Package ‘chipenrich.data’

May 2, 2024

Title Companion package to chipenrich

Version 2.29.0

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Description Supporting data for the chipenrich package. Includes predefined gene sets, gene locus definitions, and mappability estimates.

biocViews ChIPSeq, Epigenetics, FunctionalGenomics, GeneSetEnrichment, HistoneModification, Regression

Depends R (>= 3.4.0)

Imports AnnotationDbi, BiocGenerics, methods, GenomicRanges, GenomeInfoDb, IRanges, readr, rtracklayer, S4Vectors, utils

License GPL-3

Encoding UTF-8

LazyData true

Suggests BiocStyle, devtools, knitr, rmarkdown, roxygen2, testthat, GO.db, org.Dm.eg.db, org.Dr.eg.db, org.Hs.eg.db, org.Mm.eg.db, org.Rn.eg.db, TxDb.Dmelanogaster.UCSC.dm3.ensGene, TxDb.Dmelanogaster.UCSC.dm6.ensGene, TxDb.Drerio.UCSC.danRer10.refGene, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm9.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Rnorvegicus.UCSC.rn4.ensGene, TxDb.Rnorvegicus.UCSC.rn5.refGene, TxDb.Rnorvegicus.UCSC.rn6.refGene

VignetteBuilder knitr

RoxygenNote 6.1.1

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Contents

`chipenrich.data` *chipenrich.data: Data for chipenrich: gene set enrichment analysis for ChIP-seq data*

Description

Supporting data for the chipenrich package. Includes pre-defined gene sets, gene locus definitions, and mappability estimates.

`enhancer.dnase_thurman.0` *Enhancer locations*

Description

A `GRanges` with all the enhancer locations for hg19. The locations were found using a combination of DNAse data and from Thurman et al (PMID: 22955617)

Usage

`enhancer.dnase_thurman.0`

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

`gene.enh.desc` *Gene-Enhancer descriptives*

Description

A data frame with gene-level descriptions of enhancer properties using enhancers.dnase_thurman.0. Used in the adjustment of proximity test to enhancers.

gene_id The Entrez ID for the a gene

avg_denh_emp The empirical average distance to an enhancer from 90 ENCODE ChIP-seq datasets. This is used as the adjustment.

num_enh The number of enhancers assigned to the gene, defined by closest gene TSS

avgdenh The theoretical average distance to an enhancer assuming every base pair on the genome is equally likely to have a peak binding.

Usage

```
gene.enh.desc
```

Format

An object of class `data.frame` with 21600 rows and 4 columns.

`GeneSet-class` *Class* `"GeneSet"`

Description

Class for storing sets of genes and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form `new("GeneSet")`.

These objects are used internally by the `chipenrich` package and users will not likely need to create these.

Slots

`set.gene`: Object of class `"environment"`. Maps from geneset IDs to lists of Entrez gene IDs.

`type`: Object of class `"character"`. The formal name for this collection of genesets.

`set.name`: Object of class `"environment"`. Maps from geneset IDs to their descriptions/names.

`all.genes`: Object of class `"character"`. A set of all genes present across every geneset.

`organism`: Object of class `"character"`. Organism code for gene IDs.

`dburl`: Object of class `"character"`. Web URL for this collection of genesets.

Note

Not typically accessed by the user - this is used internally by the `chipenrich` package.

Author(s)

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Examples

```
# Show information about class.
showClass("GeneSet")

# What is stored inside a geneset object?
data("geneset.metabolite.hsa");
str(geneset.metabolite.hsa);

# How are the mappings from geneset IDs to gene IDs stored?
ls.str(geneset.metabolite.hsa@set.gene);
```

`geneset.biocarta_pathway.hsa` *geneset.biocarta_pathway.hsa genesets for BioCarta*

Description

BioCarta (biocarta_pathway) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:04 2017.

Usage

```
geneset.biocarta_pathway.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways

`geneset.biocarta_pathway.mmu`

geneset.biocarta_pathway.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.biocarta_pathway.rno`

geneset.biocarta_pathway.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.ctd.hsa` *geneset.ctd.hsa genesets for Comparative Toxicogenomics Database*

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:11 2017.

Usage

```
geneset.ctd.hsa
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://ctdbase.org

`geneset.ctd.mmu` *geneset.ctd.mmu genesets for Comparative Toxicogenomics Database*

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Sat Nov 10 15:56:37 2018.

