Package ‘crisprScoreData’

March 21, 2024

Version 1.6.0
Date 2022-10-12
Title Pre-trained models for the crisprScore package
Depends ExperimentHub
Imports AnnotationHub, utils
Suggests BiocStyle, knitr, rmarkdown, testthat
biocViews ExperimentHub, Homo_sapiens_Data
Description Provides an interface to access pre-trained models for on-target and off-target gRNA activity prediction algorithms implemented in the crisprScore package. Pre-trained model data are stored in the ExperimentHub database. Users should consider using the crisprScore package directly to use and load the pre-trained models.
License MIT + file LICENSE
Encoding UTF-8
RoxygenNote 7.1.2
VignetteBuilder knitr

BugReports https://github.com/crisprVerse/crisprScoreData
URL https://github.com/crisprVerse/crisprScoreData/issues
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**R topics documented:**

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| crisprScoreData | Pretrained models for several crisprScore prediction algorithms |

**Description**

Pretrained models for DeepHF and Lindel on-target prediction algorithms for Cas9 gRNA performance to be used by crisprScore package. Data were obtained using the script inst/scripts/make-data.R.

**Usage**

- DeepWt.hdf5(metadata=FALSE)
- DeepWt.T7.hdf5(metadata=FALSE)
- DeepWt.U6.hdf5(metadata=FALSE)
- hf_rnn_model.hdf5(metadata=FALSE)
- esp_rnn_model.hdf5(metadata=FALSE)
- Model_weights.pkl(metadata=FALSE)
- CRISPRa_model.pkl(metadata=FALSE)
- CRISPRi_model.pkl(metadata=FALSE)
- RFcombined.rds(metadata=FALSE)

**Arguments**

- metadata logical value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior(metadata=FALSE) loads the data.

**Format**

- character

**Value**

These accessor functions return characters specifying path of the files

**References**


Examples

DeepWt.hdf5()
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