

Introduction



연구전임교원



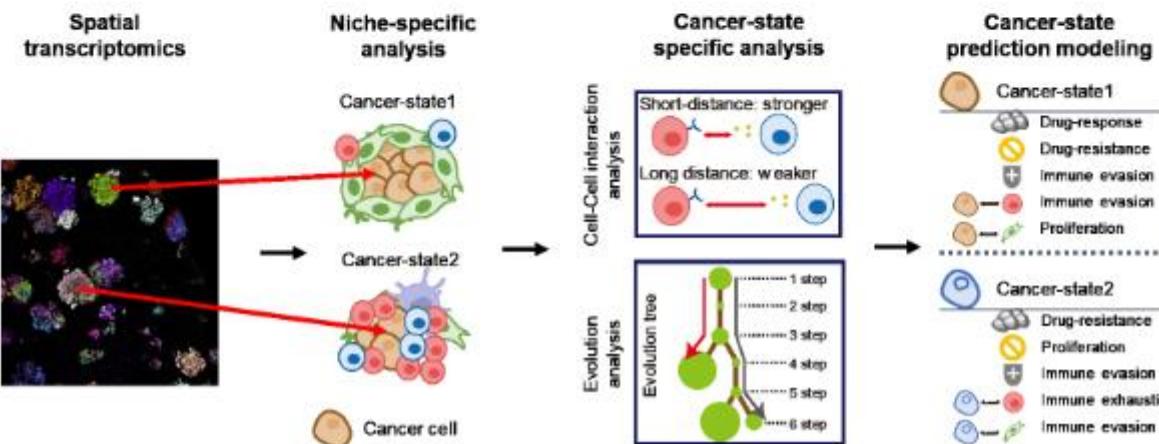
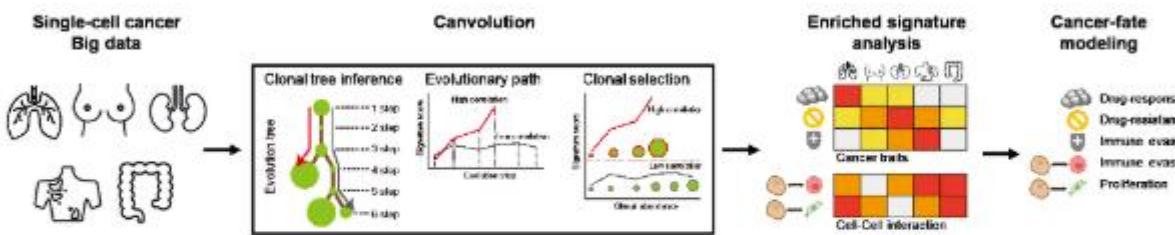
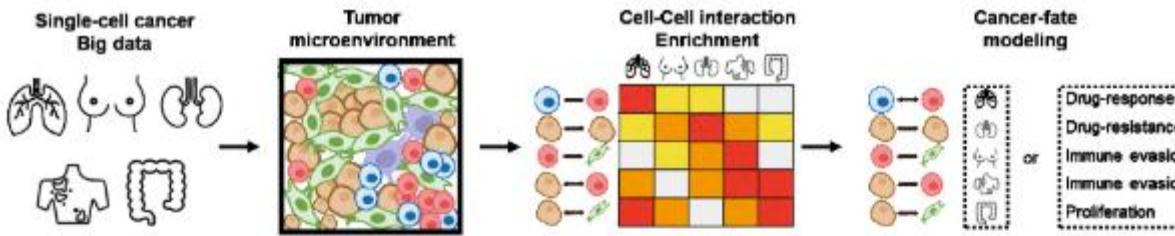
조재원 교수

