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An Improved Model of Motion-Related Signal Changes in fMRI

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Abstract

Head motion is a significant source of noise in the estimation of functional connectivity from resting-state functional MRI (rs-fMRI). Current strategies to reduce this noise include image realignment, censoring time points corrupted by motion, and including motion realignment parameters and their derivatives as additional nuisance regressors in the general linear model. However, this nuisance regression approach assumes that the motion-induced signal changes are linearly related to the estimated realignment parameters, which is not always the case. In this study we develop an improved model of motion-related signal changes, where nuisance regressors are formed by first rotating and translating a single brain volume according to the estimated motion, re-registering the data, and then performing a principal components analysis (PCA) on the resultant time series of both moved and re-registered data. We show that these “Motion Simulated (MotSim)” regressors account for significantly greater fraction of variance, result in higher temporal signal-to-noise, and lead to functional connectivity estimates that are less affected by motion compared to the most common current approach of using the realignment parameters and their derivatives as nuisance regressors. This improvement should lead to more accurate estimates of functional connectivity, particularly in populations where motion is prevalent, such as patients and young children.

Keywords

Motion; Correction; rs-fMRI; Methods

Introduction

In-scanner head motion has been shown to be one of the largest sources of noise in resting-state functional magnetic resonance imaging (rs-fMRI). This challenge has recently been a topic of tremendous interest, in large part because even small amounts of movement can cause significant distortions to estimates of functional connectivity, and because uncorrected motion-related signals can bias group results if there are differences in head motion; see

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Maclaren et al and Power et al. for review (Maclaren et al., 2013; Power et al., 2015). Small, but significant, motion-related signal changes can remain even after realigning the images using rigid-body or affine transforms.

The most common current approach to deal with the residual motion-related signal changes is to regress out the 6 rigid body realignment parameters (3 translations and 3 rotations), as well as their temporal derivatives. Other variants of this approach additionally include time-shifted and/or squared versions of these motion parameters (Friston, 1996). However, these approaches assume that the motion-related signal changes are linearly related to the realignment parameters. This is not always the case. For example, at a curved edge of image contrast where motion in one direction causes a signal increase, the same motion in the opposite direction may not produce the same decrease, or even a decrease at all. Similarly, in a region with a nonlinear gradient in image intensity, a displacement in one direction would not produce the same magnitude signal change as a displacement in the opposite direction. Motion can result in sampling different proportions of tissue classes at any given location. Depending on the proportions sampled, resulting signal changes might be positive, negative or neither.

In this study, we develop an improved model of motion-related signal changes. First, in an approach similar to Wilke et al., we derive a voxel-wise estimate of the signal changes induced by the head motion during the scan by taking one of the acquired echo-planar imaging volumes and rotating and translating it according to the negative of the estimated motion parameters (Wilke, 2012). We will call this the “motion simulated” (MotSim) dataset. This MotSim dataset models the motion-related signal changes in the original data that are entirely due to motion. The MotSim dataset is then motion corrected with rigid body volume registration (MotSimReg). This MotSimReg dataset, which has been rotated and translated according to the estimated subject motion, and then re-registered, reflects imperfections introduced by interpolation and errors in estimating the motion (Grooten et al., 2000).

Three new models of motion-related signal changes will be evaluated and compared against the current common approach of including the 6 realignment parameters and their derivatives. Specifically, we derive nuisance regressors from 1) a temporal principal components analysis (PCA) of all brain voxels in the MotSim dataset (the “forward” model), 2) a PCA of the volume registered MotSim dataset (the “backward” model), and 3) a PCA of both the “forward” and “backward” models spatially concatenated (the “both” model). The use of temporal PCA to reduce a large array of potential noise regressors has been used previously for noise reduction in fMRI (e.g. to derive nuisance regressors from CSF and white matter in the CompCor technique, (Behzadi, 2007)); the beauty with the proposed MotSim PCA approach is that the noise time series are purely derived from the estimated subject motion and thus are unlikely to contain signals of interest (unless of course the neural signals of interest are correlated with the motion).

