

Feedback on StarCellBio Prototypes

3/15/13

Assignment Overview page

March 20th, 2013

The 'Learn More' links do not work at the bottom of this page.

The Reference library and User guide links do not work at the top of this page.

Assignment overview page should say:

For this homework, you will use the new program StarCellBio, which is a cell and molecular biology experiment simulator. Use the program to answer the following questions. This assignment will review material from previous labs and help you prepare for interpreting your final blots on April 11th.

March 25th, 2013

Assignment name: Bio52 Homework Assignment

Format the text on the Assignment overview page appropriately - Source Sans pro, same font size as Assignment Detail page.

March 26th, 2013

The assignment text should be left aligned.

March 28th, 2013

7.06 Assignment: Add the 'Introduction' heading and display as much of the introduction on this page as you can without having to use the scroll bar. If a whole sentence doesn't fit on the page, then just add '...' mid-sentence.

March 28th, 2013

Indicate visually that only a portion of the assignment is shown by either "..." or the last row within the abstract is grayed out.

Assignment Detail page

March 20th, 2013

Bio52 Assignment Detail page should say:

Please use the program to design and interpret two experiments:

(1) Use the program to design an experiment to determine if the EGFR kinase inhibitor (erlotinib) blocks activation of the Ras pathway downstream of the EGFR. Print a copy of the final exposed blot(s), which should include a list of the samples you chose.

Note: Not all samples should be used in this experiment. Use the samples that will directly answer the question asked. Make sure to include a loading control.

(2) Use the program to design an experiment to determine if the Mek kinase inhibitor (U0126) blocks activation of the Ras pathway downstream of the EGFR. Print a copy of the final exposed blot(s), which should include a list of the samples you chose.

Note: Not all samples should be used in this experiment. Use the samples that will directly answer the question asked. Make sure to include a loading control.

March 25th, 2013

Assignment name: Bio52 Homework Assignment. Can be shortened to Bio52 Assignment in the green navigation bar.

Format the question numbers with the blue circle '1' and '2' - just like the usability test. There should be blue horizontal lines between the questions and there should also be a sub-heading that says 'Questions'

March 26th, 2013

The assignment text should be left aligned.

March 27th, 2013

7.06. Add the following Survey Monkey link to Question 3 in the assignment: http://www.surveymonkey.com/s/MITSpring2013_706

March 28th, 2013

Unbold "(below)" in the last paragraph of the Introduction.

Set the survey monkey link to open in a new tab or window within the web browser.

Within the Reference Information section, add a ':' after "b) Other drugs" (and remove the period). Also move Protein Phosphatase 1 (PP1) to its own line and add a bullet point so that it looks like the other three treatments in part a).

March 29th, 2013

Bio52 assignment. Change the second question to read:

2) Use the program to design an experiment to determine if Erk activation is required for EGFR phosphorylation. Print a copy of the final exposed blot(s), which should include a list of the samples you chose. Note: Not all samples should be used in this experiment. Use the samples that will directly answer the question asked. U0126 is a Mek inhibitor. Make sure to include a loading control.

Design page

March 19th, 2013

Add "Select techniques." After the sentence "What technique(s) might be best..." - I think you should move the sentence ("Please note that by selecting a technique(s)...") that is below the 3 techniques to be above the three buttons.

March 25th, 2013

Make borders around the 3 technique buttons visible at all times. The faint border that appears when hovering over it should always be apparent. Then when hovering over the box, the thicker light gray line should appear. When selected, the button should be surrounded by a thick, dark gray line.

March 26th, 2013

Remove "Select techniques." After the sentence "What technique(s) might be best..."

Show the "hand" cursor when hovering over an already selected technique box to indicate that you can unselect it.

Set up page

March 15th, 2013

Treatments: "Without PP1" should be listing before "With PP1." Maybe we should consider "-" and "+" instead of the words "Without" and "With" - I really like the + and - suggestion.

