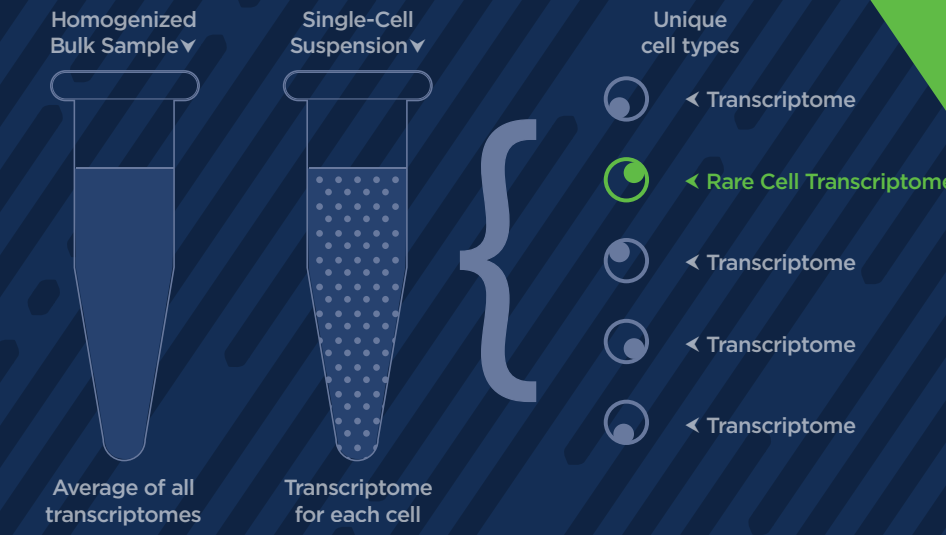


1

SINGLE-CELL RESOLUTION

A Resolution Worth Keeping

Traditional RNAseq methods analyzed the RNA of an entire population of cells, but only yielded a bulk average of the measurement instead of representing each individual cell's transcriptome. By analyzing the transcriptome of a single cell at a time, the heterogeneity of a sample is captured and resolved to the fundamental unit of living organisms—the cell.



WHY SETTLE FOR AVERAGE?

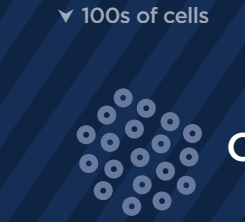
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3

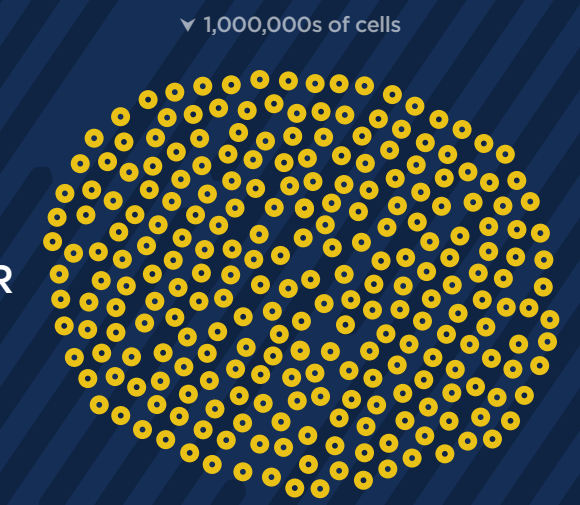
SCALE

100s to 1,000,000s

Should there be an upper or lower limit to the number of single cells that must be characterized for meaningful analyses? The newest technologies for scRNAseq enable you to catalog the cellular heterogeneity in your tissue, whether you have a scarce, rare sample of very specific cells or an abundant sample with many cell types. Droplet-based scRNAseq methods with the highest capture efficiencies ensure that you see the whole picture.



