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Background and objectives

Antibody-drug conjugates (ADCs) are a rapidly evolving class of targeted cancer therapeutics. Patients eligible for ADCs are often identified through immunohistochemistry (IHC) testing. In this study, we trained a **new lightweight foundation model (FM) on IHC-stained whole slide images (WSI) designed for efficient clinical deployment. Focusing on HER2 prediction, our IHC FM surpasses** publicly available models on 2 external validation cohorts.

★ Check **poster 8P** to see how we leverage our IHC FM for cell-level scoring

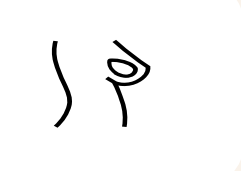
Method

We trained a deep-learning model on a proprietary cohort of breast cases with HER2-IHC scores (N=199), and further validated it on two independent multicentric cohorts (N=152, N=119). IHC WSIs were tiled into 224×224px patches at 20x magnification and encoded into feature representations using each FM. Tile-level embeddings were aggregated using an attention module to generate slide-level predictions of HER2 (0+, 1+, 2+ or 3+) following ASCO/CAP guidelines.

First iteration towards an efficient and robust FM

Our IHC FM is a 86M parameters vision transformer pre-trained with iBOT [1] on 10,000 IHC slides, from which we extracted 68M patches at 20x magnification.

The pre-training was made on 32 V100 GPUs for a total of 3,500 hours.



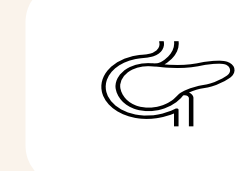
Breast Cancer



Lung Cancer



Colorectal Cancer



Gastro-Eso Cancer



Lymphoma



Ovarian Cancer



Prostate Cancer



Liver Cancer

9 indications

67 million images

3 scanners
2 continents

150 IHC Markers

10,000 slides

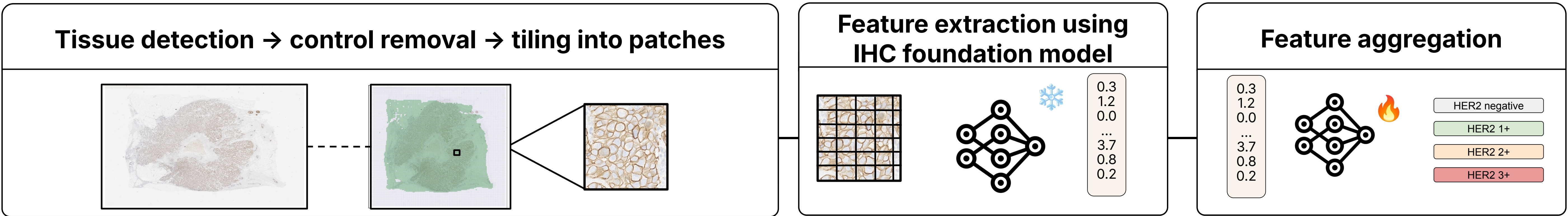
ViT-B
86M parameters

Data

Cohort	Specimen type	n _{TOTAL}	Use
Cohort 0 (France)	Surgical resections & Biopsies	199	Training
Cohort 1 (Netherlands)	Biopsies	152	Validation
Cohort 2 (UK)	Surgical resections & Biopsies	119	Validation

Breast cancer data for HER2 prediction.

HER2 prediction pipeline



Results

In cross-validation, the HER2 model based on our IHC FM achieved an AUROC of 0.897 ± 0.017, with 61.6 ± 2.6% balanced accuracy.

Model	Number of parameters (M)	Number of WSI for pre-training		Cohort 1 (Netherlands) Balanced Accuracy (95% CI)	Cohort 2 (UK) Balanced Accuracy (95% CI)
		H&E	IHC		
Our IHC FM	86	0	10k	0.529 (0.512, 0.538)	0.653 (0.646, 0.659)
Virchow2 [2]	632	2.7M	0.4M	0.460 (0.453, 0.468)	0.707 (0.702, 0.711)
H-Optimus-0 [3]	1,100	0.5M	0	0.480 (0.472, 0.488)	0.609 (0.601, 0.618)
H0-mini [4]	86	6k	0	0.477 (0.470, 0.483)	0.603 (0.597, 0.610)
UNI2-h [5]	681	350k		0.337 (0.328, 0.345)	0.738 (0.733, 0.744)

Table: Model's performance for HER2 prediction (0, 1+, 2+, 3+).
CIs are computed using bootstrapping with 10,000 repeats.

Conclusions



Efficiency: Our IHC-specific foundation model reached on par performance with current state-of-the-art pathology FMs on HER2 prediction task while being **8x smaller and trained on 30x less data**



Generalization: This model offers promising perspectives for evaluation across additional biomarkers, particularly for ADC-relevant targets.

References

[1] Zhou, J., et al. (2022). iBOT: Image BERT Pre-Training with Online Tokenizer. arXiv preprint arXiv:2111.07832.
[2] Zimmermann, E., et al. (2024). Virchow2: Scaling Self-Supervised Mixed Magnification Models in Pathology. arXiv preprint arXiv:2408.00738.
[3] Saillard, C., et al. (2024). H-optimus-0. <https://huggingface.co/bioptimus/H-optimus-0>
[4] Filiot, A., et al.(2025). Distilling foundation models for robust and efficient models in digital pathology. arXiv preprint arXiv:2501.16239v2.
[5] Chen, R. J., et al. (2024). Towards a general-purpose foundation model for computational pathology. Nature Medicine.

Affiliations & Acknowledgements

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