165.   The KBase User Experience

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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.

KBase provides several ways for scientists to access the system's functions and data including programmatically via a number of different programming languages; via a web-based scripting interface (IRIS); and using our prototype graphical user interface, the Narrative Interface (see poster on IRIS and the Narrative Interface). This poster introduces how to register as a KBase user; find documentation and tutorials; search and analyze KBase data; upload your own data; and use the first generation Narrative Interface. We explain the emerging model of how users interact with the system and with each other: how their data can be uploaded and shared as desired; how users can start projects and add narratives to them; and how users can use the Narrative Interface together with workspace (see related posters) to perform complex computational biological, human-in-the-loop workflows on heterogeneous biological data and share their processes and thoughts with the community.