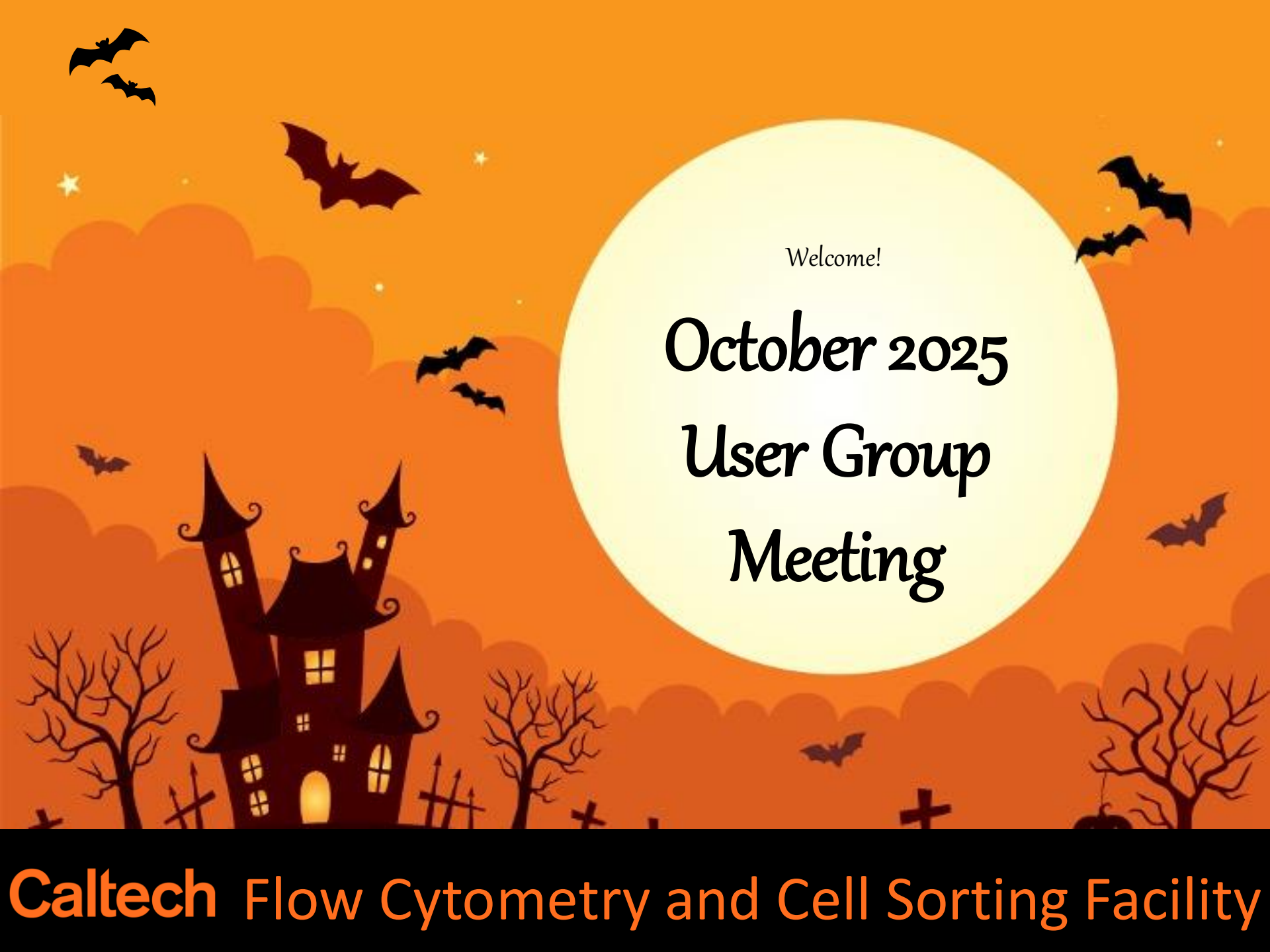




Welcome!

October 2025 User Group Meeting

Caltech Flow Cytometry and Cell Sorting Facility

Who we are?



Michael Gregory	–	Director
Maddy Adolf	–	Cytometry Technician
Olivia Finney	–	Cytometry Technician
Shelley Diamond	–	Emerita Director
Ellen Rothenberg	–	Faculty Supervisor

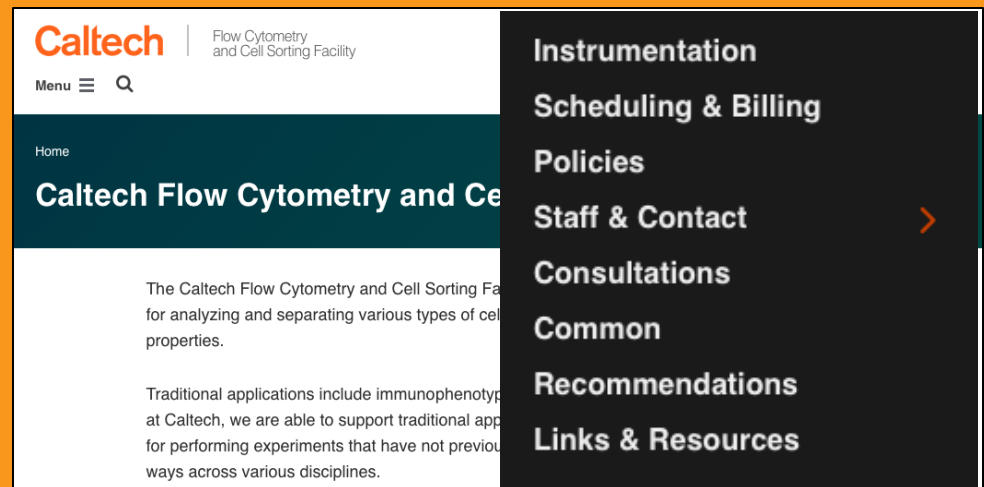
Main Contact –

cellsort@caltech.edu

Office – x3998

Mike – mikeg@caltech.edu

Cell – 561-641-5185



<https://cellsort.caltech.edu>

Getting Started



- New Project Consultation
 - Fill out our New Project form to schedule a consultation
 - Provide as much information as possible (we can update it during the meeting!)
 - Meet with the staff to discuss your project before you begin
 - BEFORE you order reagents, etc, as we may suggest changes!
- Sorts and trainings booked with staff (cellsort@caltech.edu!)
- Self-serve analysis booked directly on our scheduler



Caltech Flow Cytometry Cell Sorting Facility

Dashboard Reservations Application Management Reports

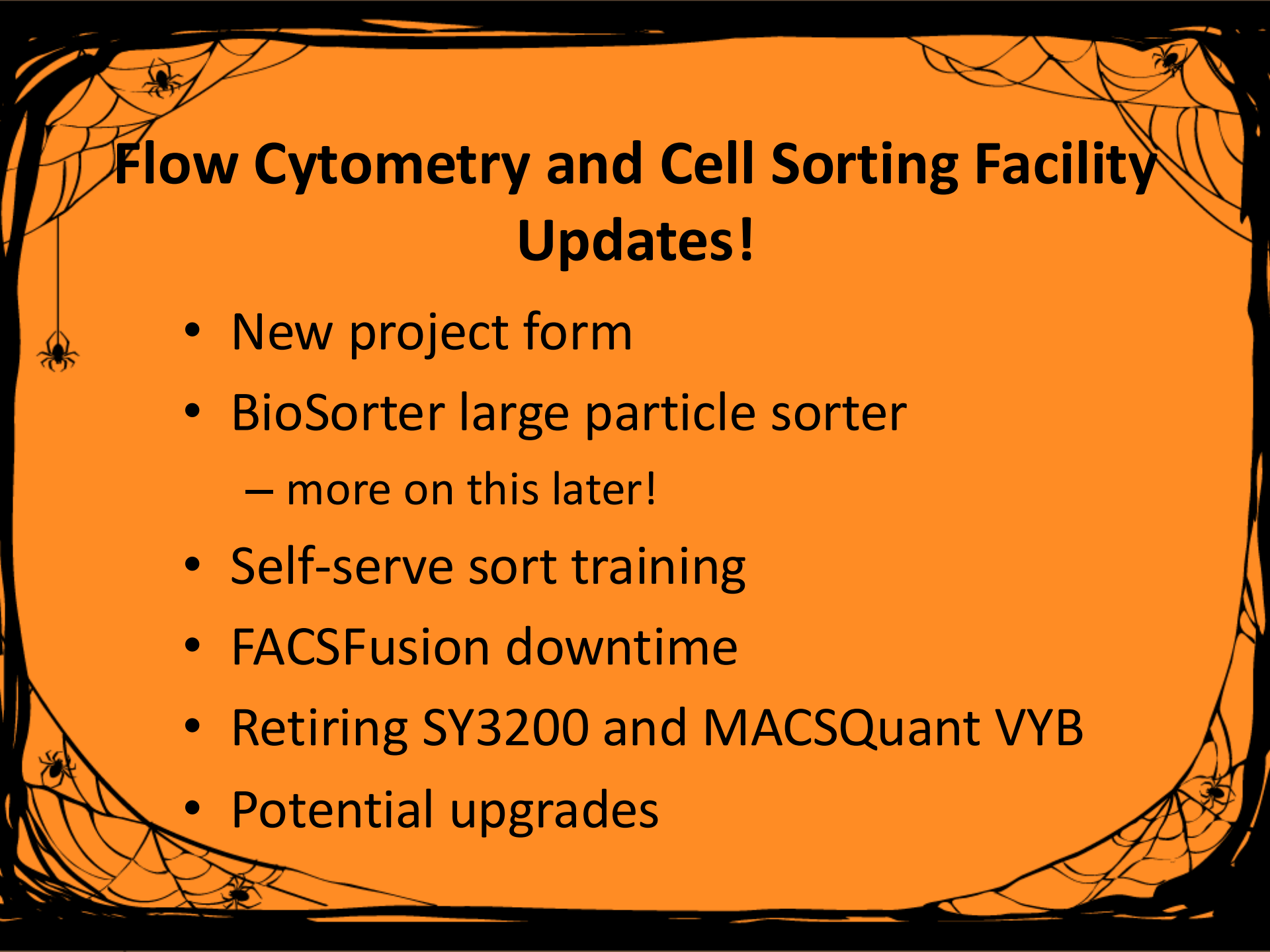
Michael

All Reservations

October 2025

Sun	Mon	Tue	Wed	Thu	Fri	Sat
28	29	30	1	2	3	
11a - 12p Cytoflex Analyzer - Laura	9:30a - 11:30a Cytoflex Analyzer - Honami (Mazmanian)	1p - 2p Consulting - Beauty Stem	10a - 12p Cytoflex Analyzer - Anthony P (Training)	2p - 5p Cytoflex SRT - Abdullah (Rothenburg)	10a - 10p Cytoflex Analyzer - Ishaan Shapiro Lab (idev@caltech.edu)	12a - 3a Cytoflex Analyzer - Ishaan
1p - 2p Cytoflex Analyzer - Jiamin	12:30p - 2:30p	1:30p - 2:30p Cytoflex SRT - Hao	1p - 4p	3:30p - 5p		

reserve.cellsort.caltech.edu



Flow Cytometry and Cell Sorting Facility Updates!

- New project form
- BioSorter large particle sorter
 - more on this later!
- Self-serve sort training
- FACSFusion downtime
- Retiring SY3200 and MACSQuant VYB
- Potential upgrades

Updates!

