Anatomical Tissue Probability Priors for Tractography

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Abstract. When visualizing streamlines produced by tractography algorithms, it is striking to observe the number of them that stop prematurely or that stop in anatomically impossible regions. We propose using the T1-weighted image tissue segmentation probability maps as a priori information for tractography to address this issue. A relaxation of the stopping criterion using tissue probabilities is first presented. It is then incorporated in a flexible sequential Monte Carlo modular add-on applicable to most streamline tractography algorithm. Results on high angular resolution diffusion imaging (HARDI) tractography show higher length on curved bundles or tight tracking paths, which agree better with known anatomy, for both deterministic and probabilistic algorithms.

1 Introduction

Tractography is the algorithmic procedure that estimates white matter (WM) fiber bundles following the local model estimated from diffusion-weighted (DW) magnetic resonance imaging (MRI). Streamline tractography outputs a sequence of tri-dimensional (3D) spatial points. Each sequence is called a streamline or tract, and represents an estimate of the link between two anatomically connected brain regions. A tractogram is the set of streamlines calculated by a tractography algorithm. Tractography algorithms are based on a set of parameters that determine which direction to follow and when to stop the tracking process.

From an initial position, the tractography algorithm follows diffusion orientations in the forward and backward directions, using a pre-determined step size ($\Delta t$), until a stopping criterion is reached. Typically, stopping criteria are: i) when the tracking takes a step outside the tracking mask, ii) when the radius of curvature between two consecutive steps is smaller than a minimum radius of curvature $R$, or iii) when the streamline length is greater than or smaller than pre-determined lengths ($\delta_{\text{min}}, \delta_{\text{max}}$). The algorithm iterates over a set of initial positions (a subset of the mask, or the whole mask) or randomly generates initial positions within the tracking mask until a fixed number of streamlines are computed [1]. Stopping parameters will determine when the streamline is included or excluded of the tractogram [1]. In general, tractography is done inside a mask defined by a WM segmentation of the T1-weighted image or fractional anisotropy (FA) thresholded mask.
But how does this tracking mask affect the tractography result? Surprisingly, few works have studied the effect of the tracking mask on tractography. Guevara et al. [2] show that a WM mask computed from a high resolution T1-weighted image produces richer and more accurate streamlines than a thresholded FA map. The discrete binary mask is an aggressive stopping criterion and can have a dramatic impact on tractography. When streamlines are visualized, a large amount of incomplete or prematurely stopping streamlines can be observed. Additionally, these streamlines stop in anatomically impossible regions [3]. For example, it is impossible that WM fibers end in the ventricles bordering large fiber bundles such as the corpus callosum (CC).

Recently, Smith et al. [4] proposed a method called Anatomically Constrained Tractography (ACT), which takes advantage of the tissue segmentation maps based on the structural T1-weighted image. They proposed relaxing the stopping criterion by using WM, Gray Matter (GM) and Cerebrospinal Fluid (CSF) probability maps. Thresholds over interpolated probability maps determine if a tract stops and if it is included or excluded from the tractogram. They also proposed a back-tracking approach to find a plausible tract when the tracking algorithm fails to find one.

Our work goes in the same direction as the work proposed in [4], using the T1-weighted image tissue probability segmentations as a priori information for tractography. Our paper provides a novel strategy using the WM, GM and CSF probability maps and changes the way tractography stopping events are triggered by taking advantage of the complete probability map. This strategy is incorporated in a general modular Sequential Monte Carlo Tractography (SMCT) framework that can be combined to most of the local streamline tractography algorithms (both deterministic and probabilistic). We show that this relaxation of the stopping criterion enhances the density of complex (e.g. high curvature or tight WM paths) streamline bundles, eliminates streamlines that are incomplete due to premature stop, increases the average length of tract bundles and can have a positive effect on brain connectivity. All this is done with a relatively low increase in computation time.

2 Streamline Tractography

This study focuses on using continuous probability maps to relax the discrete binary mask for tractography stopping criterion. Since these strategies are novel in the relaxation of the stopping criterion for tractography and do not represent new tractography algorithms as such, we compared and applied these relaxations to the state-of-the-art fibre orientation distribution function (fODF) deterministic and probabilistic algorithms. In-house implementations of these tractography algorithms is used, similar to those in MRtrix [1].

