

Data input vignette

Reading genotype data in `snpStats`

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Memory limitations

Before we start it is important to emphasise that the `SnpMatrix` objects that hold genotype data in `snpStats` are resident in memory, and limitations of the computer and of the R language impose limits on the maximum size of datasets that can be held at any one time. Each genotype reading uses only a single byte of memory so that large datasets can be read given the large memory capacity of modern computers. Originally, R imposed a limit of $2^{31} - 1 \sim 2 \times 10^9$ elements in a single array. This limit applied in both the 32-bit and 64-bit versions of R, these versions differing only in the *total* memory that could be used. For example, this would correspond to one million loci for two thousand subjects and would occupy two gigabytes of machine memory. However, version 3 of R removed the restriction on single arrays in the 64-bit version, and this was implemented for `SnpMatrix` and `XSnpMatrix` objects in version 1.19.2 of `snpStats`. However, experience of this code is limited and some caution is advised.

Reading pedfiles

A commonly encountered format for storing genotype data is the “pedfile” format, which originated some years ago in the `LINKAGE` package. Pedfiles are text files containing one line per genotyped sample, with fields separated by “white space” (`TAB` characters or `SPACES`). The first six fields contain:

1. a pedigree or family identifier, unique to the family of which this subject is a member,
2. a further identifier, unique (within the family) to each family member,
3. the member identifier of the father of the subject if the father is also present in the data, otherwise an arbitrary code (usually 0),
4. similarly, an identifier for the mother of the subject,

5. the sex of the subject (1 = Male, 2 = Female), and
6. a binary trait indicator (1 = Absent, 2 = Present).

Missing values in the last two fields are usually coded as zero.

The first few rows and columns of a sample file is shown below:

```
IBD054 430 0 0 1 0 1 3 3 1 4 1 4 2
IBD054 412 430 431 2 2 1 3 1 3 4 1 4 2
IBD054 431 0 0 2 0 3 3 3 3 1 1 2 2
IBD058 438 0 0 1 0 3 3 3 3 1 1 2 2
IBD058 470 438 444 2 2 3 3 3 3 1 1 2 2
```

Thus, the subject of line 2 has a father whose data appears on line 1 and a mother whose data is on line 3. The grandparents do not appear on the file. This subject is affected by the trait, but the trait status of her parents is not known. The genotypes of this subject at the first four loci are 1/3, 1/3, 4/1 and 4/2. Note that `snpStats` will only deal with diallelic data and, although alleles are coded 1 to 4 in this file, only two of these occur with in any one locus. In fact these data are from the sample dataset distributed with the HAPLOVIEW program (Barrett et al., 2005) which uses the numbers 1–4 to denote the four nucleotides: 1 = A, 2 = C, 3 = G, 4 = . The pedfile contains data for 20 loci on 120 subjects, and is accompanied by a second file which describes the loci, the first four lines being:

```
IGR1118a_1 274044
IGR1119a_1 274541
IGR1143a_1 286593
IGR1144a_1 287261
```

(this file is rather simple, containing just the locus name and its position on a chromosome).

The (gzipped) pedfile and the locus information file are stored in the `extdata` sub-directory of the `snpStats` package as, respectively, `sample.ped.gz` and `sample.info`. Since the precise location of these files may vary between installations, we first obtain full paths to these files using the `system.file` function

```
> pedfile <- system.file("extdata/sample.ped.gz", package="snpStats")
> pedfile

[1] "/tmp/RtmpjT1lXt/Rinst35077e436d0d75/snpStats/extdata/sample.ped.gz"

> infofile <- system.file("extdata/sample.info", package="snpStats")
```

The data can then be read in using the `read.pedfile` function

```
> sample <- read.pedfile(pedfile, snps=infofile)
```

