3D Multi-Scale Convolutional Networks
For Glioma Grading using MR Images

Chenjie Ge, Qixun Qu, Irene YH Gu, Asgeir S Jakola

1 Dept. of Electrical Eng., Chalmers Univ. of Technology, Sweden
2 Sahlgrenska University Hospital, Sweden
Contents

1. Introduction
2. Review: related work
3. Proposed method
4. Test results and evaluation
5. Conclusion
1. Introduction
Addressed issue

Deep learning for brain tumor classification using MRIs (+ biomarkers)

High Grade Glioma, HGG (in axial, coronal, sagittal views)

Low Grade Glioma, LGG
Why glioma classification using MRIs?

- Tumor grading is important to clinical planning
- Non-invasive method for diagnostics
- Determine tumor types without biomarker
2. Related Work: Review

- Using hand-crafted features [2,3]
  - e.g. size, shape, location, intensity, texture of tumors

- Using deep learning for features [4]
  - 3 layer 2D CNN structure and large size kernels

- Combined models (traditional ML and DL) [5]
  - Fish vector (through clustering) to encode DL learned features

- Using 2D CNN for learning features [Ge’18]
  - based on slice of MRIs and simple augmentation
3. Proposed Method: Motivation

- Brain tumors may vary in shape, size and location

  Tumor characterization: using multi-scale learning to capture both image-level and semantic-level features

- Tumor is relatively small in a 3D volume image

  Require: saliency-awareness for highlighting the tumor area, where deep learning can be focused on.
3. Proposed Method: Overview

Main Novelties

- Multi-scale 3D CNN architecture for feature learning.
- Fusion of multi-scale features
- Saliency-aware strategy to enhance tumor regions in MRIs.
3. Proposed method: 3D multi-scale CNN scheme

Difference from [6] (using pyramid-structure CNNs):
• Different applications: MRIs (vs Visual images)
• 3D (vs 2D), different architecture (# layers, hyper-parameters etc.).
• End-to-end scheme
c) Saliency-aware tumor enhancement

Tumor enhancement with segmentation masks, reducing intensity values in non-tumor region (to 1/3)
4. Test Results and Evaluation

a) Dataset: BraTS 2017

<table>
<thead>
<tr>
<th>class</th>
<th># subjects</th>
<th>#scans in en-T1-MRI</th>
<th>#scans in tra. set</th>
<th>#scans in val. set</th>
<th>#scans in test set</th>
</tr>
</thead>
<tbody>
<tr>
<td>HGG</td>
<td>210</td>
<td>210</td>
<td>126</td>
<td>42</td>
<td>42</td>
</tr>
<tr>
<td>LGG</td>
<td>75</td>
<td>75</td>
<td>45(90)</td>
<td>15</td>
<td>15</td>
</tr>
</tbody>
</table>

Flipping for data augmentation in LGG
4. Test Results and Evaluation

b) Setup

- Use KERAS library with TensorFlow backend
- Use “Adam” optimizer for the back propagation
- Step-wise learning rate: 0.001 for epochs 1-40; 0.0001 for epochs 41-70; 0.00001 for epochs 71-100
- Dataset partitioned randomly: \textit{training} (60%), \textit{validation} (20%), \textit{testing} (20%)
- Use drop out, L2 regularization to mitigate the overfitting
c) Performance

Performance using the proposed scheme. Left: accuracy vs. epochs; right: loss vs. epochs.

<table>
<thead>
<tr>
<th>Performance</th>
<th>training</th>
<th>validation</th>
<th>test</th>
</tr>
</thead>
<tbody>
<tr>
<td>accuracy</td>
<td>98.61%</td>
<td>94.74%</td>
<td><strong>89.47%</strong></td>
</tr>
</tbody>
</table>

Overall performance

<table>
<thead>
<tr>
<th>True/classified</th>
<th>HGG</th>
<th>LGG</th>
</tr>
</thead>
<tbody>
<tr>
<td>HGG</td>
<td><strong>90.48%</strong></td>
<td>9.52%</td>
</tr>
<tr>
<td>LGG</td>
<td>13.33%</td>
<td><strong>86.67%</strong></td>
</tr>
</tbody>
</table>

Confusion matrix on the test set

<table>
<thead>
<tr>
<th>Run</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>Average</th>
</tr>
</thead>
<tbody>
<tr>
<td>Acc. (%)</td>
<td><strong>89.47</strong></td>
<td>85.96</td>
<td>87.72</td>
<td><strong>89.47</strong></td>
<td>87.72</td>
<td>88.07</td>
</tr>
</tbody>
</table>

Performance of 5 runs on the test set (with datasets randomly re-partitioned)
d) Empirical analysis on hyper-parameters

Performance from using different learning rates. (left: training; right: validation).

Performance from using different batch sizes. (left: training; right: validation)
d) Comparison: with/without saliency enhancement

<table>
<thead>
<tr>
<th>Method</th>
<th>Without enhancement</th>
<th>With enhancement</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training accuracy(%)</td>
<td>99.01</td>
<td>98.61</td>
</tr>
<tr>
<td>Validation accuracy(%)</td>
<td>85.96</td>
<td>94.74</td>
</tr>
<tr>
<td>Test accuracy (%)</td>
<td>84.21</td>
<td>89.47</td>
</tr>
</tbody>
</table>

Remarks:
Performance of glioma classification was heavily dependent on the tumor masks
e) Comparison and Discussion

<table>
<thead>
<tr>
<th>Method</th>
<th>Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pan [4] CNN</td>
<td>73.33%</td>
</tr>
<tr>
<td>Ge [*] CNN</td>
<td>90.87%</td>
</tr>
<tr>
<td>Proposed scheme CNN</td>
<td>89.47%</td>
</tr>
</tbody>
</table>

**Comparison**: with other glioma grading methods (HGG/LGG).

<table>
<thead>
<tr>
<th>Method</th>
<th>Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Macyszyn [2]</td>
<td>SVM</td>
</tr>
<tr>
<td>Yu [3]</td>
<td>SVM</td>
</tr>
<tr>
<td>Li [5]</td>
<td>CNN</td>
</tr>
<tr>
<td>Akkus [12]</td>
<td>CNN</td>
</tr>
<tr>
<td>Ge [*]</td>
<td>CNN</td>
</tr>
</tbody>
</table>

**Related classifier**: other glioma classification methods (using biomarkers)

5. Conclusion

Proposed a 3D multi-scale CNN architecture for glioma grading using MRIs

- Characterize tumors by image- and semantic-level features
- Saliency-awareness for enhancing tumor regions
- Multi-scale feature fusion

Results showed

- Proposed network architecture is effective for brain tumor classification
- Salient region enhancement improves the performance
- Performance comparable to the state-of-the-art
Future/ongoing work

- Tests on larger datasets
- Extend to clinically more important issues: classification of different types of gliomas (e.g., IDH mutation, 1p19q codeletion …)
- Apply saliency techniques to enhance the tumor regions without requiring masks.
- Robust data augmentation for enlarging training dataset
Thank you for your attention!

Questions?