158. KBase Overview

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http://kbase.us

Project Goals: The KBase project aims to provide the computational capabilities needed to address the grand challenge of systems biology: to predict and ultimately design biological function. KBase enables users to collaboratively integrate the array of heterogeneous datasets, analysis tools and workflows needed to achieve a predictive understanding of biological systems. It incorporates functional genomic and metagenomic data for thousands of organisms, and diverse tools including (meta)genomic assembly, annotation, network inference and modeling, thereby allowing researchers to combine diverse lines of evidence to create increasingly accurate models of the physiology and community dynamics of microbes and plants. KBase will soon allow models to be compared to observations and dynamically revised. A new prototype Narrative interface lets users create a reproducible record of the data, computational steps and thought process leading from hypothesis to result in the form of interactive publications.

The Department of Energy (DOE) Systems Biology Knowledgebase (KBase) is an emerging computational environment that enables researchers to bring together the diverse data, algorithms, analytical tools, and workflows needed to achieve a predictive understanding of biological systems (see figure, KBase Overview). As a project supported by the Office of Biological and Environmental Research within the DOE Office of Science, KBase focuses on microbial and plant systems that support DOE missions in energy production and environmental science. However, the KBase approach to analyzing and modeling DOE-relevant microbes and plants can be applied to organisms from across the tree of life.
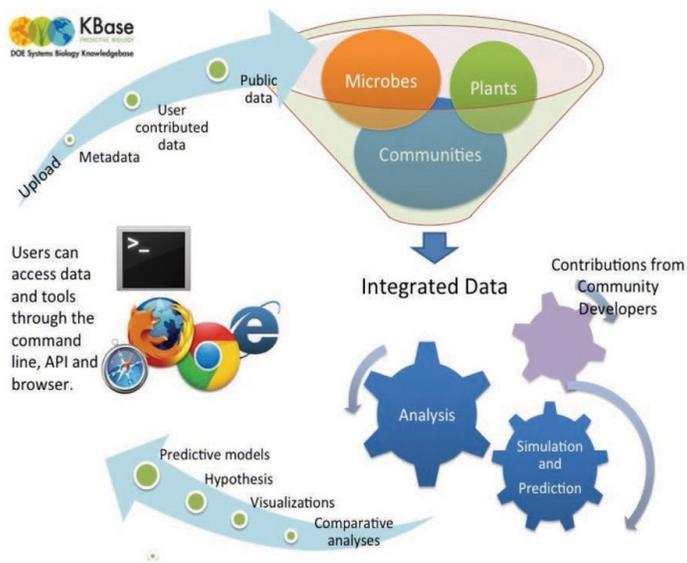
KBase Overview. This overview diagram shows how users interact with KBase by uploading biological data, analyzing it with tools developed by both KBase and the community, and using analysis results to drive experiments and a better understanding of biological systems.

KBase is also an open and extensible development environment that invites and trains community members to contribute new tools and data. Tool developers can implement their methods as new KBase services, making their tool accessible to a wide user community and placing a world of biological data at their fingertips for tool validation. Data producers can integrate their data into the KBase data model, so that all of the analysis and visualization tools available in KBase may be applied to interpret the data. By enabling members of the community to integrate and use a wide spectrum of analysis tools and datasets, KBase will serve as a catalyst for biological research, accelerating discovery for DOE missions and providing insights and benefits that can ultimately serve numerous application areas.

Systems biology is driven by the ever-increasing wealth of data resulting from new generations of genomics-based technologies. With the success of genome sequencing, biology began to generate and accumulate data at an exponential rate. In addition to the massive stream of sequencing data, each type of technology that researchers use to analyze a sequenced organism adds another layer of complexity to the challenge of understanding how different biological components work together to form a functional living system. Achieving this systems-level understanding of biology will enable researchers to predict and ultimately design how the system will function under certain conditions. Gaining this predictive understanding, however, requires an unprecedented level of collaboration among researchers in different disciplines around the world. A new collaborative computational environment is needed to bring these researchers together so they can share and integrate large, heterogeneous datasets and readily use this information to develop predictive models that drive scientific discovery.