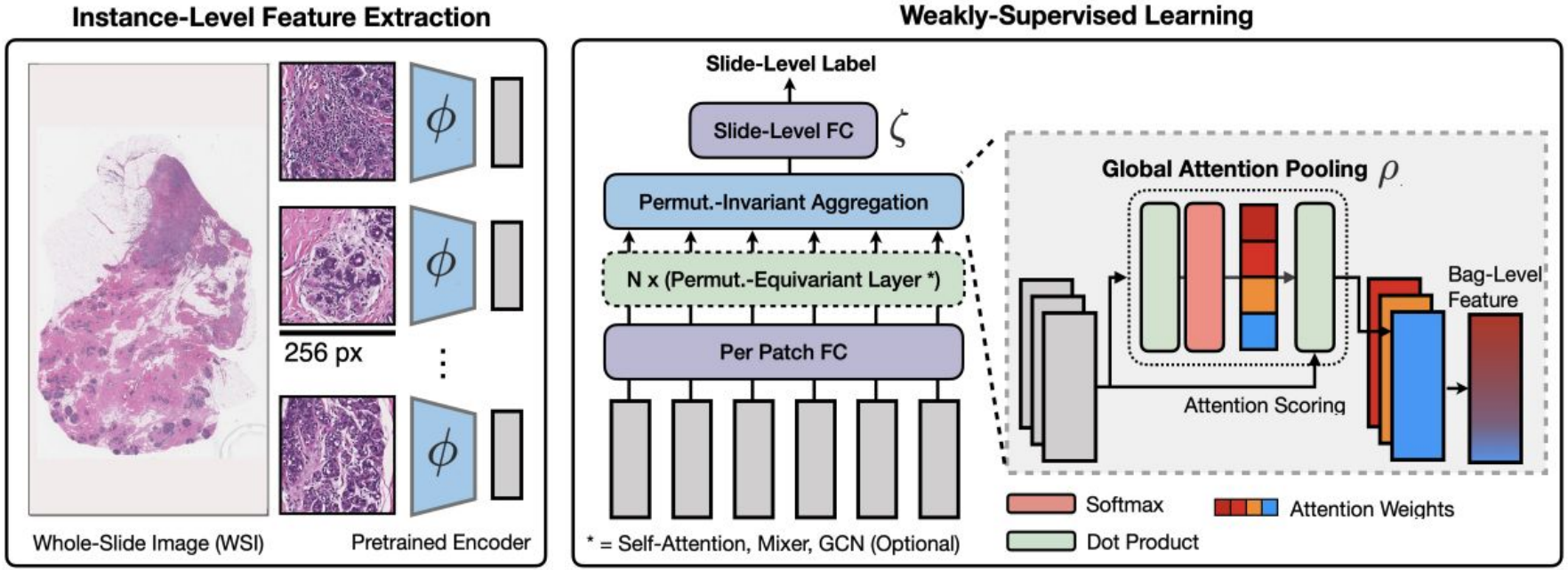
Cell-guided SSL for Histopathology

Background

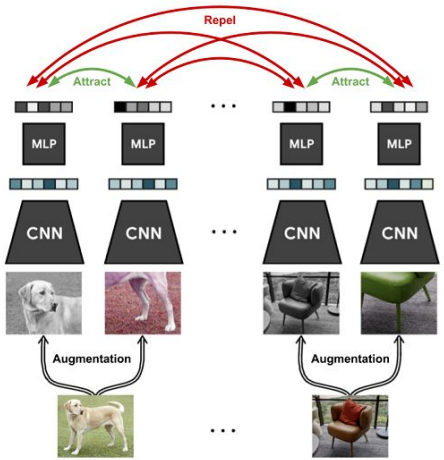
- WSIs are divided into patches.
- Followed by feature extraction using encoder, followed by MIL.



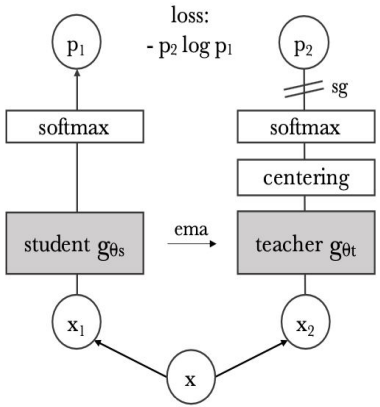
https://arxiv.org/pdf/2203.00585.pdf

Problem

- How to train the feature encoder?
  - ImageNet pretrained?
  - Self-supervised learned?
- Self-supervision has proven its superiority over Imagenet pretrained model in computational pathology.



SimCLR

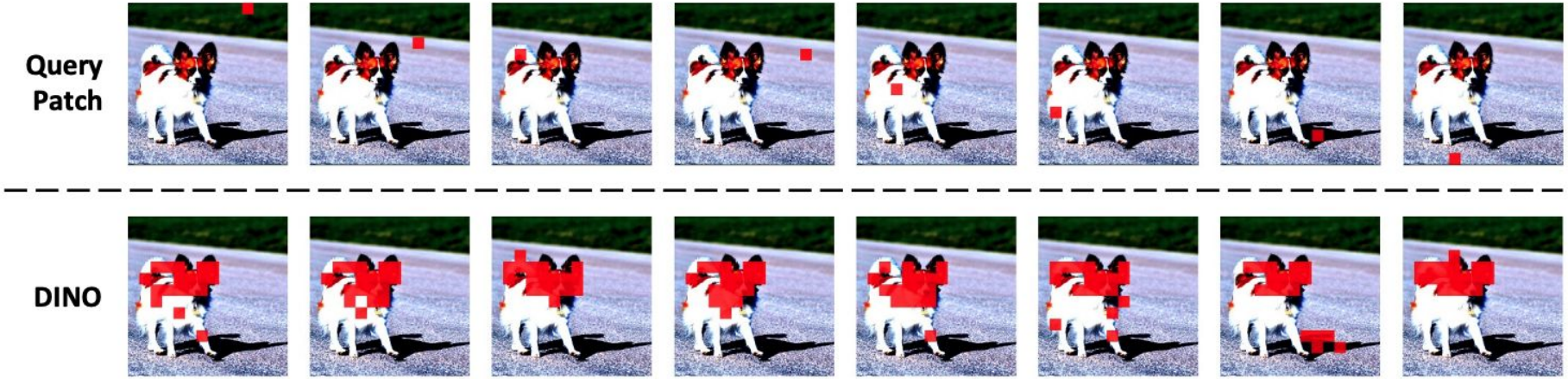


DINO

https://arxiv.org/abs/2104.14294
https://arxiv.org/abs/2002.05709

Problem

- Current SSL frameworks are trained to just match the global image-level representation of two augmented views.
- Due to no constraints and label-supervision over this matching, the SSL could match the views using fraction of region (object of invariance/sparsely).

