Package 'LEA'

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Title LEA: an R package for Landscape and Ecological Association Studies

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Author Eric Frichot <eric.frichot@gmail.com>, Olivier Francois <olivier.francois@grenoble-inp.fr>, Clement Gain <clement.gain@univ-grenoble-alpes.fr>

Maintainer Olivier Francois <olivier.francois@grenoble-inp.fr>, Eric Frichot <eric.frichot@gmail.com>

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Suggests knitr

Description LEA is an R package dedicated to population genomics, landscape genomics and genotype-environment association tests. LEA can run analyses of population structure and genome-wide tests for local adaptation. The package includes statistical methods for estimating ancestry coefficients from large genotypic matrices and for evaluating the number of ancestral populations (snmf, pca). It performs statistical tests using latent factor mixed models for identifying genetic polymorphisms that exhibit association with environmental gradients or phenotypic traits (lfmm2). {\tt LEA} also performs imputation of missing genotypes, and computes predictive values of genetic offsets based on new or future environments. The package includes factor methods for estimating ancestry coefficients from large genotypic matrices and for evaluating the number of ancestral populations (snmf, pca). LEA is mainly based on optimized programs that can scale with the dimension of large data sets.

License GPL-3

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`LEA-package` *LEA: an R package for Landscape and Ecological Associations studies.*

Description

LEA is an R package dedicated to landscape genomics and ecological association tests. LEA can run analyses of population structure and genome scans for local adaptation. It includes statistical methods for estimating ancestry coefficients from large genotypic matrices and evaluating the number of ancestral populations (snmf, pca) and identifying genetic polymorphisms that exhibit high correlation with some environmental gradient or with the variables used as proxies for ecological pressures (lfmm). LEA is mainly based on optimized C programs that can scale with the dimension of very large data sets.

Details

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Author(s)

Eric Frichot Olivier Francois Maintainer: Olivier Francois <olivier.francois@grenoble-inp.fr>

`ancestrymap` `ancestrymap` *format description*

Description

Description of the `ancestrymap` format. The `ancestrymap` format can be used as an input format for genotypic matrices in the functions `pca`, `lfmm` and `snmf`.

Details

The ancestrymap format has one row for each genotype. Each row has 3 columns: the 1st column is the SNP name, the 2nd column is the sample ID, the 3rd column is th number of alleles. Genotypes for a given SNP name are written in consecutive lines. The number of alleles can be the number of reference alleles or the number of derived alleles. Missing genotypes are encoded by the value 9.

Here is an example of a genotypic matrix using the ancestrymap format with 3 individuals and 4 SNPs:

```
rs0000    SAMPLE0    1
rs0000    SAMPLE1    1
rs0000    SAMPLE2    2
rs1111    SAMPLE0    0
rs1111    SAMPLE1    1
rs1111    SAMPLE2    0
rs2222    SAMPLE0    0
rs2222    SAMPLE1    9
rs2222    SAMPLE2    1
rs3333    SAMPLE0    1
rs3333    SAMPLE1    2
rs3333    SAMPLE2    1
```

Author(s)

Eric Frichot

See Also

ancestrymap2lfmm ancestrymap2geno geno lfmm.data ped vcf

---

ancestrymap2geno *Convert from ancestrymap to geno format*

Description

A function that converts from the ancestrymap format to the geno format.

Usage

```
ancestrymap2geno(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the ancestrymap format.
output.file	A character string containing a path to the output file, a genotypic matrix in the geno format. By default, the name of the output file is the same name as the input file with a .geno extension.

force — A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file — A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

ancestrymap geno read.geno ancestrymap2lfmm geno2lfmm ped2lfmm ped2geno vcf2geno lfmm2geno

Examples

```
# Creation of of file called "example.ancestrymap"
# a file containing 4 SNPs for 3 individuals.
data("example_ancestrymap")
write.table(example_ancestrymap,"example.ancestrymap",
col.names = FALSE, row.names = FALSE, quote = FALSE)

# Conversion    from the ancestrymap format ("example.ancestrymap")
#               to the geno format ("example.geno").
# By default,   the name of the output file is the same name
#               as the input file with a .geno extension.
# Create file:  "example.geno".
output = ancestrymap2geno("example.ancestrymap")

# Conversion    from the ancestrymap format (example.ancestrymap)
#               to the geno format with the output file called plop.geno.
# Create file:  "plop.geno".
output = ancestrymap2geno("example.ancestrymap", "plop.geno")

# As force = false and the file "example.geno" already exists,
# nothing happens.
output = ancestrymap2geno("example.ancestrymap", force = FALSE)
```

---

ancestrymap2lfmm *Convert from* ancestrymap *to* lfmm *format*

Description

A function that converts from the ancestrymap format to the lfmm format.

Usage

```
ancestrymap2lfmm(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the ancestrymap format.
output.file	A character string containing a path to the output file, a genotypic matric in the lfmm format. By default, the name of the output file is the same name as the input file with a .lfmm extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path to the output file, a genotypic matric in the lfmm format.

Author(s)

Eric Frichot

See Also

ancestrymap lfmm.data ancestrymap2geno geno2lfmm ped2lfmm ped2geno vcf2geno lfmm2geno

Examples

```
# Creation of a file called "example.ancestrymap"
# containing 4 SNPs for 3 individuals.
data("example_ancestrymap")
write.table(example_ancestrymap,"example.ancestrymap",
col.names = FALSE, row.names = FALSE, quote = FALSE)

# Conversion    from the ancestrymap format ("example.ancestrymap")
#               to the lfmm format ("example.lfmm").
# By default,   the name of the output file is the same name
#               as the input file with a .lfmm extension.
# Create file:  "example.lfmm".
output = ancestrymap2lfmm("example.ancestrymap")

# Conversion    from the ancestrymap format (example.ancestrymap)
#               to the geno format with the output file called plop.lfmm.
# Create file:  "plop.lfmm".
output = ancestrymap2lfmm("example.ancestrymap", "plop.lfmm")

# As force = false and the file "example.lfmm" already exists,
# nothing happens.
output = ancestrymap2lfmm("example.ancestrymap", force = FALSE)
```

barchart *Bar plot representation of an snmf Q-matrix*

Description

This function displays a bar plot/bar chart representation of the Q-matrix computed from an snmf run. The function can use a sort by Q option. See snmf.

Usage

```
barchart (object, K, run, sort.by.Q = TRUE, lab = FALSE, ...)
```

Arguments

object	an snmfProject object.
K	an integer value corresponding to number of ancestral populations.
run	an integer value. Usually the run number that minimizes the cross-entropy criterion.
sort.by.Q	a Boolean value indicating whether individuals should be sorted by their ancestry or not.
lab	a list of individual labels.
...	other parameters of the function barplot.default.

Value

A permutation of individual labels used in the sort.by.Q option (order). Displays the Q matrix.

Author(s)

Olivier Francois

See Also

snmf

Examples

```
# creation of a genotype file: genotypes.geno.
# 400 SNPs for 50 individuals.

data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

################
# running snmf #
################
```

```
project.snmf <- snmf("genotypes.geno",
                     K = 4, entropy = TRUE,
                     repetitions = 10,
                     project = "new")

# get the cross-entropy value for each run
ce <- cross.entropy(project.snmf, K = 4)

# select the run with the lowest cross-entropy value
best <- which.min(ce)

# plot the ancestry coefficients for the best run and K = 4

my.colors <- c("tomato", "lightblue", "olivedrab", "gold")

barchart(project.snmf, K = 4, run = best,
        border = NA, space = 0, col = my.colors,
        xlab = "Individuals", ylab = "Ancestry proportions",
        main = "Ancestry matrix") -> bp

axis(1, at = 1:length(bp$order),
      labels = bp$order, las = 3,
      cex.axis = .4)
```

`create.dataset` *create a data set with masked data*

Description

`create.dataset` creates a data set with a given percentage of masked data from the original data set. It is used to calculate the `cross.entropy` criterion.

Usage

```
create.dataset (input.file, output.file, seed = -1, percentage = 0.05)
```

Arguments

`input.file`	A character string containing a path to the input file, a genotypic matrix in the `geno` format.
`output.file`	A character string containing a path to the output file, a genotypic matrix in the `geno` format. The output file is the input file with masked genotypes. By default, the name of the output file is the same name as the input file with a _I.geno extension.
`seed`	A seed to initialize the random number generator. By default, the seed is randomly chosen.
`percentage`	A numeric value between 0 and 1 containing the percentage of masked genotypes.

Details

This is an internal function, automatically called by snmf with the entropy option.

Value

output.file — A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

geno snmf cross.entropy

Examples

```
# Creation of tuto.geno
# A file containing 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R,"genotypes.geno")

# Creation      of the masked data file
# Create file:  "genotypes_I.geno"
output = create.dataset("genotypes.geno")
```

---

cross.entropy *Cross-entropy criterion for snmf runs*

Description

Return the cross-entropy criterion for runs of snmfcwith K ancestral populations. The cross-entropy criterion is based on the prediction of masked genotypes to evaluate the fit of a model with K populations. The cross-entropy criterion helps choosing the number of ancestral populations or a best run for a fixed value of K. A smaller value of cross-entropy means a better run in terms of prediction capability. The cross-entropy criterion is computed by the snmf function when the entropy Boolean option is TRUE.

Usage

```
cross.entropy(object, K, run)
```

Arguments

object — A snmfProject object.

K — The number of ancestral populations.

run — A vector of run labels.

Value

`res` A matrix containing the cross-entropy criterion for runs with K ancestral populations.