Materials and methods

Participants

Written informed consent was obtained from subjects prior to each scanning session in accordance with a University of Wisconsin Madison IRB approved protocol. Fifty-five healthy adults (27 females; 40.9 ± 17.5 years of age on average, range: 20–77 years) with no history of neurological or psychological disorders were scanned

Data Acquisition

Each subject was instructed to lie still in the scanner while keeping her or his eyes fixated on a cross. This resting condition (eyes open and fixating) has been shown to yield slightly more reliable results compared to either eyes closed or eyes open without fixation (Patriat et al., 2013). Each subject was scanned twice within the same session. All the scans were acquired using a 3T GE MRI scanner (MR750, General Electric Medical Systems, Waukesha, WI). Each functional scan was 10 min in length and acquired with the same echo planar imaging (EPI) sequence (TR = 2.6 s, TE = 25 ms, flip angle = 60° , FOV = $224\text{mm} \times 224\text{mm}$, matrix size = 64×64 , slice thickness = 3.5 mm, number of slices = 40). T1-weighted structural images were acquired before the functional images using an MPRAGE sequence with the following parameters: TR = 8.13 ms, TE = 3.18 ms, TI = 450 ms, flip angle = 12° , FOV = $256\text{mm} \times 256\text{mm}$, matrix size = 256×256 , slice thickness = 1 mm, and number of slices = 156.

Motion Dataset (MotSim)

In this study, we introduce new motion correction methods by extracting regressors from a dataset containing signal fluctuations solely due to motion. This motion dataset, that we refer to as, MotSim, was previously suggested by Wilke (Wilke, 2012). This motion dataset is obtained by extracting one volume from the original data and creating a 4D dataset by moving this one volume according to the inverse of the estimated 6 parameters of motion (Figure 1). For the purpose of our study, the 4th volume, which also served as base for the motion realignment procedure, was chosen after the first two steps of preprocessing (removing the first three time points and performing slice-timing correction). We used linear interpolation for the resampling, the default in AFNI's 3dWarp. In a follow-up analysis, we repeated this using 5th order interpolation, and the main results were unchanged.

Motion Regressors

In this study, four motion correction models were compared, all with the same number of regressors used the current standard (see model i). The models studied here are:

- i. *12mot*: 6 parameters of motion derived from the re-alignment procedure + the derivative of each of these parameters.
- ii. *12Forw*: First 12 principal components over the whole brain of the *MotSim* dataset (“forward model”).
- iii. *12Back*: First 12 principal components over the whole brain after realigning the *MotSim* dataset, resulting in *MotSimReg* (“backward model”). Note that the

realignment is estimated from the MotSim dataset, rather than applying the inverse of the transform that created the MotSim dataset.

- iv. *12Both*: First 12 principal components over the whole brain after spatial concatenation of the motion dataset and the realigned *MotSim* dataset time series (“combined forward and backward model”).

12Forw and *12Back* differ from each other in that *12Forw* represents the *MotSim* dataset in its entirety whereas *12Back* only represents residual motion, such as interpolation errors and errors in the estimation of the amount of motion. Finally, *12Both* contains the regressors explaining the most variance across *12Forw* and *12Back*.

