



# CLIPath

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Clip for multimodal model based on WSI image and report

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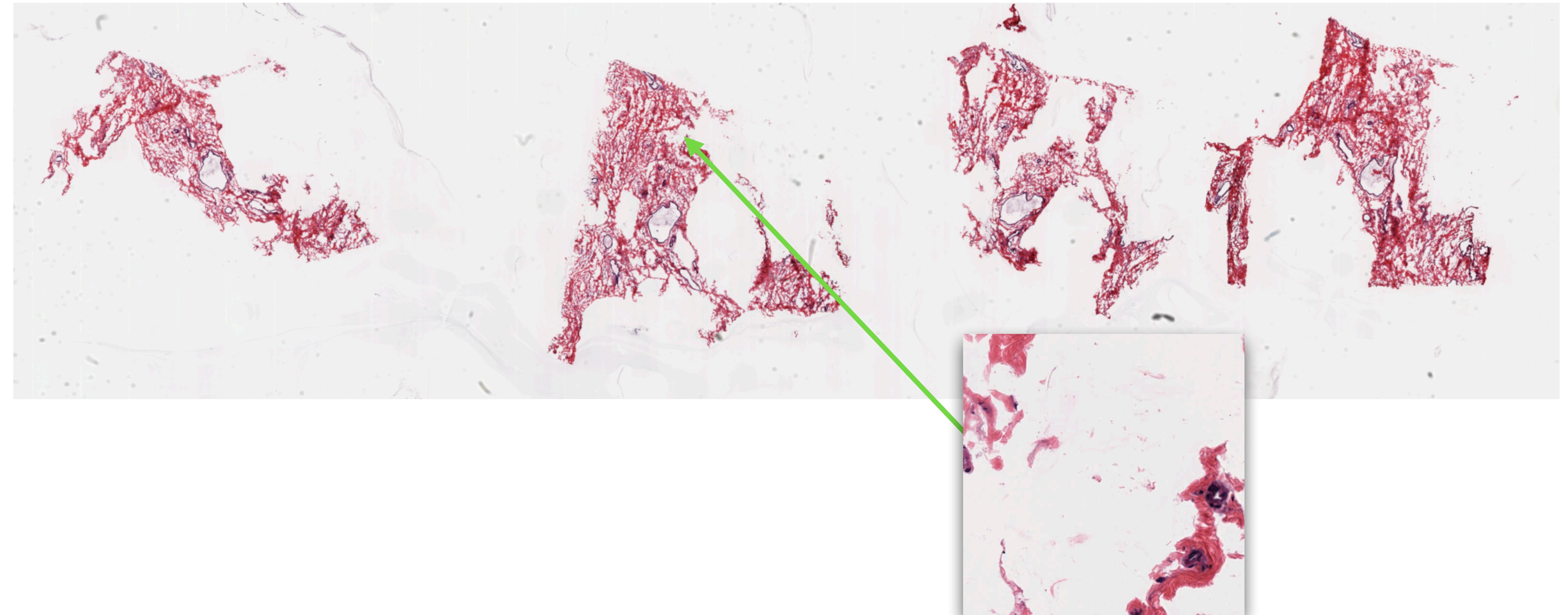
# Introduction

# WSI (Whole Slide Image)



TCGA dataset [1]

# Patch selection



TCGA dataset [1]

# Reports

## FINAL DIAGNOSIS:

### PART 1: LEFT BREAST, SEGMENTAL MASTECTOMY -

- A. INVASIVE DUCTAL CARCINOMA, NOTTINGHAM SCORE 8/9 (TUBULES 3, NUCLEI 3, MITOSIS 2), 2.6 CM.
- B. DUCTAL CARCINOMA IN SITU, MICROPAPILLARY AND SOLID TYPES WITH COMEDO NECROSIS, NUCLEAR GRADE 3, REPRESENTING 5% OF THE TUMOR VOLUME.
- C. LYMPHOVASCULAR SPACE INVOLVEMENT SEEN.
- D. INVASIVE CARCINOMA IS 0.1 CM FROM INFERIOR MARGIN.
- E. DUCTAL CARCINOMA IN SITU IS <0.1 CM (1MM) FROM INFERIOR MARGIN.
- F. MARGINS FREE OF LESION.
- G. MICROCALCIFICATION ASSOCIATED WITH BENIGN CHANGES AND TUMOR.
- H. CHANGES CONSISTENT WITH BIOPSY SITE.
- I. PROLIFERATIVE FIBROCYSTIC CHANGES WITH ATYPICAL DUCTAL EPITHELIAL HYPERPLASIA AND COLUMNAR CELL CHANGES.
- J. MICROSCOPIC PERIPHERAL PAPILLOMA AND SCLEROSING ADENOSIS.
- K. SKIN NOT REMARKABLE.

### PART 2: LEFT AXILLA, SENTINEL LYMPH NODE #1, EXCISION -

- A. ONE LYMPH NODE POSITIVE FOR METASTATIC CARCINOMA (0.9 CM).
- B. NO EXTRACAPSULAR EXTENSION SEEN.

### PART 3: LEFT AXILLA, SENTINEL LYMPH NODE #2, EXCISION -

ONE LYMPH NODE WITH RARE CLUSTERS OF METASTATIC TUMOR CELLS IN PERIPHERAL SINUS.

### PART 4: LEFT AXILLA, LYMPH NODE EXCISION -

ONE LYMPH NODE WITH EXTENSIVE THERMAL EFFECT, PROBABLY FREE OF TUMOR.