New Project Consultation form

- Input via Microsoft forms
- Responses transferred to Sharepoint list
 - Modifiable with tracking – entries are confirmed and updated during consultation or when project changes
 - Collaborative – PI and other parties can be given access to view/comment
 - Keeps all staff members up-to-date on the project details
 - Searchable

Flow Cytometry Project Form 3*

Please fill out the form below as completely as you can. This form must be approved by the Principal Investigator who accepts responsibility for the experiment prior to scheduling a consultation. This form will be kept on file and may be used for additional experiments or resubmitted to better reflect your current experiment. After completing this form, you can expect to be contacted about setting up a consultation at the earliest possible convenience. If you have any further questions or concerns, or would like to supply any additional documentation, please email us at caltech@caltech.edu, or visit our website: caltech.caltech.edu

Section 1

1. First and Last Name: *

Enter your answer

2. Caltech Email: *

Please enter an email

3. UID: *

Enter your answer

4. Phone Number:

Enter your answer

5. Name of Principal Investigator: *

Enter your answer

6. Email of Principal Investigator: *

After submitting this form, your PI will receive an email requesting their approval of your project. In order to proceed with your project, PI approval is required. Please ensure that the email you enter for this question is accurate, and that your PI is aware of your project and able to approve the form in a timely manner.

Please enter an email



Item properties

Project Description *

Immune profiling after T cell depletion:
Mice are treated with anti-CD4, anti-CD8, or isotype IgG antibody for 5 weeks to deplete CD4 or CD8 T cells.
Immune cells will be profiled with flow cytometry to validate depletion of T cells.

Item Created
9/11/2025 1:26:53 AM

First and Last Name
Honami Tanaka

Caltech Email
htanaka@caltech.edu

UID *

Phone

Name of Principal Investigator: *

Sarkis Mazmanian

Comments ▾

@mention or comment



Be the first one to add a comment



Updates!

Self-serve sort training

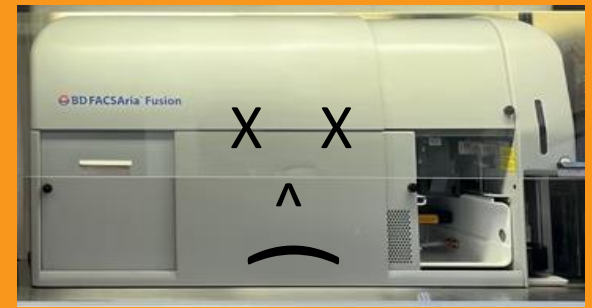
- Advantages
 - More flexible scheduling – allows for afterhours and weekend sorting with appropriate training
 - Training customized to needs
 - Less expensive/hour
- Disadvantages
 - On your own for troubleshooting
 - Longer training period, with independent use only possible once objective benchmarks are satisfied
- Possible on FACSFusion and Cytoflex SRT (requires additional setup fee). BioSorter will be primarily self-serve!



Updates!

FACSFusion excessive downtime

- Previous service provider unable to repair instrument fully in ~2.5 months. Returning to manufacturer (BD) service contract.



Retiring SY3200 sorter and MACSQuant VYB analyzer

- VYB coverage ended earlier this year. Still available, but may not be able to repair if it breaks!
- SY3200 coverage will end in December. Still available, but most sorts will need to be moved to Fusion and SRT
 - Loss of capabilities —
 - UV laser
 - stream-in-air
 - Let us know if these capabilities will be require for your future projects!



Upgrades?

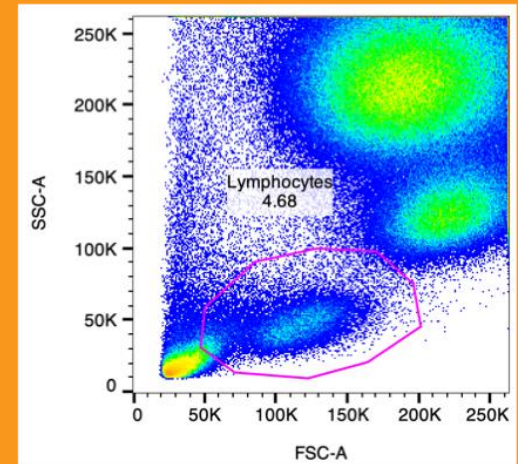
- New analyzer? Spectral instruments?
 - More colors (5 laser systems can get to ~40 colors!)
 - Full spectrum means autofluorescence can be better characterized
 - More possibility for label-free identification
 - Aurora by Cytex, ID7000 from Sony, Mosaic add-on for Cytoflex
- New Sorter? Stream-in-air? Spectral? Microfluidic? Imaging?
- Let us know your needs for upcoming projects to help us decide priorities!
- Labs with their own instrument that would rather not have to manage them? Happy to talk about mutually beneficial solutions!
- Design/development groups on campus? Please connect us!

Flow Cytometry Data

- Flow cytometry data is stored as a list mode file:

Id	Time	Plate	Row	Column	Source well	Clog	Sorted	status	In Regions	T0F	Extinction	Green	Yellow			
1	59	n/a	0	0	n/a	N	0	00001	308	76.9	0.33	0.16	0.22	9293	320	n/a
2	532	n/a	0	0	n/a	N	0	00001	395	115	0.38	0.12	0.19	11129	408	n/a
3	5156	n/a	0	0	n/a	N	0	00001	127	20.1	0.08	0.04	0.04	5184	136	n/a
4	30589	n/a	0	0	n/a	N	0	10001	3656	4593	341	33.9	16.7	50063	3672	n/a
5	30709	n/a	0	0	n/a	N	0	10001	4128	5052	207	21.9	22.4	48981	4144	n/a
6	31095	n/a	0	0	n/a	N	0	10011	3626	3889	178	33.7	411	43211	3640	n/a
7	31315	n/a	0	0	n/a	N	0	10001	4159	4877	729	75.2	31.6	47135	4168	n/a
8	31390	n/a	0	0	n/a	N	0	10101	3442	4445	158	16.4	13.2	49612	3456	n/a
9	31463	n/a	0	0	n/a	N	0	10011	3597	5072	228	52.7	761	59586	3608	n/a
10	31555	n/a	0	0	n/a	N	0	10001	3549	4684	274	27.6	19.8	53955	3560	n/a
11	31684	n/a	0	0	n/a	N	0	10001	3679	4242	350	33.0	19.2	47299	3688	n/a
12	31867	n/a	0	0	n/a	N	0	10001	3821	4105	211	20.3	15.8	47023	3832	n/a
13	31870	n/a	0	0	n/a	N	0	10001	3727	5068	345	36.8	23.5	58797	3736	n/a
14	31904	n/a	0	0	n/a	N	0	10001	3731	4332	405	47.3	21.2	48395	3744	n/a
15	32033	n/a	0	0	n/a	N	0	10001	4882	6558	613	67.8	25.2	53294	4896	n/a

- Files can get very large, depending on the number of events AND the number of parameters recorded for each event.
- Specialized software allows you to explore the data visually (also possible for RNA-seq data!)



Flow Cytometry Analysis Software

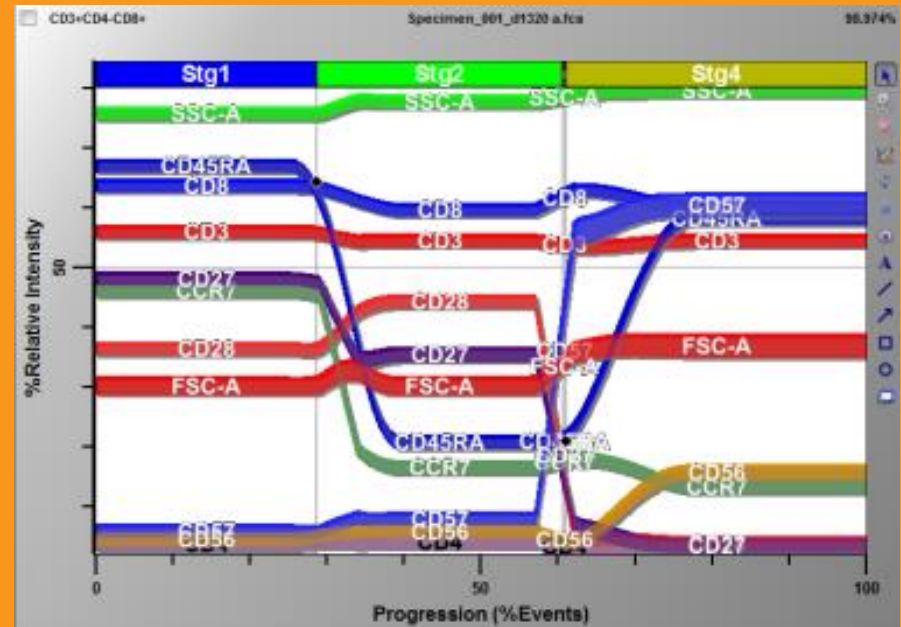
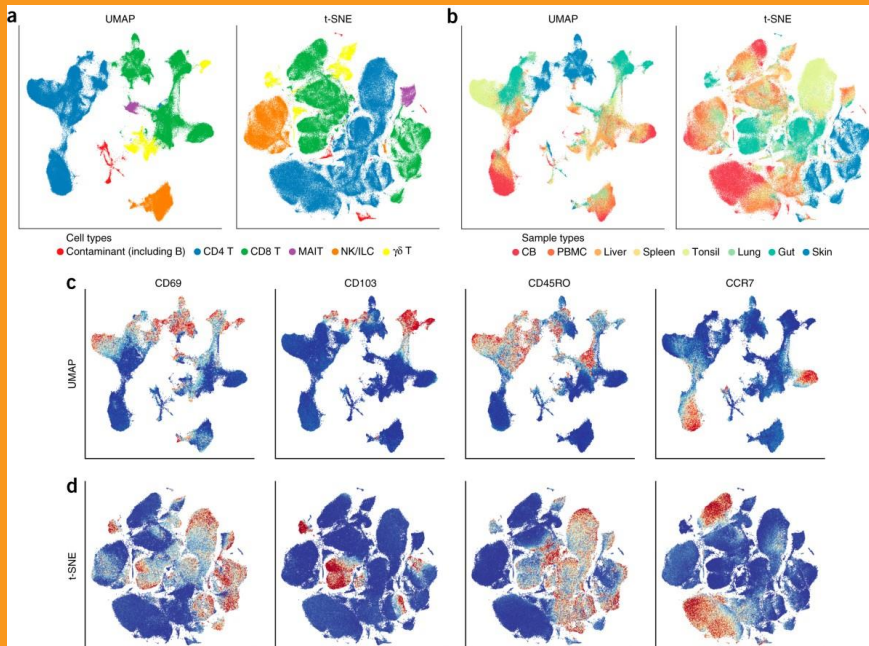
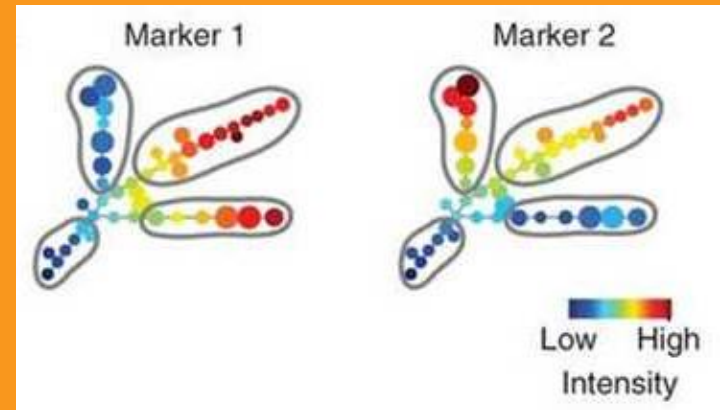
- FlowJo – Caltech site license (currently \$310/yr)
- FCSExpress & OMIQ – Dotmatics
- Modfit & Gemstone – VSH - specialty software
- Kaluza & Cytobank – Beckman Coulter
- CytoScribe – BioLegend – brand new!

