Package ‘genemodel’

February 20, 2017

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
NeedsCompilation no
Author J Grey Monroe [aut, cre]
Maintainer J Grey Monroe <greymonroe@gmail.com>
Repository CRAN
Date/Publication 2017-02-20 19:09:06

R topics documented:

AT5G62640 ......................................................... 2
genemodel.plot .................................................. 2
mutation.plot .................................................... 3

Index 4
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=1PPP6UTU17

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 "forward" 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 plots

This function plots mutations along genemodels created with genemodel.plot

Usage

```r
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

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

*Topic datasets
   AT5G62640, 2

AT5G62640, 2

genemodel.plot, 2

mutation.plot, 3