

Package: genemodel (via r-universe)

October 27, 2024

Title Gene Model Plotting in R

Date 2017-02-20

Version 1.1.0

Description Using simple input, this package creates plots of gene models. Users can create plots of alternatively spliced gene variants and the positions of mutations and other gene features.

Depends R (>= 3.2.5)

Imports stringr

License GPL-2

LazyData true

RoxygenNote 5.0.1

URL <https://github.com/greymonroe/genemodel>

Suggests knitr, rmarkdown

VignetteBuilder knitr

Repository <https://greymonroe.r-universe.dev>

RemoteUrl <https://github.com/greymonroe/genemodel>

RemoteRef HEAD

RemoteSha 22a96fd2402e8d75c4d8f9717b86a322958380cc

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 AT5G62640

Gene model for AT5G62640

Description

Gene model for AT5G62640

Usage

AT5G62640

Format

A data frame with 32 rows and 2 variables:

type feature of gene ie intron exon or UTR

coordinates start and stop of gene feature separated by a "-" ...

Source

<https://www.arabidopsis.org/servlets/TairObject?type=gene&id=1000654517>

 genemodel.plot

genemodel.plot

Description

This function plots a gene model

Usage

```
genemodel.plot(model, start, bpstop, orientation, xaxis = TRUE)
```

Arguments

model	data.frame containing model information. Required columns are "type", "coordinates"
start	start position
bpstop	stop position
orientation	either "foward" or "reverse" indicates the direction of transcription
xaxis	default is TRUE and adds axis above gene model showing position

Examples

```
data(AT5G62640)
genemodel.plot(AT5G62640, 25149433, 25152541, "reverse", xaxis=TRUE)
```

mutation.plot	<i>mutation.plot</i>
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Description

This function plots mutations along genemodels created with `genemodel.plot`

Usage

```
mutation.plot(start, stop, text = "", drop = -0.15, col = "red",  
             haplotypes = NULL)
```

Arguments

<code>start</code>	start position
<code>stop</code>	stop position
<code>text</code>	any text that you want displayed on the label
<code>drop</code>	how far below the gene model you want the mutation label to be placed
<code>col</code>	the color of the text and mutation line to be
<code>haplotypes</code>	the color of dots that you want to place along the mutation line to indicate some factor such as haplotype that the mutation belongs to

Examples

```
data(AT5G62640)  
genemodel.plot(AT5G62640, 25149433, 25152541, "reverse")  
mutation.plot(25149593, 25149593, text="P->S", col="red", haplotype="blue")
```

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