11-1-2022

An Unsupervised Autoencoder Developed from Dynamic Contrast-Enhanced (DCE)-MRI Datasets for Classification of Acute Tumor Response in an Animal Model

Hassan Bagher-Ebadian

Tavarekere N. Nagaraja

Glauber Cabral

Katelynn G. Farmer

Olivia Valadie

See next page for additional authors

Authors

Hassan Bagher-Ebadian, Tavarekere N. Nagaraja, Glauber Cabral, Katelynn G. Farmer, Olivia Valadie, P. Acharya, Benjamin Movsas, Stephen L. Brown, Indrin J. Chetty, and James R. Ewing

153

An Unsupervised Autoencoder Developed from Dynamic Contrast-Enhanced (DCE)-MRI Datasets for Classification of Acute Tumor Response in an Animal Model

H. Bagher-Ebadian,[1,2] T.N. Nagaraja,[3] G. Cabral,[3] K. Farmer,[1] O.G. Valadie,[1] P. Acharya,[2] B. Movsas,[1] S.L. Brown,[1] I.J. Chetty,[1] and J.R. Ewing[2,3]; [1]*Department of Radiation Oncology, Henry Ford Cancer Institute, Detroit, MI,* [2]*Oakland University, Rochester, MI,* [3]*Department of Neurology, Henry Ford Cancer Institute, Detroit, MI*

Purpose/Objective(s): Recent studies have shown that vascular parameters of brain tumors derived from DCE-MRI may act as potential biomarkers for radiation-induced acute effects. However, accurate characterization of the spatial regions affected by radiation therapy (RT) remains challenging. Here, we introduce an unsupervised adaptive model for classification and ranking of the RT-affected regions in an animal model of cerebral U-251n tumors.

Materials/Methods: Twenty-three immune-compromised-RNU rats were implanted with human U251n cancer cells to form an orthotopic glioma (IACUC #1509). For each rat, 28 days after implantation, two DCE-MRI studies (Dual Gradient Echo, DGE, FOV: 32×32 mm^2, $T_R/(T_{E1}\text{-}T_{E2}) = 24$ ms/(2 ms-4 ms), flip angle = 18°, 400 acquisitions, 1.55 sec interval with Magnevist contrast agent, CA injection at $\sim$ 24 sec) were performed 24h apart using a 7T MRI scanner. A single 20 Gy stereotactic radiation exposure was performed before the second MRI, which was acquired 1-6.5 hrs after RT. DCE-MRI analysis was done using a model selection technique to distinguish three different brain regions as follows: Normal vasculature (Model 1: No leakage, only plasma volume, v_p, is estimated), leaky tumor tissues with no back-flux to the vasculature (Model 2: v_p and forward volumetric transfer constant, K^{trans}, are estimated), and leaky tumor tissues with back-flux (Model 3: v_p, K^{trans}, and interstitial volume fraction, v_e, are estimated). Normalized time traces of DCE-MRI information (24 pre, and 24 post-RT for each rat, total of 64108 training datasets) of tumors and their soft surrounding normal tissues were extracted from the 3 different model regions. To eliminate high-dimensional data similarity, an unsupervised autoencoder (AE) was trained to map out the model-derived data into a feature space (latent variables, N=10). For each model, the pre and post RT latent variables were compared (by appropriate tests of significance: ANOVA/Welch, CI=95%) to reveal RT-discriminant features. Pearson correlation coefficients were used to compare the decoded data to rank the effect of RT on different models.

Results: The time trace of DCE-MRI information of rat brain in normal (Model 1, non-leaky) and highly permeable (Model 3) regions are less impacted by RT (Higher correlation between pre and post RT: r= 0.8518, p<0.0001 and r= 0.9040, p<0.0001 for Model 1 and Model 3, respectively) compared to the peritumoral regions pertaining to Model 2 (r= 0.8077, p<0.0001).

Conclusion: This pilot study suggests that among different brain regions, peritumoral zones (infiltrative tumor borders with enhanced rim) are highly affected by RT. Spatial assessment of RT-affected brain regions can play a key role in optimization of treatment planning in cancer patients, but presents a challenging task in conventional DCE-MRI. This study represents an important step toward classification and ranking the RT-affected brain spatial regions according to their vascular response following hypofractionated RT.

