

# Package: tractor.base (via r-universe)

September 13, 2024

**Version** 3.4.2

**Date** 2024-02-27

**Title** Read, Manipulate and Visualise Magnetic Resonance Images

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**Imports** methods, ore (>= 1.3.0), reportr, shades, RNifti

**Suggests** mmand, loder, divest, jsonlite, yaml, tinytest

**Enhances** oro.nifti

**Description** Functions for working with magnetic resonance images.  
Reading and writing of popular file formats (DICOM, Analyze, NIFTI-1, NIFTI-2, MGH); interactive and non-interactive visualisation; flexible image manipulation; metadata and sparse image handling.

**Encoding** UTF-8

**License** GPL-2

**URL** <https://www.tractor-mri.org.uk>, <https://github.com/tractor/tractor>

**BugReports** <https://github.com/tractor/tractor/issues>

**RoxygenNote** 7.2.3

**Roxygen** list(old\_usage=TRUE)

**Repository** <https://tractor.r-universe.dev>

**RemoteUrl** <https://github.com/tractor/tractor>

**RemoteRef** HEAD

**RemoteSha** 81e9c7f1f0fd229a6f0d17e2345a2c7f1242c707

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---

allEqual

*Test whether all elements of a vector are equal*


---

### Description

This function tests whether all elements of the specified vector are equal to each other, i.e., whether the vector contains only a single unique value. For lists, equality is determined using [equivalent](#).

### Usage

```
allEqual(x, ignoreMissing = FALSE, ...)
```

**Arguments**

x	A vector of any mode, including a list.
ignoreMissing	If TRUE, missing elements will be ignored. Otherwise the presence of missing values will result in a return value of FALSE.
...	Additional arguments to <code>all.equal</code> , via <a href="#">equivalent</a> .

**Value**

TRUE if all elements test `equivalent`; FALSE otherwise.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[equivalent](#) for elementwise equivalence of two vectors.

**Examples**

```
allEqual(c(1,1,1)) # TRUE
allEqual(c(1,1,NA)) # FALSE
allEqual(c(1,1,NA), ignoreMissing=TRUE) # TRUE
```

---

asMriImage

*Creating MriImage objects from data*

---

**Description**

Functions for creating `MriImage` objects from data, including other images. All of these functions use data from arrays or `MriImage` objects to create a new `MriImage` object. `asMriImage` is the basic function for creating an object from its constituents: an array of voxel values and some metadata (and/or a template image).

**Usage**

```
asMriImage(data, templateImage = nilObject(), imageDims = NA,
  voxelDims = NA, voxelDimUnits = NA, origin = NA, tags = NA,
  reordered = NA)
```

```
extractMriImage(image, dim, loc)
```

```
trimMriImage(image, clearance = 4, indices = NULL)
```

```
reorderMriImage(image)
```

**Arguments**

<code>data</code>	An array of pixel/voxel data.
<code>templateImage</code>	An optional MriImage object, to be used as a metadata template.
<code>imageDims, voxelDims, voxelDimUnits, origin, tags, reordered</code>	Metadata for the new image object. These values override any from the metadata object or data array. See <a href="#">MriImage</a> class documentation for details.
<code>image</code>	An MriImage object.
<code>dim, loc</code>	The dimension and location along that dimension for which data should be extracted.
<code>clearance</code>	The number of voxels' clearance left around a trimmed image.
<code>indices</code>	A list of indices to keep along each dimension. Determined from the specified clearance if NULL.

**Details**

`extractMriImage` reduces the dimensionality of the source image by one, by extracting a single “slice” of data along one dimension. `trimMriImage` trims empty space from the edges of an image, reducing the dimensions of the image and thus avoiding the storage of lots of zeroes. `reorderMriImage` reorders the image data (and corresponding metadata) to the LAS convention, an operation which is usually performed when an image is read from file.

**Value**

An MriImage object.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. [doi:10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**[MriImage](#)


---

 augmentedInfoPanel     *A simple interactive viewer for MriImage objects*


---

**Description**

The viewImages function provides a simple interactive viewer for MriImage objects. 3D and 4D images may be used.

**Usage**

```
augmentedInfoPanel(indexNames = NULL)

polarPlotPanel(directions, bValues = NULL)

viewImages(images, colourScales = NULL, point = NULL, interactive = TRUE,
  crosshairs = TRUE, orientationLabels = TRUE,
  infoPanel = RNifti::defaultInfoPanel, ...)
```

**Arguments**

indexNames	A list whose elements are either NULL or a named character vector giving the names associated with each index in the image.
directions	A matrix of 3D acquisition direction vectors, one per row.
bValues	A vector of b-values, if the image is diffusion-weighted.
images	An MriImage object, or list of MriImage objects.
colourScales	A list of colour scales to use for each image, which will be recycled to the length of images. See <a href="#">getColourScale</a> for details. The default is to use greyscale.
point	A length-3 integer vector giving the initial location of the crosshairs, in voxels.
interactive	A single logical value. If TRUE, the plot is interactive.
crosshairs	A single logical value. If TRUE, the crosshairs are displayed.
orientationLabels	A single logical value. If TRUE, orientation labels are displayed.
infoPanel	A function with at least three arguments, which must plot something to fill the bottom-right panel of the viewer after each change of crosshair location. The three mandatory arguments correspond to the current location in the image, the image values at that location, and the names of each image. The defaultInfoPanel and timeSeriesPanel functions from package RNifti are valid examples.
...	Additional arguments to infoPanel.

