

MIT Bioinformatics Seminar

Association plots, joint clustering and embedding of genes and cells

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Single-cell transcriptome analysis poses many problems in visualizing and analyzing data. Based on the geometric interpretation of correspondence analysis biplots we define "Association Plots" to depict genes that characterize ("are associated with") a cluster of cells. We further develop this geometric intuition into a method to build a nearest-neighbor graph that encompasses both genes and cells. Using this data structure one can apply clustering and embedding methods which then naturally show clusters of cells together with their associated genes. The principles of this analyses are not restricted to single-cell transcriptomics, but should apply to any data in the form of a contingency table.