FREE!

- Floreada.io – browser-based simple analysis tool
- R and Python analysis modules – these have gotten MUCH better
- Vendor acquisition software (ex CytExpert and FlowPilot)
 - Not recommended for complex analysis! Available on our Sharepoint!

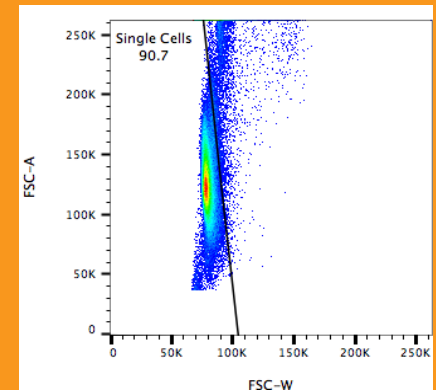
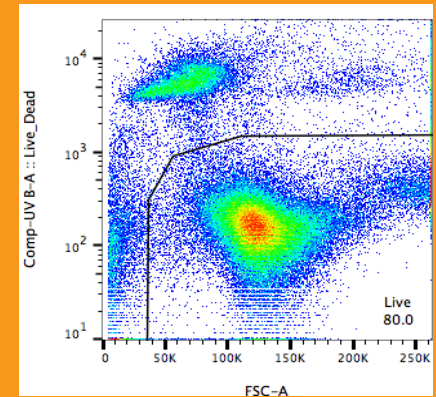
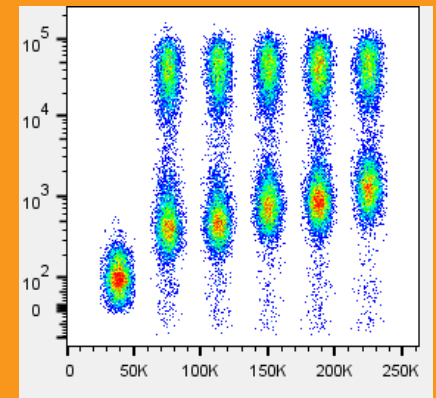
Advanced Data Analysis Tools

- Useful for exploring high dimensional datasets
 - UMAP, tSNE, and viSNE
 - Gemstone
 - Spade



Preparing Properly

- Experimental Design
 - Titrating ab/dye concentrations
 - Including a viability dye
 - Debris reduction/removal
 - Proper controls
- Instrument Setup
 - Choosing Log/Linear for FSC/SSC
 - Setting threshold
 - Optimizing detector settings
 - Screen for doublets

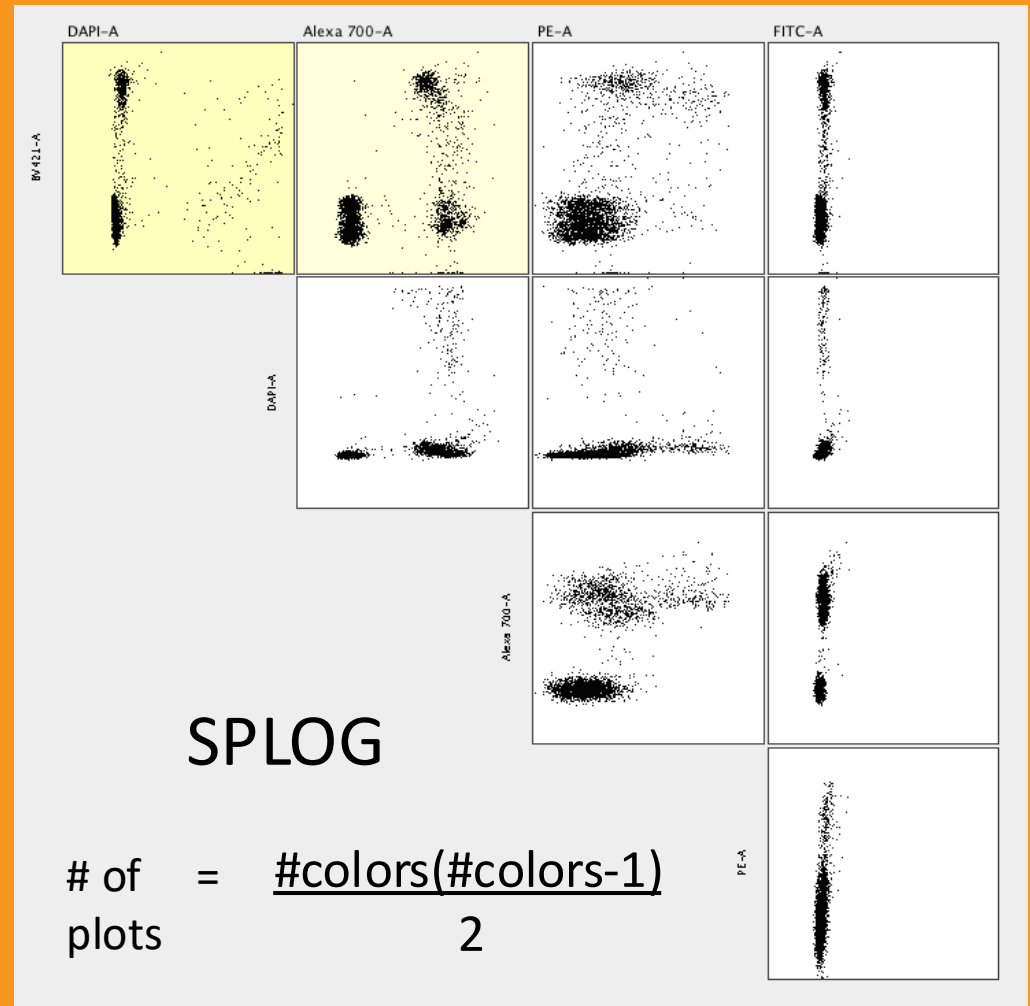


Voltages/Gains and Compensation

NXN view

Setting Voltages

- Hardware on instruments have ideal voltages
 - Starting point, may not be ideal for your cells
- Find the best signal to noise
 - Voltration?
- Set voltages with compensation in mind!

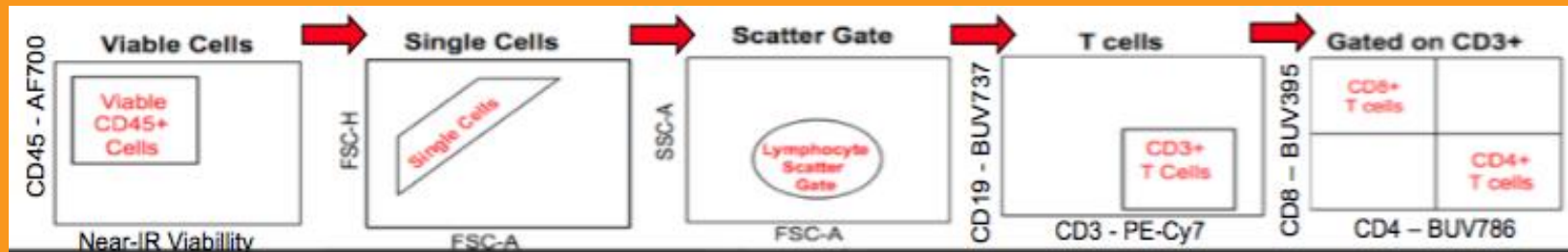


Proper Controls Ensure Good Setup and Gating

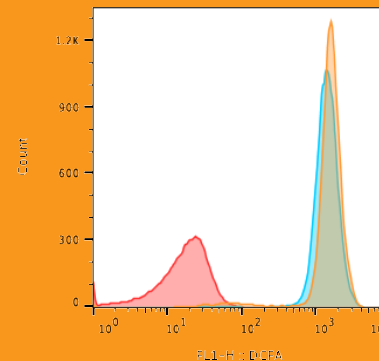
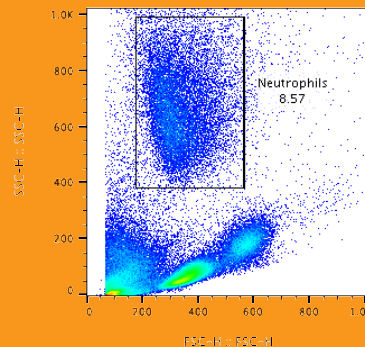
- Negative control – Cells without any staining
 - Used to set the baseline voltages for all colors in an experiment based on the natural autofluorescence of your cells
- Isotype Controls – Isotype-matched irrelevant antibodies
 - used to assess ‘non-specific’ binding of the non-antigen targeting regions of mAbs. Should NOT be used to set gating. Can inform on sample preparation issues (ie.blocking)
- Compensation Controls
 - Controls each stained with a single color, minus all others. Used to compensate for spectral overlap between fluorochromes
- FMO Controls – Fluorescence Minus One
 - Controls each stained with all colors, *except* one. Used to account for interactions between fluorochromes. A powerful & recommended gating tool for multicolor experiments

Data Analysis – How to begin?

- What's the question you're looking to answer with your data?
 - Phenotyping Subpopulations

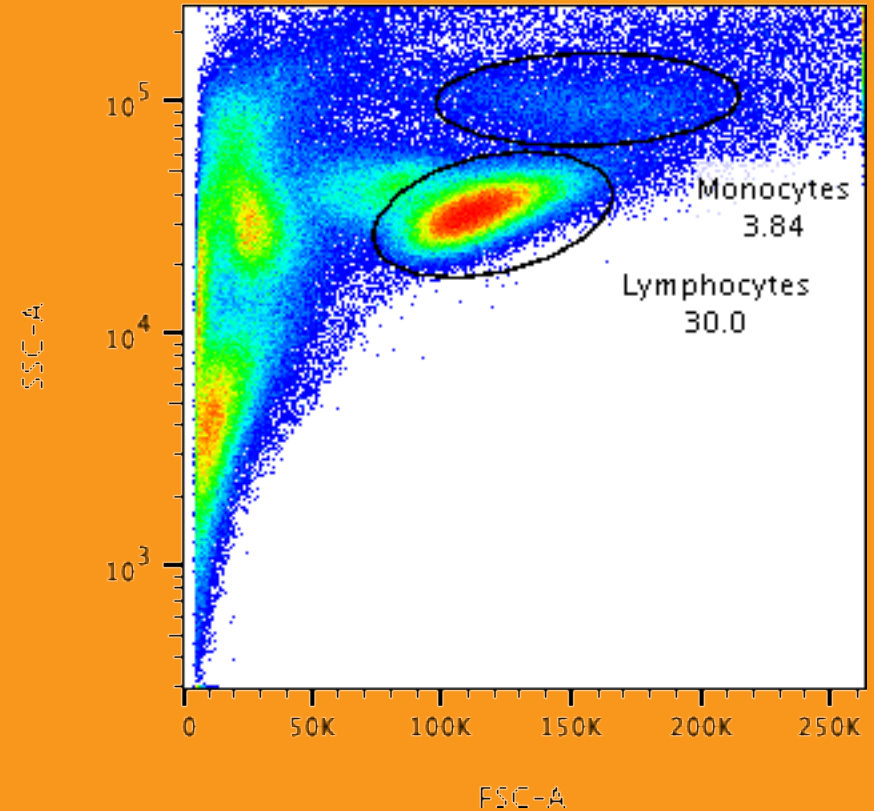
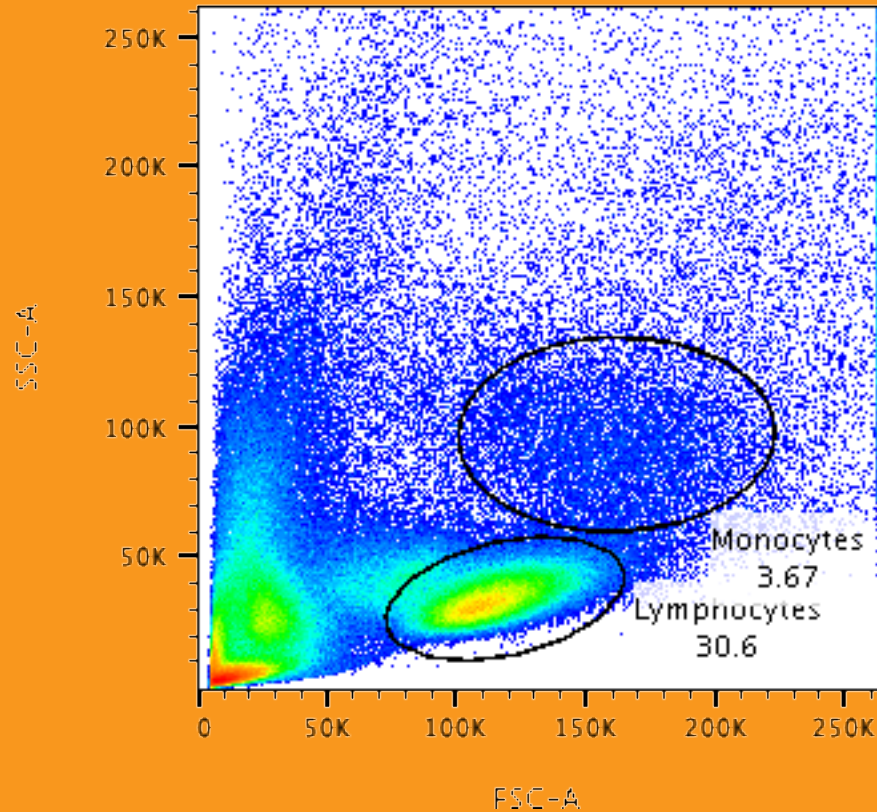


