

1. Start by choosing all the files to progress in batch mode.



NYULMC DART Cytometry and Cell Sorting ModFit Tutorial, 12/27/2016 2. Set the batch controls to not analyze but with file prompt on. This allows you to open files and alter the gates for analysis but will not try to fit the data. This lets you just look at the unfitted histograms first.

Name	Yalue	Description	OK
Analysis	No analysis 💌	Analysis option when file is opened.	Cancel
5ave report	C Off	Auto-save report?	
5ave report path	<u>C:\Documents and Settings\Administrator\My Docu</u>	Folder in which to auto-save reports.	Decet
Print report	C Off	Print report?	
5ave graphics	No	Save graphic files.	
rompts	-		
Database prompt	□ Off	Prompt to confirm save record?	
File prompt	I On	Prompt to confirm gates or histogram selection?	
Multi-dataset prompt	L_ Off	Prompt to choose a dataset from multi-dataset FCS files?	
			L La la

3. Choose the parameter for analysis (PI-A).

4. Select the first two gates and create them wide open (to cover the whole plot). This is so you can see the general position of populations and how they change between files. We can change these gates later if needed.



5. We can now set up the Synch Wizard.



It's good to start by letting the G0G1 peak position and SD adjust automatically.



G2M position looks good so no need to change this.



It's also good to maintain the S-phase default options to start, which are the simpler models.

Under the 'Other' tab you can start with having the Debris and Aggregates checked.

Synchronization Wizard	
Start G0-G1 G2-M S-Phase Other Report]
Debris and Aggregates	
Debris	Check the box if you need to model debris or aggregates.
I▼ Aggregates	
	Analyze Cancel Help

Usually there is no reason to change ModFit's defaults so this is why we want to start with them first.

6. This first file produces the following error, telling us that the GOG1 position has shifted beyond the expected amount and wants you to tell it what to do next. If the new value were close to the original position (around 50 or so), then you can let it move to the new position. However, a position of -1 does not make sense, so we will choose to lock the GOG1 position. Once the model is locked, it will stay locked until you change it.

Sync Wizard Adjustment	? ×
The Sync Wizard cannot find a peak under the G0G1 range for this sample.	
If the sample's G0G1 is visible and has shifted position, the Synch wizard can for you.	move the range
If there is no visible peak, lock the G0G1 in its last position.	
What should the Sync Wizard do?	
C Move the range over the peak at channel: -1	
Lock G0G1 in its last position at channel: 64	Ok
C Stop the analysis.	



 In some instances you will see subsequent files that have a very distinct G0G1 peak that has shifted to the right of left from this locked position so you can click the model edit button to bring up the edit dialog again.

 If it appears to have shifted back to the original, expected location then you can choose to reselect the Adjust automatically mode. Otherwise, you can just drag the arrow over the new G0G1 position. 6. If the normal control for synch experiments has a wide CV, then ModFit will be unable to go through the Synch Wizard properly and you will get high RCS values back.





Verity also mentioned that if there no black triangles present underneath the G0G1 and G2M peaks then this is another indication of CV's that are too high to use Synch Wizard with.

6. You will have to exit out of Synch Wizard and click on the Mod icon. From here you can tell ModFit to look for G2M as a visible peak.

Edit Properties for Manual Analysis									
	Name	Description	Г	Name	Value		Description		ОК
	🖻 Manual Analysis	Settings to manua		Ploidy	Diploid	-	Choose a ploidy label	_	Cancel
	Cycle1	Cell cycle		G2M S-Phase	Visible Peak		Choose a G2M state Check to enable S-Phase computatio	n	Reset
C	hoose a G2M state								Help

Keep Auto aggregates and debris on.

Name	Description		Name		Value		Description
⊡-Manual Analysis	Settings to manually a Cell cycle	4 4 1 9 M 7 7	AutoDebris AutoAggeregates Apoptosis Linearity Standards Number of cycles Model templates Range positions	On On On Comput	t Model	•	AutoDebris Compensation AutoAggeregate Compensatior Check to model apoptosis peak G2/G1 ratio (1.50 to 2.50) Number of internal standards Number of cell cycles in sample Select a model template Choose an option.



File analyzed: Specimen_001_Tube_001 Date analyzed: 22-Mar-2011 Model: 1DA0n_DSF Analysis type: Manual analysis

Ploidy Mode: First cycle is diploid

Diploid: 100.00 % Dip G1: 63.94 % at 63.49 Dip G2: 11.36 % at 146.48 Dip S: 24.70 % G2/G1: 2.31 %CV: 11.61

Total S-Phase: 24.70 % Total B.A.D.: 10.51 %

Debris: 13.32 % Aggregates: 5.53 % Modeled events: 23868 All cycle events: 19371 Cycle events per channel: 231 RCS: 1.958 RCS value went from 24.914 down to 1.958!



Synch Wizard

1. Open all the files in a batch, make the gates wide open, open Synch Wizard.

2. Set the location for GOG1 and let it adjust the position automatically (the default). Check and make sure G2M position looks good. Let the S-phase options remain the default and check the auto-aggregate and debris boxes. Click Analyze.

3. Sometimes the synch wizard doesn't do a good job at calculating aggregates automatically.



Sync Wizard Model

File: MK_030811.002 Date acquired: 08-Mar-11 Date analyzed: 22-Mar-2011

40.87 % Mean: 61.00 CV: 3.28 % 0.00 % Mean: 122.00 G2/G1: 2.00 S-Phase: 59.13 % Mean: 73.08

Compartment 1: 53.78 % Compartment 2: 5.35 % Compartment 3: 0.00 %

Debris: 8.74 % Aggregates: 37.67 % Modeled Events: 12971 RCS: 16.161

You can fix this by turning off the auto-aggregates and making your doublet-discriminator gate tight around the single cells.

Synchronization Wizard		
Start G0-G1 G2-M S-Phase	Other	Report
Debris and Aggregates		
Debris		
Aggregates		



By doing this, it brings the RCS value down to 2.601.



Sync Wizard Model

Date acquired: 08-Mar-11 Date analyzed: 23-Mar-2011

Mean: 50.21 Mean: 100.42 Mean: 74.03

Compartment 2: 10.21 % Compartment 3: 11.35 %

Modeled Events: 10107 RCS: 2.601

4. When going through the subsequent files in your batch analysis you can edit the batch properties to 'Fit with current model' so you do not have to click analyze every time. You can also uncheck the Database and File prompt so when you switch through the files you are not prompted to choose the parameter and gates every time.

Edit Properties for File	Processor		
Name	Yalue	Description	ОК
Analysis	Fit with current model	Analysis option when file is opened.	Capcel
Save report	🗖 Off	Auto-save report?	
Save report path	C:\Documents and Settings\Adminis	strator\My Docu Folder in which to auto-save reports.	Deceb
Print report	🗖 Off	Print report?	Reset
Save graphics	No	Save graphic files.	
Prompts			_
Database prompt	🗖 Off	Prompt to confirm save record?	
File prompt	🗖 Off	Prompt to confirm gates or histogram selection?	
Multi-dataset promp	t 🔲 Off	Prompt to choose a dataset from multi-dataset FCS files?	Help