Abstract: Deep Probabilistic Modeling of Glioma Growth

Jens Petersen^{1,2,3}, Paul F. Jäger¹, Fabian Isensee¹, Simon A. A. Kohl^{1*},
Ulf Neuberger², Wolfgang Wick⁴, Jürgen Debus^{5,6,7}, Sabine Heiland²,
Martin Bendszus², Philipp Kikingereder², Klaus H. Maier-Hein¹

¹Div. of Medical Image Computing, German Cancer Research Center

²Dept. of Neuroradiology, Heidelberg University Hospital

³Dept. of Physics & Astronomy, Heidelberg University

⁴Dept. of Neurooncology, Heidelberg University Hospital

⁵Div. of Molecular and Translational Radiation Oncology, Heidelberg Institute of
Radiation Oncology (HIRO)

⁶Heidelberg Ion-Beam Therapy Center (HIT), Heidelberg University Hospital

⁷Clinical Cooperation Unit Radiation Oncology, German Cancer Research Center

jens.petersen@dkfz.de

Existing approaches to modeling the dynamics of brain tumor growth, specifically glioma, employ biologically inspired models of cell diffusion, using image data to estimate the associated parameters. In this work, we propose to learn growth dynamics directly from annotated MR image data, without specifying an explicit model, leveraging recent developments in deep generative models. We further assume that imaging is ambiguous with respect to the underlying disease, which is reflected in our approach in that it doesn't predict a single growth estimate but instead estimates a distribution of plausible changes for a given tumor. In plain words, we're not interested in the question "How much will the tumor grow (or shrink)?" but instead "If the tumor were to grow (or shrink), what would it look like?". From a clinical perspective, this is relevant for example in radiation therapy, where a margin of possible infiltration around the tumor will also be irradiated. This is currently done in a rather crude fashion by isotropically expanding the tumor's outline, thus more informed estimates of growth patterns could help spare healthy tissue. In summary, our contributions are the following: 1. We frame tumor growth modeling as a model-free learning problem, so that all dynamics are inferred directly from data. 2. We present evidence that our approach learns a distribution of plausible growth trajectories, conditioned on previous observations of the same tumor. [1]

References

1. Petersen J, Jäger PF, Isensee F, et al. Deep probabilistic modeling of glioma growth. In: MICCAI 2019. vol. 11765 of LNCS. Springer; 2019. p. 806–814.

* now with DeepMind, the Karlsruhe Institute of Technology