

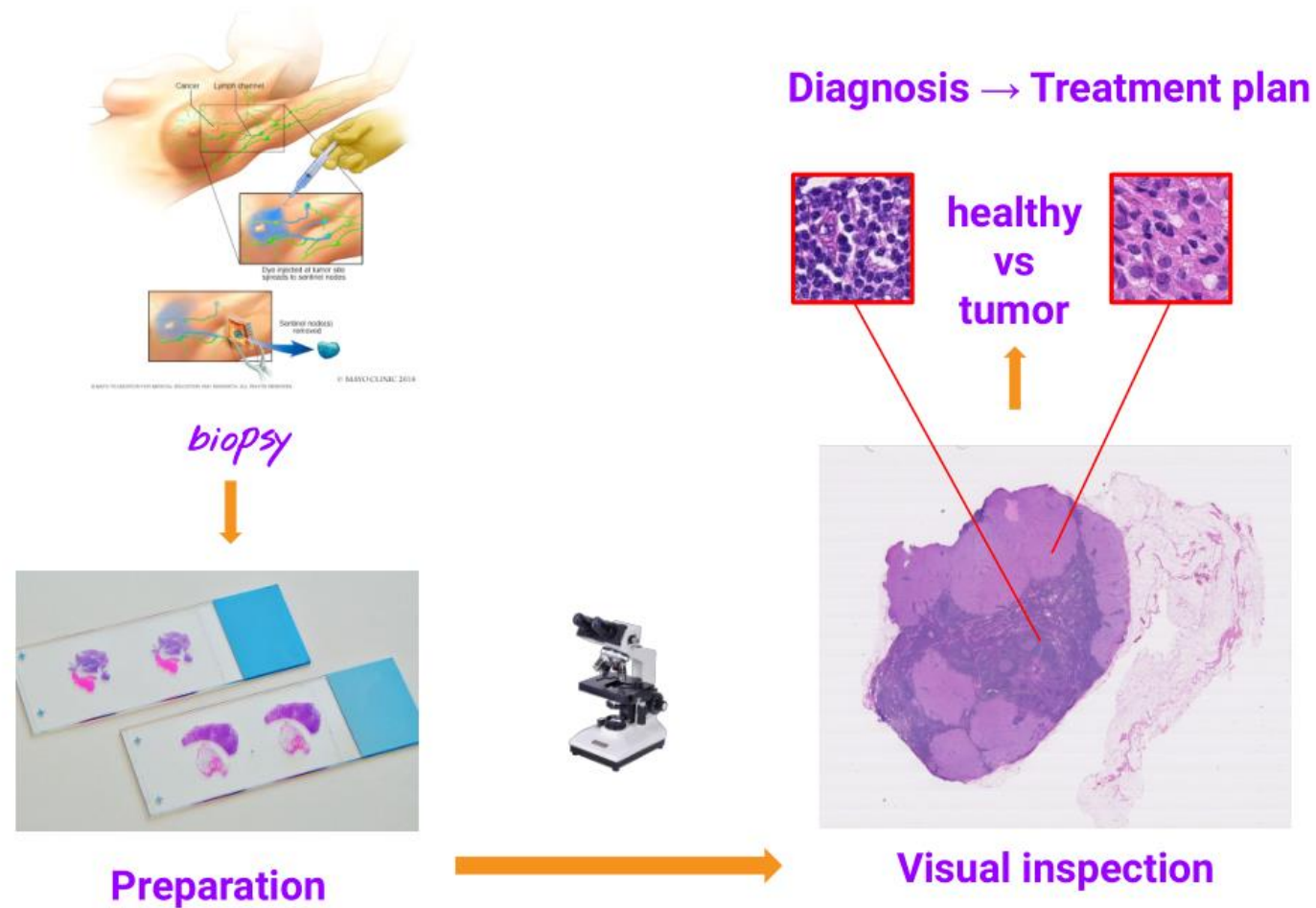
ADL Project Presentation

Detecting cancerous cells in gigapixel images

Zhizhen Cai zc2492

Context (Goal)

For **cancer**
diagnosing!



Problem: Pathologists make mistakes when diagnosing biopsied tissue

Solve: Develop a tool to assist physicians and reduce misdiagnosis rate

Context (Dataset)

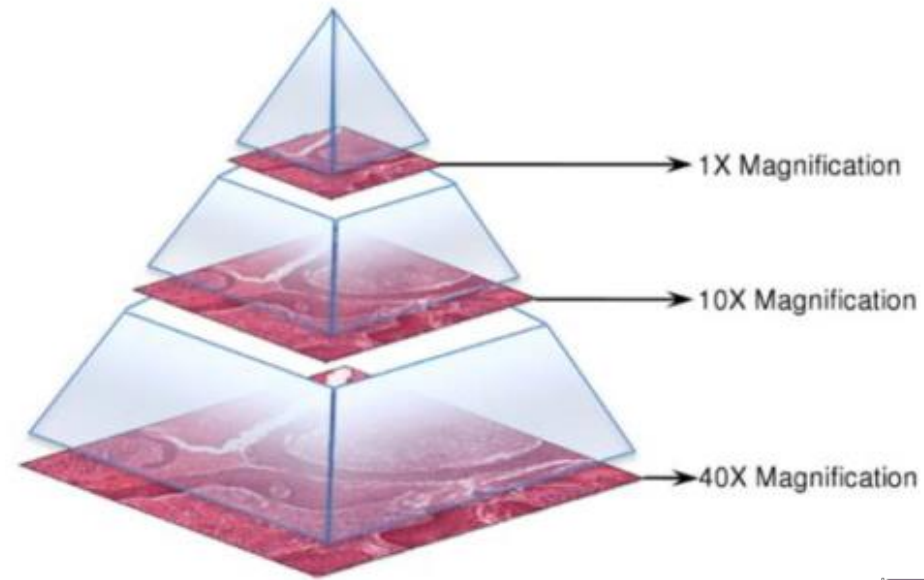
Dataset is from **CAMELYON16**: <https://camelyon16.grand-challenge.org/Data/>
(given by Professor Joshua)

Different Pathology Images

Different resolution levels(0-7)

