the PRIMER

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US DEPARTMENT OF ENERGY
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Shake 'N Plate Wins Ergonomics Prize

A team of scientists and engineers from JGI and LBNL have won the prestigious 2007 Ergo Cup, snatching victory (safely) from the jaws of 28 international

Catherine Adam, Diane Bauer, Christine Naca, and Marty Pollard take the prize at the Applied Ergonomics Conference.

finalists with their innovative "Shake 'N Plate" instrument. The 10th Annual Applied Ergonomics Conference, held March 12–15 in Dallas, Texas, hosted the awards. The Ergo Cup, presented by the Institute of Industrial Engineers, provides opportunities for institutions to highlight successful ergonomic innovations.

"Shake 'N Plate," which won in the "team-driven workplace solutions" category, is a simple device designed to alleviate upper body fatigue associated with bacterial culture plating. Operators were manually processing stacks of 22 cm x 22 cm gel-filled plates weighing up to 7 pounds. The hand-grasp forces and total weight during long processing times made this an unpleasant and fatiguing task. The "Shake 'N Plate is a lightweight sheet metal *cont. on page 5*

Establishing a Genomic Encyclopedia for the Bacteria and Archaea (GEBA)

The currently available genome sequences for bacteria and archaea are highly biased in regard to the phylogenetic diversity of the species from which they come. To tackle this bias, JGI will launch a pilot project in the next year, under the umbrella of a Genomic Encyclopedia for the Bacteria and Archaea (GEBA*), to select and sequence 100 bacterial and archaeal genomes based on the phylogenetic position of organisms in the tree of life.

Jonathan Eisen, who splits his time between JGI and UC Davis, is the champion driving the GEBA campaign.

"There is an amazing collection of genomes out there already, but they are phylogenetically biased," says Jonathan. "Despite some prior efforts focused on filling in gaps, too many gaps still exist. To really cover the ground, we need a

systematic top-down effort focused specifically on the gaps."

"This systematic phylogenomic approach will be of great value in multiple areas of DOE and general scientific interest," said JGI Director Eddy Rubin.

The plan being put forward outlines the potential benefits, including:

· Improved identification of protein families and orthology groups across species, which will improve annotation of other microbial genomes;
· Improved phylogenetic anchoring of metagenomic data;
· Gene discovery (which tends to be maximized by selecting phylogenetically novel organisms);
· A better understanding of the processes underlying the evolutionary diversification of microbes (e.g., lateral gene transfer and gene duplication)

and classification and evolutionary history of microbial species.

The organism selection process for the pilot project is being based on a combination of objective analysis of the rRNA tree of life and consultation with a scientific advisory board. All genome sequence data will be released to the community through the JGI Web site and GenBank.

The need for this project may seem surprising to some. After all, nearly 500 bacterial and archaeal genomes have been completed and another 1,000 genome projects are ongoing (see http://www. genomesonline.org). These genome projects have provided important insights into the central roles that bacteria and archaea play in global biogeochemical cycles, *cont. on page 8*

* "The best hot fudge sundae in Walnut Creek is promised to the person who comes up with a better name.

Jan-Fang Cheng — Nearly Two Decade Veteran of DOE Genomics

Jan-Fang Cheng made a rather earth-shattering first appearance in the San Francisco Bay Area—arriving with his wife on October 17, 1989. At 5:04 pm of that fateful day, while driving around the UC Berkeley campus, they wondered why everyone had instantly come piling out of all the buildings. Was this a warm Cali-fornia greeting? A rather rocky one, he'd be tempted to say of the great Loma Prieta earthquake they were experiencing.
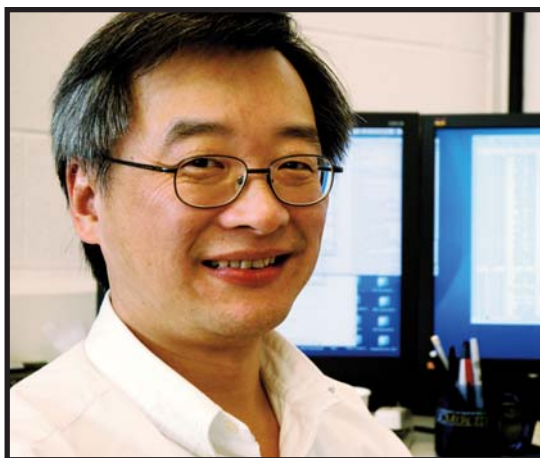
Fang had moved out from Columbia University to help set up the laboratory of Charles Cantor, the first formal director of the Human Genome Center at Lawrence Berkeley National Laboratory.

Cantor left after only one year, leaving a gap temporarily filled by Sylvia Spengler before Jasper Rine from UC Berkeley took over.

After moving up The Hill from the now defunct Stanley Hall on campus, they shifted from the emphasis on Chromosome 21 (where trisomy, or three copies, in the genome can lead to Down's Syndrome) to Chromosome 5. This was done to match the research interests of local investigators in the cytokines that are encoded on that chromosome the hormones that induce blood cells.

"We started mapping the entire Chromosome 5 after successfully building a clone map in the gene dense region of the long arm. We started with YAC [Yeast Artificial Chromosome] clones, then P1, then PAC, then BAC," he said, recounting the historic progress of cloning vectors. "My group basically built the Chromosome 5 map and JGI sequenced it."

Hailing from Taipei, Fang graduated from National Taiwan University (considered the best on the island) where he studied agronomy—where genetics was situated in those days. "Thirty years ago, that was classical genetics. Recombinant DNA had just started. I read the papers and I thought 'this is the field I want to get into—recombinant DNA is the way to improve plants.'"

