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Multiple Instance Learning Framework with Masked Hard Instance Mining for Whole Slide Image Classification

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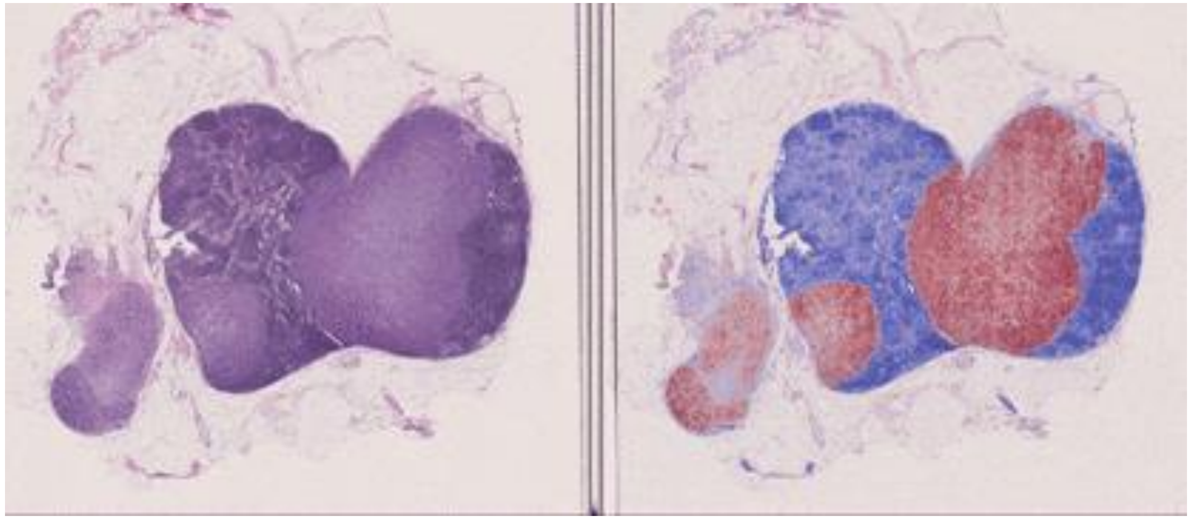
GitHub

arXiv

Background: WSI Classification

ICCV23 PARIS



[*CLAM. Nature Biomedical Engineering 2021.*]

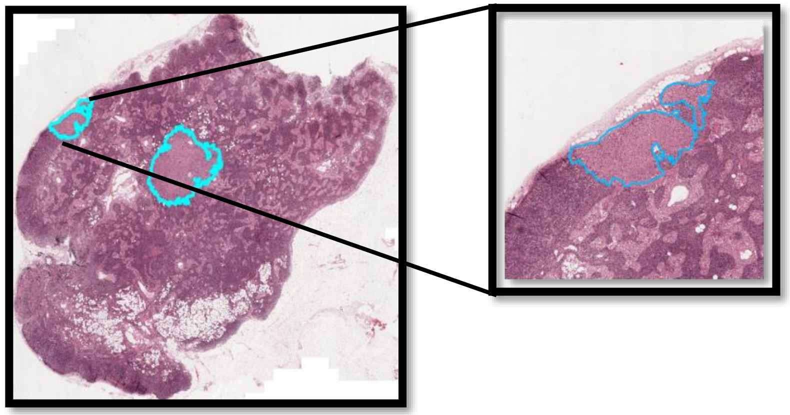
≈ 150000 × 150000 pixels per image

≈ 1000 images per Dataset

- **Whole-slide Images (WSI) Classification**
  - Many patches: **2k-20k**
  - Feature-level: use **features** as input
  - Weakly Supervised: **patch** label is **not** available
  - **Offline Feature Extractor**
  - **Redundancy**
    - **Noise fools the model**
    - **Low Efficiency (Transformer)**

Lu M Y, Williamson D F K, Chen T Y, et al. Data-efficient and weakly supervised computational pathology on whole-slide images. Nature biomedical engineering, 2021. Cite: 593

Previous Works: Only for Salient Area



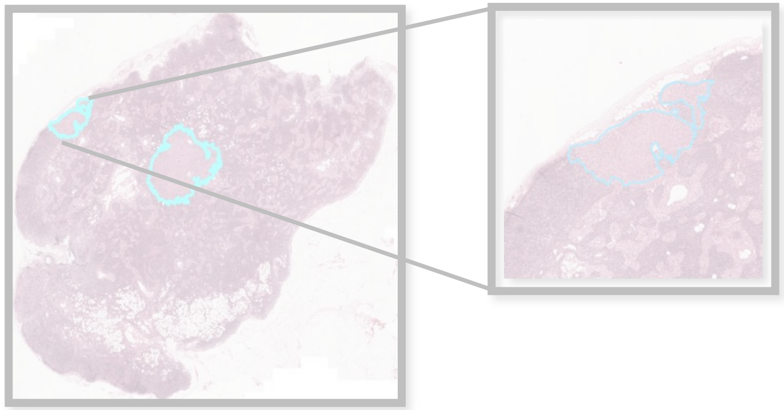
Whole-slide Image

Gigapixel resolution requires us to **zoom in**, **zoom in**, and **zoom in** again ...