## CASE SYNOPSIS:

SYNOPTIC - PRIMARY INVASIVE CARCINOMA OF BREAST

LATERALITY:

Left

PROCEDURE:

Segmental

LOCATION:

Lower outer quadrant

SIZE OF TUMOR:

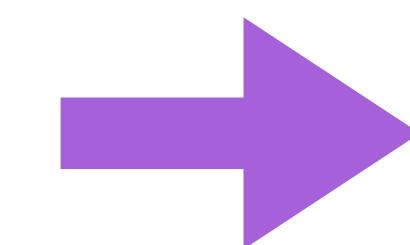
Maximum dimension invasive component: 2.6 cm

MULTICENTRICITY/MULTIFOCALITY OF INVASIVE FOCI:

No

TUMOR TYPE (Invasive component)

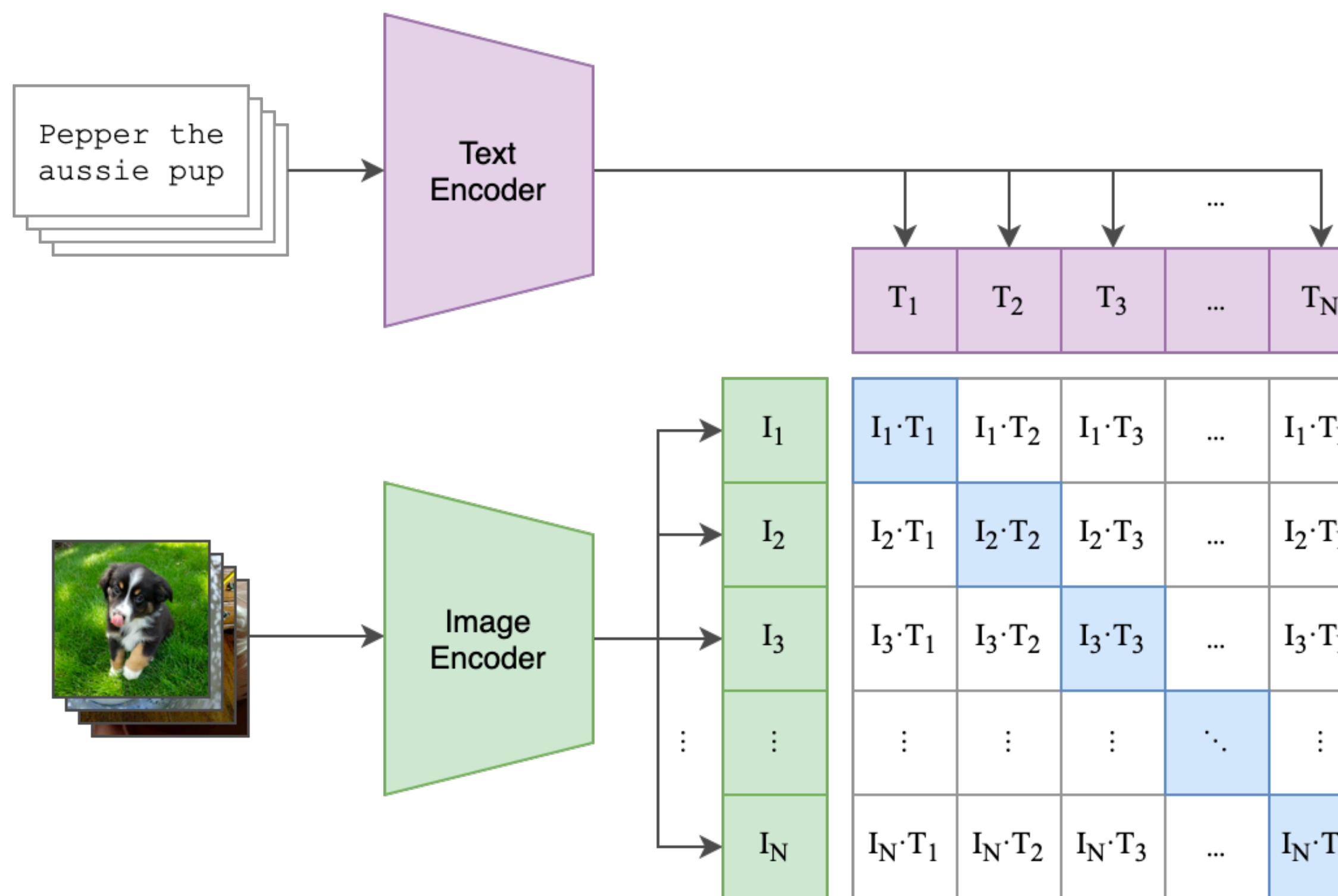
ICD-O-3  
Carcinoma, infiltrating ductal, nos 8500/3  
Site: breast, nos C50.9 3/3/11 hr



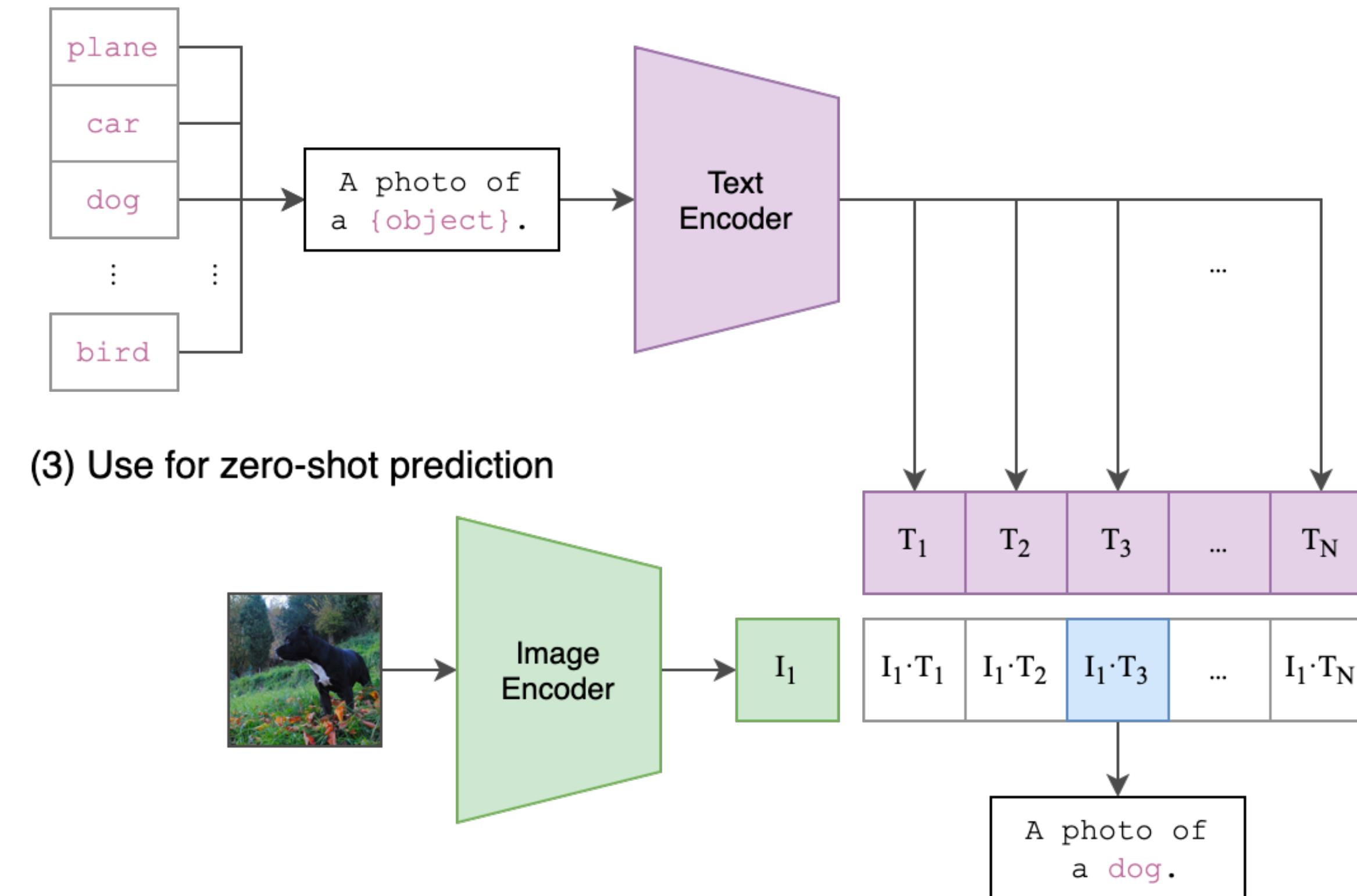
INVASIVE DUCTAL CARCINOMA,  
DUCTAL CARCINOMA IN SITU,  
MICROPAPILLARY AND SOLID  
TYPES WITH COMEDO NECROSIS.  
DUCTAL CARCINOMA IN SITU IS  
NEAR INFERIOR MARGIN.

