

# snpStats vignette

## Example of genome-wide association testing

David Clayton and Chris Wallace

May 3, 2016

### The **snpMatrix** and **snpStats** packages

The package “**snpMatrix**” was written to provide data classes and methods to facilitate the analysis of whole genome association studies in R. In the data classes it implements, each genotype call is stored as a single byte and, at this density, data for single chromosomes derived from large studies and new high-throughput gene chip platforms can be handled in memory by modern PCs and workstations. The object-oriented programming model introduced with version 4 of the S-plus package, usually termed “S4 methods” was used to implement these classes.

**snpStats** arose out of the need to store, and analyse, SNP genotype data in which subjects cannot be assigned to the three possible genotypes with certainty. This necessitated a change in the way in which data are stored internally, although **snpStats** can still handle conventionally called genotype data stored in the original **snpMatrix** storage mode. **snpStats** currently lacks some facilities which were present in **snpMatrix** (although, hopefully, the important gaps will soon be filled) but it also includes several important new facilities. This vignette currently exploits none of the new facilities; these are mainly used in the vignette which deals with imputation and meta-analysis.

For population-based studies, both quantitative and qualitative phenotypes may be analysed but, at present, rather more limited facilities are available for family-based studies. Flexible functions are provided which can carry out single SNP tests which control for potential confounding by quantitative and qualitative covariates. Tests involving several SNPs taken together as “tags” are also supported. The original **snpMatrix** package was described by Clayton and Leung (2007) *Human Heredity*, **64**: 45–51. Since this publication many new facilities have been introduced; some of these are explored in further vignettes.

### Getting started

We shall start by loading the the packages and the data to be used in the first part of this exercise, which concerns a population-based case-control study:

```
> require(snpStats)
> require(hexbin)
> data(for.exercise)
```

In addition to the `snpStats` package, we have also loaded the `hexbin` package which reduces file sizes and legibility of plots with very many data points.

The data have been created artificially from publicly available datasets. The SNPs have been selected from those genotyped by the International HapMap Project<sup>1</sup> to represent the typical density found on a whole genome association chip, (the Affymetrix 500K platform<sup>2</sup>) for a moderately sized chromosome (chromosome 10). A (rather too) small study of 500 cases and 500 controls has been simulated allowing for recombination using beta software from Su and Marchini. Re-sampling of cases was weighted in such a way as to simulate three “causal” locus on this chromosome, with multiplicative effects of 1.3, 1.4 and 1.5 for each copy of the risk allele at each locus. It should be noted that this is a somewhat optimistic scenario!

You have loaded three objects:

1. `snps.10`, an object of class “`SnpMatrix`” containing a matrix of SNP genotype calls. Rows of the matrix correspond to subjects and columns correspond to SNPs:

```
> show(snps.10)
```

```
A SnpMatrix with 1000 rows and 28501 columns
Row names:  jpt.869 ... ceu.464
Col names:  rs7909677 ... rs12218790
```

2. `snp.support`, a conventional R data frame containing information about the SNPs typed. To see its contents:

```
> summary(snp.support)
```

	chromosome	position	A1	A2
Min.	:10	Min. :1.02e+05	A:14019	C: 2349
1st Qu.:	:10	1st Qu.:2.90e+07	C:12166	G:12254
Median	:10	Median :6.74e+07	G: 2316	T:13898
Mean	:10	Mean :6.69e+07		
3rd Qu.:	:10	3rd Qu.:1.02e+08		
Max.	:10	Max. :1.35e+08		

Row names of this data frame correspond with column names of `snps.10` and comprise the (unique) SNP identifiers.

---

<sup>1</sup><http://www.hapmap.org>

<sup>2</sup>[http://www.affymetrix.com/support/technical/sample\\_data/500k\\_hapmap\\_genotype\\_data.affx](http://www.affymetrix.com/support/technical/sample_data/500k_hapmap_genotype_data.affx)

3. `subject.support`, another conventional R data frame containing further information about the subjects. The row names coincide with the row names of `snps.10` and comprise the (unique) subject identifiers. In this simulated study there are only two variables:

```
> summary(subject.support)
```

```

      cc      stratum
Min.   :0.0   CEU     :494
1st Qu.:0.0   JPT+CHB:506
Median :0.5
Mean    :0.5
3rd Qu.:1.0
Max.    :1.0

```

The variable `cc` identifies cases (`cc=1`) and controls (`cc=0`) while `stratum`, coded 1 or 2, identifies a stratification of the study population — more on this later.

In general, analysis of a whole-genome association study will require a subject support data frame, a SNP support data frame for each chromosome, and a SNP data file for each chromosome<sup>3</sup>.

A short summary of the contents of `snps.10` is provided by the `summary` function. This operation actually produces two “summaries of summaries”. First, summary statistics are calculated for each row (sample), and their results summarised. Then summary statistics are calculated for each column (SNP) and their results summarised.

```
> summary(snps.10)
```

\$rows

Call.rate	Certain.calls	Heterozygosity
Min. :0.988	Min. :1	Min. :0.000
1st Qu.:0.990	1st Qu.:1	1st Qu.:0.299
Median :0.990	Median :1	Median :0.308
Mean :0.990	Mean :1	Mean :0.307
3rd Qu.:0.990	3rd Qu.:1	3rd Qu.:0.316
Max. :0.992	Max. :1	Max. :0.339

\$cols

Calls	Call.rate	Certain.calls	RAF	MAF
Min. : 975	Min. :0.975	Min. :1	Min. :0.000	Min. :0.000
1st Qu.: 988	1st Qu.:0.988	1st Qu.:1	1st Qu.:0.230	1st Qu.:0.126
Median : 990	Median :0.990	Median :1	Median :0.503	Median :0.232

---

<sup>3</sup> Support files are usually read in with general tools such as `read.table`. The `snpStats` package contains a number of tools for reading SNP genotype data into an object of class “`SnpMatrix`”.

