

# Basic Data Analysis, Gating, and Statistics in Flow Cytometry



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# Outline

- What is an FCS File?
- Visualization and Scaling
- Gating and Controls
- Basic Statistics in Flow Data
- The Process

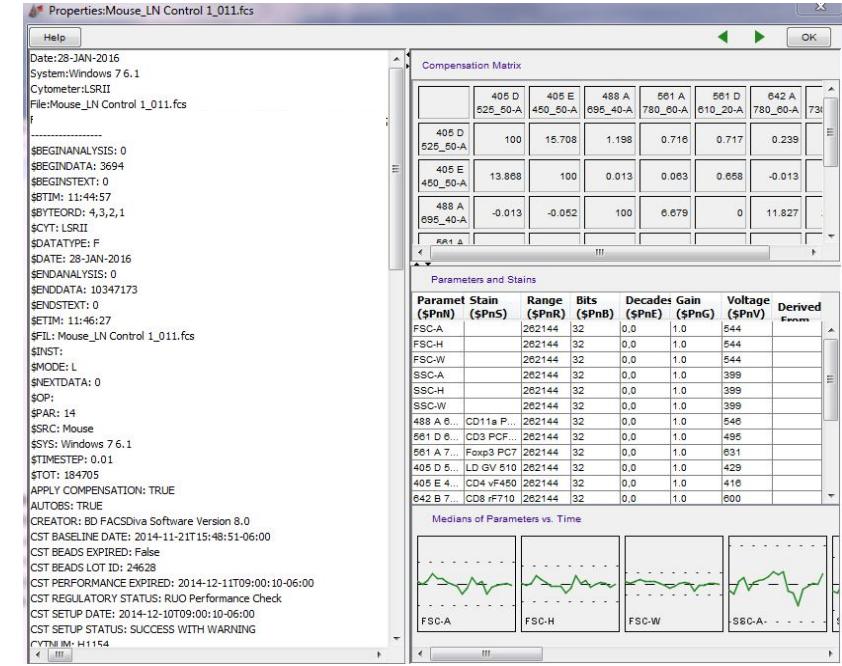
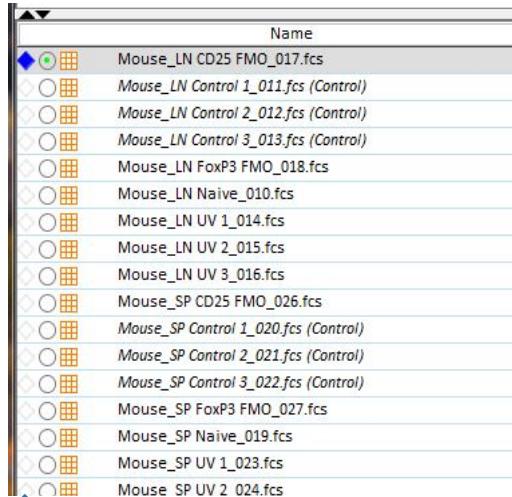
# The FCS File – Flow Cytometry Standard File

Parameter	2	3	4	5	6	7	8	9	10
Name	FSC-H	FSC-W	SSC-A	SSC-H	SSC-W	488 A 695/40	561 D 610/20	561 A 780/60	405 D 525/50
String									
Range	262144	262144	262144	262144	262144	262144	262144	262144	262144
Bits	32	32	32	32	32	32	32	32	32
1	136813.00	72175.84	100686.88	88489.00	74569.90	9000.32	15158.64	3904.32	15887.52
2	136392.00	72013.31	98798.56	86540.00	74819.30	8873.76	15250.76	3290.84	16505.28
3	136761.00	72370.88	99523.20	86557.00	75353.27	8064.00	14991.06	3386.88	16967.61
4	136288.00	72599.80	102604.32	90900.00	73974.45	8835.68	13644.54	2762.62	16658.73
5	136493.00	72679.64	102473.28	90521.00	74189.29	8384.32	14253.12	3108.56	15756.84
6	137809.00	71919.16	102944.80	91413.00	73803.40	8487.36	14612.78	3410.40	17198.28
7	136451.00	72557.54	97821.92	85559.00	74929.08	8755.04	14392.28	3188.92	15426.18
8	131217.00	73191.84	87923.36	77317.00	74526.24	7935.20	13974.80	3613.26	14421.33
9	137763.00	72796.29	98178.08	86391.00	74477.66	8622.88	14378.56	2479.40	15633.09
10	138296.00	71846.40	101661.28	90380.00	73716.24	8266.72	15017.52	3336.90	17202.24
11	138825.00	72279.32	108109.12	94829.00	74713.85	9089.92	14271.74	3181.08	16338.96
12	137084.00	71431.94	97625.92	86136.00	74278.02	9569.28	15296.82	3063.48	17455.68
13	136099.00	72974.48	94170.72	81575.00	75655.19	8542.24	16242.52	3597.58	17812.08
14	138561.00	72564.37	100914.24	87989.00	75162.98	8611.68	15122.38	3232.04	17161.65
15	120599.00	73751.43	128493.12	112851.00	74619.85	13147.68	22317.54	4793.18	23744.16
16	132646.00	73071.72	91556.64	79586.00	75393.36	7881.44	14176.68	3687.74	14792.58

- Comprised of a text segment and data segment.
- FCS Files are in a list mode data format.
- Rows = Events
- Columns = Parameters
  - H,A,W each get their own column.
- Annotate data before recording.

# The FCS File - Header

Text Segment		<input checked="" type="checkbox"/> AutoSave to .TXT
Keyword	Value	
\$ENDSTEXT	0	
\$BEGINDATA	3015	
\$ENDDATA	969014	
\$FIL	Rainbow_Beads_001.fcs	
\$SYS	Windows 7.6.1	
\$TOT	17250	
\$PAR	14	
\$MODE	L	
\$BYTEORD	4,3,2,1	
\$DATATYPE	F	
\$NEXTDATA	0	
CREATOR	BD FACSDiva Software Version 8.0	
TUBE NAME	Beads	
\$SRC	Rainbow	



- Header shows information about the data collection.
- Stores all the metadata from the instrument, including any added labels.
- Double clicking on the diamond next to a file in FlowJo will open the file information, including header information.

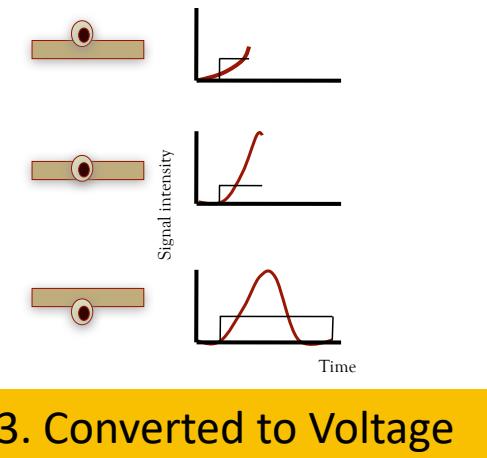
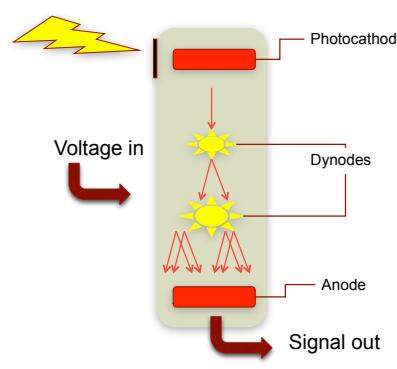
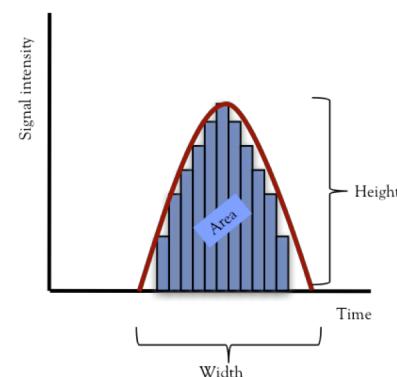
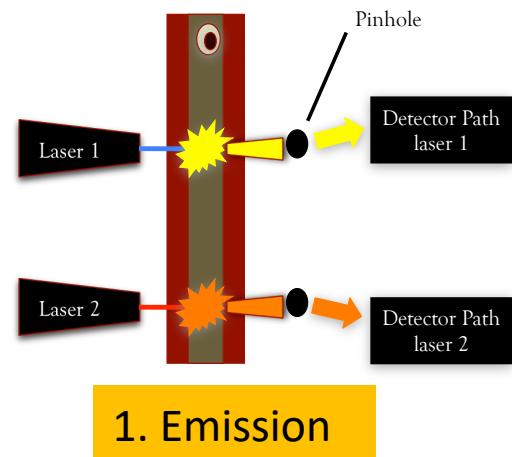
# Keywords

- All the header information can be extracted as keywords in data analysis software, allowing you to group, or sort files by keyword.
- Keywords can be added to tables with sample statistics.
- Keywords can be metadata.