Usage

```
geneset.ctd.mmu
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://ctdbase.org

`geneset.cytoband.hsa` *geneset.cytoband.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.cytoband.hsa)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.drug_bank.hsa` *geneset.drug_bank.hsa genesets for DrugBank*

Description

DrugBank (drug_bank) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:13 2017.

Usage

```
geneset.drug_bank.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

https://www.drugbank.ca

`geneset.drug_bank.mmu` *geneset.drug_bank.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.drug_bank.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.drug_bank.rno` *geneset.drug_bank.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.drug_bank.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.GOBP.dme` *geneset.GOBP.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Biological Process (GOBP) genesets for Drosophila melanogaster. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOBP.dme
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.dre` *geneset.GOBP.dre genesets for Danio rerio*

Description

Gene Ontology Biological Process (GOBP) genesets for Danio rerio. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOBP.dre
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.hsa` *geneset.GOBP.hsa genesets for Homo sapiens*

Description

Gene Ontology Biological Process (GOBP) genesets for Homo sapiens. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

```
geneset.GOBP.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.mmu` *geneset.GOBP.mmu genesets for Mus musculus*

Description

Gene Ontology Biological Process (GOBP) genesets for Mus musculus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

```
geneset.GOBP.mmu
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.rno` *geneset.GOBP.rno genesets for Rattus norvegicus*

Description

Gene Ontology Biological Process (GOBP) genesets for Rattus norvegicus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

```
geneset.GOBP.rno
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.dme` *geneset.GOCC.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Cellular Component (GOCC) genesets for Drosophila melanogaster. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOCC.dme
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.dre` *geneset.GOCC.dre genesets for Danio rerio*

Description

Gene Ontology Cellular Component (GOCC) genesets for Danio rerio. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOCC.dre
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.hsa` *geneset.GOCC.hsa genesets for Homo sapiens*

Description

Gene Ontology Cellular Component (GOCC) genesets for Homo sapiens. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

```
geneset.GOCC.hsa
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.mmu` *geneset.GOCC.mmu genesets for Mus musculus*

Description

Gene Ontology Cellular Component (GOCC) genesets for Mus musculus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

```
geneset.GOCC.mmu
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.rno` *geneset.GOCC.rno genesets for Rattus norvegicus*

Description

Gene Ontology Cellular Component (GOCC) genesets for Rattus norvegicus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

```
geneset.GOCC.rno
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.dme` *geneset.GOMF.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Molecular Function (GOMF) genesets for Drosophila melanogaster. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOMF.dme
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.dre` *geneset.GOMF.dre genesets for Danio rerio*

Description

Gene Ontology Molecular Function (GOMF) genesets for Danio rerio. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOMF.dre
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.hsa` *geneset.GOMF.hsa genesets for Homo sapiens*

Description

Gene Ontology Molecular Function (GOMF) genesets for Homo sapiens. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

```
geneset.GOMF.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.mmu` *geneset.GOMF.mmu genesets for Mus musculus*

Description

Gene Ontology Molecular Function (GOMF) genesets for Mus musculus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

```
geneset.GOMF.mmu
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.rno` *geneset.GOMF.rno genesets for Rattus norvegicus*

Description

Gene Ontology Molecular Function (GOMF) genesets for Rattus norvegicus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

```
geneset.GOMF.rno
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

`geneset.hallmark.hsa` *geneset.hallmark.hsa genesets for Hallmark (MSigDB)*

Description

Hallmark (MSigDB) (hallmark) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:15 2017.

Usage

```
geneset.hallmark.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#H

`geneset.immunologic.hsa` *geneset.immunologic.hsa genesets for Immunologic Signatures (MSigDB)*

Description

Immunologic Signatures (MSigDB) (immunologic) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:45 2017.

