Package 'gwascat'

October 14, 2021

Title representing and modeling data in the EMBL-EBI GWAS catalog

Version 2.24.0

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Description Represent and model data in the EMBL-EBI GWAS catalog.

Enhances SNPlocs.Hsapiens.dbSNP144.GRCh37

Depends R (>= 3.5.0), methods

Imports S4Vectors (>= 0.9.25), IRanges, GenomeInfoDb, GenomicRanges (>= 1.29.6), GenomicFeatures, readr, Biostrings, AnnotationDbi, BiocFileCache, snpStats, VariantAnnotation, AnnotationHub

Suggests DO.db, DT, knitr, RBGL, testthat, rmarkdown, Gviz, Rsamtools, IRanges, rtracklayer, graph, ggbio, DelayedArray, TxDb.Hsapiens.UCSC.hg19.knownGene, org.Hs.eg.db, BiocStyle

VignetteBuilder knitr

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

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LazyData no

biocViews Genetics

RoxygenNote 7.1.1

Encoding UTF-8

git_url https://git.bioconductor.org/packages/gwascat

git_branch RELEASE_3_13

git_last_commit d251baa

git_last_commit_date 2021-05-19

Date/Publication 2021-10-14

R topics documented:

`bindcadd_snv` *bind CADD scores of Kircher et al. 2014 to a GRanges instance*

Description

bind CADD scores of Kircher et al. 2014 to a GRanges instance; by default will use HTTP access at UW

Usage

```
bindcadd_snv(
  gr,
  fn = "http://krishna.gs.washington.edu/download/CADD/v1.0/1000G.tsv.gz"
)
```

Arguments

gr	query ranges to which CADD scores should be bound
fn	path to Tabix-indexed bgzipped TSV of CADD as distributed at krishna.gs.washington.edu on 1 April 2014

Details

joins CADD fields at addresses that match query; the CADD fields for query ranges that are not matched are set to NA

Value

GRanges instance with additional fields as obtained in the CADD resource

Note

This software developed in part with support from Genentech, Inc.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References

M Kircher, DM Witten, P Jain, BJ O'Roak, GM Cooper, J Shendure, A general framework for estimating the relative pathogenicity of human genetic variants, Nature Genetics Feb 2014, PMID 24487276

Examples

```
 ## Not run:
  data(ebicat_2020_04_30)
  g2 = as(ebicat_2020_04_30, "GRanges")
 # would need to lift over here
  bindcadd_snv( g2[which(seqnames(g2)=="chr2")][1:20] )

## End(Not run)
```

---

chklocs *return TRUE if all named SNPs with locations in both the SNPlocs package and the gwascat agree*

Description

return TRUE if all named SNPs with locations in both the SNPlocs package and the gwascat agree

Usage

```
chklocs(chrtag = "20", gwwl = gwrngs19)
```

Arguments

chrtag	character, chromosome identifier
gwwl	instance of {gwaswloc}

`ebicat_2020_04_30` *serialized gwaswloc instance from april 30 2020, sample of 50000 records*

Description

serialized gwaswloc instance from april 30 2020, sample of 50000 records

Usage

```
ebicat_2020_04_30
```

Format

gwaswloc instance

`g17SM` *SnpMatrix instance from chr17*

Description

SnpMatrix instance from chr17

Usage

```
g17SM
```

Format

snpStats SnpMatrix instance

getRsids *generic snp name retrieval*

Description

generic snp name retrieval

Usage

```
getRsids(x)
```

Arguments

x	gwaswloc

getRsids,gwaswloc-method *specific snp name retrieval*

Description

specific snp name retrieval

Usage

```
## S4 method for signature 'gwaswloc'
getRsids(x)
```

Arguments

x	gwaswloc

getTraits *generic trait retrieval*

Description

generic trait retrieval

Usage

```
getTraits(x)
```

Arguments

x	gwaswloc

`getTraits,gwaswloc-method` *specific trait retrieval*

Description

specific trait retrieval

Usage

```
## S4 method for signature 'gwaswloc'
getTraits(x)
```

Arguments

x	gwaswloc

`get_cached_gwascat` *use BiocFileCache to retrieve and keep an image of the tsv file*

