

Advanced Machine Learning

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ASSIGNMENT 1

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Abstract

We survey Deep Learning methods on BraTS Challenge 2015 dataset for detection of brain tumors in multimodal magnetic resonance imaging (MRI) scans. We evaluate Support Vector Machines and Deep Learning methods.

Introduction

Data comprises ample multi-institutional routine clinically-acquired pre-operative multimodal MRI scans of glioblastoma (GBM/HGG) and lower grade glioma (LGG), with pathologically confirmed diagnosis. We cast the problem as a binary classification problem, with empty outputs casted as 0 class and 1 otherwise. Each slice of a data point is considered as a separate data point. We employ 90:10 training/validation split.

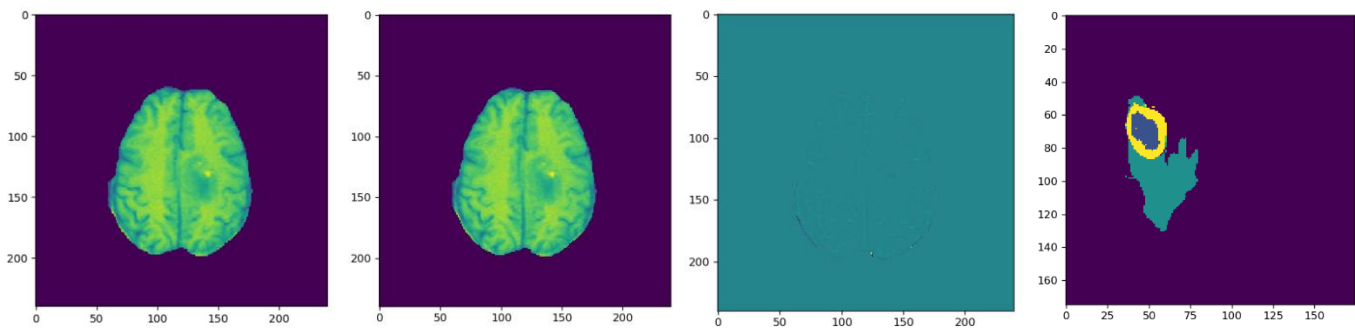


Fig. 1: a) MRI Cross Section of a Brain b) After Denoising c) Difference d) Labeled Tumor Section

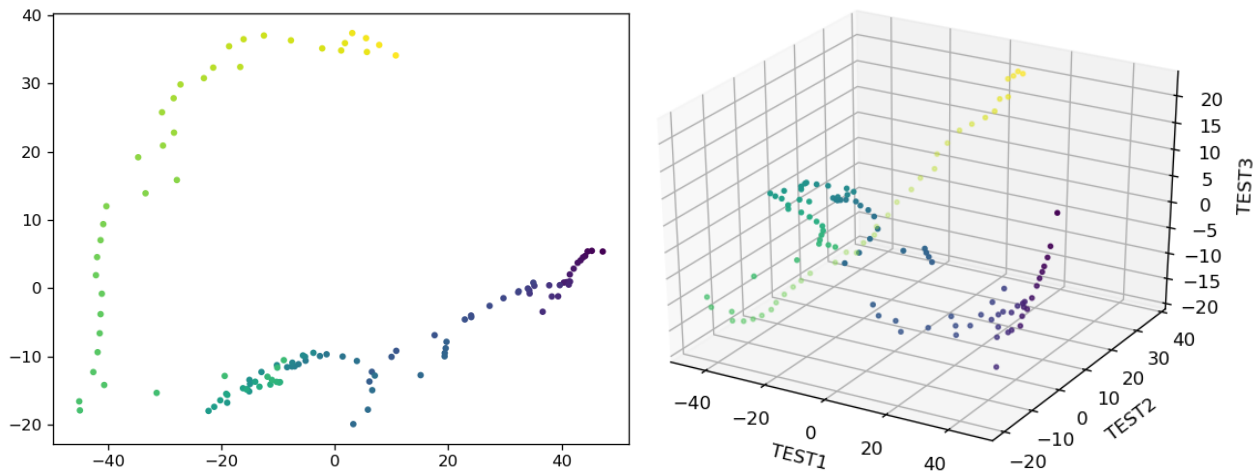


Fig. 2: Data Variation across cross-section within a single volumetric data point. PCA plots in 2D a) and 3D b)