Keyword List		
Name	Value	Explanation
\$BEGINANALYSIS	0	
\$BEGINDATA	3685	
\$BEGINTEXT	0	
\$BTIM	12:11:44	The time at the beginning of data collection, format hh:mm:ss.
\$BYTEORD	4,3,2,1	Byte Order
\$CYT	LSRII	The cytometer used to acquire the data.
\$DATATYPE	F	Data format.
\$DATE	28-JAN-2016	The date the file was created, format dd-mmm-yy.
\$ENDANALYSIS	0	
\$ENDDATA	10704836	
\$ENDSTEXT	0	
\$ETIM	12:12:13	The time at the end of data collection, format hh:mm:ss.
\$FILE	Mouse_SP Naive_0...	The name of the data file when it originally was created.
\$INST		The institution where the data were collected.
\$MODE	L	Data Mode. U = single-parameter histograms, C = correlated multi-parameter histograms.
\$NEXTDATA	0	The byte offset of additional data set included in the file.
\$OP	DeLuca	The name of the operator.
\$P10B	32	Number of bits in parameter 10.
\$P10E	0,0	The type of amplification for parameter 10 (logarithmic or linear).
\$P10G	1.0	
\$P10N	405 D 525/50-A	The name of the parameter 10.
\$P10R	262144	The range of parameter 10.
\$P10S	LD GV 510	The name of the fluorescent stain or probe used with parameter 10.
\$P10V	429	
\$P11B	32	Number of bits in parameter 11.
\$P11E	0,0	The type of amplification for parameter 11 (logarithmic or linear).
\$P11G	1.0	
\$P11N	405 E 450/50-A	The name of the parameter 11.
\$P11R	262144	The range of parameter 11.
\$P11S	CD4 vF450	The name of the fluorescent stain or probe used with parameter 11.
\$P11V	416	
\$P12B	32	Number of bits in parameter 12.
\$P12E	0,0	The type of amplification for parameter 12 (logarithmic or linear).
\$P12G	1.0	
\$P12N	642 B 730/45-A	The name of the parameter 12.
\$P12R	262144	The range of parameter 12.

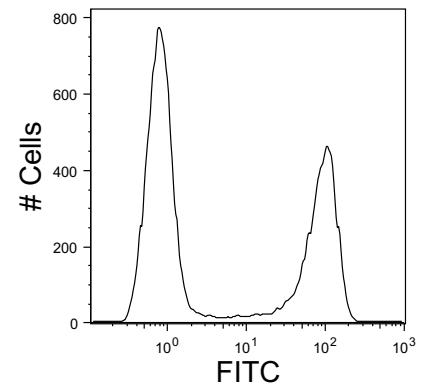
# How does the cytometer generate values?

- Detection of light from scatter or fluorescence in cells is converted into a voltage pulse.
- Each pulse generated by an object passing by the laser has a height, area and width measurement.
- Values for H, A, and W from each parameter stored in a listmode data format in FCS file.



Event	Time	FSC	SSC	FITC	PE	APC
1	0	100	500	10	650	4
2	0	110	505	700	700	6
3	0	90	480	720	670	10
4	0	95	490	700	720	15
5	0	12	76	15	15	13
6	0	120	600	14	810	785
7	0	108	530	16	595	18
8	0	117	654	12	720	12
9	1	54	276	378	576	18
10	1	193	803	690	912	790

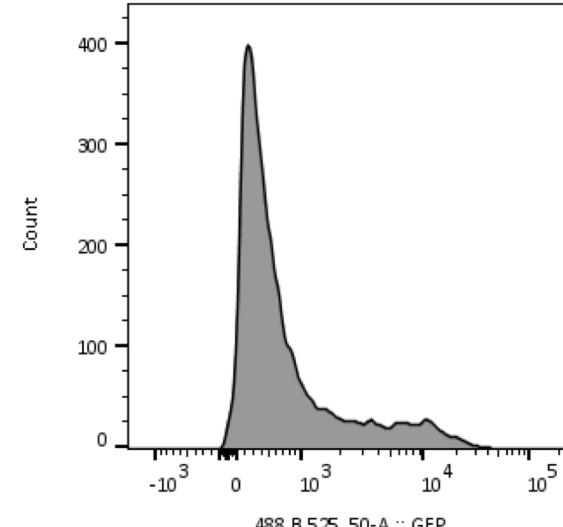
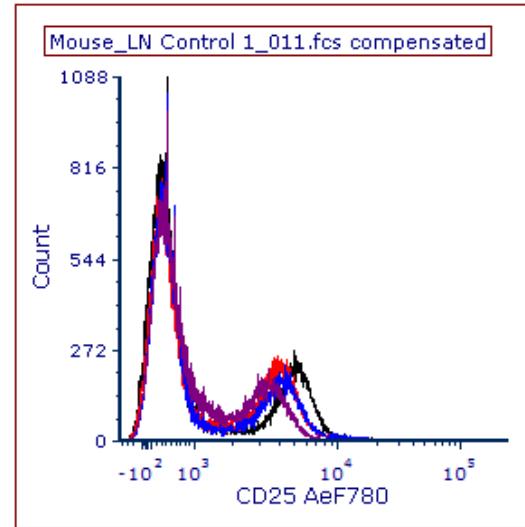
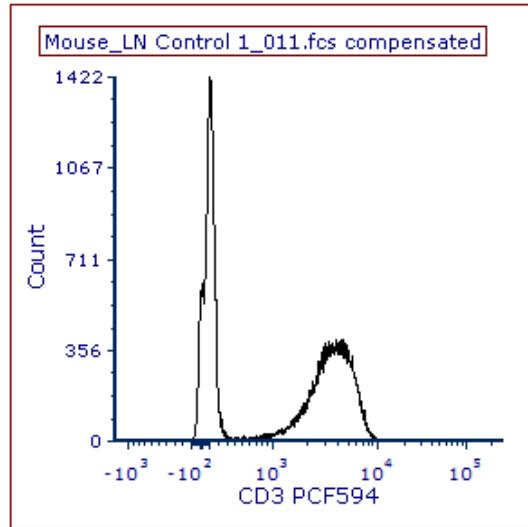
5. File Generated



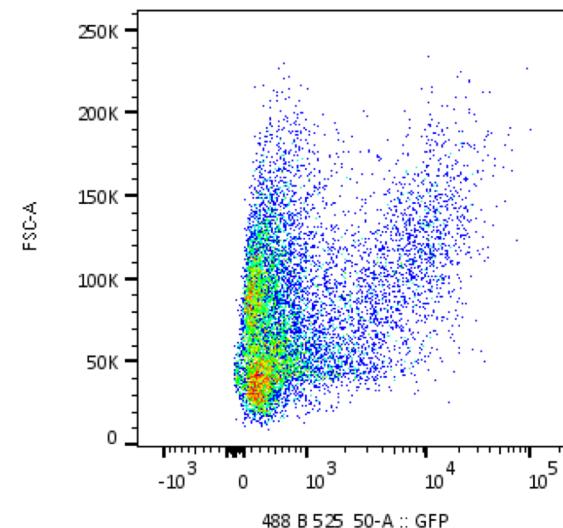
# Visualization

- We can create several types of plots with the generated data.
- Histograms, dot plots, density plots, contour plots.
- We want to display the data in a way that relates to our hypothesis.

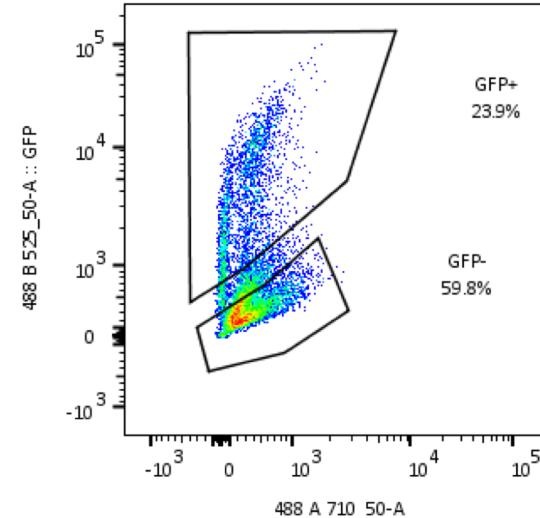
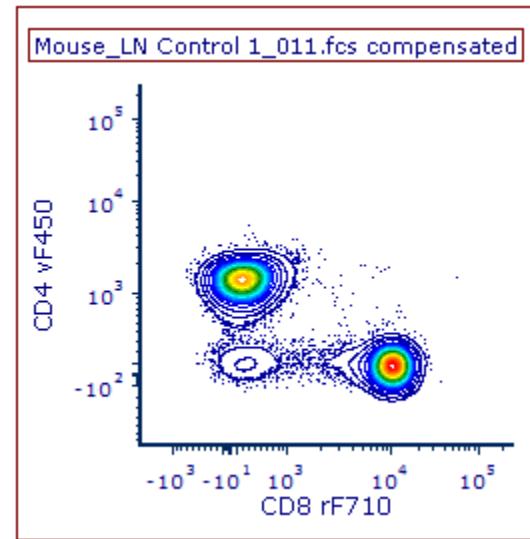
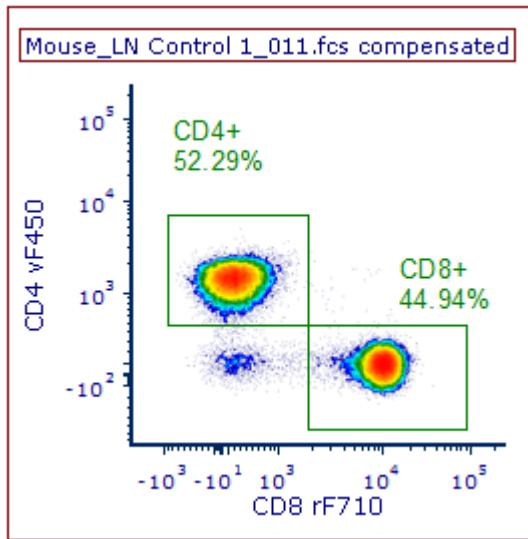
# Histograms



