9th Annual
Tumor Models San Francisco Summit
January 29-30, 2025 | San Francisco, CA

EXCLUSIVE INTERVIEW

abbvie

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Senior Bioinformatics Scientist - Computational Oncology
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What are the current bottlenecks in implementing spatial biology across oncology drug discovery & development?

I think the main bottlenecks included, but are not limited to:

- Samples for spatial omics experiment. Spatial biology often requires high-quality and well-preserved tissue samples, but current tissue fixation methods can not fully meet the criteria, especially fresh and well-annotated clinical samples are very limited
- High cost and slow. High-resolution spatial technologies like imaging mass cytometry, spatial transcriptomics, and multiplex immunofluorescence are expensive and slow
- Relatively low throughput. The scalability of the current spatial biology technologies is still limited, making it challenging to apply these techniques in large drug development studies.
- Lack of standardized analytical tools. Data processing and analysis pipelines are not yet standardized, leading to variability in results between labs and studies
- Multi-modal integration. Combining spatial omics data with bulk level and single-cell level genomics data as well as other clinical biomarker data is complex due to diverse platforms used and the lack of universal protocols
- Integration into drug development workflow. Incorporating spatial data into preclinical and clinical stages has not been standardized and well established.

What are the current bottlenecks in implementing spatial biology across oncology drug discovery & development?

I think there are definitely some very exciting developments in the field, just list some of them:

- Advances in spatial profiling technologies. Platforms like 10X Genomics's Visium and Xenium and Nanostring's GeoMx DSP and CosMx enable gene and protein profiling with spatial resolution, bringing single-cell genomics and tissue-level context, which I think very exciting.
- Single-cell and spatial convergence. Integration of single-cell RNA-seq and spatial data provides unprecedented resolution in mapping tissue heterogeneity. Some well-developed computational tools, e.g., Seurat and Cell Ranger, have made this integration more feasible.
- Integration with AI/ML. AI-driven tools like DeepCell and Cellpose improve cell segmentation, and applying ML models can also accelerate the discovery and exploration of cell-cell interaction and phenotyping in complex tissues.

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When it comes to preclinical oncology models, how can spatial biology help empower their applications in drug discovery & development?

Tap into tumor heterogeneity. Spatial biology allows for precise mapping of cellular and molecular heterogeneity within tumors and its surrounding microenvironment.

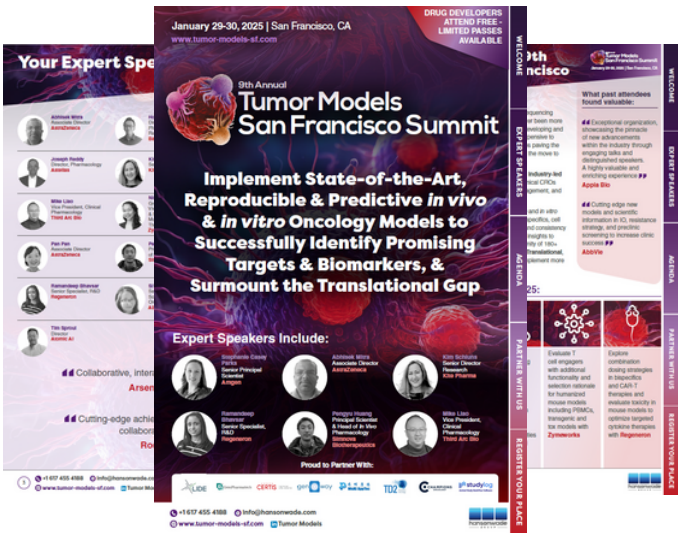
Deepen our understanding about tumor microenvironment (TME). Spatial biology can elucidate interactions between tumor cells, immune cells and stromal cells, which are critical for understanding drug efficacy and resistance.

Biomarker identification and validation. We can leverage spatial biology technologies to identify spatial distribution of predictive or prognostic biomarkers.

What is some of the exciting work you are looking forward to sharing at the 9th Tumor Models San Francisco Summit?

> *I'll share our GeoMx study on colorectal cancer state transitions and immune interactions for antigen target discovery.*

Want to find out more?



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