Package: neuroim2 (via r-universe)

October 11, 2026

Type Package

Title Data Structures for Brain Imaging Data

Version 0.19.1

LinkingTo Rcpp, RcppArmadillo, RcppParallel

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Description A collection of data structures and methods for handling volumetric brain imaging data, with a focus on functional magnetic resonance imaging (fMRI). Provides efficient representations for three-dimensional and four-dimensional neuroimaging data through sparse and dense array implementations, memory-mapped file access for large datasets, and spatial transformation capabilities. Implements methods for image resampling, spatial filtering, region of interest analysis, and connected component labeling. General introduction to fMRI analysis can be found in Poldrack et al. (2024, ``Handbook of functional MRI data analysis", <ISBN:9781108795760>).

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Encoding UTF-8

VignetteBuilder knitr, rmarkdown

Depends R (>= 4.3.0), Matrix

Collate 'RcppExports.R' 'all_generic.R' 'all_class.R' 'SparseNeuroVec-validity.R' 'affine_utils.R' 'afni_io.R' 'array_like.R' 'as_raster.R' 'axis.R' 'big_neurovec.R' 'binary_io.R' 'cgb.R' 'cgb_nuisance.R' 'clustered_neurovec.R' 'clustervol.R' 'common.R' 'conncomp.R' 'deoblique.R' 'downsample.R' 'file_format.R' 'filebacked_neurovec.R' 'globals.R' 'header_api.R' 'index_vol.R' 'mapped_neurovec.R' 'meta_info.R' 'meta_info_api.R' 'neuro_obj.R' 'neurohypervec.R' 'neuroim.R' 'neuroslice.R' 'neurospace.R' 'neurovec.R' 'neurovecseq.R' 'neurovol.R' 'nifti_extensions.R' 'nifti_io.R' 'niml_io.R' 'ops.R' 'orientation.R' 'palettes.R'

'plot-checkerboard.R' 'plot-edge-overlay.R' 'plot-engine.R'
'plot-helpers.R' 'plot-montage.R' 'plot-ortho.R'
'plot-overlay.R' 'read_image.R' 'resample.R' 'resample_to.R'
'roi.R' 'searchlight.R' 'show_helpers.R' 'simulate.R'
'space_utils.R' 'sparse_neurovec.R' 'spat_filter.R'
'summary_methods.R' 'theme.R' 'zzz.R'

RoxygenNote 7.3.3

Imports purrr, mmap, Rcpp, RcppParallel, RNifti, dbscan, stringr, methods, bigstatsr, RNiftyReg, future, future.apply, deflist, cli, ggplot2, magrittr, grid, patchwork

Suggests testthat, covr, knitr, pkgdown, ragg, roxygen2, rmarkdown, albersdown, Gmedian, R.utils, spelling, systemfonts, vdiffr, xml2

URL https://github.com/bbuchsbaum/neuroim2, https://bbuchsbaum.github.io/neuroim2/

BugReports https://github.com/bbuchsbaum/neuroim2/issues

Language en-US

Config/Needs/website bbuchsbaum/albersdown

NeedsCompilation yes

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

Date/Publication 2026-10-07 00:10:02 UTC

RemoteUrl https://github.com/cran/neuroim2

RemoteRef HEAD

RemoteSha bec765b813a5c99d849558e2a6de7c2a105eb724

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`neuroim2-package` *neuroim2: neuroimaging data structures for analysis*

Description

The neuroim2 package provides tools and functions for analyzing and manipulating neuroimaging data. It supports various neuroimaging formats and offers a range of analysis techniques.

Main functions

- `read_vol`: Read neuroimaging volumes
- `write_vol`: Write neuroimaging volumes
- `NeuroVol`: Create NeuroVol objects
- `NeuroVec`: Create NeuroVec objects

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See Also

Useful links:

- https://github.com/bbuchsbaum/neuroim2
- https://bbuchsbaum.github.io/neuroim2/
- Report bugs at https://github.com/bbuchsbaum/neuroim2/issues

[,DenseNeuroVec,numeric,numeric,ANY-method
[[

Description

This function extracts a single volume from a NeuroVec object.

Extracts a subset of data from a sparse four-dimensional brain image based on provided indices.

Usage

```
## S4 method for signature 'DenseNeuroVec,numeric,numeric,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'DenseNeuroVol,numeric,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'DenseNeuroVol,integer,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'NeuroVec,numeric'
x[[i]]

## S4 method for signature 'NeuroVec,character'
x[[i]]

## S4 method for signature 'NeuroVol,ROICoords,missing,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'NeuroVol,ROIVol,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'DenseNeuroVol,ROIVol,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'SparseNeuroVol,numeric,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,numeric,missing,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ROIVol,logical,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,ROICoords,missing,ANY'
x[i, j, k, ..., drop = TRUE]
```

```
## S4 method for signature 'ROIVol,matrix,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,missing,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,missing,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,numeric,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,logical,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,ROICoords,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROIVol,matrix,numeric,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ROICoords,numeric,missing,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'ROIVol,numeric,missing,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'NeuroVol,ROICoords,missing,ANY'
x[i, j, ..., drop = TRUE]

## S4 method for signature 'AbstractSparseNeuroVec,numeric,numeric,ANY'
x[i, j, k, m, ..., drop = TRUE]
```

Arguments

x	An object of class AbstractSparseNeuroVec
i	Numeric vector specifying the indices for the first dimension
j	Numeric vector specifying the indices for the second dimension
k	Numeric vector specifying the indices for the third dimension (optional)
m	Numeric vector specifying the indices for the fourth dimension (optional)
...	Additional arguments passed to methods
drop	Logical indicating whether to drop dimensions of length one (default: TRUE)

Value

a DenseNeuroVol object

A subset of the input object, with dimensions depending on the indexing and the ‘drop‘ parameter.

An array containing the extracted subset

`[[,AbstractSparseNeuroVec,numeric-method`
[[

Description

[[

Usage

```
## S4 method for signature 'AbstractSparseNeuroVec,numeric'
x[[i]]
```

Arguments

x	the object
i	the volume index

Value

a SparseNeuroVol object

`[[,NeuroVecSeq,numeric-method`
Extract Element from NeuroVecSeq

Description

Extracts a single volume from a NeuroVecSeq object at the specified time point.

Usage

```
## S4 method for signature 'NeuroVecSeq,numeric'
x[[i]]
```

Arguments

x	A NeuroVecSeq object
i	Numeric index specifying the time point to extract

Value

A NeuroVol object representing the extracted volume

AbstractSparseNeuroVec-class *AbstractSparseNeuroVec Class*

Description

An abstract base class for sparse four-dimensional brain image representations. This class provides the foundation for efficient storage and manipulation of large, sparse neuroimaging data.

Details

The AbstractSparseNeuroVec class serves as a template for implementing various sparse representations of 4D brain images. It combines the spatial properties of `NeuroVec` with the efficiency of sparse data structures.

Slots

`mask` An object of class `LogicalNeuroVol` defining the sparse domain of the brain image. This mask indicates which voxels contain non-zero data.

`map` An object of class `IndexLookupVol` used to map between spatial coordinates and index/row coordinates in the sparse representation.

Subclasses

Concrete implementations of this abstract class should provide specific data storage mechanisms and methods for efficient access and manipulation of sparse 4D brain image data.

See Also

`NeuroVec-class` for the parent class. `LogicalNeuroVol-class` for the mask representation. `IndexLookupVol-class` for the spatial-to-index mapping.

add_dim *Add a Dimension to an Object*

Description

This function adds a new dimension to a given object, such as a matrix or an array.

Usage

```
add_dim(x, n)

## S4 method for signature 'NeuroSpace,numeric'
add_dim(x, n)
```

Arguments

x	The NeuroSpace object
n	Numeric value specifying the size of the new dimension

Value

An object of the same class as x with the new dimension added.

Examples

```
# Create a NeuroSpace object
x <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))

# Add a new dimension with size 10
x1 <- add_dim(x, 10)

# Check the new dimension
ndim(x1) == 4
dim(x1)[4] == 10
```

---

affine_utils *Affine utility functions*

Description

Utilities for point transforms and affine decomposition/composition.

Applies a homogeneous affine transform to points where the coordinate axis is the last dimension.

Useful when expanding an affine to include additional dimensions.

For arrays ‘A, B, C, ...‘, returns ‘A

Returns per-output-axis obliquity relative to cardinal axes, in radians.

Preserves rotations/shears and world location of the center voxel.

Usage

```
apply_affine(aff, pts, inplace = FALSE)

to_matvec(transform)

from_matvec(matrix, vector = NULL)

append_diag(aff, steps, starts = numeric(0))

dot_reduce(...)

voxel_sizes(affine)
```

```
obliquity(affine)

rescale_affine(affine, shape, zooms, new_shape = NULL)
```

Arguments

aff	Base affine matrix.
pts	Points with last dimension ‘N - 1‘; shape may be vector, matrix, or higher-dimensional array.
inplace	Included for API compatibility; ignored in R.
transform	Homogeneous transform matrix.
matrix	Linear part of transform (‘N x M‘).
vector	Optional translation vector of length ‘N‘.
steps	Diagonal values for appended dimensions.
starts	Optional translations for appended dimensions.
...	Matrices/vectors compatible with %*%.
affine	Square homogeneous affine matrix.
shape	Original grid shape (spatial axes).
zooms	New voxel sizes for spatial axes.
new_shape	Optional new grid shape; defaults to ‘shape‘.

Details

These functions mirror core NiBabel affine helpers while using R-first conventions and stronger argument checks.

Value

Points transformed by ‘aff‘, with same leading shape as ‘pts‘.

A list with ‘matrix‘ and ‘vector‘.

Homogeneous affine matrix of shape ‘(N+1) x (M+1)‘.

Expanded affine matrix.

Matrix product.

Numeric vector of voxel sizes (column norms of linear block).

Numeric vector of obliquity angles.

Rescaled affine matrix.

Examples

```
aff <- diag(c(2, 3, 4, 1))
aff[1:3, 4] <- c(10, 20, 30)

pts <- rbind(c(1, 2, 3), c(4, 5, 6))
apply_affine(aff, pts)

mv <- to_matvec(aff)
from_matvec(mv$matrix, mv$vector)
```

---

anatomical_axes *Pre-defined anatomical axes*

Description

These constants define standard anatomical axes used in neuroimaging. Each axis has a defined direction vector in 3D space.

Usage

```
LEFT_RIGHT

RIGHT_LEFT

ANT_POST

POST_ANT

INF_SUP

SUP_INF
```

Format

An object of class `NamedAxis` of length 1.

An object of class `NamedAxis` of length 1.

An object of class `NamedAxis` of length 1.

An object of class `NamedAxis` of length 1.

An object of class `NamedAxis` of length 1.

An object of class `NamedAxis` of length 1.

annotate_orientation *Add L/R and A/P/S/I annotations (optional)*

Description

Add L/R and A/P/S/I annotations (optional)

Usage

```
annotate_orientation(
  plane = c("axial", "coronal", "sagittal"),
  dims,
  gp = grid::gpar(col = "white", cex = 0.9, fontface = "bold")
)
```

Arguments

plane	"axial", "coronal", or "sagittal"
dims	c(nrow, ncol) of the slice matrix
gp	grid::gpar style

Value

A ggplot2 layer with annotation_custom grobs

apply_mask *Apply a spatial mask to an image*

Description

Zeroes voxels outside a 3D spatial mask while preserving the geometry of the input object. Unlike mask, which returns an object's spatial domain, apply_mask() modifies image values.

Usage

```
apply_mask(x, mask)

## S4 method for signature 'FileBackedNeuroVec'
apply_mask(x, mask)

## S4 method for signature 'MappedNeuroVec'
apply_mask(x, mask)

## S4 method for signature 'NeuroHyperVec'
apply_mask(x, mask)
```

```
## S4 method for signature 'DenseNeuroVec'
apply_mask(x, mask)

## S4 method for signature 'AbstractSparseNeuroVec'
apply_mask(x, mask)

## S4 method for signature 'NeuroVol'
apply_mask(x, mask)

## S4 method for signature 'LogicalNeuroVol'
apply_mask(x, mask)

## S4 method for signature 'SparseNeuroVol'
apply_mask(x, mask)
```

Arguments

x	A neuroimaging object.
mask	A 3D mask supplied as a LogicalNeuroVol, numeric NeuroVol (thresholded at > 0), logical array/vector, integer voxel indices, or NULL for no masking.

Value

A masked neuroimaging object. Dense inputs remain dense; sparse inputs return a sparse object with the intersected mask.

Examples

```
sp <- NeuroSpace(c(4, 4, 4), spacing = c(1, 1, 1))
vol <- NeuroVol(array(rnorm(64), c(4, 4, 4)), sp)
msk <- LogicalNeuroVol(array(runif(64) > 0.5, c(4, 4, 4)), sp)
masked <- apply_mask(vol, msk)
```

Arith-methods *Arithmetic Operations*

Description

Methods for performing arithmetic operations on neuroimaging objects

Perform an arithmetic operation between two DenseNeuroVec objects. The input DenseNeuroVec objects must have the same dimensions and NeuroSpace objects. The method computes the elementwise arithmetic operation and returns a new DenseNeuroVec object.

Perform an arithmetic operation between a SparseNeuroVol object and a NeuroVol object. The input SparseNeuroVol and NeuroVol objects must have the same dimensions. The method performs the arithmetic operation on the non-zero values of the SparseNeuroVol and the corresponding values of the NeuroVol. The result is returned as a new DenseNeuroVol object.

Perform an arithmetic operation between a NeuroVol object and a SparseNeuroVol object. The input NeuroVol and SparseNeuroVol objects must have the same dimensions. The method performs the arithmetic operation on the values of the NeuroVol and the non-zero values of the SparseNeuroVol. The result is returned as a new DenseNeuroVol object.

Perform an arithmetic operation between two NeuroVec objects. The input NeuroVec objects must have the same dimensions. The method performs the arithmetic operation on the elements of the NeuroVec objects. The result is returned as a new DenseNeuroVec object.

This function performs arithmetic operations on a NeuroVec object and a NeuroVol object.

This function performs arithmetic operations on a NeuroVol object and a NeuroVec object.

Usage

```
## S4 method for signature 'SparseNeuroVol,SparseNeuroVol'
Arith(e1, e2)

## S4 method for signature 'ROIVol,ROIVol'
Arith(e1, e2)

## S4 method for signature 'DenseNeuroVol,DenseNeuroVol'
Arith(e1, e2)

## S4 method for signature 'DenseNeuroVec,DenseNeuroVec'
Arith(e1, e2)

## S4 method for signature 'SparseNeuroVol,NeuroVol'
Arith(e1, e2)

## S4 method for signature 'NeuroVol,SparseNeuroVol'
Arith(e1, e2)

## S4 method for signature 'SparseNeuroVec,SparseNeuroVec'
Arith(e1, e2)

## S4 method for signature 'NeuroVec,NeuroVec'
Arith(e1, e2)

## S4 method for signature 'NeuroVec,NeuroVol'
Arith(e1, e2)

## S4 method for signature 'NeuroVol,NeuroVec'
Arith(e1, e2)

## S4 method for signature 'DenseNeuroVol,numeric'
Arith(e1, e2)

## S4 method for signature 'numeric,DenseNeuroVol'
Arith(e1, e2)
```

```
## S4 method for signature 'SparseNeuroVol,numeric'
Arith(e1, e2)

## S4 method for signature 'numeric,SparseNeuroVol'
Arith(e1, e2)

## S4 method for signature 'ClusteredNeuroVol,ClusteredNeuroVol'
Arith(e1, e2)

## S4 method for signature 'ClusteredNeuroVol,numeric'
Arith(e1, e2)

## S4 method for signature 'numeric,ClusteredNeuroVol'
Arith(e1, e2)

## S4 method for signature 'ClusteredNeuroVol,NeuroVol'
Arith(e1, e2)

## S4 method for signature 'NeuroVol,ClusteredNeuroVol'
Arith(e1, e2)
```

Arguments

e1, e2	Neuroimaging operands or numeric values.

Details

ROIVol contract: element-wise arithmetic requires the same spatial support. Both operands must share the same NeuroSpace and the same set of voxel coordinates (order may differ). Missing voxels are not treated as zero, and the result does not grow to the union of the two ROIs. Values are aligned by linear voxel index before the operation.

Value

A SparseNeuroVol object representing the result of the arithmetic operation.

For the ROIVol method, an ROIVol with the same coordinates as e1, containing the element-wise result.

A DenseNeuroVec object representing the result of the arithmetic operation.

A DenseNeuroVol object representing the result of the arithmetic operation.

A DenseNeuroVol object representing the result of the arithmetic operation.

A DenseNeuroVec object representing the result of the arithmetic operation.

A DenseNeuroVec object resulting from the arithmetic operation.

A DenseNeuroVec object resulting from the arithmetic operation.

ArrayLike3D-class *ArrayLike3D Class*

Description

A virtual class for representing three-dimensional array-like objects. It provides a common interface for 3D array operations.

ArrayLike4D-class *ArrayLike4D Class*

Description

A virtual class for representing four-dimensional array-like objects. It is intended to serve as a base class for 4D array representations.

ArrayLike5D-class *ArrayLike5D Class*

Description

A virtual class for representing five-dimensional array-like objects. This class serves as an interface for objects that mimic 5D arrays.

as-ClusteredNeuroVol-DenseNeuroVol *Convert ClusteredNeuroVol to DenseNeuroVol*

Description

This method converts a ClusteredNeuroVol into an equivalent DenseNeuroVol object.

Usage

```
## S4 method for signature 'ClusteredNeuroVol,DenseNeuroVol'
coerce(from, to = "DenseNeuroVol", strict = TRUE)
```

Arguments

from	A ClusteredNeuroVol object to be converted
to	The target class, "DenseNeuroVol".
strict	Logical; whether to enforce the target class exactly.

Details

Convert a ClusteredNeuroVol Object to a DenseNeuroVol Object

Value

A DenseNeuroVol object

See Also

ClusteredNeuroVol, DenseNeuroVol

Examples

```
# Create a clustered volume
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))
clusters <- rep(1:5, length.out=sum(mask))
cvol <- ClusteredNeuroVol(mask, clusters)

# Convert to DenseNeuroVol
dvol <- as(cvol, "DenseNeuroVol")
```

---

as.array *Generic as.array Method*

Description

Coerces an object to a base array using S4 dispatch when available.

Usage

```
as.array(x, ...)
```

Arguments

x	An object to be coerced to an array.
...	Additional arguments passed to methods.

Value

An array representation of the input x.

`as.array,ClusteredNeuroVol-method`
Convert ClusteredNeuroVol to a base array

Description

Ensures that clustered volumes dispatch through the ‘as.array‘ S4 generic and return dense arrays of cluster labels aligned to the underlying space.

Provides an ‘as.array‘ S4 method so sparse volumes can be coerced with the same syntax used for dense objects.

The S4 slots of an object that extends `array` are stored as attributes on that array, so the default coercion handed back the voxel data still carrying `space`, `header` and `class`. Anyone calling `as.array()` wants the numbers without the wrapper; these methods give exactly that.

Usage

```
## S4 method for signature 'ClusteredNeuroVol'
as.array(x, ...)

## S4 method for signature 'DenseNeuroVec'
as.array(x, ...)

## S4 method for signature 'SparseNeuroVol'
as.array(x, ...)

## S4 method for signature 'DenseNeuroVol'
as.array(x, ...)

## S4 method for signature 'NeuroSlice'
as.array(x, ...)

## S4 method for signature 'SparseNeuroVec'
as.array(x, ...)
```

Arguments

`x`	A SparseNeuroVec object.
`...`	Additional arguments (currently ignored).

Value

A dense array of cluster ids.

A dense array with voxel values at their spatial locations and zeros elsewhere.

A base array with only a `dim` attribute.

A dense 4D array with sparse values inserted at mask indices and zeros elsewhere.

as.dense *Convert to dense representation*

Description

Convert to dense representation

Usage

```
as.dense(x)
```

Arguments

x	the object to densify

Value

A dense representation of the input object.

Examples

```
# Create a sparse representation
space <- NeuroSpace(c(10,10,10,4), c(1,1,1))
mask <- array(runif(10*10*10) > 0.8, c(10,10,10))  # ~20% of voxels active
data <- matrix(rnorm(sum(mask) * 4), 4, sum(mask))  # Random data for active voxels
sparse_vec <- SparseNeuroVec(data, space, mask)

# Convert to dense representation
dense_vec <- as.dense(sparse_vec)
# The dense representation has the same dimensions but stores all voxels
identical(dim(sparse_vec), dim(dense_vec))
```

as.dense,ClusteredNeuroVol-method *Convert a NeuroVecSeq to a DenseNeuroVec*

Description

Materializes a NeuroVecSeq as a single DenseNeuroVec with the sequence's combined space.

Convert a sparse volumetric image to a dense representation with the same spatial geometry. Non-zero values stored in the sparse vector are placed at their corresponding linear indices in the dense array; all other voxels are 0.

Identity method: returns a DenseNeuroVol (or subclass such as LogicalNeuroVol) unchanged.

This function provides a method to coerce an object of class ROIVol to a DenseNeuroVol using the as.dense method.

Usage

```
## S4 method for signature 'ClusteredNeuroVol'
as.dense(x)

## S4 method for signature 'NeuroVecSeq'
as.dense(x)

## S4 method for signature 'SparseNeuroVol'
as.dense(x)

## S4 method for signature 'DenseNeuroVol'
as.dense(x)

## S4 method for signature 'ROIVol'
as.dense(x)

## S4 method for signature 'SparseNeuroVec'
as.dense(x)
```

Arguments

x	An object of class ROIVol to be coerced to a DenseNeuroVol.

Value

A NeuroVol object representing the dense version of the clustered volume.

A DenseNeuroVec containing all sequence volumes concatenated in time.

A DenseNeuroVol with identical spatial dimensions and values expanded from the sparse representation.

A DenseNeuroVol object obtained by coercing the ROIVol object.

---

as.list,FileBackedNeuroVec-method

Convert FileBackedNeuroVec to List

Description

Converts a FileBackedNeuroVec object to a list of DenseNeuroVol objects.

convert SparseNeuroVec to list of DenseNeuroVol

Usage

```
## S4 method for signature 'FileBackedNeuroVec'
as.list(x)

## S4 method for signature 'NeuroVec'
```

```
as.list(x)

## S4 method for signature 'SparseNeuroVec'
as.list(x)
```

Arguments

x	the object

Details

This method creates a deferred list, where each element is a DenseNeuroVol object representing a single volume from the FileBackedNeuroVec.

Value

A list of DenseNeuroVol objects

`as.logical,NeuroVol-method` *as.logical*

Description

Convert NeuroVol to `LogicalNeuroVol`

Usage

```
## S4 method for signature 'NeuroVol'
as.logical(x)

## S4 method for signature 'ROIVol'
as.logical(x)
```

Arguments

x	the object

Details

the image values will be converted to using R base function `as.logical` and wrapped in `LogicalNeuroVol`

Value

an instance of `LogicalNeuroVol`

as.mask *Convert to a LogicalNeuroVol*

Description

Convert to a LogicalNeuroVol

Usage

```
as.mask(x, indices)
```

Arguments

x	the object to binarize
indices	the indices to set to TRUE

Value

A LogicalNeuroVol object with TRUE values at the specified indices.

Examples

```
# Create a simple 3D volume with random values
space <- NeuroSpace(c(10,10,10), spacing=c(1,1,1))
vol <- NeuroVol(array(runif(1000), c(10,10,10)), space)

# Create a mask by thresholding (values > 0.5 become TRUE)
mask1 <- as.mask(vol > 0.5)

# Create a mask by specifying indices
indices <- which(vol > 0.8)  # get indices of high values
mask2 <- as.mask(vol, indices)

# Both masks are LogicalNeuroVol objects
identical(class(mask1), class(mask2))
```

as.mask,NeuroVol,missing-method *Convert NeuroVol to a mask*

Description

This method converts a NeuroVol object to a mask by setting all positive values to TRUE and all non-positive values to FALSE.

This method converts a NeuroVol object to a mask by setting the specified indices to TRUE and the remaining elements to FALSE.

Usage

```
## S4 method for signature 'NeuroVol,missing'
as.mask(x)

## S4 method for signature 'NeuroVol,numeric'
as.mask(x, indices)
```

Arguments

x	A NeuroVol object to convert to a mask.
indices	A numeric vector containing the indices of the input NeuroVol that should be set to TRUE in the resulting mask.

Value

A LogicalNeuroVol object representing the mask created from the input NeuroVol.

A LogicalNeuroVol object representing the mask created from the input NeuroVol with specified indices.

---

as.matrix *Generic as.matrix Method*

Description

Coerces an object to a matrix.

Usage

```
as.matrix(x, ...)
```

Arguments

x	An object to be coerced to a matrix.
...	Additional arguments passed to methods.

Value

A `matrix` representation of the input `x`.

`as.matrix,ClusteredNeuroVec-method` *convert a* `NeuroVec` *to a matrix*

Description

Converts a `NeuroVecSeq` to a dense voxel-by-time matrix.

Usage

```
## S4 method for signature 'ClusteredNeuroVec'
as.matrix(x, by = c("cluster", "voxel"))

## S4 method for signature 'FileBackedNeuroVec'
as.matrix(x, ...)

## S4 method for signature 'MappedNeuroVec'
as.matrix(x)

## S4 method for signature 'NeuroVec'
as.matrix(x)

## S4 method for signature 'DenseNeuroVec'
as.matrix(x)

## S4 method for signature 'NeuroVecSeq'
as.matrix(x, ...)

## S4 method for signature 'ROIVec'
as.matrix(x)

## S4 method for signature 'AbstractSparseNeuroVec'
as.matrix(x, ...)
```

Arguments

`x`	The object to convert to a matrix
`by`	For ClusteredNeuroVec: controls the conversion target. Defaults to "cluster" to return a TxK matrix of cluster time-series. "voxel" is reserved for future use.
`...`	Additional arguments

Value

A matrix with one row per voxel and one column per time point.

A matrix representation of the object

as.numeric,SparseNeuroVol-method *Convert SparseNeuroVol to numeric*

Description

Convert SparseNeuroVol to numeric

Usage

```
## S4 method for signature 'SparseNeuroVol'
as.numeric(x)

## S4 method for signature 'ROIVol'
as.numeric(x)
```

Arguments

x	the object to convert

Value

A numeric vector of length `nrow(x@coords)`

as.raster *Generic Method for Converting Objects to Raster Format*

Description

Converts an object to a raster (bitmap) representation.

Usage

```
as.raster(x, ...)
```

Arguments

x	An object to be converted.
...	Additional arguments passed to the conversion methods.

Value

A `raster` object representing `x`.

`as.raster,NeuroSlice-method`

Convert neuroimaging objects to raster images

Description

These methods convert `NeuroSlice` and `NeuroVol` objects into `raster` images that can be displayed with `grid::grid.raster` or base `plot`.

Usage

```
## S4 method for signature 'NeuroSlice'
as.raster(
  x,
  cmap = gray(seq(0, 1, length.out = 255)),
  irange = range(x, na.rm = TRUE),
  ...
)

## S4 method for signature 'NeuroVol'
as.raster(
  x,
  zlevel = ceiling(dim(x)[3]/2),
  cmap = gray(seq(0, 1, length.out = 255)),
  irange = range(x, na.rm = TRUE),
  ...
)
```

Arguments

`x`	object to convert.
`cmap`	palette name or hex-color vector for the background (default `"grays"`). See `resolve_cmap`.
`irange`	numeric length-2 intensity range for the color scale.
`...`	additional arguments passed to methods
`zlevel`	slice index for `NeuroVol` objects. Defaults to the middle slice.

Value

A `raster` object

See Also

`plot,NeuroSlice-method`, `plot,NeuroVol-method`

as.sparse *Convert to from dense to sparse representation*

Description

Convert to from dense to sparse representation

Usage

```
as.sparse(x, mask, ...)
```

Arguments

x	the object to make sparse, e.g. DenseNeuroVol or DenseNeuroVec
mask	the elements to retain
...	additional arguments

Details

mask can be an integer vector of 1D indices or a mask volume of class LogicalNeuroVol

Value

A sparse representation of the input object, containing only the elements specified by mask.

Examples

```
bvol <- NeuroVol(array(runif(24*24*24), c(24,24,24)), NeuroSpace(c(24,24,24), c(1,1,1)))
indmask <- sort(sample(1:(24*24*24), 100))
svol <- as.sparse(bvol, indmask)


mask <- LogicalNeuroVol(runif(length(indmask)), space=space(bvol), indices=indmask)
sum(mask) == 100
```

as.sparse,DenseNeuroVec,LogicalNeuroVol-method *Convert DenseNeuroVec to sparse representation using mask*

Description

This method converts a DenseNeuroVec object to a sparse representation using a given LogicalNeuroVol mask.

This method converts a DenseNeuroVec object to a sparse representation using a given numeric mask.

Usage

```
## S4 method for signature 'DenseNeuroVec,LogicalNeuroVol'
as.sparse(x, mask)

## S4 method for signature 'DenseNeuroVec,numeric'
as.sparse(x, mask)

## S4 method for signature 'DenseNeuroVol,LogicalNeuroVol'
as.sparse(x, mask)

## S4 method for signature 'DenseNeuroVol,numeric'
as.sparse(x, mask)

## S4 method for signature 'ROIVol,ANY'
as.sparse(x)
```

Arguments

x	A DenseNeuroVec object to convert to a sparse representation.
mask	A numeric vector representing the mask to apply during conversion.

Details

For a DenseNeuroVec, numeric masks use R's vector-indexing rules: positive indices retain voxels, negative indices exclude voxels, and zeros are ignored. Repeated indices retain a voxel once. Retained voxels are stored in ascending spatial-index order, regardless of the order supplied in mask. An empty selection produces an all-zero sparse image with the original dimensions. Missing or non-finite indices and positive indices outside the spatial extent are rejected.

Value

A SparseNeuroVec object resulting from the conversion.

A SparseNeuroVec object resulting from the conversion.

---

as.vector,SparseNeuroVol-method

Convert SparseNeuroVol to a base vector

Description

Supplies an ‘as.vector‘ S4 method that flattens sparse volumes to a dense vector, keeping the same voxel ordering as ‘as.array‘.

Usage

```
## S4 method for signature 'SparseNeuroVol'
as.vector(x, mode = "any")
```

Arguments

x	A 'SparseNeuroVol' instance.
mode	Optional coercion mode (see [base::as.vector]).

Value

A vector of length 'prod(dim(x))'.

`as_canonical` *Reorient Image to Canonical (RAS+) Orientation*

Description

Reorients a neuroimaging volume or vector to the canonical RAS+ (Right-Anterior-Superior) orientation by permuting and flipping axes. This is equivalent to nibabel's `as_closest_canonical()`.

Usage

```
as_canonical(x, target = c("R", "A", "S"))
```

Arguments

x	A `NeuroVol` or `NeuroVec` object.
target	Character vector of length 3 giving the desired orientation. Default is `c("R", "A", "S")` (RAS+).

Details

Reorienting to a target that differs only in which anatomical direction each axis runs is a relabelling of the grid, not a resampling: the voxels are the same voxels, permuted and flipped. This function does exactly that, so it is exact, works on images of any size, and costs a single `aperm()`.

It used to build the target space and hand it to `resample`, which had three consequences: values were interpolated where they should merely have moved, the registration backend refused images smaller than four voxels on any axis, and – because the target space kept the source's dimensions – an axis-permuting reorientation wrote into a grid that did not contain the data and silently lost about a quarter of it.

Value

A reoriented object of the same class as `x`.

See Also

`axcodes`, `reorient`, `apply_orientation`

Examples

```
sp <- NeuroSpace(c(10L, 10L, 10L), c(2, 2, 2))
vol <- DenseNeuroVol(array(rnorm(1000), c(10,10,10)), sp)
ras_vol <- as_canonical(vol)
axcodes(ras_vol)  # "R" "A" "S"
```

---

as_mmap *Convert a NeuroVec to a memory-mapped representation*

Description

Generic for converting neuroimaging vectors to a memory-mapped `MappedNeuroVec` on disk (when possible).

Methods for the `as_mmap` generic, which convert various neuroimaging vector types to a `MappedNeuroVec` backed by an on-disk NIfTI file.

Usage

```
as_mmap(x, file = NULL, ...)

## S4 method for signature 'MappedNeuroVec'
as_mmap(x, file = NULL, ...)

## S4 method for signature 'FileBackedNeuroVec'
as_mmap(x, file = NULL, ...)

## S4 method for signature 'NeuroVec'
as_mmap(x, file = NULL, data_type = "FLOAT", overwrite = FALSE, ...)

## S4 method for signature 'SparseNeuroVec'
as_mmap(x, file = NULL, data_type = "FLOAT", overwrite = FALSE, ...)
```

Arguments

`x`	A neuroimaging vector (`NeuroVec`, `MappedNeuroVec`, or `FileBackedNeuroVec`).
`file`	Optional output file name. If `NULL`, a temporary file with extension `.nii` is created.
`...`	Additional arguments passed to methods (e.g. `data_type`, `overwrite`).
`data_type`	Character string specifying the output data type for the NIfTI file. Should be one of "UBYTE", "BYTE", "SHORT", "USHORT", "INT", "UINT", "LONG", "ULONG", "FLOAT" or "DOUBLE". Default is "FLOAT".
`overwrite`	Logical; if `TRUE`, overwrite an existing file at the specified path. Default is `FALSE`.

Value

A MappedNeuroVec (or x itself if already memory-mapped).

A MappedNeuroVec (or x itself if it is already memory-mapped).

---

as_nifti_header *Construct a Minimal NIfTI-1 Header from a NeuroVol*

Description

Given a NeuroVol object (or similar), this function builds a basic NIfTI-1 header structure, populating essential fields such as dim, pixdim, datatype, the affine transform, and the quaternion parameters.

Usage

```
as_nifti_header(
  vol,
  file_name,
  oneFile = TRUE,
  data_type = NULL,
  extensions = NULL,
  values = NULL,
  version = NULL
)
```

Arguments

vol	A NeuroVol (or 3D array-like) specifying dimensions, spacing, and affine transform.
file_name	A character string for the file name (used within the header but not necessarily to write data).
oneFile	Logical; if TRUE, sets the NIfTI magic to "n+1", implying a single-file format (.nii). If FALSE, uses "ni1" (header+image).
data_type	Character specifying the data representation, e.g. "FLOAT", "DOUBLE", "SHORT". NULL (the default) keeps the source file's datatype when vol came from one and its values are still exactly representable in it, and uses "FLOAT" otherwise.
extensions	Optional NiftiExtensionList-class object or list of NiftiExtension-class objects to include in the header.
values	Optional numeric vector of the voxel values that will be written. Used to pick a datatype and to derive scl_slope / scl_inter for integer output; taken from vol when omitted.
version	Either 1 or 2, selecting the NIfTI version to describe. NULL (the default) uses NIfTI-1 unless a dimension exceeds what its 16-bit dim field can hold, in which case NIfTI-2 is used because NIfTI-1 physically cannot represent the image.

Details

This is a convenience function that calls `createNIfTIHeader` first, then updates the fields (dimensions, `pixdim`, orientation, etc.) based on the `vol` argument. The voxel offset is set to 352 bytes (or larger if extensions are provided), and the quaternion is derived from the transform matrix via `matrixToQuatern`.

Note: This function primarily sets up a minimal header suitable for writing standard single-file NIfTI-1. If you need a more comprehensive or advanced usage, consider manually editing the returned list.

When `vol` was read from a NIfTI file, the fields that describe the acquisition rather than the array – repetition time (`pixdim[5]`), `xyzt_units`, `qform_code` and `sform_code`, `descrip`, `aux_file`, the intent fields, `cal_min`/`cal_max`, the slice timing fields and `toffset` – are carried over from that file. Only the fields the object itself determines (geometry, dimensions, datatype, offsets) are recomputed. Before this behaviour existed, a read-write round trip reset all of them, which silently dropped the TR and relabelled an MNI-space image as scanner-space.

Value

A `list` representing the NIfTI header fields, containing elements like `dimensions`, `pixdim`, `datatype`, `qform`, `quaternion`, `qfac`, `extensions`, etc. This can be passed to other functions that write or manipulate the header.

See Also

`createNIfTIHeader` for the base constructor of an empty NIfTI header. `NiftiExtension` for creating extensions.

---

automask *Compute a brain-like mask from image intensities*

Description

Builds a spatial mask from image content rather than requiring an external mask. The implementation is AFNI-inspired: it computes a clip level, applies thresholding to a representative 3D image, retains the largest connected component, and optionally applies peel/unpeel cleanup.

Usage

```
automask(
  x,
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)
```

```
## S4 method for signature 'FileBackedNeuroVec'
automask(
  x,
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)

## S4 method for signature 'MappedNeuroVec'
automask(
  x,
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)

## S4 method for signature 'DenseNeuroVec'
automask(
  x,
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)

## S4 method for signature 'AbstractSparseNeuroVec'
automask(
  x,
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)

## S4 method for signature 'NeuroVol'
automask(
  x,
```

```
  mfrac = 0.5,
  gradual = TRUE,
  representative = "mean_abs",
  peels = 1L,
  peel_threshold = 17L,
  connect = c("26-connect", "18-connect", "6-connect")
)
```

Arguments

x	A neuroimaging object.
mfrac	Fraction used in the clip-level update step.
gradual	If TRUE, use a spatially varying clip map across octants. If FALSE, use a single global clip threshold.
representative	For multi-volume inputs, the 3D summary image used for thresholding. Supported values are "mean_abs" and "median".
peels	Number of AFNI-style peel/unpeel iterations. Use 0 to disable.
peel_threshold	Minimum number of 18-neighbors required for a voxel to survive peeling.
connect	Connectivity used when retaining the largest component.

Value

A LogicalNeuroVol.

Examples

```
sp <- NeuroSpace(c(8, 8, 8), spacing = c(1, 1, 1))
arr <- array(abs(rnorm(512)), c(8, 8, 8))
arr[3:6, 3:6, 3:6] <- arr[3:6, 3:6, 3:6] + 10
vol <- NeuroVol(arr, sp)
mask <- automask(vol, gradual = FALSE, peels = 0)
```

---

axcodes *Get Orientation Axis Codes*

Description

Returns a character vector of anatomical axis direction labels for a neuroimaging object or space. For example, c("R", "A", "S") for a standard RAS-oriented image.

Usage

```
axcodes(x)

## S4 method for signature 'NeuroSpace'
axcodes(x)

## S4 method for signature 'NeuroObj'
axcodes(x)

## S4 method for signature 'matrix'
axcodes(x)
```

Arguments

x	A NeuroVol, NeuroVec, NeuroSpace, or a 4x4 affine matrix.

Value

A character vector of length 3 with axis direction codes.

Examples

```
sp <- NeuroSpace(c(10L, 10L, 10L), c(2, 2, 2))
axcodes(sp)

vol <- DenseNeuroVol(array(0, c(10,10,10)), sp)
axcodes(vol)
```

---

axes *Extract Image Axes*

Description

Extract Image Axes

Usage

```
axes(x)

## S4 method for signature 'NeuroSpace'
axes(x)
```

Arguments

x	an object with a set of axes

Value

An object representing the axes of x.

Examples

```
x <- NeuroSpace(c(10,10,10), spacing=c(1,1,1))
class(axes(x)) == "AxisSet3D"
```

AxisSet-class *AxisSet*

Description

Virtual base class representing an ordered set of named axes.

Slots

ndim the number of axes (or dimensions)

AxisSet1D-class *AxisSet1D*

Description

A one-dimensional axis set

Slots

i the first axis

AxisSet2D-class *AxisSet2D*

Description

A two-dimensional axis set representing an ordered pair of named axes.

Slots

- `i` The first axis, inherited from AxisSet1D
- `j` The second axis, of class "NamedAxis"

See Also

AxisSet1D-class, AxisSet3D-class

Examples

```
# Create an AxisSet2D object
axis1 <- new("NamedAxis", axis = "x", direction = 1)
axis2 <- new("NamedAxis", axis = "y", direction = 1)
axisSet2D <- new("AxisSet2D", i = axis1, j = axis2, ndim = 2L)
```

AxisSet3D-class *AxisSet3D Class*

Description

A class representing a three-dimensional axis set, extending the AxisSet2D class with an additional third axis.

Slots

- `k` A `NamedAxis` object representing the third axis.

See Also

AxisSet2D-class, NamedAxis-class

Examples

```
# Create NamedAxis objects for each dimension
x_axis <- new("NamedAxis", axis = "x", direction = 1)
y_axis <- new("NamedAxis", axis = "y", direction = 1)
z_axis <- new("NamedAxis", axis = "z", direction = 1)

# Create an AxisSet3D object
axis_set_3d <- new("AxisSet3D", i = x_axis, j = y_axis, k = z_axis, ndim = 3L)
```

AxisSet4D-class *AxisSet4D Class*

Description

A class representing a four-dimensional axis set, extending the AxisSet3D class with an additional fourth axis.

Slots

`l` A `NamedAxis` object representing the fourth axis.

See Also

`AxisSet3D-class`, `NamedAxis-class`

Examples

```
# Create NamedAxis objects for each dimension
x_axis <- new("NamedAxis", axis = "x", direction = 1)
y_axis <- new("NamedAxis", axis = "y", direction = 1)
z_axis <- new("NamedAxis", axis = "z", direction = 1)
t_axis <- new("NamedAxis", axis = "t", direction = 1)

# Create an AxisSet4D object
axis_set_4d <- new("AxisSet4D", i = x_axis, j = y_axis, k = z_axis,
                   l = t_axis, ndim = 4L)
```

AxisSet5D-class *AxisSet5D Class*

Description

A class representing a five-dimensional axis set, extending the AxisSet4D class with an additional fifth axis.

Slots

`m` A `NamedAxis` object representing the fifth axis.

See Also

`AxisSet4D-class`, `NamedAxis-class`

Examples

```
# Create NamedAxis objects for each dimension
x_axis <- new("NamedAxis", axis = "x", direction = 1)
y_axis <- new("NamedAxis", axis = "y", direction = 1)
z_axis <- new("NamedAxis", axis = "z", direction = 1)
t_axis <- new("NamedAxis", axis = "t", direction = 1)
v_axis <- new("NamedAxis", axis = "v", direction = 1)

# Create an AxisSet5D object
axis_set_5d <- new("AxisSet5D", i = x_axis, j = y_axis, k = z_axis,
                   l = t_axis, m = v_axis, ndim = 5L)
```

BigNeuroVec *Create a Memory-Mapped Neuroimaging Vector*

Description

Creates a BigNeuroVec object, which represents a large neuroimaging vector using memory-mapped file storage. This allows working with neuroimaging data that is too large to fit in memory.

