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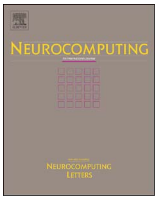

TENDER: Tensor non-local deconvolution enabled radiation reduction in CT perfusion

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ABSTRACT

Stroke is the leading cause of long-term disability and the second leading cause of mortality in the world, and exerts an enormous burden on the public health. Computed Tomography (CT) remains one of the most widely used imaging modality for acute stroke diagnosis. However when coupled with CT perfusion, the excessive radiation exposure in repetitive imaging to assess treatment response and prognosis has raised significant public concerns regarding its potential hazards to both short- and long-term health outcomes. Tensor total variation has been proposed to reduce the necessary radiation dose in CT perfusion without comprising the image quality by fusing the information of the local anatomical structure with the temporal blood flow model. However the local search in the TTV framework fails to leverage the non-local information in the spatio-temporal data. In this paper, we propose TENDER, an efficient framework of non-local tensor deconvolution to maintain the accuracy of the hemodynamic parameters and the diagnostic reliability in low radiation dose CT perfusion. The tensor total variation is extended using non-local spatio-temporal cubics for regularization, and an efficient algorithm is proposed to reduce the time complexity with speedy similarity computation. Evaluations on clinical data of patients subjects with cerebrovascular disease and normal subjects demonstrate the advantage of non-local tensor deconvolution for reducing radiation dose in CT perfusion.

1. Introduction

Stroke remains the leading cause of disability and second leading cause of mortality worldwide, thus exerting an enormous public health burden for long-term disability care costing $34 billion annually. Timely diagnosis is crucial to inform treatment decisions in acute stroke as “time is brain”. Therefore, it is critical to develop reliable in-vivo quantitative imaging markers for stroke for diagnosis and guiding treatment decisions. Computed tomography perfusion (CTP) is an ideal imaging modality to assess hemodynamic changes in the brain given its widespread availability, speed, affordability and high spatial resolution. Despite these benefits, CTP delivers one of the highest radiation doses of noninvasive imaging studies, and as a result, has raised significant public concerns because of its potential short- and long-term biological effects including cancer induction, skin damage and early cataract formation [1–4]. This is especially concerning in stroke patients whose disease requires serial monitoring of hemodynamic status with perfusion imaging to assess treatment response and prognosis [5]. Lowering the radiation exposure would reduce the potential health hazard, improve healthcare quality and safety, and make CTP modality fully utilized for a wider population. However, a major challenge in dose reduction strategies in CTP is that such approaches inevitably lead to an increase in noise and therefore less accurate hemodynamic parameter quantification given the methods used today.

In this paper, we propose an efficient framework TENDER (TEnsor Non-local Deconvolution Enabled Radiation reduction) to minimize the radiation exposure without compromising the image quality, especially the perfusion parameter accuracy. This fast deconvolution method extends the prior work of tensor total variation (TTV) [6,7] with non-local regularization to improve the image quality and interpretation of low-dose CTP. Instead of restricting the regularization of residue functions to the adjoining voxels in the spatial domain and neighboring frames in the temporal domain, we consider both long-range dependency and the global connections in the spatial and temporal dimensions. We propose to integrate the state-of-art low-dose deconvolution method together with the non-local regularization to increase the robustness of the method with efficient algorithm. To the best of our knowledge, this integration of two approaches in a

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spatio-temporal framework to regularize the flow-scaled residue impulse functions has never been proposed, and it can make significant improvement in the perfusion parameter estimation. Furthermore, the efficient algorithm to accelerate TENDER computation and optimization would make the proposed algorithm clinically valuable.

2. Related work

There are two major steps in hemodynamic parameter estimation for perfusion imaging: reconstruction and deconvolution. Therefore there are mainly two types of approaches to reduce the radiation exposure.

2.1. Reconstruction

Current state-of-the-art methods to reduce radiation exposure from CTP are problematic because they mainly focus on the reconstruction step which does not improve the parameter estimation process [8–12]. However, the stability and accuracy of the parameter estimation step is critical for the precise quantitative estimation of hemodynamic parameters. Among the few methods to improve the deconvolution step in low-dose CTP, the improvement in performance been limited without leveraging the existing high-dose data [13]. With the advent of big medical data, a data-driven mathematical approach employing a spatio-temporal model has the potential to significantly reduce the radiation exposure in CTP.

