

Contrast the Automated Brain Tumor Segmentation between Traditional Method and Deep Learning Approach

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Abstract - Accurate segmentation of brain tumors is crucial for their detection and treatment. Manual segmentation, though widely used, is labor-intensive and subject to human error. This project investigates the effectiveness of two distinct approaches: Support Vector Machine (SVM) representing traditional methods, and UNet, a deep learning approach. Through comparative analysis, we aim to evaluate their accuracy, efficiency, and performance in segmenting brain tumors from medical imaging data. By leveraging automated segmentation techniques, we seek to enhance accuracy and consistency while reducing the burden on radiologists. Our findings contribute to advancing automated brain tumor segmentation methods, with potential implications for improving diagnosis and treatment outcomes.

Key Terms: Brain tumor segmentation, SVM, UNet, Medical Imaging, Accuracy, CNNs

Brain tumor segmentation plays a pivotal role in the diagnosis and treatment planning of patients suffering from brain-related pathologies. Accurate delineation of tumor boundaries from medical imaging data is critical for precise localization, monitoring disease progression, and assessing treatment response. While manual segmentation by expert radiologists remains the gold standard, it is inherently labor-intensive, time-consuming, and subject to inter- and intra-observer variability.

In recent years, the advent of automated segmentation techniques has revolutionized medical image analysis by offering the promise of faster, more consistent, and reproducible tumor delineation. Among these techniques, machine learning-based approaches have emerged as particularly promising, owing to their ability to learn complex patterns and features directly from data.

This project focuses on comparing the efficacy of two distinct automated segmentation methodologies: Support Vector Machine (SVM), representing conventional machine learning

1. INTRODUCTION

techniques, and UNet, a state-of-the-art deep learning architecture tailored for biomedical image segmentation tasks. By contrasting these approaches, we aim to evaluate their performance in terms of accuracy, computational efficiency, and generalization across diverse datasets.

The primary objective of this study is to provide insights into the strengths and limitations of SVM and UNet for brain tumor segmentation, thereby facilitating informed decision-making regarding their adoption in clinical practice. Additionally, we seek to contribute to the growing body of knowledge in the field of medical image analysis by elucidating the comparative merits of traditional machine learning and deep learning paradigms in this context.

Through rigorous experimentation and comprehensive evaluation on benchmark datasets, we endeavor to elucidate the relative advantages and challenges associated with each methodology. Ultimately, our findings hold the potential to inform the development of more robust and reliable automated segmentation tools, with the overarching goal of improving patient care and clinical outcomes in the management of brain tumors.

2. MATERIALS AND METHODS

Support Vector Machine:

Data Collection and Preprocessing:

For SVM, the training set comprises a total of 1222 images, with 395 images labeled as

no tumor and 827 images labeled as pituitary tumor. The preprocessing begins by reshaping the features, converting each image in the dataset into a flattened, one-dimensional array while preserving the number of samples.

Following reshaping, the dataset is split into training and testing sets. Approximately 20% of the data is set aside for testing, while the remaining portion is utilized for training the model. Subsequently, normalization is applied to the pixel values of both the training and testing sets, scaling them to fall within a standardized range of 0 to 1. This standardization ensures consistent processing across the dataset and can improve the performance of machine learning algorithms.

Methodology:

The methodology involves several key steps. Firstly, the model is initialized by importing the classifier Support Vector Machine (SVC), from the scikit-learn library. An instance of the SVC, known as the Support Vector Classifier, is then created with default hyperparameters.

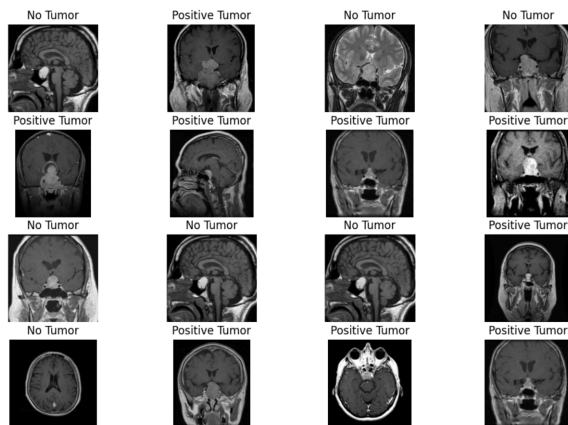
Next, the SVC model, denoted as "sv," undergoes training using the fit method, where the training data (xtrain, ytrain) is utilized. Through this process, the fit method learns the optimal decision boundary that effectively separates the classes within the feature space.

