

The ensemble average diffusion propagator (EAP) provides relevant microstructural information and meaningful descriptive maps of the white matter previously obscured by traditional techniques. Due to the huge amount of samples needed for an accurate reconstruction of the EAP, more efficient alternative techniques have been proposed in the last decade. All of them require a high number of gradients and several b-values to be calculated. In order to use the EAP in practical studies, scalar measures must be directly derived, being the most common the return-to-origin probability (RTOP), the mean-squared displacement (MSD) and the return to plane and return to axis probabilities (RTPP, RTAP). In this work, we propose an alternative method to estimate the return to axis probability (RTOP) from a single shell acquisition using a prior assumption over the diffusion signal. By applying that assumption locally, we achieve closed-form expressions of the measures using information from a only one b-value, compatible with acquisition protocols used for HARDI. Results have shown that the proposed method is highly correlated with the same measures calculated with state-of-the-art EPA estimators. In addition, due to the avoidance of EAP calculation, the execution times are highly accelerated.

The diffusion signal

In Diffusion Imaging, the probability density function of the displacement of water molecules (EAP) is given by:

$$P(\mathbf{R}|\Delta) = \int_{\mathbb{R}^3} E(\mathbf{q}) \exp(-2\pi j \mathbf{q}^T \mathbf{R}) d\mathbf{q}.$$

The measured signal in the \mathbf{q} -space is the (inverse) Fourier transform. If we apply a general diffusion model:

$$E(\mathbf{q}) = \mathfrak{F}^{-1}\{P(\mathbf{R})\}(\mathbf{q}) = \exp(-4\pi^2 \tau |\mathbf{q}|^2 D(\mathbf{q})),$$

- ▶ Direct calculation of EAP requires a very dense Cartesian sampling of \mathbf{q} -space.
- ▶ More efficient alternative techniques proposed: RBF, MAPMRI, MAPL...
- ▶ Information provided by EAP → translated to scalar measures.
- ▶ Challenge: reduce number of samples needed.

RTOP estimation

Return-to-origin-probability (RTOP): provides relevant information about the white matter structure.

$$P(\mathbf{0}) = \int_{\mathbb{R}^3} E(\mathbf{q}) d\mathbf{q}.$$

Model for diffusion: we consider a generic diffusion $D(\mathbf{q})$ that does not depend on the radial direction $D(\mathbf{q}) = D(\theta, \phi)$ and then

$$E(\mathbf{q}) = E(q_0, \theta, \phi) = \exp(-4\pi^2 \tau q_0^2 D(\theta, \phi))$$

This assumption, although restrictive, is used to define certain diffusion modalities in HARDI.

Model for RTOP:

$$\text{RTOP} = \int_0^\infty \int_0^{2\pi} \int_0^\pi \exp\{-4\pi^2 \tau q_0^2 D(\theta, \phi)\} q_0^2 \sin \theta d\phi d\theta dq_0 = \frac{1}{4} \frac{\sqrt{\pi}}{(4\pi^2 \tau)^{3/2}} \int_S D(\theta, \phi)^{3/2} dS$$

Integration in \mathbb{R}^3 reduces to integration on the surface of a single shell.

Numerical implementation:

$$\text{RTOP} = \frac{1}{(4\pi)^2 \tau^{3/2}} Y_0 \left\{ (D(\theta, \phi))^{-3/2} \right\}.$$

where $Y_0\{H(\theta, \phi)\}$ is the the zero-order coefficient of a SH decomposition of signal $H(\theta, \phi)$.

Materials and Methods

Data used: (1) Human Connectome Project (<https://ida.loni.usc.edu/login.jsp>). Five volumes (MGH 1007, MGH 1010, MGH 1016, MGH 1018 and MGH 1019), 4 different shells at $b=[1000, 3000, 5000, 10000]$ s/mm², with [64, 64, 128, 256] gradient directions, in-plane resolution 1.5 mm and slice thickness was 1.5 mm. (2) Public Kurtosis Database (<https://datadryad.org/resource/doi:10.5061/dryad.9bc43>).

