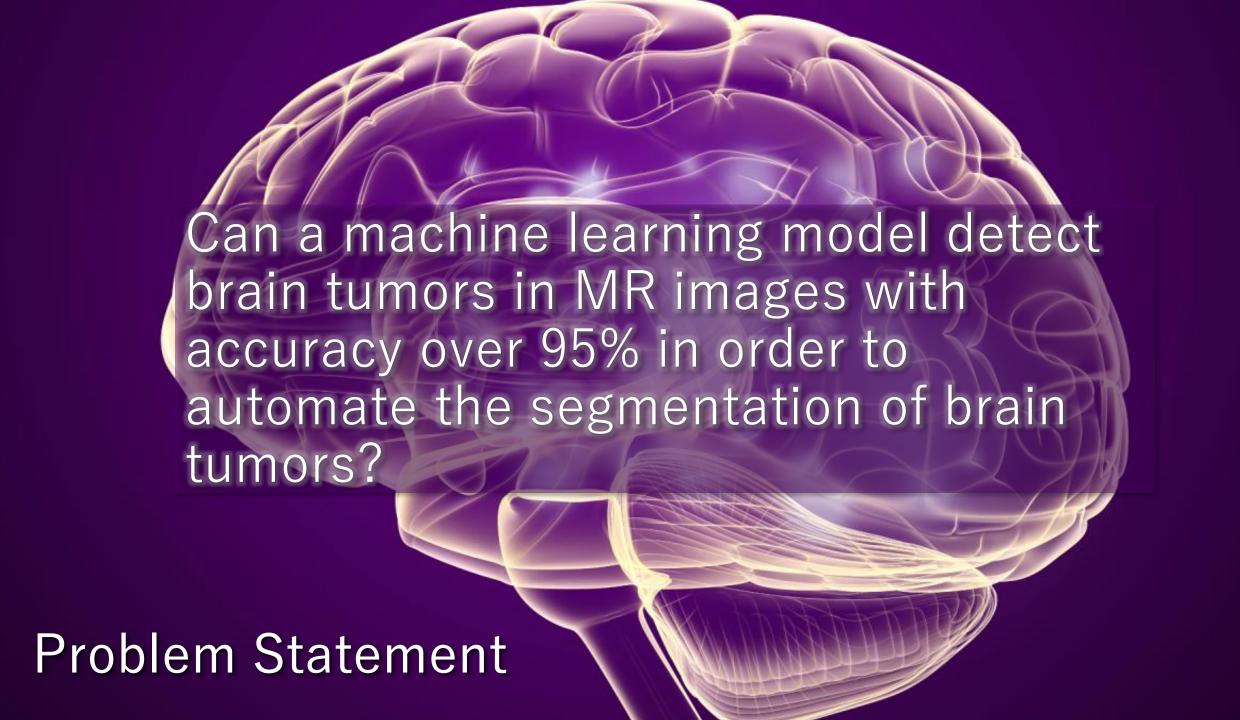
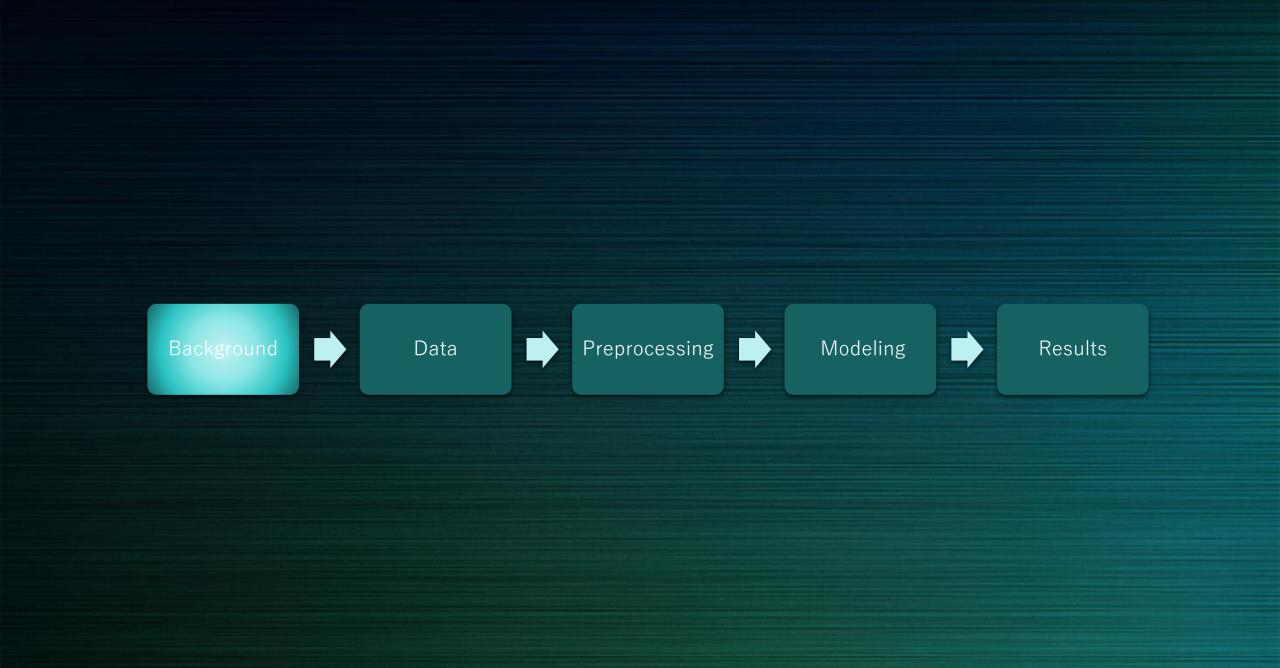
Brain Tumor Segmentation