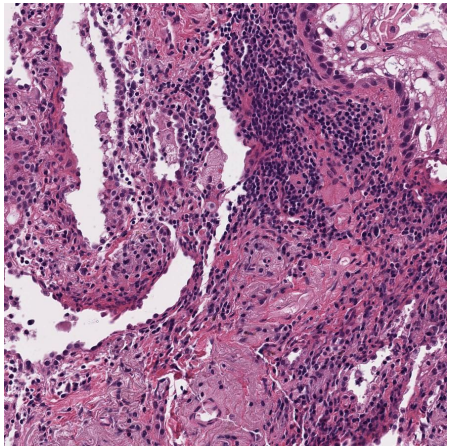


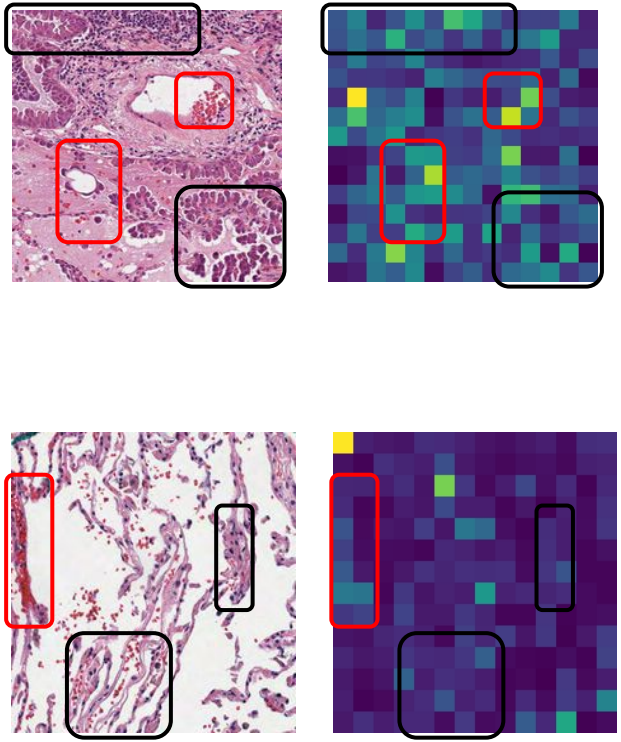
Attention Visualization in DINO

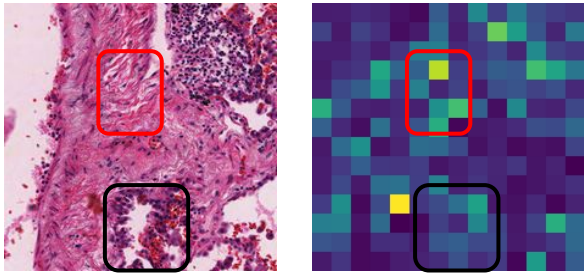
https://arxiv.org/pdf/2206.07990.pdf

Problem

- However in histopathology, there is no single or few objects of invariance. It is actually the spatial distribution of various components. (Sparse and scattered)







Introduction

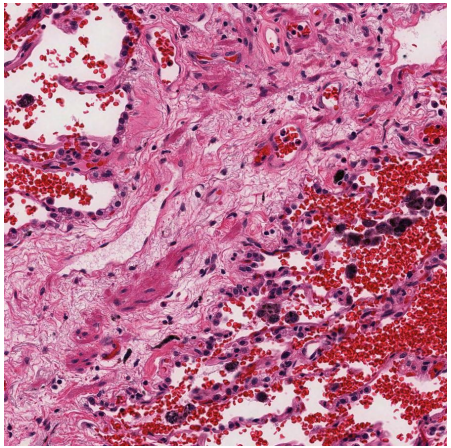
1) SSL method to learn features that explicitly encodes cell and background features by disentangling them.

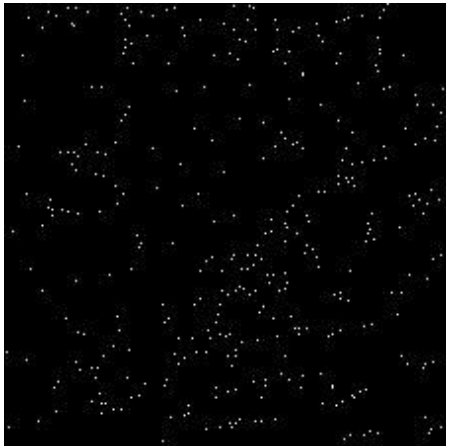
2) Model focuses on matching the cell-cell representation and background-background representation of two views in SSL pretraining.

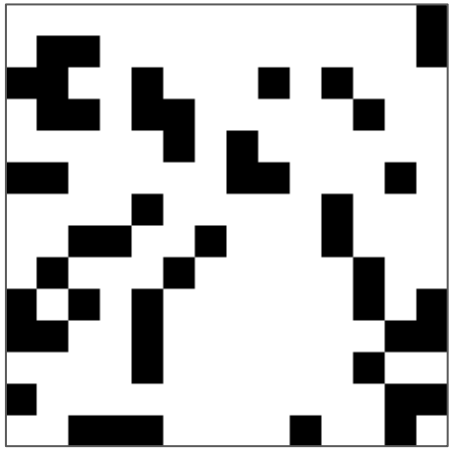
3) Introduced an block to explicitly match the spatial interaction relationship between cell and background of two views.

Prior

- Encoding cell and background representation separately, requires the need of cell segmentation prior.



