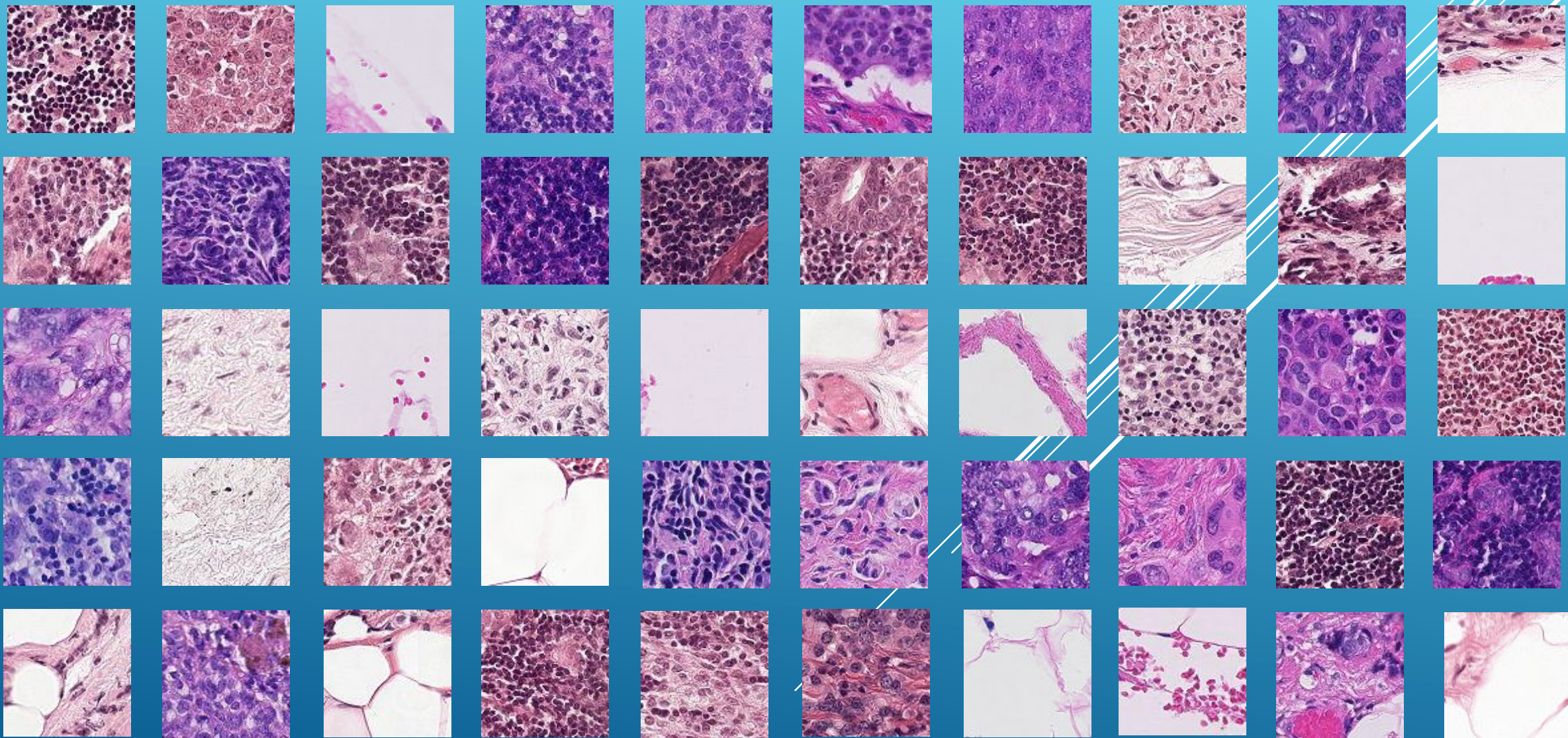


HISTOPATHOLOGIC CANCER DETECTION

<https://www.kaggle.com/c/histopathologic-cancer-detection>



DATA STRUCTURE AND PIPELINE

A series of several thin, white, parallel diagonal lines extending from the bottom right towards the top right of the slide, creating a sense of motion or a pipeline.


```
#Preview the total number of files provided and the train_labels.csv
print('Train Files =',len(os.listdir(train)), 'Validation Files =',len(os.listdir(test)))
labels.head()
```

