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Integration of multilevel OMICs data based on the identification of regulatory modules

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Complex scientific experiments provide researchers with a wealth of data from heterogeneous sources. Analyzed in its entirety, omics data provide a deep insight into the overall cellular processes of organisms. However, the integration of data from different cellular levels is challenging. Thus, there is a need for approaches dealing with this issue and in this study, we make use of transcriptome, proteome and secretome data from the human pathogenic fungus *Aspergillus fumigatus* challenged with caspofungin. Caspofungin is an antifungal drug targeting the fungal cell wall leading to a compensatory stress response. We analyze the experimental data based on two different approaches: first, we apply a simple approach based on the comparison of differentially regulated genes and proteins; secondly, we compare the cellular levels based on the identification of regulatory modules from protein-protein interaction networks. Our results show that both approaches associate the fungal caspofungin response with biological pathways like cell wall biosynthesis and carbohydrate metabolism. Compared to results of the simple approach, the regulatory modules show a notably higher consistency between the levels. The additional structural information of the networks provided by the module-based approach allows for topological analysis and the analysis of the temporal evolution of response. However, the quality of the module-based results depends on the comprehensiveness of the underlying protein-protein interaction network itself. Thus, while our results highlight the benefits and potential of a module-based analysis of multilevel omics data, future studies will have to focus on the expansion of organism specific protein-protein interaction networks.

Biography

Theresia Conrad studied bioinformatics at the Friedrich Schiller University Jena, Germany. During her studies, she spent several years at the Centre for Innovation Competence Septomics of the Jena University Hospital and Friedrich Schiller University focusing on the exploration of septic infections in consideration of the PIRO-concept. In 2015, she was awarded a Jena School for Microbial Communication (JSMC) fellowship and started her PhD in Bioinformatics at the Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute. Her research focuses on developing multilevel models to obtain a deeper understanding of host-pathogen-interactions during fungal infections.

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