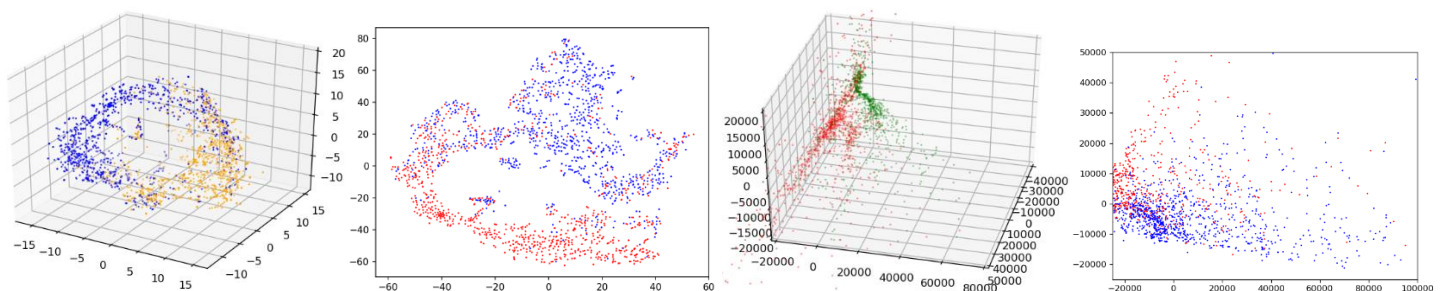


Fig. 3: tSNE 3D, tSNE 2D, PCA 3D and PCA 2D

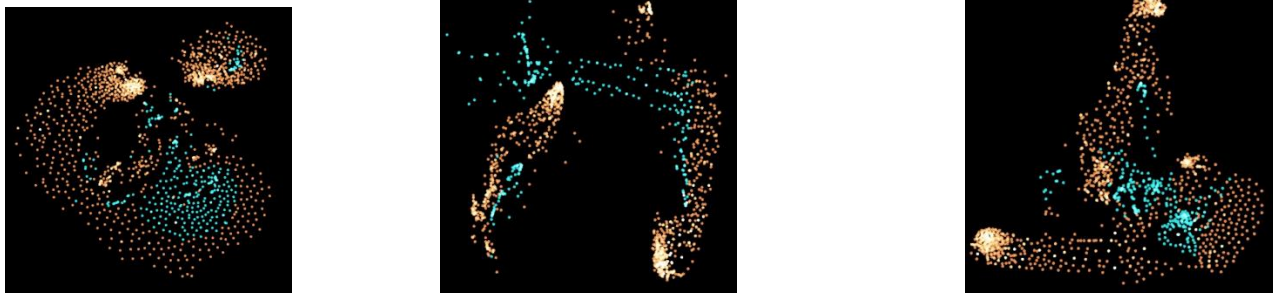


Fig. 4: TensorboardTsneVisualizations

Experimentation

| Algorithm | Train | Cross Validation and Test accuracy |
|------------------------------------|--------|------------------------------------|
| SVM on PCA | 94.1% | 83.1% (CV accuracy) |
| SVM SMOTE* | 96.85% | 79.1% (CV accuracy) |
| Fully Connected DNN after PCA | 95.01% | 86.7% (CV accuracy) |
| Conv DNN (on all the brain slices) | 98.52% | 64.8%(CV accuracy) |
| Conv DNN (with full brain slices) | 99.12% | DSC-98.355%, CV=98.01%, F1=98.55% |
| ConvDNN(Mixed 45 test samples) | 99.47% | DSC-88.41%, Test= 87.1% |