Train Files = 220025 Validation Files = 57458

	id	label
0	f38a6374c348f90b587e046aac6079959adf3835	0
1	c18f2d887b7ae4f6742ee445113fa1aef383ed77	1
2	755db6279dae599ebb4d39a9123cce439965282d	0
3	bc3f0c64fb968ff4a8bd33af6971ecae77c75e08	0
4	068aba587a4950175d04c680d38943fd488d6a9d	0

```
#Build a single dataframe that includes each of the images unique id, file path, and corresponding label (1,0)
df = pd.DataFrame({'path': glob(os.path.join(train, '*.tif'))})
df['id'] = df.path.map(lambda x: x.split('\\')[1].split(".")[0])
df_data = df.merge(labels, on = 'id')
df_data.head()
```

	path	id	label
0	D:/Kaggle/Cancer Detection/histopathologic-can...	00001b2b5609af42ab0ab276dd4cd41c3e7745b5	1
1	D:/Kaggle/Cancer Detection/histopathologic-can...	000020de2aa6193f4c160e398a8edea95b1da598	0
2	D:/Kaggle/Cancer Detection/histopathologic-can...	00004aab08381d25d315384d646f5ce413ea24b1	0
3	D:/Kaggle/Cancer Detection/histopathologic-can...	0000d563d5cfafc4e68acb7c9829258a298d9b6a	0
4	D:/Kaggle/Cancer Detection/histopathologic-can...	0000da768d06b879e5754c43e2298ce48726f722	1

```
df_data.groupby('label').id.nunique()
```

```
label
0    130908
1     89117
Name: id, dtype: int64
```

Naive Assumption = 40%



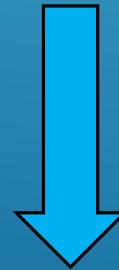
Train Directory
(160,000 Images)



Train Set
(144,000 Images)