Usage

```
BigNeuroVec(
  data,
  space,
  mask,
  label = "",
  volume_labels = character(),
  type = c("double", "float", "integer"),
  backingfile = tempfile()
)
```

Arguments

data	The input data to be stored
space	A NeuroSpace object defining the spatial properties
mask	A logical mask indicating which voxels contain data
label	Optional character string label for the vector
volume_labels	Optional character vector of per-volume labels
type	Storage type, one of "double", "float", or "integer"
backingfile	Path to the file used for memory mapping (defaults to tempfile())

Value

A new BigNeuroVec object that provides memory-efficient access to large neuroimaging data through memory mapping. The object contains the spatial properties, mask, and memory-mapped data storage.

Examples

```
# Load an example 4D brain image
example_file <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
example_4d_image <- read_vec(example_file)

# Create a mask (e.g., selecting voxels with values > 0)
mask <- array(as.vector(example_4d_image[,,,1]) > 0,
              dim = dim(example_4d_image)[1:3])

if(requireNamespace("bigstatsr", quietly = TRUE)) {
  # Create a BigNeuroVec with memory mapping
  big_vec <- BigNeuroVec(data = example_4d_image@.Data,
                         space = space(example_4d_image),
                         mask = mask,
                         label = "Example BigNeuroVec")
  print(big_vec)
}
```

BigNeuroVec-class *BigNeuroVec Class*

Description

A class representing a sparse four-dimensional brain image backed by a disk-based big matrix. BigNeuroVec objects are designed for efficient handling of large-scale brain imaging data that exceeds available memory.

Details

BigNeuroVec leverages file-backed storage to manage large 4D neuroimaging datasets that would typically exceed available RAM. It combines the sparse representation framework of `AbstractSparseNeuroVec` with the disk-based storage capabilities of `FBM`, allowing for out-of-core computations on massive datasets.

Slots

`data` An instance of class `FBM` from the `bigstatsr` package, containing time-series data. The FBM (File-Backed Big Matrix) is a matrix-like structure stored on disk, enabling efficient handling of large-scale data.

Inheritance

`BigNeuroVec` inherits from:

- `NeuroVec`: Base class for 4D brain images
- `AbstractSparseNeuroVec`: Provides sparse representation framework
- `ArrayLike4D`: Interface for 4D array-like operations

See Also

AbstractSparseNeuroVec-class for the parent sparse representation class. NeuroVec-class for the base 4D brain image class. FBM for details on File-Backed Big Matrix objects.

`bilateral_filter` *Apply a bilateral filter to a volumetric image*

Description

This function smooths a volumetric image (3D brain MRI data) using a bilateral filter. The bilateral filter considers both spatial closeness and intensity similarity for smoothing. Only in-mask, in-bounds neighbors contribute to each local weighted average.

Usage

```
bilateral_filter(
  vol,
  mask,
  spatial_sigma = 2,
  intensity_sigma = 1,
  window = 1,
  range_scale = NULL
)
```

Arguments

`vol`	A NeuroVol object representing the image volume to be smoothed.
`mask`	An optional LogicalNeuroVol object representing the image mask that defines the region where the filtering is applied. If not provided, the entire volume is considered.
`spatial_sigma`	A numeric value specifying the standard deviation of the spatial Gaussian kernel (default is 2).
`intensity_sigma`	A numeric value specifying the standard deviation of the intensity Gaussian kernel (default is 1).
`window`	An integer specifying the number of voxels around the center voxel to include on each side. For example, window=1 for a 3x3x3 kernel (default is 1).
`range_scale`	Optional positive numeric range scale used by the intensity kernel. If `NULL`, the scale is estimated as the standard deviation of the current input values inside `mask`. Supply a fixed value to apply the same range bandwidth across observed and null maps.

Details

With `range_scale = NULL`, the intensity bandwidth is estimated separately for each input volume. Equal `intensity_sigma` values therefore do not imply equal bandwidths across subjects, contrasts, or observed/null maps. For batch or group workflows, choose one positive finite `range_scale` from a reference or pooled in-mask intensity distribution and reuse it, along with the same `intensity_sigma`, for every map in comparable intensity units. The effective bandwidth is `intensity_sigma * range_scale`.

Value

A smoothed image of class `NeuroVol`.

Examples

```
brain_mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Apply bilateral filtering to the brain volume
filtered_vol <- bilateral_filter(brain_mask, brain_mask, spatial_sigma = 2,
intensity_sigma = 25, window = 1)
```

---

bilateral_filter_4d *Apply a 4D bilateral filter to a NeuroVec*

Description

This function applies a full 4D bilateral filter to a `NeuroVec`, smoothing jointly across space (x, y, z) and time (t). The filter uses spatial, temporal, and intensity kernels to preserve edges while reducing noise, leveraging a parallel C++ backend for performance. Only in-mask, in-bounds spatial neighbors contribute to each local weighted average.

Usage

```
bilateral_filter_4d(
  vec,
  mask,
  spatial_sigma = 2,
  intensity_sigma = 1,
  temporal_sigma = 1,
  spatial_window = 1,
  temporal_window = 1,
  temporal_spacing = 1,
  range_scale = NULL
)
```

Arguments

vec	A NeuroVec object (4D image).
mask	An optional LogicalNeuroVol or NeuroVol specifying the spatial region to process. If omitted, the entire spatial extent is processed.
spatial_sigma	Numeric; standard deviation of the spatial Gaussian (default 2).
intensity_sigma	Numeric; standard deviation of the intensity Gaussian (default 1).
temporal_sigma	Numeric; standard deviation of the temporal Gaussian (default 1).
spatial_window	Integer; half-width of the spatial window in voxels (default 1), e.g., 1 => 3x3x3 spatial neighborhood.
temporal_window	Integer; half-width of the temporal window in frames (default 1), e.g., 1 => 3 timepoints (t-1, t, t+1).
temporal_spacing	Numeric; spacing of the temporal dimension (e.g., TR in seconds). Default is 1. This sets the temporal scale used for the temporal kernel.
range_scale	Optional positive numeric range scale used by the intensity kernel. If NULL, the scale is estimated from all finite input values inside mask across time. Supply a fixed value to use the same range bandwidth across observed and null data.

Details

With range_scale = NULL, one intensity scale is estimated from all finite in-mask values across time in this 4-D input. It is not estimated separately for each time point, but separate calls on different subjects or contrasts can still use different bandwidths. For batch/group comparisons, reuse a positive finite range_scale and the same intensity_sigma across inputs in comparable intensity units. In contrast, bilateral_filter_vec() estimates a separate scale for each volume when range_scale = NULL.

Parameter guidance and units: - spatial_sigma: Measured in physical units (millimeters). Distances are computed using spacing(vec)[1:3], so choose spatial_sigma relative to voxel size. As a rule of thumb, set it to about 1-2 voxel sizes (e.g., 2-4 mm for 2 mm isotropic data) for moderate smoothing. - intensity_sigma: Dimensionless multiplier of the global intensity standard deviation. Internally, the filter uses exp(-(dI)^2 / (2 * (intensity_sigma * sigma_I)^2)), where sigma_I is the standard deviation of all finite voxel intensities within the mask across time. Start with 1.0 for moderate smoothing; use 0.5-0.8 to preserve more edges, or 1.5-2.0 for stronger smoothing. - temporal_sigma: Measured in temporal_spacing units (e.g., seconds). Typical values are 0.5-2 x TR. Larger values blend more across time.

Choosing the neighborhood window sizes: - spatial_window controls the discrete spatial support. A common choice is ceiling(2 * spatial_sigma / min(spacing(vec)[1:3])), which covers ~95 - temporal_window similarly can be set to ceiling(2 * temporal_sigma / temporal_spacing).

Quick presets (typical fMRI with 2-3 mm voxels and TR~2s): - Light: spatial_sigma = 1 x min(spacing), intensity_sigma = 0.8, temporal_sigma = 0.5 x TR, windows = 1 - Moderate (default-ish): spatial_sigma = 1.5 x min(spacing), intensity_sigma = 1.0, temporal_sigma = 1 x TR, windows = 1-2 - Strong: spatial_sigma = 2 x min(spacing), intensity_sigma = 1.5, temporal_sigma = 1.5 x TR, windows = 2

Tip: If your time axis has known TR, pass it via `temporal_spacing`. For NIfTI inputs, you can get TR via:

```
hdr <- read_header(nifti_path)
tr  <- hdr@header$pixdim[5]
out <- bilateral_filter_4d(vec, mask, temporal_spacing = tr)
```

Value

A NeuroVec with filtered data.

See Also

bilateral_filter, NeuroVec-class, NeuroVol-class

Examples

```
vec <- read_vec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
out  <- bilateral_filter_4d(vec, mask,
                            spatial_sigma = 2, intensity_sigma = 1,
                            temporal_sigma = 1, spatial_window = 1,
                            temporal_window = 1, temporal_spacing = 1)
```

BinaryReader *Create Binary Reader Object*

Description

Create a new instance of the BinaryReader class for reading bulk binary data.

Usage

```
BinaryReader(
  input,
  byte_offset,
  data_type,
  bytes_per_element,
  endian = .Platform$endian,
  signed = TRUE
)
```

Arguments

input	Character string (file name) or connection object to read from
byte_offset	Integer specifying bytes to skip at start of input
data_type	Character string specifying R data type ('integer', 'double', etc.)
bytes_per_element	Integer specifying bytes per data element (e.g., 4 or 8)
endian	Character string specifying endianness ('big' or 'little', default: platform-specific)
signed	Logical indicating if data type is signed (default: TRUE)

Value

An object of class BinaryReader

See Also

BinaryWriter for writing binary data

Examples

```
# Create a temporary binary file
tmp <- tempfile()
writeBin(rnorm(100), tmp, size = 8)


# Read from existing connection with offset
con <- file(tmp, "rb")
reader <- BinaryReader(con, byte_offset=0,
                       data_type = "DOUBLE", bytes_per_element = 8L)
close(reader)

# Clean up
unlink(tmp)
```

BinaryReader-class *BinaryReader Class*

Description

Class supporting reading of bulk binary data from a connection

Slots

`input` The binary input connection

`byte_offset` The number of bytes to skip at the start of input

`data_type` The data type of the binary elements

`bytes_per_element` The number of bytes in each data element (e.g. 4 or 8 for floating point numbers)

`endian` The endianness of the binary input connection

`signed` Logical indicating whether the data type is signed

`BinaryWriter` *Create Binary Writer Object*

Description

Create a new instance of the BinaryWriter class for writing bulk binary data.

Usage

```
BinaryWriter(
  output,
  byte_offset,
  data_type,
  bytes_per_element,
  endian = .Platform$endian
)
```

Arguments

`output`	Character string (file name) or connection object to write to
`byte_offset`	Integer specifying bytes to skip at start of output
`data_type`	Character string specifying R data type ('integer', 'double', etc.)
`bytes_per_element`	Integer specifying bytes per data element (e.g., 4 or 8)
`endian`	Character string specifying endianness ('big' or 'little', default: platform-specific)

Value

An object of class BinaryWriter

See Also

`BinaryReader` for reading binary data

Examples

```
tmp <- tempfile()
# Write to existing connection with offset
con <- file(tmp, "wb")
writer <- BinaryWriter(con, byte_offset = 100L,
                       data_type = "integer", bytes_per_element = 4L)
close(writer)
unlink(tmp)
```

BinaryWriter-class *BinaryWriter Class*

Description

This class supports writing of bulk binary data to a connection

Slots

`output` The binary output connection

`byte_offset` The number of bytes to skip at the start of input

`data_type` The data type of the binary elements

`bytes_per_element` The number of bytes in each data element (e.g. 4 or 8 for floating point numbers)

`endian` The endianness of the binary output connection

---

bounds *Extract Spatial Bounds of an Image*

Description

This function extracts the spatial bounds (origin + dim * spacing) of an image represented by the input object.

Usage

```
bounds(x)

## S4 method for signature 'NeuroSpace'
bounds(x)
```

Arguments

`x`	The object with the ‘bounds‘ property, typically an image.

Value

A numeric `matrix` with two columns specifying the min (column 1) and max (column 2) bounds of each dimension of `x`.

Examples

```
bspace <- NeuroSpace(c(10, 10, 10), c(2, 2, 2))
b <- bounds(bspace)
nrow(b) == ndim(bspace)
ncol(b) == 2
```

`centroid` *return the centroid of an object*

Description

return the centroid of an object

Usage

```
centroid(x, ...)

## S4 method for signature 'NeuroSpace'
centroid(x)

## S4 method for signature 'ROICoords'
centroid(x)
```

Arguments

`x`	an object with a centroid
`...`	extra args

Value

A numeric vector giving the centroid of `x`.

Examples

```
bspace <- NeuroSpace(c(10,10,10), c(2,2,2))
centroid(bspace)
```

centroids *Return a matrix of centroids of an object*

Description

Return a matrix of centroids of an object

Usage

```
centroids(x, ...)

## S4 method for signature 'ClusteredNeuroVec'
centroids(x, type = c("center_of_mass", "medoid"))

## S4 method for signature 'ClusteredNeuroVol'
centroids(x, type = c("center_of_mass", "medoid"))
```

Arguments

x	an object with multiple centroids (e.g. a ClusteredNeuroVol)
...	extra args
type	the type of center of mass: one of "center_of_mass" or "medoid"

Details

For ‘type = "center_of_mass"‘, returns arithmetic mean coordinates; for ‘"medoid"‘, returns the most central point.

Value

A numeric matrix where each row represents the coordinates of a centroid.

A matrix of coordinates where each row represents the centroid of a cluster.

cgb_filter *Correlation-guided bilateral filtering (convenience wrapper)*

Description

High-level interface that builds a correlation-guided bilateral (CGB) graph with sensible defaults (similar to the bilateral filter interface) and immediately applies it to smooth the data.

Usage

```
cgb_filter(
  runs,
  mask = NULL,
  spatial_sigma = 2,
  window = NULL,
  corr_map = c("power", "exp", "soft"),
  corr_param = 2,
  topk = 16L,
  passes = 1L,
  lambda = 1,
  leave_one_out = FALSE,
  run_weights = NULL,
  add_self = TRUE,
  time_weights = NULL,
  confounds = NULL,
  robust = c("none", "huber", "tukey"),
  robust_c = 1.345,
  return_graph = FALSE
)
```

Arguments

runs	A NeuroVec or a list of NeuroVec.
mask	Optional LogicalNeuroVol/NeuroVol or logical array for spatial masking. Defaults to in-mask voxels.
spatial_sigma	Spatial Gaussian sigma in mm. Used both for weighting and, when window is NULL, to auto-choose the neighborhood size.
window	Integer half-width of the cubic neighborhood. If NULL, it is computed as ceiling(2 * spatial_sigma / min(spacing)) and at least 1.
corr_map	Mapping from pooled correlation to affinity; one of "power", "exp", or "soft". Defaults to "power".
corr_param	Parameter for corr_map (gamma/tau/r0 respectively).
topk	Keep strongest k neighbors (0 keeps all). Defaults to 16.
passes	Number of smoothing passes (>=1). Defaults to 1.
lambda	Blend factor in [0,1] per pass. Defaults to 1 (pure diffusion).
leave_one_out	If TRUE and multiple runs are supplied, builds LORO graphs and returns a list of smoothed runs.
run_weights	Optional numeric weights per run for Fisher-z pooling.
add_self	Logical; add a tiny self-edge before normalization.
time_weights	Optional list (or single vector) of per-run time weights.
confounds	Optional list (or single matrix) of per-run confounds.
robust	One of "none", "huber", or "tukey".
robust_c	Tuning constant for robust weights.
return_graph	Logical; if TRUE, also return the graph(s) alongside the smoothed data.

Details

This is a convenience front-end to cgb_make_graph and cgb_smooth with a bilateral-like interface: - If window is NULL, it is chosen as ceiling(2 * spatial_sigma / min(spacing)) (at least 1). Larger windows allow correlations over more distant neighbors, at the cost of extra compute and memory. - spatial_sigma (in mm) controls how quickly spatial weights fall with distance. Small values emphasize very local structure; larger values mix information over a wider spatial footprint. - corr_map and corr_param set how pooled correlations are turned into edge weights: * "power": a(r) = r^gamma for r > 0. Larger gamma (e.g., 3-4) strongly emphasizes high correlations and produces more edge-preserving, patchy smoothing; smaller values (e.g., 1-2) behave more like standard correlation-weighted smoothing. * "exp": Gaussian on 1 - r with scale tau. Small tau keeps only very similar time-series; larger tau makes the filter closer to a spatial Gaussian while still respecting sign. * "soft": a(r) = max(r - r0, 0). Increasing r0 discards more weak correlations and tends to sharpen edges but can make the result more piecewise-constant. - topk limits each voxel to at most k strongest neighbors. Smaller topk yields sparser, more anisotropic graphs (cheaper but sometimes less smooth); larger topk increases mixing and memory. - passes and lambda control diffusion strength. With lambda = 1, each pass applies pure graph diffusion; multiple passes compound smoothing. Choosing lambda < 1 blends each pass with the identity and can prevent over-smoothing when using more passes. - Setting leave_one_out = TRUE for multi-run inputs builds a separate graph for each run that excludes its own correlations, which reduces information leakage in cross-validation or decoding workflows. - time_weights, confounds, and robust/robust_c adjust how time-points contribute to the correlation estimates. Down- weighting high-motion/high-DVARS frames (via make_time_weights and robust != "none") will typically yield smoother, less noisy graphs but can also reduce effective temporal degrees of freedom. - Use return_graph = TRUE when you plan to reuse the constructed graph(s) with cgb_smooth or inspect their sparsity pattern.

Value

If leave_one_out=FALSE, a smoothed NeuroVec. If leave_one_out=TRUE, a list of smoothed NeuroVec. When return_graph=TRUE, returns a list with elements result and graph (single object or lists accordingly).

Examples

```
vec <- read_vec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Auto window from spatial_sigma and spacing, single pass
out <- cgb_filter(vec, mask, spatial_sigma = 3, window = NULL, topk = 16)

# Stronger diffusion with two passes and lambda < 1
out2 <- cgb_filter(vec, mask, spatial_sigma = 4, window = NULL,
                   passes = 2, lambda = 0.7)
```

cgb_make_graph *Build a correlation-guided bilateral (CGB) graph*

Description

Computes a sparse row-stochastic graph whose weights combine spatial proximity and pooled local time-series correlations. Supports optional censoring weights, nuisance regression via weighted QR projectors, leave-one-run-out graph construction, and robust down-weighting of high-DVARS volumes.

Usage

```
cgb_make_graph(
  runs,
  mask = NULL,
  window = 1L,
  spatial_sigma = 2,
  corr_map = c("power", "exp", "soft"),
  corr_param = 2,
  topk = 16L,
  leave_one_out = FALSE,
  run_weights = NULL,
  add_self = TRUE,
  time_weights = NULL,
  confounds = NULL,
  robust = c("none", "huber", "tukey"),
  robust_c = 1.345
)
```

Arguments

runs	A NeuroVec or a list of NeuroVec objects (typically one per run).
mask	Optional LogicalNeuroVol/NeuroVol or logical array defining in-mask voxels. Defaults to all in-mask voxels.
window	Integer half-width of the cubic spatial neighborhood (e.g., 1 yields a 3x3x3 window).
spatial_sigma	Spatial Gaussian sigma in mm.
corr_map	Mapping from pooled correlation to affinity; one of "power", "exp", or "soft". The "power" and "soft" mappings rectify negative correlations, whereas "exp" preserves them (useful for sharpening more than smoothing).
corr_param	Parameter for the chosen corr_map (gamma, tau, or r0 respectively).
topk	Keep the strongest k neighbors after masking (0 keeps all).
leave_one_out	Logical; if TRUE and multiple runs are provided, returns a list of graphs where run u excludes its own correlations.

run_weights	Optional numeric weights per run used in Fisher-z pooling. Defaults to $n_k - 3$ (usable frames minus three) when omitted.
add_self	Logical; always inject a tiny self-edge before normalization.
time_weights	Optional list (or single vector) of per-run time weights $w_t \in [0, 1]$ applied before correlation estimation. An intercept is always included so correlations are computed on weighted, demeaned series.
confounds	Optional list (or single matrix) of per-run confound regressors to project out prior to correlation estimation.
robust	One of "none", "huber", or "tukey"; when not "none" an additional DVARS-style reweighting is applied.
robust_c	Tuning constant for the robust weights (Huber/Tukey).

Details

Graph construction overview: - Neighborhood: For each in-mask voxel i, consider a cubic spatial window of half-width window (i.e., (2*window+1)^3 candidates). Candidates outside the mask or bounds are ignored. - Spatial kernel: For a candidate j at physical distance d_ij (mm), assign a spatial weight w_s = exp(-d_ij^2 / (2 * spatial_sigma^2)). Distances use spacing(spatial_space). - Correlation pooling: Compute Pearson correlation r_k(i,j) within each run k (optionally after nuisance projection/weights), transform to Fisher-z, pool across runs with weights ω_k (default $n_k - 3$), then back-transform to r_pool via tanh. - Correlation-to-affinity mapping (corr_map): * "power" (mode=0): a(r) = r^gamma for r>0 else 0. Parameter = gamma. * "exp" (mode=1): a(r) = exp(-(1 - r)^2 / (2 * tau^2)). Parameter = tau. * "soft" (mode=2): a(r) = max(r - r0, 0). Parameter = r0. - Combined weight: w_ij = w_s(i,j) * a(r_pool(i,j)). If topk > 0, keep the strongest topk neighbors. Optionally inject a small self-edge when add_self=TRUE. Finally, row-normalize to obtain a stochastic W.

Parameter guidance: - spatial_sigma is in mm. A typical choice is 1-2x the voxel size (e.g., 2-4 mm for 2 mm isotropic). Larger values increase spatial mixing. - window controls support; a good rule is ceiling(2 * spatial_sigma / min(spacing)). - corr_map: use "power" with corr_param = 2 for robust smoothing; "exp" with tau ~ 0.5-1.5 retains sign information; "soft" with r0 ~ 0.1-0.3 thresholds weak correlations. - topk: 8-32 is a practical range; higher values densify the graph and increase compute/memory. - leave_one_out: for multi-run inputs, enabling this prevents a run from using its own correlations when building its graph (mitigates leakage).

Nuisance/time weights/robust options: - If confounds/time_weights specified (or robust != "none"), per-run weighted QR projectors are used; correlations are computed on the projected, weighted series. Robust options add DVARS-like down-weighting. - If the only request is an implicit intercept (no actual confounds, no time weights, no robust), the baseline builder is used for identical results.

Output and usage: - Returns CSR arrays (row_ptr, col_ind, val) that define a row-stochastic matrix W over masked voxels. Apply with cgb_smooth. - Complexity scales with number of masked voxels times neighborhood size (limited by topk). Memory proportional to number of retained edges.

Value

A list containing row_ptr, col_ind, val, dims3d, and mask_idx, or (if leave_one_out=TRUE) a list of such graphs.

Examples

```
vec <- read_vec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
# Build a graph with spatial sigma in mm and keep 16 neighbors
G <- cgb_make_graph(vec, mask, spatial_sigma = 3, window = 2, topk = 16)
# Smooth with one pass (pure diffusion)
sm <- cgb_smooth(vec, G, passes = 1, lambda = 1)
```

---

cgb_smooth *Apply a precomputed CGB graph to volumetric data*

Description

Apply a precomputed CGB graph to volumetric data

Usage

```
cgb_smooth(x, graph, passes = 1L, lambda = 1)
```

Arguments

x	A NeuroVec (4D) or NeuroVol (3D).
graph	Graph list returned by cgb_make_graph.
passes	Number of smoothing passes (>=1). Each pass multiplies by W; if lambda < 1 a simple diffusion blend (1 - lambda)I + lambda W is applied per pass.
lambda	Blend factor in $[0, 1]$ controlling diffusion strength.

Value

Smoothed object of the same class as x.

---

cgb_smooth_loro *Leave-one-run-out smoothing helper*

Description

Leave-one-run-out smoothing helper

Usage

```
cgb_smooth_loro(runs, graphs, passes = 1L, lambda = 1)
```

Arguments

runs	List of NeuroVec objects (one per run).
graphs	List of graphs returned by cgb_make_graph(..., leave_one_out=TRUE).
passes, lambda	See cgb_smooth.

Value

A list of smoothed NeuroVec objects, one per run.

---

clip_level *Estimate an image clip level*

Description

Computes an AFNI-inspired clip threshold for separating foreground from low-intensity background. For 4D images, the threshold is computed from a representative 3D volume, typically the voxelwise median across time.

Usage

```
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")

## S4 method for signature 'FileBackedNeuroVec'
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")

## S4 method for signature 'MappedNeuroVec'
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")

## S4 method for signature 'DenseNeuroVec'
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")

## S4 method for signature 'AbstractSparseNeuroVec'
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")

## S4 method for signature 'NeuroVol'
clip_level(x, mfrac = 0.5, gradual = FALSE, representative = "median")
```

Arguments

x	A neuroimaging object.
mfrac	Fraction used in the median-update step. Values outside (0, 0.99) fall back to 0.5.
gradual	If FALSE, return a scalar clip level. If TRUE, return a 3D clip map interpolated across image octants.
representative	For multi-volume inputs, the 3D summary image used for thresholding. Supported values are "median" and "mean_abs".

Value

If `gradual = FALSE`, a numeric scalar clip level. If `gradual = TRUE`, a `DenseNeuroVol` with voxel-wise clip levels.

Examples

```
sp <- NeuroSpace(c(8, 8, 8), spacing = c(1, 1, 1))
vol <- NeuroVol(array(abs(rnorm(512)), c(8, 8, 8)), sp)
clip_level(vol)
```

---

close,BinaryReader-method

Close a BinaryReader or BinaryWriter

Description

Closes the underlying connection associated with a BinaryReader or BinaryWriter object. This should be called when you're done with the reader/writer to free system resources.

Usage

```
## S4 method for signature 'BinaryReader'
close(con)

## S4 method for signature 'BinaryWriter'
close(con)
```

Arguments

`con`	The BinaryReader or BinaryWriter object to close.

Value

Invisibly returns `NULL`, called for its side effect of closing the connection.

Examples

```
# Create a temporary file and write some data
tmp <- tempfile()
writer <- BinaryWriter(tmp, byte_offset = 0L,
                       data_type = "DOUBLE", bytes_per_element = 8L)
write_elements(writer, rnorm(100))
close(writer)

# Read the data back
reader <- BinaryReader(tmp, byte_offset = 0L,
                       data_type = "DOUBLE", bytes_per_element = 8L)
data <- read_elements(reader, 100)
```

```
close(reader)

# Clean up
unlink(tmp)
```

`cluster_searchlight_series` *Cluster-centroid searchlight over cluster time-series*

Description

Iterate over clusters by their centroids and, for each seed cluster, return the time-series of the K nearest clusters (or those within a radius). This enables searchlight analysis at the cluster level rather than individual voxels.

Usage

```
cluster_searchlight_series(x, cvol = NULL, k = 10L, radius = NULL, label = "")
```

Arguments

`x`	A 'ClusteredNeuroVec' object or a 'NeuroVec' plus 'cvol'
`cvol`	A 'ClusteredNeuroVol' (required if 'x' is a 'NeuroVec')
`k`	Integer, number of nearest clusters including the seed (default: 10). Will be capped at the total number of clusters if specified value exceeds it.
`radius`	Numeric distance in mm. If given, use all clusters within this radius instead of k-nearest neighbors. Cannot be used together with `k`.
`label`	Optional character label for the returned windows

Details

The function creates a searchlight around each cluster's centroid, selecting either:

- The k nearest clusters (when `k` is specified)
- All clusters within a given radius (when `radius` is specified)

This is particularly useful for cluster-level connectivity analyses or when working with parcellated data where voxel-level searchlights would be redundant.

Value

A list of `ROIVec` objects, one per cluster, where each ROIVec contains:

values A TxN matrix where T is the number of timepoints and N is the number of neighboring clusters (including the seed itself)

coords The centroid coordinates of the neighboring clusters

The seed cluster's time-series is always the first column in each ROIVec.

See Also

ClusteredNeuroVec for creating clustered neuroimaging vectors, searchlight for voxel-level searchlight analysis, ROIVec for the structure of returned windows

Examples

```
# Create synthetic 4D data (8x8x8 volume, 10 timepoints)
sp4 <- NeuroSpace(c(8,8,8,10), c(1,1,1))
arr <- array(rnorm(8*8*8*10), dim=c(8,8,8,10))
vec <- NeuroVec(arr, sp4)

# Create a mask covering most of the volume
sp3 <- NeuroSpace(c(8,8,8), c(1,1,1))
mask_arr <- array(FALSE, dim=c(8,8,8))
mask_arr[2:7, 2:7, 2:7] <- TRUE
mask <- LogicalNeuroVol(mask_arr, sp3)

# Assign voxels to 10 clusters
n_voxels <- sum(mask_arr)
clusters <- sample(1:10, n_voxels, replace=TRUE)
cvol <- ClusteredNeuroVol(mask, clusters)

# Create clustered representation
cv <- ClusteredNeuroVec(vec, cvol)

# Get cluster searchlight with 3 nearest neighbors
windows <- cluster_searchlight_series(cv, k = 3)
length(windows)  # 10 windows (one per cluster)

# Check first window
roi1 <- windows[[1]]
dim(values(roi1))  # 10 x 3 (timepoints x neighbors)

# Use radius-based neighborhoods (5mm radius)
windows_radius <- cluster_searchlight_series(cv, radius = 5)
# Each window may have different number of neighbors
```

---

clustered_searchlight *Create a clustered searchlight iterator*

Description

This function generates a searchlight iterator that iterates over successive spatial clusters in an image volume. It allows for the exploration of spatially clustered regions within the provided mask by using either a pre-defined clustered volume or performing k-means clustering to generate the clusters.

Usage

```
clustered_searchlight(mask, cvol = NULL, csize = NULL)
```

Arguments

mask	A NeuroVol object representing the brain mask.
cvol	An optional ClusteredNeuroVol instance representing pre-defined clusters within the mask. If provided, the 'csize' parameter is ignored.
csize	An optional integer specifying the number of clusters to be generated using k-means clustering (ignored if cvol is provided).

Value

A deferred_list object containing ROIVol objects, each representing a clustered region within the image volume.

Examples

```
# Load an example brain mask
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Generate a clustered searchlight iterator with 5 clusters
clust_searchlight <- clustered_searchlight(mask, csize = 5)
```

ClusteredNeuroVec *ClusteredNeuroVec: Cluster-aware 4D neuroimaging data*

Description

'ClusteredNeuroVec' creates a 4D array-like object where voxels are grouped into clusters, with one time-series per cluster. All voxels within a cluster share the same time-series, making it ideal for parcellated analyses (e.g., Schaefer-Yeo parcellations).

Usage

```
ClusteredNeuroVec(x, cvol, FUN = mean, weights = NULL, label = "")
```

Arguments

x	Either a 'NeuroVec' object to be reduced by clusters, or a pre-computed numeric matrix of cluster time-series (T x K, where T=time points, K=clusters)
cvol	A 'ClusteredNeuroVol' object defining the cluster assignments
FUN	Reduction function to aggregate voxels within clusters (default: mean). Common choices include mean, median, or custom functions.
weights	Optional numeric vector of per-voxel weights for weighted aggregation. Must have length equal to the number of non-zero voxels in the mask.
label	Optional character label for the object (default: "")

Details

This class implements array-like 4D access while storing data efficiently as a TxK matrix instead of the full voxel x time representation. Each cluster's time-series is computed by applying the aggregation function (`FUN`) to all voxels within that cluster.

The object supports standard NeuroVec operations:

- Indexing: `x[,,,t]` to extract 3D volumes at time t
- Series extraction: `series(x, i, j, k)` for time-series at voxel (i,j,k)
- Matrix conversion: `as.matrix(x)` to get the TxK cluster matrix

Single-voxel clusters are handled efficiently without aggregation overhead.

Value

A `ClusteredNeuroVec` object containing:

cvol The input ClusteredNeuroVol defining cluster structure

ts A TxK matrix of cluster time-series (T=timepoints, K=clusters)

cl_map Integer vector mapping linear voxel indices to cluster IDs

label Character label for the object

See Also

`ClusteredNeuroVol` for creating cluster assignments, `cluster_searchlight_series` for cluster-based searchlight analysis, `series` for extracting time-series

Examples

```
# Create synthetic 4D data (10x10x10 volume, 20 timepoints)
sp4 <- NeuroSpace(c(10,10,10,20), c(1,1,1))
arr <- array(rnorm(10*10*10*20), dim=c(10,10,10,20))
vec <- NeuroVec(arr, sp4)

# Create a mask covering the central region
sp3 <- NeuroSpace(c(10,10,10), c(1,1,1))
mask_arr <- array(FALSE, dim=c(10,10,10))
mask_arr[3:8, 3:8, 3:8] <- TRUE
mask <- LogicalNeuroVol(mask_arr, sp3)

# Assign voxels to 5 random clusters
n_voxels <- sum(mask_arr)
clusters <- sample(1:5, n_voxels, replace=TRUE)
cvol <- ClusteredNeuroVol(mask, clusters)

# Create clustered representation
cv <- ClusteredNeuroVec(vec, cvol)

# Access like a regular NeuroVec
vol_t1 <- cv[,,,1]  # 3D volume at time 1
ts <- series(cv, 5, 5, 5)  # time-series at voxel (5,5,5)
```

```
# Get cluster time-series matrix
cluster_matrix <- as.matrix(cv)  # T x K matrix
dim(cluster_matrix)  # 20 x 5
```

ClusteredNeuroVec-class

ClusteredNeuroVec Class

Description

A class representing a 4D neuroimaging dataset where voxels are grouped into clusters. Each cluster has a single time-series that is shared by all voxels within that cluster.

Slots

`cvol` A `ClusteredNeuroVol` object defining cluster assignments

`ts` A numeric matrix of dimensions T x K (time points x clusters)

`cl_map` An integer vector mapping each voxel to its cluster ID (0 for outside mask)

`label` A character string label for the object

ClusteredNeuroVol-class

ClusteredNeuroVol Class

Description

This class represents a three-dimensional brain image divided into N disjoint partitions or clusters. It extends the `SparseNeuroVol` class to provide efficient storage and manipulation of clustered neuroimaging data.

Construct a `ClusteredNeuroVol` instance

Usage

```
ClusteredNeuroVol(mask, clusters, label_map = NULL, label = "")
```

Arguments

`mask`	an instance of class `LogicalNeuroVol`
`clusters`	a vector of clusters ids with length equal to number of nonzero voxels in mask `mask`
`label_map`	an optional `list` that maps from cluster id to a cluster label, e.g. (1 -> "FFA", 2 -> "PPA")
`label`	an optional `character` string used to label of the volume

Details

The ClusteredNeuroVol class is designed for efficient representation and manipulation of brain images with distinct, non-overlapping regions or clusters. It combines the memory efficiency of sparse representations with additional structures for managing cluster information.

The use case of `ClusteredNeuroVol` is to store volumetric data that has been clustered into discrete sets of voxels, each of which has an associated id. For example, this class can be used to represent parcellated neuroimaging volumes.

Value

`ClusteredNeuroVol` instance

Slots

`mask` A `LogicalNeuroVol` object representing the logical mask indicating the spatial domain of the set of clusters.

`clusters` An integer vector representing the cluster number for each voxel in the mask.

`label_map` A named list where each element represents a cluster and its name.

`cluster_map` An `environment` object that maps from cluster id to the set of 1D spatial indices belonging to that cluster.

Methods

This class inherits methods from the `SparseNeuroVol` class. Additional methods specific to cluster operations may be available.

Usage

ClusteredNeuroVol objects are particularly useful for:

- Representing parcellated brain images
- Storing results of clustering algorithms applied to neuroimaging data
- Efficient manipulation and analysis of region-based neuroimaging data

See Also

`SparseNeuroVol-class` for the parent sparse volume class. `LogicalNeuroVol-class` for the mask representation.

Examples

```
# Create a simple clustered brain volume
dim <- c(10L, 10L, 10L)
mask_data <- array(rep(c(TRUE, FALSE), 500), dim)
mask <- new("LogicalNeuroVol", .Data = mask_data,
            space = NeuroSpace(dim = dim, origin = c(0,0,0), spacing = c(1,1,1)))

clusters <- as.integer(runif(sum(mask_data)) * 5)+1
```

```
label_map <- list("Cluster1" = 1, "Cluster2" = 2, "Cluster3" = 3,
                  "Cluster4" = 4, "Cluster5" = 5)

cluster_map <- list()
for (i in 1:5) {
  cluster_map[[as.character(i)]] <- which(clusters == i)
}

clustered_vol <- ClusteredNeuroVol(
                     mask = mask,
                     clusters = clusters,
                     label_map = label_map)



# Create a simple space and volume
space <- NeuroSpace(c(16, 16, 16), spacing = c(1, 1, 1))
vol_data <- array(rnorm(16^3), dim = c(16, 16, 16))
vol <- NeuroVol(vol_data, space)

# Create a binary mask (e.g., values > 0)
mask_data <- vol_data > 0
mask_vol <- LogicalNeuroVol(mask_data, space)

# Get coordinates of masked voxels
mask_idx <- which(mask_data)
coords <- index_to_coord(mask_vol, mask_idx)

# Cluster the coordinates into 10 groups
set.seed(123)  # for reproducibility
kmeans_result <- kmeans(coords, centers = 10)

# Create the clustered volume
clustered_vol <- ClusteredNeuroVol(mask_vol, kmeans_result$cluster)

# Print information about the clusters
print(clustered_vol)
```

`ColumnReader` *Create Column Reader Object*

Description

Create a new instance of the ColumnReader class for reading column-oriented data.

Usage

```
ColumnReader(nrow, ncol, reader)
```

Arguments

nrow	Integer specifying number of rows in data
ncol	Integer specifying number of columns in data
reader	Function that takes column indices and returns matrix

Value

An object of class ColumnReader

Examples

```
reader_func <- function(cols) {
  matrix(rnorm(100 * length(cols)), 100, length(cols))
}
col_reader <- ColumnReader(nrow = 100L, ncol = 10L, reader = reader_func)
```

ColumnReader-class *ColumnReader*

Description

A class that supports reading of data from a matrix-like storage format, such as a file or a database, in a column-wise manner.

Slots

`nrow` An `integer` representing the number of rows in the matrix-like storage.

`ncol` An `integer` representing the number of columns in the matrix-like storage.

`reader` A `function` that takes a set of column indices as input and returns a `matrix` containing the requested columns from the storage.

Compare-methods *Comparison Operations*

Description

Methods for comparing neuroimaging objects. All volume comparisons return `LogicalNeuroVol` objects that preserve spatial metadata.

Usage

```
## S4 method for signature 'DenseNeuroVol,DenseNeuroVol'
Compare(e1, e2)

## S4 method for signature 'DenseNeuroVol,numeric'
Compare(e1, e2)

## S4 method for signature 'numeric,DenseNeuroVol'
Compare(e1, e2)

## S4 method for signature 'SparseNeuroVol,numeric'
Compare(e1, e2)

## S4 method for signature 'numeric,SparseNeuroVol'
Compare(e1, e2)

## S4 method for signature 'NeuroVec,NeuroVec'
Compare(e1, e2)
```

Arguments

e1, e2	Neuroimaging objects or numeric values.

Value

A LogicalNeuroVol for volume comparisons.

---

concat *Concatenate two objects in the time dimension*

Description

Concatenate two objects in the time dimension

Usage

```
concat(x, y, ...)

## S4 method for signature 'NeuroVec,NeuroVol'
concat(x, y, ...)

## S4 method for signature 'NeuroVol,NeuroVec'
concat(x, y, ...)

## S4 method for signature 'NeuroVec,NeuroVec'
concat(x, y, ...)
```

```
## S4 method for signature 'ROIVec,ROIVec'
concat(x, y, ...)

## S4 method for signature 'DenseNeuroVol,missing'
concat(x, y, ...)

## S4 method for signature 'DenseNeuroVol,DenseNeuroVol'
concat(x, y, ...)

## S4 method for signature 'AbstractSparseNeuroVec,missing'
concat(x, y, ...)

## S4 method for signature 'SparseNeuroVec,SparseNeuroVec'
concat(x, y, ...)
```

Arguments

x	the first object, typically NeuroVol or NeuroVec
y	the second object, typically NeuroVol or NeuroVec
...	additional objects

Details

The x and y images must have compatible dimensions. A NeuroVol can be concatenated to NeuroVec, and vice versa. See examples.

Value

A temporally concatenated object.

Note

dimensions of x and y must be equal

Examples

```
bv1 <- NeuroVol(rep(1,1000), NeuroSpace(c(10,10,10), c(1,1,1)))
bv2 <- NeuroVol(rep(2,1000), NeuroSpace(c(10,10,10), c(1,1,1)))
bv3 <- concat(bv1,bv2)
inherits(bv3, "NeuroVec")

bv4 <- concat(bv3, bv1)
dim(bv4)[4] == 3
bv5 <- concat(bv1, bv3)
dim(bv4)[4] == 3

bv6 <- concat(bv4,bv5)
dim(bv6)[4] == 6
```

conn_comp *Connected components*

Description

Find connected components in an image. This function identifies and labels spatially connected regions in neuroimaging data, supporting both binary masks and thresholded volumes.

Usage

```
conn_comp(x, ...)

## S4 method for signature 'NeuroVol'
conn_comp(
  x,
  threshold = 0,
  cluster_table = TRUE,
  local_maxima = TRUE,
  local_maxima_dist = 15,
  ...
)
```

Arguments

x	the image object
...	additional arguments including: • threshold - numeric value defining lower intensity bound for image mask • cluster_table - logical indicating whether to return cluster statistics • local_maxima - logical indicating whether to compute local maxima • local_maxima_dist - minimum distance between local maxima • connect - connectivity pattern ("26-connect", "18-connect", or "6-connect")
threshold	threshold defining lower intensity bound for image mask
cluster_table	return cluster_table
local_maxima	return table of local maxima
local_maxima_dist	Minimum distance, in the units of spacing(x), between reported local maxima. A voxel is reported when no other voxel of its component within this distance has a larger value, so the maxima of a component are at least local_maxima_dist apart. Default 15.

Value

A list containing:

- index - A ClusteredNeuroVol object with cluster labels

- size - A NeuroVol object with cluster sizes
- voxels - A list of cluster voxel coordinates
- cluster_table - (optional) Data frame with cluster statistics
- local_maxima - (optional) Matrix of local maxima coordinates

An object representing the connected components of x.

Examples

```
# Create a simple 3D volume with two distinct regions
space <- NeuroSpace(c(10,10,10), c(1,1,1))
vol_data <- array(0, c(10,10,10))

# Create first cluster in corner (2x2x2)
vol_data[1:2, 1:2, 1:2] <- 1

# Create second cluster in opposite corner (2x2x2)
vol_data[8:9, 8:9, 8:9] <- 1

# Create NeuroVol object
vol <- NeuroVol(vol_data, space)

# Find connected components with default 26-connectivity
# Returns components above threshold 0
comps <- conn_comp(vol, threshold=0)

# Access results
max(comps$index) == 2  # Should have 2 clusters
all(comps$size >= 0)    # All clusters should have >= 0

# Get cluster statistics
comps <- conn_comp(vol, threshold=0, cluster_table=TRUE)
# cluster_table contains: index, x, y, z, N (size), Area, value

# Find local maxima within clusters
comps <- conn_comp(vol, threshold=0, local_maxima=TRUE,
                   local_maxima_dist=2)
# local_maxima contains: index, x, y, z, value
```

---

conn_comp_3D *Extract Connected Components from a 3D Binary Mask*

Description

Identifies and labels connected components in a 3D binary mask using a two-pass algorithm. The function supports different connectivity constraints and returns both component indices and their sizes.

