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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R topics documented:

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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>

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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")
```

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