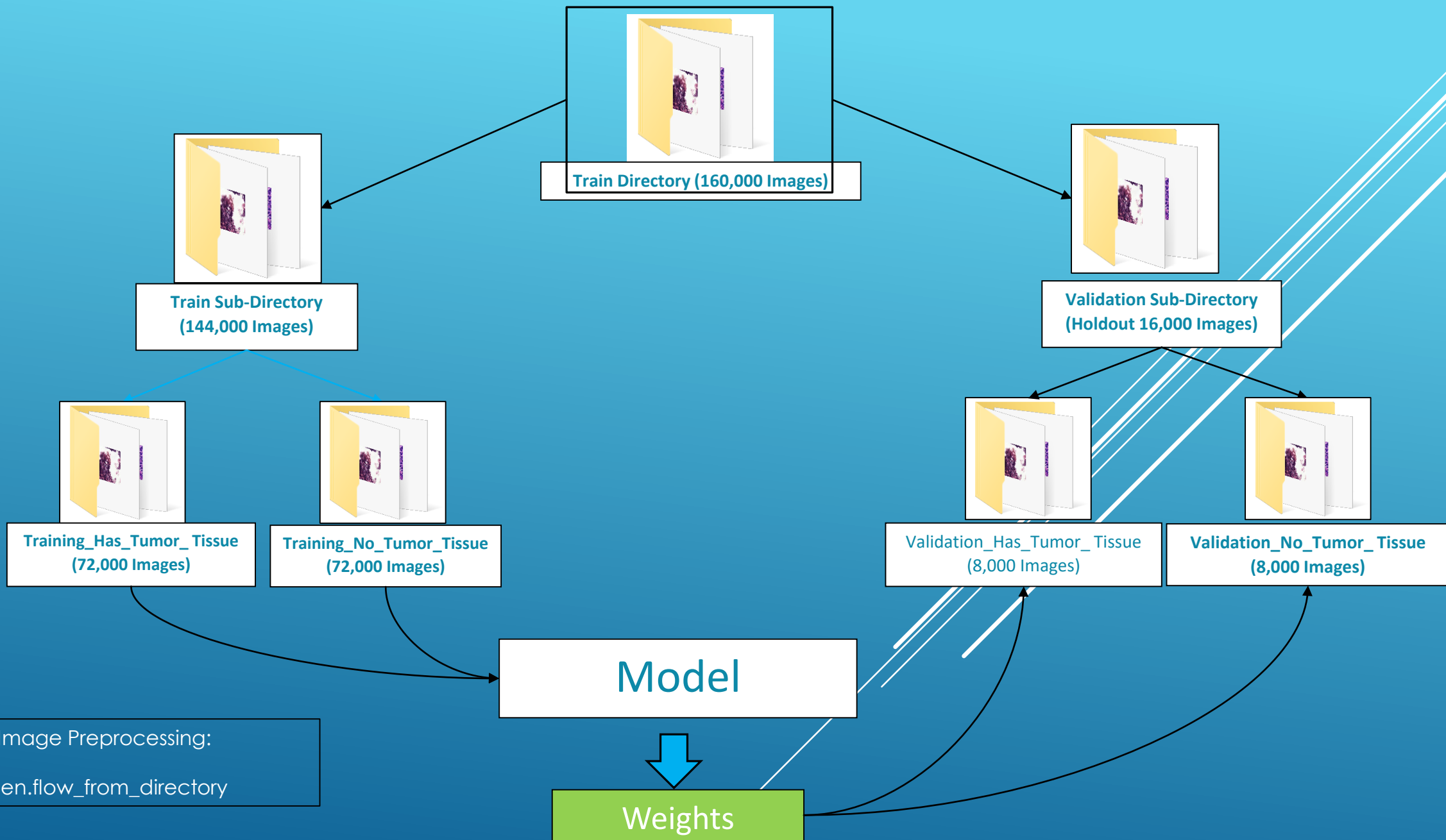


Model



Kernel Crash

Test Set
(Holdout 16,000)



Keras Image Preprocessing:
Datagen.flow_from_directory

Conceptualize and
Build our Model

Several thin, white, parallel lines of varying lengths and slight curves are positioned on the right side of the slide, extending from the top right towards the bottom right.

0	0	0	0	0	0	...
0	156	155	156	158	158	...
0	153	154	157	159	159	...
0	149	151	155	158	159	...
0	146	146	149	153	158	...
0	145	143	143	148	158	...
...

Input Channel #1 (Red)

0	0	0	0	0	0	...
0	167	166	167	169	169	...
0	164	165	168	170	170	...
0	160	162	166	169	170	...
0	156	156	159	163	168	...
0	155	153	153	158	168	...
...

Input Channel #2 (Green)

0	0	0	0	0	0	...
0	163	162	163	165	165	...
0	160	161	164	166	166	...
0	156	158	162	165	166	...
0	155	155	158	162	167	...
0	154	152	152	157	167	...
...

Input Channel #3 (Blue)

