Sliding Windows Alghorithm As Data Augmentation On Histopathology Images For Convolutional Neural Network Training

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Background & Motivation

- Convolutional Neural Network (CNN) requires large amounts of data for the learning process.

- Small data with low variation will cause over-fitting and model cannot predict new data with high accuracy
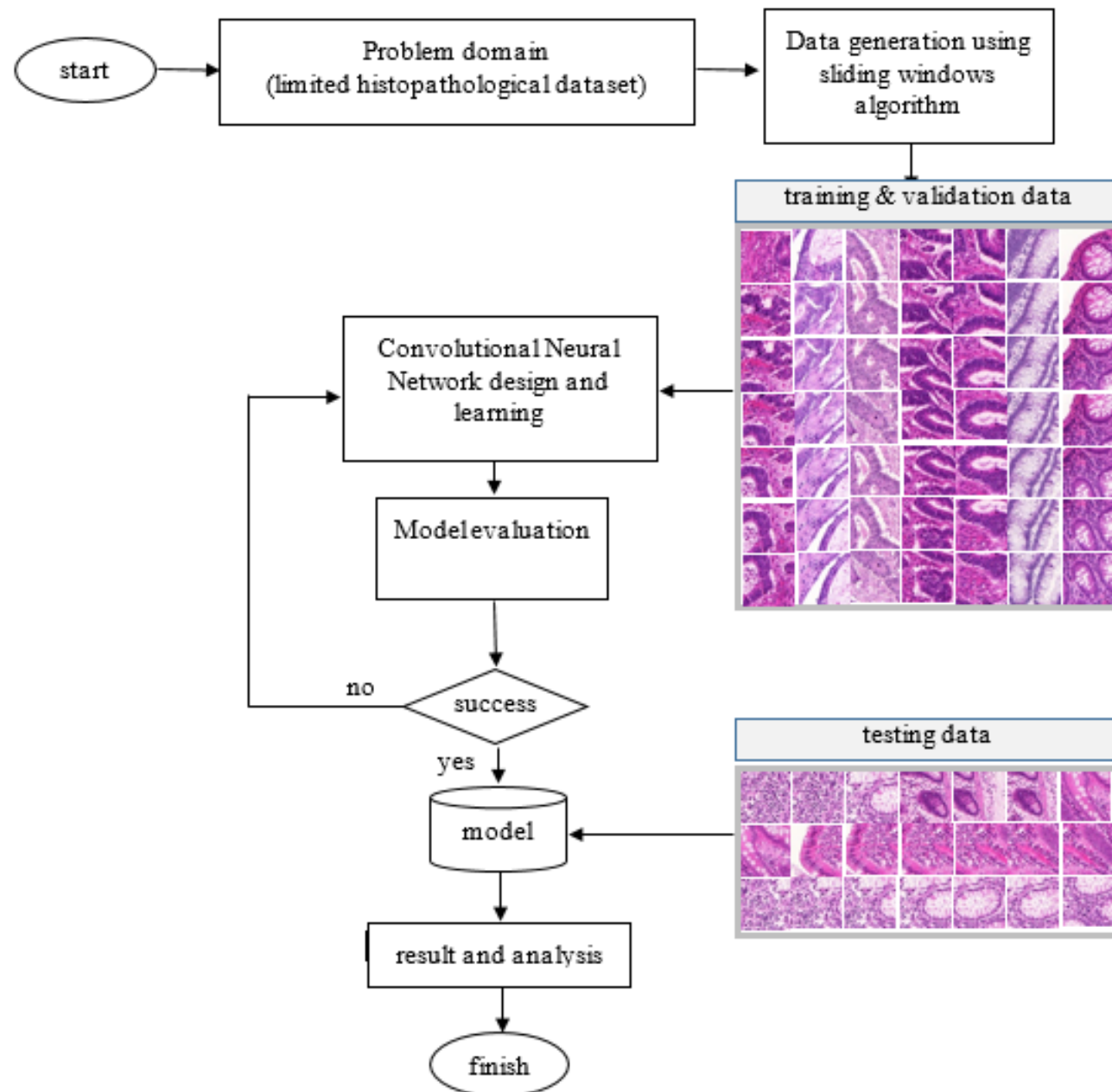
- The availability of medical data is one of the issues especially for the training process using CNN.

- This study will apply sliding windows to obtain data sub-samples on histopathological images.

