

# Package ‘ldblock’

July 29, 2021

**Title** data structures for linkage disequilibrium measures in populations

**Version** 1.22.1

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

**Description** Define data structures for linkage disequilibrium measures in populations.

**Suggests** RUnit,  
knitr,  
BiocStyle,  
gwascats,  
rmarkdown

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

**Depends** R (>= 3.5), methods

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

**License** Artistic-2.0

**LazyLoad** yes

**LazyData** yes

**BiocViews** genetics, SNP, GWAS, LinkageDisequilibrium

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/ldblock>

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 6c98ba3

**git\_last\_commit\_date** 2021-07-28

**Date/Publication** 2021-07-29

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ldblock-package	<i>c("\Sexpr[results=rd,stage=build]tools:::Rd_package_title(\`#\1\`)", "ldblock")data structures for linkage disequilibrium measures in populations</i>
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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 1.22.1\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, gwascats, rmarkdown\cr Imports: \tab Matrix, snpStats, VariantAnnotation, GenomeInfoDb, httr, 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 LazyData: \tab yes\cr BiocViews: \tab genetics, SNP, GWAS, LinkageDisequilibrium\cr VignetteBuilder: \tab knitr\cr RoxygenNote: \tab 7.1.1\cr Encoding: \tab UTF-8\cr git_url: \tab https://git.bioconductor.org/packages/\cr git_branch: \tab RELEASE_3_13\cr git_last_commit: \tab 6c98ba3\cr git_last_commit_date: \tab 2021-07-28\cr Date/Publication: \tab 2021-07-29\cr }
```

`c("\Sexpr[results=rd,stage=build]tools:::Rd_package_indices(\`#\1\`)", "ldblock")` Index of help topics: `\preformatted{ EUR_singletons singletons from EUR download-PopByChr 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`

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ulation and relationship information for 1000 genomes stack1kg couple together a group of VCFs
}
```

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	<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)
```

---

EUR_singletons	<i>singletons from EUR</i>
----------------	----------------------------

---

**Description**

singletons from EUR

**Usage**

```
EUR_singletons
```

**Format**

character vector

**Source**

[ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/working/20130606\\_sample\\_info/20130606\\_sample\\_info.xlsx](ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/working/20130606_sample_info/20130606_sample_info.xlsx), to which superpopulation codes were added

---

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(
  rsl,
  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 <a href="http://hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/">hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/</a> . It will be processed by <a href="#">read.delim</a> .
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	<i>Obtain LD statistics in region specified by a gene model.</i>
----------	--

---

**Description**

Obtain LD statistics in region specified by a gene model.

**Usage**

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

**Arguments**

sym	A standard gene symbol for use with <a href="#">genemodel</a>
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 <a href="#">readVcf</a>
stats	passed to <a href="#">ld</a>
depth	passed to <a href="#">ld</a>

**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**

```
if (interactive()) { # there is a warning owing to non-SNV present
  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**

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

**Value**

`data.frame`

**Examples**

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

---

ldmat, ldstruct-method	<i>accessor for matrix component</i>
------------------------	--------------------------------------

---

**Description**

accessor for matrix component

**Usage**

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

**Arguments**

x                      instance of ldstruct

---

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", ...)`.

**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**

chrnum	a character string denoting a chromosome, such as '22'
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

**Value**

by default, a [TabixFile](#) instance

**Examples**

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

## End(Not run)
```

---

sarpinf\_1kg

---

*population and relationship information for 1000 genomes*


---

**Description**

population and relationship information for 1000 genomes

**Usage**

```
sarpinf_1kg
```

**Format**

```
data.frame
```

**Source**

[ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/working/20130606\\_sample\\_info/20130606\\_sample\\_info.xlsx](ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/working/20130606_sample_info/20130606_sample_info.xlsx), to which superpopulation codes were added

---

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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