4-D Spatio-Temporal MR Perfusion Deconvolution via Tensor Total Variation

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Target Audience

Clinicians and researchers who wish to improve the detection and diagnosis accuracy of brain tumor or cerebral disease using MR perfusion.

Introduction

4-D dynamic susceptibility contrast (DSC) magnetic resonance imaging (MRI) is a well-established perfusion technique for non-invasive characterization of tissue dynamics, with promising applications in assessing a wide range of diseases, as well as monitoring response of therapeutic interventions). DSC-MRI provides critical real-time information by tracking the first-pass of an injected contrast-agent (e.g. gadolinium) with T2*-weighted MRI. The spatio-temproal data, consisting of contrast concentration signals for each voxel of a volume, are deconvolved from the arterial input function (AIF) and then post-processed to generate perfusion parameter maps, typically including the cerebral blood flow (CBF), cerebral blood volume (CBV), mean transit time (MTT) and time to peak (TTP). The most popular deconvolution method is truncated singular value decomposition (TSVD)[1,2] and its variants[3], which fail to exploit the spatio-temporal nature of the 4D data with both the anatomical structure and the temporal continuation. This work adapts and demonstrates the feasibility of a 4-D tensor total variation (TTV) deconvolution approach, which has been proposed for CT perfusion[4], to brain MR perfusion, with evaluation on synthetic data and clinical DSC-MRI data for glioblastomas, the most common type of brain cancer. The method is guaranteed to convergence to global optimal because of the convex cost function and presents a more elegant framework of total variation for the deconvolution, compared to recent efforts[5,6] which either do not have a global optimal solution for the non-convex case or need to handcraft spatial and temporal regularization terms.

Methods

The contrast-agent concentration signal C_v is logarithmically proportional to the change in MR signal intensity,

$$C_v(t) = -\frac{\kappa_H}{\kappa \cdot TE \cdot \rho} \ln\left(\frac{S_v(t)}{S_v(0)}\right) \quad (1)$$

where κ_H is the hematocrit correction parameter, κ is a constant assumed for all tissue voxels, TE is the echo time, ρ is the tissue density, $S_v(t)$ is the MR signal intensity at time t, and $S_v(0)$ is the pre-contrast signal intensity.

The tensor total variation approach is based on three assumptions: (1) the temporal concentration curves of the contrast agent vary smoothly; (2) the perfusion dynamics of each voxel is correlated with the neighboring region due to the non-random anatomical structure of the microvasculature for voxels in the health or diseased regions; (3) the discontinuity between the healthy and diseased regions needs to be preserved. Total variation is remarkably effective at simultaneously preserving edges while smoothing away noise at homogeneous regions, even at low SNR[5]. Imposing tensor total variation regularization on the 4-D impulse residue functions (IRF) in MR perfusion would yield piece-wise smooth IRF. The TTV approach is formulated as

$$\hat{K} = \text{armmin}_{K \in \mathbb{R}^{T \times N}} \left(\frac{1}{2}\|AK - C\|^2 + \lambda \|K\|_{TTV}\right) \quad (2)$$

where $A \in \mathbb{R}^{T \times T}$ is the Toeplitz matrix of AIF, $K \in \mathbb{R}^{T \times N}$ is the flow-scaled IRF, $C \in \mathbb{R}^{T \times N}$ is the contrast concentration curve, λ is the weighting parameter for the TTV term, T is the number of time points, and N is the number of voxels in the region of interest. The TTV term is defined as $\|K\|_{TTV} = \sum_{i,j,k,t} \sqrt{\sum_{d=1}^{4} (\nabla_d K)^2}$, as illustrated in Fig. 1. Eq. (2) is solved by an iterative algorithm consisting of three steps: (1) Adaptive gradient descent for K in the first term; (2) proximal map for the TTV term; (3) update algorithmic parameters.

Results

Synthetic data with simulated Gaussian noise with SNR = 22.6 dB to approximate the Rician distribution provide the ground truth perfusion parameters and residue functions for evaluation, following the experimental setup in Frindel. et. al.[7] where we use the gamma-variant function for AIF for more realistic simulation. Fig. 1(a) displays the example residue functions in the simulated diseased regions for four different methods (sSVD: standard singular value decomposition, bSVD: block-circulant singular value decomposition, Tikhonov regularization, TTV: tensor total variation) with the ground truth RIF. In both tissue types, the SVD-based methods and Tikhnov show unwanted oscillations which translate into large negative values without physical meaning. The oscillation was attenuated significantly by TTV to recover the ground truth RIF. Fig. 1(b) shows the peak signal-to-noise ratio (PSNR) of the RIF compared to ground truth as a function of signal-to-noise ratio (SNR) of the MRP data. We also compared to using only temporal or spatial total variation, which outperform the baseline methods but not as well as TTV with spatio-temporal regularization (Table 1). Fig. 2 shows the CBF, MTT and TTP maps computed using the four methods, where TTV preserves the smoothness of tissue within the healthy and diseased regions, and separate the two tissue types with clear-cut boundary, while overcomes the under-estimation in CBF and CBV using baseline methods.