Metodology

Data:
Total of 83 source of histopatology data with dimensions of 775x522

Colon cancer dataset

Sliding window technique (algorithm)

Sliding windows algorithm for generating histopathology images

Input   : whole images of histopathology (size 775 X 522 pixels)

Output : sub-samples of (size 224 x 224 pixels)

/*patch size initiation*/

224 ← patch_size

[ ] ← nucleus_location

[ ] ← nucleus_patch

/*loop from top left image pixel for image position */

for x in range (0, 775, 50)   /* 50 is windows-size for horizontal axis*/

*   for y in range (0,522,50)   /* 50 is windows-size for vertical axis */*

*   append.nucleus_location(x,y)*

*   end for*

end for

/*looping for image sub-samples capturing*/

for loc in nucleus_location

*   cropped = image[loc[0]:loc[0]+patch_size, loc[1]:loc[1] + patch_size*

*   /* save pixel with 224 x 224 from three channel */)*
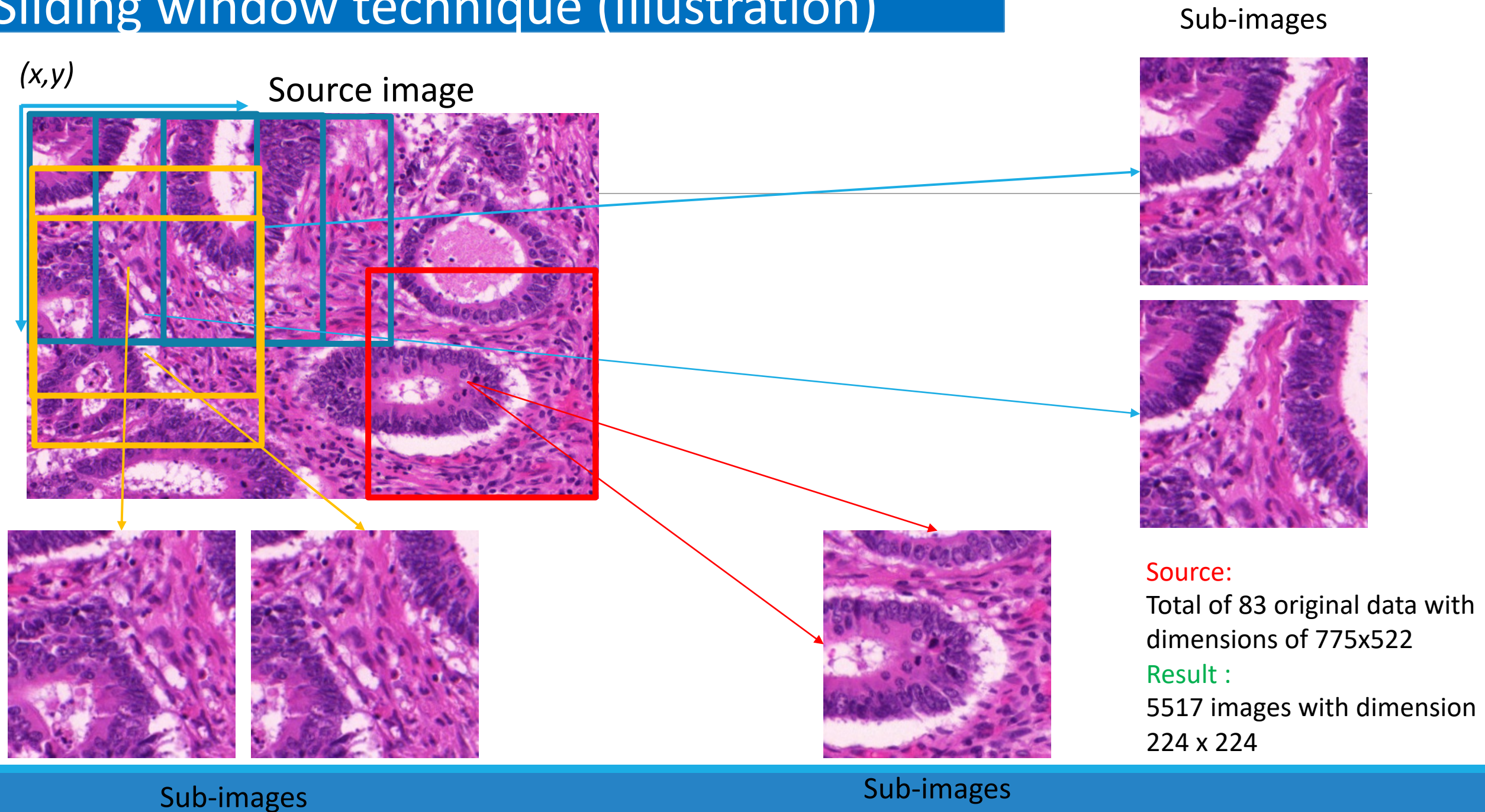
*   if cropped.size == patch_size * patch_size * 3*
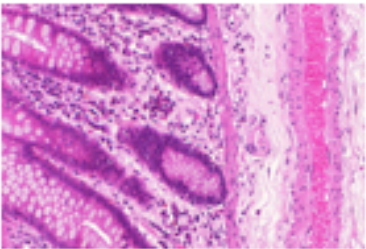
*   write(cropped)*

