

Package ‘geneObjects’

May 30, 2023

Title A Set of S4 Classes for Different Gene Types

Version 1.0.0

Description The geneObjects package implements several functions for handling various gene classes as objects with several slots based on Ensembl. It provides a way to represent different gene types (e.g., protein-coding genes, long non-coding RNAs, microRNAs) and manipulate them in a unified framework. It also provides various functions to access and modify the data stored in these objects.

License GPL (>= 2)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

VignetteBuilder knitr

Imports GenomicRanges, IRanges, methods

Suggests knitr, testthat, BiocStyle

NeedsCompilation no

Author Niccolò Bianchi [aut, cre]

Maintainer Niccolò Bianchi <niccolo.bianchi2@studenti.unimi.it>

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geneObjects-package *geneObjects* - provides a set of S4 classes for different gene types

Description

The geneObjects package implements several functions for handling various gene classes as objects with several slots based on Ensembl.

Details

Package: geneObjects
 Type: Package
 Version: 1.0.0
 Date: 2022-05-27
 License: GPL (>=2)

The geneObjects package provides a set of S4 classes to represent different types of genes (ProteinCodingGene, LncRNAGene, MicroRNAGene), all inheriting from a general Gene class. This package facilitates the handling of gene data by providing appropriate constructors, accessors, and class-specific methods for each gene class.

Author(s)

Niccolò Bianchi [aut, cre]
 UniMi + PoliMI
 Maintainer: Niccolò Bianchi
 E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

Gene-class

Gene class

Description

This is a virtual S4 class to represent a general gene with associated information.

Slots

ID The gene ID (Ensembl ID or NCBI gene ID).
 HUGO_symbol The HUGO gene symbol.
 gene_name The full gene name.
 description A brief description of the gene.
 gene_structure The gene structure represented as a GRanges object.

Author(s)

Niccolò Bianchi
UniMi + PoliMI
Maintainer: Niccolò Bianchi
E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

See Also

[ProteinCodingGene](#)
[LncRNAGene](#)
[MicroRNAGene](#)

Examples

```
# Not usually instantiated directly, used as a superclass for other gene classes.
```

getID	<i>Generic getter for gene ID</i>
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Description

This method gets the ID for the gene.
Method to get the ID for a Gene object.
Method to get the ID for a ProteinCodingGene object.
Method to get the ID for a LncRNAGene object.
Method to get the ID for a MicroRNAGene object.
This method sets the ID for the gene.
Method to set the ID for a Gene object.
Method to set the ID for a ProteinCodingGene object.
Method to set the ID for a LncRNAGene object.
Method to set the ID for a MicroRNAGene object.

Usage

```
getID(gene)  
  
## S4 method for signature 'Gene'  
getID(gene)  
  
## S4 method for signature 'ProteinCodingGene'  
getID(gene)
```

```
## S4 method for signature 'LncRNAGene'
getID(gene)

## S4 method for signature 'MicroRNAGene'
getID(gene)

setID(gene) <- value

## S4 replacement method for signature 'Gene'
setID(gene) <- value

## S4 replacement method for signature 'ProteinCodingGene'
setID(gene) <- value

## S4 replacement method for signature 'LncRNAGene'
setID(gene) <- value

## S4 replacement method for signature 'MicroRNAGene'
setID(gene) <- value
```

Arguments

gene	An object of class MicroRNAGene.
value	A character string representing the new ID for the gene.

Value

A character string representing the ID of the gene.
 A character string representing the ID of the gene.
 A character string representing the ID of the gene.
 A character string representing the ID of the gene.
 A character string representing the ID of the gene.
 An updated Gene object with the new ID.
 An updated Gene object with the new ID.
 An updated ProteinCodingGene object with the new ID.
 An updated LncRNAGene object with the new ID.
 An updated MicroRNAGene object with the new ID.

lengthProduct	<i>Generic function for length of gene product</i>
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Description

This method gets the length of the product of the gene.
 Method to get the length of the product for a ProteinCodingGene object.
 Method to get the length of the product for a LncRNAGene object.
 Method to get the length of the product for a MicroRNAGene object.

Usage

```
lengthProduct(gene)

## S4 method for signature 'ProteinCodingGene'
lengthProduct(gene)

## S4 method for signature 'LncRNAGene'
lengthProduct(gene)

## S4 method for signature 'MicroRNAGene'
lengthProduct(gene)
```

Arguments

gene An object of class MicroRNAGene.

Value

The length of the gene product.
The length of the protein sequence.
The length of the RNA sequence.
The length of the microRNA seed sequence.

LncRNAGene	<i>Constructor function for LncRNAGene class</i>
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Description

This function creates a new instance of the LncRNAGene class.

Usage

```
LncRNAGene(ID, HUGO_symbol, gene_name, description, gene_structure, lncRNA_ID, RNA_sequence)
```

Arguments

ID The gene ID (Ensembl ID or NCBI gene ID).
HUGO_symbol The HUGO gene symbol.
gene_name The full gene name.
description A brief description of the gene.
gene_structure The gene structure represented as a GRanges object.
lncRNA_ID The lncRNA ID.
RNA_sequence The RNA sequence.

Value

An instance of the LncRNAGene class.