The result, `sample`, is a list with three elements. The first is an object of class `Snpmatrix` containing the genotype data. We shall show summaries for the first few loci

```

> sample$genotypes

A SnpMatrix with 120 rows and 20 columns
Row names: 430 ... 17702
Col names: IGR1118a_1 ... IGR2020a_1

> col.summary(sample$genotypes)$MAF

[1] 0.14957265 0.14224138 0.15833333 0.15000000 0.13392857 0.15929204
[7] 0.14678899 0.14035088 0.06578947 0.14166667 0.13839286 0.15566038
[13] 0.13750000 0.14166667 0.31250000 0.26470588 0.27155172 0.50000000
[19] 0.28947368 0.02232143

> head(col.summary(sample$genotypes))

      Calls Call.rate Certain.calls      RAF      MAF      P.AA
IGR1118a_1  117 0.9750000           1 0.8504274 0.1495726 0.008547009
IGR1119a_1  116 0.9666667           1 0.1422414 0.1422414 0.724137931
IGR1143a_1  120 1.0000000           1 0.8416667 0.1583333 0.008333333
IGR1144a_1  120 1.0000000           1 0.8500000 0.1500000 0.008333333
IGR1169a_2  112 0.9333333           1 0.8660714 0.1339286 0.000000000
IGR1218a_2  113 0.9416667           1 0.8407080 0.1592920 0.008849558

      P.AB      P.BB      z.HWE
IGR1118a_1 0.2820513 0.70940171 1.175622
IGR1119a_1 0.2672414 0.00862069 1.025043
IGR1143a_1 0.3000000 0.69166667 1.375728
IGR1144a_1 0.2833333 0.70833333 1.217161
IGR1169a_2 0.2678571 0.73214286 1.636547
IGR1218a_2 0.3008850 0.69026549 1.311673

```

The second list element is a dataframe containing the first six fields of the pedigree. We'll just display the start of this:

```

> head(sample$fam)

  pedigree member father mother sex affected
430  IBD054     430   <NA>   <NA>   1      NA
412  IBD054     412     430     431   2       2
431  IBD054     431   <NA>   <NA>   2      NA
438  IBD058     438   <NA>   <NA>   1      NA
470  IBD058     470     438     444   2       2
444  IBD058     444   <NA>   <NA>   2      NA

```

Note that the zero values in the pedfile have been read as NA; this is optional, but default, behaviour of the function. Here the pedigree-member identifiers have been used as subject identifiers, since these are not duplicated while pedigree identifiers (the first choice) were duplicated (if both sets of identifiers are duplicated, they are combined). Finally, the third list element is a dataframe containing the information read from the `sample.info` file, to which have been added the two alleles found at each locus:

```
> head(sample$map)

  snp.names      V2 allele.1 allele.2
1 IGR1118a_1 274044      1      3
2 IGR1119a_1 274541      3      1
3 IGR1143a_1 286593      4      1
4 IGR1144a_1 287261      4      2
5 IGR1169a_2 299755      2      1
6 IGR1218a_2 324341      3      1
```

Here we have used the default settings of `read.pedfile`. In particular, it is not mandatory to supply a locus description file and there are further arguments which allow additional flexibility. These options are described in the on-line help page.

PLINK files

Binary PED (BED) files written by the PLINK toolset (Purcell et al., 2007) may also be read as `Snpmatrix` objects. Files of type `.bed` are written by the `plink -make-bed` command and are accompanied by two text files: a `.fam` file containing the first six fields of a standard pedfile as described above, and a `.bim` file which describes the loci. The package data directory also contains `.bed`, `.fam` and `.bim` files for the sample dataset of the last section; the following commands recover the full file paths for these files and read the files:

```
> fam <- system.file("extdata/sample.fam", package="snpStats")
> bim <- system.file("extdata/sample.bim", package="snpStats")
> bed <- system.file("extdata/sample.bed", package="snpStats")
> sample <- read.plink(bed, bim, fam)
```

The output object is similar to that produced by `read.pedfile`, a list with three elements:

```
> sample$genotypes

A Snpmatrix with 120 rows and 20 columns
Row names: 430 ... 17702
Col names: IGR1118a_1 ... IGR2020a_1

> col.summary(sample$genotypes)$MAF
```

```
[1] 0.14957265 0.14224138 0.15833333 0.15000000 0.13392857 0.15929204
[7] 0.14678899 0.14035088 0.06578947 0.14166667 0.13839286 0.15566038
[13] 0.13750000 0.14166667 0.31250000 0.26470588 0.27155172 0.50000000
[19] 0.28947368 0.02232143
```

```
> head(sample$fam)
```

```
      pedigree member father mother sex affected
430   IBD054     430     NA     NA    1       NA
412   IBD054     412    430    431    2         2
431   IBD054     431     NA     NA    2       NA
438   IBD058     438     NA     NA    1       NA
470   IBD058     470    438    444    2         2
444   IBD058     444     NA     NA    2       NA
```

```
> head(sample$map)
```

```
      chromosome snp.name cM position allele.1 allele.2
IGR1118a_1      NA IGR1118a_1 NA   274044         1         3
IGR1119a_1      NA IGR1119a_1 NA   274541         1         3
IGR1143a_1      NA IGR1143a_1 NA   286593         4         1
IGR1144a_1      NA IGR1144a_1 NA   287261         4         2
IGR1169a_2      NA IGR1169a_2 NA   299755         2         1
IGR1218a_2      NA IGR1218a_2 NA   324341         3         1
```

Usually the three input files have the same filename stub with `.bed`, `.fam` and `.bim` extensions added. In this case it is sufficient to just supply the filename stub to `read.plink`.