*   end if*
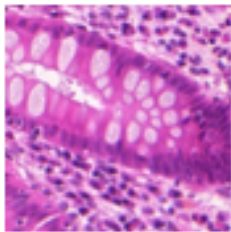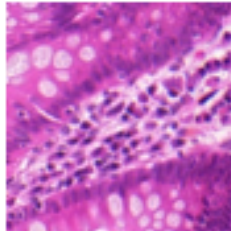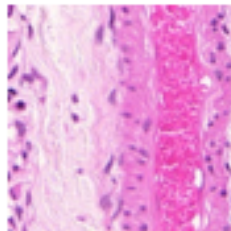
end for

Sliding window technique (Illustration)

Sub-images

(x,y)

Source image

Source:
Total of 83 original data with dimensions of 775x522
Result :
5517 images with dimension 224 x 224

Sub-images

Sub-images

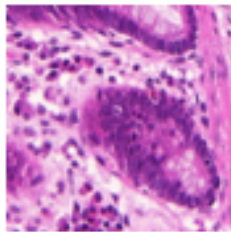# Sliding Windows Result

Real Image	invalid sub-sample image	Valid sub-sample image
size : 775x522	size:224x72 size:224x72 size:224x22	Size : 224 x 224
	X	√

CNN Design

Type	#convolution	#maxpool	#dropout	#fully-connected	#output
architecture_1	4	4	1 (0.2)	1	1
architecture_2	7	7	3 (0.3)	3	1

conv1 kernel_size:3 stride:1 pad:1	maxpool1 pool_size:2 stride:2 pad:0	conv2 kernel_size:3 stride:1 pad:1	maxpool2 pool_size:2 stride:2 pad:0	conv3 kernel_size:3 stride:1 pad:1	maxpool3 pool_size:2 stride:2 pad:0	conv4 kernel_size:3 stride:1 pad:1	maxpool4 pool_size:2 stride:2 pad:0	fully connected

(architecture 1)

conv1 kernel_size:3 stride:1 pad:1	maxpool1 pool_size:2 stride:2 pad:0	conv2 kernel_size:3 stride:1 pad:1	maxpool2 pool_size:2 stride:2 pad:0	conv3 kernel_size:3 stride:1 pad: 1	maxpool3 pool_size:2 stride:2 pad:0	conv4 kernel_size:3 stride:1 pad: 1	maxpool4 pool_size:2 stride:2 pad:0

(architecture2)

fully connected	fully connected	fully connected	maxpool7 pool_size:2 stride:2 pad:0	conv7 kernel_size:3 stride:1 pad:1	maxpool6 pool_size:2 stride:2 pad:0	conv6 kernel_size:3 stride:1 pad:1	maxpool5 pool_size:2 stride:2 pad:0	conv5 kernel_size:3 stride:1 pad:1

