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Comparing and combining various pathway analysis bioinformatics tools in the proteomics and transcriptomics studies

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Abstract

Pathway analysis is an important approach to reveal the biological meaning of the multidimensional transcriptomics and proteomics data sets. Here, we will present the comparison of the capabilities and will demonstrate the advantage of combining several pathway analysis tools, including MetaCore (GeneGO, Thomson Reuters), Pathway Studio (Ariadne Genomics, Elsevier), GeneXplain platform (GeneXplain, GmbH) and PathOlogist (Greenblum *et al*) based on three proteomics and two transcriptomics case studies. The discussed proteomics case studies are: (i) label-free quantitative LC-MS proteomics study of Alzheimer's disease and normally aged human brains, (ii) the iTRAQ-labeled LC-MS/MS study of the dynamics of human plasma proteome during leptin replacement therapy in genetically based leptin deficiency, (iii) the spectral count proteomics of the adipose tissue dynamics in leptin replacement. The discussed transcriptomics studies are: (i) the peripheral blood gene expression analysis in intestinal transplantation in adult human patients, (ii) the peripheral blood gene expression analysis in intestinal transplantation in model animals (syngeneic and allogeneic rats) without immunosuppressant treatment.

Biography

Victor P Andreev, PhD is an Associate Professor at the Department of Psychiatry & Behavioral Sciences and Department of Biochemistry & Molecular Biology, University of Miami School of Medicine. Dr. Andreev is a bioinformatician and computational scientist with a strong background in mathematics, physics, and analytical chemistry. Prior to University of Miami, he worked for the Northeastern University, Boston, and prior to this for the Institute for Analytical Instrumentation, Russian Academy of Sciences, St. Petersburg, Russia. Dr. Andreev is a member of several editorial boards, including the Journal of Pharmacogenomics and Pharmacoproteomics.