

# Package ‘scoreInvHap’

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**Title** Get inversion status in predefined regions

**Version** 1.6.0

**Description** scoreInvHap can get the samples' inversion status of known inversions. scoreInvHap uses SNP data as input and requires the following information about the inversion: genotype frequencies in the different haplotypes, R2 between the region SNPs and inversion status and heterozygote genotypes in the reference. The package include this data for two well known inversions (8p23 and 17q21.31) and for two additional regions.

**Depends** R (>= 3.4.0)

**License** file LICENSE

**Encoding** UTF-8

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**Suggests** testthat, knitr, BiocStyle, rmarkdown

**VignetteBuilder** knitr

**biocViews** SNP, Genetics, GenomicVariation

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## R topics documented:

adaptRefs . . . . .	2
classifSNPs . . . . .	2
computeScore . . . . .	3

correctAlleleTable . . . . .	4
getAlleleTable . . . . .	4
getGenotypesTable . . . . .	5
getInvStatus . . . . .	5
hetRefs . . . . .	6
prepareMap . . . . .	6
Refs . . . . .	7
scoreInvHap . . . . .	7
scoreInvHapRes . . . . .	8
SNPsR2 . . . . .	10

<b>Index</b>	<b>11</b>
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adaptRefs	<i>Adapt references to imputed data</i>
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### Description

Internal

### Usage

```
adaptRefs(Refs, alleletable, haploid = FALSE)
```

### Arguments

Refs	List with the allele frequencies
alleletable	Data.frame with the alleles per SNP (from getAlleleTable)
haploid	Logical. If TRUE, modify references for haploid samples

### Value

List with the same values than Refs but adapted to imputation data

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classifSNPs	<i>Get similarity scores and probability</i>
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### Description

This function computes the similarity scores between the sample SNPs and the haplotype's reference.

### Usage

```
classifSNPs(genos, R2, refs, BPPARAM = BiocParallel::bpparam())
```

```
classifSNPsImpute(genos, R2, refs, BPPARAM = BiocParallel::bpparam())
```

**Arguments**

genos	Matrix with the samples genotypes. It is the result of getGenotypesTable
R2	Vector with the R2 between the SNPs and the inversion status
refs	List of matrices. Each matrix has, for an SNP, the frequencies of each genotype in the different haplotypes.
BPPARAM	A BiocParallelParam instance. Used to parallelize computation

**Details**

classifSNPs computes, for each individual, similarity scores for all the present haplotypes. For each SNP, we compute as many similarity scores as haplotypes present in the reference. We have defined the similarity score as the frequency of this genotype in the different haplotype population. To compute the global similarity score, we have computed a mean of the scores by SNP weighted by the R2 between the SNP and the haplotype classification.

classifSNPsImpute is a version of classifSNPs that works with posterior probabilities of imputed genotypes.

**Value**

List with the results:

- scores: Matrix with the similarity scores of the individuals
- numSNPs: Vector with the number of SNPs used in each computation

**Examples**

```
## Simulate a table of genotypes from R0Ino.8.3
geno <- matrix(c("CC", "GG", "AA", "CG", "NN", "AC", "GG", "AA", "CC"),
  nrow = 3, dimnames = list(letters[1:3],
  c("rs141039449", "rs138092889", "rs138217047")))

## Run function using reference of inv8p23.1
classifSNPs(geno, SNPsR2$inv8p23.1, Refs$inv8p23.1)
```

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computeScore

*Compute all similarity scores for a sample*

---

**Description**

Internal

**Usage**

```
computeScore(geno, refs, R2)
```

**Arguments**

geno	Vector with the sample genotypes. It is the result of getGenotypesTable
refs	List of matrices. Each matrix has, for an SNP, the frequencies of each genotype in the different haplotypes.
R2	Vector with the R2 between the SNPs and the inversion status

**Value**

List with the results:

- scores: Vector with the similarity scores of the sample
- numSNPs: Numeric with the number of SNPs used in the computation

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correctAlleleTable      *Solve genotypes discrepancies*

---

**Description**

This function tries to solve discrepancies between the reference and sample genotypes. The cause of these discrepancies is that samples and references have used different strands to codify the SNP. This function get the complement genotypes for the discordant SNPs and checks if discordancies are solved.

**Usage**

```
correctAlleleTable(alleletable, hetRefs, map)
```

**Arguments**

alleletable	Data.frame with the alleles per SNP (from getAlleleTable)
hetRefs	Character vector with the heterozygous genotypes in the reference.
map	Data.frame with the annotation of the SNPs (from plink format)

**Value**

alleletable without discrepancies between these genotypes and the references.

