Package ‘genemodel’

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Title Gene Model Plotting in R

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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

NeedsCompilation no

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Repository CRAN

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Contents

`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` *mutation.plot*

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

`start`	start position
`stop`	stop position
`text`	any text that you want displayed on the label
`drop`	how far below the gene model you want the mutation label to be placed
`col`	the color of the text and mutation line to be
`haplotypes`	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")
```

Index