



Tensor decomposition processes for interpolation of diffusion magnetic resonance imaging



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ABSTRACT

Diffusion magnetic resonance imaging (dMRI) is an established medical technique used for describing water diffusion in an organic tissue. Typically, rank-2 or 2nd-order tensors quantify this diffusion. From this quantification, it is possible to calculate relevant scalar measures (i.e. fractional anisotropy) employed in the clinical diagnosis of neurological diseases. Nonetheless, 2nd-order tensors fail to represent complex tissue structures like crossing fibers. To overcome this limitation, several researchers proposed a diffusion representation with higher order tensors (HOT), specifically 4th and 6th orders. However, the current acquisition protocols of dMRI data allow images with a spatial resolution between 1 mm³ and 2 mm³, and this voxel size is much bigger than tissue structures. Therefore, several clinical procedures derived from dMRI may be inaccurate. Concerning this, interpolation has been used to enhance the resolution of dMRI in a tensorial space. Most interpolation methods are valid only for rank-2 tensors and a generalization for HOT data is missing. In this work, we propose a probabilistic framework for performing HOT data interpolation. In particular, we introduce two novel probabilistic models based on the Tucker and the canonical decompositions. We call our approaches: Tucker decomposition process (TDP) and canonical decomposition process (CDP). We test the TDP and CDP in rank-2, 4 and 6 HOT fields. For rank-2 tensors, we compare against direct interpolation, log-Euclidean approach, and Generalized Wishart processes. For rank-4 and 6 tensors, we compare against direct interpolation and raw dMRI interpolation. Results obtained show that TDP and CDP interpolate accurately the HOT fields in terms of Frobenius distance, anisotropy measurements, and fiber tracts. Besides, CDP and TDP can be generalized to any rank. Also, the proposed framework keeps the mandatory constraint of positive definite tensors, and preserves morphological properties such as fractional anisotropy (FA), generalized anisotropy (GA) and tractography.

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1. Introduction

Diffusion magnetic resonance imaging (dMRI) is an established medical technique that non-invasively measures water diffusion in organic tissue. The first attempt to represent this physical phenomenon was the Gaussian model proposed by Basser, Mattiello, and Le Bihan (1993); Basser, Mattiello, and Le Bihan (1994), where symmetric and positive definite tensors of rank-2 are estimated from dMRI to quantify the direction and orientation of diffusion. This model is known as diffusion tensor imaging (DTI). From

this quantification, it is possible to compute relevant physiological information (i.e. Fractional anisotropy and mean diffusivity) employed in the assessment of neurological diseases: Parkinson's disease (Butson, Moks, Walter, Vitek, & McIntyre, 2007), trauma (Ptak et al., 2003), multiple sclerosis (Hasan, Gupta, Santos, Wolinsky, & Narayana, 2005), meningitis (Nath et al., 2007), among others. Nevertheless, rank-2 tensors fail to represent accurately some complex tissue structures such as: white matter fiber bundles, crossing fibers, and bifurcated fibers (Mori, Crain, Chacko, & van Zijl, 1999; Ozarslan & Mareci, 2003).

To address these limitations in dMRI, several researchers have proposed higher order tensor (HOT) models for describing diffusion inside complex tissue structures (Barmpoutis & Vemuri, 2010; Liu, Bammer, Acar, & Moseley, 2004; Moakher, 2008; Ozarslan & Mareci, 2003). These models demonstrated accuracy and flexibility to represent dMRI with low signal to noise ratio. However, the es-

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timization of HOT requires more gradient directions for each slice in dMRI than the ones needed for DTI (Berman, Lanza, Blaskey, Edgar, & Roberts, 2013). Additionally, the current acquisition protocols of dMRI restrict the images to a voxel size in a range from 1 mm^3 to 2 mm^3 , no matter if the representation is with HOT or DTI. The problem here is that this voxel size is much bigger than tissue fibers and current acquired dMRI of the human brain have a broad resolution in comparison to anatomical structures. Therefore, the analysis of microstructural features can be difficult and some clinical procedures derived from dMRI may be inaccurate (Dirby et al., 2014).

