

Package ‘ldblock’

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Title data structures for linkage disequilibrium measures in populations

Version 1.16.0

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Description Define data structures for linkage disequilibrium measures in populations.

Suggests RUnit, knitr, BiocStyle, gwascat

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

Depends R (>= 3.5), methods

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LazyLoad yes

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

```
{ Package: \tab ldblock\cr Title: \tab data structures for linkage disequilibrium measures in populations\cr Version: \tab 1.16.0\cr Author: \tab VJ Carey <stvjc@channing.harvard.edu>\cr Description: \tab Define data structures for linkage disequilibrium measures in populations.\cr Suggests: \tab RUnit, knitr, BiocStyle, gwascat\cr Imports: \tab Matrix, snpStats, VariantAnnotation, GenomeInfoDb, httr, BiocGenerics, ensemblDb, EnsDb.Hsapiens.v75, Rsamtools, GenomicFiles (>= 1.13.6), BiocGenerics (>= 0.25.1)\cr Depends: \tab R (>= 3.5), methods\cr Maintainer: \tab VJ Carey <stvjc@channing.harvard.edu>\cr License: \tab Artistic-2.0\cr LazyLoad: \tab yes\cr BiocViews: \tab genetics, SNP, GWAS, LinkageDisequilibrium\cr VignetteBuilder: \tab knitr\cr RoxygenNote: \tab 6.1.1\cr Encoding: \tab UTF-8\cr git_url: \tab https://git.bioconductor.org/packages/ldblock\cr git_branch: \tab RELEASE_3_10\cr git_last_commit: \tab 1a9e941\cr git_last_commit_date: \tab 2019-10-29\cr Date/Publication: \tab 2019-10-29\cr }
```

`c("\Sexpr[results=rd,stage=build]tools:::Rd_package_indices("#1\"),"ldblock")` Index of help topics: `\preformatted{ 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; generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position ldByGene Obtain LD statistics in region specified by a gene model. ldblock-package c("\Sexpr[results=rd,stage=build]tools:::Rd_package_title("#1\"),"ldblock")data structures for linkage disequilibrium measures in populations ldmat use LDmat API from NCI LDlink service ldmat,ldstruct-method accessor for matrix component ldstruct-class Class "ldstruct" s3_1kg Create a URL referencing 1000 genomes content in AWS S3. stack1kg couple together a group of VCFs }`

Author(s)

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Maintainer: `c("\Sexpr[results=rd,stage=build]tools:::Rd_package_maintainer("#1\"),"ldblock")` 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%%",
  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>
--------------	--

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; generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position</i>
------	--

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 for use with genemodel
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.

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	<i>Class "ldstruct"</i>
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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	<i>Create a URL referencing 1000 genomes content in AWS S3.</i>
--------	---

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),
      tmp1 = NULL, dropchr = TRUE)
```

Arguments

<code>chrnum</code>	a character string denoting a chromosome, such as '22'
<code>tag</code>	a character string identifying the version, ignored if <code>tmp1</code> is non-null; valid tag values are the default or "20101123"
<code>wrap</code>	The URL is returned after evaluating <code>wrap</code> on it; default is useful when Tabix indexing is to be used
<code>tmp1</code>	alternate template for full URL, useful if versions prior to 2010 are of interest
<code>dropchr</code>	if TRUE <code>chrnum</code> 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	<i>couple together a group of VCFs</i>
----------	--

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  
}
```


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