- Mean (or Median) Fluorescent Intensity (MFI)
- MFIR



Sample Name	Subset Name	Count
ROS07:14.019 C3	Neutrophils	25321
ROS07:14.018 C2	Neutrophils	24801
ROS07:14.017 C1	Neutrophils	14909

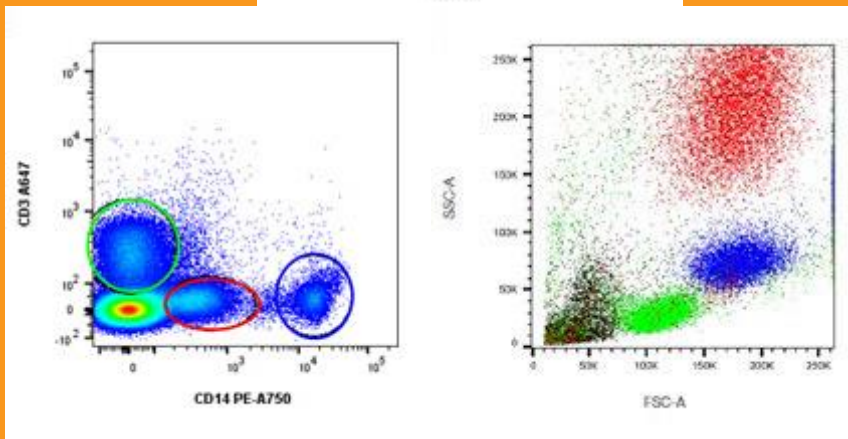
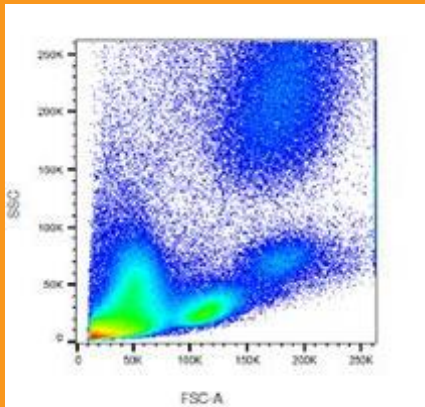
SSC - log versus linear



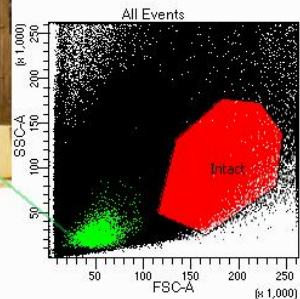
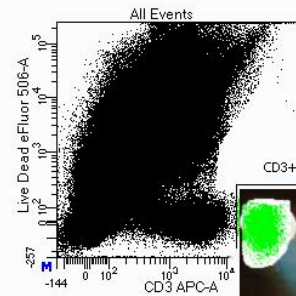
Newer instruments/software allow you to change the scaling after the fact, but if settings are optimized for one or the other you could be stuck.

Finding your Cells of Interest

- FSC v SSC – backgating – during acquisition AND/OR analysis.



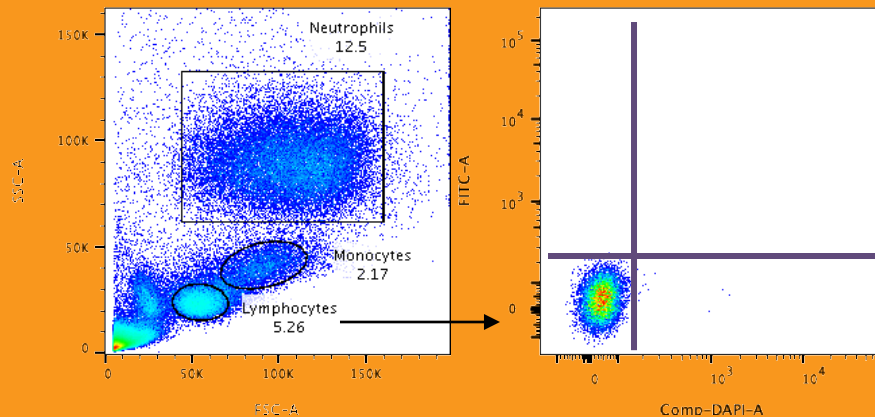
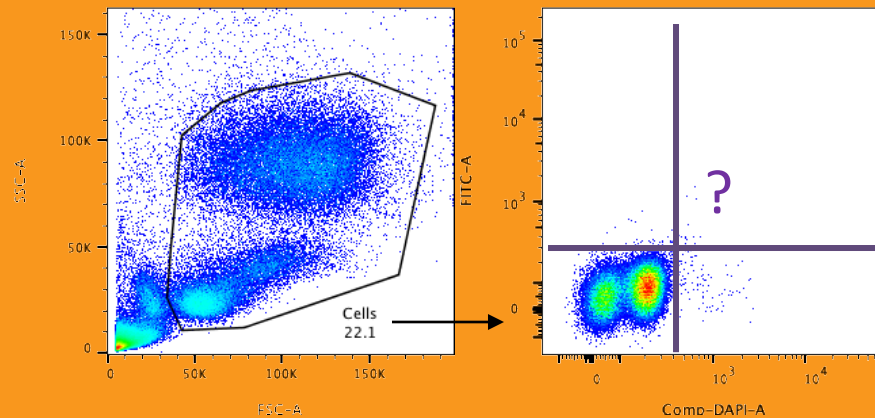
Backgating



They're ~~digging~~ ^{gating} in the wrong place.

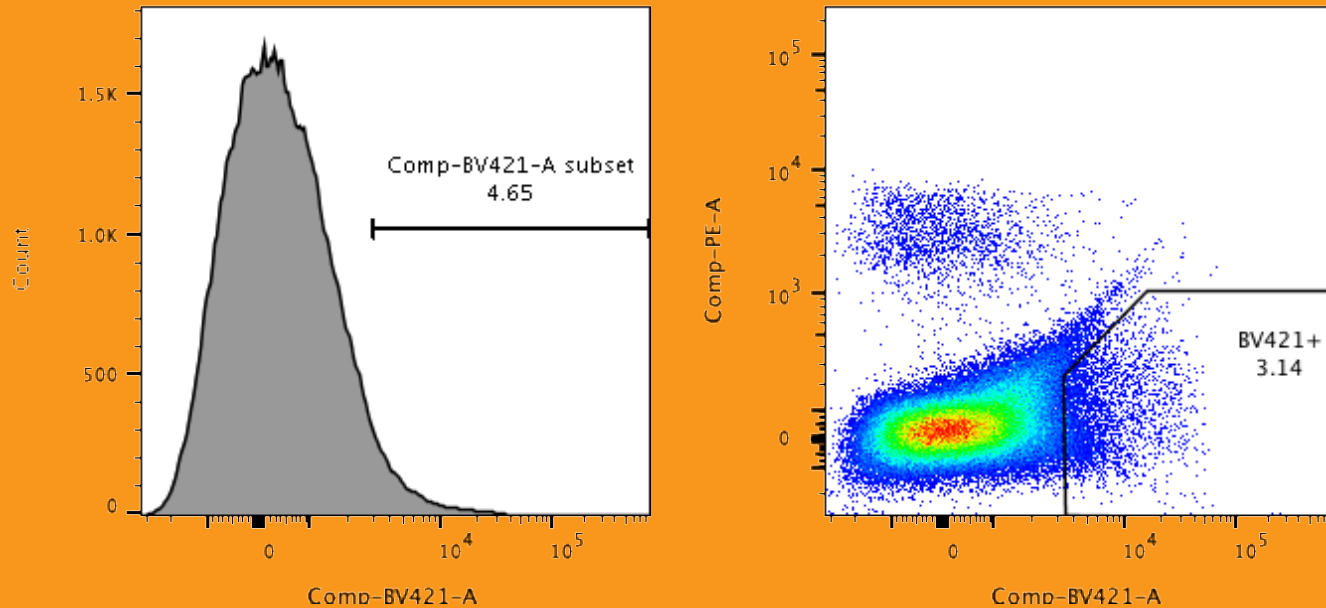
Finding your Cells of Interest

- Gating different scatter populations early?
 - Different cell populations may have different autofluorescence!



Finding your Cells of Interest

1 parameter vs 2 parameter plots help ID the real positives.



- Auto-fluorescent cells that were not removed by upstream gating can appear as a 'spike' that should be considered when gating.
- Spectral cytometers allow for autofluorescence subtraction or extraction.

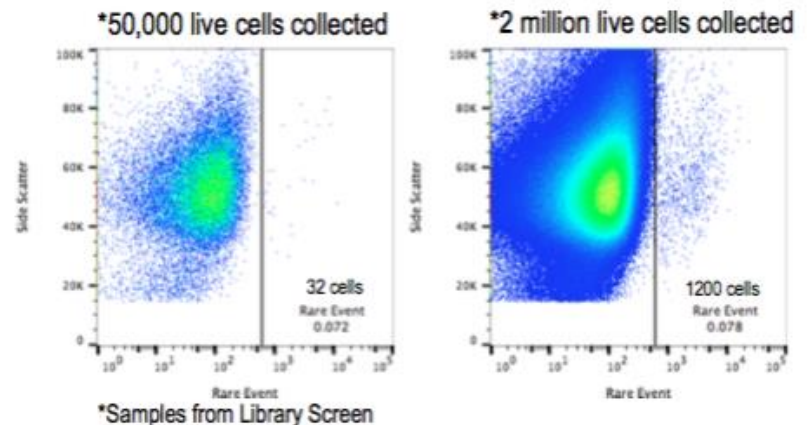
Number of cells to acquire?