---

getAlleleTable      *Compute the allele table*

---

**Description**

Get a data.frame that maps the numeric genotype of a SNPmatrix (0, 1, 2) into the real genotype. Heterozygous genotypes are ordered alphabetically.

**Usage**

```
getAlleleTable(map)
```

**Arguments**

map	Data.frame with the annotation of the SNPs (from plink format)
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**Value**

Data.frame with genotypes map

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getGenotypesTable	<i>Get genotypes table</i>
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**Description**

Get a matrix with the sample genotypes from all SNP.

**Usage**

```
getGenotypesTable(geno, allele)
```

**Arguments**

geno	SnpMatrix (from plink format)
allele	Data.frame with the alleles per SNP (from getAlleleTable)

**Value**

Character matrix with the samples genotypes

---

getInvStatus	<i>Get the inversion status of a sample</i>
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**Description**

This function estimates the inversion status of the samples using the probabilities computed in `classifSNPs`

**Usage**

```
getInvStatus(scores)
```

**Arguments**

scores	Matrix of probabilities (from <code>classifSNPs</code> )
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**Value**

List with the results:

- class: Vector with the most probable classification
- certainty: Vector with the certainty of the most probable classification

---

hetRefs	<i>Heterozygote genotypes in the references</i>
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---

**Description**

Dataset with the heterozygote genotypes of all the SNPs used in any of the references. This dataset include all the SNPs that are present inside the inversion's region in 1000 Genomes Phase 3.

**Usage**

```
hetRefs
```

**Format**

List of character vectors with the heterozygous genotypes of the SNPs present included the region of four inversions (inv8p23.1, inv17q21.31, inv7p11.2 and invXq13.2). Each element is named with the SNPs names.

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prepareMap	<i>Modify feature data from VCF</i>
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**Description**

Internal. Modify feature data from VCF to comply with scoreInvHap requirements.

**Usage**

```
prepareMap(vcf)
```

**Arguments**

vcf	VCF object
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**Value**

Data.frame with the feature data

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Refs *Genotype frequency in references*

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### Description

Dataset with the genotype frequencies in the different haplotype populations. These frequencies have been computed using the European samples of 1000 Genomes Phase 3 data. Real inversion status have been estimated using `invClust`.

### Usage

Refs

### Format

List of matrices for four inversions (`inv8p23.1`, `inv17q21.31`, `inv7p11.2` and `invXq13.2`). Each matrices has the frequency of each genotype in each haplotype.

---

`scoreInvHap` *scoreInvHap: package to get inversion status of predefined regions.*

---

### Description

`scoreInvHap` can get the samples' inversion status of known inversions. `scoreInvHap` uses SNP data as input and requires the following information about the inversion: genotype frequencies in the different inversion groups, R2 between the region SNPs and inversion status, heterozygote genotypes in the reference, allele frequencies in the reference population and inversion frequencies. The package include this data for two well known inversions (8p23 and 17q21.31) and for two additional validated regions.

This is the main function of 'scoreInvHap' package. This function accepts SNPs data in a plink or a VCF format and compute the inversion prediction.

### Usage

```
scoreInvHap(SNPlist, SNPsR2, hetRefs, Refs, R2 = 0, imputed = FALSE,
            BPPARAM = BiocParallel::bpparam(), verbose = FALSE)
```

### Arguments

<code>SNPlist</code>	List with SNPs data. It should contain genotypes (a <code>SNPmatrix</code> ) and map (a <code>data.frame</code> with the annotation)
<code>SNPsR2</code>	Vector with the R2 of the SNPs of the region
<code>hetRefs</code>	Vector with the heterozygote form of the SNP in the inversion
<code>Refs</code>	List with the allele frequencies in the references
<code>R2</code>	Vector with the R2 between the SNPs and the inversion status
<code>imputed</code>	Logical. If TRUE, scores are computed using posterior probabilities. If FALSE, scores are computed using best guess. Only applied when <code>SNPlist</code> is a VCF.
<code>BPPARAM</code>	A <code>BiocParallelParam</code> instance. Used to parallelize computation
<code>verbose</code>	Should message be shown?