Description

use BiocFileCache to retrieve and keep an image of the tsv file

Usage

```
get_cached_gwascat(
  url = "http://www.ebi.ac.uk/gwas/api/search/downloads/alternative",
  cache = BiocFileCache::BiocFileCache(),
  ...
)
```

Arguments

url	character(1) url to use
cache	BiocFileCache::BiocFileCache instance
...	passed to bfcadd

Note

will If query of cache with 'ebi.ac.uk/gwas' returns 0-row tibble, will populate cache with bfcadd. Uses readr::read_tsv on cache content to return tibble. The etag field does not seem to be used at EBI, thus user must check for updates.

gg17N *genotype matrix from chr17 1000 genomes*

Description

genotype matrix from chr17 1000 genomes

Usage

```
gg17N
```

Format

matrix

Examples

```
data(gg17N)
gg17N[1:4,1:4]
```

gr6.0_hg38 *image of locon6 in GRanges, lifted over to hg38*

Description

image of locon6 in GRanges, lifted over to hg38

Usage

```
gr6.0_hg38
```

Format

GRanges instance

gw6.rs_17 *character vector of rs numbers for SNP on chr17*

Description

character vector of rs numbers for SNP on chr17

Usage

```
gw6.rs_17
```

Format

character vector

gwascat_from_AHub *grab an image of EBI GWAS catalog from AnnotationHub*

Description

grab an image of EBI GWAS catalog from AnnotationHub

Usage

```
gwascat_from_AHub(tag = "AH91571", simple = FALSE, fixNonASCII = TRUE)
```

Arguments

tag	character(1) defaults to "AH91571" which is the 3.30.2021 image
simple	logical(1) if TRUE, just returns data.frame as retrieved from EBI; defaults to FALSE
fixNonASCII	logical(1) if TRUE, use iconv to identify and eliminate non-ASCII content

Value

If ‘simple‘, a data.frame is returned based on TSV data produced by EBI. Otherwise, non-ASCII content is processed according to the value of ‘fixNonASCII‘ and a ‘gwaswloc‘ instance is returned, which has a concise show method. This can be coerced to a simple GRanges instance with as(..., "GRanges"). The reference build is GRCh38.

Examples

```
gwcat = gwascat_from_AHub()
gwcat
```

gwastagger *GRanges with LD information on 9998 SNP*

Description

GRanges with LD information on 9998 SNP

Usage

```
gwastagger
```

Format

GRanges

gwaswloc-class *container for gwas hit data and GRanges for addresses*

Description

container for gwas hit data and GRanges for addresses

gwcat_snapshot *use AnnotationHub snapshot as basis for gwaswloc structure creation*

Description

use AnnotationHub snapshot as basis for gwaswloc structure creation

Usage

```
gwcat_snapshot(x, fixNonASCII = TRUE)
```

Arguments

x	inherits from data.frame, with columns consistent with EBI table
fixNonASCII	logical(1) if TRUE, use iconv to replace non-ASCII character, important for CMD check but perhaps not important for applied use

Examples

```
ah = AnnotationHub::AnnotationHub()
entitytab = AnnotationHub::query(ah, "gwascatData")
cand = names(entitytab)[1]
stopifnot(nchar(cand)>0)
tab = ah[[cand]]
gww = gwcat_snapshot(tab)
gww
length(gww)
```

---

gwcex2gviz *Prepare salient components of GWAS catalog for rendering with Gviz*

Description

Prepare salient components of GWAS catalog for rendering with Gviz

Usage

```
gwcex2gviz(
  basegr,
  contextGR = GRanges(seqnames = "chr17", IRanges::IRanges(start = 37500000, width =
    1e+06)),
  txrefobj = TxDb.Hsapiens.UCSC.hg19.knownGene::TxDb.Hsapiens.UCSC.hg19.knownGene,
  genome = "hg19",
  genesymobj = org.Hs.eg.db::org.Hs.eg.db,
  plot.it = TRUE,
  maxmlp = 25
)
```