When you first set up your experiment and hover over the first line, a drop down menu should appear for the temperature - and not just the drug and concentration columns. Actually the drop down menus should not appear for the drug and concentration columns if you cannot change those columns.

Treatments: replace "media only" with "growth media" and every time you add have a drug treatment then replace the name of the drug treatment with "growth media + drug". If it occupies too much space, we can abbreviate "growth media" with "media". - Should this be 'No treatment' instead?

Temperatures: change "25" to "30" and "40" to "37". - Yes, the permissive temperature is 30 and the restrictive is 37. I'm not sure where 25 and 40 are coming from.

Temperature value does not have the "C" in the add multiple treatments dialog box.

Add multiple treatments dialog box --> There should only be a single "Add multiple treatments" and "Cancel" button once the dialog box comes up.

The strains that are selected should be formatted the same way as the 7.06 assignment in the 'Add multiple treatments' window.

There should be 'Select All' buttons underneath the '+PP1' and '-PP1' columns. The 'Select All' buttons should be formatted the same way as the 'Cancel' and 'Add Multiple Treatments' buttons.

There should be an "x" in the add multiple treatments dialog box so that one can close it. - Maybe, but there is a cancel button.

Disable add new row bug - I'm not sure what this is referring to?

Too much jumping every time you change something (such as deleting a row) or changing the value of one of the treatment conditions. - I don't have jumping?

March 19th, 2013

"Add Multiple treatments" button within the "Add multiple rows" dialog box --> I am thinking that we should try to put this button underneath the other two since it is a different type of action. It appears that way for the Tufts assignment but not for the 7.06 assignment.

There should be an "x" in the add multiple treatments dialog box so that one can close it. The cancel button was confusing to me. I thought it meant "clear"

March 20th, 2013

Bio52 assignment:

The three buttons in the 'Add Multiple Rows' pop-up window need to be re-positioned. The 'Select All' button should be in the table - positioned just like the 'Add Multiple Rows' button in the experiment set up table or like the 'Select All' button on the lysate prep page. The 'Cancel' button should be much smaller and next to the 'Add Multiple Treatments' button.

March 25th, 2013

The 'x' button in the upper right hand corner of the 'Add multiple rows' window does not work.

The text 'wild type' in the pop up window should be regular font, not bold.

The copy and trash icons should be replaced with those on a transparent background.

Change the second instruction (on the Set up page) to read:

Select all of the treatment protocols for your experiment within the **Add Multiple Rows** pop up window, and then click **Add Multiple Treatments**.

Change the Confirm Set-Up message to read (Adding hyphens in set-up and also bold **Confirm Set-up and Select Technique**):

Below is your set-up for Experiment 1. ... Review the summary of your experimental set-up and then either go back to edit your set-up or click on **Confirm Set-up and Select Technique** to run your experiment.

Add in cell plate icons for each row in the experimental set-up table (just like the usability testing assignment).

March 26th, 2013

7.06 Assignment

Adjust the Add Multiple Rows pop up window so it moves, not resizes.

The Add Multiple Rows pop up window on my MacBook Air shows up half off the page- in the lower right corner. - it is still showing up very low on my screen. **we can fix this in the future.**

The 'Add multiple' text in the button within the experiment set up table should read: ADD MULTIPLE ROWS

Instructions should read:

- To setup your experiment, select **Add Multiple Rows** in the experimental set-up table below.
- Select all of the treatment protocols for your experiment within the **Add Multiple Rows** pop up window, and then click **Add Multiple Treatments**.

'SELECT ALL' button should be below each column (within each strain) in the 'Add multiple rows' window. The button should not appear at the bottom of the table - only 'Cancel' and 'Add Multiple Treatments' should be at the bottom of the window (for 7.06)

The strains should be indicated by Strain: Wild Type. With 'Strain' in bold/semi-bold and the name of the strain in the same size font, but not bold/semi-bold.

