

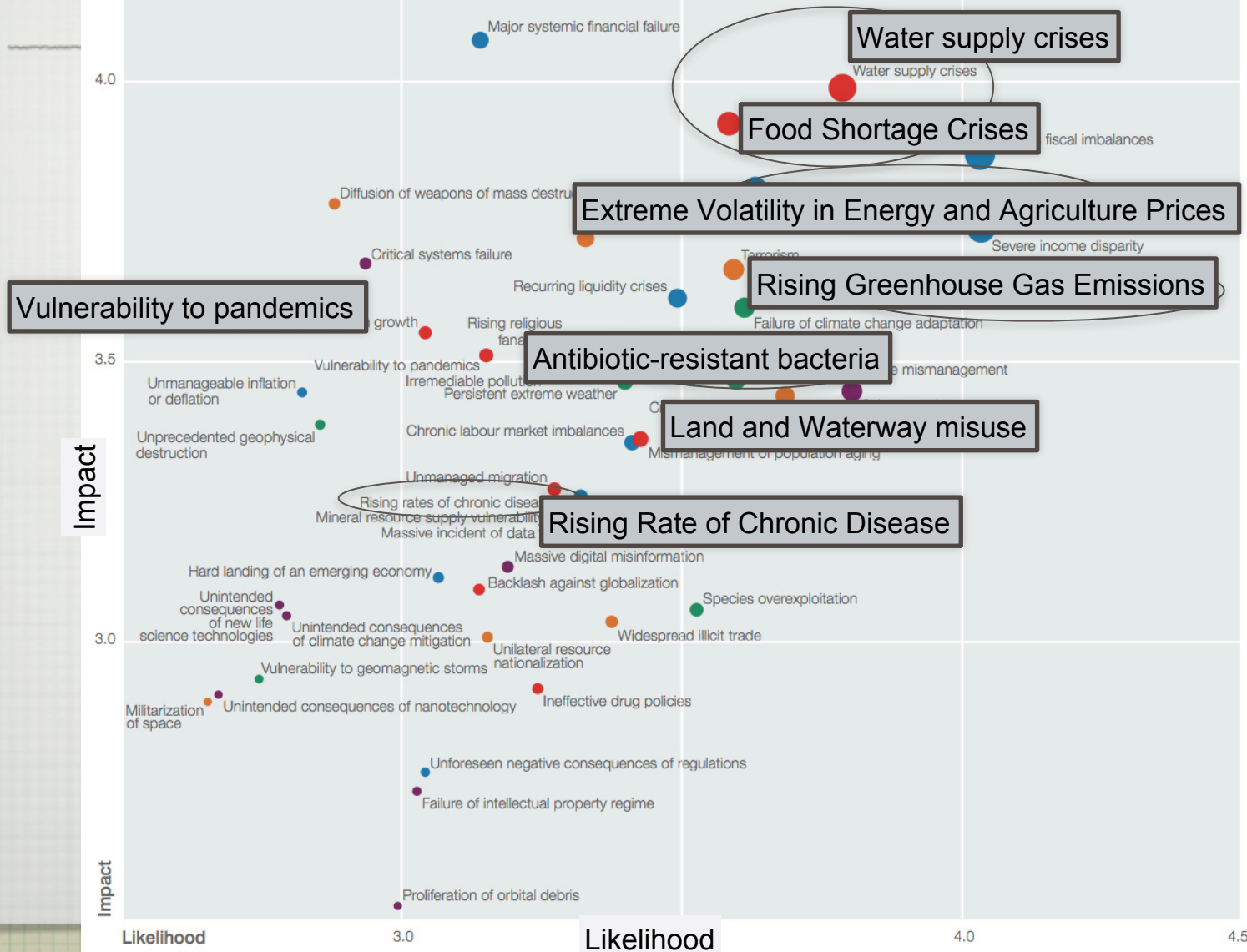


Integrative Genomics Building (IGB) Kbase and JGI

Presentation to Community Advisory Group

May 12, 2014

2012 World Economic Forum Global Risk Report



Why Is Biology a Good Source for Systems Biology & Engineering?

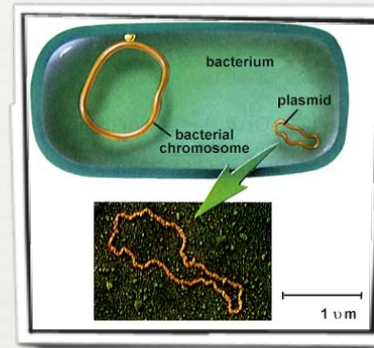
$\sim 10^{30}$ bacteria
Everywhere.



