Package ‘LDlinkR’

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Type Package

Title An R Package for Calculating Linkage Disequilibrium

Version 1.0.2

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Description Provides access to the LDlink API (<https://ldlink.nci.nih.gov/?tab=apiaccess>) using the R console. This programmatic access facilitates researchers who are interested in performing batch queries in 1000 Genomes Project data using LDlink.

License GPL (>= 2)

URL `https://ldlink.nci.nih.gov`

BugReports `https://github.com/CBIIT/LDlinkR/issues`

Encoding UTF-8

LazyData true

Imports httr (>= 1.4.0), utils (>= 3.4.2)

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.0.2

NeedsCompilation no

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Repository CRAN

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R topics documented:

`LDhap` *Query LDhap API*

Description

Query LDhap API

Usage

```
LDhap(snps, pop = "CEU", token = NULL, file = FALSE)
```

Arguments

`snps`	list of between 1 - 30 variants, using an rsID or chromosome coordinate (e.g. "chr7:24966446")
`pop`	a 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: LDhap(c("rs3", "rs4", "rs148890987"), "CEU", token = Sys.getenv("LDLINK_TOKEN"))
## Not run: LDhap("rs148890987", c("YRI", "CEU"), token = Sys.getenv("LDLINK_TOKEN"))
```

`LDmatrix` *Query LDmatrix API*

Description

Query LDmatrix API

Usage

```
LDmatrix(snps, pop = "CEU", r2d = "r2", token = NULL, file = FALSE)
```

Arguments

`snps`	list of between 2 - 1,000 variants, using an rsID or chromosome coordinate (e.g. "chr7:24966446")
`pop`	a 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU"
`r2d`	r2d, either "r2" for LD R2 or "d" for LD D', default = "r2"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: LDmatrix(c("rs3", "rs4", "rs148890987"),
                     "YRI", "r2",
                     token = Sys.getenv("LDLINK_TOKEN"))

## End(Not run)
```

`LDpair` *Query LDpair API*

Description

Query LDpair API

Usage

```
LDpair(var1, var2, pop = "CEU", token = NULL, output = "table", file = FALSE)
```

Arguments

`var1`	the first RS number or genomic coordinate (e.g. "chr7:24966446")
`var2`	the second RS number or genomic coordinate (e.g. "ch7:24966446")
`pop`	a 1000 Genomes Project population(s), (e.g. YRI or CEU), multiple allowed, default = "CEU"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`output`	two output options available, "text", which displays a two-by-two matrix displaying haplotype counts and allele frequencies along with other statistics, or "table", which displays the same data in rows and columns, default = "table"
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

text or data frame, dependning on the output option

Examples

```
## Not run: LDpair(var1 = "rs3", var2 = "rs4", pop = "YRI", token = Sys.getenv("LDLINK_TOKEN"))
## Not run: LDpair("rs3", "rs4", "YRI", token = Sys.getenv("LDLINK_TOKEN"), "text")
```

`LDpop` *Query LDpop API*

Description

Query LDpop API

Usage

```
LDpop(var1, var2, pop = "CEU", r2d = "r2", token = NULL, file = FALSE)
```

Arguments

`var1`	the first RS number or genomic coordinate (e.g. "chr7:24966446")
`var2`	the second RS number or genomic coordinate (e.g. "ch7:24966446")
`pop`	a 1000 Genomes Project population(s), (e.g. YRI or CEU), multiple allowed, default = "CEU"
`r2d`	either "r2" for LD R2 or "d" for LD D', default = "r2"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: LDpop(var1 = "rs3", var2 = "rs4",
                 pop = "YRI", r2d = "r2",
                 token = Sys.getenv("LDLINK_TOKEN"))

## End(Not run)
```

`LDproxy` *Query LDproxy API*

Description

Query LDproxy API

Usage

```
LDproxy(snp, pop = "CEU", r2d = "r2", token = NULL, file = FALSE)
```

Arguments

`snp`	an rsID or chromosome coordinate (e.g. "chr7:24966446"), one per query
`pop`	a 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU"
`r2d`	either "r2" for LD R2 or "d" for LD D', default = "r2"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: LDproxy("rs456", "YRI", "r2", token = Sys.getenv("LDLINK_TOKEN"))
```

`LDproxy_batch` *Query LDproxy API using a list of query variants, one per line.*

Description

Query LDproxy API using a list of query variants, one per line.