**Value**

These functions are called for their side effects.

**Note**

The `defaultInfoPanel` and `timeSeriesPanel` functions are not intended to be called directly. They are simple examples of valid values for the `infoPanel` argument to `viewImages`.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[getColorScale](#)

---

createNeighbourhoodInfo

*Image neighbourhoods*

---

**Description**

This function calculates information about a cuboidal region of an image, with a centre and a fixed voxel width.

**Usage**

```
createNeighbourhoodInfo(width, dim = 3, centre = rep(0, dim))
```

**Arguments**

width	An integer voxel width. Must be odd.
dim	An integer giving the dimensionality of the neighbourhood. Currently must be 3.
centre	A numeric vector giving the centre voxel of the neighbourhood. Must have exactly dim elements.

**Value**

createNeighbourhoodInfo returns a list with class "neighbourhoodInfo" and elements

**width** Copied from the width argument.

**dim** Copied from the dim argument.

**centre** Copied from the centre argument.

**vectors**  $\text{dim} \times \text{width}^{\text{dim}}$  matrix whose columns give the locations of each point in the neighbourhood.

**innerProducts** A square, symmetric matrix of inner products between every location in the neighbourhood and every other.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

---

createSliceGraphic      *Visualise MriImage objects*

---

**Description**

Visualise MriImage objects noninteractively using an R graphics device. See [viewImages](#) for an interactive alternative. These functions create 2D visualisations of 3D images by slicing or maximum intensity projection.

**Usage**

```
createSliceGraphic(image, x = NA, y = NA, z = NA,
  device = c("internal", "png"), colourScale = 1, add = FALSE,
  file = NULL, zoomFactor = 1, windowLimits = NULL)

createProjectionGraphic(image, axis, device = c("internal", "png"),
  colourScale = 1, add = FALSE, file = NULL, zoomFactor = 1,
  windowLimits = NULL)

createContactSheetGraphic(image, axis, device = c("internal", "png"),
  colourScale = 1, add = FALSE, file = NULL, zoomFactor = 1,
  windowLimits = NULL, clearance = NULL, nColumns = NULL)
```

**Arguments**

image	An <a href="#">MriImage</a> object.
x, y, z	Integer vectors, each of length 1. Exactly one of these must be specified to indicate the plane of interest.
device	Either "internal" for display on the default graphics device, or "png" for creating PNG format image file(s). Abbreviations are fine.
colourScale	A colour scale definition, of the sort generated by <a href="#">getColourScale</a> .
add	Overlay the graphic on a previous one. Used only when device is "internal".
file	A file name, to be used when device is "png".
zoomFactor	Factor by which to enlarge the image. Applies only when device is "png".
windowLimits	Numeric vector of length 2 giving the limits of the colour scale, or NULL for limits matching the range of the image data. Passed as the zlim argument to <a href="#">image</a> .
axis	A vector of axes along which slice/projection images should be created. 1 is left-right, 2 is anterior-posterior, 3 is superior-inferior.
clearance	Number of voxels' clearance to leave around each slice image in the contact sheet. Passed to <a href="#">trimMriImage</a> .
nColumns	Number of slices per row in the contact sheet grid. If NULL, the function will aim for a square grid.

**Value**

These functions are called for their side effects.

**Note**

When the device option is set to "png", the "png" and "mmand" packages are required by these functions.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**

See [viewImages](#) for an interactive alternative, and [getColourScale](#) for details of how colour scales are specified. Also [image](#), which is used as the underlying plot function.



---

deduplicate	<i>Concatenate and deduplicate vectors</i>
-------------	--

---

### Description

This function returns its arguments, after concatenating them using `c` and then removing elements with duplicate names. The first element with each name will remain, possibly with subsequent elements' content appended to it. Unnamed elements are retained.

### Usage

```
deduplicate(..., merge = FALSE)
```

### Arguments

<code>...</code>	One or more vectors of any mode, usually named.
<code>merge</code>	If <code>FALSE</code> , the default, duplicate elements will simply be discarded. If <code>TRUE</code> , additional elements with the same name will be appended to the retained one. This does not apply to unnamed elements. If this kind of deduplication actually happens, the return value will be a list, regardless of the source type.

### Value

The concatenated and deduplicated vector.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. [doi:10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

---

DicomMetadata-class     *The DicomMetadata class*

---

### Description

This class represents DICOM metadata, which typically contains detailed information about the scan parameters and subject.

### Fields

source String naming the source file  
tags Data frame of tag information  
tagOffset Starting offset for tags in the file  
dataOffset Starting offset for pixel data in the file  
dataLength Pixel data length  
explicitTypes Logical value indicating whether explicit types are used in the file  
endian String naming the endianness of the file  
asciiFields Character vector containing the contents of the ASCII header, if requested and present in the file.  
transferSyntax Transfer syntax string, if specified in the file; otherwise the empty string.

### Methods

getAsciiFields(regex = NULL) Retrieve the value of one or more fields in the ASCII header.  
Returns NA if no fields match  
getTagValue(group, element) Retrieve the value of a given tag, using an appropriate R type.  
Returns NA if the tag is missing

---

embrace                     *Combine similar strings into one*

---

### Description

Merge a vector of strings with a common prefix and/or suffix into one string with the unique parts in braces, comma-separated.

