

Package ‘BioImageDbs’

June 27, 2024

Type Package

Title Bio- and biomedical imaging dataset for machine learning and deep learning (for ExperimentHub)

Version 1.13.0

Encoding UTF-8

Depends R (>= 4.1.0)

Imports ExperimentHub, AnnotationHub, markdown, rmarkdown, EBImage, magick, magrittr, filesstrings, animation, einsum

Suggests knitr, BiocStyle, purrr

Description The package provides a bioimage dataset for the image analysis using machine learning and deep learning. The dataset includes microscopy imaging data with supervised labels. The data is provided as R list data that can be loaded to Keras/tensorflow in R.

VignetteBuilder knitr

License Artistic-2.0

URL <https://kumes.github.io/BioImageDbs/>

LazyLoad yes

biocViews ExperimentHub, ExperimentData, CellCulture, Tissue

RoxygenNote 7.1.1

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

git_branch devel

git_last_commit 9f180ad

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-06-27

Author Satoshi Kume [aut, cre] (<<https://orcid.org/0000-0001-7481-2843>>),
Koza Nishida [aut] (<<https://orcid.org/0000-0001-8501-7319>>)

Maintainer Satoshi Kume <satoshi.kume.1984@gmail.com>

Contents

BioImageDbs-package	2
Index	3

BioImageDbs-package	<i>Bio- and biomedical imaging dataset for machine learning and deep learning (for ExperimentHub)</i>
---------------------	---

Description

The package provides a bioimage dataset for the image analysis using machine learning and deep learning. The dataset includes microscopy imaging data with supervised labels. The data is provided as R list data that can be loaded to Keras/tensorflow in R.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.

Author(s)

Satoshi Kume [aut, cre] (<<https://orcid.org/0000-0001-7481-2843>>), Kozo Nishida [aut] (<<https://orcid.org/0000-0001-8501-7319>>)

Maintainer: Satoshi Kume <satoshi.kume.1984@gmail.com>

Examples

```
ls("package:BioImageDbs") # This is empty package
```

Index

* **package**

BioImageDbs-package, [2](#)

BioImageDbs (BioImageDbs-package), [2](#)

BioImageDbs-package, [2](#)