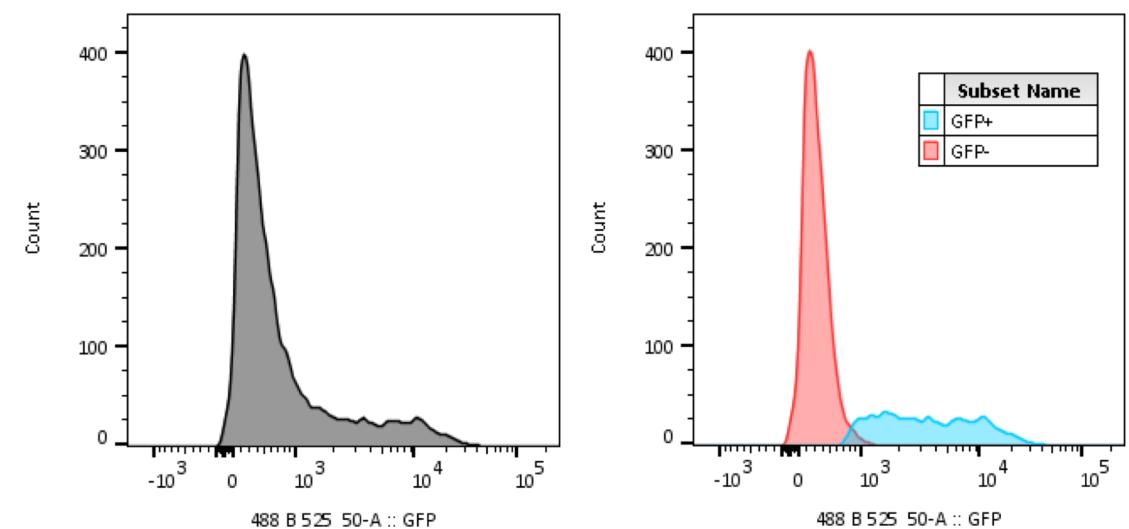
- Shows the distribution of values for a specific parameter.
- Cannot see the relationship between two populations.
- Can miss sub-populations that have similar values in one parameter.



# Bi-variate Dot Plots

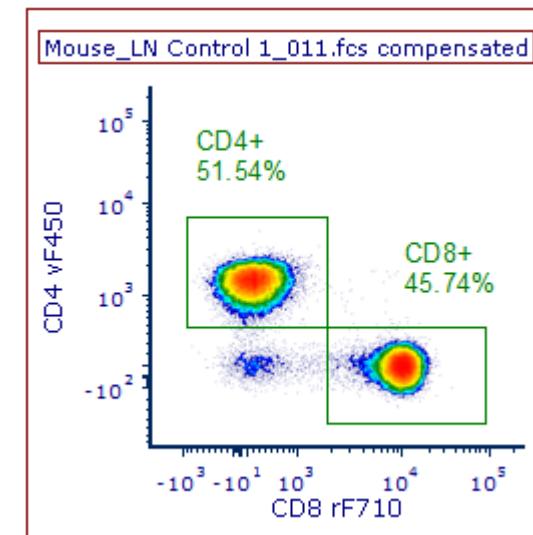
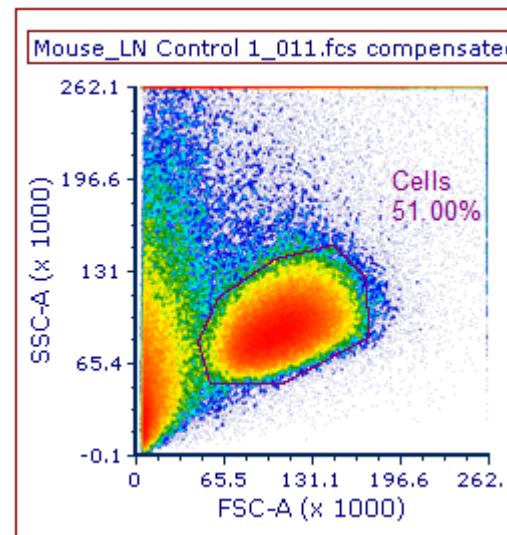


- Can see relationships between markers.
- Can see sub-populations from distinctions in two dimensions instead of one.



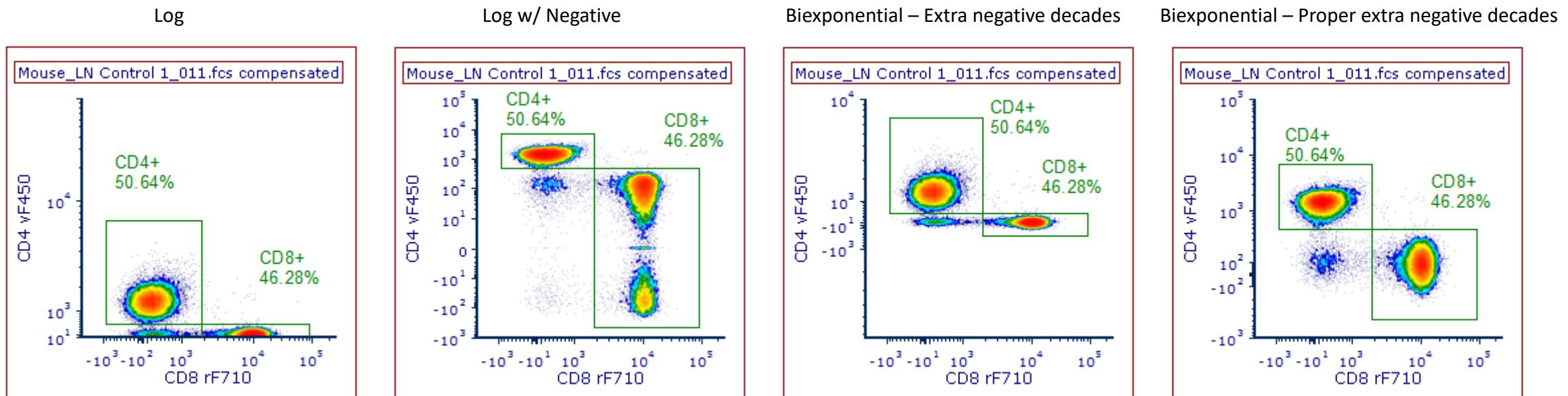
# Scaling Considerations

- Forward and Side scatter almost always displayed in **linear scale**.
  - Exception for very small things like bacteria, extracellular vesicles, and nuclei.
  - Use linear for small dynamic range.
- Fluorescence parameters almost always in **log scale**.
  - Exception for low signal increase. Ex. Cell cycle assay will only have a two-fold increase in fluorescent intensity.
  - Use log for large dynamic range.

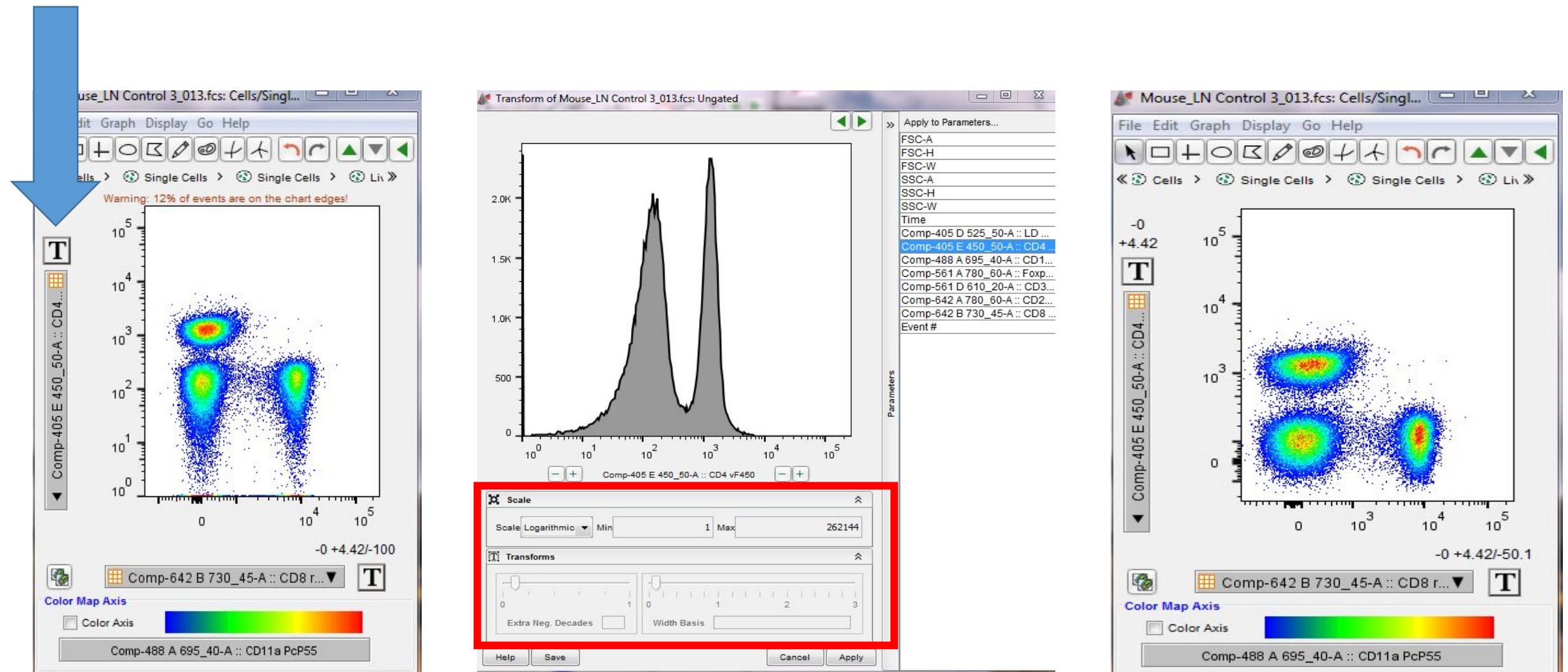


# Scaling Plots to Display Data

- Sometimes plots don't display the data in the best way.
- Changing the scaling does not change the values, just the display of the data.
- Linear, Log, Biexponential, Hyperlog.