### Usage

```
embrace(strings)
```

### Arguments

strings                     A vector, which will be coerced to mode character.

**Value**

A single merged string, with the common prefix and suffix as attributes.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**Examples**

```
embrace(c("image.hdr", "image.img"))
```

---

emptyMatrix

*The empty matrix*

---

**Description**

The empty matrix is a standard matrix of dimensions 0 x 0. It is intended to be used as a placeholder where a matrix is required but no information is stored.

**Usage**

```
emptyMatrix()
```

```
is.emptyMatrix(object)
```

**Arguments**

object          Any object.

**Value**

emptyMatrix returns the empty matrix, equivalent to `matrix(NA,0,0)`. `is.emptyMatrix` returns TRUE if its argument is identical to the empty matrix.

**Author(s)**

Jon Clayden

## References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. Journal of Statistical Software 44(8):1-18. doi:10.18637/jss.v044.i08.

---

equivalent

*Test two numeric vectors for equivalence*

---

## Description

This function is a wrapper for `isTRUE(all.equal(x, y, ...))`, but with the additional capability of doing sign-insensitive comparison.

## Usage

```
equivalent(x, y, signMatters = TRUE, ...)
```

## Arguments

<code>x</code>	The first numeric vector.
<code>y</code>	The second numeric vector.
<code>signMatters</code>	Logical value: if FALSE then equivalence in absolute value is sufficient.
<code>...</code>	Additional arguments to <code>all.equal</code> , notably tolerance.

## Value

TRUE if all elements of `x` match all elements of `y` to within tolerance, ignoring signs if required. FALSE otherwise.

## Author(s)

Jon Clayden

## References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. Journal of Statistical Software 44(8):1-18. doi:10.18637/jss.v044.i08.

## See Also

[all.equal](#)

**Examples**

```
equivalent(c(-1,1), c(1,1)) # FALSE
equivalent(c(-1,1), c(1,1), signMatters=FALSE) # TRUE
equivalent(1:2, 2:3, tolerance=2) # TRUE
```

---

fx

*Shorthand anonymous functions*

---

**Description**

These functions provide a shorthand route to simple anonymous functions.

**Usage**

```
fx(expr)
fxy(expr)
fxyz(expr)
fi(expr)
```

**Arguments**

expr            A (single or compound) expression forming the body of the function.

**Value**

The function constructed.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

---

getColourScale      *Obtaining colour scales*

---

### Description

The `getColourScale` function can be used to obtain a standard or customised colour scale for use in the package's image visualisation functions.

### Usage

```
getColourScale(n)
```

### Arguments

`n`                      A number, colour name or list (see Details).

### Details

Colour scales can be specified in any of three ways. Firstly, by a single number, representing a predefined colour scale. Currently valid values are 1 (greyscale, black background), 2 (red to yellow heat scale, red background), 3 (blue to red rainbow scale, blue background), 4 (blue to white to red diverging scale, white background), 5 (white to red, white background), 6 (white to blue, white background), 7 (yellow to orange to red) and 8 (purple to green to yellow, perceptually uniform). Secondly, a single colour name can be given (see [colours](#)); in this case the background will be black. This is useful for binary images. Thirdly, and most flexibly, a list with two named elements can be given: `colours`, a vector of colours representing the colour scale, perhaps created using the `shades` package; and `background`, a single colour representing the background.

### Value

A list with elements

**colours** A character-mode vector representing the colours in the scale, usually of length 100. This can be passed as a colour scale to R's plotting functions.

**background** A single character string representing the background colour.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[colours](#), [rgb](#), [colorRamp](#), and the [shades](#) package for colour manipulation.

**Examples**

```
getColourScale(1)
```

---

```
identifyImageFileNames
```

*Working with MRI images stored in various formats*

---

**Description**

Functions for reading, writing, locating, copying and removing MRI images stored in NIfTI, Analyze, MGH and MRtrix formats.

**Usage**

```
identifyImageFileNames(fileName, fileType = NULL, errorIfMissing = TRUE,
  auxiliaries = c("dirs", "lut", "tags"), ...)

imageFileExists(fileName, fileType = NULL)

removeImageFiles(fileName, ...)

symlinkImageFiles(from, to, overwrite = FALSE, relative = TRUE, ...)

copyImageFiles(from, to, overwrite = FALSE, deleteOriginals = FALSE, ...)

readImageFile(fileName, fileType = NULL, metadataOnly = FALSE,
  volumes = NULL, sparse = FALSE, mask = NULL, reorder = TRUE, ...)

writeImageFile(image, fileName = NULL, fileType = NA, overwrite = TRUE,
  datatype = "fit", writeTags = FALSE)
```

**Arguments**

fileName, from, to	File names, with or without appropriate extension.
fileType	A character vector of length one, giving the file type required or expected. If this option is missing, the file type used for writing images will be taken from the tractorFileType option. See Details.
errorIfMissing	Logical value: raise an error if no suitable files were found?
auxiliaries	A character vector of auxiliary file suffixes to search for.

