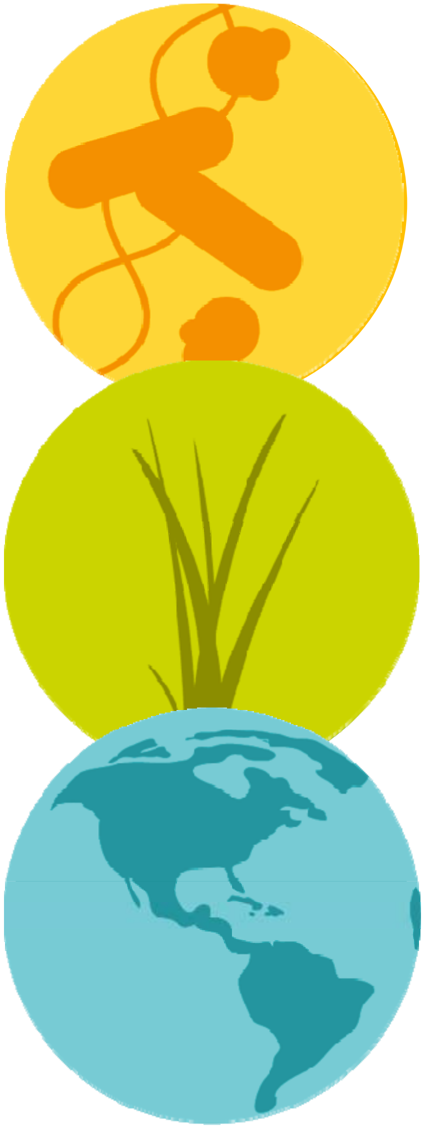


DOE Systems Biology Knowledgebase

KBASE

Data and modeling for predictive biology

BERAC Meeting
February 16, 2012

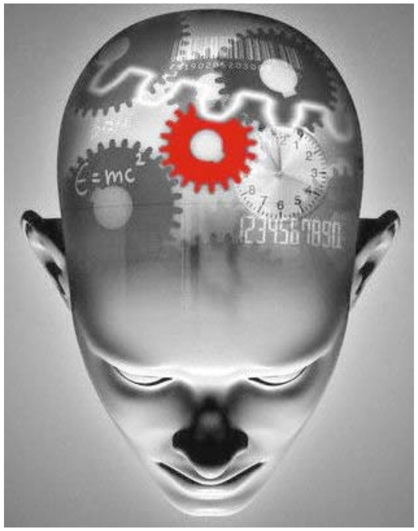
Adam P. Arkin, Ph.D.
Physical Biosciences Division
Lawrence Berkeley National Laboratory

U.S. DEPARTMENT OF ENERGY | Office of Science

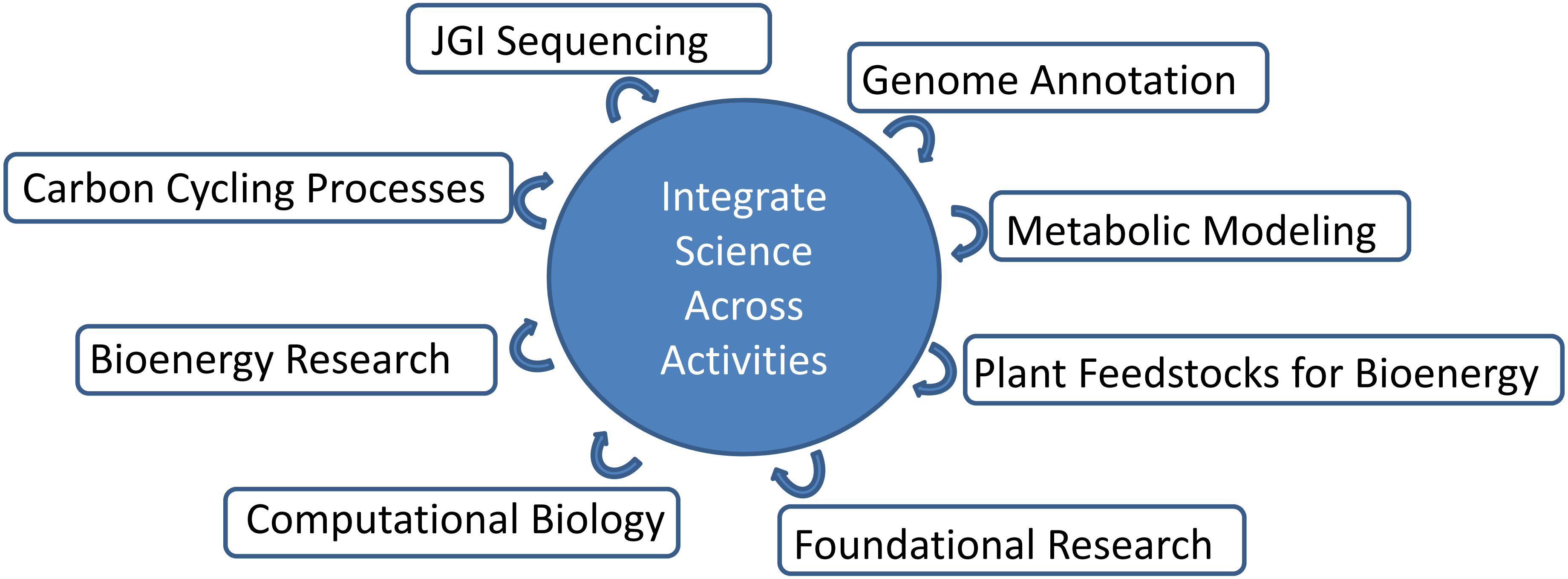
Complex Missions, Sophisticated Mission Analysis

- **DOE mission**: predict, control and design the biological components of energetic processes and environmental balance.

- Complex missions with rapidly expanding, intricately related diverse data types requires a mean to augment scientists' ability to:
  - Filter information
  - Focus attention
  - Ask the right questions
  - Leverage other minds



Integrate science and the science community



There is a tremendous wealth of data and information in the Genomic Sciences program. The Knowledgebase (Kbase) is an opportunity to integrate this data and information both within individual activities as well as to integrate together different activities.

DOE Systems Biology Knowledgebase

Components Enabling Its Development

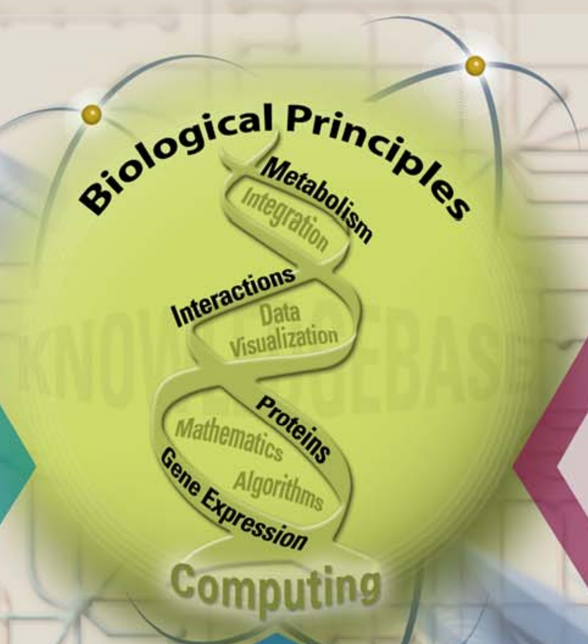
Plants and Microbes for Energy and Environment

2010 Knowledgebase R&D Project

Year-long effort funded by American Recovery and Reinvestment ACT (ARRA).

Results from this project, which was completed in September 2010, are underpinning Knowledgebase development:

- **DOE Systems Biology Knowledgebase Implementation Plan**
- **ARRA pilot projects**



User Community Data and Resources

The Knowledgebase will leverage and establish critical partnerships with other synergistic efforts:

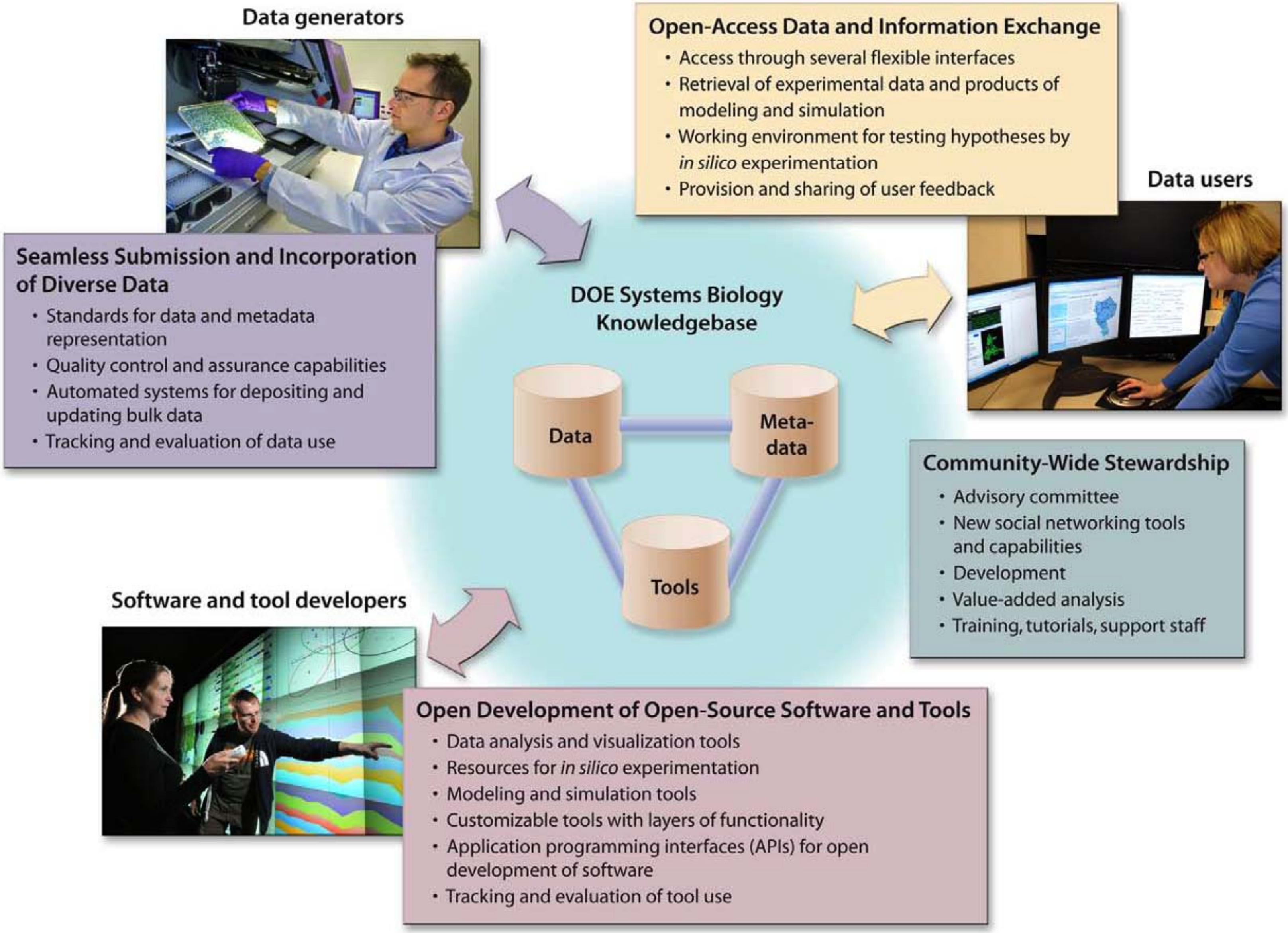
- **DOE Joint Genome Institute**
- **National Center for Biotechnology Information**
- **iPlant Collaborative**
- **DOE Office of Advanced Scientific Computing Research**
- **Others**

University-Led Projects to Develop Computational Biology and Bioinformatic Methods Enabling the Knowledgebase

In 2010, the DOE Office of Biological and Environmental Research awarded funding to 11 projects for basic research that will support Knowledgebase development in four areas:

- **Omic data integration**
- **Integrated pathway reconstruction**
- **Genomic annotation**
- **Whole cellular simulations**

Predictive Understanding


Data generators
Data users
DOE Systems Biology Knowledgebase
Data
Meta-data
Tools
Software and tool developers

Open-Access Data and Information Exchange

- Access through several flexible interfaces
- Retrieval of experimental data and products of modeling and simulation
- Working environment for testing hypotheses by *in silico* experimentation
- Provision and sharing of user feedback

Seamless Submission and Incorporation of Diverse Data

- Standards for data and metadata representation
- Quality control and assurance capabilities
- Automated systems for depositing and updating bulk data
- Tracking and evaluation of data use

Community-Wide Stewardship

- Advisory committee
- New social networking tools and capabilities
- Development
- Value-added analysis
- Training, tutorials, support staff

Open Development of Open-Source Software and Tools

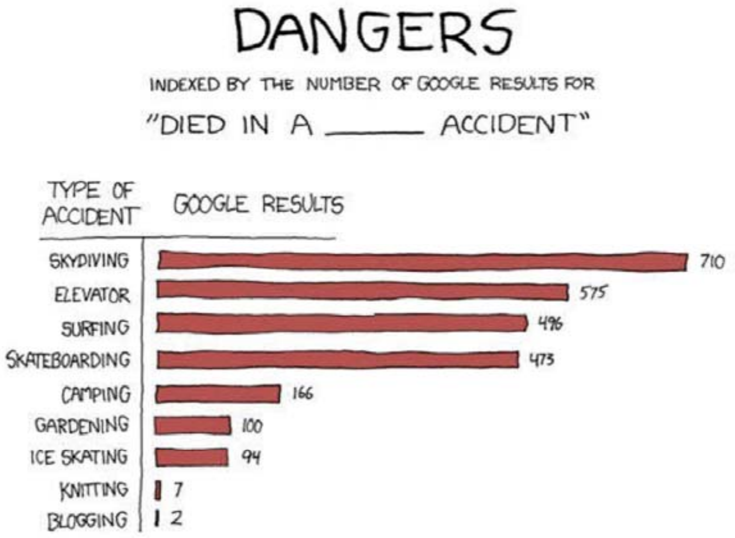
- Data analysis and visualization tools
- Resources for *in silico* experimentation
- Modeling and simulation tools
- Customizable tools with layers of functionality
- Application programming interfaces (APIs) for open development of software
- Tracking and evaluation of tool use

Kbase as an Integrative Platform

Kbase, working to build a(n)…

- ***Knowledge***base enabling ***predictive*** systems biology.
- Powerful modeling framework.
- **Community-driven**, extensible and scalable **open-source** software and application system.
- Infrastructure for integration and reconciliation of algorithms and data sources.
- Framework for standardization, search, and association of data.
- Resource to enable **experimental design** and **interpretation** of results.