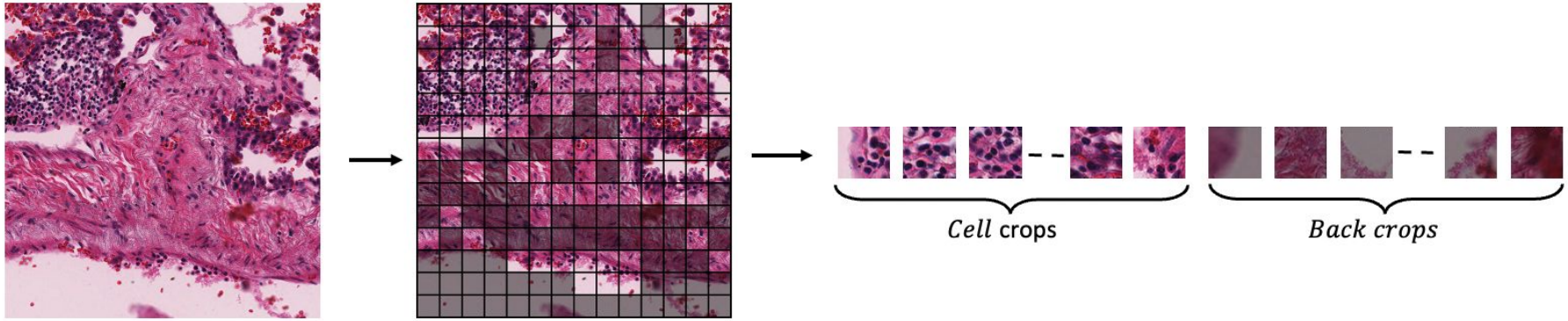




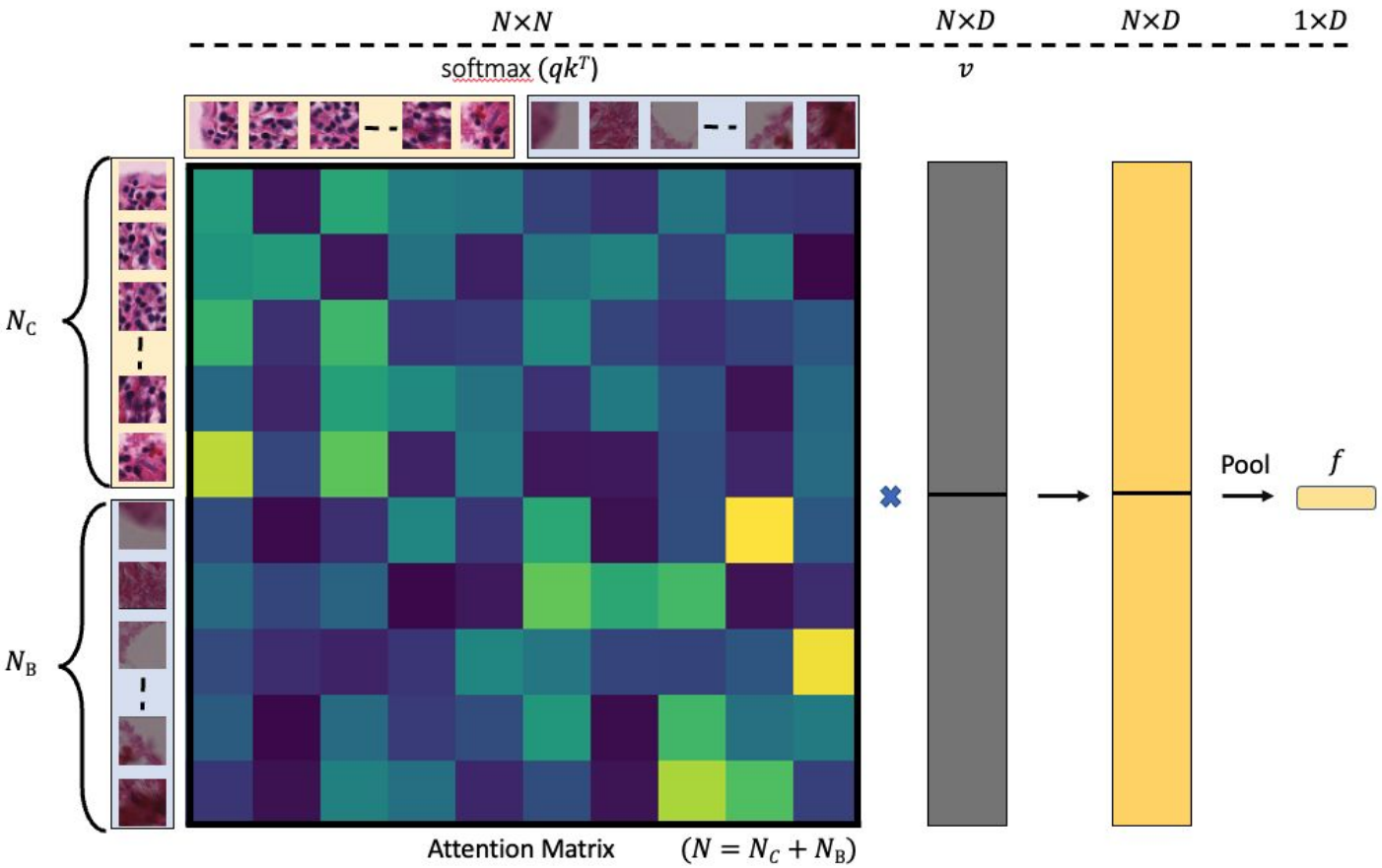
Cell segmentation
->
Centroid extraction