...	For identifyImageFileNames, additional arguments to <a href="#">resolvePath</a> . Elsewhere, additional arguments to identifyImageFileNames.
overwrite	Logical value: overwrite an existing image file? For writeImageFile, an error will be raised if there is an existing file and this is set to FALSE.
relative	Logical value: if TRUE, the path stored in the symlink will be relative (e.g. "../some_dir/some_image.nii") rather than absolute (e.g. "/path/to/some_dir/some_image.nii")
deleteOriginals	Logical value: if TRUE, copyImageFiles performs a move rather than a copy.
metadataOnly	Logical value: if TRUE, only metadata are read into the object.
volumes	An optional integer vector specifying a subset of volumes to read (generally to save memory). If given, only the requested volumes in the 4D file will be read.
sparse	Logical value: should the image data be stored in a <a href="#">SparseArray</a> object?
mask	An optional <a href="#">MriImage</a> object representing a mask, outside of which the image to be read should be considered to be zero. This can be used to save memory when only a small part of a large image is of interest. Ignored if sparse is not TRUE.
reorder	Logical value: should the image data be reordered to LAS? This is recommended in most circumstances.
image	An <a href="#">MriImage</a> object.
datatype	A datatype string, such as "uint8" or "float", specifying the pixel datatype to use when storing the data. If specified, this must be a type supported by the requested (or default) file format. The default, "fit", results in a datatype being chosen that is wide enough to fit the range of the data elements. An error will arise if there's no such type.
writeTags	Logical value: should tags be written in YAML format to an auxiliary file?

## Details

NIfTI and Analyze are related formats for storing magnetic resonance images. NIfTI is a more recent extension of Analyze, and contains more specific information about, for example, the orientation of the image. Its use is therefore recommended where possible. MGH format is used by the popular image processing package FreeSurfer, and MRtrix format by the software of the same name. These formats use a number of different file extensions, but the details are abstracted away from the user by these functions.

TractoR does not allow for files with the same basic name using multiple Analyze/NIfTI/MGH/MRtrix formats in a single directory (e.g. "foo.nii" AND "foo.img"), and these functions will produce an error if multiple compatible files exist.

Suitable values for fileType (and the tractorFileType option, which is used as a default for writing) are "NIFTI", "NIFTI\_PAIR" (the two-file NIfTI format), "MGH", and corresponding gzipped versions of these with "\_GZ" appended. File types "ANALYZE" and "MRTRIX", and "\_GZ" variants, are additionally available for reading only. "NIFTI\_GZ" is the default value for the tractorFileType option, but that can be changed using a call to [options](#), or by setting the TRACTOR\_FILETYPE environment variable before loading the tractor.base package.

Since multiple files may be involved, copying, moving or symlinking images is not trivial. copyImageFiles and symlinkImageFiles are wrappers around the standard functions [file.copy](#) and [file.symlink](#) which handle this complexity.



**Value**

readImageFile returns an `MriImage` object. imageFileExists returns TRUE if an existing file with the specified name exists (all file extensions are checked), and FALSE otherwise. removeImageFiles returns the result of `unlink` applied to all relevant files. writeImageFile and identifyImageFileNames return a list with the following elements, describing the identified or written files:

**fileStem** The file name without extension.

**headerFile** The full header file name.

**imageFile** The full image file name.

**format** The format of the files ("Nifti", "Analyze" or "Mgh"). Not returned by writeImageFile.

copyImageFiles and symlinkImageFiles are called for their side effects.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. Journal of Statistical Software 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

The NIFTI-1 standard (<http://nifti.nimh.nih.gov/nifti-1>) and `MriImage`.

---

 implode

---

*Create a character string by concatenating the elements of a vector*


---

**Description**

Create a character string by concatenating the elements of a vector, using a separator and optional final separator.

**Usage**

```
implode(strings, sep = "", finalSep = NULL, ranges = FALSE)
```

**Arguments**

strings	A vector, which will be coerced to mode character.
sep	A unit length character vector giving the separator to insert between elements.
finalSep	An optional unit length character vector giving the separator to insert between the final two elements.
ranges	Logical value. If TRUE and strings can be interpreted as integers, collapse runs of consecutive numbers into range notation.

**Value**

A character vector of length one.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. Journal of Statistical Software 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[paste](#)

**Examples**

```
implode(1:3, ", ") # "1, 2, 3"  
implode(1:3, ", ", " and ") # "1, 2 and 3"  
implode(1:2, ", ", " and ") # "1 and 2"  
implode(1:3, ", ", ranges=TRUE) # "1-3"
```

---

indexList

*Extract one or more elements from a list*

---

**Description**

Given a list-like first argument, this function extracts one or more of its elements. Numeric and character indexing are allowed.

**Usage**

```
indexList(list, index = NULL)
```

**Arguments**

**list**            A list-like object, with a `[[` indexing method.  
**index**           A vector of integers or strings, or `NULL`.

**Value**

If `index` is `NULL`, the whole list is returned. Otherwise, if `index` has length one, the corresponding element is extracted and returned. Otherwise a list containing the requested subset is returned.

**Note**

This function is not type-safe, in the sense that its return type depends on its arguments. It should therefore be used with care.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

---

infix

*Resolve a variable to a default when NULL*

---

**Description**

This is a very simple infix function for the common TractoR idiom whereby NULL is used as a default argument value, but later needs to be resolved to a meaningful value if not overridden in the call. It returns its first argument unless it is NULL, in which case it falls back on the second argument.

**Usage**

```
X %||% Y
```

**Arguments**

X, Y                    R objects, possibly NULL.

**Value**

X, if it is not NULL; otherwise Y.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**

[where](#), which resolves a value if an expression is TRUE. Several calls to that function can be conveniently chained together with this one.

