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Quantitative Analysis of DCE-MRI Data using DL model based on Signal Intensity vs Concentration Curves

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Synopsis

Keywords: Analysis/Processing, DSC & DCE Perfusion, DEEP LEARNING, BRAIN TUMOR, PERFUSION PARAMETERS

Motivation: Quantitative analysis of dynamic-contrast-enhanced MRI(DCE-MRI) is valuable approach for mapping tumor physiology; however, traditional non-linear-least squares(NLLS) methods are slow and provide noisy maps. Deep-learning(DL) approach offers solutions, yet reported models rely on signal-intensity-time-curves(SIC) which are MRI-acquisition protocol dependent.

Goal(s): To develop DL network(CNN_{CON}) that uses concentration-time-curves(CTCs) to estimate perfusion-parameters(GTKM) and compare with SIC-based DL network(CNN_{SIGNAL}).

Approach: Two CNN networks were developed using CTC and SIC data(simulations and in-vivo). Performance of models was evaluated on simulated data with different protocols and experimental data.

Results: The CNN_{CONC} outperforms NLLS & CNN_{SIGNAL} in terms of speed, accuracy and smoothness of maps.

Impact: The proposed DL framework improves DCE-MRI analysis by providing more accurate and robust results in less time. It eliminates protocol dependence and holds the potential for routine clinical use in the diagnosis and treatment planning of brain tumor patients.

Introduction

Tracer-kinetic(TK) analysis(using GTKM, LTKM, etc) of DCE-MRI data provide valuable parameters related to physiology of tumor, which have shown great potential in diagnosis of tumors including gliomas[1]. Traditionally, these models use non-linear-least squares(NLLS) fitting approach for computing TK parameter maps. However, NLLS fitting takes long processing time and generates noisy maps.

Recently, deep-learning(DL) frameworks have been explored to overcome these challenges[2–6]. However, reported DL models rely on signal-intensity-time-curves(SIC) which remain susceptible to acquisition protocol variations. Moreover, concentration-time-curves(CTC) provide a more direct representation of the actual contrast agent concentration in tissues and can be easily computed from SIC without taking much time.

Here we hypothesise that DL models based on CTC are less susceptible to imaging protocol and have better generalizability compared to SIC-based models.

Methods

First, we implemented CNN-based framework(CNN_{SIGNAL})[6], which takes SICs, arterial-input-function(AIF) and T_{10} as inputs. The proposed model (CNN_{CON}) takes input as a fusion of AIF and CTCs only to estimate TK parameters(K^{trans}, V_e & V_p). Figure 1 shows overview of the methodology. DCE-MRI data consisted of 32-time frames.

Both frameworks used Toft's GTKM model parameter values estimated using NLLS fitting as ground truth. The training was done with batch size of 32 for 200 epochs; learning rate $2x10^{-4}$ with decay of 10^{-4} for both the networks with same activation function and optimizer. GTKM physics informed loss function was used for both networks.

Synthetic Data

We synthesized 3,600,000 CTCs with synthetic noise(SNR = 5-80). Synthetic CTCs were generated using GTKM from randomly sampled TK parameters in gray matter, white matter and tumor tissues (K^{trans} =[$1x10^{-5}$- $2x10^{-1}$ min^{-1}], V_p=[0.0005-1] and V_e=[0.02-0.6]). These CTCs were then converted to SICs using GTKM and population-based AIF[7]; where TR=6.3ms, Flip Angle(FA)θ=20°, r_1 = 3.5ms, S_o=1000 & T_{10}=1500ms. Each CTC and SIC size was 1X32 with time resolution of 0.025 min^{-1}.

Patient Data

51 pre-operative glioma patients were used in this study. MR scans were performed on a 3.0T MRI scanner(Ingenia, Philips Healthcare, and The Netherlands). DCE-MRI data was acquired for 20 slices and 32 time points with FOV=230×230, TR/TE = 3.0/6.27s, FA = 20° in addition to conventional MRI sequences and pre-contrast T_{10} maps. SICs were converted to CTCs using pre-contrast T_{10}.

For training and testing purposes, 80:20 split was performed randomly on both synthetic and patient data. Additionally, variations of SICs were synthesized with different TR and FA (-25%, +25%, 50% & 100%) from baseline CTCs to mimic different acquisition protocol (Figure 2). Both the networks were first trained and tested on synthetic data followed by transfer learning for patient data. Mean Absolute Error (MAE), structural-similarity-index-measure(SSIM) and root-mean-square(RMSE) were calculated for the three predicted parameters to assess the performance of both networks.

