

# Package ‘cfToolsData’

November 28, 2024

**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.

**License** file LICENSE

**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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## 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

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`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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