- 한양생명과학기술원, 한양대학교 자연과학대학 생명과학과

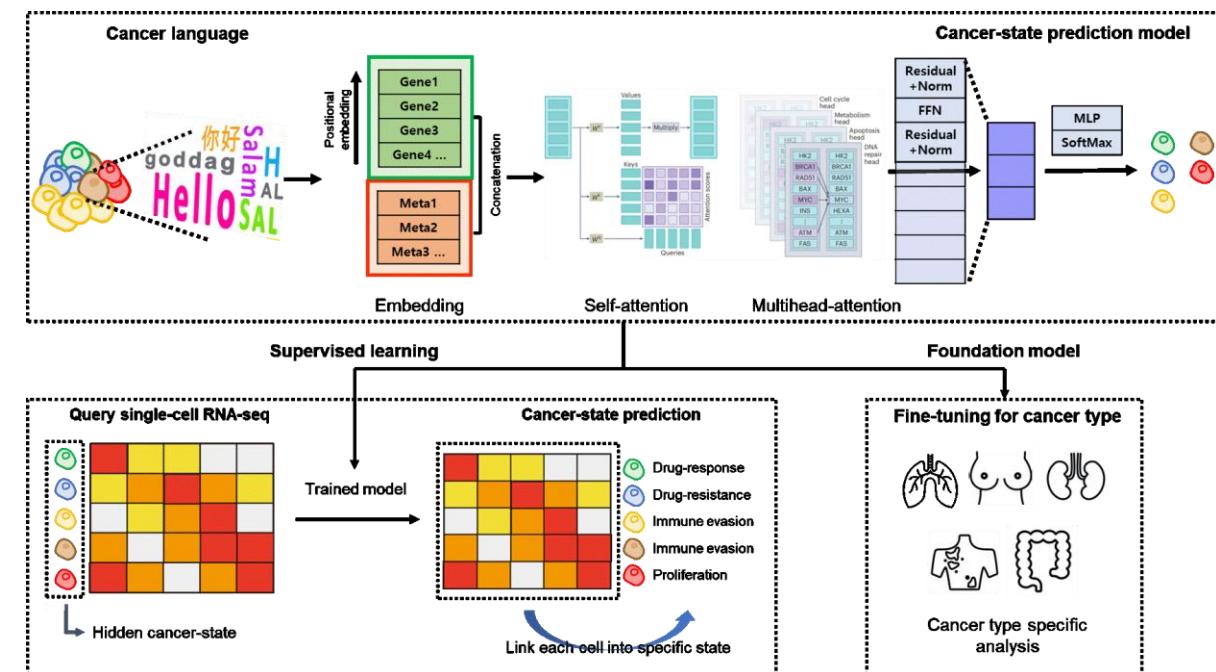
연구업적

- 단일 세포 전사체 및 공간전사체를 이용한 암-면역학 연구
- 단일 세포 기반의 분석 방법 개발

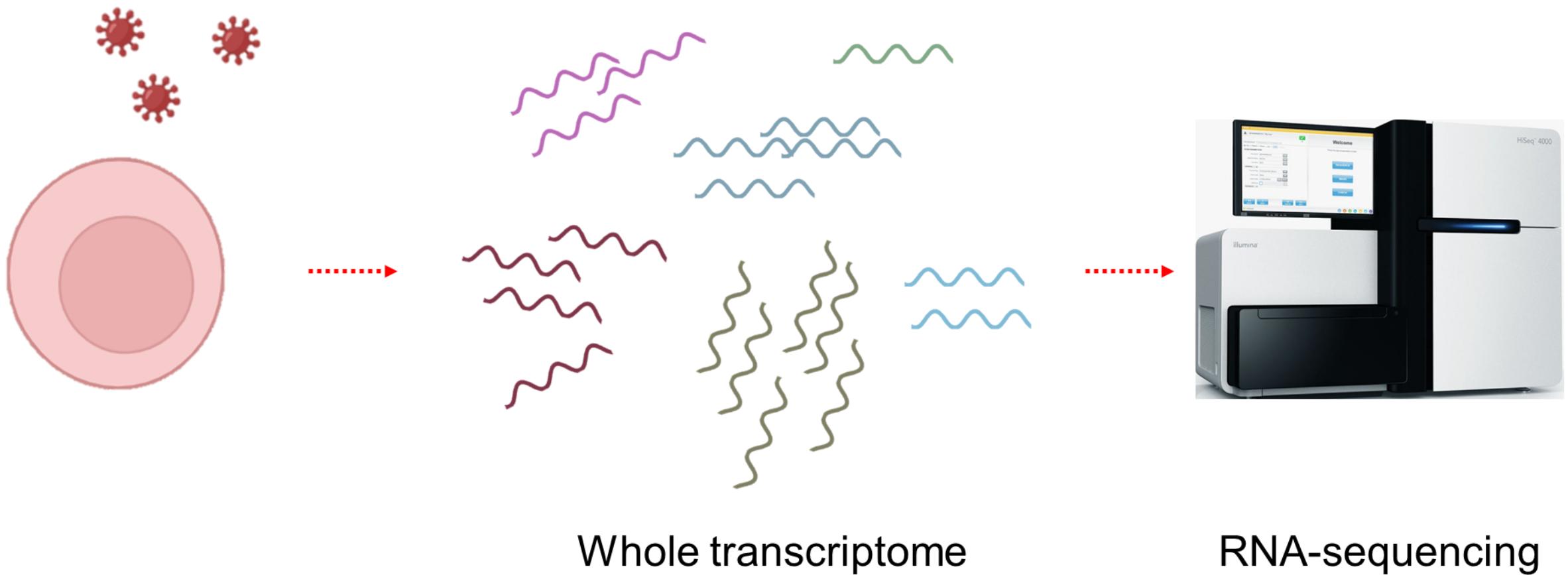
1) Bigdata analysis of cancer in scRNA / Spatial transcriptomics



