Package ‘genemodel’

October 13, 2022

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=1000654517

---

**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)
Description
This function plots mutations along genemodes 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

* datasets  
  AT5G62640, 2

AT5G62640, 2

genemodel.plot, 2

mutation.plot, 3