By Anna Douville September 15th, 2020







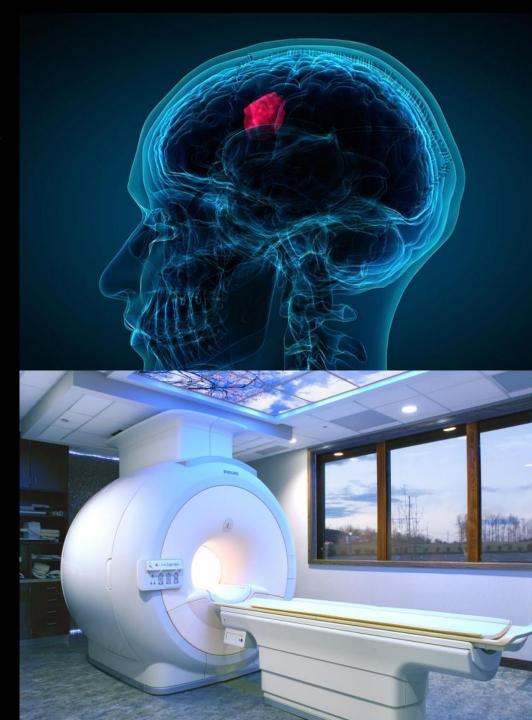
Background

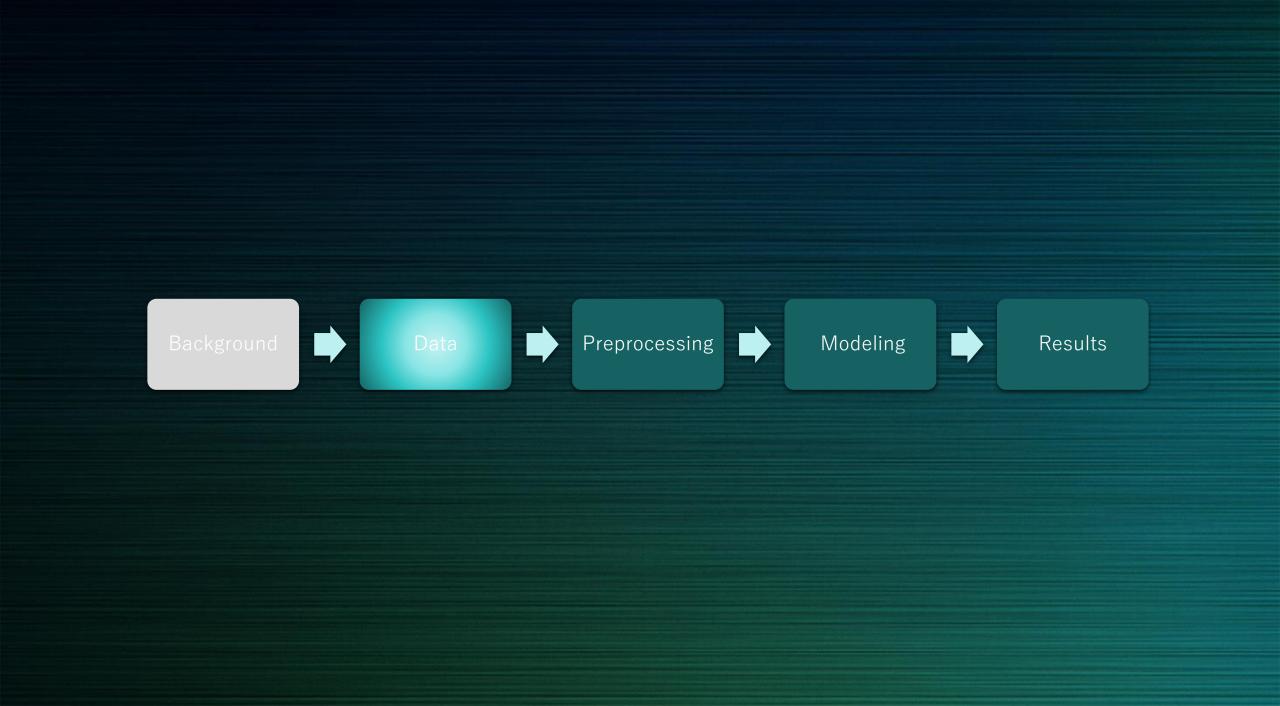
- Brain tumor: cluster of mutated cells that is potentially life-threatening
- Magnetic Resonance Imaging (MRI): non-invasive technique used to capture images of the brain
- Brain tumor segmentation: separating the tumor pixels from the non-tumor pixels in an MRI for measuring, diagnosing, informing treatment
 - Manual segmentation is extremely time consuming and difficult for radiologists

