

Package ‘TransMeta’

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Type Package
Title A novel random effect model for GWAS trans-ethnic meta-analysis
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Description A kernel regression based random effect model for testing single variant association in GWAS trans-ethnic meta-analysis.
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TransMeta-package	<i>A novel random effect model for GWAS trans-ethnic meta-analysis</i>
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Description

This package implements the kernel machine based random effect model for testing single variant association in trans-ethnic meta-analysis

Details

Package: TransMeta
Type: Package
Version: 0.2
Date: 2015-4-29
License: GPL (>= 2)

This package implements the kernel machine based random effect model for single variant test in GWAS trans-ethnic Meta-analysis. In order to get p-value of the association test, the user should provide the effect-size estimates, standard error estimates and kernel matrix K in the Get_TransMeta function.

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F_ST

K matrix of the genetic similarity kernel structure for 9 ancestry groups from HMP3 data.

Description

The kernel matrix K of the genetic similarity kernel structure for the 9 ancestry groups from HMP3 data. The 9 ancestry groups are (in the following order): CEU - Utah residents with Northern and Western European ancestry from the CEPH collection; CHD - Chinese in Metropolitan Denver, Colorado; GIH - Gujarati Indians in Houston, Texas; JPT_CHB - Japanese in Tokyo, Japan & Han Chinese in Beijing, China; LWK - Luhya in Webuye, Kenya; MXL - Mexican ancestry in Los Angeles, California; MKK - Maasai in Kinyawa, Kenya; TSI - Toscani in Italia; YRI - Yoruba in Ibadan, Nigeria.

Usage

```
data(F_ST)
```

Details

A 9×9 kernel matrix of the genetic similarity kernel structure for the 9 ancestry groups from HMP3 data. The (i,j)-th entry value in the matrix is obtained as a function of the pair-wise F_{st} value between the i-th ancestry group and the j-th ancestry group. Order of the 9 ancestry groups is arranged as follows: CEU, CHD, GIH, JPT+CHB, LWK, MEX, MKK, TSI, YRI.

Source

The pair-wise F_{st} values are obtained from Table S6 in:

<http://hapmap.ncbi.nlm.nih.gov/downloads/presentations/nature09298-s1.pdf>

Examples

```
data(F_ST)
```

get_K_Fst

Construct the genetic similarity kernel matrix K

Description

Construct the genetic similarity kernel matrix K for testing the single variant association in trans-ethnic meta-analysis.

Usage

```
get_K_Fst (FileName)
```

Arguments

FileName	A vector of characters that list the file names of summary statistics for each GWAS and the file name of a data file that identifies each study's corresponding ancestry group.
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Details

Please refer to the Vignettes PDF manual for details of the FileName argument.

Value

Returns the genetic similarity kernel matrix K for testing the single variant association in trans-ethnic meta-analysis. For example, the returned matrix can be used for the argument K in the Get_TransMeta function.

get_K_indep

Construct the group-wise independent kernel matrix K

Description

Construct the group-wise independent kernel matrix K for testing the single variant association in trans-ethnic meta-analysis.

Usage

```
get_K_indep (FileName)
```

Arguments

FileName	A vector of characters that list the file names of summary statistics for each GWAS and the file name of a data file that identifies each study's corresponding ancestry group.
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Details

Please refer to the Vignettes PDF manual for details of the FileName argument.

Value

Returns the group-wise independent kernel matrix K for testing the single variant association in trans-ethnic meta-analysis. For example, the returned matrix can be used for the argument K in the Get_TransMeta function.

Examples

```
## Please refer to the example in the Vignettes PDF manual
```

Get_TransMeta	<i>Single variant association test in the GWAS trans-ethnic meta-analysis</i>
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Description

Implementation of the kernel regression based random effect model for the single variant association test in the GWAS trans-ethnic meta-analysis

Usage

```
Get_TransMeta(FileName, type = "effect size", K.type = "Fst", K = NULL,
r.all = c(0, 0.09, 0.25, 1), method = "liu")
```

Arguments

FileName	A vector of characters that list the file names of summary statistics for each GWAS and the file name of a data file that identifies each study's corresponding ancestry group. Please refer to the Vignettes PDF manual for its details.
type	The default value is "effect size", which specifies that the input summary statistics are effect size based; otherwise, the Z-score based summary statistics will be used.
K.type	The default value is "Fst", which specifies that the K matrix is of the genetic similarity kernel structure; otherwise, the K matrix would take the group-independent kernel structure.
K	A square matrix for the kernel matrix K , for example, K can be constructed based on the HapMap3 data using the get_K_Fst function. If the user does not provide a matrix for this argument, then the K matrix will be constructed based on the input data (to estimate F.st) with its specified structure from the K.type argument.
r.all	A vector of possible values of ρ to be used, default = c(0, 0.09, 0.25, 1).
method	A method to compute the p-value (default= 'liu'). 'davies' represents an exact method that computes the p-value by inverting the characteristic function of the mixture chisq; 'liu' represents an approximation method that matches the first 3 moments; 'liu.mod' represents modified 'liu' method that matches kurtosis instead of skewness to improve tail probability approximation.

Value

SNP	The SNP id for each variant
Pval	p-value from TransMeta for the association test
Pval_rho	p-value of the score test for each ρ in the 'r.all' argument
Opt_rho	the optimal ρ in the 'r.all' argument which results in smallest p-value for the score test

Examples

```
## Please refer to the example in the Vignettes PDF manual
```

G_ind	<i>K matrix of the group-wise independent kernel structure for the 9 ancestry groups from HMP3 data.</i>
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Description

K matrix of the group-wise independent kernel structure for the 9 ancestry groups from HMP3 data. The 9 ancestry groups are (in the following order): CEU - Utah residents with Northern and Western European ancestry from the CEPH collection; CHD - Chinese in Metropolitan Denver, Colorado; GIH - Gujarati Indians in Houston, Texas; JPT_CHB - Japanese in Tokyo, Japan & Han Chinese in Beijing, China; LWK - Luhya in Webuye, Kenya; MXL - Mexican ancestry in Los Angeles, California; MKK - Maasai in Kinyawa, Kenya; TSI - Toscani in Italia; YRI - Yoruba in Ibadan, Nigeria.

Usage

```
data(G_ind)
```

Details

A 9×9 diagonal matrix. The entries correspond to the order of the 9 ancestry groups as listed above.

Examples

```
data(G_ind)
```