Patchifying
->
Presence of cells

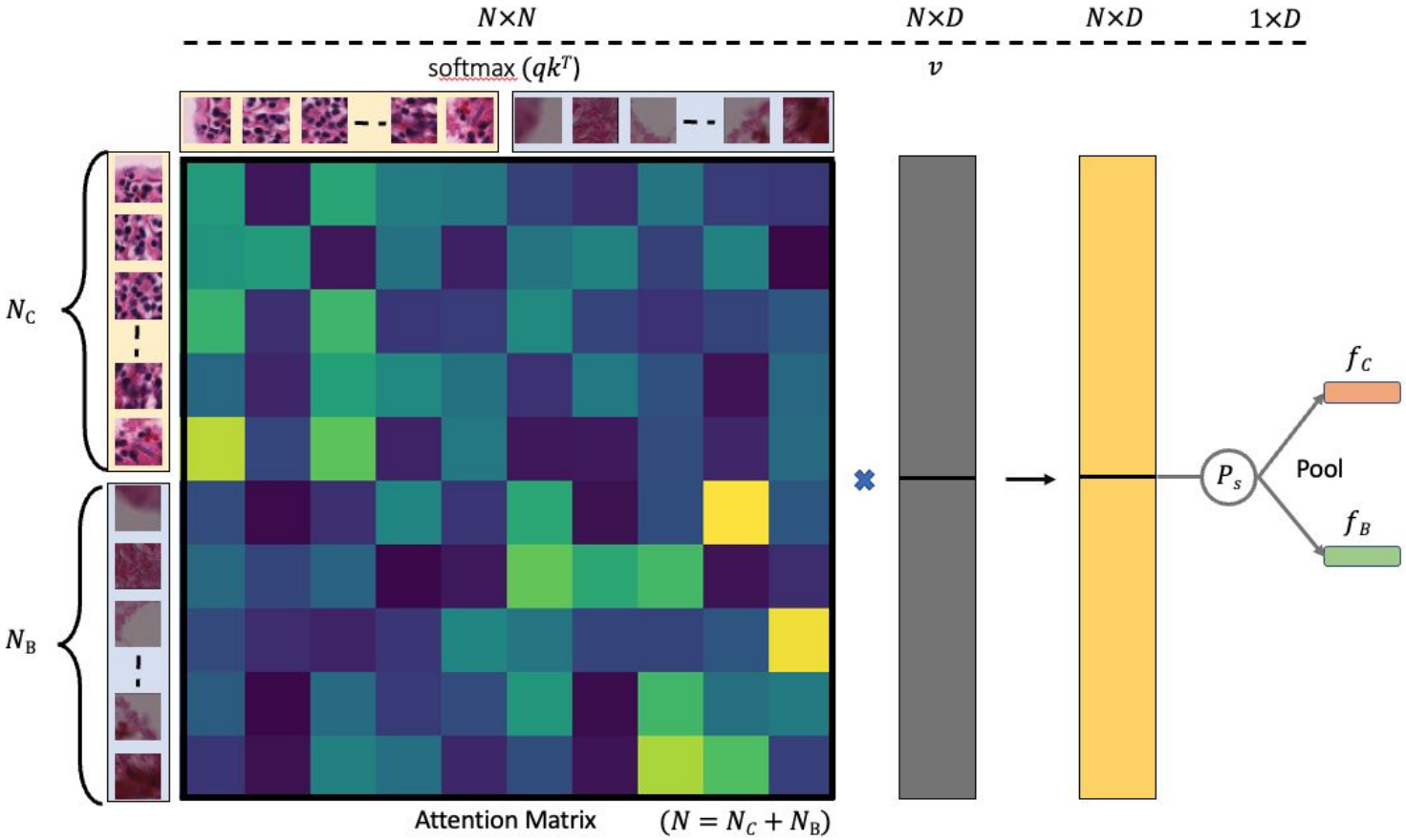
Use of Prior



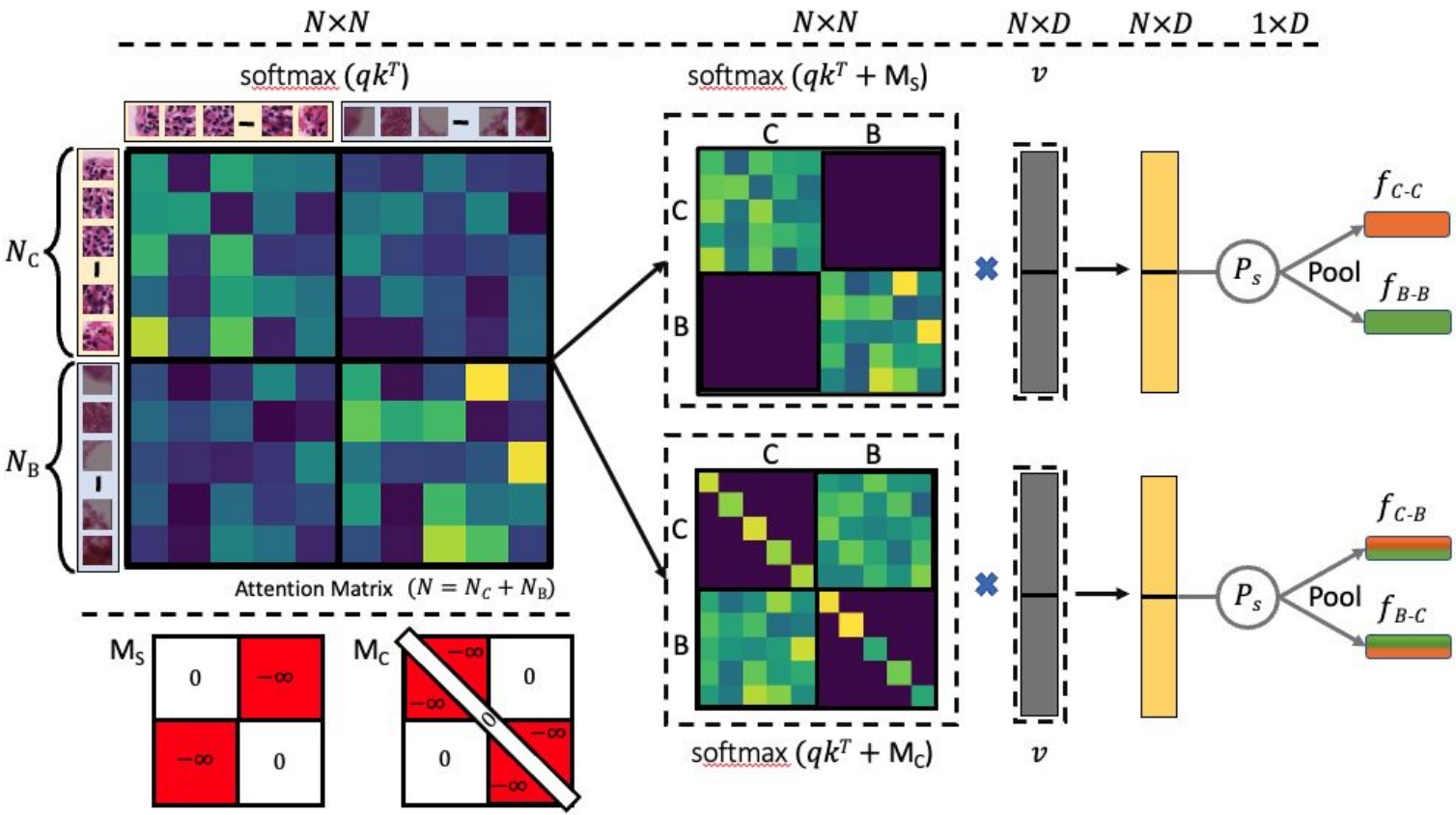
General Self-Attention followed by pooling



