

Package ‘ldblock’

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Title data structures for linkage disequilibrium measures in populations

Version 1.0.0

Author VJ Carey <stvjc@channing.harvard.edu>

Description Define data structures for linkage disequilibrium measures in populations.

Suggests RUnit, BiocGenerics, knitr

Imports Matrix, snpStats

Depends R (>= 3.1), methods

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

BiocViews genetics, SNP, GWAS

VignetteBuilder knitr

NeedsCompilation no

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ldblock-package *data structures for linkage disequilibrium measures in populations*

Description

Define data structures for linkage disequilibrium measures in populations.

Details

The DESCRIPTION file:

```
Package:          ldblock
Title:           data structures for linkage disequilibrium measures in populations
Version:         1.0.0
Author:          VJ Carey <stvjc@channing.harvard.edu>
Description:     Define data structures for linkage disequilibrium measures in populations.
Suggests:       RUnit, BiocGenerics, knitr
Imports:         Matrix, snpStats
Depends:         R (>= 3.1), methods
Maintainer:     VJ Carey <stvjc@channing.harvard.edu>
License:         Artistic-2.0
LazyLoad:       yes
BiocViews:      genetics, SNP, GWAS
VignetteBuilder: knitr
```

Index of help topics:

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downloadPopByChr  download hapmap resource with LD estimates
expandSnpSet      Given a set of SNP identifiers, use LD to
                  expand the set to include linked loci
hmlD              import hapmap LD data and create a structure
                  for its management
ldblock-package  data structures for linkage disequilibrium
                  measures in populations
ldstruct-class   Class "'ldstruct'"
```

Author(s)

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 Maintainer: VJ Carey <stvjc@channing.harvard.edu>

Examples

```
# see vignette
```

downloadPopByChr	<i>download hapmap resource with LD estimates</i>
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Description

download hapmap resource with LD estimates

Usage

```
downloadPopByChr(chrname = "chr1",  
  popname = "CEU",  
  urlTemplate = "http://hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/ld_%%CHRN%%_%%P",  
  targfolder = Sys.getenv("LDBLOCK_TXTGZ_DIR"))
```

Arguments

chrname	UCSC format tag for chromosome
popname	hapmap three letter code for population, e.g. 'CEU'
urlTemplate	pattern for creating URL given chr and pop
targfolder	destination

Details

delivers HapMap LD data to 'targfolder'

Value

just run for side effect of download.file

Examples

```
## Not run:  
  downloadPopByChr()  
  
## End(Not run)
```

expandSnpSet	<i>Given a set of SNP identifiers, use LD to expand the set to include linked loci</i>
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Description

Given a set of SNP identifiers, use LD to expand the set to include linked loci

Usage

```
expandSnpSet(rs1, lb = 0.8, ldstruct, chrn = "chr17", popn = "CEU",
  txtgzfn = dir(system.file("hapmap", package = "ldblock"), full.names = TRUE))
```

Arguments

rs1	input list – SNPs not found in the LD structure are simply returned along with those found, and the expansion list, all combined in a vector
lb	lower bound on statistic used to retrieve loci in LD
ldstruct	instance of <code>ldstruct-class</code>
chrn	chromosome identifier
popn	population identifier (one of 'CEU', 'MEX', ...)
txtgzfn	path to gzipped hapmap file with LD information

Details

direct use of elementwise arithmetic comparison

Value

character vector

Note

As of 2015, it appears that locus names are more informative than addresses for determining SNP identity across resources.

Examples

```
og = Sys.getenv("LDBLOCK_TXTGZ_DIR")
on.exit( Sys.setenv("LDBLOCK_TXTGZ_DIR" = og ) )
Sys.setenv("LDBLOCK_TXTGZ_DIR"=system.file("hapmap", package="ldblock"))
ld17 = hmlD(chr="chr17", pop="CEU")
ee = expandSnpSet( ld17@allrs[1:10], ldstruct = ld17 )
```

hmlD	<i>import hapmap LD data and create a structure for its management</i>
------	--

Description

import hapmap LD data and create a structure for its management

Usage

```
hmlD(hmgztxt, poptag, chrom, genome = "hg19", stat = "Dprime")
```

Arguments

hmgztxt	name of gzipped text file as distributed at hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/ . It will be processed by read.delim .
poptag	heuristic tag identifying population
chrom	heuristic tag for chromosome name
genome	genome tag
stat	statistic to use, "Dprime", "R2", and "LOD" are options

Details

generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position

Value

instance of ldstruct class

Examples

```
getClass("ldstruct")
# see vignette
```

ldstruct-class	<i>Class "ldstruct"</i>
----------------	-------------------------

Description

Manage information about LD statistics as reported by HapMap.

Objects from the Class

Objects can be created by calls of the form `new("ldstruct", ...)`.

Slots

ldmat: Object of class "dsCMatrix" sparse representation of statistics
chrom: Object of class "character" chromosome tag in UCSC format
genome: Object of class "character" genome tag
allpos: Object of class "numeric" coordinates
poptag: Object of class "character" hapmap founder population tag, 'CEU', 'MEX' etc.
statInUse: Object of class "character" code for statistic retrieved, one of 'Dprime', 'LOD', 'R2'
allrs: Object of class "character" all SNP identifiers, sometimes in affy format

Methods

ldmat signature(x = "ldstruct"): extract sparse matrix

Examples

```
showClass("ldstruct")
```

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