Deep Probabilistic Modeling of Glioma Growth

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Summary

- Tumor growth usually modeled from diffusion equations (bottom up), we try to model it solely from image statistics (top down).
- Probabilistic segmentation architecture [1] to predict distribution of possible tumor appearances from two previous MRI scans
- Doesn't require explicit growth model
- Qualitatively realistic growth patterns
- Can sample many hypotheses
- Open Source implementation https://github.com/jenspetersen/probabilistic-unet
- Needs lots of data
- Can't represent spatial variations or multiple foci
- Timesteps required to be equidistant

Introduction

Existing approaches usually model tumor growth using diffusion equations, evolving an initial density bottom-up. In contrast, we try to model it top-down by observing many real growth trajectories. The underlying hypothesis of our approach is that tumor growth is at least in part stochastic so that it's not possible to predict a single correct growth trajectory in time from image data alone. Hence, our aim is to model a distribution of possible changes of a tumor given the current and one previous observation.

Method

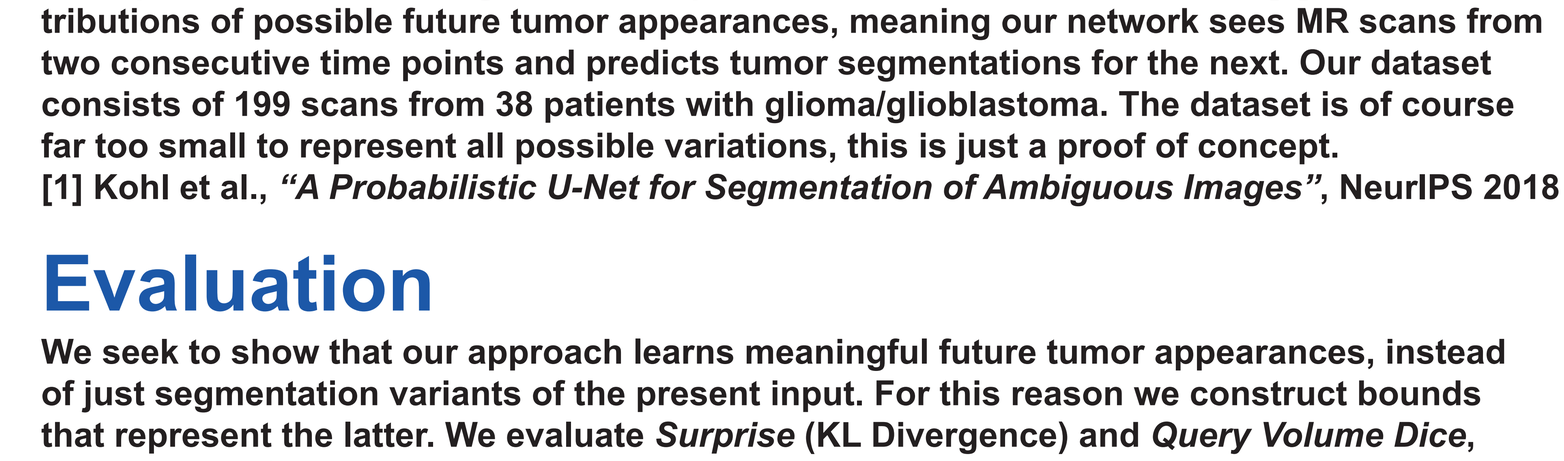
We represent tumors in segmentation space and use a Probabilistic U-Net [1] to model distributions of possible future tumor appearances, meaning our network sees MR scans from two consecutive time points and predicts tumor segmentations for the next. Our dataset consists of 199 scans from 38 patients with glioma/glioblastoma. The dataset is of course far too small to represent all possible variations, this is just a proof of concept.

