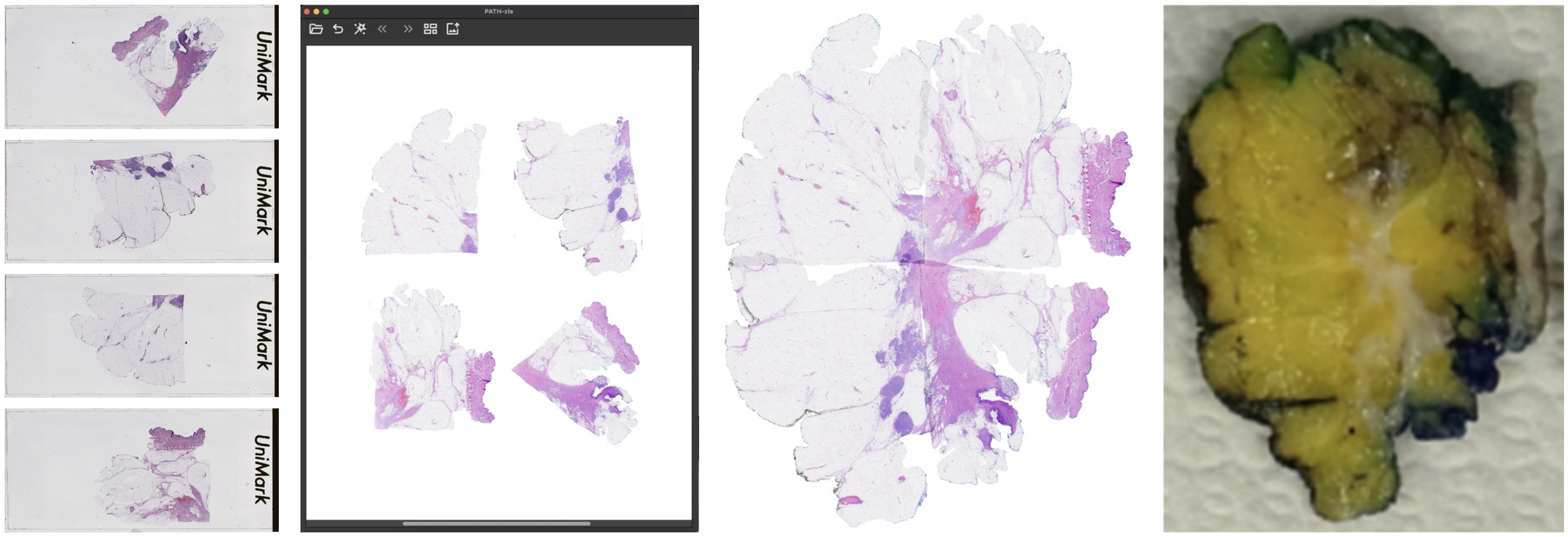
PATH-zle, an AI-based tool for histopathology Whole Slide Image reconstruction

Gabriele Abbate[1] Bernardo Forni[2,3] Luca Giudici[4] Paola Migliora[4]
Luca Mazzucchelli[4] Vittoria Martin[4] Alessandro Giusti[1]

[1]Istituto dalle Molle di Studi sull'Intelligenza Artificiale (IDSIA USI-SUPSI), Dip. di Tecnologie Innovative, SUPSI, Lugano
[2]Università della Svizzera Italiana (USI), Lugano [3]Università di Pavia, Dip. di Matematica "F. Casorati", Italia
[4]Istituto di Diagnostica Integrata della Svizzera Italiana, Clinica di Patologia – EOC, Locarno

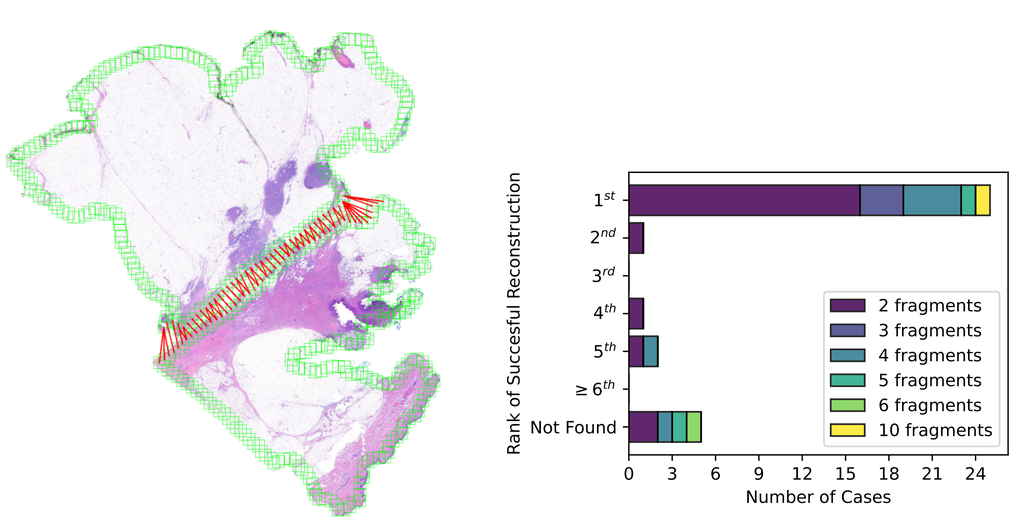
Whole-Mount Histopathology (WMH) enables comprehensive assessment of large tissue sections. However, routine workflows require cutting specimens into **fragments** that fit standard microscope slides, that are individually processed and acquired, severely complicating pathologist's analysis.



