Physio Denoise: A Model-based Tool for Modeling Physiological Noise in fMRI Data

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Abbreviations

MRI ..... Magnetic Resonance Imaging
WM ..... White matter

I. Introduction

Physiological noise is one of the significant artefacts in functional magnetic resonance imaging (fMRI). fMRI uses magnetic imaging to measure brain activity by measuring changes in local oxygenation of blood, which in turn reflects the amount of local brain activity. [1] However, physiological pulsations related to cardiac pulsation and respiration would perturb blood-oxygen level contrast (BOLD) and add nuisance to fMRI data, which are the key challenges in this area. First, respiration is inevitable. During data aquisition, even the perfect subject could not avoid chest movement from breathing, which would result in head motion in the magnetic field. So that the MR images are likely to be distorted by respiration in a way. Second, cardiac pulsation could directly influence the BOLD signal especially in the region with large blood vessels. For example, cerebrospinal fluid (CSF) flow is modulated by both the cardiac and respiratory cycles, resulting in additional signal changes. [2]

The role of physiological noise in fMRI analysis deserves discussion. Some studies prefer not performing a physiological correction on fMRI data because cardiac and respiratory related fluctuations may be correlated with variations in neuronal activity. [2] However, the spatial specificity of functional connectivity has been clearly demonstrated to be influenced by aliased physiological noise. [3] A functional connectivity study [4] by Dagli has shown that removing cardiac fluctuations resulted in a variance reduction of roughly 10%–40%, depending on the region being investigated. [4] The sensitivity of these regions near pulsatile vessels could be improved by physiological noise correction. But another unarguable evidence is that heart rate variability is widely used as a measure of emotional arousal and autonomic nervous system activity. [2] All these facts remind us that physiological noise correction shoule be used carefully especially when the key factors in experiments are related to physiological responses.

In this work, we provides a robust model-based tool named Physio Denoise in modeling physiological artefacts, which also gives back a denoised data for further use. The implementation of this tool is based on the model RETROICOR. [5] This paper introduces the modules of this tool and explains results in each step from the example subject.

II. Background

The goal of fMRI data analysis is to analyze each voxel's time series to see whether the BOLD signal changes in response to some manipulation. [1] And the method used for fMRI analysis in detection of signal changes is the general linear model(GLM). GLM, a well-developed tool of linear systems analysis, is used widely to predict the responses of certain systems to a wide variety of inputs. [6]

In this work, our approach to addressing the problem of physiological artefacts is to record cardiac and respiratory signal during the scan, and then retrospectively remove these effects from the data. [5] GLM model is used as the basis of the denoise tool to build a noise model representing physiological artefact in fMRI images, and the cleaned data is obtained by regressing out physiological components in the model.

The general linear model could be expressed as:

$$Y = X\beta + e \tag{1}$$

In the expression, X is a designed matrix containing linear variables for the model. And Y is explained by the X through weight β. And β is the weight for each varaible. The error of this model is estimated by e.

Inheritating the idea of GLM, noise model RETROICOR assumes that the signal coule be expressed by additive noise components with weights. Both cardiac signal and respiration signal are regarded as periodic signals, so that they can be expressed as a low-Fourier series expanded interms of these phases:

$$Y(t) = \sum_{m=1}^{M} a_m^c cos(m\phi_c) + b_m^c sin(m\phi_c) + a_m^r cos(m\phi_r) + b_m^r sin(m\phi_r) \tag{2}$$

In this expression, ϕ_c and ϕ_t are the phases in the respective cardiac and respiratory cycles. And the order of Fouriour expression is configureable. In this work we used $M = 2$ as default.

For the calculation of cardiac phase, it is defined as

$$\phi_c(t) = 2\pi(t - t_1)/(t_2 - t_1) \tag{3}$$

Here t_1 and t_2 is the time for the subsequent R-peak value. So the expression constrains the phase value in the range of 0 to 2π. Since recorded physiological signals are used as inputs without any preprcossing, so R peak detection will be oprerated before the calculation.