A temporal principal component analysis (PCA) generates a set of linear, uncorrelated components that reflect the main features of signal variations of the motion dataset. PCA has the benefit to minimize mutual information between the different principal components (PCs). The PCs are generated in order of decreasing variance explained (e.g. $PC1 > PC2 > PC3 \dots$). Such a PCA decomposition approach has previously been used to derive nuisance regressors from CSF and other high variance voxels, primarily to model physiological noise (Behzadi, 2007). Here we use this idea to specifically derive noise regressors that will best model the signal changes induced by subject motion, and we evaluate the effectiveness of this approach at reducing the influences of subject motion. The principal components in the MotSim models were determined from a temporal PCA of all brain voxels, including edge voxels dilated 2 voxels out from the brain. We chose the first 12 principal components of each of the MotSim models in order to keep the number of nuisance regressors the same as the commonly used *12mot* model (6 realignment parameters and their derivatives). An additional model that has been suggested is the use of the 6 realignment parameters, the realignment parameters at the previous time point, and the square of each of these regressors (Friston, 1996), which we will call *24mot*. We will additionally evaluate this model, as well as using the first 24 principal components of the ‘Both’ model (*24Both*) in order to match the number of nuisance regressors.

Data Preprocessing

Preprocessing of the rs-fMRI data was implemented using the software AFNI (Cox, 1996) (Figure 2). The preprocessing steps included: removal of the first 3 volumes of data to remove the initial transient in the MR signal; slice-timing correction to correct timing difference due to an interleaved acquisition of slices within a volume; within-run volume registration to reduce the influence of subject motion within the scanner; motion regression; T1-to-EPI alignment; normalization of T1 data to a common MNI template space, and corresponding normalization of EPI data; spatial blurring (6mm fwhm); and nuisance regression (with censoring, without global signal regression, GSR) as well as temporal filtering (0.01-0.1Hz bandpass) all in one step (using 3dTproject). The censoring step was performed using a 0.25mm threshold calculated using Euclidean norm; see Yan et al. for a comparison of the different methods of framewise displacement calculations (Yan et al., 2013). For comparison, we also processed the data using ICA-AROMA instead of the various motion-regression models (Pruim et al., 2015).

Metrics

In this study, we compare the different models described above by the means of a number of different measures. First, we compute the fraction of variance explained (R^2) by the commonly used *12mot* and the new MotSim (*12Forw*, *12Back*, *12Both*) models, and temporal signal to noise ratio (tSNR) after regressing out each of these set of regressors (Triantafyllou et al., 2006; Van Dijk et al., 2012). The fraction of variance (R^2) explained by each model was assessed on average across the whole brain as well as on a voxel-wise basis. Next, we assessed the fraction of variance explained by increasing numbers of principal components from the “Both” model, ranging from including only the first PC to including the first 24 PCs. For comparison, we computed the variance explained by an increasing numbers of regressors consisting of random noise in time (Gaussian distributed, mean=0, variance=1).

We also assessed the influence of the different motion regressors on estimates of functional connectivity. For each subject, we first computed the average time course (after nuisance regression with each motion model) across each of 264 regions of interest, as defined in Power et al. (2012). We then computed all possible pairwise correlations between these time courses to form a connectivity matrix. Finally, we performed a multiple linear regression analysis of the connectivity matrices across subjects, with the average sum squared difference (SSD) in motion as a covariate. This provides a measure of how significantly each connection is correlated (across subjects) with motion. To summarize these results for each model, we computed a histogram of the Pearson correlation coefficient with motion (mean SSD) for all connections. These connectivity matrices, and their correlation with motion, were computed for each motion model with and without censoring time points with motion (SSD>0.2mm). In addition, we compute the distance dependence of the difference in connectivity between motion-censored and -uncensored data (Power 2012).

Statistical Testing and Multiple Comparison Correction

Paired T-tests were used to determine whether differences in the above mentioned metrics (R^2 and tSNR), were significantly different between the various models. The corresponding p-values were corrected for multiple comparisons using a Bonferroni correction based on the number of tests calculated ($0.05 / [10 \text{ tests per scan} * 2 \text{ scans}]$). For the voxel-wise R^2 comparison, R^2 values were first converted to a Fisher Z and those scores were used in paired T-tests to compare the different models.