He came to the United States in 1981 after serving two years in the military, where he served as a lieutenant in an artillery regiment, commanding about 80 enlisted men. "You have to be a leader who knows what you are doing. Just a small mistake in your decision-making can have consequences—even when you're not at war. This mandatory service gave me a chance to learn how to manage people and achieve common goals."

A week after finishing his service, he was on a plane for Penn State, where he did his graduate work with Ross Hardison working on the cloning, sequencing, and expression analysis of the alpha-globin gene family. Fang received a masters degree in genetics and a PhD in molecular and cell biology in 1987.

His wife Becky received a masters in Counseling Education and found a job in New York City, so Fang settled on a position with Cantor at Columbia.

Fang's first night in the Big Apple was also momentous: he got a call from the police, reporting that his car was vandalized. With that introduction, Fang stuck to the subway as the mode of choice up the Westside to Columbia—taking the A train from Brooklyn, "the only way to get to Harlem," as the song goes.

After relocating to Berkeley and moving up The Hill, Fang and (now) JGI Director Eddy Rubin were neighbors in LBNL's Building 74, where Fang's group was mapping human Chromosome 21.

"We were building a YAC map of Chromosome 21 and Eddy proposed to generate Down's Syndrome mice using the YACs that were mapped to the DS critical region." That interaction was fruitful and many more followed.

Fang has returned to his cloning roots in his new position as head of the Process Optimization group at the JGI PGF, which includes the Technology Transfer (led by Nancy Hammon) and the Cloning Technology group (led by Eileen Dalin). He is also working with Tanja Woyke and Ze Peng who are doing R&D work for cloning technologies, "taking on the difficult projects—whole genome amplification from a single cell and fosmid ditags."

"Because we need to have a protocol in place for dealing with the unculturable organisms. An increasing number of projects being proposed are from flow-sorted cells that they want us to sequence. So far we have no way to assess the quality of the amplified DNA, and hopefully it would change in the near future."

Now, after nearly two decades cultivating the rich terrain supported by DOE genomics, Fang likes the challenge of his new position. "I like solving problems that other people can't solve."

The real challenge, Fang said, now lies ahead—putting sequence information to work in our daily life like the Biofuel project. "What is the best way to make use of the information in the genomes we're sequencing?" We shall see.

Super-Fermenting Fungus Genome Sequenced

TO BE HARNESSED FOR IMPROVED BIOFUELS PRODUCTION

On the road to making biofuels more economically competitive with fossil fuels, there are significant potholes to negotiate. For cellulosic ethanol production, one major detour has been addressed with the characterization of the genetic blueprint of the fungus *Pichia stipitis,* by JGI and collaborators at the U.S. Forest Service, Forest Products Laboratory (FPL). The research, entailing the identification of numerous genes in *P. stipitis* responsible for its fermenting and cellulose-bioconverting prowess, and an analysis of these metabolic pathways, is featured in the March 4 advanced online publication of *Nature Biotechnology.*

P. stipitis is the most proficient natural microbial fermenter in nature of the five-carbon "wood sugar" xylose—abundant in hardwoods and agricultural leftovers, which represent a mother lode of bioenergy fodder.

"Increasing the capacity of *P. stipitis* to ferment xylose, and using this knowledge for improving xylose metabolism in other microbes—such as *Saccharomyces cerevisiae,* Brewer's yeast—offers a strategy for improved production of cellulosic ethanol," said Eddy Rubin, DOE JGI Director. "In addition, this strategy could enhance the productivity and sustainability of agriculture and forestry by providing new outlets for agricultural and wood harvest residues."

Ligonocellulosic biomass, a complex of cellulose, hemicellulose, and lignin, is derived from such plant-based "feedstocks" as agricultural waste, paper and pulp, wood chips, grasses, or trees such as poplar—recently sequenced by DOE JGI. Under current strategies for generating lignocellulosic ethanol, these
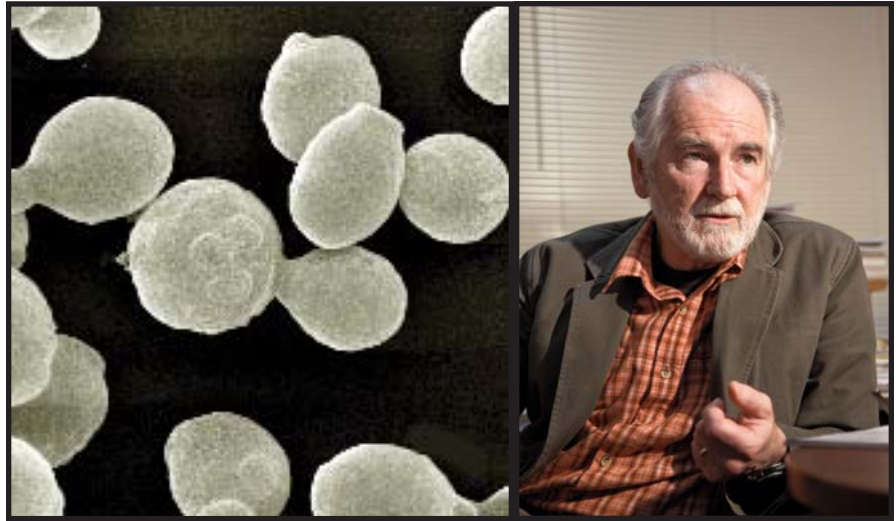
Pichia stipitis—powerful xylose fermentation microbe. Right: JGI Collaborator Thomas W. Jeffries, Ph.D., Director of the Institute for Microbial and Biochemical Technology, USDA, Forest Service, Forest Products Laboratory.

forms of biomass require expensive and energy-intensive pretreatment with chemicals and/or heat to loosen up this complex. Enzymes are then employed to break down complex carbohydrates into sugars, such as glucose and xylose, which can then be fermented to produce ethanol. Additional energy is required for the distillation process to achieve a fuel-grade product. Now, the power of genomics is being directed to optimize this age-old process.

