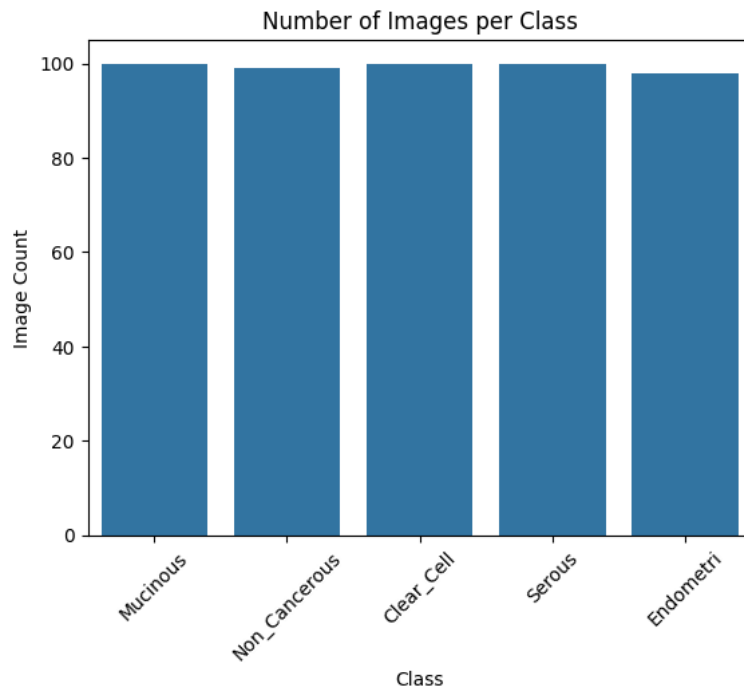
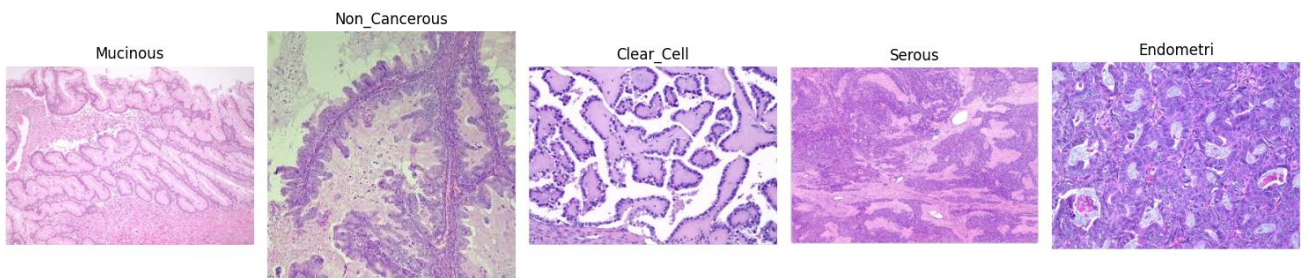


## Result & Discussion

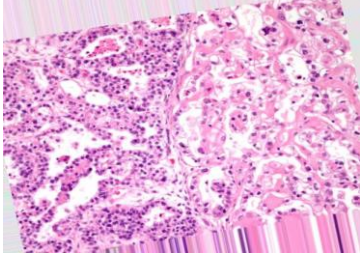
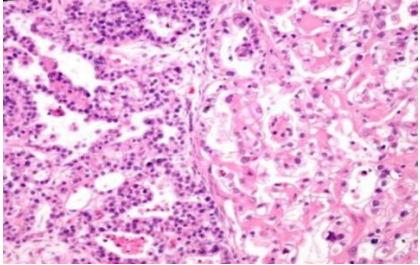
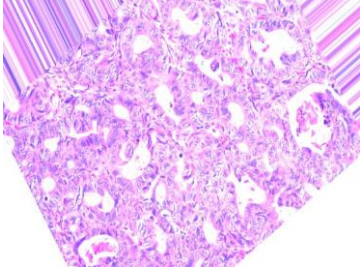
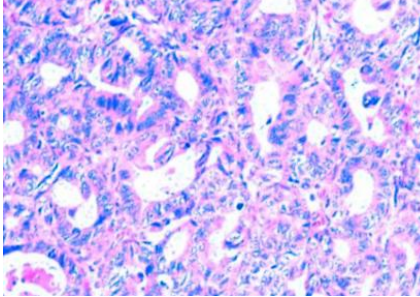
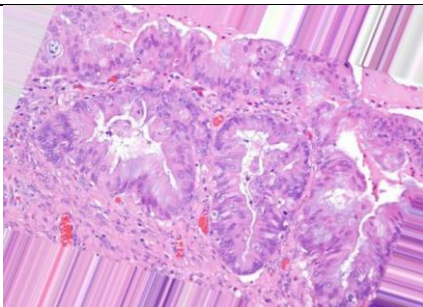
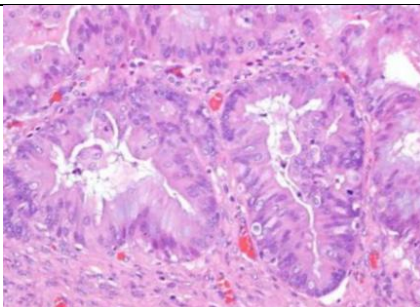
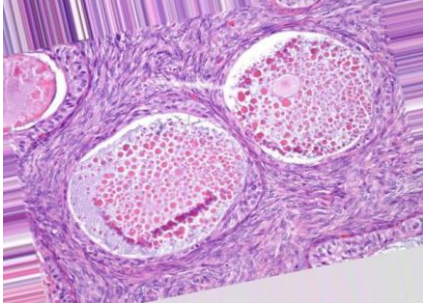
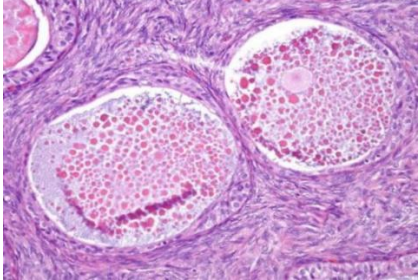
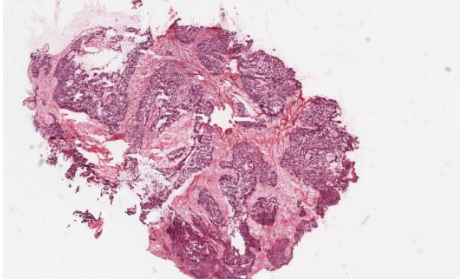
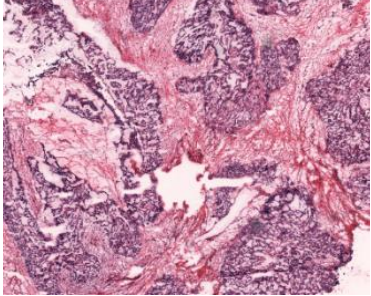
### 1. Original Histopathological Image Distribution



