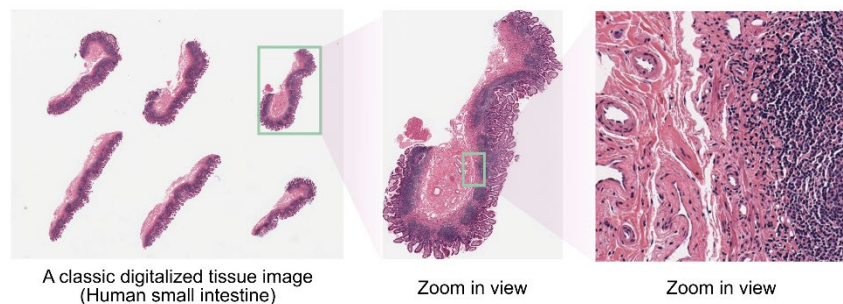


## From pathology image to biological discovery: A journey with LazySlide

Microscopic images of human tissue are a cornerstone of biomedical research and clinical diagnostics. Yet despite their importance, these images often remain difficult to analyze systematically and to connect with other types of biological data. A new study led by CeMM Principal Investigator André Rendeiro and published in *Nature Methods* (DOI: 10.1038/s41592-026-03044-7), introduces “LazySlide”, an open-source software tool that brings the power of foundation models and aims to democratize digital pathology analysis.

**(Vienna, 20 March 2026)** An inflamed artery, a tumor spreading into the lung or subtle damages in an organ - When doctors or researchers want to understand what’s happening inside a tissue, one of the most trusted tools is still the microscope. Today, they have largely gone digital: a single tissue sample can be scanned into a whole-slide image so detailed, that you can zoom from a bird’s-eye view of the entire tissue down to individual cells. These images, therefore, contain enormous information about tissues from different scales.

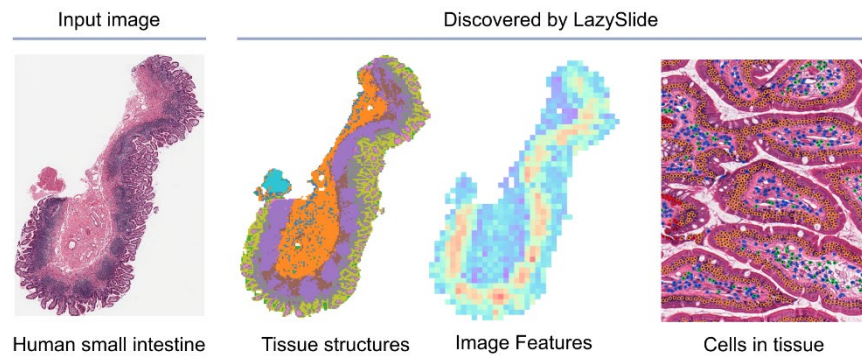


However, these images are huge, complex, and often difficult to analyze in a modern, data-driven way. While genetics and single-cell biology have developed effective ways for sharing and comparing data, digital pathology images are hard to incorporate – stored in vendor-specific formats, processed with incompatible tools, and hard to connect to molecular information like RNA sequencing. Thus, the valuable resources of digitalized tissue images are largely underutilized in many research and clinical settings.

A new study by the group of CeMM Principal Investigator André Rendeiro introduces LazySlide, an open-source application designed to make whole-slide image analysis more accessible, interoperable, and ready to plug into the same computational workflows that already drive modern genomics.

### From “pretty pictures” to searchable biology

LazySlide enables scientists to break down whole-slide images into smaller, manageable regions and analyze them using advanced artificial intelligence models. These models can recognize patterns in tissue structure, identify different cell types, and quantify subtle changes in tissue architecture, without requiring extensive manual annotation.



Crucially, the study shows that visual information from tissue images can be directly linked to molecular data such as gene expression profiles. In one example, the researchers analyzed artery tissue samples with and without calcification, a pathological process associated with cardiovascular disease. LazySlide not only distinguished healthy from diseased tissue based on image features alone, but also revealed biological pathways, such as inflammatory signalling, that became visible only when image data and RNA sequencing data were analyzed together.

“Histology contains an enormous amount of biological information, but it is often difficult to access computationally,” says Yimin Zheng, first author of the study. “With LazySlide, we wanted to provide a tool that allows researchers to explore tissue images in a systematic, quantitative way and to connect what they see under the microscope with underlying molecular processes.”

### Searching tissue with words

One particularly innovative feature of LazySlide is its ability to connect images with natural language. By using AI models that link visual patterns to text concepts, researchers can ask questions such as where signs of “calcification” appear within a tissue sample. The software then highlights relevant regions and generates quantitative scores, turning visual impressions into measurable data.

This approach also allows so-called “zero-shot” analysis: LazySlide can recognize the organ of origin of tissue samples or distinguish healthy from diseased tissue without being specifically trained for each task. This greatly lowers the barrier for applying advanced image analysis methods in biomedical research.

### An open and interoperable tool

LazySlide was designed to integrate seamlessly with existing computational biology tools widely used in genomics and single-cell research. By making digital pathology more interoperable with these established workflows, the software

helps bring tissue imaging into the broader ecosystem of data-driven life sciences.

“Our goal was to make whole-slide image analysis more accessible and more connected to the kinds of data researchers already use every day,” says André Rendeiro. “By treating tissue images as rich datasets rather than static pictures, we can gain new insights into how diseases shape human biology.”

The study, published in *Nature Methods*, highlights how open-source, flexible tools like LazySlide can accelerate research and help bridge the gap between tissue structure and molecular function – an essential step toward a more integrated understanding of health and disease.

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#### **Pictures attached**

Photo: First author Yimin Zheng and senior author André Rendeiro (© Wolfgang Däubler / CeMM)

Image: Cell detection with LazySlide in human colon tissue: Immune cells (green), connective tissue cells (blue) and epithelial cells (orange) (© Yimin Zheng)

**The Study** “*LazySlide: accessible and interoperable whole slide image analysis.*” was published in *Nature Methods* on 20 March 2026, DOI: [10.1038/s41592-026-03044-7](https://doi.org/10.1038/s41592-026-03044-7)

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