

# Semantic Segmentation of Gliomas on Brain MRIs by Graph Convolutional Neural Networks

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# Introduction

**Gliomas** are among the most common and aggressive brain tumours and are characterized by heterogeneity and rapid growth.

Glioma Segmentation from **Magnetic Resonance Imaging**(MRI) scans are critical in their diagnosis and treatment planning.

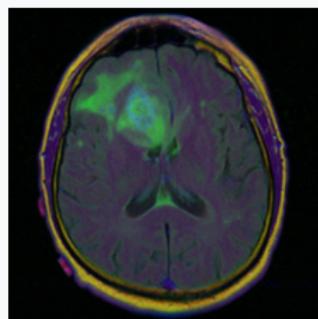
Traditional segmentation algorithms, which are pixel-based techniques, struggle with glioma occurrence's inherent complexity and variability.

This paper introduces a novel graph-based method for segmenting glioma in MRI images that leverages **Graph Neural Networks** (GNN).

# The used dataset

In our experimental activity, we employed a dataset comprising MRI scans and genomic data from 110 patients with **lower-grade glioma** (LLG).

The image size is  $256 \times 256$ . Radiologists manually annotated the images by outlining glioma abnormalities.



(a) MRI image.



(b) Mask.

Figure: A sample contained in the dataset.

# Graph construction

Let  $I \in \mathbb{R}^{H \times W \times 3}$  be an RGB MRI image where  $H$  is the height of the image,  $W$  is the width, and  $3$  is the number of channels.

Furthermore, we have  $M \in \mathbb{R}^{H \times W}$  that is a binary mask corresponding to the Region of Interest (ROI) in the image. The mask values are defined as follows:

$$M(i, j) = \begin{cases} 1 & \text{if } (i, j) \text{ is the part of the ROI} \\ 0 & \text{otherwise.} \end{cases} \quad (1)$$

# Graph construction - Step 1

In the first step, we segmented the image using the Felzenszwalb algorithm, obtaining a set of  $N_s$  so-called superpixels  $S = \{s_1, \dots, s_{N_s}\}$ .

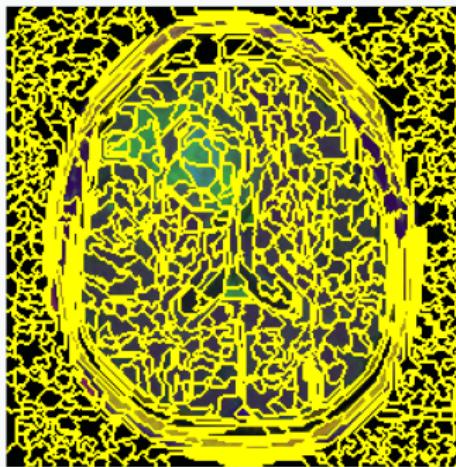


Figure: Segmentation of the image in superpixels.

## Graph construction - Step 2

For each superpixel  $s_k$ , we assign a feature vector with three components representing its mean colour defined as:

$$\mu_k = \frac{1}{|s_k|} \sum_{(i,j) \in s_k} I(i,j) \quad (2)$$

where  $|s_k|$  is the number of pixels in the superpixel  $s_k$ .

Finally, for each node, we assign a label  $l_k$  based on the most common label in the corresponding region of the binary mask:

$$l_k = \operatorname{argmax}_{l \in \{0,1\}} \left( \sum_{i,j \in s_k} M(i,j) = l \right). \quad (3)$$

# Graph construction - Step 3

Starting from the set of the obtained superpixels, we build a **Region Adjacency Graph** (RAG). Each superpixel represents a node, and each edge represents spatial adjacency between neighbouring superpixels.

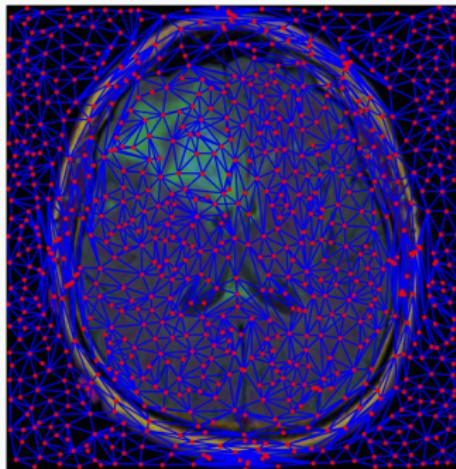


Figure: The final graph.

# Graph Neural Networks

**Graph Neural Networks** (GNN) are a particular kind of deep neural networks that processes data with a graph structure.

We tackled the problem of semantic segmentation of gliomas as a **node classification** problem in which each node represents a superpixel.

# Graph Neural Networks

A GNN is a series of stacked layers. Each one performs the following operations:

- **AGGREGATE**: aggregates the information from the neighbours of each node;
- **COMBINE**: updates the current node representation by combining the aggregated information.

