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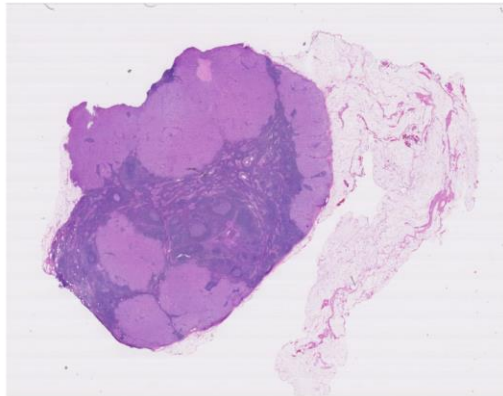
# Detecting Cancer Metastases On Gigapixel Pathology Images

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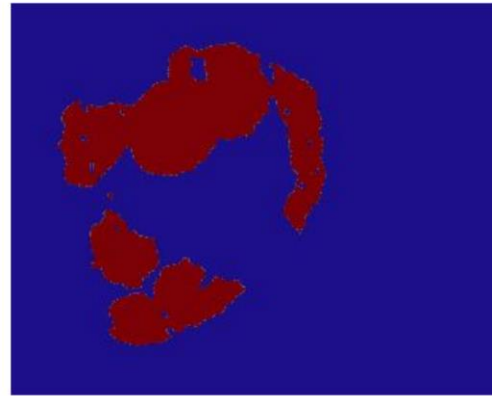
Aashish Misraa (akm2215)

# PROBLEM STATEMENT

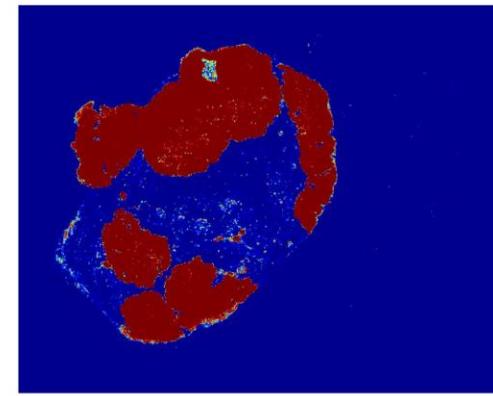
- Develop a deep learning model that outputs a heatmap showing regions of a biopsy image likely to contain cancer
- We explore different deep learning techniques to arrive at a solution that can be used to ***assist*** in diagnosis



