

## Applied Deep Learning Project - Spring, 2019

### Group Members:

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**Github Repository:** [https://github.com/luvkaggarwal/adl\\_pro](https://github.com/luvkaggarwal/adl_pro)

### Youtube Video:

### Database Link -

<https://drive.google.com/drive/folders/12yG3aijiEXHxBV3wplWBOoLz7kSRR9vo?usp=sharing>

NOTE - For privacy purposes, we have created the database on columbia account drive, to access our data, use the above link through your columbia id and add the drive folder to your own personal drive.

### Files -

- **Gen\_data:** File to generate individual train, test and validate datasets
- **Gen\_model:** File to train the model at different zoom levels
- **Heatmap:** File to create a predicted mask for a test file
- **Merge\_maps:** File that combines the predicted heat maps at different levels
- **Analyse\_maps:** Files that compares the predicted masks to the truth values

### Preprocessing:

- Identifying relevant patch in files used for training by cropping the image to the cancerous tissue. However, add a frame of 299 pixels around each patch to extract more images on higher zoom levels as some images had very less cancerous tissues ( 5 and 6 )
- Adaptive stride while extracting slices (299 x 299, requirement for InceptionV3) from each patch at different levels - to ensure that the same slice of the tissue is not over representative in the data set at lower zoom levels ( 3 and 4 )
- Considering a slice only if the tissue percentage is greater than 30 % - to reduce noisy cells
- Classify a slice as cancerous if it has even a single pixel as cancerous
- Since there is a high imbalance between healthy and cancerous tissue slices, subsample the healthy class based on tissue percentage.

However, to ensure that we have some images of low tissue percentage in the data set as well, we pick a random number between 0 and 1. If the value is above 0.8, we

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consider the image in our training set. **[Note: this is done only for healthy image slices in the training set ]**

### Training the model:

- Use image generators to augment (rotations, mirroring, lateral shifting) our training dataset so that the model generalises better on test set
- Ran our own vanilla model, a deep residual network and an Inception based Transfer Learning model. Inception model outperformed other models so use it for our current analysis. **[Note: In transfer learning, inceptionV3 outperformed VGG16, Resnet and MobileNet]**

Layer (type)	Output Shape	Param #
=====	=====	=====
inception_v3 (Model)	(None, 8, 8, 2048)	21802784
conv2d_94 (Conv2D)	(None, 8, 8, 128)	6553728
max_pooling2d_4 (MaxPooling2	(None, 1, 1, 128)	0
flatten (Flatten)	(None, 128)	0
dense (Dense)	(None, 64)	8256
dropout (Dropout)	(None, 64)	0
dense_1 (Dense)	(None, 32)	2080
dropout_1 (Dropout)	(None, 32)	0
dense_2 (Dense)	(None, 2)	66
=====	=====	=====
Total params: 28,366,914		
Trainable params: 6,564,130		
Non-trainable params: 21,802,784		

### Architecture

### Generating Heatmaps:

- Read a separate test file slice by slice (299 x 299).
- Predict on a slice only if it has at least 30% tissue percentage. Slices are picked using adaptive stride as explained before
- Now, there are intensities for each pixel. So, generate a heat map

### Merging Heatmaps:

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- Merge heat maps at different levels to incorporate surrounding context from levels 4,5 and 6 at level 3.
- Effect of each level is reduced by half as we increase the zoom level, i.e., effect of level 6 is halved when we compute intensity of level 5.

### **Analysing Heatmaps:**

- Normalise all heat maps
- Threshold the intensity of each pixel to convert to a binary value.
- Generate confusion matrix, precision - recall values and auc curves by comparing predicted heat maps with masks at different levels.
- Compare the merged heat map with mask at level 3.
- Repeat above steps with different threshold values.