# CLIP

(1) Contrastive pre-training

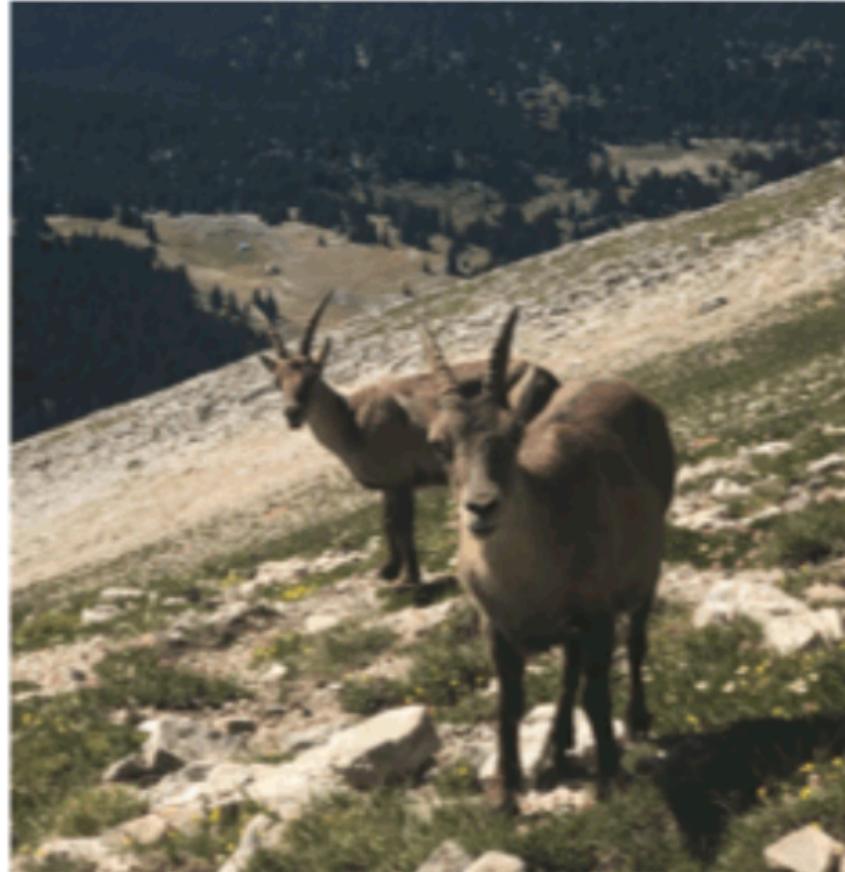


(2) Create dataset classifier from label text



# DINO

Global Crop (> 50%)  
&  
Local Crop (< 50%)



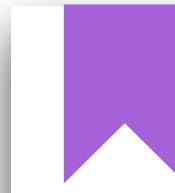
Global Crop (> 50%)

The average embedding  
subtracts the rest from this  
sample by a very small factor

# DINO



# Pathology BERT



## PathologyBERT - Pre-trained Vs. A New Transformer Language Model for Pathology Domain

Thiago Santos, MS<sup>1</sup>, Amara Tariq, Ph.D.<sup>2</sup>, Susmita Das, MS<sup>3</sup>, Kavyasree Vayalpati, MS<sup>4</sup>, Geoffrey H. Smith, MD<sup>5</sup>, Hari Trivedi, MD<sup>6</sup>, Imon Banerjee, Ph.D<sup>2,4</sup>

<sup>1</sup>Emory University, Department of Computer Science, Atlanta, Georgia, USA; <sup>2</sup>Mayo Clinic, Phoenix, Arizona, USA; <sup>3</sup>Indian Institute of Technology (IIT), Centre of Excellence in Artificial Intelligence, Kharagpur, West Bengal, India; <sup>4</sup>Arizona State University, School of Computing and Augmented Intelligence, Tempe, Arizona, USA; <sup>5</sup>Emory University, Department of Pathology, Atlanta, Georgia, USA; <sup>6</sup>Emory University, Department of Radiology, Atlanta, Georgia, USA;

