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MIMOmics

Methods for Integrated Analysis of Multi-Omics Data Sets

MIMOmics is based on our involvement in studies participating in EU funded projects, i.e. GEHA, IDEAL, Mark-Age, ENGAGE and EuroSpan. In these consortia the primary goal is to identify molecular profiles that monitor and explain complex traits with novel findings so far. Support for methodological development is missing. The state-of-the-art methodology does not match by far the complexity of the biological problem. Complex data are being analysed in a rather simple way which misses the opportunity to uncover combinations of predictive profiles among the omics data.

The objectives of MIMOmics are: to develop a statistical framework of methods for all analysis steps needed for identifying and interpreting omics-based biomarkers; and to integrate data derived from multiple omics platforms across several study designs and populations. Specific steps include: experimental design; pipelines for data gathering; cleaning of noisy spectra; predictive modeling of biomarkers; meta analysis; and causality assessment. To enhance our understanding, systems approaches will be considered for pathways and structural modelling of biological networks. The major challenge in the joint analysis of omics datasets will be to develop methods that deal with the high dimensionality, noisy spectral data, heterogeneity, and structure of these datasets.

To perform these tasks successfully we bring together established EU academic and industrial researchers in metabolomics, glycomics, biostatistics, bioinformatics, scientific computing and epidemiology, with complementary expertise. A key feature of our project is the validation of novel methodology by performing a proof of principle (Metabolic Health) . Special effort will be made for rapid uptake of methods by communication with associated consortia and development of user-friendly software.