Mean	: 990	Mean	:0.990	Mean	:1	Mean	:0.500	Mean	:0.242
3rd Qu.	: 992	3rd Qu.	:0.992	3rd Qu.	:1	3rd Qu.	:0.767	3rd Qu.	:0.358
Max.	:1000	Max.	:1.000	Max.	:1	Max.	:1.000	Max.	:0.500

	P.AA		P.AB		P.BB		z.HWE
Min.	:0.0000	Min.	:0.000	Min.	:0.0000	Min.	:-21.973
1st Qu.	:0.0656	1st Qu.	:0.208	1st Qu.	:0.0646	1st Qu.	:-2.850
Median	:0.2688	Median	:0.320	Median	:0.2749	Median	:-1.191
Mean	:0.3462	Mean	:0.307	Mean	:0.3465	Mean	:-1.861
3rd Qu.	:0.6059	3rd Qu.	:0.422	3rd Qu.	:0.6036	3rd Qu.	:-0.101
Max.	:1.0000	Max.	:0.550	Max.	:1.0000	Max.	: 3.708
						NA's	:4

The row-wise and column-wise summaries are calculated with the functions `row.summary` and `col.summary`. For example, to calculate summary statistics for each SNP (column):

```
> snpsum <- col.summary(snps.10)
> summary(snpsum)
```

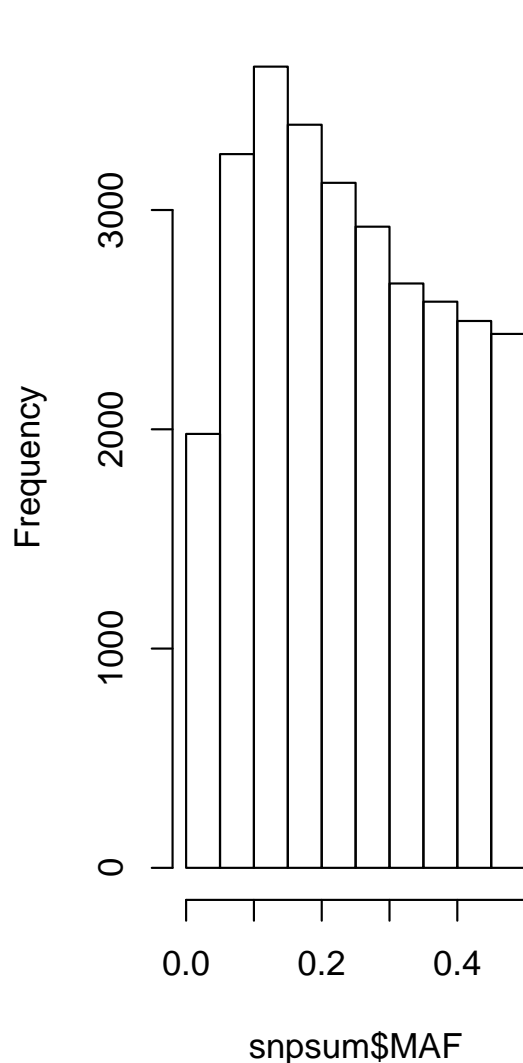
	Calls		Call.rate		Certain.calls		RAF		MAF
Min.	: 975	Min.	:0.975	Min.	:1	Min.	:0.000	Min.	:0.000
1st Qu.	: 988	1st Qu.	:0.988	1st Qu.	:1	1st Qu.	:0.230	1st Qu.	:0.126
Median	: 990	Median	:0.990	Median	:1	Median	:0.503	Median	:0.232
Mean	: 990	Mean	:0.990	Mean	:1	Mean	:0.500	Mean	:0.242
3rd Qu.	: 992	3rd Qu.	:0.992	3rd Qu.	:1	3rd Qu.	:0.767	3rd Qu.	:0.358
Max.	:1000	Max.	:1.000	Max.	:1	Max.	:1.000	Max.	:0.500

	P.AA		P.AB		P.BB		z.HWE
Min.	:0.0000	Min.	:0.000	Min.	:0.0000	Min.	:-21.973
1st Qu.	:0.0656	1st Qu.	:0.208	1st Qu.	:0.0646	1st Qu.	:-2.850
Median	:0.2688	Median	:0.320	Median	:0.2749	Median	:-1.191
Mean	:0.3462	Mean	:0.307	Mean	:0.3465	Mean	:-1.861
3rd Qu.	:0.6059	3rd Qu.	:0.422	3rd Qu.	:0.6036	3rd Qu.	:-0.101
Max.	:1.0000	Max.	:0.550	Max.	:1.0000	Max.	: 3.708
						NA's	:4

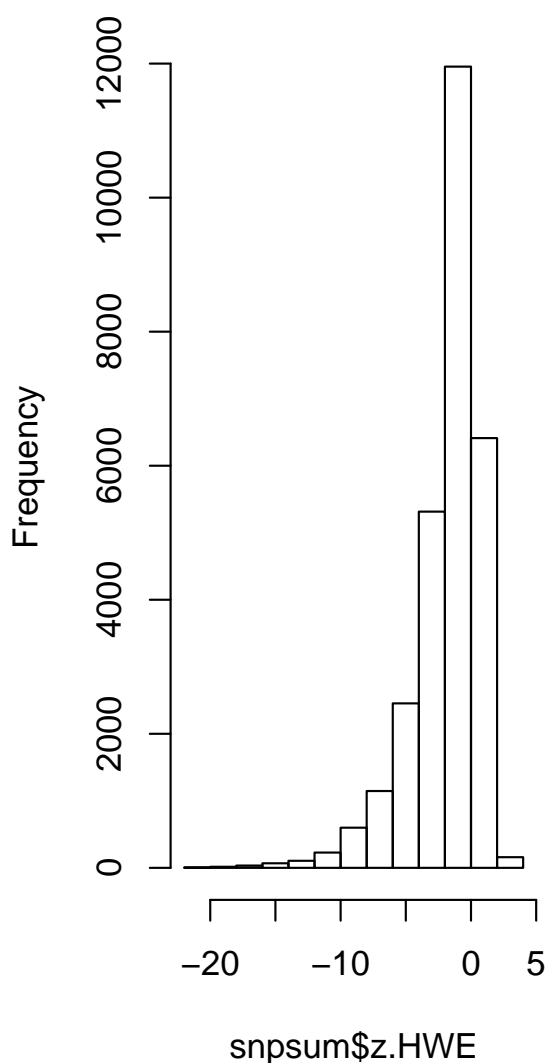
The second command duplicates the latter part of the result of `summary(snps.10)`, and the contents of `snpsum` are fairly self-explanatory. We could look at a couple of summary statistics in more detail:

```
> par(mfrow = c(1, 2))
> hist(snpsum$MAF)
> hist(snpsum$z.HWE)
```

### Histogram of snpsum\$MAF



### Histogram of snpsum\$z.HWE



The latter should represent a  $z$ -statistic. *i.e.* a statistic normally distributed with mean zero and unit standard deviation under the hypothesis of Hardy–Weinberg equilibrium (HWE). Quite clearly there is extreme deviation from HWE, but this can be accounted for by the manner in which this synthetic dataset was created.