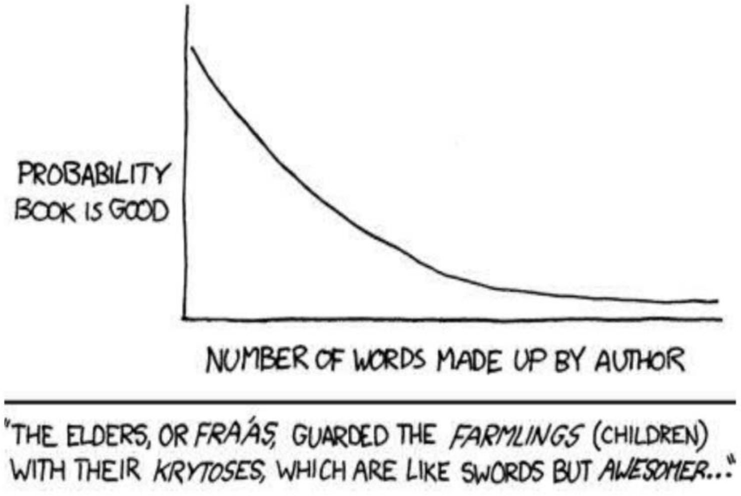
Data is extracted and displayed



This is the database model

Databases enable the rapid organization and **search** of data

Knowledge is learning & answering


PROBABILITY BOOK IS GOOD
NUMBER OF WORDS MADE UP BY AUTHOR
"THE ELDERS, OR FRAÁS, GUARDED THE FARMLINGS (CHILDREN) WITH THEIR KRYTOSES, WHICH ARE LIKE SWORDS BUT AWESOMER..."

This is the knowledgebase model

Knowledgebases should ***learn*** a "model" of the data to provide "conclusions" (hypotheses)

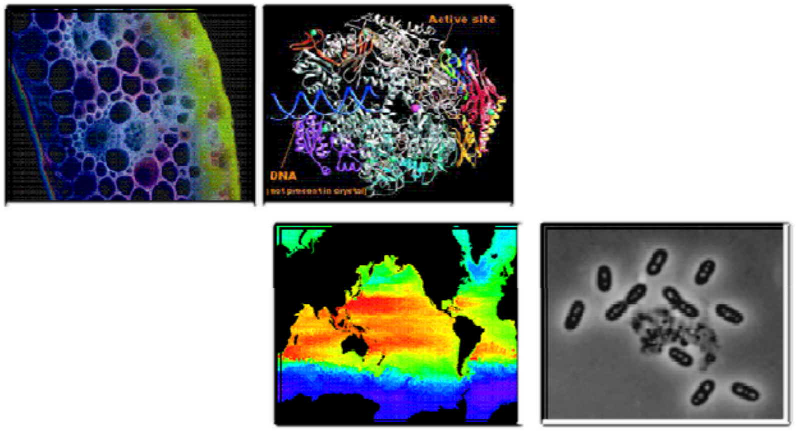
M-C Jenkins (http://www.scienceforseo.com)

Images from xkcd comics

Kbase: One Project, Four National Laboratories, and a Growing Community

Utilize existing commercial software technology and leveraging DOE internet resources (ESNet) and DOE cloud computing platforms (Magellan)

➢***Kbase is a framework for data collection, integration and analysis tools to enable the simplified use and modeling of large scale genome and genome enabled information***



By 2013 Deliver on the Initial Goals:

▪Kbase Infrastructure firmly established at 4 laboratories including high performance and cloud computing with routine 10+ Gb/s data transfer over ESNet between all Kbase sites

▪First public release includes:

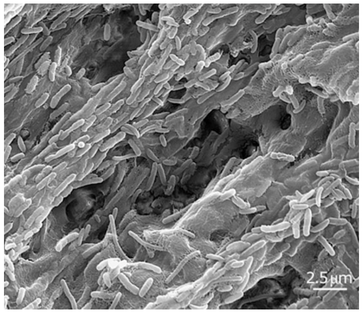
o Integration of data to reconstruct and predict metabolic and gene expression regulatory networks for up to 1,000 microbes to manipulate microbial function.

o Integration of phenotypic and experimental data for bioenergy plants to predict metabolic and regulatory genotypes enabling manipulation of biomass properties.

HOW ARE WE GOING TO DO IT?

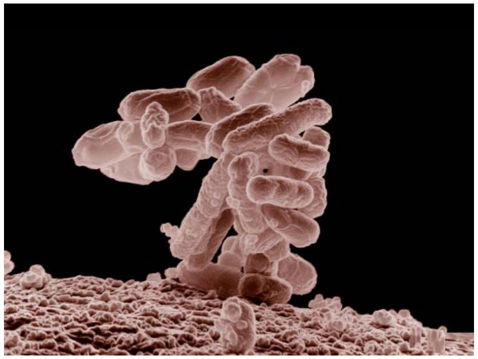
Enable DOE Mission Science

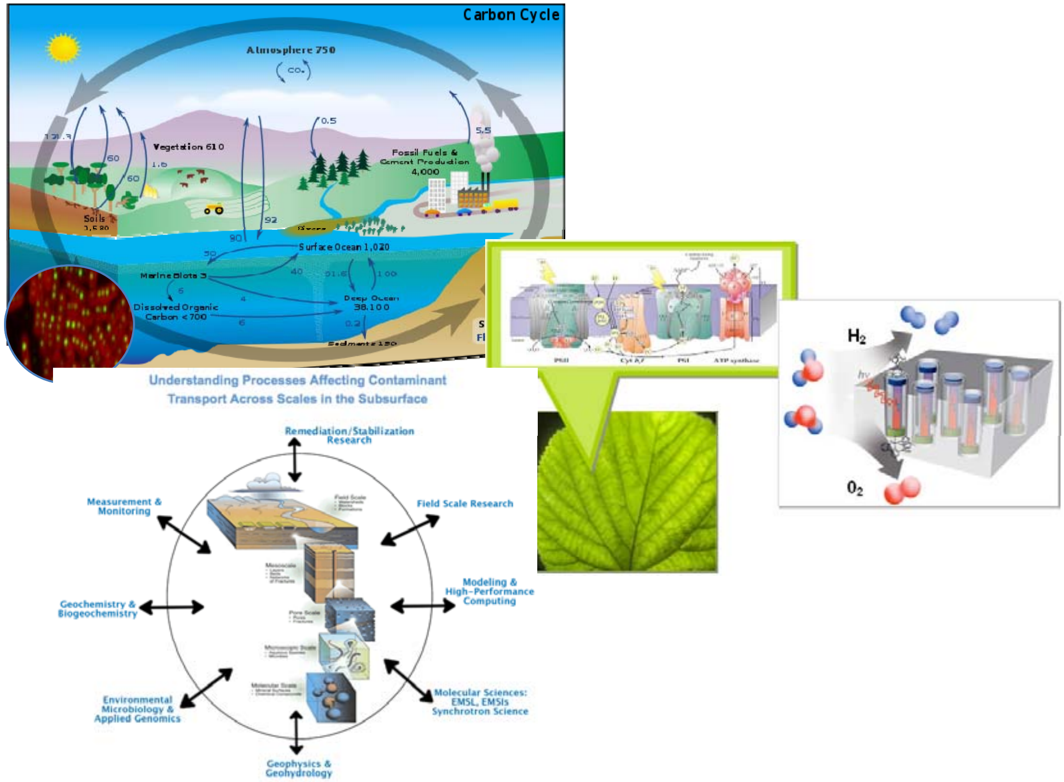
Communities



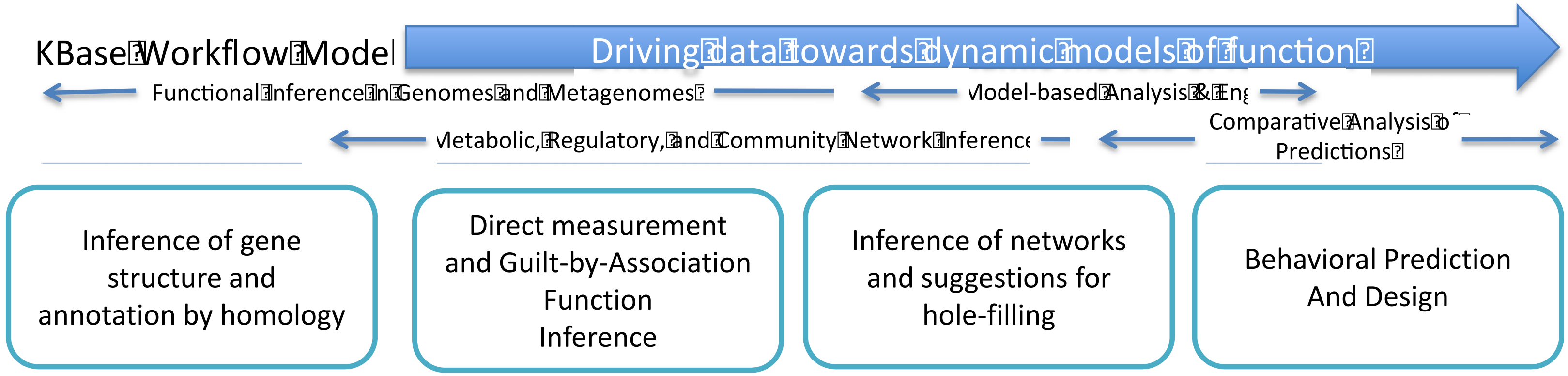
Plants

Microbes




Carbon Cycle
Atmosphere 750
CO₂
121.3
60
60
1.6
Vegetation 610
0.5
5.5
Fossil Fuels & Cement Production 4,000
Soils 1,580
92
90
Rivers
Surface Ocean 1,020
50
Marine Biota 3
40
91.6
100
6
4
Dissolved Organic Carbon <700
6
Deep Ocean 38,100
0.2
Sediments 150
Understanding Processes Affecting Contaminant Transport Across Scales in the Subsurface
Remediation/Stabilization Research
Measurement & Monitoring
Field Scale Research
Field Scale
Mesoscale
Geochemistry & Biogeochemistry
Modeling & High-Performance Computing
Pore Scale
Microscopic Scale
Molecular Scale
Environmental Microbiology & Applied Genomics
Molecular Sciences: EMSL, EMSIs Synchrotron Science
Geophysics & Geohydrology
PSII
Cyt b₆f
PSI
ATP synthase
H₂
hν
O₂

Target “Activities”