Stopping Criterion In this study, we put the emphasis on the stopping criterion and stress that using only a binary tracking mask leads to streamlines that stop in anatomically impossible regions. Namely, tracts connecting no cortical or sub-cortical GM regions.
To overcome this effect, exclusion and inclusion binary masks combined to a WM binary tracking mask can be used [1]. Tracts exiting the tracking mask and entering the CSF mask are excluded and those entering the GM masks are included. Since every voxel is either classified as WM, GM or CSF, all included tracts exiting the WM mask are those entering the GM mask. There is one exception: if the tracking process leads out of the DWI field of view (e.g. brainstem), the tracking is stopped and the tract is included since no more data is available.

Once the tractography is done, tracts with length within the interval $[\delta_{\text{min}} = 10\, \text{mm}, \, \delta_{\text{max}} = 300\, \text{mm}]$ are included in the tractogram and excluded otherwise. It is also common to see a constraint on the minimum radius $R$ of curvature [1], limiting the high angle variations of tracts and addressing the hypothesis of smoothness of WM fibers. Thus, this can lead to situations where no tracking direction is available in the aperture cone, which causes the tracking to stop. Since this always happens within the tracking mask, these tracts are excluded.

**Parameters** The deterministic and probabilistic tractography algorithms presented use a step size $\Delta t = 0.2\, \text{mm}$, which is $1/10$ of the voxel size in our DWI dataset in this work. Moreover, the minimum radius of curvature $R = 1\, \text{mm}$ for probabilistic tractography and $R = 0.26\, \text{mm}$ for deterministic tractography, as suggested in [1]. The WM binary mask is used as the seeding region.

3 Methods

In this study, we formulate the hypothesis that a discrete binary mask (WM, GM, CSF) is too strong of a stopping criterion. It should be relaxed using continuous probability maps. This section presents 2 strategies to exploit these probability maps as relaxed stopping criterion.

3.1 Continuous Maps Criterion

The T1-based FAST segmentation [5] assigns a probability of belonging to a class to each voxel. The probability at each voxel can represent an estimation of volume fraction. The resulting binary masks are the set of voxels having the highest probability for each class. Figure 1 shows the segmentation results using 3 classes (WM, GM, CSF): (b,d,f) are binary masks, (c,e,g) are probability maps. One can see that there are two major differences: i) Voxels near the boundary between distinct tissues are gray [0:black, 1:white], ii) The sub-cortical GM is mainly gray on both WM and GM maps. The discretization of these GM regions creates holes in the WM mask, which makes some WM paths tighter, making streamlines stop easily in these regions (see Figure 1 (b,d)). This problem is especially important when tracking corticospinal fibers or fibers involved in the motor system [6].

Instead of setting the probability to 1 or 0 for all classes, we propose exploiting the probabilities using a method called Continuous Maps Criterion (CMC). Let us assume the tracking process leads to the position $\text{pos}$. Trilinear interpolation can be done over the 3 probability maps in order to get the probability of each
tissue at position \( \text{pos} \): \( P_{\text{WM}}^{\text{WM}} \), \( P_{\text{pos}}^{\text{GM}} \) and \( P_{\text{pos}}^{\text{CSF}} \). The hypothesis is that the amount of tracts passing through a voxel should be proportional to \( P_{\text{WM}}^{\text{WM}} \). Similarly, the amount of included tracts should be proportional to \( P_{\text{GM}}^{\text{GM}} \), and the amount of excluded tracts proportional to \( P_{\text{CSF}}^{\text{CSF}} \). This hypothesis directly uses the tissue probability in each voxel. Thus, if the segmentation algorithm cannot surely determine the class of a voxel, the CMC method will not apply thresholds to set deterministic tracking behaviors. Rather, the probability will proportionally change the tracking behaviors. The probability of continuing the tracking process is given by the equation:

\[
P_{\text{pos}}^{\text{continu}} = \left( \frac{\alpha \cdot P_{\text{WM}}^{\text{WM}}_{\text{pos}}}{\alpha \cdot P_{\text{WM}}^{\text{WM}}_{\text{pos}} + P_{\text{GM}}^{\text{GM}}_{\text{pos}} + P_{\text{CSF}}^{\text{CSF}}_{\text{pos}}} \right)^{\frac{\Delta t}{T_{1}^{\text{res}}}},
\]

where \( \alpha \) is a weighting factor on the probability of stopping the tracking process. For example, using \( \alpha > 1 \) increases the probability of tracking in low WM partial volume fraction regions. This can help to counterbalance errors in the registration or segmentation processes, such as in [6]. In this study, we compared results for \( \alpha = 1 \) and \( \alpha = 4 \).

