

# GenomicState

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GenomicStateHub

*Access GenomicState objects through AnnotationHub*

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## 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 <a href="#">AnnotationHub-class</a> .                            |

## 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
}
```

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`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/master/data-raw/create\\_sysdata.R](https://github.com/LieberInstitute/brainflowprobes/blob/master/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/master/data-raw/create\\_sysdata.R](https://github.com/LieberInstitute/brainflowprobes/blob/master/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/master/data-raw/create\\_sysdata.R](https://github.com/LieberInstitute/brainflowprobes/blob/master/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 | <i>Locate local metadata outside of AnnotationHub</i> |
|----------------|---|

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## 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 additional 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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