Results

Motion Dataset Regressors

Figure 3 shows the fit of each model studied to the data of a high-motion subject. The motion regressors derived from the motion dataset using PCA modeled data better than the current standard, *12mot*. On average across subjects, *12Forw* and *12Both* fit the data slightly better than *12Back*. Example regressors for each model, for the subject depicted in Figure 3, are shown in Supplementary Figure 1. The mean sum-squared difference (SSD) of motion, and the percentage of time points censored for each subject are shown in Figure 4. The amount of variance in the simulated MotSim datasets explained by different numbers of

principal components are shown in the Supplementary Figure 2. For the “Both” MotSim model, 5 components explained 90% of the variance, 7 components explained 95% of the variance, and 16 components explained 99% of the variance in the combined MotSim and MotSimReg datasets (Supplementary Figure 2, values provided here are the median across subjects). For the “Forw” model, 4, 6, and 9 components explained 90%, 95%, and 99% of the variance in the MotSim model, respectively. For the “Back” model, 5, 7, and 18 components explained 90%, 95%, and 99% of the variance in the MotSimReg model. Note that these numbers are the fraction of explained variance of the simulated datasets used to derive the PCs, not the actual data. Explained variances in the actual data from increasing numbers of PCs are presented in the next section below.

Variance Explained

Figure 5 shows the differences in variance explained across the four motion correction models studied here. The models explained similar amount of variance for each of the subject’s two scans. Our three models (*12Forw*, *12Back*, and *12Both*) explained significantly more variance than the current standard *12mot* for scan 1 and scan 2 ($p < 0.005$) (Figures 5, 6, 7). On average across subjects and on average across the whole brain, the *12Both* MotSim model resulted in 4.1% more variance explained compared to the commonly used *12mot* model. Differences in explained variance between the MotSim models were relatively small, but some differences were statistically significant. Both the *12Forw* and *12Both* models explained significantly more variance than the *12Back* in scan 1 ($p < 0.05$), but not in scan 2 (Figure 6). No significant differences were observed between the *12Forw* and *12Both* models we propose in this study (Figures 5, 6).

Improvements afforded by the MotSim models varied across the brain. Figure 7 shows the results from T-tests comparing the variance explained by each motion correction model at every voxel. The MotSim models explained significantly more variance in the frontal cortex and especially towards the edges of the brain ($p < 0.005$, Figure 7). It is important to note that while on average across the whole brain only a 4.1% improvement in the explained variance was found for the MotSim models, on average across subjects, 10% of the voxels in the brain showed at least an additional 12.7% of explained variance, and 5% of the voxels showed at least an additional 17% of explained variance.

Figure 8 shows the fraction of variance explained by increasing numbers of principal components from the “Both” MotSim model. The first PC explained approximately 15% of the variance in gray matter, and 12% of the variance in white matter and CSF. These fractions increased with greater numbers of PCs. Increases in explained variance asymptotically approached a linear increase in explained variance parallel to that seen with greater numbers of random nuisance regressors.

tSNR

Figure 9 shows the differences in tSNR for each of the motion correction models for each subject’s scans. Across both scans, *12Forw*, *12Back*, and *12Both* yielded consistently higher tSNR values than the standard *12mot* method (Figure 9). The *12Both* and *12Forw* methods

yielded slightly (but statistically significant) higher tSNR than the *12Back* method for both scans ($p<0.05$, Figure 6).

Influence of motion on functional connectivity estimates

Figure 10 shows the functional connectivity matrix for each of the motion correction models. The color overlay indicates those connections whose connectivity strength is significantly correlated (across subjects) with the mean level of motion ($p<0.01$). The histograms of the Pearson correlation coefficient with motion show that the correlation with motion is reduced for the *12Both* and *24Both* models compared with the *12mot* and *24mot* models. The peak of the histogram is shifted closer to zero correlation, and fewer connections have a significant correlation with motion. ($CC=0.27$ corresponds to a significant correlation with motion at $p=0.05$). This was the case even when motion censoring was performed (keeping only those time points with $SSD<0.2\text{mm}$). The dataset exhibited only a very slight distance dependence of its connectivity (censored – uncensored) with motion. This distance dependence was not altered substantially by any of the motion regression models (Supplementary Figure 3). In the absence of motion censoring, ICA-AROMA reduced the correlation with motion more than the *12mot*, *24mot*, or MotSim models. When the MotSim models were combined with motion censoring, the correlation with motion was similar to ICA-AROMA (Figure 10).

