CYTEK® Aurora Creating an Experiment

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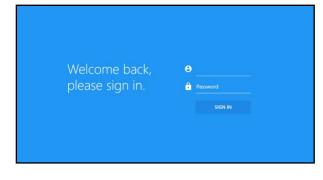
1. Setting up a new experiment

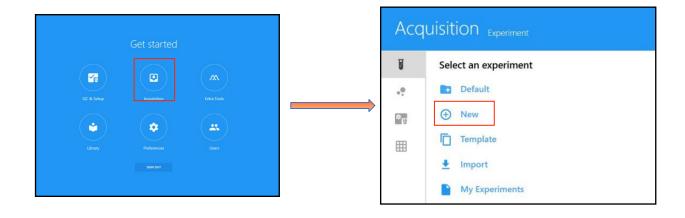
1) Launch SpectroFLO Software.

Login name: Lab name

Password: password1

- If you are the first user of the day, follow startup instructions as per UofU Aurora Startup_Clean.
 Shutdown guide.
- 3) Select Acquisition from the Get started screen.
- 4) Create a new experiment.



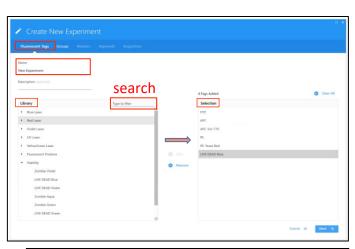


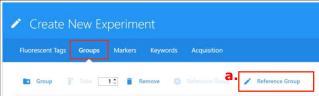
5) Fluorescent Tags Tab

- Rename your experiment
- From the fluorochrome library, search for the fluorochromes in your panel. Double click or highlight and choose add to include it in your experiment.
- To confirm the selected list, click Next.
- NOTE: DAPI, PI, Zombie or any viability dyes must also be added to your experiment and recorded as single color controls.

6) Create Reference Group Tab (ie single color controls)

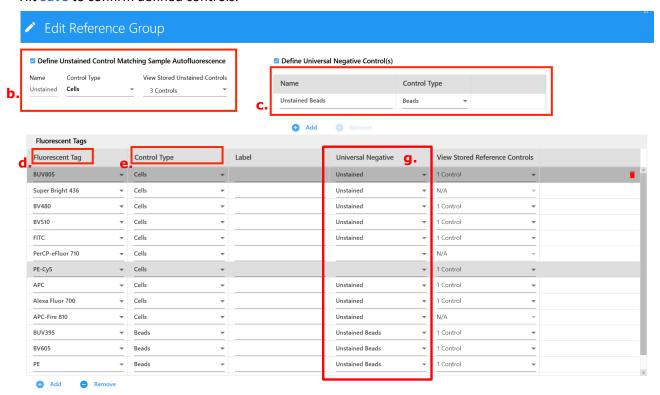
- From the Groups select reference group (a).
- SpectroFlo automatically adds an unstained and single color control tubes for each fluorochrome you've added to your experiment.





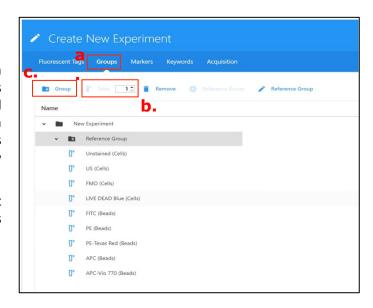
Note: An unstained sample of the same cell type as your experimental samples must be run as it is a part of the unmixing process **(b)**. You can also Define additional controls for unstained beads **(c)** if desired.

- Below the menus for the negative controls, you see your fluorescent tags listed in the left column (d). The next column is Control type (e) (beads or cells) must be selected from the dropdown menu to match the kind of control that you will be recording, for each fluorescent tag!
- Select appropriate matching autofluorescent negative (g) (eg. Unstained cells, unstained beads, or leave blank for internal negative)
- Hit Save to confirm defined controls.



