Package: CardinalCore (via r-universe)

November 17, 2026

Type Package

Title Core utilities for mass spectrometry imaging

Version 0.0.1

Date YYYY-MM-DD

Description Low-level processing and visualization utilities for mass spectrometry imaging analysis in Cardinal.

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Depends R (>= 4.6), BiocGenerics, S4Vectors

Imports methods

Suggests BiocStyle, tinytest, knitr, rmarkdown

VignetteBuilder knitr

biocViews Software, MassSpectrometry, ImagingMassSpectrometry, Normalization

URL http://www.cardinalmsi.org

BugReports https://github.com/kuwisdelu/CardinalCore/issues

Repository https://cardinalverse.r-universe.dev

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RemoteUrl https://github.com/Cardinalverse/CardinalCore

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CardinalCore-package *Short description of package*

Description

Longer description of package.

Details

Detailed description of package.

See `browseVignettes("CardinalCore")` to view a user guide and vignettes of common workflows.

Author(s)

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filt1 *Smoothing Filters in 1D*

Description

Smooth a uniformly sampled 1D signal.

Usage

```
# Moving average filter
filt1_mean(y, k = 5L)

# Linear convolution filter
filt1_conv(y, w = rep(1, 5L))
```

Arguments

y	A numeric vector.
k	The number of samples in the smoothing window. Must be positive. Must be odd.
w	The weights of the linear convolution kernel. Length must be odd.

Details

All filters documented here extend the signal by replicating the endpoints.

`filt1_mean()` performs mean filtering in O(n) time. This is fast and especially useful for calculating other filters that can be constructed as a combination of mean filters.

`filt1_conv()` performs a convolution filtering with arbitary weights. The weights are internally normalized to sum to 1.

Value

A numeric vector the same length as `y` with the smoothed result.

Author(s)

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Examples

```
set.seed(1)
x <- seq(from=0, to=6 * pi, length.out=5000)
y <- sin(x) + 0.6 * sin(2.6 * t)
y <- y + runif(length(y))
z <- filt1_mean(y, k=25)

plot(y, type="l")
lines(z, col="red")
```

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