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Gleason Grade Group Prediction for Prostate Cancer Patients with MR Images Using Convolutional Neural Network

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Introduction

- Prostate CA is the most common malignancy in men.
  - An accurate diagnosis requires a **tissue biopsy**.
- Can we eliminate this need?
  - Differentiating prostate CA from benign tissue on imaging:
    - Literature: AUC of **0.87**. Our experience: AUC of **0.90**.
- Can we predict the Gleason grade group?
  - Literature: AUC of **0.50**.
  - **Can we improve upon this?**
Objective

- To predict Gleason grade grouping from publicly available prostate MRIs using a convolutional neural network (CNN).
- A CNN is a machine learning algorithm that mimics the function of the human visual cortex.
- To design software that emulates the role of a fellowship-trained radiologist.
The **Big** Challenge

- **Paucity of publicly available data:**
  - Natural image datasets: 1,000,000+ images.
  - NIH dataset of CXRs: 100,000+ images.
  - SPIE Prostate Classification Challenge: ~200 MRIs and ~100 delineated lesions.
Solutions: Increasing the Available Data

- **Data augmentation**: Methods to *artificially* increase data size.
  - Rotation, flipping, scaling, shifting, adding noise, etc.

- **Transfer learning**: Applying solutions for one problem to a related problem.
  - Does not work well for unrelated image sets (domain shift).
  - Requires a **pre-trained model** (not available for prostate MRIs).
Step 1: Data Pre-Processing and Augmentation

Registration
- Rigid-body alignment
- Resampling

Patch Generation
- Region localization
- Cropping the region of interest (ROI)
- Augmentation: Rotation
- Intra Image Normalization [0, 1]

Validation
- 10-fold cross validation
- Channel composition

Data Set:
- DWI(D), ADC(A), Ktrans(K), T2WI (T)
Step 2: Training
Step 3: Transfer Learning

Feature Extraction

Weighted Kernel Classifier
Step 4: Feature Visualization

Model looks at the right place!
SOTA Results

Figure: t-SNE Plot Showing Data’s tendency to become more separable as Layer Propagates for Pre-trained CNN.

Table: Average cross validation results showed combining low and high level features demonstrated the best feature representation for GGG prediction task.

<table>
<thead>
<tr>
<th>GG 1 vs. 23 vs. 45 3-fold CV AVG</th>
<th>Features From C1</th>
<th>Features From C4</th>
<th>Features From FC1</th>
<th>Final Result of the CNN</th>
</tr>
</thead>
<tbody>
<tr>
<td>GG 1 Accuracy</td>
<td>0.41</td>
<td>0.95</td>
<td>0.97</td>
<td>1.00</td>
</tr>
<tr>
<td>GG 2&amp;3 Accuracy</td>
<td>0.59</td>
<td>0.68</td>
<td>0.70</td>
<td>0.68</td>
</tr>
<tr>
<td>GG 4&amp;5 Accuracy</td>
<td>0.27</td>
<td>0.80</td>
<td>0.80</td>
<td>0.87</td>
</tr>
<tr>
<td>G-mean</td>
<td>0.24</td>
<td>0.71</td>
<td>0.73</td>
<td>0.76</td>
</tr>
</tbody>
</table>
Conclusions

- Data heterogeneity and small sample size present big challenges to accurate Gleason grade prediction for prostate CA.

- We overcame these challenges and trained a convolutional neural network using data augmentation and transfer learning.

- The accuracy of our model ranged between 0.68-1.00 across different Gleason grade groups, with an overall performance of 0.76 (G-mean).
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- **Contact information:**
  - Joon Lee, MD (jlee17@hfhs.org)