Author(s)

Eric Frichot

See Also

`geno` `snmf` `G` `Q`

Examples

```
### Example of analyses using snmf ###

# creation of a genotype file: genotypes.geno.
# The data contains 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

################
# running snmf #
################

# Runs with K = 3 populations
# cross-entropy is computed for 2 runs.
project = NULL
project = snmf("genotypes.geno",
               K = 3,
               entropy = TRUE,
               repetitions = 2,
               project = "new")

# get the cross-entropy for all runs for K = 3
ce = cross.entropy(project, K = 3)

# get the cross-entropy for the 2nd run for K = 3
ce = cross.entropy(project, K = 3, run = 2)
```

---

cross.entropy.estimation

compute the cross-entropy criterion

Description

Calculate the cross-entropy criterion. This is an internal function, automatically called by `snmf`. The cross-entropy criterion is a value based on the prediction of masked genotypes to evaluate the error of ancestry estimation. The criterion will help to choose the best number of ancestral population (K)

and the best run among a set of runs in snmf. A smaller value of cross-entropy means a better run in terms of prediction capacity. The cross.entropy.estimation function displays the cross-entropy criterion estimated on all data and on masked data based on the input file, the masked data file (created by create.dataset, the estimation of the ancestry coefficients Q and the estimation of ancestral genotypic frequencies, G (calculated by snmf). The cross-entropy estimation for all data is always lower than the cross-entropy estimation for masked data. The cross-entropy estimation useful to compare runs is the cross-entropy estimation for masked data. The cross-entropy criterion can also be automatically calculated by the snmf function with the entropy option.

Usage

```
cross.entropy.estimation (input.file, K, masked.file, Q.file, G.file,
    ploidy = 2)
```

Arguments

input.file	A character string containing a path to the input file without masked genotypes, a genotypic matrix in the geno format.
K	An integer corresponding to the number of ancestral populations.
masked.file	A character string containing a path to the input file with masked genotypes, a genotypic matrix in the geno format. This file can be generated with the function, create.dataset). By default, the name of the masked data file is the same name as the input file with a _I.geno extension.
Q.file	A character string containing a path to the input ancestry coefficient matrix Q. By default, the name of this file is the same name as the input file with a K.Q extension.
G.file	A character string containing a path to the input ancestral genotype frequency matrix G. By default, the name of this file is the same name as the input file with a K.G extension (input_file.K.G).
ploidy	1 if haploid, 2 if diploid, n if n-ploid.

Value

cross.entropy.estimation returns a list containing the following components:

masked.ce	The value of the cross-entropy criterion of the masked genotypes.
all.ce	The value of the cross-entropy criterion of all the genotypes.

Author(s)

Eric Frichot

References

Frichot E, Mathieu F, Trouillon T, Bouchard G, Francois O. (2014). *Fast and Efficient Estimation of Individual Ancestry Coefficients*. Genetics, 194(4) : 973–983.

See Also

geno create.dataset snmf

Examples

```
# Creation of tuto.geno
# A file containing 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R,"genotypes.geno")

# The following command are equivalent with
# project = snmf("genotypes.geno", entropy = TRUE, K = 3)
# cross.entropy(project)

# Creation      of the masked data file
# Create file:  "genotypes_I.geno"
output = create.dataset("genotypes.geno")

# run of snmf with genotypes_I.geno and K = 3
project = snmf("genotypes_I.geno", K = 3, project = "new")

# calculate the cross-entropy
res = cross.entropy.estimation("genotypes.geno", K = 3, "genotypes_I.geno",
    "./genotypes_I.snmf/K3/run1/genotypes_I_r1.3.Q",
    "./genotypes_I.snmf/K3/run1/genotypes_I_r1.3.G")

# get the result
res$masked.ce
res$all.ce

#remove project
remove.snmfProject("genotypes_I.snmfProject")
```

---

env *Environmental input file format for* lfmm

Description

Description of the env format. The env format can be used as an input format for the environmental variables in the lfmm function.

Details

The env format has one row for each individual. Each row contains one value for each environmental variable (separated by spaces or tabulations).

Here is an example of an environmental file using the env format with 3 individuals and 2 variables:

```
0.252477 0.95250639
0.216618 0.10902647
-0.47509 0.07626694
```

Author(s)

Eric Frichot

See Also

lfmm lfmm2 read.env write.env

G *Ancestral allele frequencies from a snmf run*

Description

Return the snmf output matrix of ancestral allele frequency matrix for the chosen run with K ancestral populations. For an example, see snmf.

Usage

```
G(object, K, run)
```

Arguments

object	A snmfProject object.
K	The number of ancestral populations.
run	A chosen run.

Value

res	A matrix containing the ancestral allele frequencies for a run with K ancestral populations.

Author(s)

Eric Frichot

See Also

geno snmf Q cross.entropy

Examples

```
### Example of analyses using snmf ###

# creation of a genotype file: genotypes.geno.
# The data contain 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

#################
```

```
# running snmf #
################


# Two runs for K = 1 to 5
project.snmf = snmf("genotypes.geno",
                K = 3,
                repetitions = 2,
                project = "new")

# get the ancestral genotype frequency matrix, G, for the 2nd run for K = 3.
freq = G(project.snmf, K = 3, run = 2)
```

---

genetic.offset *Population genetic offset under new environments.*

Description

The function returns genetic offset estimates computed from user-specified population labels and new environments based on predictions of an lfmm2 model. It takes as input an object of class lfmm2Class together with the data that were used to adjust the LFMM, and a matrix of new environmental variables in the same format as the original ones.

Usage

```
genetic.offset (input, env, new.env, pop.labels, K, pca, candidate.loci)
```

Arguments

input	A genotypic matrix or a character string containing a path to the input file. The genotypic matrix must be in the lfmm{lfmm_format} format without missing values (9 or NA). See impute for completion based on nonnegative matrix factorization and consider R packages for reading large matrices.
env	A matrix of environmental covariates or a character string containing a path to the environmental file. The environment matrix must be in the env format without missing values. All variables must be encoded as numeric.
new.env	A matrix of new environmental covariates or a character string containing a path to the new environmental data file. The new environmental matrix must be in the env format without missing values, and of same dimension as the env matrix. All variables must be encoded as numeric.
pop.labels	A numeric or character vector providing population labels for all rows (individuals) of the response matrix.
K	An integer corresponding to the number of latent factors.
pca	A boolean value indicating whether genetic offsets are computed from a PCA approximation or not (default value: FALSE).
candidate.loci	A vector specifying which loci (column label) in the genotype matrix are included in the computation of the genetic offset (default value: all positions).

Value

`offset` A matrix or vector (depending on the `pca` parameter) of genetic offset values computed for every population in `pop.labels`.

Author(s)

Olivier Francois, Clement Gain

References

Gain C, Francois O. (2021). LEA 3: Factor models in population genetics and ecological genomics with R. Molecular Ecology Resources. doi.org/10.1111/1755-0998.13366.

See Also

`lfmm.data` `lfmm2`

Examples

```
### Example of offset prediction using lfmm2 ###

# Simulation with 100 target loci
# Effect sizes ranging between -10 an 10
# n = 100 individuals and L = 1000 loci

X <- as.matrix(rnorm(100)) # environmental variable
B <- rep(0, 1000)
target <- sample(1:1000, 100) # target loci
B[target] <- runif(100, -10, +10) # effect sizes

# Creating hidden factors and their loadings

U <- t(tcrossprod(as.matrix(c(-1.25,0.5,1.25)), X)) +
      matrix(rnorm(300), ncol = 3)

V <-  matrix(rnorm(3000), ncol = 3)

# Simulating a binarized matrix of haploid genotypes
# Simulation performed with a generative LFMM

Y <- tcrossprod(as.matrix(X), B) + tcrossprod(U, V) +
      matrix(rnorm(100000, sd = .5), nrow = 100)

Y <-  matrix(as.numeric(Y > 0), ncol = 1000)

######################################
# Fitting an LFMM with K = 3 factors #
######################################


# Computing genetic offset statistics for 2 populations
# defined from PCA
```

```
pop <- 1 + (prcomp(Y, scale = TRUE)$x[,1] > 0)

g.offset <- genetic.offset(input = Y,
                           env = X, new.env = 2*X + 10,
                           pop.labels = pop, K = 3)
round(g.offset, digit = 3)



# Computing genetic offset statistics for 2 populations,
# defined from ANOVA and  truly targeted loci

g.offset <- genetic.offset(input = Y,
                           env = X, new.env = 2*X + 10,
                           pop.labels = pop, K = 3,
                           pca = FALSE,
                           candidate.loci = target)

round(g.offset, digit = 3)

#rm(list = ls())
```

---

geno *Input file for* snmf

Description

Description of the geno format. The geno format can be used as an input format for genotypic matrices in the functions snmf, lfmm, and pca.

Details

The geno format has one row for each SNP. Each row contains 1 character for each individual: 0 means zero copy of the reference allele. 1 means one copy of the reference allele. 2 means two copies of the reference allele. 9 means missing data.

Here is an example of a genotypic matrix using the geno format with 3 individuals and 4 loci:

```
112
010
091
121
```

Author(s)

Eric Frichot

See Also

geno2lfmm lfmm2geno ancestrymap2geno ped2geno vcf2geno read.geno write.geno

geno2lfmm *Convert from* geno *to* lfmm *format*

Description

A function that converts from the geno format to the lfmm format.

