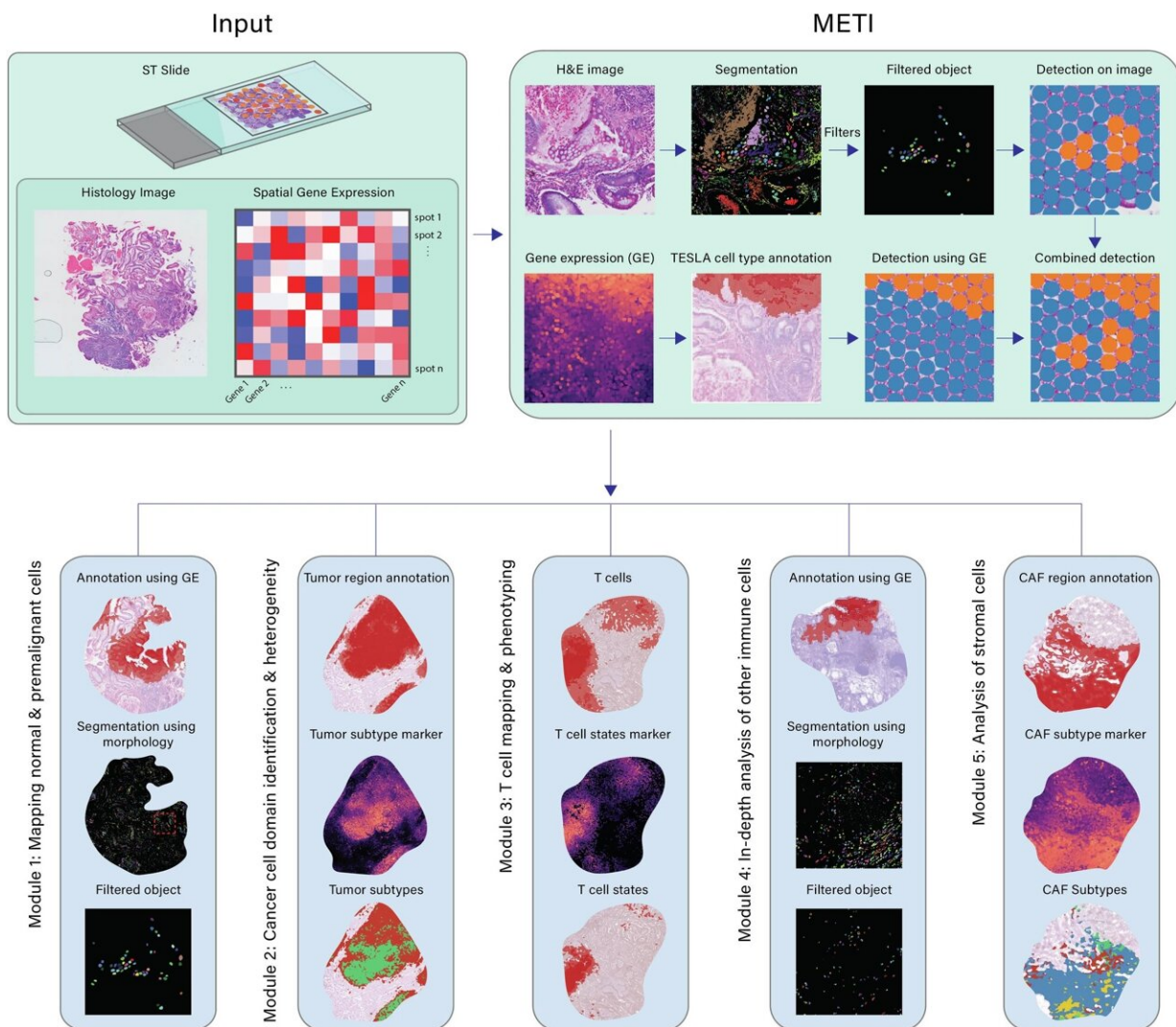


Software tool analyzes cancer cells in biopsy slides

August 29 2024, by Quinn Eastman



Workflow of METI. Credit: *Nature Communications* (2024). DOI: 10.1038/s41467-024-51708-9

An innovative software tool could advance cancer pathology by providing diagnostic insights from tissue biopsies. The tool, called METI (Morphology-Enhanced Spatial Transcriptome Analysis Integrator), was developed by researchers at MD Anderson and Emory.

METI provides a platform for integrating data based on how cells in a biopsy sample look and how they are organized (histology), as well as what genes are active inside them. It allows identification of both cancerous cells, as well as other cells, such as [healthy cells](#) or immune cells that have migrated into a tumor. The presence of [immune cells](#) and the spatial organization of the cells in a biopsy sample are often critical for diagnosis.

"METI's key contribution is its ability to accurately identify [tumor cells](#) and other components of the tumor microenvironment, by integrating both molecular and morphological information," says co-senior author Jian Hu, Ph.D., assistant professor of human genetics at Emory School of Medicine and director of the AI in Genomics lab.

To create METI, Hu worked with Linghua Wang, MD, Ph.D. and her laboratory at MD Anderson Cancer Center, and a team of experienced pathologists. They describe the software's performance in a [paper](#) published in *Nature Communications*. The software is available, with a user-friendly interface for [data visualization](#), on [GitHub](#).

The researchers evaluated METI's performance on biopsy samples from lung and bladder cancers from MD Anderson and gastric cancers from Zhejiang Cancer Hospital in China. Hu says the software can be applied to many cancer types, because it relies on [gene expression](#) and morphology signatures shared across various cancers.

METI is an unsupervised method that incorporates domain knowledge from previous publications on cancer genomics to guide its machine

learning model.

More information: Jiahui Jiang et al, METI: deep profiling of tumor ecosystems by integrating cell morphology and spatial transcriptomics, *Nature Communications* (2024). [DOI: 10.1038/s41467-024-51708-9](https://doi.org/10.1038/s41467-024-51708-9)

Provided by Emory University

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