---

isDeserialisable      *Reference object serialisation and deserialisation*

---

**Description**

Rather than using R's [save](#) and [load](#) functions directly for reference objects, TractoR uses the [SerialisableObject](#) class and these functions to save and load objects. The main difference is that this approach stores only the data in the object, and not the functions which operate on them. This helps backward compatibility when new member functions are added.

**Usage**

```
isDeserialisable(object, expectedClass = NULL)

serialiseReferenceObject(object, file = NULL)

deserialiseReferenceObject(file = NULL, object = NULL, raw = FALSE)

registerDeserialiser(className, deserialiser)
```

**Arguments**

object	For <code>serialiseReferenceObject</code> , a list or object inheriting from <a href="#">SerialisableObject</a> . For other functions, an object in (raw) serialised form. See Details.
expectedClass	A class name which the object is expected to inherit. Any class is acceptable if this parameter is NULL.
file	A file name to deserialise from.
raw	If TRUE, the raw serialised object is returned; otherwise the object is converted back to its original class.
className	A string naming a class to be handled by the specified deserialiser.
deserialiser	A function taking as its argument a list of serialised fields, and returning a suitable deserialised object.

**Details**

The `serialiseReferenceObject` function, or the `serialise` member function of the [SerialisableObject](#) class can be used to create and/or [save](#) a version of an object which contains a hierarchical representation of the data embedded in it. These serialised objects are standard R lists, with an "originalClass" attribute describing the class of the original object. The `deserialiseReferenceObject` function can be used to deserialise them. Custom deserialisers can be specified using `registerDeserialiser`, typically for legacy classes.

Note that this should generally NOT be used as the primary mechanism for saving and loading `MriImage` objects. Saving to standard NIFTI/Analyze format is usually preferable, and can be done using `writeImageFile`.

### Value

`isDeserialisable` returns TRUE if the object is deserialisable and inherits from the specified class. `deserialiseReferenceObject` returns a raw or reconstituted object after deserialisation.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

### See Also

`SerializableObject`, `save`, `load`, `writeImageFile`.

---

locateExecutable	<i>Find or run an external executable file</i>
------------------	--

---

### Description

The `execute` function is a wrapper around the `system2` function in base, which additionally echoes the command being run (including the full path to the executable) if the `reportr` output level is `Debug`. `locateExecutable` simply returns the path to an executable file on the system `PATH`.

### Usage

```
locateExecutable(fileName, errorIfMissing = TRUE)

execute(executable, params = NULL, errorOnFail = TRUE, silent = FALSE,
  ...)
```

### Arguments

<code>executable</code> , <code>fileName</code>	Name of the executable to run.
<code>params</code>	A character vector giving the parameters to pass to the executable, if any. Elements will be separated by a space.
<code>errorOnFail</code> , <code>errorIfMissing</code>	Logical value: should an error be produced if the executable can't be found?

silent            Logical value: should the executable be run without any output?  
 ...              Additional arguments to `system`.

**Value**

For `execute`, the return value of the underlying call to `system2`. For `locateExecutable`, the location of the requested executable, or NULL if it could not be found.

**Note**

These functions are designed for Unix systems and may not work on Windows.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

`system2`

---

mergeMriImages

*Merging MriImage objects*

---

**Description**

This function concatenates the data from a series of `MriImage` objects, and then attempts to work out the final dimensions of the merged image and returns it.

**Usage**

```
mergeMriImages(..., bindDim = NULL, padTags = FALSE)
```

**Arguments**

...            `MriImage` objects. They do not need to have the same dimensionality.

bindDim       An integer specifying the dimension along which to bind the data, or NULL (the default). The latter case resolves to one number higher than the last dimension common to all images.

padTags       Logical value. If TRUE, NAs will be used to pad tags which appear to be partially missing in the merged dataset. If FALSE, incomplete tags will be dropped.

**Value**

A merged image.

**Note**

Tags are retained as-is if they are identical in each image. Otherwise they are concatenated if their lengths match the number of blocks in each image, or concatenated with NAs for missing values if `padTags` is `TRUE`.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[MriImage](#)

---

MriImage-class

*The MriImage class*

---

**Description**

This class represents an MRI image. An object of this class is made up of some voxel data, stored as a sparse or dense numeric array, and some metadata, such as the file it was read from, the voxel dimensions, and so on. The group generic functions [Math](#), [Ops](#) and [Summary](#) are defined for this class, as are methods for coercing to and from a standard [array](#).

**Fields**

`imageDims` Integer vector of dimensions

`voxelDims` Numeric vector of pixel/voxel spacings

`voxelDimUnits` Character vector of spatial and/or temporal spacing units. Millimetres and seconds (i.e., `c("mm", "s")`) are typical

`source` String naming the file(s) that the image was read from. This is reset to the empty string if the image is modified

`origin` Numeric vector giving the spatial coordinate origin

`xform` Numeric matrix giving the NIfTI-style xform matrix associated with the image, which indicates its orientation

reordered Logical value indicating whether the image has been reordered. See [reorderMriImage](#)  
 tags Named list of arbitrary DICOM-style tags  
 data Sparse or dense array of data, or NULL