Usage

```
geno2lfmm(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the geno format.
output.file	A character string containing a path to the output file, a genotypic matrix in the lfmm format. By default, the name of the output file is the same name as the input file with a .lfmm extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path to the output file, a genotypic matrix in the lfmm format.

Author(s)

Eric Frichot

See Also

lfmm.data geno ancestrymap2lfmm ancestrymap2geno ped2lfmm ped2geno vcf2geno lfmm2geno read.geno write.geno

Examples

```
# Creation of a file called "genotypes.geno" in the working directory
# with 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

# Conversion    from the geno format ("genotypes.geno")
#               to the lfmm format ("genotypes.lfmm").
# By default,   the name of the output file is the same name
#               as the input file with a .lfmm extension.
# Create file:  "genotypes.lfmm".
output = geno2lfmm("genotypes.geno")
```

```
# Conversion    from the geno format ("genotypes.geno")
#               to the lfmm format with the output file called "plop.lfmm".
# Create file:  "plop.lfmm".
output = geno2lfmm("genotypes.geno", "plop.lfmm")

# As force = false and the file "genotypes.lfmm" already exists,
# nothing happens.
output = geno2lfmm("genotypes.geno", force = FALSE)
```

`impute` *Impute missing genotypes using an snmf object*

Description

Impute missing genotypes in a genotype file (.lfmm) by using ancestry and genotype frequency estimates from an `snmf` run. The function generates a new `lfmm` file. See `lfmm` and `lfmm2`.

Usage

```
impute (object, input.file, method, K, run)
```

Arguments

`object`	An snmfProject object.
`input.file`	A path (character string) to an input file in lfmm format with missing genotypes. The same input data must be used when generating the snmf object.
`method`	A character string: "random" or "mode". With "random", imputation is performed by using the genotype probabilities. With "mode", the most likely genotype is used for matrix completion.
`K`	An integer value. The number of ancestral populations.
`run`	An integer value. A particular run used for imputation (usually the run number that minimizes the cross entropy criterion).

Value

`NULL`	The function writes the imputed genotypes in an output file having the "_imputed.lfmm" suffix.

Author(s)

Olivier Francois

References

Gain C, Francois O. (2021). LEA 3: Factor models in population genetics and ecological genomics with R. Molecular Ecology Resources, doi.org/10.1111/1755-0998.13366.

See Also

snmf lfmm lfmm2

Examples

```
### Example of analysis ###

data("tutorial")
# creation of a genotype file with missing genotypes
# The data contain 400 SNPs for 50 individuals.

dat = as.numeric(tutorial.R)
dat[sample(1:length(dat), 100)] <-  9
dat <- matrix(dat, nrow = 50, ncol = 400 )
write.lfmm(dat, "genotypes.lfmm")

################
# running snmf #
################

project.snmf = snmf("genotypes.lfmm", K = 4,
        entropy = TRUE, repetitions = 10,
        project = "new")

# select the run with the lowest cross-entropy value
best = which.min(cross.entropy(project.snmf, K = 4))

# Impute the missing genotypes
impute(project.snmf, "genotypes.lfmm", method = 'mode', K = 4, run = best)

# Compare with truth
# Proportion of correct imputation results:
mean( tutorial.R[dat == 9] == read.lfmm("genotypes.lfmm_imputed.lfmm")[dat == 9] )
```

---

lfmm *Fitting Latent Factor Mixed Models (MCMC algorithm)*

Description

Latent Factor Mixed Models (LFMMs) are factor regression models in which the response variable is a genotypic matrix, and the explanatory variables are environmental measures of ecological interest or trait values. The lfmm function estimates latent factors and effect sizes based on an MCMC algorithm. The resulting object can be used in the function lfmm.pvalues to identify genetic polymorphisms exhibiting association with ecological gradients or phenotypes, while correcting for unobserved confounders. An exact and computationally efficient least-squares method is implemented in the function lfmm2 which should be the prefered option.

Usage

```
lfmm(input.file, environment.file, K,
    project = "continue",
    d = 0, all = FALSE,
    missing.data = FALSE, CPU = 1,
    iterations = 10000, burnin = 5000,
    seed = -1, repetitions = 1,
    epsilon.noise = 1e-3, epsilon.b = 1000,
    random.init = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the lfmm{lfmm_format} format. The matrix must not contain missing values. See impute for completion based on nonnegative matrix factorization.
environment.file	A character string containing a path to the environmental file, an environmental data matrix in the env format.
K	An integer corresponding to the number of latent factors.
project	A character string among "continue", "new", and "force". If "continue", the results are stored in the current project. If "new", the current project is removed and a new project is created. If "force", the results are stored in the current project even if the input file has been modified since the creation of the project.
d	An integer corresponding to the fit of an lfmm model with the d-th variable only from environment.file. By default (if NULL and all are FALSE), lfmm fits each variable from environment.file sequentially and independently.
all	A Boolean option. If TRUE, lfmm fits all variables from the environment.file at the same time. This option is not compatible with the d option.
missing.data	A Boolean option. If TRUE, the input.file contains missing genotypes. Caution: lfmm requires imputed genotype matrices. See impute.
CPU	A number of CPUs to run the parallel version of the algorithm. By default, the number of CPUs is 1.
iterations	The total number of cycles for the Gibbs Sampling algorithm.
burnin	The burnin number of cycles for the Gibbs Sampling algorithm.
seed	A seed to initialize the random number generator. By default, the seed is randomly chosen. The seed is initialized in each run of the program. For modifying the default setting, provide one seed per run.
repetitions	A number of replicate runs for the Gibbs Sampler algorithm.
epsilon.noise	A prior parameter for variances.
epsilon.b	A prior parameter for the variance of correlation coefficients.
random.init	A Boolean option. If TRUE, the Gibbs Sampler is initiliazed randomly. Otherwise, it is initialized with zero values.

Value

`lfmm` returns an object of class `lfmmProject`.

The following methods can be applied to an object of class `lfmmProject`:

`show`	Display information about all analyses.
`summary`	Summarize analyses.
`z.scores`	Return the `lfmm` output vector of z.scores for some runs.
`lfmm.pvalues`	Return the vector of adjusted p-values for a combination of runs with K latent factors, and for the d-th predictor.

`load.lfmmProject(file = "character")`
: Load the file containing an lfmmProject objet and show the object.

`remove.lfmmProject(file = "character")`
: Erase a `lfmmProject` object. Caution: All the files associated with the object will be removed.

`export.lfmmProject(file.lfmmProject)`
: Create a zip file containing the full `lfmmProject` object. It allows users to move the project to a new directory or a new computer (using import). If you want to overwrite an existing export, use the option `force == TRUE`.

`import.lfmmProject(file.lfmmProject)`
: Import and load an `lfmmProject` object from a zip file (made with the export function) into the chosen directory. If you want to overwrite an existing project, use the option `force == TRUE`.

`combine.lfmmProject(file.lfmmProject, toCombine.lfmmProject)`
: Combine `to.Combine.lfmmProject` into `file.lfmmProject`. Caution: Only projects with runs coming from the same input file can be combined. If the same input file has different names in the two projects, use the option `force == TRUE`.

Author(s)

Eric Frichot Olivier Francois

References

Frichot E, Schoville SD, Bouchard G, Francois O. (2013). *Testing for associations between loci and environmental gradients using latent factor mixed models*. Molecular biology and evolution, 30(7), 1687-1699.

See Also

`lfmm.data` `z.scores` `lfmm.pvalues` `pca` `lfmm` tutorial

Examples

```
### Example of analysis using lfmm ###

data("tutorial")
# creation of a genotype file: genotypes.lfmm.
```

```
# The file contains 400 SNPs for 50 individuals.
write.lfmm(tutorial.R, "genotypes.lfmm")

# Creation of a phenotype/environment file: gradient.env.
# One environmental predictor for 40 individuals.
write.env(tutorial.C, "gradients.env")

#################
# running lfmm #
#################

# main options, K: (the number of latent factors),
#           CPU: the number of CPUs.

# Runs with K = 6 and 5 repetitions.
# runs with 6000 iterations
# including 3000 iterations for burnin.
# Around 30 seconds per run.
project = lfmm( "genotypes.lfmm",
                "gradients.env",
                 K = 6,
                 repetitions = 5,
                 project = "new")

# get adjusted p-values using all runs
pv = lfmm.pvalues(project, K = 6)

# Evaluate FDR and POWER (TPR)
for (alpha in c(.05,.1,.15,.2)) {
    # expected FDR
    print(paste("expected FDR:", alpha))
    L = length(pv$pvalues)
    # Benjamini-Hochberg's mehod for an expected FDR = alpha.
    w = which(sort(pv$pvalues) < alpha * (1:L)/L)
    candidates = order(pv$pvalues)[w]

    # estimated FDR and True Positive Rate
    # The targets SNPs are loci 351 to 400
    Lc = length(candidates)
    estimated.FDR = length(which(candidates <= 350))/Lc
    estimated.TPR = length(which(candidates > 350))/50
    print(paste("FDR:", estimated.FDR, "True Positive Rate:", estimated.TPR))
}

###################
# Post-treatments #
###################

# show the project
show(project)

# summary of the project
summary(project)
```

```
# get the z-scores for the 2nd run for K = 6
z = z.scores(project, K = 6, run = 2)

# get the p-values for K = 6 and run 2
p = lfmm.pvalues(project, K = 6, run = 2)

##########################
# Manage an lfmm project #
##########################

# All the runs of lfmm for a given file are
# automatically saved into an lfmm project directory and a file.
# The name of the lfmmProject file is the concatenation of
# the name of the input file and the environment file
# with a .lfmmProject extension ("genotypes_gradient.lfmmProject").
# The name of the lfmmProject directory is the same name as
# the lfmmProject file with a .lfmm extension ("genotypes_gradient.lfmm/")
# There is a unique lfmm Project for each input file.

# An lfmmProject can be loaded in an R session as follows
project = load.lfmmProject("genotypes_gradients.lfmmProject")

# An lfmmProject can be exported to be imported in another directory
# or in another computer as follows
export.lfmmProject("genotypes_gradients.lfmmProject")

dir.create("test", showWarnings = TRUE)
#import
newProject = import.lfmmProject("genotypes_gradients_lfmmProject.zip", "test")

# combine projects
combinedProject <- combine.lfmmProject(
                  "genotypes_gradients.lfmmProject",
                  "test/genotypes_gradients.lfmmProject"
                  )

# remove
remove.lfmmProject("test/genotypes_gradients.lfmmProject")



# An lfmmProject can be removed as follows.
# Caution: All the files associated with the project will be removed.
remove.lfmmProject("genotypes_gradients.lfmmProject")
```

---

lfmm.data *Input file for* lfmm

Description

Description of the lfmm format. The lfmm format can be used as an input format for genotypic matrices in the functions snmf, lfmm, lfmm2, and pca.