Following training, the trained SVC model is subjected to evaluation on both the training and testing datasets. This evaluation is conducted using the score method, which computes the

accuracy of the model's predictions. The resulting accuracy scores for both the training and testing datasets are then printed to facilitate an assessment of the model's performance.

Lastly, the interpretation of the obtained scores is crucial for understanding the model's behavior. The training score provides insight into how well the model fits the training data, with a higher score potentially indicating overfitting. Conversely, the testing score offers an indication of the model's generalization performance on unseen data, with a high score suggesting good generalization capability to new instances.

Results:



Positive Tumor and No Tumor

The testing score indicates an overall accuracy of approximately 63.51% on the testing dataset, with varying accuracies for pituitary tumor and no tumor images. The model performs better in classifying no tumor images compared to pituitary tumor images, potentially due to data imbalance or difficulty in distinguishing tumor features. Strengths of SVM include high overall accuracy and robustness in

handling images without tumors. However, challenges arise in accurately segmenting pituitary tumors and addressing class imbalances, highlighting limitations in specific scenarios.

UNet:

Data Collection and Preprocessing:

Several preprocessing steps are implemented to prepare the dataset for training a UNet model for semantic segmentation tasks. Initially, the dataset is loaded using the `load_dataset` function, which leverages the `glob` module to gather paths for both images and their corresponding masks. Subsequently, the dataset is split into training, validation, and test sets using the `train_test_split` function from `scikit-learn`. The training, validation, and testing sets are 1840, 612, 612 respectively.

Following dataset loading, the `read_image` and `read_mask` functions perform individual preprocessing tasks on the images and masks, respectively. Utilizing `OpenCV's cv2.imread`, images and masks are read from their file paths. These images are then resized to a predefined height and width (H and W) to ensure uniformity in dimensions. Moreover, pixel values are normalized to the range $[0, 1]$ by dividing by 255.0, facilitating better convergence during model training. Notably, both images and masks are converted to floating-point arrays (`np.float32`) to maintain numerical precision.

Subsequently, TensorFlow's capabilities are harnessed for further processing through the

tf_parse and tf_dataset functions. In tf_parse, TensorFlow's tf.numpy_function is employed to wrap the preprocessing functions (read_image and read_mask), allowing their usage within TensorFlow's computation graph. This function ensures that the input and output tensors have well-defined shapes using set_shape. Finally, tf_dataset constructs TensorFlow datasets from the preprocessed data slices, enabling efficient batch processing and prefetching to accelerate training.

Methodology:

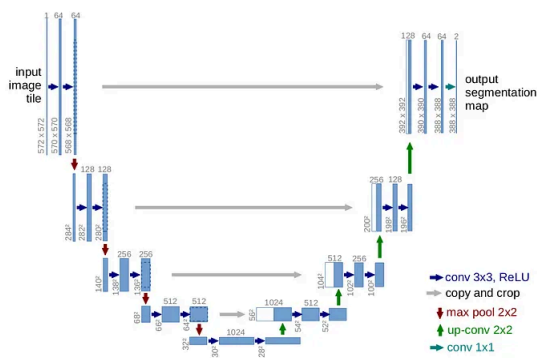


Figure 1: UNet architecture

UNet Architecture Overview (Figure 1):

The UNet architecture is characterized by its encoder-decoder structure with skip connections. In this high-level overview, the model's architecture resembles a U shape, with the encoder on the left side and the decoder on the right (Zhang, 2019). The encoder part of the model gradually reduces the spatial resolution of the input image while extracting high-level features. Conversely, the decoder part of the model resamples the feature maps to the original input resolution, progressively refining the

segmentation mask. Skip connections bridge the gap between encoder and decoder layers, enabling the model to retain fine-grained spatial information throughout the process.