2.2. Deconvolution

While the first class of approaches does not solve the inherent instability problem in the quantification (deconvolution) process of CTP, the second class of approaches directly addresses this instability issue. Among these methods, the information redundancy and sparsity is a property that has shed light into medical image analysis, ranging from deformable models [14–16], segmentation [17], fast MRI quantification [18], and low-dose quantification problems [19–21], but the sparsity frameworks need training data for dictionary learning. In another line of work, tensor total variation (TTV) deconvolution [6,7] has been recently proposed to significantly reduce the radiation dosage in CTP with improved robustness and quantitative accuracy by integrating the anatomical structure correlation and the temporal blood flow model. The anatomical structure of the brain encompasses long-range similarity of the same tissue classes, as shown in Fig. 1(a). However the locality property of the current TTV algorithm limits the search for similar patterns in the 4-connected adjacent neighborhood, neglecting the long-range or global correlations of the entire brain structure. This locality limitation has led to noticeable absence or artifact of the delicate structures, such as the capillary, the insula and the parietal lobe, which are critical indicators for the clinical diagnosis of cerebrovascular diseases. Fig. 1(b) shows the importance of accurate depiction of hemodynamic parameters. The delicate vascular and cerebral structures are critical biomarkers of the existence and severity of the cerebrovascular diseases. Naturally, integrating non-local correlation into the estimation process of the hemodynamic parameters would yield more precise depiction of the pathological regions in the brain [22,23]. As an extension of [22], this work significantly extend introduction, related work and experimental parts.

2.3. Contributions

The contribution of this work is three-fold: First, the non-local connections are explored to leverage the anatomical and structural similarity of the same tissue classes in both the spatial and the temporal dimensions. Second, efficient parallel implementation and similarity computation using window offsets reduce the computational time of the non-local algorithm. Third, extensive experiments on low-dose CTP clinical data of subjects with cerebrovascular diseases and normal subjects are performed. The experiments demonstrate the superiority of the non-local framework, compared with the local TTV method. The advantages include more accurate preservation of the fine structures and higher spatial resolution for the low-dose data.

This paper is organized as follows. Section 3 presents the current tensor total variation model for low-dose CTP deconvolution with its limitations. Section 4 introduces our proposed TENDER model for tensor non-local deconvolution to overcome the locality constraints in the TTV model, followed by Section 5 on the efficiency method for this spatio-temporal optimization problem, including fast nearest neighbor search in the non-local neighborhood, efficiency optimization, and parallel computing. Sections 6 and 7 describes the experiment setup and shows the experimental results on clinical data. The paper is concluded with Section 8.

3. Tensor total variation model

In this section, we will first briefly review the tensor total variation (TTV) model for the low-dose CTP and discuss its deficiency in accurate estimation of delicate structure and exaiming pattern complexities.

To reduce the radiation dose in CT perfusion imaging, tensor total variation (TTV) [6] is recently proposed to efficiently and robustly estimate the hemodynamic parameters. It integrates the anatomical structure correlation and the temporal continuation of the blood flow signal. The TTV algorithm optimizes a cost function with one linear

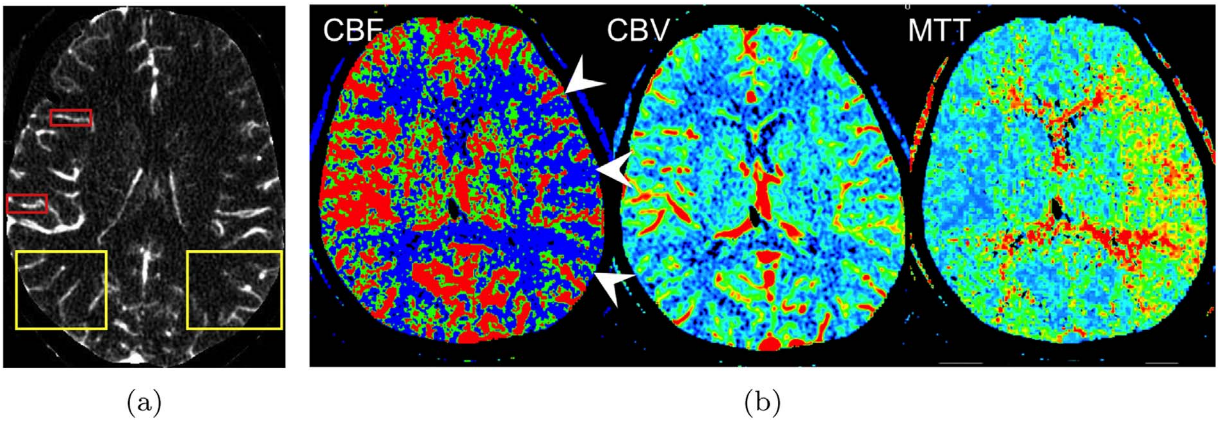

Fig. 1. (a) The illustration of long-range similarity in the brain. The red and yellow boxes show the non-local regions which have similar patterns. (b) Perfusion parameter maps (CBF – cerebral blood flow, CBV – cerebral blood volume, and MTT – mean transit time) of a 22-year old with severe left middle cerebral artery (MCA) stenosis. Arrows indicate the regions with altered hemodynamic function represented as abnormally decreased CBF and prolonged MTT. This pattern is indicative of ischemic tissue at risk of stroke in the left hemisphere (right side of the image). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)