For the calculation of respiratory phase, depth and states of breathing will be both taken into consideration. It is quite easy to imagine that a deeper breathe is more likely to bring a potential bulk motion of head. And also the phase of respiration is different from inhaling to exhaling. Therefore, respiratory phase is defined by both depth and state. State of inhaling or exhaling is more like polarity of phase, while depth is more like the amplitude value. The signal of depth is recorded by a detecting belt wrapping around subject's chest. To get the respiratory amplitude of the given time, a histogram-equalized transfer function is used, which is expressed as :

$$\phi_r(t) = \pi \frac{\sum_{b=1}^{rnd[R(t)/R_{max}]} H(b)}{\sum_{b=1}^{100} H(b)} dR/dt \tag{4}$$

First, all the signal values are normalized to the range $(0, Rmax)$. Then a histogram $H(b)$ is gained with all normalized values. In the y domain of histogram, the y value is from the normalized data. And in the x domain, the bins of histogram are defined to be 100 bins. If the normalized amplitude from the given time belongs to the nth bin, then the phase value will be calculated by dividing the sum value till nth bin by the sum of 100 bins.

In the end, value from the divisor will multiple by π, so that the phase value will be in the range of $-\pi$ to π. During data aquisition of fMRI, BOLD time series have time resolution, which refers to reprtition time or TR. And by now MRI data will be either recorded by multi-slice or single slice at a time, which means the slices constructing the whole brain volumn come from different time stamp during the TR. Therefore, a single time stamp could not represent for the whole volume. However, applying different time stamps for each slice is also not practical. Because the slices are collected in horizontal direction, and the region of interest for artefacts could be in any shape rather than only scattering on a horizontal slice. So it is not meaningful to denoise slice by slice. To simplify the slice time problem, the middle time stamp in TR is chosen to calculate the physiological phases.

III. Materials and Methods

A. Overview

This section introduces modules and workflow of this tool.

This tool consists of three main modules, as depicted in Fig.1, including preprocessing of fMRI data, preprocessing of physiological data and noise modeling. Briefly, the first modeule preprocesses the raw fMRI data with motion correction, and the second module deals with physiological data and generate the key values, physiological regressors, from these data. These two modules prepare the basic materials for the noise modeling model. Exploiting the idea of RETROICOR model, noise modeling module uses prepared regressors to build a GLM. Physiological regressors are used as independent variables in the model. So when regressing out all the physiological components, a cleaned fMRI data could be gained.

The compulsory inputs for this tool include a raw fMRI data, physiological siganls saved in text file in which three columns