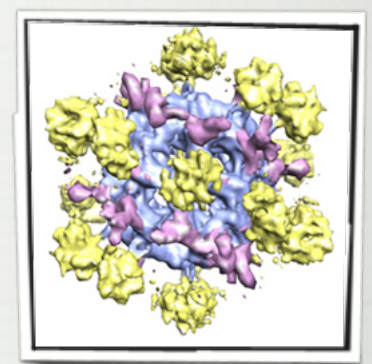
$\sim 10^6$ bacteria/g soil
 $\sim 10^5$ species



~ 4 Mb genomes
 $\sim 10^3$ genes



$\sim 10^3$ proteins
 $\sim 10^7$ interactions



$\sim 10^{11}$ stars in the
Milky Way

$\sim 10^6$ people in San
Francisco

~ 8000 genomes/flash
drive in my pocket

$\sim 10^{23}$ in the
observable universe

\sim Each person emits
 $\sim 10^6$ bacteria/hour

A sense-compute-
and-do system
contained in a 10^{-15}
liters!

$\sim 60,000$ different
classes of protein

Biology Solutions for Big Problems

Water supply crises

Land and Waterway misuse

Rising Greenhouse Gas Emissions

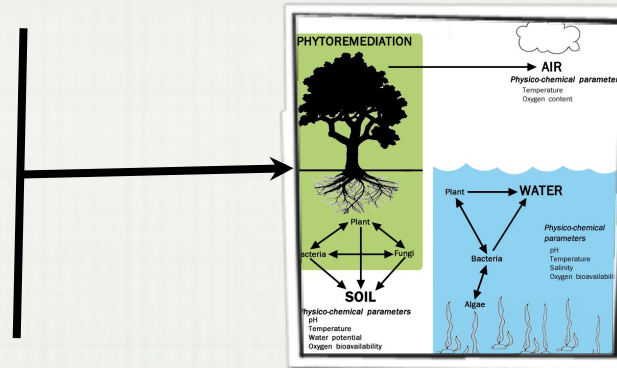
Extreme Volatility in Energy and Agriculture Prices

Food Shortage Crises

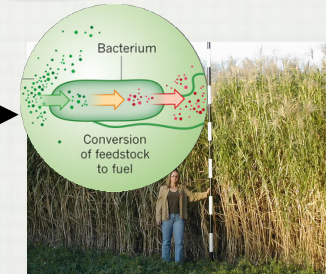
Antibiotic-resistant bacteria

Vulnerability to pandemics

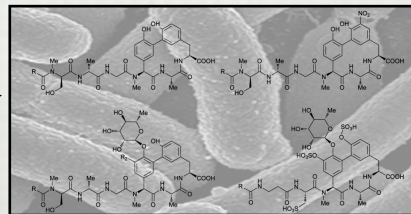
Rising Rate of Chronic Disease



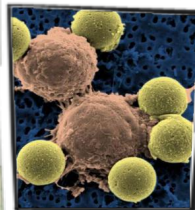
Understand biological impacts and routes to clean soil, water and air



Microbes and plants useful for renewable food and chemical production



Rapid tracking of microbes and gene flow in the environment.



Understanding microbial "gut" communities for underlying responses to environmental change

JGI Overview

User Facility for Large Scale Genomics to Enable Bioenergy and Environmental Research



- Facility
 - Walnut Creek 4-Bldgs/80,000 sq ft
- Staff
 - 284 FTE
- Funding
 - ~69 M US Dept of Energy