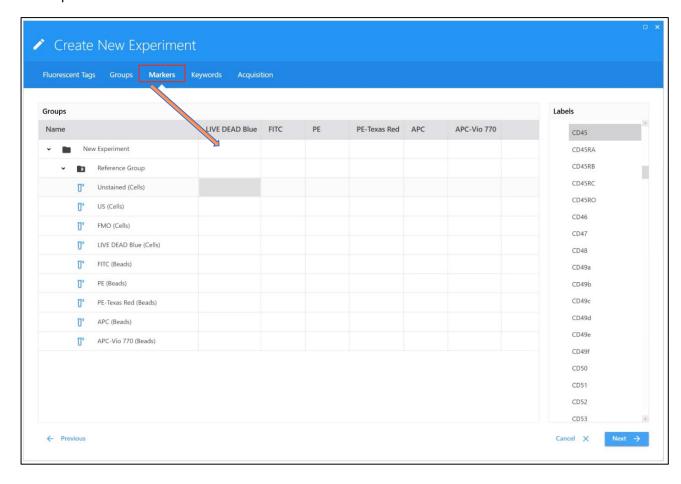
7) Create Experimental Sample Groups

- To add an experimental sample group, from the Groups (a) tab, enter the number of tubes (b) you would like to add in the group, and select + Group icon (c). NOTE: You can rename, create or delete tubes and groups later, but creating at least one here will allow you to add labels in the next step.
- If there are different conditions (e.g., different tissue, different cell lines etc.) multiple groups can be created.



8) Markers - labeling

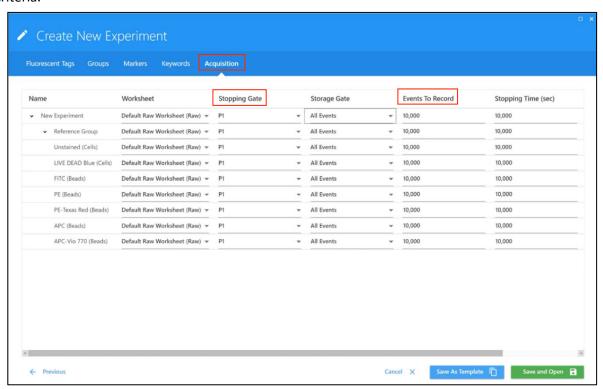
- From the "Markers" tab, set labels for each of your fluorescent tags by double clicking on the text box underneath the fluorochrome name and typing in your desired label. Hit Enter on the keyboard to confirm. NOTE: you can have group/tube specific labels; just double click on the text box by the new group name.
- When you are done labeling, click **Next**. NOTE: You can skip the "Keywords" tab and move straight to "Acquisition".



2. Adjusting User Settings

1) Acquisition Tab:

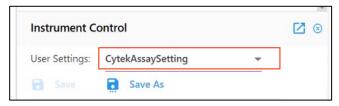
- At this stage you can define and set up the worksheet, stopping gates, events to record for references controls and experimental samples (these options can be modified at any point in the future by clicking in the "Edit" button, which should bring you back to this screen).
- For reference group samples, work from the Default Raw Worksheet. Set Stopping gate and Events to Record as needed. For cellular reference controls with rare expression, ensure that at least 1000 positive events are recorded. Storage gate is not suggested, as it will not record anything that doesn't meet that criteria.



Select Save and open.

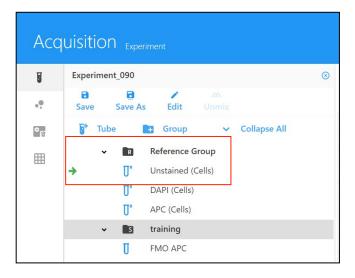
3. Recording Controls

- 1) After selecting save and open, navigate to the *Instrument Control Tab (left bottom side)* and choose "CytekAssaySetting" for the starting User Settings.
 - Importantly, "CytekAssaySetting" are the optimized starting gains for all detectors on the Aurora. Changes should only be made to bring cells on scale for FSC and SSC. (Consult Flow core staff for further conversations about fluorescent detector gain adjustments.)
- Chose desired doublet discrimination parameters in Signal tab (A, H, W)



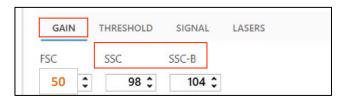


- 2) Load an unstained sample to the loading station and select the appropriate tube from the Reference Group with the green arrow.
- 3) In the Acquisition Control Window, click on the Flow Rate to adjust the acquisition speed and the number of events to display. When you first load the sample, keep the flow rate at **low** and monitor event rate.
- While Cytek says the instrument can process 30k events per second, we advise to avoid running beyond 10k events per second, and to monitor the abort rate and keep it under 5% (for example: if the flow rate is 10,000/sec, the abort rate should not be higher than 500). We always suggest clients to bring extra flow buffer to dilute their samples if needed. Refer to educational seminars about the pros and cons of running low, medium or high.