Usage

```
conn_comp_3D(mask, connect = c("26-connect", "18-connect", "6-connect"))
```

Arguments

mask	A 3D logical array representing the binary mask
connect	A character string specifying the connectivity constraint. One of "26-connect" (default), "18-connect", or "6-connect"

Details

The function implements an efficient two-pass connected component labeling algorithm:

- First pass: Assigns provisional labels and builds an equivalence table using a union-find data structure for label resolution
- Second pass: Resolves label conflicts and assigns final component labels

The connectivity options determine which voxels are considered adjacent:

- 6-connect: Only face-adjacent voxels (±1 step along each axis)
- 18-connect: Face and edge-adjacent voxels
- 26-connect: Face, edge, and vertex-adjacent voxels (all neighbors in a 3x3x3 cube)

Time complexity is O(n) where n is the number of voxels in the mask, with additional O(k) space for the union-find data structure where k is the number of provisional labels.

Value

A list with the following components:

index	A 3D array of integers. Each non-zero value represents the cluster index of the connected component for that voxel. Zero values indicate background.
size	A 3D array of integers. Each non-zero value represents the size (number of voxels) of the connected component that the voxel belongs to. Zero values indicate background.

References

Rosenfeld, A., & Pfaltz, J. L. (1966). Sequential operations in digital picture processing. Journal of the ACM, 13(4), 471-494.

See Also

array for creating 3D arrays, ClusteredNeuroVol for working with clustered neuroimaging data

Examples

```
# Create a simple 3D binary mask with two disconnected components
mask <- array(FALSE, c(4, 4, 4))
mask[1:2, 1:2, 1:2] <- TRUE  # First component
mask[3:4, 3:4, 3:4] <- TRUE  # Second component

# Extract components using different connectivity patterns
comps <- conn_comp_3D(mask, connect = "6-connect")

# Number of components
max_comps <- max(comps$index)
cat("Found", max_comps, "components\n")

# Size of each component
unique_sizes <- unique(comps$size[comps$size > 0])
cat("Component sizes:", paste(unique_sizes, collapse=", "), "\n")

# Try with different connectivity
comps_26 <- conn_comp_3D(mask, connect = "26-connect")
cat("Number of components with 26-connectivity:", max(comps_26$index), "\n")
```

---

coord_to_grid *convert n-dimensional real world coordinates to grid coordinates*

Description

convert n-dimensional real world coordinates to grid coordinates

Usage

```
coord_to_grid(x, coords)

## S4 method for signature 'NeuroSpace,matrix'
coord_to_grid(x, coords)

## S4 method for signature 'NeuroSpace,numeric'
coord_to_grid(x, coords)

## S4 method for signature 'NeuroVol,matrix'
coord_to_grid(x, coords)

## S4 method for signature 'NeuroVol,numeric'
coord_to_grid(x, coords)
```

Arguments

x	the object
coords	a matrix of real world coordinates

Value

A numeric matrix of grid coordinates.

Examples

```
# Create a simple 3D volume
bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))
coords <- matrix(c(.5,.5,.5, 1.5,1.5,1.5), ncol=3, byrow=TRUE)
grid <- coord_to_grid(bvol, coords)
world <- grid_to_coord(bvol, grid)
all.equal(coords, world)
```

---

coord_to_index *convert n-dimensional real world coordinates to 1D indices*

Description

convert n-dimensional real world coordinates to 1D indices

Usage

```
coord_to_index(x, coords)

## S4 method for signature 'NeuroSpace,matrix'
coord_to_index(x, coords)

## S4 method for signature 'NeuroSpace,numeric'
coord_to_index(x, coords)

## S4 method for signature 'NeuroVol,matrix'
coord_to_index(x, coords)
```

Arguments

x	the object
coords	a matrix of real world coordinates

Value

An integer vector of 1D indices corresponding to coords.

Examples

```
bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))
coords <- matrix(c(.5,.5,.5, 1.5,1.5,1.5), ncol=3, byrow=TRUE)
idx <- coord_to_index(bvol, coords)
coords2 <- index_to_coord(bvol, idx)
all.equal(coords, coords2)
```

coords *Extract coordinates from an object*

Description

This function extracts the coordinates from an input object.

Usage

```
coords(x, ...)
```

Arguments

x	The object to extract coordinates from.
...	Additional arguments (not used in the generic function).

Value

A numeric matrix or vector containing the coordinates of x.

Examples

```
# Create a NeuroSpace object with 3mm voxels
space <- NeuroSpace(c(10,10,10), spacing=c(3,3,3))

# Create ROI coordinates in voxel space
coords <- matrix(c(1,1,1, 2,2,2), ncol=3, byrow=TRUE)
roi_coords <- ROICoords(coords)

# Get coordinates in voxel space
vox_coords <- coords(roi_coords)
# First coordinate is (1,1,1)

# Get coordinates
cds <- coords(roi_coords)
nrow(cds) == 2
```

coords,IndexLookupVol-method
Extract Coordinates from an IndexLookupVol Object

Description

Extracts the coordinates from an IndexLookupVol object based on a given index.

Usage

```
## S4 method for signature 'IndexLookupVol'
coords(x, i)

## S4 method for signature 'ROIVol'
coords(x, real = FALSE)

## S4 method for signature 'ROICoords'
coords(x, real = FALSE)

## S4 method for signature 'AbstractSparseNeuroVec'
coords(x, i)
```

Arguments

x	An IndexLookupVol object to extract coordinates from
i	The index into the lookup volume
real	if TRUE, return coordinates in real world units

Value

A matrix of coordinates

Examples

```
space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))
ilv <- IndexLookupVol(space, c(1:100))
coords(ilv, 1)  # Extract coordinates for index 1
```

---

createNIfTIHeader *Create an Empty NIfTI-1 Header List*

Description

Initializes a list of fields following the NIfTI-1 specification with default or placeholder values. Users typically call this internally via as_nifti_header rather than using directly.

Usage

```
createNIfTIHeader(oneFile = TRUE, file_name = NULL)
```

Arguments

oneFile	Logical; if TRUE, magic is set to "n+1" indicating a single-file (.nii) approach. Otherwise set to "ni1".
file_name	Optional character string to store in the header, usually referencing the intended output file name.

Details

This function sets up the skeleton of a NIfTI-1 header, including fields for `diminfo`, `pixdim`, `qform_code`, `magic`, etc. Most fields are initialized to zero, empty characters, or standard placeholders. The `oneFile` argument controls whether `"n+1"` or `"ni1"` is used for the `magic` field.

Value

A named `list` containing approximately 30 fields that comprise the NIfTI-1 header structure. Many of these are placeholders until filled by downstream usage.

See Also

`as_nifti_header` for populating the returned header with actual data from a `NeuroVol`.

`cuboid_roi` *Create A Cuboid Region of Interest*

Description

Create A Cuboid Region of Interest

Usage

```
cuboid_roi(bvol, centroid, surround, fill = NULL, nonzero = FALSE)
```

Arguments

`bvol`	an `NeuroVol` or `NeuroSpace` instance
`centroid`	the center of the cube in *voxel* coordinates
`surround`	the number of voxels on either side of the central voxel. A `vector` of length 3.
`fill`	optional value(s) to assign to data slot.
`nonzero`	keep only nonzero elements from `bvol`. If `bvol` is A `NeuroSpace` then this argument is ignored.

Value

An instance of class `ROIVol` representing the cuboid region of interest, containing the coordinates and values of voxels within the specified region.

Examples

```
sp1 <- NeuroSpace(c(10,10,10), c(1,1,1))
cube <- cuboid_roi(sp1, c(5,5,5), 3)
vox <- coords(cube)
cube2 <- cuboid_roi(sp1, c(5,5,5), 3, fill=5)
```

`data_file` *Generic function to get the name of the data file, given a file name and a* `FileFormat` *instance.*

Description

Derives the data file name from a given file name based on the FileFormat specifications.

Usage

```
data_file(x, file_name)

## S4 method for signature 'FileFormat,character'
data_file(x, file_name)
```

Arguments

`x`	A FileFormat object specifying the format requirements
`file_name`	A character string specifying the file name to derive the data file name from

Details

The function performs the following steps:

1. If the input file_name already matches the data file format, it returns the file_name as is.
2. If the file_name matches the header file format, it constructs and returns the corresponding data file name.
3. If the file_name doesn't match either format, it throws an error.

Value

The correct data file name as a `character` string.

A character string representing the data file name

See Also

`header_file`, `strip_extension` for related file name manipulation

Examples

```
fmt <- new("FileFormat", header_extension = "hdr", data_extension = "img")
data_file(fmt, "brain_scan.img")  # Returns "brain_scan.img"
data_file(fmt, "brain_scan.hdr")  # Also Returns "brain_scan.img"
```

data_file_matches *Generic function to test whether a file name conforms to the given a* FileFormat *instance. Will test for match to data file only*

Description

Validates whether a file name conforms to the data file format specification.

Usage

```
data_file_matches(x, file_name)

## S4 method for signature 'FileFormat,character'
data_file_matches(x, file_name)
```

Arguments

x	A FileFormat object specifying the format requirements
file_name	A character string specifying the file name to validate

Details

The function performs case-sensitive pattern matching to verify that the file name ends with the specified data extension. The match is performed using a regular expression that ensures the extension appears at the end of the file name.

Value

TRUE for match, FALSE otherwise.

See Also

file_matches, header_file_matches for related file format validation

Examples

```
fmt <- new("FileFormat", header_extension = "hdr", data_extension = "img")
data_file_matches(fmt, "brain_scan.img")  # TRUE
data_file_matches(fmt, "brain_scan.hdr")  # FALSE
data_file_matches(fmt, "brain.img.gz")    # FALSE
```

data_reader *Create a Data Reader*

Description

Creates a data reader for accessing neuroimaging data from various file formats. The reader provides a unified interface for reading data regardless of the underlying format.

Usage

```
data_reader(x, offset)
```

Arguments

x	An object containing metadata required to create the reader (e.g., file path, format info)
offset	Numeric. Byte offset where data reading should begin. Default is 0.

Details

Create a Data Reader for Neuroimaging Data

The data_reader function is a generic that creates appropriate readers for different neuroimaging formats. It handles:

- File format detection and validation
- Endianness configuration
- Data type conversion
- Compression handling (e.g., gzip)
- Proper byte alignment

Value

A BinaryReader object configured for the specific data format

See Also

read_header for reading headers, BinaryReader for reading binary data

Examples

```
# Create reader for NIFTI file
meta <- read_header(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))
reader <- data_reader(meta, offset = 0)

# Read first 100 voxels
data <- read_elements(reader, 100)
close(reader)
```

data_reader,NIFTIMetaInfo-method *Create Data Reader for AFNI Format*

Description

Create Data Reader for AFNI Format

Usage

```
## S4 method for signature 'NIFTIMetaInfo'
data_reader(x, offset = 0)

## S4 method for signature 'AFNIMetaInfo'
data_reader(x, offset = 0)
```

Arguments

x	AFNIMetaInfo object
offset	Numeric byte offset

Value

BinaryReader object

DenseNeuroVec-class *DenseNeuroVec Class*

Description

A class representing a four-dimensional brain image, backed by a dense array. This class is designed for neuroimaging data where most voxels contain non-zero values.

This function constructs a DenseNeuroVec object, which represents a dense four-dimensional brain image. It handles various input data formats and ensures proper dimensionality.

Usage

```
DenseNeuroVec(data, space, label = "none", volume_labels = character())
```

Arguments

`data`	The image data. This can be: • A 4-dimensional array • A 2-dimensional matrix (either nvoxels x ntime-points or ntime-points x nvoxels) • A vector (which will be reshaped to match the space dimensions)
`space`	A `NeuroSpace` object defining the spatial properties of the image.
`label`	A character string providing a label for the DenseNeuroVec object. Default is an empty string.
`volume_labels`	Optional character vector of length `dim(space)[4]` giving per-volume labels.

Details

DenseNeuroVec objects store their data in a dense array format, which is efficient for operations that require frequent access to all voxels. This class inherits from both `NeuroVec` and `array` classes, combining spatial information with array-based storage.

The function performs several operations based on the input data type:

- For matrix input: It determines the correct orientation (voxels x time or time x voxels) and reshapes accordingly. If necessary, it adds a 4th dimension to the space object.
- For vector input: It reshapes the data to match the dimensions specified in the space object.
- For array input: It ensures the dimensions match those specified in the space object.

Note that the label parameter is currently not used in the object creation, but is included for potential future use or consistency with other constructors.

Value

A concrete instance of the `DenseNeuroVec` class.

Validity

A DenseNeuroVec object is considered valid if:

- The underlying data is a four-dimensional array.

See Also

`NeuroVec-class` for the parent class. `SparseNeuroVec-class` for a sparse representation alternative.

`NeuroVec-class` for the parent class. `SparseNeuroVec-class` for the sparse version of 4D brain images. `NeuroSpace-class` for details on spatial properties.

Examples

```
# Create a simple 4D brain image
data <- array(rnorm(64*64*32*10), dim = c(64, 64, 32, 10))
space <- NeuroSpace(dim = c(64, 64, 32,10), origin = c(0, 0, 0), spacing = c(3, 3, 4))
dense_vec <- new("DenseNeuroVec", .Data = data, space = space)

# Access dimensions
dim(dense_vec)

# Extract a single 3D volume
first_volume <- dense_vec[[1]]


# Create a simple 4D brain image
dim <- c(64, 64, 32, 10)  # 64x64x32 volume with 10 time points
data <- array(rnorm(prod(dim)), dim)
space <- NeuroSpace(dim, spacing = c(3, 3, 4))

# Create a DenseNeuroVec object
dense_vec <- DenseNeuroVec(data = data, space = space, label = "Example")
print(dense_vec)

# Create from a matrix (voxels x time)
mat_data <- matrix(rnorm(prod(dim)), nrow = prod(dim[1:3]), ncol = dim[4])
dense_vec_mat <- DenseNeuroVec(data = mat_data, space = space)
print(dense_vec_mat)
```

DenseNeuroVol-class *DenseNeuroVol Class*

Description

Represents a three-dimensional brain image backed by a dense array. This class combines the spatial properties of `NeuroVol` with the data storage capabilities of an array.

Construct a `DenseNeuroVol` instance

Usage

```
DenseNeuroVol(data, space, label = "", indices = NULL)
```

Arguments

`data`	a three-dimensional `array`
`space`	an instance of class `NeuroSpace`
`label`	a `character` string
`indices`	an optional 1-d index vector

Details

DenseNeuroVol objects are used for 3D brain images where most or all voxels contain meaningful data. They provide efficient access to individual voxel values and are suitable for operations that require frequent random access to voxel data.

Value

DenseNeuroVol instance

See Also

NeuroVol-class, SparseNeuroVol-class

Examples

```
# Create a simple 3D brain volume
vol_data <- array(rnorm(64*64*64), c(64, 64, 64))
vol_space <- NeuroSpace(dim=c(64L, 64L, 64L), origin=c(0, 0, 0), spacing=c(1, 1, 1))
brain_vol <- new("DenseNeuroVol", .Data=vol_data, space=vol_space)
```

---

deoblique *Deoblique a Neuroimaging Space or Volume*

Description

AFNI-like helper that mirrors the core behavior of `3dWarp -deoblique`:

- If `gridset` is supplied, use that as the output grid.
- Otherwise, build an axis-aligned output grid that encloses the input field-of-view.
- If `newgrid` is not supplied, use the minimum input voxel size isotropically (AFNI-style default for deobliquing).

Usage

```
deoblique(
  x,
  gridset = NULL,
  newgrid = NULL,
  method = c("linear", "nearest", "cubic"),
  engine = c("internal")
)
```

Arguments

x	A NeuroSpace or NeuroVol.
gridset	Optional output grid (a NeuroSpace or NeuroVol), analogous to AFNI's -gridset. Mutually exclusive with newgrid.
newgrid	Optional scalar output voxel size (mm), analogous to AFNI's -newgrid. If omitted and gridset is NULL, the minimum input voxel size is used isotropically.
method	Interpolation method used when x is a NeuroVol: one of "nearest", "linear", or "cubic".
engine	Resampling engine passed to resample_to.

Details

For NeuroSpace, this returns the target deobliqued space. For NeuroVol, it also resamples image data into that space.

Value

If x is a NeuroSpace, returns a deobliqued NeuroSpace. If x is a NeuroVol, returns a resampled NeuroVol in deobliqued space.

See Also

output_aligned_space, resample_to

Examples

```
sp <- NeuroSpace(c(32, 32, 20), spacing = c(2, 2, 3))
tx <- trans(sp)
tx[1, 2] <- 0.15
sp_obl <- NeuroSpace(dim(sp), spacing = spacing(sp), trans = tx)

# Build deobliqued target space (minimum spacing default)
sp_deob <- deoblique(sp_obl)

# Resample a volume to deobliqued space
vol <- NeuroVol(array(rnorm(prod(dim(sp_obl))), dim(sp_obl)), sp_obl)

vol_deob <- deoblique(vol, method = "linear")
```

dim,ClusteredNeuroVec-method
Get Dimensions of FileMetaInfo Object

Description

Get Dimensions of FileMetaInfo Object

dim of `NeuroObj` object

Usage

```
## S4 method for signature 'ClusteredNeuroVec'
dim(x)

## S4 method for signature 'FileMetaInfo'
dim(x)

## S4 method for signature 'NeuroObj'
dim(x)

## S4 method for signature 'NeuroHyperVec'
dim(x)

## S4 method for signature 'NeuroSpace'
dim(x)

## S4 method for signature 'ROIVol'
dim(x)

## S4 method for signature 'ROICoords'
dim(x)
```

Arguments

`x`	the object

Value

A numeric vector of length 2 containing the dimensions of the ROICoords object.

dim_of *Get the length of a given dimension of an object*

Description

This function returns the length of a given axis (dimension) of an object. The axis can be specified using its position or name.

Usage

```
dim_of(x, axis)

## S4 method for signature 'NeuroSpace,NamedAxis'
dim_of(x, axis)
```

Arguments

x	The NeuroSpace object
axis	The NamedAxis to query

Value

An integer representing the length of the specified `axis` of `x`.

Examples

```
x <- NeuroSpace(c(10,10,10), spacing=c(1,1,1))
stopifnot(dim_of(x, x@axes@i) == 10)
```

downsample *Downsample an Image*

Description

This function downsamples a neuroimaging object, reducing its spatial resolution while preserving the temporal dimension.

Usage

```
downsample(x, ...)

## S4 method for signature 'DenseNeuroVec'
downsample(x, spacing = NULL, factor = NULL, outdim = NULL, method = "box")

## S4 method for signature 'SparseNeuroVec'
downsample(x, spacing = NULL, factor = NULL, outdim = NULL, method = "box")
```

```
## S4 method for signature 'NeuroVec'
downsample(x, spacing = NULL, factor = NULL, outdim = NULL, method = "box")

## S4 method for signature 'DenseNeuroVol'
downsample(x, spacing = NULL, factor = NULL, outdim = NULL, method = "box")

## S4 method for signature 'NeuroVol'
downsample(x, spacing = NULL, factor = NULL, outdim = NULL, method = "box")
```

Arguments

x	A DenseNeuroVol object to downsample
...	Additional arguments passed to specific downsample methods.
spacing	Target voxel spacing (numeric vector of length 3)
factor	Downsampling factor (single value or vector of length 3, between 0 and 1)
outdim	Target output dimensions (numeric vector of length 3)
method	Downsampling method (currently only "box" for box averaging)

Value

An object of the same class as x, downsampled according to the specified parameters.

Examples

```
# Create a sample 4D image
data <- array(rnorm(64*64*32*10), dim = c(64, 64, 32, 10))
space <- NeuroSpace(dim = c(64, 64, 32, 10),
                    origin = c(0, 0, 0),
                    spacing = c(2, 2, 2))
nvec <- DenseNeuroVec(data, space)

# Downsample by factor
nvec_down1 <- downsample(nvec, factor = 0.5)

# Downsample to target spacing
nvec_down2 <- downsample(nvec, spacing = c(4, 4, 4))

# Downsample to target dimensions
nvec_down3 <- downsample(nvec, outdim = c(32, 32, 16))

# Create a sample 3D volume
data <- array(rnorm(64*64*32), dim = c(64, 64, 32))
space <- NeuroSpace(dim = c(64, 64, 32),
                    origin = c(0, 0, 0),
                    spacing = c(2, 2, 2))
vol <- DenseNeuroVol(data, space)

# Downsample by factor
vol_down1 <- downsample(vol, factor = 0.5)
```

```
# Downsample to target spacing
vol_down2 <- downsample(vol, spacing = c(4, 4, 4))

# Downsample to target dimensions
vol_down3 <- downsample(vol, outdim = c(32, 32, 16))
```

`drop` *Generic Drop Method*

Description

Provides a mechanism to remove dimensions or elements from an object.

Usage

```
drop(x)
```

Arguments

`x`	An object.

Value

An object of the same class as `x` with reduced dimensions or elements.

`drop,NeuroVec-method` *Drop a dimension*

Description

Drop a dimension

Usage

```
## S4 method for signature 'NeuroVec'
drop(x)
```

Arguments

`x`	the object to drop a dimension from

Value

An object of the same class as x with reduced dimensions or elements.

drop_dim *Drop a Dimension from an Object*

Description

This function removes a specified dimension from a given object, such as a matrix or an array.

Usage

```
drop_dim(x, dimnum)

## S4 method for signature 'AxisSet2D,numeric'
drop_dim(x, dimnum)

## S4 method for signature 'AxisSet2D,missing'
drop_dim(x, dimnum)

## S4 method for signature 'AxisSet3D,numeric'
drop_dim(x, dimnum)

## S4 method for signature 'AxisSet3D,missing'
drop_dim(x, dimnum)

## S4 method for signature 'NeuroSpace,numeric'
drop_dim(x, dimnum)

## S4 method for signature 'NeuroSpace,missing'
drop_dim(x)
```

Arguments

x	An AxisSet3D object
dimnum	Numeric index of dimension to drop (optional)

Value

An object of the same class as x with the specified dimension removed.

Examples

```
# Create a NeuroSpace object with dimensions (10, 10, 10)
x <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))

# Drop the first dimension
x1 <- drop_dim(x, 1)

# Check the new dimensions
ndim(x1) == 2
```

```
dim(x1)[1] == 10
```

---

ecode_name *Get Extension Code Name*

Description

Returns the name associated with a NIfTI extension code.

Usage

```
ecode_name(ecode)
```

Arguments

ecode	Integer extension code.

Value

Character string with the extension name, or "unknown" if not found.

Examples

```
ecode_name(4L)   # Returns "AFNI"
ecode_name(6L)   # Returns "comment"
ecode_name(999L) # Returns "unknown"
```

---

embed_kernel *Generic function to position kernel in a position in image space*

Description

Generic function to position kernel in a position in image space

Usage

```
embed_kernel(x, sp, center_voxel, ...)

## S4 method for signature 'Kernel,NeuroSpace,numeric'
embed_kernel(x, sp, center_voxel, weight = 1)
```

Arguments

x	the kernel object
sp	the space to embed the kernel
center_voxel	the voxel marking the center of the kernel in the embedded space
...	extra args
weight	multiply kernel weights by this value

Value

An object representing the embedded kernel in the specified space.

Examples

```
# Create a 3D Gaussian kernel with dimensions 3x3x3 and voxel size 1x1x1
kern <- Kernel(kerndim = c(3,3,3), vdim = c(1,1,1), FUN = dnorm, sd = 1)

# Create a NeuroSpace object to embed the kernel in
space <- NeuroSpace(c(10,10,10), c(1,1,1))

# Embed the kernel at the center of the space (position 5,5,5)
embedded_kern <- embed_kernel(kern, space, c(5,5,5))

# The result is a SparseNeuroVol with kernel weights centered at (5,5,5)
# We can also scale the kernel weights by using the weight parameter
embedded_kern_scaled <- embed_kernel(kern, space, c(5,5,5), weight = 2)

# The scaled kernel has weights twice as large as the original
max(values(embedded_kern_scaled)) == 2 * max(values(embedded_kern))
```

---

enhance_stat_map *Enhance an unsmoothed statistical map for visualization*

Description

Removes isolated speckles from a noisy ("salt-and-pepper") statistical map so it renders cleanly as an overlay, *without* the peak-depressing and cluster-smearing that a plain Gaussian blur causes. This is a display-oriented preprocessor: it is not intended to produce maps for statistical inference (it deliberately sharpens for visual punch and does not preserve the null distribution).

Usage

```
enhance_stat_map(
  vol,
  mask,
  despike = TRUE,
  despike_k = 3.5,
```

```
  despike_window = 1L,
  method = c("guided", "bilateral", "gaussian"),
  radius = 2,
  epsilon = NULL,
  spatial_sigma = 2,
  intensity_sigma = 1,
  detail_gain = 1.5,
  verbose = FALSE
)
```

Arguments

vol	A NeuroVol statistical map to enhance.
mask	An optional NeuroVol / LogicalNeuroVol restricting the region processed. If omitted, all non-zero, finite voxels of vol are used.
despike	Logical; run the selective median despike stage (default TRUE).
despike_k	Robust-deviation threshold for flagging impulses. Lower is more aggressive (default 3.5).
despike_window	Integer half-width of the despike neighbourhood (default 1L => 3x3x3).
method	Edge-preserving base filter: one of "guided" (default), "bilateral", or "gaussian".
radius	Integer box radius for the base filter and signal-weight estimation (default 2).
epsilon	Guided-filter regularisation. If NULL (default) it is set to the estimated noise variance. Only used when method = "guided".
spatial_sigma	Spatial Gaussian SD for method = "bilateral" or "gaussian" (default 2).
intensity_sigma	Intensity Gaussian SD for method = "bilateral" (default 1).
detail_gain	Strength of the signal-gated unsharp stage. 0 gives a pure denoise; 1 restores original detail in signal regions; values > 1 sharpen for display (default 1.5). Set to 0 to disable.
verbose	Logical; report the number of despiked voxels and the noise estimate (default FALSE).

Details

The enhancement runs in three stages, each reusing the package's existing filtering primitives:

1. **Selective despike.** Isolated impulsive voxels (flagged by a robust deviation from their local mean) are replaced by the median of their in-mask, non-impulse neighbours. All other voxels keep their exact value, so true clusters are preserved.
2. **Edge-preserving base smooth.** An edge-preserving filter ("guided" by default; see guided_filter / bilateral_filter / gaussian_blur) removes residual low-amplitude grain. With the guided filter, in-cluster voxels (local variance $\gg$ noise variance) are returned at essentially full amplitude, so peaks are not depressed.
3. **Signal-gated unsharp.** Local contrast is boosted by detail_gain, weighted per-voxel by a guided-style signal weight $w = \mathrm{var}/(\mathrm{var} + \sigma^2_{noise})$. Because $w \to 0$ in flat/noisy regions, the despeckled background stays smooth while real clusters gain crisp, punchy edges.

The noise scale σ_{noise} is estimated robustly (MAD of the high-frequency residual within the mask) and is used both for the default guided `epsilon` and for the signal weight, so the method adapts to the scale of the input map (e.g. a z-map versus a raw beta map).

Value

A `NeuroVol` with the enhanced map (zero outside the mask).

See Also

`guided_filter`, `bilateral_filter`, `gaussian_blur`, `plot_overlay`, `plot_ortho`

Examples

```
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
# A noisy synthetic stat map on the mask grid
set.seed(1)
noisy <- mask * 0
idx <- which(mask > 0)
vals <- rnorm(length(idx))
vals[sample(length(idx), length(idx) %/% 20)] <- 8  # salt-and-pepper spikes
noisy[idx] <- vals
stat <- NeuroVol(noisy, space(mask))

clean <- enhance_stat_map(stat, mask)
```

---

extension *Get Extension by Code*

Description

Retrieve extensions with a specific extension code from a list.

Usage

```
extension(x, ecode)

## S4 method for signature 'NiftiExtensionList,numeric'
extension(x, ecode)
```

Arguments

x	A `NiftiExtensionList-class` object.
ecode	Integer extension code to filter by.

Value

A `NiftiExtensionList-class` containing only extensions with the specified code.

extensions *Get Extensions from an Object*

Description

Generic function to retrieve NIfTI extensions from various object types.

Usage

```
extensions(x, ...)
```

Arguments

x	An object potentially containing extensions.
...	Additional arguments (currently unused).

Value

A NiftiExtensionList-class object, or NULL if no extensions.

extractor3d *Array-like access for 3-dimensional data structures*

Description

This generic function provides array-like access for 3-dimensional data structures. It allows for flexible indexing and subsetting of 3D arrays or array-like objects.

Usage

```
## S4 method for signature 'ArrayLike3D,numeric,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ArrayLike3D,matrix,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ArrayLike3D,missing,missing,ANY'
x[i, j, k, ..., drop = TRUE]

## S4 method for signature 'ArrayLike3D,missing,numeric,ANY'
x[i, j, k, ..., drop = TRUE]
```

Arguments

x	The 3-dimensional object to be accessed.
i	First index or dimension.
j	Second index or dimension.
k	Third index or dimension.
...	Additional arguments passed to methods.
drop	Logical. If TRUE, the result is coerced to the lowest possible dimension.

Value

A subset of the input object, with dimensions depending on the indexing and the ‘drop‘ parameter.

---

extractor4d *Array-like access for 4-dimensional data structures*

Description

This generic function provides array-like access for 4-dimensional data structures. It allows for flexible indexing and subsetting of 4D arrays or array-like objects.

Provides array-like access to ClusteredNeuroVec objects, supporting extraction patterns like x[,,,t] to get 3D volumes at specific time points.

Usage

```
## S4 method for signature 'ArrayLike4D,matrix,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ArrayLike4D,numeric,numeric,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ArrayLike4D,numeric,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ArrayLike4D,integer,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ArrayLike4D,missing,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ArrayLike4D,missing,numeric,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ClusteredNeuroVec,missing,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]
```

```
## S4 method for signature 'ClusteredNeuroVec,missing,missing,ANY'
x[i, j, k, m, ..., drop = TRUE]

## S4 method for signature 'ClusteredNeuroVec,numeric,numeric,ANY'
x[i, j, k, m, ..., drop = TRUE]
```

Arguments

x	The 4-dimensional object to be accessed.
i	First index or dimension.
j	Second index or dimension.
k	Third index or dimension.
m	Fourth index or dimension.
...	Additional arguments passed to methods.
drop	Logical. If TRUE, the result is coerced to the lowest possible dimension.

Value

A subset of the input object, with dimensions depending on the indexing and the ‘drop‘ parameter.

---

file_matches *Generic function to test whether a file name conforms to the given* FileFormat *instance. Will test for match to either header file or data file*

Description

Validates whether a file name conforms to the specified FileFormat and verifies the existence of both header and data files.

Usage

```
file_matches(x, file_name)

## S4 method for signature 'FileFormat,character'
file_matches(x, file_name)
```

Arguments

x	A FileFormat object specifying the format requirements
file_name	A character string specifying the file name to validate

Details

The function performs the following validation steps:

1. Checks if the file name matches either the header or data format
2. Verifies the existence of the corresponding paired file
3. Returns FALSE if either check fails

File names are validated using case-sensitive extension matching.

Value

TRUE for match, FALSE otherwise.

A logical value: TRUE if the file matches the format and both header and data files exist, FALSE otherwise

See Also

header_file_matches, data_file_matches for individual file type checking

Examples

```
# Create a FileFormat for NIFTI format

fmt <- new("FileFormat",
  file_format = "NIFTI",
  header_encoding = "raw",
  header_extension = "nii",
  data_encoding = "raw",
  data_extension = "nii")

# Create temporary file
tmp <- tempfile("brainscan", fileext = ".nii")
file.create(tmp)

# Check if files exist and match format
file_matches(fmt, tmp)

# Clean up
unlink(tmp)
```

FileBackedNeuroVec *Create a File-Backed Neuroimaging Vector*

Description

Constructs a FileBackedNeuroVec instance, which represents a file-backed neuroimaging vector object. This constructor provides memory-efficient access to large neuroimaging datasets by keeping the data on disk until needed.

Usage

```
FileBackedNeuroVec(file_name, label = basename(file_name))
```

Arguments

file_name	A character string specifying the path to the neuroimaging file. Supported formats include NIFTI (.nii) and ANALYZE (.hdr/.img).
label	Optional character string providing a label for the vector

Details

Create a FileBackedNeuroVec Object

The function performs the following operations:

- Reads the header information from the specified file
- Validates the dimensionality (must be 4D data)
- Creates a NeuroSpace object with appropriate metadata
- Initializes the file-backed vector with minimal memory footprint

Value

A new instance of class FileBackedNeuroVec.

See Also

NeuroSpace for spatial metadata management, read_header for header information extraction, sub_vector for data access methods

Examples

```
# Create a file-backed vector from a NIFTI file
fbvec <- FileBackedNeuroVec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Access specific volumes without loading entire dataset
first_vol <- sub_vector(fbvec, 1)
```

FileBackedNeuroVec-class
FileBackedNeuroVec Class

Description

A class representing a four-dimensional brain image that uses on-demand loading through memory-mapped file access. This approach enables efficient handling of large-scale brain imaging data by loading only the required portions of the data into memory when needed.

The `FileBackedNeuroVec` class represents a memory-efficient vector of neuroimaging data that is stored on disk rather than in memory. This is particularly useful for large datasets where memory constraints are a concern.

Details

FileBackedNeuroVec objects provide a memory-efficient solution for working with large 4D neuroimaging datasets. By utilizing memory-mapped file access, this class allows users to work with datasets that exceed available RAM, only loading the necessary data segments into memory as they are accessed.

Slots

`meta` An instance of class `FileMetaInfo` containing file metadata such as file path, format, and other associated information.

Inheritance

`FileBackedNeuroVec` inherits from:

- `NeuroVec`: Base class for 4D brain images
- `ArrayLike4D`: Interface for 4D array-like operations

Memory Management

Data is read from disk on-demand, reducing memory usage compared to in-memory storage. The trade-off is slightly slower access times due to disk I/O operations.

See Also

`NeuroVec-class` for the base 4D brain image class. `FileMetaInfo-class` for details on file metadata representation.

`FileBackedNeuroVec` for creating instances of this class

Examples

```
# Load example 4D image file included with package
file_path <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
fbvec <- FileBackedNeuroVec(file_path)

# Get dimensions of the image
dim(fbvec)

# Extract first volume
vol1 <- sub_vector(fbvec, 1)

# Extract multiple volumes
vols <- sub_vector(fbvec, 1:2)
```

`FileFormat-class` *FileFormat Class*

Description

This class represents a neuroimaging file format descriptor, containing information about the file format, encoding, and extensions for both header and data components.

Slots

`file_format` A `character` string specifying the name of the file format (e.g., "NIfTI").

`header_encoding` A `character` string specifying the file encoding of the header file (e.g., "raw" for binary, "gzip" for gz compressed).

`header_extension` A `character` string specifying the file extension for the header file (e.g., "nii" for NIfTI single files).

`data_encoding` A `character` string specifying the file encoding for the data file.

`data_extension` A `character` string specifying the file extension for the data file (e.g., "nii" for NIfTI single files).

Examples

```
# Create a FileFormat object for NIfTI format
nifti_format <- new("FileFormat",
                    file_format = "NIfTI",
                    header_encoding = "raw",
                    header_extension = "nii",
                    data_encoding = "raw",
                    data_extension = "nii")
```

FileFormat-operations *File Format Operations for Neuroimaging Data*

Description

A collection of methods for handling neuroimaging file formats with separate header and data files (e.g., ANALYZE, NIFTI). These methods provide functionality for file name validation, extension handling, and file path manipulation.

File Format Structure

Neuroimaging formats often use paired files:

- A header file (e.g., '.hdr') containing metadata
- A data file (e.g., '.img') containing the actual image data

Common Operations

- Validating file names against format specifications
- Converting between header and data file names
- Checking file existence and compatibility

FileMetaInfo-class *FileMetaInfo Class*

Description

This class extends MetaInfo to include file-specific metadata for neuroimaging data files.

This class extends FileMetaInfo with NIfTI-specific metadata.

This class extends FileMetaInfo with AFNI-specific metadata.

Slots

`header_file` A `character` string specifying the name of the file containing meta information.

`data_file` A `character` string specifying the name of the file containing image data.

`descriptor` A `FileFormat` object describing the image file format.

`endian` A `character` string specifying the byte order of data ('little' or 'big').

`data_offset` A `numeric` value indicating the number of bytes preceding the start of image data in the data file.

`bytes_per_element` An `integer` specifying the number of bytes per data element.

`intercept` A `numeric` vector of constant values added to image data (one per sub-image).

`slope` A `numeric` vector of multipliers for image data (one per sub-image).

`header` A `list` of format-specific attributes.

`nifti_header` A `list` of attributes specific to the NIfTI file format.

`afni_header` A `list` of attributes specific to the AFNI file format.

See Also

MetaInfo-class, NIFTIMetaInfo-class, AFNIMetaInfo-class

FileMetaInfo-class

FileMetaInfo-class

FileSource-class *FileSource Class*

Description

Base class for representing a data source for images. The purpose of this class is to provide a layer in between low level IO and image loading functionality.

Slots

`meta_info` An object of class FileMetaInfo containing meta information for the data source.

---

findAnatomy3D *Find 3D anatomical orientation from axis abbreviations*

Description

Creates a 3D anatomical orientation from axis abbreviations.

Usage

```
findAnatomy3D(axis1 = "L", axis2 = "P", axis3 = "I")
```

Arguments

axis1	Character string for first axis (default: "L" for Left)
axis2	Character string for second axis (default: "P" for Posterior)
axis3	Character string for third axis (default: "I" for Inferior)

Value

An AxisSet3D object representing the anatomical orientation

Examples

```
# Create orientation with default LPI axes
orient <- findAnatomy3D()
# Create orientation with custom axes
orient <- findAnatomy3D("R", "A", "S")
```

gaussian_blur *Gaussian Blur for Volumetric Images*

Description

This function applies an isotropic discrete Gaussian kernel to smooth a volumetric image (3D brain MRI data). The blurring is performed within a specified image mask, with customizable kernel parameters.

Usage

```
gaussian_blur(
  vol,
  mask,
  sigma = 2,
  window = NULL,
  normalize = TRUE,
  fwhm = NULL,
  truncate = 4
)
```

Arguments

vol	A NeuroVol object representing the image volume to be smoothed.
mask	An optional LogicalNeuroVol object representing the image mask. This mask defines the region where the blurring is applied. If not provided, the entire volume is processed. It must have the same dimensions as vol.
sigma	A single finite positive number specifying the standard deviation of the Gaussian kernel in the **spatial units of the image** (millimetres for a typical NIfTI), not voxels. The kernel is evaluated in physical distance using spacing(vol), so the same sigma produces the same physical smoothing regardless of voxel size. Default is 2; ignored when fwhm is given.
window	Kernel half-width in *voxels*: the number of voxels included on each side of the centre, so window = 1 is a 3x3x3 kernel. NULL (the default) derives it from sigma, truncate, and the voxel spacing, using the largest half-width over the three axes so no axis is clipped early. Supplying a number instead truncates the kernel there, which can under-smooth — see *Details*. A window larger than the volume is clamped to max(dim(vol)), which changes no result: every kernel tap that far out is out of bounds from every voxel.
normalize	A logical value controlling how the mask boundary is handled. When TRUE (the default), the blur is *insulated* to the mask: each in-mask output voxel is computed from in-mask neighbours only and the kernel is renormalized by the in-mask weight (a "smooth-in-mask" convolution, cf. AFNI 3dBlurInMask). Out-of-mask values — finite or not (including NaN/Inf) — never influence in-mask outputs, and edge voxels are not biased toward the mask exterior. When FALSE, the legacy behavior is used: the full kernel is applied with zero padding

outside the volume and out-of-mask neighbour values are read into the convolution (retained only for backward compatibility).

`fwhm` Full width at half maximum of the kernel in the image's spatial units, the form in which smoothing is usually specified. Supplying it sets `sigma` to `fwhm / (2 * sqrt(2 * log(2)))`; giving both is an error.

`truncate` How many standard deviations of the Gaussian to keep when `window` is derived. Default 4, matching `scipy.ndimage.gaussian_filter`. Smaller values are faster and smooth less than requested.

Details

The function uses a C++ implementation for efficient Gaussian blurring. The blurring is applied only to voxels within the specified mask (or the entire volume if no mask is provided).

Kernel width. A Gaussian has infinite support, so it has to be cut off somewhere, and where it is cut off changes the smoothing that is actually applied. `window` is measured in voxels while `sigma` is in millimetres, so a fixed `window` truncates at a different point on every acquisition. The old default of `window = 1` cut a `sigma = 2` mm kernel off at one standard deviation on 2 mm voxels and delivered 3.5 mm FWHM where 4.7 mm was asked for — and 1.9 mm on 1 mm voxels. Leaving `window = NULL` derives it from `sigma` instead, so the smoothing you ask for is the smoothing you get:

call	delivered	requested	shortfall
`sigma = 2, window = 1`	3.49 mm	4.71 mm	26%
`sigma = 4, window = 1`	3.76 mm	9.42 mm	60%
`sigma = 4` (derived)	9.42 mm	9.42 mm	0%

Passing `window` explicitly still truncates exactly as before, so old calls are reproducible; it is only the default that changed.

Units. `sigma` is in the spatial units of the image (millimetres for typical NIfTI data), *not* voxels: neighbour offsets are multiplied by `spacing(vol)` before the kernel is evaluated. `window`, by contrast, is a half-width counted in voxels. Mixing the two is the easy mistake — converting an FWHM to sigma in voxels and passing that as `sigma` silently under-smooths, with no error or warning. To smooth to a target FWHM:

```
fwhm_mm  <- 6
sigma_mm <- fwhm_mm / (2 * sqrt(2 * log(2)))          # ~2.55 mm
window  <- ceiling(3 * sigma_mm / mean(spacing(vol))) # cover +/- 3 sigma, in voxels
gaussian_blur(vol, mask, sigma = sigma_mm, window = window)
```

`window` must be large enough to contain the kernel: because the kernel is truncated at `window` voxels, a `window` much smaller than `3 * sigma_mm / spacing` clips the Gaussian tails and delivers less smoothing than `sigma` implies.

With the default `normalize = TRUE`, smoothing a masked statistical map (e.g. a first-level fMRI coefficient map written as `NaN` outside the brain) within its brain mask preserves the full in-mask coverage; out-of-mask `NaN`s do not erode the masked region and the renormalized edge values match the interior on their shared support.

Value

A NeuroVol object representing the smoothed image.

