

# 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*

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## 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
```

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`gencode_genomic_state` *Build a GenomicState object for Gencode TxDb objects*

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## 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
```

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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')
```

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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 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
}
```

# Index

AnnotationHub-class, [1](#)  
AnnotationHubData::makeAnnotationHubMetadata(),  
[6](#)  
  
bumphunter::annotateTranscripts(), [2](#)  
  
derfinder::annotateRegions(), [3](#)  
derfinder::makeGenomicState(), [3](#)  
  
gencode\_annotated\_genes, [2](#)  
gencode\_annotated\_genes(), [1](#), [4](#), [5](#)  
gencode\_genomic\_state, [3](#)  
gencode\_genomic\_state(), [1](#), [2](#), [5](#)  
gencode\_source\_url (gencode\_txdb), [4](#)  
gencode\_txdb, [4](#)  
gencode\_txdb(), [1-4](#)  
GenomicFeatures::TxDb, [2-4](#)  
GenomicStateHub, [1](#)  
  
local\_metadata, [5](#)