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THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY
Division of Life Science
and
Department of Chemical & Biological Engineering

Exploring Biological Dynamical Processes using Topological Data Analysis applied to Single Cell Expression Data

by

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Abstract

Transcriptional programs control cellular lineage commitment and differentiation during development. Understanding of cell fate has been advanced by studying single-cell RNA-sequencing (RNA-seq) but is limited by the assumptions of current analytic methods regarding the structure of data. We present single-cell topological data analysis (scTDA), an algorithm for topology-based computational analyses to study temporal, unbiased transcriptional regulation. Unlike other methods, scTDA is a nonlinear, model-independent, unsupervised statistical framework that can characterize transient cellular states. We applied scTDA to the analysis of murine embryonic stem cell (mESC) differentiation in vitro in response to inducers of motor neuron differentiation. scTDA resolved asynchrony and continuity in cellular identity over time and identified four transient states (pluripotent, precursor, progenitor, and fully differentiated cells) based on changes in stage-dependent combinations of transcription factors, RNA-binding proteins, and long noncoding RNAs (lncRNAs). scTDA can be applied to study asynchronous cellular responses to either developmental cues or environmental perturbations.

Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development. *Nature Biotechnology*. 2017 May. doi:10.1038/nbt.3854.

Date : 6 November 2017 (Monday)
Time : 5:00 - 6:00pm
Venue : Lecture Theatre K (Lift No. 31-32)
Host : Dr. Jiguang WANG

All Are Welcome!