"   "GT"   "CA"   "TG"   "GT"   "TG"   "CA"
```

```
> g0 == g1
```

```
          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982    TRUE   TRUE   TRUE  TRUE   TRUE    NA   TRUE
cd325285    TRUE   TRUE   TRUE  TRUE   TRUE    NA   TRUE
cd357273    TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
cd872422    TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
cd1005389   TRUE   TRUE   TRUE  TRUE   TRUE  TRUE     NA
```

If you are willing to import strand information, you can make use of the *extended* map format. In this format the strand information is added to the map-file:

```
chr  name     pos    strand coding
1    rs1001   1235   +      AG
9    rs6679   2344   +      TG
22   rs2401   3455   +      AC
X    rs123    32535  -      GT
XY   rs6679   2344   -      GT
Y    rs876    23556  +      GT
mt   mitoA1   24245  -      AC
```

The data can be converted to the internal `GenABEL-package` format with

```
> convert.snp.ped(pedfile="RData/gen0.ped",mapfile="RData/emap0.dat",out="RData/gen0ped.raw",st
```

```
Reading map from file 'RData/emap0.dat' ...
... done.  Read positions of 7 markers from file 'RData/emap0.dat'
Reading genotypes from file 'RData/gen0.ped' ...
...done.  Read information for 5 people from file 'RData/gen0.ped'
Analysing marker information ...
Writing to file 'RData/gen0ped.raw' ...
... done.
```

Note that option `strand==file` was used to specify that the extended map format should be used. The data can be loaded with

```
> df <- load.gwaa.data(phe="RData/phe0.dat",gen="RData/gen0ped.raw",force=T)

ids loaded...
marker names loaded...
chromosome data loaded...
map data loaded...
allele coding data loaded...
strand data loaded...
genotype data loaded...
snp.data object created...
assignment of gwaa.data object FORCED; X-errors were not checked!
```

We can inspect the genotypic data and check that conversion results are identical to previous runs with

```
> g1 <- as.character(df@gtdata)
> g1

          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982  "A/A"  "G/T"  "A/A"  "T/T" "G/T"  NA    "A/A"
cd325285  "A/G"  "G/G"  "C/C"  "T/G" "G/G"  NA    "C/C"
cd357273  "A/G"  "G/G"  "C/C"  "T/T" "G/G"  "T/T" NA
cd872422  "A/A"  "G/T"  "C/C"  "T/T" "G/T"  "G/G" NA
cd1005389 "G/G"  "G/G"  "C/A"  "T/T" "G/G"  "T/T" NA

> as.character(df@gtdata@strand)

rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
   "+"    "+"    "+"    "-"    "-"     "+"    "-"

> as.character(df@gtdata@coding)

rs1001 rs6679 rs2401  rs123 rs6679  rs876 mitoA1
  "AG"   "GT"   "CA"   "TG"   "GT"    "TG"   "CA"

> g0 == g1

          rs1001 rs6679 rs2401 rs123 rs6679 rs876 mitoA1
cd289982   TRUE   TRUE   TRUE   TRUE   TRUE   NA    TRUE
cd325285   TRUE   TRUE   TRUE   TRUE   TRUE   NA    TRUE
cd357273   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   NA
cd872422   TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   NA
cd1005389  TRUE   TRUE   TRUE   TRUE   TRUE   TRUE   NA
```

A.4   Converting from MACH format

The data from MACH format can be converted by using `convert.snp.mach`. This function actually calls `convert.snp.ped` in specific format. MACH software is widely used for SNP imputations. For our needs we consider two files produced by MACH: pedigree file with (the imputed) genotypic data, and info-file, containing information about quality of imputations for particular SNP.

SEE HELP FOR `convert.snp.mach` for further details.

A.5 Converting from text format

Appendix B

GenABEL internals

B.1 Internal structure of `gwaa.data-class`

Start R and load `GenABEL-package` library using command

