

How Spatial Transcriptomics Is Transforming Healthcare

The shift from single-cell to spatial techniques uncovers previously unknown insights—advancing disease research and prevention.

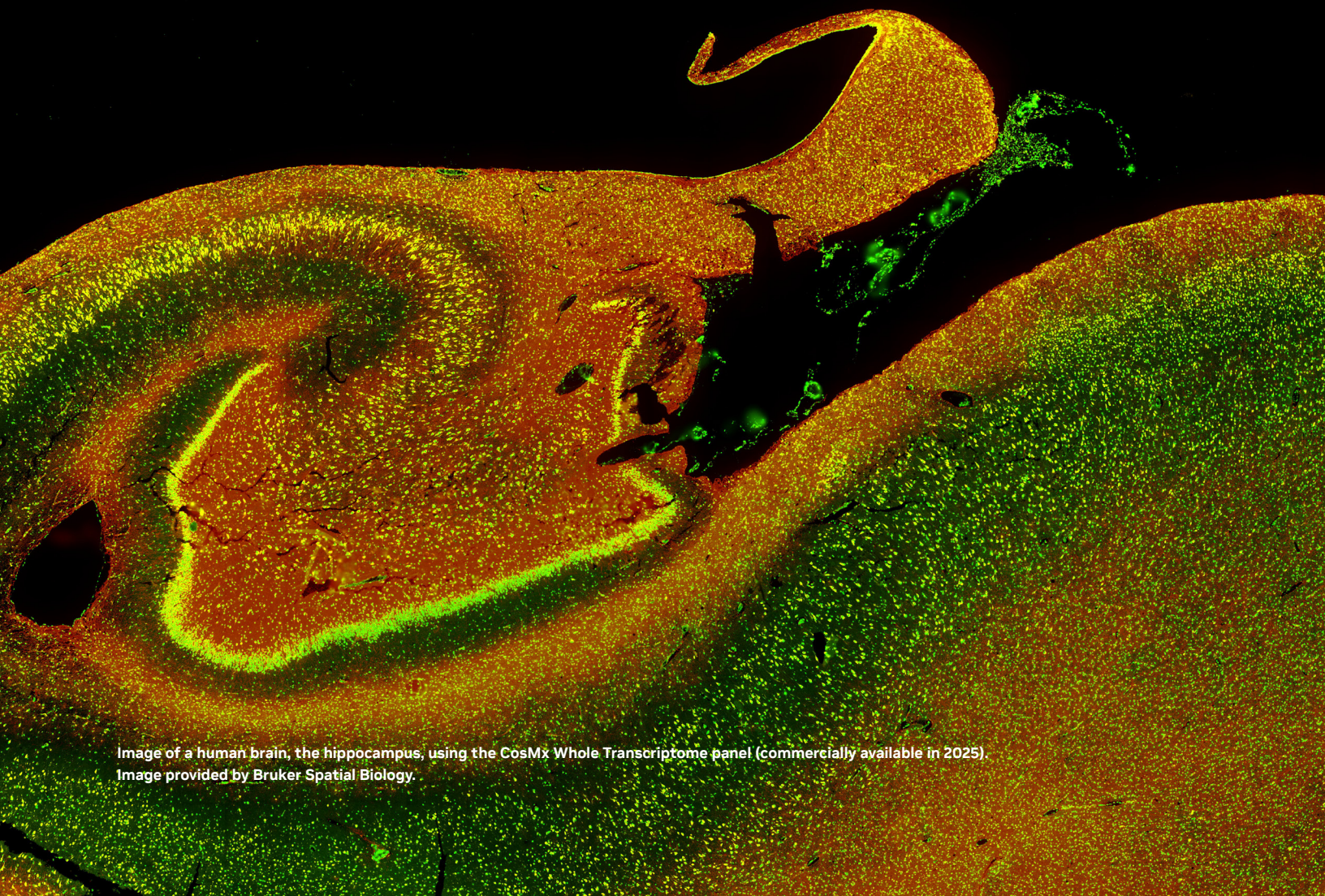


Image of a human brain, the hippocampus, using the CosMx Whole Transcriptome panel (commercially available in 2025).
Image provided by Bruker Spatial Biology.