The function `row.summary` is useful for detecting samples that have genotyped poorly. This calculates call rate and mean heterozygosity across all SNPs for each subject in turn:

```
> sample.qc <- row.summary(snps.10)
> summary(sample.qc)
```

```
Call.rate      Certain.calls Heterozygosity
```

Min.	:0.988	Min.	:1	Min.	:0.000
1st Qu.	:0.990	1st Qu.	:1	1st Qu.	:0.299
Median	:0.990	Median	:1	Median	:0.308
Mean	:0.990	Mean	:1	Mean	:0.307
3rd Qu.	:0.990	3rd Qu.	:1	3rd Qu.	:0.316
Max.	:0.992	Max.	:1	Max.	:0.339

(note that the last command yields the same as the first part of `summary(snps.10)`). The plot of heterozygosity against call rate is useful in detecting poor quality samples:

```
> par(mfrow = c(1, 1))
> plot(sample.qc)
```



There is one clear outlier.

## The analysis

We'll start by removing the 'outlying' sample above (the sample with Heterozygosity near zero):

```
> use <- sample.qc$Heterozygosity>0
> snps.10 <- snps.10[use, ]
> subject.support <- subject.support[use, ]
```

Then we'll see if there is any difference between call rates for cases and controls. First generate logical arrays for selecting out cases or controls:<sup>4</sup>

```
> if.case <- subject.support$cc == 1
> if.control <- subject.support$cc == 0
```

Now we recompute the genotype column summaries separately for cases and controls:

```
> sum.cases <- col.summary(snps.10[if.case, ])
> sum.controls <- col.summary(snps.10[if.control, ])
```

and plot the call rates, using hexagonal binning and superimposing a line of slope 1 through the origin:

```
> hb <- hexbin(sum.controls$Call.rate, sum.cases$Call.rate, xbin=50)
> sp <- plot(hb)
> hexVP.abline(sp$plot.vp, 0, 1, col="black")
```

---

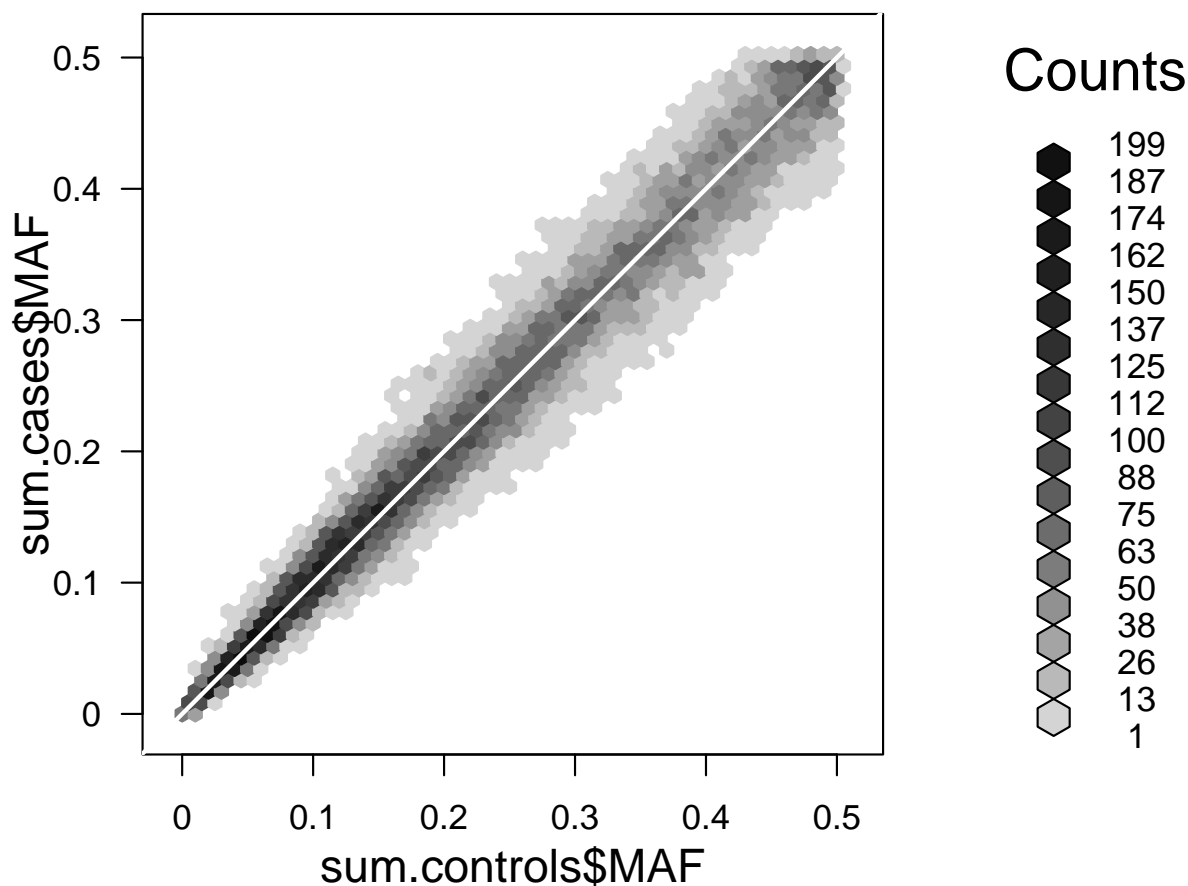
<sup>4</sup> These commands assume that the subject support frame has the same number of rows as the SNP matrix and that they are in the same order. Otherwise a slightly more complicated derivation is necessary.