References

Gaussian blur: https://en.wikipedia.org/wiki/Gaussian_blur

See Also

NeuroVol-class, LogicalNeuroVol-class, bilateral_filter

Examples

```
# Load a sample brain mask
brain_mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Apply Gaussian blurring to the brain volume
blurred_vol <- gaussian_blur(brain_mask, brain_mask, sigma = 2, window = 1)

# View a slice of the original and blurred volumes
image(brain_mask[,,12])
image(blurred_vol[,,12])

# Smooth to a target FWHM. `sigma` is in millimetres, so convert FWHM -> sigma
# in mm (NOT voxels); `window` is a voxel half-width sized to cover +/- 3 sigma.
fwhm_mm  <- 6
sigma_mm <- fwhm_mm / (2 * sqrt(2 * log(2)))
window   <- ceiling(3 * sigma_mm / mean(spacing(brain_mask)))
smoothed <- gaussian_blur(brain_mask, brain_mask, sigma = sigma_mm, window = window)
```

---

get_afni_attribute *Get AFNI Attribute from Extension*

Description

Extracts a specific attribute value from a parsed AFNI extension.

Usage

```
get_afni_attribute(ext, attr_name)
```

Arguments

ext	A NiftiExtension-class object with ecode = 4, or an xml_document from parse_afni_extension.
attr_name	Character string specifying the attribute name to retrieve (e.g., "HISTORY_NOTE", "BRICK_LABS").

Value

The attribute value, or NULL if not found. The type depends on the attribute's ni_type in the XML.

Examples

```
## Not run:
# Get the history note from an AFNI extension
history <- get_afni_attribute(afni_ext, "HISTORY_NOTE")

## End(Not run)
```

---

grid_to_coord *Generic function to convert N-dimensional grid coordinates to real world coordinates*

Description

Generic function to convert N-dimensional grid coordinates to real world coordinates

Usage

```
grid_to_coord(x, coords)

## S4 method for signature 'NeuroSpace,matrix'
grid_to_coord(x, coords)

## S4 method for signature 'NeuroSpace,matrix'
grid_to_coord(x, coords)

## S4 method for signature 'NeuroSpace,numeric'
grid_to_coord(x, coords)

## S4 method for signature 'NeuroVol,matrix'
grid_to_coord(x, coords)
```

Arguments

x	the object
coords	a matrix of grid coordinates

Value

A numeric matrix of real-world coordinates.

Examples

```
# Create a simple 3D volume
bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))
grid_coords <- matrix(c(1.5,1.5,1.5, 5.5,5.5,5.5), ncol=3, byrow=TRUE)
world <- grid_to_coord(bvol, grid_coords)
grid <- coord_to_grid(bvol, world)
all.equal(grid_coords, grid)
```

---

grid_to_grid *Generic function to convert voxel coordinates in the reference space (LPI) to native array space.*

Description

Generic function to convert voxel coordinates in the reference space (LPI) to native array space.

Usage

```
grid_to_grid(x, vox)

## S4 method for signature 'NeuroSpace,matrix'
grid_to_grid(x, vox)

## S4 method for signature 'matrix,matrix'
grid_to_grid(x, vox)
```

Arguments

x	the object
vox	a matrix of LPI voxel coordinates

Value

A numeric `matrix` of native voxel coordinates.

Examples

```
# Create a simple 3D volume in LPI orientation
space <- NeuroSpace(c(10,10,10), c(2,2,2))

# Create a reoriented space in RAS orientation
space_ras <- reorient(space, c("R", "A", "S"))

# Convert coordinates between orientations
voxel_coords <- t(matrix(c(1,1,1)))
new_coords <- grid_to_grid(space_ras, voxel_coords)
print(new_coords)
```

grid_to_index *Generic function to convert N-dimensional grid coordinates to 1D indices*

Description

Converts 2D grid coordinates to linear indices for a NeuroSlice object.

Usage

```
grid_to_index(x, coords)

## S4 method for signature 'NeuroSlice,matrix'
grid_to_index(x, coords)

## S4 method for signature 'NeuroSlice,numeric'
grid_to_index(x, coords)

## S4 method for signature 'NeuroSpace,matrix'
grid_to_index(x, coords)

## S4 method for signature 'NeuroSpace,numeric'
grid_to_index(x, coords)

## S4 method for signature 'NeuroVol,matrix'
grid_to_index(x, coords)

## S4 method for signature 'NeuroVol,numeric'
grid_to_index(x, coords)
```

Arguments

x	A NeuroSlice object
coords	Either a numeric vector of length 2 or a matrix with 2 columns, representing (x,y) coordinates in the slice grid

Details

Convert Grid Coordinates to Linear Indices

Value

An integer vector of 1D indices corresponding to coords.

See Also

index_to_grid for the inverse operation

Examples

```
# Create a 2D space (10x10)
space_2d <- NeuroSpace(c(10,10), c(1,1))

# Convert 2D grid coordinates to linear indices
coords_2d <- matrix(c(1,1, 2,2), ncol=2, byrow=TRUE)
idx_2d <- grid_to_index(space_2d, coords_2d)
# First coordinate (1,1) maps to index 1
# Second coordinate (2,2) maps to index 12 (= 2 + (2-1)*10)

# Create a 3D space (10x10x10)
space_3d <- NeuroSpace(c(10,10,10), c(1,1,1))

# Convert 3D grid coordinates to linear indices
coords_3d <- matrix(c(1,1,1, 2,2,2), ncol=3, byrow=TRUE)
idx_3d <- grid_to_index(space_3d, coords_3d)

# Single coordinate can also be converted
idx <- grid_to_index(space_3d, c(1,1,1))

slice_space <- NeuroSpace(c(10, 10))
slice_data <- matrix(1:100, 10, 10)
slice <- NeuroSlice(slice_data, slice_space)

# Convert single coordinate
idx <- grid_to_index(slice, c(5, 5))

# Convert multiple coordinates
coords <- matrix(c(1,1, 2,2, 3,3), ncol=2, byrow=TRUE)
indices <- grid_to_index(slice, coords)
```

---

guided_filter *Edge-Preserving Guided Filter for Volumetric Images*

Description

This function applies a guided filter to a volumetric image (3D brain MRI data) to perform edge-preserving smoothing. The guided filter smooths the image while preserving edges, providing a balance between noise reduction and structural preservation.

Usage

```
guided_filter(vol, radius = 4, epsilon = 0.7^2)
```

Arguments

vol	A NeuroVol object representing the image volume to be filtered.
radius	An integer specifying the spatial radius of the filter. Default is 4.

epsilon A numeric value specifying the regularization parameter. It controls the degree of smoothing and edge preservation. Default is 0.49 (0.7^2).

Details

The guided filter operates by computing local linear models between the guidance image (which is the same as the input image in this implementation) and the output. The 'radius' parameter determines the size of the local neighborhood, while 'epsilon' controls the smoothness of the filter.

The implementation uses box blur operations for efficiency, which approximates the behavior of the original guided filter algorithm.

Value

A NeuroVol object representing the filtered image.

References

He, K., Sun, J., & Tang, X. (2013). Guided Image Filtering. IEEE Transactions on Pattern Analysis and Machine Intelligence, 35(6), 1397-1409.

See Also

gaussian_blur, bilateral_filter, NeuroVol-class

Examples

```
# Load an example brain volume
brain_vol <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Apply guided filtering to the brain volume

filtered_vol <- guided_filter(brain_vol, radius = 4, epsilon = 0.49)

# Visualize a slice of the original and filtered volumes
oldpar <- par(mfrow = c(1, 2))
image(brain_vol[,,12], main = "Original")
image(filtered_vol[,,12], main = "Filtered")
par(oldpar)
```

---

has_extensions *Check if Extensions are Present*

Description

Tests whether an object has any NIfTI extensions.

Usage

```
has_extensions(x)

## S4 method for signature 'NiftiExtensionList'
has_extensions(x)

## S4 method for signature 'list'
has_extensions(x)
```

Arguments

x	An object to test.

Value

Logical indicating whether extensions are present.

---

header *Access NIfTI Header Information*

Description

Retrieves header metadata from neuroimaging objects or files. Returns a structured list with commonly needed fields like sform/qform matrices, TR, intent codes, and data scaling parameters.

For low-level access to all raw NIfTI header fields, use the `$raw` element of the returned list.

Usage

```
header(x)

## S4 method for signature 'FileMetaInfo'
header(x)

## S4 method for signature 'character'
header(x)

## S4 method for signature 'NeuroObj'
header(x)
```

Arguments

x	A NeuroVol, NeuroVec, FileMetaInfo, or a character file path.

Value

A list of class "NeuroHeader" with elements:

dim Integer dimensions.

pixdim Voxel sizes including TR.

spacing Spatial voxel sizes (first 3 pixdim values).

origin Coordinate origin.

trans 4x4 affine transform.

qform List with matrix (4x4) and code (integer).

sform List with matrix (4x4) and code (integer).

intent_code NIfTI intent code.

intent_name NIfTI intent name string.

descrip Description string.

data_type Storage data type label.

bitpix Bits per pixel.

scl_slope Data scaling slope.

scl_inter Data scaling intercept.

cal_min Display intensity minimum.

cal_max Display intensity maximum.

TR Repetition time (4th pixdim), or NA if not 4D.

raw The complete raw header list (all NIfTI fields).

Examples

```
f <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
h <- header(f)
h$dim
h$TR
h$sform
h$descrip
```

---

header_file

Generic function to get the name of the header file, given a file name and a FileFormat *instance.*

Description

Derives the header file name from a given file name based on the FileFormat specifications.

Usage

```
header_file(x, file_name)

## S4 method for signature 'FileFormat,character'
header_file(x, file_name)
```

Arguments

x	A FileFormat object specifying the format requirements
file_name	A character string specifying the file name to derive the header file name from

Details

The function performs the following steps:

1. If the input file_name already matches the header file format, it returns the file_name as is.
2. If the file_name matches the data file format, it constructs and returns the corresponding header file name.
3. If the file_name doesn't match either format, it throws an error.

Value

The correct header file name as a `character` string.

A character string representing the header file name

See Also

`data_file`, `strip_extension` for related file name manipulation

Examples

```
fmt <- new("FileFormat", header_extension = "hdr", data_extension = "img")
header_file(fmt, "brain_scan.hdr")  # Returns "brain_scan.hdr"
header_file(fmt, "brain_scan.img")  # Returns "brain_scan.hdr"
```

---

header_file_matches *Generic function to test whether a file name conforms to the given* `FileFormat` *instance. Will test for match to header file only*

Description

Validates whether a file name conforms to the header file format specification.

Usage

```
header_file_matches(x, file_name)

## S4 method for signature 'FileFormat,character'
header_file_matches(x, file_name)
```

Arguments

x	A FileFormat object specifying the format requirements
file_name	A character string specifying the file name to validate

Details

The function performs case-sensitive pattern matching to verify that the file name ends with the specified header extension. The match is performed using a regular expression that ensures the extension appears at the end of the file name.

Value

TRUE for match, FALSE otherwise.

A logical value: TRUE if the file name matches the header format, FALSE otherwise

See Also

file_matches, data_file_matches for related file format validation

Examples

```
fmt <- new("FileFormat", header_extension = "hdr", data_extension = "img")
header_file_matches(fmt, "brain_scan.hdr")  # TRUE
header_file_matches(fmt, "brain_scan.img")  # FALSE
header_file_matches(fmt, "brain.hdr.gz")    # FALSE
```

---

image *Generic Image Method for Creating Visual Representations*

Description

Creates a visual representation (or image) from an object.

Usage

```
image(x, ...)
```

Arguments

x	An object to be rendered as an image.
...	Additional arguments passed to methods.

Value

An image object representing x.

---

index_to_coord *convert 1d indices to n-dimensional real world coordinates*

Description

convert 1d indices to n-dimensional real world coordinates

Usage

```
index_to_coord(x, idx)

## S4 method for signature 'NeuroSpace,numeric'
index_to_coord(x, idx)

## S4 method for signature 'NeuroSpace,integer'
index_to_coord(x, idx)

## S4 method for signature 'NeuroVol,integer'
index_to_coord(x, idx)

## S4 method for signature 'NeuroVec,integer'
index_to_coord(x, idx)
```

Arguments

x	the object
idx	the 1D indices

Value

A numeric matrix of real-world coordinates.

Examples

```
bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))
idx <- 1:10
g <- index_to_coord(bvol, idx)
idx2 <- coord_to_index(bvol, g)
all.equal(idx, idx2)
```

index_to_grid *Convert 1d indices to n-dimensional grid coordinates*

Description

Converts linear indices to 2D grid coordinates for a NeuroSlice object.

Usage

```
index_to_grid(x, idx)

## S4 method for signature 'NeuroSlice,numeric'
index_to_grid(x, idx)

## S4 method for signature 'NeuroSpace,numeric'
index_to_grid(x, idx)

## S4 method for signature 'NeuroVec,index'
index_to_grid(x, idx)

## S4 method for signature 'NeuroVec,integer'
index_to_grid(x, idx)

## S4 method for signature 'NeuroVol,index'
index_to_grid(x, idx)

## S4 method for signature 'NeuroVol,integer'
index_to_grid(x, idx)
```

Arguments

x	A NeuroSlice object
idx	Integer vector of linear indices to convert

Details

Convert Linear Indices to Grid Coordinates

Value

A numeric matrix of grid coordinates.

See Also

grid_to_index for the inverse operation

Examples

```
 bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))
 idx <- 1:10
 g <- index_to_grid(bvol, idx)
 bvol[g]

slice_space <- NeuroSpace(c(10, 10))
slice_data <- matrix(1:100, 10, 10)
slice <- NeuroSlice(slice_data, slice_space)

# Convert single index
coords <- index_to_grid(slice, 55)

# Convert multiple indices
indices <- c(1, 25, 50, 75, 100)
coords_mat <- index_to_grid(slice, indices)
```

IndexLookupVol-class *IndexLookupVol Class*

Description

A three-dimensional brain image class that serves as a map between 1D grid indices and a table of values. This class is primarily used in conjunction with the SparseNeuroVec class to efficiently represent and access sparse neuroimaging data.

The IndexLookupVol class provides efficient indexing and coordinate lookup functionality for 3D neuroimaging data. It maintains a mapping between linear indices and 3D coordinates, optimizing memory usage and access speed for sparse volumes.

Creates an IndexLookupVol object, which provides efficient bidirectional mapping between linear indices and 3D coordinates in a neuroimaging volume. This is particularly useful for working with masked or sparse brain volumes.

Usage

```
IndexLookupVol(space, indices)
```

Arguments

space	A NeuroSpace object defining the 3D space dimensions, spacing, and orientation.
indices	An integer vector containing the linear indices of the voxels to include in the lookup volume. These should be 1-based indices within the range of the space.

Details

The IndexLookupVol class extends NeuroVol and provides a mechanism for efficient lookup and mapping of sparse 3D neuroimaging data. It stores only the indices of non-zero voxels and their corresponding mappings, allowing for memory-efficient representation of large, sparse brain images.

Create an IndexLookupVol Object

Value

An object of class IndexLookupVol containing:

- A mapping between linear indices and sparse positions
- The original space information
- The subset of included voxel indices

Slots

space A NeuroSpace object representing the 3D space of the brain image.

indices An integer vector containing the 1D indices of the non-zero voxels in the grid.

map An integer vector containing the mapping between the 1D indices and the table of values.

Methods

This class inherits methods from NeuroVol. Additional methods specific to index lookup and mapping operations may be available.

Implementation Details

The class uses an integer mapping array for O(1) lookups between linear indices and their corresponding positions in the sparse representation.

See Also

SparseNeuroVec-class for the primary class that utilizes IndexLookupVol. NeuroVol-class for the base volumetric image class.

IndexLookupVol for creating instances of this class

coords for coordinate lookup, lookup for index mapping, NeuroSpace for space representation

Examples

```
# Create a NeuroSpace object
space <- NeuroSpace(dim = c(2L, 2L, 2L), origin = c(0, 0, 0), spacing = c(1, 1, 1))

# Create a 3D mask
mask <- array(c(TRUE, FALSE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE), dim = c(2, 2, 2))

# Create indices and map for the IndexLookupVol
indices <- which(mask)
```

```
map <- seq_along(indices)

# Create an IndexLookupVol object
ilv <- IndexLookupVol(space = space, indices = as.integer(indices))

# Access the indices
print(ilv@indices)

# Access the map
print(ilv@map)


# Create a 64x64x64 space
space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))

# Create a lookup volume with random indices
indices <- sample(1:262144, 10000)  # Select 10000 random voxels
ilv <- IndexLookupVol(space, indices)

# Look up coordinates for specific indices
coords <- coords(ilv, indices[1:10])
```

`indices` *Extract indices*

Description

Extract indices

Usage

```
indices(x)
```

Arguments

`x`	the object to extract indices

Value

A `vector` of indices from `x`.

Examples

```
# Create a NeuroSpace object with 3mm voxels
space <- NeuroSpace(c(10,10,10), spacing=c(3,3,3))

# Create ROI coordinates in voxel space
coords <- matrix(c(1,1,1, 2,2,2), ncol=3, byrow=TRUE)
```

```
# Create ROI volume
roi_vol <- ROIVol(space, coords, data=c(1,2))

# Get linear indices of ROI voxels
idx <- indices(roi_vol)
# These indices can be used to index into a 3D array of size 10x10x10
```

`indices,IndexLookupVol-method`

Get Indices from an IndexLookupVol Object

Description

Retrieves the vector of indices that are included in the lookup volume.

Usage

```
## S4 method for signature 'IndexLookupVol'
indices(x)

## S4 method for signature 'ROIVol'
indices(x)

## S4 method for signature 'ROIVol'
indices(x)

## S4 method for signature 'ROIVec'
indices(x)

## S4 method for signature 'AbstractSparseNeuroVec'
indices(x)
```

Arguments

x	An IndexLookupVol object

Value

the indices of the lookup volume

Examples

```
space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))
ilv <- IndexLookupVol(space, c(1:100))
idx <- indices(ilv)  # Get included indices
```

inverse_trans *Extract inverse image coordinate transformation*

Description

Extract inverse image coordinate transformation

Usage

```
inverse_trans(x)

## S4 method for signature 'NeuroSpace'
inverse_trans(x)
```

Arguments

x	an object

Value

A numeric 4x4 matrix that maps from real-world coordinates back to grid coordinates.

Examples

```
bspace <- NeuroSpace(c(10,10,10), c(2,2,2))
itrans <- inverse_trans(bspace)
identical(trans(bspace) %*% inverse_trans(bspace), diag(4))
```

Kernel *Create a Kernel object from a function of distance from kernel center*

Description

This function creates a Kernel object using a kernel function (FUN) that takes the distance from the center of the kernel as its first argument.

Usage

```
Kernel(kerndim, vdim, FUN = dnorm, ...)
```

Arguments

kerndim	A numeric vector representing the dimensions in voxels of the kernel.
vdim	A numeric vector representing the dimensions of the voxels in real units.
FUN	The kernel function taking its first argument representing the distance from the center of the kernel (default: dnorm).
...	Additional parameters to the kernel function, FUN.

Value

A Kernel object with the specified dimensions, voxel dimensions, and kernel function.

Examples

```
kdim <- c(3, 3, 3)
vdim <- c(1, 1, 1)
k <- Kernel(kerndim = kdim, vdim = vdim, FUN = dnorm, sd = 1)
```

Kernel-class *Kernel*

Description

A class representing an image kernel for image processing, such as convolution or filtering operations in brain images.

Slots

`width` A `numeric` value representing the width of the kernel in voxels. The width is typically an odd number to maintain symmetry.

`weights` A `numeric` vector containing the weights associated with each voxel in the kernel.

`voxels` A `matrix` containing the relative voxel coordinates of the kernel. Each row represents a voxel coordinate as (x, y, z).

`coords` A `matrix` containing the relative real-world coordinates of the kernel, corresponding to the voxel coordinates.

---

labels,ClusteredNeuroVec-method *Get Labels from ClusteredNeuroVec*

Description

Get Labels from ClusteredNeuroVec

Usage

```
## S4 method for signature 'ClusteredNeuroVec'
labels(object)
```

Arguments

`object`	A ClusteredNeuroVec object

laplace_enhance *Laplacian Enhancement Filter for Volumetric Images*

Description

This function applies a multi-layer Laplacian enhancement filter to a volumetric image (3D brain MRI data). The filter enhances details while preserving edges using a non-local means approach with multiple scales.

Usage

```
laplace_enhance(
  vol,
  mask,
  k = 2,
  patch_size = 3,
  search_radius = 2,
  h = 0.7,
  mapping_params = NULL,
  use_normalization_free = TRUE
)
```

Arguments

vol	A NeuroVol object representing the image volume to be enhanced.
mask	A LogicalNeuroVol object specifying the region to process. If not provided, the entire volume will be processed.
k	An integer specifying the number of layers in the decomposition (default is 2).
patch_size	An integer specifying the size of patches for non-local means. Must be odd (default is 3).
search_radius	An integer specifying the radius of the search window (default is 2).
h	A numeric value controlling the filtering strength. Higher values mean more smoothing (default is 0.7).
mapping_params	An optional list of parameters for the enhancement mappings.
use_normalization_free	Logical indicating whether to use normalization-free weights (default is TRUE).

Value

A NeuroVol object representing the enhanced image.

length,ClusteredNeuroVec-method

Get length of NeuroVec object

Description

Returns the number of time points (4th dimension) in a NeuroVec object. This represents the temporal dimension of the neuroimaging data.

Returns the total number of time points across all vectors in the sequence

Usage

```
## S4 method for signature 'ClusteredNeuroVec'
length(x)

## S4 method for signature 'NeuroVec'
length(x)

## S4 method for signature 'NeuroVecSeq'
length(x)

## S4 method for signature 'ROIVol'
length(x)

## S4 method for signature 'ROICoords'
length(x)
```

Arguments

x	A NeuroVecSeq object

Value

Integer length (total number of time points)

An integer representing the number of coordinates in the ROICoords object.

linear_access

Extract values from an array-like object using linear indexing.

Description

This function extracts the values of the elements in an array-like object using linear indexing. Linear indexing is a way of indexing an array by a single index that is computed from multiple indices using a formula.

Usage

```
linear_access(x, i, ...)
```

Arguments

x	a data source.
i	a vector of indices.
...	additional arguments to be passed to methods.

Value

A vector containing the values at the specified linear indices of x.

Examples

```
# Create a sparse neuroimaging vector
bspace <- NeuroSpace(c(10,10,10,100), c(1,1,1))
mask <- array(rnorm(10*10*10) > .5, c(10,10,10))
mat <- matrix(rnorm(sum(mask)), 100, sum(mask))
svec <- SparseNeuroVec(mat, bspace, mask)

# Extract values using linear indices
# Get values from first timepoint at voxels 1,2,3
indices <- c(1,2,3)
vals <- linear_access(svec, indices)

# Get values from multiple timepoints and voxels
# First voxel at timepoint 1, second voxel at timepoint 2
indices <- c(1, 1000 + 2) # 1000 = prod(10,10,10)
vals <- linear_access(svec, indices)
```

---

linear_access,DenseNeuroVol,numeric-method

Linear Access Method for FileBackedNeuroVec

Description

Returns decoded values from memory-mapped data, applying the source slope and intercept exactly once.

Provides linear access to the data across all vectors in the sequence.

Usage

```
## S4 method for signature 'DenseNeuroVol,numeric'
linear_access(x, i)

## S4 method for signature 'DenseNeuroVec,numeric'
```

```
linear_access(x, i)

## S4 method for signature 'DenseNeuroVol,integer'
linear_access(x, i)

## S4 method for signature 'DenseNeuroVec,integer'
linear_access(x, i)

## S4 method for signature 'FileBackedNeuroVec,numeric'
linear_access(x, i)

## S4 method for signature 'MappedNeuroVec,numeric'
linear_access(x, i)

## S4 method for signature 'NeuroHyperVec,ANY'
linear_access(x, i, ...)

## S4 method for signature 'NeuroVecSeq,numeric'
linear_access(x, i)

## S4 method for signature 'SparseNeuroVol,numeric'
linear_access(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,numeric'
linear_access(x, i)
```

Arguments

x	A NeuroVecSeq object
i	Numeric vector of indices for linear access
...	Additional arguments (not used)

Value

Numeric vector of accessed values

Examples

```
# Create a small NeuroVec and save it
nvec <- NeuroVec(matrix(1:32, 8, 4), NeuroSpace(c(2,2,2,4)))
tmp <- tempfile(fileext = ".nii")
write_vec(nvec, tmp)

# Load as FileBackedNeuroVec and access values
fbvec <- FileBackedNeuroVec(tmp)
values <- linear_access(fbvec, 1:10)

# Clean up
unlink(tmp)
```

list_afni_attributes *List AFNI Attributes in Extension*

Description

Returns a character vector of all attribute names in an AFNI extension.

Usage

```
list_afni_attributes(ext)
```

Arguments

ext	A NiftiExtension-class object with ecode = 4, or an xml_document from parse_afni_extension.

Value

Character vector of attribute names.

Examples

```
## Not run:
# List all attributes in an AFNI extension
attrs <- list_afni_attributes(afni_ext)
print(attrs)

## End(Not run)
```

load_data,MappedNeuroVecSource-method *Load image data from a NeuroVecSource object*

Description

This function loads the image data from a NeuroVecSource object, handling various dimensionalities and applying any necessary transformations.

Usage

```
## S4 method for signature 'MappedNeuroVecSource'
load_data(x)

## S4 method for signature 'NeuroVecSource'
load_data(x)

## S4 method for signature 'NeuroVolSource'
load_data(x)

## S4 method for signature 'SparseNeuroVecSource'
load_data(x)
```

Arguments

x	The NeuroVecSource object containing the image metadata and file information.

Details

This method performs the following steps: 1. Validates the dimensionality of the metadata. 2. Reads the image data using RNifti. 3. Handles 5D arrays by dropping the 4th dimension if it has length 1. 4. Applies slope scaling if present in the metadata. 5. Constructs a NeuroSpace object with appropriate dimensions and spatial information. 6. Creates and returns a DenseNeuroVec object, handling both 3D and 4D input arrays.

Value

a DenseNeuroVec object

Note

This method currently only supports NIfTI file format through RNifti.

See Also

NeuroVecSource, DenseNeuroVec, NeuroSpace

Logic-methods *Logic Operations for Neuroimaging Volumes*

Description

Methods for performing logical operations (& and |) on neuroimaging volume objects. Results are always returned as LogicalNeuroVol objects that preserve spatial metadata.

Usage

```
## S4 method for signature 'DenseNeuroVol,DenseNeuroVol'
Logic(e1, e2)

## S4 method for signature 'SparseNeuroVol,SparseNeuroVol'
Logic(e1, e2)

## S4 method for signature 'SparseNeuroVol,NeuroVol'
Logic(e1, e2)

## S4 method for signature 'NeuroVol,SparseNeuroVol'
Logic(e1, e2)

## S4 method for signature 'NeuroVol,logical'
Logic(e1, e2)

## S4 method for signature 'logical,NeuroVol'
Logic(e1, e2)
```

Arguments

e1, e2	Neuroimaging volume objects or logical values.

Value

A LogicalNeuroVol.

Examples

```
sp <- NeuroSpace(c(5L, 5L, 5L), c(1, 1, 1))
v1 <- DenseNeuroVol(array(sample(0:1, 125, replace = TRUE), c(5, 5, 5)), sp)
v2 <- DenseNeuroVol(array(sample(0:1, 125, replace = TRUE), c(5, 5, 5)), sp)
intersection <- v1 & v2
union_mask  <- v1 | v2
```

LogicalNeuroVol-class *LogicalNeuroVol Class*

Description

This class represents a three-dimensional brain image where all values are either TRUE or FALSE. It is particularly useful for creating and managing binary masks for brain images.

This function constructs a LogicalNeuroVol instance.

Usage

```
LogicalNeuroVol(data, space, label = "", indices = NULL)
```

Arguments

data	A three-dimensional array, a 1D vector with length equal to prod(dim(space)), or a set of indices where elements are TRUE.
space	An instance of class NeuroSpace.
label	A character string.
indices	An optional 1-d index vector.

Details

The LogicalNeuroVol class extends the DenseNeuroVol class, inheriting its spatial properties and array-based storage. However, it constrains the values to be logical (TRUE or FALSE), making it ideal for representing binary masks, regions of interest (ROIs), or segmentation results in neuroimaging analyses.

Value

A LogicalNeuroVol instance.

Slots

.Data A logical array containing the binary volume data.

space A NeuroSpace object defining the spatial properties of the volume.

Methods

This class inherits methods from DenseNeuroVol. Additional methods specific to logical operations may be available.

See Also

DenseNeuroVol-class for the parent class. NeuroVol-class for the base volumetric image class.

Examples

```
# Create a simple logical brain volume (e.g., a mask)
dim <- c(64L, 64L, 64L)
mask_data <- array(sample(c(TRUE, FALSE), prod(dim), replace = TRUE), dim)
mask_space <- NeuroSpace(dim = dim, origin = c(0, 0, 0), spacing = c(1, 1, 1))
brain_mask <- new("LogicalNeuroVol", .Data = mask_data, space = mask_space)

# Check the proportion of TRUE voxels
true_proportion <- sum(brain_mask) / prod(dim(brain_mask))
print(paste("Proportion of TRUE voxels:", true_proportion))

# Load an example brain mask
brain_mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Convert the brain mask to a LogicalNeuroVol
logical_vol <- LogicalNeuroVol(brain_mask, space(brain_mask))
```

lookup *Index Lookup operation*

Description

Index Lookup operation

Usage

```
lookup(x, i, ...)
```

Arguments

x	the object to query
i	the index to lookup
...	additional arguments

Value

The value(s) at the specified index/indices of x.

Examples

```
# Create a 64x64x64 space
space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))

# Create a lookup volume with first 100 indices
ilv <- IndexLookupVol(space, 1:100)

# Look up values for indices 1, 2, and 3
# Returns their positions in the sparse representation
lookup(ilv, c(1, 2, 3))

# Look up values outside the included indices
# Returns 0 for indices not in the lookup volume
lookup(ilv, c(101, 102))
```

lookup,IndexLookupVol,numeric-method *Lookup Values in an IndexLookupVol Object*

Description

Performs a lookup operation on an IndexLookupVol object.

Usage

```
## S4 method for signature 'IndexLookupVol,numeric'
lookup(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,numeric'
lookup(x, i)
```

Arguments

x	An IndexLookupVol object
i	A numeric vector of indices to look up

Value

the values of the lookup volume

Examples

```
space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))
ilv <- IndexLookupVol(space, c(1:100))
lookup(ilv, c(1, 2, 3))  # Look up values for indices 1, 2, and 3
```

---

make_time_weights *Build smooth time weights from motion/outlier metrics*

Description

Creates per-time-point weights $w_t \in [0, 1]$ by smoothly combining framewise displacement (FD), DVARS, and spike/outlier scores. Each series is transformed through a soft logistic ramp so that values beyond the specified thresholds receive progressively lower weights instead of hard 0/1 decisions.

Usage

```
make_time_weights(
  fd = NULL,
  dvars = NULL,
  spike = NULL,
  fd_thr = 0.5,
  dvars_z = 2.5,
  spike_z = 5,
  fd_soft = 0.1,
  dvars_soft = 0.25,
  combine = c("min", "prod")
)
```

Arguments

fd	Optional numeric vector of framewise displacement values.
dvars	Optional numeric vector of DVARS values.
spike	Optional numeric vector with spike/outlier magnitudes.
fd_thr	Threshold (in mm) where FD weights start to drop (default 0.5).
dvars_z	Z-threshold applied to the standardized DVARS series (default 2.5).
spike_z	Z-threshold applied to the standardized spike series (default 5).
fd_soft	Logistic softness (in mm) controlling the slope around fd_thr.
dvars_soft	Logistic softness for the DVARS z-scores.
combine	Either "min" (take the minimum weight per TR) or "prod" (multiply all weights).

Value

Numeric vector of weights in $[0, 1]$ with length equal to the provided series. At least one of fd, dvars, or spike must be supplied.

---

map_values *Map Values from One Set to Another Using a User-supplied Lookup Table*

Description

This function maps values from one set to another using a lookup table provided by the user.

Usage

```
map_values(x, lookup)

## S4 method for signature 'NeuroVol,list'
map_values(x, lookup)

## S4 method for signature 'NeuroVol,matrix'
map_values(x, lookup)
```

Arguments

x	The object from which values will be mapped.
lookup	The lookup table. The first column is the "key" and the second column is the "value".

Value

An object of the same class as x, in which the original values have been replaced with the lookup table values.

Examples

```
x <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))
vol <- NeuroVol(sample(1:10, 10 * 10 * 10, replace = TRUE), x)

## Lookup table is a list
lookup <- lapply(1:10, function(i) i * 10)
names(lookup) <- 1:10
ovol <- map_values(vol, lookup)

## Lookup table is a matrix. The first column is the key, and the second column is the value
names(lookup) <- 1:length(lookup)
lookup.mat <- cbind(as.numeric(names(lookup)), unlist(lookup))
ovol2 <- map_values(vol, lookup.mat)
all.equal(as.vector(ovol2), as.vector(ovol))
```

---

mapf *Apply a function to an object.*

Description

This function applies a function to an object, with additional arguments passed to the function using the ... argument. The mapping object specifies how the function is to be applied, and can take many different forms, depending on the object and function used. The return value depends on the function used.

Usage

```
mapf(x, m, ...)

## S4 method for signature 'NeuroVol,Kernel'
mapf(x, m, mask = NULL)
```

Arguments

x	the object that is mapped.
m	the mapping object.
...	additional arguments to be passed to the function.
mask	restrict application of kernel to masked area

Value

The result of applying the mapping function to x.

Examples

```
# Create a simple 3D volume
bspace <- NeuroSpace(c(10,10,10), c(1,1,1))
vol <- NeuroVol(array(rnorm(10*10*10), c(10,10,10)), bspace)

# Create a 3x3x3 mean smoothing kernel
kern <- Kernel(c(3,3,3),  vdim=c(3,3,3))

# Apply the kernel to smooth the volume
smoothed_vol <- mapf(vol, kern)
```

MappedNeuroVec-class *MappedNeuroVec Class*

Description

A class representing a four-dimensional brain image backed by a memory-mapped file. This class provides efficient access to large brain images without loading the entire dataset into memory.

The MappedNeuroVec class provides memory-efficient access to large neuroimaging datasets through memory mapping. This allows processing of datasets larger than available RAM by keeping data on disk and only loading requested portions into memory.

Creates a MappedNeuroVec object that provides efficient, memory-mapped access to large neuroimaging datasets. This allows processing of data larger than available RAM by keeping it on disk and only loading requested portions into memory.

Usage

```
MappedNeuroVec(file_name, label = basename(file_name))
```

Arguments

file_name	Character string specifying the path to the neuroimaging file. Supported formats include NIFTI (.nii) and ANALYZE (.hdr/.img).
label	Optional character string providing a label for the vector

Details

MappedNeuroVec objects use memory-mapped files to store and access large 4D brain images efficiently. This approach allows for rapid access to specific portions of the data without requiring the entire dataset to be loaded into memory at once.

Create a Memory-Mapped Neuroimaging Vector

The function implements several key features:

- Zero-copy access to file data
- Automatic memory management
- Support for large datasets

- Efficient random access
- Proper cleanup on object deletion

Memory mapping is particularly useful when:

- Working with large datasets
- Only portions of data are needed at once
- Random access is required
- Multiple processes need to share data

Value

A new `MappedNeuroVec` object providing:

- Memory-mapped access to the data
- Spatial and temporal indexing
- Efficient data extraction
- Automatic memory management

Slots

`filemap` An object of class `mmap` representing the memory-mapped file containing the brain image data.

`offset` An integer representing the element offset within the memory-mapped file where the brain image data starts.

`slope` Normalized decoding slopes, either scalar or one per volume.

`intercept` Normalized decoding intercepts, either scalar or one per volume.

Methods

This class inherits methods from `NeuroVec` and implements the `ArrayLike4D` interface. Additional methods specific to memory-mapped operations may be available.

Implementation Details

The class uses the `mmap` package to establish a memory mapping between the file and memory space. Key features include:

- Zero-copy access to file data
- Automatic memory management
- Support for large datasets
- Efficient random access

See Also

`NeuroVec-class` for the parent class. `mmap` for details on memory-mapped file objects.

`MappedNeuroVec` for creating instances of this class

`mmap` for memory mapping details

Examples

```
# Create a MappedNeuroVec object (pseudo-code)
file_path <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
mapped_vec <- MappedNeuroVec(file_path)

# Access a subset of the data
subset <- mapped_vec[,,, 1:2]


# Create mapped vector from NIFTI file
mvec <- MappedNeuroVec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Extract first volume
vol1 <- mvec[[1]]

# Get dimensions
dim(mvec)

# Access specific timepoint
timepoint <- mvec[, , , 2]
```

`MappedNeuroVecSource-class`
MappedNeuroVecSource Class

Description

A class used to produce a `MappedNeuroVec` instance. It encapsulates the necessary information to create a memory-mapped representation of a 4D neuroimaging dataset.

Creates a `MappedNeuroVecSource` object that manages the memory mapping between a neuroimaging file and memory space. This is typically used internally by `MappedNeuroVec` but can be created directly for custom access patterns.

Usage

```
MappedNeuroVecSource(file_name)
```

Arguments

`file_name`	Character string specifying the path to the neuroimaging file. Supported formats include NIFTI (.nii) and ANALYZE (.hdr/.img).

Details

MappedNeuroVecSource acts as a factory for MappedNeuroVec objects. While it doesn't have any additional slots beyond its parent class, it specifies the intent to create a memory-mapped representation of the neuroimaging data. This class is typically used in data loading pipelines where large datasets need to be accessed efficiently without loading the entire dataset into memory.

Create a Memory-Mapped Source for Neuroimaging Data

The function performs several important checks:

- Validates file existence and permissions
- Reads and validates header information
- Ensures proper dimensionality (>= 3D)
- Verifies file format compatibility

Value

A new `MappedNeuroVecSource` object containing:

- Meta information about the dataset
- File format details
- Dimensional information

Inheritance

`MappedNeuroVecSource` inherits from:

- `NeuroVecSource`: Base class for NeuroVec source objects

See Also

`MappedNeuroVec` for the main user interface, `read_header` for header reading details

Examples

```
# Create a MappedNeuroVecSource
mapped_source <- new("MappedNeuroVecSource")


# Create source from NIFTI file
source <- MappedNeuroVecSource(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Check dimensions
dim(source@meta_info)

# View header information
str(source@meta_info)
```

mapToColors *Map intensity values to colors*

Description

Convert intensity values (e.g., a 2D slice) into a color representation for plotting and overlays.

Usage

```
mapToColors(
  imslice,
  col = heat.colors(128, alpha = 1),
  zero_col = "#00000000",
  alpha = 1,
  irange = range(imslice),
  threshold = c(0, 0)
)
```

Arguments

imslice	A numeric vector or array of intensities.
col	A vector of colors used as a lookup table.
zero_col	Color used for exactly-zero intensities (defaults to transparent).
alpha	Global alpha multiplier applied to all colors when alpha < 1.
irange	Intensity range used to normalize values before mapping to col.
threshold	Optional length-2 numeric vector. If diff(threshold) > 0, values within [threshold[1], threshold[2]] are set to transparent.

Value

If alpha == 1, returns a character vector/array of colors. If alpha < 1, returns an array with an added RGBA channel (last dimension length 4).

mask *Extract Mask from Neuroimaging Object*

Description

Generic function to extract or generate a mask from neuroimaging objects. For sparse objects with a @mask slot, returns the stored mask. For dense objects, returns a filled mask (all TRUE values) indicating all voxels contain valid data.

Usage

```
mask(x)

## S4 method for signature 'ClusteredNeuroVol'
mask(x)

## S4 method for signature 'FileBackedNeuroVec'
mask(x)

## S4 method for signature 'MappedNeuroVec'
mask(x)

## S4 method for signature 'NeuroHyperVec'
mask(x)

## S4 method for signature 'NeuroSlice'
mask(x)

## S4 method for signature 'DenseNeuroVec'
mask(x)

## S4 method for signature 'DenseNeuroVol'
mask(x)

## S4 method for signature 'LogicalNeuroVol'
mask(x)

## S4 method for signature 'AbstractSparseNeuroVec'
mask(x)

## S4 method for signature 'SparseNeuroVecSource'
mask(x)
```

Arguments

x	A neuroimaging object (NeuroVol, NeuroVec, or derived classes)

Details

The behavior depends on the class of the input object:

- For sparse objects (SparseNeuroVec, ClusteredNeuroVol, etc.): Returns the stored `@mask` slot
- For dense objects (DenseNeuroVol, DenseNeuroVec, etc.): Returns a LogicalNeuroVol with all TRUE values
- For ROI objects: Not implemented (use `coords()` instead)

Value

A `LogicalNeuroVol` object representing the mask

Examples

```
# Create a dense volume
vol <- NeuroVol(array(rnorm(64^3), c(64,64,64)), NeuroSpace(c(64,64,64)))
m <- mask(vol)  # Returns all TRUE mask

# Create a sparse vector with explicit mask
mask_array <- array(runif(64^3) > 0.5, c(64,64,64))
mask_vol <- LogicalNeuroVol(mask_array, NeuroSpace(c(64,64,64)))
# Data must be a matrix (time x masked voxels)
sparse_data <- matrix(rnorm(sum(mask_array) * 10), nrow = 10, ncol = sum(mask_array))
svec <- SparseNeuroVec(sparse_data, NeuroSpace(c(64,64,64,10)), mask_vol)
m2 <- mask(svec)  # Returns the stored mask
```

---

matricized_access *Extract values from a 4D tensor using a matrix of time-space indices.*

Description

This function efficiently extracts values from a 4D tensor (typically neuroimaging data) using a matrix of indices where each row contains a time index in column 1 and a spatial index in column 2. The spatial index refers to the position in the flattened spatial dimensions (x,y,z). This is primarily used internally by the `series()` method to efficiently access time series data for specific voxels.

Usage

```
matricized_access(x, i, ...)

## S4 method for signature 'SparseNeuroVec,matrix'
matricized_access(x, i)

## S4 method for signature 'SparseNeuroVec,integer'
matricized_access(x, i)

## S4 method for signature 'SparseNeuroVec,numeric'
matricized_access(x, i)

## S4 method for signature 'BigNeuroVec,matrix'
matricized_access(x, i)

## S4 method for signature 'BigNeuroVec,integer'
matricized_access(x, i)

## S4 method for signature 'BigNeuroVec,numeric'
matricized_access(x, i)
```

Arguments

x	a data source, typically a SparseNeuroVec object containing 4D neuroimaging data
i	Either: • A matrix with 2 columns: [time_index, space_index] specifying which values to extract • A numeric vector of spatial indices to extract all timepoints for those locations
...	additional arguments to be passed to methods.

Value

When i is a matrix, returns a numeric vector of values at the specified time-space coordinates. When i is a vector, returns a matrix where each column contains the full time series for each spatial index.

