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The current state and implications of tumor diagnosis from Brain MRIs

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Introducing the sumMRI platform for enhanced tumor diagnosis

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Deep dive into front-end, back-end, and ML model implementation

01 Problem

Where are we now?





250,000 Deaths Annually

Brain tumors are the 10th leading cause of death for humans, with over 250,000 dying from brain tumors annually [1]



Diagnosis Inefficiencies

ResearchDiagnostic error rates are stuck at 5%^[3]

Early assisted diagnosis can improve recovery rates by 400%^[2]

Errors

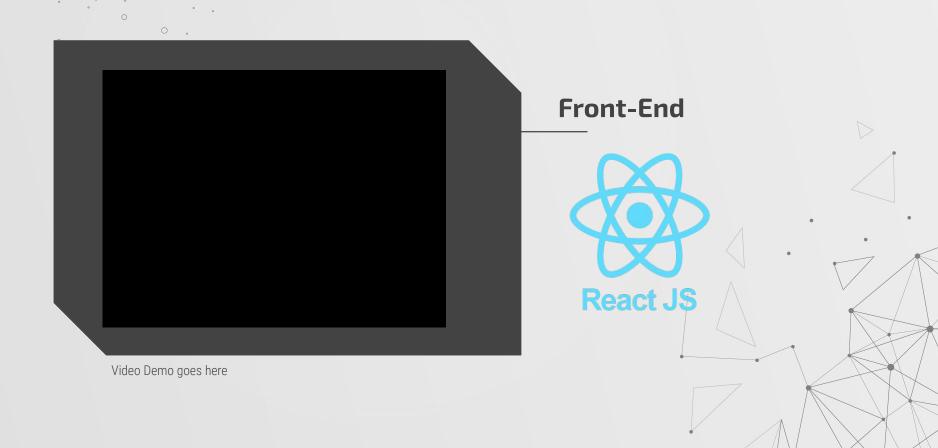
40 million diagnostic errors annually^[4]

Burnout

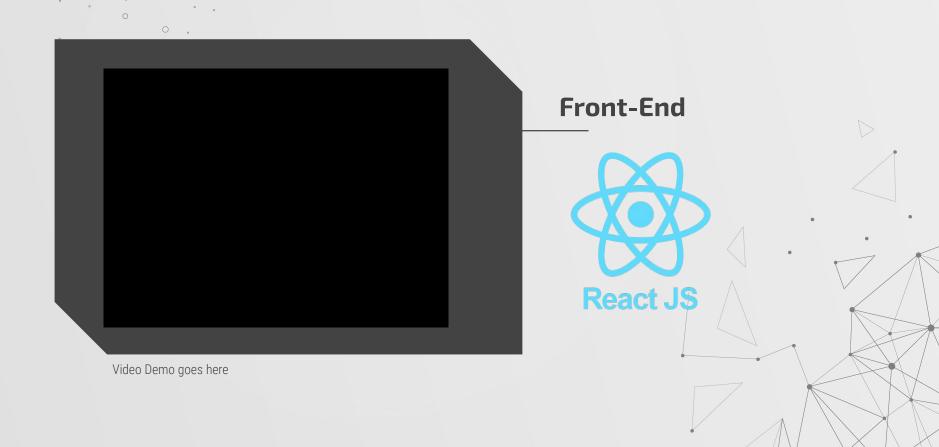
Radiologists spend 3-4 seconds/image^[5]