Author(s)

Niccolò Bianchi
 UniMi + PoliMI
 Maintainer: Niccolò Bianchi
 E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(3000, 4000), strand = "-")
LncRNAGene(ID = "ENSG000002", HUGO_symbol = "LINC00001",
            gene_name = "Long intergenic non-protein coding RNA 1",
            description = "Long non-coding RNA",
            gene_structure = gene_structure,
            lncRNA_ID = "ENST000004", RNA_sequence = "ACUGCUAGCUAGUCA...")
```

LncRNAGene-class

Long non-coding RNA gene class

Description

This is an S4 class to represent a long non-coding RNA gene, inheriting from the Gene class.

Slots

lncRNA_ID The lncRNA ID.
 RNA_sequence The RNA sequence.

Author(s)

Niccolò Bianchi
 UniMi + PoliMI
 Maintainer: Niccolò Bianchi
 E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

See Also

[ProteinCodingGene](#)
[MicroRNAGene](#)

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(start = 3000, end = 4000),
LncRNAGene(ID = "ENSG000002", HUGO_symbol = "LINC00001",
           gene_name = "Long intergenic non-protein coding RNA 1",
           description = "Long non-coding RNA",
           gene_structure = gene_structure,
           lncRNA_ID = "ENST000004", RNA_sequence = "ACUGCUAGCUAGUCA...")
```

MicroRNAGene

*Constructor function for MicroRNAGene class***Description**

This function creates a new instance of the MicroRNAGene class.

Usage

```
MicroRNAGene(ID, HUGO_symbol, gene_name, description, gene_structure, microRNA_ID, microRNA_seed_s
```

Arguments

ID	The gene ID (Ensembl ID or NCBI gene ID).
HUGO_symbol	The HUGO gene symbol.
gene_name	The full gene name.
description	A brief description of the gene.
gene_structure	The gene structure represented as a GRanges object.
microRNA_ID	The microRNA ID.
microRNA_seed_sequence	The microRNA seed sequence.

Value

An instance of the MicroRNAGene class.

Author(s)

Niccolò Bianchi
 UniMi + PoliMI
 Maintainer: Niccolò Bianchi
 E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(5000, 6000), strand = "+")
MicroRNAGene(ID = "ENSG000003", HUGO_symbol = "MIR00001",
             gene_name = "MicroRNA 1",
             description = "MicroRNA",
             gene_structure = gene_structure,
             microRNA_ID = "ENST000005", microRNA_seed_sequence = "UGAGGUAGUAGGUUGUAUGGUAG")
```

MicroRNAGene-class	<i>MicroRNA gene class</i>
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Description

This is an S4 class to represent a microRNA gene, inheriting from the Gene class.

Slots

microRNA_ID The microRNA ID.

microRNA_seed_sequence The microRNA seed sequence.

Author(s)

Niccolò Bianchi
 UniMi + PoliMI
 Maintainer: Niccolò Bianchi
 E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

See Also

[ProteinCodingGene](#)
[LncRNAGene](#)

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(start = 5000, end = 6000), strand = "+")
MicroRNAGene(ID = "ENSG000003", HUGO_symbol = "MIR00001",
             gene_name = "MicroRNA 1",
             description = "MicroRNA",
             gene_structure = gene_structure,
             microRNA_ID = "ENST000005", microRNA_seed_sequence = "UGAGGUAGUAGGUUGUAUGGUAG")
```

ProteinCodingGene	<i>Constructor function for ProteinCodingGene class</i>
-------------------	---------------------------------------------------------

Description

This function creates a new instance of the ProteinCodingGene class.

Usage

```
ProteinCodingGene(ID, HUGO_symbol, gene_name, description, gene_structure, protein_ID, protein_sequence)
```

Arguments

ID	The gene ID (Ensembl ID or NCBI gene ID).
HUGO_symbol	The HUGO gene symbol.
gene_name	The full gene name.
description	A brief description of the gene.
gene_structure	The gene structure represented as a GRanges object.
protein_ID	The protein ID.
protein_sequence	The protein sequence.

Value

An instance of the ProteinCodingGene class.

Author(s)

Niccolò Bianchi
UniMi + PoliMI
Maintainer: Niccolò Bianchi
E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(1000, 2000), strand = "+")
ProteinCodingGene(ID = "ENSG000001", HUGO_symbol = "BRCA1",
  gene_name = "Breast cancer 1",
  description = "Breast cancer type 1 susceptibility protein",
  gene_structure = gene_structure,
  protein_ID = "ENSP000003", protein_sequence = "MENSDRNSIKVAV...")
```

ProteinCodingGene-class

Protein-coding gene class

Description

This is an S4 class to represent a protein-coding gene, inheriting from the Gene class.

Slots

protein_ID The protein ID.

protein_sequence The protein sequence.

Author(s)

Niccolò Bianchi

UniMi + PoliMI

Maintainer: Niccolò Bianchi

E-Mail: niccolo.bianchi2@studenti.unimi.it

References

<https://www.ensembl.org/index.html?redirect=no>

See Also

[LncRNAGene](#)

[MicroRNAGene](#)

Examples

```
gene_structure <- GenomicRanges::GRanges(seqnames = "chr1", ranges = IRanges::IRanges(start = 1000, end = 2000))
ProteinCodingGene(ID = "ENSG000001", HUGO_symbol = "BRCA1",
  gene_name = "Breast cancer 1",
  description = "Breast cancer type 1 susceptibility protein",
  gene_structure = gene_structure,
  protein_ID = "ENSP000003", protein_sequence = "MENS DRNSIKVAV...")
```

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