Examples

```
# Create a sparse 4D neuroimaging vector
bspace <- NeuroSpace(c(10,10,10,100), c(1,1,1))
mask <- array(rnorm(10*10*10) > .5, c(10,10,10))
mat <- matrix(rnorm(sum(mask)), 100, sum(mask))
svec <- SparseNeuroVec(mat, bspace, mask)

# Extract specific timepoint-voxel pairs
# Get value at timepoint 1, voxel 1 and timepoint 2, voxel 2
idx_mat <- matrix(c(1,1, 2,2), ncol=2, byrow=TRUE)
vals <- matricized_access(svec, idx_mat)

# Get full time series for voxels 1 and 2
ts_mat <- matricized_access(svec, c(1,2))
# Each column in ts_mat contains the full time series for that voxel
```

---

matrixToQuatern *Convert a Transformation Matrix to a Quaternion Representation*

Description

Extracts the rotation and scaling components from a 3x3 (or 4x4) transformation matrix, normalizes them, and computes the corresponding quaternion parameters and a sign factor (‘qfac‘) indicating whether the determinant is negative.

Usage

```
matrixToQuatern(mat)
```

Arguments

`mat`	A numeric matrix with at least the top-left 3x3 portion containing rotation/scaling. Often a 4x4 affine transform, but only the 3x3 top-left submatrix is used in practice.

Details

This function first checks and corrects for zero-length axes in the upper-left corner of the matrix, then normalizes each column to extract the pure rotation. If the determinant of the rotation submatrix is negative, the `qfac` is set to `-1`, and the third column is negated. Finally, the quaternion parameters (a, b, c, d) are computed following standard NIfTI-1 conventions for representing the rotation in 3D.

Value

A named `list` with two elements:

`quaternion` A numeric vector of length 3, (b, c, d), which—together with a derived internally—represents the rotation.

`qfac` Either `+1` or `-1`, indicating whether the determinant of the rotation submatrix is positive or negative, respectively.

References

- Cox RW. *Analysis of Functional NeuroImages* (AFNI) and NIfTI-1 quaternion conventions. https://afni.nimh.nih.gov

See Also

`quaternToMatrix` for the inverse operation, converting quaternion parameters back to a transform matrix.

`mean-methods` *Temporal Mean of a NeuroVec*

Description

Computes the voxel-wise mean across the 4th dimension (time), returning a 3D `DenseNeuroVol` or `SparseNeuroVol`.

Usage

```
## S4 method for signature 'DenseNeuroVec'
mean(x, ..., na.rm = FALSE)

## S4 method for signature 'SparseNeuroVec'
mean(x, ..., na.rm = FALSE)
```

```
## S4 method for signature 'NeuroVec'
mean(x, ..., na.rm = FALSE)
```

Arguments

x	A NeuroVec object.
...	Additional arguments (currently unused).
na.rm	Logical; if TRUE, missing values are omitted before computing the temporal mean at each voxel.

Value

A NeuroVol containing the temporal mean at each voxel.

Examples

```
bspace <- NeuroSpace(c(10, 10, 10, 20), c(1, 1, 1))
dat <- array(rnorm(10 * 10 * 10 * 20), c(10, 10, 10, 20))
vec <- DenseNeuroVec(dat, bspace)
mean_vol <- mean(vec)
dim(mean_vol)  # 10 10 10
```

---

meta_info *Lightweight metadata for neuroimaging files*

Description

‘meta_info()‘ provides a simple, CRAN-friendly way to retrieve essential image metadata without teaching S4 details up front. It accepts a file path or a ‘FileMetaInfo‘ object and returns a normalized list containing common fields like dimensions, spacing, origin, and transform.

The function does not read image data; it only parses header information.

Usage

```
meta_info(x)

## S4 method for signature 'FileMetaInfo'
meta_info(x)

## S4 method for signature 'character'
meta_info(x)
```

Arguments

x	A character file path (e.g., ‘"image.nii.gz"‘) or an object of class FileMetaInfo.

Details

Summarize Image Metadata

Value

A named list with the following elements:

- ‘dim‘ Integer vector of image dimensions.
- ‘spacing‘ Numeric voxel spacing (mm).
- ‘origin‘ Numeric coordinate origin.
- ‘trans‘ 4x4 transformation matrix mapping grid to world (mm).
- ‘path‘ Data file path.
- ‘filename‘ Basename of ‘path‘.
- ‘format‘ File format label (e.g., "NIFTI", "AFNI").
- ‘dtype‘ Storage data type label.
- ‘bytes_per_element‘ Bytes per element.
- ‘nvox‘ Number of voxels in the spatial volume (prod of first 3 dims).
- ‘nvol‘ Number of volumes (4th dim if present, else 1).
- ‘size_bytes‘ Approximate uncompressed size in bytes (‘nvox * nvol * bytes_per_element‘).
- ‘time_step‘ Time step (TR in seconds) if available for NIfTI, else ‘NA_real_‘.

See Also

`read_header`, `trans`, `FileMetaInfo`, `NIFTIMetaInfo`

Examples

```
f <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
mi <- meta_info(f)
mi$dim
mi$spacing
mi$origin
mi$filename
# 4x4 transform
mi$trans
```

`MetaInfo` *Create Neuroimaging Metadata Object*

Description

Creates a MetaInfo object containing essential metadata for neuroimaging data, including dimensions, spacing, orientation, and data type information.

Usage

```
MetaInfo(
  Dim,
  spacing,
  origin = rep(0, length(spacing)),
  data_type = "FLOAT",
  label = "",
  spatial_axes = OrientationList3D$AXIAL_LPI,
  additional_axes = NullAxis
)
```

Arguments

`Dim`	Integer vector. Image dimensions (e.g., c(64, 64, 32) for 3D).
`spacing`	Numeric vector. Voxel dimensions in mm.
`origin`	Numeric vector. Coordinate origin. Default is zero vector.
`data_type`	Character. Data type (e.g., "FLOAT", "SHORT"). Default is "FLOAT".
`label`	Character. Image label(s). Default is "".
`spatial_axes`	Object. Spatial orientation. Default is OrientationList3D$AXIAL_LPI.
`additional_axes`	Object. Non-spatial axes. Default is NullAxis.

Details

Create MetaInfo Object

The MetaInfo object is fundamental for:

- Spatial interpretation of image data
- Data type handling and conversion
- Memory allocation and mapping
- File I/O operations

Input validation ensures:

- Dimensions are positive integers
- Spacing values are positive
- Origin coordinates are finite
- Data type is supported

Value

A MetaInfo object

See Also

NIFTIMetaInfo, AFNIMetaInfo

Examples

```
# Create metadata for 3D structural MRI
meta <- MetaInfo(
  Dim = c(256, 256, 180),
  spacing = c(1, 1, 1),
  data_type = "FLOAT",
  label = "T1w"
)

# Get image dimensions
dim(meta)

# Get transformation matrix
trans(meta)
```

MetaInfo-class *MetaInfo Class*

Description

This class encapsulates meta information for neuroimaging data types, including spatial and temporal characteristics, data type, and labeling.

Details

The MetaInfo class provides a structured way to store and access essential metadata for neuroimaging data. This includes information about the data type, spatial and temporal dimensions, voxel spacing, and coordinate system origin.

Slots

`data_type` A `character` string specifying the data type code (e.g., "FLOAT", "INT").

`dims` A `numeric` vector representing image dimensions.

`spatial_axes` An `AxisSet3D` object representing image axes for spatial dimensions (x, y, z).

`additional_axes` An `AxisSet` object representing axes for dimensions beyond spatial (e.g., time, color band, direction).

`spacing` A `numeric` vector representing voxel dimensions in real-world units.

`origin` A `numeric` vector representing the coordinate origin.

`label` A `character` vector containing name(s) of images or data series.

See Also

FileMetaInfo-class, AxisSet3D-class, AxisSet-class

Examples

```
# Create a MetaInfo object
meta_info <- new("MetaInfo",
                 data_type = "FLOAT",
                 dims = c(64, 64, 32, 100),
                 spatial_axes = new("AxisSet3D"),
                 additional_axes = new("AxisSet"),
                 spacing = c(3, 3, 4),
                 origin = c(0, 0, 0),
                 label = "fMRI_run1")
```

NamedAxis-class *NamedAxis*

Description

This class represents an axis with a name attribute

Slots

`axis` the name of the axis

`direction` of axis (-1,+1)

---

ndim *Extract the number of dimensions of an object*

Description

Extract the number of dimensions of an object

Get number of dimensions in axis set

Usage

```
ndim(x, ...)

## S4 method for signature 'AxisSet'
ndim(x, ...)

## S4 method for signature 'ClusteredNeuroVec'
ndim(x)
```

```
## S4 method for signature 'NeuroObj'
ndim(x)

## S4 method for signature 'NeuroHyperVec'
ndim(x)

## S4 method for signature 'NeuroSpace'
ndim(x)
```

Arguments

x	An AxisSet object
...	Additional arguments (not used)

Value

An integer representing the number of dimensions in x.

An integer representing the number of dimensions in x.

Examples

```
x = NeuroSpace(c(10,10,10), spacing=c(1,1,1))
ndim(x) == 3
x = NeuroSpace(c(10,10,10,3), spacing=c(1,1,1))
ndim(x) == 4
```

---

neuro-downsample *Downsampling Methods for Neuroimaging Objects*

Description

Methods for downsampling neuroimaging objects to lower spatial resolution

---

neuro-ops *Arithmetic and Comparison Operations for Neuroimaging Objects*

Description

Methods for performing arithmetic and comparison operations on neuroimaging objects

`neuro-resample` *Resampling Methods for Neuroimaging Objects*

Description

Methods for resampling neuroimaging objects to different spaces and dimensions

`NeuroBucket-class` *NeuroBucket*

Description

a four-dimensional image that consists of a sequence of labeled image volumes backed by a list

Slots

`labels` the names of the sub-volumes contained in the bucket

`data` a list of `NeuroVol` instances with names corresponding to volume labels

`NeuroHyperVec` *Constructor for NeuroHyperVec class*

Description

Constructor for NeuroHyperVec class

Usage

```
NeuroHyperVec(data, space, mask)
```

Arguments

`data`	A matrix or three-dimensional array containing the data.
`space`	A `NeuroSpace` object defining the spatial dimensions.
`mask`	A mask volume (array, vector, or `LogicalNeuroVol`).

Value

A new `NeuroHyperVec` object.

See Also

`NeuroSpace`, `LogicalNeuroVol`

Examples

```
# Create a 5D space (10x10x10 spatial, 2 trials, 2 features)
space <- NeuroSpace(c(10,10,10,2,2))

# Create a mask for the spatial dimensions
space3d <- NeuroSpace(c(10,10,10))
mask_data <- array(TRUE, dim=c(10,10,10))  # All voxels active
mask <- LogicalNeuroVol(mask_data, space3d)

# Create data in the format expected by NeuroHyperVec:
# 3D array with dimensions [features x trials x voxels]
n_features <- 2
n_trials <- 2
n_voxels <- sum(mask_data)  # 1000 voxels
data_array <- array(rnorm(n_features * n_trials * n_voxels),
                    dim = c(n_features, n_trials, n_voxels))

# Create the NeuroHyperVec object
hvec <- NeuroHyperVec(data_array, space, mask)
```

NeuroHyperVec-class *NeuroHyperVec Class*

Description

A class representing a five-dimensional brain image, where the first three dimensions are spatial, the fourth dimension is typically time or trials, and the fifth dimension represents features within a trial.

The NeuroHyperVec class provides an efficient container for five-dimensional neuroimaging data where spatial dimensions are sparse. It is particularly suited for analyses involving multiple features per trial/timepoint, such as basis functions, spectral components, or multi-modal measurements.

Usage

```
## S4 method for signature 'NeuroHyperVec,ANY,ANY,ANY'
x[i, j, k, l, m, ..., drop = TRUE]
```

Arguments

x	The NeuroHyperVec object
i, j, k, l, m	Indices for each dimension
...	Additional arguments (not used)
drop	Whether to drop dimensions of length 1

Details

Five-Dimensional Sparse Neuroimaging Data Container

The class organizes data in a 5D structure:

- Dimensions 1-3: Spatial coordinates (x, y, z)
- Dimension 4: Trials or timepoints
- Dimension 5: Features or measurements

Data is stored internally as a three-dimensional array for efficiency:

- Dimensions 1: Features (dimension 5)
- Dimensions 2: Trials (dimension 4)
- Dimensions 3: Voxels (flattened spatial)

Key features:

- Memory-efficient sparse storage of spatial dimensions
- Fast access to feature vectors and time series
- Flexible indexing across all dimensions
- Maintains spatial relationships and metadata

Slots

`mask` An object of class `LogicalNeuroVol` defining the sparse spatial domain of the brain image.

`data` A 3D array with dimensions [features x trials x voxels] containing the neuroimaging data.

`space` A `NeuroSpace` object representing the dimensions and voxel spacing of the neuroimaging data.

`lookup_map` An integer vector for O(1) spatial index lookups.

`mask` A `LogicalNeuroVol` object defining the spatial mask.

`data` A three-dimensional array with dimensions [features x trials x voxels] containing the data.

`space` A `NeuroSpace` object defining the 5D space.

`lookup_map` An integer vector for O(1) spatial index lookups.

See Also

`NeuroVec`, `LogicalNeuroVol`, `NeuroSpace`

Examples

```
# Create a simple 5D dataset (10x10x10 spatial, 5 trials, 3 features)
dims <- c(10, 10, 10)
space <- NeuroSpace(c(dims, 5, 3))

# Create a sparse mask (20% of voxels)
mask_data <- array(runif(prod(dims)) < 0.2, dims)
mask <- LogicalNeuroVol(mask_data, NeuroSpace(dims))
```

```
# Generate random data for active voxels
n_voxels <- sum(mask_data)
data <- array(rnorm(3 * 5 * n_voxels), dim = c(3, 5, n_voxels))  # [features x trials x voxels]

# Create NeuroHyperVec object
hvec <- NeuroHyperVec(data, space, mask)

# Access operations
# Get data for specific voxel across all trials/features
series(hvec, 5, 5, 5)

# Extract a 3D volume for specific trial and feature
hvec[,,,2,1]
```

`NeuroObj-class` *NeuroObj Class*

Description

Base class for all neuroimaging data objects with a Cartesian spatial representation. This class provides a foundation for more specific neuroimaging data structures.

Slots

`space` An object of class `NeuroSpace` representing the geometry of the image object.

`header` A `list` holding the raw header of the file the object was read from, empty for objects built in memory. `NeuroSpace` records the geometry; this records everything else the file said – repetition time, units, intent, description, slice timing, the qform/sform codes – so that writing the object back does not have to invent it. Use `header` to read it rather than touching the slot.

See Also

`NeuroSpace-class`, `NeuroSlice-class`, `NeuroVol-class`

`NeuroSlice` *NeuroSlice: 2D Neuroimaging Data Container*

Description

Creates a `NeuroSlice` object representing a two-dimensional slice of neuroimaging data with associated spatial information. This class is particularly useful for working with individual slices from volumetric neuroimaging data or for visualizing 2D cross-sections.

Usage

```
NeuroSlice(data, space, indices = NULL)
```

Arguments

data	A vector or matrix containing the slice data values.
space	An object of class NeuroSpace defining the spatial properties (dimensions, spacing, origin) of the slice.
indices	Optional integer vector. When data is provided as a 1D vector, indices specifies the linear indices where the data values should be placed in the 2D slice. Useful for creating sparse slices. Default is NULL.

Details

Two-Dimensional Neuroimaging Data Slice

Value

A new object of class NeuroSlice.

Input Validation

The function performs several validation checks:

- Verifies that space is 2-dimensional
- Ensures data dimensions are compatible with space
- Validates indices when provided for sparse initialization

Data Handling

The function supports two initialization modes:

- Dense mode (indices = NULL):
  - Data is reshaped if necessary to match space dimensions
  - Dimensions must match exactly after reshaping
- Sparse mode (indices provided):
  - Creates a zero-initialized matrix matching space dimensions
  - Places data values at specified indices

See Also

NeuroSpace for defining spatial properties, NeuroVol for 3D volumetric data, plot for visualization methods

Examples

```
# Create a 64x64 slice space
slice_space <- NeuroSpace(c(64, 64), spacing = c(2, 2))

# Example 1: Dense slice from matrix
slice_data <- matrix(rnorm(64*64), 64, 64)
dense_slice <- NeuroSlice(slice_data, slice_space)

# Example 2: Dense slice from vector
vec_data <- rnorm(64*64)
vec_slice <- NeuroSlice(vec_data, slice_space)

# Example 3: Sparse slice with specific values
n_points <- 100
sparse_data <- rnorm(n_points)
sparse_indices <- sample(1:(64*64), n_points)
sparse_slice <- NeuroSlice(sparse_data, slice_space, indices = sparse_indices)
```

NeuroSlice-class *NeuroSlice Class*

Description

Represents a two-dimensional brain image slice. This class extends both the `array` class for data storage and the `NeuroObj` class for spatial information.

Details

NeuroSlice objects are typically used to represent individual slices of 3D brain volumes or 2D projections of 3D data. They inherit the spatial properties from NeuroObj and the data storage capabilities from array.

See Also

`NeuroObj-class`, `NeuroVol-class`

Examples

```
# Create a simple 2D brain slice
slice_data <- matrix(rnorm(64*64), 64, 64)
slice_space <- NeuroSpace(dim=c(64L, 64L), origin=c(0, 0), spacing=c(1, 1))
brain_slice <- new("NeuroSlice", .Data=slice_data, space=slice_space)
```

NeuroSpace *NeuroSpace: Spatial Reference System for Neuroimaging Data*

Description

The NeuroSpace class defines the spatial properties and coordinate system of neuroimaging data. It encapsulates all information needed to map between voxel indices and real-world coordinates, including dimensions, voxel spacing, origin, axis orientation, and coordinate transformations.

Usage

```
NeuroSpace(dim, spacing = NULL, origin = NULL, axes = NULL, trans = NULL)
```

Arguments

dim	An integer vector specifying the dimensions of the image grid. Must be positive.
spacing	A numeric vector specifying the physical size of each voxel (typically in millimeters). Must be positive. If NULL, defaults to ones.
origin	A numeric vector specifying the real-world coordinates of the first voxel. If NULL, defaults to zeros.
axes	An AxisSet object defining the orientation and ordering of the coordinate axes. If NULL, defaults to standard neurological convention (Left-Posterior-Inferior for 3D).
trans	A transformation matrix mapping voxel indices to world coordinates. If NULL, constructed from spacing and origin.

Details

Spatial Reference System for Neuroimaging Data

Value

A new NeuroSpace object

Coordinate Systems

NeuroSpace manages two coordinate systems:

- Voxel coordinates: Zero-based indices into the image grid
- World coordinates: Real-world coordinates (typically in millimeters)

The transformation between these systems is defined by:

- Voxel spacing (physical size of voxels)
- Origin (world coordinates of first voxel)
- Axis orientation (how image axes map to anatomical directions)

Validation

The constructor performs extensive validation:

- All dimensions must be positive integers
- All spacing values must be positive
- Origin and spacing must have matching lengths
- Transformation matrix must be invertible

References

For details on neuroimaging coordinate systems:

- Brett, M., Johnsrude, I. S., & Owen, A. M. (2002). The problem of functional localization in the human brain. Nature Reviews Neuroscience, 3(3), 243-249.
- Evans, A. C., et al. (1993). 3D statistical neuroanatomical models from 305 MRI volumes. Nuclear Science Symposium and Medical Imaging Conference.

See Also

`AxisSet` for axis orientation specification, `coord_to_index` for coordinate conversion, `index_to_coord` for inverse coordinate conversion, `NeuroObj` for objects using NeuroSpace

Examples

```
# Create a standard 3D space (64x64x40 voxels, 2mm isotropic)
space_3d <- NeuroSpace(
  dim = c(64L, 64L, 40L),
  spacing = c(2, 2, 2),
  origin = c(-90, -126, -72)
)

# Check properties
dim(space_3d)           # Image dimensions
spacing(space_3d)       # Voxel sizes
origin(space_3d)        # World-space origin

# Create a 2D slice space
space_2d <- NeuroSpace(
  dim = c(128L, 128L),
  spacing = c(1.5, 1.5),
  origin = c(-96, -96)
)

# Convert between coordinate systems
world_coords <- c(0, 0, 0)
vox_idx <- coord_to_index(space_3d, world_coords)
back_to_world <- index_to_coord(space_3d, vox_idx)
```

NeuroSpace-class *NeuroSpace Class*

Description

The NeuroSpace class represents the geometric properties of a brain image, including its dimensions, origin, spacing, axes, and coordinate transformations. It provides a comprehensive framework for handling spatial information in neuroimaging data analysis.

Slots

`dim` An integer vector representing the grid dimensions of the image.

`origin` A numeric vector representing the coordinates of the spatial origin.

`spacing` A numeric vector representing the dimensions (in mm) of the grid units (voxels).

`axes` A named `AxisSet` object representing the set of spatial axes in the untransformed native grid space.

`trans` A matrix representing an affine transformation that converts grid coordinates to real-world coordinates.

`inverse` A matrix representing an inverse transformation that converts real-world coordinates to grid coordinates.

Validity

A `NeuroSpace` object is considered valid if:

- The length of the `dim` slot is equal to the lengths of the `spacing`, `origin`, and number of axes in the `axes` slots.
- The `dim` slot contains only non-negative values.

Methods

The following methods are available for `NeuroSpace` objects:

- `dim`: Get the dimensions of the space.
- `origin`: Get or set the origin of the space.
- `spacing`: Get or set the spacing of the space.
- `axes`: Get the axes of the space.
- `trans`: Apply the affine transformation to coordinates.

Usage

The `NeuroSpace` class is fundamental in representing and manipulating the spatial properties of neuroimaging data. It is used extensively throughout the package for operations that require spatial information, such as image registration, resampling, and coordinate transformations.

References

For more information on spatial transformations in neuroimaging: Brett, M., Johnsrude, I. S., & Owen, A. M. (2002). The problem of functional localization in the human brain. Nature Reviews Neuroscience, 3(3), 243-249.

See Also

AxisSet-class for details on the axis set representation. NeuroVol-class and NeuroVec-class for classes that use NeuroSpace.

Examples

```
# Create a NeuroSpace object
space <- NeuroSpace(dim = c(64L, 64L, 64L),
                    origin = c(0, 0, 0),
                    spacing = c(1, 1, 1))

# Get the dimensions
dim(space)
```

NeuroVec-class *NeuroVec Class*

Description

This S4 class represents a four-dimensional brain image, which is used to store and process time series neuroimaging data such as fMRI or 4D functional connectivity maps. The class extends the basic functionality of NeuroObj.

The NeuroVec class represents a vectorized form of neuroimaging data, supporting both in-memory and file-backed data modes. It provides efficient data storage and access methods and integrates with the spatial reference system provided by NeuroSpace.

Usage

```
NeuroVec(
  data,
  space = NULL,
  mask = NULL,
  label = "",
  volume_labels = character()
)
```

Arguments

data	The image data. This can be: • A matrix (voxels x time points) • A 4D array • A list of NeuroVol objects If a list of NeuroVol objects is provided, the geometric space (NeuroSpace) will be inferred from the constituent volumes, which must all be identical.
space	An optional NeuroSpace object defining the spatial properties of the image. Not required if data is a list of NeuroVol objects.
mask	An optional logical array specifying which voxels to include. If provided, a SparseNeuroVec object will be created.
label	A character string providing a label for the NeuroVec object. Default is an empty string.
volume_labels	Optional character vector of length dim(x)[4] giving per-volume labels.

Details

NeuroVec objects are designed to handle 4D neuroimaging data, where the first three dimensions represent spatial coordinates, and the fourth dimension typically represents time or another series dimension. This structure is particularly useful for storing and analyzing functional MRI data, time series of brain states, or multiple 3D volumes in a single object.

The function performs several operations:

- If data is a list of NeuroVol objects, it combines them into a single 4D array.
- It checks that the dimensions of data match the provided space.
- Depending on whether a mask is provided, it creates either a DenseNeuroVec or a SparseNeuroVec object.

Value

A concrete instance of the NeuroVec class:

- If mask is provided: a SparseNeuroVec object
- Otherwise: a DenseNeuroVec object

Slots

space A NeuroSpace object defining the spatial properties of the image.

label A character string providing a label for the NeuroVec object.

volume_labels An optional character vector of per-volume labels with length 0 or dim(x)[4].

Methods

Methods specific to NeuroVec objects may include operations for time series analysis, 4D data manipulation, and extraction of 3D volumes or time courses.

Usage

To create a NeuroVec object, use the constructor function `NeuroVec()`. This function should handle the appropriate initialization of the 4D data structure and associated spatial information.

See Also

`NeuroObj-class` for the parent class. `DenseNeuroVec-class` and `SparseNeuroVec-class` for specific implementations.

`NeuroSpace` for spatial information, `sub_vector` for subsetting routines, and `index_to_coord` for coordinate conversion. `DenseNeuroVec-class`, `SparseNeuroVec-class` for the specific NeuroVec types. `NeuroVol-class` for 3D volumetric data.

Examples

```
# Load an example 4D brain image
example_4d_image <- read_vec(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Create a NeuroVec object
neuro_vec <- NeuroVec(data = array(rnorm(64*64*32*10), dim = c(64, 64, 32, 10)),
                      space = NeuroSpace(dim = c(64, 64, 32,10),
                      origin = c(0, 0, 0),
                      spacing = c(3, 3, 4)))


dim(neuro_vec)

# Extract a single 3D volume (e.g., the first time point)
first_volume <- neuro_vec[[1]]


# Load an example 4D brain image
example_file <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
example_4d_image <- read_vec(example_file)

# Create a DenseNeuroVec object
dense_vec <- NeuroVec(data = example_4d_image@.Data,
                      space = space(example_4d_image))
print(dense_vec)

# Create a SparseNeuroVec object with a mask
mask <- array(runif(prod(dim(example_4d_image)[1:3])) > 0.5,
              dim = dim(example_4d_image)[1:3])
sparse_vec <- NeuroVec(data = example_4d_image@.Data,
                       space = space(example_4d_image),
                       mask = mask)
print(sparse_vec)
```

NeuroVecSeq *NeuroVecSeq: A Container for Sequential NeuroVec Objects*

Description

The NeuroVecSeq class provides a container for managing a sequence of NeuroVec objects, particularly useful for handling time series or multi-session neuroimaging data where each segment may have different lengths.

Constructs a NeuroVecSeq object to represent a variable-length sequence of NeuroVec objects. This is particularly useful for managing time series data where different segments may have different lengths.

Usage

```
NeuroVecSeq(...)
```

Arguments

...	One or more instances of type NeuroVec.

Details

NeuroVecSeq objects store:

- A list of NeuroVec objects, each potentially with different time dimensions
- The lengths of each constituent NeuroVec
- A combined NeuroSpace object representing the total space

The class provides methods for:

- Accessing individual time points across all vectors
- Extracting subsequences
- Computing statistics across the sequence
- Linear access to the underlying data

The function performs several validations:

- Ensures all inputs are NeuroVec objects
- Verifies spatial compatibility
- Combines spatial information appropriately

Value

A NeuroVecSeq object containing:

- The provided NeuroVec objects
- Associated space information
- Length information for each vector

Methods

[[Extract a single volume at a specified time point

length Get the total number of time points

sub_vector Extract a subsequence of volumes

linear_access Access data linearly across all vectors

See Also

NeuroVec for the base vector class, NeuroSpace for spatial information

Examples

```
# Create some example NeuroVec objects
v1 <- NeuroVec(array(0, c(5, 5, 5, 2)),
               space = NeuroSpace(dim = c(5, 5, 5, 2)))
v2 <- NeuroVec(array(1, c(5, 5, 5, 4)),
               space = NeuroSpace(dim = c(5, 5, 5, 4)))
v3 <- NeuroVec(array(2, c(5, 5, 5, 6)),
               space = NeuroSpace(dim = c(5, 5, 5, 6)))

# Combine them into a sequence
vs <- NeuroVecSeq(v1, v2, v3)

# Access properties
length(vs)  # Total time points
vs[[5]]     # Get the 5th volume

# Extract a subsequence
sub_seq <- sub_vector(vs, 1:5)


# Create sample vectors
v1 <- NeuroVec(array(0, c(5, 5, 5, 2)),
               space = NeuroSpace(dim = c(5, 5, 5, 2)))
v2 <- NeuroVec(array(0, c(5, 5, 5, 4)),
               space = NeuroSpace(dim = c(5, 5, 5, 4)))

# Combine into sequence
vs <- NeuroVecSeq(v1, v2)
print(vs)
```

NeuroVecSeq-class *NeuroVecSeq Class*

Description

A concatenated sequence of NeuroVec instances.

Slots

`vecs` The sequences of `NeuroVec` instances

`lens` The number of volumes in each `NeuroVec` sequence

`NeuroVecSource` *NeuroVecSource*

Description

This function constructs a NeuroVecSource object, which represents the source of a four-dimensional brain image.

Usage

```
NeuroVecSource(file_name, indices = NULL, mask = NULL)
```

Arguments

`file_name`	The name of the 4-dimensional image file.
`indices`	An optional integer vector specifying the subset of volume indices to load. If not provided, all volumes will be loaded.
`mask`	An optional logical array or `NeuroVol` object defining the subset of voxels to load. If provided, a SparseNeuroVecSource object will be created.

Details

If a `mask` is supplied, it should be a `LogicalNeuroVol` or `NeuroVol` instance. If the latter, then the mask will be defined by nonzero elements of the volume.

Value

An instance of the `NeuroVecSource` class.

`NeuroVecSource-class` *NeuroVecSource Class*

Description

A class used to produce a `NeuroVec` instance.

Slots

`indices` An `integer` vector representing the indices of the volumes to be loaded.

See Also

`FileSource-class`, `NeuroVec-class`

NeuroVol *NeuroVol: 3D Neuroimaging Volume Class*

Description

The NeuroVol class encapsulates 3D volumetric neuroimaging data. It provides methods for accessing slices, performing spatial transformations, and integrating with the spatial reference provided by NeuroSpace.

Usage

```
NeuroVol(data, space, label = "", indices = NULL)
```

Arguments

data	A 3D array containing the volumetric data.
space	An object of class NeuroSpace defining the spatial properties.
label	A character string providing a label for the volume (default: "").
indices	An optional vector of indices for sparse representation (default: NULL).

Value

A NeuroVol object.

Examples

```
bspace <- NeuroSpace(c(64,64,64), spacing=c(1,1,1))
dat <- array(rnorm(64*64*64), c(64,64,64))
bvol <- NeuroVol(dat,bspace, label="test")
```

NeuroVol-class *NeuroVol Class*

Description

Base class for representing 3D volumetric neuroimaging data. This class extends NeuroObj to provide a foundation for various types of 3D brain images.

Details

NeuroVol serves as an abstract base class for more specific 3D neuroimaging data structures. It inherits spatial properties from NeuroObj but does not specify a particular data storage method.

See Also

NeuroObj-class, DenseNeuroVol-class

NeuroVolSource *Constructor for NeuroVolSource*

Description

Constructor for NeuroVolSource

Usage

```
NeuroVolSource(input, index = 1)
```

Arguments

input	the input file name
index	the image subvolume index

Value

a new instance of type NeuroVolSource

NiftiExtension *Create a NIfTI Extension*

Description

Constructor function for creating a NiftiExtension-class object with proper padding to ensure the size is a multiple of 16 bytes.

Usage

```
NiftiExtension(ecode, data)
```

Arguments

ecode	Integer extension code. See NiftiExtensionCodes for known codes. Common values: 4 (AFNI), 6 (comment), 32 (CIFTI).
data	The extension data. Can be: • A character string (will be converted to raw with null terminator) • A raw vector (used as-is)

Details

The function automatically handles padding to ensure the total extension size (esize) is a multiple of 16 bytes, as required by the NIfTI specification. The esize includes the 8-byte header (esize + ecode fields).

Value

A NiftiExtension-class object.

See Also

NiftiExtension-class, NiftiExtensionCodes

Examples

```
# Create a comment extension
ext <- NiftiExtension(ecode = 6L, data = "This is a comment")
ext@ecode
ext@esize

# Create an AFNI extension with XML data
afni_xml <- '<?xml version="1.0"?><AFNI_attributes></AFNI_attributes>'
afni_ext <- NiftiExtension(ecode = 4L, data = afni_xml)
```

NiftiExtension-class *NiftiExtension Class*

Description

Represents a single NIfTI header extension block. NIfTI extensions allow additional metadata to be stored with the image file.

Usage

```
## S4 method for signature 'NiftiExtension'
show(object)
```

Arguments

object	A NiftiExtension object.

Details

NIfTI-1.1 extensions follow this structure:

- Bytes 0-3: esize (int32) - total extension size, must be multiple of 16
- Bytes 4-7: ecode (int32) - extension code identifying format
- Bytes 8-(esize-1): edata - the actual extension data

Extensions are chained sequentially after the NIfTI header (byte 352) until the vox_offset is reached.

Slots

`ecode` An `integer` extension code identifying the type of extension. See `NiftiExtensionCodes` for known codes.

`esize` An `integer` giving the total size of the extension in bytes, including the 8-byte header (esize + ecode). Must be a multiple of 16.

`edata` A `raw` vector containing the extension data (length = esize - 8).

See Also

`NiftiExtensionCodes` for registered extension codes. `NiftiExtensionList-class` for a collection of extensions. `parse_extension` for parsing extension data.

Examples

```
# Create a simple comment extension
comment_text <- "This is a test comment"
ext <- NiftiExtension(ecode = 6L, data = comment_text)

# Access the extension code
ext@ecode
```

NiftiExtensionCodes *Known NIfTI Extension Codes*

Description

A named integer vector of registered NIfTI extension codes. These codes identify the format/type of extension data.

Usage

```
NiftiExtensionCodes
```

Format

Named integer vector where names describe the extension type:

ignore 0 - Unknown/private format (not recommended)

DICOM 2 - DICOM format (attribute tags and values)

AFNI 4 - AFNI group (ASCII XML attributes)

comment 6 - Plain text comment

XCEDE 8 - XCEDE format

jimdiminfo 10 - JIM dimension info

workflow_fwds 12 - Workflow forwards

FreeSurfer 14 - FreeSurfer format

pypickle 16 - Python pickle

MiND_ident 18 - MiND identifier

b_value 20 - B-value (diffusion)

spherical_direction 22 - Spherical direction

DT_component 24 - DT component

SHC_degreeorder 26 - SHC degree order

voxbo 28 - VoxBo format

Caret 30 - Caret format

CIFTI 32 - CIFTI format

variable_frame_timing 34 - Variable frame timing

eval 38 - Eval

MATLAB 40 - MATLAB format

Quantiphyse 42 - Quantiphyse

MRS 44 - MRS NIfTI

Examples

```
# Get the code for AFNI extensions
NiftiExtensionCodes["AFNI"]  # Returns 4

# Get the name for a code
names(NiftiExtensionCodes)[NiftiExtensionCodes == 4]  # Returns "AFNI"
```

NiftiExtensionList-class

NiftiExtensionList Class

Description

A validated list containing zero or more NiftiExtension-class objects. This class ensures type safety when working with collections of NIfTI extensions.

Usage

```
## S4 method for signature 'NiftiExtensionList'
show(object)
```

Arguments

object	A NiftiExtensionList object.

Details

The class extends `list` and enforces that all elements must be `NiftiExtension` objects. This provides a clean container for managing multiple extensions attached to a NIfTI file.

See Also

`NiftiExtension-class` for individual extension objects. `extensions` for accessing extensions from image objects.

Examples

```
# Create an empty extension list
ext_list <- new("NiftiExtensionList")

# Create a list with extensions
ext1 <- NiftiExtension(ecode = 6L, data = "Comment 1")
ext2 <- NiftiExtension(ecode = 6L, data = "Comment 2")
ext_list <- new("NiftiExtensionList", list(ext1, ext2))
```

NIFTIMetaInfo *Create NIFTI Format Metadata Object*

Description

Creates a NIFTIMetaInfo object containing format-specific metadata for NIFTI format neuroimaging files.

Usage

```
NIFTIMetaInfo(descriptor, nifti_header)
```

Arguments

`descriptor`	NIFTIFormat object specifying file format details
`nifti_header`	List containing NIFTI header information

Details

Create NIFTIMetaInfo Object

The NIFTIMetaInfo object extends MetaInfo with NIFTI-specific features:

- NIFTI header fields (qform, sform matrices)
- Data scaling (slope, intercept)
- File organization (separate vs. single file)
- Orientation information

Validation ensures:

- Valid NIFTI format
- Consistent dimensions
- Valid transformation matrices
- Proper data scaling

Value

A NIFTIMetaInfo object

See Also

MetaInfo

Examples

```
# Read NIFTI header
header <- read_header(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Create format descriptor
fmt <- new("NIFTIFormat",
           file_format = "NIFTI",
           header_encoding = "raw",
           header_extension = "nii",
           data_encoding = "raw",
           data_extension = "nii")

# Create metadata
meta <- NIFTIMetaInfo(fmt, header@header)

# Check dimensions
dim(meta)
```

None *Pre-defined null axis*

Description

Pre-defined null axis

Usage

None

Format

An object of class NamedAxis of length 1.

not-methods *Logical Negation for Neuroimaging Volumes*

Description

Logical negation (`!`) for neuroimaging volumes. Returns a `LogicalNeuroVol` where non-zero voxels become `FALSE` and zero voxels become `TRUE`.

Usage

```
## S4 method for signature 'DenseNeuroVol'
!x

## S4 method for signature 'SparseNeuroVol'
!x
```

Arguments

`x`	A neuroimaging volume object.

Value

A `LogicalNeuroVol`.

Examples

```
sp <- NeuroSpace(c(5L, 5L, 5L), c(1, 1, 1))
mask <- LogicalNeuroVol(array(sample(c(TRUE, FALSE), 125, replace = TRUE),
                              c(5, 5, 5)), sp)
inv <- !mask
```

NullAxis *Pre-defined null axis set*

Description

Pre-defined null axis set

Usage

```
NullAxis
```

Format

An object of class `AxisSet` of length 1.

num_clusters *Number of Clusters*

Description

This function returns the number of clusters in a ClusteredNeuroVol object.

Usage

```
num_clusters(x)

## S4 method for signature 'ClusteredNeuroVec'
num_clusters(x)

## S4 method for signature 'ClusteredNeuroVol'
num_clusters(x)
```

Arguments

x	A ClusteredNeuroVol object.

Value

An integer representing the number of clusters in x.

An integer representing the number of clusters in the input object.

Examples

```
# Create a simple 3D volume and mask
space <- NeuroSpace(c(16, 16, 16), spacing = c(1, 1, 1))
vol_data <- array(rnorm(16^3), dim = c(16, 16, 16))
mask_vol <- LogicalNeuroVol(vol_data > 0, space)

# Get coordinates of masked voxels for clustering
mask_idx <- which(mask_vol)
coords <- index_to_coord(mask_vol, mask_idx)

# Cluster the coordinates into 10 groups using k-means
set.seed(123)  # for reproducibility
kmeans_result <- kmeans(coords, centers = 10)

# Create a clustered volume
clustered_vol <- ClusteredNeuroVol(mask_vol, kmeans_result$cluster)

# Get the number of clusters
n_clusters <- num_clusters(clustered_vol)
n_clusters == 10
```

numericOrMatrix-class *numericOrMatrix Union*

Description

A class union that includes both numeric vectors and matrices.

orientation_utils *Orientation utility functions*

Description

Helper functions for converting between affine matrices, axis-code representations, and array orientation transforms.

Returns the orientation transform that maps from ‘start_ornt‘ to ‘end_ornt‘.

Applies flips and permutations implied by ‘ornt‘ to the first ‘n‘ dimensions of ‘arr‘, where ‘n = nrow(ornt)‘.

Returns the affine mapping transformed array coordinates back to source array coordinates for a transform encoded by ‘ornt‘.

Usage

```
affine_to_orientation(affine, tol = NULL)

orientation_transform(start_ornt, end_ornt)

apply_orientation(arr, ornt)

orientation_inverse_affine(ornt, shape)

orientation_to_axcodes(ornt, labels = NULL)

axcodes_to_orientation(axcodes, labels = NULL)

affine_to_axcodes(affine, labels = NULL, tol = NULL)
```

Arguments

affine	Affine matrix.
tol	Optional singular-value tolerance.
start_ornt	Starting orientation matrix.
end_ornt	Target orientation matrix.
arr	Array-like object.

ornt	Orientation matrix.
shape	Shape of source array.
labels	Optional label pairs per axis.
axcodes	Character vector of axis codes. 'NA' indicates dropped axis.

Details

Orientation matrices ('ornt') use two columns:

- column 1 ('axis') stores the output axis index (1-based),
- column 2 ('flip') stores direction ('1' or '-1').

This is an R counterpart to NiBabel's orientation utilities, adapted to 'neuroim2' conventions.

Value

A 'p x 2' orientation matrix with columns 'axis' and 'flip'.

Orientation matrix representing 'start -> end'.

Reoriented array.

Homogeneous affine matrix of size '(p + 1) x (p + 1)'.

Character vector of axis codes (positive ends), with 'NA' for dropped axes.

Orientation matrix.

Character vector of axis codes.

Examples

```
aff <- diag(4)
ornt <- affine_to_orientation(aff)
orientation_to_axcodes(ornt)

arr <- array(1:24, dim = c(2, 3, 4))
tx <- orientation_transform(
  axcodes_to_orientation(c("R", "A", "S")),
  axcodes_to_orientation(c("A", "R", "S"))
)
out <- apply_orientation(arr, tx)

inv_aff <- orientation_inverse_affine(tx, dim(arr))
inv_aff
```

OrientationList2D *Pre-defined 2D orientation configurations*

Description

A list of standard 2D anatomical orientations used in neuroimaging. Each orientation defines a pair of anatomical axes.

Usage

```
OrientationList2D
```

Format

An object of class `list` of length 24.

OrientationList3D *Pre-defined 3D orientation configurations*

Description

A list of standard 3D anatomical orientations used in neuroimaging. Each orientation defines a triplet of anatomical axes.

Usage

```
OrientationList3D
```

Format

An object of class `list` of length 48.

origin *Extract Image Origin*

Description

Extract Image Origin

Usage

```
origin(x)

## S4 method for signature 'NeuroHyperVec'
origin(x)

## S4 method for signature 'NeuroSpace'
origin(x)

## S4 method for signature 'NeuroVol'
origin(x)

## S4 method for signature 'NeuroVec'
origin(x)
```

Arguments

x	an object with an origin

Value

A numeric vector giving the origin of x.

Examples

```
bspace <- NeuroSpace(c(10,10,10), c(2,2,2))
stopifnot(origin(bspace) == c(0,0,0))
```

parse_afni_extension *Parse AFNI Extension*

Description

Parses an AFNI extension (ecode = 4) containing XML-formatted attributes.

Usage

```
parse_afni_extension(ext, as_xml = TRUE)
```

Arguments

ext	A NiftiExtension-class object with ecode = 4.
as_xml	Logical; if TRUE (default) and xml2 is available, returns an xml_document object. Otherwise returns the raw XML string.