*Biopsy image*

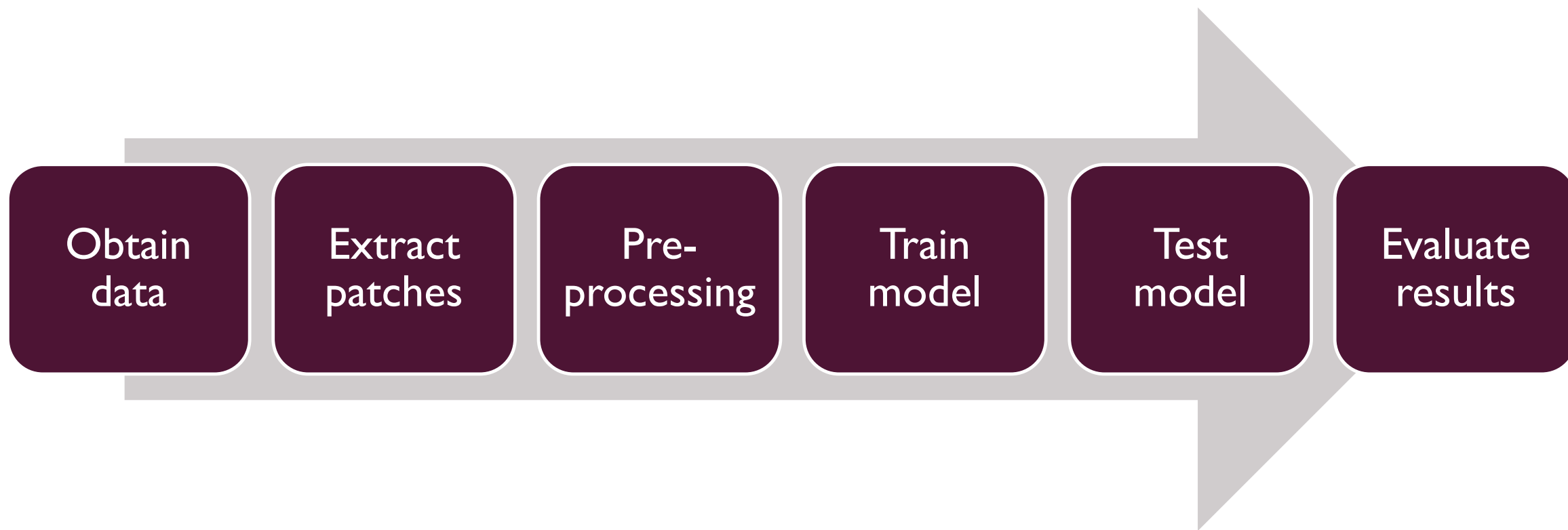


*Ground truth  
(from pathologist)*



*Model predictions*

# WORKFLOW



# OBTAINING DATA

- CAMELYON 16 dataset
- The training and testing data are a single slide each (randomly chosen)
  - Training slide : tumor\_078.tif (and associated mask)
  - Testing slide : tumor\_110.tif (and associated mask for evaluation)
- Choose two levels per slide : levels 3 and 6 (could not use more due to memory issues!)
  - Downsample factor for level 3 is 8
  - Downsample factor for level 6 is 64

# EXTRACTING PATCHES

- Patch size : 100 x 100
- Central window size : 60 x 60 (To extract the mask context, referenced from the original paper)
- Stride : 60
- Patches are extracted using a sliding window technique

# PRE - PROCESSING

- Data augmentation:
  - Rotating the patch by 90 degrees (4 times, so all rotations are obtained)
- Sampling
  - To combat the class imbalance problem – there are far more non-cancer patches than there are cancer patches (anywhere between 1 : 10 to 1 : 15, depending on the extraction method)
  - The non cancer patches were added to the training data if a randomly generated choice was above a certain threshold
    - Threshold value was set through trial-and-error

## PRE – PROCESSING (CONTD.)

- We finally obtain the patches across the different levels, shuffle them and create a final training set of patches and labels
  - Label 1 for tumor cell
  - Label 0 for normal cell
- The data is now ready to be used for training the model

## TRAIN MODEL

- Use the **same** model to train patches across both levels (Deviation from the paper, which uses different InceptionV3 towers for each level)
  - Done due to memory restrictions (Colab runs out of RAM)
- Use transfer learning with InceptionV3 (as the base)
- Model is NOT trained on ImageNet weights!
- Base is followed by Global Average Pooling, 2 Dense layers(relu and sigmoid) and 0.2 Dropout



## TRAIN MODEL (CONTD.)

- Model parameters:
  - Optimizer : RMSprop (learning rate is 0.0001)
  - Loss : Binary Crossentropy
  - Metric : Accuracy
  - Number of epochs : 20
  - Batch size : 64 (also experiment with 32)
- Use `model.fit()` 's `validation_split` feature to divide data into 75% for train, 25% for validation

# MODEL SUMMARY

Model: "sequential"

Layer (type)	Output Shape	Param #
=====		
inception_v3 (Model)	(None, 1, 1, 2048)	21802784
-----		
global_average_pooling2d (Gl	(None, 2048)	0
-----		
dense (Dense)	(None, 128)	262272
-----		
dropout (Dropout)	(None, 128)	0
-----		
dense_1 (Dense)	(None, 1)	129
=====		