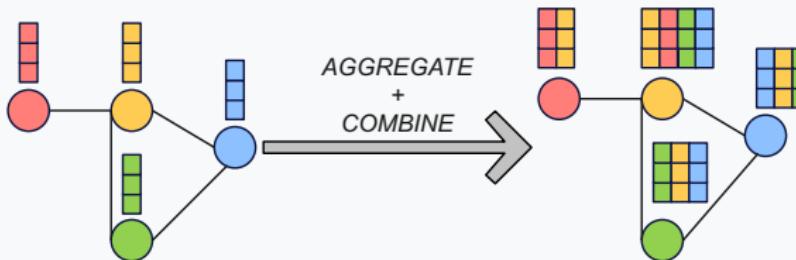


Figure: Overall mechanism of a GNN layer.

# The proposed approach

We train a GNN with two GCN layers (512-dimensional) and a final Sigmoid-activated layer for node classification.

Batch Normalization and Dropout are applied between layers to improve generalization.

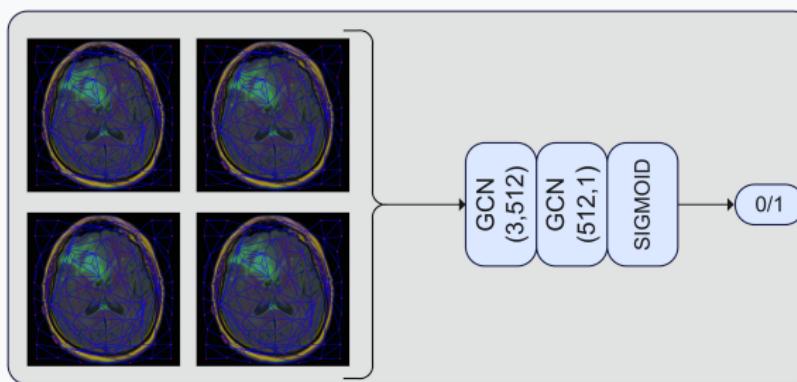


Figure: Training phase.

# The proposed approach

We train this neural net minimizing a loss function that is a combination of **Dice Loss** and **Binary Cross Entropy** (BCE) defined as:

$$\mathcal{L}_{\text{Dice}} = 1 - \frac{2 \times |P \cap M|}{|P| + |M|} \quad (4)$$

$$\mathcal{L}_{\text{BCE}} = -(M \log(S(P)) + (1 - M) \log(1 - S(P))) \quad (5)$$

$$\mathcal{L}_{\text{total}} = \mathcal{L}_{\text{BCE}} + \mathcal{L}_{\text{Dice}} \quad (6)$$

where  $M$  and  $P$  are the ground truth and predicted node/superpixels labels, and  $S(\cdot)$  is the Sigmoid activation function.

# The proposed approach

After training the GNN, given a test graph, we first perform node classification, obtaining a vector  $L = \{L_1, \dots, L_k\}$  with  $L_k \in \{0, 1\}$ . These values represent the predicted value for the node/superpixel.

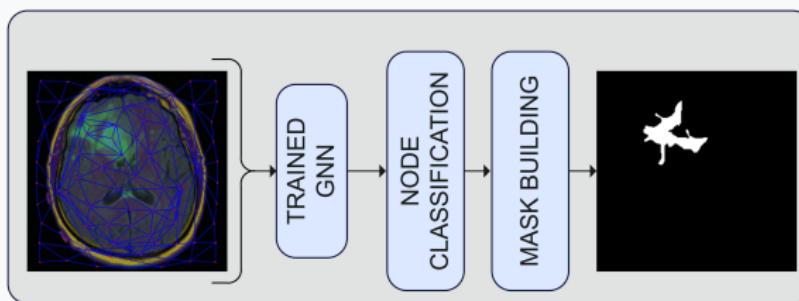


Figure: Testing phase.

# The proposed approach

We create the final predicted mask from these values and the image segmentation  $S$  stored during graph building using the following procedure:

- we create a matrix  $P$  containing zero values with the same dimension as the image;
- for each  $L_k$ , we retrieve the corresponding segment  $s_k$ ;
- find all pixels  $S(i, j)$  such as  $S(i, j) \in s_k$ ;
- assign the predicted label  $L_k$  to these pixels in the mask:  
 $M(i, j) = L_k$ .

# Experimental results

To assess the effectiveness of our proposal, we performed the following experiments:

- using the pre-trained U-Net for the image segmentation;
- fine-tuning the U-Net with the images of the considered dataset, freezing all layers except for the decoder layer;
- training the entire U-Net from scratch, starting from a random weight initial configuration;
- segmentation of the MRI scans using our approach,

# Experimental results

We divided the dataset into training and test sets using an 80:20 ratio, ensuring the split was performed at the patient level.

This approach guarantees that images from the same patient are not shared between the training and test sets. As a result, the training set contains 88 patients, while the test set includes 22 patients.

To obtain more reliable and robust results, we conducted 100 different data extractions, repeating the random patient-level split for each extraction.

