ITERATIVELY REWEIGHTED L1-FITTING FOR MODEL-INDEPENDENT OUTLIER REMOVAL AND REGULARIZATION IN DIFFUSION MRI

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ABSTRACT

Diffusion magnetic resonance imaging is negatively affected by subject motion occurring during the image acquisition. The induced data artifacts adversely influence the estimation of microstructural diffusion measures. State-of-the-art procedures for outlier removal detect and reject defective images during model fitting. These methods, however, are tailored only for specific diffusion models and excluding a varying number of diffusion-weighted images might be disadvantageous for the parameter estimation. Therefore, this work proposes a novel method based on an iteratively reweighted L1-Fitting for model-independent outlier removal with subsequent reconstruction of faulty images by modeling the signal in the continuous SHORE basis. We validate the proposed method on simulation data and clinical *in vivo* human brain scans and demonstrate its effect on diffusion parameters determined by the kurtosis and NODDI model.

Index Terms— Diffusion MRI, SHORE Basis, Sparsity, Robust Estimation, Outlier Correction, Clinical Applications

1. INTRODUCTION

Diffusion magnetic resonance imaging (dMRI) provides the possibility to investigate the structural connectivity of brain white matter non-invasively and to examine pathological conditions of the central nervous system. However, the technique is sensitive to artifacts occurring during the image acquisition. Spatially and temporally varying artifacts, e.g. induced by subject motion, potentially degrade the signal quality and complicate subsequent analysis of the complex white matter architecture. Especially in clinical applications, when data is collected from diseased patients, children in particular, measures need to be taken against the image degradation due to frequently occurring motion artifacts.

Robust estimation procedures have been introduced to reduce the influence of defective images on diffusion model parameters. Widely used in clinical applications is the RESTORE method [1] that improves the estimation of the model parameters in diffusion tensor imaging (DTI) through outlier rejection based on iteratively reweighted least squares (IRLS) regression. Consequently, microstructural features are more accurately extracted from the DT model. To this end, the RANSAC paradigm has also been investigated for robust tensor estimation and artifact detection in diffusion-weighted images [2]. Extending DTI to the popular diffusion kurtosis imaging (DKI) model [3] complements the information derived from the diffusion tensor and provides further insights on the non-Gaussianity of water diffusion in brain tissue. Recent literature shows that the dedicated outlier removal method REKINDLE [4] limits the impact of faulty DKI scans on the estimation of diffusion parameters. However, the robust estimation methods proposed in the literature so far are mainly tailored for specific diffusion models as well as limited to models than can be linearized.

The present work explores a novel approach to reduce the influence of artifacts on diffusion-weighted images (DWIs) and to provide a robust estimation of the dMRI measurements independently of the diffusion model that, specific for each application, is used to extract structural measures from the data. We use the Simple Harmonic Oscillator based Reconstruction and Estimation (SHORE) basis to capture both the angular and the radial characteristics of the diffusion process [5]. Modeling the signal in the SHORE basis not only provides a continuous signal representation but also analytical formulae for the diffusion ensemble average propagator and commonly derived diffusion parameters [6]. Promoting the sparsity of the SHORE basis coefficients by means of an L1-norm regularizer has been found to outperform linear least squares estimation of the diffusion signal modeled in the SHORE basis [6]. Nevertheless, the SHORE basis is not immune from artifacts challenging the inference of structural parameters. Therefore, we propose a novel robust estimation procedure, IRL1 SHORE, that iteratively reweights the diffusion signal to detect and reject erroneous signals based on the model residuals. State-of-the-art methods for outlier removal proceed similarly and discard faulty DWIs from the data before extracting the diffusion measures of interest. Recent literature, however, indicates that excluding DWIs due to outlier removal might negatively affect the extracted diffusion parameters [7, 8]. To account for this potential problem, the

proposed method recovers excluded DWIs by means of sparse signal reconstruction in the SHORE basis and subsequent image analysis is performed on the full data set. To evaluate the proposed method we use simulations and *in vivo* dMRI data. We demonstrate the advantages of IRL1 SHORE to correct for motion artifacts and to improve diffusion parameter estimation independently of the required diffusion model.

