A Maze-Based Computational Framework for Tumor Localization in the Brain

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Abstract

This paper presents a computational framework that models the brain as a maze-like network for tumor localization and surgical planning. Starting from an abstract structure without prior information about healthy or malignant regions, we generate a voxel-based maze. Once MRI data is available, voxel weights are assigned according to tumor probability. Multiple maze variants are generated and analyzed using A* and Minimum Spanning Tree (Prim) algorithms. This allows the identification of critical voxels—points where malignant tissue is likely concentrated—providing precise targets for neurosurgery.

1. Introduction

Accurate tumor removal in neurosurgery requires precise localization of malignant voxels while preserving healthy tissue. Early in the process, neither the exact structure of the brain nor the locations of malignant regions are known. To address this, we propose a maze-based abstraction of the brain, which provides a computational framework for analyzing neuronal connectivity and potential tumor regions. The framework leverages MRI data, maze generation algorithms, and graph search techniques to identify critical voxels for surgical intervention.

2. Maze Construction and Voxel Modeling

Let the brain be represented as a 3D grid of voxels V connected by potential synaptic edges E, forming a graph $G = (V, E)$. Initially, no voxel is labeled as healthy or malignant, and all edges have equal or undefined weight.

2.1 Maze Generation

A base maze is generated using algorithms inspired by Jamis Buck's "Maze for Programmers", such as Recursive Backtracker or Prim Maze Generation. The maze ensures all voxels are reachable and establishes a network of potential neuronal pathways.

$G_{maze} = (V, E_{maze})$

where $E_{maze} \subseteq E$ represents the edges created by the maze algorithm.

2.2 Weight Assignment from MRI

Once MRI data is available, each voxel $v \in V$ is assigned a weight $w(v)$ based on tumor likelihood. For an edge connecting voxels u and v, the edge weight is defined as:

$$w(u, v) = f(w(u), w(v))$$

where f is a function that increases weight if either voxel has high tumor probability. This weight assignment allows MST and A* algorithms to differentiate between healthy and malignant regions.

3. Generation of Multiple Maze Variants and Branch Analysis

To simulate variability and the complex connectivity of the brain, multiple maze variants $G_{maze}^{(i)}$ are generated through controlled perturbations of the base maze. Let $i = 1, \ldots, N$ with N large (e.g., 10^6). In each variant, the maze structure is slightly modified to explore alternative pathways. Branch complexity is quantified using a branching factor $b(v)$ for voxel v:

$$b(v) = \deg_{G_{\text{maze}}^{(i)}}(v)$$

Higher branching factors in the neighborhood indicate regions with more maze-like connectivity, which is associated with malignant tissue once weights are applied.

4. Pathfinding and Critical Voxel Identification

For each maze variant $G_{maze}^{(i)}$, A *pathfinding is executed between sampled voxel pairs. Let $P_{uov}^{(i)}$ denote the path found by A* from voxel u to voxel v in variant i. A frequency map $F(v)$ is defined:

$$F(v) = \sum_{i=1}^{N} \sum_{(u,v) \in S} \mathbf{1}_{v \in P_{u \to v}^{(i)}}$$

where S is the set of sampled start and goal voxel pairs, and $\mathbf{1}_{v \in P}$ is the indicator function. Voxels with high $F(v)$ are considered **critical** for surgical targeting.

4.1 MST Analysis

A Minimum Spanning Tree (Prim) is computed on each weighted maze variant. Let $T^{(i)}$ denote the MST for variant i:

$$T^{(i)} = \text{MST}(G_{\text{maze}}^{(i)}, w)$$

Regions with high MST path length and branching in weighted mazes correspond to areas of malignant tissue, demonstrating the natural **scatter effect** of tumor distribution.

5. Surgical Planning

The intersection of high-frequency voxels $F(v)$ across maze variants and MST analysis identifies precise voxel targets $V_{critical}$:

$$V_{\text{critical}} = \{v \in V \mid F(v) \geq \tau \text{ and } b(v) \geq \beta\}$$

where $ au$ is a frequency threshold and eta is a branching factor threshold. These voxels are recommended for targeted surgical intervention to remove malignant tissue while minimizing damage to healthy brain regions.

6. Computational Considerations

- **Maze construction:** $O(V)$ per variant
- **Weight assignment:** $O(V)$
- _A pathfinding:_* $O(E \log V)$ per path, parallelization recommended for large N
- **MST computation:** $O(E \log V)$ per variant
- **Critical voxel identification:** $O(V \cdot |S| \cdot N)$

Optimization strategies include: voxel sampling, variant subsampling, and GPU or multi-core parallelization.

7. Conclusion

We present a framework that integrates maze-based modeling, MRI-informed weighting, multiple maze variants, A* pathfinding, and MST analysis to identify critical voxels for tumor localization. The method accounts for natural scatter in malignant regions and provides a computationally tractable approach to guide precise neurosurgical interventions.

Keywords: Brain Maze, Tumor Localization, MRI, Prim MST, A* Pathfinding, Critical Voxels, Neurosurgical Planning