Brain Tumor Detection and Segmentation

An analysis and evaluation of the performance on U-net convolutional networks



Background

Medical field has become one of the most advanced fields in which machine learning and deep learning are applied.

Doctors need higher precision of identification to detect and then address the patient's' medical problem.

e.g. Tumor Identification



Dataset

Brain MRI segmentation

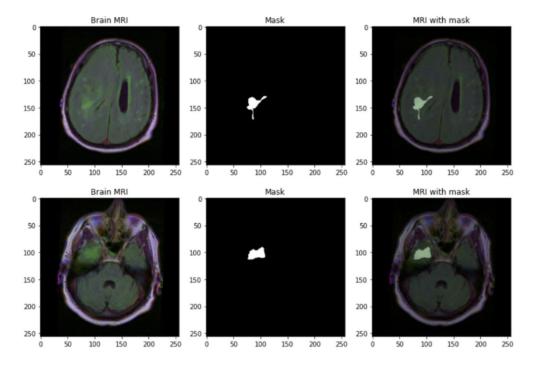
https://www.kaggle.com/mateuszbuda/lgg-mri-segmentation

The data-set contains brain MR images together with manual FLAIR abnormality segmentation masks. The images were obtained from The Cancer Imaging Archive (TCIA). They correspond to 110 patients.

The data-set is organized into 110 folders named after case ID that contains information about source institution.



Dataset





Data Processing

- A train-test split of 80% train and 10% validation, 10% test
- Each image is loaded into a custom dataset and data loader processed with PyTorch

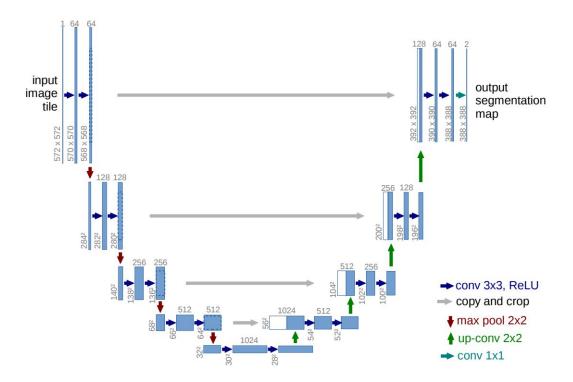


Workstation details

- Hardware
 - BU Shared Compute Cluster
 - 1x Tesla V100
 - 4x CPU Cores
 - 5 hours session
- Software
 - PyTorch 1.10
 - Python 3.8.6
 - Jupyterlab

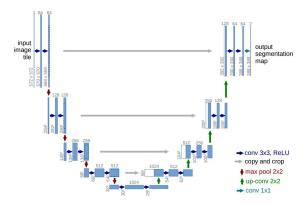


U-net





Implementation



```
class UNET(nn.Module):
   def _init_(
       self,
       in channels=3,
       out channels=1,
        features=[64, 128, 256, 512],
       super(UNET, self). init ()
       self.ups = nn.ModuleList()
       self.downs = nn.ModuleList()
       self.pool = nn.MaxPool2d(kernel size=2, stride=2)
       # Down part of UNET
       for feature in features:
            self.downs.append(DoubleConv(in channels, feature))
           in channels = feature
       # Up part of UNET
       for feature in reversed(features):
           self.ups.append(
               nn.ConvTranspose2d(
                   feature*2, feature, kernel size=2, stride=2,
           self.ups.append(DoubleConv(feature*2, feature))
       # Lowest layer connecting up and down processes
       self.bottom u = DoubleConv(features[-1], features[-1]*2)
       # Final convolution layer to output
       self.final conv = nn.Conv2d(features[0], out channels, kernel size=1)
   def forward(self, x):
       skip connections = []
       for down in self.downs:
           x = down(x)
           skip connections.append(x)
           x = self.pool(x)
       x = self.bottom u(x)
       skip connections = skip connections[::-1]
       for idx in range(0, len(self.ups), 2):
           x = self.ups[idx](x)
           skip_connection = skip_connections[idx//2]
           if x.shape != skip connection.shape:
               x = TF.resize(x, size=skip connection.shape[2:])
           concat skip = torch.cat((skip connection, x), dim=1)
           x = self.ups[idx+1](concat skip)
       return self.final conv(x)
```





