

Package ‘CardinalWorkflows’

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Type Package

Title Datasets and workflows for the Cardinal mass spectrometry imaging package

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Description Datasets and workflows for Cardinal: DESI and MALDI examples including pig fetus, cardinal painting, and human RCC.

License Artistic-2.0

Depends R (>= 2.10), Cardinal

Suggests BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

biocViews ExperimentData, MassSpectrometryData, ImagingMassSpectrometryData

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R topics documented:

| | |
|-------------------------------------|---|
| CardinalWorkflows-package | 2 |
| cardinal-data | 2 |
| pig206-data | 3 |
| rcc-data | 4 |

| | |
|--------------|----------|
| Index | 6 |
|--------------|----------|

CardinalWorkflows-package

Datasets and workflows for the Cardinal mass spectrometry imaging package

Description

Datasets and workflows for Cardinal: DESI and MALDI examples including pig fetus, cardinal farmhouse painting, and human RCC.

Details

CardinalWorkflows provides datasets and example workflows of mass spectrometry imaging experiments using the Cardinal package for MS imaging analysis.

To view the example workflows, type `browseVignettes("CardinalWorkflows")`.

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See Also

[cardinal](#), [pig206](#), [rcc](#)

cardinal-data

Cardinal Painting

Description

DESI-imaging mass spectra collected from the oil painting of a cardinal.

Usage

```
data(cardinal)
data(cardinal_analyses)
```

Format

cardinal contains the following objects:

cardinal raw dataset

cardinal.peaklist list of detected peaks

cardinal.peaks peak-picked dataset

cardinal_analyses contains the following objects:

cardinal.sscg spatial shrunken centroids clustering (Gaussian weights)

cardinal.ssca spatial shrunken centroids clustering (adaptive weights)

Source

Aston Labs (Livia S. Eberlin, Christina Ferreira, and R. Graham Cooks).

Examples

```
data(cardinal)
data(cardinal_analyses)
```

pig206-data

Cross-Section of a Whole Pig Fetus

Description

DESI-imaging mass spectra collected from the cross-section of a whole pig fetus.

Usage

```
data(pig206)
data(pig206_analyses)
```

Format

pig206 contains the following objects:

pig206 raw dataset

pig206.peaklist list of detected peaks

pig206.peaks peak-picked dataset

pig206_analyses contains the following objects:

pig206.pca principal components analysis

pig206.skmg spatially-aware k-means clustering (Gaussian weights)

pig206.skma spatially-aware k-means clustering (adaptive weights)

pig206.sscg spatial shrunken centroids clustering (Gaussian weights)

pig206.ssca spatial shrunken centroids clustering (adaptive weights)

Source

Aston Labs (Livia S. Eberlin, Christina Ferreira, and R. Graham Cooks).

Examples

```
data(pig206)
data(pig206_analyses)
```

rcc-data

Human Renal Cell Carcinoma

Description

Eight matched pairs of human renal cell carcinoma (RCC) labeled as cancer or normal.

Data are DESI-imaging mass spectra with each matched pair as a separate sample on a separate slide.

Usage

```
data(rcc)
data(rcc_analyses)
```

Format

rcc contains the following objects:

rcc raw dataset
rcc.resample dataset resampled to unit resolution
rcc.small resampled dataset without background pixels

rcc_analyses contains the following objects:

rcc.pca principal components analysis
rcc.cv.pls cross-validated PLS-DA
rcc.cv.opls cross-validated O-PLS-DA
rcc.pls PLS-DA on full dataset
rcc.opls O-PLS-DA on full dataset
rcc.cv.sscg cross-validated spatial shrunken centroids (Gaussian weights)
rcc.cv.ssca cross-validated spatial shrunken centroids (adaptive weights)
rcc.sscg spatial shrunken centroids (Gaussian weights) on full dataset
rcc.ssca spatial shrunken centroids (adaptive weights) on full dataset

Source

Aston Labs (Livia S. Eberlin and R. Graham Cooks).

References

- Dill, A. L., Eberlin, L. S., Zheng, C., Costa, A. B., Ifa, D. R., Cheng, L., et al. (2010). Multivariate statistical differentiation of renal cell carcinomas based on lipidomic analysis by ambient ionization imaging mass spectrometry. *Analytical and Bioanalytical Chemistry*, 298(7-8), 2969-2978.
- Dill, A. L., Eberlin, L. S., Zheng, C., Costa, A. B., Ifa, D. R., Cheng, L., et al. (2010). Multivariate Statistical Identification of Human Bladder Carcinomas Using Ambient Ionization Imaging Mass Spectrometry. *Chemistry - a European Journal*, 17(10), 2897-2902.

Examples

```
data(rcc)  
data(rcc_analyses)
```

Index

* datasets

cardinal-data, [2](#)

pig206-data, [3](#)

rcc-data, [4](#)

* package

CardinalWorkflows-package, [2](#)

cardinal, [2](#)

cardinal (cardinal-data), [2](#)

cardinal-data, [2](#)

cardinal_analyses (cardinal-data), [2](#)

CardinalWorkflows

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

CardinalWorkflows-package, [2](#)

data:cardinal (cardinal-data), [2](#)

data:cardinal_analyses (cardinal-data),
[2](#)

data:pig206 (pig206-data), [3](#)

data:pig206_analyses (pig206-data), [3](#)

data:rcc (rcc-data), [4](#)

data:rcc_analyses (rcc-data), [4](#)

pig206, [2](#)

pig206 (pig206-data), [3](#)

pig206-data, [3](#)

pig206_analyses (pig206-data), [3](#)

rcc, [2](#)

rcc (rcc-data), [4](#)

rcc-data, [4](#)

rcc_analyses (rcc-data), [4](#)