Return-to-axis probability calculation from single-shell acquisitions

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The Ensemble Average diffusion Propagator (EAP) provides relevant microstructural information and meaningful descriptive maps of the white matter previously obscured by traditional techniques like the Diffusion Tensor. The direct estimation of the EAP requires a dense sampling of the q-space data. Although alternative techniques have been proposed, all of them require a high number of gradients and several b-values to be calculated. Once the EAP is calculated scalar measures must be directly derived. In this work, we propose a method to drastically reduce the number of points needed for the estimation of one of the measures, the return-to-axis probability (RTAP). The proposal avoids the calculation of the EAP assuming that the diffusion does not depend on the radial direction. By applying that assumption locally, we achieve closed-form expressions of the measure using information from a only one b-value, compatible with acquisitions protocols used for HARDI. Results have shown that the measures are highly correlated with the same measures calculated with state of the art EAP estimators and highly accelerated execution times.

The diffusion signal

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

$$P(\mathbf{R}|\Delta) = \int_V E(\mathbf{q}) \exp\left(-2\pi j \mathbf{q}^T \mathbf{R}\right) d\mathbf{q}.$$

The measured signal in the **q**–space is the (inverse) Fourier transform. If we apply a general diffusion model:

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

- Direct calculation of EAP requires a very dense Cartesian sampling of **q**-space.
- More efficient alternative techniques proposed: RBF, MAP-MRI, MAPL...
- Information provided by EAP $\rightarrow$ translated to scalar measures.
- Challenge: reduce number of samples needed.

RTAP estimation

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

$$\text{RTAP} = \int_{\mathbb{R}^2} E(\mathbf{q}\perp) d\mathbf{q}\perp.$$

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

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

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

Model for RTAP:

$$\text{RTAP} = \int_0^\infty \int_0^{2\pi} \exp\{-4\pi^2\tau q_0^2 D(\theta')\}\, q_0\, d\theta'\, dq_0 = \frac{1}{8\pi^2\tau}\int_0^{2\pi} \frac{1}{D(\theta')} d\theta'$$

Using the Funk-Radon transform (FRT) $\mathscr{G}\{.\}$ we can write:

$$\text{RTAP} = \frac{1}{2\cdot 4\pi^2\tau}\mathscr{G}\left\{\frac{1}{D(\theta')}\right\}(\mathbf{r}_0) = 2\Psi(\mathbf{r}_0)$$

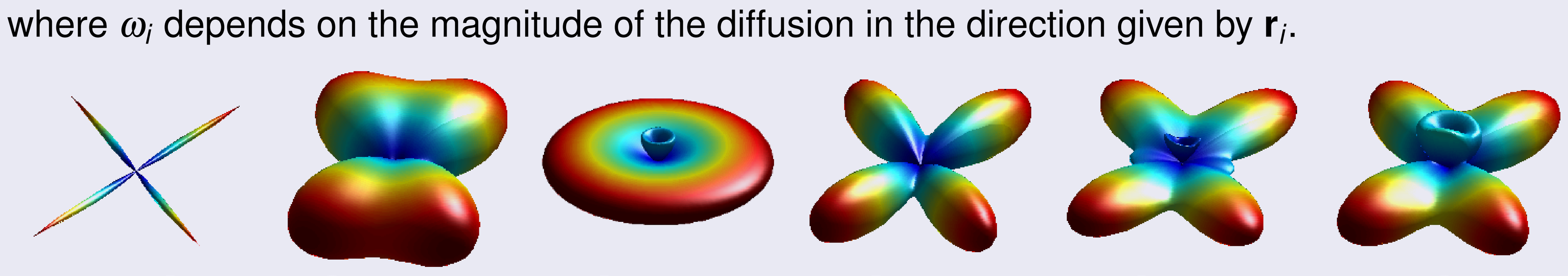
$\Psi(\mathbf{r})$ is the pQ-Balls as defined in [Tristan10] and $\mathbf{r}_0$ the direction of maximum diffusion.

Numerical implementation:

1. Other ODF-like estimators can be used instead of $\Psi(\mathbf{r})$: $\Phi(\mathbf{r})$.
2. To make it more robust, we use a weighted average:

$$\text{RTAP} = 2\frac{\sum_i \omega_i \Phi(\mathbf{r}_i)}{\sum_i \omega_i}.$$

where ω_i depends on the magnitude of the diffusion in the direction given by $\mathbf{r}_i$.



RTAP calculated with this methodology: *Apparent Return to Axis Probability* (ARTAP).