*Synthetic Minority Oversampling Technique

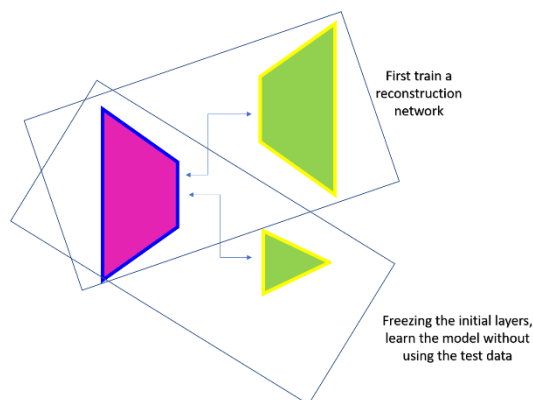
Table 1: Evaluation Metrics

Handling different distribution of Train and Test Data (Bias Correction)

- Utilizing some test data to train so that model accustoms to the new distribution

| Percentage of Test Data Used | Test Accuracy (on given test set, 942 examples) |
|------------------------------|---|
| 4.7% | 87% |
| 9.4% | 89% |
| 21.23% | 93% |
| 100% | 99.46% |

- Autoencoder based Transfer Learning (Unsupervised Way to Account for different Distribution)
Method: Train an autoencoder with some proportion of test data, freeze the weights to do Transfer Learning and learn a model, without using the test data for learning this time. Achieved 76% on the given Test Data.