Arguments

basegr	gwaswloc instance containing information about GWAS in catalog
contextGR	A GRanges instance delimiting the visualization in genomic coordinates
txrefobj	a TxDb instance
genome	character tag like 'hg19'
genesymobj	an OrgDb instance
plot.it	logical, if FALSE, just return list
maxmlp	maximum value of -10 log p – winsorization of all larger values is performed, modifying the contents of Pvalue_mlogp in the elementMetadata for the call

Examples

```
data(ebicat_2020_04_30)
# GenomeInfoDb::seqlevelsStyle(ebicat_2020_04_30) = "UCSC" # no more
GenomeInfoDb::seqlevels(ebicat_2020_04_30) = paste0("chr", GenomeInfoDb::seqlevels(ebicat_2020_04_30))
gwcex2gviz(ebicat_2020_04_30)
```

`ldtagr` *expand a list of variants by including those in a VCF with LD exceeding some threshold; uses snpStats ld()*

Description

expand a list of variants by including those in a VCF with LD exceeding some threshold; uses snpStats ld()

Usage

```
ldtagr(
  snprng,
  tf,
  samples,
  genome = "hg19",
  lbmaf = 0.05,
  lbR2 = 0.8,
  radius = 1e+05
)
```

Arguments

`snprng`	a named GRanges for a single SNP. The name must correspond to the name that will be assigned by genotypeToSnpMatrix (from VariantTools) to the corresponding column of a SnpMatrix.
`tf`	TabixFile instance pointing to a bgzipped tabix-indexed VCF file
`samples`	a vector of sample identifiers, if excluded, all samples used
`genome`	tag like 'hg19'
`lbmaf`	lower bound on variant MAF to allow consideration
`lbR2`	lower bound on R squared for regarding SNP to be incorporated
`radius`	radius of search in bp around the input range

Value

a GRanges with names corresponding to 'new' variants and mcols fields 'paramRangeID' (base variant input) and 'R2'

Note

slow but safe approach. probably a matrix method could be substituted using the nice sparse approach already in snpStats

Author(s)

VJ Carey

Examples

```
cand = GenomicRanges::GRanges("1", IRanges::IRanges(113038694, width=1))
names(cand) = "rs883593"
requireNamespace("VariantAnnotation")
expath = dir(system.file("vcf", package="gwascat"), patt=".*exon.*gz$", full=TRUE)
tf = Rsamtools::TabixFile(expath)
ldtagr( cand, tf, lbR2 = .8)
```

---

locon6 *location data for 10000 SNP*

Description

location data for 10000 SNP

Usage

```
locon6
```

Format

data.frame, coordinates are hg19

---

locs4trait *get locations for SNP affecting a selected trait*

Description

get locations for SNP affecting a selected trait

Usage

```
locs4trait(gwwl, trait, tag = "DISEASE/TRAIT")
```

Arguments

gwwl	instance of {gwaswloc}
trait	character, name of trait
tag	character, name of field to be used for trait enumeration

low17 *SnpMatrix instance from chr17*

Description

SnpMatrix instance from chr17

Usage

```
low17
```

Format

snpStats SnpMatrix instance

makeCurrentGwascat *read NHGRI GWAS catalog table and construct associated GRanges instance records for which clear genomic position cannot be determined are dropped from the ranges instance an effort is made to use reasonable data types for GRanges metadata, so some qualifying characters such as (EA) in Risk allele frequency field will simply be omitted during coercion of contents of that field to numeric.*

Description

read NHGRI GWAS catalog table and construct associated GRanges instance records for which clear genomic position cannot be determined are dropped from the ranges instance an effort is made to use reasonable data types for GRanges metadata, so some qualifying characters such as (EA) in Risk allele frequency field will simply be omitted during coercion of contents of that field to numeric.

