

gwascatData – a snapshot of the EBI/EMBL GWAS catalog

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1 Introduction

This package defines an AnnotationHub resource representing the EBI GWAS catalog on March 30 2021.

```
library(AnnotationHub)
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##   dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##   grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##   order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##   rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##   union, unique, unsplit, which.max, which.min
## Loading required package: BiocFileCache
## Loading required package: dbplyr
ahub = AnnotationHub()
## Warning: DEPRECATION: As of AnnotationHub (>2.23.2), default caching location has changed.
## Problematic cache: /Users/sarastankiewicz/Library/Caches/AnnotationHub
## See https://bioconductor.org/packages/devel/bioc/vignettes/AnnotationHub/inst/doc/TroubleshootingTheCache.html
## snapshotDate(): 2021-05-06
mymeta <- query(ahub, "gwascataData")
mymeta
## AnnotationHub with 1 record
## # snapshotDate(): 2021-05-06
## # names(): AH91571
## # $dataprovder: EBI/EMBL
## # $species: Homo sapiens
## # $rdataclass: character
## # $rdatadateadded: 2021-04-12
## # $title: gwascataData
## # $description: text file in cloud with March 30 2021 snapshot of EBI/EMBL G...
## # $taxonomyid: 9606
## # $genome: GRCh38
## # $sourcetype: TSV
## # $sourceurl: http://www.ebi.ac.uk/gwas/api/search/downloads/alternative
## # $sourcesize: NA
## # $tags: c("GWAS", "GWAS catalog")
## # retrieve record with 'object[["AH91571"]]'
```

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```
tag = names(mymeta)[1]
tag
## [1] "AH91571"
head(ahub[[tag]][,1:6])
## loading from cache
##   DATE ADDED TO CATALOG PUBMEDID FIRST AUTHOR      DATE      JOURNAL
## 1      2020-06-04 32296059      Han Y 2020-04-15      Nat Commun
## 2      2020-02-05 31666681      Zhao B 2019-10-30 Mol Psychiatry
## 3      2020-02-05 31666681      Zhao B 2019-10-30 Mol Psychiatry
## 4      2020-06-04 32296059      Han Y 2020-04-15      Nat Commun
## 5      2020-02-05 31666681      Zhao B 2019-10-30 Mol Psychiatry
## 6      2020-02-05 31666681      Zhao B 2019-10-30 Mol Psychiatry
##                                     LINK
## 1 www.ncbi.nlm.nih.gov/pubmed/32296059
## 2 www.ncbi.nlm.nih.gov/pubmed/31666681
## 3 www.ncbi.nlm.nih.gov/pubmed/31666681
## 4 www.ncbi.nlm.nih.gov/pubmed/32296059
## 5 www.ncbi.nlm.nih.gov/pubmed/31666681
## 6 www.ncbi.nlm.nih.gov/pubmed/31666681
```

The gwascata package includes tooling to transform this to a GRanges-like object.