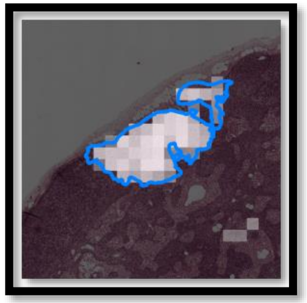
TINY details determine the classification of the **HUGE** image!

Ilse M, Tomczak J, Welling M. Attention-based deep multiple instance learning. ICLR 2018. Cite: 1245

Previous Works: Only for Salient Area



Whole-slide Image



Attention

Used Model: AB-MIL *(ResNet in MIL)*

Only for Salient Area

It seems Perfect ?

$$\hat{Y} = C(F), \qquad F = \sum_{i=1}^{N} a_i z_i$$

a_i Attention Score, z_i Patch Feature

Ilse M, Tomczak J, Welling M. Attention-based deep multiple instance learning. ICLR 2018. Cite: 1245

Previous Works: Only for Salient Area

ICCV23 PARIS

Used Model: AB-MIL *(ResNet in MIL)* Tumor Probabilities Algorithm: DTFD *(SoTA in MIL)*

Whole-slide Image Attention Tumor Probabilities

Not Perfect in Tumor Probabilities

Attention Score ≠ Tumor Probabilities

It was believed infeasible to explicitly infer instance probabilities under AB-MIL frameworks [*DSMIL. CVPR 2021 Oral*]

Zhang H, Meng Y, Zhao Y, et al. DTFD-MIL: Double-tier feature distillation multiple instance learning for histopathology whole slide image classification. CVPR 2022. Cite: 84

Previous Works: Only for Salient Area

ICCV23 PARIS

Used Model: AB-MIL *(ResNet in MIL)* / Tumor Probabilities Algorithm: DTFD *(SoTA in MIL)*

Whole-slide Image

Attention

Tumor Probabilities

Attention After Softmax

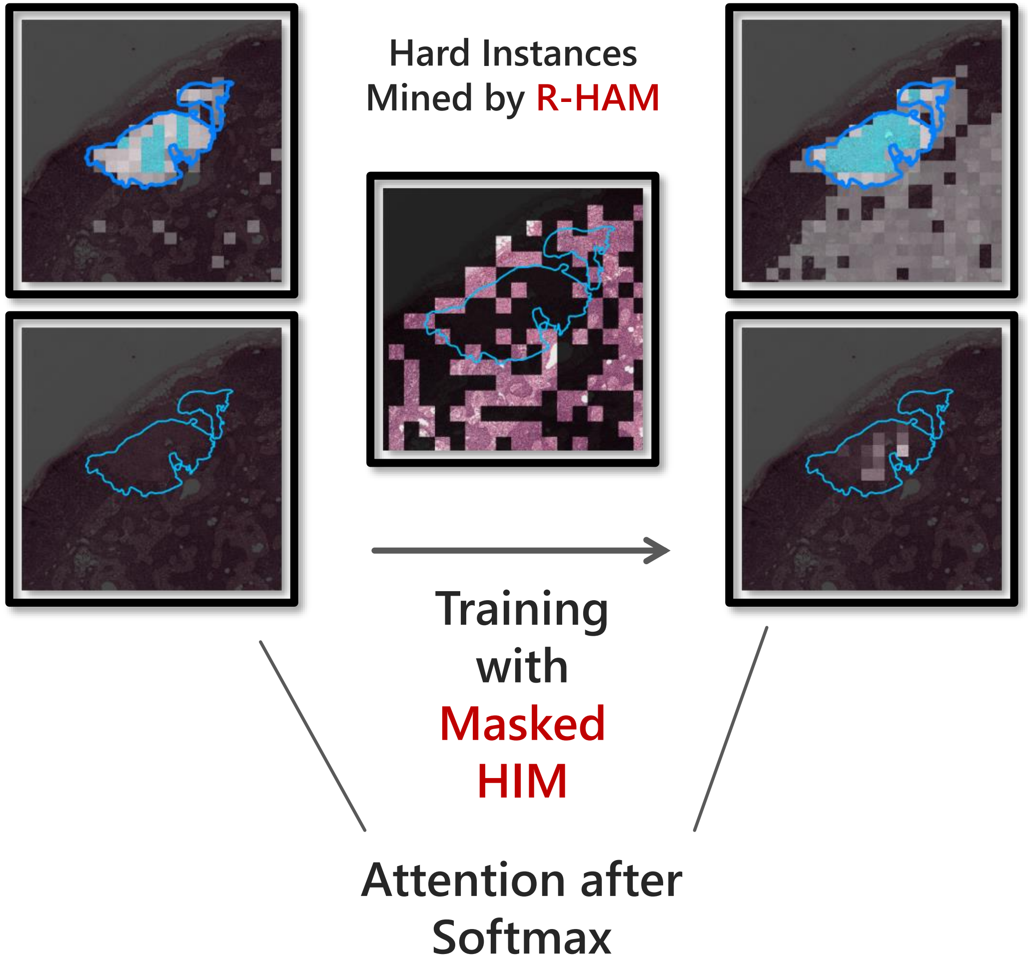
Attention Score ≠ Tumor Probabilities ≠ Final Prediction