Usage

```
geneset.immunologic.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C7

`geneset.kegg_pathway.hsa`

geneset.kegg_pathway.hsa genesets for KEGG Pathways

Description

KEGG Pathways (kegg_pathway) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:53 2017.

Usage

```
geneset.kegg_pathway.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://kegg.jp

`geneset.kegg_pathway.mmu`

geneset.kegg_pathway.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.kegg_pathway.rno`

geneset.kegg_pathway.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.hsa` *geneset.mesh.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.hsa)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.mmu` *geneset.mesh.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.rno` *geneset.mesh.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.metabolite.hsa` *geneset.metabolite.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.hsa)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.metabolite.mmu`

geneset.metabolite.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.metabolite.rno`

geneset.metabolite.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.microrna.hsa` *geneset.microrna.hsa genesets for MicroRNA Targets (MSigDB)*

Description

MicroRNA Targets (MSigDB) (microrna) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:56 2017.

Usage

```
geneset.microrna.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3

`geneset.oncogenic.hsa` *geneset.oncogenic.hsa genesets for Oncogenic Signatures (MSigDB)*

Description

Oncogenic Signatures (MSigDB) (oncogenic) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:47:23 2017.

Usage

```
geneset.oncogenic.hsa
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. GOBP.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C6

`geneset.panther_pathway.hsa`
geneset.panther_pathway.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.hsa)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.panther_pathway.mmu`

geneset.panther_pathway.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.panther_pathway.rno`

geneset.panther_pathway.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.pfam.hsa` *geneset.pfam.hsa genesets for Pfam*

Description

Pfam (pfam) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:47:28 2017.

Usage

```
geneset.pfam.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://pfam.xfam.org

`geneset.pfam.mmu` *geneset.pfam.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.pfam.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.pfam.rno` *geneset.pfam.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.pfam.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.protein_interaction_biogrid.hsa` *geneset.protein_interaction_biogrid.hsa genesets for BioGRID Protein Interactions*

Description

BioGRID Protein Interactions (protein_interaction_biogrid) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Tue Oct 24 16:05:53 2017.

Usage

```
geneset.protein_interaction_biogrid.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

https://thebiogrid.org

`geneset.reactome.dme` *geneset.reactome.dme genesets for Drosophila melanogaster*

Description

Reactome genesets for Drosophila melanogaster. All genesets are required to have >= 10 Entrez IDs. Built on Mon Mar 20 15:14:03 2017.

Usage

```
geneset.reactome.dme
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. Reactome.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

`geneset.reactome.dre` *geneset.reactome.dre genesets for Danio rerio*

Description

Reactome genesets for Danio rerio. All genesets are required to have >= 10 Entrez IDs. Built on Tue Mar 28 13:03:21 2017.

Usage

```
geneset.reactome.dre
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. Reactome.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

`geneset.reactome.hsa` *geneset.reactome.hsa genesets for Homo sapiens*

Description

Reactome genesets for Homo sapiens. All genesets are required to have >= 10 Entrez IDs. Built on Mon Mar 20 15:13:45 2017.

Usage

```
geneset.reactome.hsa
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. Reactome.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

`geneset.reactome.mmu` *geneset.reactome.mmu genesets for Mus musculus*

Description

Reactome genesets for Mus musculus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Mar 20 15:13:55 2017.

Usage

```
geneset.reactome.mmu
```

Format

A `GeneSet` object with the following slots:

- **type** A `character` indicating the type of genesets, e.g. Reactome.
- **dburl** A `character` of the URL of the database underlying the genesets.
- **organism** A `character` of the organism, e.g. Homo sapiens.
- **set.gene** An `environment` containing a `list` whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are `character` vectors of Entrez Gene IDs.
- **all.genes** A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.
- **set.name** An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

`geneset.reactome.rno` *geneset.reactome.rno genesets for Rattus norvegicus*

Description

Reactome genesets for Rattus norvegicus. All genesets are required to have >= 10 Entrez IDs. Built on Mon Mar 20 15:13:59 2017.

Usage

```
geneset.reactome.rno
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. Reactome.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

`geneset.transcription_factors.hsa` *geneset.transcription_factors.hsa genesets for Transcription Factor Targets (MSigDB)*

Description

Transcription Factor Targets (MSigDB) (transcription_factors) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:47:33 2017.

