Quantification of Structural Brain Connectivity via a Conductance Model

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Abstract

Connectomics has proved promising in quantifying and understanding the effects of development, aging and an array of diseases on the brain. In this work, we propose a new structural connectivity measure that allows us to incorporate direct brain connections as well as indirect ones that would not be otherwise accounted for by standard techniques and that may be key for the better understanding of function from structure. From our experiments on the Human Connectome Project dataset, we find that our measure of structural connectivity better correlates with functional connectivity than streamline tractography does, meaning that it provides new structural information related to function. Through additional experiments on the ADNI-2 dataset, we demonstrate the ability of this new measure to better discriminate different stages of Alzheimer's disease. Our findings suggest that this measure is useful in the study of the normal brain function and structure, and for quantifying the effects of disease on brain structure.

Keywords: brain connectivity, diffusion MRI, resting-state functional MRI, Alzheimer's disease

1. Introduction

Neurological diseases affect a large and increasing portion of the population. Recent studies on brain structural and functional connectivity have focused on various neurological diseases, to investigate their impact on the brain connections. Different neurological diseases have shown to alter brain connectivity: Alzheimer's disease (AD) (Rose et al., 2000; Buckner

[†]Data used in preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this report. A complete listing of ADNI investigators can be found at: http://adni.loni.usc.edu/wp-content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf

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et al., 2005, 2009; Prasad et al., 2015; Yu et al., 2017), late-life major depressive disorder (Smagula and Aizenstein, 2016), epilepsy (Taylor et al., 2015), Parkinsons's disease (Canu et al., 2015; Shah et al., 2017), schizophrenia (Arbabshirani et al., 2013; Cabral et al., 2013) and other psychosis (van Dellen et al., 2015; Mighdoll et al., 2015). Brain connectivity has also proven to be useful in the study of the effects of aging on the brain (Damoiseaux, 2017; Wu et al., 2013; Salat, 2011; Fjell et al., 2016).

Brain structural and functional connectivities, as measured by diffusion-weighted MRI (dMRI) and resting-state functional MRI (rs-fMRI) respectively, reveal distinct features (Park and Friston, 2013). While structural connectivity reflects the white matter fiber bundles and the axons that compose them, functional connectivity measures the temporal correlation of blood oxygenation changes. Functional connectivity is based on the premise that brain regions that are activated synchronously, and therefore undergo similar oxygenation and deoxygenation variations, are related. Consequently, functional connectivity may depend on the subject state (e.g., time of day, alertness, caffeine levels). Structural connectivity, on the other hand, is independent of the subject state, and can even be acquired *ex vivo*. Despite the fundamental differences in the processes that we observe via these two distinct measurements, structural and functional connectivity have been shown to be correlated (Damoiseaux and Greicius, 2009). Strong functional connections are, however, commonly observed between regions with no direct structural connection (Koch et al., 2002; Honey et al., 2009). Part of this variance has been shown to be due to the impact of indirect structural connections (Honey et al., 2009; Van Den Heuvel et al., 2009; Deligianni et al., 2011), i.e. between regions that are physically connected through multiple direct fiber bundles. Such indirect structural connections are usually considered only during the network analysis (Sporns, 2013), but not at the tractography step.

Differences in brain connectivity patterns between healthy and diseased populations are an indicator of change in the brain "wiring" and function due to the disease. Differences in structural connectivity between the two groups indicate changes in axon myelination, which increases conduction velocity by insulating the physical connections. A deficit in myelination causes poor signaling and eventually cell death. Therefore, knowing which structural connections of the brain are affected is key for understanding the disease, and in the long term, finding a cure. In particular, AD has been found to impact connectivity (Rose et al., 2000; Buckner et al., 2005, 2009; Prasad et al., 2015; Yu et al., 2017). The progressive neurodegeneration suffered in AD, possibly caused by the spread and accumulation of misfolded proteins along structural connections in the brain (Iturria-Medina et al., 2014), affects the functional networks detected with rs-fMRI (Buckner et al., 2005, 2009; Yu et al., 2017) and the brain connections emulated with dMRI (Rose et al., 2000; Prasad et al., 2015). Accurately modeling structural connectivity could therefore reveal the effects of AD progression in white matter degeneration.

The purpose of the present work is to derive a new structural connectivity measure that considers all possible pathways, direct and indirect, with the aim of accessing more of the information that is often only available through functional connectivity. To that end, we propose a connectivity computation method that models the white-matter pathways imaged via dMRI using the well-studied mathematics of electrical circuits (Chung et al.,

2012; Aganj et al., 2014; Chung et al., 2017; Frau-Pascual et al., 2018). Our method accounts for all possible white-matter pathways and is solved globally. It also does not require any parameter tuning and does not suffer from local minima, thereby producing consistent results with respect to the input data.

We evaluate the performance of the proposed conductance measure to test two different hypotheses, using a different dataset for each. First, we check the relationship of structural and functional connectivity, to test if our structural connectivity measure, which includes indirect connections, is more related to functional connectivity than standard measures are. Our results on 100 subjects of the WashU-UMN Human Connectome Project (HCP) (Van Essen et al., 2013) dataset support this hypothesis: our new connectivity measure provides a higher correlation to functional connectivity compared to standard methods. Second, we test if the inclusion of indirect connections in our measure and the subsequent higher similarity to functional connectivity has an impact in the classification power when comparing healthy and diseased populations. Through experiments on the second phase of Alzheimer's Disease Neuroimaging Initiative (ADNI-2) (Jack et al., 2008; Beckett et al., 2015) dataset, our connectivity measure proves useful in finding differences between the different stages of AD. This could lead to the discovery of new imaging biomarkers that help us better understand clinical data, predict the onset of disease from connectivity patterns, and deepen our insight into the human brain and how it is affected in development or by disease.

We present our conductance method for inferring a new structural brain connectivity measure from dMRI in Section 2 and put it into perspective with respect to standard tractography methods. We describe our analysis pipeline for the two datasets in Section 3 and present our results in Section 4. A discussion and conclusions follow in Sections 5 and 6. A preliminary abstract of this work was presented in (Frau-Pascual et al., 2018).