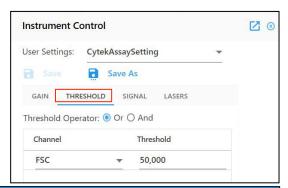


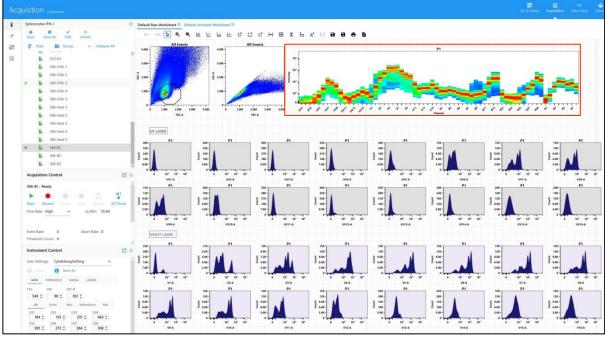
3) While running your unstained sample, (Instrument Control Window), adjust gains on the FSC and SSC and the threshold value to put cells in desired place on the plot. **Note:** The FSC and SSC settings from the CytekAssaySettings are optimized for the Spectroflo beads. Thus, reduce the FSC to bring cells on scale - typically, a **good starting point is around 50**.



• Please be aware that SSC by default is off the violet laser and that SSC-B is off the blue laser. Either can be used, but the violet SSC is preferred. NOTE: A threshold that is too high may prevent the cytometer from displaying cells of interest (dying/dead or smaller cells in heterogenous populations); a too low one would allow a lot of noise/dead cells to your file (or to your collection tube when sorting). We suggest something around 50,000 when recording bead controls, and around 100k-400k when recording cells, but play around to find something suitable for your samples.

4) After the unstained control, run a small aliquot of an experimental sample, which is expected to have the brightest signal. Check the full spectrum plot to ensure that all signal is on scale.

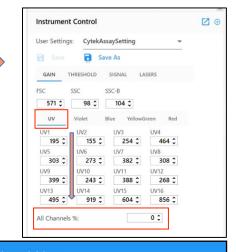


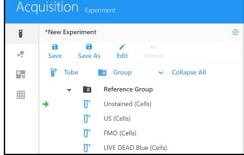


 IMPORTANT: If any data is off scale for fluorescence, never adjust that individual detector, but instead reduce the gain for "all channels%" of that laser. Gain reduction is % based and should only be reduced for all laser lines until the signal is on scale. (Consult Flow core staff for further conversations about fluorescent detector gain adjustments.)

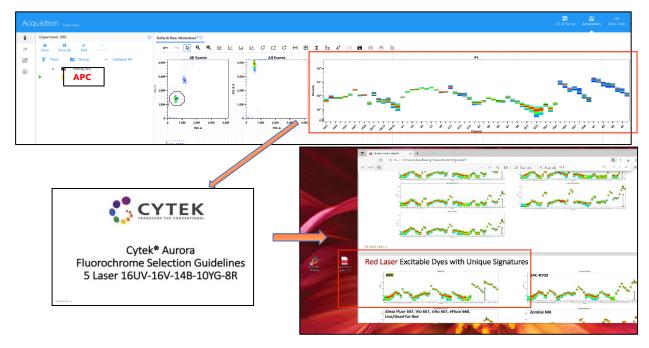
When all parameters are set properly, Reference Controls are ready for acquisition. Therefore, click Start and Record for each sample from the reference







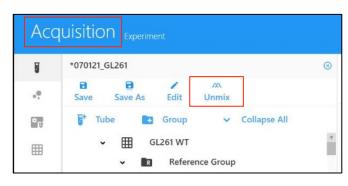
- 5) Check each reference control to ensure that the full spectrum signature matches what is expected. Compare the signature from the full spectrum plot in SpectroFlo with an image from the Cytek's fluorochrome guide:
- If a fluorochrome is not listed on Cytek's fluorochrome guide, please search for the spectra from spectrum.cytekbio.com and remember to select 5L configuration.

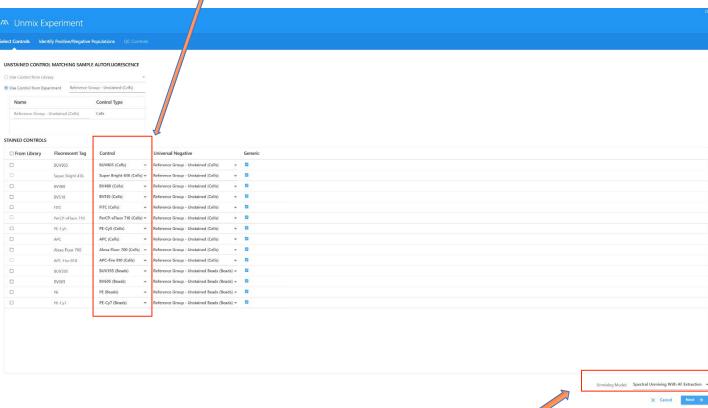


6) After all reference group samples are recorded, the "Unmix" button, that was previously greyed out, should now be clickable.