- Must determine how many cells will be enough to analyze smaller subpopulations.

Precision, most commonly expressed in coefficient of variation (**CV**) values, is defined by Shapiro* (2003) as “The extent to which identical values are obtained from measurements of identical particles.” (pg. 214)

Cell Count	Precision
10	+/- 31.6%
50	+/- 14.1%
100	+/- 10.0%
1000	+/- 3.2%
10000	+/- 1.0%

As the number of events collected increases, the variability in the precision of your data decreases.



Precision of data is determined on your gated cells of interest.

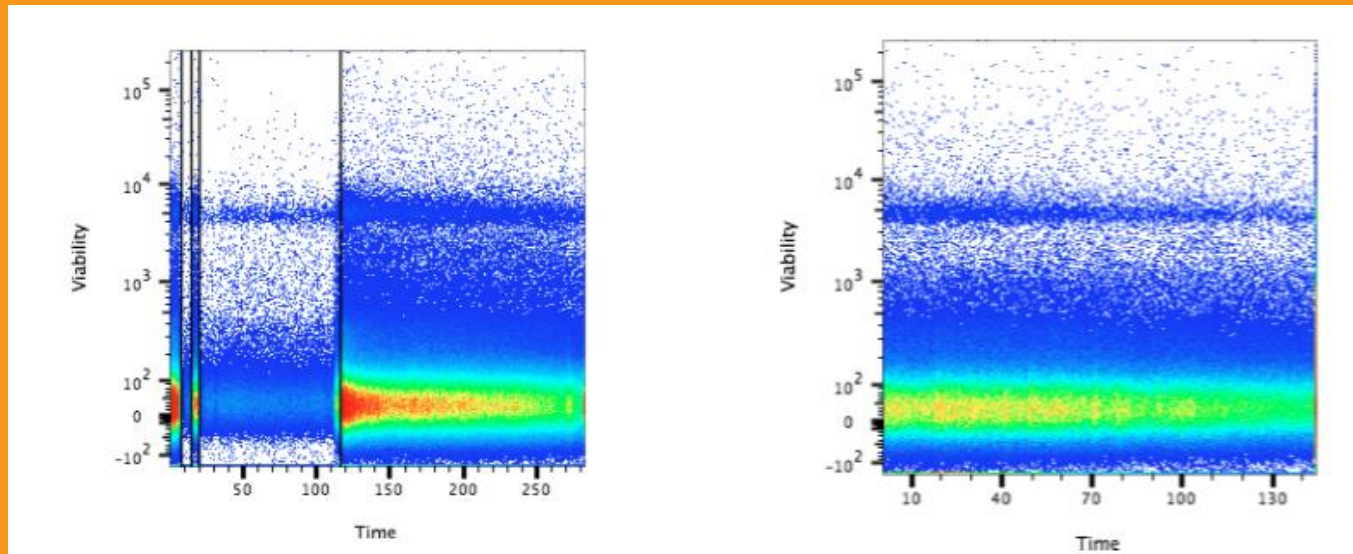
i.e. If you have 500 total events, but out of that number only 10% are your cells of interest (50 cells), your precision decreases from +/- 4.4% to +/- 14.1%.

Note: An equal number of your negative control should also be collected.

Standard is to collect at least 1,000 gated cells of interest for statistical significance.

Data QC!

- Time parameter - can use to assess and even salvage data!



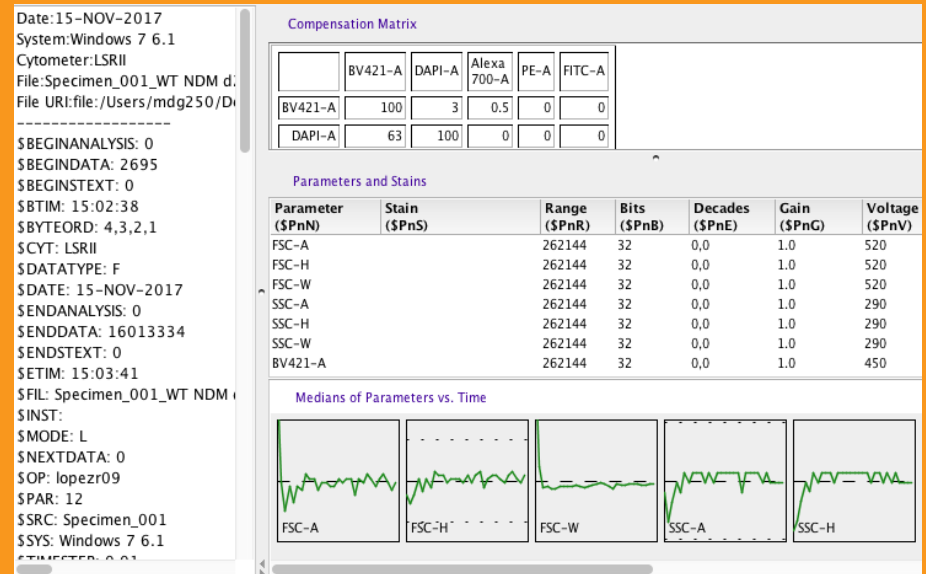
flowClean: Automated Identification and Removal of Fluorescence Anomalies in Flow Cytometry Data

[Kipper Fletez-Brant](#),^{1,3} [Josef Špidlen](#),² [Ryan R. Brinkman](#),² [Mario Roederer](#),³ and [Pratip K. Chattopadhyay](#)^{3,*}

“Tracking cell populations in centered log ratio (CLR) space” to “flag time periods with fluorescence perturbations leading to the emergence of false populations.”

Automation for Longterm Projects

- Using Keywords
 - Who's seen these windows before?
 - Can enter custom keywords to help automate analysis
 - Easily map gates to data files based on their keywords.



Keyword List

Name	△ Value	Explanation
\$BEGINANALYSIS	573376	
\$BEGINDATA	2596	
\$BEGINTEXT	0	
\$BTIM	15:12:07.1093750	The time at the beginning of data collection, format hh:mm:ss.
\$BYTEORD	1,2,3,4	Byte Order
\$CYT	BD FACSCanto II	The cytometer used to acquire the data.
\$CYTSN	V96100290	
\$DATATYPE	I	Data format.
☒ \$DATE	27-MAR-2017	The date the file was created, format dd-mmm-yy.
\$ENDANALYSIS	590897	
\$ENDDATA	573375	
\$ENDTEXT	0	
\$ETIM	15:13:07.2343750	The time at the end of data collection, format hh:mm:ss.
< Add Keyword Remove Keyword		

MIFlowCyt

Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) Compliant Manuscript Using the International Society for Advancement of Cytometry (ISAC) FCS File Repository (FlowRepository.org)

Josef Spidlen, Karin Breuer, Ryan Brinkman

First published: 01 July 2012 | <https://doi.org/10.1002/0471142956.cy1018s61> | Citations: 24

Experiment Overview	Purpose/Goal/Hypothesis
	Experiment Variables
	Conclusions
	Quality Control
Flow Sample (Specimen)	Material
	Source/Organism/Location
	Treatment
Data Analysis	Reagent/Analyte/Detector/Reporter
	List-mode Data
	Compensation
	Gating
Instrument Details	Descriptive statistics
	Instrument Identification
	Fluidics Configuration
	Optical Configuration
	Electronic Configuration

- **Minimum Information about a Flow Cytometry Experiment**
 - Published in 2012, following CYTO workshop
 - Annotates data with lots of essential information
 - Aimed to make (re-)use of public flow cytometry data sets more possible
- “Required” for FlowRepository - <http://flowrepository.org>
 - And some specific journals

Methods Section

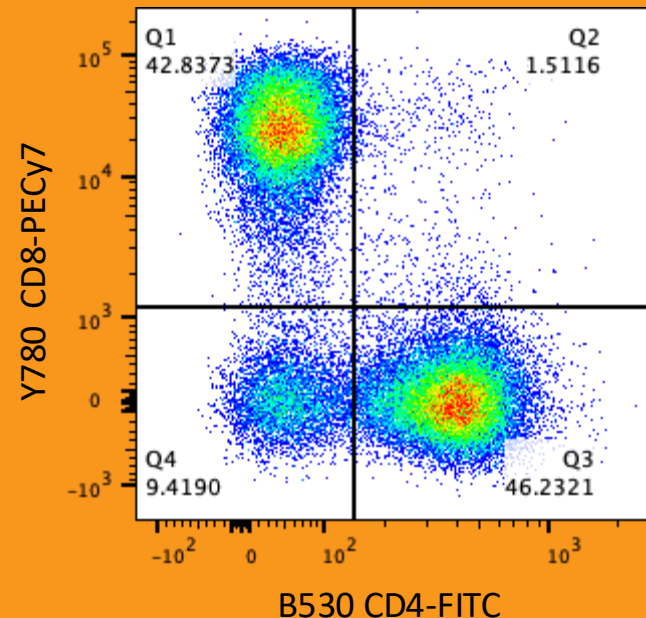
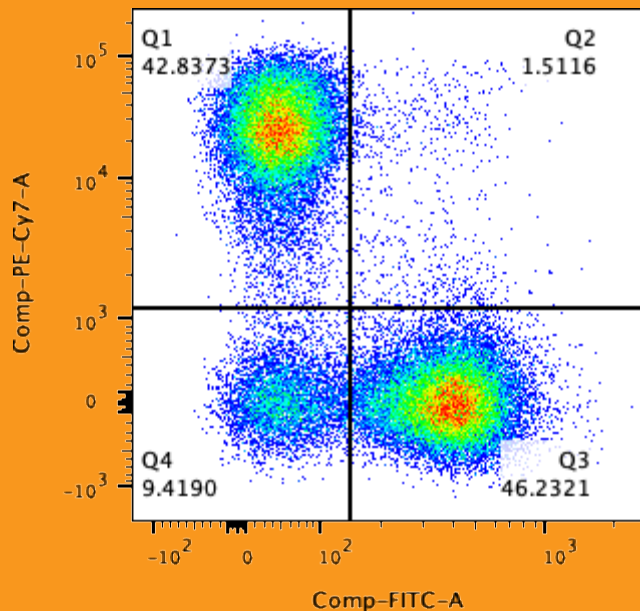
- Sample Preparation and Exp Design:
 - Sample source and preparation
 - Treatments
 - Labeling (ab clones, conc, incubation times/conditions)
 - Controls used,
- Instrument Setup:
 - Describe instrument
 - Manufacturer, model, software
 - Optical configuration
 - Fluidics setup (pressure, nozzle size, buffers used, etc)
 - Sorting conditions

Methods Section

- Data Acquisition/Analysis:
 - How compensation or unmixing was performed
 - Antibodies, cells versus beads
 - Justification of changes/modifications
 - Number of events recorded
 - Smaller populations might require more events
 - Gating scheme –
 - Gating decisions - what controls were used to set these
 - Justification for adjustments, etc
 - Statistics
 - Which populations are included?
 - MFI = mean? Median?
 - Fold increase over control vs standardizing to a bead, etc

