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Scale meets speed: a transcriptome-wide spatial analysis that runs a rapid and interactive hypothesis-driven workflow with AtoMx® SIP

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Introduction

- Whole-transcriptome spatial analysis offers unparalleled biological resolution, yet its potential is often bottlenecked by the immense computational burden and specialist expertise required for data interpretation.
- As cell counts and plex scale, the "**data-to-insight**" timeline often stretches from weeks to months.
- To bridge this gap, we reimagined the AtoMx Spatial Informatics Platform (SIP) as a **rapid, interactive, and conversational ecosystem.**
- Herein we highlight three advancements arriving in the reimagined AtoMx® Spatial Informatics Platform (SIP) and in development and highlight results found in a publicly available colon adenocarcinoma and breast cancer FFPE WTX samples.

Key Advancements

1. Spatial Discovery with LLMs. By utilizing context-aware data packaging, we bridge the gap between high-dimensional spatial data and Large Language Models (LLMs). This allows for a natural language interface where researchers can query biological pathways and spatial relationships as easily as speaking to a colleague. The LLM can act as a subject matter expert in both biological inference and spatial statistics. Researchers can ask a myriad of questions and generate reproducible, publication-quality figures from their insights.
2. New AtoMx SIP architecture. We redesigned this platform inside and out with the goal of putting biology front and center, allowing researchers to quickly observe, hypothesize, and learn iteratively. See snapshot of new features (top middle panel) and scan the QR code for a video demonstration.
3. Foundational models. We are leveraging state-of-the-art "zero-shot" foundation models to automate complex tasks, including cell-type annotation (**Box 1**) and multi-cell niche classification (**Box 2**), providing high-fidelity biological context without the need for custom training.

References

1. Bruker Spatial Biology. CosMx® Human Breast FFPE Multiomic Datasets. https://brukerspatialbiology.com/products/cosmx-spatial-molecular-imager/ffpe-dataset/cosmx-human-multiomic-breast-dataset/ (2025)
2. Blampey, Q., Benkirane, H., Bercovici, N., Andre, F. & Cournede, P.-H. Novae: A graph-based foundation model for spatial transcriptomics data. 2024.09.09.612009 (2024) doi:10.1101/2024.09.09.612009.

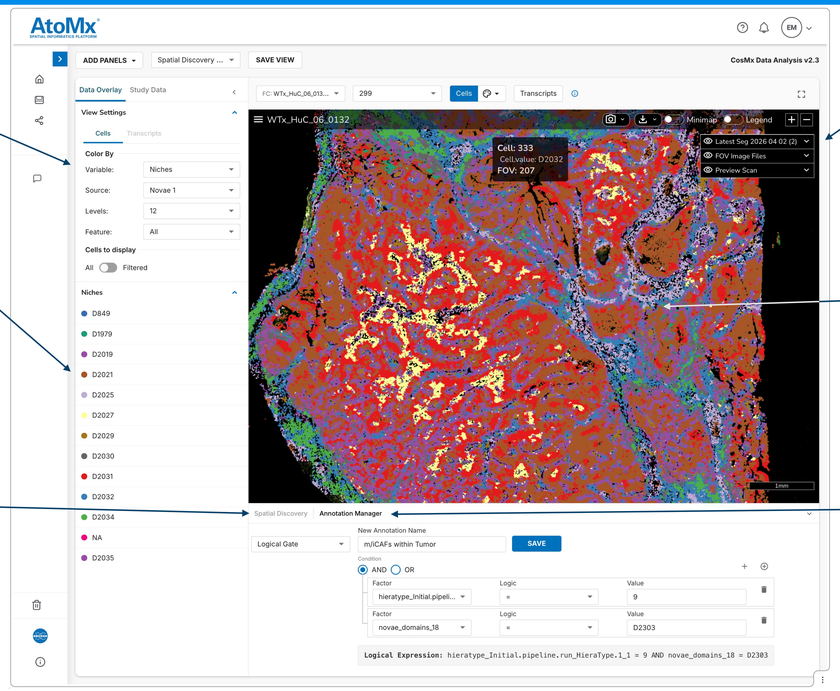
Scan here to see a demonstration

New Immersive AtoMx® SIP Experience Moves at the Speed of Scientific Curiosity

Biology ready to explore from the moment you open a study

Improved spatial domain detection using cutting-edge algorithms (Box 2)

Get AI-powered analysis insights with the new Spatial Discovery Module (see right panel)



Pan, zoom, switch between views or even slides with low-latency

View thousands of pathways, transcripts, and many other characteristics

Group and annotate cells based on a variety of attributes and use these to test your hypotheses

Fig. 1. Snapshot of the redesigned AtoMx SIP user experience using the publicly available WTX breast cancer dataset [1].