Discussion

In this study, we introduce an improved model of head motion in rs-fMRI data and we study the efficiency of these motion regressors as compared to the currently widely used correction models. The models in question include the widely used 12 parameter motion regressor model (*12mot*), and three different sets of twelve regressors derived using PCA of a data driven motion dataset (*12Forw*, *12Back*, and *12Both*). We used R^2 , tSNR, and the correlation (across subjects) of functional connectivity with motion as metrics to assess performance of these models.

12mot vs. 12Forw, 12Back, and 12Both

The proposed MotSim models (*12Forw*, *12Back*, and *12Both*) fit significantly better to the data than the current standard (*12mot*) for motion regression, explaining significantly more variance than *12mot* consistently across scans ($p<0.05$). This increased variance explained is mostly coming from voxels located at the edges of the brain largely located in the frontal cortex, where motion is most severe (Satterthwaite et al., 2013). Thus, while the *12Both* MotSim model resulted in only a 4.1% increase in explained variance compared to the *12mot* model averaged over the whole brain, and looks at first glance to be a fairly minimal improvement in explained variance (Figure 5), regionally we see a much bigger improvement. In 10% of the voxels in the brain, the *12Both* MotSim model accounts for *at least* 12.7% more variance than the *12mot* model (on average across subjects). The amount of improvement also varies across subjects. For example for the subject shown in Figure 3, some regions of the brain show almost 80% more variance explained by the *12Both* MotSim model compared to *12mot*. The better fit and variance explained also resulted in better data quality as shown by tSNR, where our PCA-derived MotSim models consistently yielded

higher tSNR across scans. Furthermore, the MotSim models yielded more reliable functional connectivity of the PCC than *12mot*.

Comparison of 12Forw, 12Back, and 12Both models

The *12Back* model explained significantly lower variance than *12Forw* and *12Both* in the first run, and significantly lower tSNR in both runs. However, these differences among the different MotSim models, while statistically significant, were small. The *12Back* model still explained a significant amount of variance, even more than the typical *12mot* model. This finding suggests that residual motion related signal changes after image registration are the result of both interpolation errors as well as errors in estimating motion from low-resolution EPI data (note that the motion is re-estimated from the MotSim data, rather than applying the inverse of the transforms that generated the MotSim dataset).

Number of nuisance regressors

Including increasing numbers of principal components from the MotSim model as nuisance regressors explained increasing amounts of variance. To a certain extent, this is to be expected as including greater numbers of nuisance regressors, even random ones, explains more variance. The fraction of variance explained by the MotSim regressors was much higher than random regressors but asymptotically approached a linear increase with the same slope seen with increasing numbers of random regressors. This asymptote is reached at about 12–15 components in the dataset used for this study. Nevertheless, the effect of motion on functional connectivity estimates is slightly reduced by increasing the number of components from 12 to 24, as seen in Figure 10. The ideal number of nuisance regressors may be different for other datasets, since this depends on the number of image volumes acquired and the level of motion.

Alternative models

In a separate follow-up analysis, we also investigated whether the MotSim dataset could be used as a voxel-specific nuisance regressor. However, we found that this single regressor, while accounting for approximately 20% of the variance, did not account for as much variance as any of the other models. This could of course be largely due to the fact that only a single regressor was used instead of twelve. It does, however, also suggest that the residual motion-related signals at each voxel in the real data are some linear combination of the simulated motion-induced signal changes from multiple voxels. While the MotSim dataset by itself did not work well as a voxel-specific model of motion, it is possible that other voxel-specific models might be comparable to our PCA-based models and, therefore, further studies should still pursue developing these strategies.