Details

The lfmm format has one row for each individual. Each row contains one value at each loci (separated by spaces or tabulations) corresponding to the number of alleles. The number of alleles corresponds to the number of reference alleles or the number of derived alleles. Missing genotypes are encoded by the value -9 or the value 9.

For the use of functions lfmm and lfmm2 missing genotypes must be removed or imputed with the function impute.

Here is an example of a genotypic matrix using the lfmm format with 3 individuals and 4 loci:

```
1 0 0 1
1 1 9 2
2 0 1 1
```

Author(s)

Eric Frichot

See Also

lfmm lfmm2 geno2lfmm lfmm2geno ancestrymap2lfmm ped2lfmm read.lfmm write.lfmm

---

lfmm.pvalues *P-values from lfmm runs*

Description

Returns a vector of p-values computed from a combination of lfmm runs. For an example, see lfmm.

Usage

```
lfmm.pvalues (object, genomic.control, lambda, K, d, all, run)
```

Arguments

object	An lfmmProject object.
genomic.control	A Boolean value. If TRUE, the p-values are automatically calibrated using genomic control. If FALSE, the p-values are calculated by rescaling the chi-squared test statistics using the lambda parameter.

lambda	A numeric value. The lambda value is used as inflation factor to rescale the chi-squared statistics in the computation of p-values. This option requires that genomic.control = FALSE. The default value of lambda is equal to 1.0 (no rescaling).
K	An integer value. The number of latent factors used in the model.
d	An integer value. Computes the p-values for the d-th covariable in the model.
all	A Boolean value. Each variable is considered separately (Obscure parameter).
run	An integer vector representing a list of runs to be combined in the computation of p-values (by default, all runs).

Value

pvalues	A vector of combined p-values for each locus.
GIF	The inflation factor value used for correcting the test statistics.

Author(s)

Eric Frichot Olivier Francois

See Also

lfmm.data lfmm

Examples

```
### Example of analyses using lfmm ###

data("tutorial")
# creation of a genotype file, "genotypes.lfmm".
# The data contain 400 SNPs for 50 individuals.
write.lfmm(tutorial.R, "genotypes.lfmm")
# creation of an environmental variable file, "gradient.env".
# The data contain one environmental variable measured for 50 individuals.
write.env(tutorial.C, "gradients.env")

################
# lfmm runs    #
################

# main options, K: (the number of latent factors),
#           CPU: the number of CPUs.

# runs with K = 3 and 2 repetitions.
# around 15 seconds per run.
project = NULL
project = lfmm("genotypes.lfmm", "gradients.env", K = 3, repetitions = 2,
    iterations = 6000, burnin = 3000, project = "new")

# get adjusted p-values using the genomic control method
p = lfmm.pvalues(project, K = 3)
```

```
hist(p$pvalues, col = "yellow3")

# get adjusted p-values using lambda = 0.6
p = lfmm.pvalues(project, genomic.control = FALSE,
    lambda = 0.6, K = 3)

hist(p$pvalues, col = "yellow3")
```

---

lfmm2 *Fitting Latent Factor Mixed Models (Least squares algorithm)*

Description

Latent Factor Mixed Models (LFMMs) are factor regression models in which the response variable is a genotypic matrix, and the explanatory variables are environmental measures of ecological interest or trait values. The `lfmm2` function estimates latent factors based on an exact least-squares approach. The resulting object can be used by the function `lfmm2.test` to identify genetic polymorphisms exhibiting association with ecological gradients or phenotypes, while correcting for unobserved confounders. An MCMC estimation algorithm is implemented in the function `lfmm`, but this version should be prefered.

Usage

```
lfmm2 (input, env, K, lambda)
```

Arguments

`input`	A genotypic matrix or a character string containing a path to the input file. The genotypic matrix must be in the `lfmm{lfmm_format}` format without missing values (9 or `NA`). See `impute` for completion based on nonnegative matrix factorization and consider R packages for reading large matrices.
`env`	A matrix of environmental covariates or a character string containing a path to the environmental file. The environment matrix must be in the `env` format without missing values. Response variables must be encoded as `numeric`.
`K`	An integer corresponding to the number of latent factors.
`lambda`	A positive numeric value for a ridge regularization parameter. The default value is set to 1e-5.

Value

`lfmm2` returns an object of class `lfmm2Class` that contains K estimated latent factors `@U` and their loadings `@V`.

The following method can be applied to an object of class `lfmm2Class`:

`lfmm2.test`	P-values adjusted for latent factors computed by lfmm2.

Author(s)

Olivier Francois

References

Caye K, Jumentier B, Lepeule J, Francois O. (2019). LFMM 2: fast and accurate inference of gene-environment associations in genome-wide studies. Molecular biology and evolution, 36(4), 852-860.

Gain C, Francois O. (2021). LEA 3: Factor models in population genetics and ecological genomics with R. Molecular Ecology Resources. doi: 10.1111/1755-0998.13366

See Also

lfmm.data impute lfmm2.test pca lfmm tutorial

Examples

```
### Example of analysis using lfmm2 ###


# Simulation with 10 target loci, with effect sizes ranging between -10 an 10
# n = 100 individuals and L = 1000 loci

X <- as.matrix(rnorm(100)) # causal environmental variable
B <- rep(0, 1000)
target <- sample(1:1000, 10) # target loci
B[target] <- runif(10, -10, +10) # effect sizes

# Creating hidden factors and loadings

U <- t(tcrossprod(as.matrix(c(-1,0.5,1.5)), X))+ matrix(rnorm(300), ncol = 3)
V <- matrix(rnorm(3000), ncol = 3)

# Simulating a binarized matrix containing haploid genotypes
# Simulation performed with the generative LFMM

Y <- tcrossprod(as.matrix(X), B) + tcrossprod(U, V) + matrix(rnorm(100000, sd = .5), nrow = 100)
Y <- matrix(as.numeric(Y > 0), ncol = 1000)

#####################################
# Fitting an LFMM with K = 3 factors #
#####################################

mod2 <- lfmm2(input = Y, env = X, K = 3)

# Computing P-values and plotting their minus log10 values
# Target loci are highlighted

pv <- lfmm2.test(object = mod2, input = Y, env = X, linear = TRUE)
plot(-log10(pv$pvalues), col = "grey", cex = .4, pch = 19)
points(target, -log10(pv$pvalues[target]), col = "red")
```

lfmm2.test *P-values adjusted for latent factors computed by* lfmm2.

Description

The function returns a vector of p-values for association between loci and environmental variables adjusted for latent factors computed by lfmm2. It takes an object of class lfmm2Class with the data that were used to adjust the LFMM.

Usage

```
lfmm2.test (object, input, env, genomic.control, linear, family)
```

Arguments

object	An object of class lfmm2Class.
input	A genotypic matrix or a character string containing a path to the input file. The genotypic matrix must be in the lfmm{lfmm_format} format without missing values (9 or NA). See impute for completion based on nonnegative matrix factorization and consider R packages for reading large matrices.
env	A matrix of environmental covariates or a character string containing a path to the environmental file. The environment matrix must be in the env format without missing values. Variables must be encoded as numeric.
genomic.control	A logical value. If TRUE, the p-values are recalibrated by using genomic control after correction for confounding.
linear	A logical value indicating whether linear or generalized linear models should be used to perform the association tests. If FALSE, family should be provided in the next argument.
family	a family for generalized linear models used in the association tests. The default is binomial(link = "logit")), which requires that y is between 0 and 1.

Value

pvalues	A matrix of p-values for each locus and each environmental variable.
zscores	A matrix of z-scores for each locus and each environmental variable.
gif	A vector of genomic inflation factors computed for each environmental variable.

Author(s)

Olivier Francois

References

Caye K, Jumentier B, Lepeule J, Francois O. (2019). LFMM 2: fast and accurate inference of gene-environment associations in genome-wide studies. Molecular biology and evolution, 36(4), 852-860.

See Also

lfmm.data lfmm2

Examples

```
### Example of analysis using lfmm2 ###

# Simulation with 10 target loci, with effect sizes ranging between -10 an 10
# n = 100 individuals and L = 1000 loci

X <- as.matrix(rnorm(100)) # environmental variable
B <- rep(0, 1000)
target <- sample(1:1000, 10) # target loci
B[target] <- runif(10, -10, +10) # effect sizes

# Creating hidden factors and loadings

U <- t(tcrossprod(as.matrix(c(-1,0.5,1.5)), X)) + matrix(rnorm(300), ncol = 3)
V <- matrix(rnorm(3000), ncol = 3)

# Simulating a binarized matrix containing haploid genotypes
# Simulation performed with the generative LFMM

Y <- tcrossprod(as.matrix(X), B) + tcrossprod(U, V) + matrix(rnorm(100000, sd = .5), nrow = 100)
Y <- matrix(as.numeric(Y > 0), ncol = 1000)

######################################
# Fitting an LFMM with K = 3 factors #
######################################

mod2 <- lfmm2(input = Y, env = X, K = 3)

# Computing P-values and plotting their minus log10 values
# Target loci are highlighted

pv <- lfmm2.test(object = mod2, input = Y, env = X, linear = TRUE)
plot(-log10(pv$pvalues), col = "grey", cex = .4, pch = 19)
points(target, -log10(pv$pvalues[target]), col = "red")
```

---

lfmm2geno *Convert from* lfmm *to* geno *format*

Description

A function that converts from the lfmm format to the geno format.