2. Methods

Brain connectivity has been previously modeled with the help of the established mathematical framework for macroscopic electrical circuits (Chung et al., 2012; Aganj et al., 2014; Chung et al., 2017). In this work, we make use of a combination of *differential* Maxwell's equations and Kirchhoff's circuit laws, resulting in an equation similar to the heat equation proposed in (ODonnell et al., 2002). As illustrated in Fig. 1, we assign to each image voxel a local anisotropic conductivity value D, which is the diffusion tensor computed from dMRI (Basser et al., 1994; Tuch et al., 2001). (See Appendix B for a formulation to use higher-order diffusion models.) By solving the partial differential equation (PDE) (Haus and Melcher, 1989)

$$-\nabla \cdot (D \nabla \phi_{i,j}) = \gamma_{i,j} \tag{1}$$

for a certain current configuration $\gamma_{i,j}$ between a pair of source (i) and sink (j) voxels (see below), we find the potential map $\phi_{i,j}$ for that specific configuration. Note that, in Eq. (1), ∇ and $\nabla\cdot$ are the gradient and the divergence operators, respectively. This differential equation describes how a current would diffuse from a source point to a sink point following the orientational information provided by the diffusion tensors. It is nonetheless important

to note that these potentials cannot be directly interpreted as connectivity. Therefore, in contrast to (ODonnell et al., 2002), we further compute the electric conductance between each pair of voxels from potential maps, to which all diffusion paths between the pair contribute. The same measure can also be computed between a pair of regions of interest (ROIs) instead of voxels, by distributing the currents γ among the ROI voxels.

We solve the PDE for a 1-ampere current between a pair of voxels i and j: $\gamma_{i,j} = \delta_i - \delta_j$, where $\delta_k(x) := \delta(x - x_k)$, with x_k the position of voxel k and $\delta(\cdot)$ the Dirac delta. To compute ROI-wise conductance, we distribute the currents among the sets of voxels I and J (the two ROIs) as: $\gamma_{I,J} = \frac{1}{|I|}\sum_{i\in I}\delta_i - \frac{1}{|J|}\sum_{j\in J}\delta_j$.

2.1. Computation of Potentials

For each source/sink current configuration $\gamma_{i,j}$, we solve the PDE[1] in Eq. (1) to find the potentials (see Fig. 1). We first discretize the linear diffusion term $-\nabla\cdot(D\nabla\phi_{i,j})$ and $\gamma_{i,j}$ (see Appendix A for more details on the discretization) and write it in the matrix form $M\phi_{i,j} = \gamma_{i,j}$, which we then invert to solve $\phi_{i,j} = M^{-1}\,\gamma_{i,j}$. We use the Neumann boundary condition: $\nabla\phi_{i,j}\cdot\mathbf{e} = 0$ for all points on the boundary, where $\mathbf{e}$ denotes the (typically exterior) normal to the boundary.

Given N voxels (or ROIs), we need a potential map for each pair of voxels, leading to N^2 potential maps, hence an intractable problem. However, by exploiting the superposition principle that derives from the linearity of the operator, we reduce the number of necessary potential maps to only N. We choose a reference sink voxel, s, and compute N potential maps, $\phi_{i,s}, i = 1, ..., N$, with i the source and s the fixed sink. Next, note that for a pair (i, j), we can compute the potentials $\phi_{i,j}$ by linearly combining the potentials of i and j to the reference sink voxel $(\phi_{i,s}, \phi_{j,s})$, as:

$$-\nabla\cdot(D\nabla(\phi_{i,s} - \phi_{j,s})) = -\nabla\cdot(D\nabla\phi_{i,s}) + \nabla\cdot(D\nabla\phi_{j,s}) \tag{2}$$

$$= (\delta_i - \delta_s) - (\delta_j - \delta_s) = \delta_i - \delta_j = -\nabla\cdot(D\nabla\phi_{i,j}) \tag{3}$$

Given that we consider the same boundary conditions for all the PDEs, we can now compute the potential map for any pair simply as $\phi_{i,j} = \phi_{i,s} - \phi_{j,s}$. Note that in the computation of $\phi_{i,j}$ for all the pairs (i, j), the inverse matrix M^{-1} needs to be computed and saved in memory only once.

2.2. Conductance as a Measure of Connectivity

The conductance between two points can be computed with Ohm's law as the ratio of the current to the potential difference. In our case, we set a 1-ampere current between two voxels (or ROIs) i and j, and the potential difference is $\phi_{i,j}(x_i) - \phi_{i,j}(x_j)$. The conductance is therefore computed, voxel-wise, as

$$C_{i,j} = \frac{1}{\phi_{i,j}(x_i) - \phi_{i,j}(x_j)}. \tag{4}$$

[1] We used the Finite Volume MATLAB toolbox (Eftekhari and Schller, 2015), and extended it so it accepts tensor-valued D.

Finally, per the aforementioned superposition principle, the conductance between any pair of voxels (i, j) is computed as

$$C_{i,j} = \frac{1}{(\phi_{i,s}(x_i) - \phi_{j,s}(x_i)) - (\phi_{i,s}(x_j) - \phi_{j,s}.(x_j))} \tag{5}$$

For ROI-wise connectivity, given that the potential map between two ROIs is $\phi_{I,J} = \phi_{I,s} - \phi_{J,s}$, where $\phi_{I,s} = M^{-1}\left(\frac{1}{|I|}\sum_{i\in I}\delta_i - \delta_s\right)$, we have:

$$C_{I,J} = \frac{1}{\frac{1}{|I|}\sum_{i\in I}\phi_{I,J}(x_i) - \frac{1}{|J|}\sum_{j\in J}\phi_{I,J}(x_j)} \tag{6}$$

$$= \underbrace{\frac{1}{\frac{1}{|I|}\sum_{i\in I}(\phi_{I,s}(x_i) - \phi_{J,s}(x_i)) - \frac{1}{|J|}\sum_{j\in J}(\phi_{I,s}(x_j) - \phi_{J,s}(x_j))}}_{\text{using superposition principle}}. \tag{7}$$

High conductance (i.e. low resistance) between two points indicates a high degree of connectivity. As shown in Fig. 1, by setting the conductivity (D) to zero outside the white-matter mask, we can compute voxel-wise conductance maps from a single voxel (in red) to the rest of the brain, as well as ROI-wise conductance maps from a single ROI (in red, indicated with arrow) to all the other ROIs[2]. Note that the ROIs are all at least weakly connected, given that indirect connections are all considered. Nevertheless, these maps can be thresholded to keep only connections stronger than a desired amount.

2.3. Comparison to standard connectivity

In standard connectomic approaches, tractography is often computed after the dMRI reconstruction to extract streamlines that represent connections between different voxels of the image (see Fig. 2). Connectivity matrices are then generated from the streamlines between different ROIs that are previously determined via segmentation of the brain. Various connectivity measures can be used to quantify these connections, leading to different connectivity matrices, e.g.: plain count of the streamlines, number of the streamlines normalized by the median length, number of tracts *crossing* the ROI or only those *ending* in the ROI, etc. The optimal choice of the type of connectivity matrix usually depends on the tractography algorithm used (choice of seeds, deterministic/probabilistic, whether sharp turns are allowed, etc.). In our approach, however, only the conductivity input will vary. This reduces the number of decisions to make (parameters to tune) in the computation of the connectivity matrix.

[2]We are currently making our codes user-friendly, and will make them publicly available on the NITRC and MATLAB Central websites before the publication of this article.