Box 1: zero-shot cell typing

We used 23 tissues (~8.6e5 cells) to train a 50-dimension cell embedding.

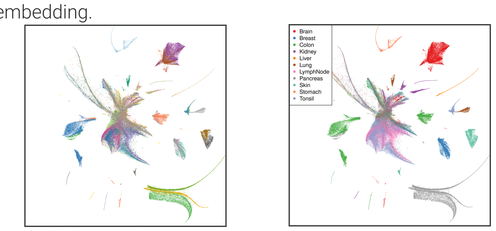


Fig. 2. Embedding-derived UMAP colored by tissue ID (left) and tissue type (right).

We then applied this embedding to the publicly-available breast cancer dataset and annotated cells based on their nearest neighbors in the two breast cancer training datasets.

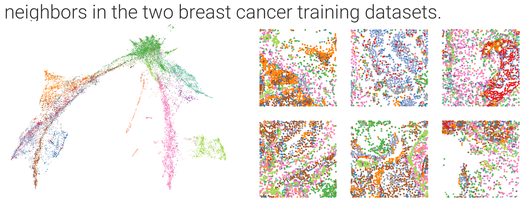
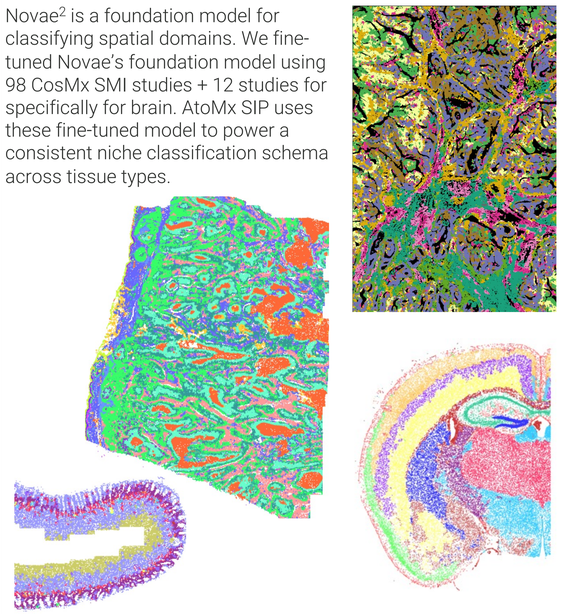


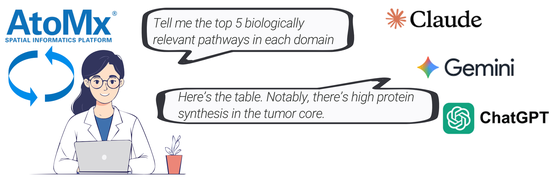
Fig. 3. Proof-of-concept results for zero-shot embedding of new data by the reference set neighbors. UMAP (left) and spatial arrangement (right).

Box 2: zero-shot niche classification

Novae[2] is a foundation model for classifying spatial domains. We fine-tuned Novae's foundation model using 98 CosMx SMI studies + 12 studies for specifically for brain. AtoMx SIP uses these fine-tuned model to power a consistent niche classification schema across tissue types.



Spatial Discovery with LLMs



AtoMx SIP's Spatial Discovery generates:

- Natural language querying. This shifts focus from coding to asking biological questions rapidly
- Context-aware data packaging. Distilled representations of spatial distributions and pathway enrichment to allow LLMs to reason over GBs of data within standard context windows
- Cross-domain synthesis. LLMs can link your results to the broader scientific literature
- Iterative discovery. LLMs suggest high-interest regions for follow-up (e.g., specific niches). Users can validate findings in the AtoMx SIP viewer and "loop" insights back into the model to refine statistical analyses like ligand-receptor signaling

Spatial Discovery is a **human-in-the-loop AI** workflow. Rather than 'black-box' automation, the LLM acts as a reasoning collaborator that facilitates, rather than replaces, the investigator's domain expertise.

Conclusion

- Accelerated Insight: The AtoMx SIP architecture removes the "bioinformatics bottleneck," enabling real-time, hypothesis-driven exploration of whole-transcriptome spatial data.
- Model-Agnostic Intelligence: By leveraging foundational models (*e.g.,* Novae) and conversational AI, researchers can move from raw images to biological synthesis without custom code.
- The New Standard: This workflow transforms spatial biology from a static data-generation exercise into an interactive, iterative collaboration between human expertise and AI-powered scale.