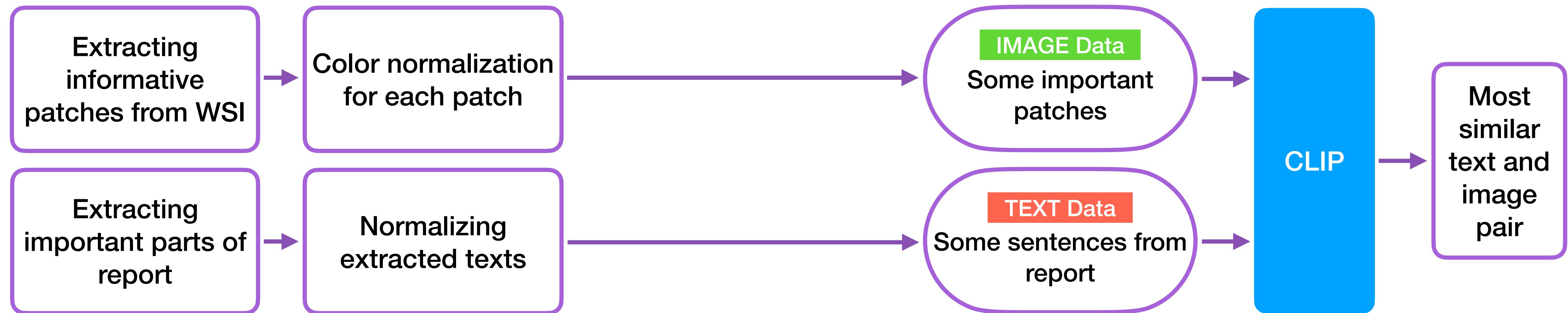
**Change Tokenizer**

**Abstract** Pathology text mining is a challenging task given the reporting variability and constant new findings in cancer sub-type definitions. However, successful text mining of a large pathology database can play a critical role to advance 'big data' cancer research like similarity-based treatment selection, case identification, prognostication, surveillance, clinical trial screening, risk stratification, and many others. While there is a growing interest in developing language models for more specific clinical domains, no pathology-specific language space exist to support the rapid data-mining development in pathology space. In literature, a few approaches fine-tuned general transformer models on specialized corpora while maintaining the original tokenizer, but in fields requiring specialized terminology, these models often fail to perform adequately. We propose PathologyBERT - a pre-trained masked language model which was trained on 347,173 histopathology specimen reports and publicly released in the Huggingface repository. Our comprehensive experiments demonstrate that pre-training of transformer model on pathology corpora yields performance improvements on Natural Language Understanding (NLU) and Breast Cancer Diagnose Classification when compared to nonspecific language models.

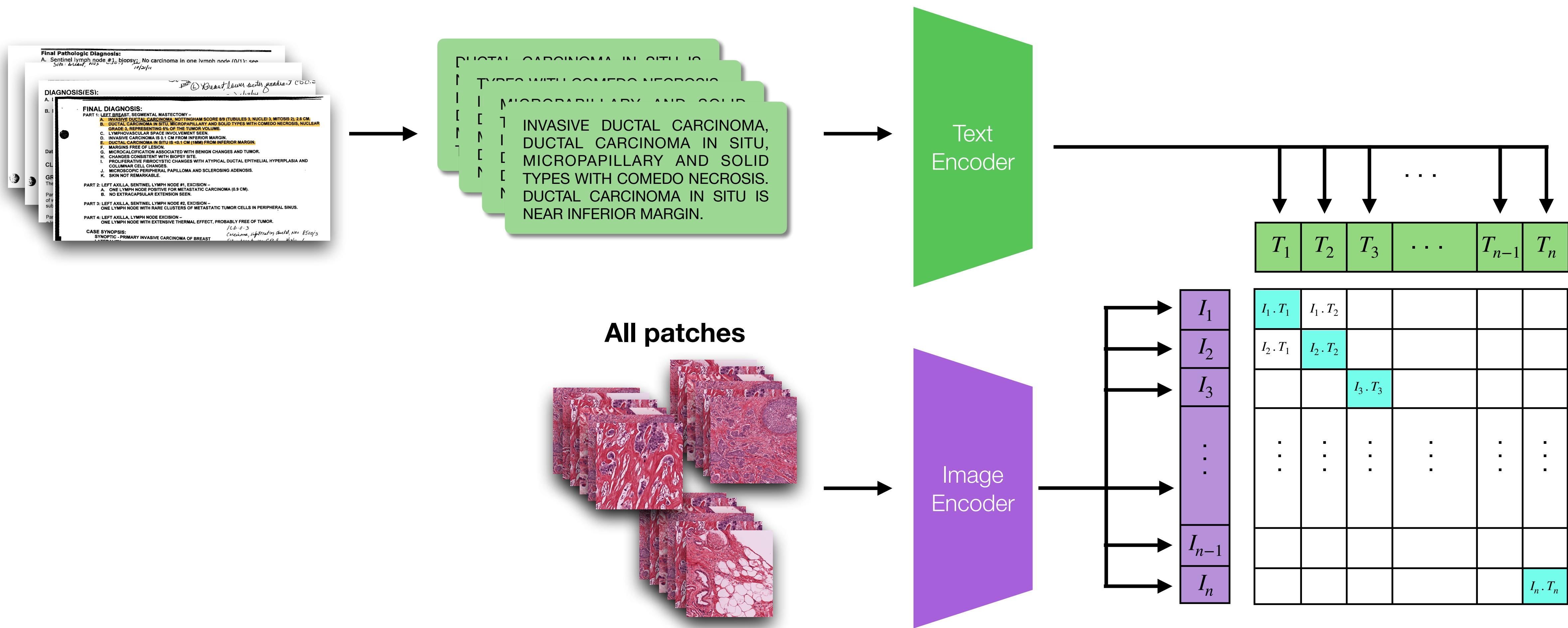
A bert model generates diagnostically relevant semantic embeddings from pathology synopses with active learning (PathologyBERT) [4]