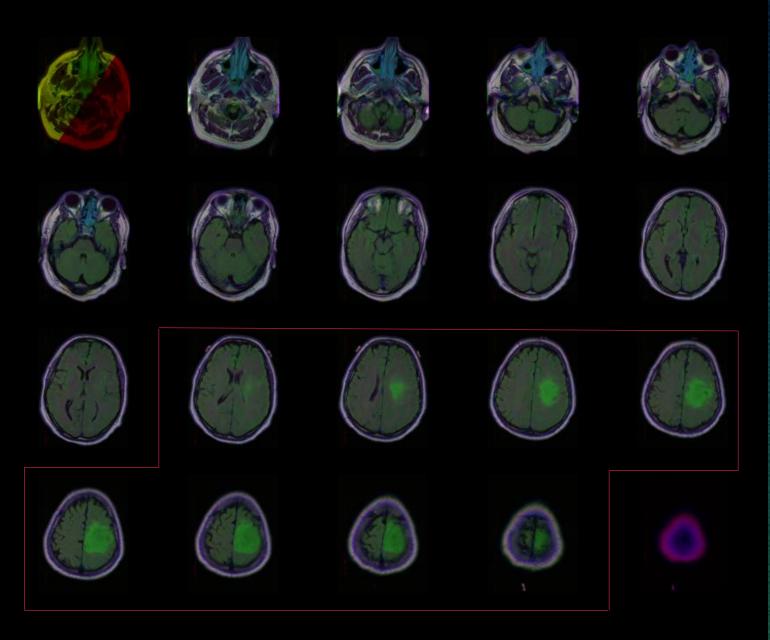
Axial Coronal Sagittal

Output

Description:

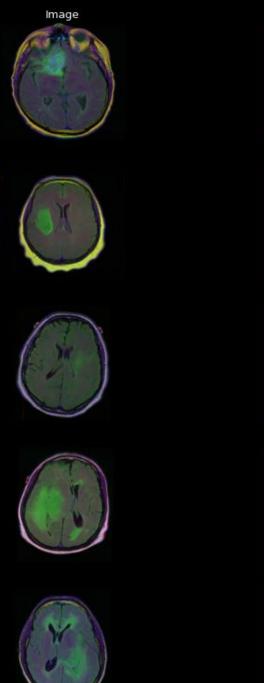


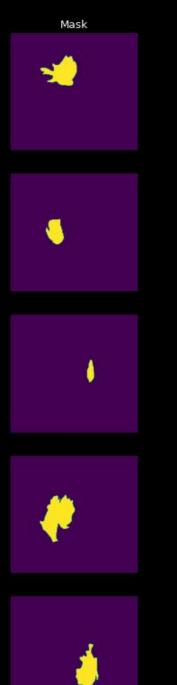


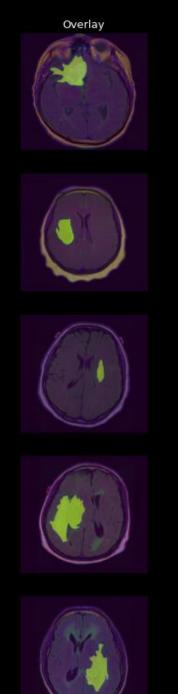


MR Images

- Subset of The Cancer Genome Atlas Low Grade Glioma (TCGA-LGG) dataset
- 3,292 MR images from 65 different patients with LGGs
- 256x256 axial cross sections
- Tumors can be seen a green mass



