

Machine Learning Tumor Segmentation for Bacteria-Based Cancer Therapy

Irika Katiyar, University of Southern California; Omar Ali, College of Marin; Qiuhong He, Purdue University; Yuanwei Jin, University of Maryland Eastern Shore; Envue Lu, Salisbury University

Abstract

Bacteria-based cancer therapy (BBCT) is a novel form of cancer therapy in which bacteria are genetically engineered to destroy tumor tissue [1]. Monitoring the tissue destruction can be accomplished using diffusion-weighted imaging (DWI), by tracking the change in area of the living portion of the tumor over the observational period. Our objective in this study is to build on current models of deep learning to develop an optimal architecture and program structure for identifying alive tumor area from DWI images.

Purpose

A 2022 study [2] utilized image segmentation methods with a U-Net architecture to predict the area of tumor tissue given a DWI image. To expand the applicability of their study and improve upon the findings, our study has two main objectives: develop a package that can be used by medical professionals, and improve upon the existing model to more accurately predict tumor masks through two parts: addressing the class imbalance issues inherent in the existing dataset, and introducing our own hand-labeled dataset to improve model generalization on new images.

Methods

We began by creating a labeled dataset to denote alive tumor tissue, and increased our dataset size to almost triple the original from data collected in [3]. We used an add_sample_weights function to deal with the class imbalance when training our model, whose weights were calculated using the following:

weight for 0 (non-tumor class): (1 / n) * (t / 2.0) weight for 1 (tumor class: (1 / p) * (t / 2.0) - offset, where n is the # of negative pixels, p is the # of positive pixels, t is the total # of pixels, and offset is a decimal number. Finally, using imaging and deep learning libraries in Python, we created an easy to use package that outputs a ground truth visualization.

Results

Our model predictions on this original dataset align with the previous years model in addition to Dr. He's team calculations in showing the success of BBCT, shown in Figure 1.

The addition of new data brought our dataset size from 1280 to 1800 with augmentation and we were able to achieve high precision with this model as well.



The introduction of class weights to the models also allowed for further improvement in results. We found with the original dataset, a weight of 3.552 for white pixels and 0.535 for black pixels yielded the best results, while weights of 5.740 for white pixels and 0.527 for black pixels were best with the addition of new data. Figure 2 displays an example of the improvement of predictions after the implementation of weighted classes.



Fig 2 Difference in predictions with class weights (new data)

Finally, we were able to successfully create a package that displayed ground truth visualization in order to validate the output of our model. Figure 3 displays an example of our final visualization, with the top row displaying contours of our prediction overlaid on the original DWI input image, and the bottom row displaying the predicted mask.



Fig 3 Final visualization output

Fig 1 Dead tumor volume over three day





Conclusions

We hope that our model is applicable to various forms of data and can be used by medical professionals for tumor area prediction. With the development of BBCT and its clear potential in the medical world, this model has the potential to be extremely impactful, not only in determining the effectiveness of novel methodologies such as BBCT but also in helping medical professionals in interpreting DWI images from the trials that are currently ongoing.

References

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- 2 Emily Hitchcock, Sarah Hodges, Kevin Zuang, Rosy J. Lu, Yuanwei Jin, Qiuhong He, and Enyue Lu. Image processing and machine learning for tumor tissue detection using mri images in bacteria based cancer therapy. In 2022 IEEE/ACM International Conference on Big Data Computing, Applications and Technologies (BDCAT), pages 288-296, 2022.
- 3 Qiuhong He, V. Chibisov, G. Ramus, H. Liu, K-T. Yung, and H. Zhu. Longitudinal diffusion-weighted mri study of the tumor tissue destruction process induced by novel attenuated salmonella typhimurium expressing protein drugs. Proceedings of the International Society for Magnetic Resonance in Medicine, 15:2836, 2007.

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