

# Package ‘BioImageDbs’

May 14, 2026

**Type** Package

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

**Version** 1.21.0

**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** 5064eca

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-14

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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**

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

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

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**Examples**

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

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