There is no obvious difference in call rates. This is not a surprise, since no such difference was built into the simulation. In the same way we could look for differences between allele frequencies, superimposing a line of slope 1 through the origin:

```
> sp <- plot(hexbin(sum.controls$MAF, sum.cases$MAF, xbin=50))
> hexVP.abline(sp$plot.vp, 0, 1, col="white")
```



This is not a very effective way to look for associations, but if the SNP calling algorithm has been run separately for cases and controls this plot can be a useful diagnostic for things going wrong (*e.g.* different labelling of clusters).

It should be stressed that, for real data, the plots described above would usually have many more outliers. Our simulation did not model the various biases and genotype failures that affect real studies.

The fastest tool for carrying out simple tests for association taking the SNP one at a time is `single.snp.tests`. The output from this function is a data frame with one line of data for each SNP. Running this in our data and summarising the results:

```
> tests <- single.snp.tests(cc, data = subject.support, snp.data = snps.10)
```

Some words of explanation are required. In the call, the `snp.data=` argument is mandatory and provides the name of the matrix providing the genotype data. The `data=` argument gives the name of the data frame that contains the remaining arguments — usually the subject support data frame<sup>5</sup>.

Let us now see what has been calculated:

```
> summary(tests)
```

	N	Chi.squared.1.df	Chi.squared.2.df	P.1df	P.2df
Min.	:974	Min. : 0.00	Min. : 0.0	Min. :0.000	Min. :0.0
1st Qu.:	987	1st Qu.: 0.17	1st Qu.: 0.8	1st Qu.:0.141	1st Qu.:0.2
Median	:989	Median : 0.77	Median : 1.9	Median :0.379	Median :0.4
Mean	:989	Mean : 1.56	Mean : 2.6	Mean :0.419	Mean :0.4
3rd Qu.:	991	3rd Qu.: 2.17	3rd Qu.: 3.7	3rd Qu.:0.678	3rd Qu.:0.7
Max.	:999	Max. :34.02	Max. :37.2	Max. :1.000	Max. :1.0
		NA's :4	NA's :830	NA's :4	NA's :830

We have, for each SNP, chi-squared tests on 1 and 2 degrees of freedom (df), together with *N*, the number of subjects for whom data were available. The 1 df test is the familiar Cochran-Armitage test for codominant effect while the 2 df test is the conventional Pearsonian test for the  $3 \times 2$  contingency table. The large number of NA values for the latter test reflects the fact that, for these SNPs, the minor allele frequency was such that one homozygous genotype did not occur in the data.

We will probably wish to restrict our attention to SNPs that pass certain criteria. For example

```
> use <- snpsum$MAF > 0.01 & snpsum$z.HWE^2 < 200
```

(The Hardy-Weinberg filter is ridiculous and reflects the strange characteristics of these simulated data. In real life you might want to use something like 16, equivalent to a 4SE cut-off). To see how many SNPs pass this filter

```
> sum(use)
```

```
[1] 28184
```

We will now throw away the discarded test results and save the positions of the remaining SNPs

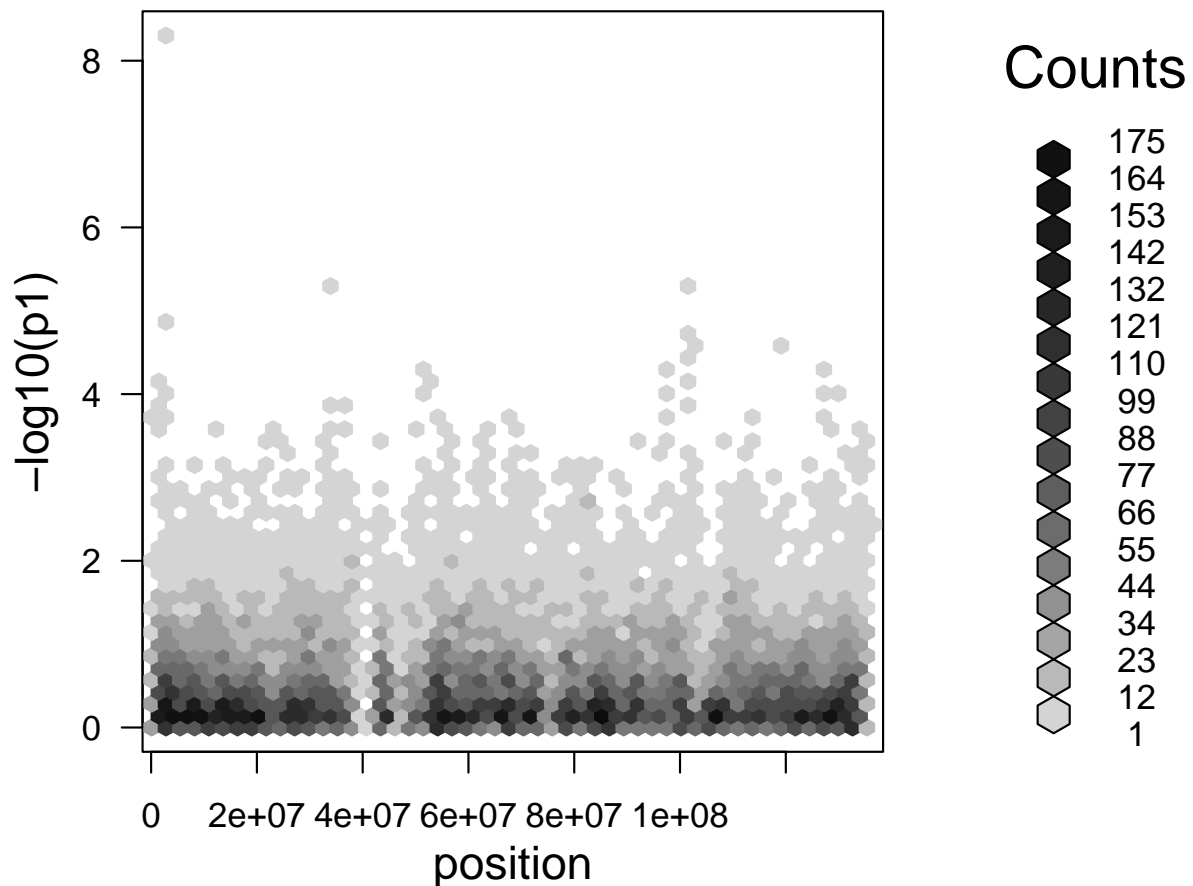
```
> tests <- tests[use]
> position <- snp.support[use, "position"]
```

