DISCUSSION OF
"FIBER DIRECTION ESTIMATION IN DIFFUSION MRI"

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We would like to congratulate the authors for their excellent and stimulating work. The proposed statistical methods address a series of important issues in the analysis of diffusion magnetic resonance imaging (dMRI) data. Their work will surely be the subject of much application and elaboration in the future.

Our discussion focuses mainly on three aspects: (1) the multiple tensor direction model, (2) the kernel smoothing method of multiple directions and (3) the fiber tracking algorithm. For each aspect, we begin with a brief summary of the contributions of the paper, then raise some questions and point out some potential alternatives and extensions.

1. Multiple tensor direction model. It is challenging to estimate multiple tensor matrices within a voxel using dMRI data, in that most existing multi-tensor models suffer the nonidentifiability issue. The multiple tensor direction model proposed in this paper focuses on a direct estimation of multiple directions within a voxel, which avoids the complications of estimating multiple tensor matrices. The proposed model is shown to be identifiable, is easy to interpret, and is to facilitate detection of crossing fiber tracts.

We raise two questions regarding this model. First, how does this model deal with label switching? According to model (2) of the paper, we write

$$\bar{S}(\mathbf{u}; \boldsymbol{\gamma}) = S_0 \sum_{j=1}^{J} \tau_j \exp\{b\alpha_j(\mathbf{u}^\mathrm{T}\mathbf{m}_j)^2\},$$

where $\boldsymbol{\gamma} = (\boldsymbol{\gamma}_1^\mathrm{T}, \boldsymbol{\gamma}_2^\mathrm{T}, \boldsymbol{\gamma}_3^\mathrm{T}, \ldots, \boldsymbol{\gamma}_J^\mathrm{T})^\mathrm{T}$, $\boldsymbol{\gamma}_j = (\tau_j, \alpha_j, \mathbf{m}_j^\mathrm{T})^\mathrm{T}$, for $j = 1, \ldots, J$. Now consider $\tilde{\boldsymbol{\gamma}} = (\boldsymbol{\gamma}_2^\mathrm{T}, \boldsymbol{\gamma}_1^\mathrm{T}, \boldsymbol{\gamma}_3^\mathrm{T}, \ldots, \boldsymbol{\gamma}_J^\mathrm{T})^\mathrm{T}$ and that $\boldsymbol{\gamma}_1 \neq \boldsymbol{\gamma}_2$. Then it is clear that $\boldsymbol{\gamma} \neq \tilde{\boldsymbol{\gamma}}$, but $\bar{S}(\mathbf{u}; \boldsymbol{\gamma}) = \bar{S}(\mathbf{u}; \tilde{\boldsymbol{\gamma}})$. We are curious how to get around this label switching issue to maintain model identifiability.

Second, the authors have developed an approximation to the log-likelihood on tessellations and used a grid search to obtain the maximum likelihood estimates