Identification of presynaptic gene clusters in synaptic signaling using functional data from genetic perturbation studies in Hippocampal autapses.

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Synaptic gene function is typically studied by measuring the effect of a (genetic) perturbation of a gene of interest on synaptic transmission. To date, many presynaptic genes are analyzed in this manner but a general framework to interpret multidimensional data sets at a systems level is lacking. We propose a new method to identify clusters of genes with similar function in the synaptic signaling process. Our method allows comparison of quantitative functional data measured under different experimental conditions, can deal with incomplete data sets, and takes into account the accuracy of data. We retrieved functional data about 58 genetic perturbations of 24 synaptic genes from 37 studies in Hippocampal autapses. Data was clustered using a mixture of probabilistic principal component analysis (PCA) (MOP) combined with Ward's hierarchical clustering algorithm. The algorithm produced stable clustering for different clustering conditions resulting in three main clusters that were in good accordance with the current view on the synaptic function of these genes, thereby validating the method. This method is generally applicable to biological systems and is expected to reveal more specific functional gene groups when more functional data on synaptic genes becomes available.