KBase Workflow Model

Driving data towards dynamic models of function

Functional Inference in Genomes and Metagenomes

Model-based Analysis & Eng

Metabolic, Regulatory, and Community Network Inference

Comparative Analysis o
Predictions

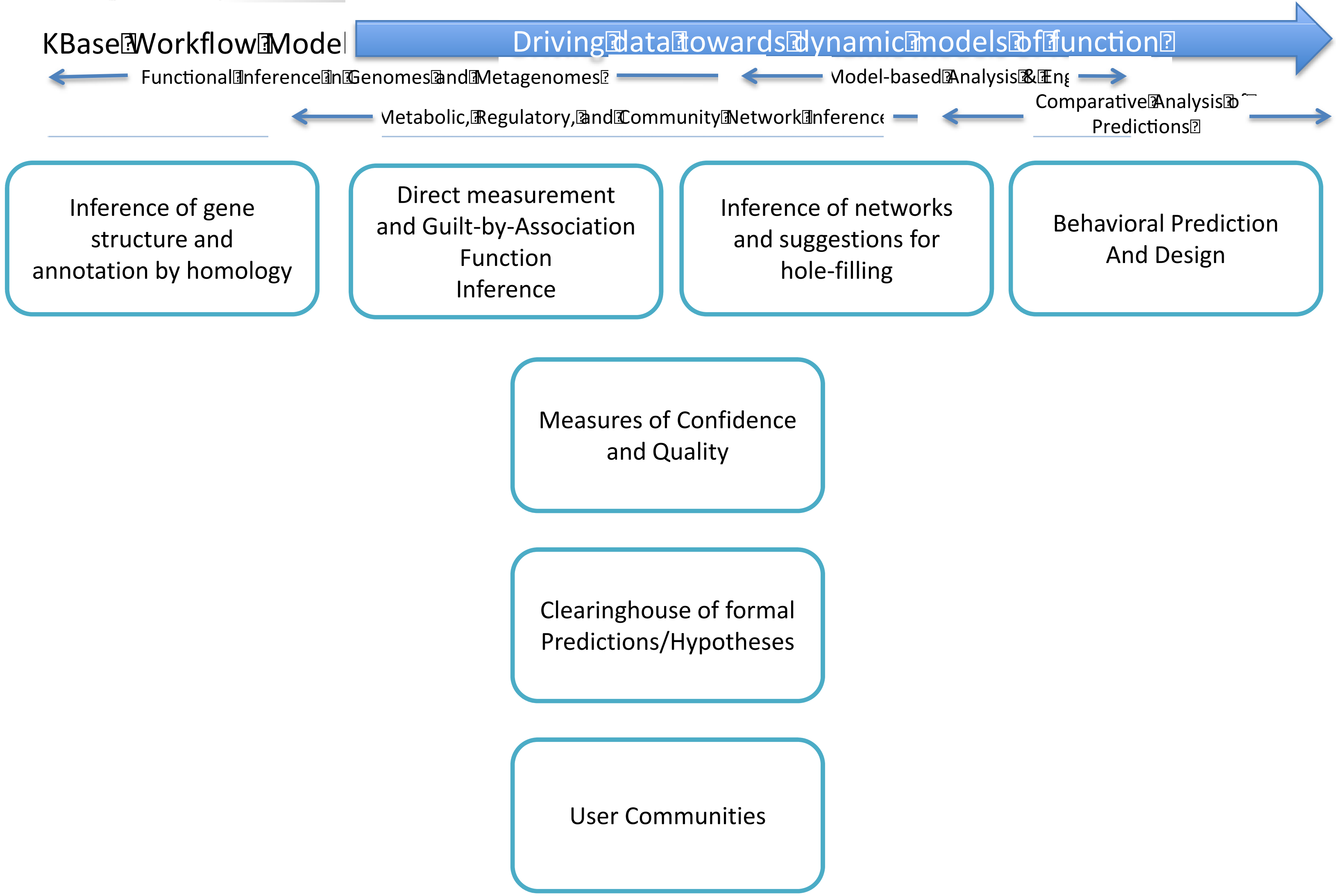
Inference of gene structure and annotation by homology

Direct measurement and Guilt-by-Association Function Inference

Inference of networks and suggestions for hole-filling

Behavioral Prediction And Design

Transformative capability



KBase Workflow Model

Driving data towards dynamic models of function

Functional Inference in Genomes and Metagenomes

Model-based Analysis & Eng

Metabolic, Regulatory, and Community Network Inferenc

Comparative Analysis o
Predictions

Inference of gene structure and annotation by homology

Direct measurement and Guilt-by-Association Function Inference

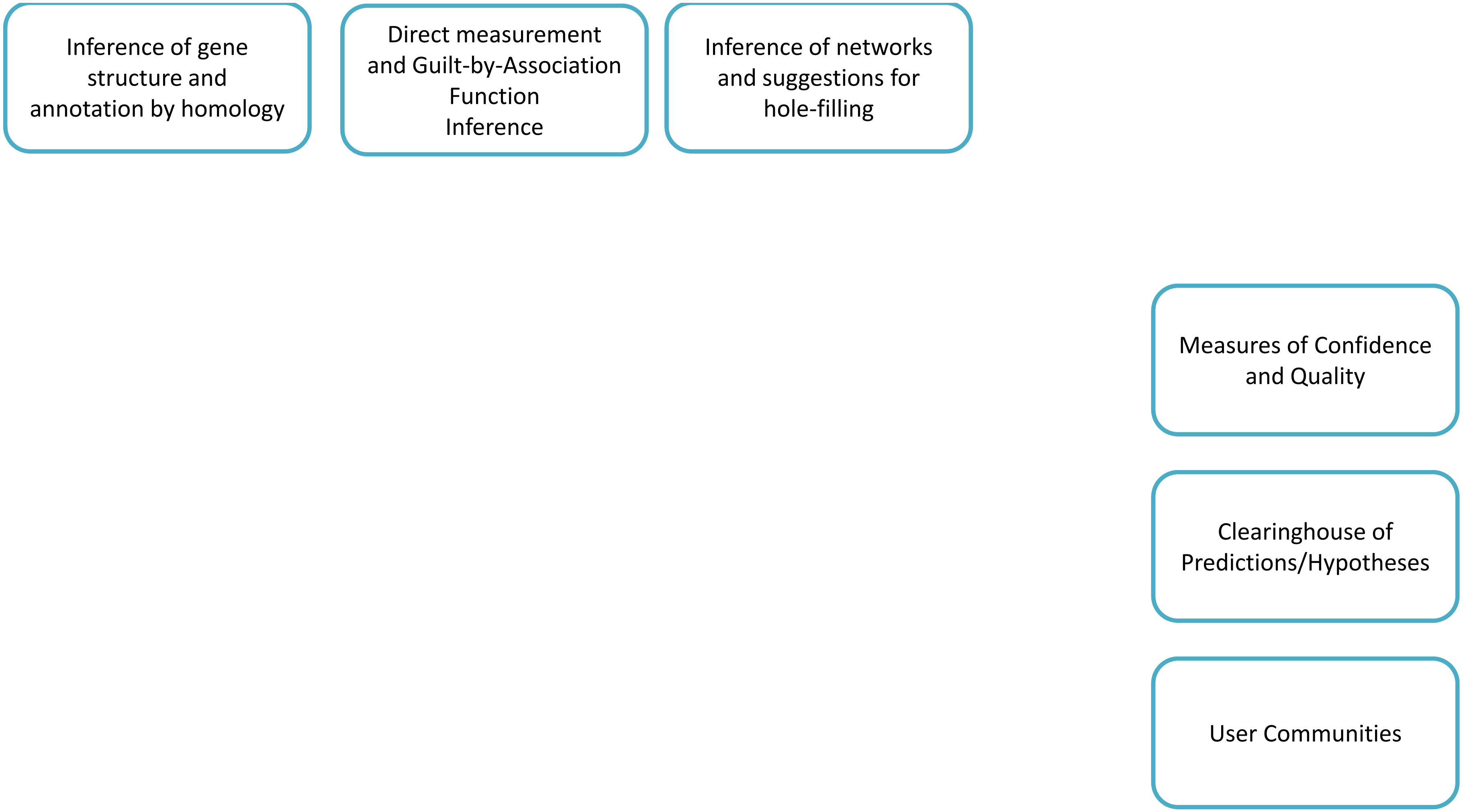
Inference of networks and suggestions for hole-filling

Behavioral Prediction And Design

Measures of Confidence and Quality

Clearinghouse of formal Predictions/Hypotheses

User Communities



Inference of gene structure and annotation by homology

Direct measurement and Guilt-by-Association Function Inference

Inference of networks and suggestions for hole-filling

Measures of Confidence and Quality

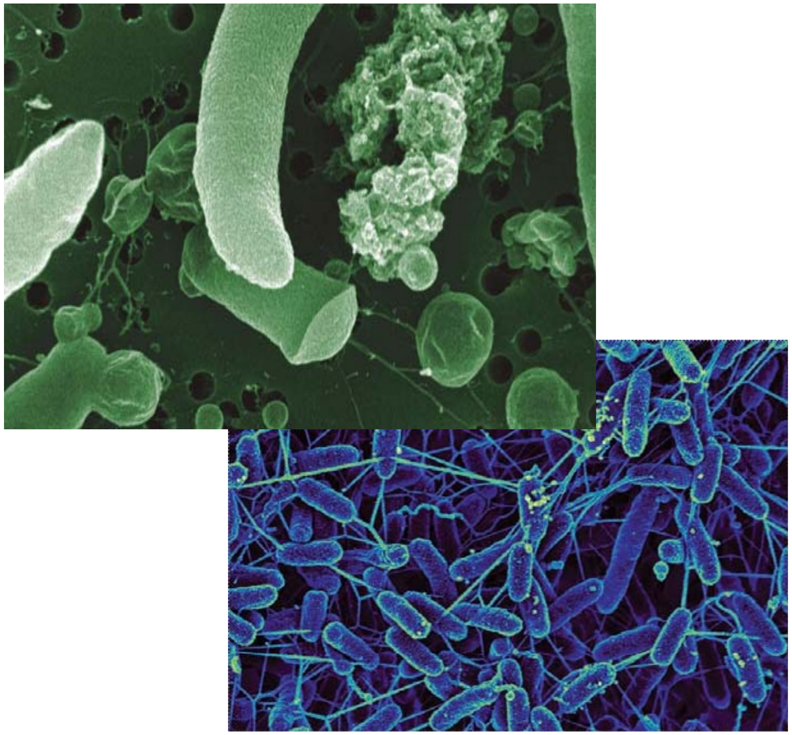
Clearinghouse of Predictions/Hypotheses

User Communities

Microbes

Our overall goals are to:

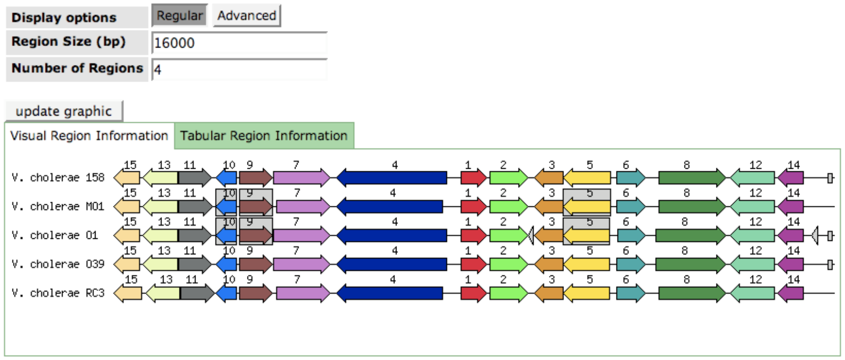
- Reconstruct and predict metabolic and gene expression regulatory networks to manipulate microbial function
- Vastly increase the capability of the scientific community to communicate and utilize their existing data
- Enable the planning of effective experiments and maximizing understanding of microbial system function



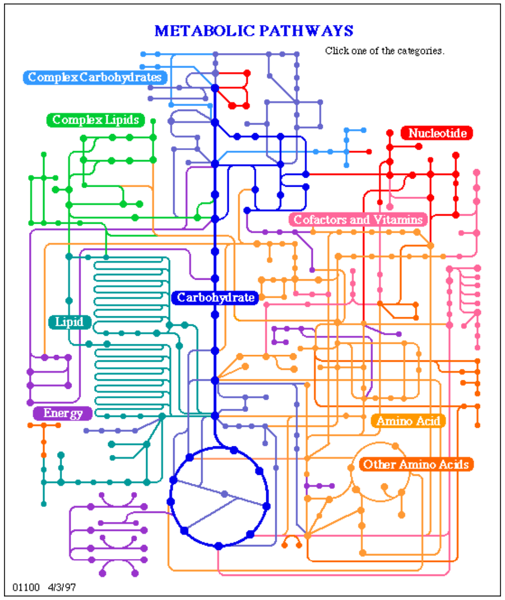
Microbes

We propose to do this by:

- Annotating genomes and assigning confidence
- Reconstructing metabolism and optimizing for function
- Reconstructing regulation and assessing agreement with expression data
- Integrating and standardizing -omics data from multiple data sources
- Constructing models of microbial organisms and interlinking models with data



