

# Package: fmriqa (via r-universe)

August 22, 2024

**Type** Package

**Title** Functional MRI Quality Assurance Routines

**Version** 0.4.0

**Date** 2019-01-10

**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>

**License** GPL-3

**LazyData** true

**RoxygenNote** 6.1.1

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

**Encoding** UTF-8

**Suggests** testthat, covr, knitr, rmarkdown

**VignetteBuilder** knitr

**Repository** <https://martin3141.r-universe.dev>

**RemoteUrl** <https://github.com/martin3141/fmriqa>

**RemoteRef** HEAD

**RemoteSha** 13943bbe77fbf2b0b343b223463bf6b87f9d607e

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fmriqa-package      *fmriqa: fMRI quality assurance routines*

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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>

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combine\_res\_glob      *Combine fmriqa csv result files into a dataframe*

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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)
```

**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)

**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)
```

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run_fmriqa_glob	<i>Run fMRI quality assurance procedure on a set of NIfTI data files</i>
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**Description**

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

**Usage**

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

**Arguments**

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

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