Has both **cells images** and **tumor mask**

Tumor mask: channel 0, value of tumor pixel is 1, other is 0



Methodology

- ① different Pathology Images with **one/different** resolution levels

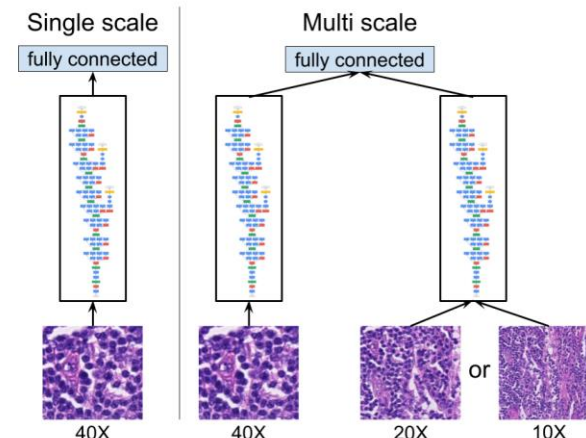
extract

patches

single or multi

Input(s)

CNN



- ② unseen Pathology Images patches (**consistent** with training)

CNN

predict tumor location

visualize

heatmap



end-to-end prototype of detecting cancer !!!

Single Input

① different Pathology Images with **specific** level (level 4)

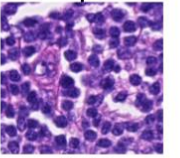
extract → patches → ^{single}Input → CNN

② unseen Pathology Images patches (**consistent** with training)

CNN → predict tumor location → visualize → heatmap

Single scale

fully connected



40X

end-to-end prototype of detecting cancer !!!

Extract patches--predefined functions

Patch size: 299 x 299
Center size: 128 X 128

def read_slide: convert a region of slide to RGB array

def find_tissue_pixels: get coordinates of tissue in this region

def apply_mask: return a image where the color of tissue pixel is (1,0,0), other are grey

def get_patches:

Get image patches, image mask patches and tissue patches based on the **center** (x0, y0) at the specific resolution level

def check_center:

Check whether the center of a patch has tumor

Extract patches---collect patches

Patch size: 299 x 299
Center size: 128 X 128

def get_dataset:

>>> Input: level, patch_size, patch_center, select_image (list)

>>> output: dataset_patch, dataset_label

Detail, for each image:

1. Get tumor and health pixels coordinates from the single resolution level
2. Pick 500 samples in both tumor and health pixels as (x0, y0)
3. If the tissue in the related patch is more than 50% of this patch, collect this patch, 100
4. Record the related label (tumor or health) of this patch

To Colab

Extract patches---collect patches

Patch size: 299 x 299
Center size: 128 X 128

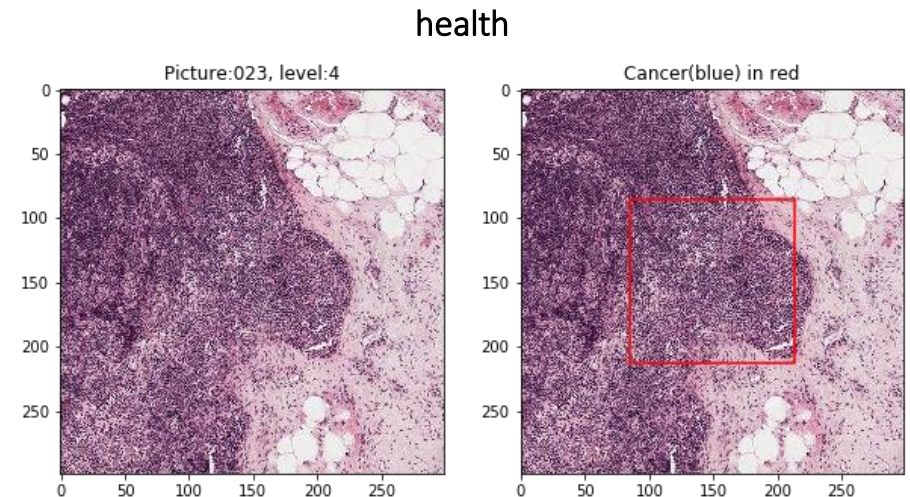
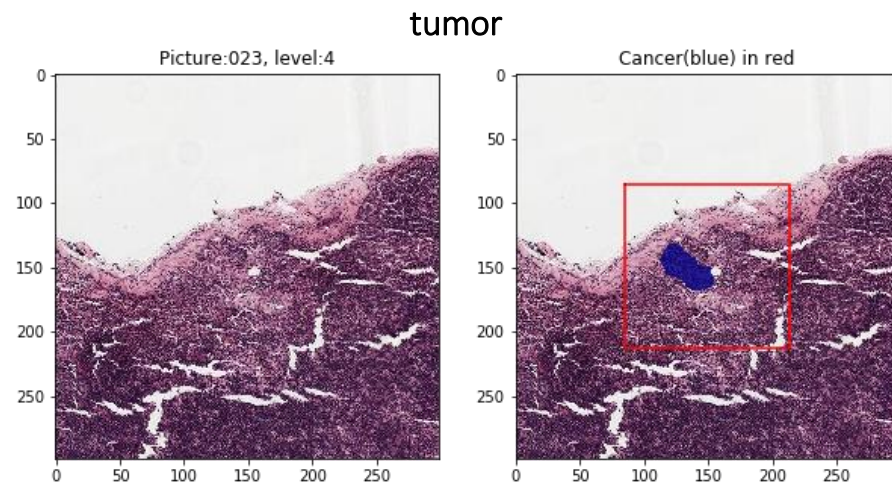
Training images: (10)

'016','023','035','057','059','064','075','081','094','096'

Test image: (1)

'110'

