Package 'lfa'

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Title Logistic Factor Analysis for Categorical Data

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Description Logistic Factor Analysis is a method for a PCA analogue on Binomial data via estimation of latent structure in the natural parameter. The main method estimates genetic population structure from genotype data. There are also methods for estimating individual-specific allele frequencies using the population structure. Lastly, a structured Hardy-Weinberg equilibrium (HWE) test is developed, which quantifies the goodness of fit of the genotype data to the estimated population structure, via the estimated individual-specific allele frequencies (all of which generalizes traditional HWE tests).

Imports methods, corpcor, RSpectra, BEDMatrix, genio

Depends R (>= 4.0)

Suggests knitr, rmarkdown, ggplot2, testthat

VignetteBuilder knitr

License GPL (>= 3)

biocViews SNP, DimensionReduction, PrincipalComponent, Regression

BugReports https://github.com/StoreyLab/lfa/issues

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Contents

`af` *Allele frequencies*

Description

Compute matrix of individual-specific allele frequencies

Usage

```
af(X, LF, safety = FALSE, max_iter = 100, tol = 1e-10)
```

Arguments

`X`	A matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, 2's and `NA`s. BEDMatrix is supported. Sparse matrices of class Matrix are not supported (yet).
`LF`	Matrix of logistic factors, with intercept. Pass in the return value from `lfa()`!
`safety`	Optional boolean to bypass checks on the genotype matrices, which require a non-trivial amount of computation. Ignored if `X` is a BEDMatrix object.
`max_iter`	Maximum number of iterations for logistic regression
`tol`	Numerical tolerance for convergence of logistic regression

Details

Computes the matrix of individual-specific allele frequencies, which has the same dimensions of the genotype matrix. Be warned that this function could use a ton of memory, as the return value is all doubles. It could be wise to pass only a selection of the SNPs in your genotype matrix to get an idea for memory usage. Use `gc()` to check memory usage!

Value

Matrix of individual-specific allele frequencies.

Examples

```
LF <- lfa( hgdp_subset, 4 )
allele_freqs <- af( hgdp_subset, LF )
```

`af_snp` *Allele frequencies for SNP*

Description

Computes individual-specific allele frequencies for a single SNP.

Usage

```
af_snp(snp, LF, max_iter = 100, tol = 1e-10)
```

Arguments

`snp`	vector of 0's, 1's, and 2's
`LF`	Matrix of logistic factors, with intercept. Pass in the return value from `lfa()`!
`max_iter`	Maximum number of iterations for logistic regression
`tol`	Numerical tolerance for convergence of logistic regression

Value

vector of allele frequencies

See Also

`af()`

Examples

```
LF <- lfa(hgdp_subset, 4)
# pick one SNP only
snp <- hgdp_subset[ 1, ]
# allele frequency vector for that SNO only
allele_freqs_snp <- af_snp(snp, LF)
```

centerscale *Matrix centering and scaling*

Description

C routine to row-center and scale a matrix. Doesn't work with missing data.

Usage

```
centerscale(A)
```

Arguments

A	matrix

Value

matrix same dimensions A but row centered and scaled

Examples

```
Xc <- centerscale(hgdp_subset)
```

hgdp_subset *HGDP subset*

Description

Subset of the HGDP dataset.

Usage

```
hgdp_subset
```

Format

a matrix of 0's, 1's and 2's.

Value

genotype matrix

Source

Stanford HGDP http://www.hagsc.org/hgdp/files.html

`lfa` *Logistic factor analysis*

Description

Fit logistic factor model of dimension `d` to binomial data. Computes `d - 1` singular vectors followed by intercept.

Usage

```
lfa(
  X,
  d,
  adjustments = NULL,
  override = FALSE,
  safety = FALSE,
  rspectra = FALSE,
  ploidy = 2,
  tol = .Machine$double.eps,
  m_chunk = 1000
)
```

Arguments

`X`	A matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, 2's and `NA`s. BEDMatrix is supported. Sparse matrices of class Matrix are not supported (yet).
`d`	Number of logistic factors, including the intercept
`adjustments`	A matrix of adjustment variables to hold fixed during estimation. Number of rows must equal number of individuals in `X`. These adjustments take the place of LFs in the output, so the number of columns must not exceed `d-2` to allow for the intercept and at least one proper LF to be included. When present, these adjustment variables appear in the first columns of the output. Not supported when `X` is a BEDMatrix object.
`override`	Optional boolean passed to `trunc_svd()` to bypass its Lanczos bidiagonalization SVD, instead using `corpcor::fast.svd()`. Usually not advised unless encountering a bug in the SVD code. Ignored if `X` is a BEDMatrix object.
`safety`	Optional boolean to bypass checks on the genotype matrices, which require a non-trivial amount of computation. Ignored if `X` is a BEDMatrix object.
`rspectra`	If `TRUE`, use `RSpectra::svds()` instead of default `trunc_svd()` or `corpcor::fast.svd()` options. Ignored if `X` is a BEDMatrix object.
`ploidy`	Ploidy of data, defaults to 2 for bi-allelic unphased SNPs
`tol`	Tolerance value passed to `trunc_svd()` Ignored if `X` is a BEDMatrix object.
`m_chunk`	If `X` is a BEDMatrix object, number of loci to read per chunk (to control memory usage).

