Towards the rewiring of the proteome during blood development

T. Will[1,2] and V. Helms[1]

[1]Center for Bioinformatics, and [2]Graduate School of Computer Science, Saarland University, Saarbrücken, Germany

Protein–protein interaction networks (PPINs) are an important component of modern systems biology. Yet, comparatively few efforts have been made to tailor their topology to the actual cellular condition being studied. We developed PPIXpress, a network construction method that exploits expression data at the transcript-level and thus reveals alterations in protein connectivity not only caused by differential gene expression but also by alternative splicing [1]. We achieved this by establishing a direct correspondence between individual protein interactions and underlying domain interactions in the full but condition-unspecific PPIN. When we compared contextualized interaction networks of matched normal and tumor samples in breast cancer, our transcript-based construction identified more significant alterations that affected proteins associated with cancerogenesis than a method that only uses gene expression data [1]. As an extension of this work, we developed the differential PPIN tool PPICompare to compare the inferred interaction networks between samples of two groups. The tool determines statistically significant between-group rewiring events and their causes. A first application of the novel software is shown in the context of hematopoiesis. To our best knowledge this work represents the first study of rewiring processes of the protein interactome during development.

[1] T. Will and V. Helms, Bioinformatics, Vol. 32, P. 571-578 (2016).