

Model-based clustering for cytometry

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High-dimensional flow and mass cytometry allow to measure the expression of several proteins on tens of thousands of immune cells of a patient. A common task is to predict patients disease status. This can be done based on characteristics of the cells clusters of each patient. Hence the need for clustering methods.

Some constraints make this problem challenging. The clusters of cells need to be interpretable as biologically meaningful profiles. Also, interesting groups of cells are typically rare populations.

We propose a procedure relying on model-based clustering and merging of clusters.

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