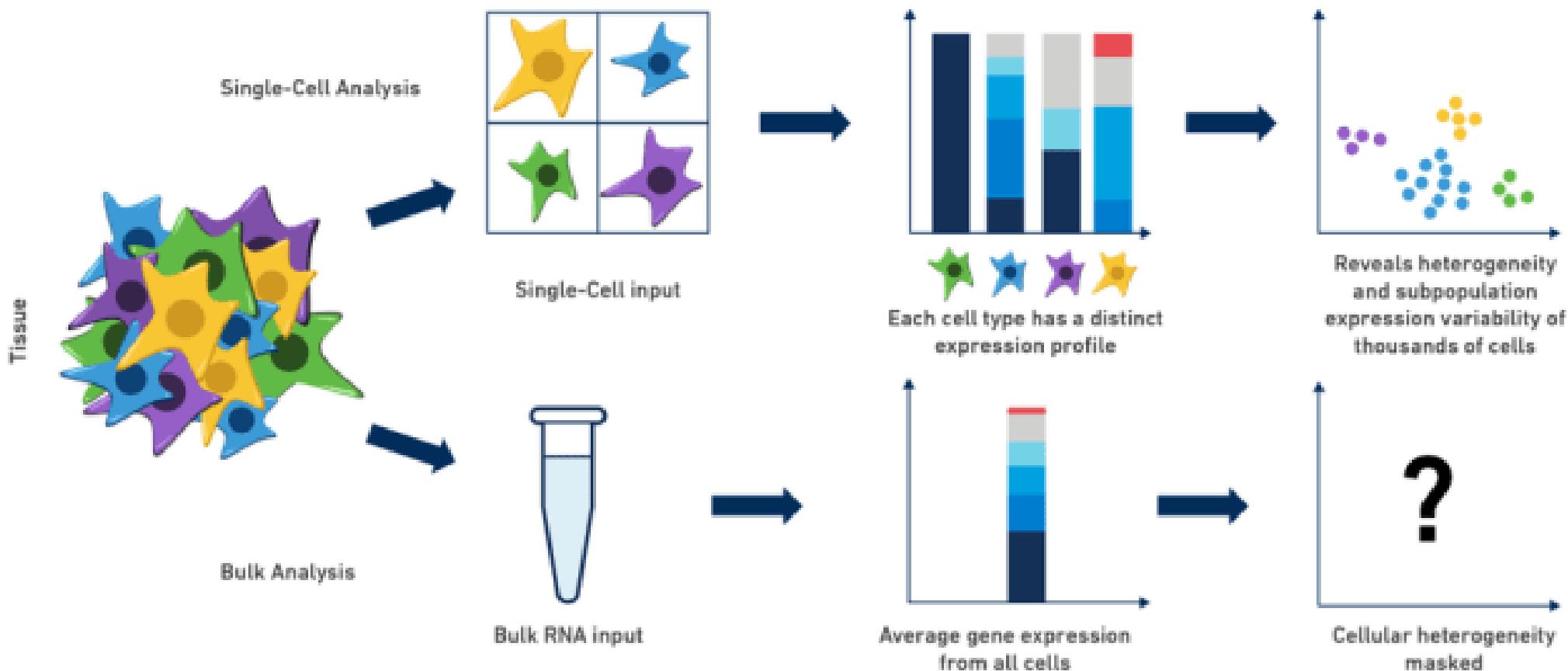
2) AI in scRNA-seq



Bulk RNA-sequencing

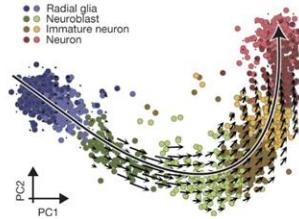


scRNA-seq

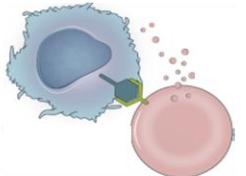


scRNA-seq

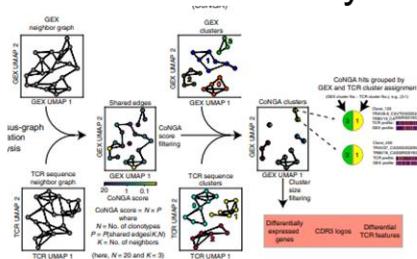
Trajectory analysis



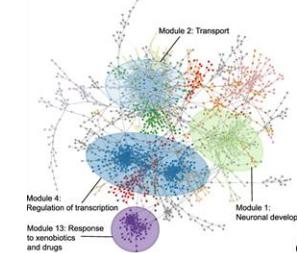
Cell-Cell interaction