# Adjusting Scaling in FlowJo



# Adjusting Scaling in FCS Express

The screenshot illustrates the process of adjusting scaling in FCS Express. A blue arrow points from the 'Axes' button in the top menu bar down to the 'Formatting Axes' dialog box.

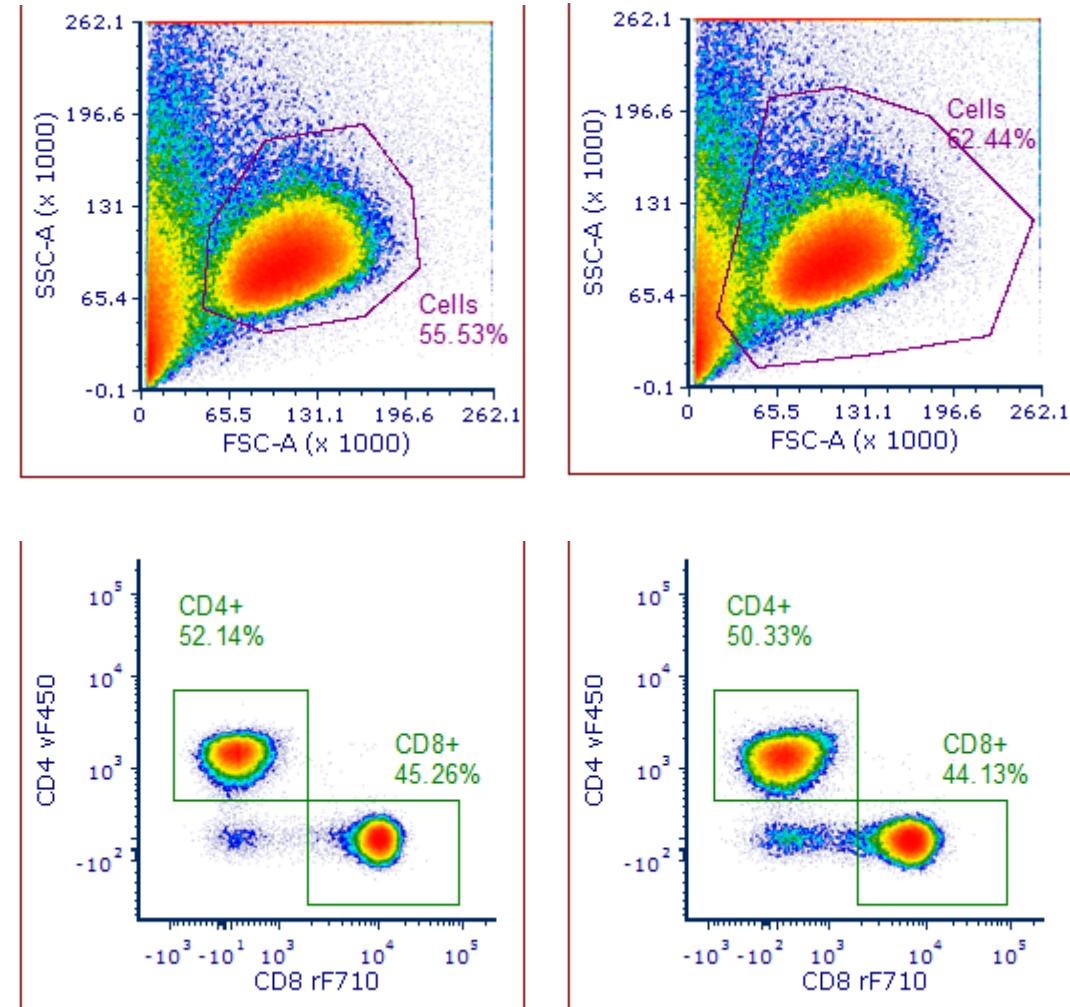
**Left Panel:** Shows the main FCS Express interface with a scatter plot titled "Mouse\_LN Control 3\_013.fcs compensated". The plot displays two populations on a log-log scale with axes labeled "CD4 vF450" and "CD8 rF710".

**Middle Panel:** The "Formatting Axes" dialog box is open, specifically the "Y Axis" tab under the "Select Axis" section. The "Scale" dropdown is set to "Log with Negative". The "Range" section shows "Automatic" selected, with "Minimum" at 0 and "Maximum" at 10000. The "Title" section has "Visible" checked. The "Axis Line" section shows "Width" at 2.00 and "Color" as dark blue. The "Grid Lines" section shows "Width" at 1.00 and "Color" as dark blue. The "Ticks" section shows "Width" at 1.00 and "Color" as dark blue.

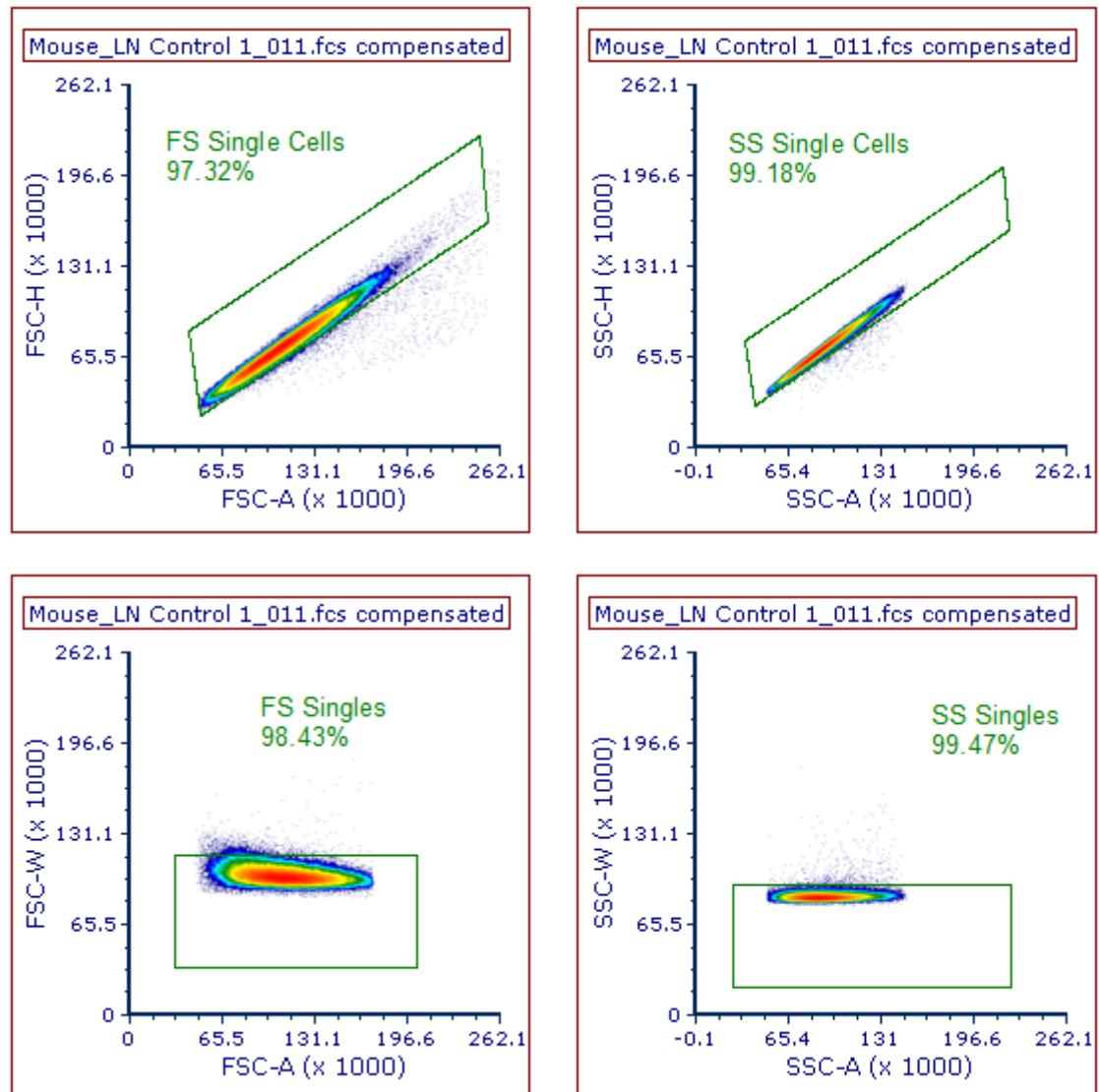
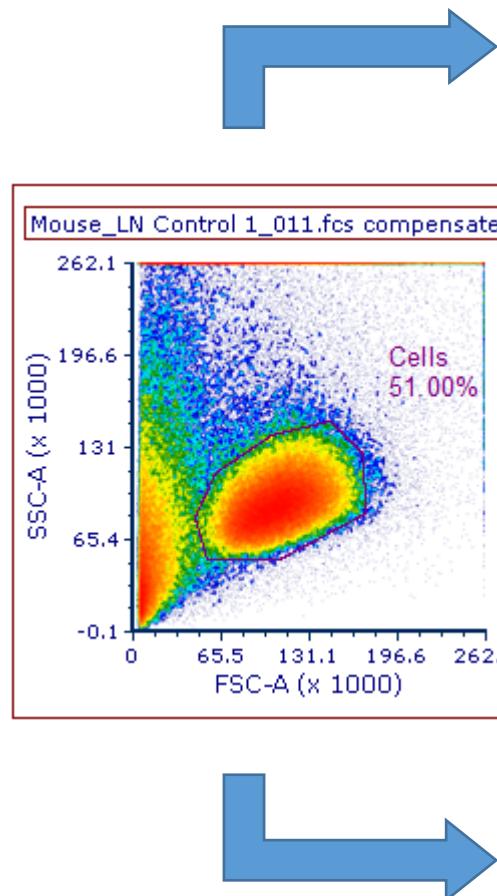
**Right Panel:** Shows the final result after applying the changes: the plot now has a visible title "Mouse\_LN Control 3\_013.fcs compensated" and a logarithmic scale from 10<sup>-4</sup> to 10<sup>5</sup>.