$$\hat{Y} = C(F), \qquad F = \sum_{i=1}^{N} a_i z_i \,, \qquad A = Softmax(A)$$

Not Perfect in Final Prediction

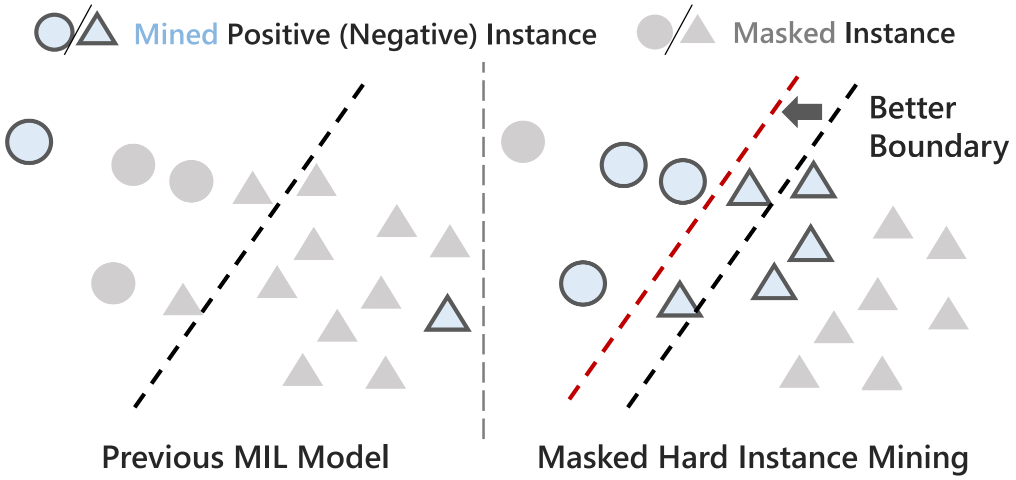
Ilse M, Tomczak J, Welling M. Attention-based deep multiple instance learning. ICLR 2018. Cite: 1245