The Omics Landscape

Overview of Single-Cell Omics

For well over a decade, scientists have used single-cell transcriptomics (commonly referred to as “single-cell omics”) to better understand biology and disease. By looking at individual-cell level, researchers can gain visibility into the full spectrum of cellular states and how they interact with each other. This helps understand gene expressions and identify rare cell types that may be linked to specific diseases.

Bulk RNA-sequencing approaches typically grind up tissues and extract information from cells to analyze everything in aggregate. Unlike bulk RNA-sequencing, which provides an average of everything happening within a tissue, single-cell approaches provide granularity on a cellular level. As a result, single-cell omics provide more precise analysis between what’s happening to individual cells in control and disease samples.

The Rise of Spatial Transcriptomics

Although single-cell techniques have helped understand diseases by evaluating cells on an individual level, they lack spatial context within the tissue surrounding these cells.

With the introduction of spatial transcriptomics, or simply spatial omics, researchers can use everything from relational data to imaging data to better understand gene expression and progression. Relational data provides context into where cells are located in relation to one another and makes it possible to overlay imaging data with molecular data.

The localization of cells and how they interact within their environment is critical for research, specifically when looking at rare cell types. However, spatial omics provide more context than how cells interact at a local level, also showcasing how a disease progresses within a tissue’s architecture. As a result, scientists are able to gain previously unknown spatial context for rare cell types and disease progression.

New Challenges From Spatial Omics

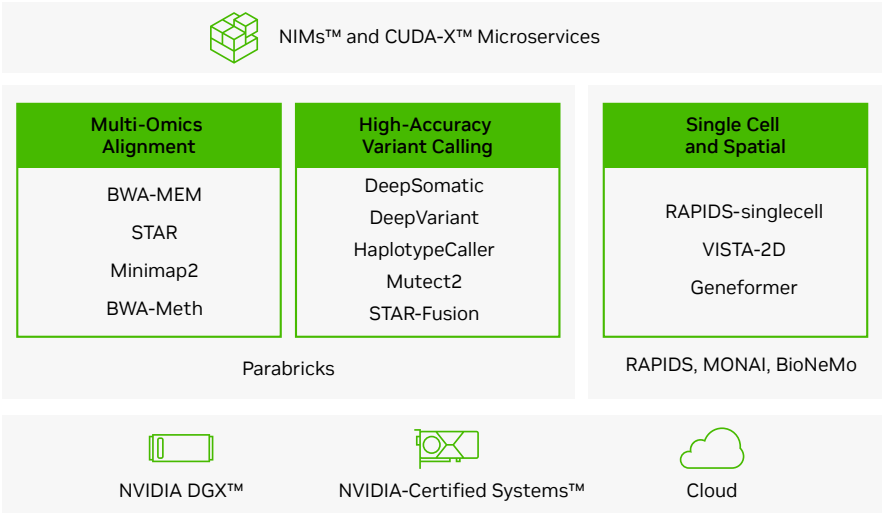
Although spatial omics unlock new insights into how cells and tissues relate to one another, the increase in data presents new challenges not seen in traditional single-cell sequencing. Spatial-omics instruments produce an immense amount of imaging—often resulting in data from millions of cells from a single run. For context, single-cell atlas projects, which often span multiple countries, investigators, and years, can produce a similar amount of data in the entirety of a project.

As a result of this volume of data, analysis can be challenging. Large datasets not only present initial computational challenges but they can become a real problem for iteration. Since pipelines are often not fixed, any additional changes to parameters require the process to be repeated. This means that analysis timelines can get longer with any additional tuning and tweaking.

Omics at NVIDIA

Accelerated Secondary and Tertiary Analysis

NVIDIA technology is used across the omics landscape, including GPUs built inside of sequencing instruments and software applications like [NVIDIA® Parabricks®](#) for accelerated secondary analysis and [NVIDIA RAPIDS™](#) for tertiary analysis. Additionally, solutions like [NVIDIA MONAI](#) and [NVIDIA BioNeMo™](#) are valuable for medical imaging and drug discovery, respectively.