2. MATERIALS AND METHODS

2.1. SHORE - an analytical model for sparse signal reconstruction

For a continuous representation, the signal is expressed as a linear combination of basis Φ that separates a radial basis X and an angular basis Y with the radial order n and, respectively, the angular order and degree l and m

$$s(q\mathbf{u}) = \sum_{l=0,even}^{N_{max}} \sum_{n=l}^{(N_{max}+l)/2} \sum_{m=-l}^{l} c_{nlm}\Phi_{nlm}(q\mathbf{u}) \quad (1)$$
$$\text{with } \Phi_{nlm}(q\mathbf{u}) = X_{nl}(q,\zeta)Y_l^m(\mathbf{u})$$

where q is the norm of the diffusion gradient vector $\mathbf{q}$, $\mathbf{u}$ a unit vector and c_{nlm} are the SHORE coefficients. A real and symmetric spherical harmonic (SH) basis Y_l^m is considered, as the diffusion signal is real and symmetric. ζ is a scale factor based on a typical diffusivity for brain tissue.

When combining analytical signal modeling with compressed sensing principles to recover the signal of sparse measurements, the SHORE basis is well suited and outperforms other continuous basis functions [6]. For sparse signal reconstruction, we use an iterative shrinkage and thresholding algorithm [9] to solve the convex optimization problem

$$\arg\min_{\mathbf{c}\in R^{n_c}} \|\mathbf{\Phi c} - \mathbf{s}\|_{l_2} + \lambda \|\mathbf{c}\|_{l_1} \quad (2)$$

where the signal vector $\mathbf{s}$ with entries $s(q\mathbf{u})$ is obtained from all the measurements through normalization by the non-diffusion weighted signal $S(0)$. The terms $\|\mathbf{\Phi c} - \mathbf{s}\|_{l_2}$ and $\|\mathbf{c}\|_{l_1}$ promote data consistency and sparsity, respectively.

2.2. Outlier detection by iteratively reweighted L1 SHORE

Similar to state-of-the-art approaches for robust signal estimation, the proposed method contains an iterative reweighting of the model residuals. Specifically, we adapt equation (2) to include an iterative reweighting of the SHORE residuals during the L1-norm fitting routine for each voxel

$$\arg\min_{\mathbf{c}\in R^{n_c}} \|\mathbf{\Omega}(\mathbf{\Phi c} - \mathbf{s})\|_{l_2} + \lambda \|\mathbf{c}\|_{l_1} \quad (3)$$

where $\mathbf{\Omega}$ is the diagonal weight matrix containing the weights $\sqrt{w_i}$ for each normalized measurement s_i. We use the Geman-McClure M-estimator and the weight function

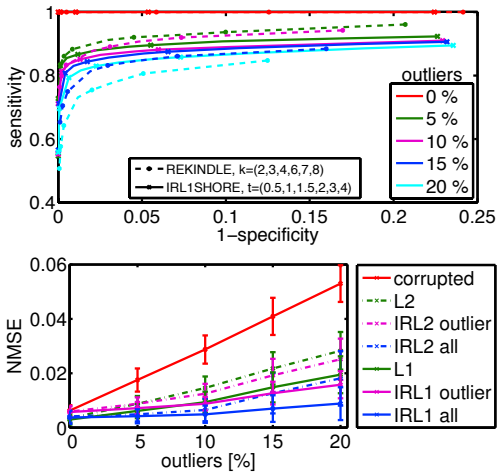

Fig. 1. Simulations with SNR=20 and varying % of outliers: (top) sensitivity and specificity of IRL1 SHORE and REKINDLE as functions of threshold t and k, respectively; (bottom) NMSE versus % of outliers for noisy data and the correction methods using L1- or L2-norm regularizers and correcting all (IRL1/2 all) or only corrupted (IRL1/2 outlier) DWIs.

$w(\hat{r}_i) = \frac{1}{(\hat{r}_i^2+1)^2}$ that have been found suitable as a robust estimator for dMRI [1, 4]. When assessing the residual magnitudes, it needs to be considered that the elements of $\mathbf{s}$ have been normalized by the signal magnitude at b = 0, which itself is a random variable estimated as part of the iterative fit, i.e. the estimate $\hat{s}(0)$. Approximating the raw signals to be Gaussian distributed with standard deviation σ, this can be corrected by normalizing the residuals according to [10]

$$\hat{r}_i = (\hat{s}(0)s_i - \hat{s}_i)/(\sigma_n\sqrt{s_i^2+1}) \quad (4)$$

where $\hat{s}$ are the SHORE estimates of the normalized signals and σ_n is the standard deviation normalized, as the measurements, by $S(0)$. In each iteration, the weights are updated from the previous residuals and a new estimate of the SHORE coefficients is determined. If convergence or the maximum number of iterations has been reached, signals are accepted if $|\hat{r}_i| <= t$. The threshold t is a critical parameter that balances sensitivity and specificity of detecting faulty data points. Signals with $|\hat{r}_i| > t$ are detected as outliers and discarded from the data set. Next, L1 SHORE is applied to the retained DWIs and rejected measurements are reconstructed.