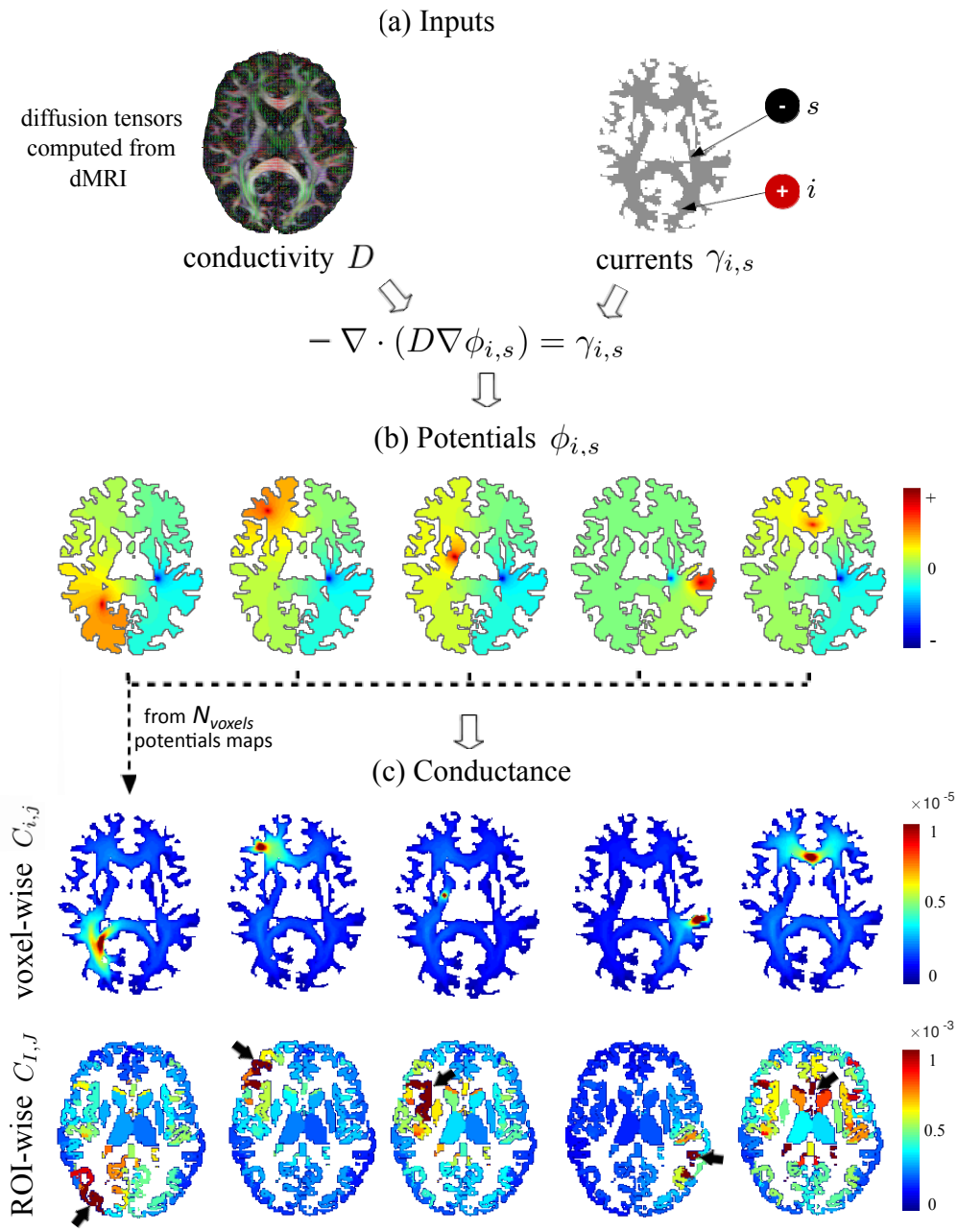


Figure 1: Conductance-based structural connectivity method. (a) We model brain connectivity globally using a combination of differential Maxwell's equations and Kirchhoff's circuit laws, with diffusion tensors computed from dMRI. (b) We first compute the potentials $\phi_{i,s}$, as depicted for five sources i and a fixed sink s. (c) Then, potential maps are superposed to generate voxel-wise conductance maps $C_{i,j}$ as shown for five voxels i (the reddest voxel), or ROI-wise conductance maps $C_{I,J}$ as shown for five ROIs I (indicated by arrows).

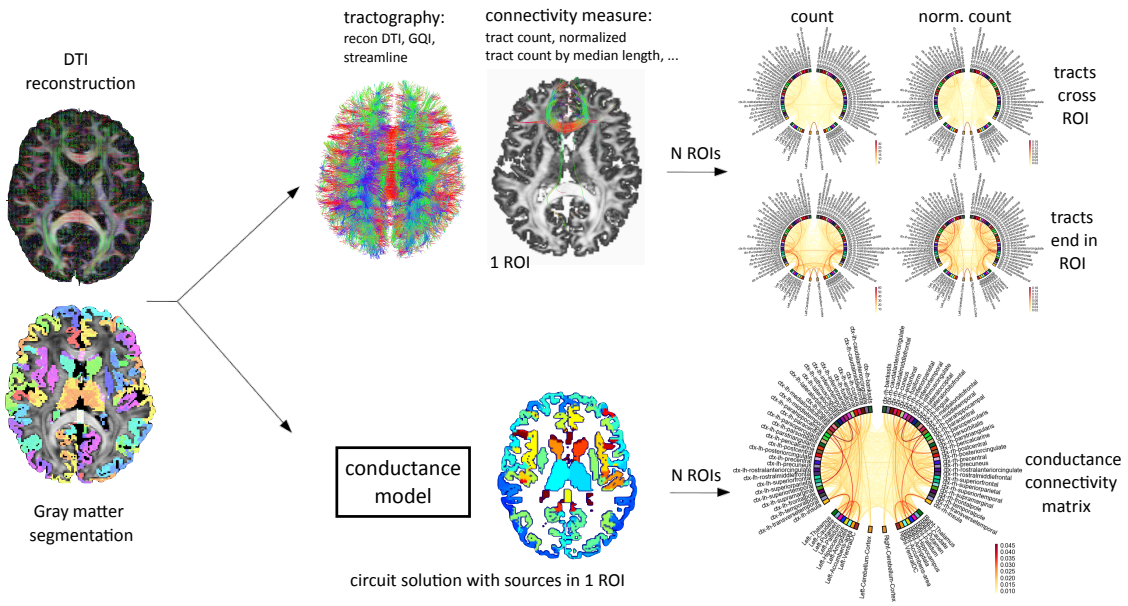


Figure 2: Comparison of the structural connectivity computation by the proposed method vs. standard tractography. The diffusion tensors reconstructed by DSI Studio and the white and gray matter segmentation and parcellation computed by FreeSurfer are given to both connectivity methods. In our conductance connectivity approach, the connectivity matrix is computed by solving a PDE for each ROI. In the standard SL connectivity approach, tractography is performed on the tensors or the GQI distributions and connectivity matrices are computed according to certain criteria.