The probability maps are calculated from the T1-weighted image at resolution \( T_{1}^{\text{res}} = 1mm \) isotropic. Using a step size \( \Delta t < T_{1}^{\text{res}} \) will exponentially increase the probability of stopping the tractography and exponentially decrease the probability using \( \Delta t > T_{1}^{\text{res}} \). For example, let positions \( \text{pos}_a \) and \( \text{pos}_b \) be at a distance of 2mm from each other, and \( P_{\text{WM}}^{\text{WM}} \) uniformly equal to 0.8. If the tractography starts at \( \text{pos}_a \) and ends at \( \text{pos}_b \), the probability of stopping with \( \Delta t = 1mm \) is \( 1 - 0.8^2 = 0.36 \), using \( \Delta t = 0.5mm \) this probability becomes \( 1 - 0.8^4 \approx 0.59 \), and using \( \Delta t = 2mm \) the probability is \( 1 - 0.8 = 0.2 \). The hypothesis of the amount of tracts passing through a voxel is thus not respected with \( \Delta t \neq T_{1}^{\text{res}} \). The step size has a strong influence on the tract propagation using CMC. In order to respect the previous hypothesis, the probability of con-
Algorithm 1 Continuous Maps Criterion Algorithm

Require: \( \text{pos} \leftarrow \text{New Tracking Position} \)
Require: \( P_{\text{continu}} \leftarrow (\text{Eq.} \ 1) \)
Require: \( P_{\text{include}} \leftarrow (\text{Eq.} \ 2) \)

\[
x_1, x_2 \sim U(0, 1) \quad \text{(uniform distribution [0, 1])}
\]

if \( x_1 < P_{\text{continu}} \) then
    return continue tracking
else
    if \( x_2 < P_{\text{include}} \) then
        return stop tracking and include
    else
        return stop tracking and exclude
    end if
end if

continuing the tracking process (Eq. 1) is adjusted to give the same tracking effect with a smaller (or bigger) \( \Delta t \).

If the tracking process stops, the probability of including the tract in the tractogram is given by the equation:

\[
P_{\text{include}} = \frac{P_{\text{GM}}}{P_{\text{GM}} + P_{\text{CSF}}},
\]

which represents the possibility of an anatomical connection stopping at \( \text{pos} \).

Algorithm 1 outlines the CMC method, determining whether the tracking continues or stops. In case of stopping, the algorithm determines if the tract is included or excluded of the tractogram.

3.2 Sequential Monte Carlo Framework

The streamline tractography can be modeled as a state system evolving over time using noisy measurements (DWI, T1, etc.), where states are both the tracking position and the tracking status (for example in the WM or stopped in the GM), and are connected over time by a Markov chain. We propose to use a Sequential Monte Carlo (SMC) framework based on the previous state model to estimate the uncertainty in a tractography stopping event. The SMC or particle filter model has been widely used for robot localization [7] using sensor measurements to estimate the robot position. Recently, it has also been used for WM tractography [8, 9]. This section presents the SMC method followed by its implementation in the context of tractography and probability maps.

SMC Method SMC methods aim to estimate a sequence of target state variables \( X_{0:t} = \{X_k, k = 0, ..., t\} \) from a sequence of observation variables \( Y_{0:t} = \{Y_k, k = 0, ..., t\} \). The goal is to sequentially estimate the posterior distribution \( p(X_k|Y_{0:k}) \). \( X_{0:t} \) is a first order Markov process such that \( X_k|X_{k-1} \sim p(X_k|X_{k-1}) \) with a known initial distribution \( p(X_0) \) and \( Y_{0:k} \) are conditionally independent if \( X_{0:k} \) are known. The key idea of SMC is to represent the posterior
distribution \( p(X_{0:t}|Y_{0:t}) \) by a set of random samples with associated weights and compute estimates based on the samples and weights \([7, 10]\). \( \{x^{(i)}_{0:k}, w^{(i)}_k\}_{i=1}^N \) denotes the set of \( N \) discrete random samples that characterize the posterior distribution, where \( \{x^{(i)}_{0:k}, i = 1, ..., N\} \) is the set of random samples, \( \{w^{(i)}_k, i = 1, ..., N\} \) their associated weights with \( \sum_{i=1}^{N} w^{(i)}_k = 1 \). The weight of a sample \( x^{(i)}_k \) at time \( k \) corresponds to its weight at time \( k-1 \) times the likelihood of the observation \( y^{(i)}_k \) (see Eq. 5). Such a discrete model suffers of degeneracy since the variance of the weights increases over time, leading to a situation where all samples except one have a weight close to zero. To overcome this problem, the number of samples can be increased or a resampling method can be applied when a significant degeneracy is observed. The latter has been chosen in this study. The degeneracy problem can be observed when the number of effective samples \( N_{eff} \), as described in Eq. 3, falls below some threshold \( N_T \) \([10]\).

