

Digital and Computational Pathology Tool Harmonization (PATH) Project

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Why HER2 and Al Matter

- HER2 is a clinically relevant biomarker in breast cancer, guiding treatment decisions
- Emerging therapies (e.g., antibody-drug conjugates) targeting HER2 are also effective in patients with "low" and "ultra-low" HER2 expression, expanding the eligible patient population and making precise, reproducible HER2 scoring increasingly important
- Al tools may help address challenges in reproducibility, accuracy, and scalability in HER2 scoring



The Role of AI Tools in HER2 Scoring

Reproducibility

Al models could help reduce inter- and intra-observer variability compared to manual scoring

Efficiency

High-throughput capabilities for analyzing and sorting large datasets

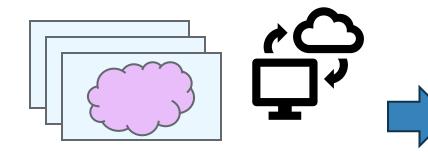
Granularity

Potential for more nuanced analyses that may be infeasible for a human eye Clinical implication Accurate HER2 scoring is increasingly important with the expansion of therapies for patients with HER2-low



Digital PATH Project Approach

The Research Question: What factors contribute to variability in biomarker assessment across computational pathology platforms and what performance metrics support improved evaluation and alignment?





Develop a common dataset of >1000 breast cancer WSIs (digital images of HER2 IHC and H&E slides) and share with tool developers

Tool developers apply independently developed AI models to assess HER2 scoring

Compare results with pathologists from a single institution and among models to evaluate variability

The structured approach enables a systematic evaluation of variability and sources of discordance



Analysis Strategy Overview

Primary Analysis

Descriptive analyses evaluating the level of agreement of ASCO/CAP HER2 categorical scores: 0, 1+, 2+, 3+

Secondary	Explorator	
Secondary	Explorator	Y Andrysis

Factor Associations Association of patient,

attributes with level of agreement of HER2 scores

Pathologist Level of Agreement

Level of agreement between models and pathologists

Quantitative Measurements

Concordance between models providing quantitative biomarker measurements

Additional Categorical Scores

Concordance between models that provide ultra-low, low, and other categories



Sample and Specimen Characteristics

Clinical/Tumor Characteristics

Histological Grade	n (%)
1	149 (13%)
2	702 (62%)
3	231 (21%)
Not Recorded	42 (4%)
Histology	
Ductal	879 (78%)
Lobular	172 (15%)
Mucinous	25 (2%)
Other	48 (4%)
Clinical Stage	
1	612 (54%)
II	363 (32%)
III	85 (8%)
IV	64 (6%)
ER Status	
Positive	963 (86%)
Weakly Positive	15 (1%)
Negative	146 (13%)
PR Status	
Positive	815 (73%)
Negative	309 (28%)
Ki-67 Status	
0-10%	537 (48%)
11-100%	523 (46%)
Unknown	64 (6%)

Demographics

	n (%)	
Age at Sample Collection (yrs)	Median: 65	
< 50	208 (19%)	
50-64	336 (30%)	
65+	580 (52%)	
Diagnosis History		
De Novo Dx of Breast Cancer	1060 (94%)	
Recurrence	64 (6%)	
Sex		
Male	16 (1%)	
Female	1108 (99%)	

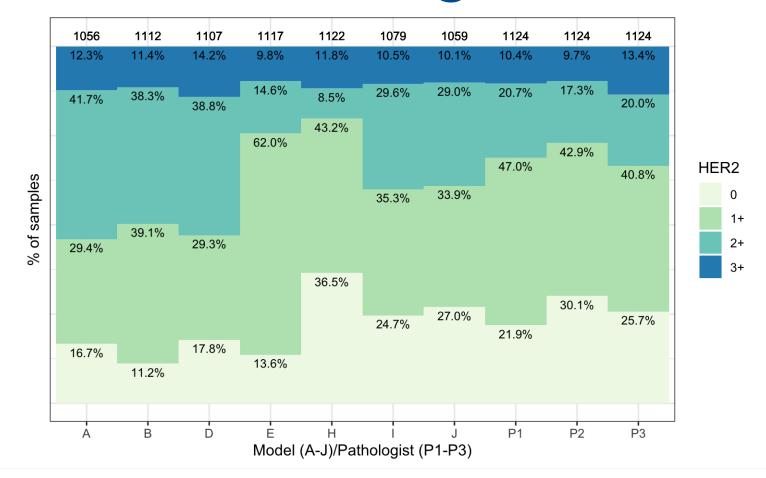
Clinical/ tumor characteristics and demographics align closely with populationlevel sources

Specimen Characteristics

Parameter	Details/Specification	
Thickness of Tissue Section	4 micron	
Fixation Type	Formaldehyde 4%	
Coverslip	Sakura TissueTek Film	
Hematoxylin Type	Hematoxylin II counterstain	
Hematoxylin Time	12 minutes	
Fixation Temperature	Room temperature	
Mounting Media	Xylene	
HER2 Antibody Clone	4B5	
HER2 Antibody Manufacturer	RocheVentura	
Scanner Type	Leica Aperio GT 450 DX	
Scanning Magnification	40x	
Scanning Software Version	4.4	

