

Visualization of metabolomics data

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In my talk, I will give an overview about modern machine learning techniques for analysing the huge number of features in metabolite data. I will introduce Independent Component Analysis (ICA) as a useful alternative to classical Principal Component Analysis. I will show in which cases a Support Vector Machine (SVM) can be appropriate for biomarker detection. And I will talk about time course analysis and how to analysis and visualize the nonlinear data structure. This will be completed by showing some examples in Matlab.