Feedback on New Flow Cytometry Functionality

5/22/2014

Setup Page

The dropdown menu under Flow Cytometry Analysis should say "Select Analysis"

Since there is only one Condition for each analysis, a third row should not appear. This is the same issue we encountered with Microscopy. The reason the two rows appear is because there are two analyses. If there weren't two analyses, then a third row wouldn't appear. The behavior here is intentional to be consistent with the Microscopy interface. If we prevent rows from automatically adding themselves with this technique, it would be confusing for users. I disagree. I think this needs to be changed for flow cytometry and microscopy. We can see what happens in usability tomorrow though.

The headings in the table should all be left aligned with the text in each column. I can't see this change in the StarCellBio Usability Test assignment for the Cell Treatment Column.

The drop down menus move left after the first item is selected in the drop down menu.

I think we should have gray horizontal lines between different analyses for the same sample and black lines between samples (like microscopy)

Run Page

I think that each analysis for a sample needs to be shown in a new tab (like microscopy). The tab would then be labeled PI or with the Antibody name, as appropriate - This is good for now since we don't have a real antibody name, but the tab label will need to be updated appropriately once a real antibody is used

The text is not appearing when hovering over a sample name to see the whole sample name.

Analyze Page

The x-axis of the graph should change with the PI and Antibody analyses. For the antibody analysis, the x-axis will need to labeled with antibody Fluorescence- This is good for now since we don't have a real antibody name, but the tab label will need to be updated appropriately once a real antibody is used

For the PI graphs, the x-axis is not correct. The two peaks should line up with the 50 and 100 marks on the x-axis The data in this problem set is not meant to be correct; it was created just to be a test for functionality. I can, however, change the peaks for the graph if you want me to. Do you still want the scale to end at 100, making the graph broader, or do you want the scale to end at 250, so the graph can look the same but the x-axis changes? I was assuming that you had just copied the data from the original usability test. I would prefer the x-axis scale to be what it was originally (going up to about 125/150 I think), but if it's easier to use the scale that we just used for the 7.06 assignment, then that's ok too.

Some graphs are off the y-axis - for example, Mutant 1 @ 37C See above explanation

Some graphs are off the x-axis - for example, Mutant 2 @ 37C See above explanation

Analysis Tools

The two tools will work in different ways:

- Single gate: click and drag
- Bisector gate: When hovering over the graph, a vertical line will appear that indicates the midpoint of the bisector gate. The user will click to set the midpoint of the bisector gate. The midpoint is then adjustable. The far right and far left sides of the bisector gate extend all the way to the right and left axes points and are unadjustable. Only one bisector gate can be on the graph at a time.

Each gate will be labeled above it with numbers (or with 1a, 1b, etc). The label will be centered above the gate and in a rather small (non-bold) font. This information will appear in the table, as below.

The information will appear in the table as follows. There will one trash can icon per row. There will be a fine dividing line between rows.

		Fluorescence	% Cells	
1	a	12-30	30	
1	b	30-45	40	
2		32-60	60	

All gates will be black.
The two sides of the bisector gates will be joined by a vertical line.
As the gate is being drawn, vertical "guides" will appear to indicate to the student the boundaries of the gates. These will also appear when adjusting the boundaries of the gates.
After drawing the gate, small dots will appear at all of the ends that are adjustable. This applies for both the single and bisector gate. I don't see these yet when you first draw a gate. Done
The headings in the table of data regarding the gates needs to be updated appropriately based on the type of flow cytometry analysis being performed. Specifically, PI fluorescence does not apply for antibody staining.
We will need to decide whether "Apply to All" means that the gates are applied to all analyses or to all analyses of a particular type (for example, PI). For right now, let's keep it so that it applies to all samples - regardless of the type of analysis being performed.
For the bisector gate, if you draw a gate near the bottom of the graph, then the second gate is off the graph entirely and doesn't show up If the gate should not appear beyond the graph, would you prefer an error message to appear, indicating the bounds and preventing the bisector gate from being drawn, or should the second gate appear somewhere else? It should just automatically appear within the graph - next to the first side of the bisector gate. **If I draw a bisector gate on the x-axis, then the right side of the bisector gate isn't really showing up. Where should the gate appear, if you draw on the x-axis itself? Theoretically, it should appear where you click.**
Can you force a scrollbar for the analysis table? This will mean that the trash can icons will need to be moved over accordingly.
When hovering over the trash can icon in the analysis table, a hand icon should appear.
If I click on a trash can icon for a sample that is far down the analysis table, then the table automatically takes me back up to the top of the table. - **It's still taking me back to the top of the table instead of staying further down the list.**

I think the table can be a little bit bigger before it starts to scroll. Another 1-2 rows will fit on my computer.
Bug: I can actually draw single gates on the graph once I click the Analyze button and before I select the gate button. Actually, I think you can draw them anytime.
Bug: I can't adjust a single gate. It draws me a new single gate (without selecting the button).
If you delete one side of the bisector gate, then the whole thing (both sides) should be deleted.
Decide if we need a confirmation message when deleting bisector gates to ask the user to confirm that both populations will be deleted.

Updated ? icon text:
To draw a single gate, click [insert image of single gate icon here]. Click and drag your cursor within the graph. The % of cells within the gate will be calculated.
To divide the entire population into two subpopulations, click [insert image of bisector gate icon here]. Click at the desired bisecting point on the graph. The % of cells within subpopulation each will be calculated.
Check **Apply to All** to apply the analysis parameters to all samples.
Bug: the two sides of a bisector gate are occasionally adding up to > 100