## Methods

apply(...) Apply a function to the margins of the image  
 binarise() Binarise the image by setting nonzero values to one  
 fill(value) Fill the image with a particular value  
 find(fun = NULL, ..., array = TRUE) Find voxels whose values are not zero, or satisfy a function  
 getDataAtPoint(...) Obtain the value of the image at a particular point  
 getMetadata() Obtain a version of the image with any data removed  
 getNonzeroIndices(array = TRUE, positiveOnly = FALSE) Find voxels whose values are not zero  
 getSlice(dim, loc) Extract data from a slice of the image along one dimension  
 getSparseness() Obtain the proportion of zeroes in the image  
 getTags(keys = NULL) Retrieve some or all of the tags stored with the image  
 getXform(implicit = TRUE) Retrieve the stored or implicit xform matrix  
 map(fun, ..., sparse = NULL) Replace the current data with the result of a function  
 mask(maskImage) Mask the image, setting zero voxels in the mask to zero  
 setData(newData) Replace the data in the image  
 setOrigin(newOrigin) Update the origin of the image  
 setSource(newSource) Update the source of the image  
 setTags(..., merge = FALSE) Add, replace or merge metadata tags  
 setXform(newXform) Update the xform matrix associated with the image  
 summarise() Summarise key aspects of the object  
 threshold(level, defaultValue = 0) Threshold the image by setting values below the threshold level to zero

---

newSparseArrayWithData

*Create a SparseArray object*

---

## Description

This function creates a [SparseArray](#) object from its constituent parts.

## Usage

```
newSparseArrayWithData(data, coordinates, dims)
```



**Arguments**

data	A vector of (nonzero) array elements.
coordinates	A matrix with as many rows as data has elements, containing the coordinates of each nonzero element in the array.
dims	The dimensions of the array.

**Value**

A [SparseArray](#) object.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

---

nilObject

*The nil object*

---

**Description**

The nil object is an empty object of class [SerialisableObject](#). It can be used as a placeholder where such an object of this class, or one of its subclasses, is required. It serialises to the empty list.

**Usage**

```
nilObject()
```

```
is.nilObject(object)
```

**Arguments**

object	Any object.
--------	-------------

**Value**

nilObject returns the nil object. is.nilObject returns TRUE if its argument is identical to the nil object, or if it is equivalent in the sense of serialising to an identical result.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[SerialisableObject](#)

---

pluralise

*Number agreement with a vector*

---

**Description**

This function chooses the singular or plural form of a word based on the length of an associated vector, or an integer.

**Usage**

```
pluralise(singular, x = NULL, n = NULL, plural = NULL)
```

**Arguments**

singular	The singular form of the word.
x	A vector of any mode, whose length is used to choose the correct word form, unless n is specified.
n	An integer which is used to choose the correct word form (singular if n = 1, plural otherwise). Take priority over x if not NULL.
plural	The plural form of the word. If NULL, an 's' is simply appended to the singular form.

**Value**

Either singular or plural, as appropriate.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

---

printLabelledValues    *Pretty print labelled information*

---

**Description**

This is a simple function to print a series of labels and associated data values, or key-value pairs.

**Usage**

```
printLabelledValues(labels, values, outputLevel = OL$Info,  
  leftJustify = FALSE)
```

**Arguments**

labels	A character vector of labels.
values	A character vector of values. Must have the same length as labels.
outputLevel	The output level to print the output to. See <code>setOutputLevel</code> , in the <code>reportr</code> package.
leftJustify	Logical value: if TRUE the labels will be left justified; otherwise they will be right justified.

**Value**

This function is called for its side effect.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using `TractoR` in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). `TractoR`: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**

[setOutputLevel](#) for the `reportr` output level system.

---

promote	<i>Promote a vector to a single-column or single-row matrix</i>
---------	---

---

### Description

The promote function promotes a vector argument to a single-column or single-row matrix. Matrix arguments are returned unmodified.

### Usage

```
promote(x, byrow = FALSE)
```

### Arguments

x	A vector or matrix.
byrow	Logical value: if TRUE, a vector will be promoted to a single-row matrix; otherwise a single-column matrix will result.

### Value

A matrix version of the x argument.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. Journal of Statistical Software 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

### See Also

[matrix](#)

---

readDicomDirectory      *Read a directory of DICOM files*

---

### Description

This function scans a directory for files in DICOM format, and converts them to a single Analyze/NIfTI-format image of the appropriate dimensionality.

### Usage

```
readDicomDirectory(dicomDir, method = c("internal", "divest"),
  readDiffusionParams = FALSE, untileMosaics = TRUE, ...)
```

### Arguments

dicomDir	Character vector of length one giving the name of a directory containing DICOM files.
method	Character string specifying whether to use the internal DICOM reading code or use the divest package.
readDiffusionParams	Logical value. Should diffusion MRI parameters (b-values and gradient directions) be retrieved from the files if possible?
untileMosaics	Logical value. Should Siemens mosaic images be converted into 3D volumes? This may occasionally be performed in error, which can be prevented by setting this value to FALSE.
...	Additional arguments to readDicom, if the divest method is used.

### Value

A list containing elements

**image** An `MriImage` object.

**bValues** Diffusion b-values, if requested. Will be NA if the information could not be found in files.

**bVectors** Diffusion gradient vectors, if requested. Will be NA if the information could not be found in the files.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[DicomMetadata](#), [MriImage](#), [sortDicomDirectories](#).