The NVIDIA AI and GPU-accelerated software suite for genomic analysis.

For alignment and high-accuracy variant calling, Parabricks is a GPU-accelerated software suite that boosts accuracy, increases speed, and reduces cost for secondary genomic analysis.

RAPIDS is an open-source suite of GPU-accelerated data science and AI libraries that improves performance across data pipelines for tertiary analysis.

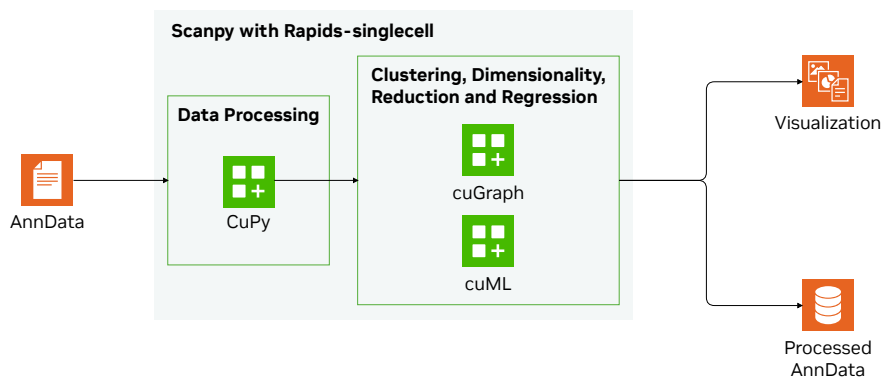
To accelerate medical image workflows, NVIDIA MONAI is a comprehensive solution for developing and deploying AI in healthcare imaging. It includes microservices and capabilities for training AI models, intelligent image labeling, and deploying medical AI applications in clinical settings. Developers can build, enhance, and deploy imaging AI solutions across healthcare and life sciences applications.

BioNeMo is a platform for building, training, and deploying AI models for drug discovery. By combining a programming framework and enterprise-grade microservices, BioNeMo dramatically accelerates computational drug discovery workflows.

Single-Cell Workflows

In addition to Parabricks' secondary analysis approaches for bulk RNA-sequencing, such as Spliced Transcripts Alignment to a Reference (STAR) for traditional transcriptomics, downstream analysis for single-cell omics can benefit from GPU acceleration. Specific models such as [RAPIDS-singlecell](#) and [Geneformer](#) are particularly impactful for processing large amounts of single-cell data.

RAPIDS-singlecell accelerates data processing, clustering, dimensionality reduction, and regression. This helps reduce the analysis time for processing large amounts of single-cell data.



RAPIDS-singlecell is built using CuPy, CuGraph, and CuML. RAPIDS-singlecell was developed by researchers at Charité.

Using transfer learning from vast single-cell transcriptome data, Geneformer predicts gene dynamics and interactions. As a result, researchers can accurately predict gene behavior and disease mechanisms with limited data.

