Package ‘fmriqa’

May 8, 2026

Type Package

Title Functional MRI Quality Assurance Routines

Version 0.5.0

Date 2026-02-20

Description Methods for performing fMRI quality assurance (QA) measurements of test objects. Heavily based on the fBIRN procedures detailed by Friedman and Glover (2006) <doi:10.1002/jmri.20583>.

BugReports `https://github.com/martin3141/fmriqa/issues`

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RoxygenNote 7.3.3

Imports viridisLite, RNifti, ggplot2, reshape2, gridExtra, grid, tidyr, optparse, tcltk, RcppEigen, imager, pracma

Encoding UTF-8

Suggests testthat, covr, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

`fmriqa-package` *fmriqa: fMRI quality assurance routines*

Description

The fmriqa package provides an implementation of the fMRI quality assurance analysis protocol detailed by Friedman and Glover (2006) <doi:10.1002/jmri.20583>.

Details

#' To learn more about fmriqa, start with the vignettes: ‘browseVignettes(package = "fmriqa")‘

For a full list of functions: ‘help(package=fmriqa, help_type="html")‘

Author(s)

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See Also

Useful links:

- Report bugs at `https://github.com/martin3141/fmriqa/issues`

`combine_res_glob` *Combine fmriqa csv result files into a dataframe*

Description

Combine fmriqa csv result files into a dataframe

Usage

```
combine_res_glob(pattern)
```

Arguments

`pattern`	glob pattern to match the csv result files (eg "*.csv")

Value

a dataframe of results

`run_fmriqa` *Run fMRI quality assurance procedure on a NIfTI data file*

Description

Run fMRI quality assurance procedure on a NIfTI data file

Usage

```
run_fmriqa(
  data_file = NULL,
  roi_width = 21,
  slice_num = NULL,
  skip = 2,
  tr = NULL,
  pix_dim = NULL,
  poly_det_ord = 3,
  spike_detect = FALSE,
  x_pos = NULL,
  y_pos = NULL,
  plot_title = NULL,
  last_vol = NULL,
  gen_png = TRUE,
  gen_res_csv = TRUE,
  gen_pdf = FALSE,
  gen_spec_csv = FALSE,
  png_fname = NULL,
  res_fname = NULL,
  pdf_fname = NULL,
  spec_fname = NULL,
  verbose = TRUE,
  bg_smooth = 12,
  bg_shrink = 25,
  t1_canny = NULL,
  t2_canny = NULL
)
```

Arguments

`data_file`	input data in nifti format, a file chooser will open if not set
`roi_width`	roi analysis region in pixels (default=21)
`slice_num`	slice number for analysis (default=middle slice)
`skip`	number of initial volumes to exclude from the analysis (default=2)
`tr`	override the TR detected from data (seconds)
`pix_dim`	override the x,y,z pixel dimensions (mm) detected from data eg pixdim=c(3,3,3)

`poly_det_ord`	polynomial order used for detrending (default=3)
`spike_detect`	generate k-space spike-detection plot (default=FALSE)
`x_pos`	x position of ROI (default=center of gravity)
`y_pos`	y position of ROI (default=center of gravity)
`plot_title`	add a title to the png and pdf plots
`last_vol`	last volume number to use in the analysis
`gen_png`	output png plot (default=TRUE)
`gen_res_csv`	output csv results (default=TRUE)
`gen_pdf`	output pdf plot (default=FALSE)
`gen_spec_csv`	output csv of spectral points (default=FALSE)
`png_fname`	png plot filename
`res_fname`	csv results filename
`pdf_fname`	pdf plot filename
`spec_fname`	csv spectral data filename
`verbose`	provide text output while running (default=TRUE)
`bg_smooth`	amount to smooth background image before calculating the maximum BG percent metric (default=12mm)
`bg_shrink`	amount to shrink the BG image away from the object to avoid residual object signal in the maximum BG percent metric (default=25mm)
`t1_canny`	threshold for weak edges for Canny edge detector (defaults to auto detect)
`t2_canny`	threshold for strong edges for Canny edge detector (defaults to auto detect)

Value

dataframe of QA metrics

Examples

```
fname <- system.file("extdata", "qa_data.nii.gz", package = "fmriqa")
res <- run_fmriqa(data_file = fname, gen_png = FALSE, gen_res_csv = FALSE, tr = 3)
```

`run_fmriqa_glob` *Run fMRI quality assurance procedure on a set of NIfTI data files*

Description

Run fMRI quality assurance procedure on a set of NIfTI data files

Usage

```
run_fmriqa_glob(pattern, ...)
```

Arguments

`pattern`	glob expresion to match analysis files
`...`	options to pass to run_fmriqa function

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