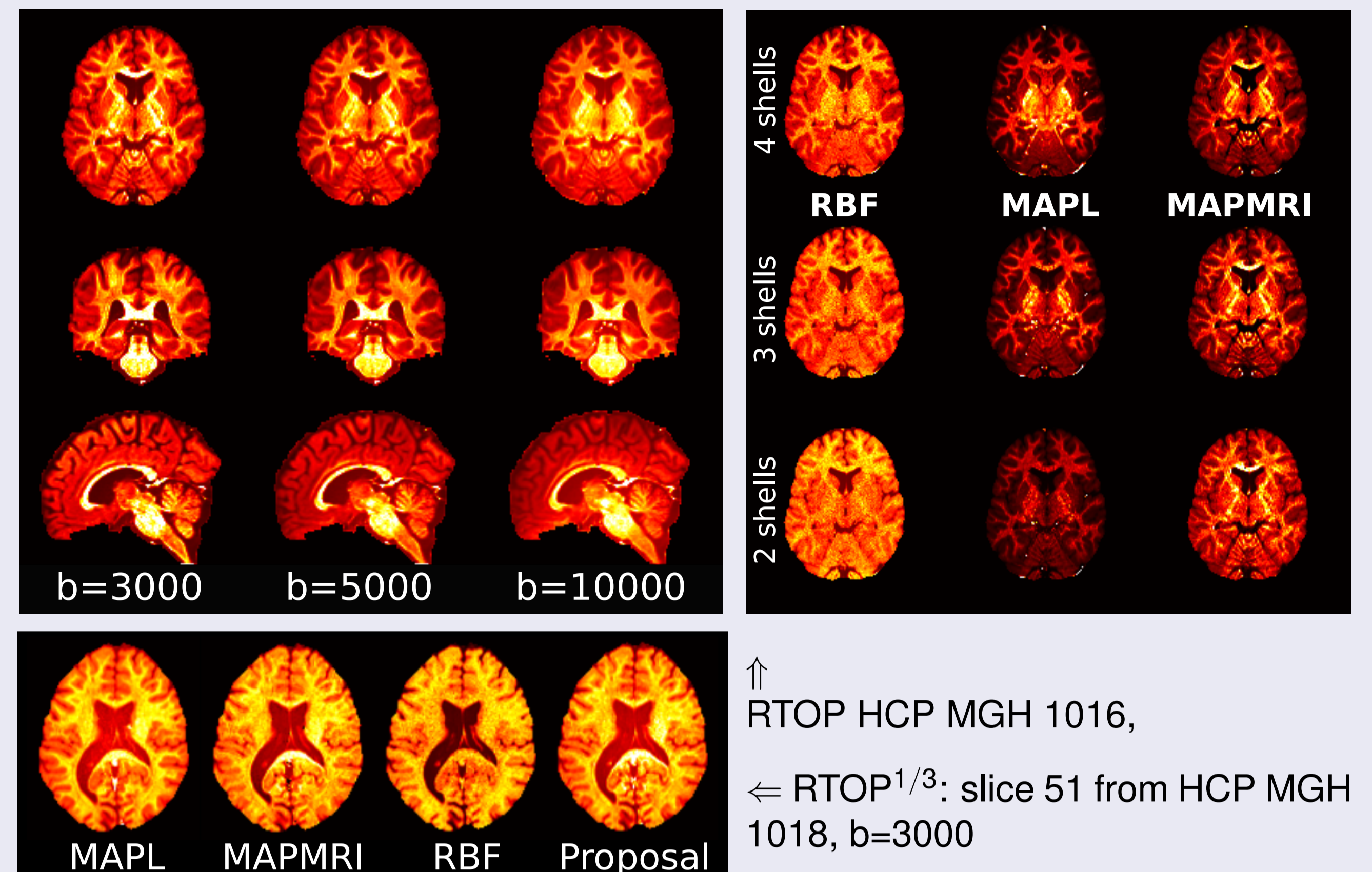
Methods: Directional radial basis functions (RBFs) [Ning15], mean apparent propagator (MAP-MRI) [Ozarslan13] and Laplacian-regularized MAP-MRI (MAPL) [Fick16].