Experimental Setup

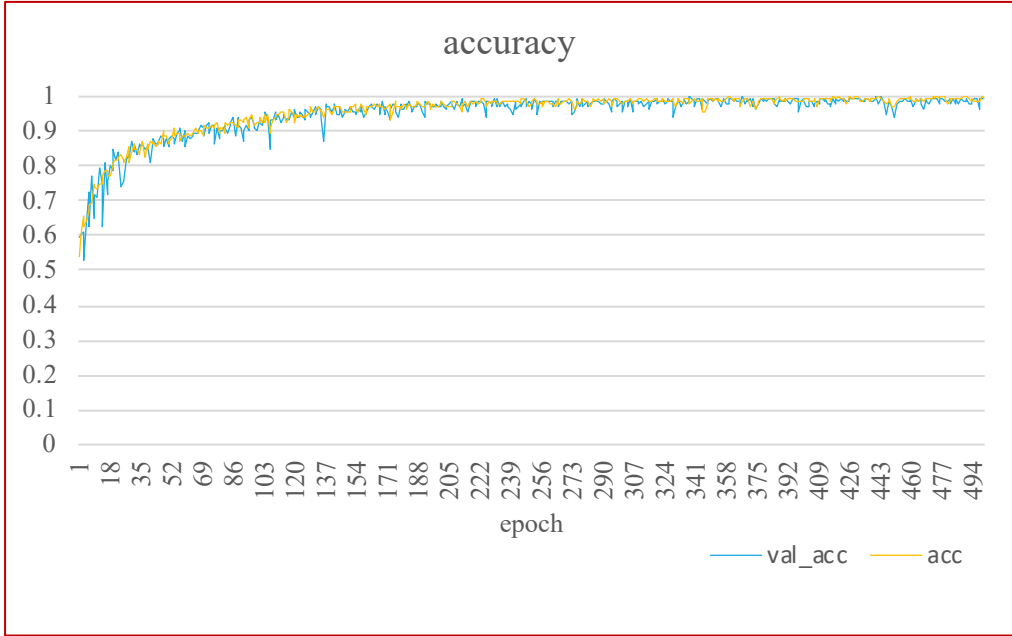| Hardware	Specification
Processor	Intel core i7® 5960X 16 cores @ 3.00 Ghz
RAM	65 GB
GPU	NVIDIA GTX-980
	Number cores : 2048
	Clock : 1,28 GHz
	GPU-RAM : 4GB

Software
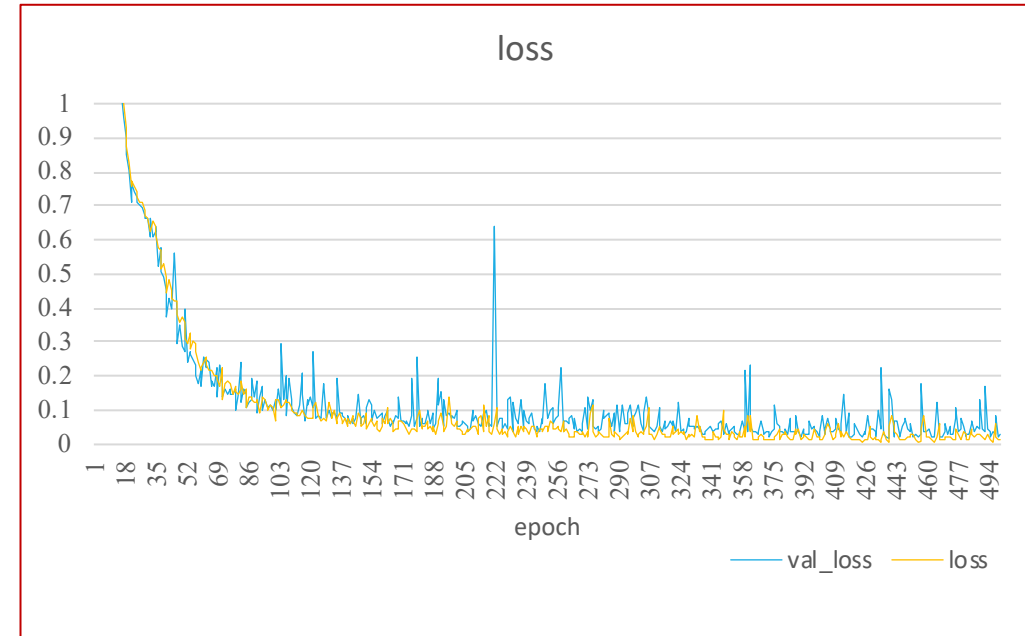
.:: Graphics of accuracy ::.