Results Section

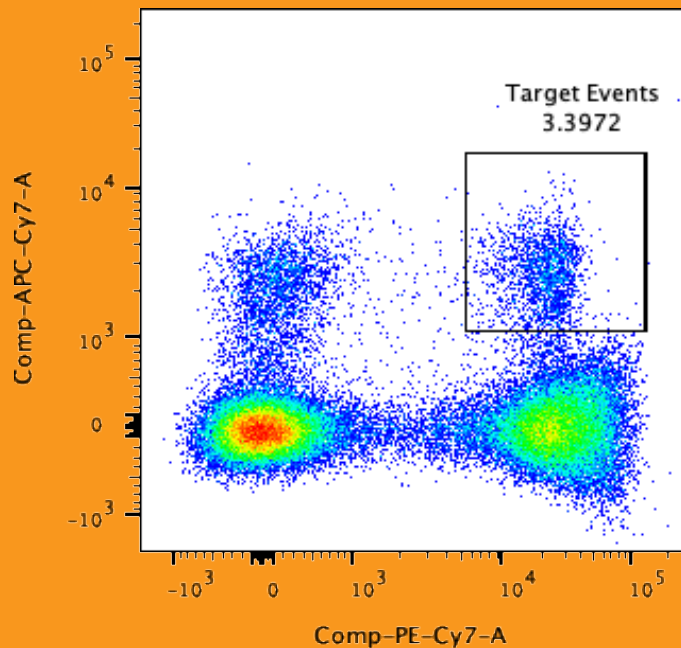
- Figures – Dot plots
 - Adjust axis labels to clearly convey what is being shown
 - Change generic names to appropriate label – usually the marker/antigen, fluorophore, detector name
 - Ex. CD45-FITC B530
 - Names can be changed using FCS editors or manually with image editors



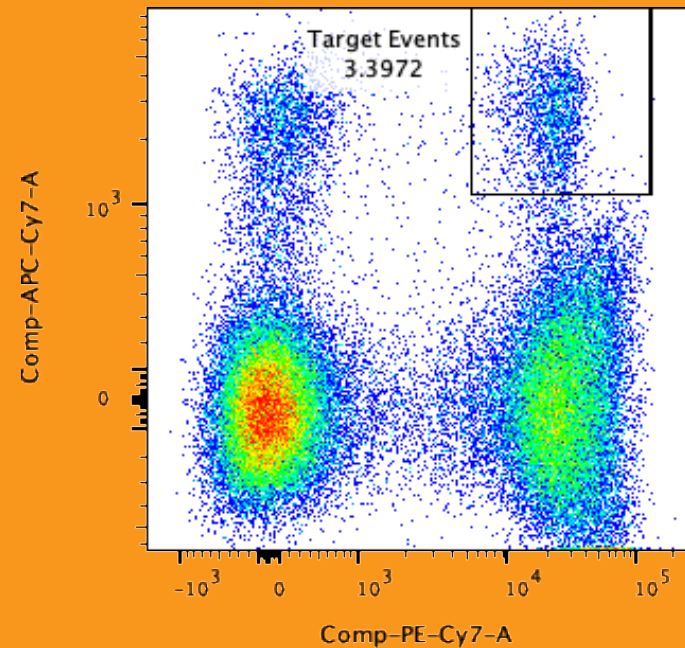
Results Section



- Figures – Dot plots
 - Scaling of axis
 - Scaling should be consistent between samples
 - Same data, but visualized differently – confusing for readers



$\neq ?$



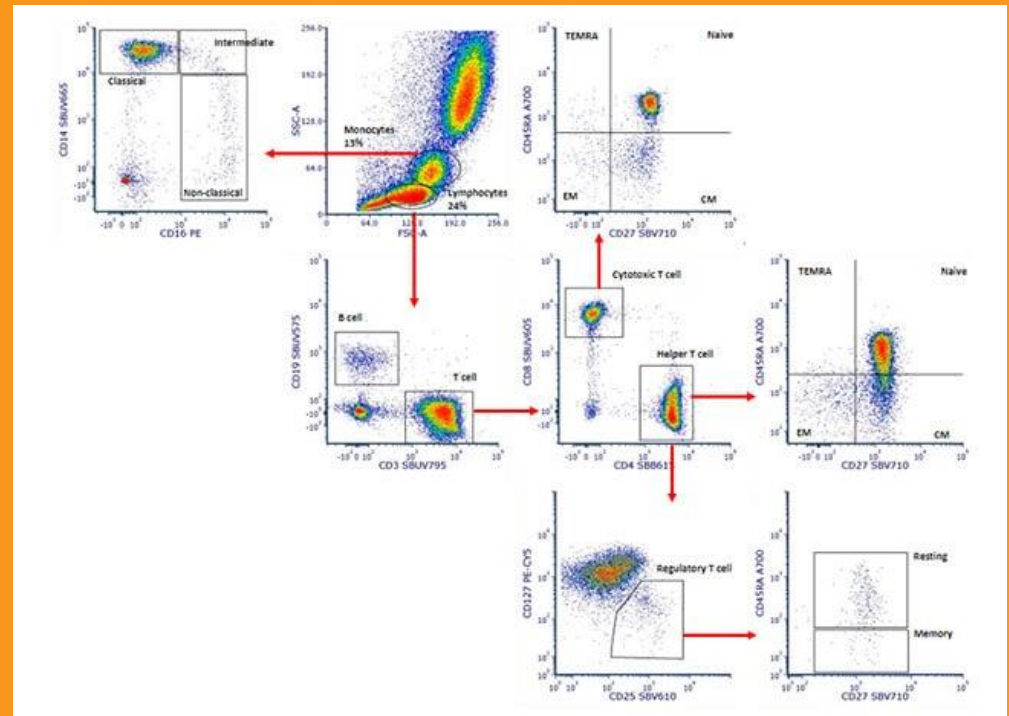
Results Section

- Gating Scheme

- Full gating scheme should be included in supplemental data
- FMO controls and other control gating may or may not be included, but raw data should be made available in public repositories like Flow Repository

- Alternative gating

- Not always necessary to start with FSC/SSC
- Start with Time, landmark gating (like CD45, DAPI, etc)



Publication Summary

- Aim to provide all information necessary to replicate experiment
 - MIFlowCyt guidelines are very comprehensive
- QC your data well and explore in a variety of analysis pathways
 - Backgate to make sure you are not missing populations
 - Be mindful of the upper right corner, cells can hide there!
 - Triple check your compensation before analyzing!
- Include gating scheme and gating justifications
 - Flow cytometry data can be presented as a generalized gating scheme, but deviations/adjustments need to be justified
- Plots
 - Label with Detector name, Marker/Antigen, and Fluorophore
 - Scale is arbitrary, but should be consistent. Be careful about over adjusting the scale to the point that tic marks are hard to understand

Large Particle Sorter

BioSorter

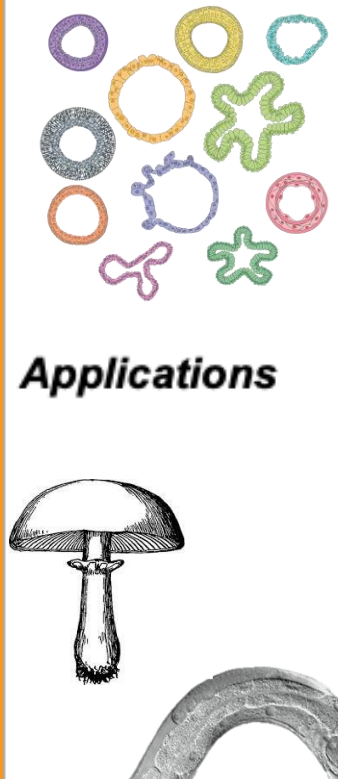
Union Biometrica

Kerckhoff B133



- Versatile instrument with 4 possible flow cells or FOCA:
 - FOCA 250
 - FOCA 500
 - FOCA 1000
 - FOCA 2000
- Large particle sorting - $\sim 30\mu\text{m}$ to $800\mu\text{m}$
- Colinear lasers at 488nm and 561nm
- 3 Detectors:
 - Bandpass Filters: 512/25, 543/22, 615/25
- Sample deposition into a variety of plates and tubes including:
 - Culture plates (6, 12, 24, 48, or 96-well + custom)
 - PCR plates
 - 384-well plates
 - 1.5 mL, 5 mL, 15 mL and 50 mL tubes
- Sorting droplet is dispensed straight down for more precision into smaller well plates

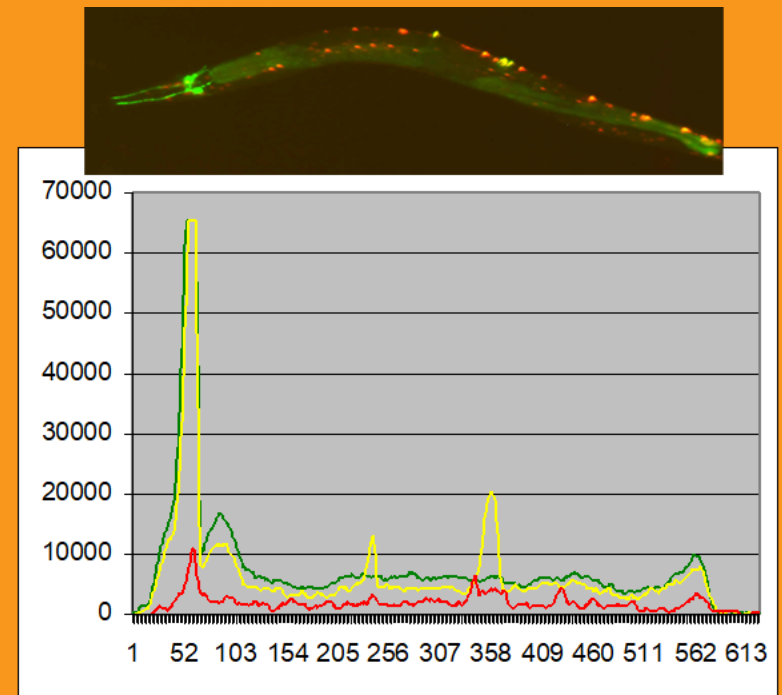
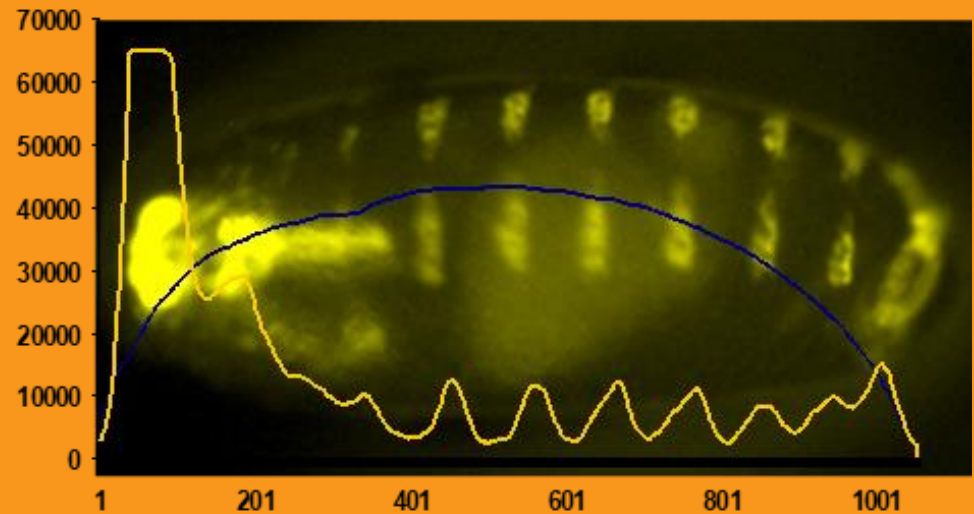
Applications

FOCA	250	500	1000	2000
Object Diameter Size Range	10-200 micron	10-350 micron	20-700 micron	40-1500 micron
 Applications		Beads (Alginate, Chemistry. Cells on Beads)		
	<i>C.elegans</i>	<i>C.elegans</i>	Zooplankton	Zebrafish (embryos and larvae)
	Sea Urchin embryos	<i>Drosophila</i> (embryos and 1st instar larvae)	<i>Drosophila</i> (embryos, L1 and L2 instar larvae)	<i>Drosophila</i> (up to 3rd instar larvae)
		Mosquito (embryos and first instar larvae)	Mosquito (embryos and first, second and third instar larvae)	<i>Xenopus</i> , <i>Medaka</i> , <i>Daphnia</i>
	Stem cell	Pancreatic islet (mouse & rat)	Pancreatic islet (mouse, rat & human)	
	Hepatocyte	Embryoid body		
	Kidney duct cell	Adipocyte		
	Pollen	Pancreatic duct cell	Arabidopsis seed	

BioSorter

Special Features

- Straight down dispensing (only one population at a time)
- Very gentle sorting
- Recovery of unsorted 'waste' to rerun
- Plate/tray sorting
- Profiler 
- Future?
 - More colors? Sterile enclosure?
 - Additional FOCA?