Architecture

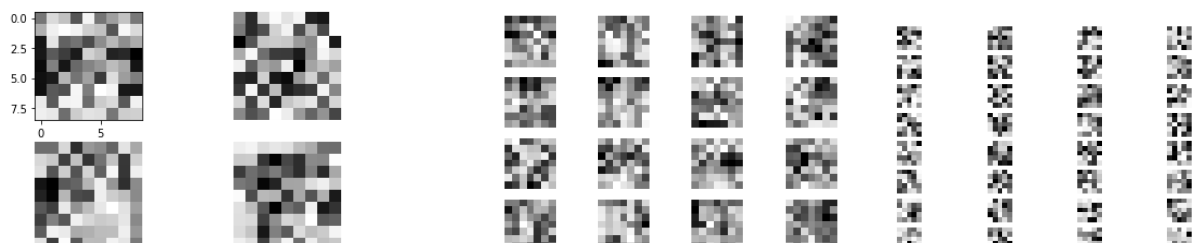


Fig. 5: Feature Maps for First, Second, Third Convolutional Layer

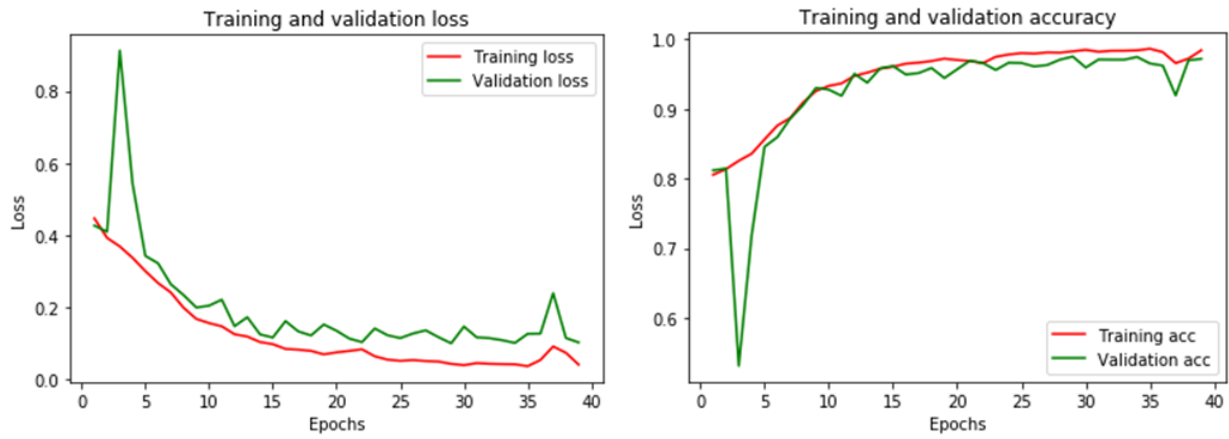


Fig. 6: Training Loss and Accuracy

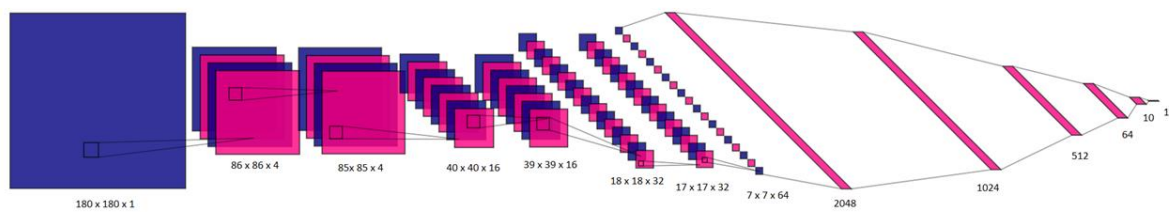


Fig. 7: DNN Architecture

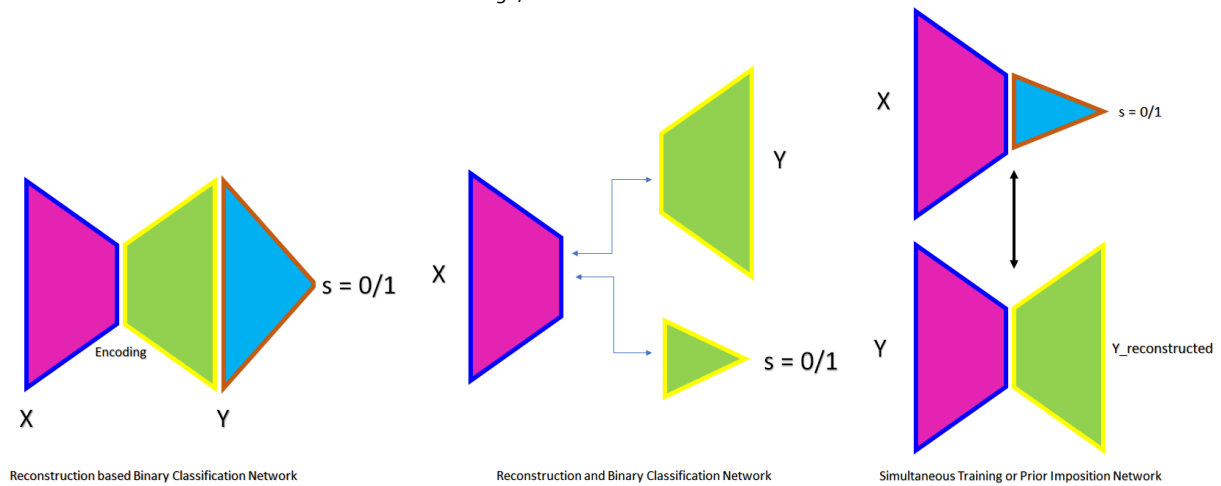


Fig. 7: Further Extensions

Note- We also experimented with the first architecture and code for same has also been submitted.

Learnings from the Assignment

- We learnt that applied Deep Learning is a highly empirical process and requires wide experimentation.
- We observe within a single volumetric scan, there is huge variation in the data distribution. This is evident from the figure no.
- We also employ data augmentation.
- SMOTE has a disadvantages of overfitting the classifier.