Usage

```
geneset.transcription_factors.hsa
```

Format

A `GeneSet` object with the following slots:

type A `character` indicating the type of genesets, e.g. GOBP.

dburl A `character` of the URL of the database underlying the genesets.

organism A `character` of the organism, e.g. Homo sapiens.

set.gene An `environment` containing a `list` whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are `character` vectors of Entrez Gene IDs.

all.genes A `character` vector of all the Entrez Gene IDs contained over all the genesets in this `type`.

set.name An `environment` containing a `list` whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3

`geneset.transcription_factors.mmu` *geneset.transcription_factors.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.transcription_factors.mmu)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.transcription_factors.rno`

geneset.transcription_factors.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.transcription_factors.rno)
```

Format

See `GeneSet-class` for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`locusdef.danRer10.10kb`

locusdef.danRer10.10kb locus definition

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.10kb_outside`

locusdef.danRer10.10kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.10kb_outside_upstream`

locusdef.danRer10.10kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.1kb` *locusdef.danRer10.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.1kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.1kb_outside` *locusdef.danRer10.1kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.1kb_outside_upstream`

locusdef.danRer10.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.5kb` *locusdef.danRer10.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.5kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, danRer10.
- **organism** A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.5kb_outside` *locusdef.danRer10.5kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, danRer10.
- **organism** A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.5kb_outside_upstream` *locusdef.danRer10.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.exon`

locusdef.danRer10.exon locus definition

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.danRer10.exon
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:24 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.intron` *locusdef.danRer10.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.danRer10.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.nearest_gene` *locusdef.danRer10.nearest_gene locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.danRer10.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:23 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.danRer10.nearest_tss`

locusdef.danRer10.nearest_tss locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.danRer10.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, danRer10.

organism A `character` indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:22 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`locusdef.dm3.10kb` *locusdef.dm3.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.dm3.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.10kb_outside` *locusdef.dm3.10kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:06 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.10kb_outside_upstream` *locusdef.dm3.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.dm3.10kb_outside_upstream`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.1kb` *locusdef.dm3.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

`locusdef.dm3.1kb`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.1kb_outside`

locusdef.dm3.1kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.1kb_outside_upstream` *locusdef.dm3.1kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm3.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.5kb` *locusdef.dm3.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.dm3.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.5kb_outside`

locusdef.dm3.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.5kb_outside_upstream` *locusdef.dm3.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm3.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm3.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.exon` *locusdef.dm3.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.dm3.exon
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm3.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.intron` *locusdef.dm3.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.dm3.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.nearest_gene`

locusdef.dm3.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.dm3.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm3.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm3.nearest_tss`

locusdef.dm3.nearest_tss locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.dm3.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm3.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.10kb` *locusdef.dm6.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.dm6.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.10kb_outside` *locusdef.dm6.10kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.dm6.10kb_outside`

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.10kb_outside_upstream`
locusdef.dm6.10kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.dm6.10kb_outside_upstream`

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.1kb` *locusdef.dm6.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.dm6.1kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.1kb_outside` *locusdef.dm6.1kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.1kb_outside_upstream` *locusdef.dm6.1kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.5kb` *locusdef.dm6.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.dm6.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.5kb_outside`

locusdef.dm6.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.5kb_outside_upstream` *locusdef.dm6.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.exon` *locusdef.dm6.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.dm6.exon
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.intron` *locusdef.dm6.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.dm6.intron
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.nearest_gene`

locusdef.dm6.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.dm6.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.nearest_tss` *locusdef.dm6.nearest_tss locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.dm6.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, dm6.

organism A `character` indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.hg19.10kb` *locusdef.hg19.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.hg19.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.10kb_outside`

locusdef.hg19.10kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:59 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.10kb_outside_upstream` *locusdef.hg19.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg19.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.1kb` *locusdef.hg19.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.hg19.1kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg19.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.1kb_outside` *locusdef.hg19.1kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.1kb_outside_upstream`

locusdef.hg19.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.5kb` *locusdef.hg19.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.hg19.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.5kb_outside` *locusdef.hg19.5kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.5kb_outside_upstream` *locusdef.hg19.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.hg19.5kb_outside_upstream`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.exon` *locusdef.hg19.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

`locusdef.hg19.exon`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:53 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.intron` *locusdef.hg19.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.hg19.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.nearest_gene` *locusdef.hg19.nearest_gene locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.hg19.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg19.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg19.nearest_tss` *locusdef.hg19.nearest_tss locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.hg19.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg19.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`locusdef.hg38.10kb` *locusdef.hg38.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.hg38.10kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg38.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.10kb_outside`

locusdef.hg38.10kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.10kb_outside_upstream` *locusdef.hg38.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.1kb` *locusdef.hg38.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.hg38.1kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.1kb_outside`

locusdef.hg38.1kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:40 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.1kb_outside_upstream`

locusdef.hg38.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg38.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.5kb` *locusdef.hg38.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.hg38.5kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg38.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.5kb_outside` *locusdef.hg38.5kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.5kb_outside_upstream` *locusdef.hg38.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.exon` *locusdef.hg38.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.hg38.exon