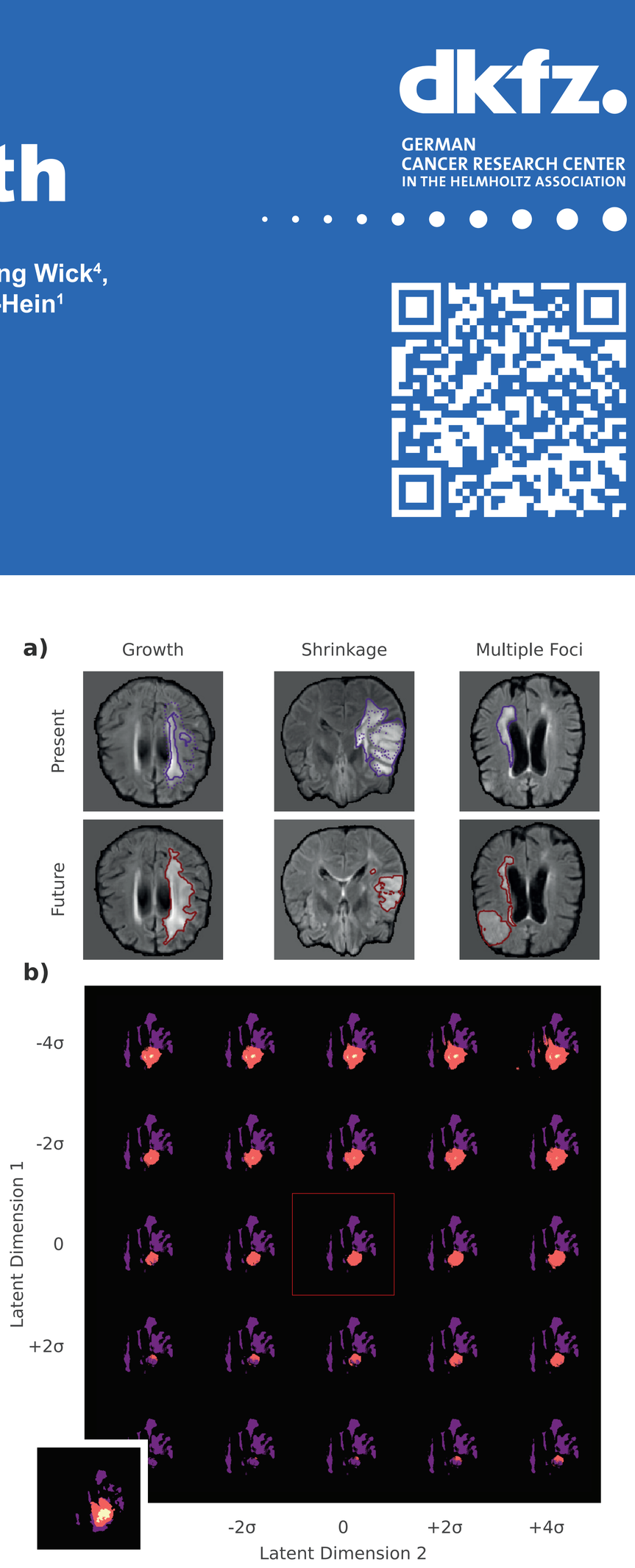
[1] Kohl et al., *"A Probabilistic U-Net for Segmentation of Ambiguous Images"*, NeurIPS 2018

Evaluation

We seek to show that our approach learns meaningful future tumor appearances, instead of just segmentation variants of the present input. For this reason we construct bounds that represent the latter. We evaluate *Surprise* (KL Divergence) and *Query Volume Dice*, i.e. the score from the sample that best matches the ground truth in volume. Large change = Highest 10%, Moderate change = Above mean without previous.

	Input	Output	Evaluation
Our Model	Past & Present	Future	Future
Upper Bound	Future	Future	Future
Lower Bound	Present	Present	Future





Results

Qualitative

(a) Prior mean prediction (solid purple) and sample with best volume match (dashed purple) as well as future ground truth (red). The approach is able to model growth or shrinkage, but is unable to represent tumors with both growth and shrinkage in different locations. (b) Regular grid samples from prior, with mean highlighted in red and ground truth inlay in bottom left corner (unrelated to (a)). Dimension 1 encodes tumor core size (enhancing tumor and necrosis) while dimension 2 encodes enhancing tumor size. The third latent dimension, not shown here, captures small variations in edema size. Purple – Edema, Orange – Enhancing, Yellow – Necrosis

Quantitative

Median indicated in red, p-values from Wilcoxon ranksum test. For large changes, our approach can represent the future much better than the lower bound. The low surprise in our model indicates that our model's learned prior assigns higher likelihood than the lower bound to the real future tumor appearance.

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