

## Computational models to integrate transcriptomic and proteomic data for predict abundance of undetected proteins

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The last decade has seen significant growth in technologies pertaining to molecular biological assays to measure gene expression profiles. However, evidence suggests that transcriptomic profiling is necessary but not sufficient to characterize biological system complexity. Therefore, in addition to studying gene expression at the transcriptional level, large-scale proteomic analysis should be considered as a means to understand the systems and pathways in living organisms. Integrated analysis of global scale transcriptomic and proteomic data can provide important insights into the metabolic mechanisms underlying complex biological systems. However, because the relationship between protein abundance and mRNA expression level is complicated by many cellular and physical processes, sophisticated statistical models need to be developed to capture their relationship. In the past several years, our group has been using transcriptomic and proteomics data generated from bacterial *Desulfovibrio vulgaris* and *Shewanella oneidensis* to develop novel statistical tools for integrative transcriptomic and proteomic analysis, and results showed that a better biological interpretation can be achieved by using these statistical methods.

### Biography

Dr. Zhang is a professor in School of Chemical Engineering and Technology of Tianjin University in China. Prior to joining Tianjin University, Prof. Zhang was a faculty with Biodesign Institute of Arizona State University, and a Senior Research Scientist II and Senior Principal Investigator at Microbiology Department with the Pacific Northwest National Laboratory of the U.S. Department of Energy (DOE). Dr. Zhang has broad research experience in microbial genetics, physiology and ecology, has authored more than 90 peer-reviewed papers. His recent research focuses on microbial metabolic engineering, applying metatranscriptomics and single-cell transcriptomics for complex microbial community, and developing computational tools for integrating various post-genomic datasets.