# Baseline

# Pipeline

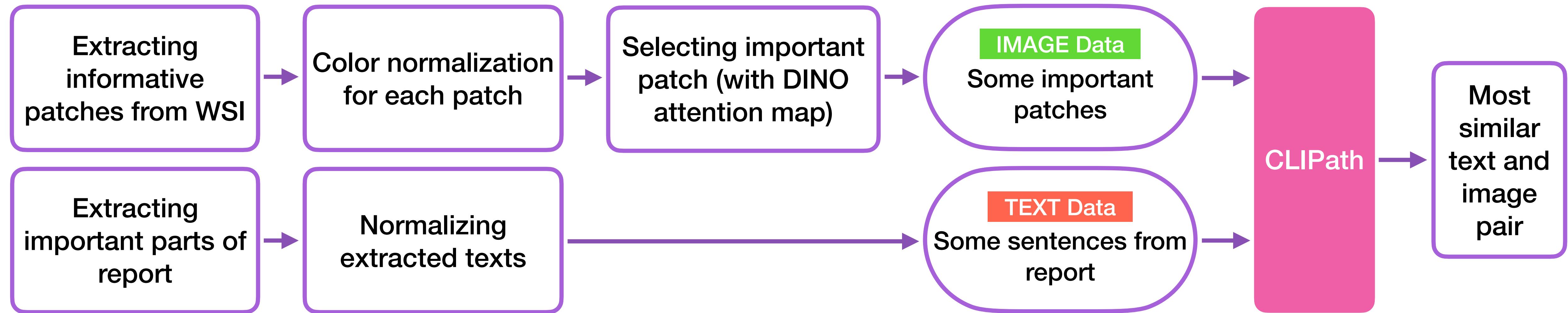


# Baseline model

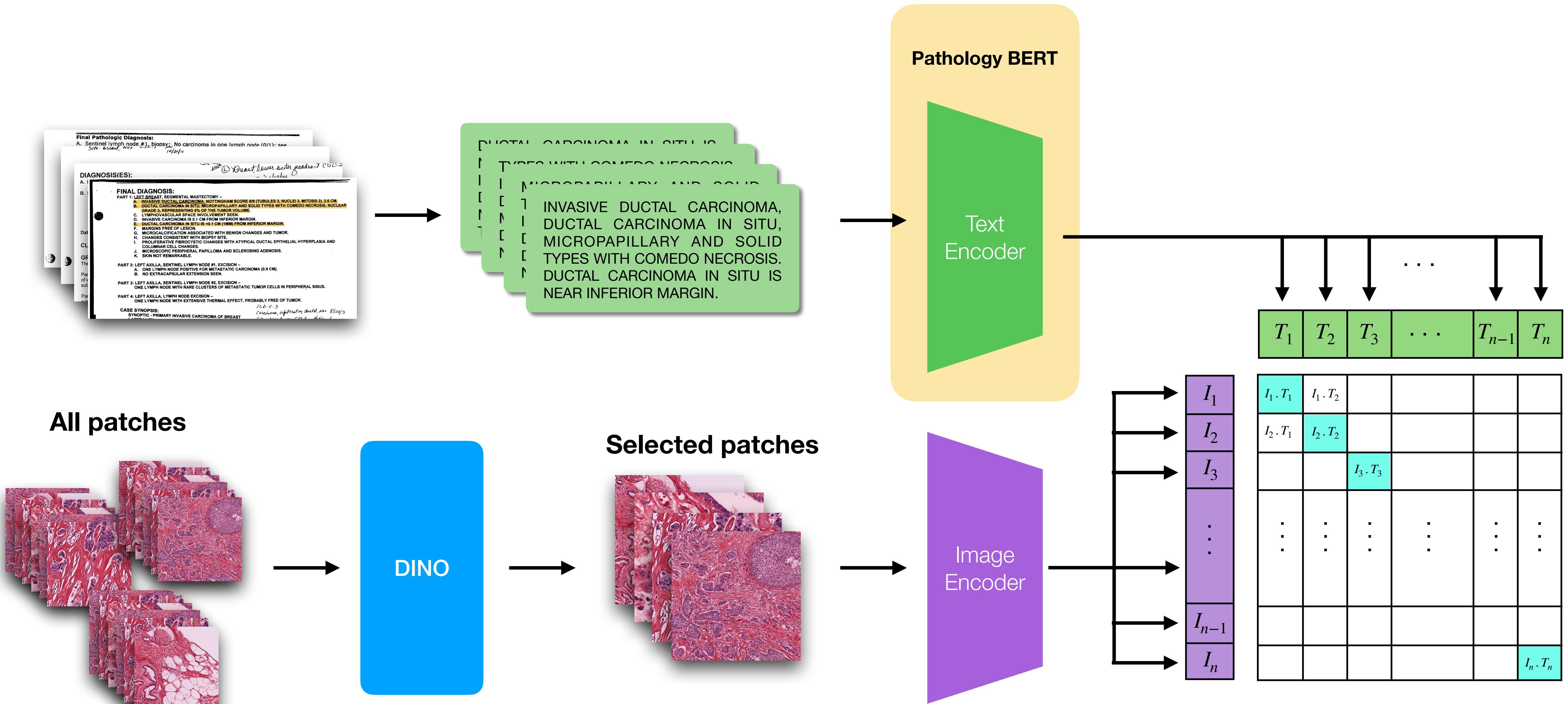


# Proposed Model

# Pipeline



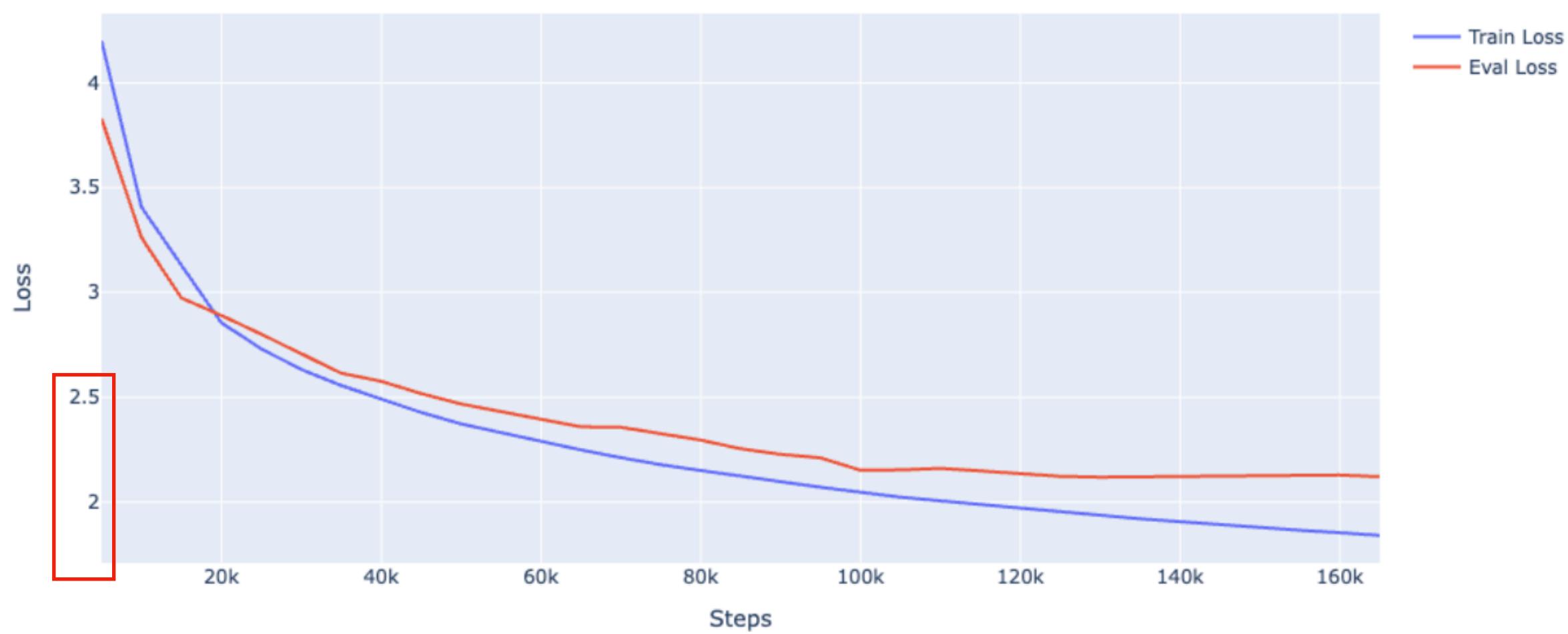
# CLIPPath



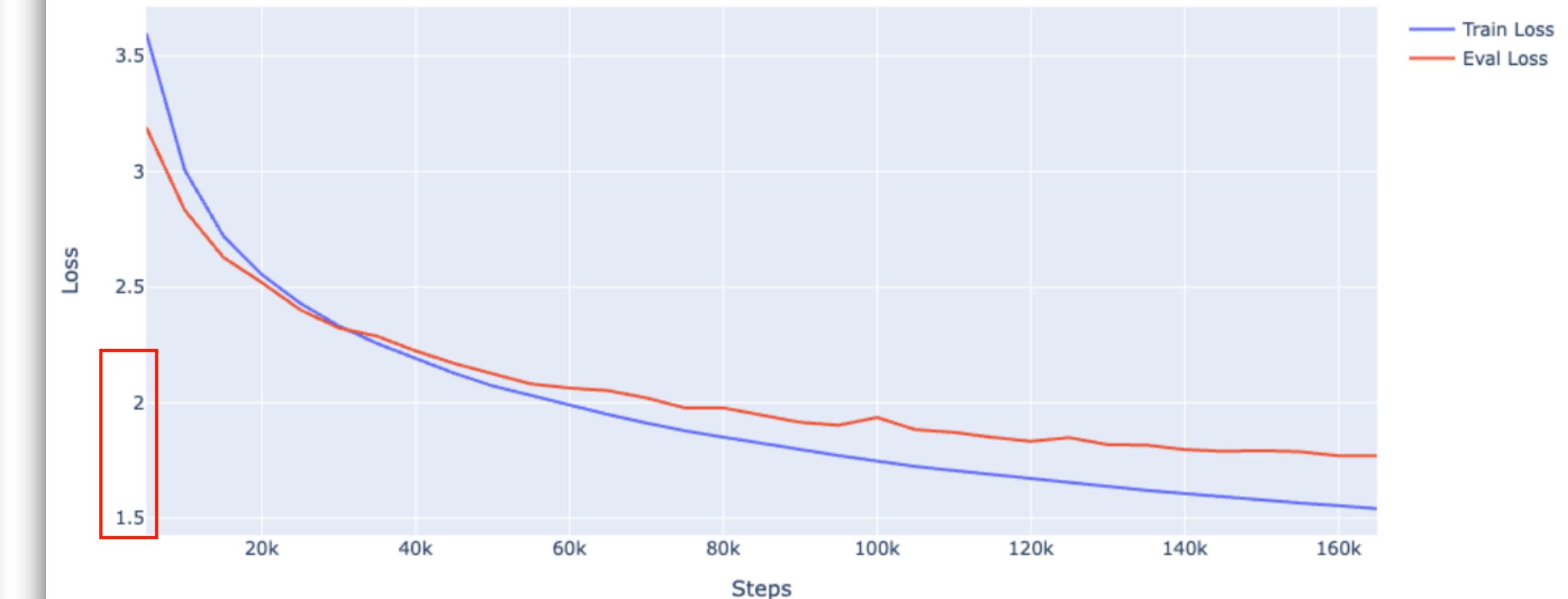
# Results

# Results

Train Loss vs Eval Loss baseline Model



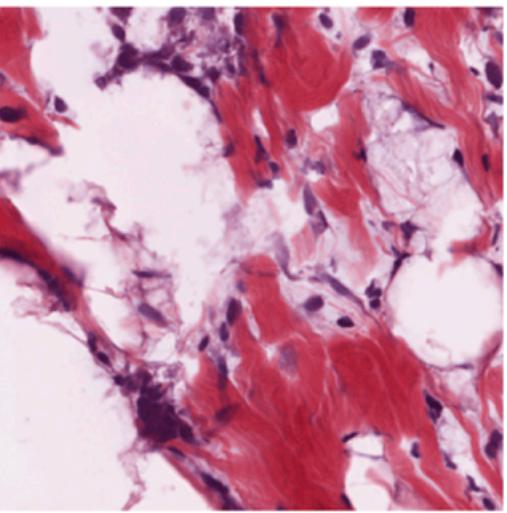
Train Loss vs Eval Loss proposed Model



# Results

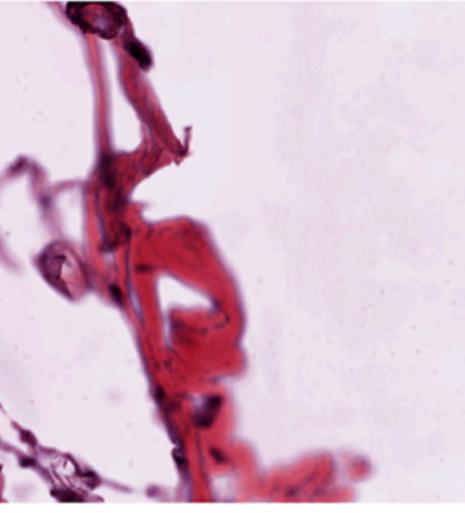
	<b>Baseline model</b>	<b>CLIPPath model</b>
Accuracy	0.525	0.698
Top-5 Accuracy	0.57	0.72

# Results



38%
invasive ductal carcinoma, ducal carcinoma in situ
36%
invasive ductal carcinoma with lobular features.
25%
invasive lobular carcinoma in greatest linear dimension.