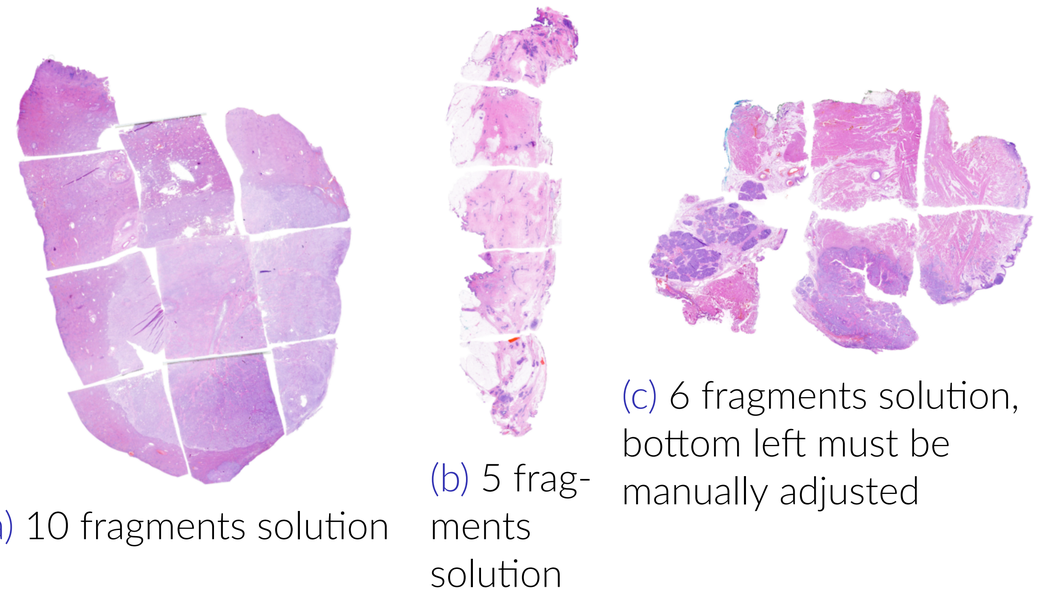
Left to right: microscope slides with fragments of a large specimen; PATH-zle shows the fragments to assemble in the pathologist interface; automatically reconstructed section; specimen before it was cut into fragments.

We propose PATH-zle, a novel method that combines **geometric** and **semantic** cues to digitally reconstruct the whole-mount section from an arbitrary number of fragments.

1. For a given pair of fragments, a set of candidate configurations is generated by sampling possible pairs of edges (one belonging to each fragment).
2. Each candidate configuration is assigned a cost based on a *geometric cost* that penalizes non-compact configurations and a *semantic cost* that penalizes visual differences of the tissue across a seam, using UNI [1] embeddings (a **Visual Foundation Model** for pathology) of patches sampled along the shared contour.
3. We reconstruct whole sections by iteratively combining pairs that have low cost and little overlap between them.
4. A dedicated graphical interface provides a ranked list of candidate reconstructions and enables pathologists to resolve ambiguities and validate the reconstruction.



Left: candidate configuration with patch matching. Right: rank distribution of the correct reconstruction for our dataset.



(a) 10 fragments solution

(b) 5 fragments solution

(c) 6 fragments solution, bottom left must be manually adjusted

We **publicly release** a new dataset of 34 cases acquired in-house (each composed by 2–10 fragments), which significantly extends the only similar public dataset (4 cases).

Whole-section reconstruction accuracy.

		PATH-zle		PythoStitcher[2]		SemanticStitcher[3]
Dataset	**Sect.**	top-1	top-5	top-1	top-5	top-1
Ours (all sections)	34	76%	85%	-*	-*	35%
Ours (only 2&4 frag)	27	74%	89%	48%	48%	44%
Schouten et al. [2]	4	100%	100%	100%	100%	75%

Our method outperforms **state-of-the-art** alternatives and runs in less than 5 s per case, with a gain in top-1 accuracy of +41%.

[1] Chen, Richard J., et al. "A General-Purpose Self-Supervised Model for Computational Pathology". *arXiv:2308.15474* (2023).

[2] Schouten, Daan, et al. "Full resolution reconstruction of whole-mount sections from digitized individual tissue fragments". *Scientific Reports* 14.1 (2024): 1497.

[3] Brandstätter, Stefan, et al. "Semantic Mosaicing of Histo-Pathology Image Fragments using Visual Foundation Models". *arXiv:2508.03524* (2025).

gabriele.abbate@idsia.ch bernardo.forni01@universitadipavia.it