The temperatures should be labeled with the appropriate degree symbol followed by a 'C' as follows: 37 °C

Even though the pop up window has 'Growth Media' the treatment within the Experiment Set-Up Table says 'Buffer only'. They should both say 'Growth Media'

If multiple treatments are selected within the pop up window, they should get input to the experiment set up table from left to right, top to bottom. - ?A? Sorry my mistake - this is because in my head the -PP1 column should be on the left, not the right.

Please have the -PP1 column on the left and the +PP1 column on the right in the pop up window. :)

The growth media treatment does not have a concentration associated with it. This should just be blank.

March 27th, 2013

Tufts Bio52 Assignment

The 'Select All', 'Cancel' and 'Add Multiple rows' buttons in the pop up window are not aligned properly.

March 29th, 2013

Tufts Bio52 Assignment

Display stimulation time in the Experiment Setup table. No need to show it in the pop up window. Here is the info: EGF - 10 minutes

Change 'um' to the symbol 'µm'.

April 1, 2013

The new copy and trash icons are getting cut off at the bottom.

Are the new copy and trash icons not on a transparent background? It still looks like they are on a gray background.

The temperature value in the experiment setup table should not be editable.

Select Techniques page

March 26th, 2013

The text within the Flow Cytometry window should read:

No available flow cytometry techniques.

Select **New Flow Cytometry** below.

Once there is a Flow Cytometry technique, the text should read: F.C. 1, F.C. 2 (not FACS Exp. 1, etc.)

When the cursor hovers over 'F.C. 1' etc, the text should be blue.

The text for F.C. 1 should have the same margins as the W.B. 1, W.B. 2, etc. in the Western Blot technique window.

Navigation

March 26th, 2013

Bug: when on 7.06 Spring assignment and I click back to 'Assignments' in the green navigation bar, the Bio52 assignment is automatically selected. The current assignment should be selected in the Assignment overview page.

Western Blot

March 15th, 2013

Sample Prep

_If there is no alternative choice for the type of lysate provided, then it should not be in a drop down menu. It should just appear as a given value within the column. **Let's make the outline of the drop down menu opaque (but keep the font black) so it is clear that OTHER assignments have options, but the current assignment does not. This should be the case whenever there is only option in a particular assignment.**

Prepare Gel

_Do not automatically load samples, this is very not intuitive. Place a marker that says "Load Samples" and then have the image of a loaded gel appear. - **Let's see how the students respond this year and talk to Cheryl after this semester's implementation.**

Develop

Measuring tool should not appear if a student does not load a marker.

March 19th, 2013

Sample Prep

Bug: After selecting all the samples to prepare lysate from, I clicked on the "X" button. The box was still selected.

Prepare Gel

_Only show a blank gel before students choose gel type.

Blot

_Within the blot tabs you have to click at the name of the blot to be able to switch to that tab. Simply clicking within the tab but outside of the name does not work. Is this a bug? I found that to be very annoying and at first thought that switching back and forth between tabs was not working.

Develop

Measuring tool should say "N/A" if a student does not load a marker and not "NaN"

March 20th, 2013

Blot

For the TUFTS assignment only: The secondary antibody should say: goat anti rabbit HRP

For the TUFTS assignment: Add a secondary antibody that is: goat anti mouse HRP. This secondary antibody will not recognize the primary antibody and will lead to blank blots under all conditions.

Develop

Should only see phosphorylation of Erk when cells are treated with serum starvation & agonist (EGF) treatment. P-Erk should not appear under any other conditions.

Bug: if you perform a second western blot, then the gel will not have the correct number of samples in it. It will have the same number of samples as your first western blot experiment. -- CANNOT REPLICATE - IT SEEMS OK NOW.

March 25th, 2013

Develop

_The protein measurement tool should only be apparent when hovering over the blot. It seems to appear even when adjusting the Exposure time slider. Also it appears even when hovering above the blot - and includes protein sizes that don't make sense.

Now that there are 2 secondary antibodies for the Tufts assignment, the blots need to be distinguished at the top (or in the drop down menu if there are more than 5 blots). I think we should just call them 'Tubulin - rabbit', 'Tubulin - mouse', etc. What do you think?