\[
N_{eff} = 1/ \sum_{i=1}^{N} (w^{(i)}_k)^2.
\] (3)

The resampling idea is to eliminate samples with small weights and concentrate on samples that have large weights. The resampling generates \( N \) new samples with equal weights from the current discrete estimation of \( p(X_{0:t}|Y_{0:t}) \). This method is also known as Sequential Importance Sampling particle filter \([7, 10]\).

**SMC Tractography** This section presents a Sequential Monte Carlo Tractography (SMCT) framework to estimate a likely tract using probability maps whenever the tractography reaches a stopping criterion. The key idea is to back track \( K_b \) steps and compute a better likely tract after \( K = K_b + K_f \) steps, where \( K_b \) and \( K_f \) are respectively the number of backward and forward steps. If there are less tracking steps done than \( K_b \), \( K_b \) is set to the number of tracking steps done so far. The goal is to estimate a likely tract initialized with \( K_b \) steps before the stopping criterion is reached, and then go \( K_f \) forward steps to ensure the local stopping event is solved. That is, the tract stops correctly in the GM or the tract continues its propagation in the WM. If the tract stops in the GM, the tracking is done. If the tract is in the WM, the tractography continues normally until another stopping criterion is reached.

In the context of tractography \( x_k = [pos_k, \ status_k] \), where \( pos_k \) is the tracking position at time \( k \) and \( status_k \in \{\text{active}, \text{inactive}\} \) represents the tracking process propagating in the WM (active) or stopped in the GM (inactive). If \( status_k = \text{active} \) then \( pos_{k-1} \) propagates to \( pos_k \) following a probabilistic method, otherwise the tracking reaches the GM and is stopped (\( pos_k = pos_{k-1} \)) in this case. The \( status_k \) becomes inactive following equation:

\[
P_{\text{inactive}}^{\text{pos}} = \left( \frac{P_{\text{GM}}^{\text{pos}}}{P_{\text{GM}}^{\text{pos}} + \alpha \cdot P_{\text{WM}}^{\text{pos}}} \right)^{\frac{\Delta t}{\tau_{\text{res}}}},
\] (4)

otherwise, it remains constant over time (\( status_k = status_{k-1} \)). The probability of CSF is the observation \( Y_k \) in our model, thus, the weight \( w_k \) of a tract at position \( p_k \) is computed following equation:
\[ w_k^{(i)} = w_{k-1}^{(i)} \cdot p(y_k^{(i)}|x_k^{(i)}) = w_{k-1}^{(i)} \cdot (1 - P_{pos_k}^{CSF}) \Delta t. \]  (5)

Equations 4 and 5 are related to $\Delta t$ to ensure the step size does not change the weighting and stopping event of the algorithm, as it is in section 3.1. The SMCT uses a fixed number $N$ of samples to estimate $p(X_k)$. The weight $w_k^{(i)}$ of each sample $x_k^{(i)}$ at time $k$ is normalized over all samples to ensure that $\sum_{i=1}^{N} w_k^{(i)} = 1$.

The SMCT will estimate the valid tract distribution around the stopping event and iteratively learn subsequent valid tract distribution from the previous one. The resulting tract is drawn from the final valid tract distribution. The key elements of the algorithm are:

1. Whenever a stopping criterion excluding a tract is reached, set $p(X_{k=0})$ to $N$ samples with position $pos_0^{(i)}$ set to the $K_b$ previous tracking position, its status $^{(i)}$ = active and $w_0^{(i)} = 1/N$. Thus, all samples have the same initial position and weight.
2. Propagate the $N$ samples from $p(X_{k=0})$, the initial tracts distribution, using a probabilistic method.
3. Update $w_k^{(i)} \forall x_k^{(i)}$ samples using Eq. 5 and normalize $w_k^{(i)}$ in order to have that $\sum_{i=1}^{N} w_k^{(i)} = 1$.
4. Resample the distribution if $N_{eff} < N/10$.
5. Propagate the status of each drawn sample from the previous iteration. The status becomes inactive following Eq. 4.
6. Update the position $pos_k^{(i)} \forall x_k^{(i)}$ samples using a probabilistic method if the status $^{(i)} = active$, otherwise $pos_k^{(i)} = pos_k^{(i)}$.
7. Repeat steps 3 to 6 $K$ times, $k = k + 1$.
8. Draw a single sample from $p(X_K)$. If status = active, the tracking continues using the principal tractography algorithm, otherwise the tracking is done and the tract is included in the tractogram.