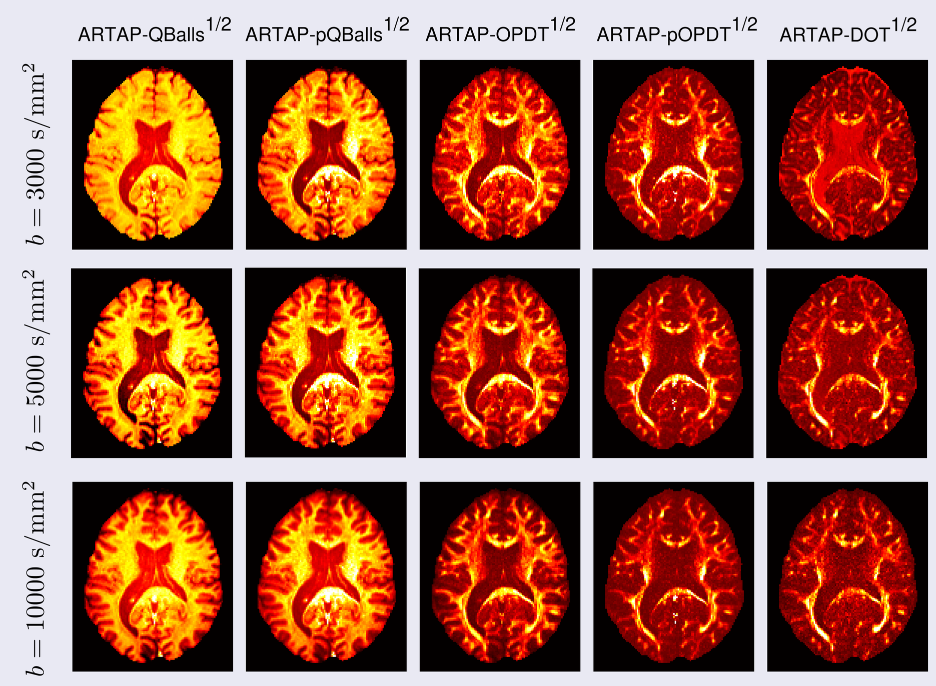
Materials and Methods

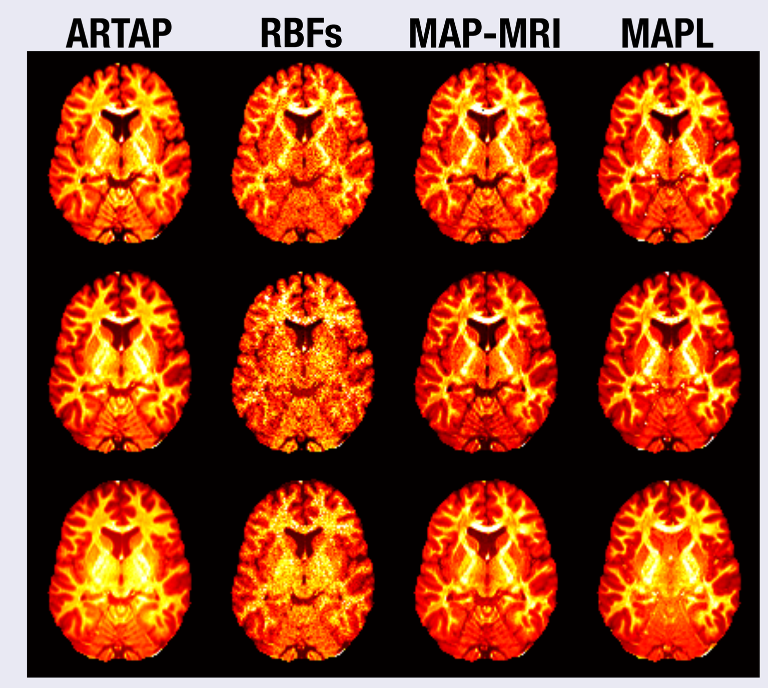
Data used: Human Connectome Project (https://ida.loni.usc.edu/login.jsp). Five volumes (MGH 1007, MGH 1010, MGH 1016, MGH 1018 and MGH 1019), 4 different shells at b=[1000, 3000, 5000, 10000] s/mm^2, with [64, 64, 128, 256] gradient directions, in-plane resolution 1.5 mm and slice thickness was 1.5 mm.

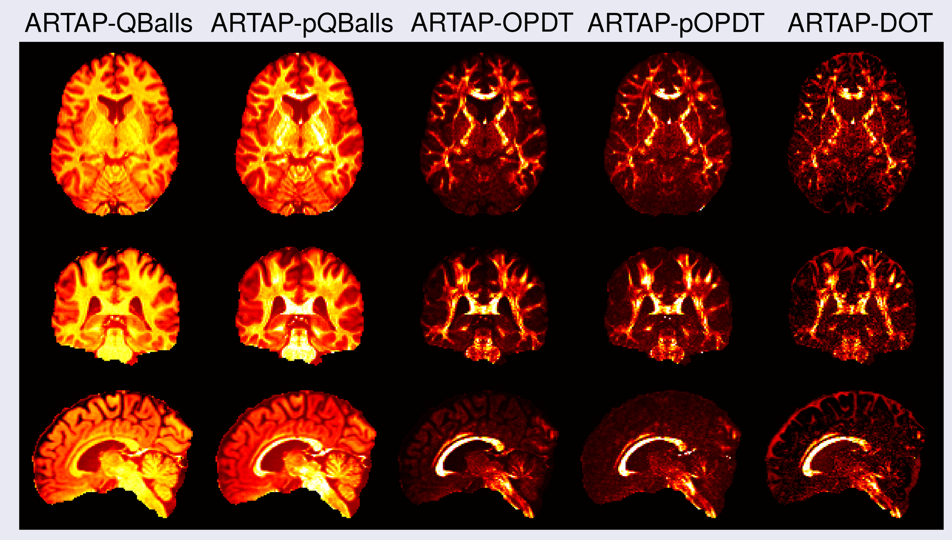
Methods: Directional radial basis functions (RBFs) [Ning15], mean apparent propagator (MAP-MRI) [Ozarslan13] and Laplacian-regularized MAP-MRI (MAPL) [Fick16].