Dynamic learning rate adjustment

Algorithm 1 Learning rate adjustment

```
1: learning rate ← 1e-3
 2: highest dice score ← 0
 3: worsen streak \leftarrow 0
 4: if worsen streak < 30 then
       train model for one epoch
       dice score ← model dice score
       if dice score > highest dice score then
           highest dice score ← dice score
           worsen streak \leftarrow 0
           Save model checkpoint
10:
11:
       else
12:
           worsen streak+=1
           Decay learning rate by one step
13:
           if worsen streak == 5 then
14:
15:
               learning rate ← 1e-3
           if worsen streak == 15 then
16:
17:
               learning rate \leftarrow 1e-3
```

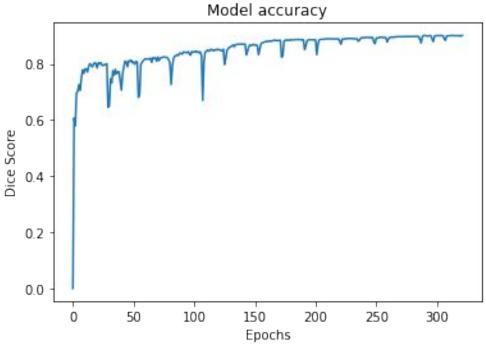


Result measurement

- Key metrics
 - Pixel accuracy
 - Not a good metric
 - Dice coefficient
 - (2 x intersection) / (union + intersection)
 - Emphasizes correct pixel prediction on intersections

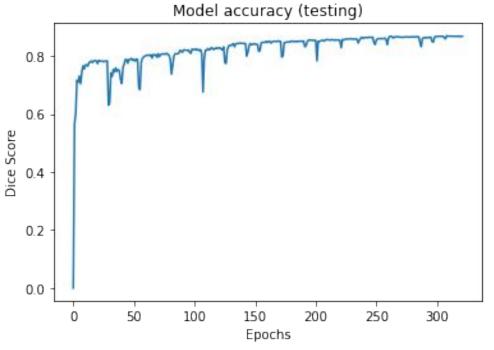


Model accuracy, validation, 91.2%



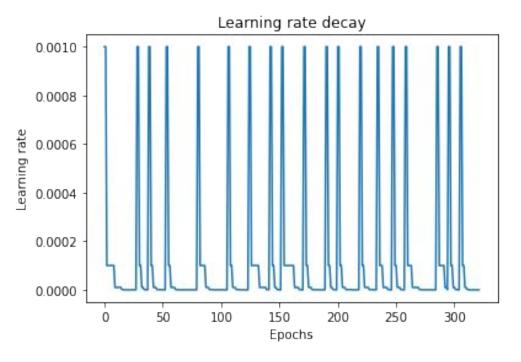


Model accuracy, testing, 86.4%



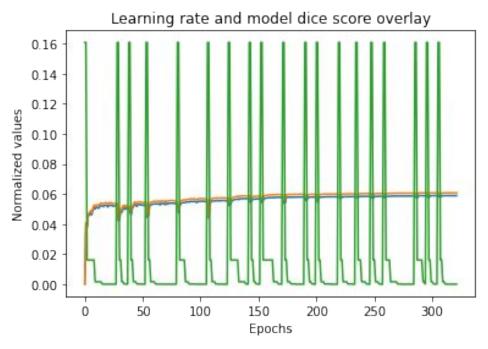


Learning rate decay





Dice coefficient and learning rate normalized





Previous Achievements

 Mateusz Buda, Ashirbani Saha, Maciej A. Mazurowski. 2019. Association of genomic subtypes of lower-grade gliomas with shape features automatically extracted by a deep learning algorithm. Computers in Biology and Medicine (June 2019), 218-225.