In the absence of motion censoring, ICA-AROMA reduced the correlation with motion more than any of the motion models we investigated. When the MotSim models were combined with motion censoring, the correlation with motion was similar to ICA-AROMA. This suggests that the residual errors in the dataset after MotSim regression are coming from image volumes occurring at the time of the motion, e.g. intra-volume motion which MotSim was not designed to correct. It should also be kept in mind that ICA-AROMA is fundamentally a different method of denoising – it is data driven, while MotSim is model-

based. There are values to both approaches. For example, if one is interested in examining the functional connectivity of regions near an edge in the brain, ICA-AROMA could remove the effect of interest while MotSim only attempts to remove signal changes related to the estimated bulk head motion. Our goal in this study was to derive a more accurate model of one critical part of motion-induced signal changes – the signal changes due to between-volume motion. Future work could build on these models by including the effects of spin-history, B0-field changes, and intra-volume motion (assuming an independent higher temporal resolution measure motion is available). Recent work has also shown alternative approaches to motion censoring, for example by estimating the residual error after realignment (Christodoulou et al., 2013), and alternative data-based nuisance regressors, for example the use of time courses from the edge of the brain (Patriat et al., 2015). Similarly, modified acquisition strategies, such as multi-echo fMRI, can provide alternative or complementary methods of reducing the effects of motion (Kundu et al., 2012).

Limitations

While our methods proved to perform better than the current standard, our methods were only tested on healthy subjects; therefore, future studies should focus on applying these methods on a patient population and young patients, a population known to move a lot. An additional limitation is that the creation of the simulated motion (MotSim) dataset relied on an accurate estimate of the subject's head motion. Motion *during* the acquisition of a volume would not be accurately captured. A potential avenue to improve the motion correction models introduced in this study would be to create the motion dataset using external measures of motion (such as cameras and other in-scanner tracking systems). These systems have a much faster temporal resolution, which would allow for the estimation of slice-wise motion. This approach could then be further extended by incorporating models and corrections for spin-history effects. The current approach also does not consider changes in the B0-field, and the associated variation in EPI distortions, resulting from head motion. Such B0-field signal changes, however, would be less prevalent for small head motions, particularly those of only a few millimeters or less, which continue to be a problem in resting-state functional connectivity.

Conclusion

Taken together, these results show that motion reduction using the current common approach of regressing out the 6 realignment parameters and their derivatives can be significantly improved by using time series derived from a PCA decomposition of simulated motion-induced signal changes. That is, instead of using the realignment parameters themselves, we are using an estimate of the signal changes that this motion would produce. More specifically, our data show that nuisance regressors derived from a PCA decomposition of a simulated motion dataset and a realigned version of this dataset, the *12Forw* and *12Both* models introduced here, yield significantly better data quality (as identified by R^2 and tSNR), lead to functional connectivity estimates that are less affected by motion, and offer better fit of real data. This improvement should lead to more accurate estimates of functional connectivity, particularly in populations where motion is prevalent, such as patients and young children.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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References