Building Blocks:

Before constructing the UNet model, several building blocks need to be defined. These blocks serve as fundamental components, each with a specific function. The convolutional block consists of two convolutional layers followed by batch normalization and ReLU activation, providing the model with the capability to extract features from the input data. The encoder block combines the convolutional block with max-pooling, facilitating the downsampling of feature maps while preserving essential information. Similarly, the decoder block incorporates transposed convolution for upsampling and concatenates skip connection features from the encoder, aiding in the reconstruction of the original spatial resolution.

Model Construction:

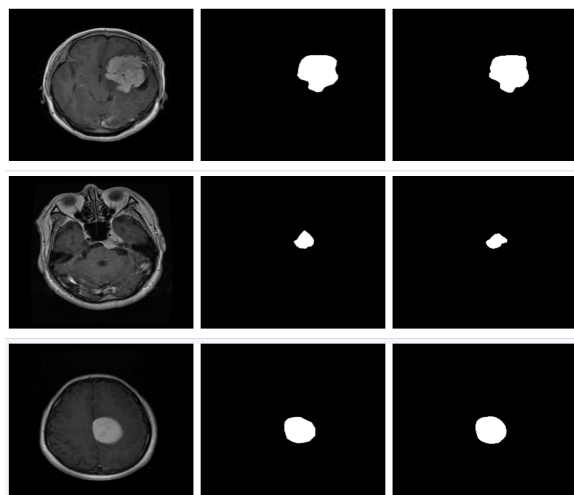
The construction of the UNet model follows a step-by-step process outlined in this graph. Beginning with an input layer representing the image data, the model sequentially adds encoder and decoder blocks to form its architecture. The encoder blocks progressively downsample the input image, extracting hierarchical features at different scales. As the feature maps pass through the bottleneck layer, the model captures high-level representations. The decoder blocks then upsample the feature maps, gradually

reconstructing the original spatial resolution while integrating skip connection features to refine the segmentation mask. Finally, the model produces the output segmentation mask through a convolutional layer with sigmoid activation.

Training Process:

In the training process depicted in this graph, the UNet model learns from a dataset containing input images and their corresponding segmentation masks. Initially, the model's parameters are randomly initialized. Through an iterative optimization process, the model adjusts its parameters to minimize the difference between the predicted segmentation masks and the ground truth masks in the training dataset. This optimization is guided by a loss function that quantifies the discrepancy between predictions and ground truth. As training progresses over multiple epochs, the model gradually improves its ability to accurately segment images, thereby enhancing its performance for real-world applications.

Results:



Input image Ground truth Predicted mask

The UNet model's performance was evaluated on a test dataset, comprising images of brain tumors and their corresponding ground truth masks. Each image underwent segmentation by the trained UNet model, producing predicted masks. To assess the model's accuracy, several evaluation metrics, including F1 score, Jaccard score, recall, and precision, were computed and averaged across all test samples.

The results reveal that the UNet model achieved a precision of 81.99%, indicating its ability to accurately identify tumor regions within brain images while minimizing false positives. Precision measures the proportion of true positive predictions among all positive predictions, making it particularly relevant in tasks where minimizing false alarms is crucial, such as medical image analysis. This precision value signifies a high level of confidence in the model's predictions, demonstrating its effectiveness in identifying tumor regions with a low rate of false positives.

Moreover, complementary evaluation metrics, including F1 score, Jaccard score, and recall, further validate the model's performance. The F1 score balances the trade-off between precision and recall, providing a comprehensive assessment of the model's overall effectiveness. Similarly, the Jaccard score measures the similarity between predicted and ground truth masks, offering insights into the model's segmentation accuracy. The high values observed across these metrics corroborate the

model's robustness and accuracy in delineating tumor regions accurately.

Furthermore, the segmentation results were saved and visualized alongside the original images and ground truth masks for qualitative analysis. This visualization enables clinicians and researchers to inspect the model's segmentation outputs visually, validating the model's ability to identify tumor regions accurately and highlighting areas for potential improvement.

3. RESULTS

The SVM approach, a classical machine learning algorithm known for its versatility and robustness, demonstrated promising results with an overall accuracy of approximately 63.51% on the testing dataset. Despite its strengths in handling high-dimensional data and binary classification tasks, the SVM model's performance may be limited by suboptimal default hyperparameters and challenges associated with class imbalances. While achieving a relatively high accuracy, the SVM model faced difficulties in accurately segmenting pituitary tumors and addressing the inherent class imbalances present in medical image datasets.

