

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: 0:56s

End time: 1:57s

Asks if she needs to click on the gene id. Notices "History and discussion" link. Scrolls to see what else is there and finally clicks. Examines history page.

- 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: 1:10s

End time: 5:03s

Notes: Scrolls the page up and down, and then clicks on “Update Annotation.” Logs in with the username/password provided. Looks at the “Update Annotation” page and says “OK.” Goes for the Compare and Transfer box right away. Ponders a bit, selects a few, and clicks on “Compare and Transfer” button. Says, “Interesting,” and checks radio-buttons. Transfers, submits. On “Preview” page says: “Yes,” and clicks on “Submit.”

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: 5:05s

End time: 5:11s

Notes: Clicks on “I disagree.” (Says, she noticed it before.)

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: 6:22s

End time: 7:14s

Notes: Clicks on “Update.” Says, “Any COG Group? One of these?” Goes for “Compare and Transfer.” Follows already familiar steps. Adds the gene to the list of watched annotations by clicking on the check-box on the “Update Annotation” page.

Task Set 4.

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

Start time: 7:20s

End time: 7:35s

Notes: Noticed that they all the genes in the “Gene Card” were selected. Clicks on “Discuss Selected.” Types in a comment and submits.

Task Set 5.

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

Start time: 7:40s

End time: 8:29s

Notes: Goes for My Annotations

Task Set 6.

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

Says: “I never used IMG. I would want to look at homolog alignments (scrolls up and down), Evidence – Pfam, COG. I would want to know more about homologs.” Goes to “Compare and Transfer” that she remembers from the previous tasks. Comments that there is % Identity but no visualisation tool on IMG. “That’s what I’m used to: a way to go look at these genes and how they were determined (NCBI?), when it was deposited, who did it, how, what center, was it **experimentally-described or based on homology.**”

B. DEBRIEFING

What did you think of this application?

It’s cool. Not familiar with IMG system, admires “Evidence for Functional Prediction.”

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

Transferring – I loved it; and especially if you could pull up any number of homologs. I would prefer a way to visualize alignment. I would want to link out to the original data [Center].

Worst? Hard to say, I wasn’t doing a real annotation. Having numbers [gene ids] is not very useful, having the terms show up needs to be there. I don’t like the visualization of alignment on IMG (in Evidence for Function Prediction).

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

Yes, they were, it’s just it not a good simulation because there was no critical analysis.

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

No.

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

I don’t know. (Asks what Gene Cart is.)

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?

Visualization tools, I am used to having that – graphic for staring my analysis. I find them very helpful. (Doesn’t like little green alignments on IMG system.)

While using this system, did you ever feel lost?

A little bit – trying to find “My Watched Annotations” – I guessed, it wasn’t very obvious.

And you feel lost when you don't know the system. But it didn't seem to take that much time to get used to it. (What was I doing when I was making an annotation 'Watched'? I am not sure.)

D. DEMOGRAPHICS

1. Age: 35-45
2. Highest level of education: Bachelors
3. Field of study or work: Genome annotation [participated in Human Genome Project]
4. Used JGI's IMG system before: Never
5. Other comparative genomics tools you are familiar with:
6. Familiarity with functional gene annotation: I have annotated a gene before.
7. Computer user: I use computers routinely and have a good understanding of them, but I do not do programming.