

# fbat

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## R topics documented:

checkMarkers . . . . .	1
checkMendelian . . . . .	3
fbat . . . . .	4
getFounders . . . . .	6
missGFreq . . . . .	6
pedAFreq . . . . .	7
pedFlagHomo . . . . .	8
pedGFreq . . . . .	9
pedHardyWeinberg . . . . .	10
readHapMap . . . . .	12
readLink . . . . .	13
readPed . . . . .	14
sampleInfoCEU . . . . .	15
sampleInfoCHB . . . . .	15
sampleInfoJPT . . . . .	16
sampleInfoYRI . . . . .	17
summaryPvalue . . . . .	17
viewFlagHomo . . . . .	18
viewHW . . . . .	19
viewstat . . . . .	20
<b>Index</b>	<b>21</b>

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checkMarkers	<i>Basic data quality checks for markers</i>
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### Description

Basic data quality checks for markers.

### Usage

```
checkMarkers(geneSetObj, founderOnly=TRUE, thrsh=0.05, quiet=TRUE)
checkMarkers.default(pedObj, founderOnly=TRUE, thrsh=0.05, quiet=TRUE)
```

**Arguments**

geneSetObj	a geneSet object.
pedObj	a list with five elements: ped, columns, markerNames, Position, and filename. ped is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; columns are the names of the first 5 (or 6) columns of ped file. It should be either equal to c("family", "pid", "father", "mother", "sex", "affected") or equal to c("family", "pid", "father", "mother", "sex"); founderOnly indicates if using only founder info; markerNames is a vector of marker names; Position is a vector of marker positions; fileName is the pedigree file name
founderOnly	indicates if using only founder info
thrsh	threshold for Hardy-Weinberg test. If the pvalue of the HW test for a marker is greater than thrsh, then the marker is a good marker.
quiet	print intermediate results if quiet=FALSE.

**Value**

a data frame contains components:

Name	marker names.
Position	marker positions.
ObsHET	marker's observed heterozygosity (i.e., proportion of heterozygotes at markes). Missing alleles are excluded in the calculation.
PredHET	marker's predicted heterozygosity (i.e., $2 * MAF * (1 - MAF)$ ). Missing alleles are excluded in the calculation.
HWpval	pvalues for Hardy-Weinberg test
pGeno	percentage of non-missing genotypes for markes
MAF	minor allele frequencies. missing allele are excluded from calculation
Rating	Rating[i]=1 means that the <i>i</i> -th marker passes HW test (do not reject H0 that HW equilibrium holds). Rating[i]=0 means HW equilibrium does hold for the <i>i</i> -th marker.

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**Examples**

```
data(CAMP)
res<-checkMarkers(CAMP)
print(res)
```

---

checkMendelian	<i>Check Mendelian Errors</i>
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### Description

Check Mendelian errors.

### Usage

```
checkMendelian(geneSetObj, quiet = TRUE)

checkMendelian.default(pedObj, quiet=TRUE)
```

### Arguments

geneSetObj	a geneSet object.
pedObj	a list with five elements: ped, columns, markerNames, Position, and filename. ped is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; columns are the names of the first 5 (or 6) columns of ped file. It should be either equal to c("family", "pid", "father", "mother", "sex", "affected") or equal to c("family", "pid", "father", "mother", "sex"); founderOnly indicates if using only founder info; markerNames is a vector of marker names; Position is a vector of marker positions; fileName is the pedigree file name
quiet	print intermediate results if quiet=FALSE.

### Details

check the following errors:

- 1 father id = subject id
- 2 mother id = subject id
- 3 could not determine if an individual is a parent or a child in a family
- 4 inconsistent parental sex in a family
- 5 parental genotypes are not compatible with childrens' genotypes in a family
- 6 all childrens' genotypes are missing in a family
- 7 inconsistent sib genotypes in a family

### Value

A list with following elements:

errorFlag	errorFlag=1 indicates the occurrence of errors; errorFlag=0 indicates no error.
compatibleFlag	compatibleFlag=0 indicates the occurrence of non-compatibility; compatibleFlag=1 indicates compatibility.

