

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: II- 13.22s

End time: II- 14.34s

Notes: Clicks to Gene Details. Clicks on version link. Says it's Wiki-like.

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

Start time: 00:50s

End time: 08:15

Notes: First, is looking for GO function on the gene details page. Scrolls down and looks at the "Evidence for Function Prediction." After scrolling the page up and down, clicks on "Update Annotation." Scrolls up and down again, examines "Compare and Transfer"

gene list. Selects a homolog and on the list, but says that he is not sure how he would get the EC number. After some hesitation, clicks on “Compare Selected.” Clicks on EC number, GO function, etc. of the homolog. Clicks on “Transfer.” Submits. Looks at Preview, sees that the EC number is not there, cancels, and repeats the sequence of steps. [Bug on “Preview”: EC number does not show up]. Submits. Closes “Update Annotation” window. Notices that the data in main window hasn’t changed [the page needs to be reloaded].

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: 08:30s

End time: 09:10s

Notes: Clicks on “I disagree” and says out loud “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: 10:36s

End time: 12:20s

Notes: Clicks on “Update” button. Goes to already familiar “Compare and Transfer.” Clicks on a radio-button of a COG group for a homolog and transfers. Scrolls up and down the “Update” page. Clicks on “Add to My Watched Annotations.” Submits. Reviews “Preview,” submits.

Task Set 4.

- * Start from the Gene Cart: <http://groups.sims.berkeley.edu/annotation/genecart.php>
- * Comment on annotations for multiple genes.

Start time: 12:32s

End time: 13:41s

Notes: Selects two genes on the list (number 2 and number 4), says that that’s what he wants to comment on. Wonders if discuss button next to one of the genes would work, says: “No, it won’t work.” Scrolls down, finds “Discuss selected” below the fold. Clicks on the button, types his comment in the Discussion window and submits.

Task Set 5.

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

Start time: 13:40s

End time: 14:00s

Notes: Clicks on “My Annotations” link on the nav bar. Looks at “My Watched Annotation.” Comments on how he perceives the difference between the two.

Task Set 6.

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

14:44s

25:23s

Starts on “Gene List,” clicks on gene id to go to “Gene Details.” Scrolls down, examines the “Evidence for Function Prediction.” Says: “They look the same to me.” Says that COG number looks consistent. Clicks on Pfam info for one (and is taken off site), goes back to “Gene Details.” Comments, that it would have been nice if the back click landed where you were before (on the page). Clicks on Phylogentic Profile Similarity Search. Wants to have a list of homologs. Wants to be able to have descriptions for the EC numbers, COG numbers, etc. Looks at the Last Annotator name. Wonders what 60% agreement is. (Thinks that 60% agreement might have to do with % similarity). No evidence to why homolog has this annotation on “Compare and Transfer.” Wonders if there is any other way to annotate rather than simply transfer annotation. Realizes that you could type the data in. Clicks on email icon to pull up email. Wants to be able to look up descriptions in the course of the actual annotation. Says that he needs more data.

B. DEBRIEFING

What did you think of this application?

It was pretty good. I had trouble starting the first place, it was not intuitive, I spent too much time on the first task.

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

The actual act of annotating was easy, once you knew what you were doing. In that sense, it's good. There are two ways, he noticed, that the genes could be annotated – to type in data and to compare/transfer – didn't notice what was the basis for those genes to be selected. Didn't notice if there was a degree of similarity. Says that it didn't say what the criteria for homology was; he would want to have actual data of why it was chosen. He noted that it was hard to read the subsection in the multiple select box – he would want a description of why it is the best homolog (based on the...). And he would want function description next to the EC, GO, etc. Says that best scores would be useful.

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

Yes. Especially the part about disagreeing.

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

There should be different ways for annotation. InterProt Hits is another useful way. There are 3 ways: 1) taking it from homolog; 2) taking it from InterProt hit; 3) doing it manually. All 3 ways could be supported.

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

No, I didn't see. No, I want more information. But there is a problem of too much stuff on one page.

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?

Too creative of a question. Score card for disagreement is helpful. I want a field where you can say why you disagree. [It is there]. People should say why they disagree – it is fundamental to the scientific discourse (explain why or give me an alternative).

While using this system, did you ever feel lost?

In the beginning, I was. Once I saw how it worked, I realized how the person who designed it was thinking.

D. DEMOGRAPHICS

1. Age: 35-45
2. Highest level of education: PhD
3. Field of study or work: Annotation group at JGI; training and experience as molecular biologist
4. Used JGI's IMG system before: Never
5. Other comparative genomics tools you are familiar with: None.
6. Familiarity with functional gene annotation: I have annotated a gene before. (Manual annotation of a eukaryotic genome, automated annotation at JGI.)
7. Computer user: I use computers often and do computer programming. (Perl script only.)