So I totally have $200 \times 10 = 2000$ training samples
200 test samples



Preprocessing

Patch size: 299 x 299
Center size: 128 X 128

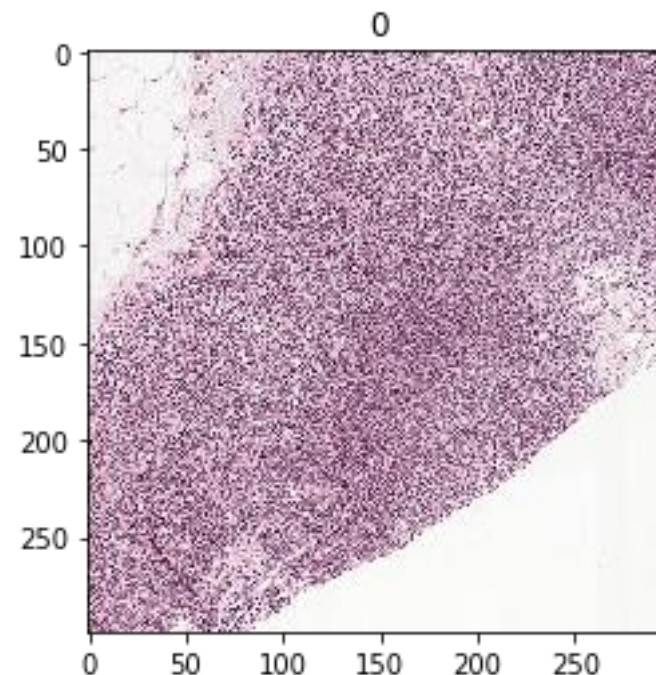
Split training data
training : validation = 8 : 2



```
patch_train shape:(1600, 299, 299, 3)
patch_val shape:(400, 299, 299, 3)
patch_test shape:(200, 299, 299, 3)
```

rescale image to [0,1]

set batch = 32



Model

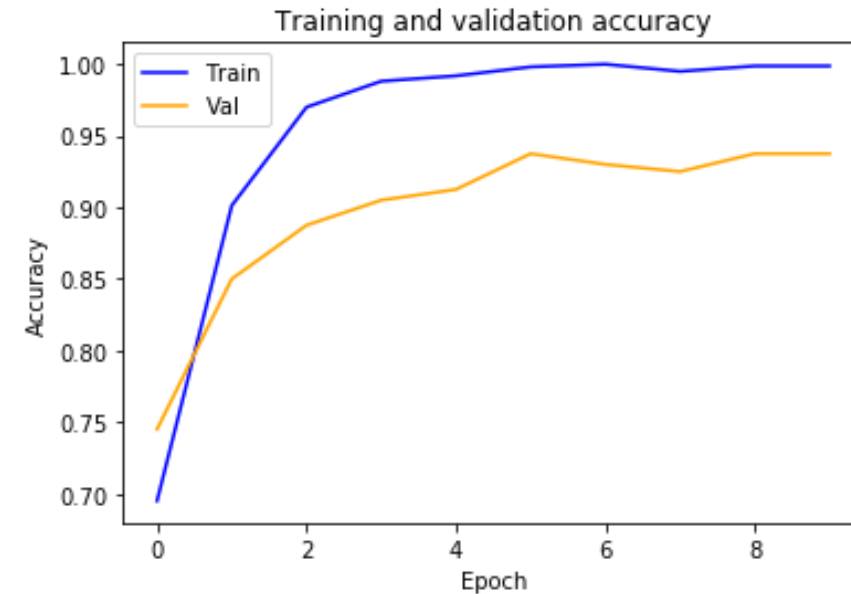
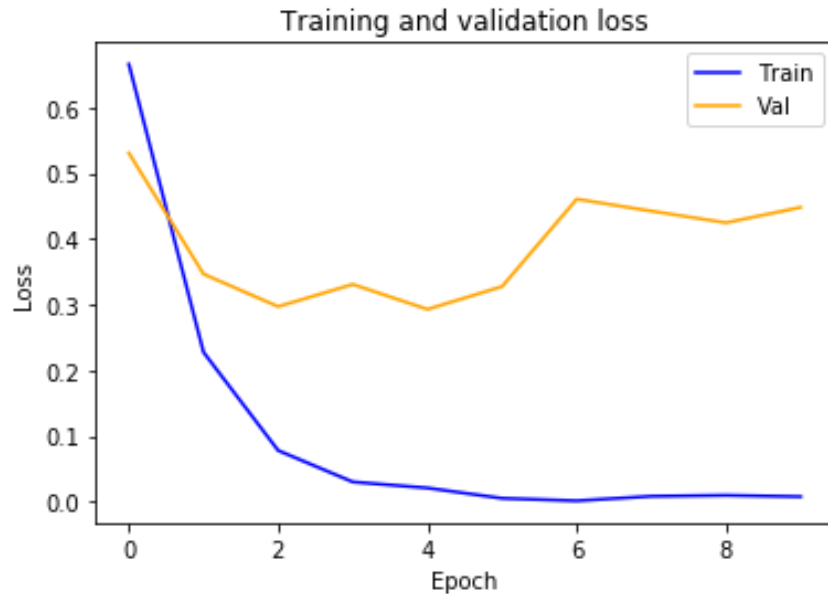
To Colab

Patch size: 299 x 299
Center size: 128 X 128

Use CNN model defined by myself:

Epoch 10/10

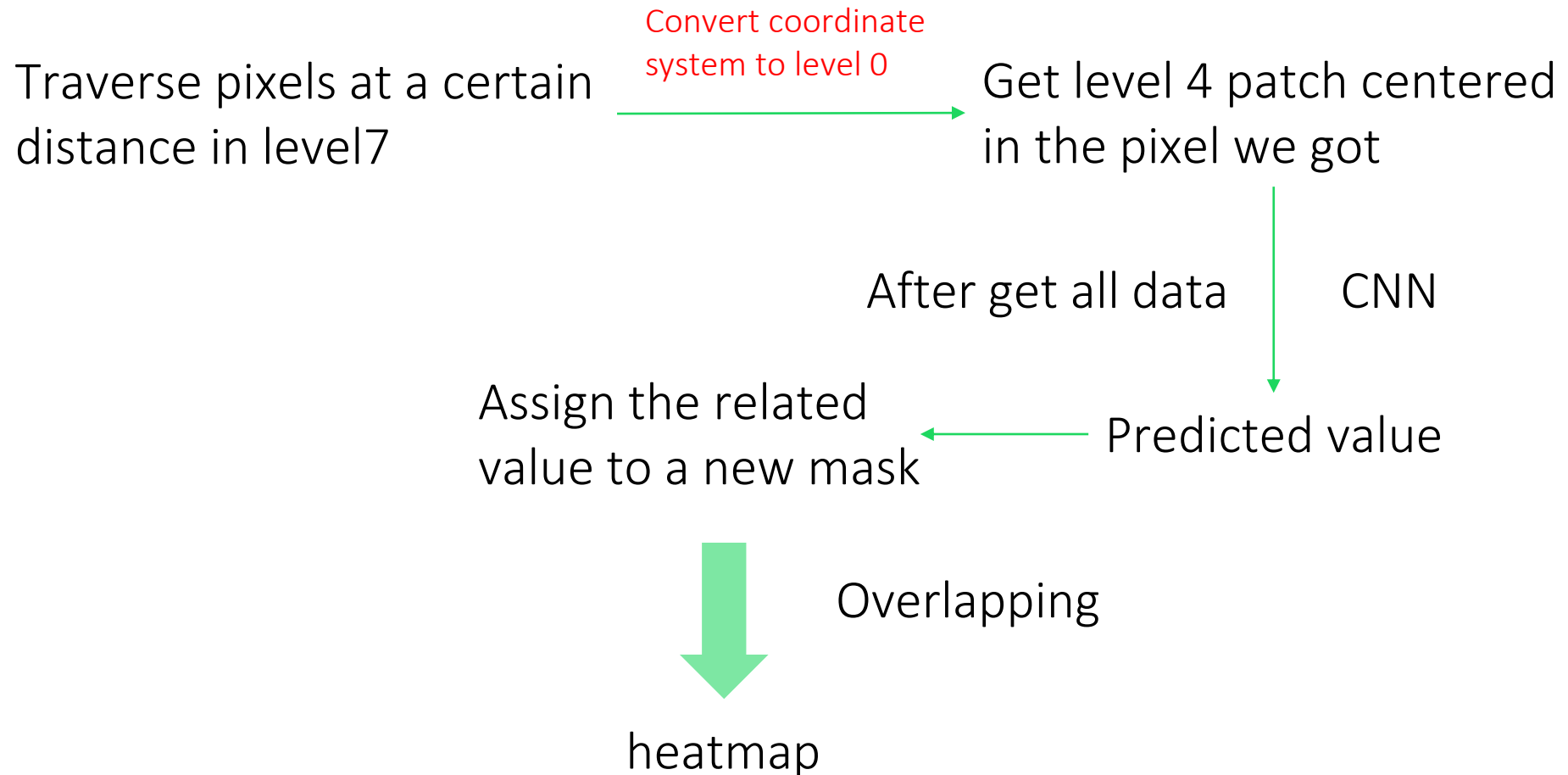
50/50 [=====] - 14s 286ms/step - loss: 0.0078 - accuracy: 0.9987 - val_loss: 0.4480 - val_accuracy: 0.9375



Evaluate the model: Test loss: 0.280, accuracy: 0.835

end-to-end heatmap

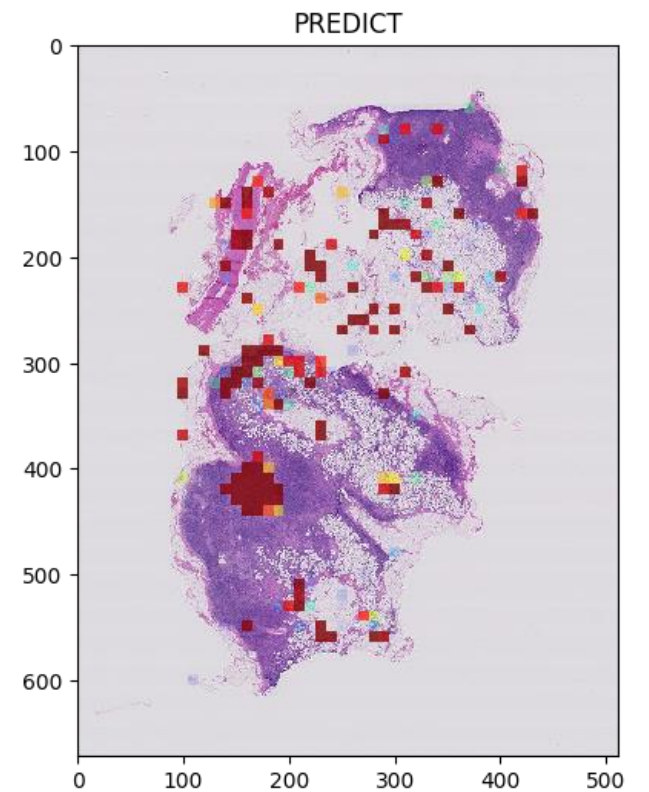
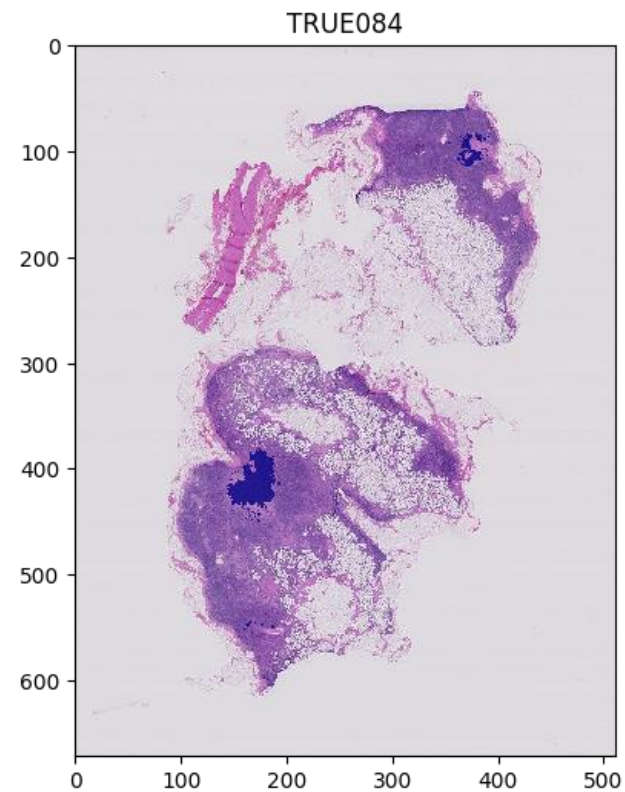
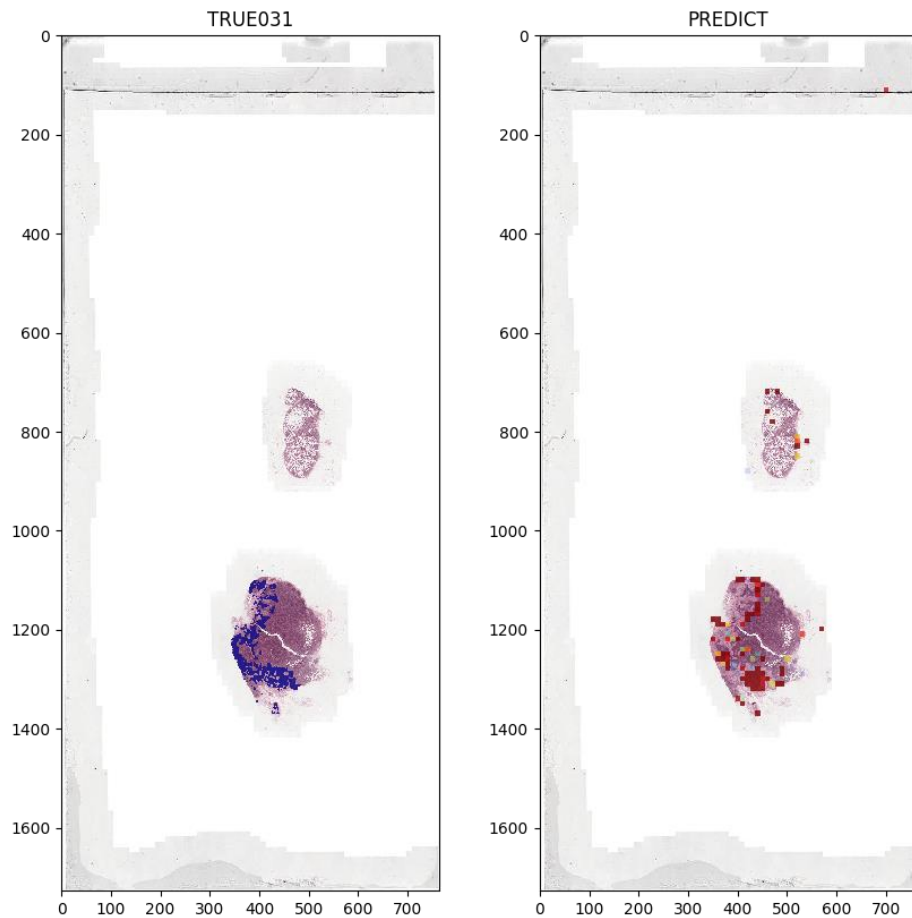
To Colab