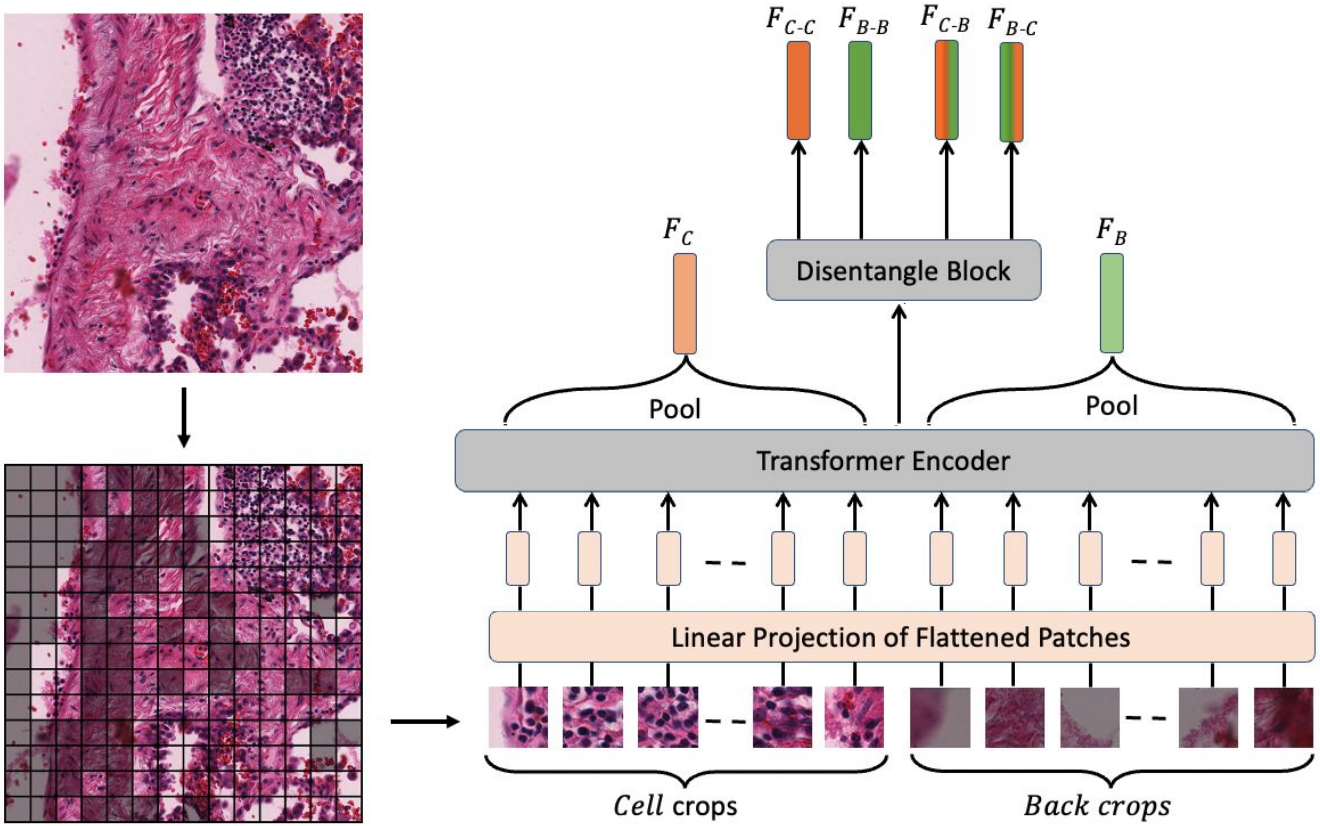
Self-attention followed by use of prior for pooling



Disentangle attention



Proposed pipeline



Pipeline

1. This mechanism will enforce the consistency between cell-cell and background-background representation in two views in SSL method.

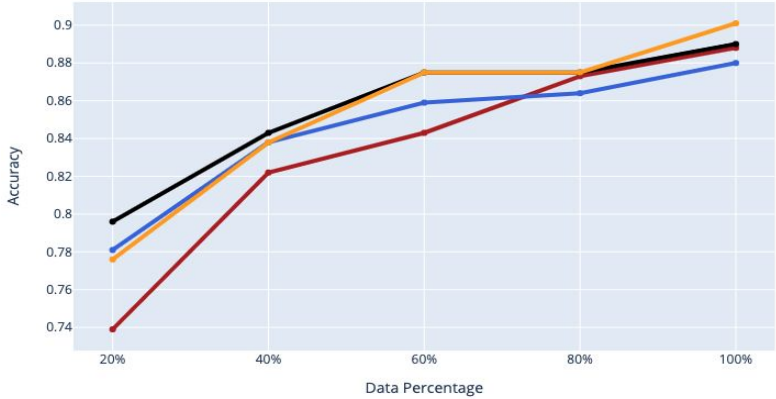
2. Disentanglement of interaction between cell and background followed by matching them between two views, enhances the encoding capabilities through focusing on discriminative diverse information available in the WSI crops.

