Package 'ldblock'

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Title data structures for linkage disequilibrium measures in populations

Version 1.14.3

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

Description Define data structures for linkage disequilibrium measures in populations.

Suggests RUnit, BiocGenerics, knitr, gQTLstats

Imports Matrix, snpStats, VariantAnnotation, GenomeInfoDb, Rsamtools, GO.db, GenomicFiles (>= 1.13.6), BiocGenerics (>= 0.25.1), EnsDb.Hsapiens.v75, ensembldb, httr

Depends R (>= 3.1), methods, Homo.sapiens

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

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LazyLoad yes

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`ldblock-package` *c("\Sexpr[results=rd,stage=build]tools:::Rd_package_title(\"#1\")", "ldblock")data structures for linkage disequilibrium measures in populations*

Description

c("\Sexpr[results=rd,stage=build]tools:::Rd_package_description(\"#1\")", "ldblock")Define data structures for linkage disequilibrium measures in populations.

Details

The DESCRIPTION file: c("\Sexpr[results=rd,stage=build]tools:::Rd_package_DESCRIPTION(\"#1\")", "ldblock")This package was not yet installed at build time.\cr c("\Sexpr[results=rd,stage=build]tools:::Rd_package_indic "ldblock") Index: This package was not yet installed at build time.\cr

Author(s)

c("\Sexpr[results=rd,stage=build]tools:::Rd_package_author(\"#1\")", "ldblock")VJ Carey <stvjc@channing.harvard.edu

Maintainer: c("\Sexpr[results=rd,stage=build]tools:::Rd_package_maintainer(\"#1\")", "ldblock")VJ Carey <stvjc@channing.harvard.edu>

Examples

```
# see vignette
```

`downloadPopByChr` *download hapmap resource with LD estimates*

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

Description

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

Usage

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

Arguments

`rsl`	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 `ldstruct-class`
`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` *import hapmap LD data and create a structure for its management; generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position*

Description

import hapmap LD data and create a structure for its management; generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position

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

Value

instance of ldstruct class

Examples

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

ldByGene *Obtain LD statistics in region specified by a gene model.*

Description

Obtain LD statistics in region specified by a gene model.

Usage

```
ldByGene(sym = "MMP24", vcf = system.file("vcf/c20exch.vcf.gz", package
  = "gQTLstats"), flank = 1000, vcfSLS = "NCBI", genomeSLS = "hg19",
  stats = "D.prime", depth = 10)
```

Arguments

sym	A standard gene symbol
vcf	Path to a tabix-indexed VCF file
flank	number of basepairs to flank gene model for search
vcfSLS	seqlevelsStyle (SLS) token for VCF; will be imposed on gene model
genomeSLS	character tag for genome, to be used with readVcf
stats	passed to ld
depth	passed to ld

Value

sparse matrix representation of selected LD statistic, as returned by ld

Note

Uses an internal function genemod4ldblock, that relies on EnsDb.Hsapiens.v75 to get gene model. Default VCF comes from gQTLstats

Examples

```
ld1 = ldByGene(depth=150)
image(ld1[1:200,1:200], col.reg=heat.colors(120), colorkey=TRUE,
 main="SNPs in MMP24 (chr20)")
```

ldmat *use LDmat API from NCI LDlink service*

Description

use LDmat API from NCI LDlink service

Usage

```
ldmat(rsvec, pop = "CEU", type = "d",
  token = Sys.getenv("LDLINK_TOKEN"))
```

Arguments

rsvec	character vector of SNP ids
pop	three letter code for HapMap population, defaults to CEU
type	'r2' or 'd', defaults to 'd' implying d-prime
token	the API token provided by NCI, defaults to value of environment variable LDLINK_TOKEN

Value

data.frame

Examples

```
if (interactive()) ldmat(c("rs77749396","rs9303279","rs9303280","rs9303281"))
```

ldmat,ldstruct-method *accessor for matrix component*

Description

accessor for matrix component

Usage

```
## S4 method for signature 'ldstruct'
ldmat(x)
```

Arguments

x	instance of ldstruct

ldstruct-class *Class* "ldstruct"

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",...)`.

Examples

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

s3_1kg *Create a URL referencing 1000 genomes content in AWS S3.*

Description

stack1kg produces a VcfStack instance with references to VCF for 1000 genomes autosomal chrs. S3-resident VCF files with version "v5a.20130502" are used.

Usage

```
s3_1kg(chrnum, tag = "20130502", wrap = function(x) TabixFile(x),
  tmpl = NULL, dropchr = TRUE)
```

Arguments

chrnum	a character string denoting a chromosome, such as '22'
tag	a character string identifying the version, ignored if tmpl is non-null; valid tag values are the default or "20101123"
wrap	The URL is returned after evaluating wrap on it; default is useful when Tabix indexing is to be used
tmpl	alternate template for full URL, useful if versions prior to 2010 are of interest
dropchr	if TRUE chrnum will have 'chr' removed if present

Value

by default, a TabixFile instance

Examples

```
s3_1kg("22")
## Not run:
 require(VariantAnnotation)
 scanVcfHeader(s3_1kg("22"))

## End(Not run)
```

stack1kg *couple together a group of VCFs*

Description

couple together a group of VCFs

Usage

```
stack1kg(chrs = as.character(1:22), index = FALSE, useEBI = TRUE)
```

Arguments

chrs	a vector of chromosome names for extraction from 1000 genomes VCF collection
index	logical telling whether VcfStack should attempt to create the local index; for 1000 genomes, the tbi are in the cloud and will be used by readVcf so FALSE is appropriate
useEBI	logical(1) defaults to TRUE ... use tabix-indexed vcf from EBI

Value

VcfStack instance

Note

The seqinfo component of returned stack will have NA for genome. Please set it manually; for useEBI=TRUE this would be GRCh38.

Examples

```
if (interactive()) {
  st1 = stack1kg()
  st1
  }
```

Index