This algorithm generates multiple probabilistic tracts, encouraging tracts to follow the WM or end in the GM, and discouraging tracts to propagate in CSF. The output of the SMCT is either an inactive tract ending in the GM or an active tract in the WM. Otherwise, if at any iteration $k$ the weights $w_k^{(i)} = 0 \forall x_k^{(i)}$ samples, the tract is excluded from the tractogram because no valid tract is found (e.g. $P_{pos_k}^{CSF} = 1, x_k^{(i)}$).

In our implementation, we used both the fODF deterministic and probabilistic tractography algorithms as principal algorithm and the probabilistic fODF algorithm within the SMCT, see section 2 for details on these algorithms. The principal tractography algorithm is done until the tracking reaches a stopping criterion excluding the tract, as determined by the CMC method of section 3.1 or if there is no valid tracking direction. Whenever it happens, the SMCT is used. When no valid tracking direction is found for a sample within SMCT, the sample $x_k^{(i)}$ is still in the WM, but cannot propagate further, thus his weight $w_k^{(i)} = 0$.

Other parameters are $N = 100$ samples, $K_b = 10$ and $K_f = 5$, which corresponds to the tracking distance of 2 voxels in T1-weighted space, respectively 1
voxel using a $\Delta t = 0.2\text{mm}$. Estimating likely tracts after a tracking distance of three $T_{1\text{res}}$ voxels is sufficient to find a plausible path for many tracts previously excluded due to stopping criterion. It also keeps computation time low.

4 Dataset

Diffusion-weighted images were acquired on a single volunteer along 64 uniformly distributed directions using a b-value of $b = 1000\text{s/mm}^2$ and a single $b = 0\text{s/mm}^2$ image using the single-shot echo-planar imaging (EPI) sequence on a 1.5 Tesla SIEMENS Magnetom (128x128 matrix, 2mm isotropic resolution, TR/TE 11000/98 ms and GRAPPA factor 2). An anatomical T1-weighted 1mm isotropic MPRAGE (TR/TE 6.57/2.52 ms) image was also acquired.

Diffusion data was first corrected for eddy currents and head motion using FSL (www.fmrib.ox.ac.uk/fsl), then upsampled to 1mm isotropic resolution using a trilinear interpolation [1, 11]. Diffusion Tensor (DT) estimation and corresponding Fractional Anisotropy (FA) map generation were done using MRtrix [1]. From this, the single fiber response function was estimated from all FA values above a threshold of 0.7, within the WM binary mask. This single fiber response was used as input to spherical deconvolution [12, 13] to compute the fiber orientation distribution function (fODF), with spherical harmonic order 8, at every voxel of the brain. In this work, we used the efficient implementation publicly available in MRtrix.

The T1-weighted image was registered to a 1mm isotropic DWI using FLIRT. The Brain Extraction tool (BET) and FAST [5] of FSL were also used to extract both binary and probabilistic maps of the WM, GM and CSF.

5 Results and discussion

We compared the results using binary mask, CMC and the recently proposed method ACT [4]. ACT is adapted to only use 3 maps (WM, GM, CSF) and not use the subcortical GM criterion to compare with our proposed methods. The results of 12 tractograms each containing 50,000 tracts are discussed: both deterministic (Det.) and probabilistic (Prob.) tractograms using a binary mask (bin.), ACT, CMC and SMCT. CMC* and SMCT* denote the use of $\alpha = 4$.

Table 1 shows the proportion of seeds resulting in included tracts in the tractograms as well as the proportion of tracts excluded due to the stopping criterion and length criterion. The use of CMC with the fODF deterministic tractography decreases the proportion of tracts excluded due to the stopping criterion by 10% with respect to its binary version and decreases this proportion by 36% using SMCT (10% and 39% respectively using fODF Prob. CMC and SMCT). Table 1 shows high percentage of excluded tract for tractography using ACT. We hypothesize that this is mainly due to not using subcortical GM maps, which, after visualization, can cause tract to propagate through subcortical GM and end in the CSF. Nonetheless, we compared our results to ACT.
Seeds resulting in tracts near complex tracking configurations (high curvature or tight WM paths) have more chance of being excluded due to stopping criterion and thus, an increase of the included tracts could provide a better representation of the actual WM fiber distribution. Note that this does not address the seeding issue of long bundles that traverse more voxels and result in an over estimation of longer bundles compared to shorter bundles with similar fiber density.