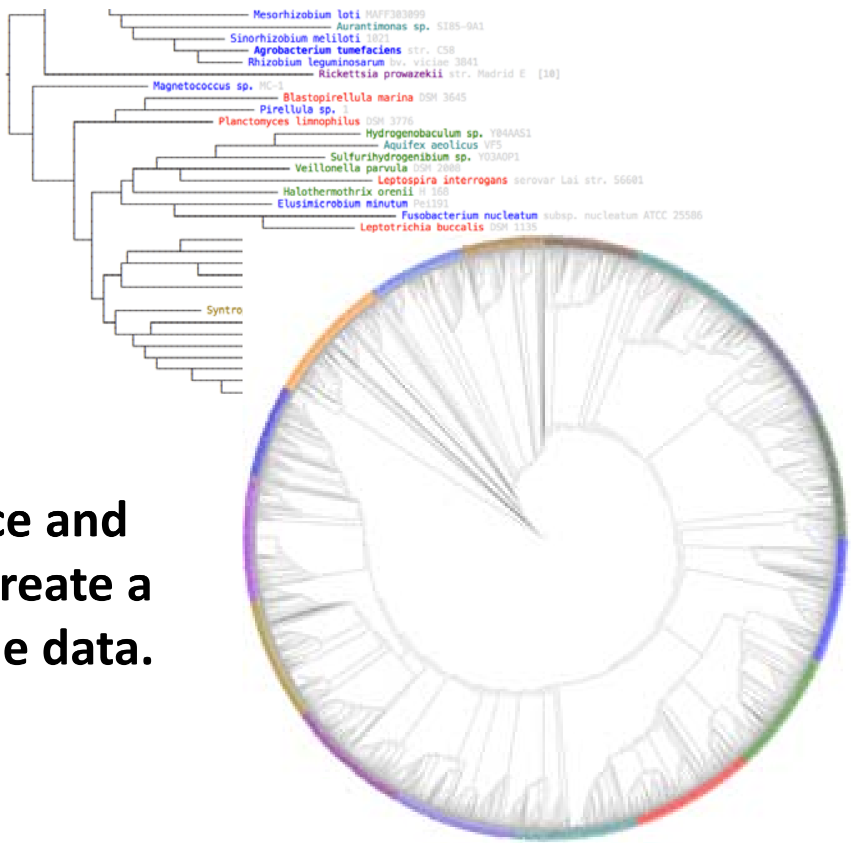
Display options: Regular | Advanced
Region Size (bp): 16000
Number of Regions: 4
update graphic
Visual Region Information | Tabular Region Information



Microbes Demos

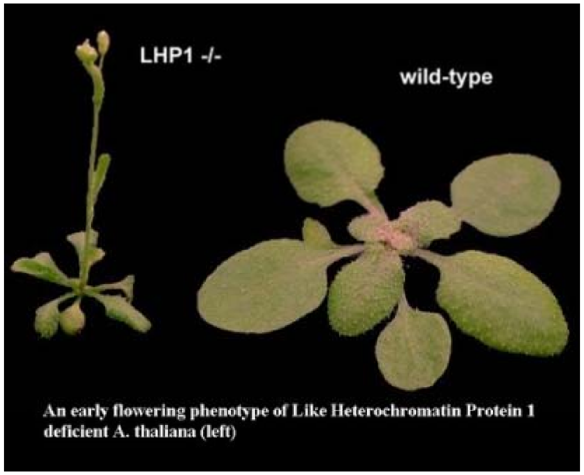
Within 13 months, we will be able to demonstrate use of the following:

- Data integration and data model
- Next generation organism pages
- Phylogenetic tree services
- Next generation gene pages
- Metabolic modeling
- Regulatory/Transcriptional networks


Mesorhizobium loti MAFF303099
Aurantimonas sp. SI85-9A1
Sinorhizobium meliloti 1021
Agrobacterium tumefaciens str. C58
Rhizobium leguminosarum bv. viciae 3841
Rickettsia prowazekii str. Madrid E [10]
Magnetococcus sp. MC-1
Blastopirellula marina DSM 3645
Pirellula sp. 1
Planctomyces limnophilus DSM 3776
Hydrogenobaculum sp. Y04AAS1
Aquifex aeolicus VF5
Sulfurihydrogenibium sp. YO3AOP1
Veillonella parvula DSM 2008
Leptospira interrogans serovar Lai str. 56601
Halothermothrix orenii H 168
Elusimicrobium minutum Pei191
Fusobacterium nucleatum subsp. nucleatum ATCC 25586
Leptotrichia buccalis DSM 1135
Syntro

A microbiologist with a genome sequence and phenotypic growth data will be able to create a metabolic model fully reconciled with the data.

Plants



An early flowering phenotype of Like Heterochromatin Protein 1 deficient A. thaliana (left)

Our overall goals:

In order to extract knowledge from the wealth of high-throughput data in plant biology we need the ability to meaningfully integrate data.

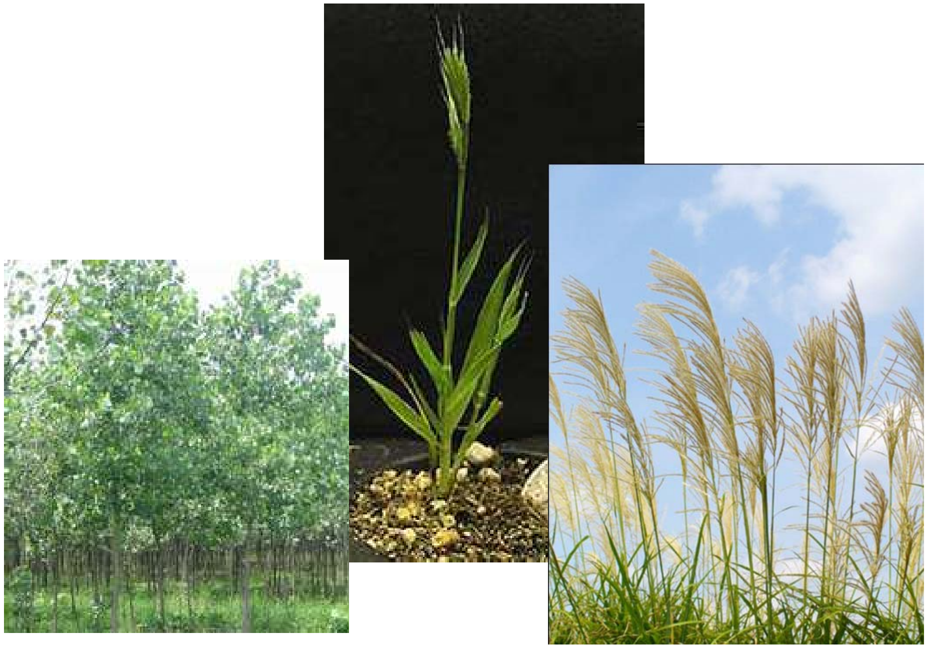
Therefore we aim to:

- Deploy Kbase capability that will allow for interactive, data-driven analysis and exploration across multiple -omics experiments.
- Provide researchers in plant sciences access to comprehensive datasets from high-throughput experiments together with relevant analytical tools and resources.
- Provide a platform for researchers to analyze their own experimental data, and have these results incorporated into the data exploration framework.

Plants Demos

We will accomplish this by using:

- Advance storage and indexing strategies for fast but persistent retrieval of large-scale genomics data
- Massively parallel processing of raw data using cloud compute resources
- Interactive charting libraries
- Using controlled vocabularies and ontologies for describing and storing genomic data



Plants Demos

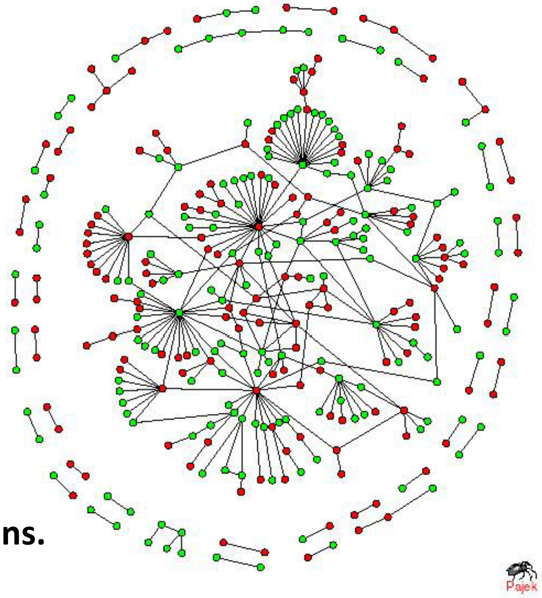
Within 13 months, we will have the following capabilities:

Genotyping Workflow

- Create a workflow for rapidly converting sequencing reads into genotypes
- Demonstrate more than 100-fold speedup over serial version by leveraging capabilities of KBase cloud
- Workflows will be developed as part of the KBase CyberInfrastructure

Data exploration: Linking of gene targets from phenotype and genotype studies with co-expression, protein-protein interaction, and metabolic models

- Allow users to narrow candidate gene lists based on these integrated data types
- Recommender system based on "guilt-by-association" principle: identify other genes, expression datasets, etc. associated with the user-selected group of genes
- Project genetic variations and network edges onto metabolic pathways
- Visualize co-expression network and node Interactions among subnetworks correlated to phenotype of interest



Plants work is cross-cutting with microbial and communities data and predictions.

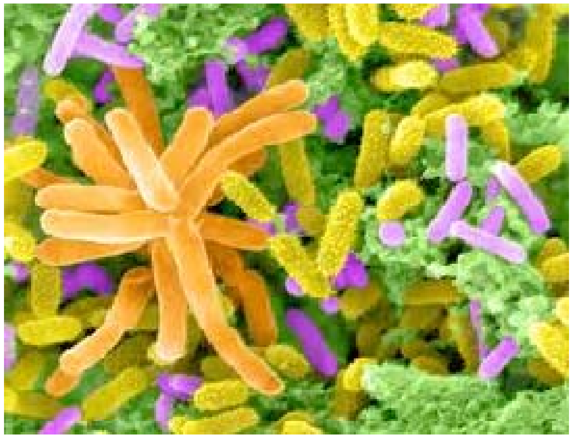
Microbial Communities

There has been an explosion of metagenomics data:

- Systems biology is driven by the ever-increasing wealth of data
- Metagenomics is >90% of the data
- Computation needs to be smarter

Our overall goal is to build a Kbase metagenomic platform that provides:

- Scalable, flexible analyses, link physiological and metadata sets to metagenomic sequences
- Data QC and GSC compliant data and standards for data collection
- Enable modeling of metabolic processes within a community
- Predict microbial growth in isolation and in a community



Microbial Communities

Within 13 months, we will have the following capabilities:

Metagenomic Experimental Design Wizard

The foundation laid will enable researchers to perform *in silico* experimentation and hypothesis testing

Bioprospecting

- Find communities with similar alpha diversity
- Find communities in similar biomes
- Locate novel proteins (unknowns)
- Suggest functions (based on metadata) that might be encoded in "abundant unknowns"
- Identify optimal candidates for screening

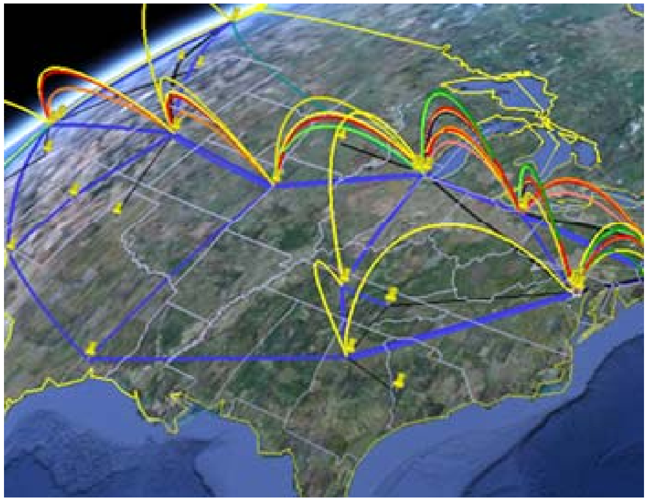
Communities work is cross-cutting with microbial and plant data and predictions.