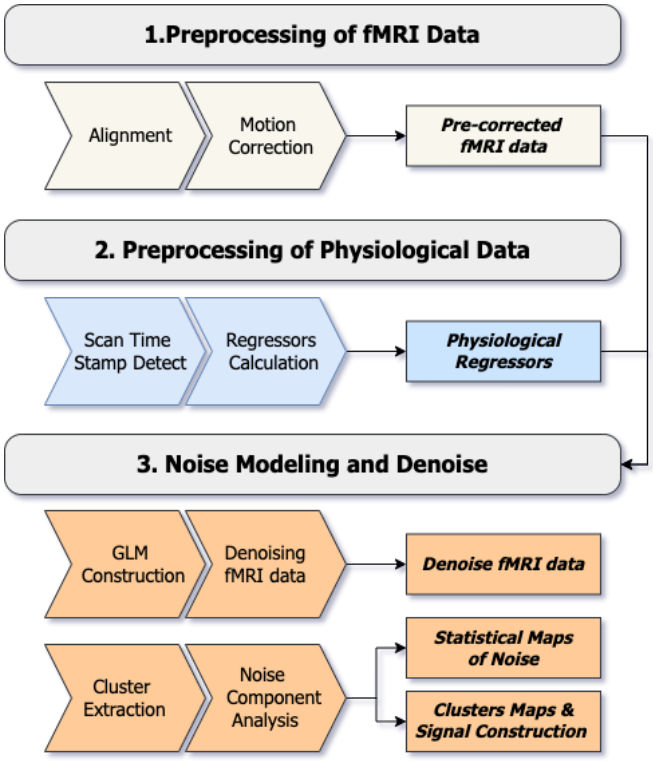

Fig. 1. Workflow of Denoise Tool

respectively stand for cardiac signal, respiration signal and time stamps, TR time, sample rate and working directory.

B. Softwares and Packages

HeartPy [7],

C. Data Preprocessing

1) Alignment:

2) Motion Correction:

D. Processing of Physiological data

The main idea of processing physiological data is to extract needed regressors for the noise model.

1) Scan Time Detection: The whole denoising process aims at correcting fMRI data for each scan. So the time stamp of the beginning of each scan could be used to represent each volume image. Using scan time detection part also synchronizs physiological signals to each volume in fMRI data, which is essential to get regressors in the modeling part.

Segmentation is also applied on input physiological data which limits the length of signals to be consistent with fMRI data. Because during the data aquisition the physiological data could be collected by external equipments such as Biopac rather than MRI device. So length of signals may not be the same as fMRI data. Moreover, as mentioned in the background, the respiratory phase calculation partly depends on the a histogram of the amplitude during the whole scan. So a uncompatible length of respiratory signal might influences the phase values which indirectly effects the noise model. To

be specific, a period of unexpected unstable signal could be accidently collected when subjects taking off the device, which may change the distribution of histogram in a way.

After scan time detection, the length of physiological signals will be limited to be 2 TR time longer than the fMRI data. And a csv file recording each scan time will be generated in the working directory.

2) Cardiac Regressors: In Physio Denoise, we choose a less invasive method of assess cardiac cycles, which is Photoplethysmogram (PPG). PPG devices employ an optical sensor to measure the changes in coloration of the skin as blood perfuses through the arteries and capillaries with each heartbeat. [7]

With the help of HeartPy, the peak of the signal could be detected and marked, as it shows in Fig.2

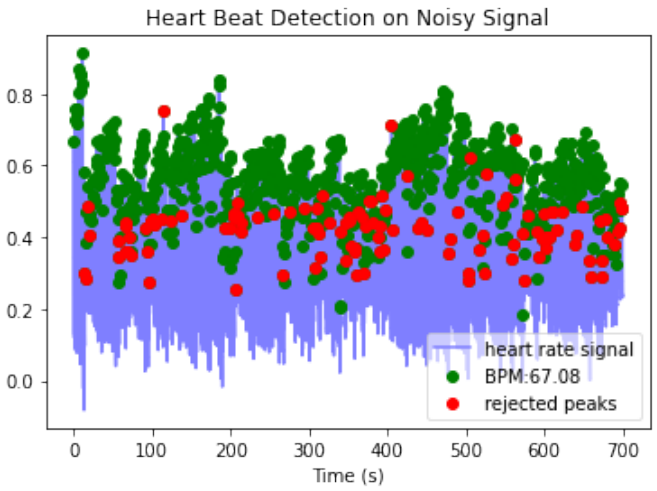

Fig. 2. An example of PPG signal analyzed by HeartPy. The green points represent the accepted peaks, while the red points are rejected by HeartPy. Peaks are considered low confidence if the interval created between two adjacent peaks deviates by more than 30% of the mean peak-peak interval of the analysed segment. [7]

While a sequence of peaks from PPG signal is generated, two continous accepted peaks are found for the time stamp of each scan. The scan time will locate between these two peaks. So that cardiac phase value in the formula 3 could be gained.

3) Respiration Regressors:

IV. Results and discussion

V. Conclusion

References

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