Computational Proteomics and Applied Bioinformatics

Forskningsleder Veit Schwämmle

Gruppens kerneforskningsområder

The Computational Proteomics Group develops and applies computational solutions for improved data analysis in large-scale omics experiments with focus on proteins and their post-translational modifications (PTMs).
We investigate functional protein states to determine, confirm and predict their contribution to cell behavior and disease.
Given the continuous increase in data amounts and availability, we implement solutions for large-scale (re)analysis and usage of deep learning (AI) tools.

Main research lines:
- *Analysis of data from protein mass spectrometry experiments*: development of software tools, implementation and benchmarking of workflows, PTM quantification
- *Tools for quantification and interpretation of omics data*: data clustering, statistical testing, smart visualization of complex data
- *Re-processing and integration of public data sets*: quantification of protein complexes, modifications, co-regulation across hundreds of cell types
- *Simulation of molecular pathways*: computer models for PTM crosstalk, moderated protein function and biological pathways.

Experience in programming, for example in R, is advised but not necessary
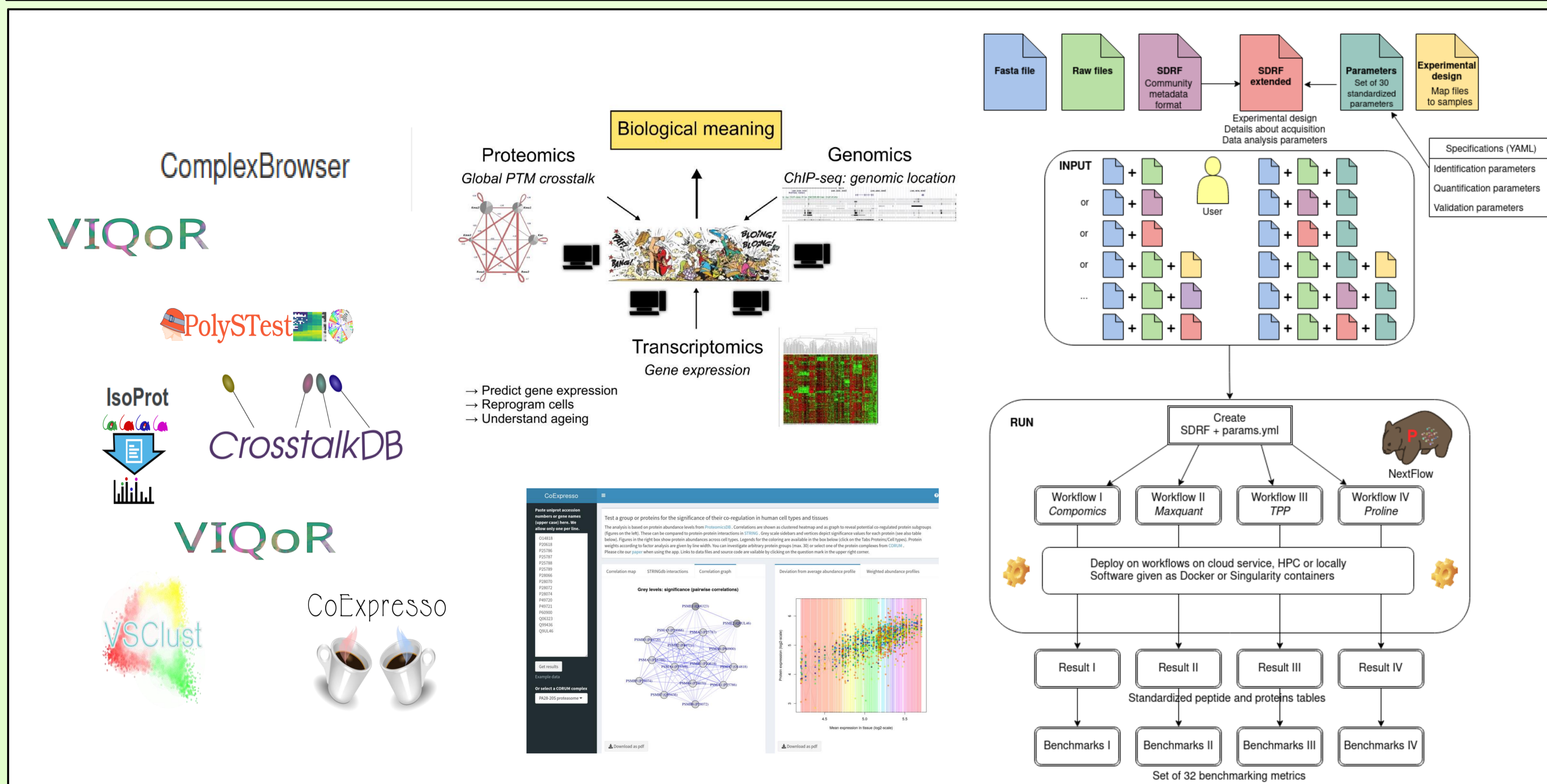
Er du interesseret i at skrive projekt i gruppen, så kontakt :
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Project	Description
Smart visualization of PTMomics data	Use smart and interactive visualization methods to help understanding protein function from complex multi-layered data, e.g. histone profiles for different tissues, histone variants, PTMs.
Biomarker detection in public proteomics data	Employ public tumor proteomics to identify and validate specific biomarkers for various tumor subtypes via machine learning on different data levels like PTMs, peptides, proteins and protein complexes.
Extracting peptide properties from AI models	Develop the "Great Hypothesis Tester", a tool designed to automate the generation and evaluation of hypotheses regarding the physicochemical characteristics of peptides. Do this by summarizing thousands of peptide features after predicting them with modern AI models.
Co-regulatory behavior of protein complexes	Use large-scale quantitative protein profiles to study the co-regulation of groups of proteins. Run rigorous statistical validation and investigate the role of post-translational modifications.
Data analysis with missing values	Develop novel algorithms designed to include missing values in omics data analysis without making assumptions that could compromise biological interpretation.
Lego Bioinformatics	Implement, test and run data analysis workflows that a built on the recent most powerful software tools, to be run on high-end computers for the analysis of thousands of samples.