GenomicState

November 6, 2026

GenomicStateHub *Access GenomicState objects through AnnotationHub*

Description

This function uses AnnotationHub to obtain the objects provided by this package. These are: the TxDb object made with gencode_txdb(), the annotated genes object made with gencode_annotated_genes() or the GenomicState object made with gencode_genomic_state().

Usage

```
GenomicStateHub(
  version = "31",
  genome = c("hg38", "hg19"),
  filetype = c("TxDb", "AnnotatedGenes", "GenomicState"),
  ah = AnnotationHub::AnnotationHub()
)
```

Arguments

version	A character(1) with the Gencode version number.
genome	A character(1) with the human genome version number. Valid options are 'hg38' or 'hg19'.
filetype	A character() with either TxDb, AnnotatedGenes or GenomicState.
ah	An AnnotationHub object AnnotationHub-class.

Value

The AnnotationHub-class query for the file you requested.

Author(s)

Leonardo Collado-Torres

See Also

gencode_txdb() gencode_annotated_genes() gencode_genomic_state()

Examples

```
## Query AnnotationHub for the GenomicState object for Gencode v31 on
## hg19 coordinates
hub_query_gs_gencode_v31_hg19 <- GenomicStateHub(
    version = "31",
    genome = "hg19",
    filetype = "GenomicState"
)
hub_query_gs_gencode_v31_hg19


## Check the metadata
mcols(hub_query_gs_gencode_v31_hg19)

## Access the file through AnnotationHub
if (length(hub_query_gs_gencode_v31_hg19) == 1) {
    hub_gs_gencode_v31_hg19 <- hub_query_gs_gencode_v31_hg19[[1]]

    hub_gs_gencode_v31_hg19
}
```

---

gencode_annotated_genes

Annotation the genes for a given Gencode TxDb object

Description

Based on a TxDb object built by gencode_txdb() this function annotates the genes. This information is then used by packages like derfinder and derfinderPlot.

Usage

```
gencode_annotated_genes(txdb)
```

Arguments

txdb	A GenomicFeatures::TxDb object built with gencode_txdb().

Value

The annotated genes resulting from bumphunter::annotateTranscripts().

Author(s)

Leonardo Collado-Torres.

References

Based on code for the brainflowprobes package at: https://github.com/LieberInstitute/brainflowprobes/blob/devel/data-raw/create_sysdata.R

See Also

gencode_txdb() gencode_genomic_state()

Examples

```
## Start from scratch if you want:
## Not run:
txdb_v31_hg19_chr21 <- gencode_txdb("31", "hg19", chrs = "chr21")

## End(Not run)

## or read in the txdb object for hg19 chr21 from this package
txdb_v31_hg19_chr21 <- AnnotationDbi::loadDb(
    system.file("extdata", "txdb_v31_hg19_chr21.sqlite",
        package = "GenomicState"
    )
)

## Obtain the annotated genes for the Gencode TxDb object
genes_v31_hg19_chr21 <- gencode_annotated_genes(txdb_v31_hg19_chr21)

## Explore the result
genes_v31_hg19_chr21
```

---

gencode_genomic_state *Build a GenomicState object for Gencode TxDb objects*

Description

Based on a TxDb object built by gencode_txdb() this function builds a GenomicState object which you can then use with derfinder::annotateRegions(). This information is then used by packages like derfinderPlot.

Usage

```
gencode_genomic_state(txdb)
```

Arguments

txdb	A GenomicFeatures::TxDb object built with gencode_txdb().

Details

Note that not all genes will have symbols as many will be NA.

Value

A GenomicState object with the gene symbols as built using derfinder::makeGenomicState().

Author(s)

Leonardo Collado-Torres

References

Based on code for the brainflowprobes package at: https://github.com/LieberInstitute/brainflowprobes/blob/devel/data-raw/create_sysdata.R

See Also

gencode_txdb() gencode_annotated_genes()

Examples

```
## Start from scratch if you want:
## Not run:
txdb_v31_hg19_chr21 <- gencode_txdb("31", "hg19", chrs = "chr21")

## End(Not run)

## or read in the txdb object for hg19 chr21 from this package
txdb_v31_hg19_chr21 <- AnnotationDbi::loadDb(
    system.file("extdata", "txdb_v31_hg19_chr21.sqlite",
        package = "GenomicState"
    )
)

## Now build the GenomicState object
gs_v31_hg19_chr21 <- gencode_genomic_state(txdb_v31_hg19_chr21)

## Explore the result
gs_v31_hg19_chr21
```

---

gencode_txdb *Create a Gencode TxDb object*

Description

This function builds a transcript database (TxDb) object which you can then use to build a Gencode GenomicState object. This function will download the data from Gencode, import it into R, process it and build the TxDb object.

Usage

```
gencode_txdb(
  version = "31",
  genome = c("hg38", "hg19"),
  chrs = paste0("chr", c(seq_len(22), "X", "Y", "M"))
)

gencode_source_url(version = "31", genome = c("hg38", "hg19"))
```

Arguments

version	A character(1) with the Gencode version number.
genome	A character(1) with the human genome version number. Valid options are 'hg38' or 'hg19'.
chrs	A character() vector with the chromosome (contig) names to keep.

Value

A GenomicFeatures::TxDb object.

A `character(1)` with the URL for the GTF Gencode file of interest.

Author(s)

Leonardo Collado-Torres

References

Based on code for the `brainflowprobes` package at: https://github.com/LieberInstitute/brainflowprobes/blob/devel/data-raw/create_sysdata.R

See Also

`gencode_annotated_genes()` `gencode_genomic_state()`

Examples

```
## Start from scratch if you want:
## Not run:
txdb_v31_hg19_chr21 <- gencode_txdb("31", "hg19", chrs = "chr21")

## End(Not run)

## or read in the txdb object for hg19 chr21 from this package
txdb_v31_hg19_chr21 <- AnnotationDbi::loadDb(
    system.file("extdata", "txdb_v31_hg19_chr21.sqlite",
        package = "GenomicState"
    )
)

## Explore the result
txdb_v31_hg19_chr21

## Locate the GTF file for Gencode version 31 for hg19
gencode_source_url(version = "31", genome = "hg19")
```

`local_metadata` *Locate local metadata outside of AnnotationHub*

Description

Locate local metadata outside of AnnotationHub

Usage

```
local_metadata(local_path = "/dcl01/lieber/ajaffe/lab/GenomicState/data-raw")
```

Arguments

`local_path`	A `character(1)` pointing to where the data is stored locally

Value

The AnnotationHub metadata `data.frame()` for the data in this package with `RDataPath` updated to point to the `local_path`. It includes an addtional column called `loadCode` which you can evaluate with `eval(parse(text = entry))`.

Author(s)

Leonardo Collado-Torres

See Also

`AnnotationHubData::makeAnnotationHubMetadata()`

Examples

```
## Get the local metadata
meta <- local_metadata()

## Subset to the data of interest, lets say hg19 TxDb for v31
interest <- subset(meta, RDataClass == "TxDb" & Tags == "Gencode:v31:hg19")

## Inspect the result
interest

## Next you can load the data
if (file.exists(interest$RDataPath)) {
    ## This only works at JHPCE
    eval(parse(text = interest$loadCode))

    ## Explore the loaded object (would be gencode_v31_hg19_txdb in this case)
    gencode_v31_hg19_txdb
}
```

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