---

<sup>5</sup>This is not mandatory — we could have made `cc` available in the global environment. However we would then have to be careful that the values are in the right order; by specifying the data frame, order is forced to be correct by checking the order of the row names for the `data` and `snp.data` arguments.

We now calculate  $p$ -values for the Cochran-Armitage tests and plot minus logs (base 10) of the  $p$ -values against position

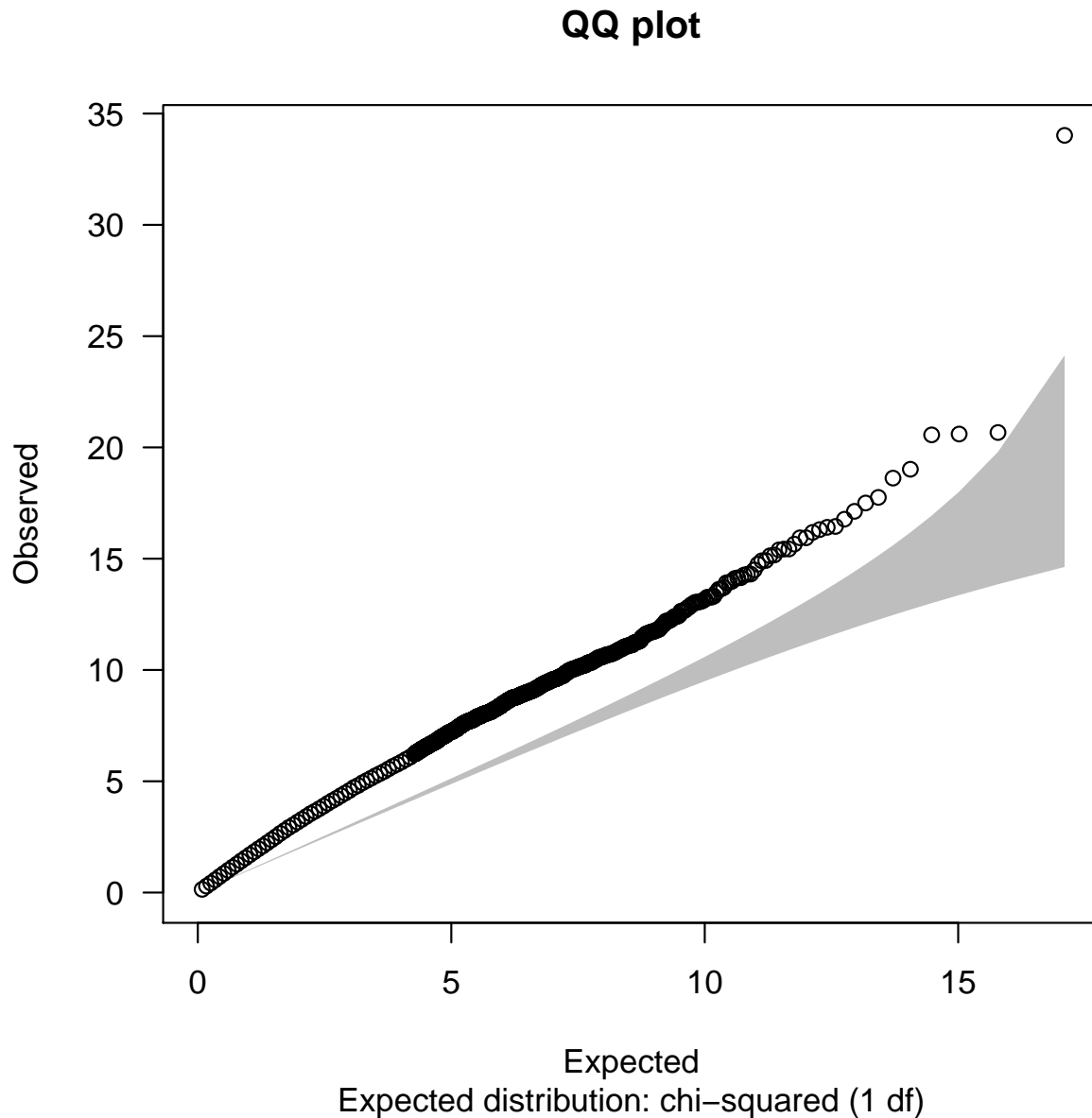
```
> p1 <- p.value(tests, df=1)
> plot(hexbin(position, -log10(p1), xbin=50))
```



Clearly there are far too many “significant” results, an impression which is made even clearer by the quantile-quantile (QQ) plot:

```
> chi2 <- chi.squared(tests, df=1)
> qq.chisq(chi2, df = 1)
```

N	omitted	lambda
28184.000	0.000	1.677



The three numbers returned by this command are the number of tests considered, the number of outliers falling beyond the plot boundary, and the slope of a line fitted to the smallest 90% of values (*i.e.* the multiple by which the chi-squared test statistics are over-dispersed). The “concentration band” for the plot is shown in grey. This region is defined by upper and lower probability bounds for each order statistic. The default is to use the 2.5% and 95.7% bounds<sup>6</sup>.