"The information embedded in the genome sequence of *Pichia* has helped us identify several gene targets to improve xylose metabolism," said *Pichia* paper lead author Thomas W. Jeffries of the Forest Products Laboratory in Madison, Wisconsin. "We are now engineering these genes to increase ethanol production." Jeffries said that yeast strains like *Pichia* have evolved to cope with the oxygen-limited environment rich in partially digested wood that is

encountered in the gut of insects, from where the sequenced strain was originally isolated.

FPL has a Cooperative Research and Development Agreement (CRADA) in place with a New York City-based bioenergy company, Xethanol Corporation, which plans to integrate Dr. Jeffries' findings into its large-scale biofuels production processes.

Pichia joins white rot fungus in the growing portfolio of bioenergy-relevant fungus genomes sequenced by DOE JGI through its user programs and contributed freely to the worldwide scientific community.

The JGI effort was led by the Microbial Program Lead and Genomics Technologies Program head Paul Richardson, and included Igor Grigoriev, Andrea Aerts, Asaf Salamov, Erika Lindquist, Paramvir Dehal, Harris Shapiro, along with Jane Grimwood and Jeremy Schmutz of Stanford.

LabAutomation 2007 Conference

MARTY POLLARD

Six staff members from the JGI Production Department attended the LabAutomation 2007 vendor exhibits in Palm Springs, CA on January 28–29. Each year, the LabAutomation conference provides JGI with a great opportunity to see new equipment or look at familiar equipment in new ways. It is also a time when we can talk to vendor sales and technical staff about the directions that JGI is heading in so they can tailor their products and sales pitches to our needs.

In the past couple of years, the LabAutomation conference technical sessions have moved toward addressing topics of more interest to the pharmaceutical industry and a lot less toward DNA sequencing. In a sense, the LabAutomation conference is returning to its roots because this was the focus of the conference when I first started attending in 1998. However, the vendor show has remained the premier venue to see instrumentation relevant to JGI production and research needs. The vendor show had 224 booths for us to visit. For those who have not seen much equipment outside of the JGI, the LabAutomation show is a great way to see what's in use out there. For those of us who have attended the LabAutomation show year after year, the general consensus was that there weren't any dramatic new instrument releases or new technology. Familiar sales people have changed employers, companies have bought other companies, and major robots have had relatively minor improvements. I think we all saw enough to give us something to think about as the JGI moves into an era of new sequencing technologies.

JGI JUDGES SCIENCE FAIR

Students from 11 local middle and high schools presented 95 projects at the Intel-Affiliated Contra Costa 2007 Science and Engineering Fair held at Heald Conference Center on March 22-24. JGI's Diane Bauer and Khela Weiler joined 60 other judges from industry and academia to provide invaluable feedback to the students. JGI's own Karen Kelly, a Clayton Valley High School teacher, served as one of the organizers of the event along with April Treece, Project Director Contra Costa Economic Partnership Workforce Initiative. Karen is seen here with her students who earned top honors.

AWARDS

WENDY SHACKWITZ, ERIKA LINDQUIST
Developed and Implemented JGI Emergency Response Program

RENÉ PERRIER
Contributions to JGI Emergency Response Program

CHRISTINE NACA
Contributions as Ergo Working Group Chair

STEVEN WILSON
Contributions as Safety Culture Group Chair

EILEEN DALIN
Cloning Tech Project Mgmt Efforts

GENOME ASSEMBLY TEAM
New EST Process Pipeline

GREG STANLEY
QuickResponse Avoided Potential Bldg Disaster

HARRIS SHAPIRO, HANK TU, MICHAEL ZHANG, JASMYN PANGILINAN, ED KIRTON
Design and Implementation New Process

CHARLOTTE CANILAO, BETTE HERRERA, REBEKAH SEHORN, ALICIA ROSARIO
JGI New Hire Orientation Process Team

JASON BAUMOHL, KECIA DUFFY-WEI, BRUCE GRAY, STEVE WILSON, SIMONA NECULA
Vendor Barcode Project Team

JGI PROMOTIONS

TANJA WOYKE
Biologist Scientist
PR/Process Optimization

JEFF FROULA
CSE Trainee
IF/Genome Assembly

EILEEN DALIN
Sequencing Supv
PR/Process Optimization

MATTHEW HAMILTON
Sr. Research Associate
Production

LENA PHILIP
Biosciences Tech II
PR/Capillaries

LATEST ARRIVALS

To: Jane
Grimwood &
Jeremy Schmutz
Molly Rose
9/14/06
8lbs 5oz

To: Deepa &
Jayant Patil
Karan
11/11/06
6 lbs 2 oz

To: Maria-Ines
Benito &
Jonathan Eisen
Andrés Benjamin
1/30/07
7 lbs 14 oz

Shake 'N Plate Wins Ergonomic Prize

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The award-winning Shake N' Plate.

platform mounted on a ball joint similar to a camera tripod. In fact, one of the operators used the camera tripod idea as her original design suggestion to the JGI Instrumentation Group. The design was quickly fabricated in the LBNL shops and put into production use. The device removes almost all of the weight from the operator's arms and actually improves the process throughput.