Details

AFNI stores dataset attributes in an XML format within the NIfTI extension. The XML contains elements like HISTORY_NOTE, volume labels, tagged points, and other AFNI-specific metadata.

Value

If as_xml = TRUE and xml2 is available, returns an xml_document. Otherwise returns a character string containing the XML.

See Also

get_afni_attribute for extracting specific AFNI attributes.

Examples

```
## Not run:
# Read a NIfTI file with AFNI extension
hdr <- read_nifti_header("afni_file.nii")
afni_ext <- hdr$extensions[[1]]
parsed <- parse_afni_extension(afni_ext)

## End(Not run)
```

---

parse_extension *Parse NIfTI Extension Data*

Description

Parses the raw data in a NIfTI extension based on its extension code. Provides specialized parsing for known extension types.

Usage

```
parse_extension(ext, ...)
```

Arguments

ext	A NiftiExtension-class object.
...	Additional arguments passed to type-specific parsers.

Value

Parsed data in an appropriate format:

- ecode 4 (AFNI): An XML document (if xml2 available) or character string
- ecode 6 (comment): Character string
- Other codes: Raw vector (unchanged)

See Also

parse_afni_extension for AFNI-specific parsing.

Examples

```
# Parse a comment extension
ext <- NiftiExtension(ecode = 6L, data = "Test comment")
parse_extension(ext)  # Returns "Test comment"
```

---

partition *Partition an image into a set of disjoint clusters*

Description

This function partitions an image into a set of disjoint clusters using k-means clustering.

Usage

```
partition(x, k, ...)

## S4 method for signature 'LogicalNeuroVol,integer'
partition(x, k)

## S4 method for signature 'LogicalNeuroVol,numeric'
partition(x, k)

## S4 method for signature 'DenseNeuroVol,numeric'
partition(x, k)
```

Arguments

x	the image to partition, represented as a 3D array.
k	the number of clusters to form.
...	additional arguments passed to the kmeans function.

Value

a 3D array where each voxel is assigned to a cluster.

See Also

kmeans

Examples

```
# Load an example 3D image
library(neuroim2)
img <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Partition the image into 5 clusters using default options
clusters <- partition(img, 5)
```

---

patch_set *Generate a set of coordinate "patches" of fixed size from an image object.*

Description

Generate a set of coordinate "patches" of fixed size from an image object.

Usage

```
patch_set(x, dims, mask, ...)
```

Arguments

x	the object to extract patches from
dims	a vector indicating the dimensions of the patches
mask	mask indicating the valid patch area
...	additional args

Value

A list of coordinate patches, each representing a fixed-size region of the input object.

Examples

```
# Create a simple 3D volume
space <- NeuroSpace(c(10,10,10), spacing=c(1,1,1))
vol <- NeuroVol(array(rnorm(1000), c(10,10,10)), space)

# Create a mask with some active voxels
mask <- LogicalNeuroVol(vol > 0, space)

# Extract 3x3x3 patches centered at each active voxel
patches <- patch_set(vol, dims=c(3,3,3), mask=mask)
```

```
# Access the first patch
patch1 <- patches[[1]]
dim(patch1)  # Should be c(27) (flattened 3x3x3 patch)
```

---

patch_set,NeuroVol,numeric,missing-method *Create a patch set from a NeuroVol object*

Description

This function creates a patch set from a NeuroVol object given specified dimensions

This function creates a patch set from a NeuroVol object given specified dimensions and a mask.

Usage

```
## S4 method for signature 'NeuroVol,numeric,missing'
patch_set(x, dims, mask, ...)

## S4 method for signature 'NeuroVol,numeric,LogicalNeuroVol'
patch_set(x, dims, mask, ...)
```

Arguments

x	a NeuroVol object
dims	the dimensions of the patch
mask	the mask defining the valid patch centers
...	additional args

Value

A deferred list of patches.

A deferred list of patches.

---

perm_mat *Extract permutation matrix associated with an image*

Description

A permutation matrix defines how the native voxel coordinates can be transformed to standard (LPI) orientation.

Usage

```
perm_mat(x, ...)

## S4 method for signature 'AxisSet2D'
perm_mat(x, ...)

## S4 method for signature 'AxisSet3D'
perm_mat(x, ...)

## S4 method for signature 'NeuroSpace'
perm_mat(x, ...)
```

Arguments

x	A NeuroSpace object
...	Additional arguments (not used)

Details

a permutation matrix can be used to convert between cardinal image orientations. For example, if an image is stored in "RPI" (Right-Posterior-Inferior) format, a coordinate in this space can be converted to LPI (Left-Posterior-Inferior) by multiplying a coordinate vector by the permutation matrix.

Value

A numeric N x N `matrix` representing the permutation transform, where N is the dimensionality of the image.

A matrix representing the axis directions

A matrix representing the axis directions

A numeric N x N `matrix` representing the permutation transform, where N is the dimensionality of the image.

Examples

```
fname <- system.file("extdata", "global_mask_v4.nii", package="neuroim2")
vol <- read_vol(fname)
pmat <- perm_mat(space(vol))

vox <- c(12,12,8)
pvox <- vox %*% perm_mat(space(vol))

stopifnot(all(pvox == c(-12,12,8)))
```

plot,NeuroSlice-method *Plot a NeuroSlice*

Description

Display slices of a NeuroVol as a faceted montage.

Usage

```
## S4 method for signature 'NeuroSlice,ANY'
plot(
  x,
  cmap = gray(seq(0, 1, length.out = 255)),
  irange = range(x, na.rm = TRUE),
  legend = TRUE
)

## S4 method for signature 'NeuroVol,missing'
plot(
  x,
  y,
  cmap = "grays",
  zlevels = NULL,
  along = 3L,
  irange = range(x, na.rm = TRUE),
  thresh = c(0, 0),
  alpha = 1,
  legend = TRUE
)

## S4 method for signature 'NeuroVol,NeuroVol'
plot(
  x,
  y,
  cmap = "grays",
  zlevels = NULL,
  along = 3L,
  ov_cmap = NULL,
  ov_alpha = 0.5,
  ov_thresh = 0
)
```

Arguments

x	the background volume to display.

cmap	palette name or hex-color vector for the background (default "grays"). See resolve_cmap.
irange	numeric length-2 intensity range for the color scale.
legend	logical; show the colour bar?
y	optional overlay volume (same dimensions as x). When supplied, the plot is rendered as a background + overlay composite.
zlevels	integer slice indices to display. Default: 9 evenly-spaced slices (3×3 grid).
along	native voxel-grid axis along which to slice. For canonically ordered images, 1 = sagittal, 2 = coronal, and 3 = axial (the default). Display orientation is inferred from the image affine.
thresh	a 2-element vector indicating the lower and upper transparency thresholds.
alpha	opacity for the background layer (0–1).
ov_cmap	overlay palette; NULL (default) chooses a two-sided palette for signed maps and a sequential one otherwise.
ov_alpha	overlay opacity (default 0.5).
ov_thresh	overlay threshold; values with $\|v\| <$ ov_thresh become transparent (default 0).

Details

The plot method uses ggplot2 to create a raster visualization of the slice data. The slice's anatomical axis metadata determines permutation and flips, so right/anterior/superior point toward increasing screen coordinates. The intensity values are mapped to colors using the specified colormap and range.

when 'x' is a NeuroSlice object, the plot method returns a ggplot2 object containing the raster visualization of the slice data. The plot can be further customized using standard ggplot2 functions.

When a second volume y is supplied it is treated as an overlay (e.g.\ a statistical map) composited on top of x with adjustable transparency. This delegates to plot_overlay.

Value

a ggplot2 object

See Also

as.raster

as.raster

Examples

```
# Create example slice
slice_space <- NeuroSpace(c(100, 100))
slice_data <- matrix(rnorm(100*100), 100, 100)
slice <- NeuroSlice(slice_data, slice_space)

# Basic plot
plot(slice)
```

```
dat <- matrix(rnorm(100*100), 100, 100)
slice <- NeuroSlice(dat, NeuroSpace(c(100,100)))

plot(slice)
```

---

plot_checkerboard *Checkerboard comparison of two registered volumes*

Description

Alternates tiles from a background volume and a comparison volume on matched slices. This is useful for visual registration QC.

Usage

```
plot_checkerboard(
  bgvol,
  overlay,
  zlevels = NULL,
  along = 3L,
  tile = NULL,
  cmap = "grays",
  bg_range = c("robust", "data"),
  ov_range = c("robust", "data"),
  probs = c(0.02, 0.98),
  ncol = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  draw = FALSE,
  style = c("light", "dark", "report"),
  labels = c("fixed", "moving"),
  legend = TRUE,
  crop = TRUE,
  mask_background = TRUE,
  unit = c("index", "mm"),
  annotate = TRUE,
  assemble = TRUE,
  n_slices = 6L,
  match_intensity = TRUE,
  canvas = NULL,
  interpolate = TRUE,
  focus_brain = TRUE
)
```

Arguments

bgvol	Background/reference 3D volume.
overlay	Comparison 3D volume on the same NeuroSpace grid as 'bgvol'.
zlevels	Slices to plot: indices along 'along' (unit = "index") or world coordinates (unit = "mm"). NULL (default) picks n_slices slices spread over the brain.
along	Native voxel-grid axis for slicing. Display orientation is inferred from the image affine.
tile	Tile width in voxels (the key states the equivalent in mm). NULL (default) picks a clean size in mm giving about ten tiles across the head.
cmap	Palette used to render the normalized checkerboard image.
bg_range, ov_range	Intensity scaling of each image: "robust" (computed over head voxels), "data", or numeric c(lo, hi). Each image is windowed independently so tissue contrast, not a brightness step, is what differs between tiles.
probs	Quantiles for robust scaling.
ncol	Number of columns (NULL = chosen to fill the canvas).
title, subtitle, caption	Optional layout-level labels used when drawing.
draw	Logical; if TRUE, also print the figure immediately (and return it invisibly). By default the figure is returned visibly.
style	Visual style: "light", "dark" or "report".
labels	Length-2 character vector naming the two images in the key.
legend	Logical; draw the key under the panels.
crop	Logical; crop panels to the head bounding box.
mask_background	Logical; show the checker pattern only inside the head (union of both images' foreground), leaving air black.
unit	"index" or "mm": how zlevels is interpreted. Panels are labelled in world coordinates.
annotate	Logical; draw orientation letters on the first panel.
assemble	Logical; return one **patchwork** figure (default) or the list of panel ggplots.
n_slices	Number of automatically chosen slices.
match_intensity	Logical; map the comparison image's intensities onto the reference image's distribution (quantile matching over head voxels) before interleaving, so a brightness or contrast difference between the images does not masquerade as misalignment. Default TRUE.
canvas	Optional c(width, height) in inches to fit the layout to (default: the open device).
interpolate	Logical; smooth the rendered checkerboard (default TRUE), which also softens the head outline.

focus_brain — Logical; interleave tiles only inside the (dilated) bright-tissue mask of bgvol and show the fixed image alone on the scalp, so the seams where registration is judged dominate the figure instead of the stair-stepped head outline. Default TRUE.

Value

A figure (class neuro_fig, a **patchwork** whose layout is re-fitted to the device it is drawn on) when assemble = TRUE or a named list of panel ggplots (assemble = FALSE); invisibly when draw = TRUE.

See Also

Other plot_neuro: plot_edge_overlay(), plot_montage(), plot_ortho(), plot_overlay()

Examples

```
fixed <- read_vol(system.file("extdata", "mni_downsampled.nii.gz", package = "neuroim2"))
moving <- fixed
moving[] <- sqrt(fixed[c(2:dim(fixed)[1], 1), , ])   # shifted, different contrast
p <- plot_checkerboard(fixed, moving)
ggplot2::ggsave(tempfile(fileext = ".png"), p, width = 8, height = 6)
```

---

plot_edge_overlay *Overlay fixed and moving edge maps on a background volume*

Description

Displays a structural/reference background with two edge channels rendered in distinct colors. This is intended for registration QC where fixed/template edges and moving/result edges should coincide.

Usage

```
plot_edge_overlay(
  bgvol,
  fixed_edges,
  moving_edges,
  zlevels = NULL,
  along = 3L,
  bg_cmap = "grays",
  fixed_color = "#2bb8f0",
  moving_color = "#ff3b30",
  agree_color = "#ffd23f",
  bg_range = c("robust", "data"),
  edge_range = c("robust", "data"),
  probs = c(0.02, 0.98),
  edge_thresh = 0,
```

```
  edge_alpha = 0.9,
  ncol = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  draw = FALSE,
  style = c("light", "dark", "report"),
  labels = c("fixed", "moving"),
  legend = TRUE,
  bg_dim = 0.75,
  crop = TRUE,
  unit = c("index", "mm"),
  annotate = TRUE,
  assemble = TRUE,
  n_slices = 6L,
  thin = TRUE,
  compute_edges = FALSE,
  canvas = NULL,
  interpolate = TRUE,
  focus_brain = TRUE
)
```

Arguments

bgvol	Background 3D volume.
fixed_edges	Edge map for the fixed/reference image on the same NeuroSpace grid as 'bgvol'.
moving_edges	Edge map for the moving/result image on the same NeuroSpace grid as 'bgvol'.
zlevels	Slices to plot: indices along 'along' (unit = "index") or world coordinates (unit = "mm"). NULL (default) picks n_slices slices spread over the brain.
along	Native voxel-grid axis for slicing. Display orientation is inferred from the image affine.
bg_cmap	Background palette.
fixed_color, moving_color	Overlay colors for the two edge maps.
agree_color	Colour for contour pixels present in both edge maps (where the images agree), keyed "both"; NA turns the agreement layer and its key entry off.
bg_range, edge_range	"robust" or "data" intensity scaling.
probs	Quantiles for robust scaling.
edge_thresh	Values below this edge magnitude are transparent.
edge_alpha	Global alpha for edge overlays.
ncol	Number of columns (NULL = chosen to fill the canvas).
title, subtitle, caption	Optional layout-level labels used when drawing.

draw	Logical; if TRUE, also print the figure immediately (and return it invisibly). By default the figure is returned visibly.
style	Visual style: "light", "dark" or "report".
labels	Length-2 character vector naming the fixed and moving edge maps in the key (e.g. c("MNI template", "registered EPI")).
legend	Logical; draw the colour key under the panels.
bg_dim	Brightness multiplier (0–1) for the background so the edge colours read clearly.
crop	Logical; crop panels to the head bounding box.
unit	"index" or "mm": how zlevels is interpreted. Panels are labelled in world coordinates.
annotate	Logical; draw orientation letters on the first panel.
assemble	Logical; return one **patchwork** figure (default) or the list of panel ggplots.
n_slices	Number of automatically chosen slices.
thin	Logical; thin edge bands to their ridge lines (1–2 pixels) so the two contours can be compared precisely. Default TRUE.
compute_edges	Logical; if TRUE, fixed_edges and moving_edges are ordinary intensity images (e.g. the template and the registered image) and their edges are computed per slice as the in-plane gradient magnitude, keeping the strongest 12% of head voxels.
canvas	Optional c(width, height) in inches to fit the layout to (default: the open device).
interpolate	Logical; smooth the background and anti-alias the edge contours (default TRUE).
focus_brain	Logical; fade edges that lie outside the (dilated) brain mask of bgvol (bright tissue connected to the centre of the head, which excludes scalp fat), so scalp and skull contours do not dominate the comparison. Default TRUE.

Value

A figure (class neuro_fig, a **patchwork** whose layout is re-fitted to the device it is drawn on) when assemble = TRUE or a named list of panel ggplots (assemble = FALSE); invisibly when draw = TRUE.

See Also

Other plot_neuro: plot_checkerboard(), plot_montage(), plot_ortho(), plot_overlay()

Examples

```
fixed <- read_vol(system.file("extdata", "mni_downsampled.nii.gz", package = "neuroim2"))
moving <- fixed
moving[] <- fixed[c(2:dim(fixed)[1], 1), , ]   # a one-voxel shift
p <- plot_edge_overlay(fixed, fixed, moving, compute_edges = TRUE,
                       labels = c("template", "registered"))
ggplot2::ggsave(tempfile(fileext = ".png"), p, width = 8, height = 6)
```

plot_montage *Montage of slices through a volume*

Description

Draws a grid of slices through one volume (typically a structural image) in the same style as plot_overlay: black tiles cropped to the head, world-coordinate labels, L/R markers on the first tile, and a grid that fills the canvas. Also accepts a list of NeuroSlice objects or plain matrices.

Usage

```
plot_montage(
  x,
  zlevels = NULL,
  along = 3L,
  cmap = "grays",
  range = c("robust", "data"),
  probs = c(0.02, 0.98),
  ncol = NULL,
  downsample = 1L,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  style = c("light", "dark", "report"),
  crop = TRUE,
  interpolate = TRUE,
  cbar_title = "value",
  colorbar = NULL,
  unit = c("index", "mm"),
  annotate = TRUE,
  n_slices = 12L,
  draw = FALSE,
  canvas = NULL
)
```

Arguments

x	A 3D volume, or a list of NeuroSlice objects / matrices.
zlevels	Slices to plot when x is a volume: indices along along (unit = "index", the default) or world coordinates (unit = "mm"). NULL (default) picks n_slices slices spread over the brain.
along	Native voxel-grid axis along which to slice. For canonically ordered images, 1 = sagittal, 2 = coronal, and 3 = axial. Display orientation is inferred from the image affine.
cmap	Palette name or vector (see [resolve_cmap()]).
range	"robust" (quantile-based), "data" (min/max), or an explicit numeric c(lo, hi).

probs — Quantiles for 'range="robust"'.

ncol — Number of columns in the facet layout.

downsample — Integer decimation for speed.

title, subtitle, caption — Optional ggplot labels.

style — Visual style: "light", "dark", or "report" (light card, dark cropped tiles, typography, and a colorbar – matching plot_overlay's report look).

crop, interpolate — Logical; crop to the head bounding box (volume input) / smooth the raster. Both default to TRUE.

cbar_title — Character; the quantity label drawn above the colorbar. Supplying it explicitly also turns the colorbar on.

colorbar — Logical or NULL. NULL (default) shows a slim colorbar only for non-grayscale palettes or when cbar_title is supplied; arbitrary structural intensity units carry no information.

unit — "index" (default) or "mm": how zlevels is interpreted for volume input. Panels are always labelled in world coordinates (mm).

annotate — Logical; draw L/R (or A/P) orientation letters on the first panel.

n_slices — Number of slices chosen automatically when zlevels is NULL. Automatic slices are spread over the extent of the brain (bright tissue), skipping neck, scalp-only and empty planes.

draw — Logical; if TRUE, also print the figure immediately (and return it invisibly). By default it is returned visibly, like any ggplot.

canvas — Optional c(width, height) in inches to fit the layout to (default: the open device, else 10 x 7.5 in).

Value

A figure (class neuro_fig, a **patchwork** wrapping one faceted ggplot with one facet per slice), returned visibly; invisibly when draw = TRUE. Its layout is re-fitted to the device it is drawn on, so ggsave() at any size gives a filled, centred grid.

See Also

Other plot_neuro: plot_checkerboard(), plot_edge_overlay(), plot_ortho(), plot_overlay()

Examples

```
bg <- read_vol(system.file("extdata", "mni_downsampled.nii.gz", package = "neuroim2"))
p <- plot_montage(bg, title = "MNI152 (downsampled)")
ggplot2::ggsave(tempfile(fileext = ".png"), p, width = 8, height = 6)
```

plot_ortho *Orthogonal three-plane view with optional crosshairs and overlay*

Description

Draws sagittal, coronal and axial sections through one point, optionally with a thresholded statistical map on top (the classic "stat map" view). All three views share one physical scale and one head-bounding-box crop, so the crosshair lines up across views.

Usage

```
plot_ortho(
  vol,
  coord = NULL,
  unit = c("index", "mm"),
  cmap = "grays",
  range = c("robust", "data"),
  probs = c(0.02, 0.98),
  crosshair = TRUE,
  annotate = TRUE,
  downsample = 1L,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  draw = FALSE,
  style = c("light", "dark", "report"),
  enhance = FALSE,
  crop = TRUE,
  interpolate = TRUE,
  cbar_title = "value",
  colorbar = NULL,
  assemble = TRUE,
  overlay = NULL,
  ov_thresh = 0,
  ov_cmap = NULL,
  ov_range = c("robust", "data"),
  ov_alpha = 1,
  ov_alpha_mode = c("binary", "proportional", "ramp", "soft"),
  ov_symmetric = NULL,
  ov_cap = NULL,
  canvas = NULL
)
```

Arguments

vol	A 3D background volume.

`coord` Length-3 coordinate of the target point: voxel indices (`unit = "index"`, default) or world coordinates in mm (`unit = "mm"`). `NULL` (default) uses the peak absolute value of `overlay` when one is given, otherwise the volume centre.

`unit` `"index"` or `"mm"`: how `coord` is interpreted.

`cmap` Palette for the background.

`range` Background intensity limits shared by all panels: `"robust"` (computed over head voxels), `"data"`, or numeric `c(lo, hi)`.

`probs` Quantiles for robust scaling.

`crosshair` Logical; draw the (gapped) crosshair.

`annotate` Logical; draw orientation letters on every view.

`downsample` Integer decimation for speed.

`title, subtitle, caption` Optional figure labels.

`draw` Logical; if `TRUE`, also print the figure immediately (and return it invisibly). By default the figure is returned visibly.

`style` Visual style: `"light"`, `"dark"`, or `"report"`.

`enhance` Display-only enhancement of an unsmoothed statistical `vol`; see `plot_overlay`.

`crop` Logical; crop views to the head bounding box.

`interpolate` Logical; smooth the background raster (default `TRUE`).

`cbar_title` Character; the quantity label drawn above the colorbar. Supplying it explicitly also turns the colorbar on.

`colorbar` Logical or `NULL`. `NULL` (default) shows a colorbar when it carries information: an `overlay` is given, the background uses a non-grayscale palette, or `cbar_title` is supplied.

`assemble` Logical; if `TRUE` (default) return one assembled **patchwork** figure; if `FALSE` return the named list of the `axial`, `coronal` and `sagittal` ggplots.

`overlay` Optional 3D statistical volume on the same grid as `vol`, drawn over all three views.

`ov_thresh, ov_cmap, ov_range, ov_alpha, ov_alpha_mode, ov_symmetric, ov_cap` Overlay threshold, palette, scaling, opacity and opacity mode; identical in meaning to the same arguments of `plot_overlay`.

`canvas` Optional `c(width, height)` in inches to fit the layout to (default: the open device).

Details

The affine determines which native voxel axis is nearest each anatomical plane and how that plane must be permuted or flipped for display. Oblique images are shown on their regular native voxel planes; values are not silently resampled. Use `deoblique()` or `resample_to()` first when true cardinal-plane sections are required.

Each view is labelled with the world coordinate of its plane (mm).

Value

A figure (class `neuro_fig`, a **patchwork** whose layout is re-fitted to the device it is drawn on) when `assemble = TRUE` or a named list of ggplots (`assemble = FALSE`); invisibly when `draw = TRUE`.

See Also

Other plot_neuro: `plot_checkerboard()`, `plot_edge_overlay()`, `plot_montage()`, `plot_overlay()`

Examples

```
bg <- read_vol(system.file("extdata", "mni_downsampled.nii.gz", package = "neuroim2"))
p <- plot_ortho(bg, coord = c(24, 26, 26))
ggplot2::ggsave(tempfile(fileext = ".png"), p, width = 9, height = 3.5)
```

---

plot_overlay *Composite a statistical map on a structural background*

Description

Draws a grid of slices through a structural background (e.g. a T1) with a thresholded statistical map on top, in the style of a journal figure: black tiles cropped to the head, world-coordinate slice labels, L/R markers, and a compact colorbar that marks the threshold.

Usage

```
plot_overlay(
  bgvol,
  overlay,
  zlevels = NULL,
  along = 3L,
  bg_cmap = "grays",
  ov_cmap = NULL,
  bg_range = c("robust", "data"),
  ov_range = c("robust", "data"),
  probs = c(0.02, 0.98),
  ov_thresh = 0,
  ov_alpha = 1,
  ov_alpha_mode = c("binary", "proportional", "ramp", "soft"),
  ov_symmetric = NULL,
  alpha_gamma = NULL,
  ov_cap = NULL,
  ncol = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  draw = FALSE,
```

```
  style = c("light", "dark", "report"),
  enhance = FALSE,
  assemble = TRUE,
  colorbar = TRUE,
  legend = NULL,
  crop = TRUE,
  interpolate = TRUE,
  cbar_title = "value",
  unit = c("index", "mm"),
  annotate = TRUE,
  n_slices = 12L,
  canvas = NULL,
  alpha_knee = NULL,
  alpha_cap = NULL,
  alpha_floor = NULL,
  alpha_mid = 0.2,
  gamma_min = 1.5,
  gamma_max = 5
)
```

Arguments

bgvol	Background 3D volume.
overlay	Overlay 3D volume on the same NeuroSpace grid as 'bgvol'.
zlevels	Slices to plot, as indices along 'along' (unit = "index", the default) or world coordinates in mm (unit = "mm"). NULL (default) chooses n_slices slices spread over the extent of the supra-threshold overlay.
along	Native voxel-grid axis for slicing. Display orientation and anatomical plane labels are inferred from the image affine.
bg_cmap	Background palette (e.g., "grays").
ov_cmap	Overlay palette. NULL (default) chooses automatically: the two-sided "cold_hot" map for signed data, "hot" otherwise. Any name accepted by [resolve_cmap()] or a vector of colours.
bg_range, ov_range	Background/overlay scaling. Either a mode string, "robust" or "data", or an explicit numeric c(lo, hi) to pin the scale (e.g. ov_range = c(-6, 6)) for consistent colouring across figures and subjects. The robust background window is computed over head voxels only; the robust overlay scale is computed once from the whole overlay volume (supra-threshold values when a threshold is set) and rounded to two significant digits, so a given map always gets the same scale whichever slices are shown.
probs	Quantiles for robust scaling.
ov_thresh	Numeric threshold; values with |v| < thresh are not drawn.
ov_alpha	Global opacity of the overlay (0..1).
ov_alpha_mode	One of "binary" (default: every supra-threshold voxel fully opaque), "proportional", "ramp", or "soft" (opacity rises nonlinearly with magnitude; the curve alpha =

floor + (1 - floor) * t^gamma self-tunes gamma from the data). In the graded modes every voxel that passes a threshold keeps at least 60% opacity, and the colorbar is faded with the same curve so it matches the picture.

ov_symmetric — Logical or NULL. NULL (default) uses symmetric limits around zero when the overlay has both signs.

alpha_gamma — Optional exponent for ov_alpha_mode = "soft". NULL (default) auto-tunes it from the data.

ov_cap — Optional numeric; the magnitude at the upper end of the colour/opacity scale. Defaults to the data-driven limit.

ncol — Number of columns. NULL (default) picks the layout that best fills the canvas.

title, subtitle, caption — Optional figure labels, left-aligned with the tiles.

draw — Logical; if TRUE, also print the figure immediately (and return it invisibly). By default the figure is returned visibly, like a ggplot, so it prints at the console or in a knitr chunk.

style — Visual style: "light" (white card), "report" (warm off-white card with the key strip on), or "dark" (black card). Tiles are black in every style.

enhance — Display-only enhancement of the (unsmoothed) statistical overlay. FALSE (default) leaves it untouched; TRUE applies enhance_stat_map with defaults; a named list is forwarded as arguments to enhance_stat_map().

assemble — Logical; if TRUE (default), return one assembled **patchwork** figure. If FALSE, return the list of per-slice ggplots.

colorbar — Logical; draw the colorbar (default TRUE).

legend — Logical or NULL; add a one-line key under the tiles (plane, neurological convention, and what the threshold shows). NULL (default) shows it for style = "report" only.

crop — Logical; crop every panel to the head bounding box (shared across slices, and always containing every supra-threshold voxel).

interpolate — Logical; smooth the background raster (default TRUE). The overlay itself is always drawn with crisp voxels.

cbar_title — Character; the quantity label drawn above the colorbar. Defaults to "value"; set it to the statistic actually shown (e.g. "t", "Semipartial r").

unit — "index" or "mm": how zlevels is interpreted. Panels are always labelled in world coordinates (mm).

annotate — Logical; draw L/R orientation letters on the first panel.

n_slices — Number of slices chosen when zlevels is NULL.

canvas — Optional c(width, height) in inches to freeze the layout for one size. By default (NULL) the layout is re-fitted to whatever device the figure is drawn on, including ggsave().

alpha_knee, alpha_cap — Optional lower (non-negative) and upper (positive) magnitude anchors of the soft opacity curve, independent of the colour limits. NULL uses the threshold (or median magnitude) and the colour-scale cap. Fix both and alpha_gamma to reproduce one opacity mapping across figures; see soft_alpha_params.

`alpha_floor` Minimum soft opacity (0–1) above the knee, before `ov_alpha`; values below `ov_thresh` stay transparent. `NULL` (default) uses 0.6 when a threshold is set, otherwise 0.

`alpha_mid`, `gamma_min`, `gamma_max`
Auto-gamma policy passed to `soft_alpha_params` (0.2 at the median supra-knee magnitude, gamma clamped to [1.5, 5]).

Details

Signed maps. For overlays with both signs (t/z/contrast maps), the default palette is two-sided and the limits symmetric, so negative values are as visible as positive ones. With a threshold, the colour ramp starts at a saturated colour at ±threshold and brightens toward the cap; the colorbar shows the sub-threshold band in a neutral tone and ticks the threshold and cap. When the data exceed the cap, the end tick reads ≥ cap.

Soft opacity. In `ov_alpha_mode = "soft"` the resolved curve is recorded in `attr(result, "soft_alpha")` for either return form; pass it back through `alpha_knee`, `alpha_cap`, `alpha_gamma` and `alpha_floor` to reuse it.

Saving. The figure's layout is fitted to the device it is drawn on: `p <- plot_overlay(...); ggsave("fig.png", p, width = 6, height = 9)` re-arranges the tiles for a 6 x 9 in page, and additions such as `p + patchwork::plot_annotation(title = "...")` are kept. Pass `canvas` only to freeze the layout for one size.

Value

A figure (class `neuro_fig`, a **patchwork** whose layout is re-fitted to the device it is drawn on) when `assemble = TRUE` or a list of ggplots (`assemble = FALSE`); invisibly when `draw = TRUE`.

See Also

Other plot_neuro: `plot_checkerboard()`, `plot_edge_overlay()`, `plot_montage()`, `plot_ortho()`

Examples

```
bg <- read_vol(system.file("extdata", "mni_downsampled.nii.gz", package = "neuroim2"))
stat <- bg
stat[] <- rnorm(length(stat)) * (bg[] > stats::quantile(bg[], 0.6))
p <- plot_overlay(bg, stat, ov_thresh = 1.5, cbar_title = "z")
tf <- tempfile(fileext = ".png")
ggplot2::ggsave(tf, p, width = 7, height = 5)
```

---

prepare_confounds *Prepare weighted nuisance projectors for each run*

Description

Converts per-run confound matrices and time weights into orthonormal projectors that can be consumed directly by the C++ graph builder. Each run produces Q_k (columns spanning the weighted confound space) and $\sqrt{w_k}$ (per-time-point square-root weights). Supplying a `NULL` confound matrix yields a zero-column projector, enabling pure time-weighting without regression.

Usage

```
prepare_confounds(
  confounds,
  time_weights = NULL,
  run_lengths,
  include_intercept = TRUE,
  center_cols = TRUE,
  scale_cols = FALSE
)
```

Arguments

`confounds`	List of matrices ($T_k \times p_k$), or a single matrix reused for all runs. Each row corresponds to a time point.
`time_weights`	Optional list of numeric vectors (length T_k) or a single vector reused for every run. If `NULL`, unit weights are used.
`run_lengths`	Integer vector with the number of time points per run. Required when any run has both `confounds=NULL` and `time_weights=NULL`.
`include_intercept`	Logical; prepend a column of ones before QR (default TRUE).
`center_cols`	Logical; center each confound column before weighting (default TRUE).
`scale_cols`	Logical; scale columns to unit variance before weighting (default FALSE).

Value

A list with elements `Q_list` (list of matrices) and `sqrtw_list` (list of numeric vectors). Each entry has the same length as `run_lengths`.

`quaternToMatrix` *Convert Quaternion Parameters to a Transformation Matrix*

Description

Given a quaternion (`b`, `c`, `d`), a scalar offset (origin), voxel step sizes, and the `qfac` sign, reconstructs a 4x4 affine matrix representing rotation, scaling, and translation as used in NIfTI-1.

Usage

```
quaternToMatrix(quat, origin, stepSize, qfac)
```

Arguments

quat	A numeric vector of length 3 containing the quaternion parameters (b, c, d). The scalar part a is computed internally.
origin	A numeric vector of length 3 specifying the translation components (often the real-space origin or offset).
stepSize	A numeric vector of length 3 giving the voxel dimensions along each axis (e.g., `(dx, dy, dz)`).
qfac	Either `+1` or `-1`, indicating the sign from the determinant check in `matrixToQuatern`.

Details

This function uses the quaternion formalism common in neuroimaging, adding the offset (translation) into the 4th column, and applying the voxel sizes along each axis. If `qfac` is `-1`, the z scale is negated. The resulting 4x4 matrix is typically used as an affine transform for voxel-to-world coordinate mapping.

Value

A 4x4 numeric affine transformation matrix. The top-left 3x3 submatrix encodes rotation and scaling, and the 4th column encodes translation.

See Also

`matrixToQuatern` for converting a matrix back to quaternion form.

`random_searchlight` *Create a spherical random searchlight iterator*

Description

This function generates a spherical random searchlight iterator for analyzing local neighborhoods of voxels within a given radius in a brain mask.

Usage

```
random_searchlight(mask, radius, nonzero = TRUE)
```

Arguments

mask	A `NeuroVol` object representing the brain mask.
radius	A numeric value specifying the radius of the searchlight sphere in voxel units.
nonzero	Logical; if `TRUE` (default) discard zero-valued voxels in the mask when forming each searchlight.

Value

A list of `ROIVolWindow` objects, each representing a spherical searchlight region.

Examples

```
# Create a simple brain mask
mask_data <- array(TRUE, c(10, 10, 10))
mask_data[1, 1, 1] <- FALSE
mask <- LogicalNeuroVol(mask_data, NeuroSpace(c(10,10,10)))

# Generate random searchlight iterator with a radius of 2 voxels

searchlights <- random_searchlight(mask, radius = 6)
```

---

read_header *read header information of an image file*

Description

read header information of an image file

Usage

```
read_header(file_name)
```

Arguments

file_name	the name of the file to read

Value

an instance of class FileMetaInfo

Examples

```
hdr <- read_header(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
dim(hdr)                  # image dimensions
hdr@header$pixdim[5]      # TR in seconds
```

read_hyper_vec *Read a 5D image as a NeuroHyperVec*

Description

Read a 5D image as a NeuroHyperVec

Usage

```
read_hyper_vec(file_name, mask = NULL)
```

Arguments

file_name	Path to a single NIfTI file.
mask	Optional spatial mask (logical array/vector, NeuroVol, or LogicalNeuroVol). When provided, only masked voxels are stored.

Value

A NeuroHyperVec.

read_image *read_image*

Description

Convenience wrapper that inspects the file header(s) and dispatches to the appropriate specialized reader: read_vol for a single 3D file, read_vec for 4D data or for any multi-file input, or read_hyper_vec for 5D data.

Usage

```
read_image(
  file_name,
  type = c("auto", "vol", "vec", "hyper"),
  index = 1,
  indices = NULL,
  mask = NULL,
  mode = c("normal", "mmap", "bigvec", "filebacked")
)
```

Arguments

file_name	Character vector of one or more file paths.
type	One of "auto", "vol", "vec", or "hyper" to override header-based dispatch.
index	Integer volume index. Used as the single-volume selector for read_vol (when dispatching to it) and, when indices is NULL, forwarded to read_vec as indices so you can pull out a subset of time points while still receiving a NeuroVec.
indices	Optional integer vector of sub-volume indices forwarded to read_vec. Takes precedence over index.
mask	Optional spatial mask passed through to the vector or hyper-vector readers. Ignored by read_vol.
mode	IO mode forwarded to read_vec; see that function for details. Ignored for 3D and 5D dispatch.

Details

Auto-dispatch (type = "auto") uses the following rules:

- length(file_name) > 1: always routed to read_vec, so the result is a NeuroVecSeq regardless of whether the individual files are 3D, 4D, or a mix. See read_vec for the return-type details.
- Single file with a 5th dimension > 1: routed to read_hyper_vec, returning a NeuroHyperVec.
- Single file with a 4th dimension > 1: routed to read_vec, returning a NeuroVec. If index is supplied (and indices is not), it is forwarded as indices so you can pull out a subset while still getting a NeuroVec back.
- Single effectively-3D file (either truly 3D or 4D with dim[4] == 1): routed to read_vol, returning a DenseNeuroVol.

Explicit type values bypass header inspection:

- type = "vol": requires a single file; always returns a DenseNeuroVol. The index argument picks the sub-volume when the file is 4D.
- type = "vec": forwards to read_vec. Multi-file input yields a NeuroVecSeq. A single 3D file is promoted to a NeuroVec with dim[4] == 1.
- type = "hyper": requires a single file; returns a NeuroHyperVec.

Value

The return type depends on dispatch:

- **3D dispatch** (single effectively-3D file, or type = "vol"): a DenseNeuroVol.
- **4D dispatch** (single 4D file, or type = "vec" with one file): a NeuroVec (concrete subclass depends on mode).
- **Multi-file dispatch** (length(file_name) > 1, or type = "vec" with multiple files): a NeuroVecSeq, which extends NeuroVec but stores each file as a distinct segment rather than concatenating into a single contiguous 4D array. Mixed 3D/4D inputs are allowed; each 3D file contributes one time point to the sequence.
- **5D dispatch** (single 5D file, or type = "hyper"): a NeuroHyperVec.

See Also

read_vol, read_vec, read_hyper_vec

Examples

```
# 3D file -> DenseNeuroVol
vol <- read_image(system.file("extdata", "global_mask2.nii.gz", package = "neuroim2"))

# 4D file -> NeuroVec
vec <- read_image(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))

# Multiple files (any mix of 3D and 4D) -> NeuroVecSeq
fn <- system.file("extdata", "global_mask_v4.nii", package = "neuroim2")
seq_vec <- read_image(c(fn, fn))
class(seq_vec)  # "NeuroVecSeq"
```

---

read_meta_info *Generic function to read image meta info given a file*

Description

Reads meta information from image files based on their format (NIFTI or AFNI).

Usage

```
read_meta_info(x, file_name)

## S4 method for signature 'NIFTIFormat'
read_meta_info(x, file_name)

## S4 method for signature 'AFNIFormat'
read_meta_info(x, file_name)
```

Arguments

x	A FileFormat object (either NIFTIFormat or AFNIFormat)
file_name	A character string specifying the file name to read meta information from

Details

These methods use format-specific functions to read the header information and create the appropriate meta information object. The '.read_meta_info' helper function is used internally to streamline the process for both formats.

Value

A list containing the meta information read from the file.

An object of class NIFTIMetaInfo or AFNIMetaInfo, depending on the input format

Examples

```
# Create a NIFTI format descriptor
fmt <- new("NIFTIFormat",
           file_format = "NIFTI",
           header_encoding = "raw",
           header_extension = "nii",
           data_encoding = "raw",
           data_extension = "nii")

# Read metadata from a NIFTI file

fname <- system.file("extdata", "global_mask_v4.nii", package="neuroim2")
meta <- read_meta_info(fmt, fname)

# Access metadata properties
dim(meta)          # Image dimensions
trans(meta)        # Transformation matrix
```

`read_vec` *read_vec*

Description

Loads a neuroimaging volume from one or more files, with support for various input formats and memory management strategies.

Usage

```
read_vec(
  file_name,
  indices = NULL,
  mask = NULL,
  mode = c("normal", "mmap", "bigvec", "filebacked")
)
```

Arguments

`file_name`	A character vector of one or more file paths to load. A 3D file is promoted to a 4D `NeuroVec` with a single time point (see Details). When multiple paths are supplied the result is always a `NeuroVecSeq` (which itself extends `NeuroVec`), regardless of whether the individual files are 3D, 4D, or a mix of both.
`indices`	The indices of the sub-volumes to load (e.g. if the file is 4-dimensional). Only supported in "normal" mode.
`mask`	A logical mask defining which spatial elements to load. Required for "bigvec" mode and optional for other modes.

mode — The IO mode which is one of: * "normal": Standard in-memory loading * "mmap": Memory-mapped access (more memory efficient) * "bigvec": Optimized for large datasets with masking * "filebacked": File-backed storage with on-demand loading

Details

This function supports multiple file formats: * .nii: Standard NIfTI format * .nii.gz: Compressed NIfTI (not supported in mmap mode)

Memory management modes: * "normal": Loads entire dataset into memory. Best for smaller datasets or when memory is not a constraint. * "mmap": Memory-maps the file, providing efficient access for large files without loading entirely into memory. Not available for compressed files. * "bigvec": Optimized for large datasets where only a subset of voxels are of interest. Requires a mask to specify which voxels to load. * "filebacked": Similar to mmap but with more flexible caching strategies.

Which mode to use. `"normal"` is the default because it is the simplest thing that works, but it is the wrong default once the data stops being small. An R image always holds `doubles`, so a 56 MB int16 run becomes 236 MB in memory and a session-worth of runs will not fit. Two cheaper routes exist and both are usually *faster*, not just smaller:

* **Pass a** `mask` when the analysis only touches part of the brain – which is nearly every analysis. Only the in-mask voxels are read, and the result is a sparse `NeuroVec` that `series` and the searchlight iterators consume directly. * **Use** `mode = "mmap"` when voxels are visited in a scattered order, as in searchlight, ROI and connectivity work. The file is not read up front and pages are served on demand.

On an ordinary single run (64 x 64 x 36 x 200), extracting 5,000 scattered voxel time series measured 44 ms with `mask=`, 144 ms via `"mmap"` including the open, and 4.8 s by loading the whole image first. Reach for `"normal"` when you genuinely need every voxel of a small image in memory at once.

3D inputs: A path pointing at a 3D image is not rejected. It is promoted to a 4D `NeuroVec` whose fourth dimension has length 1, so the return type is always a `NeuroVec`, never a `NeuroVol`. If you want a true volume, use `read_vol` (or `vec[[1]]`).

Multiple files: When `file_name` has length > 1, each file is loaded independently and the results are wrapped with `NeuroVecSeq`. No data is copied or re-concatenated into a single dense 4D array; the returned `NeuroVecSeq` holds the constituent `NeuroVecs` in its `@vecs` slot and exposes them as a single logical time series. Time-point lookups (e.g. `x[[i]]`, `sub_vector(x, i)`, `linear_access(x, i)`) transparently walk across the segments. The per-file time lengths may differ (e.g. a 3D file contributes 1 time point, a 4D file contributes `dim(file)[4]`); all spatial dimensions must match.

