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High-throughput bioinformatics for large-scale proteomics

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The life sciences are being revolutionized by major technological developments that are taking place since the past decade. This transition allowed to move from the analysis of individual genes, transcripts and proteins to whole-genome, -transcriptome and -proteome studies. The technological advances, however, are widening the gap between data production and data analysis. In many cases manual data analysis is not possible and dedicated software is required to analyze the high-throughput data in an automated fashion. This requires efficient bioinformatics methods, robust tools and innovative statistical approaches. Furthermore, besides the analysis of single data sets, an important next step will be the integration of diverse data types collected at different levels of biological organization.

We established new ways to integrate and analysis modern high-throughput data with state-of-the-art bioinformatics methods. The presented work will focus on bioinformatics methods for the rapid processing of large proteomics datasets and their integration with other OMICS technologies. We apply modern ways for distributed data storage, data-and project management and a portal-based user interface for the construction and execution of processing and analysis workflows. These workflows range from the generation of quality control measures, over different quantification methods and peptide/protein identification to statistical and downstream analysis (e.g., pathway mapping). Fast turn-around times can be guaranteed through dedicated workflow systems and a high-performance-computing cluster. Furthermore, visualization portlets for proteomics data to enable efficient scientific collaboration. We show that our established infrastructure is especially dedicated to large, heterogeneous and distributed proteomics studies.

Biography

Sven Nahnsen has completed BSc degree in Biomathematics from the University of Greifswald, Germany, a MSc degree in Biotechnology from the University of Strasbourg, France and a PhD in Bioinformatics from the University of Tuebingen, Germany in 2010. After a short postdoc in the Computer Science Department of the same University, in 2012, he became the head of the Quantitative Biology Center in Tuebingen, Germany.

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