**Editorial**

# Biological Systems and Pathway Modeling Approaches

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## Editorial

Working together as a biomedical scientist, chemist, modelers, experimentalist, computational scientist, clinician and discuss how maultifactorial diseases (including cancer, cardiovascular disease, diabetes, multiple sclerosis, kidney diseases, sepsis, infection, neuro degeneration, immune-related and other disorders) in human and other living organisms can be modeled and analyzed with the current available knowledge sources [1-4].

Field experts covers the paradigm of genomic, proteomic, interactomic, molecular network modeling, pharmacokinetic, pharmacodynamic and agent based modeling in design and development of the conceptual frame work of metabolic pathway and analysis to view the diagrammatic representation of the disease model and further analysis and study of its core components. Successful modeling of disease, infection spread and implementation of concepts is greatly assisted by the data standards [5,6].

### Biological pathways and implications

Biological diagrams are optimum effort since ancestral period to till date in communicating the complex ideas of biological system [7]. Biological pathways signify a series of molecular interactions with in a cell at diverse circumstances and points that leads to the different biological functions. Internal chemical reactions are triggered by the signals from the external environment that affects the biological pathway to specific and responsible tasks. Activity such as phosphorylation and dephosphorylation in MAPK complex alters their function from deactivation to activation and vice-versa [8]. Over the last few decades due to the technical advancements and need of computational modeling has digged out a massive knowledge from the large experiments of genomics and proteomics [8].

Metabolic network expresses the relationship between gene, enzyme (proteins) and small biomolecules (metabolites) interactions that catalyzes a biochemical reaction or transports a metabolite in the system. Metabolic modeling and control network study in genome wide construction holds a central part in the systems biology [1,2].

### Pathway modeling approaches

Computational based modeling of biological pathway can be carried out using two types of modeling methods: mathematical modeling and network based analysis.

In mathematical modeling concept, the system learns and analyzes the network by transforming the reactions and entities in to the matrix form. Numerous mathematical formulation and approaches have been designed and developed to study and analyze the diverse biochemical pathway with their inter and intra interactions. Boolean network, Ordinary differential equation and stoichiometric methods are used to model large scale signaling pathway, genome scale network, metabolic pathway and small size gene regulatory networks [9].

Network based methods relate graph theory to discover and connect associations between nodes in the pathway, typical node and internodes interaction. Where each biological entity such as gene or protein represents a node and each edge represents the interaction type between the node pairs. The graph based network model could be a represented as directed or undirected graph. Bayesian networks are implemented in probabilistic graph model to learn cellular network from gene expression data [10] other networks such as Gaussian Network, Maximum Likelihood, Density Estimation, Helmholtz Machine, Latent Variable Models, Generative Topographic Mapping and Hidden Markov Model [11].

### Metabolic network databases and tools

Organism specific metabolic network databases such as EcoCyc (*E. coli*), HinCyc (H. influenza) and PseudoCyc (P. aeruginosa). Metabolic network database covering numerous group of organisms are KEGG, MPW and MetaCyc. Databases concentrate on single reaction are BRENDA, ENZYME, INTERACTOME, BioModel system. Numerous tools such as BioTapestry, Cytoscape, GenMapp, MEGA, PathVisio, Simbiology tool box by Matlab and etc are available to successfully model, analyze and study the genome, proteome and metabolome data.

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