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Dpath: a novel software for classification and quantification of cellular states in single-cell transcriptomics

A software for classification and quantification of cell types during stage transitions from stem cells to differentiated cells. This software can further classify and quantify the progenitor and committed states in single-cell RNA-sequence data in a non-biased manner.

IP Status: US Patent Issued; Issued Patent No. 11,127,484

Applications

- Independent post-processing software for transcriptomic data analysis for developmental, stem cell and cancer biologists interested in cellular differentiation.

Key Benefits & Differentiators

- **Cell ranking based on differentiation potential:** The novel method of metagene entropy allows accurate classification of cells
- **Quantitative assessment of progenitor and committed cell states:** The self-organizing map (SOM) and random walk with restart (RWR) algorithms embedded in Dpath can separate progenitor from differentiated cells and reconstruct the lineage hierarchies in an unbiased manner
- **Facilitates speed and resolution of single-cell RNA-seq data analysis** Dpath addresses the problem of dropout events using a weighted Poisson non-negative matrix factorization (wp-NMF) method and provides fast and high resolution single-cell transcriptomics

Technology Summary

Single-cell RNA sequencing represents a transformational advance for global gene analyses. However, technical hurdles such as the computational management of dropout events, the reconstruction of biological pathways, and the isolation of target cell populations have not been fully resolved yet. Researchers at the University of Minnesota have developed a novel program called Dpath that can successfully address the dropout events, quantitatively assess the cellular states, and prioritizes genes for both progenitor and committed cellular states. This post processing software constitutes a powerful tool for biologists interested in cellular differentiation.

Unlike existing software, Dpath uses metagene entropy to rank cells based on their differentiation potential. Dpath uses the self-organizing map (SOM) and the random walk with restart (RWR) algorithms to separate the progenitors from the differentiated cells and reconstruct the lineage hierarchies in an unbiased manner. This software also resolves the problem of dropout events by using a weighted Poisson non-negative matrix factorization (wp-NMF) method. This novel software is easy to use, and provides fast and high resolution single-cell transcriptomics. The Dpath software is a valuable tool for developmental, stem cell and cancer biologists and can further discoveries in the biological mechanisms that govern stem cell

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Category
Life Sciences/Diagnostics & Imaging
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Software & IT/Algorithms
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and progenitor cell populations.

Phase of Development

TRL: 4-6

A complete version of Dpath has been developed as an R package and tested. A direct comparison with commonly used factorization methods and pseudotime inference algorithms have demonstrated the superiority of the Dpath program.Dpath was tested using single cells from Etv2-EYFP transgenic mouse embryos and revealed specific molecular pathways that directed differentiation programs involving the haemato-endothelial lineages.

Desired Partnerships

This technology is now available for:

- License
- Sponsored research
- Co-development

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Researchers

- **Daniel Garry, MD, PhD** Professor of Medicine, Lillehei Heart Institute
- **Wuming Gong, PhD** Assistant Professor, Department of Medicine
- **Naoko Koyano-Nakagawa, PhD,MS** Associate Professor, Department of Medicine

References

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