March 26th, 2013

Blot

_Display the protein marker (colorful bands) on the membrane. The colorful bands indicating the marker are not displayed on the membrane (after selecting 'Blot & Develop') anymore.

7.06 assignment - Place the primary antibodies in alphabetical order

Develop

_Swap the image of the film out for the image that Jamie gave us (a square that is a darker gray than the image of the membrane).

Adjust the protein marker on the side of the film so that it is outside of the film and is also Source Sans Pro.

Bug: Can't rename Western blots within the small folder containing the gel/membrane/film.

Can rename the smaller tabs now, but it just doesn't look like a text box. A text box should appear - like when you rename the larger windows for the western blotting experimental techniques (W.B. 1, W.B. 2, etc)

Please review the document provided by Terry to display the western blot bands correctly.

April 1, 2013

The tab labels are not displayed correctly for the western blot data.

The tabs for the larger western blot experimental technique window are also mis-aligned. More so than usual.

Change the cursor to be a hand when hovering over the trash can icon in the western blotting tabs (big and small tabs).

April 8, 2013

Allow for 4 blots to fit within the re-probe window before moving them to a drop down menu.

FACS

March 15th, 2013

Sample Prep

_Font size is too small, should match the font size within the western blot sample prep - The whole table needs to be formatted exactly the same way - headings in semi-bold, similar spacing between columns, the headings should be one font size bigger than the font in the table.

If there is no alternative choice for the type of lysate provided, then it should not be in a drop down menu. It should just appear as a given value within the column. **Let's make the outline of the drop down menu opaque (but keep the font black) so it is clear that OTHER assignments have options, but the current assignment does not. This should be the case whenever there is only option in a particular assignment.**

March 26th, 2013

Please review the Flow Cytometry document as originally provided to you.

The 'X' should not appear (or be opaque) to delete the sample in the Flow Cytometry Samples window unless there is more than one type of sample selected.

The headings in the Sample Prep window should be: Select, Samples, Cell Treatment, DNA Content Treatment

The tabs should be labeled 'F.C. 1', 'F.C. 2' etc.

The blue button on the Sample Prep page should read: 'Prepare Samples'

In the green navigation bar, the text should read 'Flow Cytometry', not 'FACS'

The whole Sample Prep table needs to be formatted appropriately - headings in semi-bold, similar spacing between columns, the headings should be one font size bigger than the font in the table (compare to sample table in western blotting)

'Run Samples' button should be a blue navigation button.

The Run Samples button looks strange - it looks like it is outlined in a darker gray than normal.

Please confirm the formatting is ok. -otherwise they are on gray bg - it still looks funny to me.

Samples window needs to display Strain, Treatment +/-PPI and Temperature. Does not need to display live (should be fixed) cells, but should display PI. This is what it should say:

Wild Type, Growth Media -PPI, 30 °C - PI

All samples should have fixed cells, not live cells.

Analyze

Select first sample by default when click on "Run Samples" button.

Numbers with the graphs need to be a bigger font.

X-axis should be labeled "DNA Copy number (C)" - The peaks in the X axis needs to be labeled as 1C and 2C.

Y-axis should be labeled _____ (number of cells?) - Yes, numbers of cells. I don't know what the current labels mean.

Tools for analysis:

1. Ability to draw bins. The program calculates for you the number of cells within the bin and % of the total population. Student should be allowed to label the bins with different names (G1, S, etc). Student should be able to edit size of bin after drawing them.

Need to come up with a quick and dirty way to be able to see multiple FACS at the same time or export all of your analysis in a summarized graphical representation where they can easily see all of their analysis.

Generate some variability within samples so that the same treatment done twice gives you a slightly different FACS plot. - Yes, there needs to be slight variability in terms of numbers of cells that are analyzed (Y- axis) and also slight variation in peaks - no more than 5% either direction. -- is bias consistent between peaks - i.e. shift 5% or variable bias over 1C-2C?