Interpolation of tensor fields is a feasible methodology to reduce the voxel size in dMRI and achieves clinical relevance in reconstruction of tissue fiber bundles for tractography. Furthermore, interpolation of tensor fields is important in any application where estimating data among nearby tensors is required, including image registration (Yassine & McGraw, 2009). A considerable number of methods for tensorial interpolation have been proposed in the literature, including direct linear interpolation (Pajevic, Aldroubi, & Basser, 2002), log-Euclidean space (Arsigny, Fillard, Pennec, & Ayache, 2006), b-splines (Barmpoutis, Vemuri, Shepherd, & Forder, 2007), Riemannian manifolds (Fletcher & Joshi, 2007; Pennec, Fillard, & Ayache, 2006), feature-based framework (Yang et al., 2012), geodesic loxodromes (Kindlmann, Estepar, Nithammer, Haker, & Westin, 2007) and generalized Wishart processes (Vargas Cardona, Alvarez, & Orozco, 2015). They have different shortcomings. For example, linear interpolation does not ensure positive definite tensors (Pajevic et al., 2002), and the works of Arsigny et al. (2006); Fletcher and Joshi (2007) and Pennec et al. (2006) are highly affected by the intrinsic Rician noise added in dMRI during acquisition. Remarkably, the most significant limitation for all the approaches mentioned is that they are exclusively valid for rank-2 tensors (DTI), and only the linear interpolation can easily be employed on HOT fields. As we pointed out before, DTI is deficient to represent complex tissue structures. For this reason, it is necessary a tensorial interpolation methodology that can be generalized to any order. The aim is to achieve a more accurate representation of the brain tissue.

Regarding HOT field interpolation, the authors of Yassine and McGraw (2008, 2009) developed a method based on tensor subdivision and minimization of two properties (curl and divergence) of the field for interpolation of 4th-order tensors. However, the works in Yassine and McGraw (2008, 2009) only reported outcomes for rank-4 tensor fields, and the methods do not have a clear extension to higher orders, lacking generalization. Another valid approach is to interpolate the dMRI before the tensor reconstruction. For example, in Dirby et al. (2014), it was demonstrated that interpolation of raw dMRI with conventional methods (linear, bicubic and b-spline) can reveal anatomical details only seen in very high resolution images. Though, this framework may produce the undesirable swelling effect in tensors (Yang et al., 2014) and blurs the tract boundaries (Dirby et al., 2014). Also, authors in Astola and Florack (2009); Astola, Jalba, Balmashnova, and Florack (2011) introduced an approach to perform probabilistic tractography in HOT data. In particular, they developed a Finsler geometry-based methodology for multi-fiber analysis. The Finsler geometry model is able to perform probabilistic tractography in HOT fields using the orientation distribution function (ODF), and it is a generalization of the streamline method applied on DTI (Astola et al., 2011). Nevertheless, a derived method of Finsler geometry for interpolation has not been developed yet.

To the best of our knowledge, there is not a generalized methodology for interpolating HOT fields (no matter the rank), that retains all mandatory constraints for tensorial representation of dMRI. In this work, we propose a novel methodology to perform interpolation in HOT fields of any order. In this regard, we employ

