



System Biology-A Computational Platform for Biological Research

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Abstract: System biology uses computational tools to assess and analyze how biological components interact with one another and it's surrounding in a precise manner displaying unique structural and functional characteristics to exhibit an appropriate response, contributing towards the stability of a specific biological system. Biological entities are dynamic and sophisticated.it is difficult to predict how these biological entities might behave when placed in a functional frame work. Therefore to investigate their systematic interacting properties, computational platform is utilized to describe and predict their dynamical behavior.

Keywords: HGP; Systems Biology Markup Language; Systems Biology Graphical Notation

1. INTRODUCTION

System biology is a subfield of bioinformatics which involves the use of mathematical and computational modelling to understand the dynamics of a biological system along with its interacting sub components for the precise representation of a functional biological system [1]. This discipline permits in silico interpretation of biological system by employing knowledge from different fields of science such as applied statistics, mathematics, informatics, engineering and life sciences. For example HGP (Human Genome Project) is one of the most significant contribution of this field [2, 3]. Employing mathematical and computational modeling approaches for data storage, for development of informatics tools for simulation, analysis and visualization of system units etc. Quantitative assessments of biological system is shaped in to valid mathematical models for the purpose of accurate analysis [4]. Therefore Systems Biology Markup Language (SBML) was designed for the development of computer-readable format for the representation of biological processes [5]. This computational language provides a unique format for addressing biological pathways using different tools that aids in exhibiting the biological framework with high reliability and accuracy [6, 7]. The graphical notation for the representation of biological processes has been proposed recently by Systems Biology Graphical Notation (SBGN) [8].As scientific research is increasing through the development of new technologies and instrumentation, biological databases such as primary and secondary have become an essential partner in such research for acquisition, management and analysis of biological information [9].Such *in silico* analysis of biological system is crucial since increasingly biological research relies on information science and hence is managed by computational tools and databases. Therefore, these systems biology databases are crucial for quantitative modeling of biological systems [10].Mathematical depiction of the biological pathway depends on the knowledge of the system and the aim of the modeling process [11]. Figure 1 illustrates how system biology works. System biology approaches for modeling biological pathways could be achieved either by means of network-based analysis or mathematical modeling [12]. Network-based analyzing approaches uses graph theory to determine relation among biological entity (nodes) in the pathways. Such nodal networks appeared as directed or undirected graphs e.g. probabilistic graph model [13]. Mathematical modeling on the other hand transforms the reactions and entities into matrix form [14].

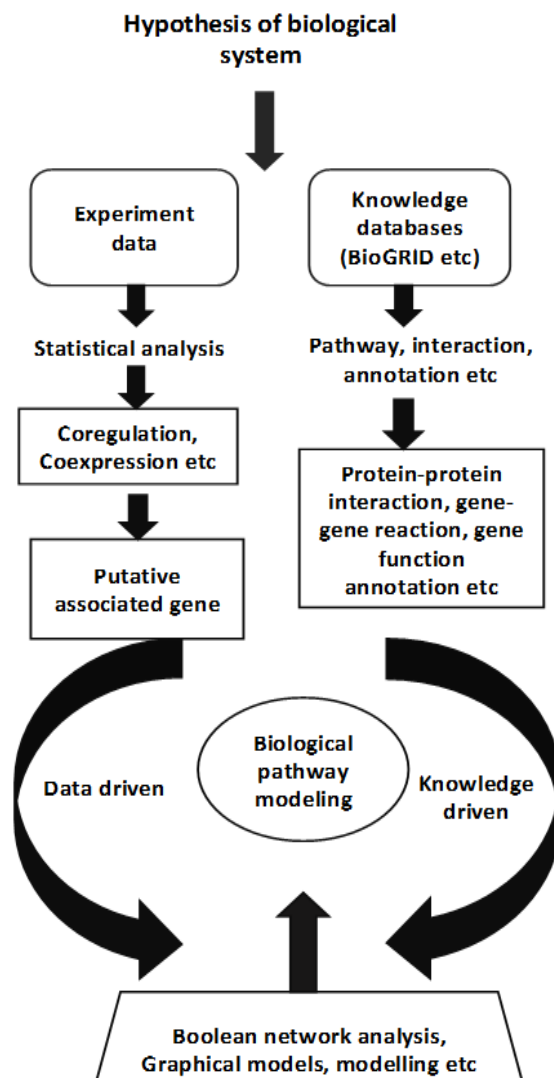


Figure1. Illustrates of system biology

Enlisted below is few system biology tools and database.

Table1. System biology tools and database

Bioinformatics tools for system biology	Purpose
BioFNet	Database for analysis and synthesis of biological systems [15]
BioModels Database	Warehouse of computational models of biological processes [16].
BioSystems	Database provides data on biological systems and their component [17].
ESCAPE Embryonic Stem Cells Atlas of Pluripotency Evidence	Integrates data based on mouse and human embryonic stem cells from diverse high-throughput studies [18]
Genome Proteome Search engine (GPSe)	Retrieve data from different biological databases [19]
InnateDB	Database providing information relating to signaling pathways involved in the innate immune responses[20]
IPAD	Database for Systematic Enrichment Analysis [21].
JWS Online Cellular Systems Modelling	Provides access to a database of curated models of biological systems [22]
KBase	Provides secure sharing of data, tools, and scientific conclusions in predictive and systems biology [23].
MEMOSys	Database for Genome-scale metabolic models [24].
PANTHER (Protein ANalysis Through Evolutionary Relationships)	Classify proteins (and their genes) [25].
PhosphoPep 2.0	Provides interactive cross-examination of MS-derived phosphorylation data from 4 different organisms [26].

Plant Systems Biology Modelling (PlaSMo)	Permit scientists to share reviews, annotations and enhancements of models [27].
PlateletWeb	For the analysis of platelet signaling [28].
SABIO-RK Biochemical Reaction Kinetics Database	Database that contains data about biochemical reactions, their kinetic rate etc [29].
SysMO-DB	For determining, sharing and exchanging data, models and processes in systems biology [30].
Systems Biology and Medicine Database (SBM DB)	Database of gene expression profiles [31].
Systems Biology Ontology (SBO)	Contain commonly used terms in Systems Biology [32].
SYSTOMONAS genome Database	Store data related to metabolome, proteome and transcriptome data and gene-regulatory networks [33].
The Systems Biology Researcher Database (SysBioDB)	Offers exchange of information worldwide for all systems biology scientists [34]

2. CONCLUSION

Therefore system biology provides a computational approach for understanding the fundamentals of biological pathways using different modeling tools for simulation and visualization of biological processes on computational platform

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