Value

The return type depends on how many files are supplied:

- **Single 3D file** — a `NeuroVec` with `dim(x)[4] == 1` (concrete class depends on `mode`: e.g. `DenseNeuroVec` for `"normal"`, `MappedNeuroVec` for `"mmap"`, `BigNeuroVec` for `"bigvec"`, `FileBackedNeuroVec` for `"filebacked"`).
- **Single 4D file** — a `NeuroVec` of the same concrete class as above, with `dim(x)[4]` equal to the 4th dimension of the file (or `length(indices)` when `indices` is supplied).

- **Multiple files (any mix of 3D and 4D)** — a NeuroVecSeq wrapping one NeuroVec per input file in the order given. Because NeuroVecSeq extends NeuroVec, it can be used wherever a NeuroVec is accepted, but its underlying storage is segmented rather than a single contiguous 4D array. For example, `read_vec(c(vol, vec, vec, vol))` returns a 4-element NeuroVecSeq whose segments have time lengths `c(1, T2, T3, 1)`.

Note

* Memory-mapping (.mmap mode) is not supported for gzipped files * The bigvec mode requires a mask to be specified * When loading multiple files, they must have compatible dimensions

Examples

```
# Load a single NIfTI file
img <- read_vec(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))


# Memory-mapped loading for large files
big_img <- read_vec(system.file("extdata", "global_mask_v4.nii", package="neuroim2"), mode="mmap")

# Load masked data for memory efficiency
mask <- as.logical(big_img[[1]])
masked_data <- read_vec(system.file("extdata", "global_mask_v4.nii", package="neuroim2"),
               mask=mask, mode="bigvec")
```

---

read_vol *Load a single 3D image volume from a file*

Description

Reads exactly one 3D volume from a neuroimaging file and returns it as a DenseNeuroVol. Accepts both 3D files (where only `index = 1` is valid) and 4D files (where `index` selects a single sub-volume along the 4th dimension).

Usage

```
read_vol(file_name, index = 1)
```

Arguments

`file_name`	Path to a single image file (NIfTI `.nii` or `.nii.gz`). A character vector of length > 1 is not supported — use read_vec if you need to read multiple files, or call `read_vol` in a loop.
`index`	Integer giving the index of the sub-volume to load. Must be 1 for a 3D file. For a 4D file, must satisfy `1 <= index <= dim(file)[4]`.

Value

A DenseNeuroVol (always 3D, always dense). The associated NeuroSpace has three spatial dimensions even when the source file is 4D.

See Also

read_vec for loading 4D data as a NeuroVec, read_image for automatic dimensionality-based dispatch, and read_hyper_vec for 5D data.

Examples

```
# Read the first volume from a 4D file
fname <- system.file("extdata", "global_mask_v4.nii", package="neuroim2")
x <- read_vol(fname)
print(dim(x))    # 3D
space(x)

# Read the 3rd sub-volume from the same 4D file
x3 <- read_vol(fname, index = 3)
```

---

read_vol_list *read_vol_list*

Description

This function loads a list of image volumes and returns a NeuroVec object.

Usage

```
read_vol_list(file_names, mask = NULL)
```

Arguments

file_names	A list of file names to load.
mask	An optional mask defining the subset of voxels to load.

Value

An instance of the NeuroVec class.

`reorient` *Remap the grid-to-world coordinates mapping of an image.*

Description

Remap the grid-to-world coordinates mapping of an image.

Usage

```
reorient(x, orient)

## S4 method for signature 'NeuroSpace,character'
reorient(x, orient)
```

Arguments

`x`	the object
`orient`	the orientation code indicating the "remapped" axes.

Details

When `x` is a `NeuroSpace` object, the `orient` argument should be a character vector of length 3 specifying the desired anatomical orientation using single-letter codes. Each letter represents an anatomical direction:

- First position: "R" (Right) or "L" (Left)
- Second position: "A" (Anterior) or "P" (Posterior)
- Third position: "S" (Superior) or "I" (Inferior)

For example, `c("R", "A", "S")` specifies Right-Anterior-Superior orientation, while `c("L", "P", "I")` specifies Left-Posterior-Inferior orientation. The orientation codes determine how the voxel grid coordinates map to real-world anatomical space.

Value

A reoriented version of `x`.

Examples

```
# Create a NeuroSpace object in LPI (Left-Posterior-Inferior) orientation
space <- NeuroSpace(c(64, 64, 40), c(2, 2, 2))

# Reorient to RAS (Right-Anterior-Superior) orientation
# Use individual axis codes: "R" for Right, "A" for Anterior, "S" for Superior
space_ras <- reorient(space, c("R", "A", "S"))

# The transformation matrix will be updated to reflect the new orientation
# Original and reoriented spaces will have different coordinate mappings
```

```
coords <- c(32, 32, 20)
orig_world <- grid_to_coord(space, coords)
new_world <- grid_to_coord(space_ras, coords)
```

`resample` *Resample an Image to Match the Space of Another Image*

Description

This function resamples a source image to match the spatial properties (dimensions, resolution, and orientation) of a target image.

This method resamples a NeuroVol object (`source`) to match the dimensions and orientation of a NeuroSpace object (`target`).

This method preserves discrete cluster labels and label mappings when resampling clustered volumes to a new space.

Usage

```
resample(source, target, ...)

## S4 method for signature 'NeuroVol,NeuroVol'
resample(source, target, interpolation = 3L)

## S4 method for signature 'NeuroVol,NeuroSpace'
resample(source, target, interpolation = 3L)

## S4 method for signature 'ClusteredNeuroVol,NeuroSpace'
resample(source, target, interpolation = 0L)

## S4 method for signature 'ClusteredNeuroVol,NeuroVol'
resample(source, target, interpolation = 0L)
```

Arguments

`source`	A NeuroVol object representing the source volume to be resampled.
`target`	A NeuroSpace object representing the target space to match the dimensions and orientation of the source volume.
`...`	Additional arguments passed to the resampling function, such as interpolation method, boundary handling, or other resampling options.
`interpolation`	A single integer specifying the type of interpolation to be applied to the final resampled image. May be 0 (nearest neighbor), 1 (trilinear), or 3 (cubic spline). No other values are valid.

Value

An object representing the resampled `source` image, with the same spatial properties as `target`.

See Also

NeuroVol for the base volume class

Examples

```
img <- read_vol(system.file("extdata", "global_mask_v4.nii", package = "neuroim2"))
rspace <- space(img)


newtrans4X3 <- trans(img)[1:4, 1:3]
newtrans4X3 <- newtrans4X3 * c(.5,.5,.5,1)
newtrans <- cbind(newtrans4X3, c(space(img)@origin,1))

rspace <- NeuroSpace(rspace@dim*2, rspace@spacing/2, origin=rspace@origin, trans=trans(img))

rvol <- resample(img, rspace)



# Create source and target volumes
src_vol <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))
targ_vol <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Resample source to match target
resampled <- resample(src_vol, targ_vol, interpolation=1)
```

---

resample_to *Resample an image with readable method names*

Description

A convenience front-end to [resample()] that accepts human-friendly method names and an engine switch. Internally delegates to the S4 ‘resample(source, target, interpolation = 0/1/3)‘ methods.

Usage

```
resample_to(
  source,
  target,
  method = c("nearest", "linear", "cubic"),
  engine = c("internal"),
  ...
)
```

Arguments

source	A ‘NeuroVol‘ (source image)
target	A ‘NeuroVol‘ or ‘NeuroSpace‘ to match
method	Interpolation method: ‘"nearest"‘, ‘"linear"‘, or ‘"cubic"‘
engine	Resampling engine. For now only ‘"internal"‘ is supported.
...	Reserved for future options

Value

A ‘NeuroVol‘ in the target space

Examples

```
img <- read_vol(system.file("extdata","global_mask_v4.nii", package="neuroim2"))
sp  <- space(img)
sp2 <- NeuroSpace(sp@dim*2, sp@spacing/2, origin=sp@origin, trans=trans(img))
r1  <- resample_to(img, sp2, method = "linear")
```

---

resampled_searchlight *Create a resampled searchlight iterator*

Description

This function generates a resampled searchlight iterator by sampling regions from within a brain mask. By default it builds spherical searchlights, but users can provide a custom `shape_fun` to return ellipsoids, cubes, or arbitrary irregular searchlight shapes. Centers are drawn with replacement, so the same voxel (and its neighborhood) may appear multiple times. Each searchlight can also draw its radius from a user-specified set of radii.

Usage

```
resampled_searchlight(
  mask,
  radius = 8,
  iter = 100,
  shape_fun = NULL,
  nonzero = TRUE
)

bootstrap_searchlight(mask, radius = 8, iter = 100)
```

Arguments

mask	A NeuroVol object representing the brain mask.
radius	A numeric scalar or vector specifying candidate radii (in voxel units) for the searchlight sphere. If a vector is supplied, a radius is sampled uniformly (with replacement) for each searchlight. All radii must be positive. Default is 8.
iter	An integer specifying the total number of searchlights to sample (with replacement). Default is 100.
shape_fun	Either NULL (default spherical kernel), a character keyword ("sphere", "ellipsoid", "cube", "blobby"), or a custom function. Custom functions are called as shape_fun(mask, center, radius, iter, nonzero) and must return either a ROIVolWindow or an n x 3 integer matrix of voxel coordinates. This enables anisotropic or irregular searchlights.
nonzero	Logical; if TRUE (default), the generated searchlight is intersected with the nonzero voxels of mask. Applies to both the default sphere and any shape_fun that returns coordinates.

Details

Searchlight centers are sampled with replacement, so the same center (and its surrounding voxels) can be selected multiple times. When multiple radii are provided, each searchlight independently samples one radius from the supplied values. Supplying shape_fun lets you draw non-spherical searchlights (e.g., ellipsoids, cubes, blobby deformations, or task-specific kernels). Built-in shortcuts are available via shape_fun = "ellipsoid", "cube", and "blobby"; "sphere" or NULL uses the default spherical kernel.

Value

A deferred_list object containing ROIVolWindow objects, each representing a sampled searchlight region drawn from within the mask.

Examples

```
# Load an example brain mask
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Generate a resampled searchlight iterator with radii drawn from {4,6,8}
searchlights <- resampled_searchlight(mask, radius = c(4, 6, 8))

# Use a custom shape: random ellipsoid scaled along each axis
ellipsoid_fun <- function(mask, center, radius, iter, nonzero) {
  scales <- runif(3, 0.5, 1.5)        # axis-wise stretch/compress
  vox <- spherical_roi(mask, center, radius, nonzero = FALSE)@coords
  ctr_mat <- matrix(center, nrow(vox), 3, byrow = TRUE)
  keep <- rowSums(((vox - ctr_mat) * scales)^2) <= radius^2
  vox[keep, , drop = FALSE]
}
ellip_searchlights <- resampled_searchlight(mask, radius = c(4, 6),
                                            iter = 50, shape_fun = ellipsoid_fun)
```

```
# Or use built-in named shapes
ellip_builtin <- resampled_searchlight(mask, radius = 6, shape_fun = "ellipsoid")
cube_builtin  <- resampled_searchlight(mask, radius = 6, shape_fun = "cube")
```

`resolve_cmap` *Neuroimaging color palettes and helpers*

Description

Lightweight, perceptually-uniform color tools with safe fallbacks.

Usage

```
resolve_cmap(name = "grays", n = 256)
```

Arguments

`name`	Palette name (e.g., "grays", "viridis", "inferno", "magma", "plasma", "turbo", "cividis", "coldhot", "blue-red", "coolwarm"). Any palette in `grDevices::hcl.pals()` (e.g. "RdBu", "Spectral", "Reds") is also accepted. Case- and punctuation-insensitive. Unknown names emit a warning and fall back to a viridis-like ramp. If you pass a vector of colors, it's returned unchanged.
`n`	Number of colors to generate.

Value

A character vector of hex colors.

`ROI-class` *ROI*

Description

Base marker class for a region of interest (ROI)

ROICoords *Create ROI Coordinates Object*

Description

Creates an ROICoords object from a matrix of coordinates representing points in 3D space.

Usage

```
ROICoords(coords)
```

Arguments

coords	A matrix with 3 columns representing (x, y, z) coordinates

Details

ROI Coordinates

Value

An ROICoords object

Examples

```
coords <- matrix(c(1,2,3, 4,5,6), ncol=3, byrow=TRUE)
roi_coords <- ROICoords(coords)
```

ROICoords-class *ROICoords*

Description

A class representing a region of interest (ROI) in a brain image, defined by a set of coordinates. This class stores the geometric space of the image and the coordinates of the voxels within the ROI.

Slots

space An instance of class NeuroSpace representing the geometric space of the image data.

coords A matrix containing the coordinates of the voxels within the ROI. Each row represents a coordinate as, e.g. (i, j, k).

ROIVec *Create an instance of class* ROIVec

Description

This function constructs an instance of the ROIVec class, which represents a region of interest (ROI) in a 4D volume. The class stores the NeuroSpace object, voxel coordinates, and data values for the ROI.

Usage

```
ROIVec(vspace, coords, data = matrix(1, nrow = 1, ncol = nrow(coords)))
```

Arguments

vspace	An instance of class NeuroSpace with four dimensions, which represents the dimensions, voxel spacing, and time points of the 4D volume.
coords	A 3-column matrix of voxel coordinates for the region of interest.
data	The matrix of data values associated with the region of interest, with each row representing a voxel and each column representing a time point. By default, it is a matrix with a number of rows equal to the number of rows in the 'coords' matrix and a single column filled with ones.

Value

An instance of class ROIVec, containing the NeuroSpace object, voxel coordinates, and data values for the region of interest.

Examples

```
# Create a NeuroSpace object
vspace <- NeuroSpace(dim = c(5, 5, 5, 10), spacing = c(1, 1, 1))

# Define voxel coordinates for the ROI
coords <- matrix(c(1, 2, 3, 2, 2, 2, 3, 3, 3), ncol = 3)

# Create a data matrix for the ROI
data <- matrix(rnorm(30), nrow = 10, ncol = 3)

# Create a ROIVec object
roi_vec <- ROIVec(vspace, coords, data)
```

ROIVec-class *ROIVec*

Description

A class representing a vector-valued volumetric region of interest (ROI) in a brain image.

Slots

`coords` A `matrix` containing the 3D coordinates of the voxels within the ROI. Each row represents a voxel coordinate as (x, y, z).

`.Data` A `matrix` containing the data values associated with each voxel in the ROI. Each row corresponds to a unique vector value, and the number of rows should match the number of rows in the `coords` matrix.

Validity

An object of class `ROIVec` is considered valid if: - The `coords` slot is a matrix with 3 columns. - The `.Data` slot is a matrix. - The number of rows in the `.Data` matrix is equal to the number of rows in the `coords` matrix.

ROIVecWindow-class *ROIVecWindow*

Description

A class representing a spatially windowed, vector-valued volumetric region of interest (ROI) in a brain image.

Slots

`coords` A `matrix` containing the 3D coordinates of the voxels within the ROI. Each row represents a voxel coordinate as (x, y, z).

`.Data` A `matrix` containing the data values associated with each voxel in the ROI. Each row corresponds to a unique vector value, and the number of rows should match the number of rows in the `coords` matrix.

`parent_index` An `integer` representing the 1D index of the center voxel in the parent space.

`center_index` An `integer` representing the location in the coordinate matrix of the center voxel in the window.

Validity

An object of class `ROIVecWindow` is considered valid if: - The `coords` slot is a matrix with 3 columns. - The `.Data` slot is a matrix. - The number of rows in the `.Data` matrix is equal to the number of rows in the `coords` matrix.

ROIVol *Create ROI Volume Object*

Description

Creates an ROIVol object representing a set of values at specific 3D coordinates within a spatial reference system.

Usage

```
ROIVol(space, coords, data)
```

Arguments

space	A NeuroSpace object defining the spatial reference
coords	A matrix with 3 columns representing (x,y,z) coordinates
data	A numeric vector of values corresponding to each coordinate

Details

ROI Volume

Value

An ROIVol object

Examples

```
space <- NeuroSpace(c(64,64,64))
coords <- matrix(c(1,2,3, 4,5,6), ncol=3, byrow=TRUE)
data <- c(1.5, 2.5)
roi_vol <- ROIVol(space, coords, data)
```

ROIVol-class *ROIVol*

Description

A class representing a volumetric region of interest (ROI) in a brain image, defined by a set of coordinates and associated data values.

Slots

`coords` A `matrix` containing the 3D coordinates of the voxels within the ROI. Each row represents a voxel coordinate as (x, y, z).

`.Data` A `numeric` vector containing the data values associated with each voxel in the ROI. The length of this vector should match the number of rows in the `coords` matrix.

Validity

An object of class `ROIVol` is considered valid if: - The `coords` slot is a matrix with 3 columns. - The `.Data` slot is a numeric vector. - The length of the `.Data` vector is equal to the number of rows in the `coords` matrix.

`ROIVolWindow-class` *ROIVolWindow*

Description

A class representing a spatially windowed volumetric region of interest (ROI) in a brain image, derived from a larger parent ROI.

Slots

`parent_index` An `integer` representing the 1D index of the center voxel in the parent space.

`center_index` An `integer` representing the location in the coordinate matrix of the center voxel in the window.

`coords` A `matrix` containing the 3D coordinates of the voxels within the ROI. Each row represents a voxel coordinate as (x, y, z).

`.Data` A `numeric` vector containing the data values associated with each voxel in the ROI. The length of this vector should match the number of rows in the `coords` matrix.

Validity

An object of class `ROIVolWindow` is considered valid if: - The `coords` slot is a matrix with 3 columns. - The `.Data` slot is a numeric vector. - The length of the `.Data` vector is equal to the number of rows in the `coords` matrix.

`scale_fill_neuro` *A ggplot2 fill scale with neuroimaging-friendly defaults*

Description

A ggplot2 fill scale with neuroimaging-friendly defaults

Usage

```
scale_fill_neuro(
  cmap = "grays",
  range = c("robust", "data"),
  probs = c(0.02, 0.98),
  limits = NULL,
  na.value = "transparent",
  guide = "colorbar"
)
```

Arguments

`cmap`	Palette name or vector of colors. See [resolve_cmap()].
`range`	Either "robust" (quantiles) or "data" (min/max) to determine the default scale limits when ‘limits‘ is not provided.
`probs`	Two-length numeric vector of quantiles for ‘range="robust"‘.
`limits`	Optional numeric limits (min, max). Overrides ‘range‘.
`na.value`	Color for NA.
`guide`	Legend guide (default "colorbar").

Details

Values outside ‘limits‘ are clamped to the nearest color endpoint rather than converted to ‘NA‘. This keeps robust display limits from creating transparent holes in bright or dark image regions.

Value

A ggplot2 scale object.

scale_series *Generic functions to scale (center and/or normalize by standard deviation) each series of a 4D image That is, if the 4th dimension is 'time' each series is a 1D time series.*

Description

Generic functions to scale (center and/or normalize by standard deviation) each series of a 4D image That is, if the 4th dimension is 'time' each series is a 1D time series.

Usage

```
scale_series(x, center, scale)

## S4 method for signature 'NeuroVec,logical,missing'
scale_series(x, center, scale)

## S4 method for signature 'DenseNeuroVec,logical,logical'
scale_series(x, center, scale)

## S4 method for signature 'SparseNeuroVec,logical,logical'
scale_series(x, center, scale)

## S4 method for signature 'NeuroVec,logical,logical'
scale_series(x, center, scale)

## S4 method for signature 'NeuroVec,missing,logical'
scale_series(x, center, scale)

## S4 method for signature 'NeuroVec,missing,missing'
scale_series(x, center, scale)
```

Arguments

x	a four dimensional image
center	a logical value indicating whether series should be centered
scale	a logical value indicating whether series should be divided by standard deviation

Value

An object of the same class as x, with each time series centered and/or scaled.

Examples

```
bvec <- NeuroVec(array(rnorm(24*24*24*24), c(24,24,24,24)), NeuroSpace(c(24,24,24,24), c(1,1,1)))
res <- scale_series(bvec, TRUE, TRUE)
```

searchlight *Create an exhaustive searchlight iterator*

Description

This function generates an exhaustive searchlight iterator that returns either voxel coordinates or ROIVolWindow objects for each searchlight sphere within the provided mask. The iterator visits every non-zero voxel in the mask as a potential center voxel.

Usage

```
searchlight(mask, radius, eager = FALSE, nonzero = FALSE, cores = 0)
```

Arguments

mask	A NeuroVol object representing the brain mask.
radius	A numeric value specifying the radius (in mm) of the spherical searchlight.
eager	A logical value specifying whether to eagerly compute the searchlight ROIs. Default is FALSE, which uses lazy evaluation.
nonzero	A logical value indicating whether to include only coordinates with nonzero values in the supplied mask. Default is FALSE.
cores	An integer specifying the number of cores to use for parallel computation. Default is 0, which uses a single core.

Value

A deferred_list object containing either matrices of integer-valued voxel coordinates or ROIVolWindow objects, each representing a searchlight region.

Examples

```
# Load an example brain mask
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Generate an exhaustive searchlight iterator with a radius of 6 mm

searchlights <- searchlight(mask, radius = 6, eager = FALSE)
```

searchlight-methods *Searchlight Analysis Methods*

Description

Methods for performing searchlight analyses on neuroimaging data

searchlight_coords *Create an exhaustive searchlight iterator for voxel coordinates using spherical_roi*

Description

This function generates an exhaustive searchlight iterator that returns voxel coordinates for each searchlight sphere within the provided mask, using 'spherical_roi' for neighborhood computation. The iterator visits every non-zero voxel in the mask as a potential center voxel.

Usage

```
searchlight_coords(mask, radius, nonzero = FALSE, cores = 0)
```

Arguments

mask	A NeuroVol object representing the brain mask.
radius	A numeric value specifying the radius (in mm) of the spherical searchlight.
nonzero	A logical value indicating whether each searchlight should be restricted to voxels with nonzero values in the supplied mask. Default is FALSE. It does not affect which voxels are used as centres: every nonzero voxel of the mask is a centre, as in searchlight.
cores	An integer specifying the number of cores to use for parallel computation. Default is 0, which uses a single core.

Value

A deferred_list object containing matrices of integer-valued voxel coordinates, each representing a searchlight region. Its length is the number of nonzero voxels in mask, matching searchlight called with the same arguments.

Examples

```
# Load an example brain mask
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Generate an exhaustive searchlight iterator with a radius of 6 mm

searchlights <- searchlight_coords(mask, radius = 6)
```

searchlight_indices *Compile spherical searchlights to full-volume linear indices*

Description

Returns the geometry of every spherical searchlight centred on a nonzero voxel of mask, without constructing ROI objects, extracting analysis data, or changing parallel execution state. Neighborhoods are compiled sequentially by the same cached-offset and compiled clipping machinery used by searchlight_coords.

Usage

```
searchlight_indices(mask, radius, nonzero = TRUE)
```

Arguments

mask	A NeuroVol object defining the searchlight centres and, when nonzero = TRUE, the allowed neighborhood members.
radius	A positive numeric scalar giving the spherical radius in millimetres.
nonzero	A single logical value. If TRUE (the default), each neighborhood is restricted to finite, nonzero voxels of mask. It never changes the centres: every nonzero mask voxel is a centre.

Details

The full-volume index contract means an input whose first three dimensions contain more than .Machine$integer.max voxels is rejected. The function has no cores argument and never inspects or modifies future::plan().

Value

A list-like object of class searchlight_indices with one integer vector per centre. Every value is a stable, 1-based full-volume linear index using R's column-major array order. Centre order is which(mask != 0). The result carries the following documented attributes: center_indices, space, radius, and nonzero. The object is eagerly compiled but contains indices only.

Examples

```
mask_data <- array(FALSE, c(7, 7, 7))
mask_data[2:6, 2:6, 2:6] <- TRUE
mask <- LogicalNeuroVol(mask_data, NeuroSpace(c(7, 7, 7)))

neighborhoods <- searchlight_indices(mask, radius = 2)
length(neighborhoods)
attr(neighborhoods, "center_indices")
index_to_grid(mask, neighborhoods[[1]])
```

searchlight_shape_functions
Convenience shape generators for resampled_searchlight()

Description

Helpers that return ready-to-use shape_fun callbacks for resampled_searchlight(), covering a few sensible non-spherical defaults.

Usage

```
ellipsoid_shape(scales = c(1, 1, 1), jitter = 0)

cube_shape()

blobby_shape(drop = 0.3, edge_fraction = 0.7)
```

Arguments

scales	Length-3 positive numeric vector scaling the x/y/z axes relative to a sphere (for ellipsoid_shape). Values >1 stretch; <1 compress.
jitter	Non-negative numeric; standard deviation of multiplicative Gaussian noise applied to scales each draw (ellipsoid).
drop	Numeric in [0,1]; probability of dropping a voxel (blobby).
edge_fraction	Numeric in (0,1]; fraction of farthest voxels (by Euclidean distance from the center, in voxel units) considered "edge" and eligible for random dropping (blobby).

Details

Each returned function has signature function(mask, center, radius, iter, nonzero) and should return an $n \times 3$ integer coordinate matrix. The coordinates are later converted to a ROIVolWindow internally.

Value

A function suitable for the shape_fun argument of resampled_searchlight().

Examples

```
mask <- read_vol(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))

# Ellipsoid stretched along z with modest per-iteration jitter
sl_ellip <- resampled_searchlight(mask, radius = 6,
                                  shape_fun = ellipsoid_shape(scales = c(1, 1, 1.4),
                                                              jitter = 0.1))

# Simple axis-aligned cube (Chebyshev ball)
```

```
sl_cube <- resampled_searchlight(mask, radius = 5, shape_fun = "cube")

# Blobby sphere with 40% dropout on boundary voxels
sl_blob <- resampled_searchlight(mask, radius = 6,
                                 shape_fun = blobby_shape(drop = 0.4, edge_fraction = 0.6))
```

`series` *Extract one or more series from object*

Description

This function extracts time series data from specific voxel coordinates in a 4D neuroimaging object. It supports multiple ways of specifying the coordinates:

- Linear indices (1D)
- Grid coordinates (3D matrix)
- Individual x,y,z coordinates

Usage

```
series(x, i, ...)

## S4 method for signature 'ClusteredNeuroVec,numeric'
series(x, i, j, k, ...)

## S4 method for signature 'NeuroHyperVec,ANY'
series(x, i, j, k, ...)

## S4 method for signature 'NeuroVec,matrix'
series(x, i)

## S4 method for signature 'NeuroVec,matrix'
series_roi(x, i)

## S4 method for signature 'NeuroVec,ROICoords'
series(x, i)

## S4 method for signature 'NeuroVec,ROICoords'
series_roi(x, i)

## S4 method for signature 'NeuroVec,LogicalNeuroVol'
series(x, i)

## S4 method for signature 'NeuroVec,NeuroVol'
series(x, i)
```

```
## S4 method for signature 'NeuroVec,LogicalNeuroVol'
series_roi(x, i)

## S4 method for signature 'NeuroVec,integer'
series(x, i, j, k, drop = TRUE)

## S4 method for signature 'DenseNeuroVec,matrix'
series(x, i)

## S4 method for signature 'DenseNeuroVec,integer'
series(x, i, j, k, drop = TRUE)

## S4 method for signature 'NeuroVec,numeric'
series(x, i, j, k, drop = TRUE)

## S4 method for signature 'NeuroVec,numeric'
series_roi(x, i, j, k, drop = TRUE)

## S4 method for signature 'NeuroVecSeq,integer'
series(x, i, j, k, drop = TRUE)

## S4 method for signature 'NeuroVecSeq,numeric'
series(x, i, j, k, drop = TRUE)

## S4 method for signature 'NeuroVecSeq,matrix'
series(x, i)

## S4 method for signature 'NeuroVecSeq,matrix'
series_roi(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,ROICoords'
series(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,matrix'
series(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,numeric'
series(x, i, j, k)

## S4 method for signature 'AbstractSparseNeuroVec,integer'
series(x, i, j, k, drop = TRUE)
```

Arguments

x	A NeuroVecSeq object
i	A matrix of ROI coordinates (n x 3)
...	Additional arguments (not used)
j	second dimension index

k	third dimension index
drop	whether to drop dimension of length 1

Details

when x is a NeuroHyperVec object, the series method returns a 2D array with dimensions [features x trials]

Value

A list or array containing the extracted series.

A 2D array with dimensions [features x trials]

A matrix where each column represents a voxel's time series

A ROIVec object containing the time series for the specified ROI

See Also

series_roi

Examples

```
# Create a simple 4D neuroimaging vector (10x10x10 volume with 20 timepoints)
space <- NeuroSpace(c(10,10,10,20), c(1,1,1))
vec <- NeuroVec(array(rnorm(10*10*10*20), c(10,10,10,20)), space)

# Extract time series using linear indices
ts1 <- series(vec, 1:10)  # Get time series for first 10 voxels

# Extract time series using 3D coordinates
coords <- matrix(c(1,1,1, 2,2,2, 3,3,3), ncol=3, byrow=TRUE)
ts2 <- series(vec, coords)  # Get time series for 3 specific voxel locations

# Extract single time series using x,y,z coordinates
ts3 <- series(vec, 5, 5, 5)  # Get time series from middle voxel
```

---

series_roi *Extract time series from specific voxel coordinates and return as ROI object*

Description

Extracts time series data from a NeuroVec object at specified voxel coordinates and returns it as an ROI object.

Usage

```
series_roi(x, i, ...)
```

Arguments

x	The NeuroVec object
i	Numeric index for the first dimension
...	Additional arguments

Value

A ROIVec object containing the time series data for the specified coordinates.

See Also

series

Examples

```
# Create a simple 4D neuroimaging vector
space <- NeuroSpace(c(10,10,10,20), c(1,1,1))
vec <- NeuroVec(array(rnorm(10*10*10*20), c(10,10,10,20)), space)

# Extract time series for first 100 voxels as ROI
roi1 <- series_roi(vec, 1:100)

# Extract time series using 3D coordinates
coords <- matrix(c(1,1,1, 2,2,2, 3,3,3), ncol=3, byrow=TRUE)
roi2 <- series_roi(vec, coords)
```

---

show,NamedAxis-method *Show method for NamedAxis objects*

Description

Show method for NamedAxis objects

Usage

```
## S4 method for signature 'NamedAxis'
show(object)

## S4 method for signature 'AxisSet1D'
show(object)

## S4 method for signature 'AxisSet2D'
show(object)

## S4 method for signature 'AxisSet3D'
show(object)
```

```
## S4 method for signature 'AxisSet4D'
show(object)

## S4 method for signature 'ClusteredNeuroVec'
show(object)

## S4 method for signature 'ClusteredNeuroVol'
show(object)

## S4 method for signature 'IndexLookupVol'
show(object)

## S4 method for signature 'MappedNeuroVec'
show(object)

## S4 method for signature 'FileMetaInfo'
show(object)

## S4 method for signature 'NeuroHyperVec'
show(object)

## S4 method for signature 'NeuroSlice'
show(object)

## S4 method for signature 'NeuroSpace'
show(object)

## S4 method for signature 'NeuroVecSource'
show(object)

## S4 method for signature 'NeuroVec'
show(object)

## S4 method for signature 'DenseNeuroVec'
show(object)

## S4 method for signature 'NeuroVecSeq'
show(object)

## S4 method for signature 'DenseNeuroVol'
show(object)

## S4 method for signature 'NeuroVol'
show(object)

## S4 method for signature 'SparseNeuroVol'
show(object)
```

```
## S4 method for signature 'Kernel'
show(object)

## S4 method for signature 'ROIVol'
show(object)

## S4 method for signature 'ROICoords'
show(object)

## S4 method for signature 'ROIVec'
show(object)

## S4 method for signature 'SparseNeuroVec'
show(object)
```

Arguments

object	A NamedAxis object

Value

Invisibly returns NULL, called for its side effect of displaying the object.

`simulate_fmri` *Simulate fMRI Data*

Description

Generates synthetic 4D fMRI data with realistic spatiotemporal properties including temporal autocorrelation, spatial smoothness, heteroscedasticity, and optional global signal fluctuations and latent components.

Usage

```
simulate_fmri(
  mask,
  n_time,
  TR = 2,
  spatial_fwhm = 6,
  ar_mean = 0.45,
  ar_sd = 0.08,
  noise_sd = 1,
  hetero_fwhm = 20,
  hetero_strength = 0.6,
  global_amp = 0.2,
  global_rho = 0.85,
  n_factors = 4,
```

```
  factor_fwhm = 12,
  factor_rho = 0.8,
  seed = NULL,
  return_centered = TRUE
)
```

Arguments

mask	A NeuroVol object defining the brain mask region. Can be binary or continuous (non-zero values define the mask).
n_time	Integer specifying the number of time points to simulate.
TR	Numeric value for the repetition time in seconds (default = 2.0). Currently used only for metadata.
spatial_fwhm	Numeric value specifying the spatial smoothness in mm (full width at half maximum) applied to each timepoint (default = 6).
ar_mean	Numeric value for the mean of the AR(1) coefficient distribution across voxels (default = 0.45).
ar_sd	Numeric value for the standard deviation of the AR(1) coefficient distribution (default = 0.08).
noise_sd	Numeric value for the baseline noise standard deviation (default = 1.0).
hetero_fwhm	Numeric value for the spatial scale (FWHM in mm) of the heteroscedasticity field (default = 20).
hetero_strength	Numeric value controlling the strength of spatial heteroscedasticity on log scale (default = 0.6).
global_amp	Numeric value for the amplitude of global signal fluctuations as a fraction of median noise (default = 0.2). Set to 0 to disable.
global_rho	Numeric value for the AR(1) coefficient of global signal (default = 0.85).
n_factors	Integer specifying the number of latent spatial components (default = 4). Set to 0 to disable.
factor_fwhm	Numeric value for the spatial smoothness (FWHM in mm) of latent component maps (default = 12).
factor_rho	Numeric value for the AR(1) coefficient of latent component time courses (default = 0.8).
seed	Integer seed for random number generation (default = NULL for no seed).
return_centered	Logical indicating whether to center each voxel's time series to mean zero (default = TRUE).

Details

The simulation combines several realistic features:

- Voxel-wise AR(1) temporal autocorrelation with spatial variation
- Spatial smoothing applied to innovations for realistic spatial correlation

- Heteroscedastic noise with smooth spatial modulation
- Optional low-frequency global signal fluctuations
- Optional latent spatial components resembling resting-state networks

The spatial smoothing uses the package's optimized `gaussian_blur` function for efficiency. Set any FWHM argument to `0` to disable that smoothing step.

Value

A `NeuroVec` object containing the simulated 4D fMRI data.

References

Welvaert, M., & Rosseel, Y. (2013). On the definition of signal-to-noise ratio and contrast-to-noise ratio for fMRI data. PloS one, 8(11), e77089.

Examples

```
# Create a simple spherical mask
dims <- c(32, 32, 20)
mask_array <- array(FALSE, dims)
center <- dims / 2
for (i in 1:dims[1]) {
  for (j in 1:dims[2]) {
    for (k in 1:dims[3]) {
      if (sum(((c(i,j,k) - center) / (dims/3))^2) <= 1) {
        mask_array[i,j,k] <- TRUE
      }
    }
  }
}

mask <- NeuroVol(mask_array, NeuroSpace(dims, c(3,3,3)))

# Simulate 100 time points
sim_data <- simulate_fmri(mask, n_time = 100, seed = 42)

# Check dimensions
dim(sim_data)  # Should be c(32, 32, 20, 100)
```

---

slice *Extract image slice*

Description

Extract a 2D slice from an image volume

Usage

```
slice(x, zlevel, along, orientation, ...)

## S4 method for signature 'NeuroVol,numeric,numeric,missing'
slice(x, zlevel, along, orientation)

## S4 method for signature 'NeuroVol,numeric,NeuroSpace,AxisSet3D'
slice(x, zlevel, along, orientation)
```

Arguments

x	the object
zlevel	coordinate (in voxel units) along the sliced axis
along	the axis along which to slice
orientation	the target orientation of the 2D slice
...	additional arguments

Value

A 2D slice from the image volume.

---

slices *Extract an ordered series of 2D slices from a 3D or 4D object*

Description

This function extracts an ordered series of 2D slices from a 3D or 4D object. The returned slices are in the order they appear in the original object.

Usage

```
slices(x, ...)

## S4 method for signature 'NeuroVol'
slices(x)
```

Arguments

x	A NeuroVol object
...	Additional arguments to be passed to the underlying methods

Value

A `list` of 2D `matrices`, each containing a slice from the input `x`.

A deflist object containing functions that return 2D slices of the volume along the z-axis. The length of the deflist equals the number of slices in the z dimension.

Examples

```
# Create a simple 3D volume
space <- NeuroSpace(c(10,10,10), c(1,1,1))
vol <- NeuroVol(array(rnorm(10*10*10), c(10,10,10)), space)

# Get all slices along the z-axis
slc <- slices(vol)

# Number of slices equals the z dimension
length(slc) == dim(vol)[3]

# Each slice is a 2D matrix
dim(slc[[1]]) == c(10,10)
```

---

soft_alpha_params *Self-tuning nonlinear opacity curve for statistical overlays*

Description

Parameters of the curve used by `plot_overlay(ov_alpha_mode = "soft")`. For magnitude m, opacity is

$$alpha(m) = f + (1 - f)\,\mathrm{clamp}((m - lo)/(hi - lo), 0, 1)^{\gamma},$$

where f is `alpha_floor`. Plotting then hides values below the hard threshold and multiplies by `ov_alpha`.

Usage

```
soft_alpha_params(
  mags,
  thresh = 0,
  cap = NULL,
  gamma = NULL,
  alpha_mid = 0.2,
  gamma_min = 1.5,
  gamma_max = 5,
  knee = NULL,
  alpha_floor = 0
)
```

Arguments

`mags`	Numeric vector of overlay magnitudes (typically `abs(values)`).
`thresh`	Hard threshold; used as the knee when `> 0` and `knee` is not given.
`cap`	Optional upper magnitude anchor (opacity 1).
`gamma`	Optional fixed exponent; `NULL` auto-tunes it.
`alpha_mid`	Target opacity for the median supra-knee magnitude when `gamma` is tuned.

gamma_min, gamma_max
: Clamp range for the tuned exponent.

knee
: Optional non-negative lower magnitude anchor, overriding the threshold/median policy. Use `0` to ramp from zero.

alpha_floor
: Minimum opacity (0 to 1) above the knee, before `ov_alpha` and the hard threshold are applied.

Details

The knee `lo` defaults to the threshold or, when no threshold is set, to the median non-zero magnitude (a robust noise-floor proxy). The cap `hi` defaults to the largest magnitude. When `gamma` is not given it is tuned so the median supra-knee magnitude maps to `alpha_mid` (before the floor), and clamped to `[gamma_min, gamma_max]` so the default curve stays convex; an explicit `gamma` bypasses the clamp. Fix `knee`, `cap` and `gamma` to reuse one curve across datasets.

Value

A list with `lo`, `hi`, `gamma` and `alpha_floor`.

See Also

plot_overlay

Examples

```
p <- soft_alpha_params(0:8, knee = 0, cap = 3, gamma = 0.7, alpha_floor = 0.15)
m <- c(0, 1.6, 2.1, 3, 8)
p$alpha_floor + (1 - p$alpha_floor) *
  pmin(pmax((m - p$lo) / (p$hi - p$lo), 0), 1)^p$gamma
```

---

space *Extract Geometric Properties of an Image*

Description

This function retrieves the geometric properties of a given image, such as dimensions and voxel size.

Retrieves the NeuroSpace object associated with an IndexLookupVol object.

Usage

```
space(x, ...)

## S4 method for signature 'ClusteredNeuroVec'
space(x)

## S4 method for signature 'IndexLookupVol'
```

```
space(x)

## S4 method for signature 'ROICoords'
space(x)

## S4 method for signature 'NeuroObj'
space(x)

## S4 method for signature 'NeuroHyperVec'
space(x)

## S4 method for signature 'NeuroSpace'
space(x)
```

Arguments

x	An IndexLookupVol object
...	Additional arguments, if needed.

Value

A NeuroSpace object representing the geometric space of x.

Examples

```
# Create a NeuroSpace object with dimensions (10, 10, 10) and voxel size (1, 1, 1)
x <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))

# Create a NeuroVol object with random data and the specified NeuroSpace
vol <- NeuroVol(rnorm(10 * 10 * 10), x)

# Retrieve the geometric properties of the NeuroVol object
identical(x, space(vol))

space <- NeuroSpace(c(64, 64, 64), c(1, 1, 1), c(0, 0, 0))
ilv <- IndexLookupVol(space, c(1:100))
space(ilv)  # Get the associated NeuroSpace object
```

---

space_utils *Space utility functions*

Description

Utilities for reasoning about mapped voxel spaces and slice embeddings.

Returns a voxel space with positive diagonal affine that encloses all mapped input voxel centers.

Returns the affine mapping slice coordinates to 3D volume coordinates.

Usage

```
output_aligned_space(mapped_voxels, voxel_sizes = NULL)

vox2out_vox(mapped_voxels, voxel_sizes = NULL)

slice_to_volume_affine(index, axis, shape = NULL, index_base = c("R", "zero"))

slice2volume(index, axis, shape = NULL, index_base = c("R", "zero"))
```

Arguments

mapped_voxels	A 'NeuroSpace', 'NeuroVol', 'NeuroVec', object with 'shape' and 'affine', or length-2 sequence '(shape, affine)'.
voxel_sizes	Optional output voxel sizes for spatial axes. If scalar, treated as isotropic.
index	Slice index.
axis	Slice axis ('1..3' or '0..2').
shape	Optional volume shape for bounds validation.
index_base	Either '"R"' (1-based, default) or '"zero"'.

Details

Compared to NiBabel-style helpers, these functions add a few R-friendly improvements:

- Accept 'NeuroSpace', 'NeuroVol', and list/object '(shape, affine)' inputs.
- Handle inputs with more than 3 dimensions by using first 3 spatial dims.
- Support both R-style (1-based) and zero-based slice indexing.

Value

A named list with:

- 'shape': output spatial shape.
- 'affine': output 4x4 affine (positive diagonal).
- 'bounds': world-space min/max of mapped corners.

Same as 'output_aligned_space()'.

A '4 x 3' affine matrix from slice coordinates to volume coordinates.

Same as 'slice_to_volume_affine()'.

Examples

```
sp <- NeuroSpace(c(10L, 8L, 6L), spacing = c(2, 2, 2))
out <- output_aligned_space(sp)
out$shape
out$affine

slice_aff <- slice_to_volume_affine(index = 3, axis = 3, shape = c(10, 8, 6))
slice_aff
```

spacing *Extract Voxel Dimensions of an Image*

Description

This function extracts the voxel dimensions of an image represented by the input object.

Usage

```
spacing(x)

## S4 method for signature 'ROICoords'
spacing(x)

## S4 method for signature 'NeuroObj'
spacing(x)

## S4 method for signature 'NeuroHyperVec'
spacing(x)

## S4 method for signature 'NeuroSpace'
spacing(x)
```

Arguments

x	The object representing the image.

