# Package 'BioImageDbs'

October 16, 2021

**Type** Package

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

**Version** 1.0.5

**Encoding** UTF-8

**Depends** R (>= 4.1.0)

**Imports** ExperimentHub (>= 1.16.1), 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://github.com/kumeS/BioImageDbs

**LazyLoad** yes

**biocViews** ExperimentHub, ExperimentData, CellCulture, Tissue

**RoxygenNote** 7.1.1

**git_url** https://git.bioconductor.org/packages/BioImageDbs

**git_branch** RELEASE_3_13

**git_last_commit** 6d39648

**git_last_commit_date** 2021-09-18

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**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>

## R topics documented:

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#### 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

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#### Author(s)

NA

Maintainer: NA

#### Examples

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

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