

Package ‘crisprScoreData’

March 30, 2023

Version 1.3.0

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>

git_url <https://git.bioconductor.org/packages/crisprScoreData>

git_branch devel

git_last_commit 666db07

git_last_commit_date 2022-11-01

Date/Publication 2023-03-30

Author Jean-Philippe Fortin [aut, cre, cph]

Maintainer Jean-Philippe Fortin <fortin946@gmail.com>

R topics documented:

crisprScoreData 2

crisprScoreData	<i>Pretrained models for several crisprScore prediction algorithms</i>
-----------------	--

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(<code>metadata=FALSE</code>) loads the data.
----------	--

Format

character

Value

These accessor functions return characters specifying path of the files

References

Wang, D., Zhang, C., Wang, B. et al. Optimized CRISPR guide RNA design for two high-fidelity Cas9 variants by deep learning. *Nat Commun* 10, 4284 (2019). <https://doi.org/10.1038/s41467-019-12281-8>

Wei Chen, Aaron McKenna, Jacob Schreiber, Maximilian Haeussler, Yi Yin, Vikram Agarwal, William Stafford Noble, Jay Shendure, Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair, *Nucleic Acids Research*, Volume 47, Issue 15, 05 September 2019, Pages 7989–8003, <https://doi.org/10.1093/nar/gkz487>.

Examples

```
DeepWt.hdf5()
```

Index

* datasets

- crisprScoreData, [2](#)

- CRISPRa_model.pkl (crisprScoreData), [2](#)
- CRISPRi_model.pkl (crisprScoreData), [2](#)
- crisprScoreData, [2](#)
- crisprScoreData-package
 - (crisprScoreData), [2](#)

- DeepWt.hdf5 (crisprScoreData), [2](#)
- DeepWt_T7.hdf5 (crisprScoreData), [2](#)
- DeepWt_U6.hdf5 (crisprScoreData), [2](#)

- esp_rnn_model.hdf5 (crisprScoreData), [2](#)

- hf_rnn_model.hdf5 (crisprScoreData), [2](#)

- Model_weights.pkl (crisprScoreData), [2](#)

- RFcombined.rds (crisprScoreData), [2](#)