Data visualization algorithm reduces dimensions and retains high resolution

Single-cell technologies reveal many details about diseased and normal tissue, producing high-dimensional biological data. Unfortunately, algorithms to visualize high-dimensional data often lose important information on data structure. This technology is an algorithm, viSNE, that maps high-dimensional data into a 2-D representation with color as a third dimension, without simplifying or clustering the input data. The technology provides an elegant method of viewing data from flow cytometry and other high-throughput, single-cell methods, allowing users to identify rare subsets of cells, track tumor progression, and study tumor heterogeneity. By reducing dimensionality while retaining relationships among cells, viSNE promotes applications in many fields, including oncology and biomedical research.

Algorithm produces a single map that retains local and global data geometry, preserving information in a human-readable visualization.

This technology achieves the difficult task of reducing high-dimensional single cell data to a 2-D plot that retains relationships between cells. While standard algorithms that use linear dimensionality reduction do not account for the relationship between points in high-dimensional space, viSNE performs nonlinear dimensionality reduction based on t-distributed stochastic neighbor embedding (t-SNE). This technology assigns each cell a coordinate in high-dimensional space, grouping very similar cells into a single point, and then projecting into a lower dimensional space. To reduce overcrowding in the low-dimension representation, this technology can subsample data while projecting.

A prototype of the technology has been tested on flow cytometry data and was able to identify acute lymphoblastic leukemia cells from normal cells in a simulation of minimal residual disease detection. This technology was also able to accurately group other subsets of cells and enable high-resolution analysis of cancer cell samples.

Lead Inventor:

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Applications:

- Visualizes flow cytometry and other single cell data
- Detects minimal residual disease (MRD) cell subpopulations
- Identifies rare cell populations
- Tracks tumor progression
- Analyzes tumor heterogeneity
- Visualizes single-cell gene expression data

Advantages:

- Retains high-dimensional geometry of cells
- Single map retains input data’s nonlinearity
- Robust algorithm distinguishes cell subpopulations across different technologies and biomarkers
- Identifies multivariate relationships within data that are often missed with pairwise cytometry plots

Patent Information:

Patent Pending (US 20140336942) Tech Ventures Reference: IR CU13134

Related Publications:


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Images: Turn in images in separate files; put labels, alt-text, and captions here.

Image name: acute myeloid leukemia cell mapping.png Alt-text: visualization of AML single cells using viSNE Caption: viSNE mapped single cell AML data in low dimensional space to reveal specific cell types and expression patterns Source: Published Patent Application

Inventors

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