- `nMerrMarker` A  $nMarkers \times 1$  vector records the numbers of families with non-compatible genotypes, where  $nMarkers$  is the number of markers.
- `nMerrFamily` A  $nFamily \times 1$  vector records the numbers of markers with non-compatible genotypes, where  $nFamily$  is the number of families.
- `nErrFamilySample`  
A  $nFamily \times 1$  vector records the numbers of times that father id is equal to subject id or mother id is equal to subject id in a family.

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### Examples

```
data(CAMP)
checkMendelian(CAMP, quiet = TRUE)
```

---

fbat *Family-Based Association Tests*

---

### Description

Family-Based Association Tests for biallelic markers.

### Usage

```
fbat(geneSetObj,
     model="a",
     traitMethod=3,
     traitOffset=0,
     quiet=TRUE)

fbat.default(pedObj,
             model="a",
             traitMethod=3,
             traitOffset=0,
             quiet=TRUE)
```

### Arguments

- `geneSetObj` an object of `geneSet`.
- `pedObj` a list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `filename`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of `ped` file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name

model	Genotype coding method. model="d" means GDOM (dominant) coding; model="r" means GREC (recessive) coding; model="g" means GEN (genotype) coding; model="a" or otherwise means GTDT (additive) coding.
traitMethod	Trait coding method. traitMethod=1 means $T=y-\text{offset}$ , where $y$ is the trait and offset is an offset. In a .ped file, $y=2$ if affected; $y=1$ if unaffected; and $y=0$ if unknown. traitMethod=2 means $T=1$ if affected, $T=0$ otherwise.
traitOffset	Offset if traitMethod=1.
quiet	Print some intermediate results if quiet=FALSE.

### Value

statPvalue	A $m$ by 3 matrix with the 3 columns: test statistics, degree of freedom and pvalues, where $m$ is the number of markers.
S.list	A list of S scores for markers.
ES.list	A list of expected S scores for markers.
CovS.list	A list of covariance matrix of S scores for markers.
alleles.list	A list of alleles for markers
familySize	size of nuclear families
flagMarkers	A vector of flags. flagMarkers[i]=1 if for marker i, all children genotypes in all families are missing. Otherwise flagMarkers[i]=0.
numInfoFamily	number of informative families at each marker

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- Horvath et al. The family based association test method: computing means and variances for general statistics. *Technical report* <http://www.biostat.harvard.edu/~fbat/fbattechreport.ps>.
- Rabinowitz and Laird (2000). A Unified Approach to Adjusting Association Tests for Population Admixture with Arbitrary Pedigree Structure and Arbitrary Missing Marker Information. *Human Heredity* **50**:211-223.
- Laird et al. (2000). Implementing a Unified Approach to Family-Based Tests of Association. *Genetic Epidemiology* **19**(Suppl 1):S36-S42.
- Schaid (1996). General Score Tests for Associations of Genetic Markers With Disease Using Cases and Their Parents. *Genetic Epidemiology* **13**:423-449.

### Examples

```
data (CAMP)
tmp<-fbat (CAMP)
summaryPvalue (tmp)
```

---

getFounders *Get founders' information*

---

### Description

Get a subset of pedigree object containing only founders' information.

### Usage

```
getFounders (pedObj)
```

### Arguments

`pedObj` a list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `filename`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), `pid` (patient id), `father` (father id), `mother` (mother id), `sex`, `affected` (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of `ped` file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name

### Value

An pedigree object contains only founders' information.

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### References

~put references to the literature/web site here ~

---

missGFreq *Count frequencies of missing genotypes*

---

### Description

Count frequencies of missing genotypes

### Usage

```
missGFreq(geneSetObj, founderOnly = TRUE, quiet = FALSE)
```

```
missGFreq.default(pedObj, founderOnly=TRUE)
```

**Arguments**

**geneSetObj** a `geneSet` object.  
**pedObj** a list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `filename`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), `pid` (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of `ped` file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name  
**founderOnly** indicates if using only founder info  
**quiet** print intermediate results if `quiet=FALSE`.

