

Physiological noise correction for the GE scanners at CFMRI

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Overview:

This document describes the procedure for using **physioGE**[®] Matlab package to remove cardiac and respiratory noises from fmri datasets acquired on GE 3T scanners at CFMRI. The cardiac and respiratory waveforms are recorded with the GE built-in pulse sensor and respiratory bellow. The fmri datasets can be either BOLD data from GE product EPI or arterial spin labeling (ASL) data from our in-house SPEP sequence. A retrospective image-based method (RETROICOR)^{1,2} is used for correcting the GE BOLD data, and extensions² of this method are used for removing physiological noise in ASL data.

The output of the **physioGE**[®] program can be a new fmri dataset with physiological noise removed, or a set of files containing physiological noise regressors. The latter is designed for users who wish to regress out physiological noise using their own deconvolution methods.

NOTE: We currently offer two systems for recording physiological signals during fMRI scans: a Labview-based system and a GE built-in system. The procedure described in this document works only for data acquired using the GE built-in system. For data acquired with the Labview-based system, another program **physio**[®] should be used and can be downloaded from our website <http://fmri.ucsd.edu/Howto/physio.shtml> .

System Requirement and Software Installation

1. SYSTEM REQUIREMENTS:
 - Redhat Enterprise Linux 5.x or above is recommended.
 - Matlab 7.7 or above is required.
 - AFNI 2006_6_30 or above is required.
2. DOWNLOAD and INSTALLATION:
 - Download physioGE.tar <http://fmri.ucsd.edu/download/physioGE.tar>.
 - Untar the file (on Linux: tar -xvf physioGE.tar).
 - Add the physioGE folder to Matlab path.

Required Data Files

1. fMRI data set: either an AFNI Brik or NIFTI .
2. Physiological data: PPGData and RESPData files from the GE scanner.
3. Paradigm file: a text file containing columns of stimulus patterns or predicted hemodynamic responses. Each column represents one stimulus/event type, and each row is one time point. The time points must fall on the same grid as the input fMRI dataset.

¹ Glover et al , Magn Reson Med 44(1): 162-7, 2000

² Khaled Restom, Yashar Behzadi and Thomas T Liu, submitted for review,2005 (tliu@ucsd.edu)

Physiological Noise Correction (Step-by-step Instructions)

1. Create AFNI Briks or NIFTI from fMRI DICOM images
to3d -prefix prefix -time:zt #slices #reps TR alt+z i*

NOTE: to3d is an AFNI command for converting dicom images. If the prefix name contains .nii or .nii.gz suffix, to3d will convert the dicom images to NIFTI format; otherwise it creates an AFNI Brik. You can also use other available software for converting dicom to NIFTI.

If the dataset is acquired with our in-house SPEP sequence, use the AFNI Brik created on the scanner directly. NIFTI is not supported for the in house sequence at this time.

2. Remove physiological noise in MATLAB
 - OPTION 1: Deconvolution (Appendix A)

physioGE(brikIn, PPGDatafile, RESPDatafile, brikOut, ref, model, sflag);

- OPTION 2: No deconvolution (Appendix B)

This option is designed for users who wish to regress out physiological noise using their own deconvolution methods. The outputs are a set of text files containing physiological noise regressors for each slice. These regressors can be used for decomvolution.

physioGERG(brikIn, PPGDatafile, RESPDatafile, outfile, model sflag);

APPENDIX A:

physioGE(brikIn, PPGDatafile, RESPDatafile, brikOut, ref, model, slflag);

Required Inputs:

brikIn - Input AFNI Brik (prefix without '+orig') or NIFTI (with .nii or .nii.gz suffix);
PPGDatafile - PPG data filename;
RESPDatafile - RESP data filename;
brikOut - prefix of the output dataset (without '+orig', or .nii. or .nii.gz);
The output dataset is saved in the same format as the input dataset,
e.g., if input is an AFNI Brik, output will also be an AFNI brik.

Optional Inputs:

ref - Paradigm/reference function (DEFAULT: [])
• Either a vector: [head on off cycles tail]
total scan time = (head + (on+off)*cycles + tail).
• Or a file:
The file must be a text file containing columns of stimulus pattern (or predicted hemodynamic response). Each column represents one stimulus, and each row is one time point. The time points must fall on the same grid as the input dataset.
• Or [] if the fMRI data is from a baseline scan without a task.
Model - Data type (DEFAULT: 'raw')
'raw' : if data is GE EPI BOLD;
'd3': if data is an ASL FLOW time course requiring d3 operation;
'a3': if data is an ASL BOLD time course requiring a3 operation;
slflag - slice order (DEFAULT: 1 interleaved)
0: sequential;
1: interleaved;

Output:

A new dataset (an AFNI Brik or NIFTI) with physiological noise removed.

Example:

```
brikIn='example/epifunc.nii';  
PPGfile='example/physio/PPGData_fmri_0709201011_58_03_867';  
RESPfile='example/physio/RESPData_fmri_0709201011_58_03_867';  
brikOut='epifunc_phys';  
ref='example/ref_epifunc.1D'; %reference is defined in ref_epifun.1D  
model='raw'; %bold  
slflag=1; %interleaved slices
```

```
physioGE(brikIn, PPGfile, RESPfile, brikOut, ref, model, slflag) %remove physio noise
```

Output dataset:

```
example/epifunc_phys.nii
```

APPENDIX B:

physioGERG(brikIn, PPGDatafile, RESPDatafile, outfile, model sflag);

Required Inputs:

brikIn - Input AFNI Brik (prefix without '+orig') or NIFTI (with .nii or .nii.gz suffix);
PPGDatafile - PPG data filename;
RESPDatafile - RESP data filename;
outfile - name of the output regressor file (outfile.1D.slice#);

Optional Inputs:

Model - Data type (DEFAULT: 'raw')
'raw' : if data is GE EPI BOLD;
'd3' : if data is ASL FLOW requiring d3 operation;
'a3' : if data is ASL BOLD requiring a3 operation;
sflag - slice order (DEFAULT: 1 interleaved)
0: sequential;
1: interleaved ;

Output:

A set of text files containing physiological noise regressors for each slice (.1D.slice#).

Example:

```
brikIn='example/epifunc.nii';  
PPGfile='example/physio/PPGData_fmri_0709201011_58_03_867';  
RESPfile='example/physio/RESPData_fmri_0709201011_58_03_867';  
fileout='epifunc_RG';  
model='raw'; %bold  
sflag=1; %interleaved slices
```

physioGERG(brikIn, PPGfile, RESPfile, fileout, model, sflag)

Output files:

```
Example/epifunc_RG.1D.01  
Example/epifunc_RG.1D.02  
Example/epifunc_RG.1D.03  
Example/epifunc_RG.1D.04  
.  
.  
.
```

Please report bugs and send suggestions to kunlu@ucsd.edu.