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CytoTrace2: Methods and Systems for Determining Phenotypic States from Genomic Data with Interpretable AI

Researchers at Stanford have developed a novel deep-learning-based tool called CytoTRACE2 that interprets single-cell RNA sequencing (scRNA-seq) to enable the discovery of regenerative cells across all tissue types and novel targets in cancer and other diseases.

CytoTRACE2 has been validated across 31 human and mouse scRNA-seq datasets encompassing 28 tissue types, outperforming existing methods in recapitulating experimentally determined potency levels and differentiation states. Moreover, it reconstructed the temporal hierarchy of mouse embryogenesis across 62 timepoints and facilitated discovery of cellular phenotypes in cancer linked to survival and immunotherapy resistance.

This technology has broad applicability for drug and biomarker discovery for diseases where developmental phenotypes and hierarchies play a role, especially cancer. It is also a powerful research tool for understanding the biology of these phenotypically complex diseases.

Stage of Development
Prototype

Applications

- Drug & target discovery platform for cancer & other diseases involving developmental phenotypes
- Discovery and measurement of disease-relevant biomarkers

- Research tool for discovering molecular features underlying complex biological phenotypes
- Research tool for optimizing stem cell biology experiments

Advantages

- Powerful: Direct biological interpretability from complex single cell RNA sequencing data
- Novel: No existing methods can predict cell potency (absolute developmental potential) from single-cell RNA sequencing data
- General: Discovery and recovery of nuanced molecular programs from any genomic data type

Patents

- Published Application: WO2025188815

Innovators

- Aaron Newman
- Minji Kang
- Gunsagar Gulati
- Jose Almagro Armenteros
- Erin Brown

Licensing Contact

Sam Rubin

Licensing Associate, Life Science

Email