3. Data analysis

We used two publicly available datasets in our analysis, from the WashU-UMN Human Connectome Project (HCP) (Van Essen et al., 2013) and the second phase of Alzheimer's Disease Neuroimaging Initiative (ADNI-2) (Jack et al., 2008; Beckett et al., 2015). These two datasets allowed us to evaluate the proposed method from different aspects: HCP data was used to measure the relationship between structural and functional connectivities, and ADNI-2 enabled the assessment of the utility of our measure in discriminating healthy and diseased populations. We preprocessed both datasets similarly.

MR processings: We performed tissue segmentation and parcellation of the cortex into ROIs using FreeSurfer[3] (Fischl, 2012). The parcellation used in this work is the Desikan-Killiany atlas (Desikan et al., 2006).

Diffusion MRI processings: The diffusion preprocessing pipeline used for ADNI-2 involved the FSL software[4] (Jenkinson et al., 2012) and included BET brain extraction (Smith, 2002) and EDDY (Andersson and Sotiropoulos, 2016) for eddy current and subject motion correction. For HCP, there were more steps involved (Glasser et al.,

[3]FreeSurfer software https://surfer.nmr.mgh.harvard.edu/
[4]FSL software https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/

2013), namely: B0 intensity normalization, EPI distortion correction with TOPUP (Andersson et al., 2003), eddy current and subject motion correction with EDDY, and gradient non-linearity correction. From the preprocessed dMRI images, we reconstructed the diffusion tensors using the Diffusion Tensor Imaging (DTI) (Basser et al., 1994) reconstruction of DSI Studio[5], which we then used as input to our conductance approach. To compare with standard approaches (see Fig. 2), we also ran streamline (SL) tractography (Yeh et al., 2013) using DTI, for direct comparison with our approach, and generalized q-sampling imaging (GQI) (Yeh et al., 2010), which, as opposed to DTI, can model multiple axon populations per voxel. We generated 10000 fiber tracts and used default values for the rest of the parameters. Then, we computed connectivity matrices according to various connectivity conventions: plain tract count, tract count normalized by the median length, both considering tracts *crossing* the ROI or *ending* in the ROI.

rs-fMRI processings: The rs-fMRI data, already projected to the surface and preprocessed as in (Glasser et al., 2013), was detrended, bandpass-filtered at 0.01-0.08Hz, and smoothed with a kernel with a full width at half maximum of 6mm. We stacked four sessions of rs-fMRI data, and computed the correlation matrix for the ROIs.

Note that we used rs-fMRI only in our HCP experiments, for which the data was already preprocessed as described in (Glasser et al., 2013).

4. Results

We evaluate the performance of the proposed conductance measure through experiments that answer two different questions:

(a) Relationship between structural and functional connectivity (Section 4.1): Is our structural connectivity measure, which considers both direct and indirect connections, more correlated to functional connectivity than standard measures are?

(b) Discrimination of healthy and diseased populations (Section 4.2): Does our measure provide additional information that better distinguish different stages of AD?

In the following subsections, we attempt to answer these questions using the HCP and ADNI-2 datasets, respectively.

4.1. HCP dataset

We evaluate our method on 100 subjects from the publicly available WashU-UMN HCP dataset (Van Essen et al., 2013), which contains rs-fMRI and dMRI data, while comparing our approach with standard SL tractography in regards to the relation to functional connectivity.

[5]DSI Studio software http://dsi-studio.labsolver.org

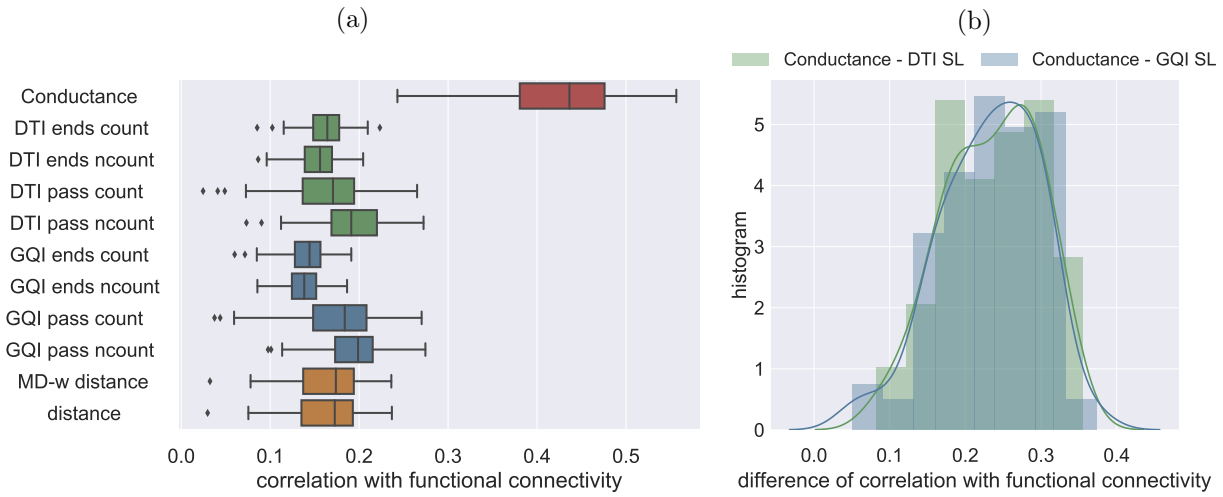


Figure 3: Correlation of structural and functional connectivities considering different approaches and metrics. (a) Distribution of correlations across 100 subjects. DSI Studio measures computed using DTI and GQI are compared: 'count' means plain count, 'ncount' means normalized fiber count by the median length, 'ends' means that only fibers *ending* in the ROI are considered, and 'cross' that fibers *crossing* an ROI are also considered. The 'distance' method is our approach ran with constant isotropic tensors, and the 'MD-w distance' is our approach ran with isotropic tensors and weighted by the mean diffusivity. For each box, the central line is the median, the left/right edges are the 25th and the 75th percentiles, the whiskers extend to the most extreme data points not considered outliers, and the outliers are plotted individually. (b) Histogram of the difference of structural/functional correlation, for conductance minus DTI SL and GQI SL tractographies. The DSI Studio measure giving the highest correlation with functional connectivity is used: tract count normalized by median length, considering tracts *crossing* an ROI.