**Value**

A matrix with the following three columns:

**column 1** counts of genotypes, of which both alleles are missing.  
**column 2** counts of genotypes, of which the first allele is missing and the second allele is not missing.  
**column 3** counts of genotypes, of which the first allele is not missing and the second allele is missing.

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**Examples**

```

data(CAMP)
res<-missGFreq(CAMP, founderOnly=FALSE)
# number of missing genotypes per marker
print(res$nMissMarkers)
# number of missing genotypes per subject
print(res$nMissSubjects[1:10,])

```

---

pedAFreq                      *get allele frequencies*

---

**Description**

Get allele frequencies (missing alleles allowed).

**Usage**

```

pedAFreq(geneSetObj, founderOnly=TRUE, missingOutput=FALSE, quiet=FALSE)

pedAFreq.default(pedObj,
                 founderOnly=TRUE,
                 missingOutput=FALSE,
                 quiet=FALSE)

```

**Arguments**

`geneSetObj` a `geneSet` object.  
`pedObj` a list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `filename`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), `pid` (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of `ped` file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name  
`founderOnly` indicates if using only founder info.  
`missingOutput` indicates if missing allele frequency should be output.  
`quiet` print intermediate results if `quiet=FALSE`.

**Value**

`aFreqMat` allele frequencies.  
`aPercMat` allele percentages.  
`missingOutput` indicates if missing allele frequency should be output.

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**Examples**

```

data(CAMP)
res<-pedAFreq(CAMP)
res$aFreqMat
res$aPercMat
res$missingOutput
  
```

---

pedFlagHomo      *flag homo/heterozygotes*

---

**Description**

Flag homo/heterozygotes.

**Usage**

```

pedFlagHomo(geneSetObj, founderOnly=TRUE, quiet=FALSE)

pedFlagHomo.default(pedObj,
                    founderOnly=TRUE,
                    quiet=FALSE)
  
```



**Arguments**

geneSetObj	a geneSet object.
pedObj	a list with five elements: ped, columns, markerNames, Position, and filename. ped is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; columns are the names of the first 5 (or 6) columns of ped file. It should be either equal to c("family","pid","father","mother","sex","affected") or equal to c("family","pid","father","mother","sex"); founderOnly indicates if using only founder info; markerNames is a vector of marker names; Position is a vector of marker positions; fileName is the pedigree file name
founderOnly	indicates if using only founder info
quiet	print intermediate results if quiet=FALSE.

**Value**

countMat	Count the number of homo/heterozygotes.
flagHomoMat	Flag homo/heterozygotes. 1 – homozygotes; 0 – heterozygotes; -1 – genotype contains one missing allele; -2 – genotype contains two missing alleles.
markerNames	marker names.

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**Examples**

```
data (CAMP)
res<-pedFlagHomo (CAMP)
res$countMat
res$flagHomoMat
res$markerNames
```

---

pedGFreq                      *get genotype frequencies*

---

**Description**

Get genotype frequencies (missing alleles allowed).

**Usage**

```
pedGFreq(geneSetObj, founderOnly=TRUE, missingOutput=FALSE, quiet=FALSE)

pedGFreq.default (pedObj,
                  founderOnly=TRUE,
                  missingOutput=FALSE,
                  quiet=FALSE)
```

**Arguments**

`geneSetObj` a `geneSet` object.  
`pedObj` a list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `filename`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), `pid` (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of `ped` file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name  
`founderOnly` indicates if using only founder info.  
`missingOutput` indicates if missing allele frequency should be output.  
`quiet` print intermediate results if `quiet=FALSE`.

**Value**

`gFreqMat` genotype frequencies.  
`gPercMat` genotype percentages.  
`missingOutput` indicates if missing allele frequency should be output.

**Author(s)**

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**Examples**

```

data (CAMP)
res<-pedGFreq (CAMP)
res$gFreqMat
res$gPercMat
  
```

---

`pedHardyWeinberg` *Test Hardy-Weinberg equilibrium for each marker based on parental data*

---

**Description**

Test Hardy-Weinberg equilibrium for each marker based on parental data.

