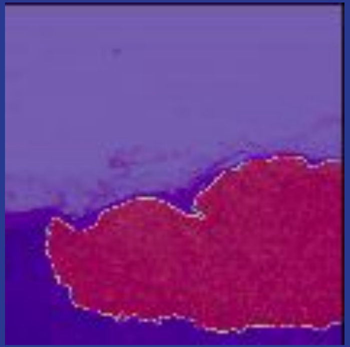
Applied Deep Learning

Final Project: Detecting Cancer Metastases on Gigapixel Pathology Images



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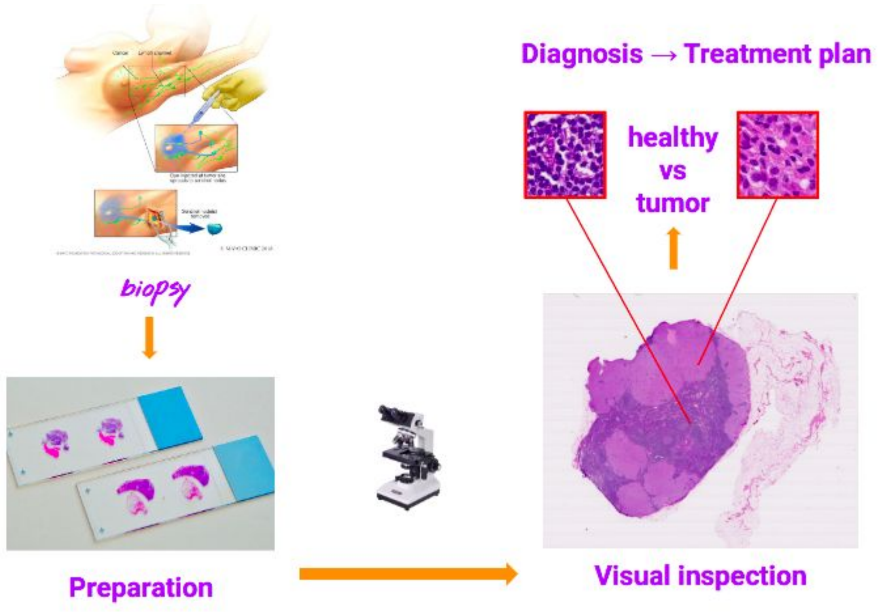
Contents

Motivation

Source: Lecture Slides

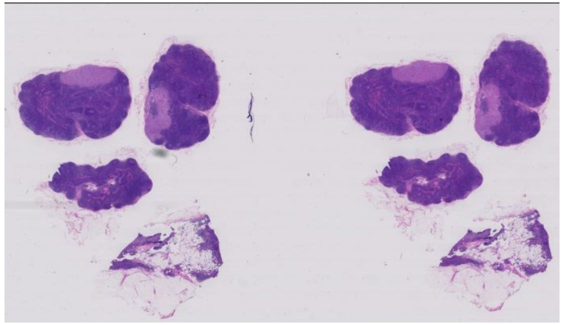
- Metastasis detection is currently performed by pathologists by examining large expansions of biological issues.
- This is a very labor intensive and error prone process and only skilled pathologists are able to make accurate predictions.



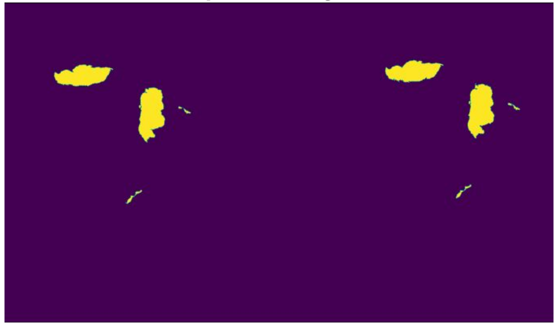
Data Pre-Processing

- We have 22 Gigapixel Pathology images wherein each image has it’s corresponding tumor mask as shown below (except for tumor_038, which we remove from our dataset)