Implementational Details and Ideas Tried

- Taking slices which have major part of the brain visible.
- Crop each slice from 240×240 to 180×180 .
- Normalize each image by its maximum, or Mean-Variance Normalization, Image Denoising
- Experimenting different activation functions, loss functions, early stopping, batch normalization, learning rate decay

- Note on Data Skewness: The data has a class imbalance in a certain sense, but per person. We discard the images with incomplete brain as we were not doing segmentation. The slides in which tumor is not visible, the ground truth corresponding to that slide is completely black. Thus, as far as the model input is concerned, the skew will be less than what it is for a person.
- We use different medical purpose specific metrics for evaluation.

References

1. Deep Learning for Medical Image Processing: Overview, Challenges and Future Muhammad Imran Razzak, SaeedaNaz and Ahmad Zaib
2. Deep Learning for Brain MRI Segmentation: State of the Art and Future Directions: ZeynettinAkkus, AlfiiaGalimzianova, AssafHoogi, Daniel L. Rubin, Bradley J. Erickson
3. Brain Tumor Segmentation with Deep Neural Networks: Mohammad Havaeia,AxelDavyb , David Warde-Farleyc , Antoine Biardc, Aaron Courvillec, YoshuaBengioc , Chris Palc, Pierre-Marc Jodoina , Hugo Larochellea

Acknowledgments

We thank Mayank Mishra for useful discussion.

Appendix

Model summary

| Layer (type) | Output Shape | Param # |
|------------------------------|---------------------|---------|
| ===== | | |
| input_2 (InputLayer) | (None, 180, 180, 1) | 0 |
| <hr/> | | |
| conv2d_5 (Conv2D) | (None, 86, 86, 4) | 328 |
| <hr/> | | |
| max_pooling2d_4 (MaxPooling2 | (None, 85, 85, 4) | 0 |
| <hr/> | | |
| activation_4 (Activation) | (None, 85, 85, 4) | 0 |
| <hr/> | | |
| conv2d_6 (Conv2D) | (None, 40, 40, 16) | 3152 |
| <hr/> | | |
| max_pooling2d_5 (MaxPooling2 | (None, 39, 39, 16) | 0 |
| <hr/> | | |
| activation_5 (Activation) | (None, 39, 39, 16) | 0 |
| <hr/> | | |
| conv2d_7 (Conv2D) | (None, 18, 18, 32) | 12832 |
| <hr/> | | |
| max_pooling2d_6 (MaxPooling2 | (None, 17, 17, 32) | 0 |
| <hr/> | | |
| activation_6 (Activation) | (None, 17, 17, 32) | 0 |
| <hr/> | | |
| conv2d_8 (Conv2D) | (None, 7, 7, 64) | 51264 |
| <hr/> | | |
| flatten_2 (Flatten) | (None, 3136) | 0 |
| <hr/> | | |
| dense_7 (Dense) | (None, 2048) | 6424576 |
| <hr/> | | |
| batch_normalization_5 (Batch | (None, 2048) | 8192 |
| <hr/> | | |
| dense_8 (Dense) | (None, 1024) | 2098176 |
| <hr/> | | |
| batch_normalization_6 (Batch | (None, 1024) | 4096 |
| <hr/> | | |
| dense_9 (Dense) | (None, 512) | 524800 |

| | | |
|-----------------------|--------------------|-------|
| <hr/> | | |
| batch_normalization_7 | (Batch (None, 512) | 2048 |
| <hr/> | | |
| dense_10 | (Dense) (None, 64) | 32832 |
| <hr/> | | |
| batch_normalization_8 | (Batch (None, 64) | 256 |
| <hr/> | | |
| dense_11 | (Dense) (None, 10) | 650 |
| <hr/> | | |
| dense_12 | (Dense) (None, 1) | 11 |
| <hr/> | | |
| ===== | | |