"Shake 'N Plate" upstaged such big competitors as Boeing, GE, Harley Davidson, and Toyota to take home the prize. The winning team of JGI and LBNL Engineering Division staff was comprised of Christine Naca, Martin Pollard, Diane Bauer, Catherine Adam, Simon Roberts, Karl Petermann, Charlie Reiter, Ira Janowitz, Karli Ikeda, Miranda Harmon-Smith, Sanna Anwar, and Damon Tighe.

For more about the Applied Ergonomics Conference and the Ergo Cup competition, see http://www.appliedergo.org/conference/ErgoCup.htm.

JGI New Employees

KATHRYN BOWSER
Biosciences Tech 1
PR/Sequencing

MIKE CANTOR
Computer Scientist
IF/Genome Data Systems

**DHARSHANI
DHARMAWARDENA**
Student Assistant
PR/Capillaries

CINDY EHSAN
Senior Admin
*Procurement, Finance &
Materials*

BRIAN FOSTER
Systems Analyst 2
GT/Microbial Genomics

JACOB (YAKOV) GOLDER
Computer Systems
Manager II
Informatics

JAMES HAN
Biosciences Tech II
PR/QC

SEAN HOOPER
Computational Biologist
Postdoc
Programs/Genome Biology

CHERYL KERFELD
Biologist Staff Scientist
Programs/Education

KURT LABUTTI
Systems Analyst 2
GT/Microbial Genomics

DAVID LAI
Desktop Systems
Specialist 2
IF/Systems Admin

RACHEL MACKELPRANG
Visiting Postdoc
Programs/Vertebrate

ABBY NGAU
Software Developer 3
IF/Genome Data Systems

SIRISHA SUNKARA
Systems Analyst 2
GT/Sequencing Tech

BRIDGET SWIFT
Biosciences Tech 1
PR/Capillaries

AIJAZUDDIN SYED
Software Developer 3
IF/Genome Assembly

SUSAN TAYLOR
Computer Scientist
Genome Data Systems

PAUL WINWARD
Computer Scientist
*IF/Genome Assembly*

QUIYAN XU
GSRA
PR/QA_QC

ZHIYING ZHAO
Sr Research Associate
GT/Sequencing Tech

Puzzling Plankton Yield Secrets to Role in Evolution/Global Photosynthesis

The analysis of DNA sequences from tiny green algae have provided insights into the mystery of how new species of plankton evolve—and further highlights their critical role in managing the global carbon cycle. These findings—from a group led by JGI, the University of California, San Diego, and the Pierre & Marie Curie University—were published the week of April 23, 2007 in the *Proceedings of the National Academy of Sciences* (PNAS).

Ocean-dwelling phytoplankton from the genus *Ostreococcus* emerge at the primitive root of the green plant lineage, dating back nearly 1.5 billion years. Today, these microscopic, free-living creatures, among the smallest eukaryotes ever characterized—barely a micron in diameter—are major contributors to nearly half of the world's total photosynthetic activity. These "picophytoplankton" also exhibit great diversity that contrasts sharply with the dearth of ecological
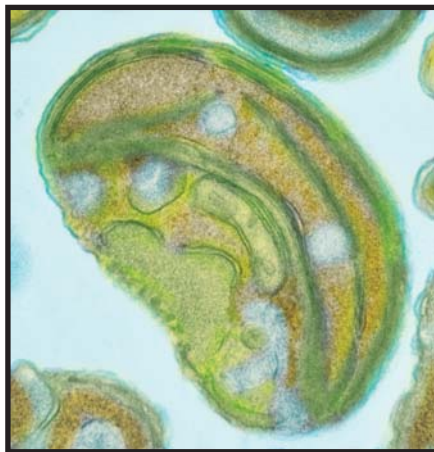
Ostreococcus yields secrets

niches available to them in aquatic ecosystems. This observation, known as the "paradox of the plankton," has long puzzled biologists.

Plumbing the depths of molecular-level information of related species, genomics offers a novel glimpse into this paradox. The researchers compared the genomes of two *Ostreococcus* species, *O. lucimarinus* and *O. tauri,* and saw dramatic changes in genome structure and metabolic capabilities.

"We found several striking features of genome organization," said JGI's Igor Grigoriev, the PNAS paper's senior author. "Overlapping genes conserved across the species may enable them to cross-regulate their expression, while species-specific chromosomes with horizontally-transferred genes can account for changes in the cell surface to adapt to different ecological niches." Grigoriev and his colleagues noted the abundance of selenium-rich proteins that surfaced in their analysis, which he said allows the organisms to horde nutrients and reduced their appetite for iron—an adaptive process in *Ostreococcus.*

"This work builds on the community's emerging understanding about how carbon fixation is car- *cont. on page 11*

IMG 2.1 Data Management System Released

As interest mounts in the rising number of newly characterized microbial genomes, powerful computational tools become critical for the management and analysis of these data to enable strategies for such challenges as harvesting the potential of carbon-neutral bioenergy sources and for coping with global climate change. JGI's Integrated Microbial Genomes (IMG) data management system addresses this challenge with the release of version 2.1. Released on the second anniversary of its launch, the content of IMG 2.1 is updated with new microbial genomes from the latest release of the National Center for Biotechnology Information's (NCBI) Reference Sequence collection (RefSeq), Version 21. Other enhancements feature model eukaryotic genomes, including several well-characterized yeast species, and plasmids, the double-stranded circular DNA molecules independent of any sequenced microbes—significantly expanding the utility of the system for comparative genome analysis.