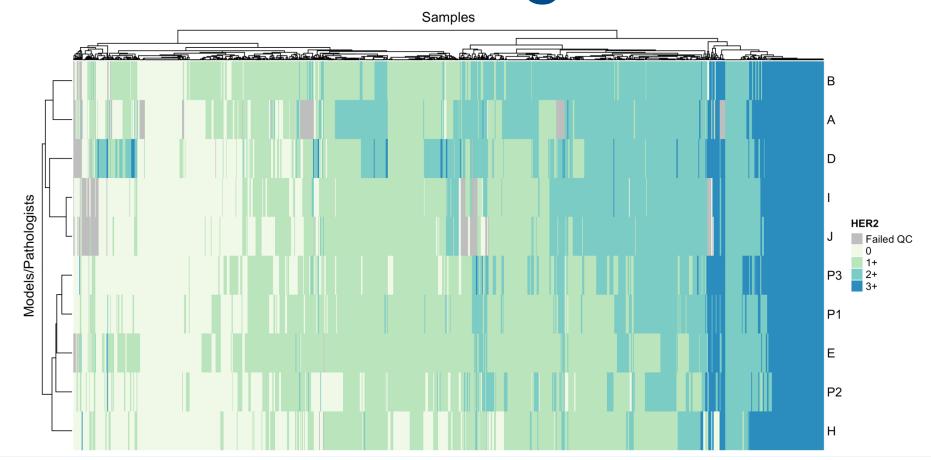
The specimen characteristics are homogenous to determine sources of variability in the model outputs.

HER2 Scoring Distribution Across AI Models and Pathologists



Finding: There is variability in HER2 outputs across models/pathologists, with more variability in 1+ and 2+ calls compared to 3+ calls.

HER2 Scoring Variability Across AI Models and Pathologists



Finding: HER2 outputs show variability across AI models and pathologists, with the highest variability observed in 1+ and 2+ scores, while 3+ scores demonstrate greater consistency.

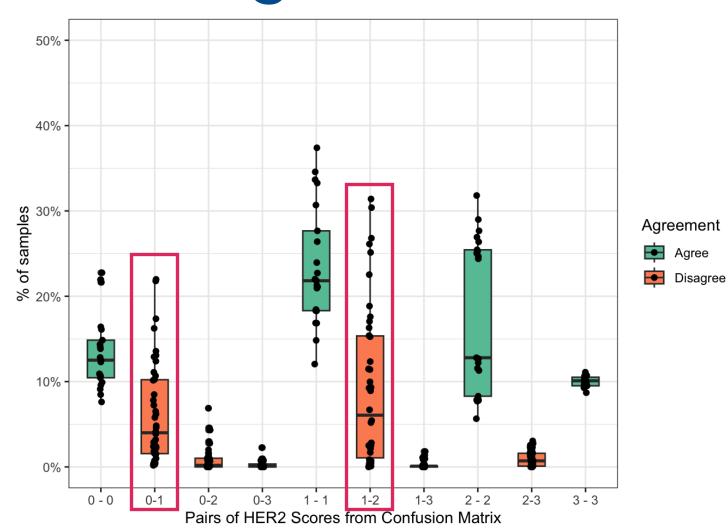
HER2 Scoring Agreement Across Al Models and Pathologists



	# of pairwise	Agreement	Categorical (ASCO/CAP)	Binary		
	comparisons	Measure, Median	(0, 1+, 2+, 3+)	(0 vs. 1+, 2+, 3+)	(0, 1+ vs. 2+, 3+)	(0, 1+, 2+ vs. 3+)
Models Only (7)	21		65.1	85.6	79.9	97.3
Models (7) vs. Pathologists (3)	21	OPA (%)	65.1	84.6	81.1	96.7
Pathologists Only (3)	3		70.4	85.1	86.3	96.6
Models Only (7)	21		0.51	0.57	0.59	0.86
Models (7) vs. Pathologists (3)	21	Карра	0.51	0.57	0.58	0.84
Pathologists Only (3)	3		0.57	0.61	0.67	0.84

Finding: AI models and pathologists show similar HER2 scoring agreement, with the highest concordance for 3+ cases.

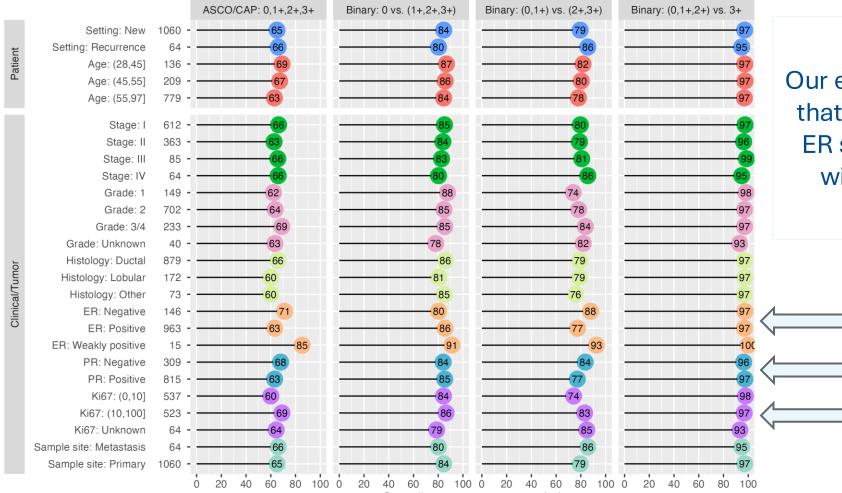
Pairwise Agreement in HER2 Scoring Across Models



