

Spatially resolved multi-omics

“Spatially resolved multi-omics” refers to a set of cutting-edge technologies that integrate multiple omics approaches (such as [genomics](#), [transcriptomics](#), [proteomics](#), and [metabolomics](#)) while preserving the spatial context of biological samples. This means that instead of analyzing bulk molecular data from homogenized tissue, these techniques allow scientists to study the spatial organization of cells and biomolecules within their native tissue environment.

Key Aspects

- **Spatial Resolution:** Unlike traditional omics methods that lose spatial information, these approaches retain the localization of molecular data within a tissue or cell structure. - **Multi-omics Integration:** Combines different layers of biological data (e.g., DNA mutations, RNA expression, protein levels, and metabolic changes) to provide a comprehensive view of cellular and tissue function. - **Technologies Used:**

1. **Spatial Transcriptomics:** Maps gene expression across tissue sections.
2. **Spatial Proteomics:** Determines protein distribution at high resolution.
3. **Spatial Metabolomics:** Tracks metabolite changes in different tissue regions.
4. **Spatial Epigenomics:** Investigates chromatin modifications and DNA accessibility within tissues.

- Applications:

1. Understanding tumor microenvironments and heterogeneity in cancer.
2. Mapping cellular architecture in developing tissues and organs.
3. Investigating disease mechanisms in neuroscience, immunology, and regenerative medicine.
4. Identifying spatial biomarkers for precision medicine.

This approach is transforming biomedical research by enabling scientists to study the intricate molecular landscapes of tissues with unprecedented detail.

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