---

readDicomFile	<i>Read a DICOM file into a DicomMetadata object</i>
---------------	--

---

**Description**

This function reads a DICOM file into a [DicomMetadata](#) object. Only DICOM files from magnetic resonance scanners are supported.

**Usage**

```
readDicomFile(fileName, checkFormat = TRUE, stopTag = NULL,
              ignoreTransferSyntax = FALSE, ascii = TRUE)
```

**Arguments**

fileName	The name of a DICOM file.
checkFormat	If TRUE, the function will check for the magic string "DICM" at byte offset 128. This string should be present, but in reality not all files contain it.
stopTag	An integer vector giving the group and element numbers (in that order) of a DICOM tag, or NULL. If not NULL, the function will stop parsing the DICOM file if the specified tag is encountered. This can be used to speed up the process if a specific tag is required.
ignoreTransferSyntax	If TRUE, any transfer syntax stored in the file will be ignored, and the code will try to deduce the transfer syntax using heuristics. This may occasionally be necessary for awkward DICOM files, but is not generally recommended.
ascii	If TRUE, the function will attempt to read an embedded Siemens ASCII header, if one exists.

**Value**

readDicomFile returns a [DicomMetadata](#) object, or NULL on failure.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. [doi:10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**

The DICOM standard, found online at <https://www.dicomstandard.org/>. (Warning: may produce headaches!) Also [readDicomDirectory](#) for information on how to create [MriImage](#) objects from DICOM files.

---

 resolvePath

*Functions for file name and path manipulation*


---

**Description**

Functions for expanding file paths, finding relative paths and ensuring that a file name has the required suffix.

**Usage**

```

resolvePath(path, ...)

relativePath(path, referencePath)

matchPaths(path, referencePath)

registerPathHandler(regex, handler)

expandFileName(fileName, base = getwd())

ensureFileSuffix(fileName, suffix, strip = NULL)

```

**Arguments**

path, referencePath	Character vectors whose elements represent file paths (which may or may not currently exist).
...	Additional arguments to custom path handlers.
regex	A Ruby-style regular expression.
handler	A function taking and returning a string.
fileName	A character vector of file names.
base	If fileName is a relative path, this option gives the base directory which the path is relative to. If fileName is an absolute path, this argument is ignored.
suffix	A character vector of file suffixes, which will be recycled if shorter than fileName.
strip	A character vector of suffixes to remove before appending suffix. The intended suffix does not need to be given here, as the function will not append it if the specified file name already has the correct suffix.

**Details**

The `resolvePath` function passes its arguments elementwise through any matching path handler, and returns the resolved paths. Nonmatching elements are returned as-is. `registerPathHandler` registers a new path handler for special syntaxes, and is for advanced use only. `relativePath` returns the specified path, expressed relative to `referencePath`. `matchPaths` resolves a vector of paths against a vector of reference paths. `expandFileName` returns the full path to the specified file name, collapsing "." elements if appropriate. `ensureFileSuffix` returns the specified file names with the requested suffixes appended (if they are not already).

**Value**

A character vector.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:[10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

**See Also**

[normalizePath](#) does most of the work for `expandFileName`.

---

resolveVector

*Miscellaneous vector functions*

---

**Description**

These functions provide the (Euclidean) length of a vector, the vector cross product or angle between two vectors.

**Usage**

```
resolveVector(len, ...)
```

```
vectorLength(vector)
```

```
vectorCrossProduct(a, b)
```

```
angleBetweenVectors(v1, v2)
```



**Arguments**

len	The expected length of the vector.
...	Elements of the vector, to be concatenated together.
vector, v1, v2	Numeric vectors of any length.
a, b	Numeric 3-vectors.

**Value**

For `vectorLength`, the Euclidean norm or length of the specified vector, given by `sqrt(sum(vector^2))`. For `vectorCrossProduct`, the vector cross product of the two specified vectors; and for `angleBetweenVectors`, the angle (in radians) between the two specified vectors. The `resolveVector` function concatenates the values given in `...{}`, and if the result is a vector of length `len` then it is returned. If not, `NULL` is returned.

**Author(s)**

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

[crossprod](#) for the matrix cross product.

---

SerialisableObject-class

*The SerialisableObject class*

---

**Description**

This reference class extends [TractorObject](#) by adding a function for simple serialisation of the data fields of an object, either to a list or a file. This is intended to be used for classes whose state can meaningfully be restored from a list of standard R objects (not including transient C/C++ pointers, for example). A serialised object may be deserialised using the [deserialiseReferenceObject](#) function.

**Methods**

`serialise(file = NULL)` Serialise the object to a list or file

**See Also**

[save](#)

---

sortDicomDirectories    *Sort a directory of DICOM files into series*

---

### Description

This function sorts a directory containing DICOM files into subdirectories by series UID (DICOM tag 0x0020,0x000e), subject name (0x0010,0x0010) and/or scan date (0x0008,0x0020). Each unique identifier, together with its description for series, will be used as the name for a new subdirectory, and all relevant files will be copied into that subdirectory. Duplicate file names are disambiguated if necessary.

