Studying cells in reduced dimensions

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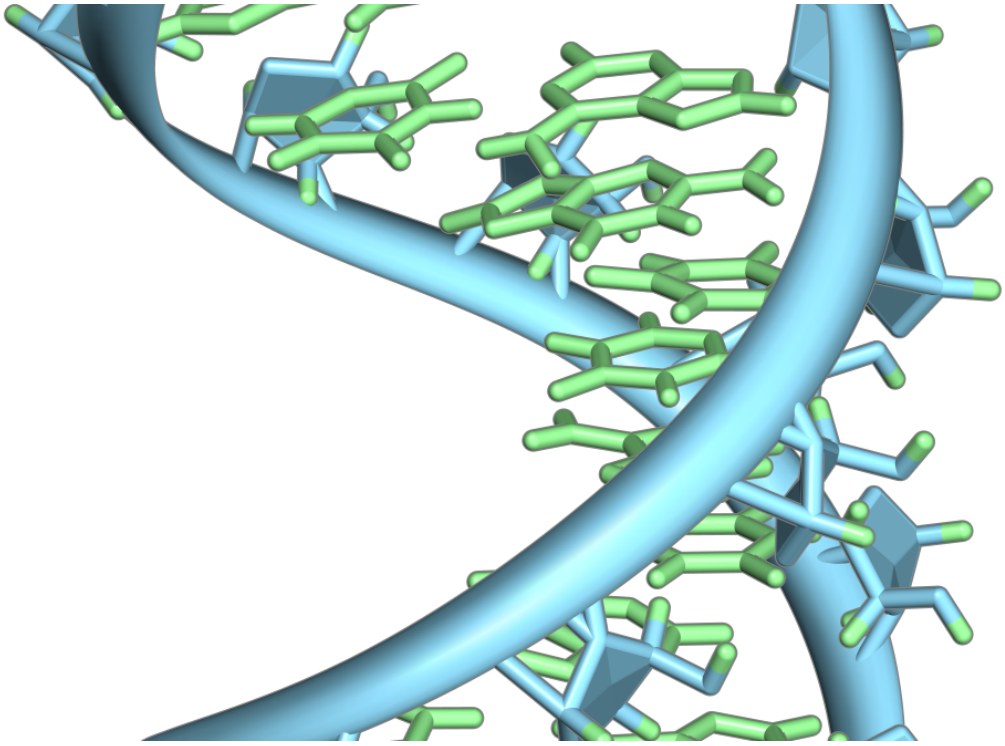

A hairpin loop from a pre-mRNA. Highlighted are the nucleobases (green) and the ribose-phosphate backbone (blue). Note that this is a single strand of RNA that folds back upon itself. Credit: Vossman/ Wikipedia

Single-cell RNA sequencing is a powerful tool for identifying transcriptomic variations and developmental trajectories in cell types that determine the course of diseases like cancer, with the goal of eventually improving diagnosis and treatment.

To aid visualization and analysis, computational techniques have been developed that provide low-dimensional representations of single-cell data. However, these techniques can result in dampened or exaggerated similarities between cells.

Maintenance of global and local structure inherent to each single-cell dataset is central to producing reliable low-dimensional representations for downstream analyses.

Now Cody Heiser and Ken Lau, Ph.D., have developed an unbiased, quantitative framework for evaluating the preservation of single-cell data structure by various "dimensionality reduction" techniques.

Writing in the journal *Cell Reports*, they suggest that the performance of these techniques can be determined by evaluating alterations to underlying data distributions. They show that the relative performance of dimensionality reduction tools such as t-SNE and UMAP varies as a function of data types and measurement modalities used.

More information: Cody N. Heiser et al. A Quantitative Framework for Evaluating Single-Cell Data Structure Preservation by Dimensionality Reduction Techniques, *Cell Reports* (2020). DOI: 10.1016/j.celrep.2020.107576

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