TuMore: Generation of Synthetic Brain Tumor MRI Data for Deep Learning Based Segmentation Approaches

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INTRODUCTION

Accurate segmentation and measurement of brain tumors plays an important role in clinical practice and research, as it is critical for treatment planning and monitoring of tumor growth. However, brain tumor segmentation is one of the most challenging tasks in medical image analysis. Since manual segmentations are subjective, time consuming and neither accurate nor reliable, there exists a need for objective, robust and fast automated segmentation methods that provide competitive performance. Therefore, deep learning based approaches are gaining interest in the field of medical image segmentation. When the training data set is large enough, deep learning approaches can be extremely effective, but in domains like medicine, only limited data is available in the majority of cases. Due to this reason, we propose a method that allows to create a large dataset of brain MRI (Magnetic Resonance Imaging) images containing synthetic brain tumors - glioblastomas more specifically - and the corresponding ground truth, that can be subsequently used to train deep neural networks.

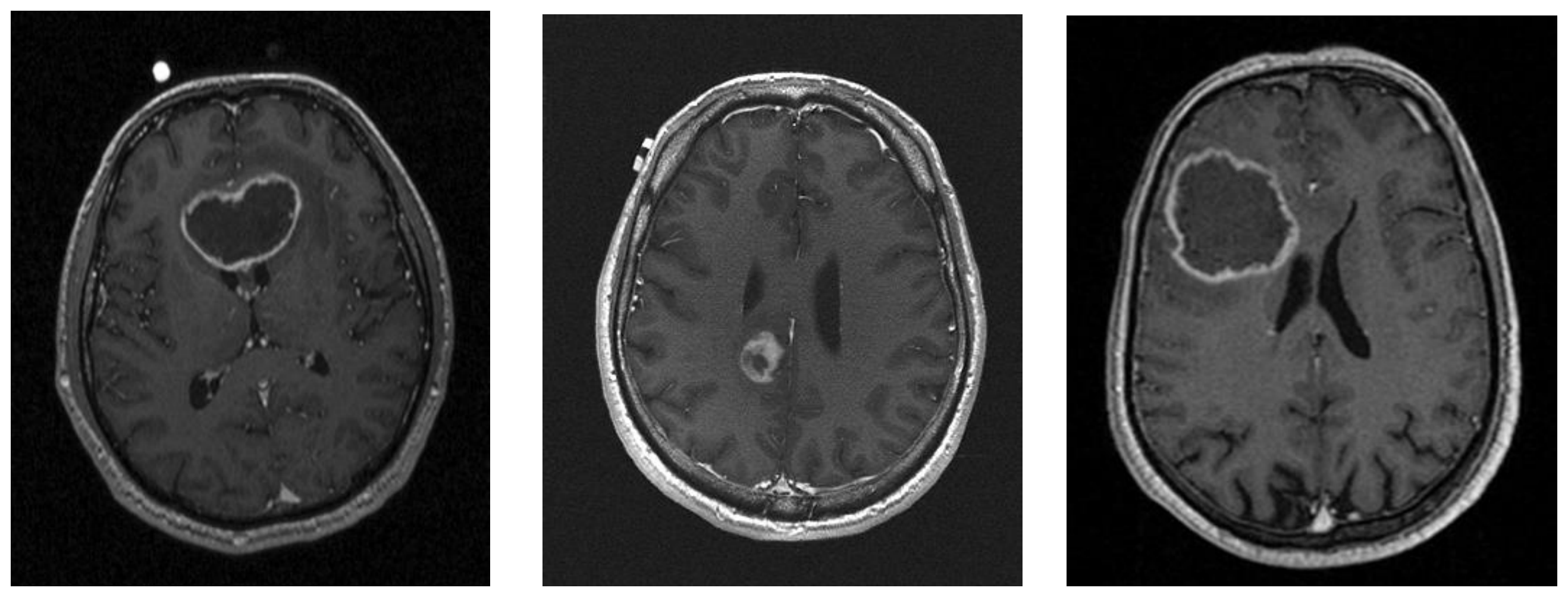

Fig. 1 Three examples of brain MRI images (T1 weighted, contrast enhanced) with real glioblastomas and a tumor mass effect

Typical radiographic features of glioblastomas:

→ thick, irregular-enhancing margins
→ central necrotic core

In Figure 1, three examples of brain MRI images with real glioblastomas and a real tumor mass effect can be seen. The typical radiographic features of glioblastomas are clearly visible.

