Pilot Usability Study

Welcome. The purpose of this interview is to examine the usability of this collaborative gene annotation tool, not you. Any problem you encounter will help us improve it. You can quit at any time.

Tell us your thoughts as you are working. If you forget to think aloud, we may remind you. Please ask questions as they occur to you, but we will not be able to answer them until the end of the test.

Your feedback is highly appreciated. Thank you for participating in this test.

A. ORIENTATION

We are currently developing an add-on to the existing JGI IMG portal, which you should already be familiar with. Basically, we have received many requests, throughout the lifetime of the IMG system, for a system which would allow users to annotate genes, upload these annotations for others to see, view other people's annotations, and discuss any points of contention. The current system implements only functional annotation; for the present time, structural annotation remains outside of the scope of this project. You can think of this as an additional feature set which will be tightly integrated with the existing IMG system. However, since we want your feedback on the new features, and not the existing system, we will be directing you to certain "starting pages," from which you will try to execute certain tasks. Do you have any questions?

A. TASKS

Task Set 1
   * Start from the gene list: http://groups.sims.berkeley.edu/annotation/
   • View the annotation history for the first gene on the list.

Start time: 11:16am
End time: 11:16am
Notes: Clicks on gene id, examines the "Gene Details" page, and clicks on "V1.1 (current)." Scrolls "Annotation History."

   • Modify the existing annotation for that gene with data from a homolog:
        o GO function; EC number; COG group; Gene Name.
   * Submit your annotation.

Start time: 11:17am
End time: 11:20am

Notes: Clicks on "Update Annotation," and goes for the "Compare and Transfer" tool. Selects a homolog from the list, clicks "Compare Selected." Recognizes that the subject and homolog are in separate columns. Checks GO, EC, etc., clicks radio buttons for the data he wants to transfer. Notices that "Transfer nothing" radio-button is still selected in the subject column as he gets ready to transfer annotation. Hesitates a bit and then clicks on "Transfer Annotation." Submits, checks "Preview," submits.

Task Set 2.
   * Start from the gene list: http://groups.sims.berkeley.edu/annotation/
   * Express your opposition to the annotation for the first gene on the list.

Start time: 11:20am
End time: 11:21am
Notes: Clicks on "I disagree."

Task Set 3.
   * Start from the Gene Cart: http://groups.sims.berkeley.edu/annotation/genecart.php
   * Change an annotation by adding a COG group.
   * Add this gene to your list of watched annotations.

Start time: 11:21am
End time: 11:24am
Notes: Clicks through to "Gene Details," clicks on "Update Annotation." Goes to "Compare and Transfer." Clicks the radio button for the closest homolog COG group, transfers. Before submitting, clicks on the homolog drop-down under "Evidence," ads gene to "My Watched Annotations" by clicking on the check-box, submits, reviews, submits, closes the window.

Task Set 4.
   * Start from the Gene Cart: http://groups.sims.berkeley.edu/annotation/genecart.php
   * Comment on annotations for multiple genes.

Start time: 11:24am
End time: 11:25am
Notes: Scrolls "Gene Cart" page up and down looking for a way to comment. Says "They are all selected and I want to comment…" Finds the "Discuss Selected" button, clicks, types in a comment, submits.

Task Set 5.
   * Starting from anywhere on the site, find where you can view your watched annotations.

Start time: 11:25am
End time: 11:27am
Notes: Clicks on "Add to My Watched Annotations" check-box then remembers that there was "My Annotations" link on the nav bar.

Task Set 6.
How would you go about determining whether this annotation is a valid one or not?

Says, " I want to know, good or not…" Looks at the "Evidence for Function Prediction." Goes to "Update"/"Compare and Transfer," comes back to "Gene Details" and examines % Identity. Says, "I am not seeing anything I disagree with. I think it's good. So, I'd vote for it." Clicks on "I agree." Then goes to look at the "Annotation History."

B. DEBRIEFING
What did you think of this application?

The system is very intuitive and it is integrated very well with the IMG.

What were the best (most useful?) parts? What were the worst (least useful?) ?

Compare and Transfer was very useful. But I wasn't sure it was transferring the homolog data. I liked the color on "Agree/Disagree" buttons. Precompiled analysis on IMG is great, the platform is increadibly easy. I didn't notice e-mail right away, that's great. SATCHIMO is great, is it on IMG currently? [It's not].

Did these sets of tasks feel natural to you? Why or why not?

Yes.

Do you feel there are other tasks that you think this interface should support?

Being able to compare %ID, COGs, ECs is the most straight-forward way. Nothing that's noticeably absent.

Do you feel there is anything that should be removed from the current design?

I confused the annotation version with the system version [standard JGI footer] at first.

What other kinds of functionality would you like to see in a collaborative gene annotation tool, either in the current system or in a no-holds-barred system of the future?

A way to have user-directed refined annotations updated on other systems throughout the community. Name/Password – to be accountable for the work you do -- is good. I'd say within a single platform your system is well resolved. Another useful thing would be to see where the gene starts and stops.

While using this system, did you ever feel lost?

No.

D. DEMOGRAPHICS

1. Age: 25-35

2. Highest level of education: PhD

3. Field of study or work: Environmental Genomics

4. Used JGI's IMG system before: A few times a month

5. Other comparative genomics tools you are familiar with: BLAST, Mummer, and many, many others.

6. Familiarity with functional gene annotation: I annotate genes regularly. (A few genomes plus metagenomes.)

7. Computer user: I use computers often and do computer programming.