**Usage**

```

pedHardyWeinberg(geneSetObj, threshold=3, founderOnly=TRUE, quiet=FALSE)

pedHardyWeinberg.default(pedObj,
  threshold=3, founderOnly=TRUE, quiet=FALSE)
  
```

**Arguments**

geneSetObj	a geneSet object.
pedObj	a list with five elements: ped, columns, markerNames, Position, and filename. ped is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; columns are the names of the first 5 (or 6) columns of ped file. It should be either equal to c("family", "pid", "father", "mother", "sex", "affected") or equal to c("family", "pid", "father", "mother", "sex"); founderOnly indicates if using only founder info; markerNames is a vector of marker names; Position is a vector of marker positions; fileName is the pedigree file name
threshold	a threshold to check if expected frequencies of genotypes are too small.
founderOnly	indicates if using only founder info
quiet	print intermediate results if quiet=FALSE.

**Value**

resMat	A matrix records the following quantities for all markers (rows correspond to markers): nInfoInd (number of informative individuals, i.e. individuals whose genotypes contain no missing alleles for the specified marker), nGenotype (number of possible genotypes), nHET (number of heterozygous genotypes), nHOM (number of homozygous genotypes), nAllele (number of alleles), nMissing (number of missing alleles), chi2 (chi square test statistic), df (degree of freedom of the chi square test statistic under H0), p-value (pvalue of the test).
genotype	A list of possible genotypes and their frequencies for all markers.
nGenotype.vec	A vector of numbers of possible genotypes for all markers.
piVec	Allele frequencies for all markers.

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**Examples**

```
data(CAMP)
res<-pedHardyWeinberg(CAMP)
viewHW(res, "m709")
viewHW(res, "m654")
viewHW(res, "m47")
viewHW(res, "p46")
viewHW(res, "p79")
viewHW(res, "p252")
viewHW(res, "p491")
viewHW(res, "p523")
```

---

readHapMap                      *Import HapMap data*

---

### Description

Import HapMap data and convert it to pedigree format.

### Usage

```
readHapMap(hapmapfile, race="CEU", skip = 2, comment.char = "&", quiet = FALSE)
```

### Arguments

hapmapfile	the hapmap file name
race	can take values CEU, YRI, CHB, and JPT
skip	first skip lines in the file hapmapfile will be skipped.
comment.char	hapmapfile snp names contain the symbol # which is the comment command of R. So by default, we set comment.char as “&”.
quiet	print intermediate results if quiet=FALSE.

### Details

HapMap files are those snp files output by HapMap browsers.

### Value

A list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `fileName`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of ped file. It should be either equal to `c("family","pid","father","mother","sex","affected")` or equal to `c("family","pid","father","mother","sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name.

### Author(s)

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---

readLink	<i>Import file with PLINK data format</i>
----------	---

---

### Description

Import file with PLINK data format and convert it to a pedigree object.

### Usage

```
readLink(pedfile, gmfile, columns = c("family", "pid", "father", "mother", "sex"))
```

### Arguments

pedfile	pedigree data file with no marker info
gmfile	marker info files. It contains three columns: marker IDs, marker names, and marker positions
columns	By default, the first five columns of pedfile are sample information: family id, patient id, father id, mother id, patient sex.
quiet	print intermediate results if quiet=FALSE.

### Details

The data format is used by the software PLINK.

### Value

A list with five elements: ped, columns, markerNames, Position, and fileName. ped is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; columns are the names of the first 5 (or 6) columns of ped file. It should be either equal to c("family","pid","father","mother","sex","affected") or equal to c("family","pid","father","mother","sex"); founderOnly indicates if using only founder info; markerNames is a vector of marker names; Position is a vector of marker positions; fileName is the pedigree file name.

### Author(s)

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---

`readPed`*Import pedigree file from standard pedigree file format*

---

### Description

Import pedigree file from standard pedigree file format.

