scLT-kit: a versatile toolkit for automated processing and analysis of single-cell lineage tracing data

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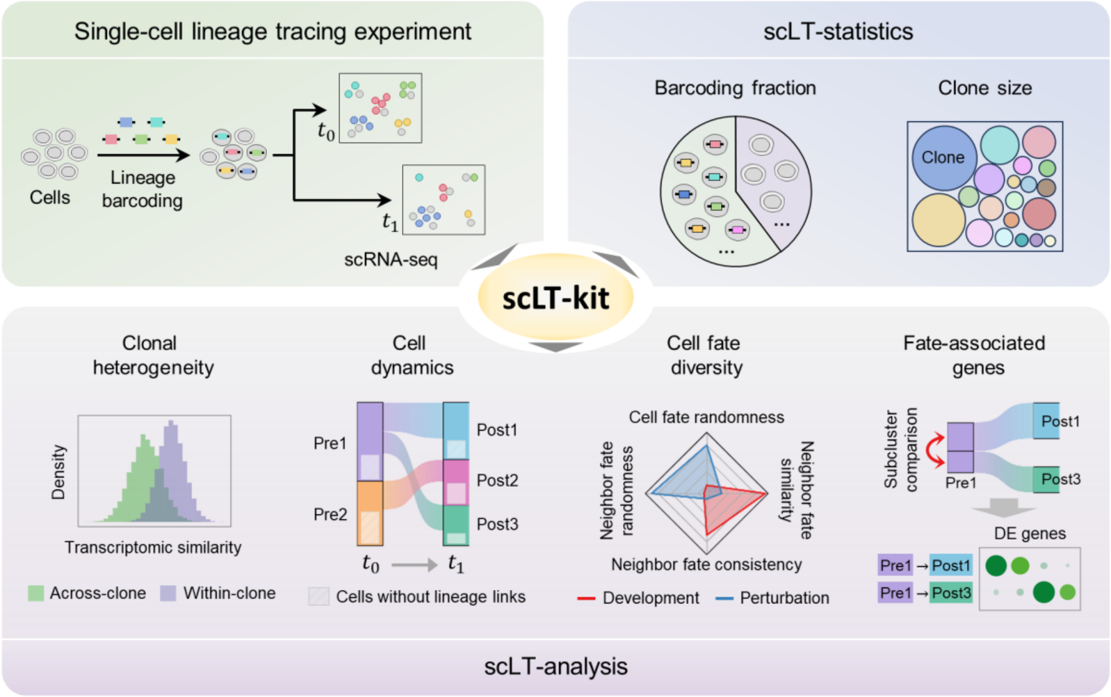
Problems & Ideas

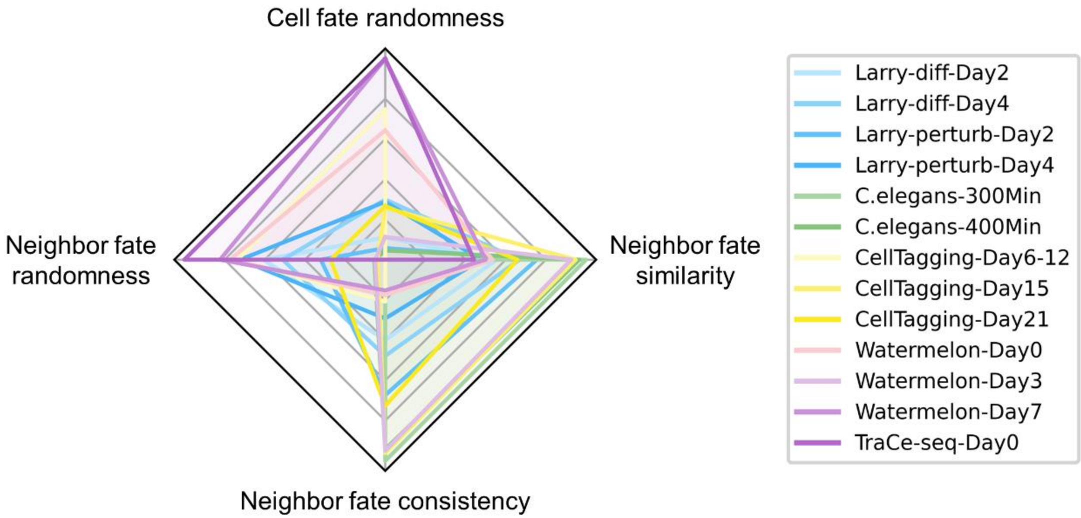
- Problems of single-cell lineage tracing data analysis:
  - Diverse data features.
  - Complex cell dynamics.
- Ideas: A user-friendly Python package, named scLT-kit, for automated processing and analysis of scLT data.



The workflow of scLT-kit. Based on the time-series lineage tracing single-cell data (top left panel), scLT-kit calculates the barcoding fraction and clone sizes (top right panel, scLT-statistics module), and analyze clonal heterogeneity, cell dynamics, cell fate diversity, and fate-associated genes (bottom panel, scLT-analysis module).

Main Contributions

- Contributions:
  - An overview of data quality and features (barcoding fraction, clone size, etc.) of scLT data.
  - Comprehensive perspectives for cell dynamics, including clonal heterogeneity, dynamic relationships, fate diversity, and the mechanisms governing cell fates.
  - Systemic comparation between the dynamic characteristics in normal developmental processes with those occurring in response to external perturbations.



Radar plot displaying the indicators of cell fate diversity in developmental datasets and tumor drug response datasets.