Deep Learning Framework to Predict Gene Expression

Tech ID: 32918 / UC Case 2022-826-0

BACKGROUND

The gene expression profile of a cell can indicate the current status of the cell, such as its cell type, proliferation status, and degree of maturation or differentiation. The health of a cell in tissues is always in transition, such as diseased state (e.g., tumor cells), healthy state, and states in between. To fully understand and leverage the nature and pathways of cell states towards better diagnosis, treatment, and medical outcomes, it may be beneficial to forecast cell health as a function of certain gene-related configuration. Traditionally it has been difficult to predict ad hoc whole transcriptome alterations caused by gene-related perturbations.

TECHNOLOGY DESCRIPTION

To overcome this research challenge, investigators at UC Santa Cruz (UCSC) have developed a modeling framework to predict whole transcriptome alterations caused by perturbations. Building on the Variational Autoencoder (VAE) and certain RNA sequencing techniques, the UCSC researchers measure certain gene expression profile (transcriptome) with high precision and accuracy. These measurements correlate with certain transcription factor (TF) activity from the thousands of genes in a cell. By leveraging VAE's deep learning means, UCSC's *in silico* perturbation approach can use candidate TFs of interest to simulate genetic or chemical perturbations on TFs, resulting in the prediction gene expression alterations. Preliminary research results hold promise in terms of deploying efficient and powerful strategies for gene expression experimentation and profiling.

APPLICATIONS

- cell research
- genome engineering
- drug discovery

ADVANTAGES

- no specialized hardware for setup
- can be used with a broad range of cell types

INTELLECTUAL PROPERTY INFORMATION

Country	Type	Number	Dated	Case
Patent Cooperation Treaty	Reference for National Filings	WO 2024/025950	02/01/2024	2022-826

Patent Pending

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OTHER INFORMATION

KEYWORDS

genetics, gene expression, transcriptome, Variational Autoencoder, VAE, drug discovery, transcription factor, perturbations, perturbation, gene perturbations, prediction, multiomics, multi-omics

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Genomics
- **Computer**
  - Software

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