# Basic Gating Considerations

- Gating on cells only
  - Exclude debris.
- Doublet Discrimination
  - Removes events that are two cells stuck together.
- Live/Dead gating
  - Dead cells soak up antibody.
- Each of these things lead to double positive or strange events!

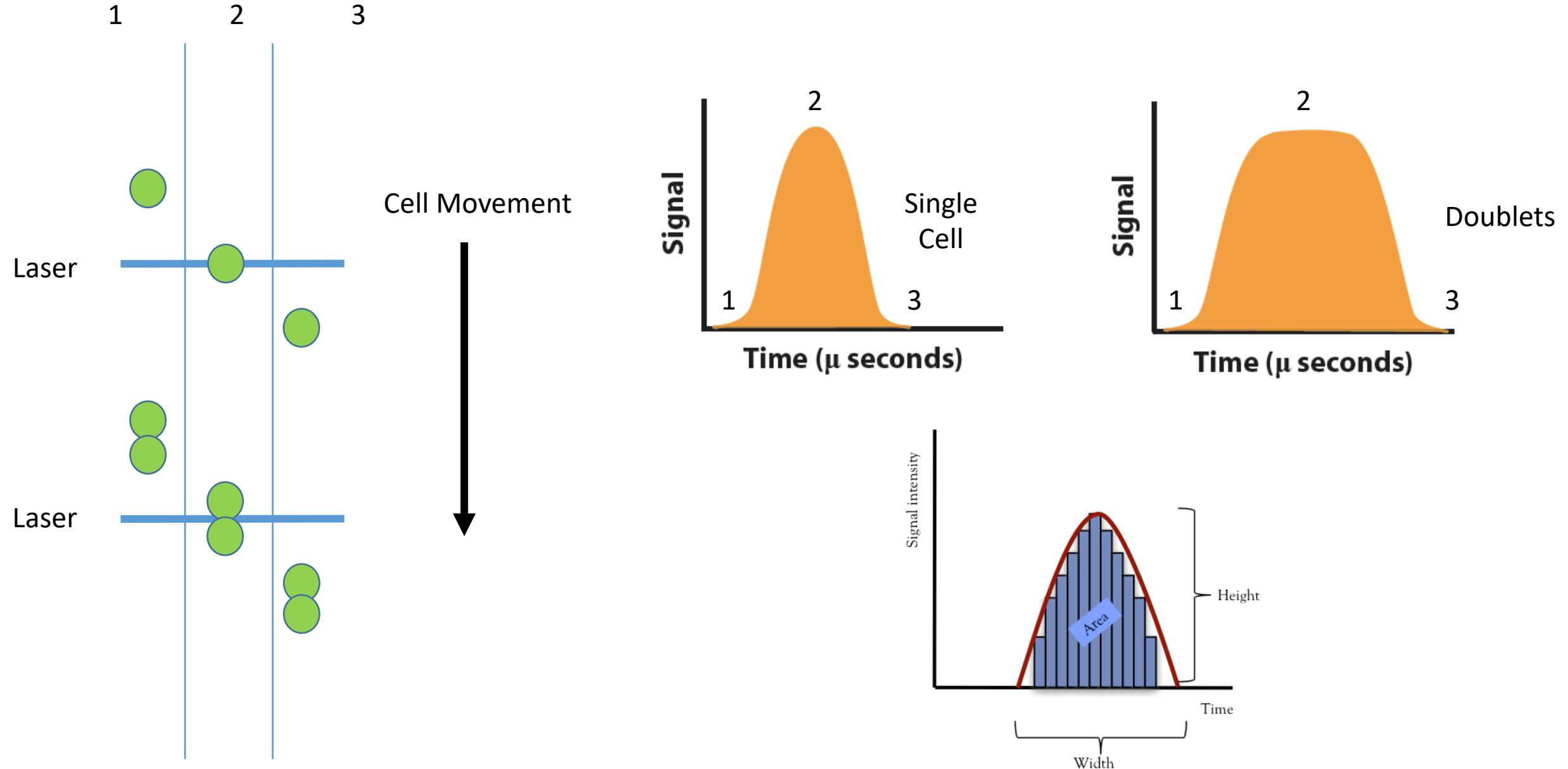


# Doublet Discrimination

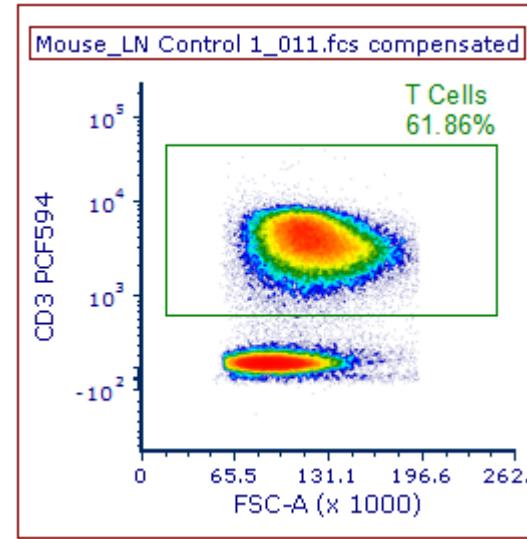
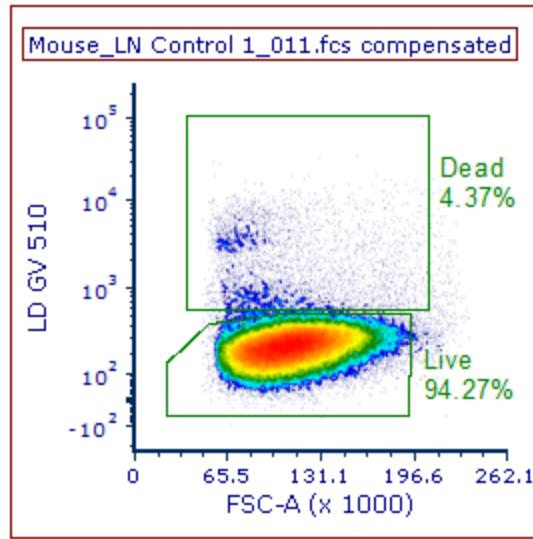


- Helps remove events that are two or more cells stuck together.
- Reduces contribution to false positive or double positive events.