Infrastructure

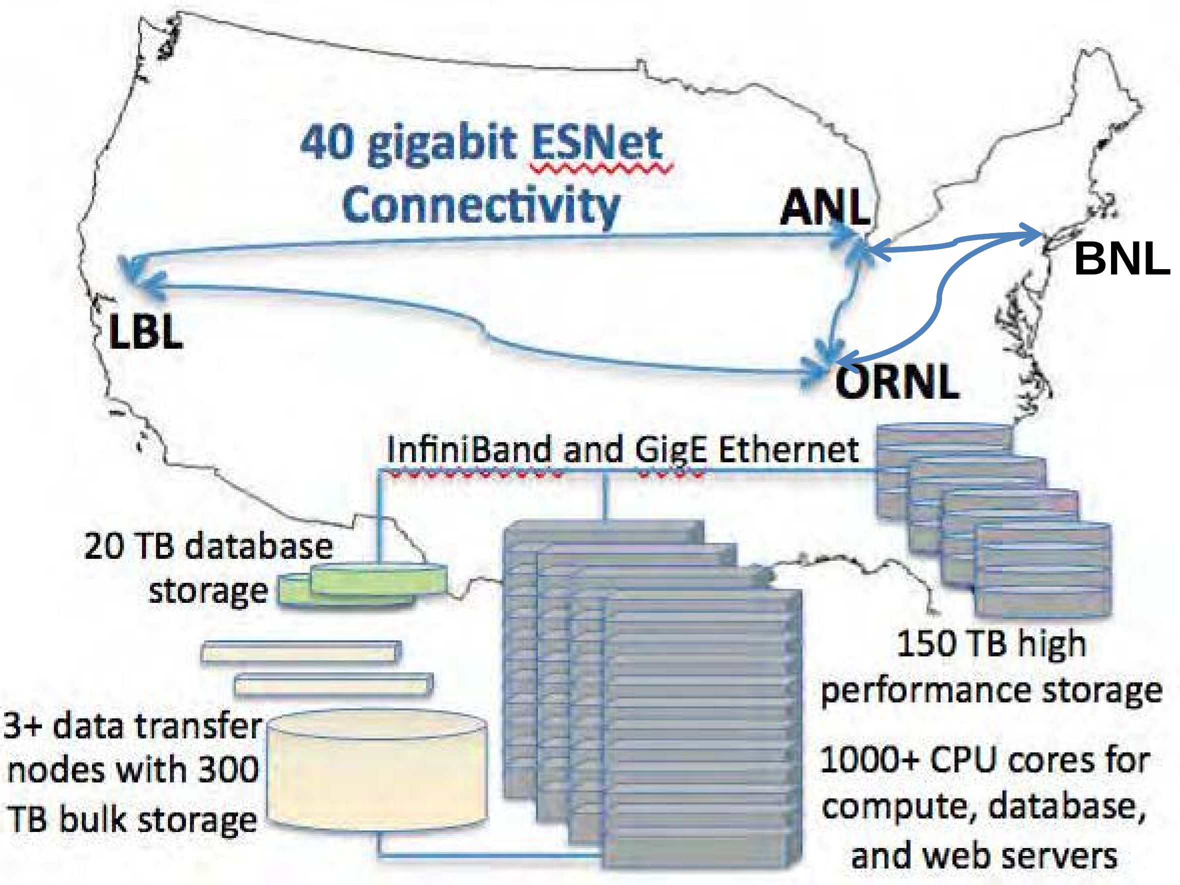
KBase is providing robust and scalable infrastructure to support new science by offering…

- High speed data transfers will enable better response times
- Access to back end storage systems for large data sets
- Remote compute services for HPC, cluster and cloud based
- Workflow support
- Web UX access to data and computing
- Persistent and transient data management capabilities
- Support for users, teams, projects and cross talk

Energy Sciences Network (ESNet)



Kbase leverages ESNet for 10+ Gb/s data transfer between all nodes


40 gigabit ESNet Connectivity
ANL
BNL
LBL
ORNL
InfiniBand and GigE Ethernet
20 TB database storage
150 TB high performance storage
3+ data transfer nodes with 300 TB bulk storage
1000+ CPU cores for compute, database, and web servers

•ESnet backbone (ESnet4) is anational 10 Gbps optical circuit infrastructure

•ESnet shares its optical network with Internet2

•ESnet's IP network functions as a Tier 1 internet service provider

KBASE predictive biology

DOE Systems Biology Knowledgebase

The DOE KBase Cloud

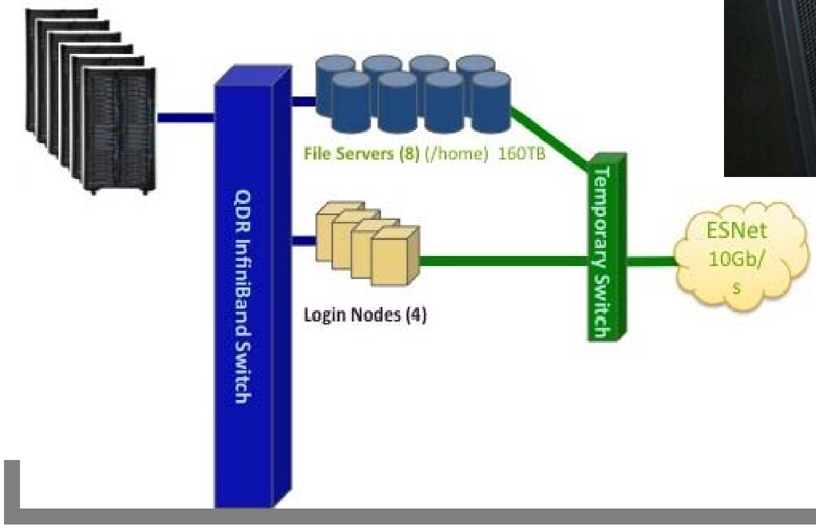
Argonne Magellan Hardware

Built on DOE Magellan Cloud

Magellan Goals:

Establish a nationwide scientific mid-range distributed computing and data analysis testbed.

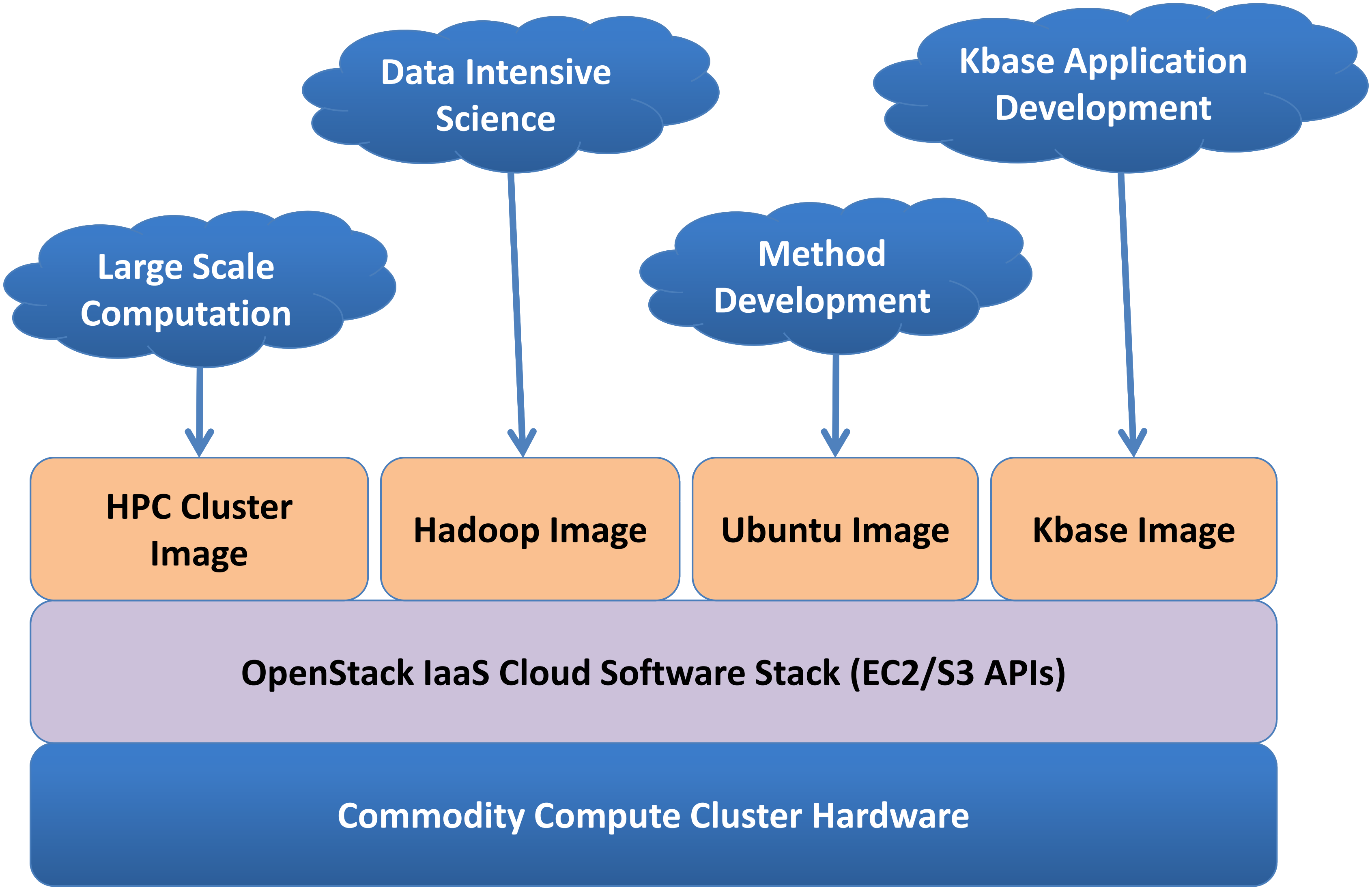
http://magellan.alcf.anl.gov/
http://science.energy.gov/ascr



Current config at 252nodes
Expected to reach ~700 nodes in FY12

Smaller system housed at ORNL with around ~70 nodes

The Kbase Cloud Architecture



Data Intensive Science

Kbase Application Development

Large Scale Computation

Method Development

HPC Cluster Image

Hadoop Image

Ubuntu Image

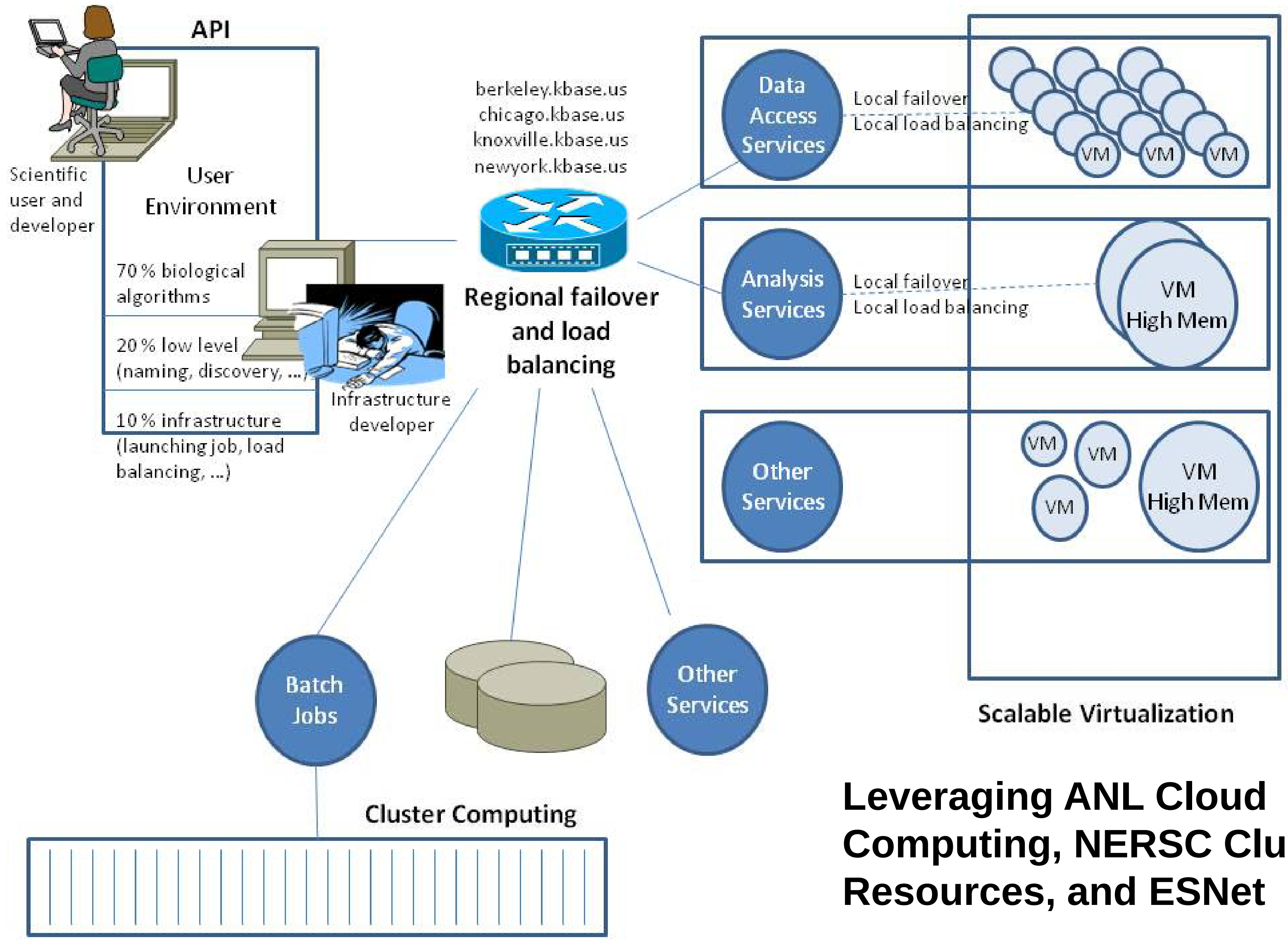
Kbase Image

OpenStack IaaS Cloud Software Stack (EC2/S3 APIs)