Details

Genotype matrix should have values in 0, 1, 2, or NA. The coding of the SNPs (which case is 0 vs 2) does not change the output.

Value

The matrix of logistic factors, with individuals along rows and factors along columns. The intercept appears at the end of the columns, and adjustments in the beginning if present.

Examples

```
LF <- lfa(hgdp_subset, 4)
dim(LF)
head(LF)
```

---

lfa-defunct *Defunct functions in package* lfa.

Description

These functions are defunct and no longer available.

Details

Defunct functions are: read.bed, read.tped.recode, model.gof, center

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pca_af *PCA Allele frequencies*

Description

Compute matrix of individual-specific allele frequencies via PCA

Usage

```
pca_af(X, d, override = FALSE, ploidy = 2, tol = 1e-13, m_chunk = 1000)
```

Arguments

X	A matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, 2's and NAs. BEDMatrix is supported. Sparse matrices of class Matrix are not supported (yet).
d	Number of logistic factors, including the intercept
override	Optional boolean passed to trunc_svd() to bypass its Lanczos bidiagonalization SVD, instead using corpcor::fast.svd(). Usually not advised unless encountering a bug in the SVD code. Ignored if X is a BEDMatrix object.
ploidy	Ploidy of data, defaults to 2 for bi-allelic unphased SNPs
tol	Tolerance value passed to trunc_svd() Ignored if X is a BEDMatrix object.
m_chunk	If X is a BEDMatrix object, number of loci to read per chunk (to control memory usage).

Details

This corresponds to algorithm 1 in the paper. Only used for comparison purposes.

Value

Matrix of individual-specific allele frequencies.

Examples

```
LF <- lfa(hgdp_subset, 4)
allele_freqs_lfa <- af(hgdp_subset, LF)
allele_freqs_pca <- pca_af(hgdp_subset, 4)
summary(abs(allele_freqs_lfa-allele_freqs_pca))
```

---

sHWE *Hardy-Weinberg Equilibrium in structure populations*

Description

Compute structural Hardy-Weinberg Equilibrium (sHWE) p-values on a SNP-by-SNP basis. These p-values can be aggregated to determine genome-wide goodness-of-fit for a particular value of d. See doi:10.1101/240804 for more details.

Usage

```
sHWE(X, LF, B, max_iter = 100, tol = 1e-10, m_chunk = 1000)
```

Arguments

X	A matrix of SNP genotypes, i.e. an integer matrix of 0's, 1's, 2's and NAs. BEDMatrix is supported. Sparse matrices of class Matrix are not supported (yet).
LF	matrix of logistic factors
B	number of null datasets to generate, B = 1 is usually sufficient. If computational time/power allows, a few extra B could be helpful
max_iter	Maximum number of iterations for logistic regression
tol	Tolerance value passed to trunc_svd() Ignored if X is a BEDMatrix object.
m_chunk	If X is a BEDMatrix object, number of loci to read per chunk (to control memory usage).

Value

a vector of p-values for each SNP.

Examples

```
# get LFs
LF <- lfa(hgdp_subset, 4)
# look at a small (300) number of SNPs for rest of this example:
hgdp_subset_small <- hgdp_subset[ 1:300, ]
gof_4 <- sHWE(hgdp_subset_small, LF, 3)
LF <- lfa(hgdp_subset, 10)
gof_10 <- sHWE(hgdp_subset_small, LF, 3)
hist(gof_4)
hist(gof_10)
```

---

trunc_svd *Truncated singular value decomposition*

Description

Truncated SVD

Usage

```
trunc_svd(
  A,
  d,
  adjust = 3,
  tol = .Machine$double.eps,
  override = FALSE,
  force = FALSE,
  maxit = 1000
)
```

Arguments

A	matrix to decompose
d	number of singular vectors
adjust	extra singular vectors to calculate for accuracy
tol	convergence criterion
override	TRUE means we use corpcor::fast.svd() instead of the iterative algorithm (useful for small data or very high d).
force	If TRUE, forces the Lanczos algorithm to be used on all datasets (usually corpcor::fast.svd() is used on small datasets or large d)
maxit	Maximum number of iterations

Details

Performs singular value decomposition but only returns the first d singular vectors/values. The truncated SVD utilizes Lanczos bidiagonalization. See references.

This function was modified from the package irlba 1.0.1 under GPL. Replacing the crossprod() calls with the C wrapper to dgemv is a dramatic difference in larger datasets. Since the wrapper is technically not a matrix multiplication function, it seemed wise to make a copy of the function.

Value

list with singular value decomposition. Has elements 'd', 'u', 'v', and 'iter'

Examples

```
obj <- trunc_svd( hgdp_subset, 4 )
obj$d
obj$u
obj$v
obj$iter
```

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