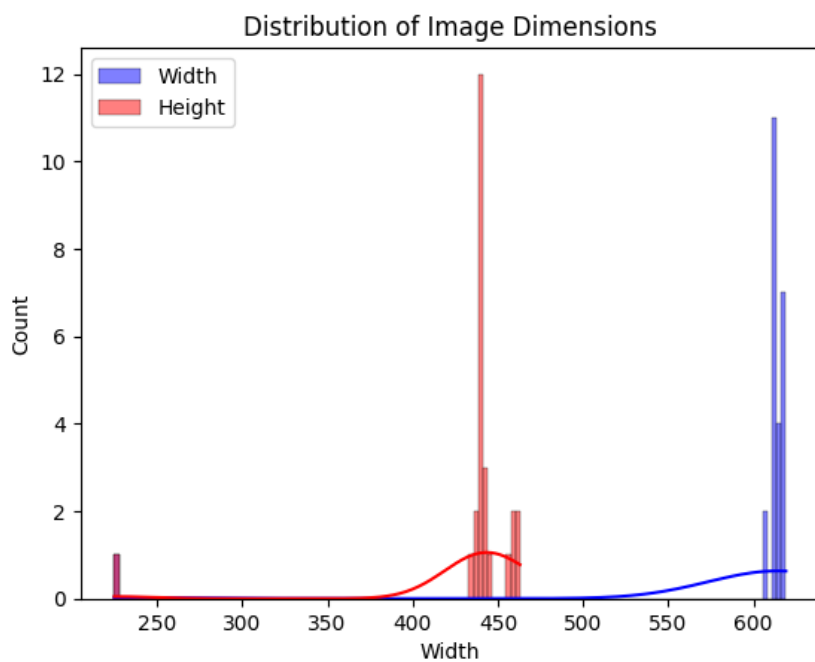
### 2. Sample Images



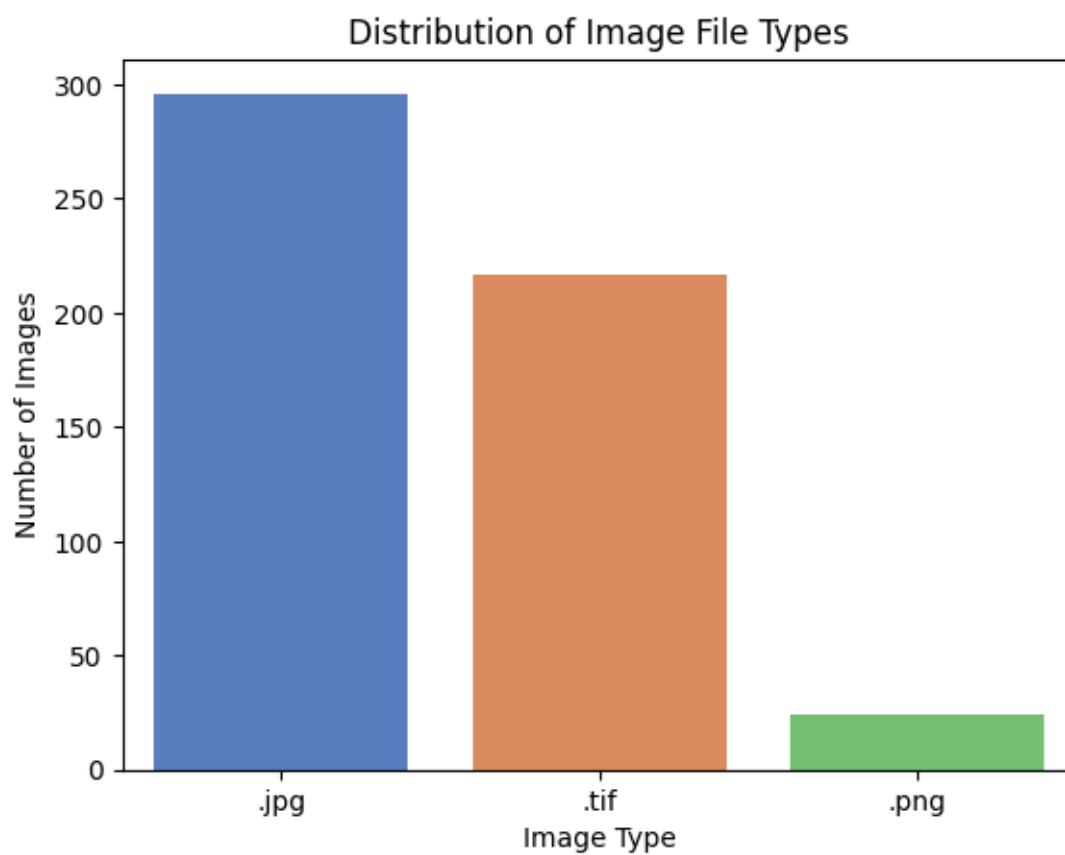
By manually inspection on data images we could find unusable, noisy images among the data set and then we have to process this data by cropping, rotating, Spliting or removing entire image to maintain data usability. We use "ImageJ" software to acheive this target and restore the images in folder called "Pre-Processed Data"

Subtype	Original Noisy Images	Processed Images
Clear Cell		
Endometrioid		
Mucinous		
Non_Cancerous		
Serious		

### 3. Image Size Distribution



### 4. Image Extension Distribution



## Model Performance Metrics

### 1. Random Forest

Random Forest Classification Report on Separate Test Data:				
	precision	recall	f1-score	support
Clear_Cell	0.64	0.75	0.69	100
Endometri	0.80	0.83	0.81	100
Mucinous	0.64	0.66	0.65	100
Non_Cancerous	0.68	0.70	0.69	100
Serous	0.85	0.61	0.71	100
accuracy			0.71	500
macro avg	0.72	0.71	0.71	500
weighted avg	0.72	0.71	0.71	500
Random Forest Model Accuracy on Test Data: 0.71				

### 2. XG Boost

Fine-Tuned XGBoost Classification Report:				
	precision	recall	f1-score	support
Clear_Cell	0.66	0.76	0.70	100
Endometri	0.85	0.85	0.85	100
Mucinous	0.64	0.71	0.67	100
Non_Cancerous	0.74	0.70	0.72	100
Serous	0.87	0.68	0.76	100
accuracy			0.74	500
macro avg	0.75	0.74	0.74	500
weighted avg	0.75	0.74	0.74	500