"Our work on the genomes of *Chlorobi* and *Chloroflexi* has resulted in more than a dozen genomes through JGI, and members of my research group use the IMG site daily, if not hourly," said Don Bryant, Ernest C. Pollard Professor of Biotechnology and Professor of Biochemistry and Molecular Biology at Penn State University.

EVOLUTIONARY BOOKMARKING

BY RENÉ PERRIER

A bookmark is a marker that identifies a Web document or a specific place in such document. But, unlike genes, bookmarks have evolved quite rapidly since their first appearance during the last millennium (or just 13 years ago, depending on how you look at it).

PHASE 1: PRIMITIVE BOOKMARKING

In the old days, a typical Internet user on her computer at work would "bookmark" a Web page on her browser that she wanted to revisit later. She would then revisit the same page from the same browser a few weeks later. Or she would try to remember how to find that page again from her home computer since the "bookmark" was stored on her work computer...

PHASE 2: ONLINE BOOKMARKING

Many companies started to offer free services that would let users store their bookmarks online and access them from anywhere. Most of these companies died when the Internet bubble burst (evolution on the Internet can be cruel, too)

PHASE 3: SOCIAL BOOKMARKING

This is when bookmarking merges with the social software revolution. Some smart people realized that sharing bookmarks would increase the value of these bookmarks and allow everyone to discover new pages that were deemed interesting enough by their friends, peers, mentors, or even just strangers.

FOLKSONOMY

A folksonomy is a user-generated taxonomy used to categorize and retrieve Web pages, photographs, Web links, and other Web content using open-ended labels called tags." These tags became very useful when users realized that they needed some way of organizing their bookmarks. Browsers and early online bookmarking tools would let them organize their bookmarks in some kind of list or tree structure, but it clearly became insufficient for organizing hundreds of bookmarks.

Using the folksonomy concept, users now are able to organize their bookmarks using "tags." These tags are just collections of words the users associate with the bookmarks. For instance, I could bookmark an article in an online magazine about sequencing termite guts to produce better and cheaper biofuels. I would tag this article with words like "energy," "metagenomics," "biofuels," "environment," and "jgi"—even if the word "jgi" is not technically a word and the word "metagenomics" does not appear in the article.

Social bookmarking tools generally provide search capabilities so that anyone could find this article when looking for all the pages tagged with the word "metagenomics." If the article does not contain the word "metagenomics," a similar search with a tool like Google would not return it. With an index-based search engine like Google, searching for "humor" pages will only return pages that do contain the word "humor." Using a folksonomy-based engine, it will return all the pages that were tagged with the word "humor" by the "folks" using the system.

These tools are also evolving and now provide features like:
· When searching using one or more tags, the search results are ordered by popularity. The more a given page gets tagged, the higher it will be in the results list.
· It is possible to see the list of people that tagged a given page and see the other pages they tagged as well. This allows users to explore the bookmarks of others who share their affinities.
· When tagging a page, the tagging engine will make a list of suggestions based on the tags used for the same page by other folks. This increases the chances of using similar tags for similar pages, as opposed to having a collection of similar words like "fun," "funny," "joke," "jokes".
· Some bookmarks can be kept private and others shared.
· Query-based RSS feeds (see previous edition of the Primer) can be built (notify me as soon as a new page is being bookmarked with the tag "jgi").
· Lists of the most popular bookmarked pages, tags, etc.
· Some tools even provide an API that developers can use to access the services programmatically.

EXAMPLES

http://del.icio.us

Del.icio.us is one of the first social bookmarking tools that came online and is the one that is likely to be most popular for the time being.

http://www.connotea.org/

Connotea is a free online reference management service for scientists, researchers, and clinicians, created in December 2004 by Nature Publishing Group. In other words, a tagging engine for the scientific community.

Genomic Encyclopedia for the Bacteria and Archaea (GEBA)

cont. from page 1

health, agriculture, and evolution. Much microbial genomics work has now moved beyond sequencing particular organisms to functional genomic studies and/or metagenomic sequencing of DNA isolated directly from the environment.

"Though metagenomic and functional genomic studies are critical to understanding the role of microbes in the wild, there is still much work needed in terms of the characterization of the genomes of particular organisms" says Jonathan. Though there are many projects that focus on particular phenotypes, like extremophiles and pathogens, no projects focus on filling in the gaps in the tree of life. "We believe that this gap filling is a critical need because genomes from these organisms will aid almost all aspects of comparative and metagenomic studies, such as genome annotation and identification of organisms in the environment."

AMOUNT OF SEQUENCING AND SELECTION CRITERIA

Overall, the long-term goal of this project would be to generate reference genomes for every major and minor group of bacteria and archaea. This could represent on the order of 5,000 genomes. This amount of sequencing is not beyond the capabilities of the current capacity of major genome sequencing centers, says Jonathan. "If we assume that the average genome size is four megabases, which is probably an overestimate, then to sequence 5,000 genomes would be the equivalent of sequencing a 20 billion base pair genome. So, basically, this is the equivalent of a few mammalian genomes. However, though the sequencing itself is within current capacities, there are management and quality control issues associated with carrying out such a project including growth, DNA isolation, library construction, etc. Therefore, we are using our pilot project to test some of these issues."

For current and past sequencing projects, a large number of criteria have been employed, including societal importance relevant to funding agency mission, physiological uniqueness, and size of the research commu-


Jonathan Eisen at the 2007 JGI User Meeting explaining the motivation behind the launch of GEBA.

nity working on an organism.