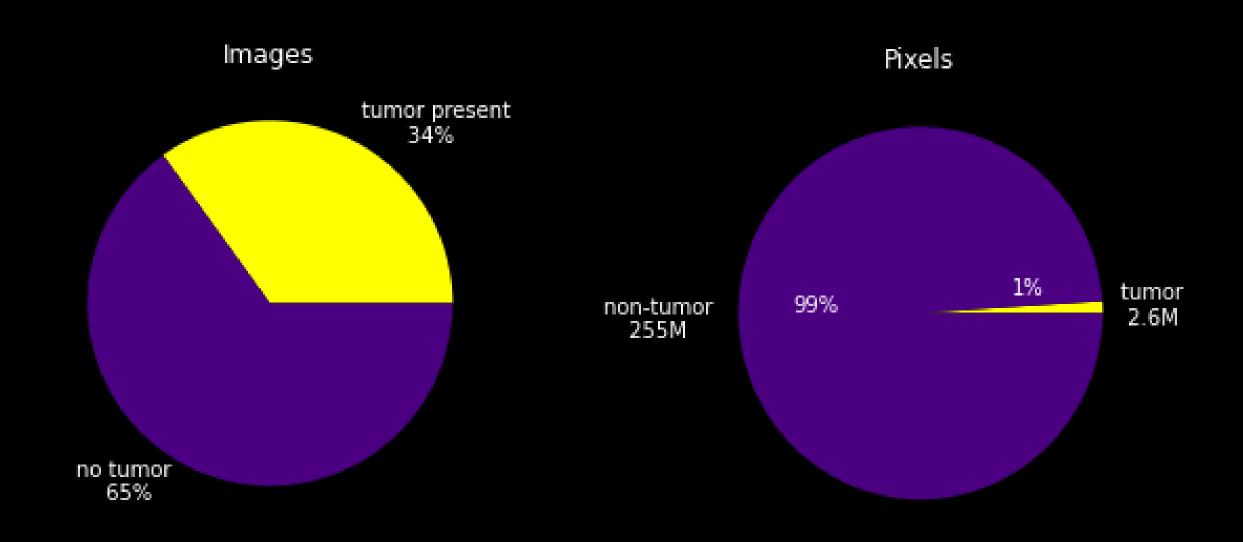


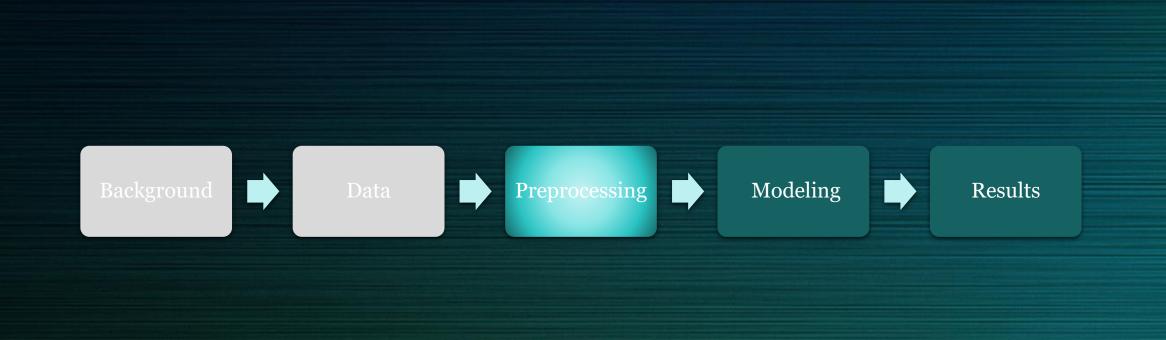




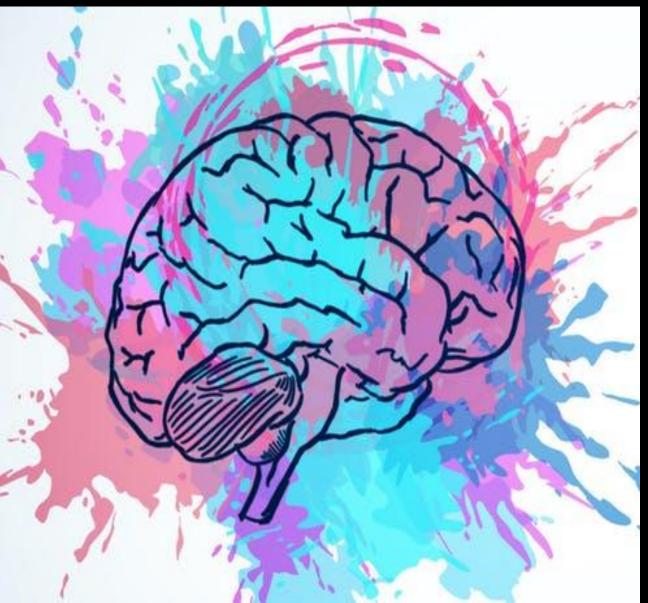
- Each MRI has a corresponding mask
- Masks label all tumor pixels (yellow) as 255 and all non-tumor pixels (purple) as 0
- Validated by board-certified radiologist

