Automating the JGI's Community Sequencing Program

Jayant Patil[1], Joni Fazo[2], Art Kobayashi[2], Annette Greiner[1], Arkady Voloshin[1], Pat Kale[2], Marsha Fenner[1], David Bruce[3], Jan-Feng Cheng[1] and Jim Bristow[1]

[1]Lawrence Berkeley National Laboratory / DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598

[2]Lawrence Livermore National Laboratory / DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598

[2]Los Alamos National Laboratory / DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598

March 26, 2007

ACKNOWLEDGMENTS:

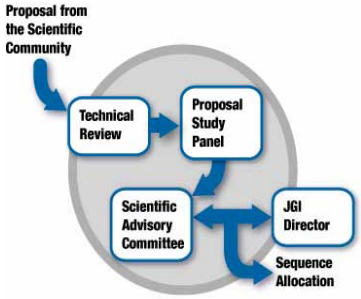
The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231

Automating the JGI's Community Sequencing Program

Jayant Patil[1], Joni Fazo[2], Art Kobayashi[2], Annette Greiner[1], Arkady Voloshin[1], Pat Kale[2], Marsha Fenner[1], David Bruce[3], Jan-Fang Cheng[1], and Jim Bristow[1]

What is the Community Sequencing Program?

The Community Sequencing Program (CSP) provides the scientific community at large with access to high throughput sequencing at the Department of Energy's Joint Genome Institute (JGI) for projects of relevance to DOE missions. Through this program, the Department of Energy aims to advance sequence-based scientific research from a broad range of disciplines.



How does the review process work?

All proposals undergo the following reviews:

- *Technical review*
- *Proposal Study Panel (PSP) review*
- *Scientific Advisory Committee (SAC) review*

Proposals are evaluated on scientific merit and relevance to DOE mission.

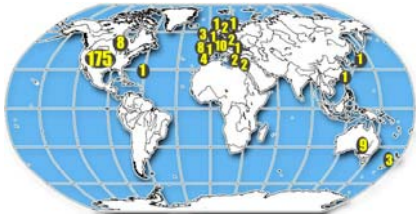
DOE Mission

✓Bioremediation ✓Global carbon recycling
✓Alternative energy production

What happens after proposals are accepted?

- Scope of Work, User Agreement and other required documents are approved.
- Proposals are converted to projects.
- Sequence traces are released to the Genbank Trace Archive on a regular basis.
- The JGI makes the assemblies, gene annotations, and analyses available to the community at large.

CSP 2007 submissions



Web User Interface

How to participate?

Established in 2004 as a manual process, we have since moved to an automated system that manages the proposal submission, review, and notification process. Scientists from around the world submit proposals through our website, http://www.jgi.doe.gov/CSP/proposals.

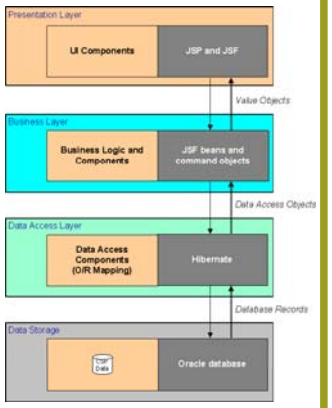
[1] DOE Joint Genome Institute - BACE Division, Lawrence Livermore National Laboratory
[2] DOE Joint Genome Institute - Genomics Division, Lawrence Berkeley National Laboratory
[3] DOE Joint Genome Institute - Los Alamos National Laboratory

Technology behind the CSP application

The automated CSP application is based on a J2EE multi-tier architecture:

- The *Presentation Layer* with web UI components built in Java Server Faces (JSF) and Java Server Pages (JSP).
- The *Business Layer* consists of JSF beans, servlets, and Java command classes.
- The *Data Access Layer* is an O/R mapping layer developed with the open-source technology Hibernate.
- *Oracle database.*

Application architecture



Iterative development

We are using an iterative software process with a focus on ***Just In Time*** software delivery to best support this exciting and important program.

2 to 3 weeks iterations that span multiple disciplines.

- Requirements
- Implementation
- Testing
- Deployment

We are using Twiki for frequent team and user communication and documentation.

Support

- Development team provides daily support to worldwide CSP users.
- We are using the RequestTracker tool for management and tracking of requests and follow-up customer communications.

What's next?

- All JGI proposals will be accepted through the CSP application.
- Improve the user interface with AJAX technology.
- Enhance analytical reporting.

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231