User Projects



- Sally Ireri, Ph.D.

Mengyi Cao Lab

- Vera Beilinson

Margaret McFall-Ngai/Pachter
Labs

- Helena Awad

Linda Hsieh-Wilson Lab

- Amy Chow, Ph.D.

Mitchell Guttman Lab

Bacterial scRNA-seq isolated from host

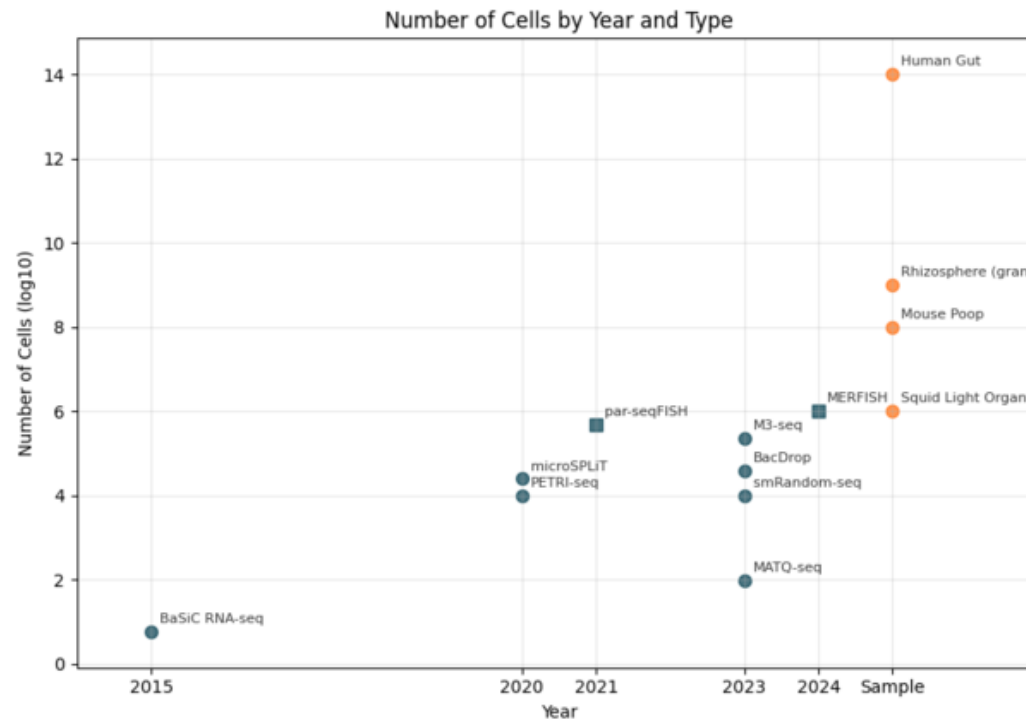
Vera Beilinson

McFall-Ngai/Pachter Labs

Flow Cytometry Facility Lab Meeting

Oct 27, 2025

Bacterial scRNA-seq methods are increasing



NGS

Untargeted

Captures tmRNAs

Not all methods are reproducible (BacDrop)

Imaging

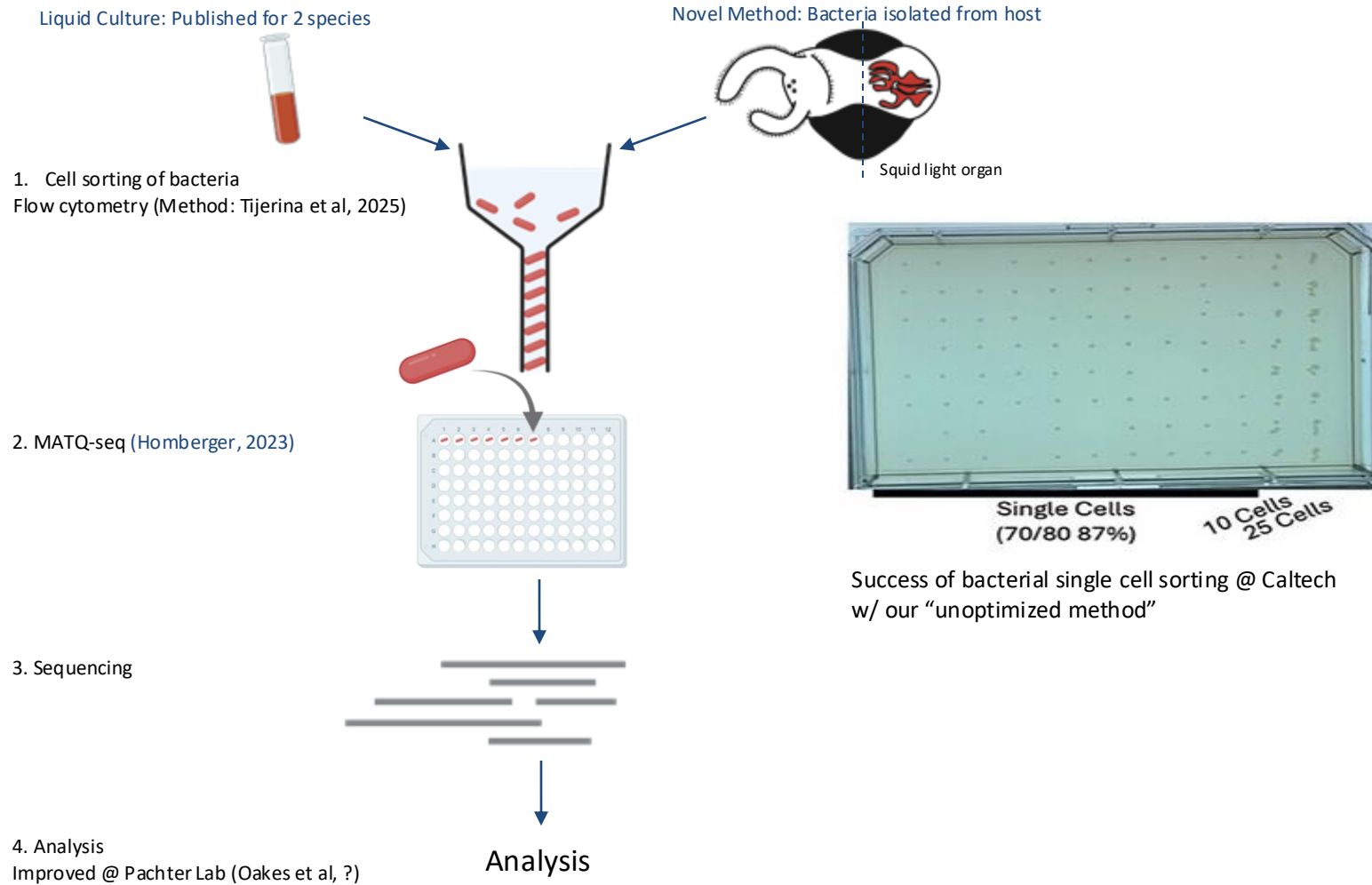
Targeted (price ↑ w/ # of genes, # of cells depends on user)

Methods performed from *liquid culture* samples (no debris).

What about bacteria from a host?

Host debris is an issue

Goal: perform MATQ-seq on bacteria isolated from a host



Goal: More accurate cells sorting

Previous sorting: size + presence of RFP plasmid → better to have counterstain to avoid debris in well

Goal: Identify a counterstain that is compatible for growth AND RNALater safe

→ Current no information online!!

→ RFP is RNALater safe (GFP and YFP is not)

Why:

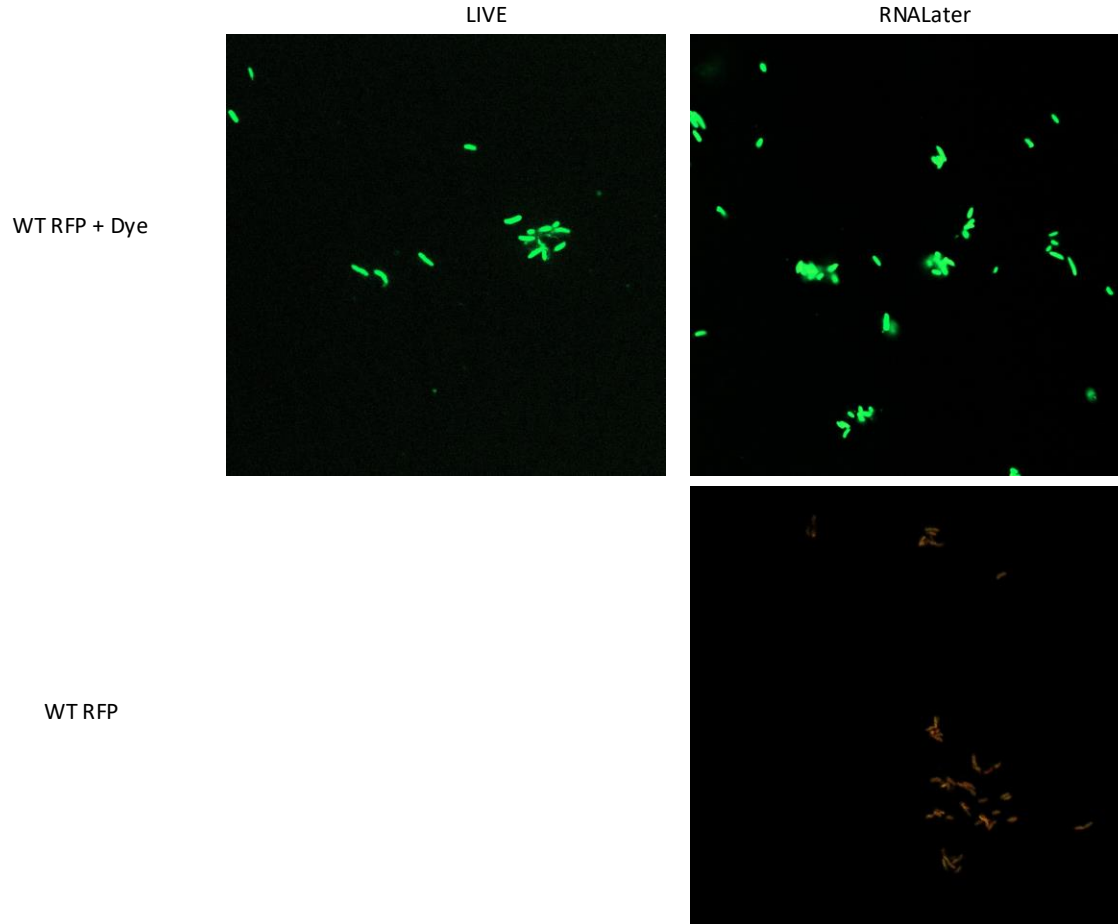
→ Sorting live onto agar plates is a good sorting control to know success

→ For MATQ-seq it is ideal if the samples are fixed in RNALater prior to sorting since bacteria change transcription fast

Dye (1:250 and 0.2:250)	Liquid culture low OD	Liquid culture high OD	Isolated from host (squid)
SYTO9	No/minor growth	No/minor growth	No/minor growth
Bactoview Green	No growth	No growth	No growth
Calcein Violet	Growth	Growth	Growth
Hoescht	No growth	No growth	?