OR



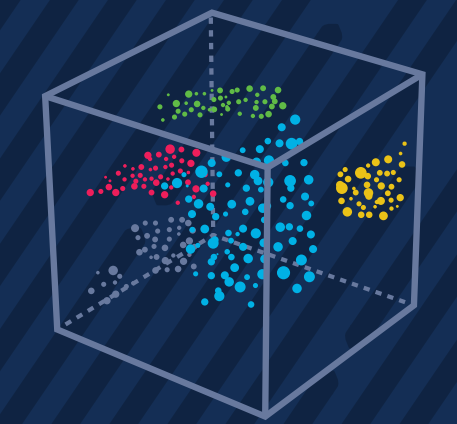
EXPERIMENT WITHOUT LIMITS

REVOLUTIONIZING GENE EXPRESSION

with Single-Cell RNAseq



▲Tissue specimen with a spatial relationship between cells.



▲Relationship between cells by similarity of gene expression.

CELL BY CELL

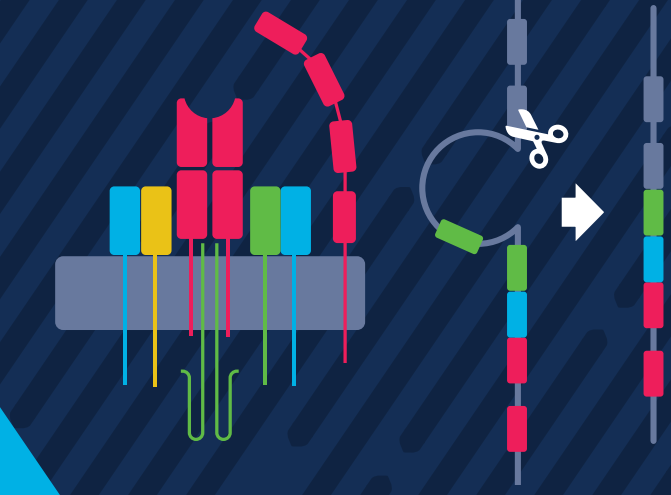
Revealing Hidden Differences

Whether you're working with tumor cells, stem cells, T cells, or embryonic cells, heterogeneity is ever-present. scRNAseq allows you to analyze the complexity of biological systems, both within a population and over time, at the single-cell level. Single-cell transcriptome analysis has enabled a detailed and unbiased look at these dynamic processes in all their forms.

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4

Characterize the complexities of T-cell receptors from full-length, paired V(D)J sequences.▼



