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Welcome to a labolution-The application of data mining and systems biology for personalized medicine

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High-throughput technologies ranging from high-content microscopy screening to automated mass spectrometry pipelines and peptide microarray assays enable the generation of big medical data sets in a brief period of time with the requirement of very small analyte volumes. As a result, extremely large multiomics data sets can be generated which are ideally suited for statistical learning procedures using well established classifiers such as random forests or multivariate logistic regression models. To extract meaningful information from the data, a major challenge comprises the dimensionality reduction and unsupervised pattern recognition via machine learning algorithms including Fisher discriminant analysis, shrunken centroid analysis or clustering. Another problem to be tackled is represented by multivariate feature collinearities and ways have to be identified to remove this ambiguity. Yet, the reward for this mathematical rigor is the generation of reliable classifiers which can quickly stratify individual patients into disease/treatment subpopulations with acceptable sensitivity and specificity from multiomics data sets. Above all, technology suppliers such as opentrons and Oxford Nanopore Technologies promise the automated generation of multiomics data sets for a reasonable price.

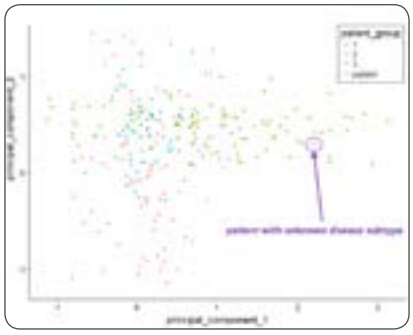

Figure 1: Example data: principal component analysis of simulated peptide microarray data of corresponding to serum responses from different patient collectives. The groups correspond to the microarray serum signals detected for patients with different known pathogenic subtypes of the disease. The principal component dimensionality reduced data is used for the training of classifiers such as random forests or multiple logistic regression models. The PCA data for a patient serum with unknown disease subtype is shown

Biography

Christoph Hiemenz has completed his MSc from Ruprecht-Karls University Heidelberg. He work as a bioinformatician at PEPperPRINT GmbH and is the scientific instructor of the iGEM Team Heidelberg 2019. He has worked on diverse research projects:

-DKFZ Heidelberg, Prof. Jörg Hoheisel- Kinase activity profiling with peptide arrays

-BioQuant Heidelberg, Prof. Roland Eils/Prof. Barbara Di Ventura- Optogenetic nuclear protein shutteling and ODE modeling

-KTH Stockholm, Prof. Stefan Ståhl – Surface functionalization of E.coli cells via sortases and inteins

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