Usage

```
LDproxy_batch(snp, pop = "CEU", r2d = "r2", token = NULL, append = FALSE)
```

Arguments

`snp`	a character string or data frame listing rsID's or chromosome coordinates (e.g. "chr7:24966446"), one per line
`pop`	a 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU"
`r2d`	either "r2" for LD R2 or "d" for LD D', default = "r2"
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`append`	logical. If TRUE, output for each query variant is appended to a text file. If FALSE, output of each query variant is saved in its own text file.

Value

text file(s) are saved to the current working directory.

Examples

```
## Not run: snps_to_upload <- c("rs3", "rs4")
## Not run: LDproxy_batch(snp = snps_to_upload, token = Sys.getenv("LDLINK_TOKEN"), append = FALSE)
```

`list_chips` *List available SNP Chip Arrays*

Description

List available SNP Chip Arrays

Usage

```
list_chips()
```

Value

a data frame listing the names and abbreviation codes for available SNP Chip Arrays from Illumina and Affymetrix

Examples

```
list_chips()
```

`list_pop` *List available reference populations*

Description

List available reference populations

Usage

```
list_pop()
```

Value

a data frame listing the available reference populations, continental (ex: European, African, and Admixed American) and sub-populations (ex: Finnish, Gambian, and Peruvian)

Examples

```
list_pop()
```

`SNPchip` *Query SNPchip API*

Description

Query SNPchip API

Usage

```
SNPchip(snps, chip = "ALL", token = NULL, file = FALSE)
```

Arguments

`snps`	between 1 - 5,000 variants, using an rsID or chromosome coordinate (e.g. "chr7:24966446")
`chip`	chip or arrays, platform code(s) for a SNP chip array, ALL_Illumina, ALL_Affy or ALL, default=ALL
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: SNPchip(c("rs3", "rs4", "rs148890987"), "ALL",
                  token = Sys.getenv("LDLINK_TOKEN"))

## End(Not run)
## Not run: SNPchip(c("rs3", "rs4", "rs148890987"),
                  c("A_CHB2", "A_SNP5.0"),
                  token = Sys.getenv("LDLINK_TOKEN"))

## End(Not run)
## Not run: SNPchip("rs148890987", "ALL_Affy", token = Sys.getenv("LDLINK_TOKEN"))
```

`SNPclip` *Query SNPclip API*

Description

Query SNPclip API

Usage

```
SNPclip(
  snps,
  pop = "CEU",
  r2_threshold = "0.1",
  maf_threshold = "0.01",
  token = NULL,
  file = FALSE
)
```

Arguments

`snps`	a list of between 1 - 5,000 variants, using an rsID or chromosome coordinate (e.g. "chr7:24966446")
`pop`	a 1000 Genomes Project population, (e.g. YRI or CEU), multiple allowed, default = "CEU"
`r2_threshold`	LD R2 threshold between 0-1, default = 0.1
`maf_threshold`	minor allele frequency threshold between 0-1, default = 0.01
`token`	LDlink provided user token, default = NULL, register for token at `https://ldlink.nci.nih.gov/?tab=apiaccess`
`file`	Optional character string naming a path and file for saving results. If file = FALSE, no file will be generated, default = FALSE.

Value

a data frame

Examples

```
## Not run: SNPclip(c("rs3", "rs4", "rs148890987"), "YRI", "0.1", "0.01",
                    token = Sys.getenv("LDLINK_TOKEN"))

## End(Not run)
```

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