COMPLEXITY

Beyond Cell Type

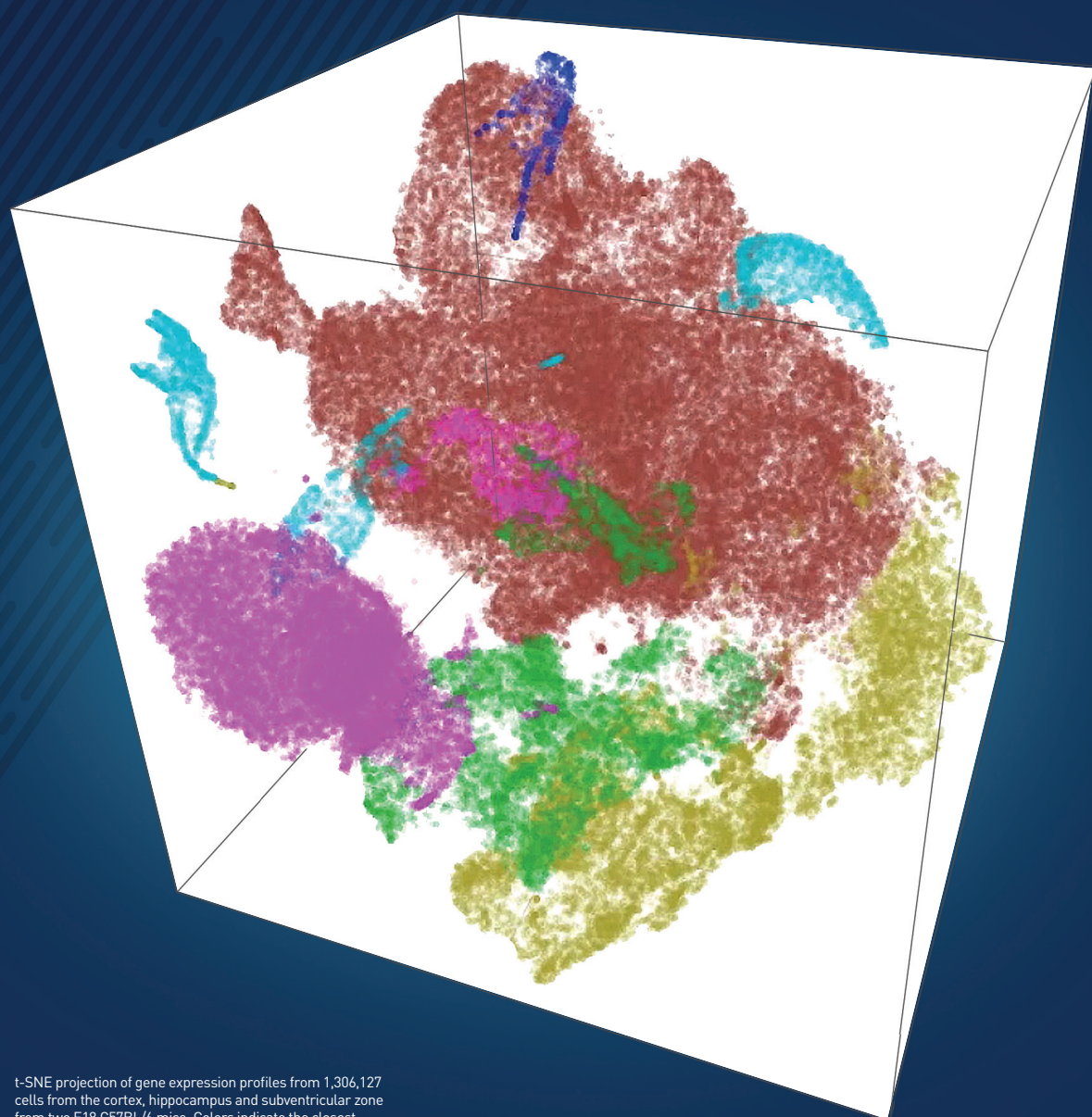
For the first time, scRNAseq is enabling a cell-by-cell molecular and cellular characterization of hundreds of thousands of cells within the same sample. Complex systems, like those found in the immune system, can be explored without limits.

scRNAseq can now be applied to:
Immunology • Neurology • Stem Cell Biology • Oncology • Immuno-oncology

CLARIFY COMPLEX SYSTEMS

TRACKING THE TRAJECTORY
OF CELL FATES

2



t-SNE projection of gene expression profiles from 1,306,127 cells from the cortex, hippocampus and subventricular zone from two E18 C57BL/6 mice. Colors indicate the closest match in a panel of sorted reference cell types.

For more information, visit:
<http://go.10xgenomics.com/1-million-brain-cells>

LEARN MORE AT 10XGENOMICS.COM/SINGLE-CELL



10X GENOMICS IS CHANGING THE DEFINITION OF SEQUENCING.

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REVOLUTIONIZING GENE EXPRESSION with Single-Cell RNAseq

Transcriptome analysis has made the leap from bulk population-based studies to the single cell, and scientists are harnessing this new degree of resolution with remarkable ingenuity. Single-cell RNA sequencing (scRNAseq) allows you to ask and answer questions that require single-cell resolution on a scale that suits your experimental needs, from hundreds to millions of cells. Are you truly tracking your cells' transcriptomes, or are you just reading into the averages?



Reveal Cellular Heterogeneity from Hundreds to Millions of Cells with Single-Cell RNA-seq

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Perform deep profiling of complex cell populations with flexible throughput digital gene expression on a cell-by-cell basis with the Chromium Single Cell 3' Solution. Assign expression profiles to individual cells to ensure biologically relevant signals are not masked by bulk average measurements.



The Chromium™ System
 The Chromium System, powered by GemCode™ Technology, is an innovative system that transforms the capability of existing short-read sequencers. With millions of uniquely addressable partitions, the Chromium System unlocks critical genomic information.