Table 1 PSNR(dB) of the residue functions

Methods	Healthy	Diseased	All
sSVD	26.00	16.88	26.56
bSVD	22.25	16.62	23.16
Tikhonov	18.10	8.61	18.60
Temporal	34.14	25.88	35.72
Spatial	35.11	29.75	36.04
TTV	**39.04**	**30.33**	**39.65**

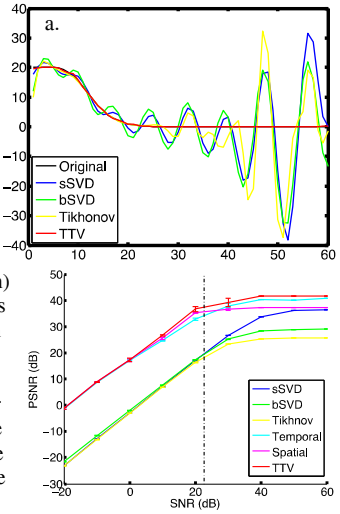

Fig. 1 (a) Residue functions at CBF=20 mL/100g/min; (b) PSNR of residue functions as a function of the SNR of the data. The dotted line indicates the SNR in our clinical data.

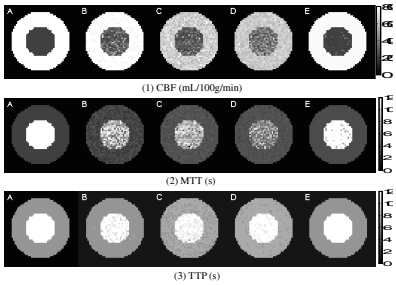

Fig. 2 Perfusion maps (CBF, MTT, TTP) computed using (B) sSVD (C) bSVD (D) Tikhonov (E) TTV. (A) are the true maps.

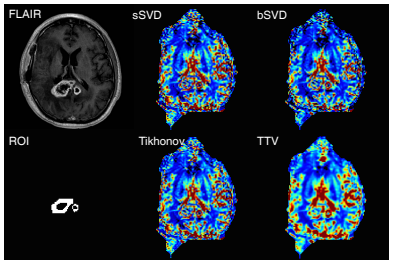

Fig. 3 Deconvolution of MRP data from gliobastoma subject using four methods with cancer mask delineated from FLAIR image as the ground-truth.

Real DSC T2* MR perfusion data of patients with a cerebral gliomas from TCGA-gliobastoma multiforme (GBM)[8] were selected. They were acquired on a 1.5T whole-body scanner (Signa; GE Medical Systems, Milwaukee, Wisconsin) using a gradient echo sequence (TE=40 ms, TR=1900 ms). Each subject data is 128 x 128x17 voxels x 95 time points. We also have the tumor (gliomas) region delineated by a physician from three-month follow-up T1 FLAIR imaging as the ground truth. Fig. 3 shows the CBV maps of a slice with both active cancer and necrosis tissue in the posterior region of the brain and estimated using four methods. TTV reduces the noise in the necrosis region while improving the contrast between the cancer (high-grade gliomas) and the necrosis regions. The segmentation accuracy using a moving threshold improves the area-under-curve (AUC) from 86% to 91% using TTV.

Conclusion

4-D tensor total variation can effectively improve the quantification accuracy for MR perfusion. The algorithm is guaranteed to converge to global optimal since it is convex and experimental results on both synthetic and real data show its superiority in residue function estimation, hemodynamic map quantification and localization of tumor.

References

[1] Østergaard et. al. 1996; MRM 36(5):715-7325. [2] Østergaard et. al. 1996; MRM 36(5):726-736. [3] Wu. et. al. MRM; 50(1):164-174. [4] Fang. et.al. MICCAI 2014; 8673:154-161. [5] He et. al. TMI, 2010; 29(5):1182-1191. [6] Frindel, et. al. MedIA, 2014; 18:144-160. [8] Strong el. al. *Inverse problems* 2003; 19(6): 165. [9] https://wiki.cancerimagingarchive.net/display/Public/DSC+T2*+MR+Perfusion+Analysis.