March 19th, 2013

Analyze

Y-axis should be labeled "Number of cells" - Test

March 26th, 2013

Bug: Can't rename Flow cytometry experiments - If click on the name of the Flow Cytometry experiment in the tab, then you get an internal server message.

When a sample is selected in the Samples window, it should still be numbered, and not return to a bullet point.

The y-axis should not be labeled in terms of 0, 0.01 etc. No labels needed or they need to be in terms of 10's of thousands. You could label the graph as 25, 50, 75, 100, etc. And then label the Y axis as: Number of cells (thousands) -- It is actually Probability

Instead of changing the y-axis labels between samples, make the peaks shorter or taller to account for more or less cells. -- It is actually Probability

Eliminate the horizontal and vertical cross lines in the graphs. -- When I hide grid axis values disappear - I think it's fine if the y-axis values disappear. Let's just label the y-axis on our own.

Remove the key for the graph (yellow box with the label DNA content)

The overall flow cytometry tabs are not formatted correctly. I can't figure out what is happening but it looks like there are two tabs of different heights?

The 2C peak should be higher- about 1/3 the height of the 1C peak when a "normal" DNA content plot is displayed.

When a broad peak between 1C and 2C is displayed, the peak needs to be more broad and the left side of the peak needs to match the right side of the peak (a more gradual increase than a sharp peak). - I think this is ok now.

X-axis should be labeled 'PI Fluorescence'. The number values on the X axis should be 0, 50, 100 (with the 1C peak centered at 50 and the 2C peak centered at 100).

Add more variation in the peaks in flow cytometry. There can be shifts 10% or more. All the data will shift the same way.

The tops of the peaks should be wider. Instead of being a sharp peak, create a peak that is spread out more (5%)?

Samples window needs to display Strain, Treatment +/-PPI and Temperature. Does not need to display live (should be fixed) cells, but should display PI. This is what it should say:

Wild Type, Growth Media -PP1, 30 °C - PI

When hovering over (and selecting) sample names in the Samples window - to look at different flow cytometry plots, the cursor needs to look like a hand.

Add the following text when the user is simply looking at the flow cytometry plots. This text will be on the right side of the plot in the tab window:

- To view the flow cytometry data for each sample, select the sample name in the Samples window to the left.

Add an 'Analyze Data' button at the bottom center of the right side of the tab window. Button should be gray with text in all caps (like 'Add Multiple Rows' and 'Select All' buttons)

Once the 'Analyze Data' button is selected, the following instructions should appear in the right side of this tab window:

- The flow cytometry analysis tool will divide the flow cytometry plot into segments and calculate the percentage of cells that are found within each segment of your plot.
- To analyze your data, click within the flow cytometry experimental results graph at the position where you would like to create a segment. The tool will vertically divide the graph into segments at that position and display the percentage of cells that are within each section of your plot below. Create another segment by clicking at the next position at which you would like to create another segment.
- To delete a particular data analysis point, click the 'x' to the right ...
- To alter the position of the segment, click on the numerical value below and type the desired position of the segment in terms of levels of PI Fluorescence.

FACS Analysis Tool

March 28th, 2013

Display the boundaries of the segments as you are making them. After the first click in the graph, the first vertical line need to appear to indicate to students that they are in fact doing something in the graph.

Change the mouse from the arrow pointer to the hand when the data analysis tool is activated and the cursor is hovered over the graph.

Build in the ability to adjust the position of the vertical lines using the mouse. (If this is possible, the pointer would need to change to a hand when the mouse hovers over the vertical lines)

Bug: I added three segments and they displayed in yellow, blue and then red (in that order). When I delete the yellow segment, the other two segments need to stay as the original colors and not transition to blue -> yellow and red -> blue. This switch in colors can be very confusing.

Bug: There's a bug in the formatting of the Flow Cytometry Analysis table that I uncovered as I was navigating back and forth in the program between flow cytometry techniques within different experiments. See the attached screenshots of what the table looked like in the email I sent you. As you can see, I didn't even analyze specific graphs (the first screenshot) and yet a table was being displayed with 'undefined' values. In the second and third screenshots, I had analyzed the graphs but I believe that the data was not saved as I switched between experiments and between flow cytometry techniques within an experiment.