METHODS

The software application was developed using the medical imaging and visualization platform MeVisLab, which provides an interface for connecting existing and new, proprietary algorithms using a dataflow network. In order to receive an approximation of a sphere, an icosahedron was recursively refined [1]-[3] and a special displacement algorithm was applied to the resulting vertices. The idea behind this displacement algorithm is to randomly choose a vertex (*V_chosen*) according to a uniform distribution. Then, the distance between *V_chosen* and the center of the polyhedron is increased. This results in an elevation of the corresponding vertex. To make the deformation look natural, also the remaining vertices are displaced accordingly. In order to determine the strength of displacement for each vertex, all vertices are categorized in displacement levels k, according to the minimum number of edges that are required to reach *V_chosen*. Finally, the displacement of *V_chosen* and the remaining vertices is achieved by multiplying the x, y and z coordinate of each vertex with factor ε(k) (see formula 1), where k denotes the displacement level, d (which is randomly chosen according to a uniform distribution on the interval [1, 2.5]) indicates the initial strength of displacement and m is a decay factor of 0.97.

$$\varepsilon(k) = \begin{cases} 1+d, & k=0 \\ 1+d\cdot m, & k=1 \\ 1+d\cdot m^{2k}, & k>1 \end{cases} \qquad (1)$$

This process is repeated for seven times. Then, the synthetic tumor is inserted into a brain MRI image of a healthy subject.

A simplified tumor mass effect was simulated by deforming the brain MRI image around the artificial glioblastoma according to a displacement field. Since the force, that is applied to the brain by a tumor mass, is an outward radial force, that originates from the initial tumor region and weakens by distance, the required displacement field was constructed in the following way: First, the 3D Euclidean distance transform of the sphere was calculated to receive a gradually decreasing intensity from the tumor center to the edges. Then, a gradient filter was applied to the Euclidian distance transform, leading to a dense vector field. Afterwards, the Euclidian distance transform was normalized and multiplied with a factor, that can be varied depending on the desired strength of deformation. Finally, the result was multiplied with the previously calculated gradient field. This leads to a displacement field that lets the strength of the deformation weaken by distance.

RESULTS

In Figure 2 three brain MRI images containing synthetic glioblastomas with a simulated tumor mass effect can be seen. The typical radiographic features of glioblastomas are clearly visible in the synthetic brain MRI data. As can be seen by comparing the real MRI images (figure 1) and the synthetic MRI images (figure 2), the proposed method allows to generate quite realistic looking glioblastomas, that comply with the basic radiographic features of real glioblastomas.