Discussion

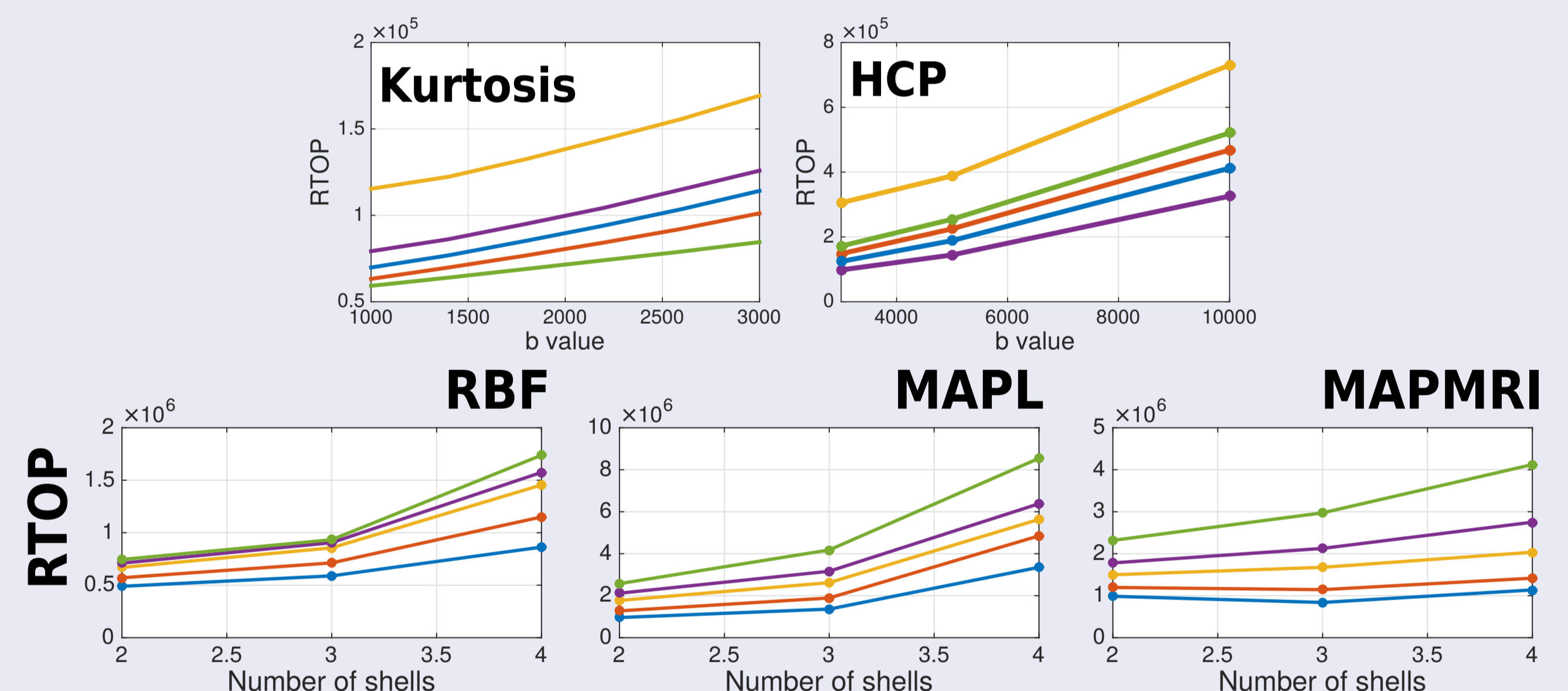
- ▶ Main advantage: reduction of acquisition time, number of samples and processing time
- ▶ Compatible with some standard diffusion acquisitions: DKI, CHARMED and HARDI.
- ▶ Counterpart: dependence with b-value selected; other methods similar behavior.
- ▶ Loss of radial information of EAP. (Really used here?)
- ▶ Extension of the method to RTPP, RTAP and QMSD.

Results

RTOP (Visual comparison)