---

<sup>6</sup>Note that this is not a simultaneous confidence region; the probability that the plot will stray outside

This over-dispersion of chi-squared values was built into our simulation. The data were constructed by re-sampling individuals from *two* groups of HapMap subjects, the CEU sample (of European origin) and the JPT+CHB sample (of Asian origin). The 55% of the cases were of European ancestry as compared with only 45% of the controls. We can deal with this by stratification of the tests, achieved by adding the **stratum** argument to the call to `single.snp.tests` (the remaining commands are as before)

```
> tests <- single.snp.tests(cc, stratum, data = subject.support,  
+      snp.data = snps.10)  
> tests <- tests[use]  
> p1 <- p.value(tests, df = 1)  
> plot(hexbin(position, -log10(p1), xbin=50))
```

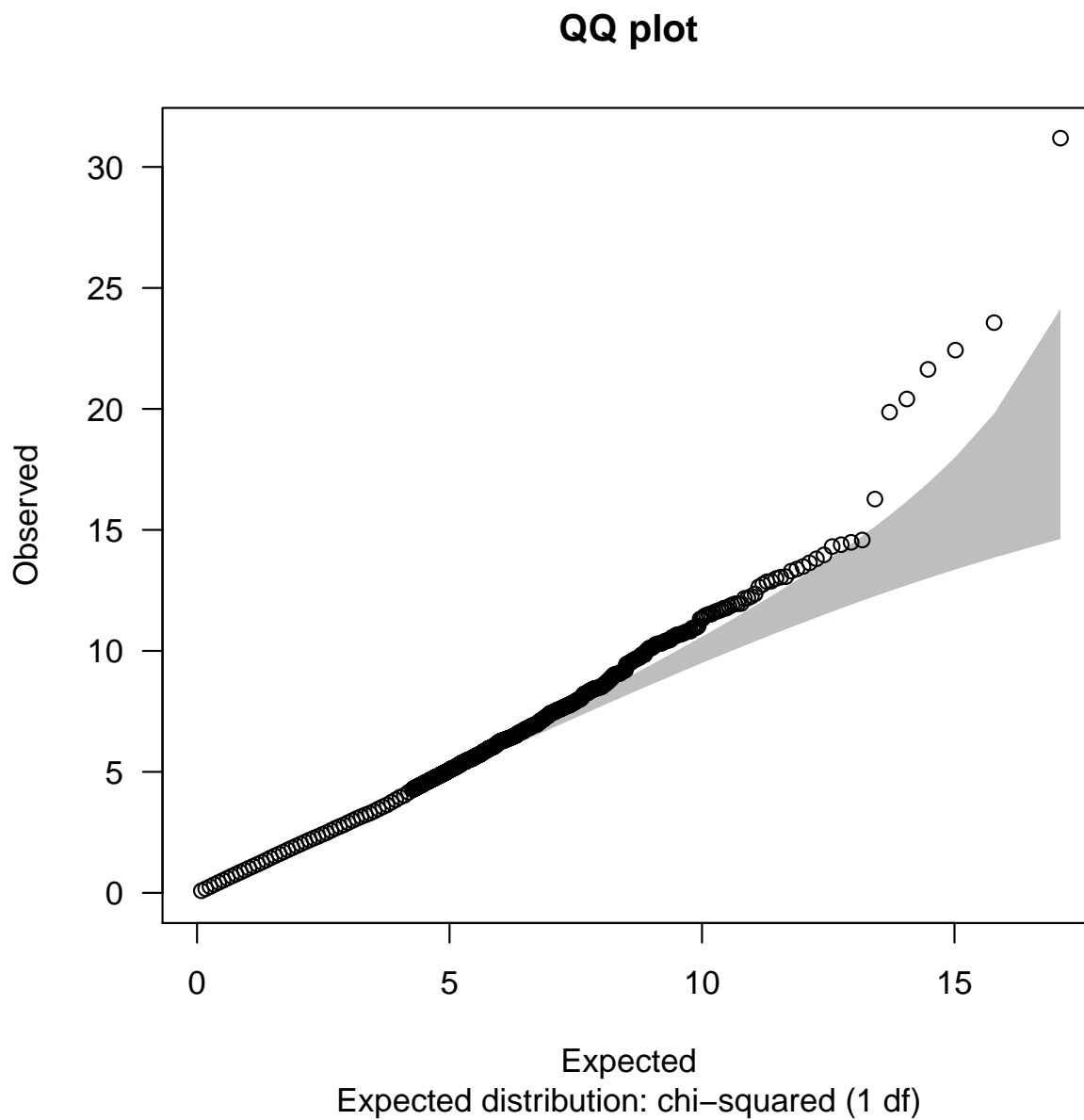
---

the band at some point exceeds 95%.



```
> chi2 <- chi.squared(tests, df=1)
> qq.chisq(chi2, df = 1)
```

N	omitted	lambda
28184.000	0.000	1.007



Most of the over-dispersion of test statistics has been removed (the residual is probably due to “cryptic relatedness” owing to the way in which the data were simulated).

Now let us find the names and positions of the most significant 10 SNPs. The first step is to compute an array which gives the positions in which the first, second, third etc. can be found

```
> ord <- order(p1)
> top10 <- ord[1:10]
> top10
```

```
[1] 459 20174 20175 20173 20170 20171 20172 21134 26269 7981
```



We now list the 1 df  $p$ -values, the corresponding SNP names and their positions on the chromosome:

```
> names <- tests@snp.names
> p1[top10]

      rs870041 rs10882596 rs7088765 rs4918933 rs4918928 rs2025850 rs2274491
2.337e-08  1.207e-06  2.179e-06  3.296e-06  6.249e-06  8.307e-06  5.478e-05
rs17668255  rs7085895 rs11596495
1.341e-04  1.411e-04  1.486e-04

> names[top10]

[1] "rs870041"    "rs10882596" "rs7088765"   "rs4918933"   "rs4918928"
[6] "rs2025850"   "rs2274491"   "rs17668255"  "rs7085895"   "rs11596495"

> position[top10]

[1] 2075671 97190034 97191413 97189084 97179410 97185949 97186968
[8] 101990691 127661165 33024457
```

The most associated SNPs lie within two small regions of the genome. To concentrate on the rightmost region (the most associated region on the left contains just one SNP), we'll first sort the names of the SNPs into position order along the chromosome and select those lying in the region approximately one mega-base either side of the second most associated SNP:

```
> posord <- order(position)
> position <- position[posord]
> names <- names[posord]
> local <- names[position > 9.6e+07 & position < 9.8e+07]
```

The variable `posord` now contains the permutation necessary to sort SNPs into position order and `names` and `position` have now been reordered in this manner. The variable `local` contains the names of the SNPs in the selected 2 mega-base region.