Demo: Tumor Found



Demo: Tumor Not Found



Model Performance

126 — Images Tested On

0.65 Loss

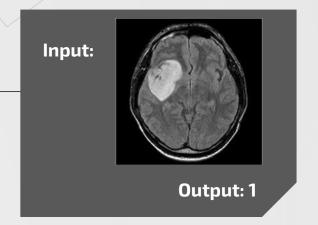
83.33%

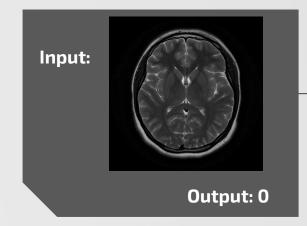
Accuracy



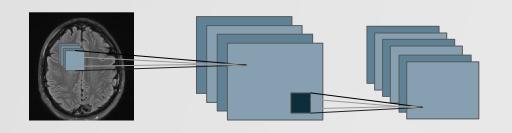


CLASSIFICATION





Convolutional Neural Network



INPUT IMAGE

Takes an MRI scan of a brain as input

FEATURE MAPS

Identify relevant features

POOLING

Abstract away irrelevant features





FLATTENING

Produce a 1d array of numbers

VALIDATION

Check if model works for new, unseen data

CLASSIFICATION

Outputs 1 if tumor is present, 0 if not

Building and Training a Neural Net

```
# creates model for exactly one input and one output
model = Sequential()
# layer that normalizes inputs
model.add(BatchNormalization(input_shape = (28,28,3)))
# convolution layer - forms a representation of part of an image:
# 32 - filters: the number of output filters in the convolution
# (3, 3) - kernel size: height, width of convolution window
   activation function. relu = rectified linear unit
model.add(Convolution2D(32, (3,3), activation = 'relu', input shape = (28, 28, 3)))
# pooling layer - abstracts away irrelevant parts of the image
# pool size = size over which to take the max value (2x2)
model.add(MaxPooling2D(pool size=2))
# padding = 'same' -> even padding to the left/right/up/down of input such that
# the output has the same dimensions as input
model.add(Convolution2D(filters=64, kernel size=4, padding='same', activation='relu'))
model.add(MaxPooling2D(pool size=2))
model.add(Convolution2D(filters=128, kernel size=3, padding='same', activation='relu'))
model.add(MaxPooling2D(pool size=2))
model.add(Convolution2D(filters=128, kernel size=2, padding='same', activation='relu'))
model.add(MaxPooling2D(pool size=2))
# dropout layer - randomly sets input units to 0 w frequency of rate (0.25)
# at each step during training time
model.add(Dropout(0.25))
# flattening layer - values are compressed into a vector to be processed
model.add(Flatten())
# densely connected NN layer
# units = dimensionality of output space
model.add(Dense(units=128,activation = 'relu'))
model.add(Dense(units = 64, activation = 'relu'))
model.add(Dense(units = 32, activation = 'relu'))
model.add(Dense(units = 2, activation = 'softmax'))
```

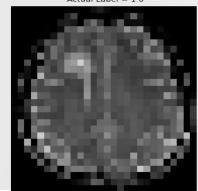
model.compile(optimizer='adam', loss = 'categorical crossentropy',metrics = ['accuracy'])

CNN Model Output

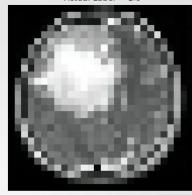
Prediction Class = 0.0 Actual Label = 0.0



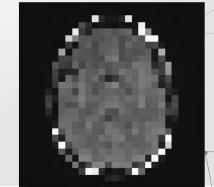
Prediction Class = 1.0 Actual Label = 1.0



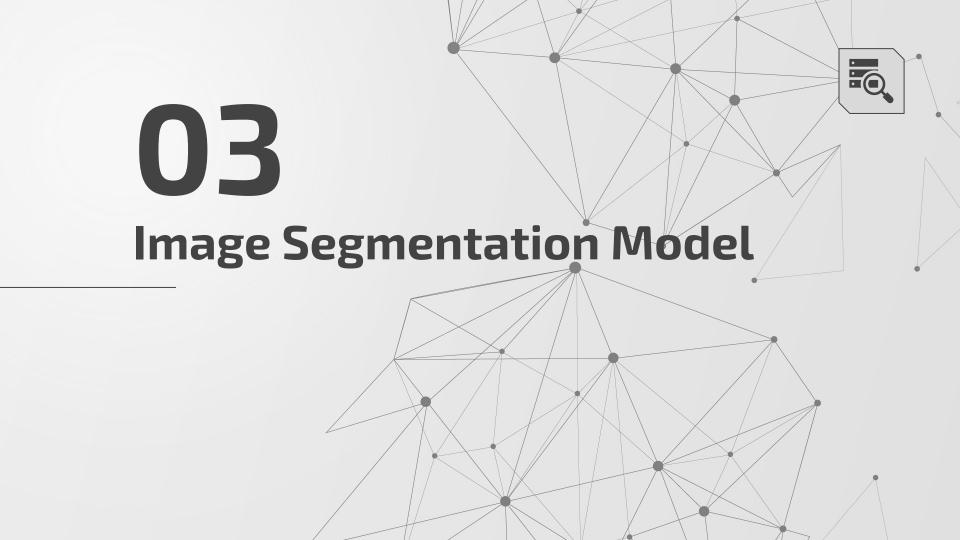
Prediction Class = 1.0 Actual Label = 1.0