```
> library(GenABEL)
```

After that, load the data with the command

```
> data(srdta)
```

The object you have loaded, `srdta`, belongs to the `gwaa.data` class. This is a special class developed to facilitate GWA analysis.

In GWA analysis, different types of data are used. These include the phenotypic and genotypic data on the study participants and chromosome and location of every SNP. For every SNP, it is desirable to know the details of coding (what are alleles? – A, T, G, C? – and what is the strand – '+' or '-', 'top' or 'bot'? – this coding is for).

One could attempt to store all phenotypes and genotypes together in a single table, using, e.g. one row per study subject; than the columns will correspond to study phenotypes and SNPs. For a typical GWA data set, this would lead to a table of few thousands rows and few hundreds of thousands of columns. Such a format is generated when one downloads HapMap data for a region. To store GWA data in such tables internally, within R, proves to be inefficient. In `GenABEL-package`, special data class, `gwaa.data-class` is used to store GWA data. The structure of this data class is shown at the figure B.1.

An object of some class has "slots" which may contain actual data or objects of other classes. The information stored at a particular `slot` of an `object` can be accessed by command `object@slot`.

At the first level, a `gwaa.data-class` object has slot `phdata`, which contains all phenotypic information in a data frame (`data.frame-class` object). The rows of this data frame correspond to study subjects, and the columns correspond to the variables. There are two default variables, which are always present in `phdata`. The first of these is "id", which contains study subject identification code. This identification code can be arbitrary character, but every person must be coded with an unique ID. The second default variable is "sex", where males are coded with ones ("1") and females are coded with zero ("0"). It is important
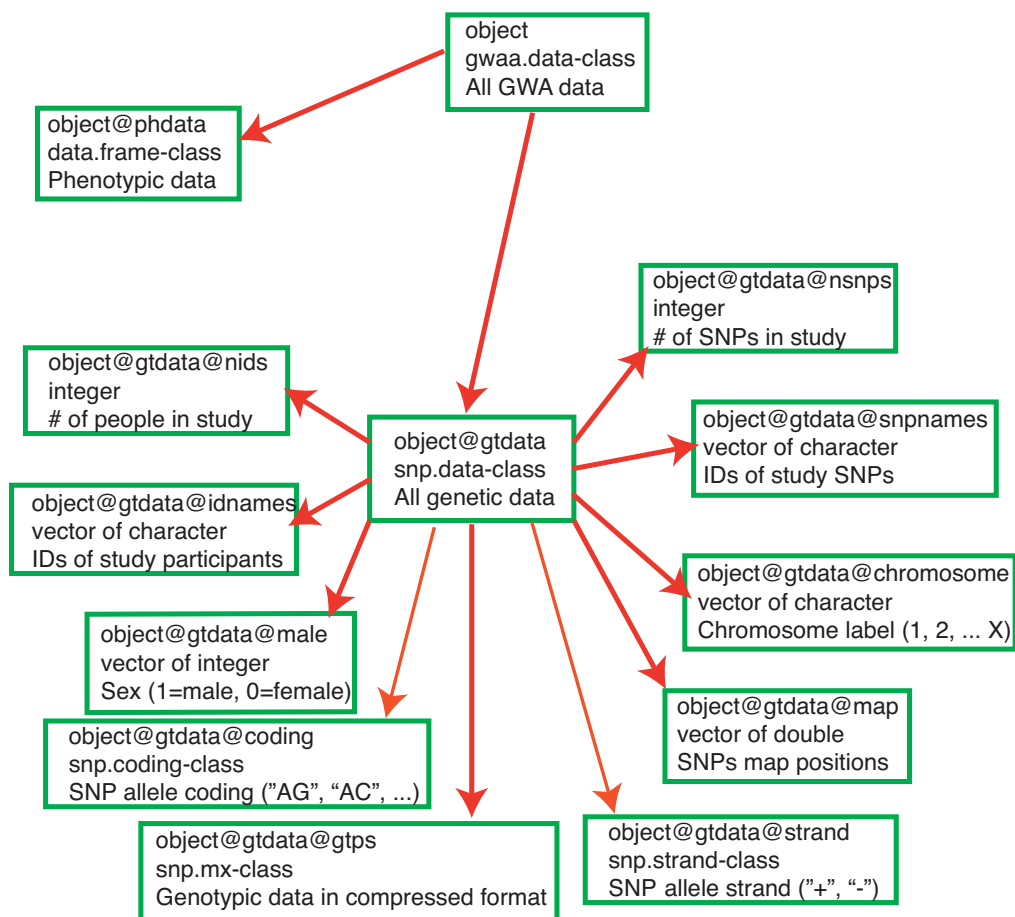
Figure B.1: Structure of gwaa.data-class. In every box, first line contains the object and slot names, second line describes the class of this object, and third line describes what information is contained.

to understand that this data frame is not supposed to be directly modified by the user. In particular, it is extremely important to remember that one should not directly add subjects to the table, change the values of "id" and "sex", and change the order of subjects in `phdata` unless this one is really understands the way `GenABEL-package` works. One also should not run such data manipulation functions as `merge`, `cbind` and `rbind` – exactly because they may change the number of subjects or interfere with the order. On the other hand, it is OK to add more variables to the data frame through direct computations, for example, if one wishes to add computed body mass index, it is OK to run the command like

