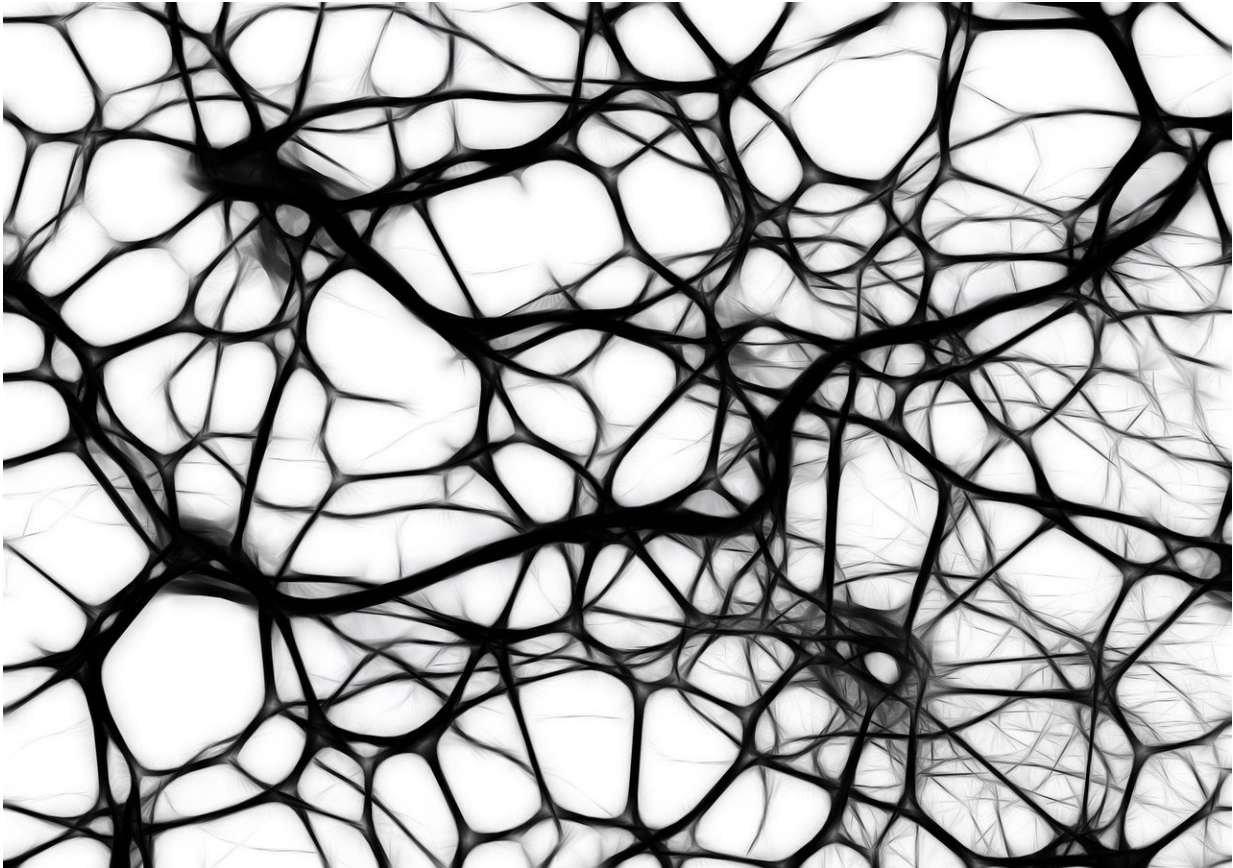


Analyzing single-cell landscapes

December 3 2018, by Leigh Macmillan



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Single-cell RNA sequencing is a powerful tool for studying cellular diversity, for example in cancer where varied tumor cell types determine diagnosis, prognosis and response to therapy. Single-cell technologies generate hundreds to thousands of data points per sample, generating a

need for new methods to define cell populations across different single-cell landscapes.

Qi Liu, Ph.D., Ken Lau, Ph.D., and colleagues have developed a new tool, sc-UniFrac, to quantify diverse cell types in single-cell studies. The tool compares hierarchical trees that represent single-cell landscapes and allows [cells](#) that drive differences to be identified as unbalanced branches on the trees.

Reporting in *PLOS Biology*, the investigators demonstrated the utility of sc-UniFrac in multiple applications, including regional specification of brain cells and identification of altered cells in tumor samples. The authors expect that sc-UniFrac will facilitate single-cell studies, in particular studies aimed at tracking how tumor [cell populations](#) evolve during [disease progression](#) and respond to drug treatments.

More information: Qi Liu et al. Quantitative assessment of cell population diversity in single-cell landscapes, *PLOS Biology* (2018). [DOI: 10.1371/journal.pbio.2006687](https://doi.org/10.1371/journal.pbio.2006687)

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