

# Package ‘LDlinkR’

August 1, 2019

**Type** Package

**Title** Access LDlink API with R

**Version** 1.0.0

**Maintainer** Timothy A. Myers <myersta@mail.nih.gov>

**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>

**Encoding** UTF-8

**LazyData** true

**Imports** httr (>= 1.4.0), utils (>= 3.5.2)

**Suggests** testthat

**RoxygenNote** 6.1.1

**NeedsCompilation** no

**Author** Timothy A. Myers [cre],  
Mitchell J. Machiela [aut]

**Repository** CRAN

**Date/Publication** 2019-08-01 12:50:17 UTC

## R topics documented:

LDhap . . . . .	2
LDmatrix . . . . .	2
LDpair . . . . .	3
LDpop . . . . .	4
LDproxy . . . . .	5
LDproxy_batch . . . . .	6
list_chips . . . . .	6
list_pop . . . . .	7
SNPchip . . . . .	7
SNPclip . . . . .	8

**Index** **10**


---

LDhap	<i>Query LDhap API</i>
-------	------------------------

---

**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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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	<i>Query LDmatrix API</i>
----------	---------------------------

---

**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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>

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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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	<i>Query LDproxy API using a list of query variants, one per line.</i>
---------------	------------------------------------------------------------------------

---

### 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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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	<i>List available SNP Chip Arrays</i>
------------	---------------------------------------

---

### 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()
```

---

<code>list_pop</code>	<i>List available reference populations</i>
-----------------------	---------------------------------------------

---

**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()
```

---

<code>SNPchip</code>	<i>Query SNPchip API</i>
----------------------	--------------------------

---

**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 <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a>
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)
```

# Index

LDhap, [2](#)  
LDmatrix, [2](#)  
LDpair, [3](#)  
LDpop, [4](#)  
LDproxy, [5](#)  
LDproxy\_batch, [6](#)  
list\_chips, [6](#)  
list\_pop, [7](#)  
  
SNPchip, [7](#)  
SNPclip, [8](#)