Results

RTAP (Visual comparison)



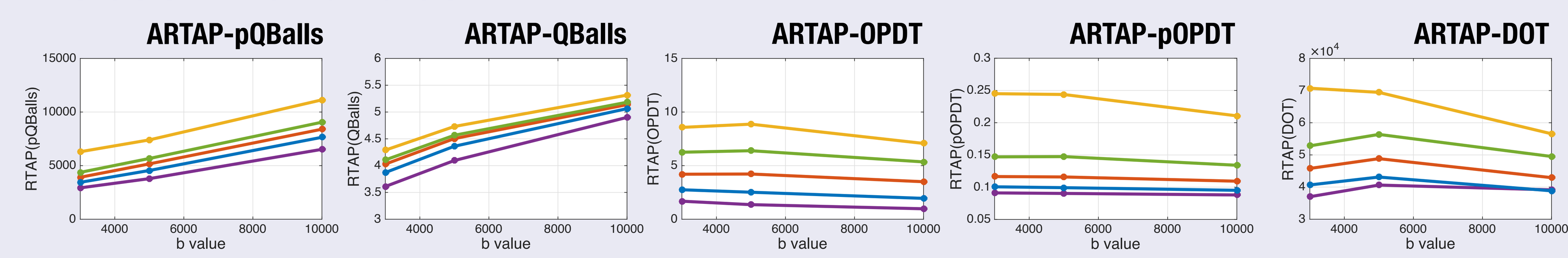


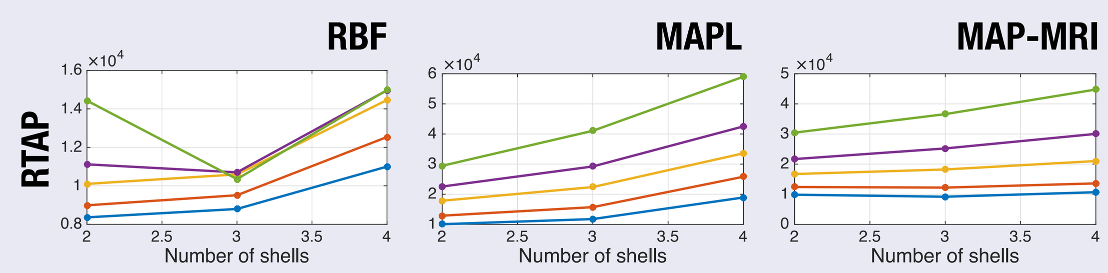


$\Uparrow$ RTAP$^{1/2}$ HCP-MGH 1018, and RTAP HCP-MGH 1016

$\Leftarrow$ RTAP: slice from HCP MGH 1016, b=3000

Evolution with b-value





Correlation and execution times

		pQBalls			OPDT		
		RBF	MAPL	MAPMRI	RBF	MAPL	MAPMRI
4 shells	**ARTAP** (b=3000)	0.58	0.75	**0.84**	0.50	0.75	**0.89**
	ARTAP (b=5000)	0.67	**0.84**	**0.86**	0.46	0.75	**0.88**
	ARTAP (b=10000)	0.65	**0.87**	0.79	0.45	0.77	**0.88**
	RBF	–	0.58	0.53			
	MAPL	–	–	**0.88**			
		RBF	MAPL	MAPMRI	RBF	MAPL	MAPMRI
3 shells	**ARTAP** (b=3000)	0.43	0.82	0.84	0.42	0.83	**0.85**
	ARTAP (b=5000)	0.45	**0.88**	**0.86**	0.45	0.85	**0.87**
	ARTAP (b=10000)	0.36	0.81	0.75	0.47	0.83	**0.86**
	RBF	–	0.41	0.39			
	MAPL	–	–	**0.92**			
		RBF	MAPL	MAPMRI	RBF	MAPL	MAPMRI
2 shells	**ARTAP** (b=3000)	0.68	0.84	**0.87**	**0.83**	0.82	**0.86**
	ARTAP (b=5000)	0.67	**0.85**	0.82	**0.82**	0.80	**0.84**
	ARTAP (b=10000)	0.56	0.77	0.71	**0.83**	0.79	**0.83**
	RBF	–	0.79	0.81			
	MAPL	–	–	**0.86**			

Correlation coefficient (HCP data).

Execution time (HCP-MGH 1016)

Method	**2 shells**	**3 shells**	**4 shells**
RBFs	118h	332h	577h
MAP-MRI	13h	13h	16h
MAPL	2h	2h	2h
ARTAP	**3.3min**	**3.5min**	**4min**

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?)
- Variability between ODFs: weakness or strength?

Acknowledgements

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