A useful feature of `read.plink` is the ability to select a subset of data from a large PLINK dataset. This is demonstrated in our small example below

```
> subset <- read.plink(bed, bim, fam, select.snps=6:10)
> subset$genotypes
```

```
A SnpMatrix with 120 rows and 5 columns
Row names: 430 ... 17702
Col names: IGR1218a_2 ... IGR1373a_1
```

```
> col.summary(subset$genotypes)$MAF
```

```
[1] 0.15929204 0.14678899 0.14035088 0.06578947 0.14166667
```

```
> subset$map
```

	chromosome	snp.name	cM	position	allele.1	allele.2
IGR1218a_2	NA	IGR1218a_2	NA	324341	3	1
IGR1219a_2	NA	IGR1219a_2	NA	324379	4	2
IGR1286a_1	NA	IGR1286a_1	NA	358048	3	2
TSC0101718	NA	TSC0101718	NA	366811	4	3
IGR1373a_1	NA	IGR1373a_1	NA	395079	2	4

Note that, in order to select certain SNPs, the input PLINK file must be in SNP-major order *i.e.* all individuals for the first SNP, all individuals for the second SNP, and so on. This is the default mode in PLINK. However, to select certain individuals, the input PLINK file must be in individual-major order.

Long format data

The least compact, but perhaps most flexible, input format is the “long” format in which each genotype call takes up a single line. Such data can be read using the function `read.snps.long`. A simple example is provided by the small gzipped data file `sample-long.gz` provided with the package:

```
> longfile <- system.file("extdata/sample-long.gz", package="snpStats")
> longfile

[1] "/tmp/RtmpjTllXt/Rinst35077e436d0d75/snpStats/extdata/sample-long.gz"
```

The first 5 lines of the file are listed as follows:

```
> cat(readLines(longfile, 5), sep="\n")

snp1      subject1      1      1.000
snp1      subject2      2      1.000
snp1      subject3      1      1.000
snp1      subject4      1      1.000
snp1      subject5      2      1.000
```

The first field gives the SNP identifier (`snp1` to `snp18`), the second gives the sample, or subject, identifier (`subject1` to `subject100`), the third field gives the genotype call (1=A/A, 2=A/B, 3=B/B), and the last field gives a confidence measure for the call (here always 1.000). To read in this file and inspect the data:

```
> gdata <- read.long(longfile,
+   fields=c(snp=1, sample=2, genotype=3, confidence=4),
+   gcodes=c("1", "2", "3"),
+   threshold=0.95)
> gdata
```

```
A SnpMatrix with 100 rows and 18 columns
Row names: subject1 ... subject100
Col names: snp1 ... snp18
```

```
> summary(gdata)
```

```
$rows
```

Call.rate	Certain.calls	Heterozygosity
Min. :1	Min. :1	Min. :0.1111
1st Qu.:1	1st Qu.:1	1st Qu.:0.2778
Median :1	Median :1	Median :0.3333
Mean :1	Mean :1	Mean :0.3478
3rd Qu.:1	3rd Qu.:1	3rd Qu.:0.3889
Max. :1	Max. :1	Max. :0.6667

```
$cols
```

Calls	Call.rate	Certain.calls	RAF	MAF
Min. :100	Min. :1	Min. :1	Min. :0.0450	Min. :0.0450
1st Qu.:100	1st Qu.:1	1st Qu.:1	1st Qu.:0.2700	1st Qu.:0.1087
Median :100	Median :1	Median :1	Median :0.4475	Median :0.2850
Mean :100	Mean :1	Mean :1	Mean :0.4383	Mean :0.2739
3rd Qu.:100	3rd Qu.:1	3rd Qu.:1	3rd Qu.:0.5913	3rd Qu.:0.4300
Max. :100	Max. :1	Max. :1	Max. :0.9100	Max. :0.4900

P.AA	P.AB	P.BB	z.HWE
Min. :0.0000	Min. :0.0700	Min. :0.0000	Min. :-1.85573
1st Qu.:0.1525	1st Qu.:0.2025	1st Qu.:0.0875	1st Qu.: -0.62145
Median :0.2850	Median :0.4000	Median :0.1750	Median : 0.25448
Mean :0.3878	Mean :0.3478	Mean :0.2644	Mean : 0.09661
3rd Qu.:0.5475	3rd Qu.:0.4600	3rd Qu.:0.3350	3rd Qu.: 0.86390
Max. :0.9200	Max. :0.5500	Max. :0.8200	Max. : 1.19206

```
A few remarks:
```