Image Dimensions
96x96x3

-1	-1	1
0	1	-1
0	1	1

Kernel Channel #1



308

1	0	0
1	-1	-1
1	0	-1

Kernel Channel #2



-498

0	1	1
0	1	0
1	-1	1

Kernel Channel #3



164

+

+

+ 1 = -25



Bias = 1

Feature Map
Output

-25				...
				...
				...
				...
...


```
kernel_size = (3,3) #Height and Width of the convolution window.  
pool_size= (2,2) #Size of the max pooling windows  
first_filters = 32  
second_filters = 64  
third_filters = 128
```

```
dropout_conv = 0.3  
dropout_dense = 0.3
```

```
model = Sequential()  
model.add(Conv2D(first_filters, kernel_size, activation = 'relu', input_shape = (96, 96, 3)))  
model.add(Conv2D(first_filters, kernel_size, activation = 'relu'))  
model.add(MaxPool2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

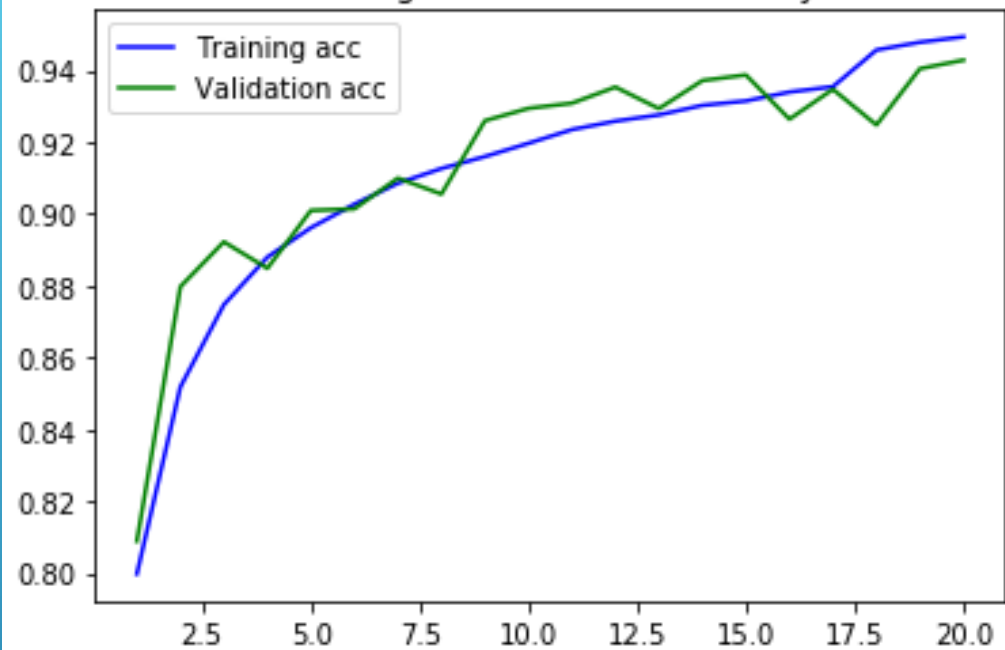
```
model.add(Conv2D(second_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(second_filters, kernel_size, activation = 'relu'))  
model.add(MaxPool2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

```
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(Conv2D(third_filters, kernel_size, activation = 'relu'))  
model.add(MaxPool2D(pool_size = pool_size))  
model.add(Dropout(dropout_conv))
```

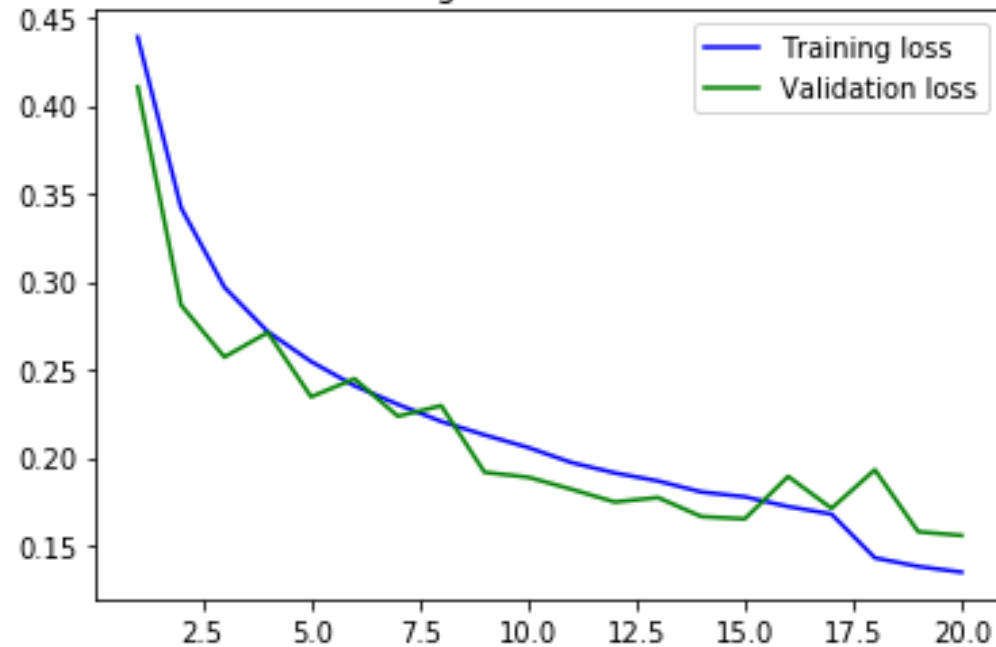
```
model.add(Flatten())  
model.add(Dense(256, activation = "relu"))  
model.add(Dropout(dropout_dense))  
model.add(Dense(1, activation = "sigmoid"))
```

```
model.summary()
```