4.1.1. Relationship with functional connectivity

To test the hypothesis that indirect connections can explain some of the variability between structural and functional connectivity, we compared the structural connectivity matrices – computed from our conductance and the standard approaches – to the functional connectivity matrix. We computed the Pearson correlation coefficient between the elements of the structural and functional connectivity matrices per subject, and then compared the distribution of these correlation values, as depicted in Fig. 3(a) and reported in Table 1. As can be seen, functional connectivity is much more strongly correlated with the proposed conductance-based structural connectivity than with all DSI Studio methods. Next, to make sure that our method makes use of the actual white-matter fiber orientations, and not just the physical distance between ROIs, we repeated the experiments using isotropic tensors; once with a constant tensor magnitude (denoted by distance), and again by weighting the tensor with mean diffusivity (denoted by MD-w distance). Figure 3(b) shows the histogram of the correlations of functional connectivity with two DSI Studio approaches subtracted (subject-wise) from correlations of functional connectivity with the proposed conductance-based connectivity. The positive range of values shows how much more the conductance connectivity is correlated with the functional connectivity than the DSI Studio metrics are. A two-tailed paired t-test between these two distributions revealed a statistic of $t = 37$ and a significance value of $p = 10^{-60}$ in the DTI case, and $t = 35$ and $p = 10^{-58}$ in the GQI case.

Table 1: Cross-subject mean correlation of functional and the proposed conductance-based structural connectivity with all structural connectivity metrics. Here 'ncount' indicates that the number of tracts were normalized by the median length.

	conductance	DTI				GQI			
		end in ROI		cross ROI		end in ROI		cross ROI	
		count	ncount	count	ncount	count	ncount	count	ncount
functional	**0.427**	0.163	0.152	0.165	0.192	0.141	0.138	0.175	**0.195**
conductance	1	0.304	0.346	0.353	**0.439**	0.251	0.336	0.356	**0.453**

Table 2: HCP inter-hemispheric connections ratios with respect to all connections, for different connectivities. Reported results were averaged across 98 subjects.

connectivity	ratio of cortical inter-hemispheric to all
MD-weighted distance connections	0.3278 ± 0.0131
functional connections	0.3356 ± 0.0310
conductance model connections	0.2849 ± 0.0071
GQI pass ncount connections	0.0613 ± 0.0119

4.1.2. Modeling of inter-hemispheric connections

One of the well-known issues in standard tractography methods is the mismodeling of inter-hemispheric connections, as such long tracts can be mistakenly cut short (Sinke et al., 2018). As can be seen in Table 2, DSI Studio methods model a low quantity of cortical inter-hemispheric (only 6% of all) connections. Our conductance method results in a higher ratio of inter-hemispheric connections, close to that of functional connectivity measures and the mean diffusivity weighted (MD-w) distance.

Next, we again considered the correlation of the different structural connectivity measures with functional connectivity, but this time separately for three connection groups cortical inter-hemispheric, cortical intra-hemispheric, and all subcortical connections, with the results illustrated in Fig. 4. Regarding the cortical inter-hemispheric connections, we observe a much lower correlation of the DSI Studio measures compared to the conductance-based measure. Note here that our measure of distance gives a low correlation too. This difference decreases for the intra-hemispheric connections, although conductance-based connectivity still correlates much more than the rest. For subcortical connections, we observe that the distance correlates much more with functional connectivity than DSI Studio measures do, and that the conductance-based connectivity has a very large standard deviation.

4.2. ADNI-2 dataset

We test the impact of our global conductance-based structural connectivity measure in the detection of white-matter differences in populations in different stages of AD and in the classification of dMRI images according to AD stage. A better modeling of structural connections could lead to a better understanding of the progression of this and other diseases, and to the discovery of new imaging biomarkers for the study of AD.

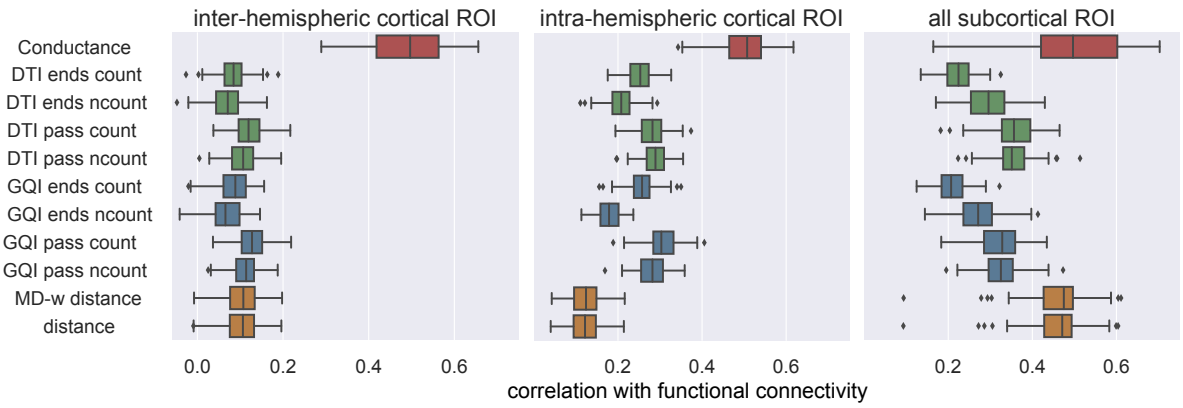


Figure 4: Structure/function correlation for three groups of connections: cortical inter-hemispheric, cortical intra-hemispheric and all subcortical connections. Comparison of conductance model, the DSI Studio measures and *distance* and *MD-w distance*.

We analyzed 213 subjects of the ADNI-2 dataset in different stages: 78 cognitively normal (CN), 89 with mild cognitive impairment (MCI), and 47 with AD dementia (Fig. 5). Data used in this section were obtained from the Alzheimers Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). The ADNI was launched in 2003 as a public - private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment (MCI) and early Alzheimers disease (AD).

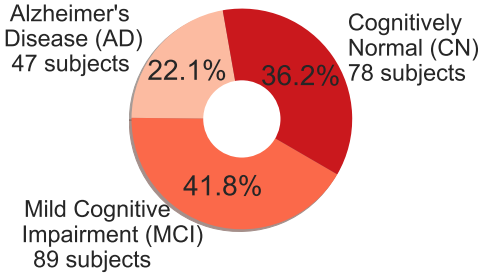


Figure 5: ADNI-2 data demographics.

4.2.1. Pair-wise classification of disease stage

We verified the suitability of our connectivity measure for disease stage classification, which would allow inferring the disease stage from connectivity measures derived from dMRI. We used Feature Selection with a Random Forest classifier to choose the most relevant features (with importance higher than the mean), and then performed the classification with a Random Forest classifier with balanced class weight (Pedregosa et al., 2011). We cross-validated with a shuffle split cross-validation strategy with 200 splits considering a 10% of the data for testing (Varoquaux et al., 2017).