Architecture 1

Architecture 2

Result
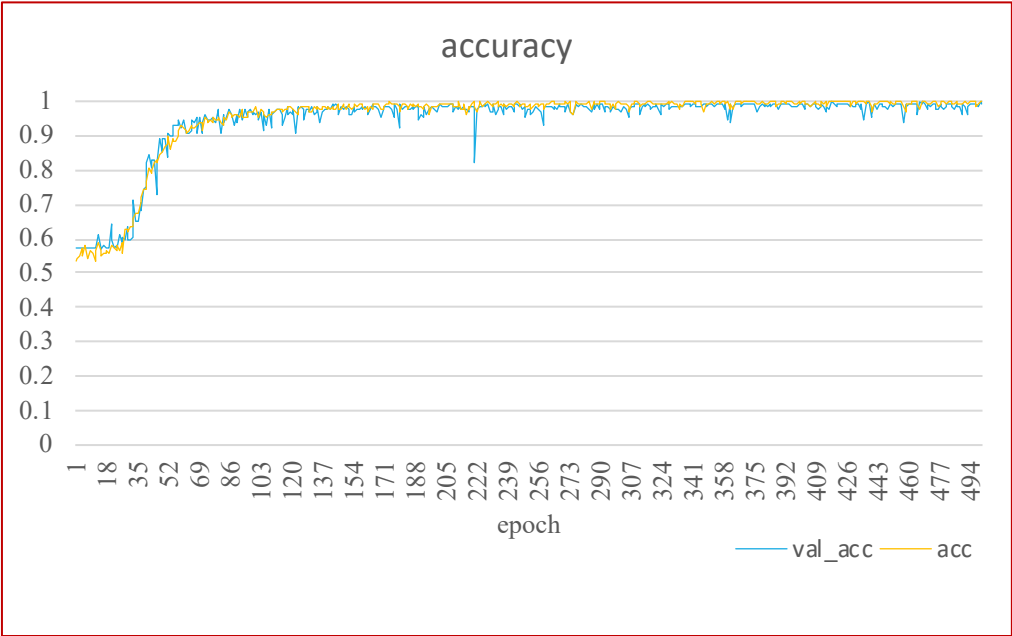
.:: Graphics of loss ::.

Architecture 1

Architecture 2

Result
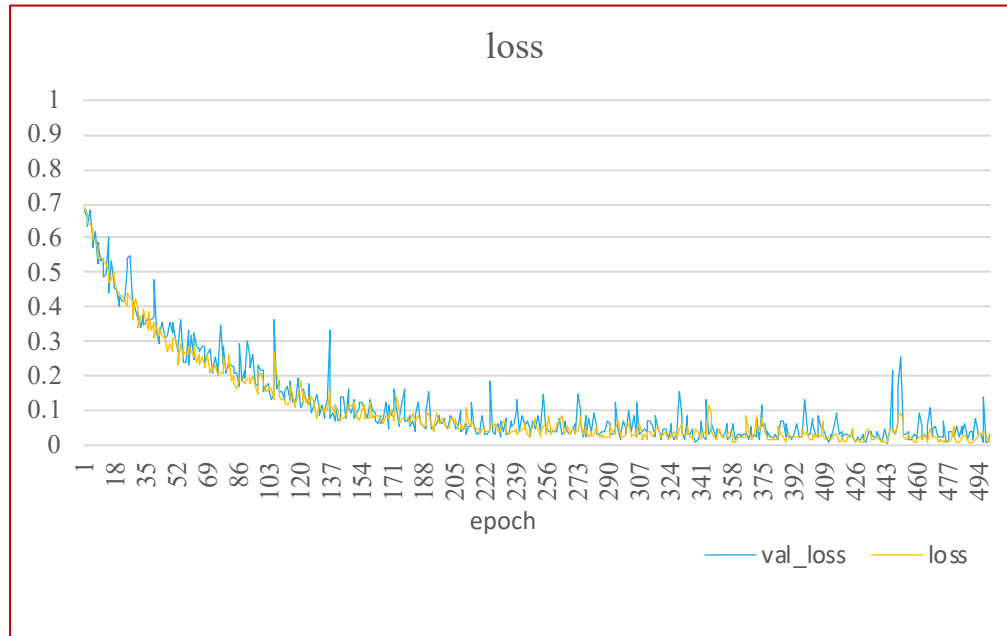
		Predicted	
		benign	malignant
actual	benign	444	281
	malignant	116	861