Users

DOE
Mission
Areas



Bioenergy



Carbon Cycling

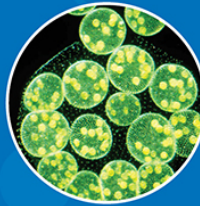


Biogeochemistry

JGI
Programs



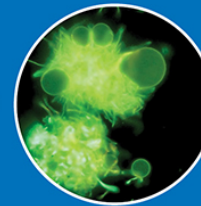
Metagenomes



Plants



Fungi



Microbes

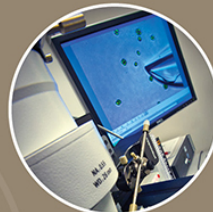


DNA Synthesis
Science

JGI
Infrastructure



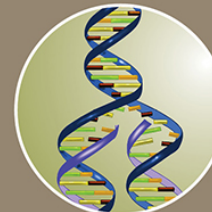
DNA
Sequencing



Advanced
Genomic
Technologies

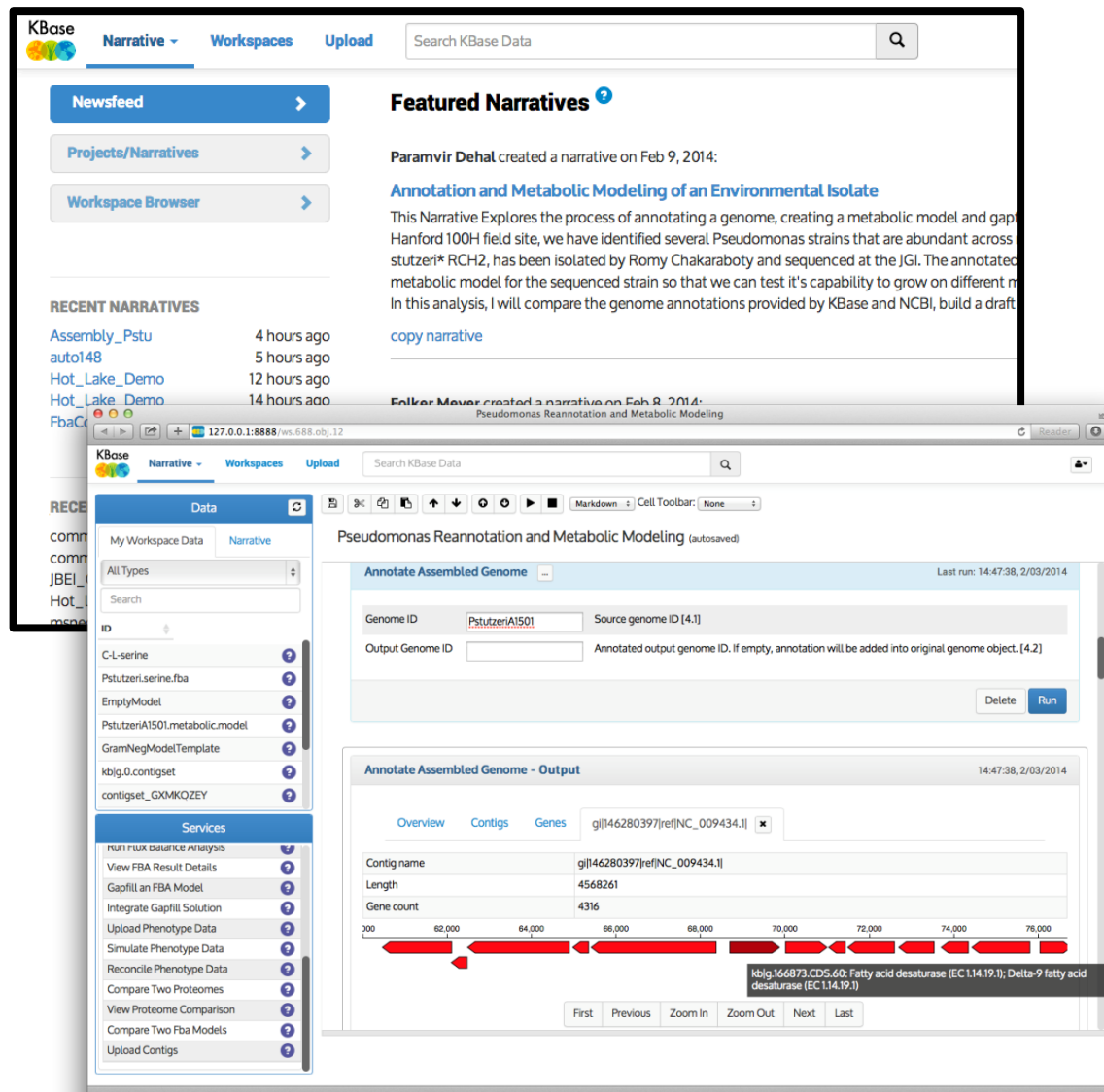


Computational
Analysis



DNA Synthesis

- Novel “Narrative Interface” allows researchers to share their thoughts, methods, and results in an active, persistent document.
- Enables access to hundreds of data access and analysis methods and large public and private datasets in a unified model.
- Allows open, transparent, reproducible science with complex heterogeneous data sets.
- Enables sharing and project management.



The screenshot displays the KBase Narrative Interface, which is a web-based platform for collaborative model-building. The interface is divided into several sections:

- Navigation Bar:** Includes tabs for 'Narrative', 'Workspaces', and 'Upload', along with a search bar for 'Search KBase Data'.
- Newsfeed:** A section on the left with links to 'Projects/Narratives' and 'Workspace Browser'.
- Featured Narratives:** A section on the right highlighting recent work. One featured narrative is titled 'Annotation and Metabolic Modeling of an Environmental Isolate' by Paramvir Dehal, created on Feb 9, 2014. The description states: 'This Narrative Explores the process of annotating a genome, creating a metabolic model and gap-filling. At the Hanford 100H field site, we have identified several Pseudomonas strains that are abundant across stutzeri* RCH2, has been isolated by Romy Chakaraboty and sequenced at the JGI. The annotated metabolic model for the sequenced strain so that we can test it's capability to grow on different media. In this analysis, I will compare the genome annotations provided by KBase and NCBI, build a draft...'.
- RECENT NARRATIVES:** A list of recent narratives including 'Assembly_Pstu', 'auto148', 'Hot_Lake_Demo', and 'FbaC'.
- Main Narrative View:** The central area shows a narrative titled 'Pseudomonas Reannotation and Metabolic Modeling (autosaved)'. It includes a 'Data' panel on the left with a list of datasets (e.g., 'C-L-serine', 'Pstutzeri.serine.fba', 'EmptyModel', 'PstutzeriA1501.metabolic.model', 'GramNegModelTemplate', 'kblg.0.contigset', 'contigset_GXMKQZEY') and a 'Services' panel with various analysis tools (e.g., 'Pant flux balance analysis', 'View FBA Result Details', 'Gapfill an FBA Model', 'Integrate Gapfill Solution', 'Upload Phenotype Data', 'Simulate Phenotype Data', 'Reconcile Phenotype Data', 'Compare Two Proteomes', 'View Proteome Comparison', 'Compare Two Fba Models', 'Upload Contigs').
- Workflow Steps:** The main area shows a workflow for 'Annotate Assembled Genome'. It includes input fields for 'Genome ID' (PstutzeriA1501) and 'Source genome ID' (4.1), and an 'Output Genome ID' field. A 'Run' button is visible.
- Output View:** Below the workflow, the 'Annotate Assembled Genome - Output' section shows a detailed view of the results. It includes a table with columns for 'Contig name', 'Length', and 'Gene count'. The 'Contig name' is 'gll146280397[ref]NC_009434.1', the 'Length' is 4568261, and the 'Gene count' is 4316. A genomic map is shown below the table, with a red arrow indicating the direction of the gene. A tooltip for the gene 'kblg.166873.CDS.60: Fatty acid desaturase (EC 1.14.19.1); Delta-9 fatty acid desaturase (EC 1.14.19.1)' is visible.



Integrative Genomics Building (IGB)

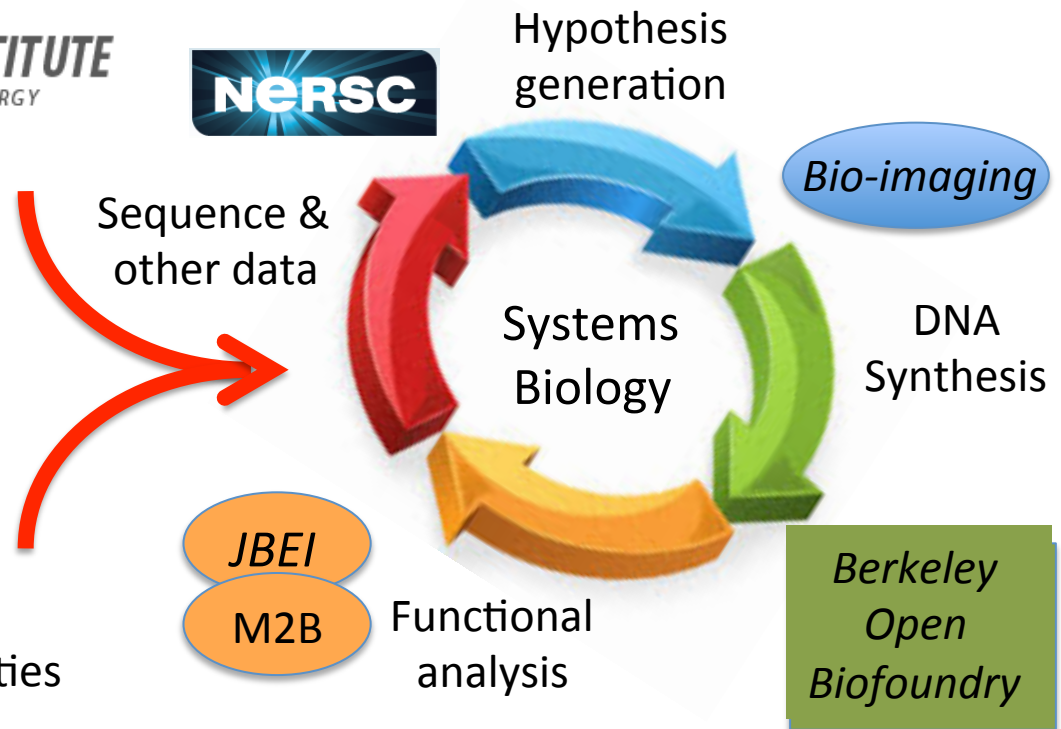
Providing essential infrastructure for systems biology for bioenergy and the environment



HTP sequencing & analysis
DNA synthesis capability
Converting sequence to function



DOE Systems Biology Knowledgebase
Data sharing & integration
Modeling of organisms & communities
Supporting predictive biology





Thank You

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