Usage

```
lfmm2geno(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the lfmm format.
output.file	A character string containing a path to the output file, a genotypic matrix in the geno format. By default, the name of the output file is the same name of the input file with a .geno extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

lfmm.data geno ancestrymap2lfmm ancestrymap2geno geno2lfmm ped2lfmm ped2geno vcf2geno

Examples

```
# Creation of a file called "genotypes.lfmm" in the working directory,
# with 400 SNPs for 50 individuals.
data("tutorial")
write.lfmm(tutorial.R, "genotypes.lfmm")

# Conversion    from the lfmm format ("genotypes.lfmm")
#               to the geno format ("genotypes.geno").
# By default,   the name of the output file is the same name
#               as the input file with a .geno extension.
# Create file:  "genotypes.geno".
output = lfmm2geno("genotypes.lfmm")

# Conversion    from the lfmm format ("genotypes.lfmm")
#               to the geno format with the output file called "plop.geno".
# Create file:  "plop.geno".
output = lfmm2geno("genotypes.lfmm", "plop.geno")

# As force = false and the file "genotypes.geno" already exists,
```

```
# nothing happens.
output = lfmm2geno("genotypes.lfmm", force = FALSE)
```

---

pca *Principal Component Analysis*

Description

The pca function performs a principal component analysis of a genotypic matrix encoded in one of the following formats: lfmm, geno, ancestrymap, ped or vcf. The pca function computes eigenvalues, eigenvectors, and standard deviations for all principal components and the projections of individuals on each component. Thepca function returns an object of class "pcaProject" containing the output data and the input parameters.

Usage

```
pca (input.file, K, center = TRUE, scale = FALSE)
```

Arguments

input.file	A character string containg the path to the genotype input file, a genotypic matrix in the lfmm format.
K	An integer corresponding to the number of principal components calculated. By default, all principal components are calculated.
center	A boolean option. If TRUE, the data matrix is centered (default: TRUE).
scale	A boolean option. If TRUE, the data matrix is centered and scaled (default: FALSE).

Value

pca returns an object of class pcaProject containing the following components:

eigenvalues	The vector of eigenvalues.
eigenvectors	The matrix of eigenvectors (one column for each eigenvector).
sdev	The vector of standard deviations.
projections	The matrix of projections (one column for each projection).

The following methods can be applied to the object of class pcaProject returned by pca:

plot	Plot the eigenvalues.
show	Display information on analysis.
summary	Summarize analysis.
tracy.widom	Perform Tracy-Widom tests for eigenvalues.
load.pcaProject(file.pcaProject)	Load the file containing a pcaProject object and return the pcaProject object.

`remove.pcaProject(file.pcaProject)`
: Erase a `pcaProject` object. Caution: All the files associated with the `pcaProject` object will be removed except the genotype file.

`export.pcaProject(file.pcaProject)`
: Create a zip file containing the full `pcaProject` object. It allows users to move the project to a new directory or a new computer (using import). If you want to overwrite an existing export, use the option `force == TRUE`.

`import.pcaProject(file.pcaProject)`
: Import and load an `pcaProject` object from a zip file (made with the export function) into the chosen directory. If you want to overwrite an existing project, use the option `force == TRUE`.

Author(s)

Eric Frichot

See Also

`lfmm.data` `snmf` `lfmm` `lfmm2` `tutorial`

Examples

```
# Create a genotype file "genotypes.lfmm"
# with 1000 SNPs for 165 individuals.
data("tutorial")
write.lfmm(tutorial.R,"genotypes.lfmm")

#################
# Perform PCA   #
#################

# run PCA
# Available options: K (the number of PCs),
#                    center and scale.
# Creation of  genotypes.pcaProject - the pcaProject object.
#               a directory genotypes.pca containing:
#  genotypes.eigenvalues - eigenvalues,
#  genotypes.eigenvectors - eigenvectors,
#  genotypes.sdev - standard deviations,
#  genotypes.projections - projections,

# Create a pcaProject object: pc.
pc <- pca("genotypes.lfmm", scale = TRUE)

######################
# Display information #
######################

# Display information on analysis.
show(pc)
```

```
# Summarize analysis.
summary(pc)

#####################
# Graphical outputs #
#####################

par(mfrow=c(2,2))

# Plot eigenvalues.
plot(pc, lwd=5, col="blue", cex = .7, xlab=("Factors"), ylab="Eigenvalues")

# PC1-PC2 plot.
plot(pc$projections)
# PC3-PC4 plot.
plot(pc$projections[,3:4])

# Plot standard deviations.
plot(pc$sdev)

############################
# Perform Tracy-Widom tests #
############################

# Perfom Tracy-Widom tests for all eigenvalues.
# Create file: genotypes.tracyWidom - tracy-widom test information,
#          in the directory genotypes.pca/.
tw <- tracy.widom(pc)

# Plot the percentage of variance explained by each component.
plot(tw$percentage)

# Show p-values for the Tracy-Widom tests.
tw$pvalues

#########################
# Manage a pca project   #
#########################

# All the project files for a given input matrix are
# automatically saved into a pca project directory.
# The name of the pcaProject file is the same name as
# the name of the input file with a .pcaProject extension
# ("genotypes.pcaProject").
# The name of the pcaProject directory is the same name as
# the name of the input file with .pca extension ("genotypes.pca/")
# There is only one pca Project for each input file including all the runs.

# An pcaProject can be load in a different session.
project = load.pcaProject("genotypes.pcaProject")

# An pcaProject can be exported to be imported in another directory
# or in another computer
```

```
export.pcaProject("genotypes.pcaProject")

dir.create("test", showWarnings = TRUE)
#import
newProject = import.pcaProject("genotypes_pcaProject.zip", "test")
# remove
remove.pcaProject("test/genotypes.pcaProject")


# A pcaProject can be erased.
# Caution: All the files associated with the project will be removed.
remove.pcaProject("genotypes.pcaProject")
```

---

ped ped *format description*

Description

Description of the ped format. The ped format can be used as an input format for genotypic matrices in the functions `snmf`, `lfmm`, and `pca`.

Details

The ped format has one row for each individual. Each row contains 6 columns of information for each individual, plus two genotype columns for each SNP. Each column must be separated by spaces or tabulations. The genotype format must be either 0ACGT or 01234, where 0 means missing genotype. The first 6 columns of the genotype file are: the 1st column is the family ID, the 2nd column is the sample ID, the 3rd and 4th columns are the sample IDs of parents, the 5th column is the gender (male is 1, female is 2), the 6th column is the case/control status (1 is control, 2 is case), the quantitative trait value or the population group label.

The ped format is described here.

Here is an example with 3 individuals and 4 SNPs:

```
1    SAMPLE0 0 0 2 2 1 2 3 3 1 1 2 1
2    SAMPLE1 0 0 1 2 2 1 1 3 0 4 1 1
3    SAMPLE2 0 0 2 1 2 2 3 3 1 4 1 2
```

Author(s)

Eric Frichot

See Also

`ped2lfmm` `ped2geno` `geno` `lfmm.data` `ancestrymap` `vcf`

ped2geno *Convert from ped to geno format*

Description

A function that converts from the ped format to the geno format.

Usage

```
ped2geno(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the ped format.
output.file	A character string containing a path to the output file, a genotypic matrix in the geno format. By default, the name of the output file is the same name as the input file with a .geno extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

ped geno ancestrymap2lfmm ancestrymap2geno geno2lfmm ped2lfmm vcf2geno lfmm2geno

Examples

```
# Creation of a file called "example.ped"
# with 4 SNPs for 3 individuals.
data("example_ped")
write.table(example_ped,"example.ped",
    col.names = FALSE, row.names = FALSE, quote = FALSE)

# Conversion    from the ped format ("example.ped")
#               to the geno format ("example.geno").
# By default,   the name of the output file is the same name
#               as the input file with a .geno extension.
# Create file:  "example.geno".
output = ped2geno("example.ped")
```

```
# Conversion    from the ped format ("example.ped")
#               to the geno format with the output file called "plop.geno".
# Create file:  "plop.geno".
output = ped2geno("example.ped", "plop.geno")

# As force = false and the file "example.geno" already exists,
# nothing happens.
output = ped2geno("example.ped", force = FALSE)
```

---

ped2lfmm *Convert from* ped *to* lfmm *format*

Description

A function that converts from the ped format to the lfmm format.

Usage

```
ped2lfmm(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the ped format.
output.file	A character string containing a path for the output file, a genotypic matricx in the lfmm format. By default, the name of the output file is the same name as the input file with a .lfmm extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path for the output file, a genotypic matricx in the lfmm format.

Author(s)

Eric Frichot

See Also

ped lfmm.data ancestrymap2lfmm ancestrymap2geno geno2lfmm ped2geno vcf2geno lfmm2geno

Examples

```
# Creation of a file called "example.ped"
# with 4 SNPs for 3 individuals.
data("example_ped")
write.table(example_ped,"example.ped",
    col.names = FALSE, row.names = FALSE, quote = FALSE)

# Conversion    from the ped format ("example.ped")
#               to the lfmm format ("example.lfmm").
# By default,   the name of the output file is the same name
#               as the input file with a .lfmm extension.
# Create file:  "example.lfmm".
output = ped2lfmm("example.ped")

# Conversion    from the ped format ("example.ped")
#               to the geno format with the output file called "plop.lfmm".
# Create file:  "plop.lfmm".
output = ped2lfmm("example.ped", "plop.lfmm")

# As force = false and the file "example.lfmm" already exists,
# nothing happens.
output = ped2lfmm("example.ped", force = FALSE)
```

Q *Admixture coefficients from a snmf run*

Description

Return the `snmf` output matrix of admixture coefficients for the chosen run with K ancestral populations. For an example, see `snmf`.

Usage

```
Q(object, K, run)
```

Arguments

`object`	A snmfProject object.
`K`	The number of ancestral populations.
`run`	A chosen run.

Value

`res`	A matrix containing the admixture coefficients for the chosen run with K ancestral populations.

Author(s)

Eric Frichot

See Also

geno snmf G cross.entropy

Examples

```
### Example of analysis using snmf ###

# Creation of the genotype file: genotypes.geno.
# The data contain 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

#################
# running snmf #
#################

project.snmf <- snmf("genotypes.geno",
                K = 3,
                repetitions = 2,
                project = "new")

# get the ancestry coefficients for the 2nd run for K = 3.
Q.3 <- Q( project.snmf, K = 3, run = 2)

# cluster assignment for each individual
cluster <- apply( Q.3, 1, which.max)
table(cluster)
```

---

read.env *Read environmental file in the* env*format*

Description

Read a file in the env format.

Usage

```
read.env(input.file)
```

Arguments

input.file	A character string containing a path to the input file, an environmental data matrix in the env format.

Value

R	A matrix containing the environmental variables with one line for each individual and one column for each environmental variable.

Author(s)

Eric Frichot

See Also

env write.env lfmm

Examples

```
# Creation of an environmental matrix, C
# containing 2 environmental variables for 3 individuals.
# C contains one line for each individual and one column for each variable.
C = matrix(runif(6), ncol=2, nrow=3)

# Write C in a file called "example.env".
# Create file:    "example.env".
write.env(C,"example.env")

# Read the file "example.env".
C = read.env("example.env")
```

---

read.geno *read a file in the geno format*

Description

Read a file in the geno format.

Usage

```
read.geno(input.file)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the geno format.