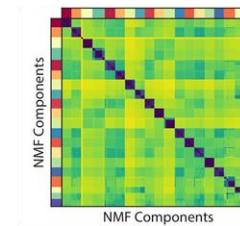
T/B cell clonality



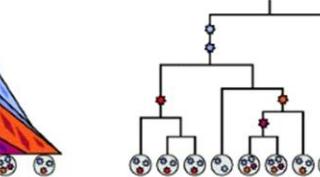
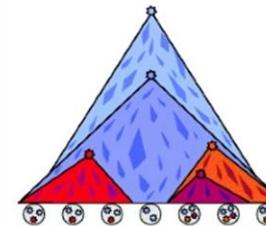
Network analysis



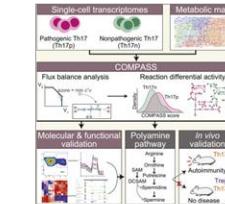
Signature analysis



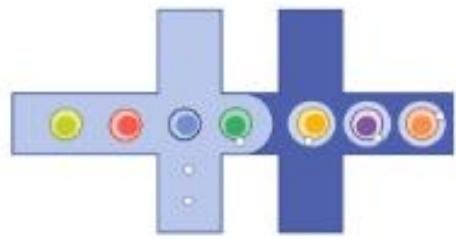
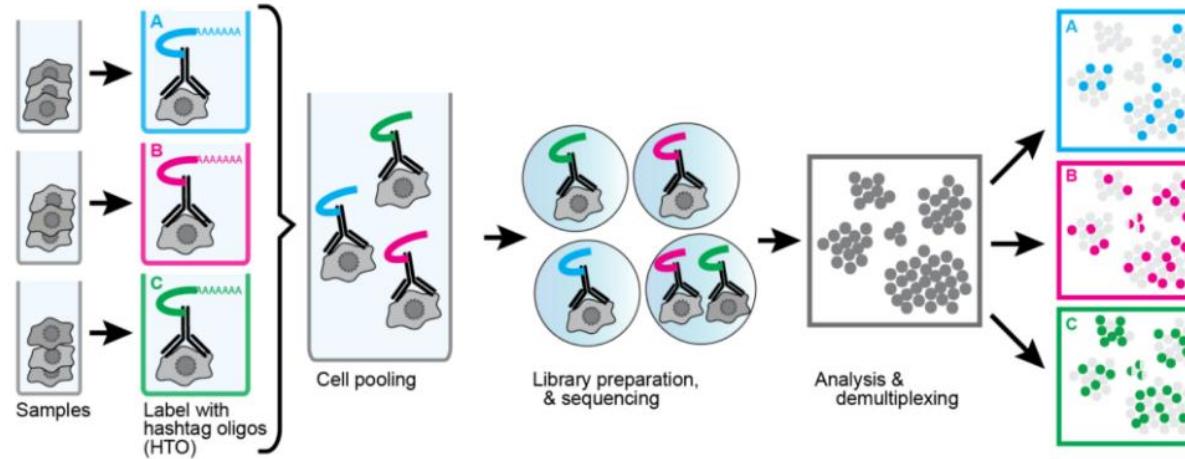
Cancer evolution