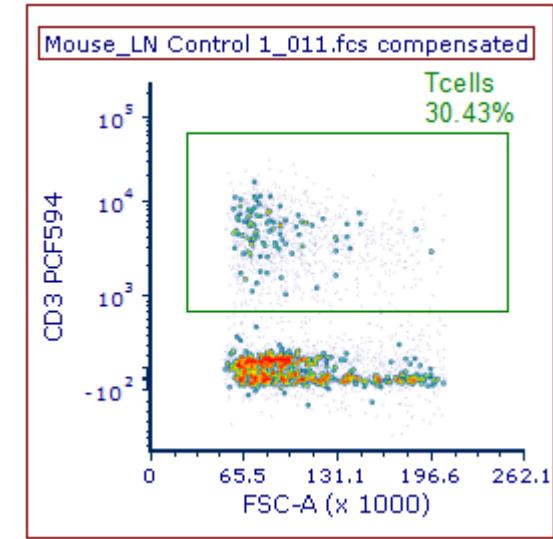
# Why Doublet Discrimination Works



# Live/Dead Gating



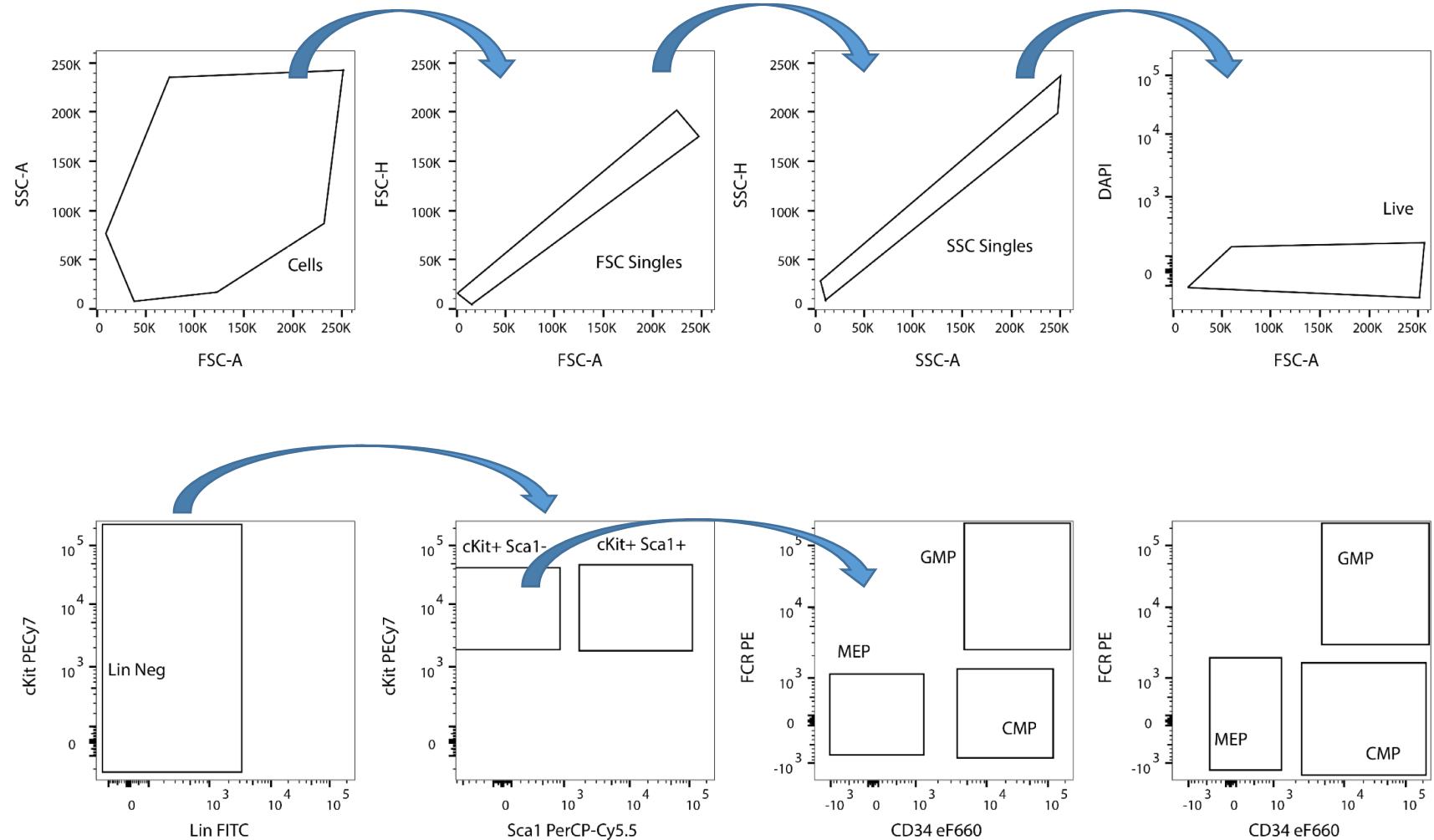
From Live gate



From Dead gate

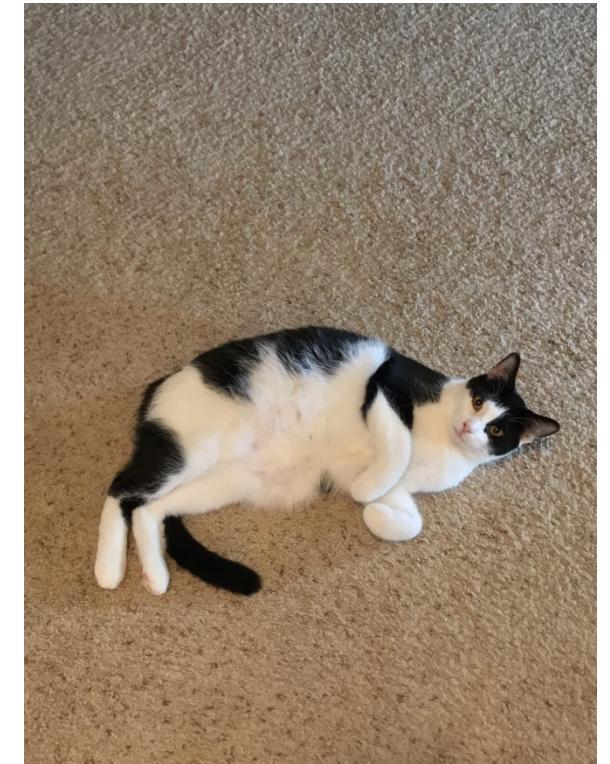
# Gating Strategies

- General gating strategy
  - Doesn't have to be in this order.

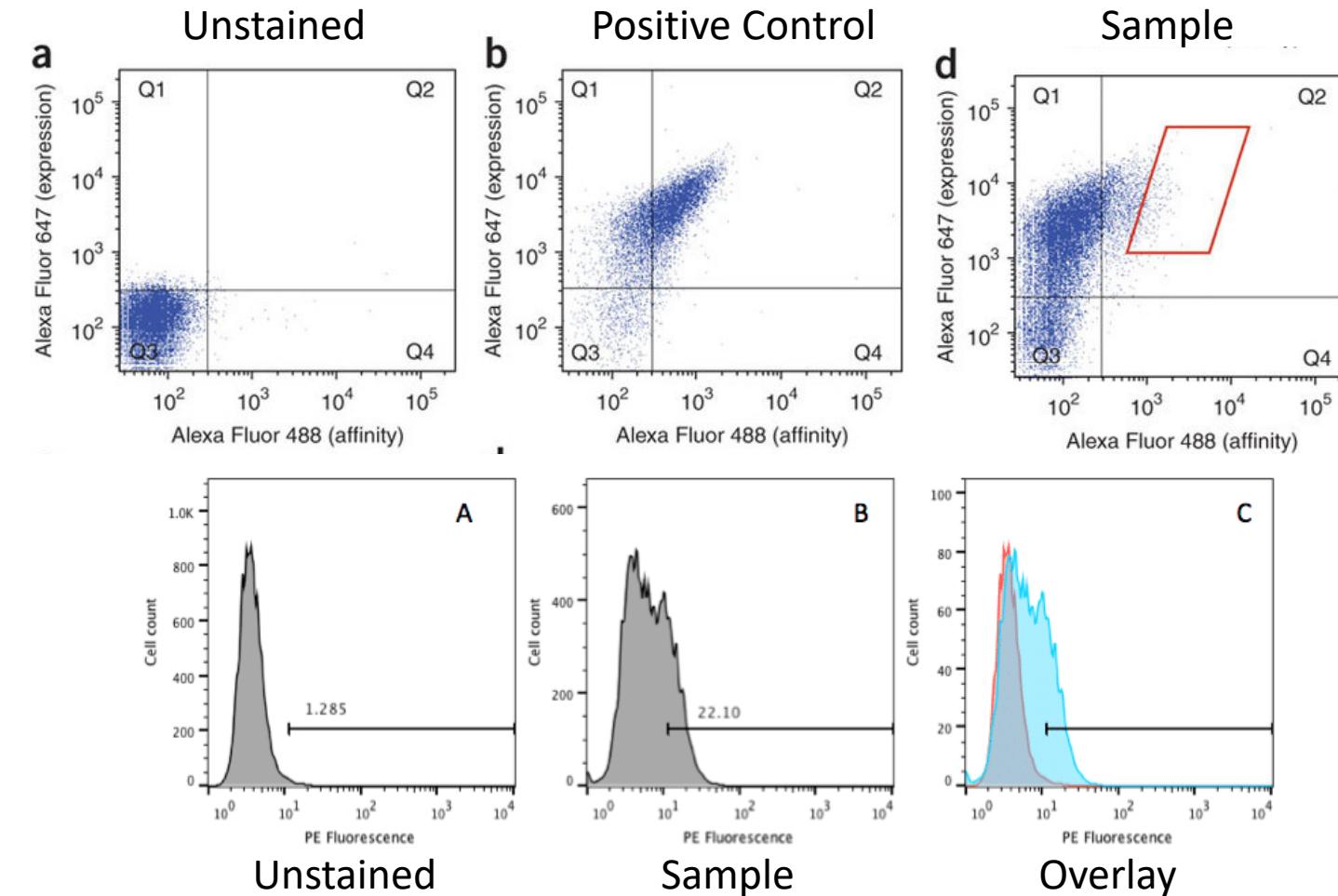


# Common Gating Controls

- Fluorescence minus one (FMO) Control
  - Gating control, shows the background and contributions from neighboring fluorescence spillover.
- Positive Control
  - Standardize gating procedure and observe staining profile.
  - Treated to induce positivity.
- Biological Controls
  - Stim vs. Unstim, T0 vs. Time course, Treated vs. Untreated.
  - Any control you need to prove your hypothesis.
- Unstained control
  - To evaluate inherent background and autofluorescence.