Next we shall estimate the size of the effect at the most associated SNPs for each region (rs870041, rs10882596). In the following commands, we extract each SNP from the matrix as a numerical variable (coded 0, 1, or 2) and then, using the `glm` function, carry out a logistic regression of case-control status on this numerical coding of the SNP and upon stratum. The variable `stratum` must be included in the regression in order to allow for the different population structure of cases and controls. We first make copies of the `cc` and `stratum` variables in `subject.support` in the current working environment (where the other variables reside):

```
> cc <- subject.support$cc
> stratum <- subject.support$stratum
> top <- as(snps.10[, "rs870041"], "numeric")
> glm(cc ~ top + stratum, family = "binomial")
```

Call: glm(formula = cc ~ top + stratum, family = "binomial")

Coefficients:

(Intercept)	top	stratumJPT+CHB
-0.405	0.510	-0.230

Degrees of Freedom: 988 Total (i.e. Null); 986 Residual  
(10 observations deleted due to missingness)

Null Deviance: 1370

Residual Deviance: 1330 AIC: 1340

The coefficient of top in this regression is estimated as 0.5100, equivalent to a relative risk of  $\exp(.5100) = 1.665$ . For the other top SNP we have:

```
> top2 <- as(snps.10[, "rs10882596"], "numeric")
> fit <- glm(cc ~ top2 + stratum, family = "binomial")
> summary(fit)
```

Call:

glm(formula = cc ~ top2 + stratum, family = "binomial")

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.472	-1.075	-0.877	1.111	1.511

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-0.245	0.123	-2.00	0.04556 *
top2	0.458	0.095	4.82	1.4e-06 ***
stratumJPT+CHB	-0.512	0.136	-3.76	0.00017 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1373.8 on 990 degrees of freedom  
Residual deviance: 1343.9 on 988 degrees of freedom  
(8 observations deleted due to missingness)  
AIC: 1350

Number of Fisher Scoring iterations: 4

This relative risk is  $\exp(0.4575) = 1.580$ . Both estimates are close to the values used to simulate the data.

You might like to repeat the analysis above using the 2 df tests. The conclusion would have been much the same. A word of caution however; with real data the 2 df test is less robust against artifacts due to genotyping error. On the other hand, it is much more powerful against recessive or near-recessive variants.

The **snpStats** package includes its own functions to fit generalized linear models. These are much faster than **glm**, although not yet as flexible. They allow for a each of series of SNPs to be entered into a GLM, either on the left hand side (*i.e.* as the dependent variable) or on the right-hand side (as a predictor variable). In the latter case several SNPs can be entered in each model fit. For example, to fit the same GLM as before, in which each SNP is entered in turn on the right-hand side of a logistic regression equation, for each of the SNPs in the 2 megabase “local” region:

```
> localest <- snp.rhs.estimates(cc~stratum, family="binomial", sets=local,
+                               data=subject.support, snp.data=snps.10)
```

This function call has computed 371 GLM fits! The parameter estimates for the first five, and for the second best SNP analyzed above (rs10882596) are shown by

```
> localest[1:5]
```

Model	Y-variable	Parameter	Estimate	S.E.	z-value
rs9787457	cc	rs9787457	0.14176	0.1016	1.395
rs7919320	cc	rs7919320	0.15527	0.10145	1.530
rs4918184	cc	rs4918184	0.075481	0.10391	0.726
rs11187837	cc	rs11187837	-0.031994	0.12002	-0.267
rs7084339	cc	rs7084339	0.10027	0.10235	0.980

```
> localest["rs10882596"]
```

Model	Y-variable	Parameter	Estimate	S.E.	z-value
rs10882596	cc	rs10882596	0.4575	0.094955	4.818

The parameter estimate for rs1088259 and its standard error agree closely with the values obtained earlier, using the `glm` function.

The GLM code within `snpStats` allows a further speed-up which is not available in the standard `glm` function. If a variable is to be included in the model as a “factor” taking many levels then a more efficient algorithm can be invoked by using the `strata` function in the model formula. For example, the following command fits the same model for all the 28184 SNPs we have decided to use in these analyses:

```
> allest <- snp.rhs.estimates(cc~strata(stratum), family="binomial", sets=use,
+                             data=subject.support, snp.data=snp.10)
> length(allest)
```

```
[1] 28184
```

As expected, the parameter estimates and standard errors are unchanged, for example:

```
> allest["rs10882596"]
```

Model	Y-variable	Parameter	Estimate	S.E.	z-value
rs10882596	cc	rs10882596	0.4575	0.094955	4.818

Note that `strata()` can only be used once in a model formula.

## Multi-locus tests

There are two other functions for carrying out association tests (`snp.lhs.tests` and `snp.rhs.tests`) in the package. These are somewhat slower, but much more flexible. For example, the former function allows one to test for differences in allele frequencies between more than two groups. An important use of the latter function is to carry out tests using *groups* of SNPs rather than single SNPs. We shall explore this use in the final part of the exercise.