### Usage

```
readPed (
  filename,
  columns=c("family", "pid", "father", "mother",
            "sex", "affected"),
  quiet=FALSE
)
```

### Arguments

<code>filename</code>	File containing genotype data
<code>columns</code>	column names for sample info
<code>quiet</code>	indicates if intermediate output should be printed

### Value

A list with five elements: `ped`, `columns`, `markerNames`, `Position`, and `fileName`. `ped` is a pedigree data frame whose first 6 columns are family (pedigree id), pid (patient id), father (father id), mother (mother id), sex, affected (affection status). The remaining columns are pairs of marker alleles. Each row corresponds to an individual; `columns` are the names of the first 5 (or 6) columns of ped file. It should be either equal to `c("family", "pid", "father", "mother", "sex", "affected")` or equal to `c("family", "pid", "father", "mother", "sex")`; `founderOnly` indicates if using only founder info; `markerNames` is a vector of marker names; `Position` is a vector of marker positions; `fileName` is the pedigree file name.

### Author(s)

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### See Also

[read.table](#), etc

---

sampleInfoCEU	<i>Information about HapMap CEU subjects</i>
---------------	--

---

**Description**

Information about HapMap CEU subjects.

**Usage**

```
data(sampleInfoCEU)
```

**Format**

A data frame with 90 observations on the following 6 variables.

**pedID** a numeric vector

**id** a numeric vector

**fid** a numeric vector

**mid** a numeric vector

**sex** a numeric vector

**sampleID** a factor with levels NA06985 NA06991 NA06993 NA06994 NA07000 NA07019  
 NA07022 NA07029 NA07034 NA07048 NA07055 NA07056 NA07345 NA07348 NA07357  
 NA10830 NA10831 NA10835 NA10838 NA10839 NA10846 NA10847 NA10851 NA10854  
 NA10855 NA10856 NA10857 NA10859 NA10860 NA10861 NA10863 NA11829 NA11830  
 NA11831 NA11832 NA11839 NA11840 NA11881 NA11882 NA11992 NA11993 NA11994  
 NA11995 NA12003 NA12004 NA12005 NA12006 NA12043 NA12044 NA12056 NA12057  
 NA12144 NA12145 NA12146 NA12154 NA12155 NA12156 NA12234 NA12236 NA12239  
 NA12248 NA12249 NA12264 NA12707 NA12716 NA12717 NA12740 NA12750 NA12751  
 NA12752 NA12753 NA12760 NA12761 NA12762 NA12763 NA12801 NA12802 NA12812  
 NA12813 NA12814 NA12815 NA12864 NA12865 NA12872 NA12873 NA12874 NA12875  
 NA12878 NA12891 NA12892

**Examples**

```
data(sampleInfoCEU)
```

---

sampleInfoCHB	<i>Information about HapMap CHB subjects</i>
---------------	--

---

**Description**

Information about HapMap CHB subjects

**Usage**

```
data(sampleInfoCHB)
```

**Format**

A data frame with 45 observations on the following 6 variables.

**pedid** a numeric vector

**id** a numeric vector

**fid** a numeric vector

**mid** a numeric vector

**sex** a numeric vector

**sampleID** a factor with levels NA18524 NA18526 NA18529 NA18532 NA18537 NA18540  
 NA18542 NA18545 NA18547 NA18550 NA18552 NA18555 NA18558 NA18561 NA18562  
 NA18563 NA18564 NA18566 NA18570 NA18571 NA18572 NA18573 NA18576 NA18577  
 NA18579 NA18582 NA18592 NA18593 NA18594 NA18603 NA18605 NA18608 NA18609  
 NA18611 NA18612 NA18620 NA18621 NA18622 NA18623 NA18624 NA18632 NA18633  
 NA18635 NA18636 NA18637

**Examples**

```
data(sampleInfoCHB)
```

---

sampleInfoJPT	<i>Information about HapMap JPT subjects</i>
---------------	--

---

**Description**

Information about HapMap JPT subjects

**Usage**

```
data(sampleInfoJPT)
```

**Format**

A data frame with 45 observations on the following 6 variables.