Exploratory Analysis



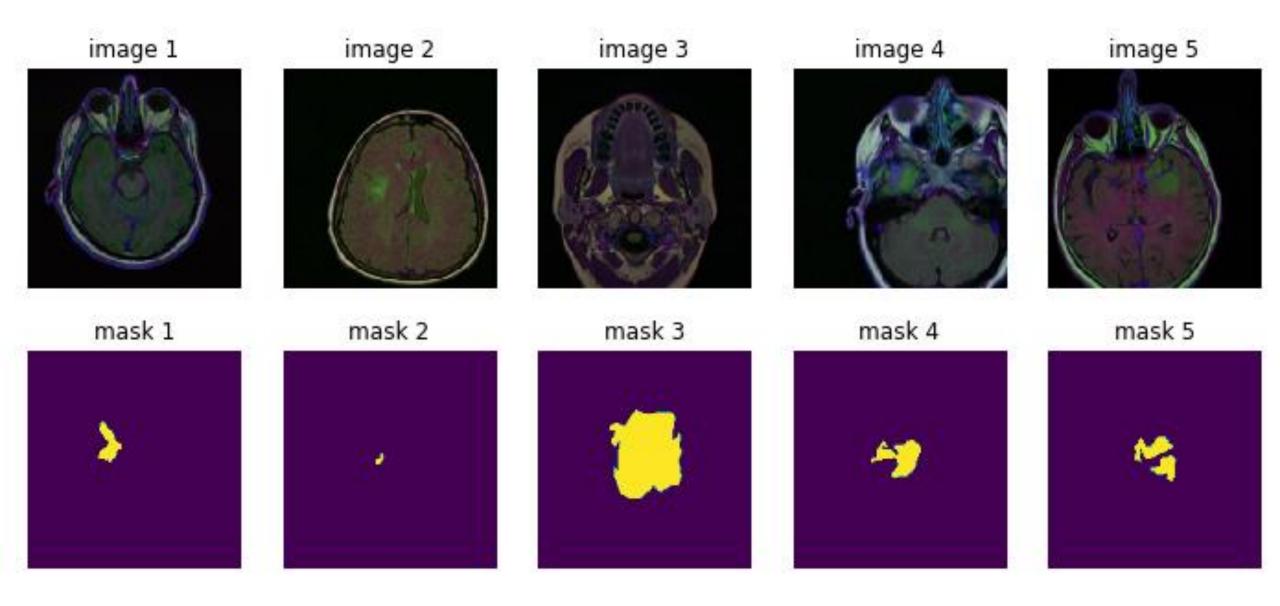


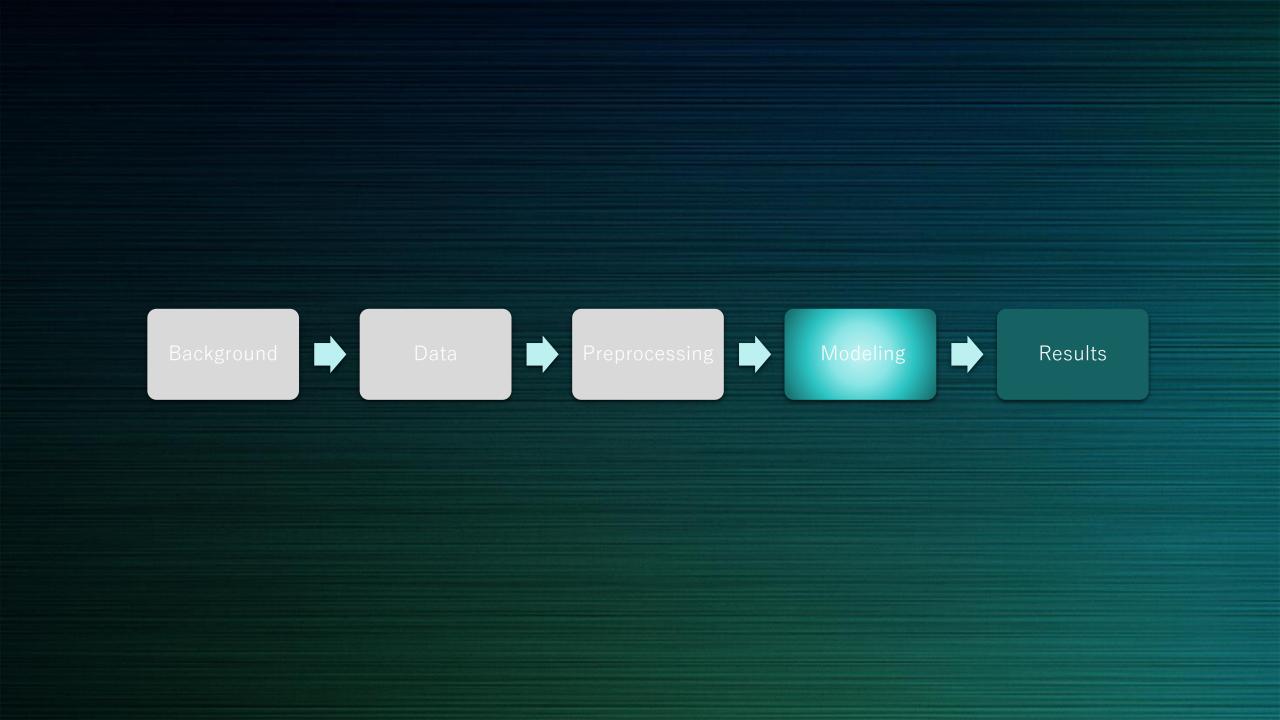
Preprocessing

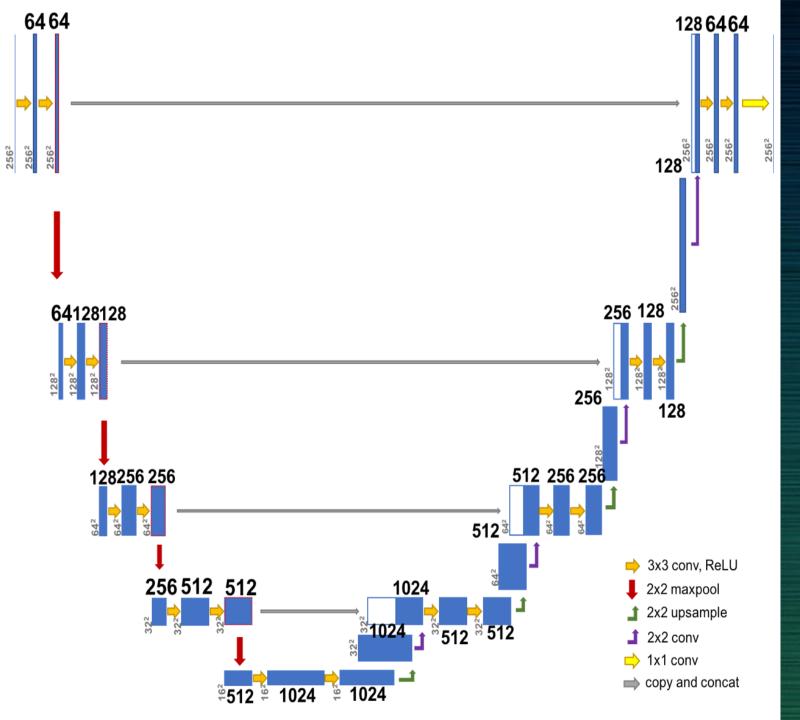


- Dropped all 2,556 images w/o a tumor present
 - increased the percentage of tumor pixels to 2.9%
 - decreased size of the dataset to 1,373 image & mask pairs
- Cropped images around the tumor w/ random amount of padding on each side
 - Increased percentage of tumor pixels to 6% w/o sacrificing too much context
- Resized images back to 256x256
- Scaled images by 255 to normalize data from 0 to 1

