

Package ‘divest’

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Title Get Images Out of DICOM Format Quickly

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Imports Rcpp (>= 0.11.0), RNifti (>= 0.3.0)

Suggests testthat, covr

LinkingTo Rcpp, RNifti

Description Provides tools to sort DICOM-format medical image files, and convert them to NIfTI-1 format.

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URL <https://github.com/jonclayden/divest>

BugReports <https://github.com/jonclayden/divest/issues>

Encoding UTF-8

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readDicom

*Read one or more DICOM directories***Description**

These functions are R wrappers around the DICOM-to-NIfTI conversion routines provided by `dcm2niix`. They scan directories containing DICOM files, potentially pertaining to more than one image series, read them and/or merge them into a list of `niftiImage` objects.

Usage

```
readDicom(path = ".", subset = NULL, flipY = TRUE, crop = FALSE,
          forceStack = FALSE, verbosity = 0L, labelFormat = "%t_N%n_S%s",
          interactive = base::interactive())

sortDicom(path = ".", forceStack = FALSE, verbosity = 0L,
          labelFormat = "%t_N%n_S%s", nested = TRUE, keepUnsorted = FALSE)

scanDicom(path = ".", forceStack = FALSE, verbosity = 0L,
          labelFormat = "%t_N%n_S%s")
```

Arguments

<code>path</code>	A character vector of paths to scan for DICOM files. Each will be examined in turn. The default is the current working directory. <code>readDicom</code> (only) will accept paths to individual DICOM files, rather than directories. Alternatively, for <code>readDicom</code> and <code>sortDicom</code> , a data frame like the one returned by <code>scanDicom</code> , from which file paths will be read.
<code>subset</code>	If <code>path</code> is a data frame, an expression which will be evaluated in the context of the data frame to determine which series to convert. Should evaluate to a logical vector.
<code>flipY</code>	If <code>TRUE</code> , the default, then images will be flipped in the Y-axis. This is usually desirable, given the difference between orientation conventions in the DICOM and NIfTI-1 formats.
<code>crop</code>	If <code>TRUE</code> , then <code>dcm2niix</code> will attempt to crop excess neck slices from brain images.
<code>forceStack</code>	If <code>TRUE</code> , images with the same series number will always be stacked together as long as their dimensions are compatible. If <code>FALSE</code> , the default, images will be separated if they differ in echo, coil or exposure number, echo time, protocol name or orientation.
<code>verbosity</code>	Integer value between -1 and 3, controlling the amount of output generated during the conversion. A negative value will suppress all output from <code>dcm2niix</code> except warnings and errors.
<code>labelFormat</code>	A <code>sprintf</code> -style string specifying the format to use for the final image labels. See Details.

interactive	If TRUE, the default in interactive sessions, the requested paths will first be scanned and a list of DICOM series will be presented. You may then choose which series to convert.
nested	For sortDicom, should the sorted files be created within the source directory (TRUE, the default), or in the current working directory (FALSE)?
keepUnsorted	For sortDicom, should the unsorted files be left in place, or removed after they are copied into their new locations? The default, FALSE, corresponds to a move rather than a copy. If creating new files fails then the old ones will not be deleted.

Details

The scanDicom function parses directories full of DICOM files and returns information about the acquisition series they contain. readDicom reads these files and converts them to (internal) NIfTI images (whose pixel data can be extracted using `as.array`). sortDicom sorts the files into subdirectories by series, but does not convert them.

The labelFormat argument describes the string format used for image labels and sorted subdirectories. Valid codes, each escaped with a percentage sign, include a for coil number, c for image comments, d for series description, e for echo number, f for the source directory, i for patient ID, l for the procedure step description, m for manufacturer, n for patient name, p for protocol name, q for scanning sequence, s for series number, t for the date and time, u for acquisition number and z for sequence name.

Value

The readDicom function returns a list of niftiImage objects, which can be easily converted to standard R arrays or written to NIfTI-1 format using functions from the RNifti package. The scanDicom function returns a data frame containing information about each DICOM series found. sortDicom is called for its side-effect, and so returns NULL.

Author(s)

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Examples

```
path <- system.file("extdata", "raw", package="divest")
scanDicom(path)
readDicom(path, interactive=FALSE)
```

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