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:37 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.intron` *locusdef.hg38.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.hg38.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:38 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.nearest_gene` *locusdef.hg38.nearest_gene locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.hg38.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.hg38.nearest_tss` *locusdef.hg38.nearest_tss locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.hg38.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, hg38.

organism A `character` indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`locusdef.mm10.10kb` *locusdef.mm10.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.mm10.10kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm10.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.10kb_outside` *locusdef.mm10.10kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm10.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.10kb_outside_upstream` *locusdef.mm10.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.mm10.10kb_outside_upstream`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.1kb` *locusdef.mm10.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

`locusdef.mm10.1kb`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.1kb_outside`

locusdef.mm10.1kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm10.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.1kb_outside_upstream` *locusdef.mm10.1kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm10.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.5kb` *locusdef.mm10.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.mm10.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.5kb_outside`

locusdef.mm10.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm10.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.5kb_outside_upstream` *locusdef.mm10.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm10.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.exon` *locusdef.mm10.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.mm10.exon
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm10.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:35 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.intron` *locusdef.mm10.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.mm10.intron
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm10.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:36 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.nearest_gene`

locusdef.mm10.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.mm10.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm10.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm10.nearest_tss`

locusdef.mm10.nearest_tss locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.mm10.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm10.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`locusdef.mm9.10kb` *locusdef.mm9.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.mm9.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.10kb_outside` *locusdef.mm9.10kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.10kb_outside_upstream` *locusdef.mm9.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.1kb` *locusdef.mm9.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.mm9.1kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm9.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.1kb_outside` *locusdef.mm9.1kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm9.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.1kb_outside_upstream` *locusdef.mm9.1kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.5kb` *locusdef.mm9.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.mm9.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.5kb_outside`

locusdef.mm9.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.5kb_outside_upstream` *locusdef.mm9.5kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.exon` *locusdef.mm9.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.mm9.exon
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.intron` *locusdef.mm9.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.mm9.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.nearest_gene`

locusdef.mm9.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.mm9.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm9.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.nearest_tss` *locusdef.mm9.nearest_tss locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.mm9.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, mm9.

organism A `character` indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.rn4.10kb` *locusdef.rn4.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.rn4.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.10kb_outside`

locusdef.rn4.10kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.10kb_outside_upstream` *locusdef.rn4.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.1kb` *locusdef.rn4.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn4.1kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.1kb_outside` *locusdef.rn4.1kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.rn4.1kb_outside`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.1kb_outside_upstream`

locusdef.rn4.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.rn4.1kb_outside_upstream`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.5kb` *locusdef.rn4.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn4.5kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.5kb_outside`
locusdef.rn4.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.5kb_outside_upstream`
locusdef.rn4.5kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.exon` *locusdef.rn4.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn4.exon
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.intron` *locusdef.rn4.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn4.intron
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.nearest_gene`

locusdef.rn4.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn4.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.nearest_tss`

locusdef.rn4.nearest_tss locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.rn4.nearest_tss`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn4.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.10kb` *locusdef.rn5.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.rn5.10kb`

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.10kb_outside`

locusdef.rn5.10kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.10kb_outside_upstream` *locusdef.rn5.10kb_outside_upstream locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.1kb` *locusdef.rn5.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.1kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.1kb_outside`

locusdef.rn5.1kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.1kb_outside_upstream`

locusdef.rn5.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.5kb` *locusdef.rn5.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.5kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.5kb_outside` *locusdef.rn5.5kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.5kb_outside_upstream`

locusdef.rn5.5kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.exon` *locusdef.rn5.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn5.exon
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:17 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.intron` *locusdef.rn5.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn5.intron
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.nearest_gene`

locusdef.rn5.nearest_gene locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn5.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.nearest_tss`

locusdef.rn5.nearest_tss locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn5.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn5.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.10kb` *locusdef.rn6.10kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.10kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.10kb_outside` *locusdef.rn6.10kb_outside locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.10kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:40 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.10kb_outside_upstream`

locusdef.rn6.10kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.10kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.1kb` *locusdef.rn6.1kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.1kb
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.1kb_outside`

locusdef.rn6.1kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.1kb_outside
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.1kb_outside_upstream`

locusdef.rn6.1kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.1kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.5kb` *locusdef.rn6.5kb locus definition*

Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.5kb
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.5kb_outside`

locusdef.rn6.5kb_outside locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.5kb_outside
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.5kb_outside_upstream`

locusdef.rn6.5kb_outside_upstream locus definition

Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.5kb_outside_upstream
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.exon` *locusdef.rn6.exon locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn6.exon
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:36 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.intron` *locusdef.rn6.intron locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn6.intron
```

Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:37 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.nearest_gene` *locusdef.rn6.nearest_gene locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn6.nearest_gene
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:35 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.nearest_tss` *locusdef.rn6.nearest_tss locus definition*

Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn6.nearest_tss
```

Format

A `LocusDefinition` object with the following slots:

granges A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A `character` indicating the genome build. In this case, rn6.

organism A `character` indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:34 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

`LocusDefinition-class` *Class* `"LocusDefinition"`

Description

A storage class representing gene locus definitions and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form `new("LocusDefinition")`. These objects are used internally by the `chipenrich` package and users will not likely need to create these.

Slots

`dframe`: Object of class `"data.frame"`. Each row represents a locus for a particular geneid.

`granges`: Object of class `"GenomicRanges"`. Locus definitions stored as a GenomicRanges object.

`genome.build`: Object of class `"character"`. Genome build these definitions were generated from.

`organism`: Object of class `"character"`. Organism code.

Note

Not typically accessed by the user - this is used internally by the `chipenrich` package.

Author(s)

Ryan Welch `<welchr@umich.edu>`

Examples

```
# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss)
lapply(attributes(locusdef.mm9.nearest_tss), head)
```

`mappa.hg19.10kb.100mer` *mappa.hg19.10kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.24mer` *mappa.hg19.10kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.10kb.24mer)`

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.10kb.36mer)`

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.75mer` *mappa.hg19.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.100mer` *mappa.hg19.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.24mer` *mappa.hg19.1kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.36mer` *mappa.hg19.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.40mer` *mappa.hg19.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.50mer` *mappa.hg19.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.1kb.75mer` *mappa.hg19.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.100mer` *mappa.hg19.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.24mer` *mappa.hg19.5kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.24mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.36mer` *mappa.hg19.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.36mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.40mer` *mappa.hg19.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.50mer` *mappa.hg19.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.5kb.75mer` *mappa.hg19.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.100mer` *mappa.hg19.exon.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.24mer` *mappa.hg19.exon.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.36mer` *mappa.hg19.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.40mer` *mappa.hg19.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.50mer` *mappa.hg19.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.exon.75mer` *mappa.hg19.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.100mer`

mappa.hg19.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.100mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.24mer`

mappa.hg19.intron.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.intron.24mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.36mer`

mappa.hg19.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.intron.36mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.40mer` *mappa.hg19.intron.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.50mer` *mappa.hg19.intron.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.intron.75mer`

mappa.hg19.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.100mer`

mappa.hg19.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.24mer`

mappa.hg19.nearest_gene.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.24mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.36mer`

mappa.hg19.nearest_gene.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.36mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.40mer` *mappa.hg19.nearest_gene.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.50mer` *mappa.hg19.nearest_gene.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_gene.75mer`

mappa.hg19.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.100mer`

mappa.hg19.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.24mer`

mappa.hg19.nearest_tss.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.36mer`

mappa.hg19.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.40mer` *mappa.hg19.nearest_tss.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.50mer` *mappa.hg19.nearest_tss.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.nearest_tss.75mer`

mappa.hg19.nearest_tss.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.10kb.100mer` *mappa.mm9.10kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.10kb.36mer` *mappa.mm9.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.36mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.10kb.40mer` *mappa.mm9.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.10kb.50mer` *mappa.mm9.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.10kb.75mer` *mappa.mm9.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.10kb.75mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.100mer` *mappa.mm9.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.1kb.100mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.36mer` *mappa.mm9.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.40mer` *mappa.mm9.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.50mer` *mappa.mm9.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.75mer` *mappa.mm9.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.100mer` *mappa.mm9.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.100mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.36mer` *mappa.mm9.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.36mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.40mer` *mappa.mm9.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.50mer` *mappa.mm9.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.75mer` *mappa.mm9.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.100mer` *mappa.mm9.exon.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.36mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.40mer` *mappa.mm9.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.50mer` *mappa.mm9.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.intron.100mer`

mappa.mm9.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.intron.36mer`

mappa.mm9.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.intron.40mer`

mappa.mm9.intron.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.40mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.intron.50mer`

mappa.mm9.intron.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.intron.75mer`

mappa.mm9.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.100mer`

mappa.mm9.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.nearest_gene.100mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.36mer` *mappa.mm9.nearest_gene.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.nearest_gene.36mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.40mer`

mappa.mm9.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.50mer`

mappa.mm9.nearest_gene.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.50mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.75mer`

mappa.mm9.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.100mer`

mappa.mm9.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.36mer`

mappa.mm9.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.40mer`

mappa.mm9.nearest_tss.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.50mer`

mappa.mm9.nearest_tss.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <`welchr@umich.edu`>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.75mer`

mappa.mm9.nearest_tss.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.75mer)
```