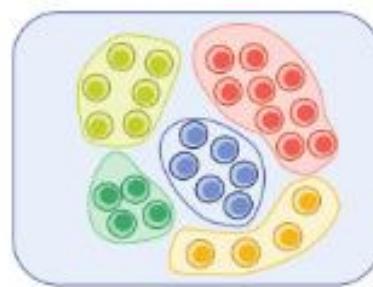
**Single-cell
technology**



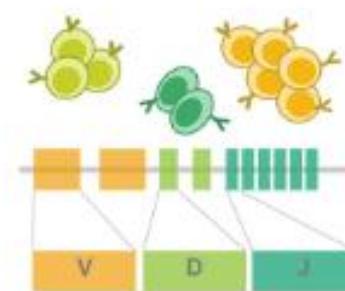
CITE-seq & TCR/BCR



Drop Isolation of
single cell

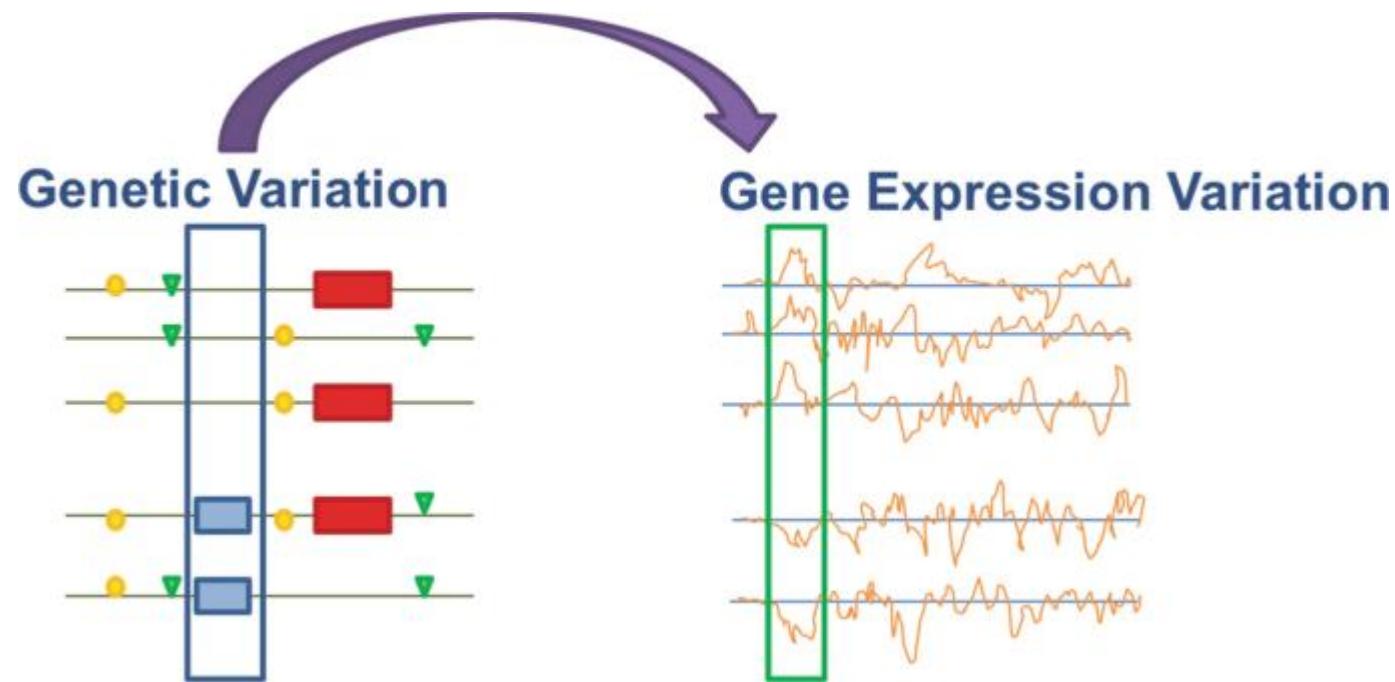
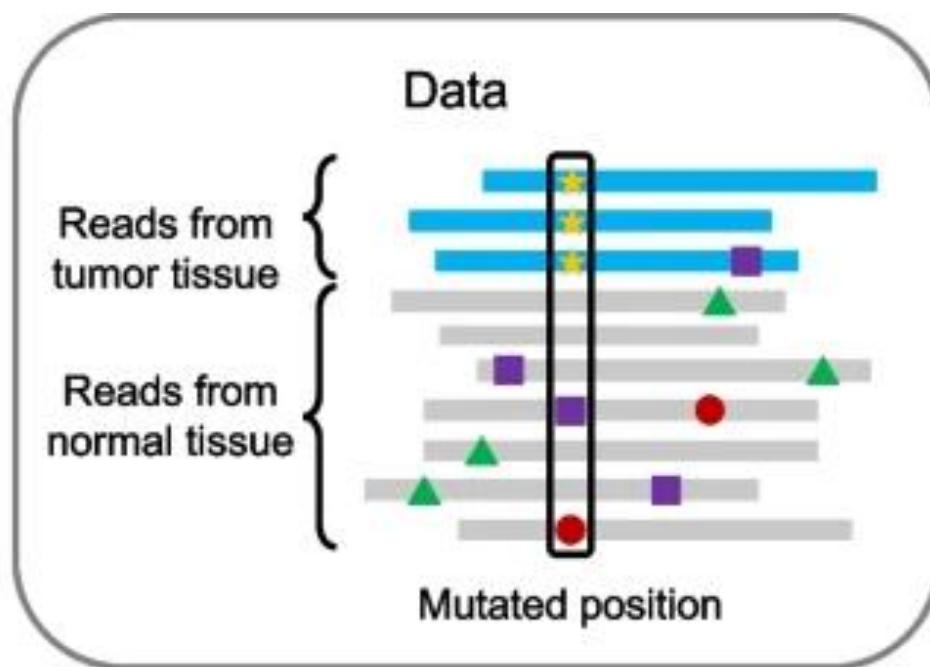