- Behzadi Y, Restom K, Liao J, Liu TT. A Component Based Noise Correction Method (CompCor) for BOLD and Perfusion Based fMRI. *Neuroimage*. 2007; 37:90–101. [PubMed: 17560126]
- Christodoulou AG, Bauer TE, Kiehl KA, Feldstein Ewing SW, Bryan AD, Calhoun VD. A quality control method for detecting and suppressing uncorrected residual motion in fMRI studies. *Magnetic Resonance in Imaging*. 2013; 31:707–717.
- Cox R. AFNI: Software for Analysis and Visualization of Functional Magnetic Resonance Neuroimages. *Computers and Biomedical Research*. 1996; 29:162–173. [PubMed: 8812068]
- Friston. Movement-related effects in fMRI time-series. *Resonance in Medicine*. 1996; 35:346–355.
- Grootenboer S, Hutton C, Ashburner J, Howseman AM, Josephs O, Rees G, Friston KJ, Turner R. Characterization and correction of interpolation effects in the realignment of fMRI time series. *Neuroimage*. 2000; 11:49–57. [PubMed: 10686116]
- Kundu P, Inati SJ, Evans JW, Luh WM, Bandettini PA. Differentiating BOLD and non-BOLD signals in fMRI time series using multi-echo EPI. *Neuroimage*. 2012; 60:1759–1770. [PubMed: 22209809]
- Maclaren J, Herbst M, Speck O, Zaitsev M. Prospective motion correction in brain imaging: a review. *Magnetic Resonance Medicine*. 2013; 69:621–636.
- Patriat R, Molloy EK, Birn RM. Using Edge Voxel Information to Improve Motion Regression for rs-fMRI Connectivity Studies. *Brain Connect*. 2015; 5:582–595. [PubMed: 26107049]
- Patriat R, Molloy EK, Meier TB, Kirk GR, Nair VA, Meyerand ME, Prabhakaran V, Birn RM. The effect of resting condition on resting-state fMRI reliability and consistency: a comparison between resting with eyes open, closed, and fixated. *Neuroimage*. 2013; 78:463–473. [PubMed: 23597935]
- Power JD, Schlaggar BL, Petersen SE. Recent progress and outstanding issues in motion correction in resting state fMRI. *Neuroimage*. 2015; 105:536–551. [PubMed: 25462692]
- Pruim RH, Mennes M, van Rooij D, Llera A, Buitelaar JK, Beckmann CF. ICA-AROMA: A robust ICA-based strategy for removing motion artifacts from fMRI data. *Neuroimage*. 2015; 112:267–277. [PubMed: 25770991]
- Satterthwaite TD, Elliott MA, Gerraty RT, Ruparel K, Loughead J, Calkins ME, Eickhoff SB, Hakonarson H, Gur RC, Gur RE, Wolf DH. An improved framework for confound regression and filtering for control of motion artifact in the preprocessing of resting-state functional connectivity data. *Neuroimage*. 2013; 64:240–256. [PubMed: 22926292]
- Triantafyllou C, Hoge RD, Wald LL. Effect of spatial smoothing on physiological noise in high-resolution fMRI. *Neuroimage*. 2006; 32:551–557. [PubMed: 16815038]
- Van Dijk KR, Sabuncu MR, Buckner RL. The influence of head motion on intrinsic functional connectivity MRI. *Neuroimage*. 2012; 59:431–438. [PubMed: 21810475]
- Wilke M. An alternative approach towards assessing and accounting for individual motion in fMRI timeseries. *Neuroimage*. 2012; 59:2062–2072. [PubMed: 22036679]
- Yan CG, Cheung B, Kelly C, Colcombe S, Craddock RC, Di Martino A, Li Q, Zuo XN, Castellanos FX, Milham MP. A comprehensive assessment of regional variation in the impact of head micromovements on functional connectomics. *Neuroimage*. 2013; 76:183–201. [PubMed: 23499792]

Figure 1. Motion dataset generation. One volume from the acquired and re-aligned dataset is extracted, and then the estimated motion parameters are used to rotate and translate the extracted volume in time to create the Motion Simulated (MotSim) dataset.

Figure 2.

Preprocessing and processing pipeline. Green cells indicate single subject preprocessing and analysis of the rs-fMRI data. Grey cells indicate single subject processing of the anatomical data. Black cells indicate group level analysis.

Figure 3.

