# Path\_Metrics\_Clustering\_R

Here we provide source code for a clustering and visualization method for single-cell RNA-seq data sets, that exploits \*\*path metrics\*\*. Using this method, distances between cells are measured in a data-driven way that is both density-sensitive (decreasing distances across high-density regions) and respects the underlying data geometry.

By combining path metrics with multidimensional scaling, a low-dimensional embedding of the data is obtained, which respects both the global geometry of the data and preserves cluster structure.