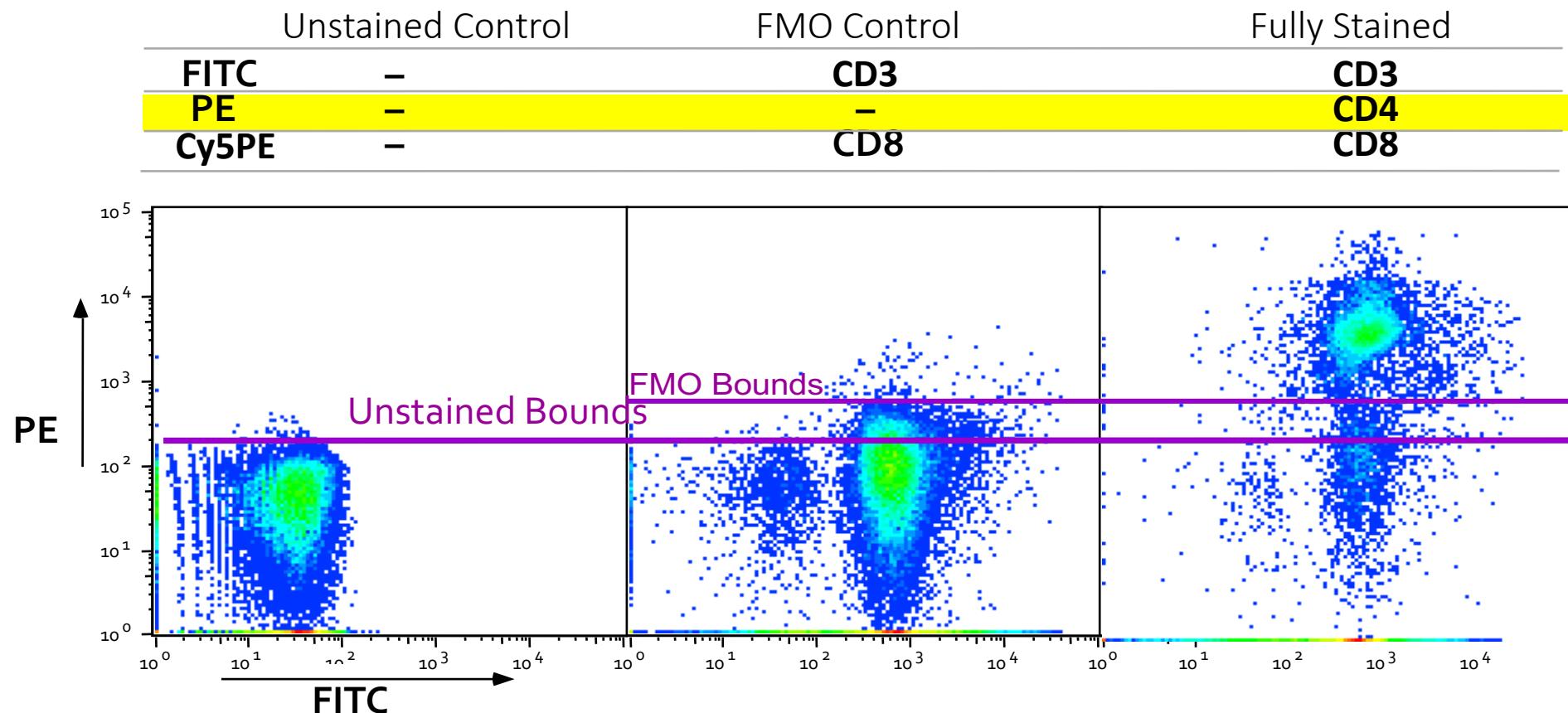


# Negative and Positive controls slide



- **Positive controls**
  - Biological control to assess what the signal looks like when the antigen of interest is present.
  - Useful for rare positive populations or when antigen expression is variable between samples.
- **Unstained/Negative control**
  - Helps make gating decisions.
    - Visualizing autofluorescence.

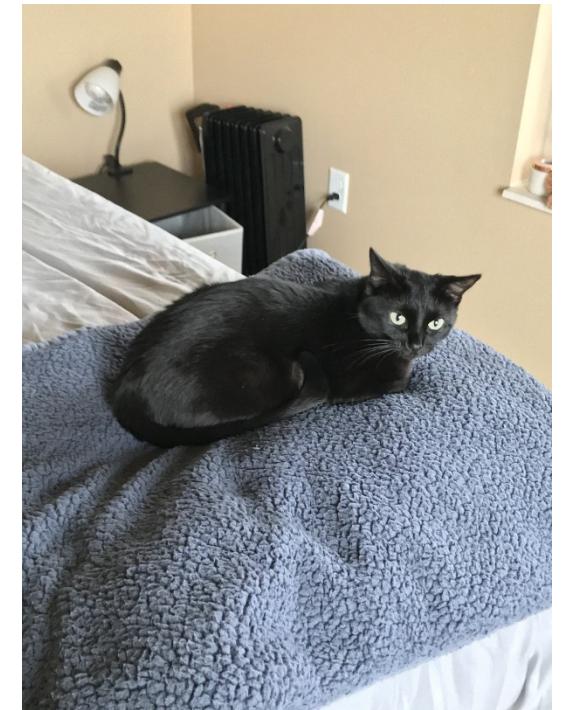
# FMOs



From Excyte Expert Cytometry (Courtesy of M. Roederer, Ph.D, NIH Vaccine Center)

# Why NOT Isotype Controls?

- Nearly impossible to determine if the isotype antibody has the same number of average fluorophores attached per Ab as experimental Ab.
- Different antibody than test sample, different binding properties.
- Maecker HT, and Trotter J. Flow cytometry controls, instrument setup and determination of positivity. Cytometry Part A 2006; 69A:1037–1042
  - Flow Server (T drive) > Flowdata > Flow Resources > Flow References > Isotypes.
- Can use isotype control to test how well the blocking buffer worked.

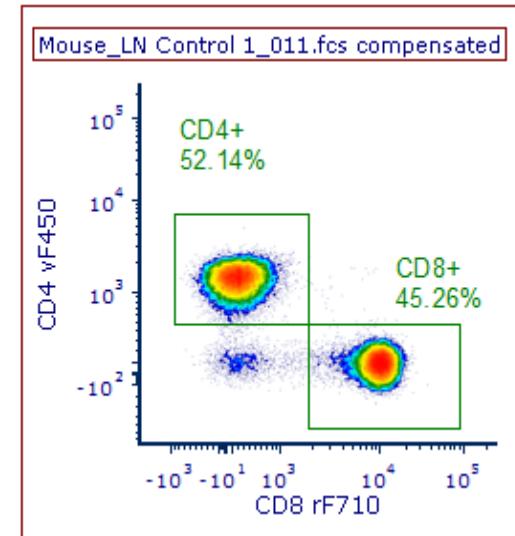
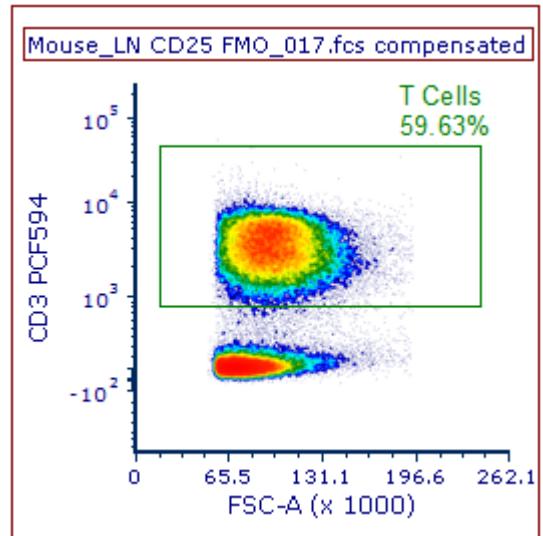


# Basic Statistics in Flow Cytometry

- Typically described using frequencies and fluorescence intensity.
- Frequency
  - Number of events in the target population within a larger population.
- MFI (Median Fluorescence Intensity)
  - NOT mean. Mean is subject to outliers, median is less affected.
- Statistical modeling (Following Seminars)
  - DNA Cell Cycle analysis
  - Proliferation analysis
- Absolute counts
  - Volumetric based acquisition cytometer or counting beads spiked in sample at known concentration. (Counting beads tend to be problematic)

# Frequency

- Ex. Number of CD4+ cells in a population of Live, single, CD3+ positive cells.
- Used to analyze presence of antigen/marker.



