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Complex Gaussian Noise for Efficient Visualization of Fiber Tracking Uncertainty

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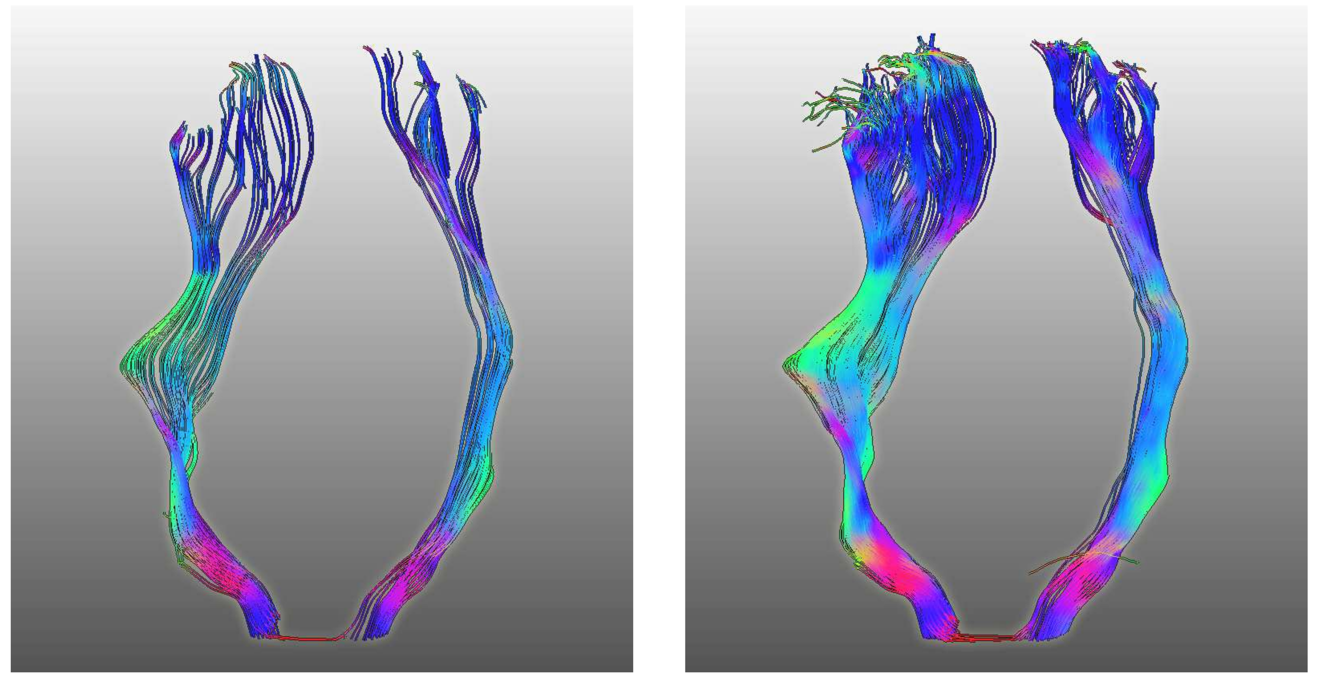
Problem

White matter fiber tracts obtained by fiber tracking can differ from the true pathways of the patient due to several factors. One determining factor, which is examined in this paper, is the susceptibility to noise in DTI.

Bootstrapping [1,2] allows for visualizing uncertainty:

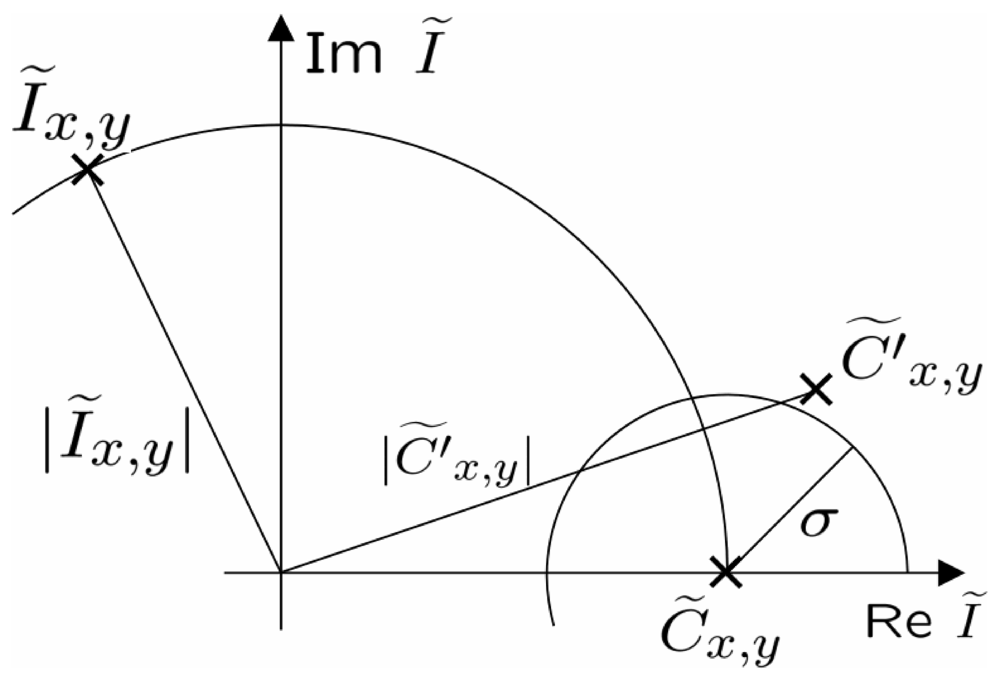
- acquire equivalent data sets of the same patient.
- compute average of randomly chosen images (repeat this, e.g., 50 x).
- track fibers for each new data set.



Left: initial fiber set, right: tracking result for 50 new data sets (seed points identical to left).

Problems of Bootstrapping method:

- time-consuming acquisition step.
- computational complexity: O($m \cdot s$) with
  m = # randomly chosen images
  s = number of slices of the data set.



Complex Gaussian noise of width σ added to pixel value $|\widetilde{I}_{x,y}|$. The result is $|\widetilde{C'}_{x,y}|$.

Methods

Noise distribution of MR images, even after 2D inverse Fourier transformation, is commonly assumed to be Gaussian [3].

However, after magnitude calculation, the data is no more complex; noise is Rician distributed [4].

We propose to add complex Gaussian noise to the magnitude images, so that noise distribution is equivalent to those of standard MR images:

$\widetilde{C}_{x,y} = |\widetilde{I}_{x,y}| + 0i$ (complex number to pixel value)

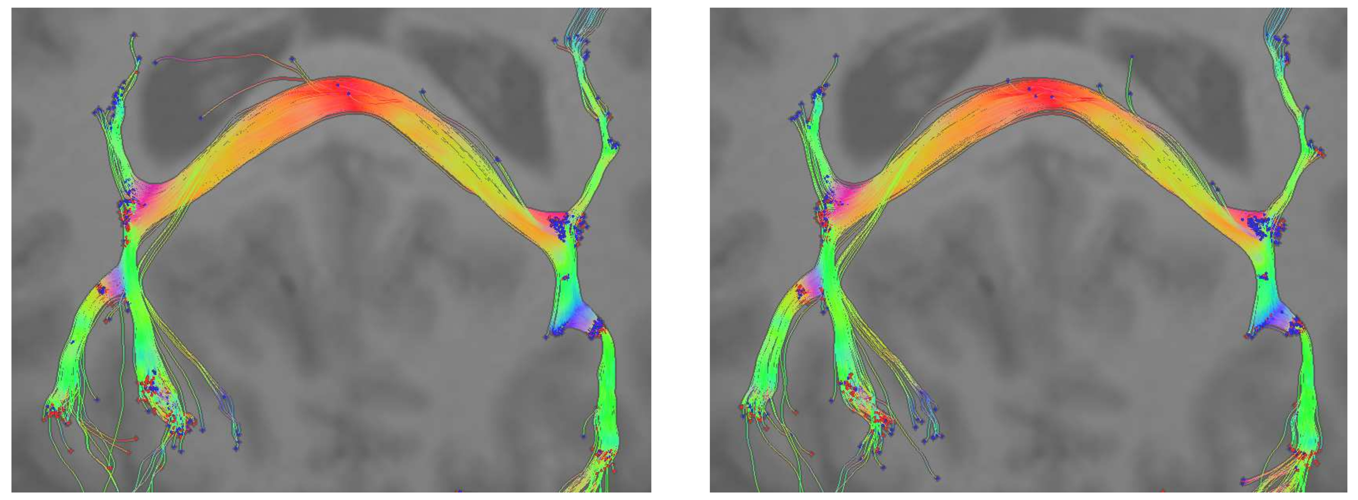
$\widetilde{C'}_{x,y} = \widetilde{C}_{x,y} + \widetilde{N}(0, \Sigma),\ \ \Sigma = \sigma^2 E$ (noise added)