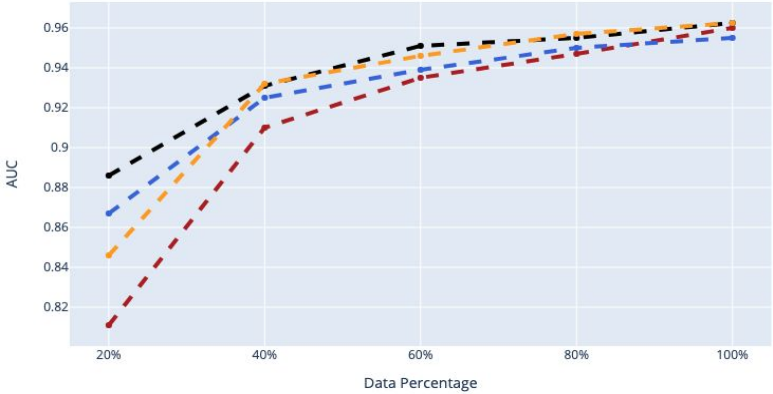
Results

	Lung Cancer		**BRCA**		**PAAD**		**Bright (3 Class)**		**Bright (6 Class)**	
	Acc	AUC	Acc	AUC	Acc	AUC	Acc	AUC	Acc	AUC
Baseline	0.911	0.967	0.896	0.947	0.821	0.704	0.637	0.835	0.475	0.787
Cell-Back	0.921	0.966	**0.927**	**0.955**	0.821	0.719	**0.675**	**0.854**	**0.525**	**0.813**
Cell-Back (Disentangle)	**0.927**	**0.973**	**0.927**	0.95	**0.839**	**0.733**	**0.650**	0.852	**0.500**	0.799

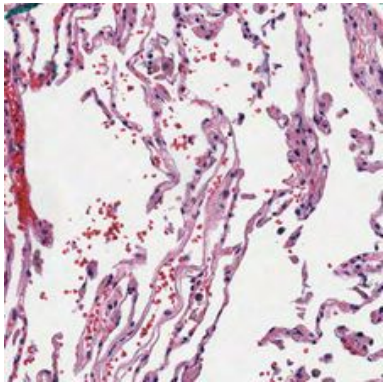
Percentage data study (TCGA-Lung)

No Prior

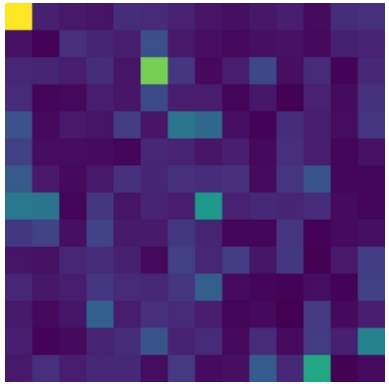




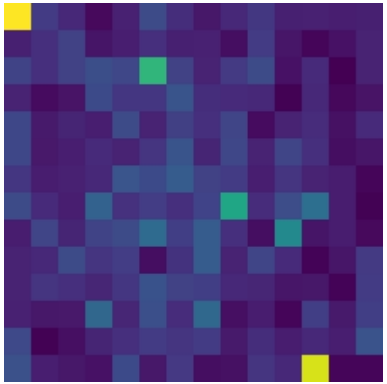
Qualitative analysis



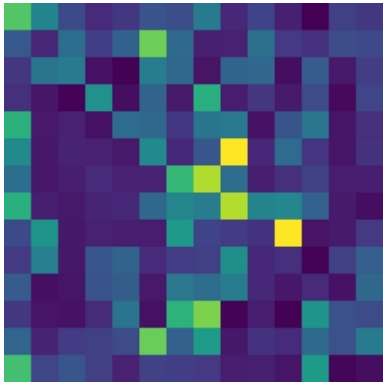
WSI Crop



Baseline

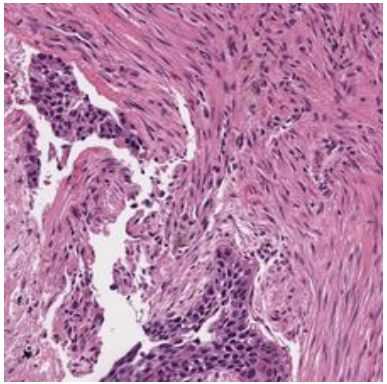


Cellback



Cellback
Disentangle

Qualitative analysis



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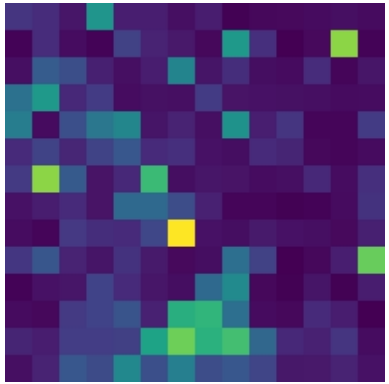

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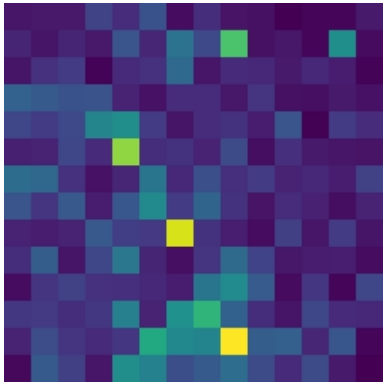

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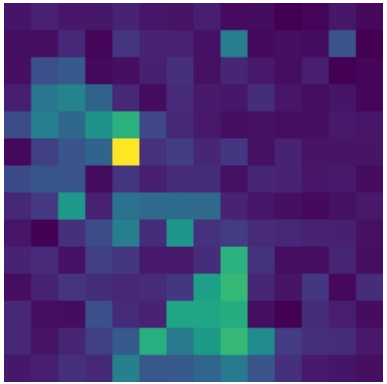
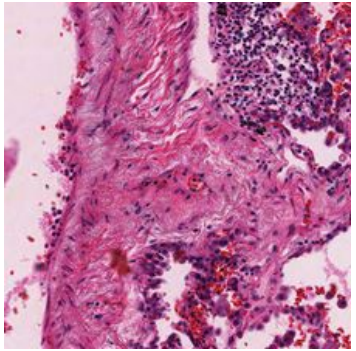


Cellback
Disentangle

Qualitative analysis



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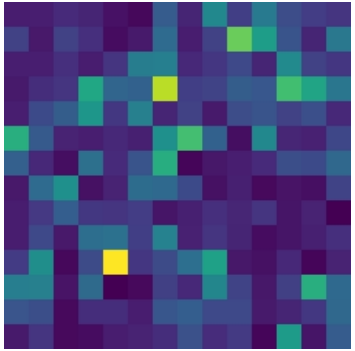