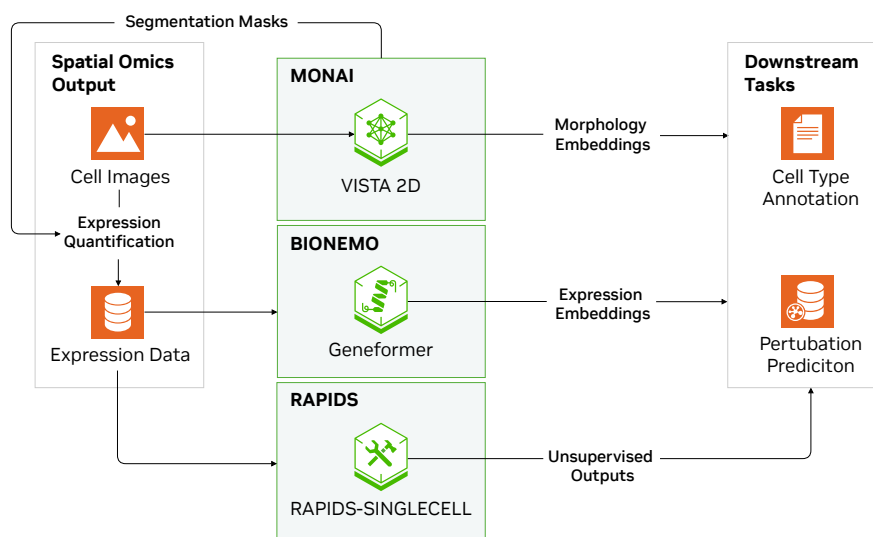
Spatial Workflows

At its simplest definition, spatial omics is spatially resolved single-cell omics. This means that single-cell methods can be used for spatial since they produce expression data. However, not all spatial methods can be used for single cell, since they produce additional imaging and spatial data. As a result, imaging tools are often required for analysis in spatial omics.

To accelerate bottlenecks and increase accuracy, NVIDIA Parabricks includes a single-cell and spatial-omics workflow that can enable novel methods of analysis. Software across NVIDIA (including imaging, generative AI, and data science) is combined to power rapid and high-accuracy analysis.

Generative AI is specifically applied to spatial-omics analysis with [VISTA-2D](#), an NVIDIA AI Foundation model for high-accuracy segmentation in cell imaging. Since it impacts the accuracy of downstream tasks, high-accuracy segmentation is imperative for attributing expression to the correct cell.

Unlike specialist models, VISTA-2D works on multiple types of cells, since it was trained as a generalist foundation model. In addition to being a robust deep learning algorithm based on transformers, it supports multiple datasets, modalities, and GPUs.



Single-cell and spatial-omics reference workflow.

The explosion of data from single-cell and spatial sequencing has made it more important than ever to address computational challenges. However, an increase in data does not immediately translate to an increase in understanding. Researchers need to be able to effectively and efficiently analyze data. GPU-accelerated data science libraries and specially designed workflows enable researchers to gain insights from these enormous datasets that would have previously taken significantly more time and resources.

Leaders in Spatial Omics

From instrument and sequencing providers to research institutes and labs, leaders in spatial omics are building industry-changing technology and conducting breakthrough scientific research that are making a profound impact on the world.

Instrument and Sequencing Providers

10x Genomics

10x Genomics is a leader in single-cell, spatial, and in-situ technologies that enable scientific discoveries across a range of disciplines, from oncology to neuroscience. Their instruments and software offer end-to-end solutions that help analyze complex biological systems at large scale and high resolution to advance human health. One of their powerful instruments, the Xenium Analyzer, allows scientists to characterize thousands of genes in cells and tissues with ultra-precise and sensitive single-cell spatial imaging and explore data immediately, since the data is processed onboard during the run.

“We built the Xenium Analyzer to help cutting-edge researchers rapidly move from instrument to insight with our powerful onboard analysis, enabled by NVIDIA GPUs. The combination of Xenium with NVIDIA RAPIDS further accelerates our best-in-class workflows and enables more precise analysis so researchers can go from run to result and data to discovery even faster,” explained Adrian Benjamin, global spatial marketing lead at 10x Genomics.



The 10x Genomics Xenium Analyzer. Image provided by 10x Genomics.

Bruker Spatial Biology

Bruker Spatial Biology is a pioneer in spatial biology and has worked to create end-to-end solutions that enable scientific exploration. Their instruments—including the CosMx SMI, a spatial molecular imager that elevates single-cell research—have introduced vital technology to research institutes and have helped unlock new imaging capabilities.

“Spatial-omics technology (CosMx Spatial Molecular Imaging) can now image the entire transcriptome inside cells and tissues, generating data at a density and scale that has never before been accomplished (~150TB per cm²). This data will play a critical role in transforming our understanding of both health and disease, radically accelerating drug development and spatial diagnostics,” said Joseph Beechem, PhD, the chief scientific officer and senior vice president of research and development at Bruker Spatial Biology.

“In reality, generative AI will be required to explore the true information content of these images. We’re thrilled to work in partnership with NVIDIA at all levels of the data-to-information pipeline.”