(a) validation dataset

		Predicted	
		benign	malignant
actual	benign	27	10
	malignant	12	31

(b) new dataset

Figure 7. Model testing of Architecture_1; (a) Validation dataset and (b) new dataset

Architecture 1 :
Validation dataset
Accuracy : 76%

New dataset
Accuracy : 72 %

		Predicted	
		benign	malignant
actual	benign	666	59
	malignant	15	962

(b) validation dataset

		Predicted	
		benign	malignant
actual	benign	31	6
	malignant	12	31

(b) new dataset

Architecture 2 :
Validation dataset
Accuracy : 95%

New dataset
Accuracy : 77%

Discussion

- Miss-classification of Maliganant tissues classified to benign
- From 12 miss-classification there are 10 (highlight) similar result by architecture 1 and architecture 2
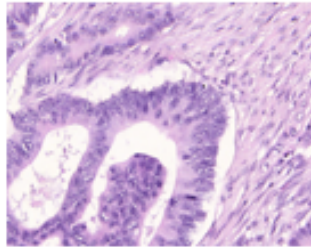
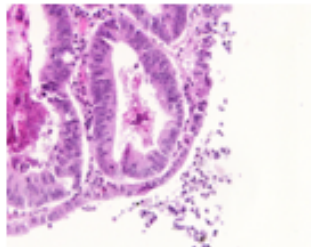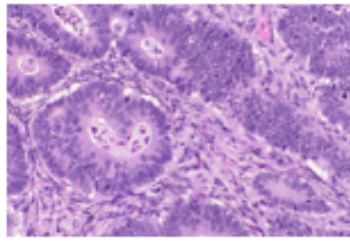| Architecture_1			Architecture_2		
File_name			File_name		
test45	testB_18	testA_38	testB_19	testA_38	testA_3
testA_3	test_A_48	testA_16	testA_48	testA_16	testB_14
testB_14	testB_6	testB_1	testB_6	testB_1	testA_56
testA_56	testA_34	testA_23	testA_34	testB_9	testA_23

Discussion
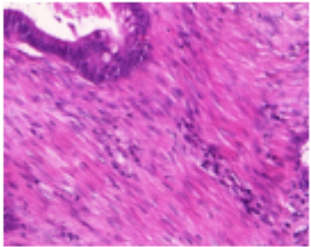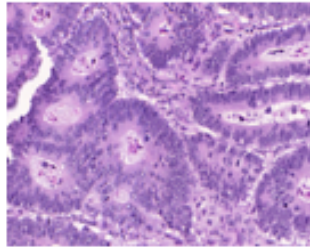
testA_38 testA_3 testA_48 testA_16 TestA_14
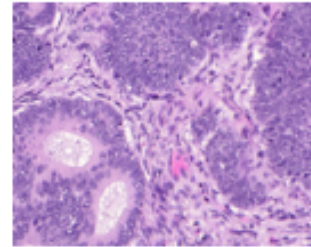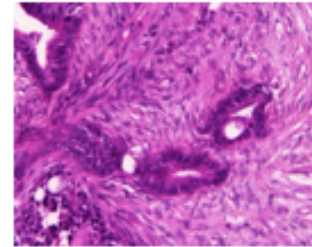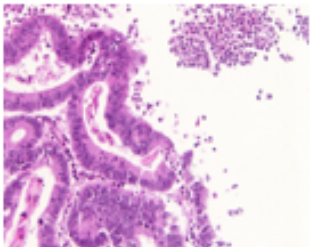
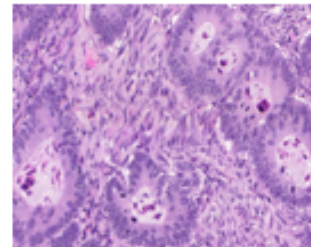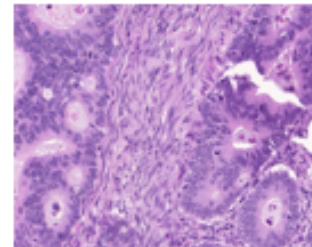tetstB_6 testB_1 testA_56 testA_34 testA_23

List of mialigant tissued that classiefied to benign by both of model architecture 1 and architecture 2

Acknowledgment

Conclusion & Future Direction

❖ **Sliding windos can be implemented to produce histopathology dataset for CNN training**

❖ **Data and architecture of CNN is still improved**

❖ **Next, using pre-trained model can be implemented**

Thank You