MHIM: More ‘Useless’, More Powerful

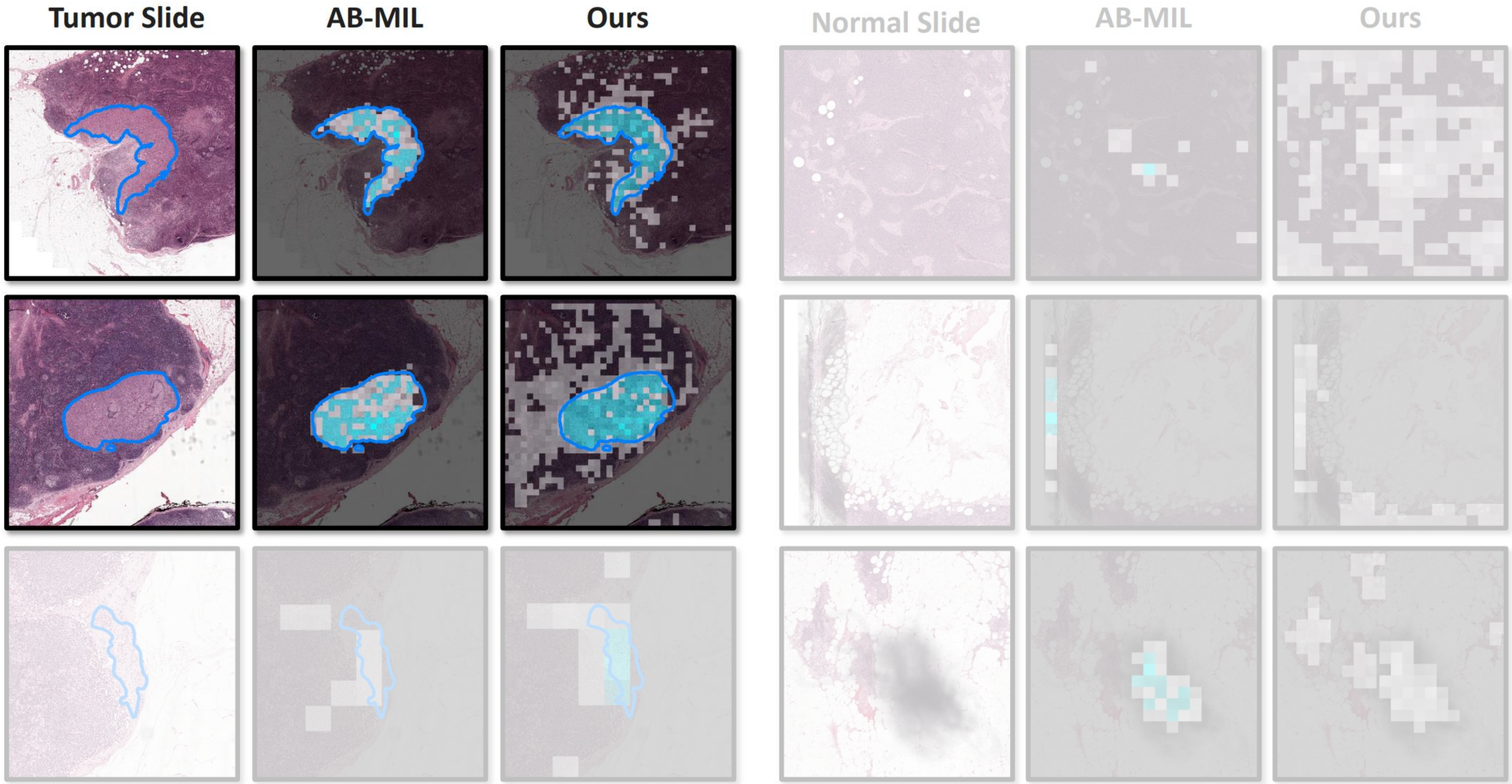


Intuitive: Only focus on salient area， but fail to detect complete tumor area, and fail to get better prediction

Counter-intuitive: Focus on more “useless area”， and make more complete prediction