Transformations

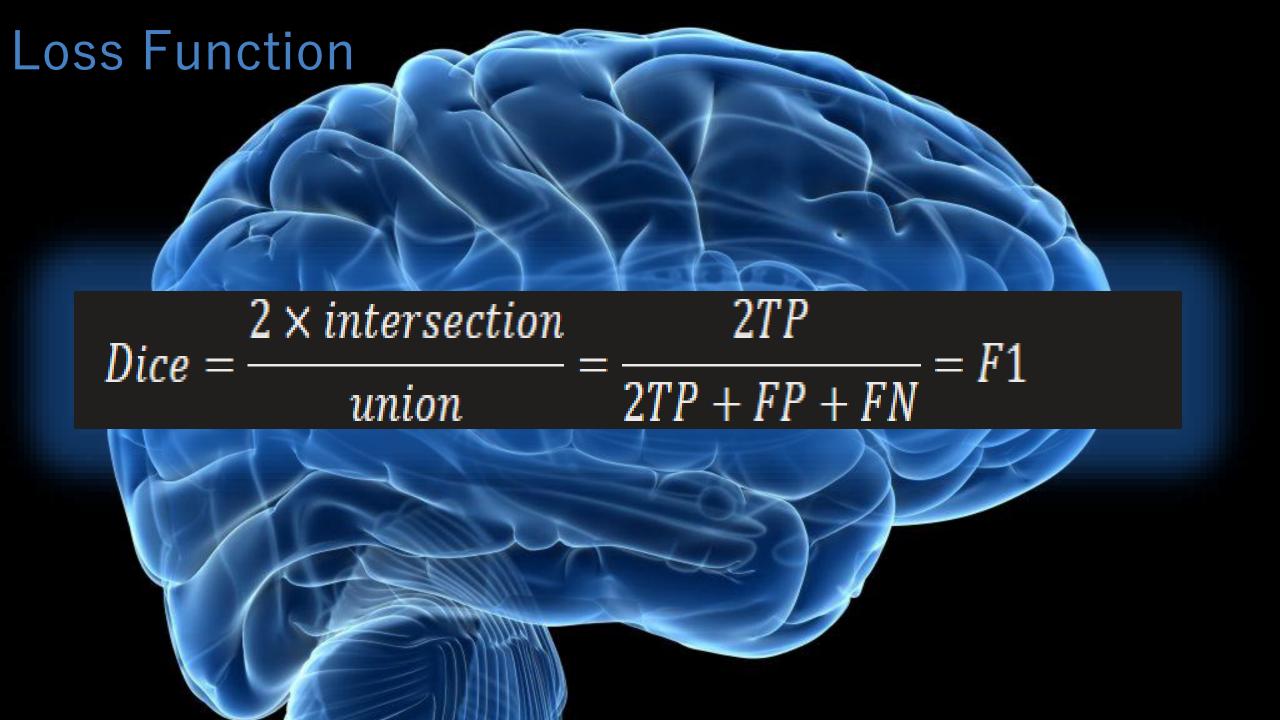






U-Net

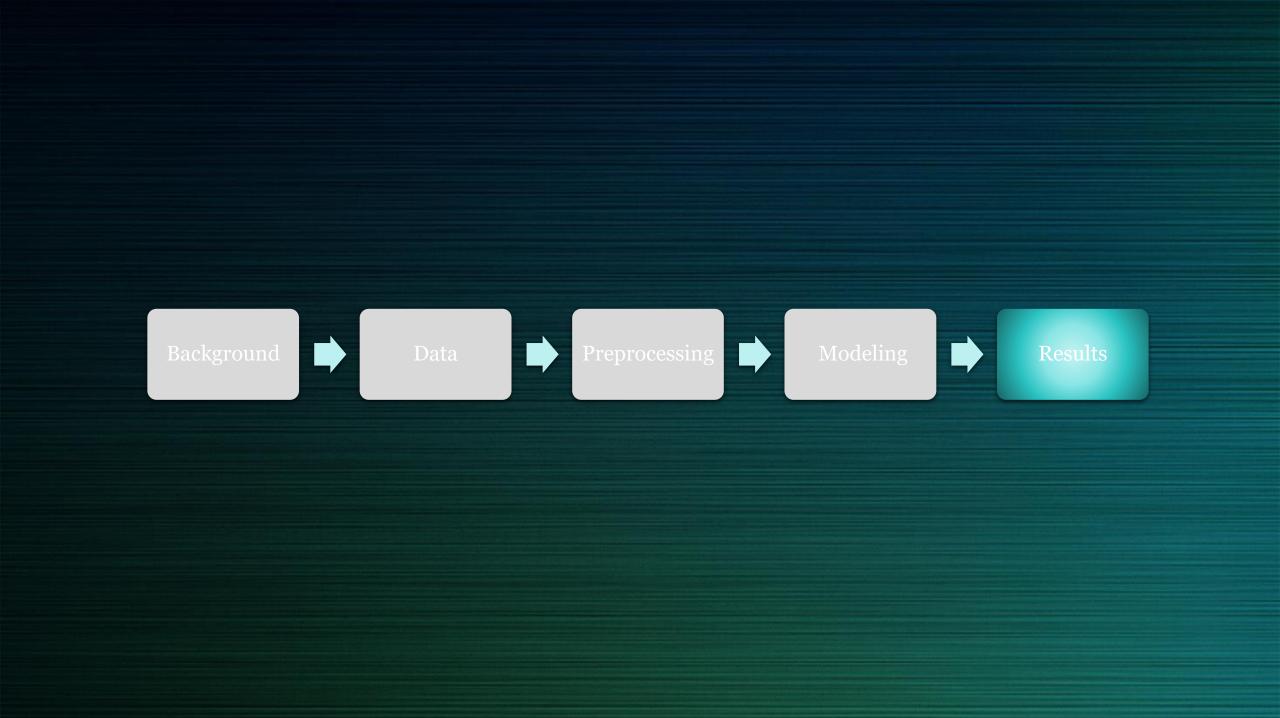
- FCN developed for biomedical image segmentation
- Encoder path
 - pooling
 - convolutions
 - provides context information
- Decoder path
 - upsampling
 - convolutions
 - provides spatial information
- Skip connections
 - ensure context is not lost
- Binary output for every pixel
- 22,384,577 parameters to train