2.3. Simulations and experiments

Synthetic data is generated using the Camino Monte-Carlo simulator [11] to validate the proposed method. For 600 instances of a 55° crossing microstructure of well-defined, but random orientation, we simulate diffusion signals for two b = 0 scans and for two shells in q-Space with 30 and 64 uniformly distributed diffusion-weighting directions with

b-values 700 and 2000 s/mm^2, respectively. We reduce the signal intensities by 70% to simulate signal dropouts due to subject motion in a well-defined amount of data. Rician noise is added with SNR of 20 defined on the non-diffusion weighted image, i.e. $\text{SNR}_{\text{DWI}} < 20$. We calculate sensitivity and specificity of the outlier detection and the normalized mean square error (NMSE) between the signal reconstructed with IRL1 SHORE and the ground truth simulation data.

Furthermore, we investigate the impact of IRL1 SHORE on *in vivo* clinical dMRI scans that are affected by strong motion artifacts because they were acquired from children suffering from metachromatic leukodystrophy, a rare neurodegenerative disease. Parents gave informed written consent for the scientific use of the data. The images were collected on a 3.0T SIEMENS MAGNETOM Skyra scanner using a twice-refocused echo planar imaging sequence. The imaging protocol has the same parameters as used for simulations with a spatial resolution of 2x2x2mm^3, TR/TE = 9100/89 and FOV = 96x96mm^2 for 50 contiguous slices. To validate the performance of IRL1 SHORE, we extract common diffusion features such as fractional anisotropy (FA), kurtosis anisotropy (KA) and mean and radial kurtosis (MK, RK) using ExploreDTI [12]. This toolbox also enables the comparison of our method with the REKINDLE approach for outlier removal [4]. We apply REKINDLE with the default settings for outlier removal and a constraint that promotes positive diagonal elements of the kurtosis tensor. In addition, a measure for the fiber density is obtained from the NODDI model [13].

3. RESULTS AND DISCUSSION

3.1. Simulations

We investigate the performance of the proposed method using simulated data corrupted by artificial signal dropouts. In IRL1 SHORE, a critical parameter is the threshold, t, that separates outliers from good data. REKINDLE applies the corresponding threshold parameter k. We compute the sensitivity and specificity of both methods based on the applied threshold and the number of outliers in the data (Fig. 1, top row). For the proposed method, a threshold of $t = 2.0$ is found to provide a good balance of these two properties independently of the amount of outliers in the data. In contrast, the optimal threshold value for REKINDLE varies with the outlier percentage. IRL1 SHORE, further, provides superior outlier detection for increased percentage of outliers. Applying $t = 2.0$ and varying the amount of artificial outliers, we determine the NMSE between noise-free simulations and noisy simulations with and without outlier correction. REKINDLE is not considered because it only detects faulty signals but does not recover discarded DWIs. We also compare SHORE using L2-norm and L1-norm regularization as well as two different strategies for correcting the DWIs: correcting (1) only voxels detected as outliers or (2) all measurements. The results shown in figure 1 (bottom row) indicate that the SHORE basis already regularizes the dMRI signal, which is known to be SNR sensitive, especially at high b-values. The detection of outliers by iteratively reweighting the model residuals and the subsequent recovery of corrupted data further reduce the NMSE. The L1-norm regularizer leads to more accurate SHORE signal estimation and therefore lower NMSE than L2 SHORE, a finding confirming recent literature [6]. Modeling all DWIs rather than only the voxels detected as outliers, further improves the signal estimation and reduces the NMSE.

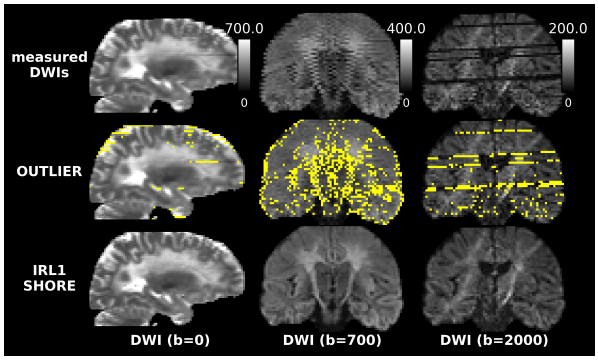

Fig. 2. DWIs with outliers (top) that are detected (middle) and corrected (bottom) by IRL1 SHORE (b = 0, 700, 2000s/mm^2)