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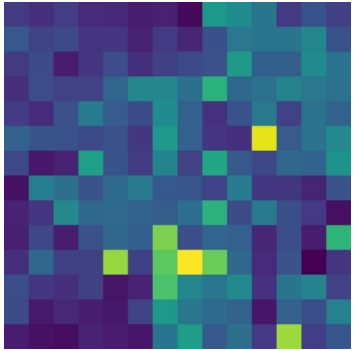
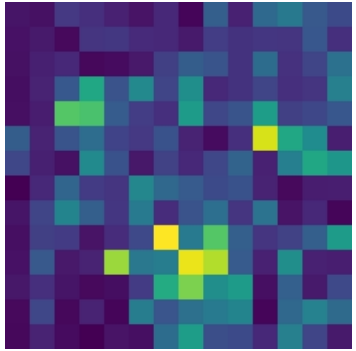
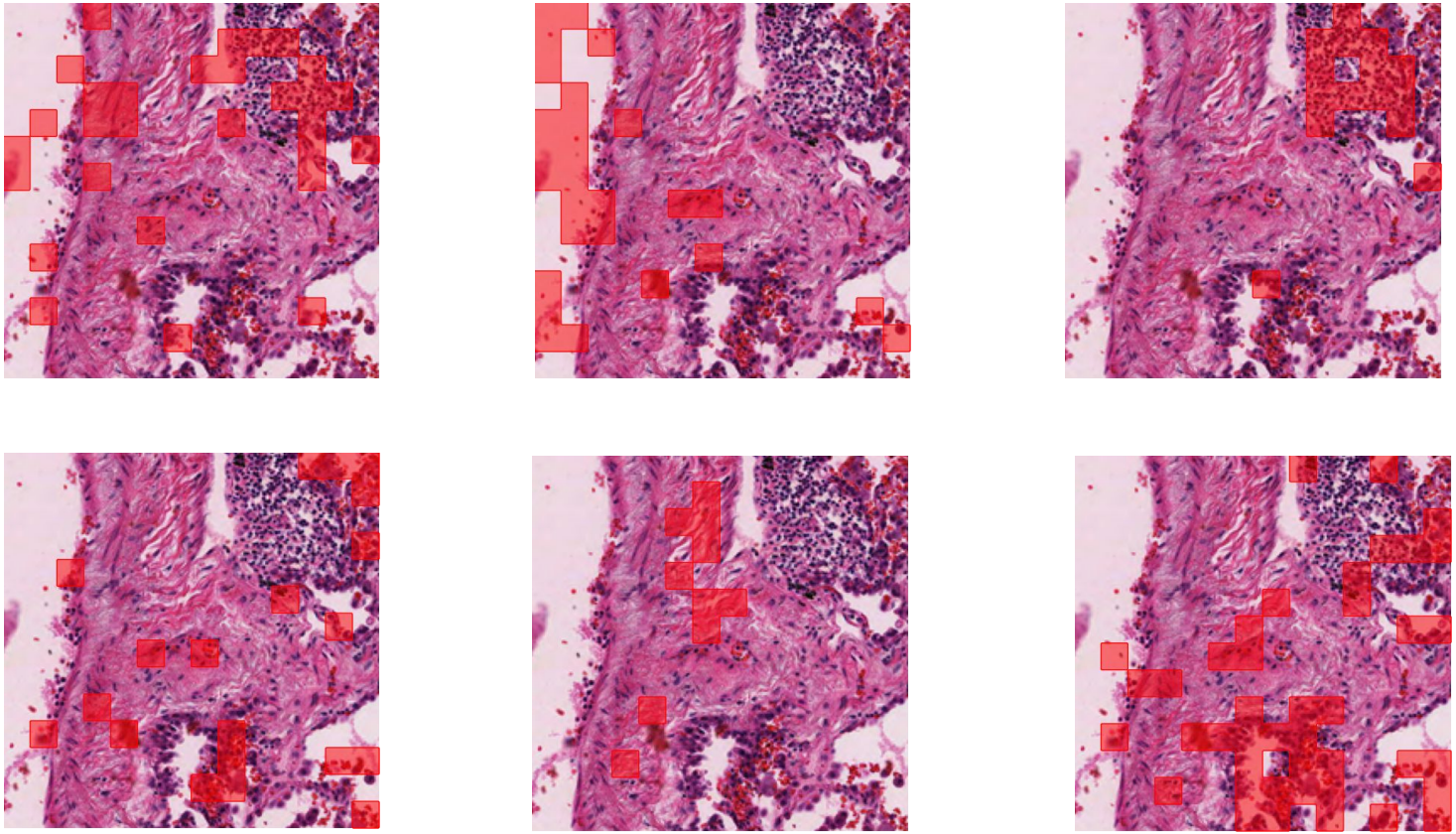