Table 1 also provides the tract density and average tract length of the whole tractogram, the pyramidal tracts (PYT), the cingulum (Cg) and the superior longitudinal fasciculus (SLF). The CMC has little effect on the density and length of tracts. ACT and CMC* provide results with longer length than bin. and CMC. We hypothesize that this is due to the wider tracking area defined by the stopping criterion of ACT and the relaxed stopping probability of CMC*. SMCT, and especially SMCT*, also increase the average tract length of the 3 selected tract bundles and increase the tract density of the SLF.

One can see from Figure 2 (a) that most of the tracts stop early when entering in the brainstem. This is mainly due to the binarization of the probability maps (see Figure 1), which cuts several pathways through the brainstem. ACT, CMC and SMCT using the full probability maps can be observed in Figure 2 (b,c,d,e,f), where tracts more efficiently traverse the brainstem and some exit the image field of view, as expected. The use of SMCT provided a more uniform and dense PYT, providing longer tracts and producing qualitatively the best PYT reconstruction. We observed the same effect on probabilistic results (not shown due to space restriction).
SMCT increases tract densities on complex tract configurations as shown on the SLF in Figure 3 and expressed quantitatively in Table 1. SMCT also produces longer tracts than other methods on the Cg bundle (Figure 4), finding the full curving extent of the Cg. By helping the tracking of complex bundles, SMCT not only contributes to a more uniform tract density but also to find new tracts or longer paths that qualitatively agree better with known anatomy.

Finally, the back-tracking approach proposed by Smith et al. [4] was tested and showed a general increase in the number of seeds resulting in included tracts in the tractograms using binary mask, ACT or CMC for both probabilistic and deterministic tractography. This incremental back-tracking idea offers even more relaxation of the stopping criterion. We believe that combined to SMCT, it could potentially increase the general quality of the tractography. This issue will be further investigated and quantified in the future.
Fig. 4. The 6 deterministic tractograms of the Cg. a) det. bin, b) det. ACT, c) det. CMC, d) det. CMC*, e) det. SMCT, f) det. SMCT*.

Computational Cost Using our dataset, the SMCT was called on average 1.1 times per seed, resulting in an average computation time increase by a factor of 4 to obtain the same total number of tracts in the tractogram.

6 Conclusion

The results show that the use of the full probabilistic tissue segmentation maps increases the quality of tractograms compared to tractography done with binarized mask versions. Even more importantly, tissue probability maps allow the integration of a general framework solving local stopping issues by providing a likely plausible path when the tractography algorithm fails to find one. The SMCT takes advantages of global tractography algorithms [8, 9] and applies these advantages in a local manner. The results show that this approach increases the proportion of seeds resulting in actual tracts, which could be beneficial for connectivity studies. The SMCT combined with a fODF deterministic algorithm provides a hybrid tractography taking advantage of the regularity of the deterministic algorithm and richness of the probabilistic scheme. In our opinion, this gives a promising extension for deterministic tractography.

We think the CMC approach offers a more accurate way of dealing with the tractography mask than the use of a binary mask. This approach is of course dependent on the segmentation algorithm, as any method based on WM segmentation. FAST [5] provides good results, but other tools should be investigated, such as SPM (www.fil.ion.ucl.ac.uk/spm/). In particular, it would be of interest to study how CMC and ACT methods are sensitive to noise and perturbations, and how these methods can deal with less reliable tissue probability maps. Furthermore, the use of subcortical GM could be incorporated to CMC in a similar way as it proposed by Smith et al. [4]. Although CMC uses a probabilistic strategy and ACT uses a dynamic thresholding strategy, they both showed similar results in this study.
Since SMCT is a flexible modular add-on to most of the local streamline tractography algorithms, its implementation based on the DT is of interest, as DT tractography is still most commonly used in neuroscience applications. It could also be quite interesting to see how the CMC could be integrated to the particle filtering algorithm of Zhang et al. [8] and Pontabry et al. [9]. Conversely, it could be interesting to integrate the ingredients of their work on particle filtering for WM tractography to the SMCT framework.

One on the next challenge in tractography is to properly use a priori information from anatomy to improve the results and perform better brain connectivity. We think SMCT and CMC are a step forward to address this challenge.

References