Author Disclosure: H. Bagher-Ebadian: None. T.N. Nagaraja: None. G. Cabral: None. K. Farmer: None. O.G. Valadie: None. P. Acharya: None. B. Movsas: None. S.L. Brown: None. I.J. Chetty: Research Grant; Varian Medical Systems, Inc, Philips Healthcare, ViewRay Inc. Honoraria; ViewRay Inc. Speaker's Bureau; ViewRay Inc. Travel Expenses; Varian Medical Systems, Inc, ViewRay Inc. Board member; Indo-American Society of Medical Physicists (IASMP. Member of the ASTRO Nominating Committee; ASTRO Nominating Committee. J.R. Ewing: None.

154

Deep Learning-Driven Real-Time Liver Tumor Localization via Optical Surface Imaging and Biomechanical Modeling

H.C. Shao,[1] T. Mengke,[1] H. Chen,[2] J. Wang,[1] and Y. Zhang[1]; [1]*UT Southwestern Medical Center, Dallas, TX,* [2]*Perception Vision Medical Technology, Guangzhou, Guangdong, China*

Purpose/Objective(s): To track liver tumors in real time via a deep learning-based framework, by exploring patient-specific correlations between patients' body surface maps and internal anatomical motion.

Materials/Methods: Real-time liver tumor localization was achieved via deformable registration-based motion estimation, in a two-step framework: (a) liver boundary motion estimation via deep features learnt from optical body surface imaging; and (b) intra-liver motion propagation via deep learning-based biomechanical modeling from liver boundary motion. In step (a), a patient-specific, fully-connected convolutional neural network (SurfCNN) predicts the motion of nodes residing on the boundary of a patient-specific reference liver mesh, by extracting saliency features from curvature entropy maps derived out of real-time optical body surface images. Subsequently, step (b) uses the liver boundary motion solved in (a) to infer intra-liver tumor motion, using a U-Net-style model (UNet-Bio) inspired by biomechanical modeling via finite element analysis (FEA). The cascaded framework was evaluated using a dataset of 8 liver cancer patients from our institute. Each patient had a 10-phase, contrast-enhanced 4D-CT set with liver and liver tumor contoured. To generate sufficient motion variations to train and test the patient-specific SurfCNN model, we augmented the dataset of each patient by simulating varying real-time motion patterns and magnitudes. The augmentation was achieved via a principal component analysis-based statistical model, expanding the nine inter-phase deformation-vector-fields (DVFs) of each 4D-CT into 1,728 different motion states including both rigid and deformable motion. Optical surface imaging was simulated from each motion state via extracted body surface maps, while corresponding liver boundary motion was derived via the augmented DVFs to supervise the training of SurfCNN. UNet-Bio, on the other hand, could be trained as a population-based model using supervisions from intra-liver DVFs solved by FEA-based biomechanical modeling. The liver tumor localization accuracy was assessed through Dice similarity coefficient (DSC), Hausdorff distance (HD), and center-of-mass-error (COME), by comparing the augmentation DVF-propagated 'ground-truth' liver tumor volumes against ones deformed by the cascaded framework.

Results: Tested using 576 unseen scenarios for each patient case, the cascaded SurfCNN and UNet-Bio scheme can localize liver tumors to 0.791 (mean) $\pm$ 0.141 (s.d.) in DSC, 3.6 $\pm$ 1.9 mm in HD, and 2.3 $\pm$ 1.7 mm in COME. In comparison, the prior reference image without deformable registration yielded 0.534 $\pm$ 0.277 in DSC, 8.3 $\pm$ 6.1 mm in HD and 6.8 $\pm$ 5.8 mm in COME. The whole model inference time was less than 100 milliseconds, satisfying the temporal constraints of real-time imaging.

Conclusion: The deep learning-based framework allows accurate 3D liver tumor tracking in real-time via non-ionizing, marker-less, and high frame-rate optical surface imaging.

Author Disclosure: H. Shao: None. T. Mengke: None. H. Chen: None. J. Wang: Research Grant; NIH, CPRIT. Y. Zhang: Research Grant; NIH.

155

Voxel-Wise GBM Recurrence Prediction Based on Sparse Attention Multi-Modal MR Image Fusion Coupling with Stem Cell Niches Proximity Estimation

C. Jiao,[1] Y. Lao,[2] A. Vassantachart,[3] M. Shiroishi,[4] G. Zada,[5] E.L. Chang,[1] Z. Fan,[4] K. Sheng,[6] and W. Yang[1]; [1]*Department of Radiation Oncology, Keck School of Medicine, University of Southern California, Los Angeles, CA,* [2]*Department of Radiation Oncology, University of California, Los Angeles, Los Angeles, CA,* [3]*Department of Radiation Oncology, LAC+USC Medical Center, Los Angeles, CA,* [4]*Department of Radiology, Keck School of Medicine, University of Southern California, Los Angeles, CA,* [5]*Department of*