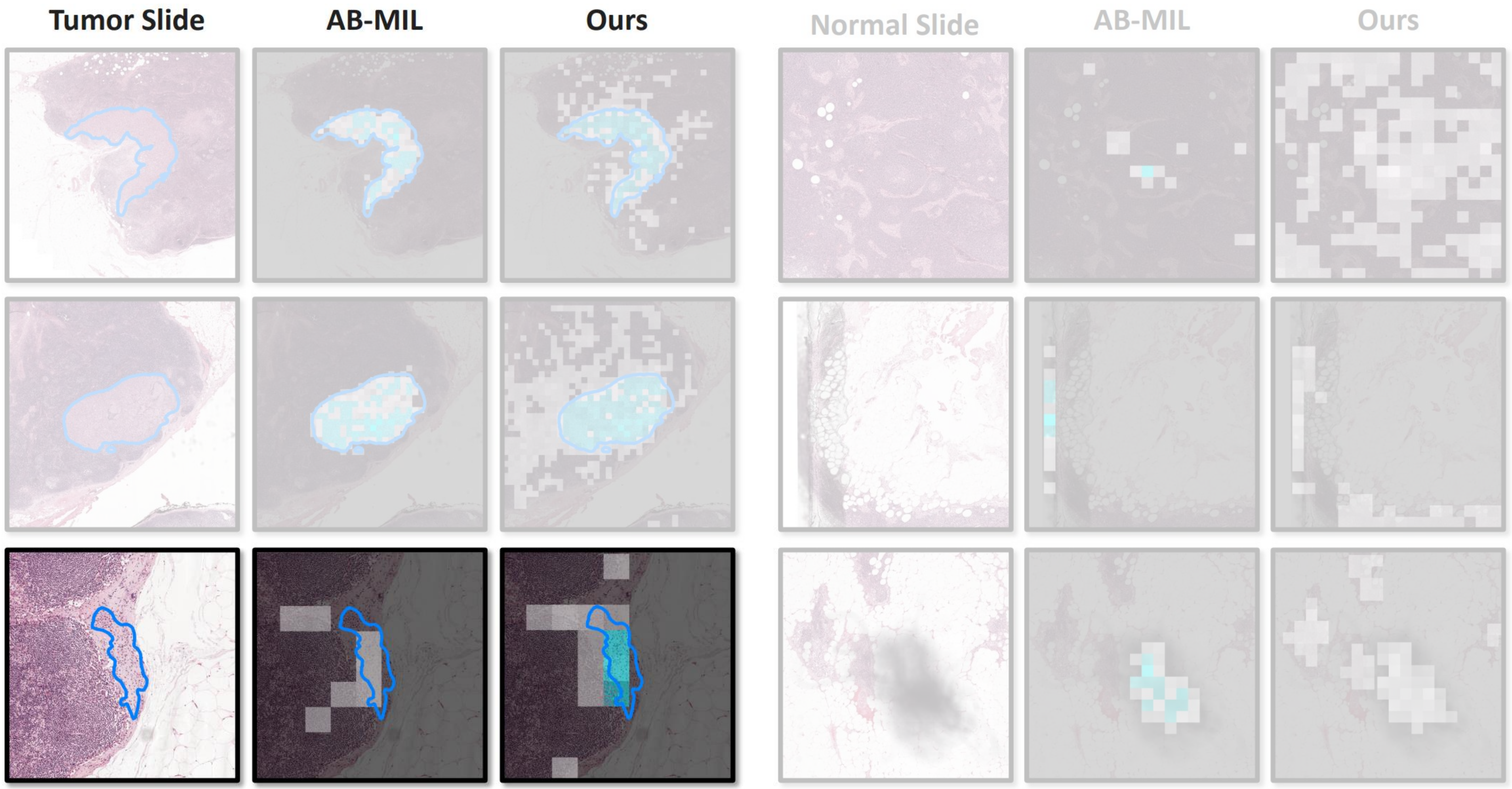


MHIM: More 'Useless', More Powerful



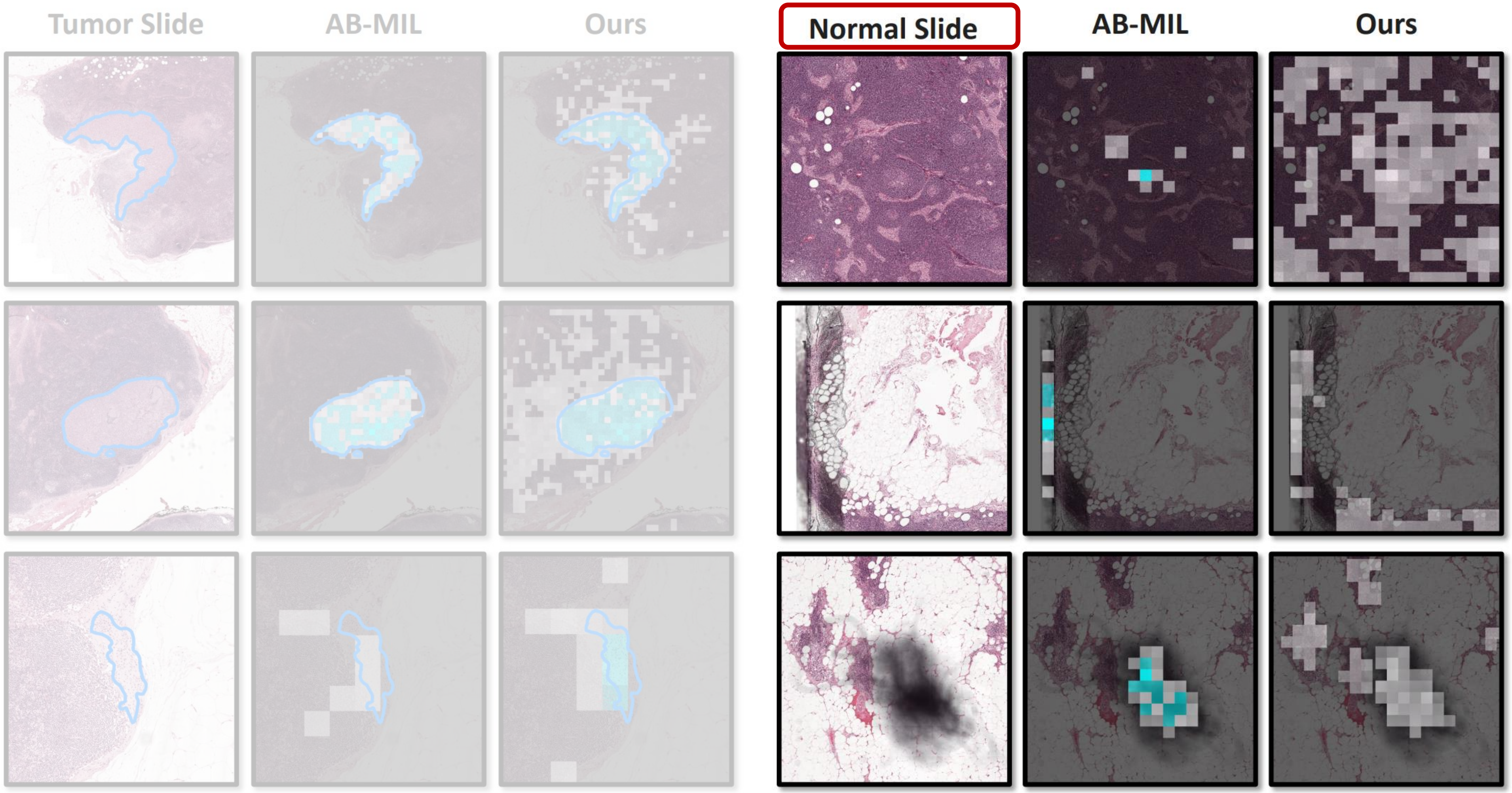
More Complete Prediction

MHIM: More 'Useless', More Powerful



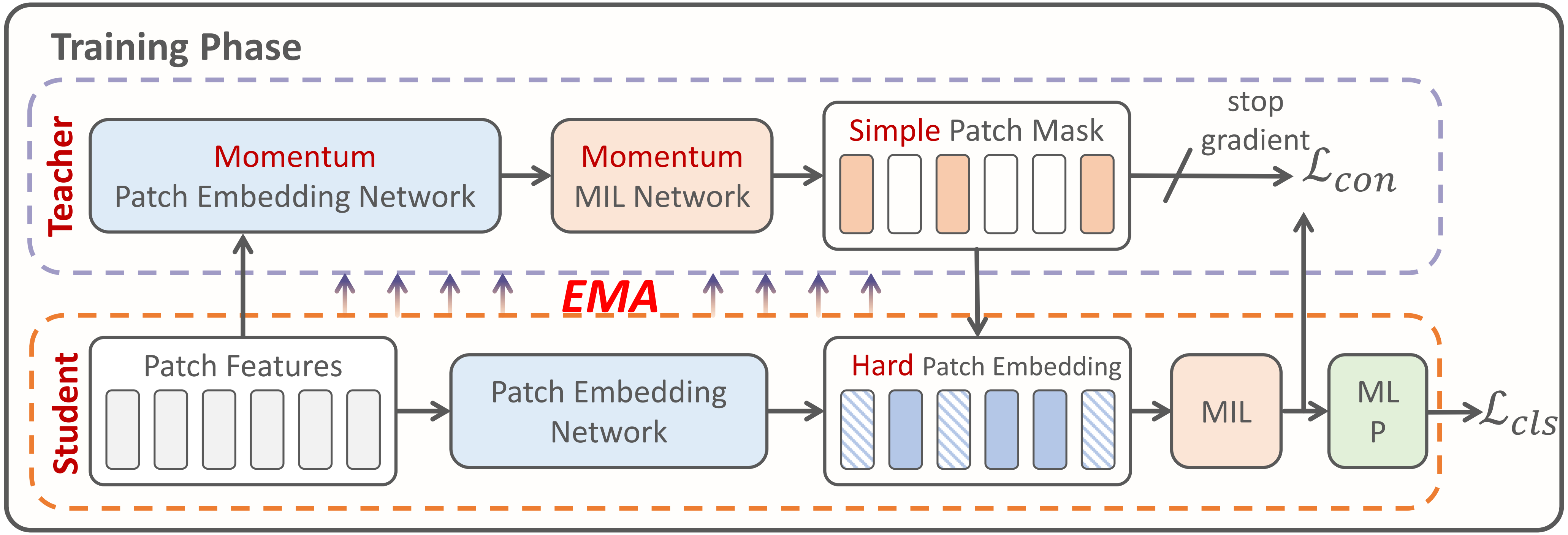
More Accurate Prediction

MHIM: More 'Useless', More Powerful



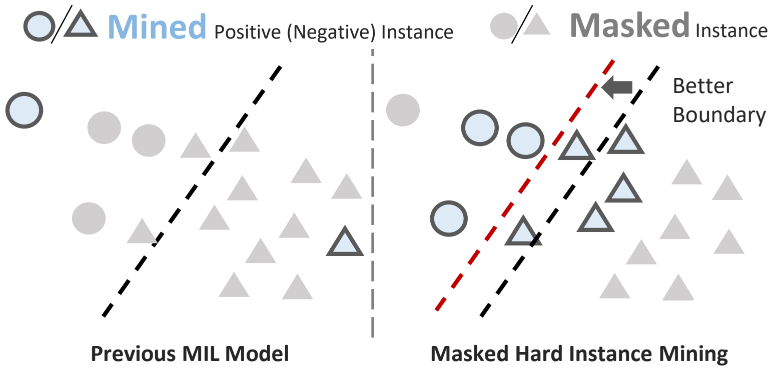
More Robust Prediction

MHIM: More 'Useless' and More Powerful

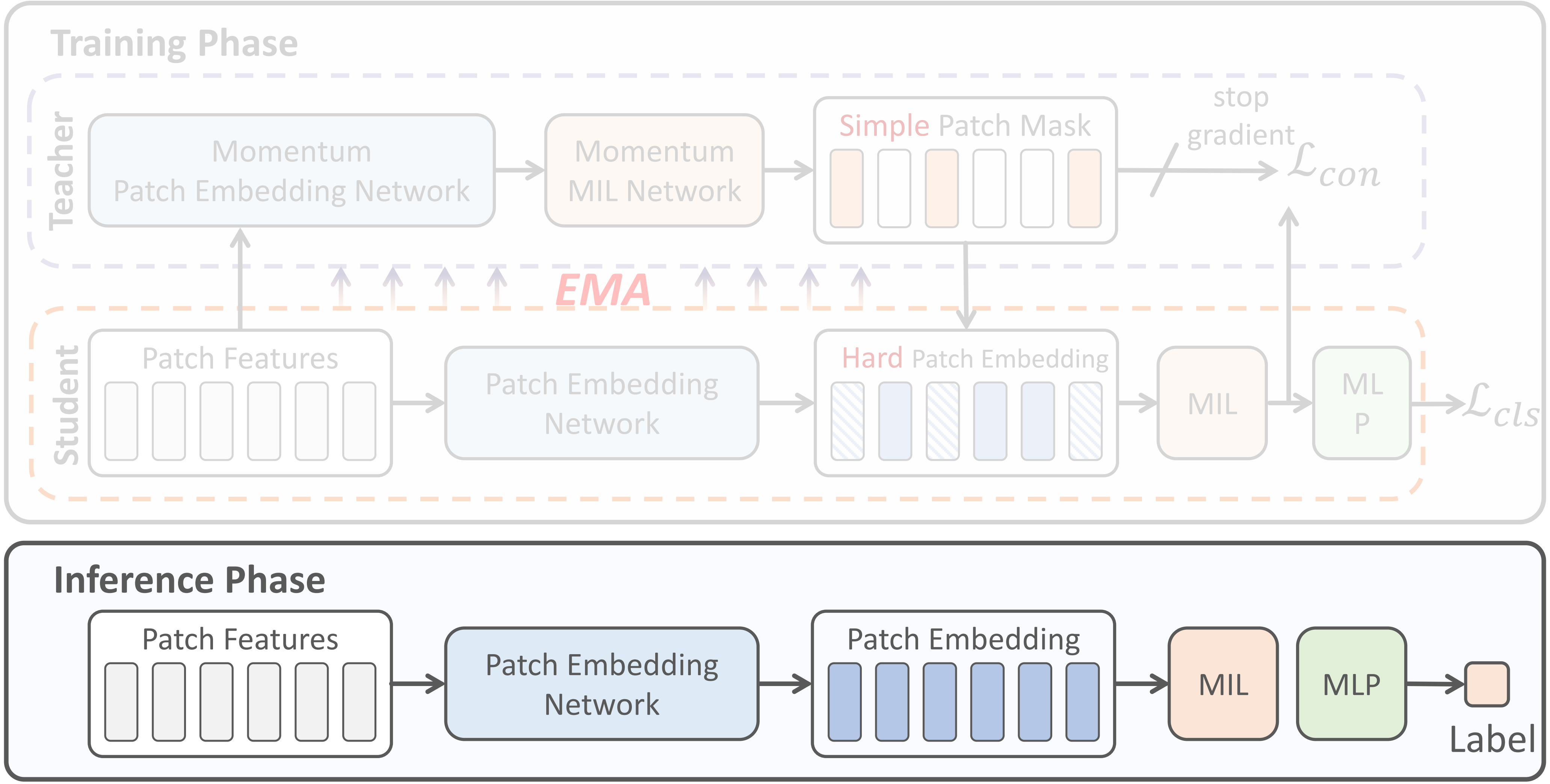


How to **effectively** mine **hard** instances **without** instance label ?

