

Package ‘ldblock’

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Title data structures for linkage disequilibrium measures in populations

Version 1.8.1

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

Description Define data structures for linkage disequilibrium measures in populations.

Suggests RUnit, BiocGenerics, knitr

Imports Matrix, snpStats, erma, VariantAnnotation, GenomeInfoDb, Rsamtools, GO.db, GenomicFiles (>= 1.13.6)

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

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

License Artistic-2.0

LazyLoad yes

BiocViews genetics, SNP, GWAS, LinkageDisequilibrium

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:

```

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Author:       VJ Carey <stvjc@channing.harvard.edu>
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Suggests:    RUnit, BiocGenerics, knitr
Imports:      Matrix, snpStats, erma, VariantAnnotation, GenomeInfoDb, Rsamtools, GO.db, GenomicFiles (>= 1.1)
Depends:      R (>= 3.1), methods, Homo.sapiens
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License:      Artistic-2.0
LazyLoad:    yes
BiocViews:    genetics, SNP, GWAS, LinkageDisequilibrium
VignetteBuilder: knitr
  
```

Index of help topics:

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
ldByGene	obtain LD statistics in region specified by a gene model
ldblock-package	data structures for linkage disequilibrium measures in populations
ldstruct-class	Class "'ldstruct'"
s3_1kg	Create a URL referencing 1000 genomes content in AWS S3

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

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Examples

```
# see vignette
```

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

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

import hapmap LD data and create a structure for its management

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
```

 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](#)

Examples

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

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")
```

s3_1kg

Create a URL referencing 1000 genomes content in AWS S3

Description

Create a URL referencing 1000 genomes content in AWS S3.

Usage

```
s3_1kg(chrnum, tag = "20130502", wrap = function(x) TabixFile(x), tmp1 = NULL, dropchr = TRUE)
stack1kg(chrs=as.character(1:22), index=FALSE)
```

Arguments

chrnum	a character string denoting a chromosome, such as '22'
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
tag	a character string identifying the version, ignored if tmp1 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
tmp1	alternate template for full URL, useful if versions prior to 2010 are of interest
dropchr	if TRUE chrnum will have 'chr' removed if present

Details

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

Value

by default, a [TabixFile](#) instance

Examples

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

## End(Not run)
```

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