"We believe that this project should be driven largely by taxonomic criteria—that is, organisms should be selected to increase the coverage of genomes across the diversity of bacteria and archaea. Such a taxonomic approach could be balanced in various ways by other criteria, such as technical feasibility or societal importance. For example, one could identify a taxonomic group for sequencing, let's say a particular phylum, and then the choice of which organism to sequence from within that phylum could be refined by other criteria."

"This is a pilot," says Jonathan, "We are hoping to learn a lot from this pilot, but we want to turn this into a broad community-guided effort to coordinate the sequencing of genomes across the tree. We will convene a meeting soon to solicit active community input."

Phylogenetic tree showing major lines of bacterial descent. Most of these lineages have not been sequenced (pale blue), and of those, most only have a few sequenced representatives (green). Only three of more than 40 lineages have significant numbers of representatives with sequenced genomes (in red): the Proteobacteria, Firmicutes, and Actinobacteria.
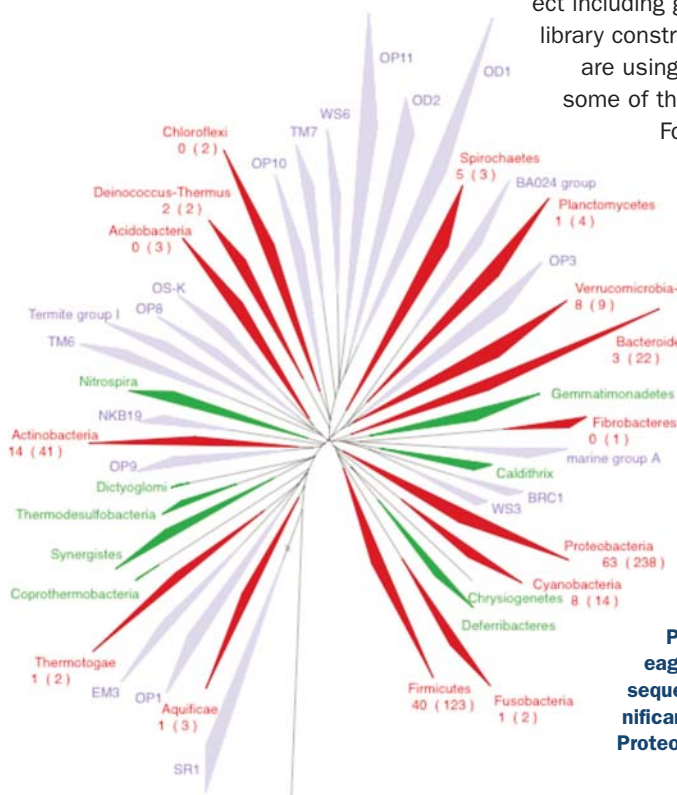
JGI Researchers Teach UC Merced Students

With the help of researchers from JGI, Miriam Barlow and Mónica Medina of UC Merced's School of Natural Sciences are coordinating an innovative theoretical and experimental course in genomics.

"For undergraduate students, working directly with top biomedical research scientists is a rare and valuable opportunity, and the collaborative approach in our genomics course is groundbreaking," said Dean of Natural Sciences Maria Pallavicini. "It's the kind of opportunity UC Merced was built to offer."

This semester, 14 students are studying with 20 JGI researchers led by JGI's Pilar Francino.

"We had a great response from everybody," said Pilar. "Actually, for some topics, we had to choose among several potential lecturers that were interested in teaching."

JGI scientists take turns visiting the UC Merced campus to teach procedures involved in genome projects. They do this by working with students on several small projects that illustrate different aspects of genome science, like DNA preparation, library construction, sequencing, genome assembly, gene prediction, and annotation.

JGI collaborating scientists, Jerry Tuskan from Oak Ridge National Laboratory and Ellen Panisko from Pacific Northwest National Laboratory, are also slated to participate in teaching the course.

The small projects for teaching the course all originated with UC Merced researchers.

Medina's contribution is a project sequencing DNA from microbes in coral reefs, with the aim of finding out why coral reefs are becoming sick.

Barlow's project involves sequencing plasmids—circular DNA found in bacteria
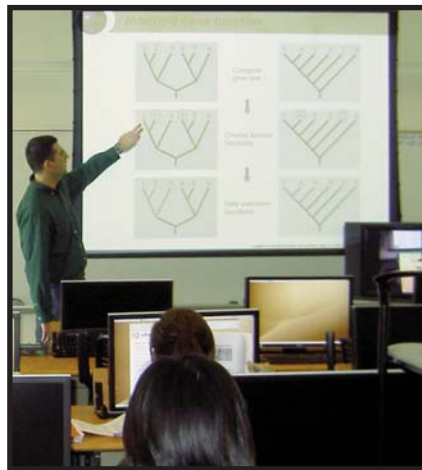
Konstantinos (Kostas) Mavrommatis of the JGI's Genome Biology Program presents an introduction to bioinformatics at UC Merced on March 1st.

—that contain multiple copies to resistance genes to determine if and how plasmids remove resistance genes.

Graduate student Shinichi Sunagawa defined a project sequencing genes expressed in sea anemones to study the cell biology of symbiosis.

Professor Andrés Aguilar's project

aims to determine how species of rockfish have formed by sequencing expressed genes in that group of fish.

Finally, Professor Benoît Dayrat contributed a project involving sequencing the mitochondrial genomes of gastropods to determine how they are related to each other.

The students in the course will analyze and interpret these sequencing projects under the direction of their UC Merced professors and scientists from the JGI.

"This course involves hands-on training to familiarize our students with the protocols in use at the Joint Genome Institute," said Mónica, who was with the JGI before accepting a faculty appointment at UC Merced in 2005.

