https://doi.org/10.1038/s41588-023-01621-6

A call for spatial omics submissions

The field of spatial omics is developing rapidly, with a potentially transformative effect across many areas of biology. *Nature Genetics* invites authors to submit papers that use these techniques to answer questions of broad interest to researchers working in genetics and genomics.

The discipline of genomics is a child of technological progress: from the DNA microarrays that first enabled genome-scale experiments, to the step change offered by high-throughput sequencing, and more recently the revolution triggered by single-cell methods. At each stage, the initial breakthrough was followed by the rapid development of assays for further biomolecules and features such as RNA, DNA methylation, histone modifications, chromatin accessibility, and so forth.

The resolution of single-cell methods offered an unprecedented opportunity to explore and characterize the diversity of cell types and states at scale, but it was also recognized that these dissociation-based techniques have a major drawback: spatial information, long-understood as an important factor in cellular biology, is lost. As just one example, the function of tissue stem cells is dependent on the niche provided by their neighbors, in terms of intracellular ligand–receptor signaling and other characteristics of the local tissue environment.

This has motivated the development of 'spatial transcriptomics': sequencing- and fluorescent in situ hybridization (FISH)-based methods to assay cell transcriptomes while preserving the spatial context, generally by working with tissue sections. These high-throughput methods build on the legacy of previous efforts that generated whole-mount in situ hybridization atlases for model organisms, as noted by a review of the field's history. Initially, the resolution of these methods could be low — for example, the commercially available Visium spatial transcriptomics kit uses 50-µm spots that capture multiple cells — but further development has led to the generation of rich, transcriptome-scale, cellular-resolution data, with some methods even achieving subcellular resolution. And as observed for single-cell genomics, as the RNA assays matured and were recognized as a paradigmatic shift, new methods for spatially analyzing chromatin accessibility, proteomes, metabolomes and DNA variation have appeared, giving rise to the broader field of spatial omics.

As this area of spatially resolved omics methods develops further, *Nature Genetics* is issuing a call for submissions that apply these techniques to further our understanding of fundamental biology and disease mechanisms. It is not hard to imagine scientific questions where applications of spatial methods will be vital, such as disentangling the complex ecosystem of the tumor microenvironment (TME), or the tightly choreographed cellular interplay of organismal development. Beyond that, much as single-cell progress led to an explosion of computational tools to analyze such data — adapted from extant bulk genomics methods, as well as mixing in novel approaches from machine learning and population genetics, among others — it seems clear to us that the spatial field is similarly poised for an exciting period of rapid progress.

We have already published various manuscripts that use spatial omics; for example, in single-cell atlases of the human lung and endometrium, and whole-embryo maps of mouse development. Unsurprisingly, given its past prominence for driving progress in genomics, cancer biology has taken with alacrity to spatial technologies, as exemplified in our pages by studies that characterize pan-cancer expression programs and their intercellular interactions, exploring breast cancer and its TME, relating pancreatic cancer therapy responses to spatial structures and identifying stem-like niches in diffuse midline gliomas.

In particular, the journal has an interest in computational analysis tools, such as SpiceMix. Although methods developed for single-cell RNA data have been successfully transferred to the spatial realm, the full richness of spatially resolved data has yet to be comprehensively leveraged, which suggests that there are plentiful opportunities for researchers to capitalize on by applying approaches from disciplines in which spatially resolved data is the norm, such as geology and ecology. Given that there is a lack of strong ground truths to benchmark performance and a lack of metrics to assess said performance, we are especially keen to contribute to establishing norms for these studies, as exemplified by a community-run biohackathon occurring this month in Germany that will focus on spatial clustering.

As seen from this selection of examples, the journal has a broad interest in this area, from the basic methodology through to new analytic tools and incorporating these into larger works: for instance, it is increasingly clear that having spatial analyses to complement single-cell data can add considerably to our understanding of fundamental biological processes at the cellular and tissue levels, as well as offering substantial resource value for the broader field to reuse. We eagerly welcome manuscripts that fully utilize the potential power of spatial data, and not only as a complement to other omic data.

Spatial omics is at an inflection point, and *Nature Genetics* sees immense potential for it to be harnessed by the wider field. We are especially interested in, and will prioritize, submissions that apply spatial omics to address timely questions of broad interest to our core audience working in the fields of genetics and genomics.

Published online: 02 January 2024