

An open-source tool for the integrated analysis, visualization and reconstruction of metabolic networks

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Genome-scale metabolic network models have become an important field of systems biology for understanding cellular behaviors. Three major components: network reconstruction, simulation and visualization are usually indispensable for a metabolic network model of high quality. Therefore, various bioinformatics tools were provided to facilitate the complicated needs. Although some of the required functions have been served separately by existing tools, a free software resource that simultaneously serves the needs of the three major components is not yet available. Here we present a software platform to provide functionalities of easy metabolic network drafting and editing, amenable network visualization for experimental data integration, and flux balance analysis tools for simulation studies. The tool comes with downloadable, ready-to-use public-domain metabolic models, reference metabolite/reaction databases, and metabolic network maps, all of which can be imported to the tool as the starting materials for network construction or simulation analyses. Furthermore, all of the metabolic models, analysis results and on-going projects generated by this tool can be easily exchanged in the research community. All together, the open-source tool is a powerful integrative resource that may facilitate the development of systems biology studies.

Biography

Yu-Chieh Liao has completed her Ph.D at National Cheng Kung University and postdoctoral studies at National Health Research Institutes in Taiwan. She is now an assistant investigator at National Health Research Institutes and working on the fields of bioinformatics and systems biology.