Evolution with b-value

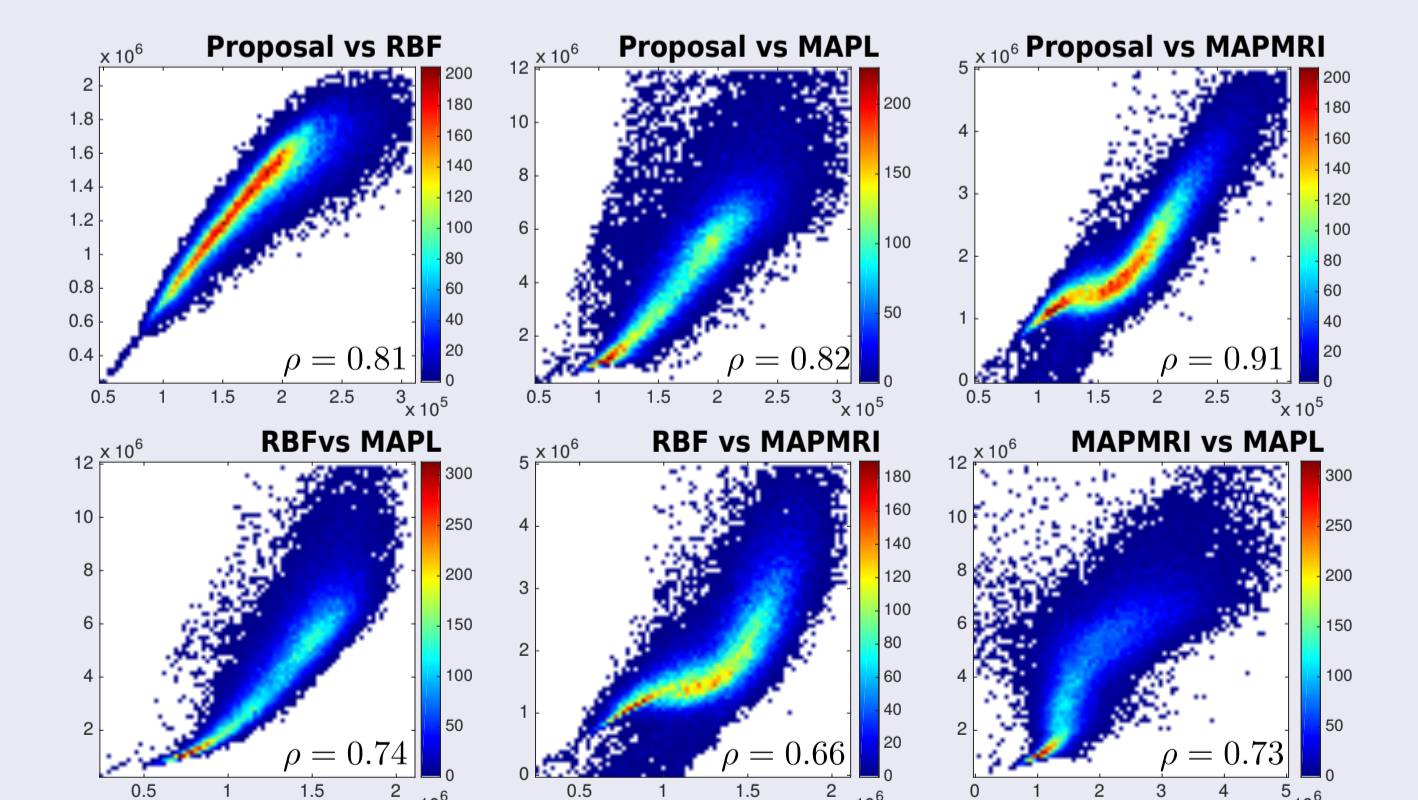


Correlation

	RBF	MAPL	MAPMRI	
4 shells	Proposal (b=3000)	0.7421	0.6826	0.9134
	Proposal (b=5000)	0.8141	0.8257	0.9117
	Proposal (b=10000)	0.7807	0.9296	0.8730
	RBF	–	0.7407	0.6616
3 shells	Proposal (b=3000)	0.6888	0.8616	0.9202
	Proposal (b=5000)	0.6635	0.9538	0.9151
	Proposal (b=10000)	0.5255	0.8963	0.8273
	RBF	–	0.6548	0.5532
2 shells	Proposal (b=3000)	0.6462	0.9047	0.90270
	Proposal (b=5000)	0.5370	0.8950	0.8278
	Proposal (b=10000)	0.3433	0.8032	0.7075
	RBF	–	0.6488	0.5899
MAPL	–	–	0.7747	

Correlation coefficient (HCP data).

	Execution time (HCP-MGH 1016)		
Method	Two shells	Three shells	Four shells
RBFs	118h 10min	332h 40min	577h 12min
MAPMRI	13h 43min	13h 46min	16h 20min
MAPL	2h 11min	2h 14min	2h 22min
Proposal	16s	29s	54s



2D histogram of RTOP calculated with different methods (4 shells vs b=5000).

Acknowledgements

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References

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