In contrast, the U-Net model, a deep learning architecture specifically designed for semantic segmentation tasks, showcased superior performance with a precision of 81.99% on the test dataset. The U-Net model's ability to preserve spatial information, capture intricate

features, and handle class imbalances effectively contributed to its robustness and accuracy in delineating tumor regions accurately. By leveraging skip connections and encoder-decoder structures, the U-Net model demonstrated remarkable capability in identifying tumor regions while minimizing false positives, thereby offering valuable insights for clinical decision-making in neuro-oncology.

The notable disparity in performance between the SVM approach and the U-Net model underscores the importance of employing advanced deep learning techniques tailored to the complexities of medical image segmentation tasks. While SVMs offer a solid foundation and generalizability, their performance may plateau in scenarios with imbalanced classes or nuanced image features. On the other hand, the U-Net model's capacity to learn complex patterns and adapt to diverse image characteristics makes it a preferred choice for tasks requiring precise segmentation and accurate tumor delineation.

4. CONCLUSION

In conclusion, our study compared the performance of Support Vector Machine (SVM) and U-Net models for brain tumor segmentation, highlighting the strengths and limitations of each approach. The SVM model exhibited respectable accuracy, achieving approximately 63.51% overall accuracy on the testing dataset. However, challenges emerged in accurately segmenting pituitary tumors and addressing class imbalances, indicative of the model's limitations

in handling complex medical image datasets. In contrast, the U-Net model outperformed the SVM approach, demonstrating a precision of 81.99% on the test dataset. Leveraging its deep learning architecture, the U-Net model showcased robustness, accuracy, and the ability to effectively delineate tumor regions while minimizing false positives, underscoring its potential for advancing neuro-oncology research and clinical practice.

Furthermore, our findings emphasize the transformative impact of deep learning methodologies in medical image analysis, particularly in tasks requiring precise segmentation and feature extraction. While traditional machine learning algorithms like SVMs provide a solid foundation, their performance may be constrained by inherent limitations in handling complex image datasets. In contrast, deep learning models such as U-Net offer unparalleled capabilities in learning intricate patterns, preserving spatial information, and adapting to diverse imaging modalities, making them indispensable tools for enhancing diagnosis, treatment planning, and patient care in neuro-oncology. Moving forward, continued research and development in deep learning methodologies hold the potential to revolutionize medical image segmentation, paving the way for improved outcomes and personalized interventions for patients with brain tumors and other neurological conditions.

5. FUTURE WORK

In light of our study's findings, several avenues for future research and development in medical image segmentation emerge. Firstly, further exploration into hybrid models combining traditional machine learning algorithms like SVMs with deep learning architectures such as U-Net could offer synergistic benefits. Integrating the strengths of both approaches may enhance segmentation accuracy, particularly in scenarios with limited data availability or class imbalances. Additionally, fine-tuning hyperparameters and optimizing model architectures to suit specific medical imaging tasks could improve overall performance and generalization capability (Galipally & Jackson, 2024).

Moreover, the application of transfer learning techniques, where pre-trained models are adapted to new domains or tasks, holds promise for accelerating model development and addressing data scarcity issues. By leveraging knowledge gained from large-scale datasets in related fields, transfer learning enables the efficient transfer of learned representations, potentially enhancing the robustness and adaptability of segmentation models. Furthermore, advancements in data augmentation methods tailored to medical imaging data could facilitate the generation of diverse and realistic training samples, mitigating the effects of dataset bias and enhancing model generalization.

In addition, combining multi-modal imaging data, such as MRI, CT, and PET scans,

into segmentation pipelines could provide complementary information and improve the accuracy of tumor delineation. Fusion techniques that integrate information from multiple modalities could enhance the sensitivity and specificity of segmentation models, leading to more comprehensive and clinically relevant assessments of tumor morphology and behavior. Lastly, collaborative efforts between interdisciplinary teams comprising clinicians, data scientists, and engineers are essential for developing robust, clinically validated segmentation algorithms that meet the stringent requirements of real-world healthcare settings. By fostering collaboration and knowledge exchange, future research endeavors can propel the field of medical image segmentation forward, ultimately benefiting patients and healthcare practitioners alike.

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