Package ‘BioImageDbs’

May 23, 2024

Type Package

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

Version 1.12.0

Encoding UTF-8

Depends R (>= 4.1.0)

Imports ExperimentHub, AnnotationHub, markdown, rmarkdown, EBImage, magick, magrittr, filestrings, 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 RELEASE_3_19

git_last_commit cc38446

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-23

Author 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>
BioImageDbs-package

Contents

BioImageDbs-package ..................................................... 2

Index 3

Index

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

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