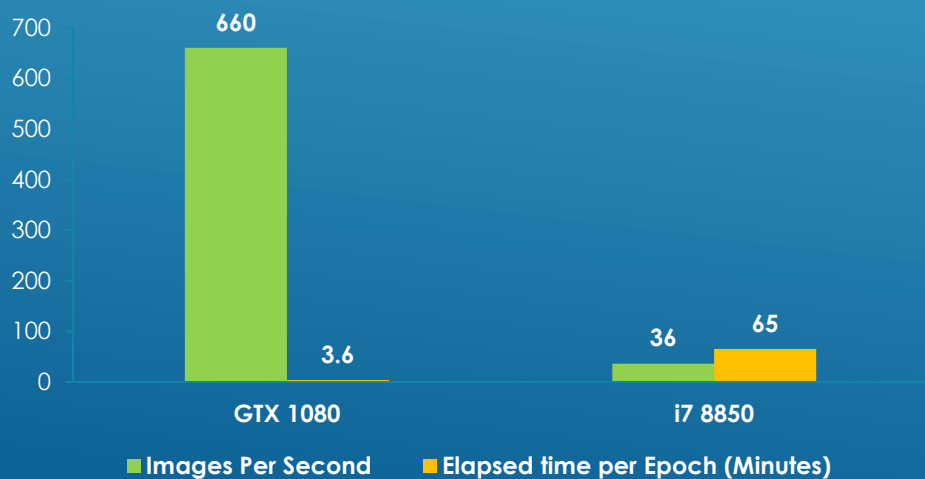
Training and validation accuracy



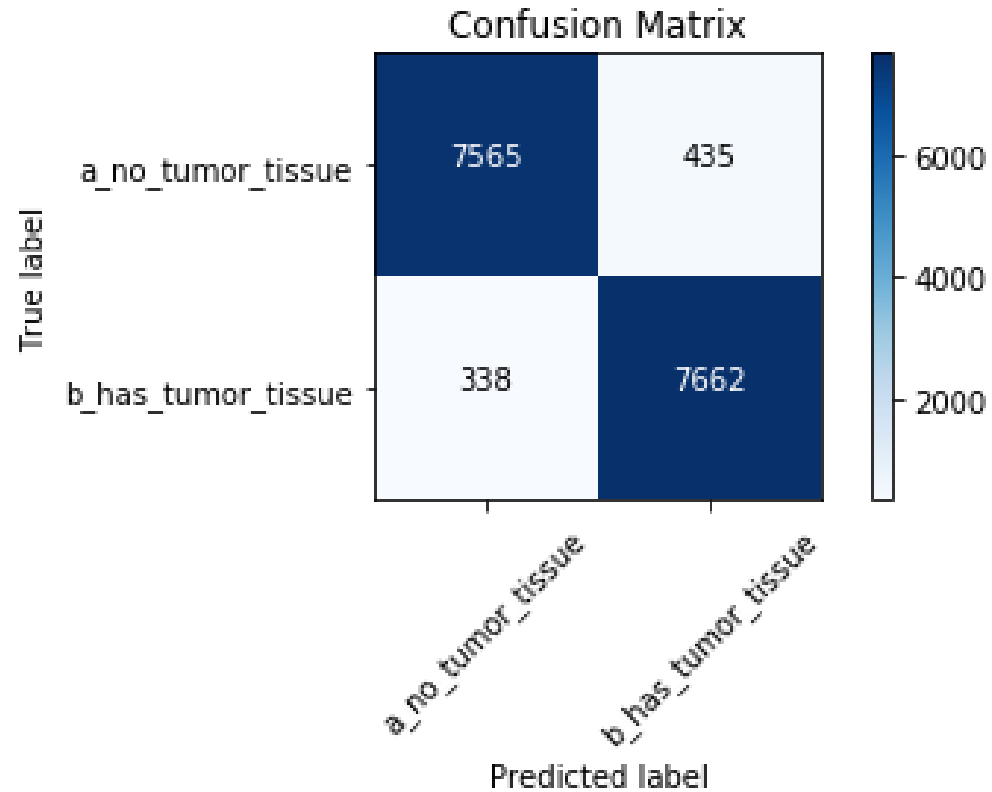
Training and validation loss



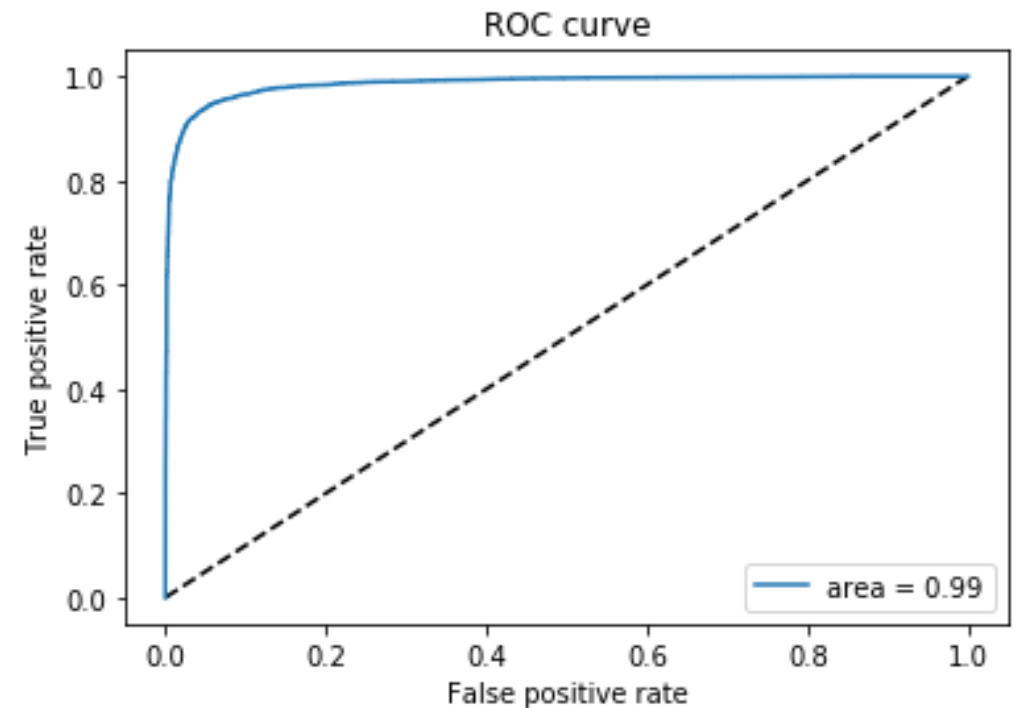
Time to Train



Model Validation



AUC = 0.989



	precision	recall	f1-score	support
a_no_tumor_tissue	0.96	0.95	0.95	8000
b_has_tumor_tissue	0.95	0.96	0.95	8000
micro avg	0.95	0.95	0.95	16000
macro avg	0.95	0.95	0.95	16000
weighted avg	0.95	0.95	0.95	16000

REFERENCES

- **Stanford CNN Overview** - <http://cs231n.github.io/convolutional-networks/>
 - **Public Kernel Referenced** - <https://www.kaggle.com/vbookshelf/cnn-how-to-use-160-000-images-without-crashing>
 - **Keras Documentation** - <https://keras.io/>
- 
- Several white lines of varying lengths and angles are drawn in the bottom right corner of the slide, creating a modern, abstract graphic element.