Commodity Compute Cluster Hardware

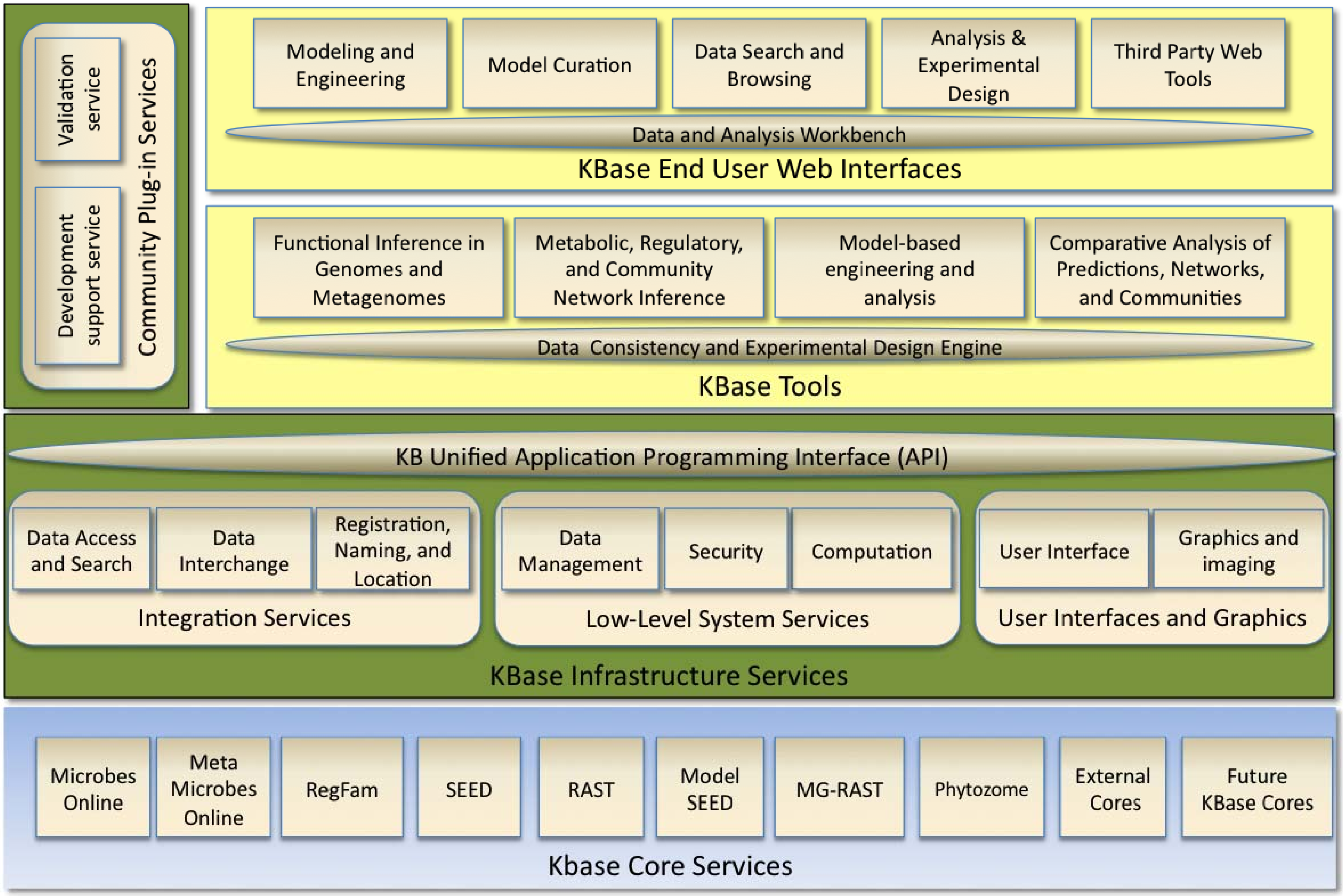
KBASE
predictive biology
DOE Systems Biology Knowledgebase

The Kbase Infrastructure



Leveraging ANL Cloud Computing, NERSC Cluster Resources, and ESNet

The Kbase Infrastructure and Services



Community Plug-in Services

Validation service

Development support service

Modeling and Engineering

Model Curation

Data Search and Browsing

Analysis & Experimental Design

Third Party Web Tools

Data and Analysis Workbench

KBase End User Web Interfaces

Functional Inference in Genomes and Metagenomes

Metabolic, Regulatory, and Community Network Inference

Model-based engineering and analysis

Comparative Analysis of Predictions, Networks, and Communities

Data Consistency and Experimental Design Engine

KBase Tools

KB Unified Application Programming Interface (API)

Data Access and Search

Data Interchange

Registration, Naming, and Location

Integration Services

Data Management

Security

Computation

Low-Level System Services

User Interface

Graphics and imaging

User Interfaces and Graphics

KBase Infrastructure Services

Microbes Online

Meta Microbes Online

RegFam

SEED

RAST

Model SEED

MG-RAST

Phytozome

External Cores

Future KBase Cores

Kbase Core Services

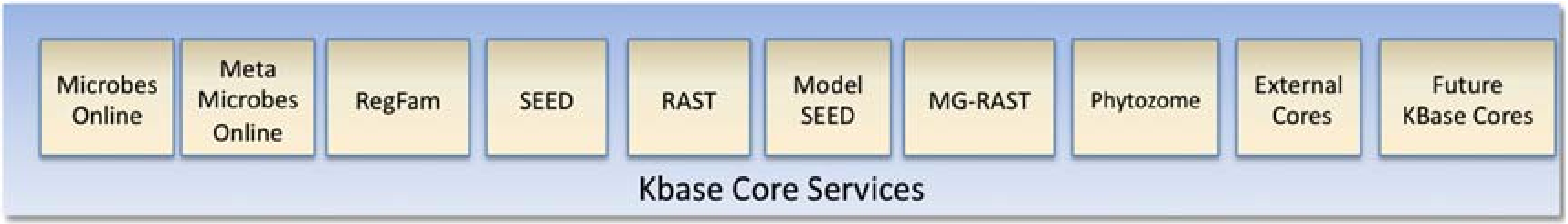
Building Kbase Services

➢*KBase will integrate initial f core services and enable KBase Unified Application Programming Interface (API)*

➢The *KBase Unified API is the primary programming target for KBase tools and applications*

➢*KBase Unified API provides*

–Access to core functions and data
–Low-level systems services
–User interface and graphics services and
–Integration services



Microbes Online | Meta Microbes Online | RegFam | SEED | RAST | Model SEED | MG-RAST | Phytozome | External Cores | Future KBase Cores

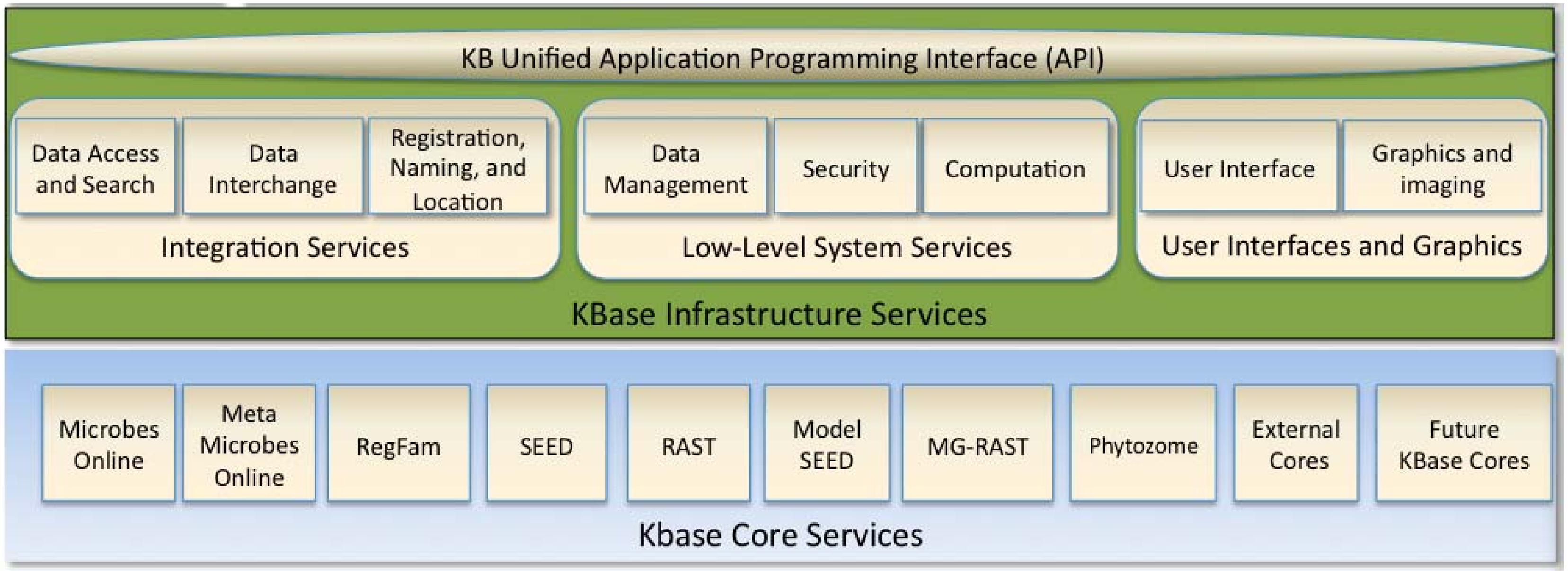
Kbase Core Services

Building a Kbase Unified API

- Uniform view of KBase core services

- Access to data management, security and computational services in the KBase infrastructure

- Rich set of standard graphics and UX components for building web applications with single look and feel



KB Unified Application Programming Interface (API)

Integration Services: Data Access and Search; Data Interchange; Registration, Naming, and Location

Low-Level System Services: Data Management; Security; Computation

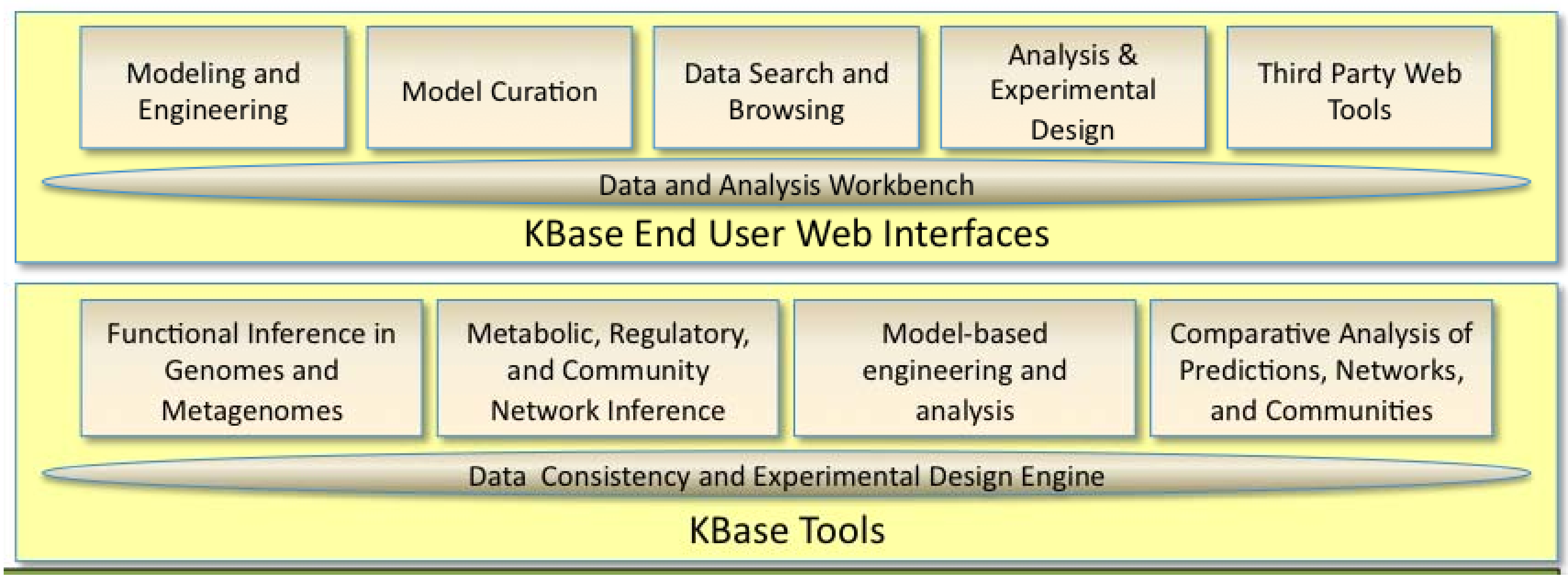
User Interfaces and Graphics: User Interface; Graphics and imaging

KBase Infrastructure Services

Kbase Core Services: Microbes Online; Meta Microbes Online; RegFam; SEED; RAST; Model SEED; MG-RAST; Phytozome; External Cores; Future KBase Cores

Building a Kbase User Experience

- ➢Most KBase code development will be layered on top of the KBase Unified API
- ➢Supports a layered architecture consisting of collections of KBase Tools and End User Web Interfaces
- ➢Each layer extends the API by providing additional support for high-level functions