Fit of the motion correction models for a high motion subject. Top: voxel-wise difference in fraction of explained variance (R^2) between 12Both and 12mot models. Red-orange voxels represent higher variance accounted for by the 12Both model. Blue-cyan voxels represent higher variance accounted for by the 12mot model. Colors are thresholded at a R^2 difference of 0.2. Bottom: Black time series represent the aligned EPI data. Red time series represent the best fit of the various motion models. 12mot = 6 realignment parameters and their derivatives, 12Forw = first 12 principal components (PCs) of the MotSim dataset, 12Back =

first 12 PCs of the MotSimReg dataset, 12Both = first 12 PCs of the spatially concatenated MotSim and MotSimReg datasets.

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Figure 4. Mean sum-squared difference (SSD) of motion realignment parameters for the 55 subjects scanned, as well as the percentage of data retained after censoring time points with $SSD < 0.2\text{mm}$, sorted by the mean SSD.

Variance Explained (scan 1)

Variance Explained (scan 2)

Figure 5.

Fraction of variance (R^2) explained by the motion correction models for each scan, averaged across subjects and across the whole brain. Error bars represent the standard error deviation from the mean. (Note that these are average values across all subjects and across the whole brain. Improvements vary across the brain and across subjects, and can be much higher (see Figures 3 and 6).)

R2	12mot	12Forw	12Back	12Both
12mot		12Forw	12Back	12Both
12Forw	12Forw		12Forw	
12Back	12Back	12Forw		12Both
12Both	12Both		12Both	

tSNR	12mot	12Forw	12Back	12Both
12mot		12Forw	12Back	12Both
12Forw	12Forw		12Forw	
12Back	12Back	12Forw		12Both
12Both	12Both		12Both	

	Scan 1
	Scan 2

Figure 6.

Significance testing results for fraction of variance explained and tSNR between pairs of motion models. Cells in the upper triangle of each table represent results for scan 1, while cells in the lower triangle represent results for scan2. Shaded cells (orange for scan 1, purple for scan2) indicate significant difference. White, or non-shaded, cells indicate lack of significant difference using a paired T-test correction at $p < 0.05$ using Bonferroni correction based on the number of tests.

Figure 7.

Voxel-wise map of the fraction of variance explained, across all subjects, by the MotSim models (12Forw, 12Back, 12Both) compared to the 6 realignment parameters and their derivatives (12mot). The maps are thresholded at a voxel-wise $p = 0.005$, and the color reflects the mean difference in explained variance (max range = 0.1).

Figure 8.

Fraction of variance explained by using increasing numbers of principal components from the “Both” model. Plotted values are averaged across subjects and either gray matter (GM), white matter (WM), or cerebral spinal fluid (CSF). For comparison, the relationship between fraction of explained variance and number of regressors is computed for increasing numbers of random regressors (regressors consisting of Gaussian-distributed random noise in time with zero mean and unit standard deviation). The dashed line is parallel to the relationship from the random regressors and is provided as a visual aid.

Figure 9. Temporal signal-to-noise ratio (tSNR) of the fMRI data after regressing out each of the motion models, on average across the whole brain and across all subjects. Error bars reflect standard error deviation from the mean (whole brain) tSNR across subjects.

Figure 10.

(top) Functional connectivity matrices for 264 seed regions from Power et al. (2012). The color overlay indicates connections significantly correlated, across subjects, with the mean amount of motion (mean SSD) thresholded at $p < 0.01$. Connectivity matrices and their correlation with motion are shown for 4 motion correction methods: 12mot – 6 realignment parameters and their derivatives; 24mot – 6 realignment parameters, the realignment parameters at the preceding time point, and these 12 regressors squared; 12Both – the first 12 principal components of the “Both” MotSim model; 24Both – the first 24 principal

components of the “Both” MotSim model. (bottom) Histograms of the correlation (across subjects) between functional connectivity and mean motion, for all 264×264 functional connections. The correlations with motion for 12Both and 24Both models is reduced (shifted closer to a mean correlation with motion = zero) compared to the 12mot and 24mot models.