Find **Simple** First, **Mask** it Then, Remaining is **Hard**.



MHIM: More 'Useless' and More Powerful



Plain Inference Pipeline Enhanced Efficiency

MHIM: More 'Useless' and More Powerful

ICCV23 PARIS

Model	C16	TCGA	Para.	Time	Mem.
AB-MIL	94.00	93.17	**657K**	**4.0s**	2.4G
CLAM-MB	94.70	93.69	789K	4.3s	2.7G
DTFD-MIL	95.15	93.83	987K	5.2s	**2.1G**
MHIM-MIL	**96.14**	**94.97**	**657K**	4.3s	2.3G
TransMIL	93.51	92.51	2.67M	13.1s	10.6G
MHIM-MIL	**96.49**	**94.87**	**2.67M**	**10.1s**	**5.5G**

Module	CAMELYON-16		TCGA	
	AB.	Trans.	AB.	Trans.
Baseline	94.00	93.51	93.17	92.51
+MHIM	95.86	96.06	94.14	93.75
+MHIM+Siam.	95.82	96.24	94.55	94.13
+MHIM+Siam.+Con.	**96.14**	**96.49**	**94.97**	**94.87**

	C16	TCGA
DSMIL	94.57±0.40	93.71±1.82
MHIM	96.22±0.28 (+1.65)	95.27±1.66 (+1.56)
MHIM[‡]	96.49±0.65 (+1.92)	95.53±1.74 (+1.82)

Strategy	CAMELYON-16		TCGA	
	AB.	Trans.	AB.	Trans.
Baseline	94.00	93.51	93.17	92.51
HAM	95.68	95.90	93.83	94.54
R-HAM	**96.14**	95.88	94.79	94.60
L-HAM	95.81	**96.49**	94.33	94.67
LR-HAM	95.92	96.33	**94.97**	**94.87**