Visualization of
single cell sequencing

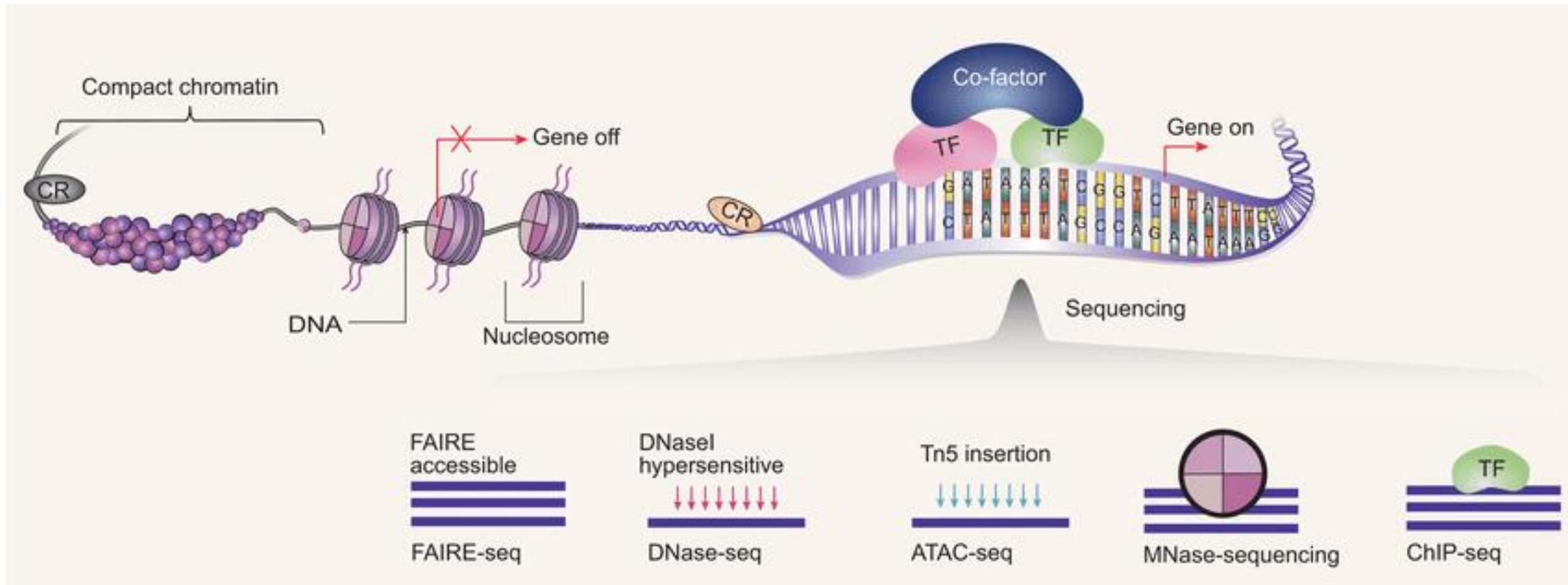


Detection of VDJ
recombination

scDNA-seq



scATAC-seq

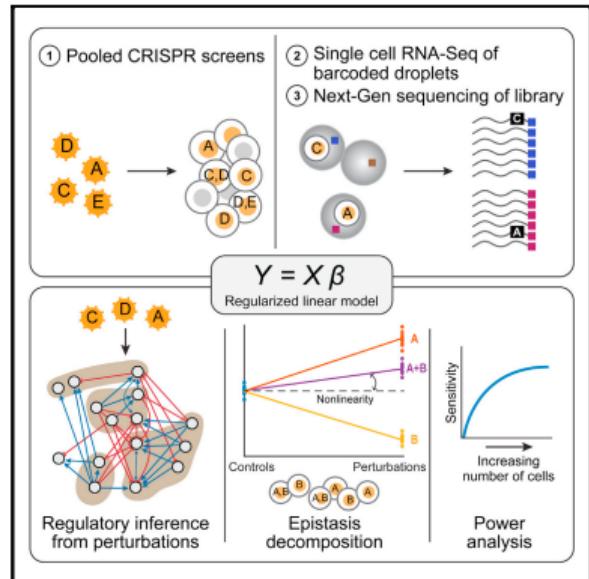


Perturb-sequencing

Cell

Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens

Graphical Abstract



Resource

Authors

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Correspondence

