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(54) Title: METHODS FOR CHARACTERIZING CELLS USING GENE EXPRESSION AND CHROMATIN ACCESSIBILITY

Profiling Different Modalities to Gain Better Understanding of Complex Biological Systems

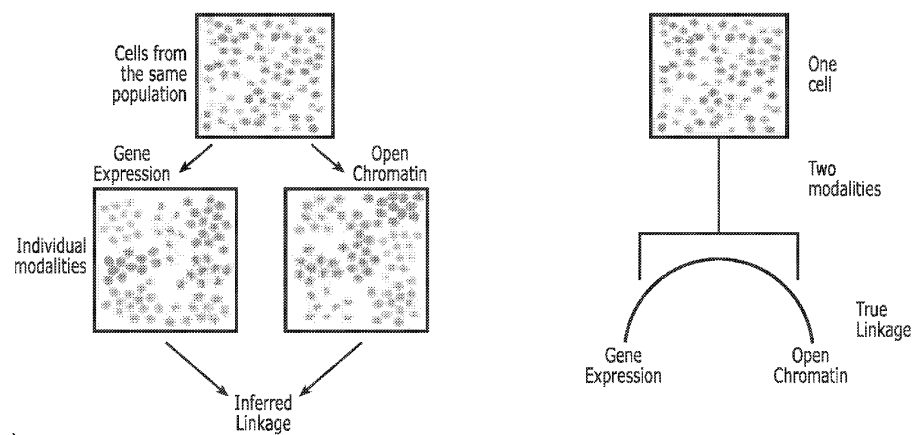


FIG. 24

(57) Abstract: While robust high-throughput systems for assaying either transcription or chromatin accessibility (e.g., using ATAC-seq) at single cell resolution are now widespread, researchers and clinicians typically must split cell samples and analyze each modality separately and computationally infer linkages between the gene expression and chromatin accessibility data. The present disclosure provides a high-throughput solution that simultaneously measures gene expression and chromatin accessibility from single cells or nuclei and methods of using this data to directly infer linkages between gene expression and chromatin accessibility data to chart regulatory pathways and functional characterization of complex disease pathology.

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