Cellback

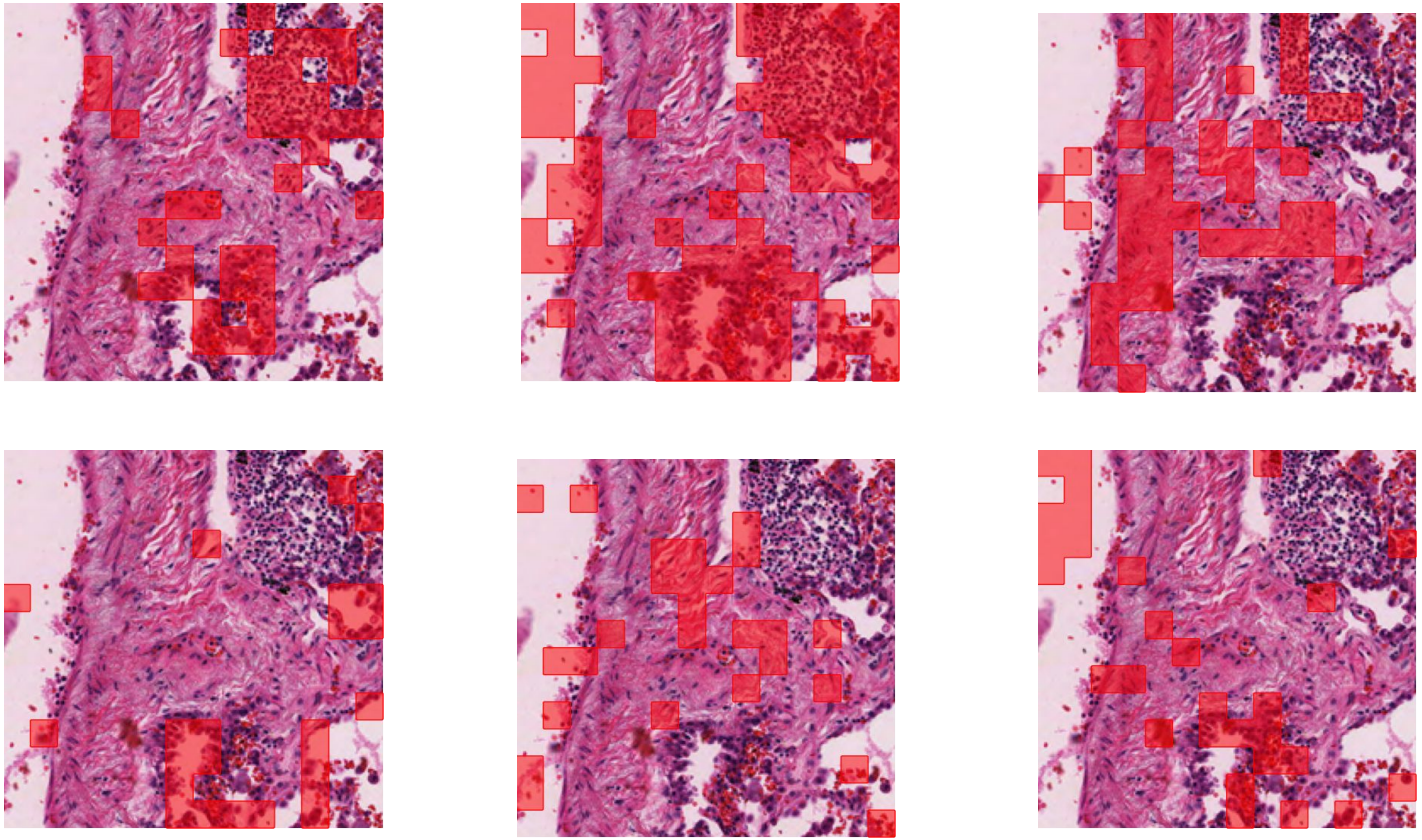
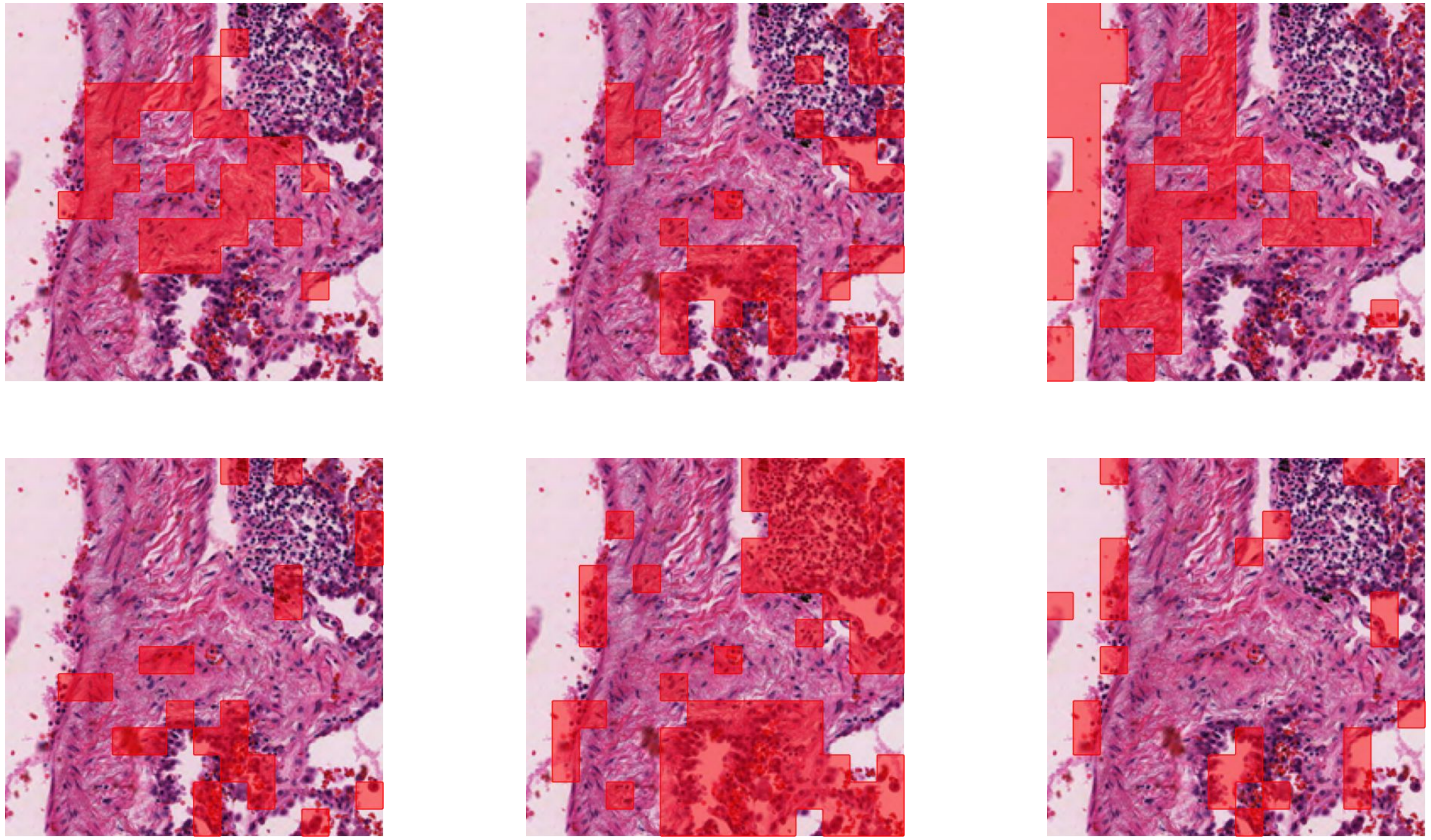


Cellback
Disentangle

Baseline



Cellback



Disentanle with cellback