We classified each pair of stages and then all stages together, and report the results in Fig. 6. We compare our conductance measure to different connectivity measures computed with DSI Studio, using DTI and GQI reconstruction methods. Note that, in general, classification performance is affected by class size, even though we used balanced weights in our classification. In all cases, our conductance measure has a higher prediction accuracy. Our conductance method provides a higher prediction accuracy than DSI Studio does, especially in the case of CN vs AD. When classifying all stages simultaneously, one must keep in mind

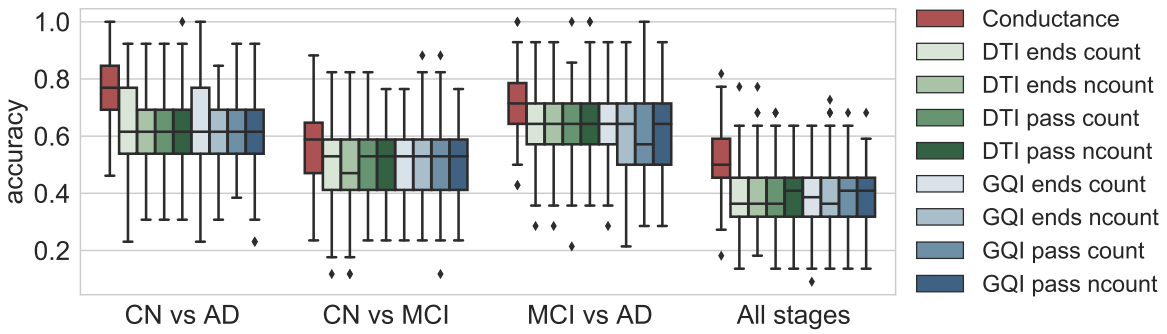


Figure 6: Prediction accuracies of different stages of AD, when using a Random Forest classifier, with balanced weights and previous Feature Selection. Cross-validation was used: Shuffle Split with 200 splits considering a 10% of the data for testing.

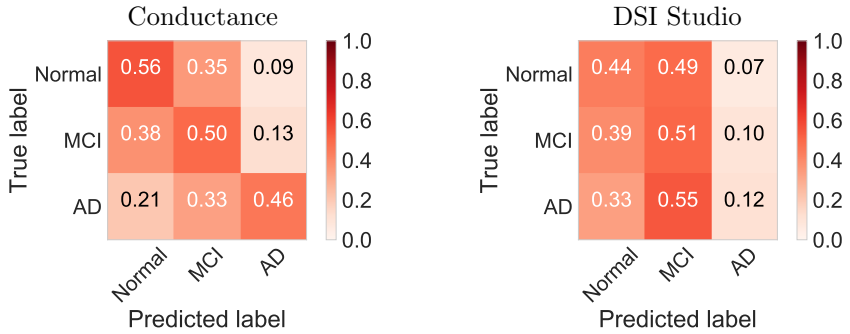


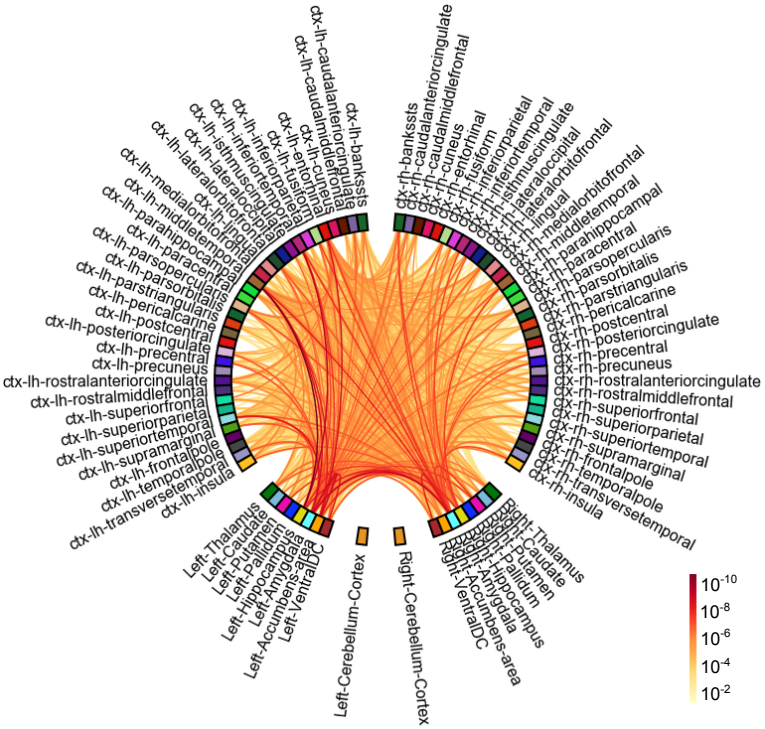
Figure 7: Confusion matrices and prediction accuracy in the classification of disease stages using standardized data, Feature Selection, and Random Forest classifier, on the conductance method connectivity matrix and the DSI Studio with GQI and the metric fiber count normalized by the median tract length.

that we have 3 classes, so a prediction accuracy of 0.5 is still informative. For the case of all-stage classification, Fig. 7 shows the confusion matrices for our conductance measure and the DSI Studio measure (here only considering the measure from GQI with SL tractography, counting the number of tracts crossing a ROI normalizing by the median length). We observe that our conductance method correctly classifies 46% of the AD cases whereas DSI Studio only 12%. For the rest of the disease stages, the two methods had comparable performance.

4.2.2. CN vs AD connectivities

Next, we searched for pairs of regions where the structural connectivity significantly differed between the CN and AD groups. Figure 8 shows the p-values resulting from a 2-sample t-test between the AD and CN groups per ROI. Connections with significant differences ($p < 0.05$, after Bonferroni correction) between the AD and CN groups for the conductance measure (Fig. 8(a)) involve regions that are known to be affected by AD, namely hippocampus and amygdala (Barnes et al., 2006; Prestia et al., 2011). Regarding differences between the MCI and AD groups, only the connections of right pars opercularis with insula and amygdala were significant, and when considering the CN and MCI groups, no connection was significantly different.