53%
invasive ductal carcinoma with lobular features.
26%
invasive ductal carcinoma, ducal carcinoma in situ
21%
invasive lobular carcinoma in greatest linear dimension.

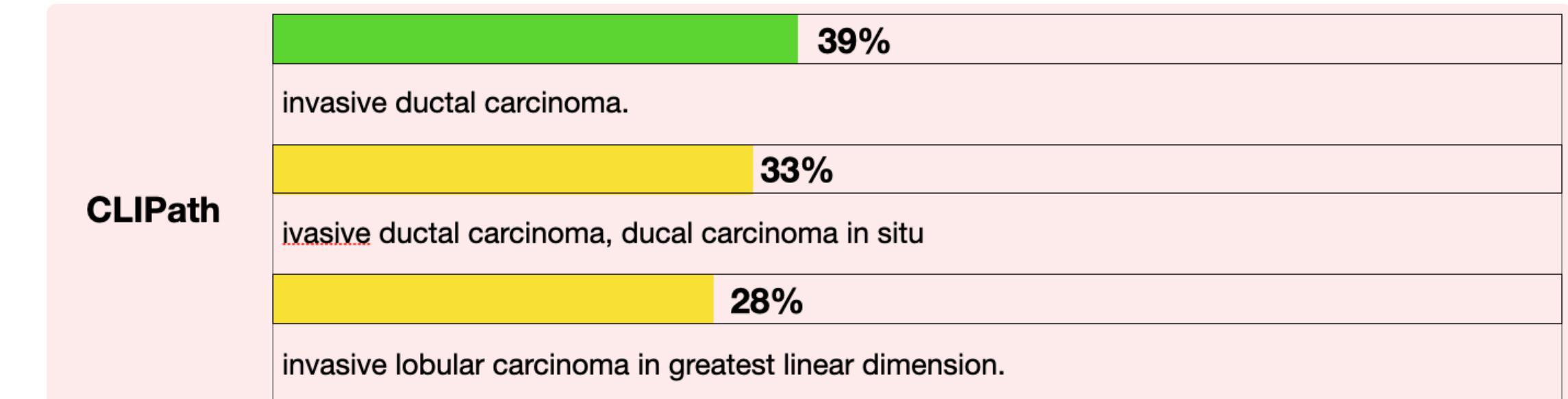
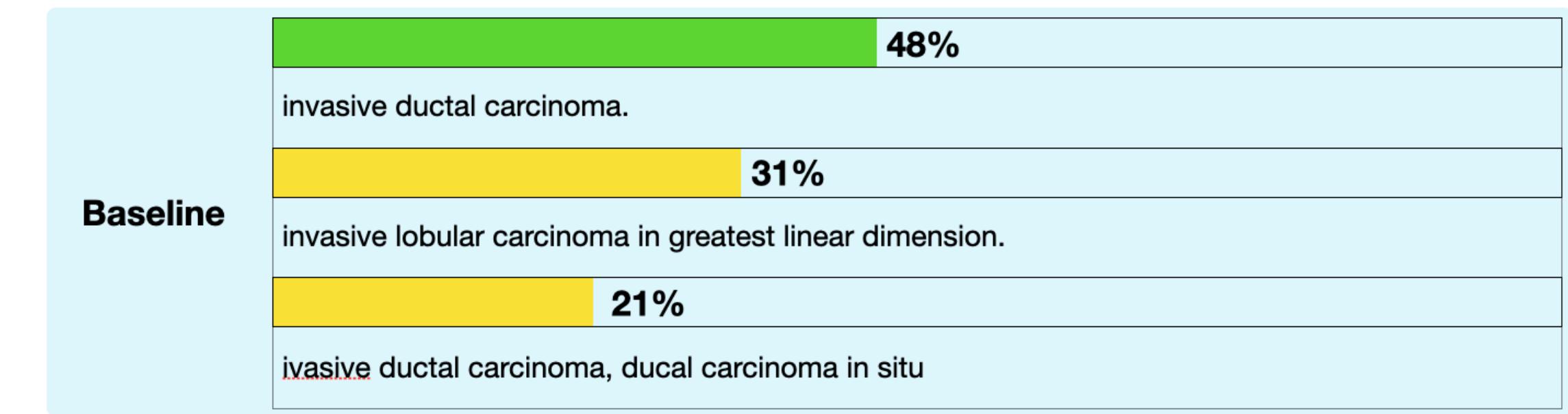
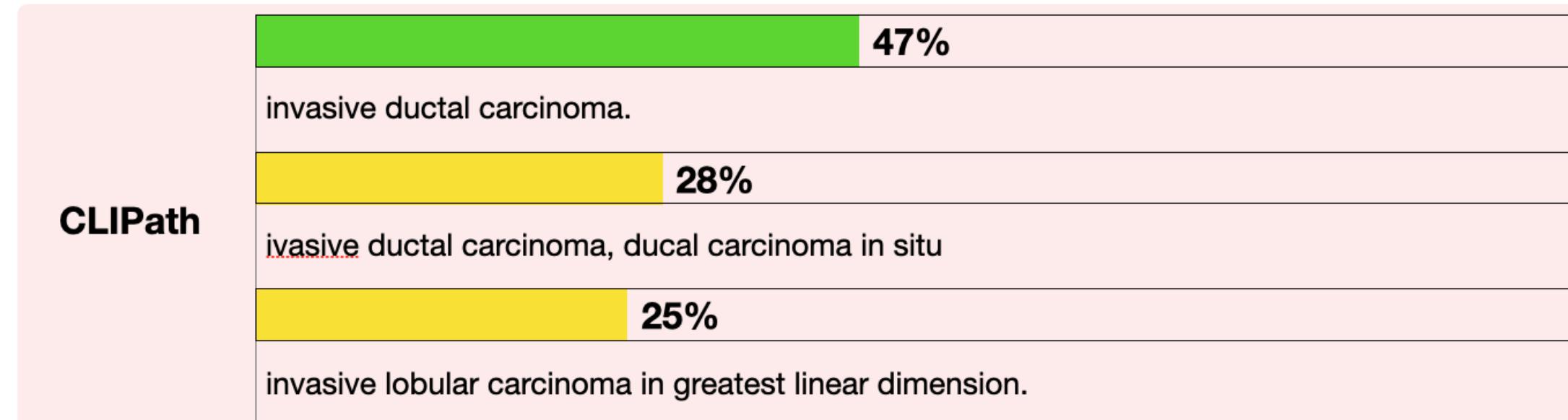
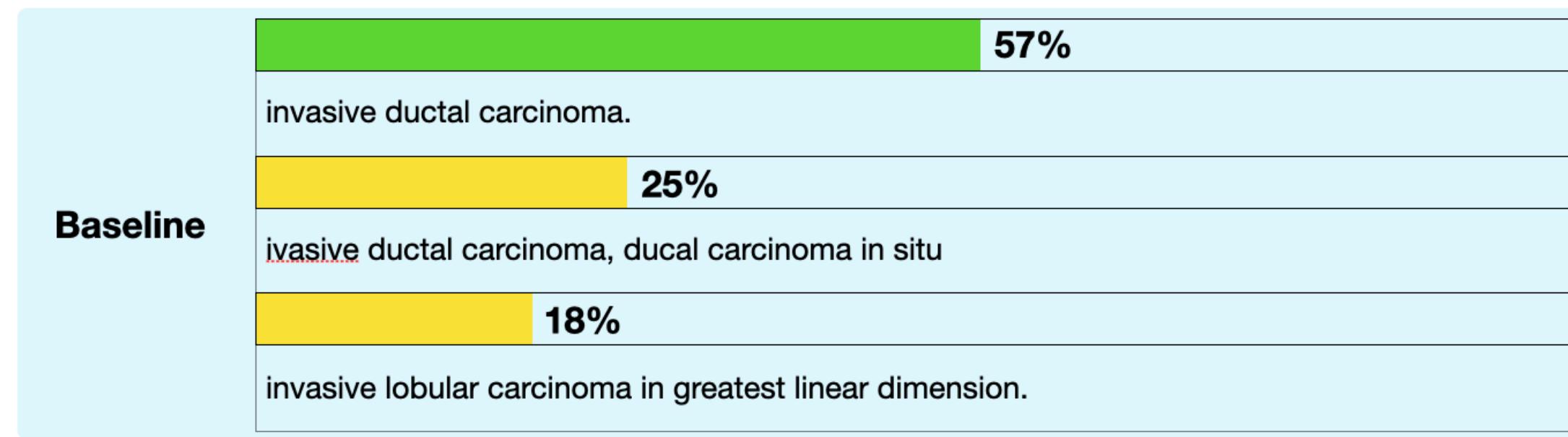
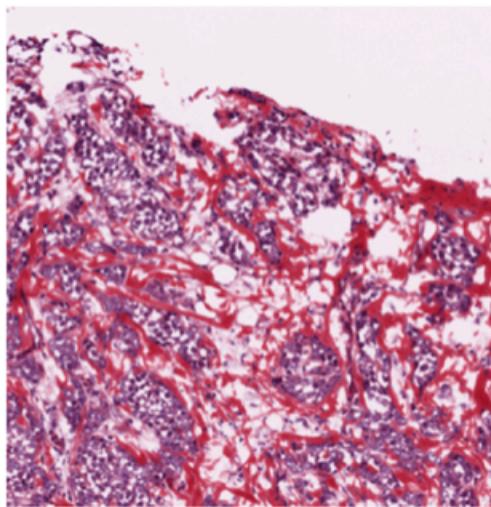