Value

R	A matrix containing the genotypes with one line for each individual and one column for each SNP.

Author(s)

Eric Frichot

See Also

write.geno geno snmf geno2lfmm lfmm2geno ancestrymap2geno ped2geno vcf2geno

Examples

```
# tutorial contains a matrix of genotypes R with 1000 SNPs for 165 individuals.
# and a matrix with an environmental variable C.
data("tutorial")

# Write R in a file called "genotypes.geno".
# Create file:    "genotypes.geno".
write.geno(tutorial.R,"genotypes.geno")

# Read the file "genotypes.geno".
R = read.geno("genotypes.geno")
```

`read.lfmm` *Read files in the* `lfmm` *format*

Description

Read a file in the `lfmm` format.

Usage

```
read.lfmm(input.file)
```

Arguments

`input.file`	A character string containing a path to the input file, a genotypic matrix in the `lfmm` format.

Value

`R`	A matrix containing the genotypes with one line per individual and one column per SNP.

Author(s)

Eric Frichot

See Also

`write.lfmm` `lfmm.data` `lfmm` `geno2lfmm` `lfmm2geno` `ancestrymap2lfmm` `ped2lfmm`

Examples

```
# tutorial contains a matrix of genotypes R with 1000 SNPs for 165 individuals.
# and a matrix with an environmental variable C.
data("tutorial")

# write R in a file called "genotypes.lfmm"
# Create file:    "genotypes.lfmm".
```

```
write.lfmm(tutorial.R,"genotypes.lfmm")

# read the file "genotypes.lfmm".
R = read.lfmm("genotypes.lfmm")
```

`read.zscore` *Read the output files of* `lfmm`

Description

Read the output file from `lfmm`. This is an internal function. Zscores of a run can be accessed using the function `z.scores`.

Usage

```
read.zscore(input.file)
```

Arguments

`input.file`	a character string containing a path to the output of `lfmm`.

Value

`R`	A matrix containing the `lfmm` results with one line per SNP. The first column is the zscore. The second column is the -log10(p-value). The third column is the p-value.

Author(s)

Eric Frichot

See Also

`zscore.format` `lfmm`

Examples

```
### Example of analyses using lfmm ###

data("tutorial")
# creation of the genotype file, genotypes.lfmm.
# It contains 400 SNPs for 50 individuals.
write.lfmm(tutorial.R, "genotypes.lfmm")
# creation of the environment file, gradient.env.
# It contains 1 environmental variable for 40 individuals.
write.env(tutorial.C, "gradients.env")

#################
# runs of lfmm #
```

```
################

# main options, K: (the number of latent factors),
#           CPU: the number of CPUs.

# Toy runs with K = 3 and 2 repetitions.
# around 15 seconds per run.
project = NULL
project = lfmm("genotypes.lfmm", "gradients.env", K = 3,
        iterations = 6000, burnin = 3000, project = "new")

res = read.zscore("./genotypes_gradients.lfmm/K3/run1/genotypes_r1_s1.3.zscore")
```

---

snmf *Estimates individual ancestry coefficients and ancestral allele frequencies.*

Description

snmf estimates admixture coefficients using sparse Non-Negative Matrix Factorization algorithms, and provides STRUCTURE-like outputs.

Usage

```
snmf (input.file, K,
    project = "continue",
    repetitions = 1, CPU = 1,
    alpha = 10, tolerance = 0.00001, entropy = FALSE, percentage = 0.05,
    I, iterations = 200, ploidy = 2, seed = -1, Q.input.file)
```

Arguments

input.file	A character string containing a the path to the input file, a genotypic matrix in the geno format.
K	An integer vector corresponding to the number of ancestral populations for which the snmf algorithm estimates have to be calculated.
project	A character string among "continue", "new", and "force". If "continue", the results are stored in the current project. If "new", the current project is removed and a new one is created to store the result. If "force", the results are stored in the current project even if the input file has been modified since the creation of the project.
repetitions	An integer corresponding with the number of repetitions for each value of K.
CPU	A number of CPUs to run the parallel version of the algorithm. By default, the number of CPUs is 1.
alpha	A numeric value corresponding to the snmf regularization parameter. The results can depend on the value of this parameter, especially for small data sets.

tolerance	A numeric value for the tolerance error.
entropy	A boolean value. If true, the cross-entropy criterion is calculated (see create.dataset and cross.entropy.estimation).
percentage	A numeric value between 0 and 1 containing the percentage of masked genotypes when computing the cross-entropy criterion. This option applies only if entropy == TRUE (see cross.entropy).
I	The number of SNPs to initialize the algorithm. It starts the algorithm with a run of snmf using a subset of nb.SNPs random SNPs. If this option is set with nb.SNPs, the number of randomly chosen SNPs is the minimum between 10000 and 10 % of all SNPs. This option can considerably speeds up snmf estimation for very large data sets.
iterations	An integer for the maximum number of iterations in algorithm.
ploidy	1 if haploid, 2 if diploid, n if n-ploid.
seed	A seed to initialize the random number generator. By default, the seed is randomly chosen.
Q.input.file	A character string containing a path to an initialization file for Q, the individual admixture coefficient matrix.

Value

snmf returns an object of class snmfProject.

The following methods can be applied to the object of class snmfProject:

plot	Plot the minimal cross-entropy in function of K.
show	Display information about the analyses.
summary	Summarize the analyses.
Q	Return the admixture coefficient matrix for the chosen run with K ancestral populations.
G	Return the ancestral allele frequency matrix for the chosen run with K ancestral populations.
cross.entropy	Return the cross-entropy criterion for the chosen runs with K ancestral populations.
snmf.pvalues	Return the vector of adjusted p-values for a run with K ancestral populations.
impute	Return a geno or lfmm file with missing data imputation.
barchart	Return a bar plot representation of the Q matrix from a run with K ancestral populations .
load.snmfProject(file.snmfProject)	Load the file containing an snmfProject objet and return the snmfProject object.
remove.snmfProject(file.snmfProject)	Erase a snmfProject object. Caution: All the files associated with the object will be removed.
export.snmfProject(file.snmfProject)	Create a zip file containing the full snmfProject object. It allows to move the project to a new directory or a new computer (using import). If you want to overwrite an existing export, use the option force == TRUE.

`import.snmfProject(file.snmfProject)`
: Import and load an `snmfProject` object from a zip file (made with the export function) into the chosen directory. If you want to overwrite an existing project, use the option `force == TRUE`.

`combine.snmfProject(file.snmfProject, toCombine.snmfProject)`
: Combine `to.Combine.snmfProject` into `file.snmfProject`. Caution: Only projects with runs coming from the same input file can be combined. If the same input file has different names in the two projects, use the option `force == TRUE`.

Author(s)

Eric Frichot

References

Frichot E, Mathieu F, Trouillon T, Bouchard G, Francois O. (2014). *Fast and Efficient Estimation of Individual Ancestry Coefficients*. Genetics, 194(4): 973–983.