The CosMx SMI. Image provided by Bruker Spatial Biology.

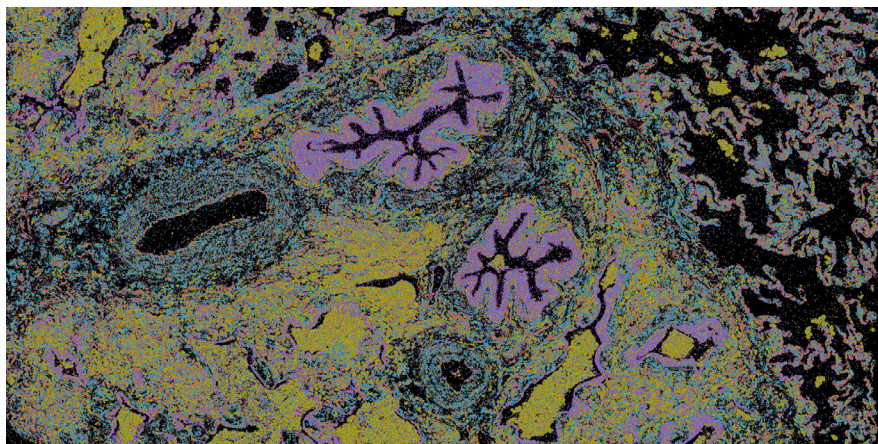
Research Institutes and Labs

TGen

Part of City of Hope, the Translational Genomic Research Institute (TGen) conducts research on a variety of diseases ranging from neuro and cancer genomics to basic genomics of complex diseases. By conducting research that accelerates translational solutions using genomics, TGen always works to impact patient care.

Computational challenges arose for TGen with the increase of data from multi-omics sequencing. TGen was able to cut the analysis time on a dataset of 4 million cells from 10 hours to four minutes with NVIDIA RAPIDS.

“As we look forward, we’re talking about generating datasets with tens of millions or maybe even hundreds of millions of cells. Scalability across datasets of that size is only possible because we’ve been able to use this RAPIDS implementation,” said Nicholas Banvoich, PhD, associate professor in the Integrated Cancer Genomics Division at TGen.



Human lung samples run on the 10x Genomics Xenium Analyzer. Image provided by TGen.

Weill Cornell Medicine

Since 1898, Weill Cornell Medicine has provided world-class clinical care and cutting-edge research. This commitment to patient care and scientific discovery connects patients to the latest treatment and prevention strategies.

To map cellular and molecular landscapes, Weill Cornell Medicine worked on the Spatial Atlas of Human Anatomy (SAHA) project, resulting in best practices and data standards for spatial analysis.

“Comparing multiple cancer samples and spatial platforms demonstrates the power of SAHA data in revealing insights into organ development, homeostasis, and cancer progression. This perspective paves the way for early disease detection and personalized therapeutic interventions, laying the groundwork for precision medicine,” stated Christopher E. Mason, PhD, WorldQuant professor of genomics and computational biomedicine at Weill Cornell Medicine.

“To increase the accessibility and usability of our extensive data, with NVIDIA, we also are developing a generative AI model, spatialGPT, trained on SAHA data. It leverages deep learning algorithms to predict cell types and niche labels, infer cross-modal information, and identify novel spatial patterns associated with disease progression.”

Powering Research With Accelerated Spatial Omics

The evolution of analysis from single-cell to spatial omics has helped provide crucial context into cell locations and interactions. Sequencing providers continue to build innovative technology and instrumentation that enable research institutes and labs to conduct breakthrough scientific research.

Although spatial omics is helping to advance our understanding of diseases, the amount of data produced is also increasing computational challenges. To solve these challenges, GPU-accelerated software and prebuilt workflows help researchers analyze these large datasets in a fraction of the time previously required.

Understanding the localization of cells and spatial context is now possible with spatial omics. As a result, spatial omics continue to fuel new scientific research and advance disease understanding and prevention.

Ready to Get Started?

To download and get started today, visit:

nvidia.com/download-parabricks

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