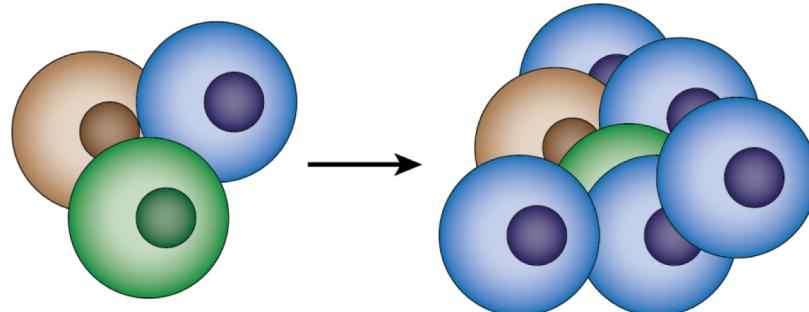
From Live Single Cells

49.81% of CD3+ cells are CD4+  
44.86% of CD3+ cells are CD8+

# Frequency Hypotheses

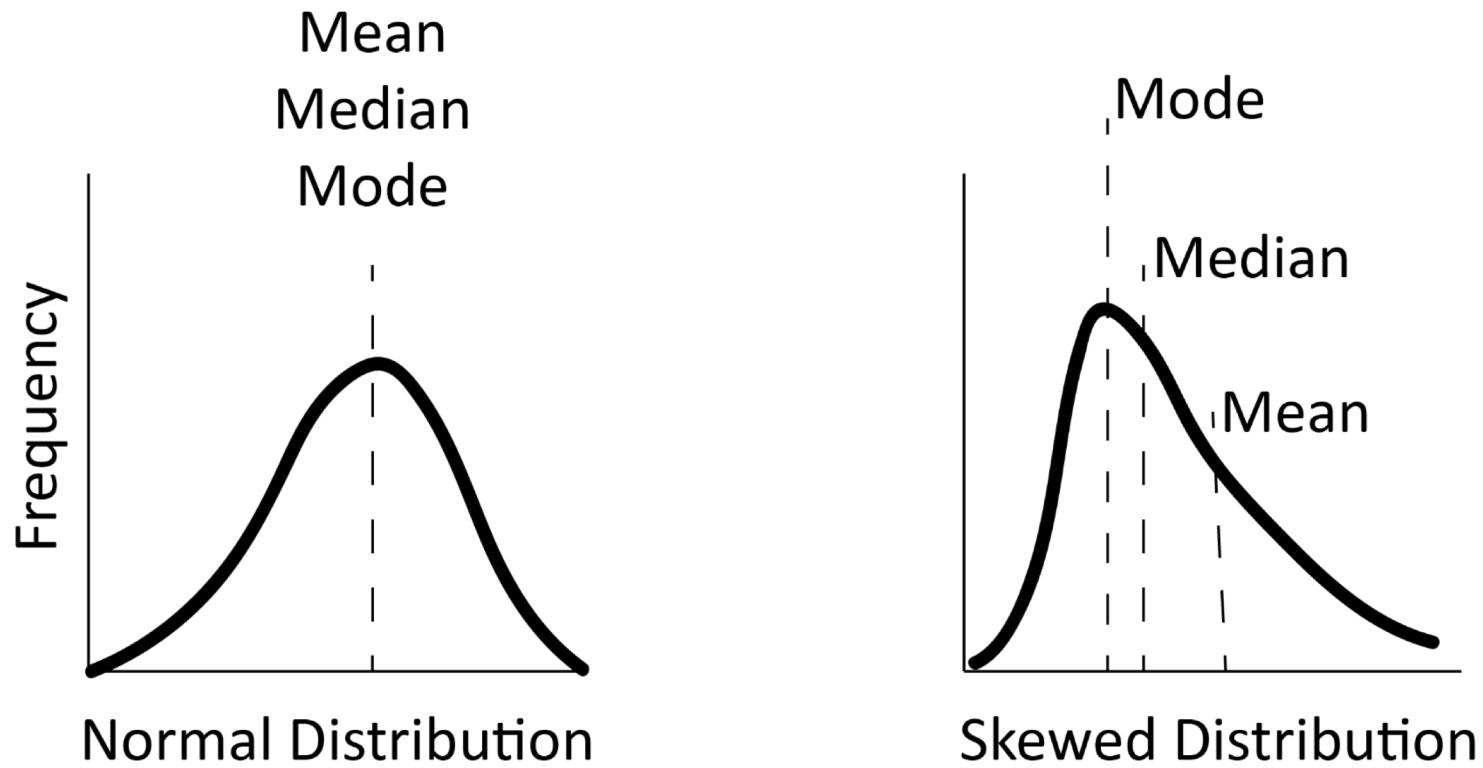
**Treatment increases numbers of cell type Y**

**Cell type Y is more prevalent in disease state A**



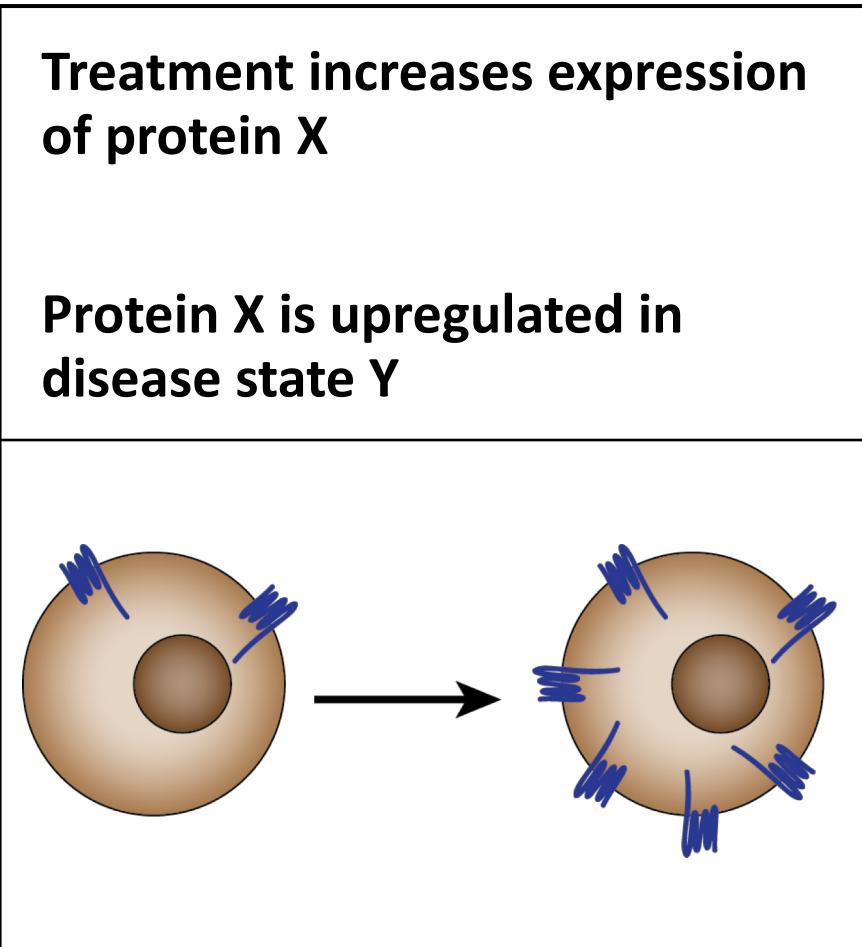
Report **% positive** to evaluate changes in composition of cell populations

# Central Tendency



Most flow cytometry data is displayed on a Logarithmic scale –  
What looks symmetrical is actually skewed!

# Median Fluorescence Intensity



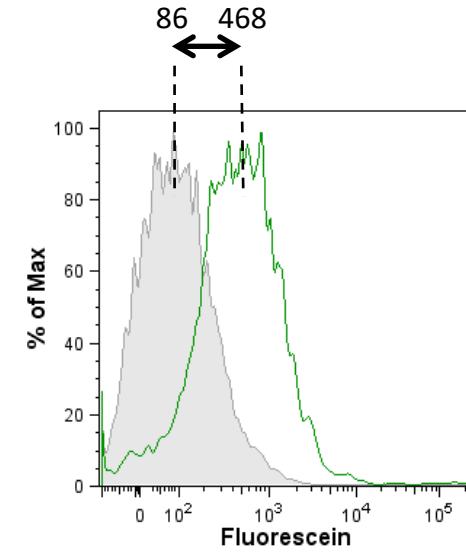
- Use the MFI to assess *levels* of target protein expression
  - Median for logarithmic data.
  - Mean is ok for linear only.
- Standardizing your assay is critical
  - Reference Standard for PMT sensitivity (Rainbow Beads).
  - Can compare samples run on different days.
  - [https://cancer.wisc.edu/research/wp-content/uploads/2017/03/Flow\\_TechNotes\\_Rainbow-Standard-Tech-Note\\_20170918.pdf](https://cancer.wisc.edu/research/wp-content/uploads/2017/03/Flow_TechNotes_Rainbow-Standard-Tech-Note_20170918.pdf)
- Fold increase?

# Fold-change in MFI

- Used in comparison of expression level of antigen/marker between samples.
  - Fold-change in MFI =  $MFI(\text{sample})/MFI(\text{control})$
  - Can compare fold-change in MFI between treatments/samples.

## Caution:

- In order to use Fold-change in MFI, need to be aware of potential skewing of data due to log scale.
- Small changes in negative can translate into large changes in the fold.



Control MFI = 86

Experimental MFI = 468

Fold-change in MFI =  $468/86 = 5.44$

# The Data Analysis Process

1. Have a specific Hypothesis. ASK A SPECIFIC QUESTION!
  1. Need to know which statistics you are after.
2. Gate on live, single cells and use controls to gate each fluorescent parameter.
3. Gather statistics from plots and gates.
4. Perform Analyses.

# Acknowledgements

- Thank you to the DeLuca Lab for data used in this presentation.
- Excyte Expert Cytometry for graphics used in this presentation.

# Mark your calendars for upcoming UWCCC Flow Lab Seminars!

## Rigor and Reproducibility in Flow Cytometry

Friday, December 14, 2018  
10am, WIMR 7001A

## Overview of Computational Data Analysis Platforms for Flow Cytometry

Friday, January 11, 2019  
10am, WIMR 7001A

## Flow Cytometry – Compensation with Confidence

Friday February 1, 2019  
10am, WIMR 7001A

## Flow Cytometry Current Best Practices for PIs

Thursday, February 14, 2019  
7:30am, WIMR 7170

## Multicolor Panel Design for Flow Cytometry

Tuesday, March 5, 2019  
2pm, WIMR 7001A

## Data Analysis with Alex II

Tuesday, March 7, 2019  
10am, WIMR 7170

## Data Analysis with Alex III

Wednesday, May 16, 2019  
10am, WIMR 7170