Prediction Class = 0.0 Actual Label = 0.0



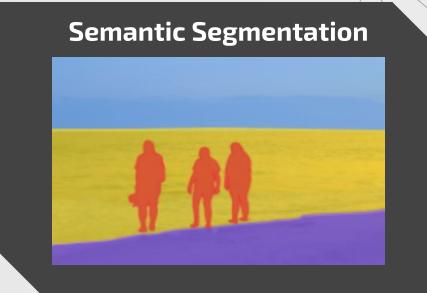




Semantic Segmentation

Use a CNN to classify each pixel in a grid.

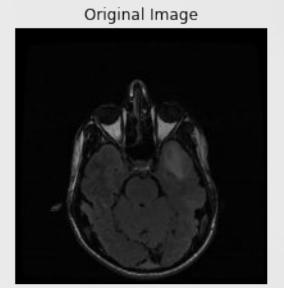




Our Semantic Segmentation

Issue #1: Not a lot of Training Data (relative to Population Needs)

Issue #2: Small Details need to be Segmented

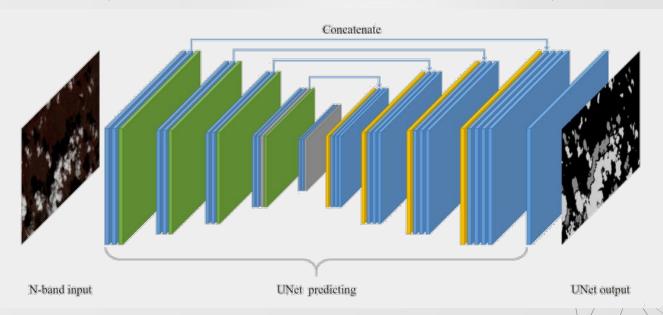




U-Net

Convolutional Network for Biomedical Image Segmentation

- Detects structures with low contrast
- Fast (Model can process an image in 1 second)



U-Net

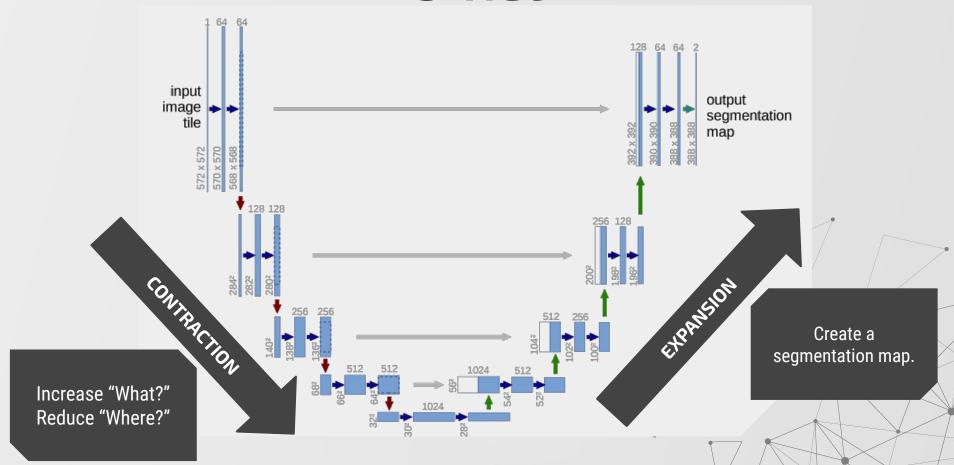


Image Segmentation Model Output