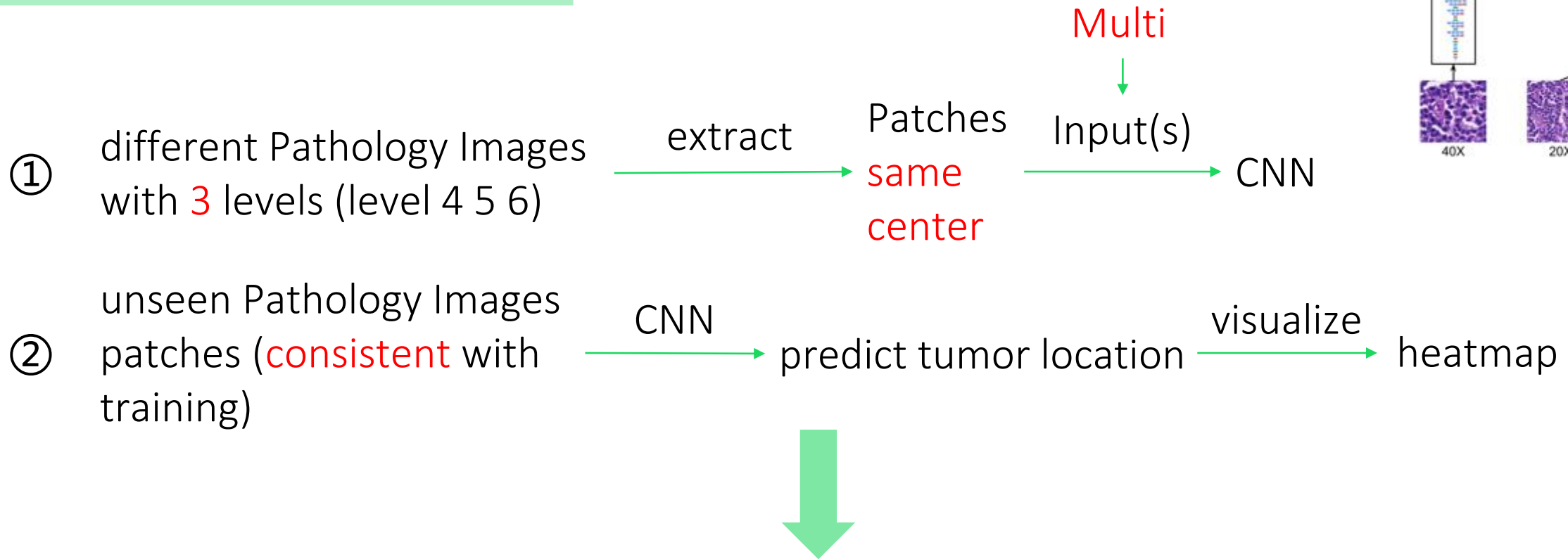
end-to-end prototype of detecting cancer !!!

end-to-end heatmap

Heatmap with single input (unseen data)



Multi Input



end-to-end prototype of detecting cancer !!!