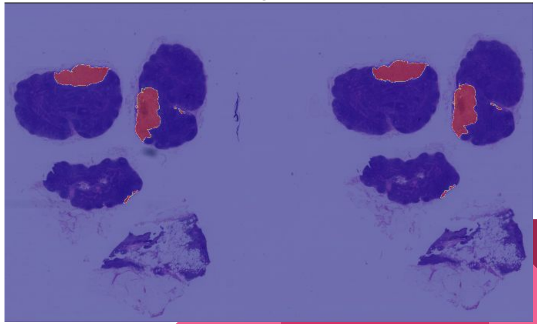
Original Image



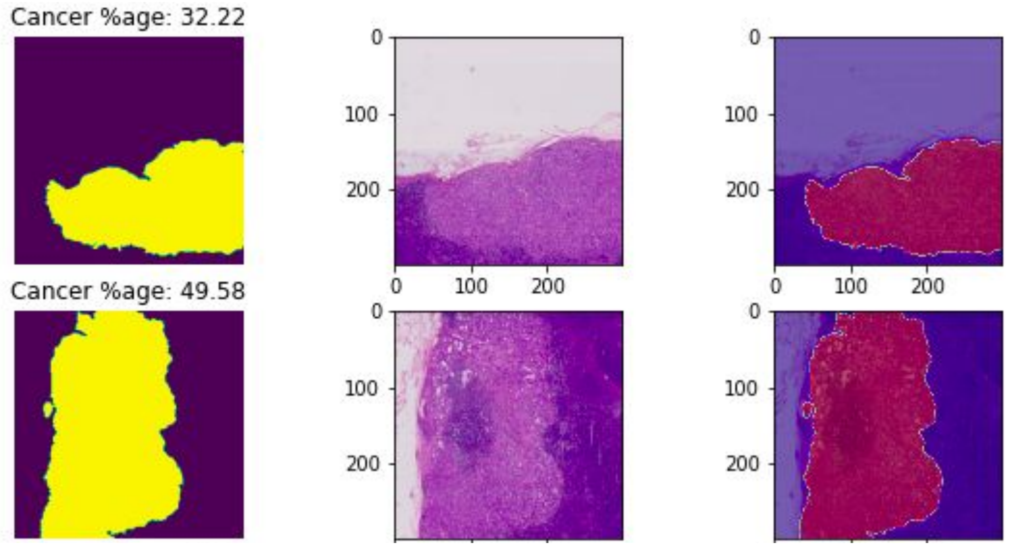
Corresponding mask



Overlay of original and mask to show cancerous regions



- Due to lack of computational resources, we only use 10 out of the 21 slides we have by splitting them into train (5 slides), validation (3 slides) and test (2 slides).
- To create the train/validation/test set we sample **non overlapping** patches of size **(299,299)** from the slides at different zoom levels **(level 3 and 4)** and save them in the drive. We also apply a **tissue threshold of 25%** to filter the patches.

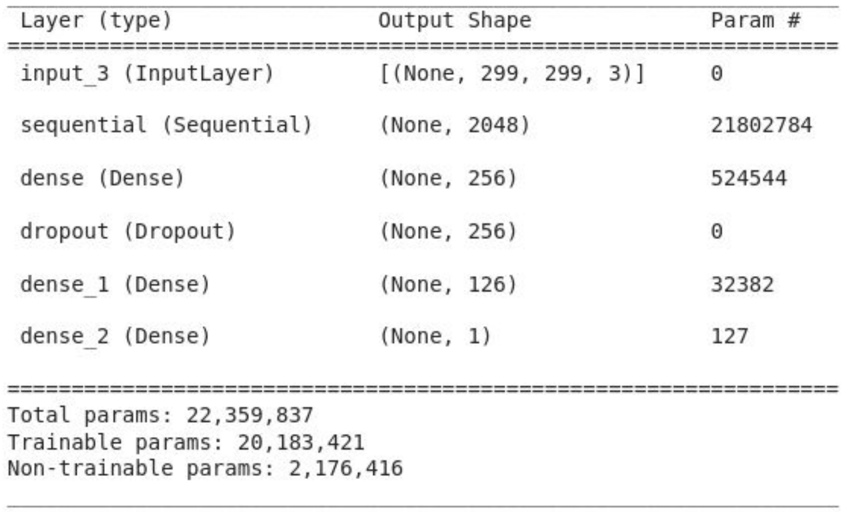


Showing the mask (left most), original image patch and the overlay (right most). All these images are of size (299,299)

Modeling

- We use the concept of **transfer learning and fine tuning** for the purpose of modelling.
- Using the weights from the **Inception V3** model **we freeze 100 layers** in the base model and fine tune the others while training.
- Adding **Global Average Pooling** between the inception model and the first dense layer reduces the trainable parameters by a significant amount and speeds up the training process.
- We also add a **dropout layer** to prevent overfitting (as shown in the model summary on the right).