1. In our example, the entire file has been read. However, subsets of data may be extracted by specifying the required SNP or sample identifiers.
2. Any calls for which the call confidence is less than `threshold` is set to `NA` (this did not affect any calls in this simple example).
3. Here, calls were represented by a single genotype code. It is also possible to read calls as pairs of alleles. The function then returns a list whose first argument is the `SnpMatrix` object, and whose second object is a dataframe containing the allele codes. This option is demonstrated below, using an alternative coding of the same data (all SNPs are CT SNPs):

```
> allelesfile <- system.file("extdata/sample-long-alleles.gz", package="snpStats")
> cat(readLines(allelesfile, 5), sep="\n")
```

```
snp1      subject1      C      C      1.000
snp1      subject2      C      T      1.000
snp1      subject3      C      C      1.000
snp1      subject4      C      C      1.000
snp1      subject5      C      T      1.000
```

```
> gdata <- read.long(allelesfile,
+   fields=c(snp=1, sample=2, allele.A=3, allele.B=4, confidence=5),
+   threshold=0.95)
> gdata
```

\$genotypes

A SnpMatrix with 100 rows and 18 columns
Row names: subject1 ... subject100
Col names: snp1 ... snp18

\$alleles

	allele.A	allele.B
snp1	C	T
snp2	C	T
snp3	C	T
snp4	C	T
snp5	C	T
snp6	C	T
snp7	T	C
snp8	C	T
snp9	T	C
snp10	T	C
snp11	C	T
snp12	T	C
snp13	C	T
snp14	T	C
snp15	C	T
snp16	C	T
snp17	C	T
snp18	C	T

```
> gdata$genotypes
```

A SnpMatrix with 100 rows and 18 columns
Row names: subject1 ... subject100
Col names: snp1 ... snp18


```

> gdata$alleles

      allele.A allele.B
snp1         C         T
snp2         C         T
snp3         C         T
snp4         C         T
snp5         C         T
snp6         C         T
snp7         T         C
snp8         C         T
snp9         T         C
snp10        T         C
snp11        C         T
snp12        T         C
snp13        C         T
snp14        T         C
snp15        C         T
snp16        C         T
snp17        C         T
snp18        C         T

```

Note that the assignment of alleles depends on the order in which they were encountered. This function has many options and the online help page needs to be read carefully.

Other formats

Imputation

A further source of input data is programs which can *impute* genotype data for a set of study individuals, using genome-wide SNP-chip data for the study subjects plus HapMap or 1,000 genomes project datasets. `snpStats` provides the functions `read.beagle`, `read.impute`, and `read.mach` to read in files produced by the leading imputation programs. For more details of such data, see the imputation and meta-analysis vignette.

VCF format

The 1,000 genomes data are released in the VCF format. `snpStats` does not yet include a function to read data files in this format, but the `GGtools` package does contain such a function (`vcf2sm`).

X, Y and mitochondrial SNPs

The `SnpMatrix` class is designed for diploid SNP genotypes. SNPs which can be haploid are stored in objects of the `XSnpMatrix` class, which has an addition slot, named `diploid`. Since, for the X chromosome, ploidy depends on sex and may vary from row to row, this (logical) vector has the same number of elements as the number of rows in the SNP data matrix. Most input routines do not allow for reading an `XSnpMatrix` and simply read into a `SnpMatrix`, coding haploid calls as (homozygous) diploid. Such objects may then be coerced into the `XSnpMatrix` class using `as(..., "XSnpMatrix")` or `new("XSnpMatrix", ..., diploid=...)`. If `as` is used, ploidy is inferred from homozygosity while, if `new` is used, it must be supplied (if all rows have the same ploidy, this argument can be a scalar). In either case, calls presumed to be haploid but coded as heterozygous will be set to `NA`.

Reference

Barrett JC, Fry B, Maller J, Daly MJ.(2005) Haploview: analysis and visualization of LD and haplotype maps. *Bioinformatics*, 2005 Jan 15, [PubMed ID: 15297300]

Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR, Bender D, Maller J, Sklar P, de Bakker PIW, Daly MJ and Sham PC (2007) PLINK: a toolset for whole-genome association and population-based linkage analysis. *American Journal of Human Genetics*, **81**