Hyperparameters

- Adam Optimizer
 - Learning rate = .001
 - Decay = learning rate / # epochs
 - Epsilon = None
- Convolution Layers
 - Activation = ReLU
 - Kernel initializer = HeNormal
 - Padding = Same
- Batch size: 32
- Epochs: 100
- Callbacks: ModelCheckpoints





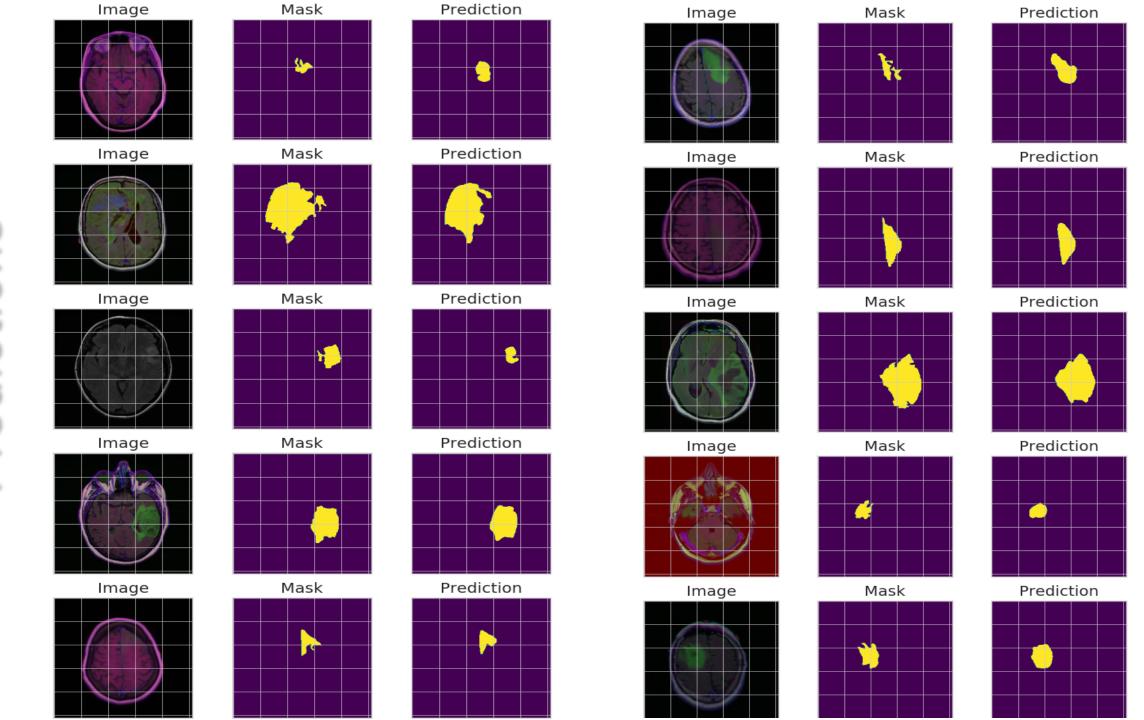
Model Performance

Accuracy: .98

Dice Coefficient: .68

	loss	accuracy	dice
train	0.200864	0.986188	0.799399
test	0.331611	0.983733	0.677358





Summary

- Brain tumor segmentation is crucial for the proper measurement, treatment, and diagnosis of a tumor
- Previously, radiologists had to spend hours manually segmenting brain tumors from MRI
- Radiologists can use a deep learning model with a U-Net architecture for semiautomated brain tumor segmentation with a binary accuracy of 98%
- Model performance may improve with a much larger dataset or with different variations of the U-Net that may allow for fully automated brain tumor segmentation