```
obj@phdata$bmi <- obj@phdata$weight/((obj@phdata$height)^2)
```

To add many variables to `phdata`, special GenABEL function `add.phdata` should be used.

The other slot of an object of `gwaa.data-class` is slot `gtdata`, which contains all GWA genetic information in an object of class `snp.data` class (figure B.1). This class, in turn, has slots `nids`, containing the number of study subjects, `idnames`, containing all ID names of these subjects, `nsnps`, containing the number of SNPs typed, `snpnames`, containing the SNP names, `chromosome`, containing the name of the chromosome the SNPs belong to and slot `map` with map position of SNPs, and slot `male`, containing the sex code for the subjects (1=male, 0=female). The latter is identical to the "sex" variable contained in the `phdata`, but is duplicated here because many operations with purely genetic data, in particular these concerning analysis of sex chromosomes, depend on the sex. The strand information is presented in the slot `strand`. `GenABEL-package` codes strand as "+" (forward), "-" (reverse) or "u" (unknown). Of cause, if you prefer top/bottom coding, this information may be stored in the same form – you will just need to remember that "+" corresponds to e.g. "top", and "-" to "bottom" strand. The allelic coding is presented in slot `coding`. Coding for every allele is presented with a pair of characters, for example "AG". Thus, for such polymorphism, you may expect "AA", "AG" and "GG" genotypes to be found in population. The order (that is "AG" vs "GA") is important – the first allele reported is the one which will be used as a reference in association analysis, and thus the effects are reported for the second allele. To avoid memory overheads, the strand and coding information is internally stored as `snp.strand-class` and `snp.coding-class`. Information can be converted to human-readable format using `as.character` function.

If, for example, you would like to know, how many SNPs were included in the study (slot `nsnps` of the slot `gtdata` of `srdta`), you need to run command

```
> srdta@gtdata@nsnps
```

```
[1] 833
```

Thus, 833 SNPs were typed in the study. You can access information stored in any slot in this manner.

You may want to read the general `GenABEL-package` man page using `help(GenABEL)`. To see help on `gwaa.data-class`, you can use `help("gwaa.data-class")` (mind the quotation marks!).

Summary:

- An object of some class has "slots" which may contain actual data or objects of other classes. The information stored at a particular `slot` of an `object` can be accessed by command `object@slot`.

- `GenABEL-package` uses special data class, `gwaa.data-class`, to store GWA data.

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