

Tumor Progression Mapping: An Intuitive Visualization of Glioblastoma Progression in MR Follow-ups

Christian Weber¹, Bram Stieljes², Joanna Polanska³, Franciszek Binczyk^{3,4}, Rafal Tarnawski⁴, Barbara Bobek-Billewicz⁴, Timo Rodi², Sebastian Regnery², and Klaus H. Maier-Hein^{1,2}

¹Medical and Biological Informatics, German Cancer Research Center, Heidelberg, Baden Württemberg, Germany, ²Quantitative Image-based Disease Characterization, German Cancer Research Center, Heidelberg, Baden Württemberg, Germany, ³Silesian University of Technology, Gliwice, Poland, ⁴Maria Skłodowska-Curie Memorial Cancer Center and Institute of Oncology, Gliwice, Poland

Target audience: Radiologists evaluating tumor growth.

Purpose: Tumor growth is commonly monitored by following the tumor diameter. However, this is infeasible for glioblastomas that commonly feature erratic growth and unsharp margins [1]. Due to the complex shape and short observation interval, the changes in tumor volume from time step to time step may be subtle and progression can easily be overlooked, even more so as this task is highly challenging involving to revisit previous acquisitions to capture a sense of the progression. Often steady growth is only recognized after several subsequent examinations, when the progression becomes apparent. We present a method that aims at providing a compact overview of the history of a patient's tumor development and highlight areas of potential change in the MRI. This may aid the neuroradiological diagnostic process by providing an intuitive visualization that reduces the complexity of the data and in which regions of interest are pin-pointed that are relevant for further investigation, thereby saving time and increasing sensitivity in detection of tumor progression.

Methods: Twenty glioblastoma patients were included and followed with a mean of 10.5 follow ups per patient with a mean time between follow ups of 2.3 months. We used the T2w FLAIR for tumor segmentation (SIEMENS Aera 1.5T) with the following parameters: 21 slices with an in-plane voxel size of $0.625 \times 0.625 \text{ mm}^2$ and 5mm slice thickness (1mm gap); TR/TE/TI=90/108/25 ms. For all patients and time steps, the gross tumor volume was manually segmented by an expert were resampled to a standard reference of $1 \times 1 \times 1 \text{ mm}^3$ voxel size to account for the variety of different image resolutions present in the data set. In a second step, all images were registered to the first T2w image acquired of the according patient using a rigid registration algorithm of ITK [4]. Segmentations were interpolated using the shape-based method described in [3] and on the result the respective transformation was applied in order to minimize artifacts. All data of one patient was then visualized in a grid, where different slices of an MRI were represented as rows and different time points are represented by columns, providing a condensed view over the complete spatiotemporal course of the progression. The segmentations were overlaid via shifting reference: The segmentation of the previous time point was depicted in green and the current time point was depicted in red. The overlap between both was shown in yellow (c.f. Fig. 1).

Results: Using the above described method we constructed progression maps for all 20 data sets to visualize the individual growth patterns. As can be taken from Fig. 2, the maps provide an intuitive visualization of the history of tumor volume changes where progression and shrinking are mapped as red and green respectively. However, not all indicated areas were caused by actual volume changes and occasionally reflect other effects such as topological changes due to surgery or segmentation inaccuracies. We found that these effects could easily be recognized by examining the original data sets. In Fig. 2, the maps resemble states before ($t=0$) and after ($t=1$) tumor resection as well as consecutive reduction of the post-operative edema (green area, $t>1$) and finally re-growth of the tumor (red area, $t>1$).

Discussion: Progression maps provide an intuitive and compact visualization of the complex evolution of glioblastomas over time, thus reducing the complexity of the 4D data in a way that supports radiologists in their clinical routine of retracing changes in brain tissue due to several complex interactions such as treatment, edema and tumor growth. Furthermore, they may aid radiologists to recognize subtle growth patterns that can be easily overlooked. Currently there are two major limitations. First, strong effects on brain geometry (e.g. a resection) cannot be fully encompassed using a rigid registration and thus can lead to areas of misalignment and consecutive artifacts in the color-coded maps. Secondly, even though the shape-based interpolation of segmentations reduces artifacts, interpolation between thick slices is prone to errors and may also introduce artifacts to the maps. Therefore these maps have to be seen as overviews that highlight regions that should be considered with extra attention.

Conclusion: Tumor progression maps are able to effectively summarize complex growth patterns and highlight subtle changes in tumor volume.

References:

[1] Osborn, A. G. *Diagnostic neuroradiology* (Vol. 343). 1994. St. Louis: Mosby. [2] Nolden *et al.* *Int J Comput Assist Radiol Surg.* 2013 Jul;8(4):607-20. [3] Herman *et al.* *IEEE Computer Graphics and Applications* 1992; 12(3), 69-79. [4] Yoo *et al.* *Studies in health technology and informatics* 2002; 586-592.

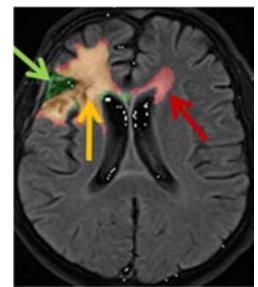


Fig.1: Depiction of the temporal tissue change: axial T2w FLAIR with previous (green), current(red) and overlap (yellow).

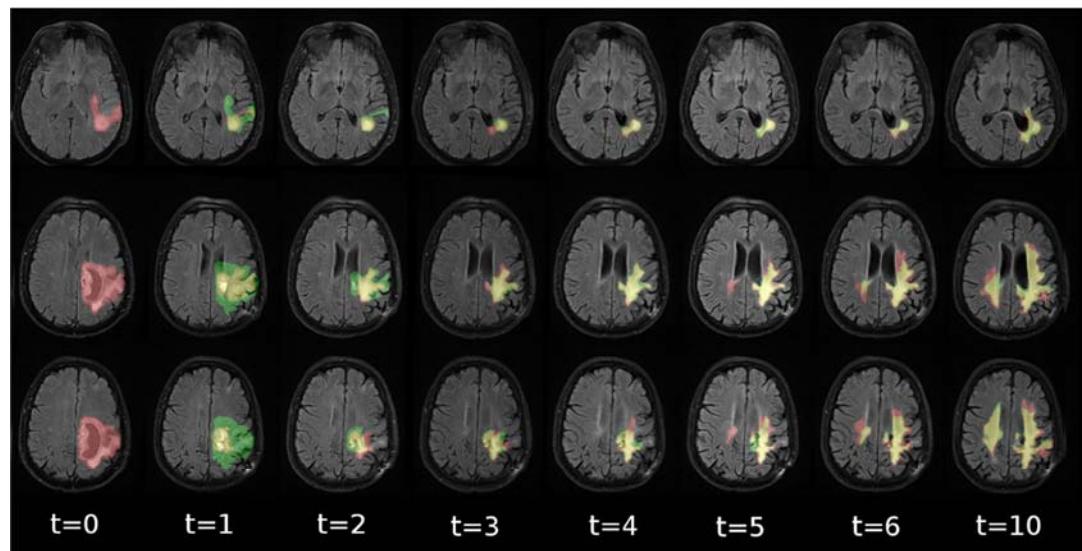


Fig.2: Display of the color-coded time course of tumor volume change (color coding as defined in Fig. 1). Note the smooth transition from time point to time point and the comprehensive overview offered by these maps.