**pedid** a numeric vector

**id** a numeric vector

**fid** a numeric vector

**mid** a numeric vector

**sex** a numeric vector

**sampleID** a factor with levels NA18940 NA18942 NA18943 NA18944 NA18945 NA18947  
 NA18948 NA18949 NA18951 NA18952 NA18953 NA18956 NA18959 NA18960 NA18961  
 NA18964 NA18965 NA18966 NA18967 NA18968 NA18969 NA18970 NA18971 NA18972  
 NA18973 NA18974 NA18975 NA18976 NA18978 NA18980 NA18981 NA18987 NA18990  
 NA18991 NA18992 NA18994 NA18995 NA18997 NA18998 NA18999 NA19000 NA19003  
 NA19005 NA19007 NA19012

**Examples**

```
data(sampleInfoJPT)
```



---

sampleInfoYRI	<i>Information about HapMap YRI subjects</i>
---------------	--

---

**Description**

Information about HapMap YRI subjects

**Usage**

```
data(sampleInfoYRI)
```

**Format**

A data frame with 90 observations on the following 6 variables.

**pedID** a numeric vector

**id** a numeric vector

**fid** a numeric vector

**mid** a numeric vector

**sex** a numeric vector

**sampleID** a factor with levels NA18500 NA18501 NA18502 NA18503 NA18504 NA18505  
 NA18506 NA18507 NA18508 NA18515 NA18516 NA18517 NA18521 NA18522 NA18523  
 NA18852 NA18853 NA18854 NA18855 NA18856 NA18857 NA18858 NA18859 NA18860  
 NA18861 NA18862 NA18863 NA18870 NA18871 NA18872 NA18912 NA18913 NA18914  
 NA19092 NA19093 NA19094 NA19098 NA19099 NA19100 NA19101 NA19102 NA19103  
 NA19116 NA19119 NA19120 NA19127 NA19128 NA19129 NA19130 NA19131 NA19132  
 NA19137 NA19138 NA19139 NA19140 NA19141 NA19142 NA19143 NA19144 NA19145  
 NA19152 NA19153 NA19154 NA19159 NA19160 NA19161 NA19171 NA19172 NA19173  
 NA19192 NA19193 NA19194 NA19200 NA19201 NA19202 NA19203 NA19204 NA19205  
 NA19206 NA19207 NA19208 NA19209 NA19210 NA19211 NA19221 NA19222 NA19223  
 NA19238 NA19239 NA19240

**Examples**

```
data(sampleInfoYRI)
```

---

summaryPvalue	<i>summarize the test statistics and p-values</i>
---------------	---

---

**Description**

summarize the test statistics and p-values

**Usage**

```
summaryPvalue(fbatObject)
```

**Arguments**

fbatObject    Object for Family Based Association Tests. See references.

**Details**

Print summary of test statistics and p-value.

**Author(s)**

Weiliang Qiu <stwxq@channing.harvard.edu>, Ross Lazarus <ross.lazarus@channing.harvard.edu>, Gregory Warnes <warnes@bst.rochester.edu>, Nitin Jain <nitin.jain@pfizer.com>

**References**

<http://www.biostat.harvard.edu/~fbat/fbat.htm>

**Examples**

```
data (CAMP)
tmp<-fbat (CAMP)
summaryPvalue (tmp)
```

---

viewFlagHomo            *flag homo/heterozygotes for specified marker*

---

**Description**

Flag homo/heterozygotes for specified marker.

**Usage**

```
viewFlagHomo (flagHomo.object, markerName)
```

**Arguments**

flagHomo.object            object returned by the function pedFlagHomo().

markerName            name of the specified marker.

**Value**

countMatM            Count the number of homo/heterozygotes for the specified marker.

flagHomoMatM            Flag homo/heterozygotes for the specified marker. 1 – homozygotes; 0 – heterozygotes; -1 – genotype contains one missing allele; -2 – genotype contains two missing alleles.