See Also

`geno` `pca` `lfmm` `Q` `barchart` `tutorial`

Examples

```
### Example of analysis using snmf ###

# Creation of the genotype file: genotypes.geno.
# The data contain 400 SNPs for 50 individuals.
data("tutorial")
write.geno(tutorial.R, "genotypes.geno")

################
# running snmf #
################

project.snmf = snmf("genotypes.geno",
                K = 1:10,
                entropy = TRUE,
                repetitions = 10,
                project = "new")

# plot cross-entropy criterion of all runs of the project
plot(project.snmf, cex = 1.2, col = "lightblue", pch = 19)

# get the cross-entropy of the 10 runs for K = 4
ce = cross.entropy(project.snmf, K = 4)

# select the run with the lowest cross-entropy for K = 4
best = which.min(ce)

# display the Q-matrix
```

```
my.colors <- c("tomato", "lightblue",
               "olivedrab", "gold")

barchart(project.snmf, K = 4, run = best,
        border = NA, space = 0, col = my.colors,
        xlab = "Individuals", ylab = "Ancestry proportions",
        main = "Ancestry matrix") -> bp

axis(1, at = 1:length(bp$order),
    labels = bp$order, las = 3, cex.axis = .4)

###################
# Post-treatments #
###################

# show the project
show(project.snmf)

# summary of the project
summary(project.snmf)

# get the cross-entropy for all runs for K = 4
ce = cross.entropy(project.snmf, K = 4)

# get the cross-entropy for the 2nd run for K = 4
ce = cross.entropy(project.snmf, K = 4, run = 2)

# get the ancestral genotype frequency matrix, G, for the 2nd run for K = 4.
freq = G(project.snmf, K = 4, run = 2)

############################
# Advanced snmf run options #
############################


# Q.input.file: init a run with a given ancestry coefficient matrix Q.
# Here it is initialized with the Q matrix from the first run with K=4
project.snmf = snmf("genotypes.geno", K = 4,
    Q.input.file = "./genotypes.snmf/K4/run1/genotypes_r1.4.Q")

# I: init the Q matrix of a run from a smaller run with 100 randomly chosen
# SNPs.
project.snmf = snmf("genotypes.geno", K = 4, I = 100)

# CPU: run snmf with 2 CPUs.
project.snmf = snmf("genotypes.geno", K = 4, CPU = 2)

# percentage: run snmf and calculate the cross-entropy criterion with 10% of
# masked genotypes, instead of 5% of masked genotypes.
project.snmf = snmf("genotypes.geno", K = 4, entropy = TRUE, percentage = 0.1)

# seed: choose the seed for the random generator.
project.snmf = snmf("genotypes.geno", K = 4, seed = 42)
```

```
# alpha: choose the regularization parameter.
project.snmf = snmf("genotypes.geno", K = 4, alpha = 100)

# tolerance: choose the tolerance parameter.
project.snmf = snmf("genotypes.geno", K = 4, tolerance = 0.0001)


##########################
# Manage an snmf project #
##########################

# All the runs of snmf for a given file are
# automatically saved into an snmf project directory and a file.
# The name of the snmfProject file is the same name as
# the name of the input file with a .snmfProject extension
# ("genotypes.snmfProject").
# The name of the snmfProject directory is the same name as
# the name of the input file with a .snmf extension ("genotypes.snmf/")
# There is only one snmf Project for each input file including all the runs.

# An snmfProject can be load in a different session.
project.snmf = load.snmfProject("genotypes.snmfProject")

# An snmfProject can be exported to be imported in another directory
# or in another computer
export.snmfProject("genotypes.snmfProject")

dir.create("test", showWarnings = TRUE)
#import
newProject = import.snmfProject("genotypes_snmfProject.zip", "test")
# combine projects
combinedProject = combine.snmfProject("genotypes.snmfProject", "test/genotypes.snmfProject")
# remove
remove.snmfProject("test/genotypes.snmfProject")


# An snmfProject can be erased.
# Caution: All the files associated with the project will be removed.
remove.snmfProject("genotypes.snmfProject")
```

`snmf.pvalues` *P-values for snmf population differentiation tests*

Description

Returns a vector of p-values computed from an `snmf` run.

Usage

```
snmf.pvalues (object, genomic.control, lambda, ploidy, entropy, fisher, K, run)
```

Arguments

`object`	An snmfProject object.
`genomic.control`	A Boolean value. If `TRUE`, the p-values are automatically calibrated using genomic control. If `FALSE`, the p-values are calculated by rescaling the chi-squared test statistics using the `lambda` parameter.
`lambda`	A numeric value. The lambda value is used as an inflation factor to rescale the chi-squared statistics in the computation of p-values. This option requires that `genomic.control = FALSE`. The default value of `lambda` is equal to 1.0 (no rescaling).
`ploidy`	An integer value among 1 or 2. Tests are implemented for haploids and diploids (to be extended to polypoids).
`entropy`	A Boolean value. If `TRUE`, the run of minimum entropy is used for computing the p-values.
`fisher`	A Boolean value. If `TRUE`, F-distributions are used to test the null-hypothesis, Chi-squared otherwise.
`K`	An integer value. The number of genetic clusters.
`run`	An integer for the run number used the computation of p-values (by default, the minimum entropy run).

Value

`p.values`	A vector of p-values for each locus for the population differentiation test.
`GIF`	The inflation factor value used in the test.

Author(s)

Olivier Francois

References

Martins, H., Caye, K., Luu, K., Blum, M. G. B., Francois, O. (2016). Identifying outlier loci in admixed and in continuous populations using ancestral population differentiation statistics. Molecular Ecology, 25(20), 5029-5042.

See Also

`snmf`

Examples

```
### Example of analyses using snmf ###

data("tutorial")
# creation of a genotype file, "genotypes.lfmm".
# The data contain 400 SNPs for 50 individuals.
write.geno(tutorial.R, "genotypes.geno")


################
# snmf runs    #
################

# main options, K: the number of ancestral populations,
#        entropy: cross-entropy criterion,
#        CPU: the number of CPUs.

project.snmf = snmf("genotypes.geno",
                    K = 4,
                    entropy = TRUE,
                    ploidy = 2,
                    repetitions = 10,
                    project = "new")

# genome scan using adjusted p-values (genomic control method)

p = snmf.pvalues(project.snmf, entropy = TRUE, ploidy = 2, K = 4)
p$GIF

par(mfrow = c(2,1))
hist(p$pvalues, col = "orange")

plot(-log10(p$pvalues), pch = 19, col = "blue", cex = .7)
```

`struct2geno` *Conversion from the STRUCTURE format to the geno format.*

Description

The function converts a multiallelic genotype file in the STRUCTURE format into a file in the 'geno' for `snmf` and the 'lfmm' format for `lfmm`.

Usage

```
struct2geno (input.file, ploidy, FORMAT, extra.row, extra.column)
```

Arguments

input.file	A character string. A path to a STRUCTURE or a TESS input file of multiallelic markers (eg, microsatellites) for haploid or diploid individuals. Missing data must be encoded as "-9" or as any negative value. Individual genotypes are encoded using either one or two rows of data.
ploidy	An integer value (1 or 2). Value 2 for diploids and 1 for haploids.
FORMAT	An integer value equal to 1 for markers encoded using one row of data for each individual, and 2 for markers encoded using two rows of data for each individual.
extra.row	An integer value indicating the number of extra rows in the header of the input file (eg, marker ids).
extra.column	an integer value indicating the number of extra columns in the input file. Extra columns can include individual ids, pop ids, geographic coordinates, etc.

Value

NULL. Output files in the 'geno' and the 'lfmm' format record individual genotypes for each allele at each marker.

Author(s)

Olivier Francois

See Also

lfmm.data geno lfmm snmf

Examples

```
### Example of conversion from a STRUCTURE format ###
### Artificial data with 10 diploid individuals and 10 STR markers
### FORMAT = 1
### Input file: 'dat.str'

dat.str  <- matrix(sample(c(101:105,-9),
                  200, prob = c(rep(1,5), 0.1),
                  replace = TRUE),
                  nrow = 10, ncol = 20)
write.table(dat.str,
            file = "dat.str",
            col.names = FALSE,
            row.names = FALSE,
            quote = FALSE)

### Conversion
struct2geno("dat.str", ploidy = 2, FORMAT = 1)

### snmf run and barplot
s  <- snmf("dat.str.geno", K = 2, project = "new")
barchart(s, K = 2, run = 1, xlab = "Individuals")
```

`tracy.widom` *Tracy-Widom test for eigenvalues*

Description

Perform tracy-widom tests on a set of eigenvalues to determine the number of significative eigenvalues and calculate the percentage of variance explained by each principal component. For an example, see `pca`.

Usage

```
tracy.widom (object)
```

Arguments

`object`	a pcaProject object.

Value

`tracy.widom` returns a list containing the following components:

`eigenvalues`	The sorted input vector of eigenvalues (by descreasing order).
`twstats`	The vector of tracy-widom statistics.
`pvalues`	The vector of p-values associated with each eigenvalue.
`effecn`	The vector of effective sizes.
`percentage`	The vector containing the percentage of variance explained by each principal component.

Author(s)

Eric Frichot

References

Tracy CA and Widom H. (1994). *Level spacing distributions and the bessel kernel*. Commun Math Phys. 161 :289–309. Patterson N, Price AL and Reich D. (2006). *Population structure and eigenanalysis*. PLoS Genet. 2 :20.

See Also

`pca` `lfmm.data` `lfmm`

Examples

```
# Creation of the genotype file "genotypes.lfmm"
# with 1000 SNPs for 165 individuals.
data("tutorial")
write.lfmm(tutorial.R,"genotypes.lfmm")

#################
# Perform a PCA #
#################

# run of PCA
# Available     options, K (the number of PCs calculated),
#               center and scale.
# Creation of   genotypes.pcaProject - the pcaProject object.
#               a directory genotypes.pca containing:
# Create files: genotypes.eigenvalues - eigenvalues,
#               genotypes.eigenvectors - eigenvectors,
#               genotypes.sdev - standard deviations,
#               genotypes.projections - projections,
# Create a pcaProject object: pc.
pc = pca("genotypes.lfmm", scale = TRUE)

############################
# Perform Tracy-Widom tests #
############################

# Perfom Tracy-Widom tests on all eigenvalues.
# Create file:  genotypes.tracyWidom - tracy-widom test information,
#               in the directory genotypes.pca/.
tw = tracy.widom(pc)

# Plot the percentage of variance explained by each component.
plot(tw$percentage)

# Display the p-values for the Tracy-Widom tests.
tw$pvalues

# remove pca Project
remove.pcaProject("genotypes.pcaProject")
```

`tutorial` *Example tutorial data sets*

Description

This dataset is composed of a genotypic matrix stored tutorial.R with 50 individuals genotyped for 400 SNPs. The last 50 SNPs are correlated with an environmental variable (tutorial.C). This dataset is a subset of the data shown in the computer note associated with the package (Frichot and Francois 2015).

Usage

```
tutorial
```

Value

`tutorial.R`	A genotypic matrix for 50 individuals genotyped at 400 SNPs. The last 50 SNPs are correlated with an environmental variable stored in tutorial.C.
`tutorial.C`	An environmental variable for 50 invdividuals.

`vcf` `vcf` *format description*

Description

Description of the `vcf` format. The `vcf` format can be used as an input format for genotypic matrices in the functions `snmf`, `lfmm`, and `pca`.

Details

The vcf format is described here.