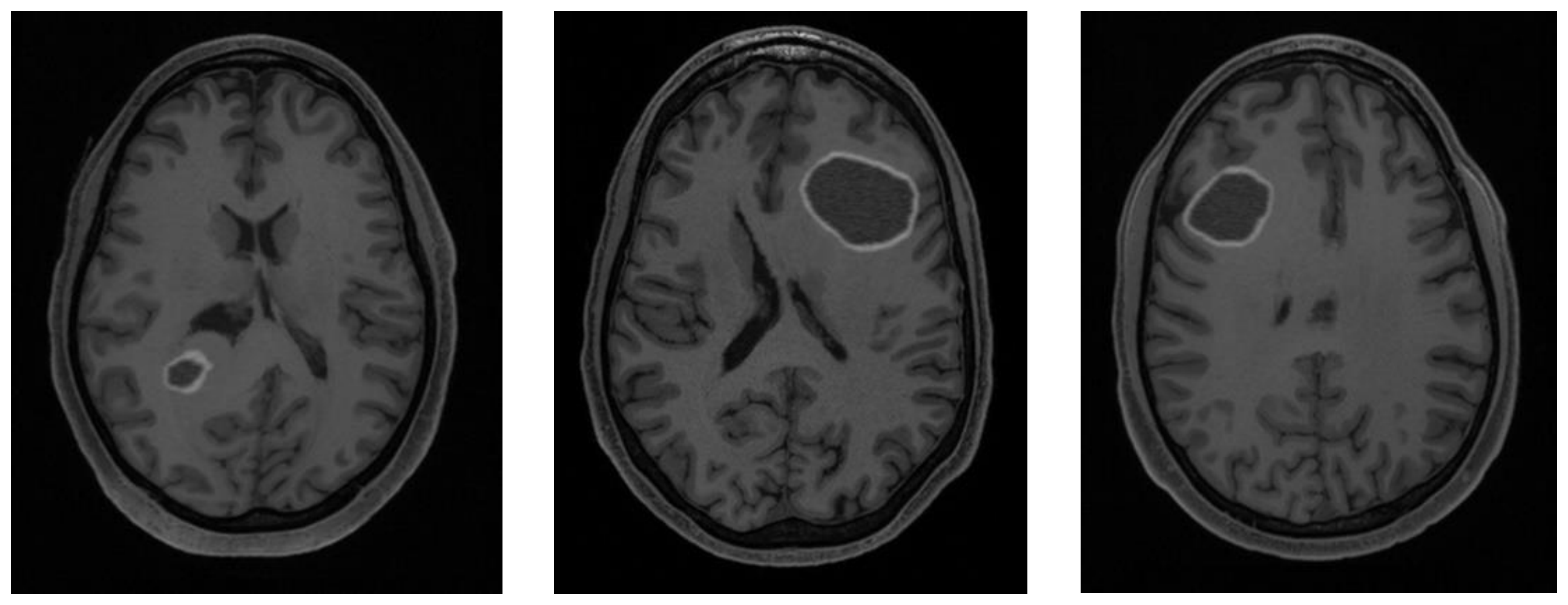

Fig. 2 Brain MRI images containing synthetic glioblastomas with a simulated tumor mass effect

CONCLUSIONS

1. **With the proposed method it is possible to generate realistic looking glioblastomas, insert them into brain MRI images of healthy subjects and simulate the tumor mass effect;**
2. **The position, shape and size of the tumor is already exactly known. Therefore, a very precise ground truth can easily be created without any action of a human expert;**
3. **The proposed method is simple, but still has the ability to simulate all crucial characteristics of glioblastomas (appearance of the enhancing tumor and the necrotic core) in T1 weighted contrast-enhanced MRI images;**
4. **An easy application via MeVisLab is presented.**

Further adaptations of the proposed approach could be to simulate the effect of Gadolinium to the brain in MRI images and simulate edema or fiber bundles. The proposed approach may also be applied for other areas of clinical oncology and diagnostic medicine)

REFERENCES

1. Egger, J., Mostarkic, Z., Grosskopf, S. and Freisleben, B. “A Fast Vessel Centerline Extraction Algorithm for Catheter Simulation,” 20th IEEE International Symposium on Computer-Based Medical Systems, Maribor, Slovenia, pp. 177-182, IEEE Press (2007).
2. Egger, J. et al. “GBM Volumetry using the 3D Slicer Medical Image Computing Platform,” Sci Rep., Nature Publishing Group (NPG), 3:1364 (2013).
3. Egger, J. et al. “Integration of the OpenIGTlink network protocol for image guided therapy with the medical platform MeVisLab,” The international Journal of medical Robotics and Computer assisted Surgery, 8(3):282-390 (2012).

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