Fine-Tuned XGBoost Model Accuracy: 0.74				

The fine-tuned XGBoost model achieved the highest accuracy (74%) among the tested models (Random Forest, Decision Tree, SVM), indicating it best captured the patterns in the data.

#### ❖ Best classified

- Serous (Precision- 0.87) and Endometrioid (F1-score- 0.85) show high precision and recall, indicating the model distinguishes these subtypes well.

### ❖ Challenging subtypes

- Mucinous and Clear\_Cell had lower F1-scores (0.67 and 0.70), suggesting more misclassifications possibly due to overlapping features or fewer unique patterns.
- Non\_Cancerous had moderate results, with balanced precision and recall (~0.70).

### 3. Decision Tree

Decision Tree Classification Report on Test Data:				
	precision	recall	f1-score	support
Clear_Cell	0.55	0.61	0.58	100
Endometri	0.70	0.69	0.70	100
Mucinous	0.52	0.53	0.52	100
Non_Cancerous	0.59	0.59	0.59	100
Serous	0.60	0.53	0.56	100
accuracy			0.59	500
macro avg	0.59	0.59	0.59	500
weighted avg	0.59	0.59	0.59	500
Decision Tree Model Accuracy on Test Data: 0.59				

### 4. SVM Classifier

SVM Classification Report:				
	precision	recall	f1-score	support
Clear_Cell	0.37	0.37	0.37	100
Endometri	0.52	0.67	0.59	100
Mucinous	0.39	0.43	0.41	100
Non_Cancerous	0.31	0.31	0.31	100
Serous	0.68	0.43	0.53	100
accuracy			0.44	500
macro avg	0.46	0.44	0.44	500
weighted avg	0.46	0.44	0.44	500
SVM Model Accuracy: 0.44				