Adapt to All Major Baselines *(AB-MIL, TransMIL, DSMIL)*

More Powerful and More Efficient *(+1.7% AUC on TCGA, -48% Mem.)*

MHIM: More 'Useless' and More Powerful

ICCV23 PARIS

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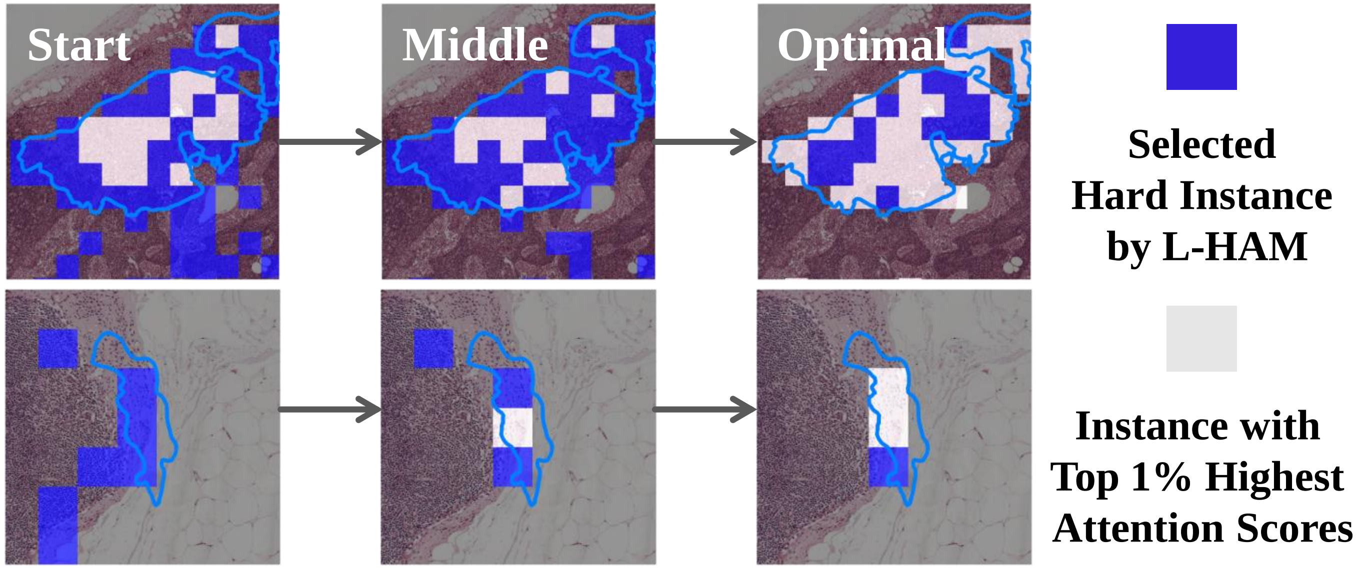


Can teacher really provide hard instances through Mask strategies?

Take Home Message

Background: **WSI Classification**

- Gigapixel Resolution, Low-Data Dataset
- Offline Feature Extractor
- Redundancy

Previous Work: **Only for Salient Area**

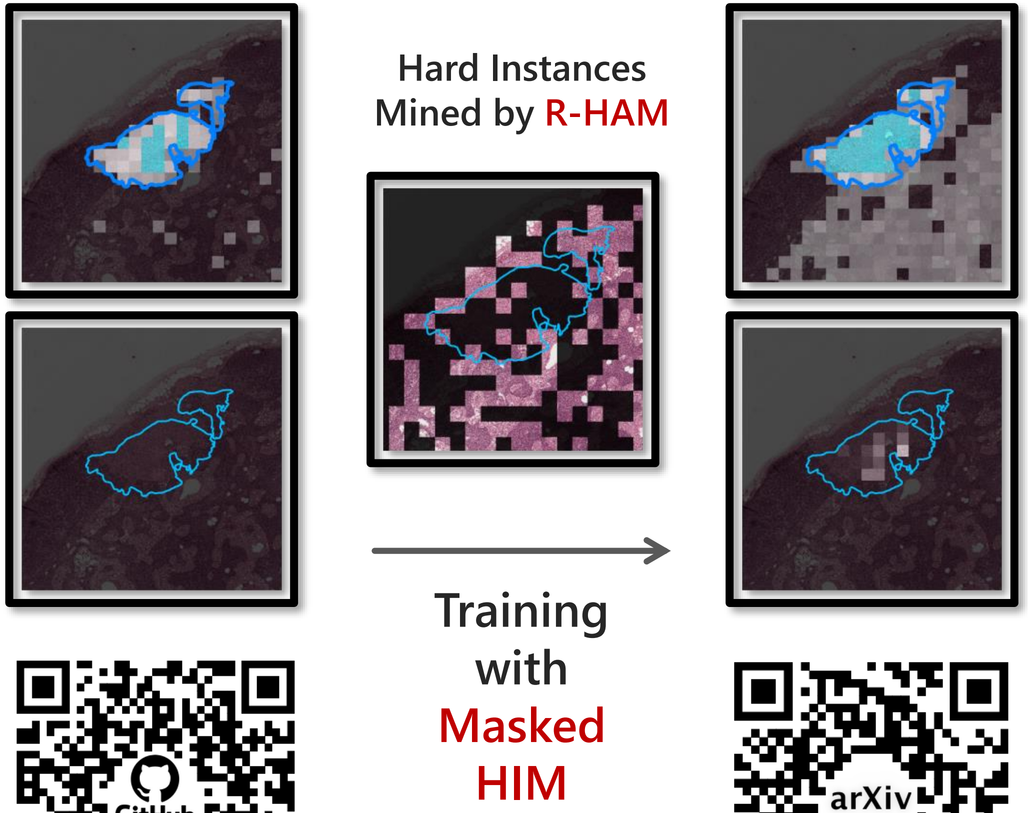
- Not Perfect in Tumor Probabilities
- Not Perfect in Final Prediction

MHIM: **More 'Useless', More Powerful**

- More Complete Prediction
- More Accurate Prediction
- More Robust Prediction

Welcome to MHIM: **Look for More about**

- Masked Strategy, Experiment, Visualization
- Dataset, Pre-process, Implement Detail



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