Value

A numeric vector specifying the voxel dimensions of x.

Examples

```
bspace <- NeuroSpace(c(10, 10, 10), c(2, 2, 2))
all.equal(spacing(bspace), c(2, 2, 2))
```

SparseNeuroVec-class *SparseNeuroVec Class*

Description

A class representing a sparse four-dimensional brain image, optimized for efficient storage and access of large, sparse neuroimaging data.

Constructs a SparseNeuroVec object for efficient representation and manipulation of sparse neuroimaging data with many zero or missing values.

Usage

```
SparseNeuroVec(
  data,
  space,
  mask,
  label = "",
  volume_labels = character(),
  orientation = c("auto", "voxels_x_time", "time_x_voxels")
)
```

Arguments

data	A matrix or a 4-D array containing the neuroimaging data. For matrix input, rows/columns must match either voxels-by-time or time-by-voxels relative to mask; when unambiguous, orientation = "auto" infers the layout from mask cardinality. When the matrix is square (n_voxels == n_timepoints), auto mode assumes voxels-by-time and warns – pass orientation explicitly if the matrix is time-by-voxels (as from series). For 4-D arrays, axes are always $x, y, z, time$.
space	A NeuroSpace object representing the dimensions and voxel spacing of the neuroimaging data.
mask	A 3D array, 1D vector of type logical, or an instance of type LogicalNeuroVol, which specifies the locations of the non-zero values in the data.
label	Optional character string providing a label for the vector
volume_labels	Optional character vector of length dim(space)[4] giving per-volume labels.
orientation	Matrix orientation: "auto" (default) infers it from mask cardinality; a square matrix is interpreted as voxels by time. Use "time_x_voxels" for output from series, or "voxels_x_time" to declare rows as voxels explicitly. Ignored for 4-D arrays.

Details

SparseNeuroVec objects store data in a compressed format, where only non-zero values are retained. This approach significantly reduces memory usage for sparse brain images. The class leverages the mask and mapping from its parent class AbstractSparseNeuroVec to efficiently manage the spatial structure of the data.

Value

A SparseNeuroVec object, containing the sparse neuroimaging data, mask, and associated NeuroSpace information.

Slots

data A matrix where each column represents a non-zero vector spanning the fourth dimension (e.g., time series for each voxel). Rows correspond to voxels in the sparse domain defined by the mask.

Inheritance

SparseNeuroVec inherits from:

- NeuroVec: Base class for 4D brain images
- AbstractSparseNeuroVec: Provides sparse representation framework
- ArrayLike4D: Interface for 4D array-like operations

See Also

AbstractSparseNeuroVec-class for the parent sparse representation class. NeuroVec-class for the base 4D brain image class.

Examples

```
# Create a sparse 4D brain image
mask <- LogicalNeuroVol(array(runif(64*64*32) > 0.7, c(64,64,32)), NeuroSpace(c(64,64,32)))
data <- matrix(rnorm(sum(mask) * 100), nrow=sum(mask), ncol=100)
sparse_vec <- SparseNeuroVec(data=data, mask=mask, space=NeuroSpace(dim=c(64,64,32,100)))

# Access a subset of the data
subset <- sparse_vec[,,, 1:10]


bspace <- NeuroSpace(c(10,10,10,100), c(1,1,1))
mask <- array(rnorm(10*10*10) > .5, c(10,10,10))
mat <- matrix(rnorm(sum(mask)), 100, sum(mask))
svec <- SparseNeuroVec(mat, bspace, mask)
length(indices(svec)) == sum(mask)
```

SparseNeuroVecSource-class

SparseNeuroVecSource Class

Description

A class used to produce a SparseNeuroVec instance. It encapsulates the necessary information to create a sparse representation of a 4D neuroimaging dataset.

Details

SparseNeuroVecSource acts as a factory for SparseNeuroVec objects. It holds the spatial mask that determines which voxels will be included in the sparse representation. This class is typically used in data loading or preprocessing pipelines where the sparse structure of the data is known or determined before the full dataset is loaded.

Slots

mask An object of class LogicalNeuroVol representing the subset of voxels that will be stored in memory. This mask defines the sparse structure of the resulting SparseNeuroVec.

Inheritance

SparseNeuroVecSource inherits from:

- NeuroVecSource: Base class for NeuroVec source objects

See Also

SparseNeuroVec-class for the resulting sparse 4D neuroimaging data class. LogicalNeuroVol-class for the mask representation.

Examples

```
# Create a simple mask
mask_data <- array(runif(64*64*32) > 0.7, dim = c(64, 64, 32))
mask <- LogicalNeuroVol(mask_data, space = NeuroSpace(dim = c(64, 64, 32)))

# Create a SparseNeuroVecSource
sparse_source <- new("SparseNeuroVecSource", mask = mask)
```

SparseNeuroVol-class *SparseNeuroVol Class*

Description

This class represents a three-dimensional brain image using a sparse data representation. It is particularly useful for large brain images with a high proportion of zero or missing values, offering efficient storage and processing.

Construct a SparseNeuroVol instance

Usage

```
SparseNeuroVol(data, space, indices = NULL, label = "")
```

Arguments

data	a numeric vector or ROIVol
space	an instance of class NeuroSpace
indices	a index vector indicating the 1-d coordinates of the data values
label	a character string

Details

The SparseNeuroVol class extends the NeuroVol class and implements the ArrayLike3D interface. It uses a sparseVector from the Matrix package to store the image data, which allows for memory-efficient representation of sparse 3D neuroimaging data.

Image data is backed by Matrix::sparseVector.

Value

SparseNeuroVol instance

Slots

data A sparseVector object from the Matrix package, storing the image volume data in a sparse format.

References

Bates, D., & Maechler, M. (2019). Matrix: Sparse and Dense Matrix Classes and Methods. R package version 1.2-18. https://CRAN.R-project.org/package=Matrix

See Also

NeuroVol-class for the base volumetric image class. DenseNeuroVol-class for a dense representation of 3D brain images.

Examples

```
# Create a sparse 3D brain image
dim <- c(64L, 64L, 64L)
space <- NeuroSpace(dim = dim, origin = c(0, 0, 0), spacing = c(1, 1, 1))
sparse_data <- Matrix::sparseVector(x = c(1, 2, 3),
                                    i = c(100, 1000, 10000),
                                    length = prod(dim))
sparse_vol <- new("SparseNeuroVol", space = space, data = sparse_data)
sparse_vol[1000] == 1

data <- 1:10
indices <- seq(1,1000, length.out=10)
bspace <- NeuroSpace(c(64,64,64), spacing=c(1,1,1))
sparsevol <- SparseNeuroVol(data,bspace,indices=indices)
densevol <- NeuroVol(data,bspace,indices=indices)
sum(sparsevol) == sum(densevol)
```

---

spatial-filter *Spatial Filtering Methods for Neuroimaging Data*

Description

Methods for applying spatial filters to neuroimaging data

spherical_roi *Create a Spherical Region of Interest*

Description

Creates a Spherical ROI based on a centroid.

Usage

```
spherical_roi(
  bvol,
  centroid,
  radius,
  fill = NULL,
  nonzero = FALSE,
  use_cpp = TRUE
)
```

Arguments

bvol	an NeuroVol or NeuroSpace instance
centroid	the center of the sphere in positive-coordinate (i,j,k) voxel space.
radius	the radius in real units (e.g. millimeters) of the spherical ROI
fill	optional value(s) to store as data
nonzero	if TRUE, keep only nonzero elements from bvol
use_cpp	Deprecated and ignored; the compiled implementation is always used. Passing FALSE warns. The former fallback returned neighbourhoods offset by one voxel and missing boundary voxels.

Value

an instance of class ROIVol

See Also

[spherical_roi_set()] for efficiently creating many spherical ROIs, [series_roi()] and [coords()] for extracting time series and coordinates from ROIs, and the vignette: `vignette("regionOfInterest", package = "neuroim2")`.

Examples

```
sp1 <- NeuroSpace(c(10,10,10), c(1,2,3))
# create an ROI centered around the integer-valued positive voxel coordinate: i=5, j=5, k=5
cube <- spherical_roi(sp1, c(5,5,5), 3.5)
vox <- coords(cube)
cds <- coords(cube, real=TRUE)
```

```
## fill in ROI with value of 6
cube1 <- spherical_roi(sp1, c(5,5,5), 3.5, fill=6)
all(cube1 == 6)

## Create multiple spherical ROIs at once (preferred):
centers <- rbind(c(5,5,5), c(3,3,3), c(7,7,7))
vols <- spherical_roi_set(bvol = sp1,
                          centroids = centers, radius = 3.5, fill = 1)
length(vols)  # 3

## Equivalent, less efficient lapply variant:
vols2 <- lapply(seq_len(nrow(centers)), function(i) {
  spherical_roi(sp1, centers[i,], radius = 3.5, fill = 1)
})

# create an ROI centered around the real-valued coordinates: x=5, y=5, z=5
vox <- coord_to_grid(sp1, c(5, 5, 5))
cube <- spherical_roi(sp1, vox, 3.5)
```

`spherical_roi_set` *Create Multiple Spherical Regions of Interest*

Description

This function generates multiple spherical ROIs simultaneously, centered at the provided voxel coordinates. It is more efficient than calling `spherical_roi` multiple times when you need to create many ROIs.

Usage

```
spherical_roi_set(bvol, centroids, radius, fill = NULL, nonzero = FALSE)
```

Arguments

`bvol`	A `NeuroVol` or `NeuroSpace` instance
`centroids`	A matrix of voxel coordinates where each row represents a centroid (i,j,k)
`radius`	The radius in real units (e.g. millimeters) of the spherical ROIs
`fill`	Optional value(s) to store as data. If provided, must be either a single value or a vector with length equal to the number of ROIs
`nonzero`	If `TRUE`, keep only nonzero elements from `bvol`

Value

A list of `ROIVolWindow` objects, one for each centroid

Examples

```
# Create a NeuroSpace object
sp1 <- NeuroSpace(c(10,10,10), c(1,2,3))

# Create multiple ROIs centered at different voxel coordinates
centroids <- matrix(c(5,5,5, 3,3,3, 7,7,7), ncol=3, byrow=TRUE)
rois <- spherical_roi_set(sp1, centroids, 3.5)

# Create ROIs with specific fill values
rois <- spherical_roi_set(sp1, centroids, 3.5, fill=c(1,2,3))
```

---

split_blocks *Cut a vector-valued object into a list of sub-blocks*

Description

Splits a vector-valued object into a list of sub-blocks defined by a vector of indices.

Usage

```
split_blocks(x, indices, ...)

## S4 method for signature 'NeuroVec,integer'
split_blocks(x, indices, ...)

## S4 method for signature 'NeuroVec,factor'
split_blocks(x, indices, ...)

## S4 method for signature 'NeuroVec,factor'
split_blocks(x, indices, ...)
```

Arguments

x	a vector-valued object
indices	a vector of indices defining the sub-blocks. Must match the length of the input vector.
...	additional arguments

Value

A list of sub-blocks, where each sub-block contains the elements from x corresponding to the matching indices.

Examples

```
# Create a 4D neuroimaging vector with 20 timepoints
space <- NeuroSpace(c(10,10,10,20), c(1,1,1))
vec <- NeuroVec(array(rnorm(10*10*10*20), c(10,10,10,20)), space)

# Split into 4 blocks by assigning timepoints to blocks 1-4 repeatedly
block_indices <- rep(1:4, length.out=20)
blocks <- split_blocks(vec, block_indices)
```

---

split_clusters *Cut an object into a list of spatial or spatiotemporal clusters*

Description

This function cuts an object into a list of sub-objects based on a vector of cluster indices. The resulting list contains each of the clusters as separate objects.

These methods split a NeuroVec object into multiple ROIVec objects based on cluster assignments.

Usage

```
split_clusters(x, clusters, ...)

## S4 method for signature 'NeuroVec,ClusteredNeuroVol'
split_clusters(x, clusters, ...)

## S4 method for signature 'NeuroVec,integer'
split_clusters(x, clusters, ...)

## S4 method for signature 'NeuroVol,ClusteredNeuroVol'
split_clusters(x, clusters)

## S4 method for signature 'NeuroVol,integer'
split_clusters(x, clusters)

## S4 method for signature 'NeuroVol,numeric'
split_clusters(x, clusters)

## S4 method for signature 'ClusteredNeuroVol,missing'
split_clusters(x, clusters)

## S4 method for signature 'NeuroVec,integer'
split_clusters(x, clusters, ...)

## S4 method for signature 'NeuroVec,numeric'
split_clusters(x, clusters, ...)
```

```
## S4 method for signature 'NeuroVec,ClusteredNeuroVol'
split_clusters(x, clusters, ...)
```

Arguments

x	A NeuroVec object to be split.
clusters	Either a ClusteredNeuroVol object or an integer vector of cluster assignments.
...	Additional arguments to be passed to methods.

Details

There are two methods for splitting clusters:

- Using a ClusteredNeuroVol object: This method uses the pre-defined clusters in the ClusteredNeuroVol object.
- Using an integer vector: This method allows for custom cluster assignments.

methods return a deflist, which is a lazy-loading list of ROIVec objects.

Value

A `list` of sub-objects, where each sub-object corresponds to a unique cluster index.

A deflist (lazy-loading list) of ROIVec objects, where each element corresponds to a cluster.

See Also

NeuroVec-class, ClusteredNeuroVol-class, ROIVec-class

Examples

```
# Create a synthetic 3D volume and its NeuroSpace
space <- NeuroSpace(c(10, 10, 10,4))
vol_data <- array(rnorm(10 * 10 * 10 * 4), dim = c(10, 10, 10,4))
neuro_vec <- NeuroVec(vol_data, space)

# Create a binary mask (e.g., select voxels with values > 0)
mask_data <- as.logical(neuro_vec[[1]] > .5)
mask_vol <- LogicalNeuroVol(mask_data, NeuroSpace(c(10, 10, 10)))

# Extract indices and coordinates for the masked voxels
mask_idx <- which(mask_data)
coords <- index_to_coord(mask_vol, mask_idx)

# Perform k-means clustering on the coordinates (e.g., 3 clusters)
set.seed(123)  # for reproducibility
k_res <- kmeans(coords, centers = 3)

# Create a ClusteredNeuroVol using the mask and k-means cluster assignments
clustered_vol <- ClusteredNeuroVol(mask_vol, k_res$cluster)

# Split the NeuroVec by clusters using the ClusteredNeuroVol method
```

```
  split_result_clust <- split_clusters(neuro_vec, clustered_vol)

  # Calculate and print the mean value for each cluster
  means_clust <- sapply(split_result_clust, function(x) mean(values(x)))
  print(means_clust)

  # Alternatively, create an integer vector of cluster assignments:
  cluster_assignments <- numeric(prod(dim(space)[1:3]))
  cluster_assignments[mask_idx] <- k_res$cluster
  split_result_int <- split_clusters(neuro_vec, as.integer(cluster_assignments))

  # Verify that both splitting methods yield the same cluster means
  means_int <- sapply(split_result_int, function(x) mean(values(x)))
  print(all.equal(sort(means_clust), sort(means_int)))



# Create a simple example space and data
space <- NeuroSpace(c(10, 10, 10,4))
data <- array(rnorm(1000*4), dim = c(10, 10, 10,4))
vec <- NeuroVec(data, space)

# Create a mask for clustering (e.g., values > 0)
mask <- vec[,,,1] > 0
mask_vol <- LogicalNeuroVol(as.array(mask), NeuroSpace(c(10, 10, 10)))

# Get coordinates of masked voxels for clustering
mask_idx <- which(mask)
coords <- index_to_coord(mask_vol, mask_idx)

# Perform clustering on the coordinates (3 clusters for example)
set.seed(123) # for reproducibility
kmeans_result <- kmeans(coords, centers = 3)

# Create a ClusteredNeuroVol
clustered_vol <- ClusteredNeuroVol(mask_vol, kmeans_result$cluster)

# Split the NeuroVec by clusters
split_result <- split_clusters(vec, clustered_vol)

# Calculate mean value for each cluster
cluster_means <- sapply(split_result, function(x) mean(values(x)))
print(cluster_means)

# Alternative: using integer cluster assignments
cluster_indices <- numeric(prod(dim(space)[1:3]))
cluster_indices[mask_idx] <- kmeans_result$cluster
split_result2 <- split_clusters(vec, as.integer(cluster_indices))

# Verify both methods give same results
cluster_means2 <- sapply(split_result2, function(x) mean(values(x)))
print(all.equal(sort(cluster_means), sort(cluster_means2)))
```

split_fill *Fill Disjoint Sets of Values with the Output of a Function*

Description

This function splits an object into disjoint sets of values based on a factor, applies a specified function to each set, and returns a new object with the original values replaced by the function's output.

Usage

```
split_fill(x, fac, FUN)

## S4 method for signature 'NeuroVol,factor,function'
split_fill(x, fac, FUN)
```

Arguments

x	The object to split.
fac	The factor to split by.
FUN	The function used to summarize the sets.

Details

The FUN function can either return a scalar for each input vector or a vector equal to the length of the input vector. If it returns a scalar, every voxel in the set will be filled with that value in the output vector.

Value

An object of the same class as x, with values replaced by the output of FUN.

Examples

```
## Summarize with mean -- FUN returns a scalar
x <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))
vol <- NeuroVol(rnorm(10 * 10 * 10), x)
fac <- factor(rep(1:10, length.out=1000))
ovol.mean <- split_fill(vol, fac, mean)
identical(dim(ovol.mean), dim(vol))
length(unique(as.vector(ovol.mean))) == 10

## Transform by reversing vector -- FUN returns a vector
ovol2 <- split_fill(vol, fac, rev)
```

split_reduce *Summarize Subsets of an Object by Splitting by Row and Applying a Summary Function*

Description

This function summarizes subsets of a numeric matrix or matrix-like object by first splitting the object by row and then applying a summary function.

Usage

```
split_reduce(x, fac, FUN)

## S4 method for signature 'matrix,integer,function'
split_reduce(x, fac, FUN)

## S4 method for signature 'matrix,factor,missing'
split_reduce(x, fac)

## S4 method for signature 'matrix,factor,function'
split_reduce(x, fac, FUN)

## S4 method for signature 'NeuroVec,factor,function'
split_reduce(x, fac, FUN)

## S4 method for signature 'NeuroVec,factor,missing'
split_reduce(x, fac, FUN)
```

Arguments

x	A numeric matrix or matrix-like object.
fac	A factor to define subsets of the object.
FUN	The summary function to apply to each subset. If not provided, the mean of each sub-matrix column is computed.

Details

If 'FUN' is supplied, it must take a vector and return a single scalar value. If it returns more than one value, an error will occur.

If 'x' is a NeuroVec instance, voxels (dimensions 1:3) are treated as columns and time-series (dimension 4) as rows. The summary function is then applied to groups of voxels. However, if the goal is to apply a function to groups of time-points.

Value

A matrix (or matrix-like object) containing the summarized values after applying FUN.

Examples

```
mat = matrix(rnorm(100*100), 100, 100)
fac = factor(sample(1:3, nrow(mat), replace=TRUE))
## Compute column means of each sub-matrix
ms <- split_reduce(mat, fac)
all.equal(row.names(ms), levels(fac))

## Compute column medians of each sub-matrix
ms <- split_reduce(mat, fac, median)

## Compute time-series means grouped over voxels.
## Here, 'length(fac)' must equal the number of voxels: 'prod(dim(bvec)[1:3])'
bvec <- NeuroVec(array(rnorm(24*24*24*24), c(24,24,24,24)), NeuroSpace(c(24,24,24,24), c(1,1,1)))
fac <- factor(sample(1:3, prod(dim(bvec)[1:3]), replace=TRUE))
ms <- split_reduce(bvec, fac)
ms2 <- split_reduce(bvec, fac, mean)
all.equal(row.names(ms), levels(fac))
all.equal(ms, ms2)
```

---

split_scale *Center and/or Scale Row-subsets of a Matrix or Matrix-like Object*

Description

This function centers and/or scales the row-subsets of a numeric matrix or matrix-like object.

Usage

```
split_scale(x, f, center, scale)

## S4 method for signature 'matrix,factor,logical,logical'
split_scale(x, f, center = TRUE, scale = TRUE)

## S4 method for signature 'matrix,factor,missing,missing'
split_scale(x, f)

## S4 method for signature 'DenseNeuroVec,factor,missing,missing'
split_scale(x, f)

## S4 method for signature 'DenseNeuroVec,factor,logical,missing'
split_scale(x, f, center)

## S4 method for signature 'DenseNeuroVec,factor,logical,logical'
split_scale(x, f, center, scale)
```

Arguments

x	A numeric matrix or matrix-like object.
f	The splitting object, typically a factor or a set of integer indices. Must be equal to the number of rows in the matrix.
center	Should values within each submatrix be centered? If TRUE, the mean is removed from each column of the submatrix.
scale	Should values be scaled? If TRUE, the vector is divided by the standard deviation for each column of the submatrix.

Value

An object of the same class as x, with row-subsets centered and/or scaled according to f.

Examples

```
M <- matrix(rnorm(1000), 10, 100)
fac <- factor(rep(1:2, each=5))
Ms <- split_scale(M, fac)

## Correctly centered
all(abs(apply(Ms[fac == 1,], 2, mean)) < .000001)
all(abs(apply(Ms[fac == 2,], 2, mean)) < .000001)

## Correctly scaled
all.equal(apply(Ms[fac == 1,], 2, sd), rep(1, ncol(Ms)))
all.equal(apply(Ms[fac == 2,], 2, sd), rep(1, ncol(Ms)))
```

---

square_roi *Create a square region of interest*

Description

This function creates a square region of interest (ROI) in a 3D volume, where the z-dimension is fixed at one voxel coordinate. The ROI is defined within a given NeuroVol or NeuroSpace instance.

Usage

```
square_roi(bvol, centroid, surround, fill = NULL, nonzero = FALSE, fixdim = 3)
```

Arguments

bvol	A NeuroVol or NeuroSpace instance representing the 3D volume or space.
centroid	A numeric vector of length 3, representing the center of the square ROI in voxel coordinates.
surround	A non-negative integer specifying the number of voxels on either side of the central voxel.

fill	An optional value or values to assign to the data slot of the resulting ROI. If not provided, no data will be assigned.
nonzero	A logical value indicating whether to keep only nonzero elements from bvol. If bvol is a NeuroSpace instance, this argument is ignored.
fixdim	A logical value indicating whether the fixed dimension is the third, or z, dimension. Default is TRUE.

Value

An instance of class ROIVol representing the square ROI.

Examples

```
sp1 <- NeuroSpace(c(10, 10, 10), c(1, 1, 1))
square <- square_roi(sp1, c(5, 5, 5), 1)
vox <- coords(square)
## a 3 X 3 X 1 grid
nrow(vox) == 9
```

---

strip_extension *Generic function to strip extension from file name, given a* FileFormat *instance.*

Description

Removes the file extension from a given file name based on the FileFormat specifications.

Usage

```
strip_extension(x, file_name)

## S4 method for signature 'FileFormat,character'
strip_extension(x, file_name)
```

Arguments

x	A FileFormat object specifying the format requirements
file_name	A character string specifying the file name to strip the extension from

Details

The function performs the following steps:

1. If the file_name matches the header file format, it removes the header extension.
2. If the file_name matches the data file format, it removes the data extension.
3. If the file_name doesn't match either format, it throws an error.

Value

A `character` string `file_name` without its extension.

A character string representing the file name without the extension

See Also

`header_file`, `data_file` for related file name manipulation

Examples

```
# Create a FileFormat for NIFTI files
fmt <- new("FileFormat",
           header_extension = "nii",
           data_extension = "nii")

# Strip extension from a NIFTI file
strip_extension(fmt, "brain_scan.nii")  # Returns "brain_scan"
```

---

sub_clusters *Select a Subset of Clusters*

Description

Return a new object containing only the requested clusters. Clusters can be identified by integer ID or by name (matched against the label map).

Usage

```
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVec,integer'
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVec,numeric'
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVec,character'
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVol,integer'
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVol,numeric'
sub_clusters(x, ids, ...)

## S4 method for signature 'ClusteredNeuroVol,character'
sub_clusters(x, ids, ...)
```

Arguments

x	A clustered neuroimaging object.
ids	Integer cluster IDs, numeric (coerced to integer), or character cluster names to retain.
...	Additional arguments (currently unused).

Value

An object of the same class as x containing only the selected clusters.

Examples

```
sp <- NeuroSpace(c(10L, 10L, 10L), c(1, 1, 1))
mask <- LogicalNeuroVol(array(c(rep(TRUE, 500), rep(FALSE, 500)),
                              c(10, 10, 10)), sp)
clusters <- rep(1:5, length.out = 500)
cvol <- ClusteredNeuroVol(mask, clusters,
          label_map = list(A = 1, B = 2, C = 3, D = 4, E = 5))
# By integer ID
sub <- sub_clusters(cvol, c(1L, 3L))
# By name
sub2 <- sub_clusters(cvol, c("A", "C"))
```

---

sub_vector *Generic function to extract a sub-vector from a* NeuroVec *object.*

Description

Extracts a subset of volumes from a file-backed neuroimaging vector and returns them as a dense (in-memory) vector.

Extracts a subsequence of volumes from a NeuroVecSeq object.

Usage

```
sub_vector(x, i, ...)

## S4 method for signature 'FileBackedNeuroVec,numeric'
sub_vector(x, i)

## S4 method for signature 'NeuroVec,numeric'
sub_vector(x, i)

## S4 method for signature 'NeuroVec,character'
sub_vector(x, i)

## S4 method for signature 'NeuroVecSeq,numeric'
```

```
sub_vector(x, i)

## S4 method for signature 'NeuroVecSeq,numeric'
sub_vector(x, i)

## S4 method for signature 'AbstractSparseNeuroVec,numeric'
sub_vector(x, i)
```

Arguments

x	A NeuroVecSeq object
i	Numeric vector of indices specifying the time points to extract
...	additional arguments

Details

This method efficiently reads only the requested volumes from disk, converting them to an in-memory representation. The spatial metadata is preserved but adjusted to reflect the new number of volumes.

Memory usage is proportional to the number of volumes requested, not the size of the full dataset.

Value

A NeuroVec object that is a sub-sequence of the supplied object.

A NeuroVecSeq object containing the extracted subsequence

Examples

```
bvec <- NeuroVec(array(rnorm(24*24*24*24), c(24,24,24,24)), NeuroSpace(c(24,24,24,24), c(1,1,1)))
vec <- sub_vector(bvec,1:2)
all.equal(2, dim(vec)[4])

vec <- sub_vector(bvec, c(1,3,5,7))
all.equal(4, dim(vec)[4])

mask <- LogicalNeuroVol(rep(TRUE, 24*24*24), NeuroSpace(c(24,24,24), c(1,1,1)))
svec <- SparseNeuroVec(array(rnorm(24*24*24*24), c(24,24,24,24)),
NeuroSpace(c(24,24,24,24), c(1,1,1)), mask)
vec <- sub_vector(svec, c(1,3,5))
all.equal(3, dim(vec)[4])
```

Summary-methods *Summary Methods for Neuroimaging Objects*

Description

Methods for the Summary group generic (e.g., sum, min, max, range, prod, any, all) applied to neuroimaging data objects.

Usage

```
## S4 method for signature 'SparseNeuroVec'
Summary(x, ..., na.rm = FALSE)

## S4 method for signature 'SparseNeuroVol'
Summary(x, ..., na.rm = FALSE)

## S4 method for signature 'DenseNeuroVol'
Summary(x, ..., na.rm = FALSE)
```

Arguments

x	A neuroimaging object (SparseNeuroVec, SparseNeuroVol, or DenseNeuroVol)
...	Additional arguments passed to methods
na.rm	Logical indicating whether to remove NA values before computation

Value

The result of the summary operation

Examples

```
# Create a simple volume
vol <- DenseNeuroVol(array(1:27, c(3,3,3)),
                     NeuroSpace(c(3L,3L,3L), c(1,1,1)))
sum(vol)
range(vol)
```

summary-neuro-methods *Summary of Neuroimaging Objects*

Description

Provides a concise summary of neuroimaging volume and vector objects, including spatial metadata and data statistics.

Usage

```
## S4 method for signature 'NeuroVol'
summary(object, ...)

## S4 method for signature 'DenseNeuroVec'
summary(object, ...)

## S4 method for signature 'SparseNeuroVec'
summary(object, ...)
```

Arguments

object	A neuroimaging object.
...	Additional arguments (currently ignored).

Value

An object of class "summary.NeuroVol" or "summary.NeuroVec" (invisibly), with a print method.

Examples

```
vol <- DenseNeuroVol(array(rnorm(27), c(3,3,3)),
                     NeuroSpace(c(3L,3L,3L), c(1,1,1)))
summary(vol)
```

temporal_access *Extract full sparse rows across time.*

Description

This function extracts one or more rows from the sparse time-by-voxel backing representation used by sparse neuroimaging vectors. It complements matricized_access(), which is the column-oriented accessor.

Usage

```
temporal_access(x, i, ...)

## S4 method for signature 'SparseNeuroVec,integer'
temporal_access(x, i)

## S4 method for signature 'SparseNeuroVec,numeric'
temporal_access(x, i)

## S4 method for signature 'BigNeuroVec,integer'
temporal_access(x, i)

## S4 method for signature 'BigNeuroVec,numeric'
temporal_access(x, i)
```

Arguments

x	a data source, typically a SparseNeuroVec object containing 4D neuroimaging data
i	a numeric vector of temporal indices to extract
...	additional arguments to be passed to methods.

Value

A matrix with one row per requested time index and one column per sparse voxel in the backing representation.

---

theme_neuro *A minimal, publication-friendly theme for image slices*

Description

Quiet axes, thin panel border, no grid, generous margins, slim legend.

Usage

```
theme_neuro(base_size = 10, base_family = "", style = c("light", "dark"))
```

Arguments

base_size	Base font size.
base_family	Base font family.
style	Visual style, either "light" or "dark".

TIME *Time axis*

Description

Represents the temporal dimension in neuroimaging data

Usage

```
TIME
```

Format

An object of class `NamedAxis` of length 1.

TimeAxis *Time axis set*

Description

A one-dimensional axis set representing time

Usage

```
TimeAxis
```

Format

An object of class `AxisSet1D` of length 1.

trans *Extract image coordinate transformation*

Description

Extract image coordinate transformation

Get transformation matrix

Usage

```
trans(x)

## S4 method for signature 'MetaInfo'
trans(x)

## S4 method for signature 'NeuroObj'
trans(x)

## S4 method for signature 'NeuroHyperVec'
trans(x)

## S4 method for signature 'NeuroSpace'
trans(x)
```

Arguments

x	an object with a transformation

Details

This function returns a transformation that can be used to go from "grid coordinates" to "real world coordinates" in millimeters. see NeuroSpace

Value

A numeric 4x4 matrix that maps from grid coordinates to real-world coordinates.

Examples

```
bspace <- NeuroSpace(c(10,10,10), c(2,2,2))
trans(bspace)
all.equal(dim(trans(bspace)), c(4,4))
```

---

values *Extract Data Values of an Object*

Description

Extract Data Values of an Object

Usage

```
values(x, ...)

## S4 method for signature 'ClusteredNeuroVec'
values(x)
```

```
## S4 method for signature 'DenseNeuroVol'
values(x)

## S4 method for signature 'SparseNeuroVol'
values(x)

## S4 method for signature 'ROIVol'
values(x, ...)

## S4 method for signature 'ROIVec'
values(x, ...)
```

Arguments

x	the object to get values from
...	additional arguments

Value

A vector or array containing the values extracted from x.

Examples

```
x <- NeuroSpace(c(10,10,10), c(1,1,1))
vol <- NeuroVol(rnorm(10 * 10 * 10), x)
values(vol)
```

---

vec_from_vols *Create NeuroVec from list of NeuroVol objects*

Description

Factory function to create a NeuroVec object from a list of NeuroVol objects. This is a convenience wrapper around the NeuroVec constructor that combines multiple 3D volumes into a single 4D NeuroVec.

Usage

```
vec_from_vols(vols, mask = NULL)
```

Arguments

vols	A list of NeuroVol objects. All volumes must have identical spatial dimensions.
mask	An optional logical array or LogicalNeuroVol object defining the subset of voxels to include. If provided, a SparseNeuroVec will be created.

Value

A NeuroVec object (either DenseNeuroVec or SparseNeuroVec depending on whether a mask is provided).

See Also

NeuroVec, NeuroVol

Examples

```
# Create a simple NeuroVec from list of volumes
spc <- NeuroSpace(c(10, 10, 10))
vol1 <- NeuroVol(rnorm(10*10*10), spc)
vol2 <- NeuroVol(rnorm(10*10*10), spc)
vec <- vec_from_vols(list(vol1, vol2))
print(dim(vec))  # Should be c(10, 10, 10, 2)
```

---

vectors *Extract an ordered list of 1D vectors.*

Description

This function extracts an ordered list of 1D vectors from an object that supplies vector data. The `subset` argument specifies the subset of vectors to extract, and can be a vector of indices or a logical vector. The return value is a list containing the extracted vectors in the same order as the specified indices.

Usage

```
vectors(x, subset, ...)

## S4 method for signature 'NeuroVec,missing'
vectors(x)

## S4 method for signature 'DenseNeuroVec,missing'
vectors(x)

## S4 method for signature 'NeuroVec,numeric'
vectors(x, subset)

## S4 method for signature 'NeuroVec,logical'
vectors(x, subset)

## S4 method for signature 'NeuroVecSeq,missing'
vectors(x)
```

```
## S4 method for signature 'NeuroVecSeq,numeric'
vectors(x, subset)

## S4 method for signature 'NeuroVecSeq,logical'
vectors(x, subset)

## S4 method for signature 'ROIVec,missing'
vectors(x)

## S4 method for signature 'matrix,missing'
vectors(x)

## S4 method for signature 'ROIVec,integer'
vectors(x, subset)

## S4 method for signature 'matrix,integer'
vectors(x, subset)

## S4 method for signature 'matrix,numeric'
vectors(x, subset)

## S4 method for signature 'ROIVec,numeric'
vectors(x, subset)

## S4 method for signature 'ROIVec,logical'
vectors(x, subset)

## S4 method for signature 'SparseNeuroVec,missing'
vectors(x, nonzero = FALSE)
```

Arguments

x	the object that supplies the vector data.
subset	the subset of vectors to extract.
...	additional arguments to be passed to methods.
nonzero	only include nonzero vectors in output list

Value

A `list` containing the extracted vectors from `x` in the same order as `subset`.

A deflist object where each element is a function that returns the time series for a voxel. The length of the deflist equals the total number of voxels.

Examples

```
file_name <- system.file("extdata", "global_mask_v4.nii", package="neuroim2")
vec <- read_vec(file_name)
v <- vectors(vec)
mean(v[[1]])
```

vols *Extract an ordered series of 3D volumes.*

Description

This function extracts an ordered series of 3D volumes from an object that supplies volume data. The `indices` argument specifies the subset of volumes to extract, and can be a vector of indices or a logical vector. The return value is a list containing the extracted volumes in the same order as the specified indices.

Usage

```
vols(x, indices, ...)

## S4 method for signature 'NeuroVec,numeric'
vols(x, indices)

## S4 method for signature 'NeuroVec,missing'
vols(x)
```

Arguments

`x`	the object that supplies the volume data.
`indices`	the subset of volumes to extract.
`...`	additional arguments to be passed to methods.

Value

A `list` containing the extracted 3D volumes from `x` in the same order as `indices`.

Examples

```
vec <- read_vec(system.file("extdata", "global_mask_v4.nii", package="neuroim2"))
vs <- vols(vec)
length(vs) == dim(vec)[4]

vs <- vols(vec, indices=1:3)
length(vs) == 3
```

volume_labels *Get per-volume labels for a* NeuroVec.

Description

Get per-volume labels for a NeuroVec.

Usage

```
volume_labels(x)

## S4 method for signature 'NeuroVec'
volume_labels(x)
```

Arguments

x	A NeuroVec or compatible object.

Value

A character vector of labels. Returns `character(0)` when no labels are defined.

A character vector of per-volume labels, or `character(0)` if none are set.

Examples

```
sp <- NeuroSpace(c(2, 2, 2, 3), c(1, 1, 1))
vec <- NeuroVec(array(1:24, dim = c(2, 2, 2, 3)), sp,
                volume_labels = c("baseline", "task", "rest"))
volume_labels(vec)
```

voxels *extract voxel coordinates*

Description

extract voxel coordinates

Usage

```
voxels(x, ...)

## S4 method for signature 'Kernel'
voxels(x, center_voxel = NULL)
```

Arguments

x	the object to extract voxels from
...	additional arguments to function
center_voxel	the absolute location of the center of the voxel, default is (0,0,0)

Value

A matrix or vector representing voxel coordinates from x.

Examples

```
# Create a 3D kernel with dimensions 3x3x3 and voxel size 1x1x1
kern <- Kernel(kerndim = c(3,3,3), vdim = c(1,1,1))

# Get voxel coordinates centered at origin (0,0,0)
vox <- voxels(kern)
# Returns a matrix where each row is a voxel coordinate
# relative to the kernel center

# Get voxel coordinates centered at specific point (5,5,5)
vox_centered <- voxels(kern, center_voxel = c(5,5,5))
# Returns coordinates shifted to be centered at (5,5,5)
```

---

which_dim *Find Dimensions of a Given Axis*

Description

This function returns the dimension of the specified axis for a given object, such as a matrix or an array.

Usage

```
which_dim(x, axis)

## S4 method for signature 'NeuroSpace,NamedAxis'
which_dim(x, axis)
```

Arguments

x	The NeuroSpace object
axis	The NamedAxis to find

Value

An integer representing the dimension index of the specified axis for the object x.

Examples

```
x <- NeuroSpace(c(10,10,10), spacing=c(1,1,1))
which_dim(x, x@axes@j) == 2
```

`write_elements` *Write a sequence of elements from an input source*

Description

Write a sequence of elements from an input source

Usage

```
write_elements(x, els)

## S4 method for signature 'BinaryWriter,numeric'
write_elements(x, els)
```

Arguments

`x`	the output channel
`els`	the elements to write

Value

Invisibly returns `NULL` after writing the elements.

Examples

```
# Create a temporary binary file for writing
tmp <- tempfile()
writer <- BinaryWriter(tmp, byte_offset = 0L,
                       data_type = "DOUBLE", bytes_per_element = 8L)

# Write some random data
data <- rnorm(100)
write_elements(writer, data)
close(writer)

# Read back the data to verify
reader <- BinaryReader(tmp, byte_offset = 0L,
                       data_type = "double", bytes_per_element = 8L)
read_data <- read_elements(reader, 100)
close(reader)

# Verify data was written correctly
all.equal(data, read_data)

# Clean up
```

```
unlink(tmp)

# Create a temporary binary file for writing
tmp <- tempfile()
writer <- BinaryWriter(tmp, byte_offset = 0L,
                       data_type = "DOUBLE", bytes_per_element = 8L)
# Write some data
write_elements(writer, rnorm(100))
close(writer)

# Clean up
unlink(tmp)
```

`write_vec` *Write a 4d image vector to disk*

Description

Write a 4d image vector to disk

Usage

```
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroHyperVec,character,missing,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroHyperVec,character,character,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroHyperVec,character,missing,character'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'ROIVec,character,missing,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVec,character,missing,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVec,character,character,missing'
write_vec(
  x,
  file_name,
  format,
  nbit = FALSE,
  compression = 5,
  chunk_dim = c(10, 10, 10, dim(x)[4]),
```

```
  ...
)

## S4 method for signature 'NeuroVec,character,missing,character'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'ROIVec,character,missing,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVec,character,missing,missing'
write_vec(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVec,character,character,missing'
write_vec(
  x,
  file_name,
  format,
  nbit = FALSE,
  compression = 5,
  chunk_dim = c(10, 10, 10, dim(x)[4]),
  ...
)

## S4 method for signature 'NeuroVec,character,missing,character'
write_vec(x, file_name, format, data_type, ...)
```

Arguments

x	an image object, typically a NeuroVec instance.
file_name	output file name.
format	file format string. Since "NIFTI" is the only currently supported format, this parameter can be safely ignored and omitted.
data_type	the numeric data type. If specified should be one of "UBYTE", "BYTE", "SHORT", "USHORT", "INT", "UINT", "LONG", "ULONG", "FLOAT" or "DOUBLE". Defaults to the datatype of the file the image was read from when its values are still exactly representable in it, and to "FLOAT" otherwise; integer targets are fitted with scl_slope / scl_inter rather than truncated. Otherwise output format will be inferred from R the datatype of the image.
...	extra args
nbit	set nbit compression
compression	compression level 1 to 9
chunk_dim	the dimensions of each chunk

Value

Invisibly returns NULL after writing the vector to disk.

Examples

```
bvec <- NeuroVec(array(0, c(10,10,10,10)), NeuroSpace(c(10,10,10,10), c(1,1,1)))

# Create temporary files
tmp1 <- tempfile(fileext = ".nii")

# Write vectors to temporary files
write_vec(bvec, tmp1)

# Clean up
unlink(tmp1)
```

`write_vol` *Write a 3d image volume to disk*

Description

Write a 3d image volume to disk

Usage

```
write_vol(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVol,character,missing,missing'
write_vol(x, file_name, format, data_type, ...)

## S4 method for signature 'ClusteredNeuroVol,character,missing,missing'
write_vol(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVol,character,character,missing'
write_vol(x, file_name, format, data_type, ...)

## S4 method for signature 'ROIVol,character,character,missing'
write_vol(x, file_name, format, data_type, ...)

## S4 method for signature 'NeuroVol,character,missing,character'
write_vol(x, file_name, format, data_type, ...)
```

Arguments

`x`	an image object, typically a `NeuroVol` instance.
`file_name`	output file name
`format`	file format string. Since "NIFTI" is the only currently supported format, this parameter can be safely ignored and omitted.

data_type	output data type, If specified should be one of "UBYTE", "BYTE", "SHORT", "USHORT", "INT", "UINT", "LONG", "ULONG", "FLOAT" or "DOUBLE". Defaults to the datatype of the file the image was read from when its values are still exactly representable in it, and to "FLOAT" otherwise; integer targets are fitted with scl_slope / scl_inter rather than truncated. Otherwise output format will be inferred from R the datatype of the image.
...	additional arguments passed to the format-specific writer.

Details

The output format will be inferred from file extension.

The output format will be inferred from file extension. `write_vol(x, "out.nii")` outputs a NIFTI file. `write_vol(x, "out.nii.gz")` outputs a gzipped NIFTI file.

No other file output formats are currently supported.

Value

Invisibly returns `NULL` after writing the volume to disk.

Examples

```
bvol <- NeuroVol(array(0, c(10,10,10)), NeuroSpace(c(10,10,10), c(1,1,1)))

tmp1 <- tempfile(fileext = ".nii")
write_vol(bvol, tmp1)
unlink(tmp1)
```

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