Usage

```
makeCurrentGwascat(
  table.url = "http://www.ebi.ac.uk/gwas/api/search/downloads/alternative",
  fixNonASCII = TRUE,
  genome = "GRCh38",
  withOnt = TRUE
)
```

Arguments

table.url	string identifying the .txt file curated at EBI/EMBL
fixNonASCII	logical, if TRUE, non-ASCII characters as identified by iconv will be replaced by asterisk
genome	character string: 'GRCh38' is default and yields current image as provided by EMBL/EBI; 'GRCh37' yields a realtime liftOver to hg19 coordinates, via AnnotationHub storage of the chain files. Any other value yields an error.
withOnt	logical indicating whether 'alternative' (ontology-present, includes repetition of loci with one:many ontological mapping) or 'full' (ontology-absent, one record per locus report) version of distributed table

Value

a GRanges instance

Author(s)

VJ Carey

Examples

```
# if you have good internet access
  if (interactive()) {
     newcatr = makeCurrentGwascat()
     newcatr
     }
```

---

obo2graphNEL *convert a typical OBO text file to a graphNEL instance (using Term elements)*

Description

convert a typical OBO text file to a graphNEL instance (using Term elements)

Usage

```
obo2graphNEL(
  obo = "human-phenotype-ontology.obo",
  kill = "\\[Typedef\\]",
  killTrailSp = TRUE
)
```

Arguments

obo	string naming a file in OBO format
kill	entity types to be excluded from processing – probably this should be in a 'keep' form, but for now this works.
killTrailSp	In the textual version of EFO ca. Aug 2015, there is a trailing blank in the tag field defining EFO:0000001, which is not present in references to this term. Set this to TRUE to eliminate this, or graphNEL construction will fail to validate.

Details

Very rudimentary list and grep operations are used to retain sufficient information to map the DAG to a graphNEL, using formal term identifiers as node names and 'is-a' relationships as edges, and term names and other metadata are assigned to nodeData components.

Value

a graphNEL instance

Note

The OBO for Human Disease ontology is serialized as text with this package.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References

For use with human disease ontology, http://www.obofoundry.org/cgi-bin/detail.cgi?id=disease_ontology

Examples

```
data(efo.obo.g)
requireNamespace("graph")
hn = graph::nodes(efo.obo.g)[1:5]
hn
graph::nodeData(efo.obo.g, hn[5])
```

process_gwas_dataframe *convert GWAS catalog data.frame to gwaswloc, a GRanges extension with simple show method*

Description

convert GWAS catalog data.frame to gwaswloc, a GRanges extension with simple show method

Usage

```
process_gwas_dataframe(df)
```

Arguments

df	data.frame

riskyAlleleCount *given a matrix of subjects x SNP calls, count number of risky alleles*

Description

given a matrix of subjects x SNP calls, count number of risky alleles for various conditions, relative to NHGRI GWAS catalog

Usage

```
riskyAlleleCount(
  callmat,
  matIsAB = TRUE,
  chr,
  gwwl,
  snpap = "SNPlocs.Hsapiens.dbSNP144.GRCh37",
  gencode = c("A/A", "A/B", "B/B")
)
```

Arguments

callmat	matrix with subjects as rows, SNPs as columns; entries can be generic A/A, A/B, B/B, or specific nucleotide calls
matIsAB	logical, FALSE if nucleotide codes are present, TRUE if generic call codes are present; in the latter case, gwascat:::ABmat2nuc will be run
chr	code for chromosome, should work with the SNP annotation getSNPlocs function, so likely "ch[nn]"
gwwl	an instance of {gwaswloc}
snpap	name of a Bioconductor SNPlocs.Hsapiens.dbSNP.* package
gencode	codes used for generic SNP call

Value

matrix with rows corresponding to subjects , columns corresponding to SNP

Examples

```
## Not run:
data(gg17N) # translated from GGdata chr 17 calls using ABmat2nuc
data(ebicat37)
library(GenomeInfoDb)
seqlevelsStyle(ebicat37) = "UCSC"
h17 = riskyAlleleCount(gg17N, matIsAB=FALSE, chr="ch17", gwwl=ebicat37)
h17[1:5,1:5]
table(as.numeric(h17))

## End(Not run)
```