### Usage

```
sortDicomDirectories(directories, method = c("internal", "divest"),
  deleteOriginals = FALSE, sortOn = "series", seriesId = c("UID",
    "number", "time"), nested = TRUE, ...)
```

### Arguments

directories	A character vector giving the directories to search for DICOM files. Subdirectories will also be searched.
method	Character string specifying whether to use the internal DICOM reading code or use the divest package.
deleteOriginals	A single logical value. If TRUE, then the source files will be deleted after being copied to their new locations, making the operation a move rather than a copy. Nothing will be deleted if the copy fails.
sortOn	The string "series", "subject" or "date", or any combination in the order desired. This will be the basis of the sort, which will be nested if more than one type is specified.
seriesId	A string describing the kind of series identifier to use for sorting by series: "UID" (DICOM tag 0x0020,0x000e; the default), "number" (0x0020,0x0011) or "time" (0x0008,0x0031).
nested	Logical value. If TRUE and directories is of length 1, subdirectories will be created within the specified original directory. Otherwise they will be created in the working directory.
...	Additional arguments to pass to <a href="#">readDicomFile</a> .

### Value

This function is called for its side effect.

### Author(s)

Jon Clayden

## References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

## See Also

[readDicomDirectory](#) for reading DICOM files into an MriImage object.

---

SparseArray-class      *The SparseArray class*

---

## Description

This class represents an array with any number of dimensions, in which a significant proportion of entries are zero. The coordinates of nonzero entries are stored along with their values, with all remaining entries assumed to be zero. Methods are provided to index into the array in the standard way, using matrix or vector indices; and for coercing between SparseArray objects and standard (dense) arrays.

## Fields

data Vector of nonzero data values  
coords Integer matrix of nonzero data locations, one per row  
dims Integer vector of dimensions

## Methods

aperm(perm) Permute the dimensions of the array  
apply(margin, fun, ...) Apply a function to margins of the array  
flip(dimsToFlip) Flip the array along one or more directions  
setCoordinatesAndData(newCoords, newData) Update the nonzero locations and data values in the array  
setDimensions(newDims) Change the dimensions of the image  
summarise() Summarise key aspects of the object

---

threadSafeTempFile	<i>Obtain thread-safe temporary file names</i>
--------------------	--

---

### Description

This function is a wrapper around `tempfile`, which creates temporary file names whose path contains the process ID of the calling process. This avoids clashes between threads created by functions such as `mclapply` (in the “parallel” package), which can easily occur with the standard `tempfile` function.

### Usage

```
threadSafeTempFile(pattern = "file")
```

### Arguments

`pattern`            Character vector giving the initial part of each file name.

### Value

A character vector of temporary file names. No files are actually created.

### Author(s)

Jon Clayden

### References

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. [doi:10.18637/jss.v044.i08](https://doi.org/10.18637/jss.v044.i08).

### See Also

[tempfile](#)

---

TractorObject-class    *The TractorObject class*

---

### Description

This reference class extends the standard [envRefClass](#) class, adding methods for finding all of the field or methods available for an object. There is also a method for summarising key elements of the object as a named character vector, which can be suitable overridden by inheriting classes. The `show` method prints this summary as a labelled list.

### Methods

`fields()` Retrieve a list of all field names  
`methods()` Retrieve a list of all method names  
`summarise()` Summarise key aspects of the object

---

`where`                      *Compact conditional values*

---

### Description

This simple function checks whether its first argument is a logical value that evaluates to TRUE. If so, it returns its second argument. If not, it returns its third argument.

### Usage

```
where(condition, value, fallback = NULL)
```

### Arguments

`condition`            An expression that resolves to a single logical value.  
`value, fallback`    Any expression.

### Details

This function differs from the standard [ifelse](#) function in that it does not act elementwise, and that the third argument is optional, defaulting to NULL.

### Value

value, if condition evaluates to TRUE; otherwise fallback.

### Author(s)

Jon Clayden

**References**

Please cite the following reference when using TractoR in your work:

J.D. Clayden, S. Muñoz Maniega, A.J. Storkey, M.D. King, M.E. Bastin & C.A. Clark (2011). TractoR: Magnetic resonance imaging and tractography with R. *Journal of Statistical Software* 44(8):1-18. doi:10.18637/jss.v044.i08.

**See Also**

ifelse

---

[,SparseArray,ANY,ANY-method

*Indexing methods*

---

**Description**

Indexing methods for [SparseArray](#) and [MriImage](#) objects. For the latter class, arguments are passed to the equivalents for array or [SparseArray](#), except where *i* is another [MriImage](#) object, where its nonzero region will be used to provide the indices. For [SparseArray](#), indexing may be blank, or by numeric vector or matrix.

**Usage**

```
## S4 method for signature 'SparseArray,ANY,ANY'
x[i, j, ..., drop = TRUE]

## S4 replacement method for signature 'SparseArray,ANY,ANY'
x[i, j, ...] <- value

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

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

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

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

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

## S4 replacement method for signature 'MriImage,missing,missing'
x[i, j, ...] <- value
```

```
## S4 replacement method for signature 'MriImage,ANY,missing'  
x[i, j, ...] <- value  
  
## S4 replacement method for signature 'MriImage,missing,ANY'  
x[i, j, ...] <- value  
  
## S4 replacement method for signature 'MriImage,ANY,ANY'  
x[i, j, ...] <- value  
  
## S4 replacement method for signature 'MriImage,MriImage,missing'  
x[i, j, ...] <- value
```

### Arguments

x	An object of the appropriate type.
i, j, ...	Indexing objects.
drop	Scalar value: should unitary dimensions be dropped?
value	New value(s) for replacement forms.

### Value

A vector, array or [SparseArray](#).

### Author(s)

Jon Clayden

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