DOI: https://doi.org/10.1016/j.compbiomed.2019.05.002
In addition to segmentation, utilized biological identification.

- In addition to segmentation, utilized biological identification to classify characteristics of these tumors
- Dice coefficient of 82%
- We achieved 86.4%, improvement of ~4.4%



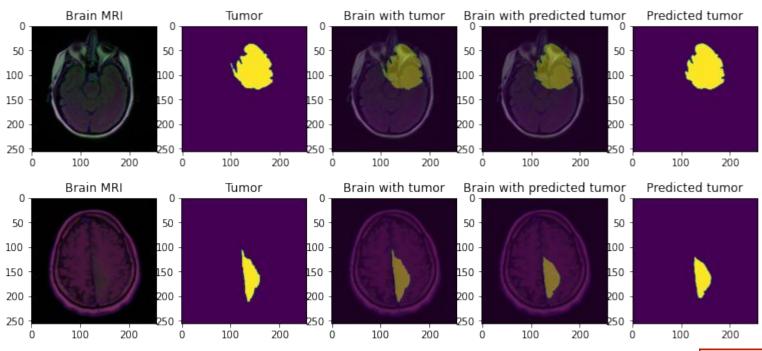
Model Performance

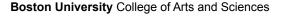
Categorized problems into three sections

- 1. Expected performance
- 2. Excellent performance
- 3. Incorrect performance



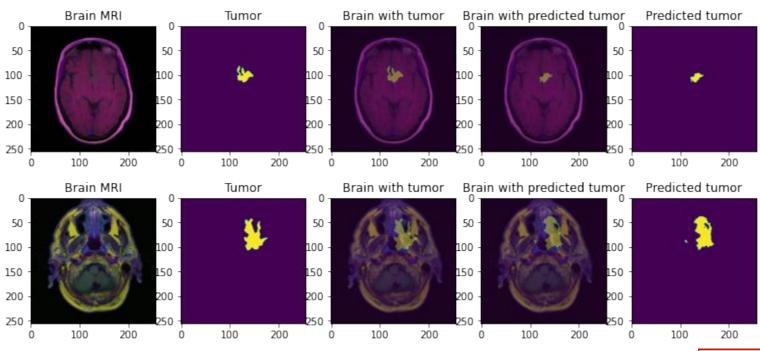
Expected performance

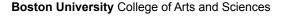






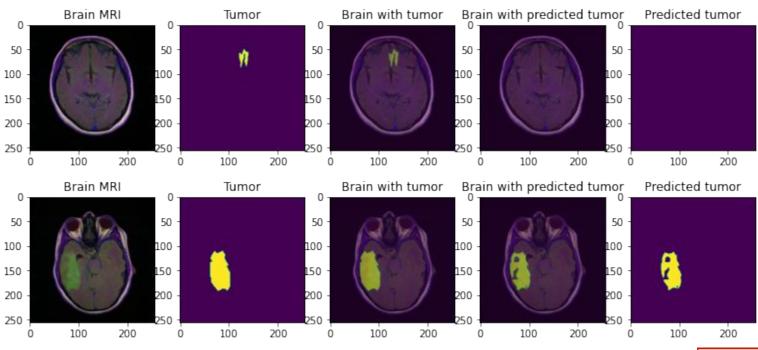
Excellent performance

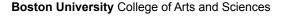






Incorrect performance







Limitations

- Data size limitations
 - 1007 MB total, 110 patients
- Network architecture
 - Not a "faithful" recreation



Future Work

- Test other model architectures
 - GoogLeNet (didn't have enough time to implement and test)
- Packaging
 - FaaS?
 - Edge deployment?
- Data improvements
- Network modifications



Q&A

Questions are welcome:)



Thank you!