UC Merced opened September 5, 2005 as the 10th campus in the University of California system and the first American research university of the 21st century. The campus significantly expands access to the UC system for students throughout the state, with a special mission to increase college-going rates among students in the San Joaquin Valley.

UC MERCED LECTURERS FROM JGI

JGI sequencing process	Damon Tighe
Library creation	Jennifer Kuehl
Genome maps	Jan-Fang Cheng
Sequencing technology	Sue Lucas
Microbial genomes	Thanos Lykidis
Unix overview	Wayne Huang
Animal genomes	Dario Boffelli
QC and Genome assembly	Alla Lapidus, Eugene Golstman
EST libraries	Erika Lindquist, Ed Kirton
Transcriptomics	Rick Baker
Microbial biodiversity	Falk Warnecke
Gene prediction	Asaf Salamov
Genome annotation	Igor Grigoriev, Astrid Terry
Metagenomics	Susannah Tringe, Tanja Woyke
Comparative genomics	Pilar Francino, Paramvir Dehal

JGI Springs into Jamborees

Bracketing the User Meeting, JGI coordinated four recent genome annotation jamborees—workshops designed to computationally assign biological features and function to the genomes being sequenced.

During the User Meeting, the Production Genomics Facility hosted a Eukaryotic Annotation Jamboree for JGI 2005-2007 eukaryotic genome project proposers, their collaborators, and new members of those communities for which genomes will be annotated during 2007. Some 90 Users participated in this workshop. The JGI Genome Portal offers an interface to several bioinformatics tools for analysis of genomes sequenced, assembled, and annotated at JGI. Genome Portals for over 20 eukaryotic genomes are publicly available and support distributed community-driven manual curation and analysis for all of them.

The PGF also held the *Micromonas pusilla* Jamboree April 2-4. Three dozen *Micromonas* researchers from around the world gathered to annotate from *Micromonas pusilla. Micromonas,* phytoplankton abundant in oceans that play a critical role in global management of

CO_2, are among the smallest known eukaryotes (one to three microns).

Before the JGI User Meeting, a *Postia placenta* (brown rot) Jamboree was held March 18-19 in Pacific Grove, California, in conjunction with the Asilomar Fungal Genetics Meeting. This Jamboree was organized by Jean Challacombe and Diego Martinez from JGI LANL.

On March 20, 2007, the last day of Oomycetes Conference preceding the Fungal Meeting, the JGI Annotation Team (Andrea Aerts, Alan Kuo, Diego Martinez, and Igor Grigoriev) trained two dozen *Phytophthora* researchers on analysis of initial annotations of *Phytophthora capsici* genome. During the next two days of the conference, Alan Kuo reported on annotation results at the *Phycomyces*

blakesleaanus and *Nectria haematococca* workshops and Igor Grigoriev gave talks at the *Dothideomycetes* workshop and comparative genomics session of the conference. These jamborees not only helped to develop plans for further work for individual genomes sequenced at JGI, but the significant presence of JGI troops enabled stronger interactions with JGI User Communities. At the end of the meeting, Scott Baker of PNNL and other external users said that they were glad that JGI had infiltrated the larger meeting.

Finally, 20 students and staff from the UC Merced Genomics Course made a field trip to the PGF to participate in a custom annotation jamboree on Saturday, April 14.

2007 JGI User Meeting

They gathered in Walnut Creek, from Adney to Zhou, spanning the globe from New Zealand to Sweden:

Registrations: 404
Posters: 71
Tour participants: 181
Reception participants: 296
IMG workshop attendees: . . . 137
JGI workshop participants: . . 248

POPLAR VERNALIZATION

JERRY TUSKAN, ORNL &
JGI LSP LEAD

Perennial plants such *Populus* differ from annual plants in several ways. One of the most obvious is the ability to grow over many years, sometimes over many centuries. To accomplish this in a temperate region such as the United States or Europe, most perennial plants go through a dormancy period where nutrients are reallocated to below-ground tissues, while aboveground tissues accumulate solutes to assure their survival during freezing or sub-freezing wintertime conditions. This transition leads to the sometimes brilliant fall colors we see on trees and

A bud from the JGI's sentinel poplar tree which is now 60.5 inches tall.

shrubs and is triggered by shortening day lengths witnessed in the fall. Once a plant has gone dormant, it usually requires a period of cold temperature to break dormancy and to initiate the redistribution of nutrients to the apical portion of the plant. This process is known as *vernalization.* The warmer temperatures and longer days in the spring lead to bud flush and sometimes flowering. Nisqually-1, the first perennial woody plant to have its genome sequenced, like all temperate perennial plants, is following this same schedule and will flush new leaves in the spring, grow in the summer, lose its leaves in the fall, and remain dormant in the winter.

JGI EXPANDS HORIZONS

On Saturday, March 3, 2007, a female contingent of JGI staff helped nurture the next generation of young women in genomics through the "Expanding Your Horizons" program at Diablo Valley College in Pleasant Hill, CA. The "Build a Berry" exercise enabled participants to extract DNA from fresh strawberries, build a simulated strawberry gene using a giant DNA model, and conduct online BLAST searches to elaborate the functions of genes. The JGI team included: Eileen Dalin, Pilar Francino, Karen Kelly, Susan Lucas (below), Wendy Schackwitz, Kristen Taylor, Susannah Tringe.
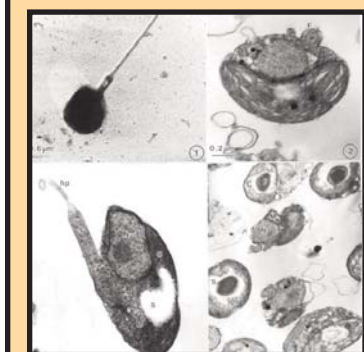
Micromonas particpantii

Several of the *Micromonas* jamboree participants took a break to gather on the steps of the PGF. Front row: Hervé Moreau, Evelyn Derelle, Andy Allen, Sarah McDonald; middle row: Uwe John, Marie Cuvelier, Micaela Parker, Meredith Everett, Alex Worden; back row: Thomas Mock, Rory Welsh, Kemin Zhou, Igor Grigoriev, Pierre Rouze

Puzzling Plankton Yield Secrets

ried out by picoplankton," said Brian Palenik, lead author and researcher at Scripps Institution of Oceanography, University of California, San Diego.