Modeling and Engineering

Model Curation

Data Search and Browsing

Analysis & Experimental Design

Third Party Web Tools

Data and Analysis Workbench

KBase End User Web Interfaces

Functional Inference in Genomes and Metagenomes

Metabolic, Regulatory, and Community Network Inference

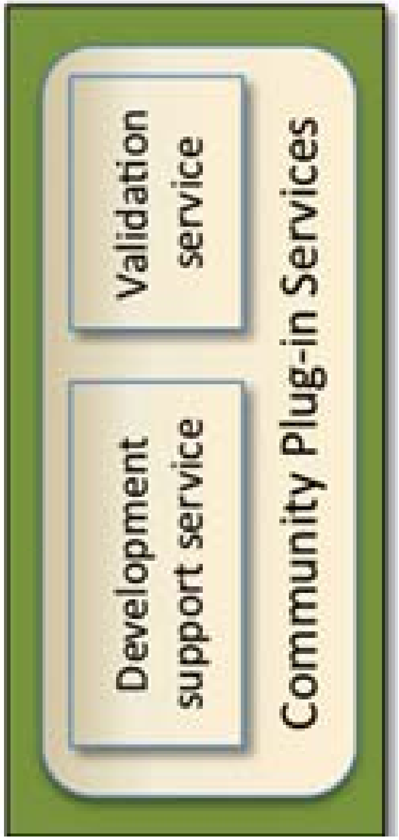
Model-based engineering and analysis

Comparative Analysis of Predictions, Networks, and Communities

Data Consistency and Experimental Design Engine

KBase Tools

Building a Kbase Developer Community



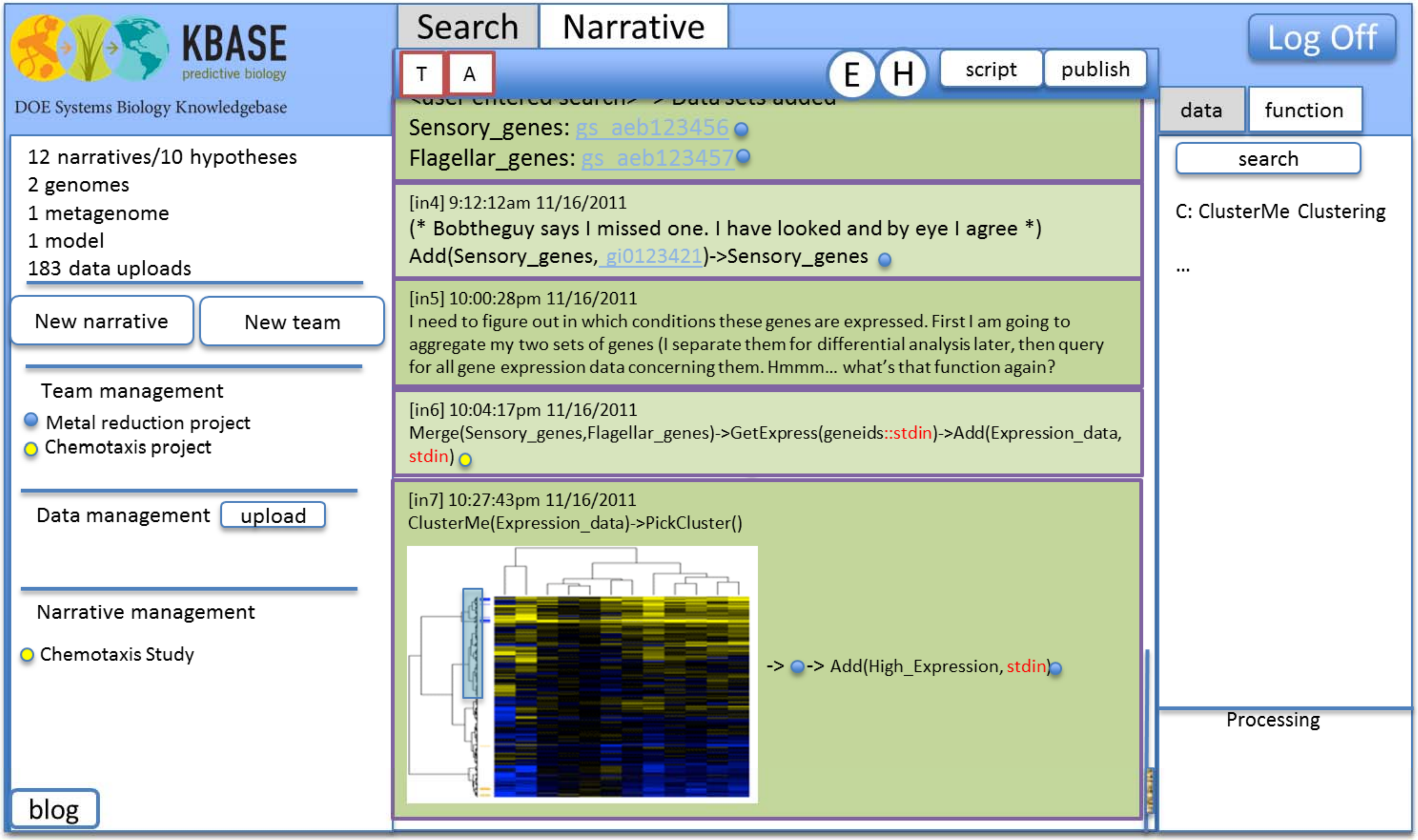
Two ways to work with KBase

➢Extend from below with additional core services that ***extend the KBase API***

➢Extend from above by plugging in applications that ***use the KBase API***

KBASE
predictive biology
DOE Systems Biology Knowledgebase

Concept: Kbase User Experience



12 narratives/10 hypotheses
2 genomes
1 metagenome
1 model
183 data uploads

Team management
● Metal reduction project
○ Chemotaxis project

Data management

Narrative management
○ Chemotaxis Study

<user entered search> -> Data sets added
Sensory_genes: gs_aeb123456 ●
Flagellar_genes: gs_aeb123457 ●

[in4] 9:12:12am 11/16/2011
(* Bobtheguy says I missed one. I have looked and by eye I agree *)
Add(Sensory_genes, gi0123421)->Sensory_genes ●

[in5] 10:00:28pm 11/16/2011
I need to figure out in which conditions these genes are expressed. First I am going to aggregate my two sets of genes (I separate them for differential analysis later, then query for all gene expression data concerning them. Hmmm… what's that function again?

[in6] 10:04:17pm 11/16/2011
Merge(Sensory_genes,Flagellar_genes)->GetExpress(geneids::stdin)->Add(Expression_data, stdin) ○

[in7] 10:27:43pm 11/16/2011
ClusterMe(Expression_data)->PickCluster()

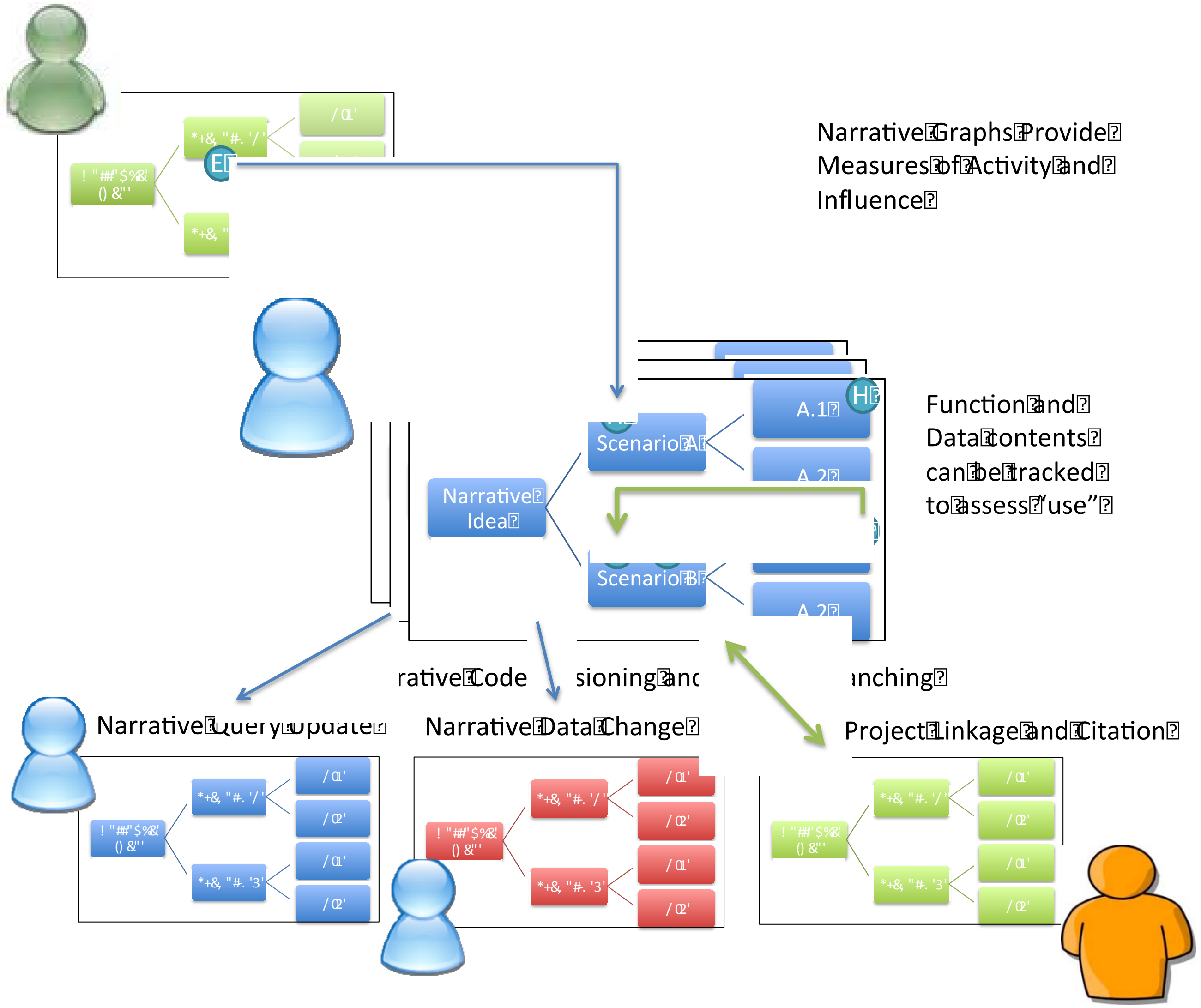
-> ●-> Add(High_Expression, stdin)●

C: ClusterMe Clustering

…

Processing

Concept: Interactive community knowledge



Narrative Graphs Provide Measures of Activity and Influence

Function and Data contents can be tracked to assess "use"

Goals for the User Experience

KBase will allow users to…

- Keep pace with the rate of data generation.
- Use interrelated data of different types.
- Develop analytical tools.
- Perform rapid comparisons across multiple genomes.
- Allow free and open access to KBase data, models and simulations.
- Grow partners, developers, data generators, or users.
- Coordinate with other researchers to target what experimental work is needed, and to share results.
- Learn how to use KBase features of models and move into predictive systems biology.

BUILDING THE KBASE COMMUNITY

Who are the Kbase core developers

The KBase Team:

BERKELEY LAB

Argonne NATIONAL LABORATORY

BROOKHAVEN NATIONAL LABORATORY

OAK RIDGE National Laboratory

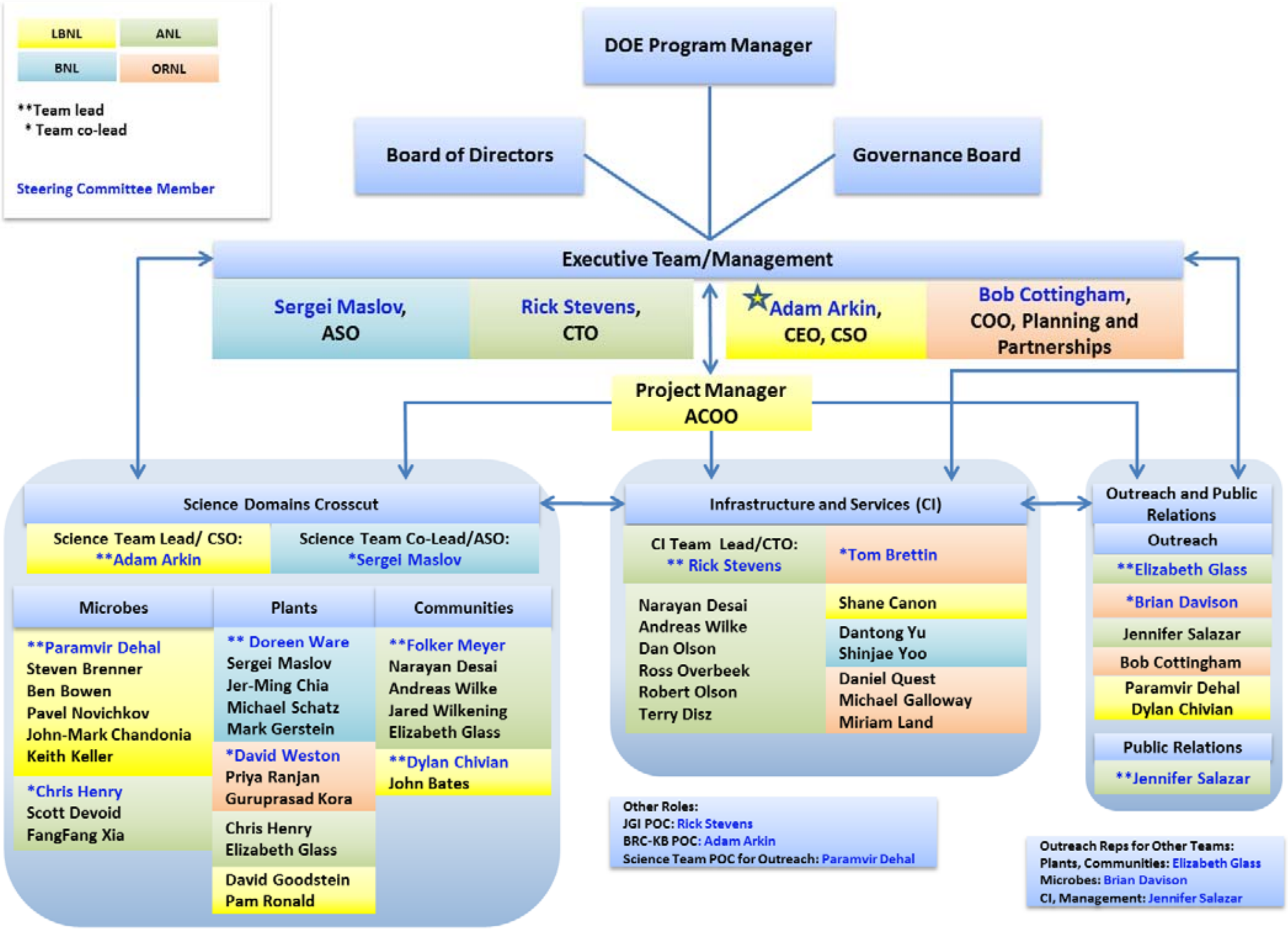
Collaborators:

- Cold Spring Harbor Laboratory
- University of California, Davis
- Hope College in Michigan
- University of Illinois at Urbana-Champaign
- Yale University
- The Joint Genome Institute
- InterBRC Knowledgebase
- Several University Knowledgebase Projects

→New Partners and Collaborators from Users and Stakeholders

Funding: This work is supported by the U.S. Department of Energy, Office of Biological and Environmental Research under Contract DE-AC02-06CH11357.

There *is* an org-chart but…



LBNL | ANL | BNL | ORNL

**Team lead
* Team co-lead

Steering Committee Member

DOE Program Manager

Board of Directors

Governance Board

Executive Team/Management

Sergei Maslov, ASO

Rick Stevens, CTO

☆Adam Arkin, CEO, CSO

Bob Cottingham, COO, Planning and Partnerships

Project Manager ACOO

Science Domains Crosscut

Science Team Lead/ CSO: **Adam Arkin

Science Team Co-Lead/ASO: *Sergei Maslov

Microbes
**Paramvir Dehal
Steven Brenner
Ben Bowen
Pavel Novichkov
John-Mark Chandonia
Keith Keller
*Chris Henry
Scott Devoid
FangFang Xia

Plants
** Doreen Ware
Sergei Maslov
Jer-Ming Chia
Michael Schatz
Mark Gerstein
*David Weston
Priya Ranjan
Guruprasad Kora
Chris Henry
Elizabeth Glass
David Goodstein
Pam Ronald

Communities
**Folker Meyer
Narayan Desai
Andreas Wilke
Jared Wilkening
Elizabeth Glass
**Dylan Chivian
John Bates

Infrastructure and Services (CI)

CI Team Lead/CTO: ** Rick Stevens

*Tom Brettin

Narayan Desai
Andreas Wilke
Dan Olson
Ross Overbeek
Robert Olson
Terry Disz

Shane Canon
Dantong Yu
Shinjae Yoo
Daniel Quest
Michael Galloway
Miriam Land

Outreach and Public Relations

Outreach
**Elizabeth Glass
*Brian Davison
Jennifer Salazar
Bob Cottingham
Paramvir Dehal
Dylan Chivian

Public Relations
**Jennifer Salazar

Other Roles:
JGI POC: Rick Stevens
BRC-KB POC: Adam Arkin
Science Team POC for Outreach: Paramvir Dehal

Outreach Reps for Other Teams:
Plants, Communities: Elizabeth Glass
Microbes: Brian Davison
CI, Management: Jennifer Salazar

Formal project management under 413-lite

We are nucleators.

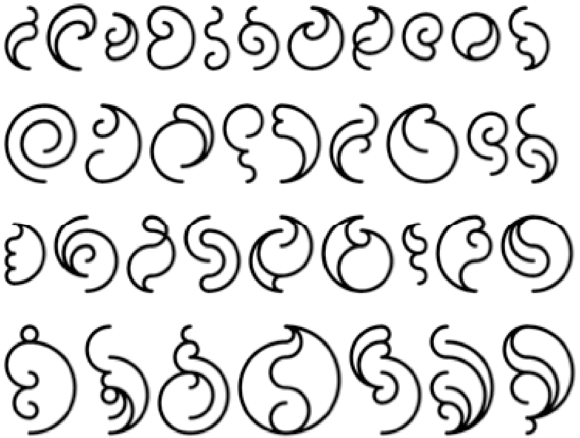
The Kbase core team is creating the initial infrastructure to:

- Allow effective and easy data federation and centralization.
- Lower the bar to adding and accessing new algorithms and analyses
- Enable nimble use of of advanced DOE network and compute resources
- Create a community framework for development and biological knowledge sharing
- Enable *their own research and yours!*

Everyone should be a contributor!

KBASE:

A. Professional Computational Biologists
B. Data generators and basic analysts
C. Knowledge Seekers
D. Knowledge Generators



instances of “minimum inventory/maximum diversity” systems, a term coined by Peter Pearce in his book, Structure in Nature Is a Strategy for Design (MIT Press, 1978).

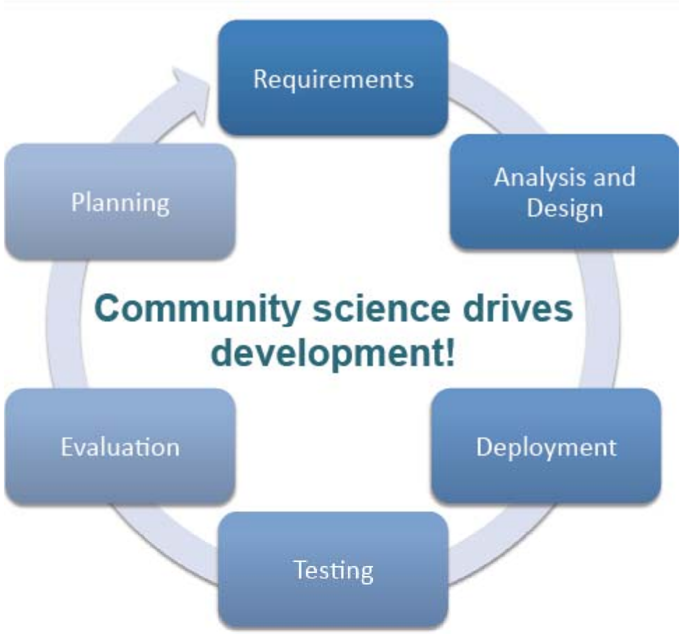
Therefore we aim to:

- Create a powerful framework for programmatic access to data and functions of Kbase. (Users A,B)
  - Ultimately provide stubs for use in PERL, PYTHON, R, MATLAB, Galaxy, etc.
- Create a set of packaged “Widgets” that make placement and recognizable display of Kbase “functions” on web pages (or within perhaps other apps), easy and identifiable. (Users B)
- Create a “simplified” portal for search and aggregation of data for data consumers and Knowledge Seekers. (Users C,D)
- *Create a innovative platform for knowledge creation, evolution and sharing.*

Outreach to the Community

We will build a diverse community of users by…

- Creating a unique a powerful resource for people to share new analyses and data and the use of these to produce new science.
- Advertising and informing via:
  - Online communication
  - Conference workshops
  - Press releases
- Interacting with the community and fostering relationships
- Collecting feedback from the community to ensure we are meeting their needs
- Measuring our impact
- Participating in standards groups



Visit us at kbase.science.energy.gov

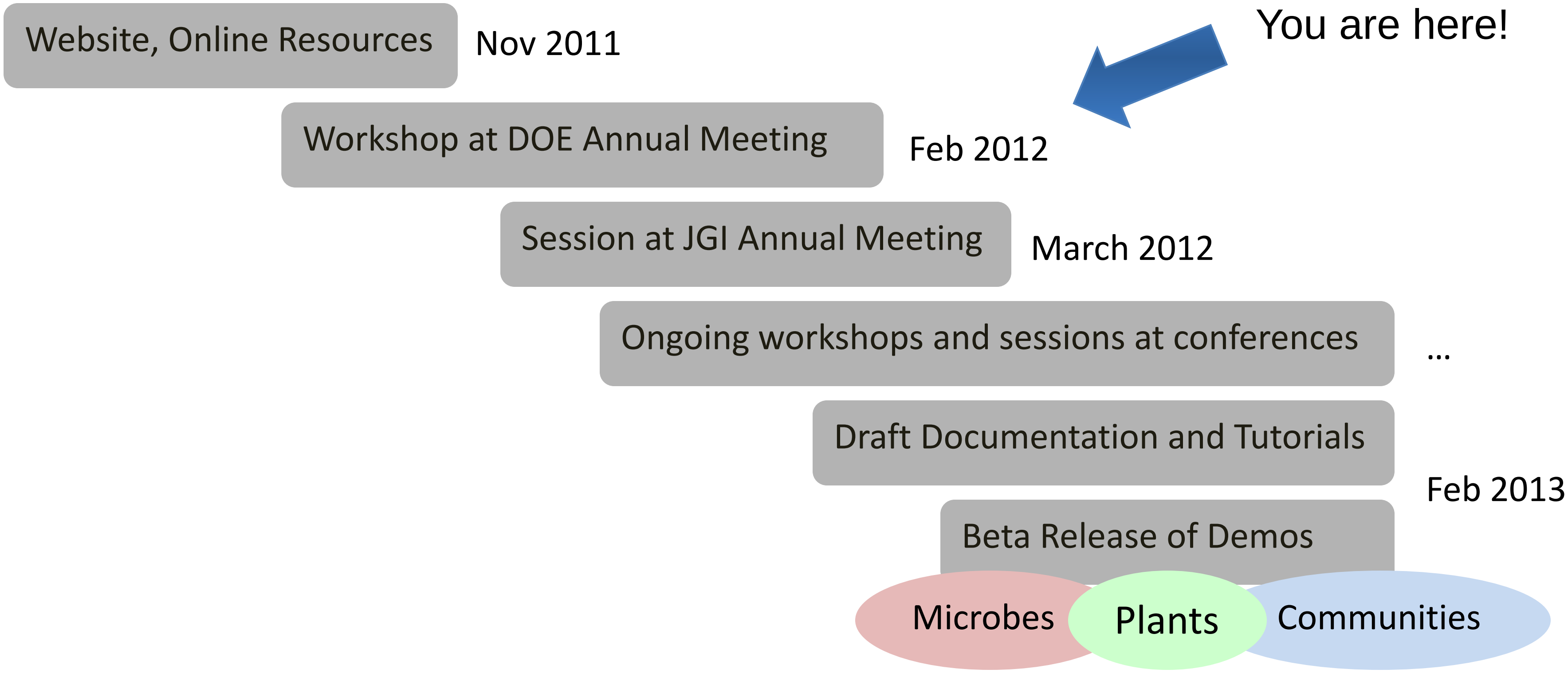
Contact us at outreach@kbase.us

WHEN WILL WE DO IT?

KBase Release/Build Timeline

- Feb 2012 – Development release (internal target)
  - debug release engineering, prototype deployments, initial data models and data loads, non-unified API, performance testing, architecture refinement
- May 2012 – Alpha release (internal target, limited invited testing)
  - draft tutorials, v0.0 database loads, draft API (performance and ubiquity unified prototypes), draft UI library, domain workflow drafts, cloud and cluster services
- Aug 2012 – Beta Release (early adopter beta testing)
  - workflow function complete, API refinement, v1.0 database loads, prototype plugin interfaces, prototype galaxy support, performance debugging
- Nov 2012 – Production Release Candidate (public beta testing)
  - draft website, draft documentation, full functionality API, draft UI v1.0, database loads v2.0, significant number of external beta test users
- Feb 2013 – KBase Production Release
  - public website, unified API, initial production UI, database loads v3.0 (microbes, community, plant databases), production demonstration workflows, replication and fail over services,

Outreach Timeline?



Website, Online Resources Nov 2011

Workshop at DOE Annual Meeting Feb 2012

You are here!

Session at JGI Annual Meeting March 2012

Ongoing workshops and sessions at conferences …

Draft Documentation and Tutorials

Feb 2013

Beta Release of Demos

Microbes Plants Communities

For more information, and to follow our progress, please visit

http://kbase.science.energy.gov/

http://outreach.kbase.us

Thank you!

Visit us at kbase.science.energy.gov

Contact us at outreach@kbase.us