# Experimental results

For the evaluation, we used the following metrics:

- **Dice Coefficient** (DC): is a statistical measure used to gauge the similarity between two sets;
- **Pixel Error** (PE): measures the proportion of misclassified pixels;
- **Rand Error** (RE): measures the proportion of misclassified pixel pairs relative to each other regarding their segmentation

# Experimental results

Method/Metric	DC ↑	PE ↓	RE ↓
U-Net Pred.	$0.5279 \pm 0.0258$	$0.0126 \pm 0.0017$	$0.0057 \pm 0.0008$
U-Net FT	$0.4154 \pm 0.0917$	$0.0188 \pm 0.0027$	$0.0165 \pm 0.0035$
U-Net Train.	$0.3093 \pm 0.1231$	$0.0406 \pm 0.0215$	$0.0559 \pm 0.0358$
Our proposal	$0.6743 \pm 0.0329$	$0.0107 \pm 0.0029$	$0.0200 \pm 0.0050$

Table: The obtained results. ↑ signifies higher is better, vice versa ↓ lower is better.

# Experimental results

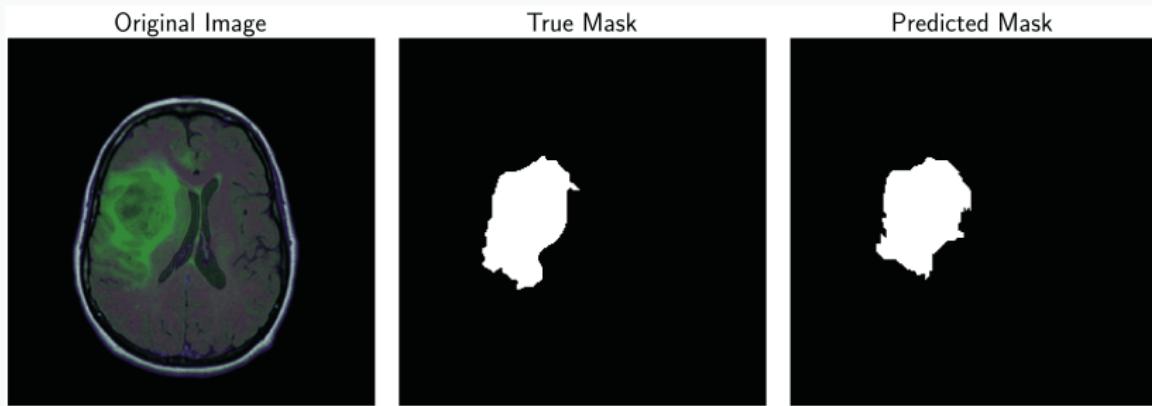


Figure: Segmentation example 1.

# Experimental results



Figure: Segmentation example 2.

# Experimental results

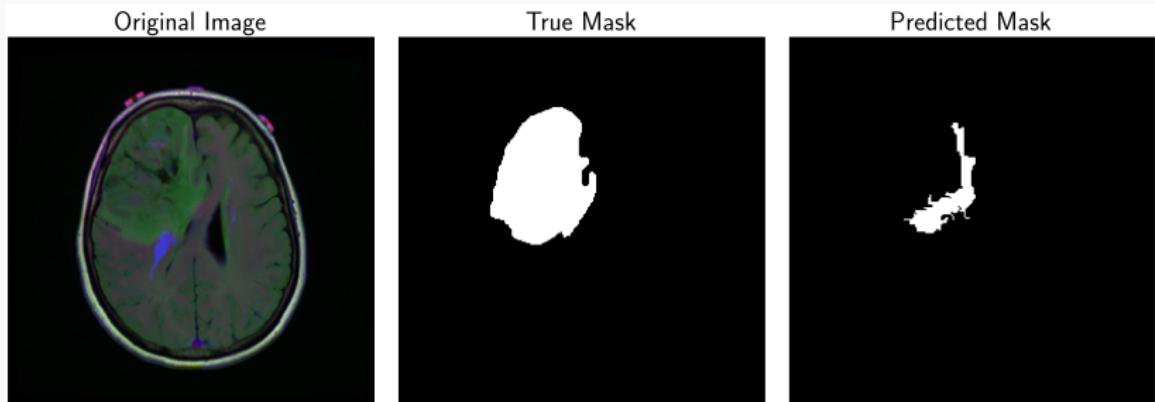


Figure: Segmentation example 3.

# Conclusions

This paper presents a novel graph-based method for glioma segmentation in MRI scans. It utilizes GNN to model complex spatial and contextual relationships between tumour regions and surrounding tissues.

The approach demonstrates superior performance compared to U-Net-based methods in tumour segmentation.

Future work will focus on enhancing the segmentation capabilities of this framework by incorporating multimodal data, such as genetic profiles and clinical information, to provide a more comprehensive understanding of the tumour's biological and anatomical context.

Thank you for your attention!