"From an applied perspective, we are learning some of the tricks nature has employed to 'engineer' an extremely small eukaryote to thrive in nature—which may well find applications in bioengineering," said Palenik. "It was particularly interesting to see the predicted use of selenium-containing enzymes as one of the tricks to maintain such tiny cells. There are many mechanisms that can account for species formation in photosynthetic phytoplankton and this

is just one of the major pieces to this long-standing puzzle for biologists."

"Assimilation of atmospheric CO_2 by marine phytoplankton is a global-scale process that is responsible for about half of the biosphere net primary production," said collaborator and co-author Hervé Moreau of the Pierre & Marie Curie University Oceanic Observatory in Banyuls-sur-mer, France. "This active absorption of hundreds of millions of tons of carbon per day is essential for maintaining the control of the planet's climate by counteracting greenhouse effects due to human activities. Clearly, this storage capacity is affected by

changes in the photosynthetic efficiency of the algae, which in turn is linked to the environmental conditions experienced by these organisms in their environment."

The ecology of picoeukaryotes has thus become an intense field of investigation over the last decade as these microalgae, although representing a minor component of the plankton, nevertheless play major roles in oceanic biomass production.

Other JGI authors include Andrea Aerts, Jane Grimwood, Jeremy Schmutz, Asaf Salamov, Nicholas Putnam, Kemin Zhou, Robert Otillar, Gregory Werner, Inna Dubchak, and Daniel Rokhsar.

RECENT NOTABLE JGI-ENABLED PUBLICATIONS

Strain-resolved Community Proteomics Reveals Recombining Genomes of Acidophilic Bacteria

Nature 446, 537-541 (29 March 2007) | doi:10.1038/nature05624

> Ian Lo, Vincent J. Denef, Nathan C. VerBerkmoes, Manesh B. Shah, Daniela Goltsman, Genevieve DiBartolo, Gene W. Tyson, Eric E. Allen, Rachna J. Ram, J. Chris Detter, Paul Richardson, Michael P. Thelen, Robert L. Hettich & Jillian F. Banfield

Genomic data sets used to identify, with strain specificity, expressed proteins from the dominant member of a genomically uncharacterized, natural, acidophilic biofilm.

Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments

Science 23 February 2007: Vol. 315. no. 5815, pp. 1126 – 1130 doi: 10.1126/science.1133420

> C. von Mering, P. Hugenholtz, J. Raes, S. G. Tringe, T. Doerks, L. J. Jensen, N. Ward, P. Bork

Protein-coding marker genes, extracted from large-scale environmental shotgun sequencing data, provided a more direct, quantitative, and accurate picture of community composition than that provided by traditional ribosomal RNA–based approaches depending on the polymerase chain reaction.

**The *Calyptogena magnifica* Chemoautotrophic Symbiont Genome**

Science 16 February 2007: Vol. 315. no. 5814, pp. 998 - 1000 zDOI: 10.1126/ science.1138438

> I. L. G. Newton, T. Woyke, T. A. Auchtung, G. F. Dilly, R. J. Dutton, M. C. Fisher, K. M. Fontanez, E. Lau, F. J. Stewart, P. M. Richardson, K. W. Barry, E. Saunders, J. C. Detter, D. Wu, J. A. Eisen, C. M. Cavanaugh

The *Calyptogena magnifica* (clam) symbiont, *Candidatus Ruthia magnifica*, is the first intracellular sulfur-oxidizing endosymbiont to have its genome sequenced, revealing a suite of metabolic capabilities.

PUBLICATION FACTOID (CARE OF JGI WEB DEVELOPER ANNETTE GREINER):

DOI numbers can be used to build a "permanent" URL (technically a URI) for an article published online. You can find DOI numbers for *Science* and *Nature* articles by looking at the top of the article on the *Science* or *Nature* web site. Then you just add the DOI number to the address of a doi server. Annette uses dx.doi.org. So, for an article with DOI number 10.1038/nb51290, the "permanent" URL is http://dx.doi.org/10.1038/nbt1290.

The first part of the DOI number is always the code for that particular journal, so everything published by *Nature* starts with 10.1038. DOI numbers are starting to show up in citations. There's a more thorough explanation at: http://www.doi.org/index.html.
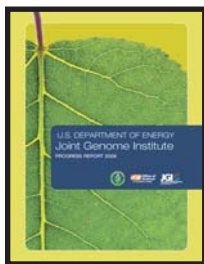
The 2006 edition of the JGI Progress Report is now available. For hardcopies, contact David Gilbert: gilbert21@llnl.gov

FINISHING IN THE FUTURE

The second annual "Finishing in the Future" meeting wil be held June 18–20 in historic Santa Fe, New Mexico. To register, please visit our Web site at http://finishingfuture.lanl.gov/. If you have any questions, please contact Chris Detter at (505) 667-1326 or cdetter@lanl.gov.