Extract patches---collect patches

Patch size: 299 x 299
Center size: 128 X 128

def get_dataset:

>>> Input: level, patch_size, patch_center, select_image (list)

>>> output: dataset_patch, dataset_label

Detail, for each image:

1. Get tumor and health pixels coordinates from the single resolution level
2. Pick 500 samples in both tumor and health pixels as (x0, y0)
3. If the tissue in the related patch is more than 50% of this patch, collect this patch
- 3.5 add the patch in level 5 and 6 with same size, centered in same (x0, y0)
4. Record the related label (tumor or health) of this patch

To Colab

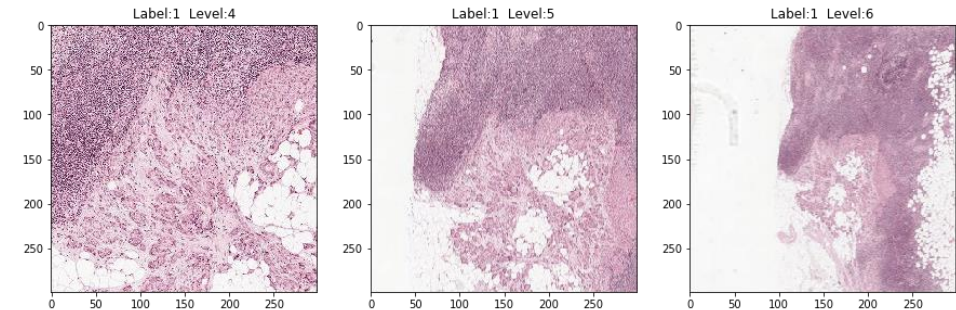
Extract patches---collect patches

Patch size: 299 x 299
Center size: 128 X 128

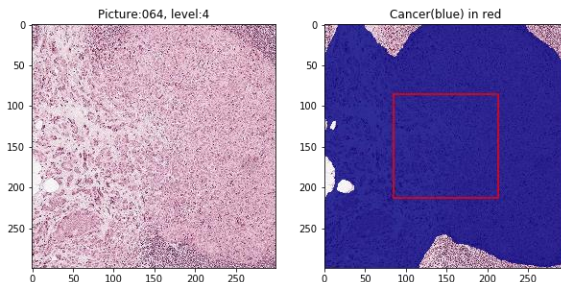
So I totally have $200 \times 10 \times 3 = 6000$ training samples
600 test samples

After split:

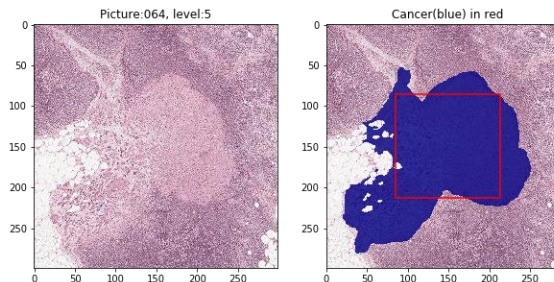
```
patch_train_4 shape:(1600, 299, 299, 3)
patch_val_4 shape:(400, 299, 299, 3)
patch_test_4 shape:(200, 299, 299, 3)
patch_train_5 shape:(1600, 299, 299, 3)
patch_val_5 shape:(400, 299, 299, 3)
patch_test_5 shape:(200, 299, 299, 3)
patch_train_6 shape:(1600, 299, 299, 3)
patch_val_6 shape:(400, 299, 299, 3)
patch_test_6 shape:(200, 299, 299, 3)
```



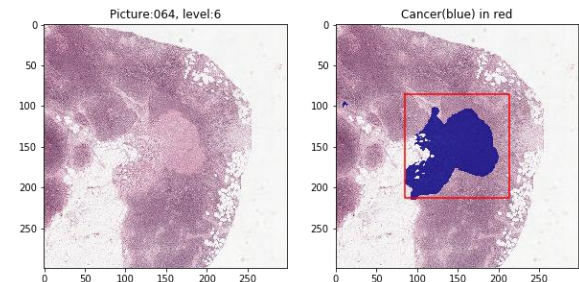
Tumor in level 4



Tumor in level 5



Tumor in level 6



Model

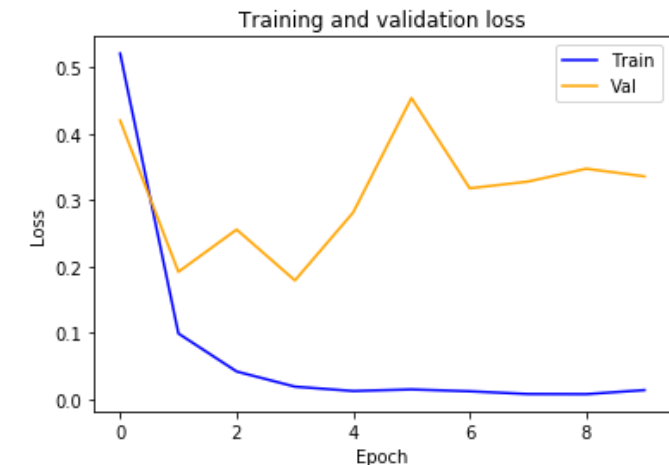
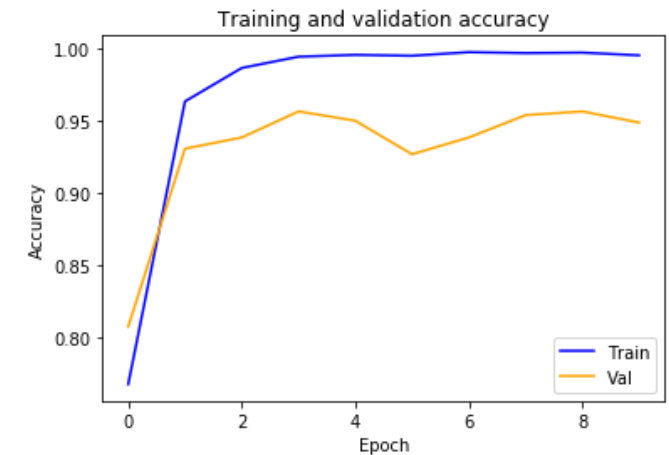
To Colab