**Value**

A scoreInvHap object

**Examples**

```
if(require(VariantAnnotation)){
  vcf <- readVcf(system.file("extdata", "example.vcf", package = "scoreInvHap"), "hg19")
  res <- scoreInvHap(vcf, SNPsR2$inv7p11.2, hetRefs = hetRefs$inv7p11.2,
                    Refs$inv7p11.2)
}
```

---

scoreInvHapRes

*scoreInvHapRes instances*

---

**Description**

Container with the results of the classification pipeline

**Usage**

```
## S4 method for signature 'scoreInvHapRes'
classification(object, minDiff = 0, callRate = 0,
               inversion = FALSE)

## S4 method for signature 'scoreInvHapRes'
certainty(object)

## S4 method for signature 'scoreInvHapRes'
diffscores(object)

## S4 method for signature 'scoreInvHapRes'
maxscores(object)

## S4 method for signature 'scoreInvHapRes'
numSNPs(object)

## S4 method for signature 'scoreInvHapRes'
plotCallRate(object, callRate = 0.9, ...)

## S4 method for signature 'scoreInvHapRes'
plotScores(object, minDiff = 0.1, ...)

## S4 method for signature 'scoreInvHapRes'
propSNPs(object)

## S4 method for signature 'scoreInvHapRes'
scores(object)
```



**Arguments**

object	scoreInvHapRes
minDiff	Numeric with the threshold of the minimum difference between the top and the second score. Used to filter samples.
callRate	Numeric with the threshold of the minimum call rate of the samples. Used to filter samples.
inversion	Logical. If true, haplotypes classification is adapted to return inversion status.
...	Further parameters passed to plot function.

**Value**

A scoreInvHapRes instance

**Methods (by generic)**

- classification: Get classification
- certainty: Get classification certainty
- diffscores: Get maximum similarity scores
- maxscores: Get maximum similarity scores
- numSNPs: Get number of SNPs used in computation
- plotCallRate: Plot call rate based QC
- plotScores: Plot scores based QC
- propSNPs: Get proportions of SNPs used in computation
- scores: Get similarity scores

**Slots**

classification Factor with the individuals classification  
 scores Similarity scores for the different haplotypes.  
 numSNPs Numeric with SNPs used to compute the scores.  
 certainty Numeric with the certainty of the classification for each individual.

**Examples**

```
if(require(VariantAnnotation)){
  vcf <- readVcf(system.file("extdata", "example.vcf", package = "scoreInvHap"), "hg19")

  ## Create scoreInvHapRes class from pipeline
  res <- scoreInvHap(vcf, SNPsR2$inv7p11.2, hetRefs = hetRefs$inv7p11.2,
  Refs$inv7p11.2)

  ## Print object
  res

  ## Get haplotype classification
  classification(res)

  ## Get similarity scores
  scores(res)
}
```

---

SNPsR2

*R2 between the SNPs and the inversion status*

---

**Description**

Dataset with R2 between the SNPs and the inversion status. These values are used to weigh similarity scores. These values have been computed using the European samples of 1000 Genomes Phase 3 data. Real inversion status have been estimated using invClust.

**Usage**

SNPsR2

**Format**

List of numeric vectors for 6 inversions (inv8p23.1, inv17q21.31, inv7p11.2 and invXq13.2).

# Index

## \*Topic **datasets**

- hetRefs, [6](#)
  - Refs, [7](#)
  - SNPsR2, [10](#)
- adaptRefs, [2](#)
- certainty (scoreInvHapRes), [8](#)
- certainty, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- classification (scoreInvHapRes), [8](#)
- classification, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- classifSNPs, [2](#)
- classifSNPsImpute (classifSNPs), [2](#)
- computeScore, [3](#)
- correctAlleleTable, [4](#)
- diffscores (scoreInvHapRes), [8](#)
- diffscores, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- getAlleleTable, [4](#)
- getGenotypesTable, [5](#)
- getInvStatus, [5](#)
- hetRefs, [6](#)
- maxscores (scoreInvHapRes), [8](#)
- maxscores, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- numSNPs (scoreInvHapRes), [8](#)
- numSNPs, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- plotCallRate (scoreInvHapRes), [8](#)
- plotCallRate, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- plotScores (scoreInvHapRes), [8](#)
- plotScores, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- prepareMap, [6](#)
- propSNPs (scoreInvHapRes), [8](#)
- propSNPs, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- Refs, [7](#)
- scoreInvHap, [7](#)
- scoreInvHap-package (scoreInvHap), [7](#)
- scoreInvHapRes, [8](#)
- scoreInvHapRes-class (scoreInvHapRes), [8](#)
- scoreInvHapRes-methods (scoreInvHapRes), [8](#)
- scores (scoreInvHapRes), [8](#)
- scores, scoreInvHapRes-method (scoreInvHapRes), [8](#)
- SNPsR2, [10](#)