

Flow Cytometry Data Assessment with L2 Discrepancy Learning Process

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We developed a L2 discrepancy learning process to assess how flow cytometry data are spatially distributed. This discrepancy learning process is able to recover the spatial distribution where the individual events are either clumped or scarce. It is simple to numerically implement and provides a quantitative level of information to track the most outliers [Khettabi 2007]. We applied the L2 discrepancy learning process to K-Means clustering method. The discrepancy K-Means does not require the estimation of the number of clusters or other parameters and the L2 discrepancy learning process defines the means/modes as insiders automatically.

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References:

F. El Khettabi and P. Kyriakidis, the L2 Discrepancy Framework to Mine High-Throughput Screening Data for Targeted Drug Discovery: Application to AIDS Antiviral Activity Data of The National Cancer Institute, Data Mining for Biomedical Informatics, in conjunction with the 7th SIAM International Conference on Data Mining(SDM 2007).