$\sigma = \sqrt{{\sigma_2}^2 - {\sigma_1}^2}$, ${\sigma_1}^2$ = noise of source,
${\sigma_2}^2$ = bootstrap noise.

Computational complexity: O(s).

Results & Conclusions

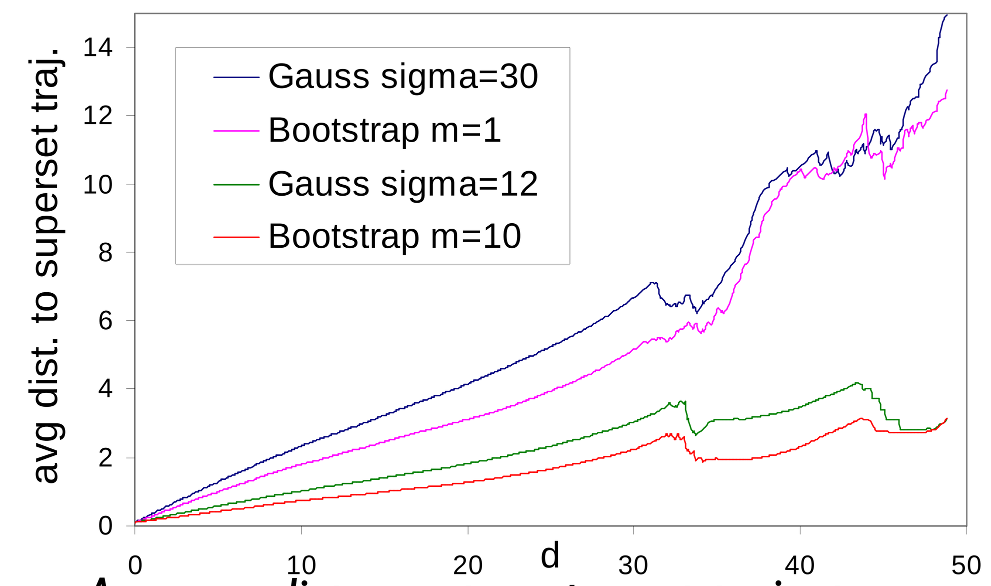
The figures below give a first impression that Bootstrap noise can be simulated appropriately by complex Gaussian noise.



*Old method: m = 10
20 seed points, 50 data sets.*

*New method: σ =12
20 seed points, 50 data sets.*

The plot supports this observation. For all points lying on the streamlines that have the same geodesic distance *d* to a seed point, their average distance to the superset trajectory is determined.



Average distance to superset trajectory

Our method constitutes an alternative to the Bootstrap method. It does not need multiple acquisitions of DTI data and hence makes the visualization process more efficient.

[1] D. K. Jones et al., Magn. Reson. Med. 2005, 53:1462-1467
[2] M. Lazar et al., Neuroimage 2005, 24:524-532
[3] J. Sijbers et al., Magn. Reson. Imaging 1998, 16(1):87-90
[4] H. Gudbjartsson et al., Magn. Reson. Med.1995, 24:1910-1914