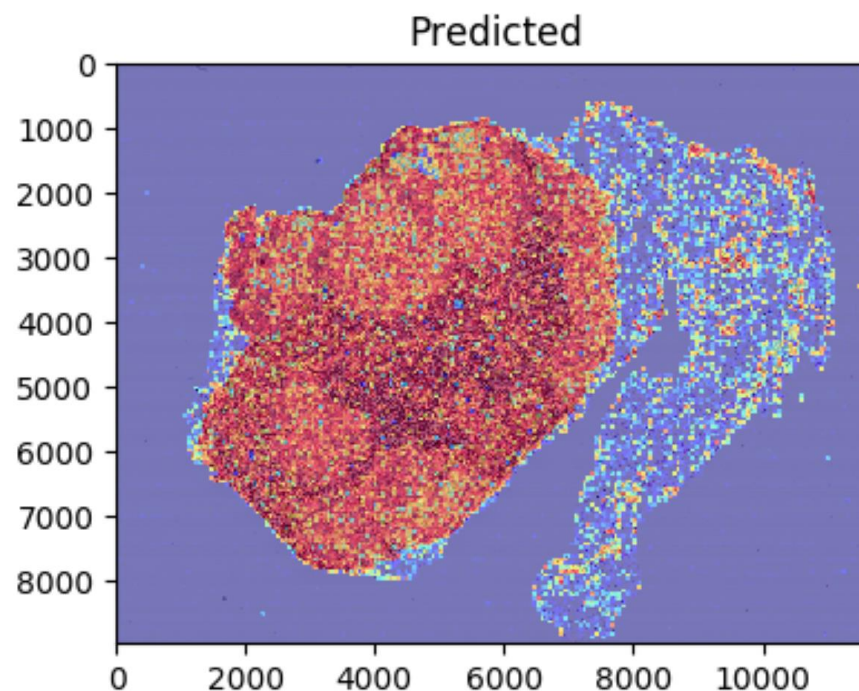
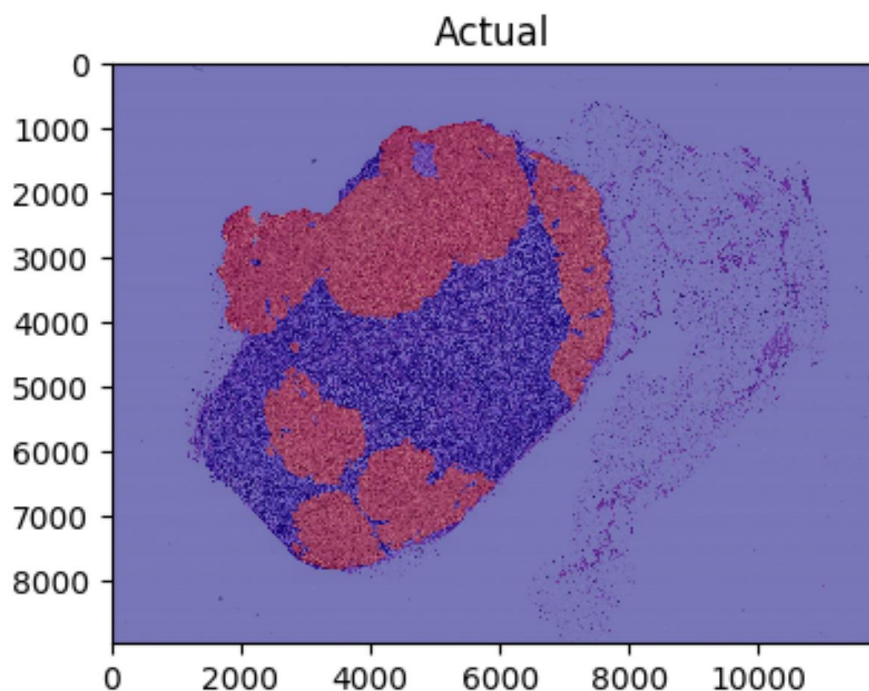
Total params: 22,065,185

Trainable params: 262,401

Non-trainable params: 21,802,784

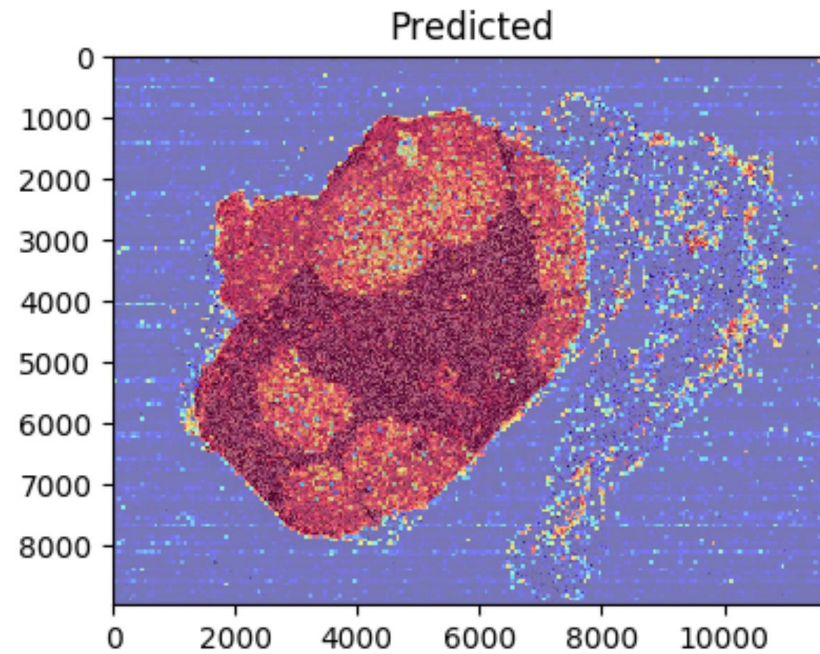
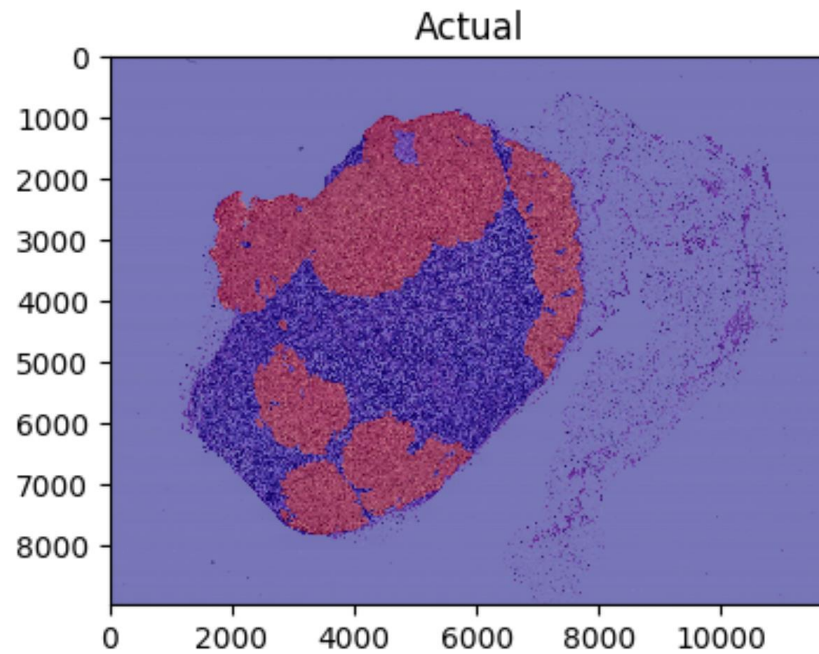
## TEST MODEL

