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Methods for guiding projection pursuit clustering and matching clusters over samples

The technologies described in this patent address a critically important deficit in the statistical methods available to enable comparison of outcomes measured by flow cytometry or similar, data intensive technologies. Most of flow and mass cytometry applications are based on comparison between control and experiment sample(s) to reveal (dis)similarity(s) due to drug treatment, progression of disease, response to radiotherapy, etc. To define these dissimilarities across samples, the populations of cells in each sample are usually clustered to reveal phenotypically distinct cell subsets that can then be matched, quantified and compared between samples.

We developed computationally efficient cluster matching method based on the quadratic form (QF) distance metric. For a given cell cluster defined in one sample, QF allows one to find a matching cluster in another sample in multidimensional space.

Applications

- These technologies can be used with any method that enables identification and isolation of cellular (or other) subsets on/in which markers are expressed, e.g., flow cytometry, mass cytometry.

Advantages

- The accuracy of QF is independent of population shape (Gaussian, skewed, bimodal, etc.);

- This method accommodates cases when the location of a population varies significantly from sample to sample in two-dimensional display, or when populations disappear or appear between samples;
- It is computationally efficient.

Patents

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