(a) Conductance method



(b) DSI Studio

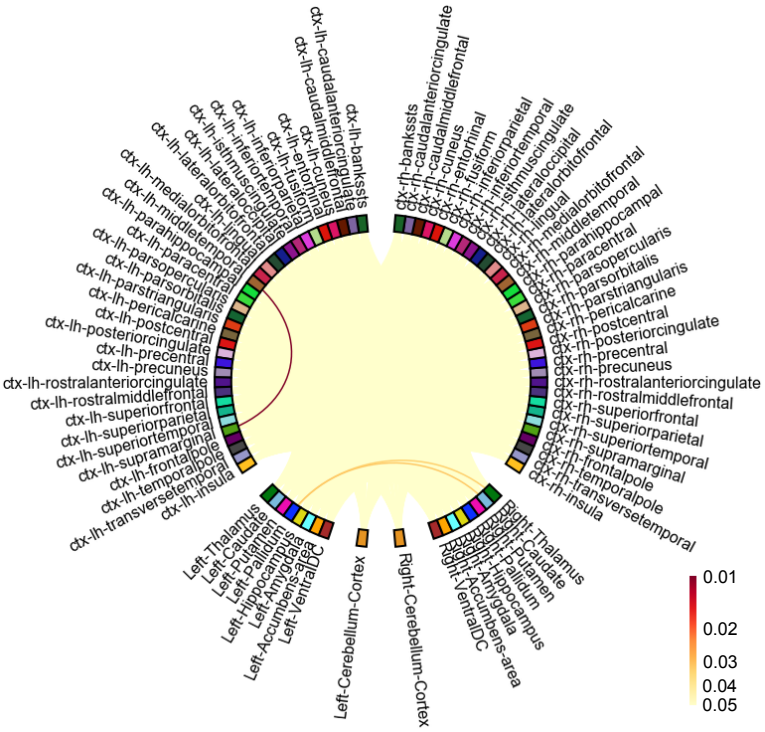


Figure 8: p-values showing significant differences in connectivity per ROI between the AD and CN groups, when using the conductance method and DSI Studio (DTI measure counting the number of fibers crossing a ROI).

We performed the same analysis with DSI Studio (Fig. 8(b)), and only some of the DTI measures revealed a few significantly different connections in the comparison of AD and CN groups. DTI counting the number of fibers *crossing* an ROI and the same normalized by the median length revealed differences in a few connections, as depicted in Fig. 8(b). When counting the number of fibers either *crossing* or *ending* in an ROI, only the left middle-temporal to supramarginal connection was significantly different. No differences were found in the other pairs of groups, and none with any of the GQI SL measures.

5. Discussion

We have proposed a new approach to measure brain structural connectivity, which – directly from the reconstructed dMRI data – accounts for indirect brain connections that would not otherwise be inherently considered by standard techniques. The proposed methodology is solved globally and considers all possible paths when computing the connectivity measure, and as such, it may be including some implausible paths as well. However, we expect orientational information from dMRI and the distance between distant regions to reduce the impact of such erroneous pathways. Note that we do not suggest that the conductance method is an appropriate model for the brain's biological wiring. We only use the mathematical framework provided by this model to account for indirect white-matter connections.

Another advantage of our method is that we have fewer decisions to make and parameters to tune in the connectivity analysis pipeline. Standard tractography-based connectivity analysis includes different steps that require a certain decision making when quantifying connectivity. Therefore, connectivity results will vary depending on the decisions made along this pipeline: modeling of one or several fiber bundle populations, the choice of the probabilistic or deterministic tractography, number of seeds, number of streamlines, the allowed turning angle, how we count the tracts, etc. This introduces a large amount of variability in the results, in a field where the scarcity of ground truth is one of the biggest challenges (Cheng et al., 2012; Maier-Hein et al., 2017). Our methodology, however, computes connectivity from the diffusion tensors without the need for any parameter tuning.

We have shown in Section 4.1 that one can compute structural connectivity measures that, using our method that accounts for indirect pathways, are significantly more correlated with functional connectivity than compared to more standard approaches. This supports the hypothesis on the role of indirect connections in the relationship between functional and structural connectivity, i.e. that part of the variance between these two connectivity measures lies within indirect connections, usually not accounted for in structural connectivity (Honey et al., 2009; Deligianni et al., 2011). Although the conductance measure was significantly more correlated with functional connectivity than standard measures were, the mean correlation was merely 0.43 (see Fig. 3). The reason for this is that structural and functional connectivities describe quite different processes: while the former describes physical connections, the latter only reflects how synchronously different regions in the brain function and considers such synchrony as a surrogate for connectivity. Nevertheless, increased similarity to functional connectivity implies that the proposed measure may be more informative about

brain function.

We observed through our experiments that our approach captures more of the inter-hemispheric connections (see Section 4.1.2). These connections, which are mostly – but not always (Roland et al., 2017) – through the corpus callosum (Zarei et al., 2006), have proved challenging for standard tractography methods. Inter-hemispheric connections have been shown to be affected by disease and shown correlations with clinical changes in some disorders (e.g. AD) (Wang et al., 2013, 2015; Saar-Ashkenazy et al., 2016; Xue et al., 2018). In fact, the proposed conductance measure has proven useful (see Section 4.2) in distinguishing normal and AD subjects and in better classification among AD stages. This could potentially lead to dMRI-derived biomarkers for early detection of AD.

Our approach could also be employed in a more general-purpose connectivity analysis, as an alternative to classic tractography algorithms, since it can be regarded as a global tractography algorithm. However, the conductance values may not fit the definition of either streamlines or probability measures. As we have shown in Section 2, the proposed method can also enable the computation of voxel-wise and thus parcellation-independent connectivity (Moyer et al., 2017), which allows us to compute conductance between any pairs of points of the white matter as well.

One of the limitations of the proposed conductance measure is that it derives from tensors, and therefore does not make use of the information provided by higher-order models. Even so, we make use of the whole tensor and not just the main direction of the axon population. Therefore, our tensors are actually used as low-order orientation distribution functions (ODFs). Nevertheless, our approach can be extended to exploit multiple axon population models to deal with crossing and kissing fibers, using a multi-tensor approach or general ODFs (Seunarine and Alexander, 2014; Aganj et al., 2015) instead. We propose a framework to implement this work with ODFs in Appendix B.

6. Conclusion

In this work, a new structural connectivity measure – directly derived from dMRI data – has been proposed that accounts for all possible pathways, when quantifying connectivity between a pair of regions. The method is global, contains no local minima and has no parameter that require setting by the user. Using this methodology, we computed structural connectivity measures that were significantly more correlated with functional connectivity than by using more standard approaches. In the study of diseased populations, our novel connectivity measure allows us to better classify different stages of Alzheimer's disease. Our results suggest that the proposed method provides new information that is not accounted for in standard streamline-based connectivity measures, and highlights the importance of its further development.

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BF has a financial interest in CorticoMetrics, a company whose medical pursuits focus on brain imaging and measurement technologies. BFs interests were reviewed and are managed by Massachusetts General Hospital and Partners HealthCare in accordance with their conflict of interest policies.

Appendix A. Discretization of the diffusion term.

For the discretization of $\nabla.(D\nabla\Phi)$, we find the values in the mid points of the mesh before computing the derivatives, so we can correctly derive in the corresponding points for potentials and conductivity values.