- Model predicts on a test slide at level 3 (uses a similar patch extraction approach)
- Model performance can be improved!



For 20 epochs

## TEST MODEL (CONTD.)

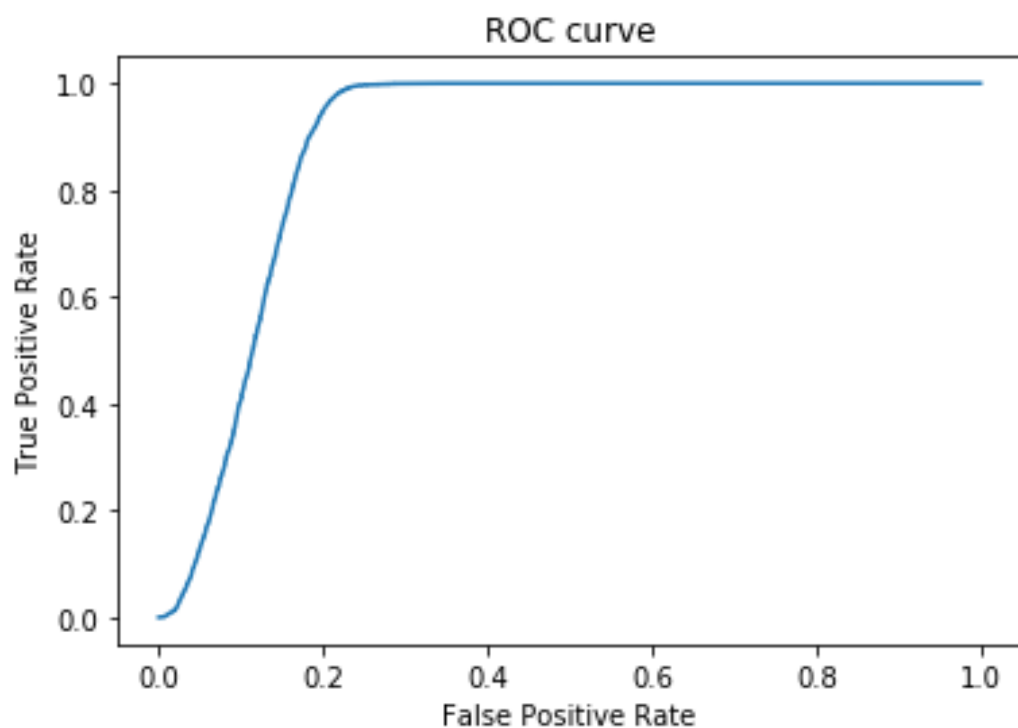


For 60 epochs

# EVALUATION

- Use Precision, Recall and AUC score
- Plot an ROC curve
- Display the confusion matrix

