

Package ‘fmriqa’

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Type Package

Title Functional MRI Quality Assurance Routines

Version 0.5.0

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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](https://doi.org/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, tidy, optparse, tcltk, RcppEigen, imager, pracma

Encoding UTF-8

Suggests testthat, covr, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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fmriqa-package	<i>fmriqa: fMRI quality assurance routines</i>
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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	<i>Combine fmriqa csv result files into a dataframe</i>
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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

<code>data_file</code>	input data in nifti format, a file chooser will open if not set
<code>roi_width</code>	roi analysis region in pixels (default=21)
<code>slice_num</code>	slice number for analysis (default=middle slice)
<code>skip</code>	number of initial volumes to exclude from the analysis (default=2)
<code>tr</code>	override the TR detected from data (seconds)
<code>pix_dim</code>	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, ...)
```

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Arguments

pattern	glob expression to match analysis files
...	options to pass to run_fmriqa function

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