A prerequisite to multi-locus analyses is to decide on how SNPs should be grouped in order to “tag” the genome rather more completely than by use of single markers. Hopefully, the `snpMatrix` package will eventually contain tools to compute such groups, for example, by using HapMap data. The function `ld.snp`, which we encountered earlier, will be an essential tool in this process. However this work is not complete and, for now, we demonstrate the testing tool by grouping the 28184 SNPs we have decided to use into 20kB blocks. The following commands compute such a grouping, tabulate the block size, and remove empty blocks:

```
> blocks <- split(posord, cut(position, seq(100000, 135300000, 20000)))
> bsize <- sapply(blocks, length)
> table(bsize)
```

```

bsize
  0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19
803 732 895 869 801 665 581 417 316 192 170 102 72 41 43 20 13 9 5 5
 20 21 22 24
  1  6  1  1

```

```
> blocks <- blocks[bsize>0]
```

You can check that this has worked by listing the column positions of the first 20 SNPs together with the those contained in the first five blocks

```
> posord[1:20]
```

```
[1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
```

```
> blocks[1:5]
```

```
$`(1e+05,1.2e+05)`
```

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

```
$`(1.2e+05,1.4e+05)`
```

```
[1] 4
```

```
$`(1.4e+05,1.6e+05)`
```

```
[1] 5 6 7 8 9 10
```

```
$`(1.6e+05,1.8e+05)`
```

```
[1] 11 12 13 14
```

```
$`(1.8e+05,2e+05)`
```

```
[1] 15 16 17 18
```

Note that these positions refer to the reduced set of SNPs after application of the filter on MAF and HWE. Therefore, before proceeding further we create a new matrix of SNP genotypes containing only these 27,828:

```
> snps.use <- snps.10[, use]
```

```
> remove(snps.10)
```

The command to carry out the tests on these groups, controlling for the known population structure differences is

```

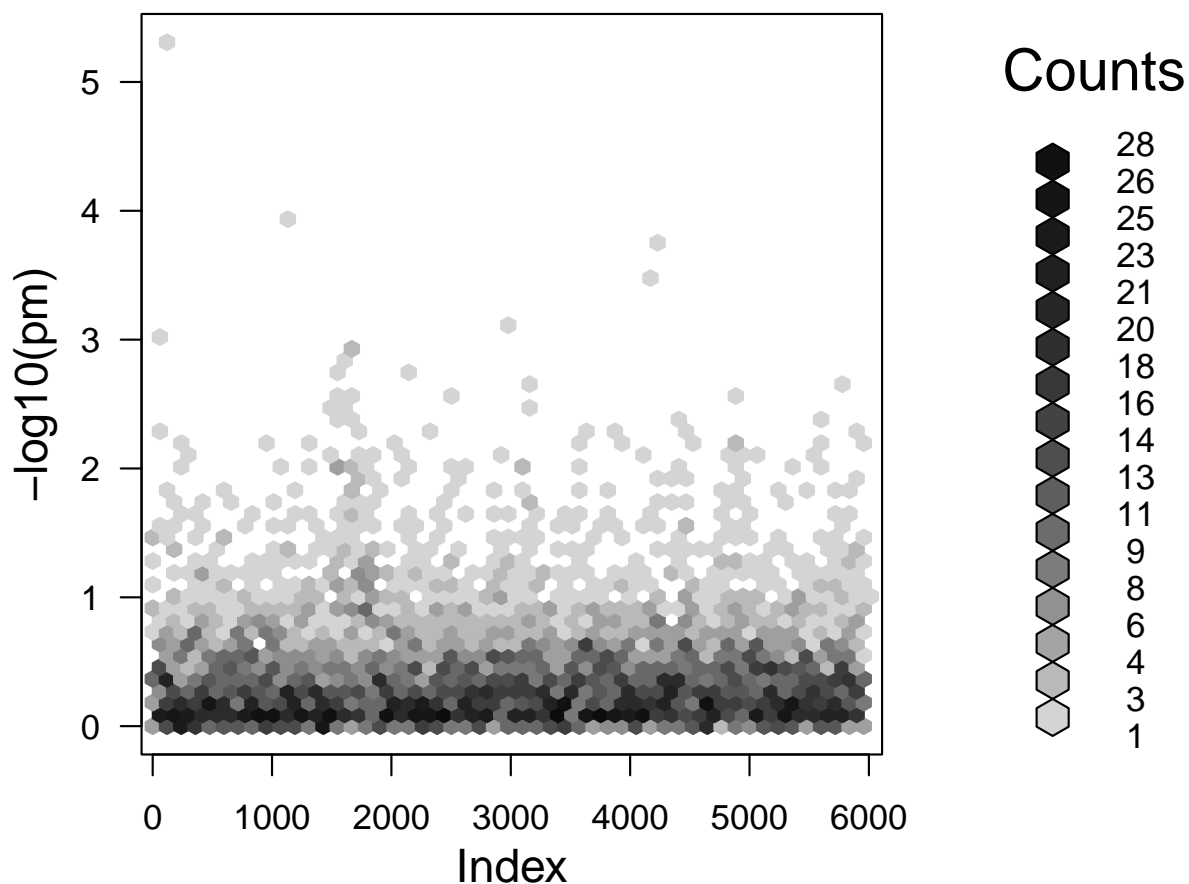
> mtests <- snp.rhs.tests(cc ~ stratum, family = "binomial",
+   data = subject.support, snp.data = snps.use, tests = blocks)
> summary(mtests)

```

Chi.squared	Df	p.value
Min. : 0.00	Min. : 1.00	Min. :0.000
1st Qu.: 1.44	1st Qu.: 2.00	1st Qu.:0.258
Median : 3.48	Median : 4.00	Median :0.487
Mean : 4.52	Mean : 4.51	Mean :0.495
3rd Qu.: 6.53	3rd Qu.: 6.00	3rd Qu.:0.741
Max. :32.29	Max. :24.00	Max. :1.000

The first argument, together with the second, specifies the model which corresponds to the null hypothesis. In this case we have allowed for the variation in ethnic origin (**stratum**) between cases and controls. We complete the analysis by extracting the  $p$ -values and plotting minus their logs (base 10):

```
> pm <- p.value(mtests)
> plot(hexbin(-log10(pm), xbin=50))
```



The same associated region is picked out, albeit with a rather larger  $p$ -value; in this case the multiple df test cannot be powerful as the 1 df test since the simulation ensured that the “causal” locus was actually one of the SNPs typed on the Affymetrix platform. QQ plots are somewhat more difficult since the tests are on differing degrees of freedom. This difficulty is neatly circumvented by noting that, under the null hypothesis,  $-2\log p$  is distributed as chi-squared on 2 df:

```
> qq.chisq(-2 * log(pm), df = 2)
```

N	omitted	lambda
5957.000	0.000	1.056

QQ plot