4. Unmixing

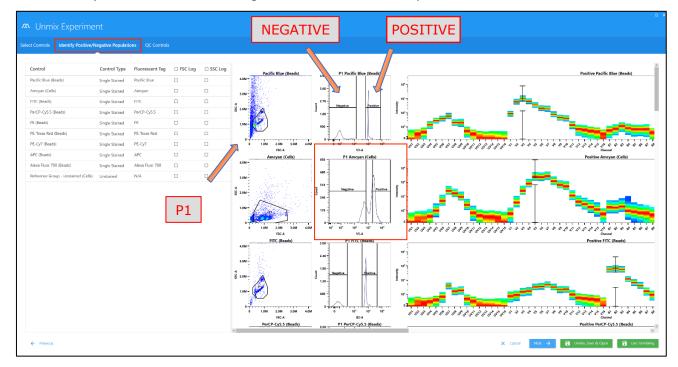
- 1) From the Acquisition Control Window click on unmix.
- After that, you will have to select which controls (beads or cells) that are going to be used for the unmixing.





- Cytek Aurora allows to extract a sample's auto fluorescence and treat it as a separate
 parameter, which can improve the resolution for <u>specific</u>, <u>well defined</u> cell types. Therefore,
 you can click the box "Auto Fluorescence as a Fluorescent Tag" and click on Next. NOTE: this
 can get tricky if your cells have a complex autofluorescence profile. (Consult Flow core staff
 for further conversations about AF extraction.)
- 3) Click Next

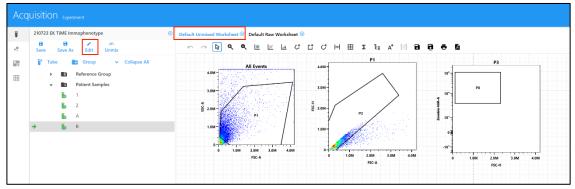
3) After selecting all controls, identify an appropriate P1 gate and positive and negative regions for each single color control. If you used "unstained/universal negative" as the negative in setup window there wont be a negative gate to adjust. If the positive peaks are not well defined (wide or double peaks merging) or you have a dimly expressed marker we suggest you to draw your bars around the brightest end of them, as depicted in the second line below:

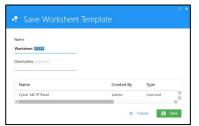


Once finished, you can hit Live Unmixing

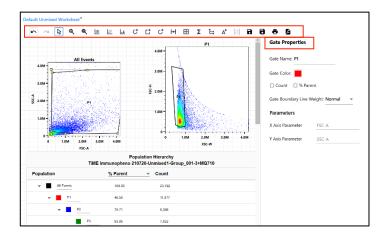
5. Recording Experimental Samples

1) After unmixing, a new "**Default Unmixed Worksheet**" tab is created in the acquisition tab. Please <u>never</u> make adjustments to the Default unmixed worksheet and then save/overwrite the worksheet. Instead *Save as* under a different name. After worksheet is saved it will need to be applied to the appropriate groups by "editing" the experiment.





2) At this point you can start recording your experimental samples, edit the experimental setup, create plots, edit gates properties, and analyze your data.



6. Data export

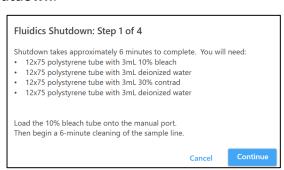
You have a few options while exporting your experimental data.

1) Exporting FCS files:

• FCS files (both RAW and Unmixed) are automatically saved once samples are recorded. FCS files can be found in this path C:CytekbioExport→FcsFiles→Experiments→lab folder

7. Cleaning

- 1) If you are not the last user for the day: Clean the flow cell after your experiment is finished. Go to the Acquisition module and select Clean Flow Cell. Prepare fresh new tubes of 10% bleach and DI water and follow on-screen prompts.
- 2) If you are the last user for the day: Clean the analyzer after your experiment. Go to the Acquisition module and select Fluidics Shutdown.
- Prepare fresh new tubes containing:
- 3 mL of 10% bleach
- · 3 mL of DI water
- 3 mL of 30% Contrad 70
- 3 mL of DI water



Follow the on-screen prompts and turn off the cytometer at the end of cleaning. A pop-up window should tell you when to do so.