

## Dynamic Contrast Enhanced MRI for Informing Cancer Treatment: Challenges and Outlook for Use in Cancer Modeling

Ryan T. Woodall<sup>\*1</sup>, Russell C. Rockne<sup>2</sup>, and Jennifer M. Munson<sup>3</sup>

<sup>1</sup> City of Hope, Division of Mathematical Oncology, Department of Computational and Quantitative Medicine, Beckman Research Institute, City of Hope, 1500 E Duarte Rd, Bldg 74, Duarte, CA 91010, USA, rwoodall@coh.org

<sup>2</sup> City of Hope, Division of Mathematical Oncology, Department of Computational and Quantitative Medicine, Beckman Research Institute, City of Hope, 1500 E Duarte Rd, Bldg 74, Duarte, CA 91010, USA, rrockne@coh.org

<sup>3</sup> Fralin Biomedical Research Institute, Virginia Polytechnic Institute and State University, Roanoke, VA, USA, munsonj@vt.edu

**Key Words:** *Medical Imaging, Cancer, Computing Methods, Treatment Prediction*

DCE-MRI contains a wealth of information concerning perfusion and fluid transport within tissues, especially in tumors where abnormal vessel development allows for contrast agent accumulation. Most researchers using DCE-MRI rely on compartmental models of contrast agent, fitting individual voxels to an ordinary differential equation (ODE). While parameters derived from this type of model fitting have been useful in applications such as delineating responders from non-responders[1], in test-retest analysis of DCE-MRI Tofts-Kety parameterization of patients undergoing treatment for glioblastoma, it was found that changes in  $K^{trans}$  must be greater than 72% to detect a physiological change, increased to 83% when hand-drawn vascular input functions (VIFs) are used instead of automated methodologies[2]. It is our goal to use mathematical methods to further leverage the information from DCE-MRI, and increase standardized utilization in the clinic through understanding of underlying physics.

In this abstract we a VIF-free method of DCE-MRI parameterization using auto-encoding neural networks (ANNs). Such methods, when applied to data from the QIN glioblastoma treatment response dataset, extract similar parametric information from compartmental ODE methods ( $CCC_{K^{trans}} = 0.82$ ) without the use of an arterial input function. We anticipate that standardized ANN architecture will lead to better prediction of treatment response, or delineating disease type from perfusion data, while preserving physical interpretability of the ANN embeddings. Additionally, we present a data-driven inverse model of DCE-MRI which (while requiring a VIF) allows for extracting local perfusion parameters, and the maximum likelihood steady-state interstitial fluid velocity field within the tumor stroma. In a mouse K-Luc glioma model, our inverse model reproduces spatiotemporal DCE-MRI data from initial conditions with high accuracy ( $CCC = 0.88$ ). We anticipate further development of these methods will guide personalized treatments for CAR-T infusions, stereotactic radiation therapy, and systemic drug delivery.

### REFERENCES

- [1] J. Zhang *et al.*, “Clinical Applications of Contrast-Enhanced Perfusion MRI Techniques in Gliomas: Recent Advances and Current Challenges,” *Contrast Media Mol. Imaging*, vol. 2017, pp. 1–27, 2017, doi: 10.1155/2017/7064120.
- [2] R. T. Woodall *et al.*, “Repeatability of tumor perfusion kinetics from dynamic contrast-enhanced MRI in glioblastoma,” *Neuro-Oncology Adv.*, vol. 3, no. 1, Jan. 2021, doi: 10.1093/oaajnl/vdab174.