Results

The training and testing for synthetic data shows that proposed model predicted parameters with lower MAEs for K^{trans}, V_p and V_e(Figure 3). Similar performance translated onto patient dataset as well (Table 1) with better SSIM and RMSE scores for CNN_{CON}. The average processing time reduced from 45min (NLLS) to less than 5 min (for both CNN models) on regular desktop computer. Figure 4 shows that proposed network maps are even less noisy than other two approaches with higher precision and accuracy.

Discussion

The proposed network reduces the computational time substantially when compared with NLLS method. It additionally reduces variability associated with acquisition protocols by choosing CTCs over SICs(Figure 2) for capturing reliable physiological information from the tissues. Experimentation on synthetic data demonstrates how error propagates by variations in TR & FA when SICs are used as the input(Table 1).
The study suggest that CTCs should be preferred choice for DL frameworks to estimate faster and less noisy TK maps. However, it has been assessed on the simulation data and needs to be investigated on same patient's data acquired with variations in acquisition protocols. In future, proposed CNN_{CON} framework will be used to evaluate performance on other brain tumors from multiple centres and DCE-MRI data of different time frames or temporal resolutions.

Conclusion

The proposed DL network (CNN_{CON}) performs quantitative analysis of DCE-MRI data rapidly and with more accuracy compared to traditional NLLS fitting. It is insensitive to imaging protocols compared to reported DL model(CNN_{SIGNAL}). And hence offer better generalizability.

Acknowledgements

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Figures

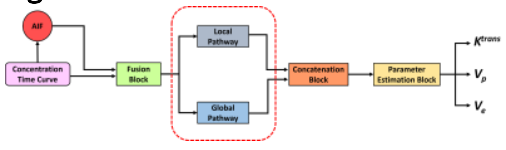

Figure 1 : Proposed Architecture Overview

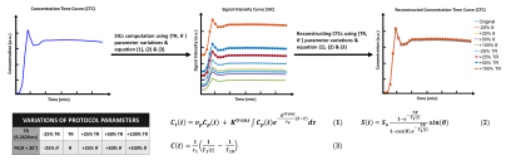

Figure 2 : Comparison between SICs and CTCs(baseline and reconstructed) computed using different variations of protocol parameters (TR & θ)

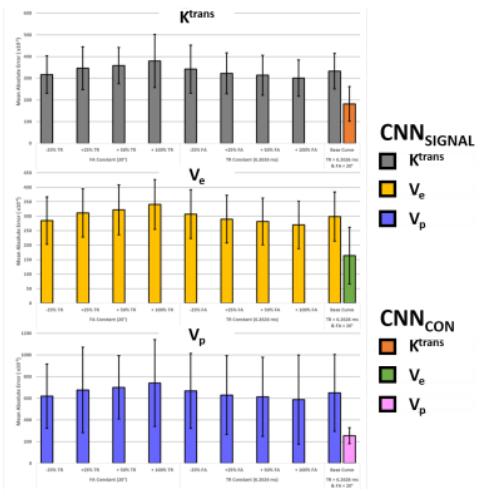

Figure 3 : Mean Absolute Error of CNN_{SIGNAL} and CNN_{CON} (all protocol parameter variations will have same MAEs)for K^{trans}, Vp & V_e

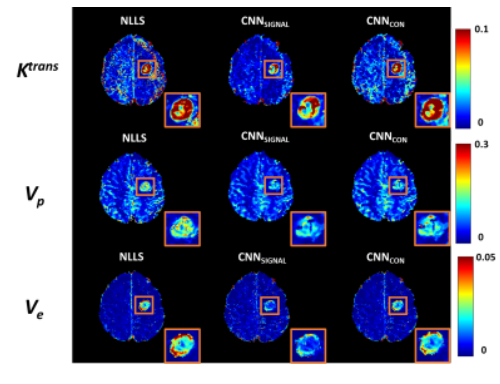

Figure 4 : TK Parametric maps : each row shows K^{trans}, Vp & V_e of NLLS(ground truth), CNN_{SIGNAL} and $CNN_{CONCENTRATION}$ respectively of representative case of High Grade Glioma(HGG)

	CNN_{SIGNAL}		CNN_{CON}	
	SSIM	RMSE	SSIM	RMSE
K^{trans}	0.91 ± 0.062	0.045 ± 0.0044	0.94 ± 0.027	0.040 ± 0.0026
V_p	0.89 ± 0.053	0.0079 ± 0.0002	0.93 ± 0.053	0.0078 ± 0.0003
V_e	0.90 ± 0.070	0.023 ±0.0039	0.88 ± 0.050	0.010 ± 0.0013

Table 1: SSIM & RMSE values of predicted TK parametric maps (K^{trans}, V_p & V_e respectively) on the test patient data for both the networks CNN_{SIGNAL} and CNN_{CON}