**Author(s)**

Weiliang Qiu <stwxq@channing.harvard.edu>, Ross Lazarus <ross.lazarus@channing.harvard.edu>, Gregory Warnes <warnes@bst.rochester.edu>, Nitin Jain <nitin.jain@pfizer.com>

**Examples**

```
data (CAMP)
res<-pedFlagHomo (CAMP)
viewFlagHomo (res, "p79")
```

---

viewHW	<i>View allele frequencies, Hardy-Weinberg equilibrium test statistics for specified marker</i>
--------	---

---

**Description**

View allele frequencies, Hardy-Weinberg equilibrium test statistics for specified marker.

**Usage**

```
viewHW(HW.object, markerName)
```

**Arguments**

HW.object	object returned by the function 'pedHardyWeinberg'.
markerName	a character string indicating the name of marker whose statistics are to be viewed

**Value**

resM	A vector records the following quantities for the specified marker: nInfoInd (number of informative individuals, i.e. individuals whose genotypes contain no missing alleles for the specified marker), nGenotype (number of possible genotypes), nHET (number of heterozygous genotypes), nHOM (number of homozygous genotypes), nAllele (number of alleles), nMissing (number of missing alleles), chi2 (chi square test statistic), df (degree of freedom of the chi square test statistic under H0), p-value (pvalue of the test).
nGenotypeM	number of possible genotypes for the specified marker.
genotypeM	possible genotypes and their frequencies.
piVecM	allele frequencies.

**Author(s)**

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**Examples**

```
data (CAMP)
res<-pedHardyWeinberg (CAMP)
viewHW (res, "m709")
viewHW (res, "m654")
viewHW (res, "m47")
viewHW (res, "p46")
viewHW (res, "p79")
viewHW (res, "p252")
viewHW (res, "p491")
viewHW (res, "p523")
```

---

`viewstat`*view statistics for a marker*

---

**Description**

view statistics for a marker

**Usage**

```
viewstat(fbatObject, markerName)
```

**Arguments**

`fbatObject` Object for Family Based Association Tests. See references.  
`markerName` name(s) of the marker(s) for which statistics is needed

**Details**

Print various stats for a marker, such as: family size, number of people in the family, number of informative families in the marker, the alleles of marker, scores for marker, expected score for marker, covariance matrix of the score for the marker, Moore-Penrose generalized inverse of covariance matrix and P-value.

**Author(s)**

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**References**

<http://www.biostat.harvard.edu/~fbat/fbat.htm>

**Examples**

```
data(CAMP)
res<-fbat(CAMP)
viewstat(res, "m709")
viewstat(res, "m654")
viewstat(res, "m47")
viewstat(res, "p46")
viewstat(res, "p79")
viewstat(res, "p252")
viewstat(res, "p491")
viewstat(res, "p523")
```

# Index

## \*Topic **datasets**

sampleInfoCEU, [14](#)  
sampleInfoCHB, [15](#)  
sampleInfoJPT, [15](#)  
sampleInfoYRI, [16](#)

## \*Topic **htest**

checkMarkers, [1](#)  
fbat, [4](#)  
pedAFreq, [7](#)  
pedFlagHomo, [8](#)  
pedGFreq, [9](#)  
pedHardyWeinberg, [10](#)  
viewFlagHomo, [17](#)  
viewHW, [18](#)

## \*Topic **misc**

checkMendelian, [2](#)  
getFounders, [5](#)  
missGFreq, [6](#)  
readHapMap, [11](#)  
readLink, [12](#)  
readPed, [13](#)  
summaryPvalue, [17](#)  
viewstat, [19](#)

checkMarkers, [1](#)  
checkMendelian, [2](#)

fbat, [4](#)

getFounders, [5](#)

missGFreq, [6](#)

pedAFreq, [7](#)  
pedFlagHomo, [8](#)  
pedGFreq, [9](#)  
pedHardyWeinberg, [10](#)

read.table, [14](#)  
readHapMap, [11](#)  
readLink, [12](#)  
readPed, [13](#)

sampleInfoCEU, [14](#)  
sampleInfoCHB, [15](#)

sampleInfoJPT, [15](#)  
sampleInfoYRI, [16](#)  
summaryPvalue, [17](#)

viewFlagHomo, [17](#)  
viewHW, [18](#)  
viewstat, [19](#)