3.2. *In vivo* clinical data

In human *in vivo* images tainted by motion artifacts, we show the advantages of IRL1 SHORE. Figure 2 highlights that the proposed method succeeds in locating faulty signals and substantially corrects the DWIs. In contrast to state-of-the-art methods for outlier removal that discard corrupted images, IRL1 SHORE corrects and recovers all DWIs before diffusion parameter estimation. Due to this, the proposed method is potentially less susceptible to errors that might occur if diffusion measures are calculated from a reduced number of DWIs [7, 8]. As for simulations, we compare the two different strategies for correcting DWIs. Visually, no significant difference is noticeable. However, future work will investigate these strategies more thoroughly and quantitatively, also with respect to their influence on diffusion parameters. Figure 3 shows that IRL1 SHORE reduces the influence of artifacts in the DWIs on diffusion parameters extracted by means of different diffusion models. Compared to the DWIs (Fig. 2), the improvement is less pronounced. Nevertheless, the white matter structure is much better defined using IRL1 SHORE, especially in the color-encoded FA map. For DT and kurtosis measures, we also compare IRL1 SHORE to the REKINDLE method for outlier removal. On our challenging clinical data, REKINDLE appears to reduce, rather than increase the quality of kurtosis fits. Given the relatively low number of acquired DWIs, it appears that simply discarding outliers leaves a set of measurements that is insufficient to reli-

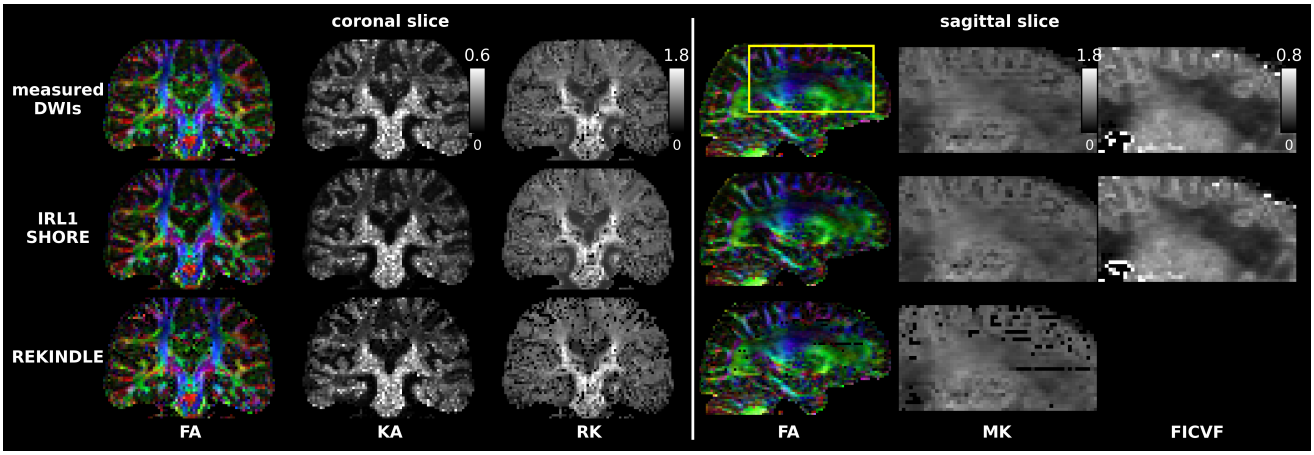

Fig. 3. Color-encoded FA, KA, RK, MK and FICVF maps determined for the measured DWIs (top) and for the proposed IRL1 SHORE (middle) and the competing REKINDLE method (bottom).

ably fit the kurtosis model using the iteratively weighted LLS (IWLLS) approach used by REKINDLE. In contrast, our proposed method uses a sparsifying basis and an L1-regularized fit. This makes it particularly suited to restore and denoise the full set of DWIs from the sparse set of inliers. Standard methods can then be used for the final model fit. Finally, figure 3 depicts that IRL1 SHORE corrects for artifacts in the parameter map of the intra-cellular volume fraction, FICVF, a measure for the fiber density obtained from the NODDI model. Our results demonstrate that, in contrast to state-of-the-art methods for outlier removal, IRL1 SHORE improves diffusion features independently of the required diffusion model.

4. CONCLUSION

In this work, we propose a new method for model-independent outlier removal and robust sparse signal reconstruction that corrects dMRI data for motion artifacts, reduces the impact of defective DWIs on diffusion measures and thus improves the quality of parameter maps. Future work will apply this method to more imaging data and other diffusion models.

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