Patch size: 299 x 299
Center size: 128 X 128

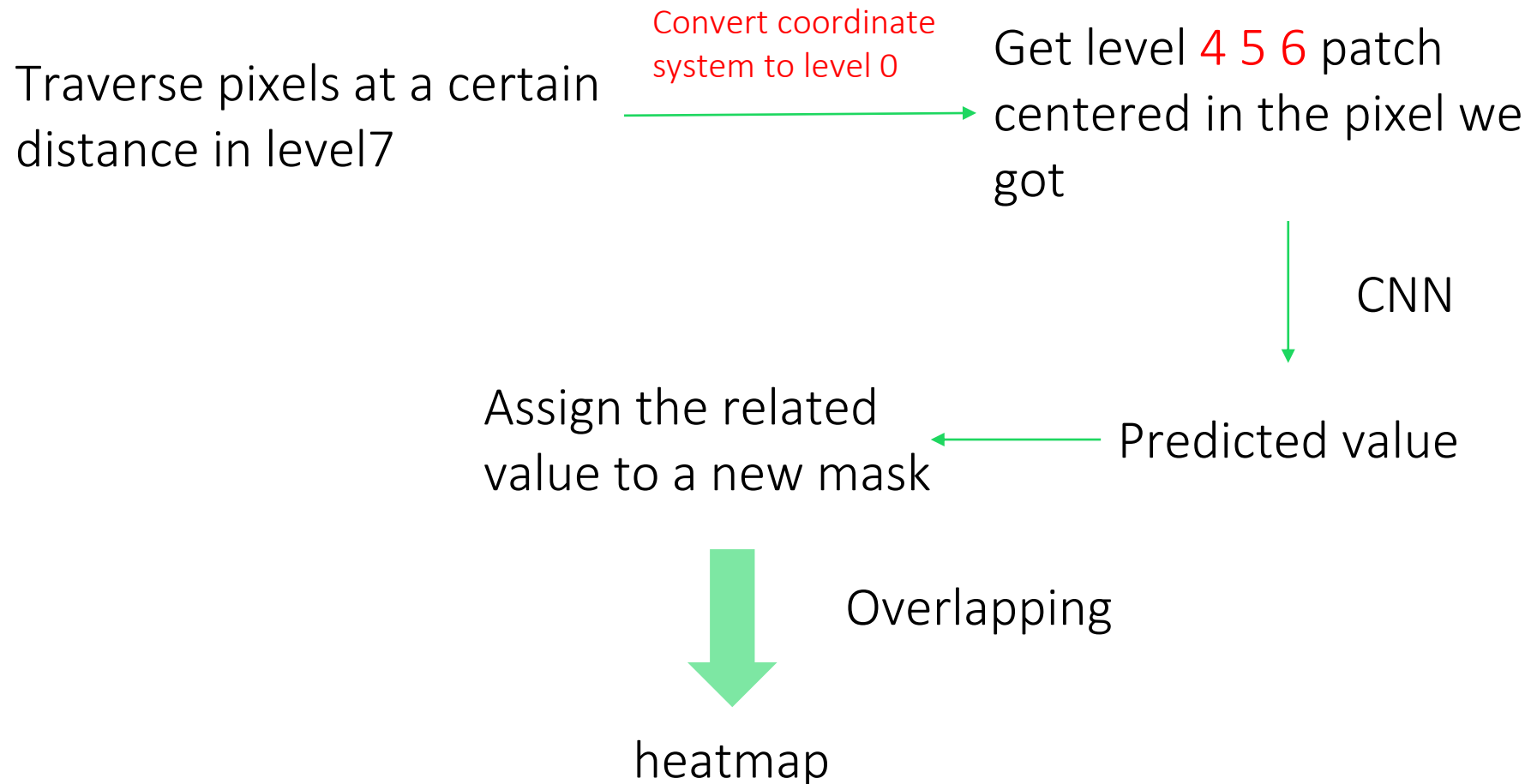
Use CNN model defined by myself: have **three** inputs

Layer (type)	Output Shape	Param #	Connected to
input_1 (InputLayer)	[(None, 299, 299, 3)]	0	
input_2 (InputLayer)	[(None, 299, 299, 3)]	0	
input_3 (InputLayer)	[(None, 299, 299, 3)]	0	
sequential (Sequential)	(None, 74, 74, 32)	11936	input_1[0][0]
sequential_1 (Sequential)	(None, 74, 74, 32)	11936	input_2[0][0]
sequential_2 (Sequential)	(None, 74, 74, 32)	11936	input_3[0][0]
concatenate (Concatenate)	(None, 74, 74, 96)	0	sequential[0][0] sequential_1[0][0] sequential_2[0][0]
flatten (Flatten)	(None, 525696)	0	concatenate[0][0]
dense (Dense)	(None, 128)	67289216	flatten[0][0]
dropout (Dropout)	(None, 128)	0	dense[0][0]
dense_1 (Dense)	(None, 1)	129	dropout[0][0]
Total params: 67,325,153			
Trainable params: 67,324,769			
Non-trainable params: 384			

Evaluate the model: Test loss: 1.938, accuracy: **0.809**



end-to-end heatmap

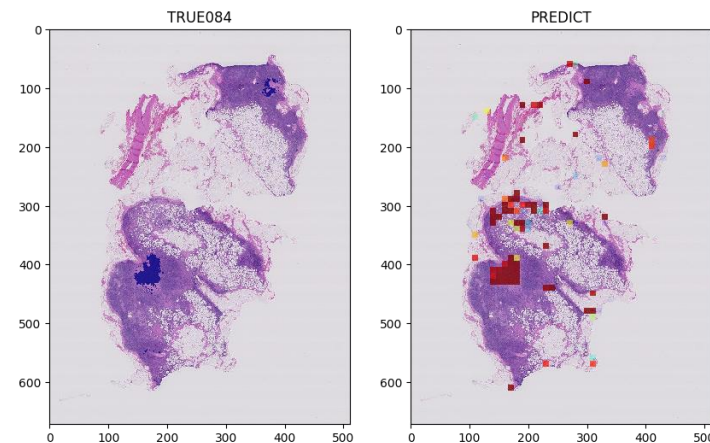
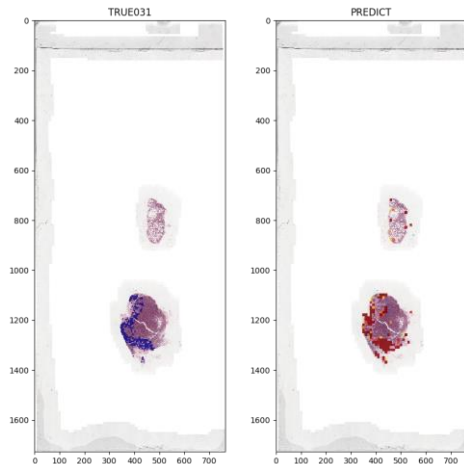


end-to-end prototype of detecting cancer !!!