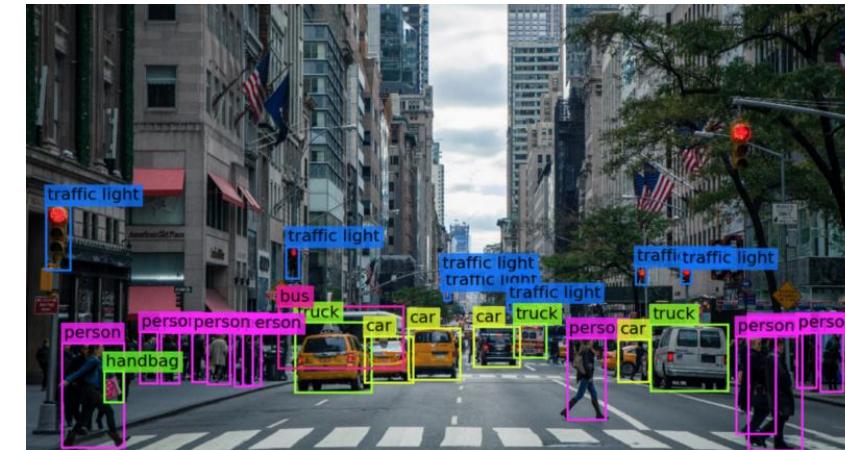
aregev@broadinstitute.org

In Brief

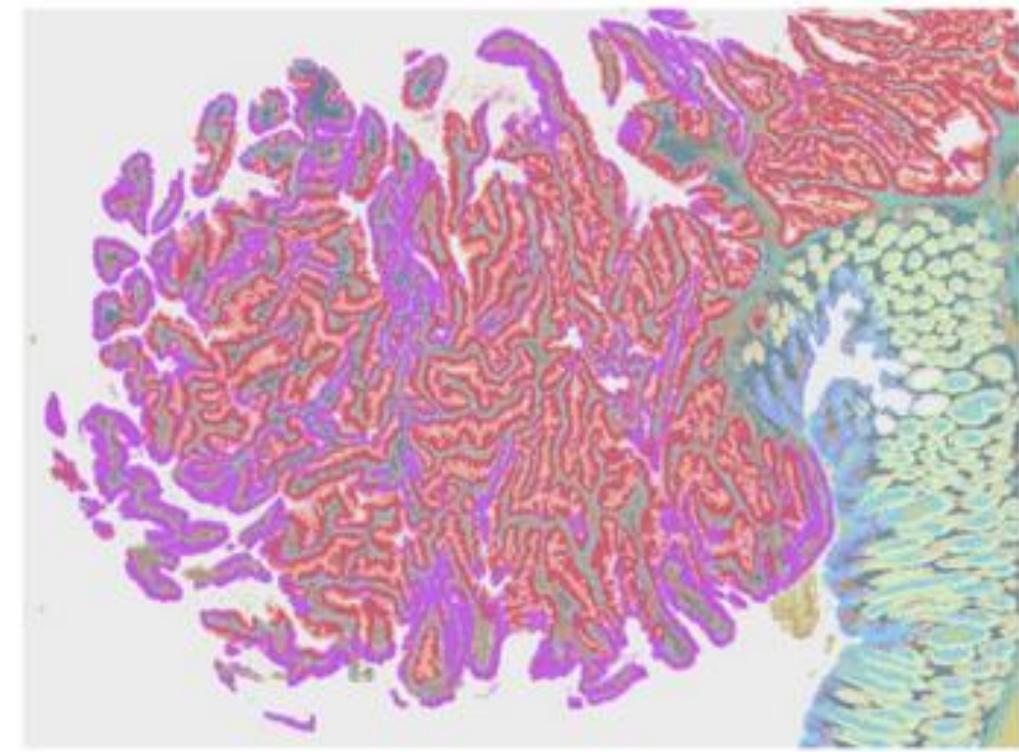
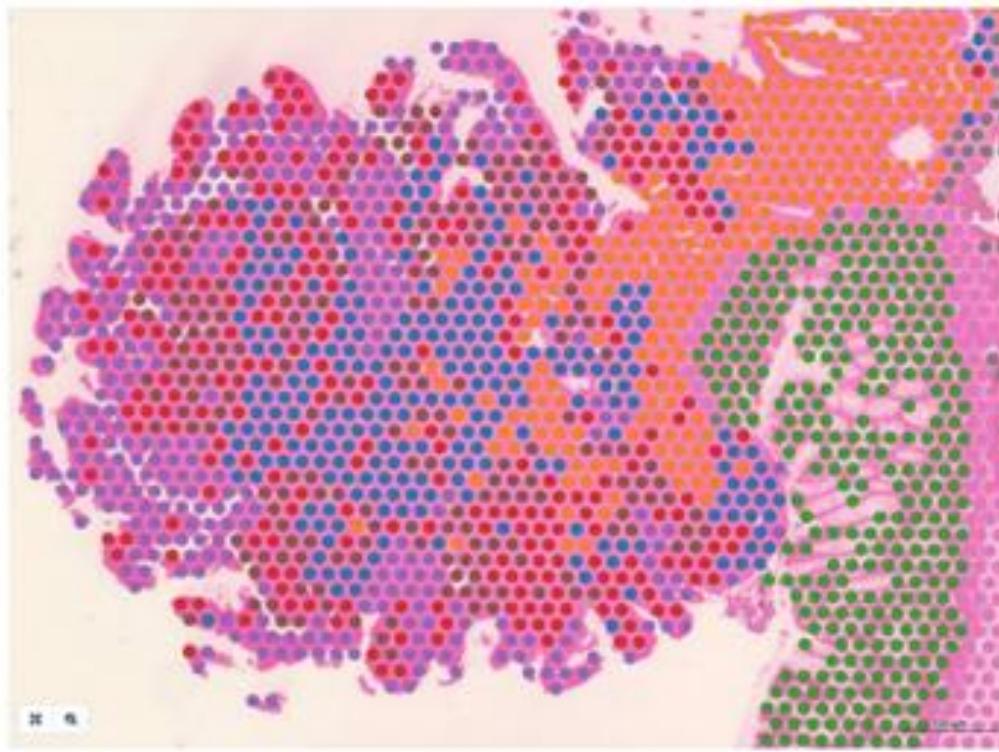
A technology combining single-cell RNA sequencing with CRISPR-based perturbations termed Perturb-seq makes analyzing complex phenotypes at a large scale possible



OpenAI
ChatGPT 4.0



Spatial transcriptomics



Homepage:
<https://jaewon-cho.github.io/>

System Single-cell Biology Lab

Research Publications News People Resources Job Opportunities Contact **Teaching**



!!Submit a **summary of research** (1 or 2 sentences)

Lab information

→ Tell your preference

- 1) Mid-term presentation (scRNA + CITE/Immune)
- 2) Final presentation (others)
 - 15 minute-presentation
 - < 25 minutes including Q&A