Improving the clinical followup of meningiomas with mathematical modeling and AI

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Meningiomas rank among the most common intracranial tumors. Because they are usually benign, patients are routinely monitored by surgeons until the growth of these tumors poses a significant health risk. Continuous monitoring of these tumors is recognized as an important aspect of patient care. After the discovery of a meningioma, surgeons usually schedule multiple MRI examinations. The timing and frequency of these exams are determined by the medical team depending on their expertise and familiarity with this type of tumor. Usually, the decisions are made based on some characteristics that result from the segmentation of the tumor. Thus, the effectiveness of patient follow-up depends on the accuracy of these segmentation assessments. Currently, this challenging and time-consuming task is performed by surgeons. To assist them in this work, we evaluated different neural network architectures using a dataset of 333 meningiomas. Our goal was to use 5-fold crossvalidation to identify the neural network that best delineated the meningiomas. Comparing Dice, AUC, and volumetric scores –three metrics commonly used to evaluate segmentation network performance– showed that a Basic Unet architecture with an average Dice score of 0.74 produced the best results. This model shows that it can handle meningiomas of different shapes and sizes, although it may encounter difficulties in identifying meningiomas in certain positions.

Because monitoring tumor development remains essential for decision making, it may be useful for clinicians to understand the growth patterns of meningiomas. To facilitate this understanding, we investigated four mathematical models: exponential, linear, power, and Gompertz models, which are commonly used to characterize the growth of intracranial tumors using at leat 3 MRI exams obtained at different times. These models were evaluated twice using a robust mixed-effects approach: once with volumes obtained from our segmentation model and a second time with segmentations provided by neurosurgeons. In both cases, the Gompertz model produced better and more reliable results. Consequently, the growth rate of meningiomas can be calculated based on the estimated Gompertz parameters and reported to the surgeons.

To further this work, our goal was to predict the previously computed growth rates using less MRI exams. First, we applied the same population-based approach as before, using a leave-one-out method for prediction and the Gompertz model. In this method, we temporarily excluded the last images of each patient from the cohort and applied the same protocol as described previously. These results were then compared with those obtained by deep learning techniques. In this last approach, the intermediate features calculated by our segmentation model were fed into a regression network to predict the desired growth rate. The two approaches are compared in this presentation.