tensor representations and modulate their parameters with Gaussian processes (GPs), aiming to estimate new data with robustness, considering that GPs are functions of a multi-dimensional input variable. Specifically, we introduce two probabilistic models, that we refer to as the Tucker decomposition process (TDP) and the canonical decomposition process (CDP). Our models are based on the Tucker and canonical decomposition of tensors (Carroll & Chang, 1970; Gulliksen & Frederiksen, 1964), respectively. The main advantage of tensor decompositions is the transformation of a complex mathematical object in a superposition of scalars, vectors or matrices. These simple representations allow to index a tensor in an independent variable (i.e. spatial coordinates), facilitating the probabilistic modeling of tensor fields, no matter the order (rank). We test the TDP and CDP in 2nd, 4th and 6th rank HOT fields. For rank-2 tensors, we compare against direct interpolation (Pajevic et al., 2002), log-Euclidean approach (Arsigny et al., 2006), and Generalized Wishart processes (Vargas Cardona et al., 2015). For rank-4 and rank-6 tensors we compare against direct interpolation and raw dMRI interpolation with b-splines (Dirby et al., 2014). Results obtained show that TDP and CDP interpolate accurately the HOT fields, and generalize to any rank. Importantly, the proposed framework safeguards the mandatory constraint of positive definite tensors, and preserve morphological properties such as fractional anisotropy (FA), white matter (WM) segmentation, generalized anisotropy (GA), and tractography.

2. Materials and methods

In this section, we first define the proposed framework. Second, we briefly explain the main concepts of a Gaussian process. Then, we introduce the Tucker and canonical decomposition of a tensor, and we describe the priors that we use to represent tensorial fields by combining the Tucker and canonical decomposition with Gaussian processes. Also, we introduce the higher order tensors for modeling dMRI data. Bayesian inference for the proposed probabilistic models is then discussed. Finally, we give details of the experimental setup.

2.1. Proposed approach for tensor interpolation

A tensor is a geometric or physical object specified by a set of coefficients $\mathcal{T}_{i_1 i_2 \dots i_l}$ of a multi-linear form $\mathcal{T} = \phi(\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_l) \in \mathbb{K}^{I_1 \times I_2 \times \dots \times I_l}$ of l vector arguments $\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_l$ written in some orthonormal basis, where \mathbb{K} may refer to \mathbb{R} (real) or \mathbb{C} (complex). The number l is known as the order or rank of the tensor and each vector argument has an independent (may be different) dimensionality. Alternatively, a tensor can be represented in several forms employing vectorial or matrix approximations:

$$\mathcal{T} \sim \mathbf{M}(\boldsymbol{\alpha}_1, \boldsymbol{\alpha}_2, \dots, \boldsymbol{\alpha}_m),$$

being $\mathbf{M} \in \mathbb{K}^{I_1 \times I_2 \times \dots \times I_l}$ any vectorial or matrix decomposition of \mathcal{T} , and $\boldsymbol{\alpha}_1, \boldsymbol{\alpha}_2, \dots, \boldsymbol{\alpha}_m$ parameters of the given representation. Following this notion, our main goal is to develop probabilistic models (PM) using tensors indexed by an independent variable $\mathbf{z} = [z_1, z_2, \dots, z_J]^T$, being J the dimensionality of \mathbf{z} . For example, if \mathbf{z} refers to spatial coordinates, then, $\mathbf{z} = [x, y, z]^T$ and $J = 3$. The PM can be seen as probability distributions over a tensor field, this is, a grid of interconnected and related tensors. Furthermore, such probability distributions allow the interpolation of new tensor data for any input locations (\mathbf{z}_*), according to the following definition:

$$\mathcal{T}(\mathbf{z}) \sim \mathcal{M}(\boldsymbol{\alpha}_1(\mathbf{z}), \boldsymbol{\alpha}_2(\mathbf{z}), \dots, \boldsymbol{\alpha}_m(\mathbf{z})), \quad (1)$$

where \mathcal{M} is a tensor representation, and $\boldsymbol{\alpha}_1(\mathbf{z}), \boldsymbol{\alpha}_2(\mathbf{z}), \dots, \boldsymbol{\alpha}_m(\mathbf{z})$ are free parameters that depend on the mathematical definition of \mathcal{M} . The probabilistic nature of \mathcal{M} arises because the parameters $\boldsymbol{\alpha}_1(\mathbf{z}), \boldsymbol{\alpha}_2(\mathbf{z}), \dots, \boldsymbol{\alpha}_m(\mathbf{z})$ are realizations of stochastic processes.

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