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## MetDisease - A disease-centric view of metabolic networks

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Recent progress in the field of metabolomics has created an opportunity to advance our understanding of physiological and pathological processes. It also created a number of bioinformatics challenges associated with data analysis and interpretation. Experience with genomic data has shown that automated annotations linking genes, transcripts and proteins to published biomedical literature is useful for a wide range of bioinformatics applications including pathway analysis and identification of disease genes. With this in mind we recently developed Metab2MeSH, a web-based tool that uses a statistical approach (Fisher's exact test) to annotate compounds with Medical Subject Headings (MeSH) used by the National Library of Medicine to manually index articles for MEDLINE/PubMed. The resulting data set contains statistically significant associations (p-value<0.005) between compounds and MeSH terms linked to PubMed articles (http://metab2mesh.ncibi.org).

To demonstrate the utility of Metab2MeSH, we focused on the subset of MeSH terms related to disease and used them to annotate human metabolic networks. To visualize these data we developed MetDisease, a plugin for the open-source tool Cytoscape (http://cytoscape.org). MetDisease allows users to highlight and explore parts of metabolic networks related to one or more MeSH disease terms and provides links to relevant PubMed literature. It can be used in concert with our other Cytoscape plug-in, Metscape, used for visualizing metabolites, genes and pathways from experimental data, and visualize changes in the gene/metabolite data. MetDisease in combination with Metscape can help identify metabolites with known connection to diseases and link them to relevant PubMed articles.

### Biography

Dr. Karnovsky got her Ph.D. from Russian Academy of Sciences. She did postdoctoral work at the University of Colorado at Boulder, followed by nine years of bioinformatics research in pharmaceutical industry (at Pharmacia and at Pfizer). Since 2007 she has been a research investigator at the Center for Computational Medicine and Bioinformatics at the University of Michigan. Her research interests include analysis of high throughout omics data, focusing primarily on metabolomics, and the development of computational methods and tools for the analysis and integration of metabolomics data with other types of high throughput data.