Package ‘cfToolsData’

February 27, 2025

Title ExperimentHub data for the cfTools package

Version 1.5.0

Description The cfToolsData package supplies the data for the cfTools package. It contains two pre-trained deep neural network (DNN) models for the cfSort function. Additionally, it includes the shape parameters of beta distribution characterizing methylation markers associated with four tumor types for the CancerDetector function, as well as the parameters characterizing methylation markers specific to 29 primary human tissue types for the cfDeconvolve function.

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LazyData False

Encoding UTF-8

Depends R (>= 4.3.0)

RoxygenNote 7.2.3

VignetteBuilder knitr

Imports utils, ExperimentHub

Suggests BiocStyle, knitr, rmarkdown, ExperimentHubData, testthat (>= 3.0.0)

biocViews ExperimentHub, ExperimentData, ReproducibleResearch, DiseaseModel, CancerData, Tissue

URL `https://github.com/jasminezhoulab/cfToolsData`

BugReports `https://github.com/jasminezhoulab/cfToolsData/issues`

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Contents

`cfToolsData` *ExperimentHub datasets for the cfTools package*

Description

The cfToolsData package supplies data for the cfTools package. It contains two pre-trained deep neural network (DNN) models for the cfSort function. Additionally, it includes the shape parameters of beta distribution characterizing methylation markers associated with four cancer types and 29 primary human tissue types as example files for the CancerDetector and the cfDeconvolve function.

For more information, see https://doi.org/10.1038/s41467-022-32995-6 and https://doi.org/10.1073/pnas.2305236120.

Value

Downloads and caches '.txt.gz' or HDF5-formatted '.h5' files.

Author(s)

Ran Hu

`COAD.tumorMarkerParams.hg19` *Parameters of COAD markers*

Description

The shape parameters of beta distribution characterizing methylation markers associated with colon adenocarcinoma (COAD)

Value

Downloads and caches a '.txt.gz' file.

Examples

```
COADMarkerParams <- COAD.tumorMarkerParams.hg19()
COADMarkerParams
```

`DNN1` *Model DNN1*

Description

The 1st deep neural network in cfSort.

Value

Downloads and caches a '.h5' file in HDF5 format.

Examples

```
modelDNN1 <- DNN1()
modelDNN1
```

`DNN2` *Model DNN2*

Description

The 2nd deep neural network in cfSort.

Value

Downloads and caches a ‘.h5‘ file in HDF5 format.

Examples

```
modelDNN2 <- DNN2()
modelDNN2
```

`LIHC.tumorMarkerParams.hg19` *Parameters of LIHC markers*

Description

The shape parameters of beta distribution characterizing methylation markers associated with liver hepatocellular carcinoma (LIHC)

Value

Downloads and caches a ‘.txt.gz‘ file.

Examples

```
LIHCMarkerParams <- LIHC.tumorMarkerParams.hg19()
LIHCMarkerParams
```

`LUNG.tumorMarkerParams.hg19` *Parameters of lung cancer markers*

Description

The shape parameters of beta distribution characterizing methylation markers associated with lung cancer

Value

Downloads and caches a ‘.txt.gz‘ file.

Examples

```
LUNGMarkerParams <- LUNG.tumorMarkerParams.hg19()
LUNGMarkerParams
```

`STAD.tumorMarkerParams.hg19` *Parameters of STAD markers*

Description

The shape parameters of beta distribution characterizing methylation markers associated with stomach adenocarcinoma (STAD)

Value

Downloads and caches a ‘.txt.gz‘ file.

Examples

```
STADMarkerParams <- STAD.tumorMarkerParams.hg19()
STADMarkerParams
```

`tissueMarkerParams.annot`

Annotation of tissue markers

Description

The annotation of strategies used to identify tissue markers.

Value

Downloads and caches a ‘.txt.gz‘ file.

Examples

```
tissueMarkerAnnot <- tissueMarkerParams.annot()
tissueMarkerAnnot
```

`tissueMarkerParams.hg19`

Parameters of tissue markers

Description

The shape parameters of beta distribution characterizing methylation markers specific to 29 primary human tissue types

Value

Downloads and caches a ‘.txt.gz‘ file.

Examples

```
tissueMarkerParams <- tissueMarkerParams.hg19()
tissueMarkerParams
```

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