# EVALUATION FOR 20 EPOCHS



AUC : 0.885454056201899

Threshold : 0.4063341021537781

CONFUSION MATRIX

```
[[69306304 19757455]
```

```
 [ 246256 16202945]]
```

True Positive : 16202945

True Negative : 69306304

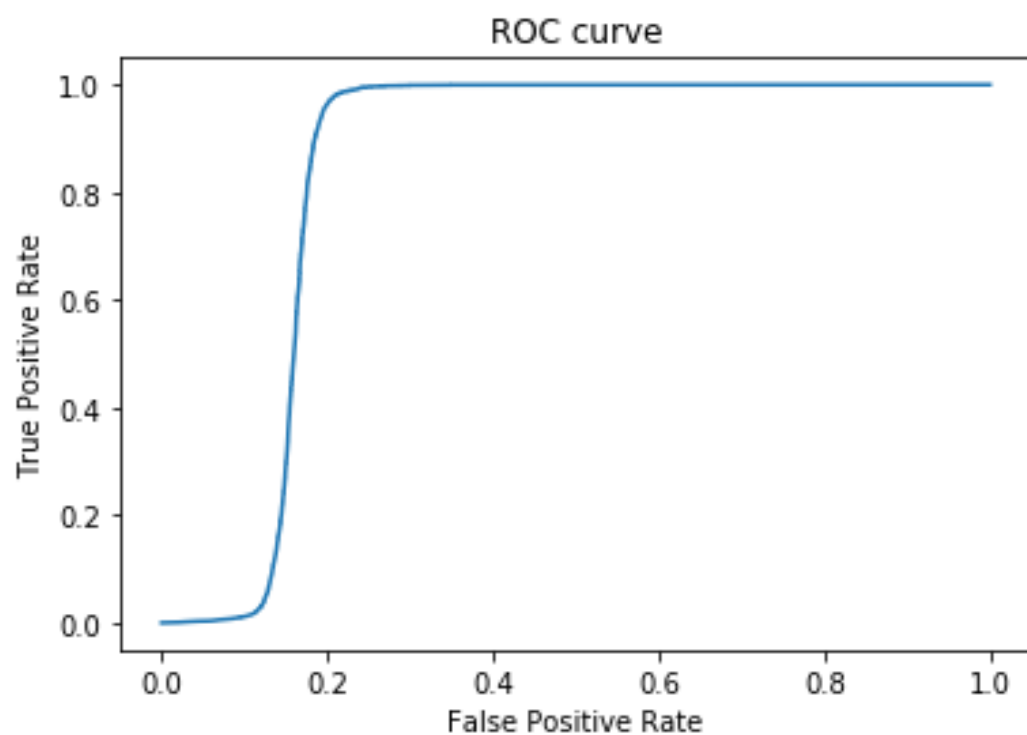
False Positive : 19757455

False Negative : 246256

Precision : 0.45057744074037

Recall : 0.9850293032470088

# EVALUATION FOR 60 EPOCHS



AUC : 0.8401566635430748

Threshold : 0.45884621143341064

CONFUSION MATRIX

```
[[70509827 18553932]
```

```
 [ 342333 16106868]]
```

True Positive : 16106868

True Negative : 70509827

False Positive : 18553932

False Negative : 342333

Precision : 0.46469983381803076

Recall : 0.9791884724370503

## OBSERVATIONS AND TAKEAWAYS

- Smaller patch sizes seem to work better
  - Tried various patch sizes from 90 x 90 to 200 x 200 – smaller patches yielded best results
- Model can identify tissue correctly (no red patches outside the tissue)
- Model performs well on cancerous cells
  - Evidenced from high recall and relatively lower false negatives
- Model does not perform well on non-cancerous cells
  - Evidenced from high false positives
- KEY TAKEAWAY : Model performs reasonably well, but can be improved
  - Better to mislabel cell as cancerous than the other way round – can compromise on precision if it leads to high recall (which our model follows)



## OTHER APPROACHES ATTEMPTED

- Approach : Select only patches from the slide with tissue percent above a specified threshold (say 10%)
  - Observation : Did not significantly impact performance
- Approach : Use patches from multiple slides (10+), at a higher level, say 7
  - Observation : Yielded less accurate results

## OTHER APPROACHES ATTEMPTED (CONTD.)

- Approach : Train different models for different levels, and then ensemble them
  - Observation : Ran out of RAM in Colab
- Approach : Extreme case – set patch stride as 1 (Extracted 200000+ patches per slide at level 7)
  - Observation : Ran out of RAM in Colab

## FUTURE WORK

- Experiment with more architectures
  - We used only VGG16 and InceptionV3 – increasing the number of epochs did not necessarily improve the performance
- Better data extraction techniques – leading to more *diverse* and *balanced* training data
- Possibly better metric ?
  - Using accuracy to train the model led to large red patches because model optimized for accuracy



# Code Walkthrough