Format

A data frame containing:

`geneid`	Entrez Gene IDs
`mappa`	Gene locus mappability

Author(s)

Ryan Welch `<welchr@umich.edu>`

See Also

For more information about gene locus definitions: `chipenrich.data`

`peaks_E2F4` *ChIP-seq Peaks for the E2F4 Transcription Factor*

Description

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

Usage

```
peaks_E2F4
```

Format

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." Nucleic Acids Res 39(9): 3558-3573.

Examples

```
# Load E2F4 peak data.
data(peaks_E2F4)

# Print the first 10 peaks in the dataset.
print(head(peaks_E2F4))
```

`peaks_H3K4me3_GM12878` *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

Usage

```
peaks_H3K4me3_GM12878
```

Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found at the following ENCODE URL:

http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878H

Examples

```
# Load H3K4me3 in GM12878 peak data.
data(peaks_H3K4me3_GM12878)

# Print the first 10 peaks in the dataset.
print(head(peaks_H3K4me3_GM12878))
```

`spline.log_dtss.90ENCODE` *DTSS Spline adjustment*

Description

A mgcv::gam object on a combined data of 90 ENCODE ChIP-seq datasets that modeled the relationship between a gene's locus length the distance from a peak to the gene's transcription start site, using a cubic spline. This is used to adjust for the proximity to TSSes test.

Usage

```
spline.log_dtss.90ENCODE
```

Format

An object of class `gam` (inherits from `glm`, `lm`) of length 46.

`tss.danRer10` *tss.danRer10 TSS locations*

Description

A `GRanges` with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.danRer10
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`tss.dm3` *tss.dm3 TSS locations*

Description

A `GRanges` with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.dm3
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`tss.dm6` *tss.dm6 TSS locations*

Description

A `GRanges` with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.dm6
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`tss.hg19` *tss.hg19 TSS locations*

Description

A `GRanges` with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.hg19
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

`tss.hg38` *tss.hg38 TSS locations*

Description

A `GRanges` with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.hg38
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`tss.mm10` *tss.mm10 TSS locations*

Description

A `GRanges` with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.mm10
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`tss.mm9` *tss.mm9 TSS locations*

Description

A `GRanges` with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.mm9
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

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`tss.rn4` *tss.rn4 TSS locations*

Description

A `GRanges` with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn4
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`tss.rn5` *tss.rn5 TSS locations*

Description

A `GRanges` with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn5
```

Format

A `GRanges` object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`tss.rn6` *tss.rn6 TSS locations*

Description

A `GRanges` with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn6
```

Format

A `GRanges` object with the following `mcols`:

gene_id	The Entrez ID for the TSS
symbol	The gene symbol for the TSS

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

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