Model Summary (we create another identical model trained on a different zoom level)

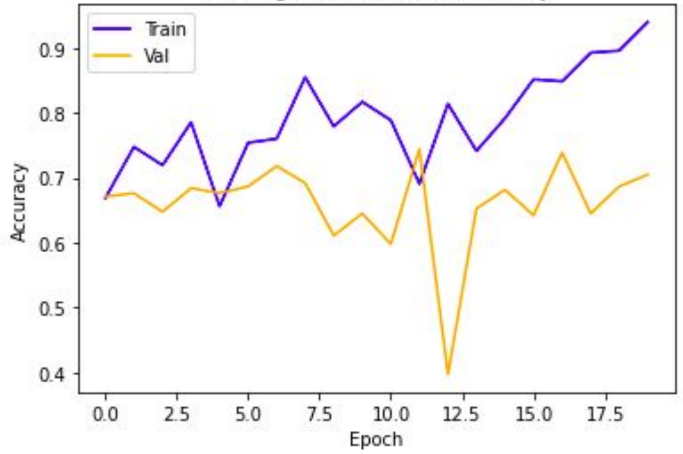


```
 Layer (type)                Output Shape              Param #
=================================================================
 input_3 (InputLayer)        [(None, 299, 299, 3)]     0

 sequential (Sequential)     (None, 2048)              21802784

 dense (Dense)               (None, 256)               524544

 dropout (Dropout)           (None, 256)               0

 dense_1 (Dense)             (None, 126)               32382

 dense_2 (Dense)             (None, 1)                 127

=================================================================
Total params: 22,359,837
Trainable params: 20,183,421
Non-trainable params: 2,176,416
_________________________________________________________________
```

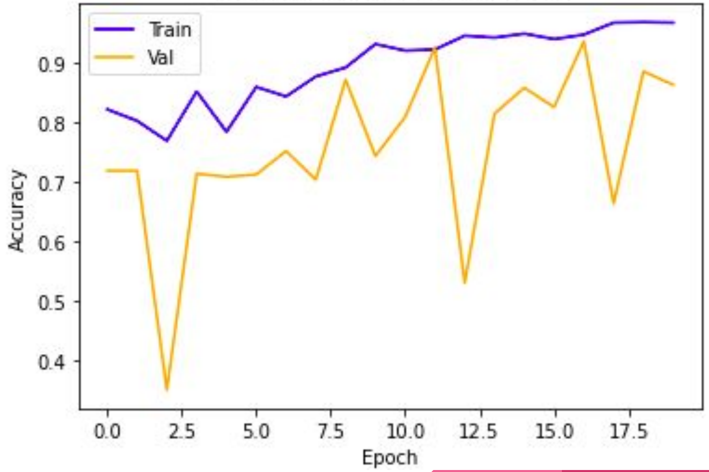
Results

- Below we can see how the **training and validation accuracy** changes over the number of epochs for both the models.

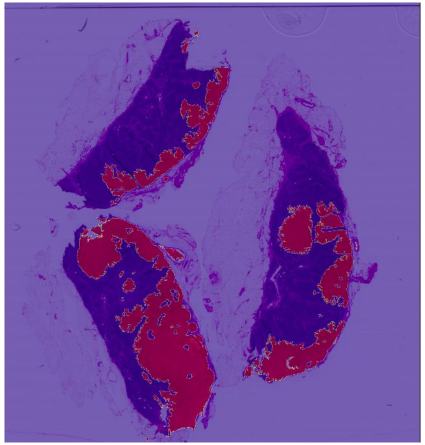
Model 1 (Zoom Level 4)



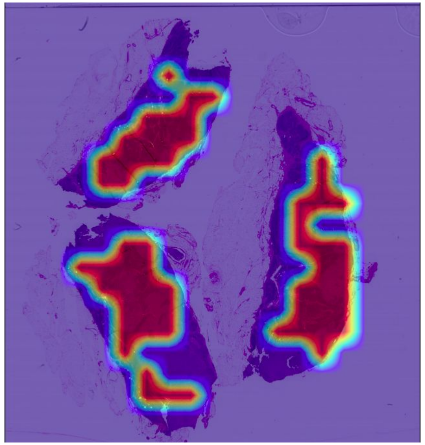
Model 2 (Zoom Level 3)



- On evaluating the model on the test set we created by the sliding window approach on 2 slides we get the following results:
  - Model1 (trained at zoom level 4) gives a **78.51%*** of test accuracy
  - Model2 (trained at zoom level 3) gives a **91.84%*** of test accuracy
- We also created a mask using our trained models (as shown below).



On the left we have the original slide with the original mask overlapped over it. On the right is the original slide overlapped with the predicted mask.



*** such high test accuracy is because of the fact that the test set is very small and does not have a lot of cancerous cells present in it. It is not indicative of how the model would perform in the real world.**

Conclusion and possible Improvements

- The models above work well enough to vaguely identify cancerous regions in tissue slides but are not accurate or robust enough to replace a highly skilled pathologist.
- The following steps can be taken to improve the accuracy and robustness of the model:
  - Use even higher zoom levels (level 2, 1 or 0) to get more number of patches and balance the dataset by removing patches which do not have cancer (Data Augmentation can also be used to balance these datasets).
  - Try different tissue and cancer thresholds and see which one gives better results.
  - Try out different modelling approaches.