Here is an example of a genotypic matrix using the vcf format with 3 individuals and 4 loci:

```
##fileformat=VCFv4.1
##FORMAT=<ID=GM,Number=1,Type=Integer,Description="Genotype meta">
##INFO=<ID=VM,Number=1,Type=Integer,Description="Variant meta">
##INFO=<ID=SM,Number=1,Type=Integer,Description="SampleVariant meta">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT SAMPLE0 SAMPLE1 SAMPLE2
1 1001 rs0000 T C 999 . VM=1;SM=100 GT:GM 1/0:1 0/1:2 1/1:3
1 1002 rs1111 G A 999 . VM=2;SM=101 GT:GM 0/0:6 0/1:7 0/0:8
1 1003 notres G AA 999 . VM=3;SM=102 GT:GM 0/0:11 ./.:12 0/1:13
1 1004 rs2222 G A 999 . VM=3;SM=102 GT:GM 0/0:11 . 1/0:13
1 1003 notres GA A 999 . VM=3;SM=102 GT:GM 0/0:11 ./.:12 0/1:13
1 1005 rs3333 G A 999 . VM=3;SM=102 GT:GM 1/0:11 1/1:12 0/1:13
```

Author(s)

Eric Frichot

See Also

`vcf2geno` `vcf2lfmm` `geno` `lfmm` `ped` `ancestrymap`

vcf2geno *Convert from vcf to geno format*

Description

A function that converts from the vcf format to the geno format. Note: This function may be obsolete. Conversion in accepted format such as ped can be obtained with the program vcftools.

Usage

```
vcf2geno(input.file, output.file = NULL, force = TRUE)
```

Arguments

input.file	A character string containing a path to the input file, a genotypic matrix in the vcf format.
output.file	A character string containing a path to the output file, a genotypic matrix in the geno format. By default, the name of the output file is the same name as the input file with a .geno extension.
force	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

output.file	A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

vcf geno ancestrymap2lfmm ancestrymap2geno ped2lfmm ped2geno lfmm2geno geno2lfmm

Examples

```
# Creation of a file called "example.vcf"
# with 4 SNPs for 3 individuals.
data("example_vcf")
write.table(example_vcf,"example.vcf",col.names =
    c("#CHROM", "POS", "ID", "REF", "ALT", "QUAL", "FILTER", "INFO",
    "FORMAT", "SAMPLE0", "SAMPLE1", "SAMPLE2"),
    row.names = FALSE, quote = FALSE)

# Conversion    from the vcf format ("example.vcf")
#               to the geno format ("example.geno").
# By default,   the name of the output file is the same name
```

```
#               as the input file with a .geno extension.
# Create files: "example.geno",
#               "example.vcfsnp" - SNP informations,
#               "example.removed" - removed lines.
output = vcf2geno("example.vcf")

# Conversion    from the vcf format ("example.vcf")
#               to the geno format with the output file called "plop.geno".
# Create files: "plop.geno",
#               "plop.vcfsnp" - SNP informations,
#               "plop.removed" - removed lines.
output = vcf2geno("example.vcf", "plop.geno")

# As force = false and the file "example.geno" already exists,
# nothing happens.
output = vcf2geno("example.vcf", force = FALSE)
```

`vcf2lfmm` *Convert from* `vcf` *to* `lfmm` *format*

Description

A function that converts from the `vcf` format to the `lfmm` format. Note: This function may be obsolete. Conversion in accepted format such as ped can be obtained with the program `vcftools`.

Usage

```
vcf2lfmm(input.file, output.file = NULL, force = TRUE)
```

Arguments

`input.file`	A character string containing a path to the input file, a genotypic matrix in the `vcf` format.
`output.file`	A character string containing a path to the output file, a genotypic matrix in the `lfmm` format. By default, the name of the output file is the same name as the input file with a .lfmm extension.
`force`	A boolean option. If FALSE, the input file is converted only if the output file does not exist. If TRUE, convert the file anyway.

Value

`output.file`	A character string containing a path to the output file, a genotypic matrix in the `lfmm` format.

Author(s)

Eric Frichot

See Also

vcf lfmm.data ancestrymap2lfmm ancestrymap2geno ped2lfmm ped2geno vcf2geno

Examples

```
# Creation of a file called "example.vcf"
# with 4 SNPs for 3 individuals.
data("example_vcf")
write.table(example_vcf,"example.vcf",col.names =
    c("#CHROM", "POS", "ID", "REF", "ALT", "QUAL", "FILTER", "INFO",
    "FORMAT", "SAMPLE0", "SAMPLE1", "SAMPLE2"),
    row.names = FALSE, quote = FALSE)

# Conversion    from the vcf format ("example.vcf")
#               to the lfmm format ("example.lfmm").
# By default,   the name of the output file is the same name
#               as the input file with a .lfmm extension.
# Create files: "example.lfmm",
#               "example.vcfsnp" - SNP informations,
#               "example.removed" - removed lines.
output = vcf2lfmm("example.vcf")

# Conversion    from the vcf format ("example.vcf")
#               to the lfmm format with the output file called "plop.lfmm".
# Create files: "plop.lfmm",
#               "plop.vcfsnp" - SNP informations,
#               "plop.removed" - removed lines.
output = vcf2lfmm("example.vcf", "plop.lfmm")

# As force = false and the file "example.lfmm" already exists,
# nothing happens.
output = vcf2lfmm("example.vcf", force = FALSE)
```

---

write.env *Write files in the env format*

Description

Write a file in the env format.

Usage

```
write.env(R, output.file)
```

Arguments

R	A matrix containing the environmental variables with one line for each individual and one column for each environmental variable. The missing genotypes have to be encoded with the value 9.

output.file A character string containing a path to the output file, an environmental data matrix in the env formt.

Value

output.file A character string containing a path to the output file, an environmental data matrix in the env formt.

Author(s)

Eric Frichot

See Also

read.env env lfmm

Examples

```
# Creation of an environmental matrix C
# containing 2 environmental variables for 3 individuals.
# C contains one line for each individual and one column for each variable.
C = matrix(runif(6), ncol=2, nrow=3)

# Write C in a file called "tuto.env".
# Create file:    "tuto.env".
write.env(C,"tuto.env")

# Read the file "tuto.env".
C = read.env("tuto.env")
```

---

write.geno *Write files in the geno format*

Description

Write a file in the geno format.

Usage

```
write.geno(R, output.file)
```

Arguments

R A matrix containing the genotypes with one line for each individual and one column for each SNP. The missing genotypes have to be encoded with the value 9.

output.file A character string containing a path to the output file, a genotypic matrix in the geno format.

Value

output.file — A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

read.geno geno snmf geno2lfmm lfmm2geno ancestrymap2geno ped2geno vcf2geno

Examples

```
# Creation of a file called "genotypes.geno" in the working directory,
# with 1000 SNPs for 165 individuals.
data("tutorial")

# Write R in a file called "genotypes.geno".
# Create file:    "genotypes.geno".
write.geno(tutorial.R,"genotypes.geno")

# Read the file "genotypes.geno".
R = read.geno("genotypes.geno")
```

---

write.lfmm *Write files in the lfmm format*

Description

Write a file in the lfmm format.

Usage

```
write.lfmm(R, output.file)
```

Arguments

R — A matrix containing the genotypes with one line for each individual and one column for each SNP. The missing genotypes have to be encoded with the value 9.

output.file — A character string containing a path to the output file, a genotypic matrix in the lfmm format.

Value

output.file — A character string containing a path to the output file, a genotypic matrix in the geno format.

Author(s)

Eric Frichot

See Also

read.lfmm lfmm.data lfmm geno2lfmm lfmm2geno ancestrymap2lfmm ped2lfmm

Examples

```
# Creation of a file called "genotypes.geno" in the working directory,
# with 1000 SNPs for 165 individuals.
data("tutorial")

# write R in a file called "genotypes.lfmm"
# Create file:    "genotypes.lfmm".
write.lfmm(tutorial.R,"genotypes.lfmm")

# read the file "genotypes.lfmm".
R = read.lfmm("genotypes.lfmm")
```

---

z.scores *z-scores from a lfmm run*

Description

Return the lfmm output matrix of zscores for the chosen runs with K latent factors, the d-th variable and the all option. For an example, see lfmm.

Usage

```
z.scores (object, K, d, all, run)
```

Arguments

object	A lfmmProject object.
K	The number of latent factors.
d	The d-th variable.
all	A Boolean option. If true, the run with all variables at the same time. If false, the runs with each variable separately.
run	A list of chosen runs.

Value

res	A matrix containing a vector of z-scores for the chosen runs per column.

Author(s)

Eric Frichot

See Also

lfmm lfmm.data

Examples

```
### Example of analyses using lfmm ###

data("tutorial")
# creation of the genotype file, genotypes.lfmm.
# It contains 400 SNPs for 50 individuals.
write.lfmm(tutorial.R, "genotypes.lfmm")
# creation of the environment file, gradient.env.
# It contains 1 environmental variable for 40 individuals.
write.env(tutorial.C, "gradients.env")

#################
# runs of lfmm #
#################

# main options, K: (the number of latent factors),
#           CPU: the number of CPUs.

# Toy runs with K = 3 and 2 repetitions.
# around 15 seconds per run.
project = NULL
project = lfmm("genotypes.lfmm", "gradients.env", K = 3, repetitions = 2,
    iterations = 6000, burnin = 3000, project = "new")

# get the z-scores for all runs for K = 3
z = z.scores(project, K = 3)

# get the z-scores for the 2nd run for K =3
z = z.scores(project, K = 3, run = 2)

# remove
remove.lfmmProject("genotypes_gradients.lfmmProject")
```

---

zscore.format *Output file format for* lfmm

Description

Description of the zscore output format of lfmm.

Details

The zscore format has one row for each SNP. Each row contains three values: The first value is the zscore, the second value is the -log10(pvalue), the third value is the p-value (separated by spaces or tabulations).

Author(s)

Eric Frichot

See Also

lfmm lfmm.data env

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