Formatting changes of the right panel of the flow cytometry tab window:

- Add additional space between the button to show/hide instructions and the table itself. 10 px?
- Make the 'Apply to all' text bigger. It should be the same font size as the primary and secondary antibody names once a western blot is developed.
- Change the 'Click here to show/hide instructions' to say 'Show Instructions' and 'Hide Instructions'. Can you format this button in gray with text in all caps?
- Format 'Flow Cytometry Analysis' to be smaller font size - exactly the same as 'Blotting Conditions' in the western blot tool.
- Reduce the left margin on the instructions
- Move the default position of the table lower in the window so that maybe the instructions can be viewed above the table.

Table headings (flow cytometry analysis tool):

- The DNA% heading needs to change to be '% Cells'.
- Delete the 'Colors' and 'Actions' headings. I don't think they are necessary to understand the table.
- How much room do we have in the headings? Instead of 'From' and 'To' just have a single heading that says PI Fluorescence and then display the values in the table as a range. For example: '0 - 25'.

Segment Colors:

The color-coding of the sections with this tool seems to be less bright than the other analysis tool. For example, the blue rendering on the graph itself is not very blue. I do like the colors of the vertical lines themselves.

I don't think you need to color code the graph itself - just the vertical lines. It can be confusing since you can create segments that are overlapping and these will be a mix of the three colors (the two different segments and the yellow graph itself).

Bug: I added three segments and they displayed in yellow, blue and then red (in that order). When I delete the yellow segment, the other two segments need to stay as the original colors and not transition to blue -> yellow and red -> blue. This switch in colors can be very confusing.

Instructions to use the flow cytometry analysis tool:

Remove the instruction that says "To view the flow cytometry data for each sample, select the same name in the samples window". **[I still worry that viewing all of the data may not be completely obvious for all students.]**

Instructions for the right side of the flow cytometry analysis: [we may not need the second instruction below based on how intuitive the tool is.]

- To calculate the percentage of cells within segments of the graph, click on the graph and draw a segment bounded by the vertical lines provided. Repeat to create another segment.
- To alter the position of the segment, drag the vertical line into the appropriate position.
- To apply the analysis to all of your samples, select **Apply to All**. To make changes to an individual graph, ensure that **Apply to All** is not checked.

April 1, 2013

Flow Cytometry Analysis Tool:

Remove the dotted lines that appear when adjusting the position of already-drawn vertical lines. These dotted lines are not necessary since the double headed arrow indicate this.

As you're drawing the segment boundaries, don't display the segment as a box. Instead display it as a horizontal line - maybe even with arrowheads on either end to display the boundaries of the segment.

MAJOR BUG: once you click 'Apply to all', all of the graphs (and NOT just the analysis) are the same. This seems relevant for the first several samples that are listed in the samples window, but not all of the samples if you have many samples.

April 8, 2013

Instructions for the Flow Cytometry Analysis Tool:

- Click and drag to draw a segment in the graph. The % of cells within the segment will be calculated.
- Drag the vertical lines that define a segment to change its width.
- Select **Apply to All** to apply the same analysis to all samples.

BUG: Resizing after unchecking "Apply to all" applies to other graphs in certain circumstances (appears to be a problem for Lourdes, not Alison in Chrome but for both in Firefox)

Flow Cytometry Graphs:

Display the data in a dark gray line. The yellow line conflicts with the first data analysis section displaying in yellow.

General Notes

Ivan, please be very careful when you combine all three of our versions back into one working version. I believe that the CORRECT Tufts assignment is only found at <http://edison.mit.edu>. I can tell this based on question 2 in the assignment.

Other

There is a very faint white line that appears above the tabs within the FACS plots and the blots. This should be removed.

Remove jumpiness from the browser in almost every page.