Finding: Disagreements were more frequent between adjacent HER2 scores (e.g., 0 vs. 1+ or 1+ vs. 2+) rather than between more distant scores (e.g., 0 vs. 2+, 0 vs. 3+, or 2+ vs. 3+).



What Drives Variability in HER2 Scoring?



Finding:

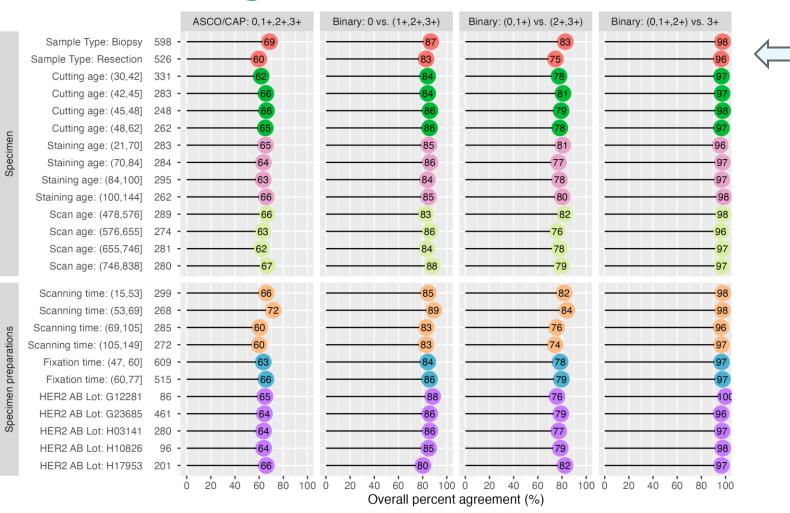
FRIENDS

of CANCER RESEARCH

Our exploratory analyses suggest that sample type, Ki67, PR, and ER status could be associated with the level of agreement among models.

Overall percent agreement (%)

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Evaluating WSIs to Identify Drivers of Variability

Criterion 1	Criterion 2	Criterion 3
At least one model scored 0 and one model scored 3+ on the same sample	Discordance across pathologists (at least two HER2 score categories away, e.g., 0 and 2+) AND Discordance across models (any discordant calls, does not have to be 2 steps)	All models agree and all pathologists agree, but models and pathologists do not agree
32 samples*	17 samples*	4 samples

- A trained pathologist reviewed WSIs and provided a summary of observations
- Tool developers reviewed these images (without knowing their scores/which image they were) and provided updated scoring



Key Observations: Sources of Variability in HER2 Scoring

Artifacts and Sample Quality

- Common issues included staining artifacts, crushed cells, and difficulty visualizing cancer cells
- Benign or DCIS cells
 exhibited positive staining

Heterogeneous Staining Patterns

- Samples with variable staining intensity across tumor regions
- Particularly impactful for HER2 1+ and 2+ cases

Model and Pathologist Alignment

Cases with HER2 categories
 0 or 3+ showed higher
 agreement, while HER2
 categories 1+ or 2+ had less
 agreement

Impact of Review Process

- Post-review, agreement among models generally improved when addressing ambiguities, such as artifacts or DCIS staining
- Persistent discordance generally remained in complex cases (e.g., Paget's disease, cytology samples with sparse tumor cells) highlighting opportunities for further model refinement



Conclusions and Next Steps

Key Findings from the Digital PATH Project

- Al tools demonstrate promise in HER2 scoring with highest agreement for HER2 3+ category
- Variability is more pronounced for HER2 0, 1+ and 2+ categories, which has become increasingly relevant with newer HER2-targeted treatments
- A common dataset enabled robust, rapid comparisons across models, helping identify potential sources of variability and informing best practices

The Role of Reference Data Sets

- Enable transparent evaluation of AI tools
- Provide a foundation for aligning methodologies and identifying variability

Next Steps

- Leverage project findings to propose best practices for AI tool development and validation
- Further explore how reference data sets can be leveraged to support AI tools



Project Partners

4D Path, Inc.

Indica Labs

Amgen

AstraZeneca

BostonGene

Bristol Myers Squibb

Caris Life Sciences

Daiichi Sankyo

EMD Serono, Inc. Emory University GA Green Consulting LLC GSK Johnson and Johnson Innovative Medicine

Karolinska Institutet

Kulig Consulting

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Lunit

Molecular Characterization Laboratory at Frederick National Laboratory

MD Anderson Cancer Center

Merck and Co., Inc.

National Cancer Institute

Nucleai

Common Data Set Provider

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U.S. Food and Drug Administration

Verily

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