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Integrative bioinformatics for knowledge discovery of PTM networks

Cathy H. Wu
University of Delaware, USA

Abstract

Facilitated by proteomic and other high-throughput studies, the number of protein phosphorylation related resources has been growing along with pertinent literature. However, our understanding of phosphorylation events in signaling networks is still fragmented. The iPTMnet (http://proteininformationresource.org/iPTMnet) is a new bioinformatics resource being developed for integrative understanding of protein post-translational modifications (PTMs) in systems biology context, with the initial focus on phosphorylation. The iPTMnet bioinformatics framework consists of: (i) the PIR iProClass database for molecular and omics data integration, including many phosphorylation, pathway, and interaction databases, (ii) the RLIMS-P/eFIP text mining system for knowledge extraction from scientific literature, (iii) the Protein Ontology (PRO) for knowledge representation of specific protein PTM forms, and (iv) a web portal linking data and analysis tools with Cytoscape network visualization for scientific queries and exploration. The text mining system allows researchers to provide a list of PubMed IDs or proteins of interest as input, and returns a ranked list of abstracts with evidence tagging for phosphsorylation information (kinase, substrate, phosphorylation site) and its functional impact, particularly interaction partners of phosphorylated proteins. The user interface further supports community annotation to validate text mining results and capture knowledge about PTM forms in PRO. A PTM database is under development to combine text mining results and data extracted from related databases to capture relevant kinase-substrate information and their functional impact and biological context. Scientific use cases have been developed to demonstrate the integrative bioinformatics approach for exploring and discovering PTM networks.

Biography

Cathy H. Wu is the Edward G. Jefferson Chair and Director of the Center for Bioinformatics & Computational Biology, Professor of Departments of Computer & Information Sciences and of Biological Sciences, and Director of Bioinformatics Graduate Programs at the University of Delaware. She has conducted bioinformatics research for over 20 years and led the Protein Information Resource (PIR) since 1999. She is the PI/Co-PI on several large consortium projects, has served on many scientific advisory boards, including the HUPO council, published about 180 peer-reviewed papers and eight books and conference proceedings, and given about 140 invited talks.