Package 'GenePackage'

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Type Package

Title A Package for Gene Objects

Version 0.1.0

Description This package provides S4 classes for different gene types.

Imports methods

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.2

biocViews Genomics, Transcriptomics

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Contents

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createGene   *Create a Gene Object*

Description

This function creates a gene object of the specified type.

Usage

```
createGene(type, ...)
```

Arguments

type
: A character string specifying the type of gene ('protein_coding', 'lncRNA', 'miRNA', 'transcript').

...
: Additional parameters for the gene object.

Value

An object of the specified gene class.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", symbol = "TP53",
            name = "Tumor protein p53", description = "Plays a role in cell cycle regulation",
                chromosome = "17", start = 7565097, end = 7590856, strand = "+",
                proteinID = "NP_000537", proteinSequence = "MDM2", exonCount = 11L)
getSymbol(gene)
lengthProduct(gene)
gcContent(gene)
```

---

gcContent   *Calculate the GC Content of a Gene Sequence*

Description

This method calculates the GC content (percentage of G and C nucleotides) of a gene's sequence.

Usage

```
gcContent(object)
```

Arguments

object
: An object of class ProteinCodingGene or Transcript.

Value

The GC content as a percentage.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", symbol = "TP53",
                    proteinSequence = "MDM2")
gcContent(gene)
transcript <- createGene("transcript", ID = "ENST000002", sequence = "ATGCATGC")
gcContent(transcript)
```

Gene-class   *Gene Class*

Description

A class representing a general gene structure with various attributes.

Slots

ID A character string representing the gene ID.

symbol A character string representing the gene symbol.

name A character string representing the gene name.

description A character string representing the gene description.

chromosome A character string representing the chromosome.

start A numeric value representing the start position of the gene.

end A numeric value representing the end position of the gene.

strand A character string representing the DNA strand.

---

getSymbol   *Get the Symbol of a Gene Object*

Description

This method returns the symbol of a gene object.

Usage

```
## S4 method for signature 'Gene'
getSymbol(object)
```

Arguments

object   An object of class Gene.

Value

The symbol of the gene.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", symbol = "TP53")
getSymbol(gene)
```

---

lengthProduct   *Get the Length of the Gene Product*

Description

This method returns the length of the gene product, depending on the gene type.

Usage

```
lengthProduct(object)
```

Arguments

object   An object of a specific gene class.

Value

The length of the gene product.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", symbol = "TP53",
                   proteinSequence = "MDM2")
lengthProduct(gene)
```

LongNonCodingRNA-class

Long Non-Coding RNA Gene Class

Description

A class representing a long non-coding RNA gene with specific attributes.

Slots

lncRNAID A character string representing the lncRNA ID.

RNASequence A character string representing the RNA sequence.

MicroRNA-class   *MicroRNA Gene Class*

Description

A class representing a microRNA gene with specific attributes.

Slots

miRNAID A character string representing the miRNA ID.

seedSequence A character string representing the miRNA seed sequence.

```
ProteinCodingGene-class
```
Protein-Coding Gene Class

Description

A class representing a protein-coding gene with specific attributes.

Slots

proteinID A character string representing the protein ID.

proteinSequence A character string representing the protein sequence.

exonCount An integer representing the number of exons.

```
setChromosome
```
Set the Chromosome of a Gene Object

Description

This method sets the chromosome of a gene object.

Usage

```
setChromosome(object, value)
```

Arguments

object   An object of class Gene.

value   The new chromosome value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", chromosome = "17")
gene <- setChromosome(gene, "18")
```

---

setDescription   *Set the Description of a Gene Object*

Description

This method sets the description of a gene object.

Usage

```
setDescription(object, value)
```

Arguments

object   An object of class Gene.

value   The new description value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", description = "Tumor protein p53")
gene <- setDescription(gene, "New Description")
```

---

setEnd   *Set the End Position of a Gene Object*

Description

This method sets the end position of a gene object.

Usage

```
setEnd(object, value)
```

Arguments

object   An object of class Gene.

value   The new end position value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", end = 7590856)
gene <- setEnd(gene, 7591000)
```

---

setName *Set the Name of a Gene Object*

Description

This method sets the name of a gene object.

Usage

```
setName(object, value)
```

Arguments

object   An object of class Gene.

value   The new name value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", name = "Tumor protein p53")
gene <- setName(gene, "New Gene Name")
```

---

setStart *Set the Start Position of a Gene Object*

Description

This method sets the start position of a gene object.

Usage

```
setStart(object, value)
```

Arguments

object   An object of class Gene.

value   The new start position value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", start = 7565097)
gene <- setStart(gene, 7566000)
```

---

setStrand   *Set the Strand of a Gene Object*

Description

This method sets the strand of a gene object.

Usage

```
setStrand(object, value)
```

Arguments

object   An object of class Gene.

value   The new strand value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", strand = "+")
gene <- setStrand(gene, "-")
```

---

setSymbol   *Set the Symbol of a Gene Object*

Description

This method sets the symbol of a gene object.

Usage

```
setSymbol(object, value)
```

Arguments

object   An object of class Gene.

value   The new symbol value to assign.

Value

The modified gene object.

Examples

```
gene <- createGene("protein_coding", ID = "ENSG000001", symbol = "TP53")
gene <- setSymbol(gene, "NEW_SYMBOL")
```

Transcript-class   *Transcript Class*

Description

A class representing a transcript, inheriting from the Gene class.

Slots

transcriptID A character string representing the transcript ID.

sequence A character string representing the transcript sequence.

Index