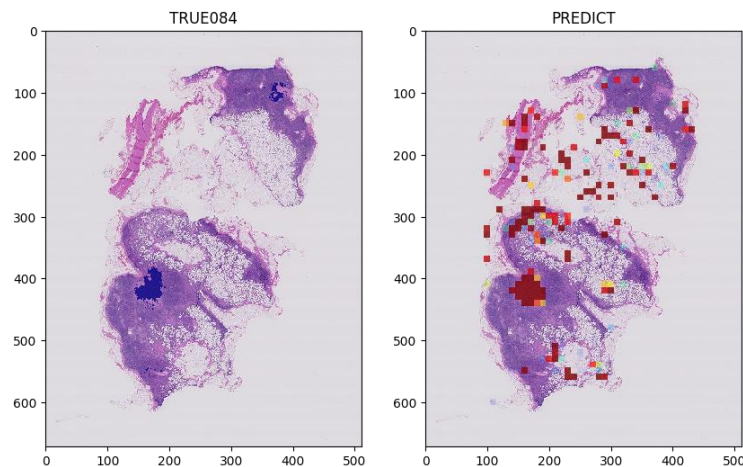
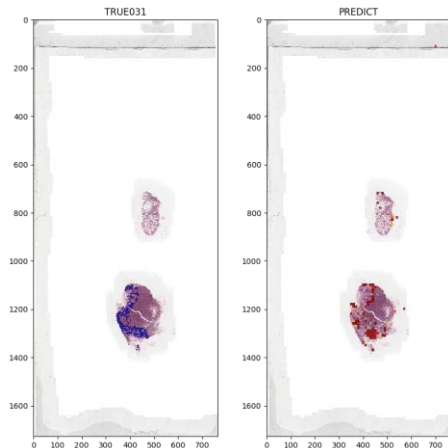
end-to-end heatmap

Heatmap with multi inputs (unseen data)

multi



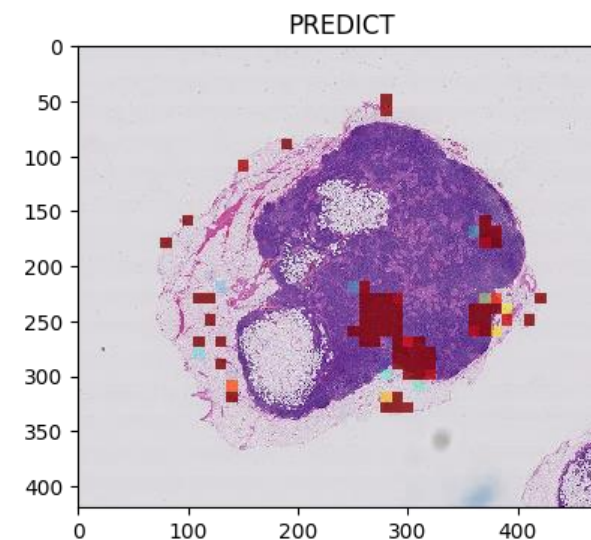
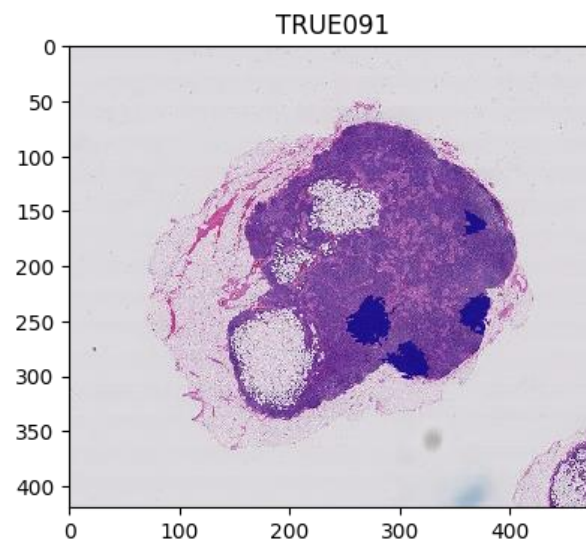
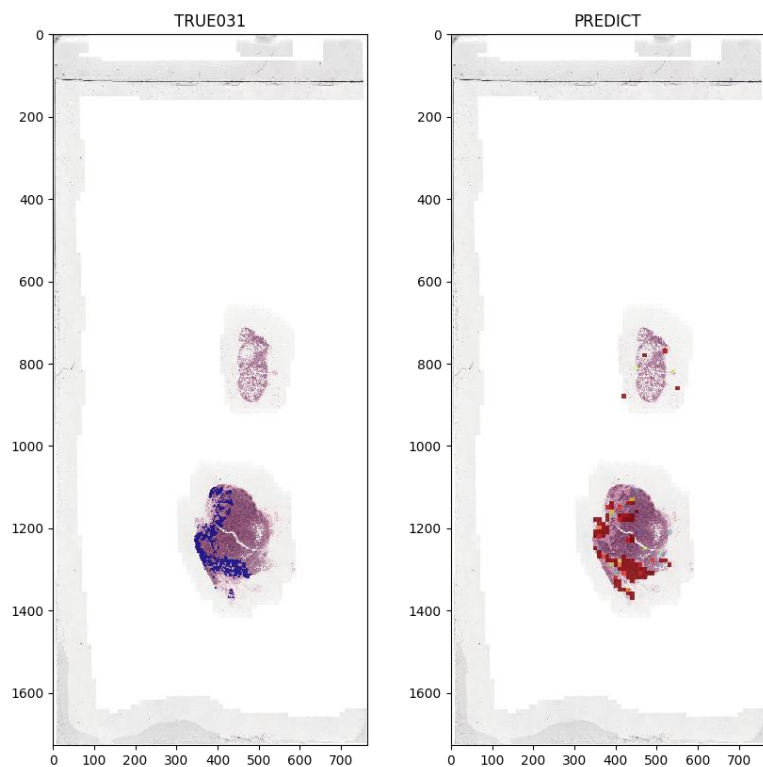
single



Multi perform
better than single

end-to-end heatmap

More heatmap with multi inputs (unseen data)



Improve

Increase the number of training set

Use data augmentation to generate more data since tumor number is small

Thank
you