For tensor $D = \begin{pmatrix} D^{11} & D^{12} & D^{13} \\ D^{21} & D^{22} & D^{23} \\ D^{31} & D^{32} & D^{33} \end{pmatrix}$ in 3D, with $\tilde{D}_{n,m,p} = \frac{D_{n,m,p}+D_{n-1,m,p}}{2}$, $\hat{D}_{n,m,p} = \frac{D_{n,m,p}+D_{n,m-1,p}}{2}$ and $\bar{D}_{n,m,p} = \frac{D_{n,m,p}+D_{n,m,p-1}}{2}$, we have:

$$
\begin{aligned}
\nabla.(D\nabla\Phi) &= \frac{\partial}{\partial x}\left(D^{11}\frac{\partial}{\partial x}\Phi + D^{12}\frac{\partial}{\partial y}\Phi + D^{13}\frac{\partial}{\partial z}\Phi\right) \\
&+ \frac{\partial}{\partial y}\left(D^{21}\frac{\partial}{\partial x}\Phi + D^{22}\frac{\partial}{\partial y}\Phi + D^{23}\frac{\partial}{\partial z}\Phi\right) + \frac{\partial}{\partial z}\left(D^{31}\frac{\partial}{\partial x}\Phi + D^{32}\frac{\partial}{\partial y}\Phi + D^{33}\frac{\partial}{\partial z}\Phi\right) \\
&= \frac{-1}{\Delta x^2}\begin{pmatrix} -\tilde{D}^{11}_{n,m,p} \\ \tilde{D}^{11}_{n,m,p} + \tilde{D}^{11}_{n+1,m,p} \\ -\tilde{D}^{11}_{n+1,m,p} \end{pmatrix}^T \begin{pmatrix} \phi_{n-1,m,p} \\ \phi_{n,m,p} \\ \phi_{n+1,m,p} \end{pmatrix} - \frac{1}{\Delta y^2}\begin{pmatrix} -\hat{D}^{22}_{n,m,p} \\ \hat{D}^{22}_{n,m,p} + \hat{D}^{22}_{n,m+1,p} \\ -\hat{D}^{22}_{n,m+1,p} \end{pmatrix}^T \begin{pmatrix} \phi_{n,m-1,p} \\ \phi_{n,m,p} \\ \phi_{n,m+1,p} \end{pmatrix} \\
&- \frac{1}{\Delta z^2}\begin{pmatrix} -\bar{D}^{33}_{n,m,p} \\ \bar{D}^{33}_{n,m,p} + \bar{D}^{33}_{n,m,p+1} \\ -\bar{D}^{33}_{n,m,p+1} \end{pmatrix}^T \begin{pmatrix} \phi_{n,m,p-1} \\ \phi_{n,m,p} \\ \phi_{n,m,p+1} \end{pmatrix} + \frac{1}{4\Delta x\Delta y}\begin{pmatrix} -D^{12}_{n+1,m,p} - D^{21}_{n,m-1,p} \\ D^{12}_{n+1,m,p} + D^{21}_{n,m+1,p} \\ D^{12}_{n-1,m,p} + D^{21}_{n,m-1,p} \\ -D^{12}_{n-1,m,p} - D^{21}_{n,m+1,p} \end{pmatrix}^T \begin{pmatrix} \phi_{n+1,m-1,p} \\ \phi_{n+1,m+1,p} \\ \phi_{n-1,m-1,p} \\ \phi_{n-1,m+1,p} \end{pmatrix} \\
&+ \frac{1}{4\Delta x\Delta z}\begin{pmatrix} -D^{13}_{n+1,m,p} - D^{31}_{n,m,p-1} \\ D^{13}_{n+1,m,p} + D^{31}_{n,m,p+1} \\ D^{13}_{n-1,m,p} + D^{31}_{n,m,p-1} \\ -D^{13}_{n-1,m,p} - D^{31}_{n,m,p+1} \end{pmatrix}^T \begin{pmatrix} \phi_{n+1,m,p-1} \\ \phi_{n+1,m,p+1} \\ \phi_{n-1,m,p-1} \\ \phi_{n-1,m,p+1} \end{pmatrix} \\
&+ \frac{1}{4\Delta y\Delta z}\begin{pmatrix} -D^{23}_{n,m-1,p} - D^{32}_{n,m,p+1} \\ D^{23}_{n,m+1,p} + D^{32}_{n,m,p+1} \\ D^{23}_{n,m-1,p} + D^{32}_{n,m,p-1} \\ -D^{23}_{n,m+1,p} - D^{32}_{n,m,p-1} \end{pmatrix}^T \begin{pmatrix} \phi_{n,m-1,p+1} \\ \phi_{n,m+1,p+1} \\ \phi_{n,m-1,p-1} \\ \phi_{n,m+1,p-1} \end{pmatrix}
\end{aligned}
\tag{A.1}
$$

Appendix B. Extension for high-angular-resolution diffusion imaging (HARDI).

Assuming that $\vec{u}$ is the b-vector and $b = \tau q^2$ the b-value, with q and τ the q-vector and the diffusion time, the measured diffusion signal values according to the mono-exponential model are

$$S(\vec{q}) = S_0\ e^{-\tau q^2 A(\vec{u})}, \tag{B.1}$$

where $\vec{q} = q\hat{u}$ and A is the apparent diffusion coefficient. Note that

$$q^2 A(\vec{u}) = -\frac{1}{\tau} ln\left(\frac{S(\vec{q})}{S_0}\right).$$

In DTI, we model A as a quadratic function:

$$A(\vec{u}) \approx \vec{u}^T D\vec{u} \tag{B.2}$$

$$q^2 A(\vec{u}) \approx \vec{q}^T D\vec{q} \;\rightarrow\; S(\vec{q}) = S_0\; e^{-\tau \vec{q}^T D\vec{q}} \tag{B.3}$$

By deriving this equation with respect to $\vec{q}$, we get:

$$\nabla_{\vec{q}} \left(q^2 A(\vec{u})\right) = 2D\vec{q} \tag{B.4}$$

$$\frac{1}{2}\nabla \left(v^2 A(\vec{u})\right) = D\vec{v}, \text{ where } \vec{v} = v\hat{u} \text{ and } v = \|\vec{v}\|_2 \tag{B.5}$$

For HARDI, we can approximate the left-hand-side of Eq. (1) as follows:

$$-\nabla \cdot (D\nabla\Phi) = -\nabla. \left[\frac{1}{2}\nabla_v \left(v^2 A(\vec{u})\right)|_{\vec{v}=\nabla\Phi}\right] \tag{B.6}$$

$$= -\nabla. \left[\frac{1}{2}\nabla_v \left(\|\vec{v}\|_2^2 A\left(\frac{\vec{v}}{\|\vec{v}\|_2}\right)\right)|_{\vec{v}=\nabla\Phi}\right] \tag{B.7}$$

Equation (B.7) is no longer linear with respect to the potentials, and therefore cannot be solved as easily as in the case of DTI. Moreover, due to nonlinearity, the superposition property no longer holds either. Iterative optimization approaches may be used to approximate the solution to this equation.

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