---

si.hs.37 *Seqinfo for GRCh37*

Description

Seqinfo for GRCh37

Usage

```
si.hs.37
```

Format

GenomeInfoDb Seqinfo instance

---

si.hs.38 *Seqinfo for GRCh38*

Description

Seqinfo for GRCh38

Usage

```
si.hs.38
```

Format

GenomeInfoDb Seqinfo instance

subsetByChromosome *generic trait subsetting*

Description

generic trait subsetting

Usage

```
subsetByChromosome(x, ch)
```

Arguments

x	gwaswloc
ch	character vector of chromosomes

subsetByChromosome,gwaswloc-method *specific trait subsetting*

Description

specific trait subsetting

Usage

```
## S4 method for signature 'gwaswloc'
subsetByChromosome(x, ch)
```

Arguments

x	gwaswloc
ch	character vector of chromosomes

`subsetByTraits` *generic trait subsetting*

Description

generic trait subsetting

Usage

```
subsetByTraits(x, tr)
```

Arguments

`x`	gwaswloc
`tr`	character vector of traits

`subsetByTraits,gwaswloc-method` *specific trait subsetting*

Description

specific trait subsetting

Usage

```
## S4 method for signature 'gwaswloc'
subsetByTraits(x, tr)
```

Arguments

`x`	gwaswloc
`tr`	character vector of traits

topTraits *operations on GWAS catalog*

Description

operations on GWAS catalog

Usage

```
topTraits(gwwl, n = 10, tag = "DISEASE/TRAIT")
```

Arguments

gwwl	instance of {gwaswloc}
n	numeric, number of traits to report
tag	character, name of field to be used for trait enumeration

Value

topTraits returns a character vector of most frequently occurring traits in the database

locs4trait returns a {gwaswloc} object with records defining associations to the specified trait

chklocs returns a logical that is TRUE when the asserted locations of SNP in the GWAS catalog agree with the locations given in the dbSNP package SNPlocs.Hsapiens.dbSNP144.GRCh37

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
data(ebicat_2020_04_30)
topTraits(ebicat_2020_04_30)
```

traitsManh *use ggbio facilities to display GWAS results for selected traits in genomic coordinates*

Description

use ggbio facilities to display GWAS results for selected traits in genomic coordinates

Usage

```
traitsManh(
  gwr,
  selr = GRanges(seqnames = "chr17", IRanges(3e+07, 5e+07)),
  traits = c("Asthma", "Parkinson's disease", "Height", "Crohn's disease"),
  truncmlp = 25,
  ...
)
```

Arguments

gwr	GRanges instance as managed by the gwaswloc container design, with Disease.Trait and Pvalue_mlog among elementMetadata columns
selr	A GRanges instance to restrict the gwr for visualization. Not tested for noncontiguous regions.
traits	Character vector of traits to be exhibited; GWAS results with traits not among these will be labeled "other".
truncmlp	Maximum value of -log10 p to be displayed; in the raw data this ranges to the hundreds and can cause bad compression.
...	not currently used

Details

uses a ggbio autoplot

Value

autoplot value

Note

An xlab is added, concatenating genome tag with seqnames tag.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```
# do a p-value truncation if you want to reduce compression
## Not run:   # ggbio July 2018
data(ebicat_2020_04_30)
library(GenomeInfoDb)
seqlevelsStyle(ebicat_2020_04_30) = "UCSC"
traitsManh(ebicat_2020_04_30)

## End(Not run)
```

`[,gwaswloc,ANY,ANY,ANY-method` *extractor for gwaswloc*

Description

extractor for gwaswloc

Usage

```
## S4 method for signature 'gwaswloc,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]
```

Arguments

`x`	gwaswloc
`i`	index
`j`	index
`...`	addtl indices
`drop`	logical(1)

Index