46%
infiltrating ductal carcinoma.
27%
invasive ductal carcinoma, ducal carcinoma in situ
27%
invasive lobular carcinoma in greatest linear dimension.

49%
infiltrating ductal carcinoma.
27%
invasive ductal carcinoma, ducal carcinoma in situ
23%
invasive lobular carcinoma in greatest linear dimension.

1024×1024

# Results



3072×3072

# Discussion

# Discussion

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- We create new dataset (selected part of report and informative patch of WSI)
- Our proposed model get better Accuracy and lower Loss within all reports
- The limitation of computing resources was one of the challenges of this project, which did not allow testing better and more methods.
- There is still a lot of work to be done and it is possible to provide better solutions to improve the model.

# Future works

# Future works

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- More effective way for first stage of patch selection
- Using other method for main model (e.g. MIL, Ava. Pool, ...)
- Using creative method to select important part of report automated (e.g. MIL)
- Using more powerful computational units (e.g. GPU with more memory)

# References

# References

- [1] National Cancer Institute 2023, The Cancer Genome Atlas Program (TCGA), accessed 9 March 2023, <https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga>
- [2] Radford, A., Kim, J. W., Hallacy, C., Ramesh, A., Goh, G., Agarwal, S., ... & Sutskever, I. (2021, July). Learning transferable visual models from natural language supervision. In *International conference on machine learning* (pp. 8748-8763). PMLR.
- [3] Caron, M., Touvron, H., Misra, I., Jégou, H., Mairal, J., Bojanowski, P., & Joulin, A. (2021). Emerging properties in self-supervised vision transformers. In *Proceedings of the IEEE/CVF international conference on computer vision* (pp. 9650-9660).
- [4] Mu, Y., Tizhoosh, H. R., Tayebi, R. M., Ross, C., Sur, M., Leber, B., & Campbell, C. J. (2021). A bert model generates diagnostically relevant semantic embeddings from pathology synopses with active learning. *Communications Medicine*, 1(1), 11.

Thanks For  
Your  
Attention :)