→ Calcein Violet is the only counterstain that allows for growth

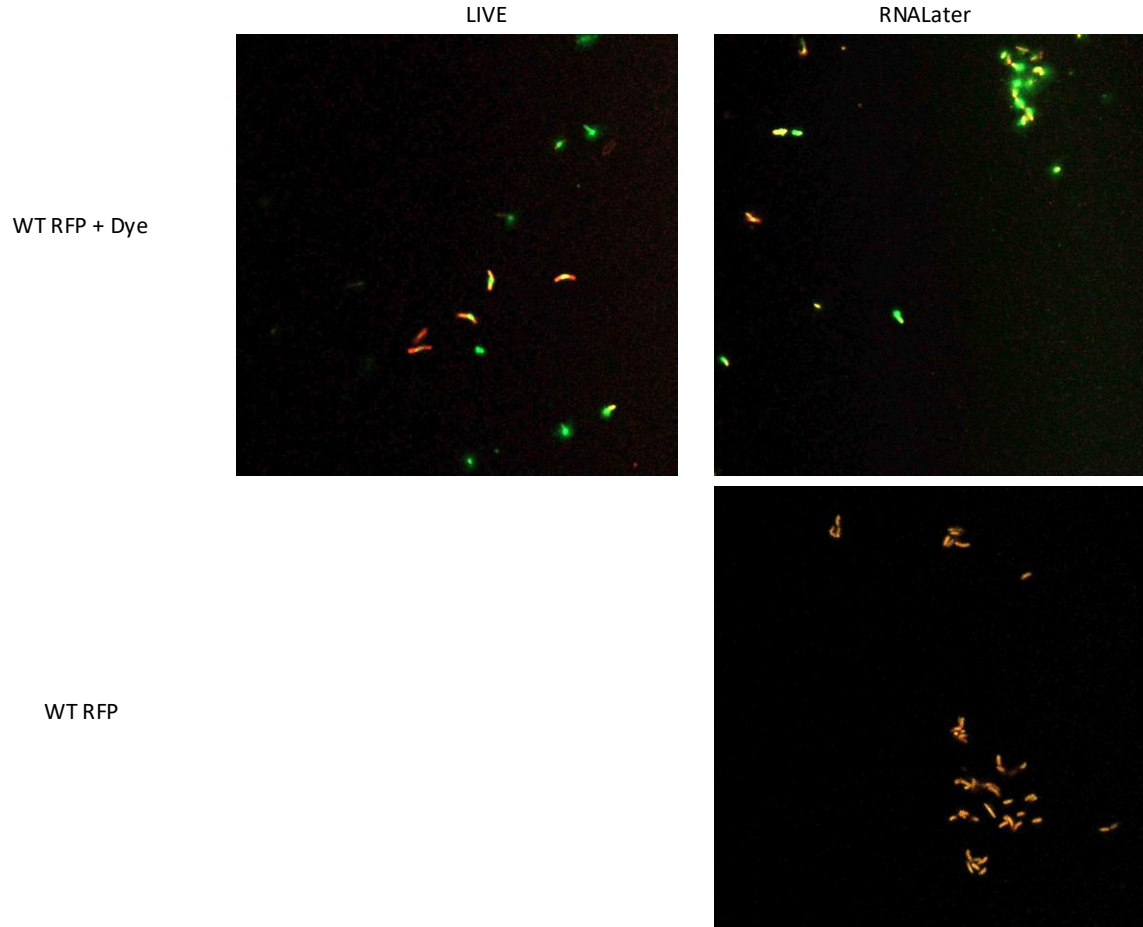
Which dyes are RNALater compatible



→ **Syto9** is present in live and RNALater but Syto9 obliterated RFP

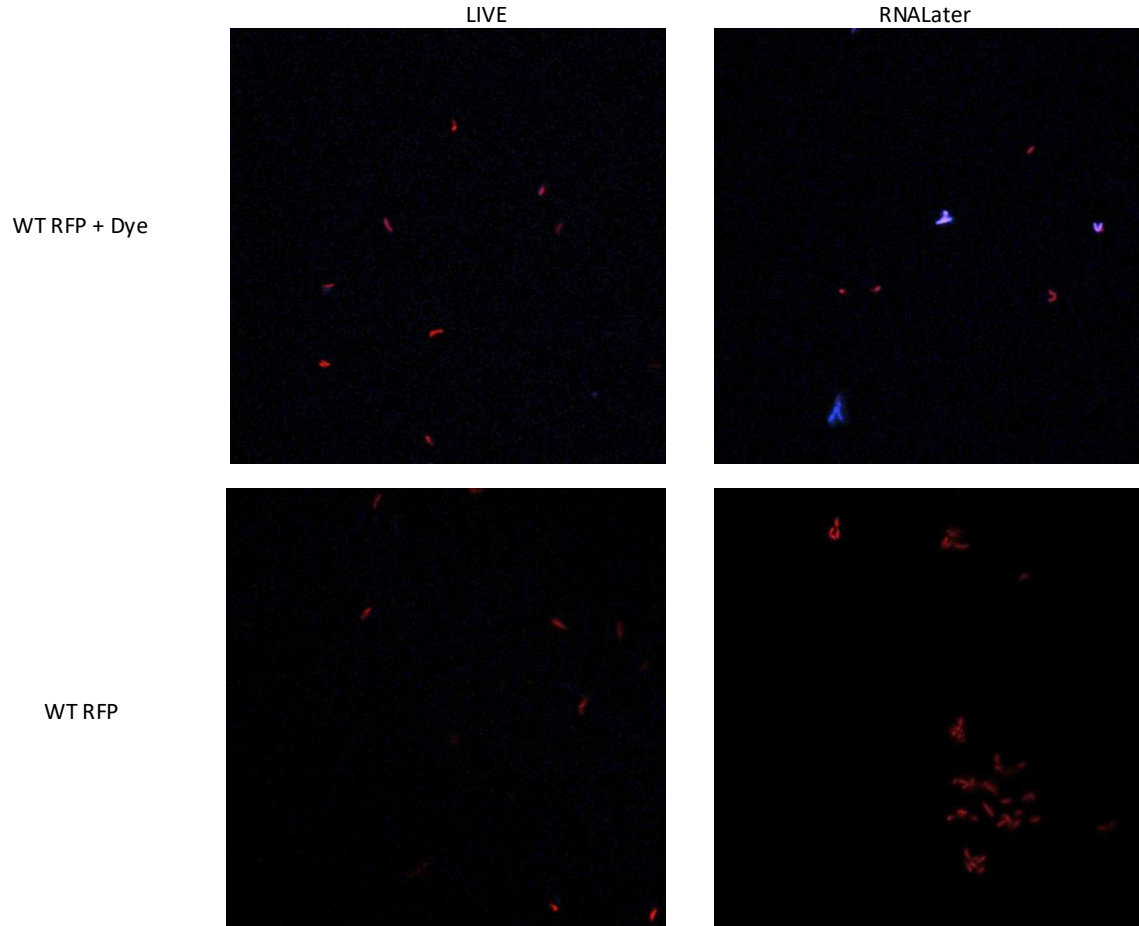
→ Some background in Syto9 channel

Which dyes are RNALater compatible



- **Bactoview** is present in live and RNALater
- Some background in Bactoview (FITC) channel

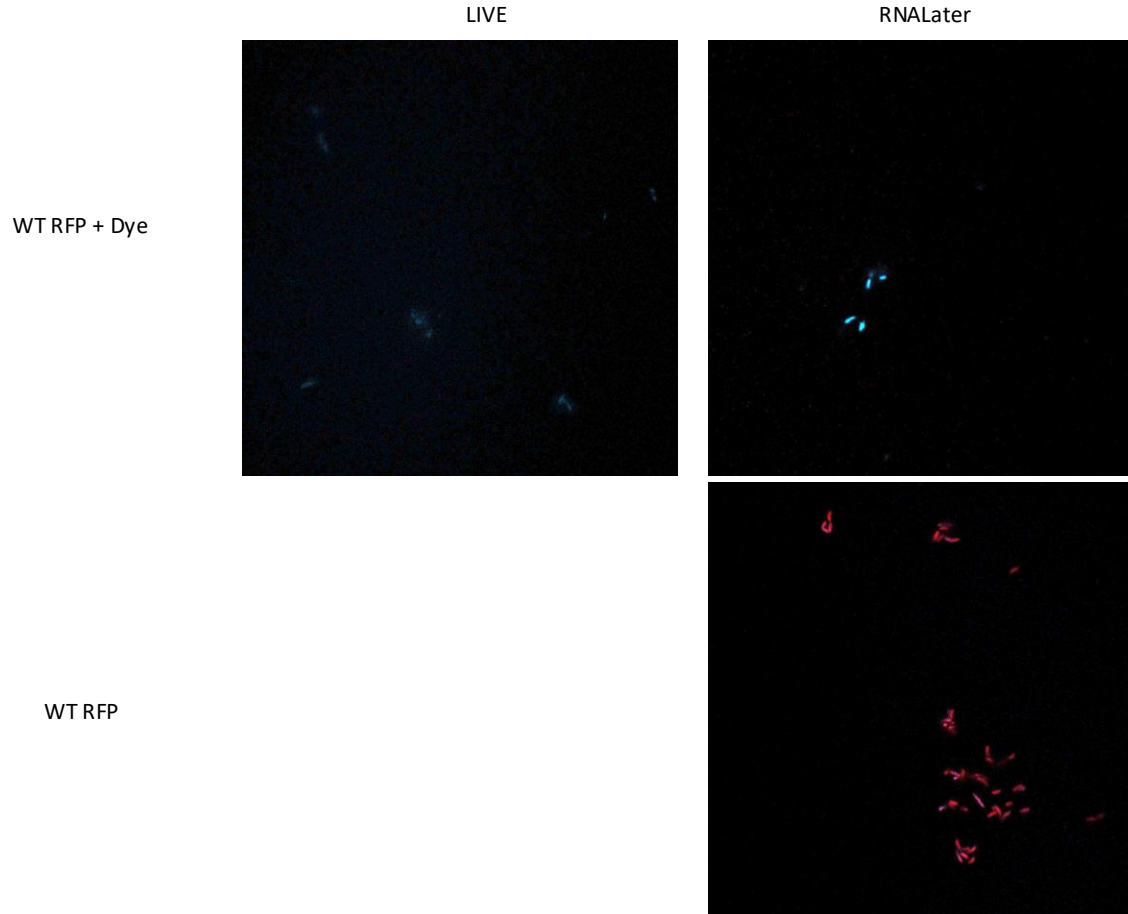
Which dyes are RNALater compatible



→ **Calcein Violet** is present in live and RNALater (possibly brighter in RNALater)

→ Little background in violet channel

Which dyes are RNALater compatible



- **Hoescht** is present in live and RNALater but obliterates RFP signal
- Little background in Hoescht channel

Conclusion

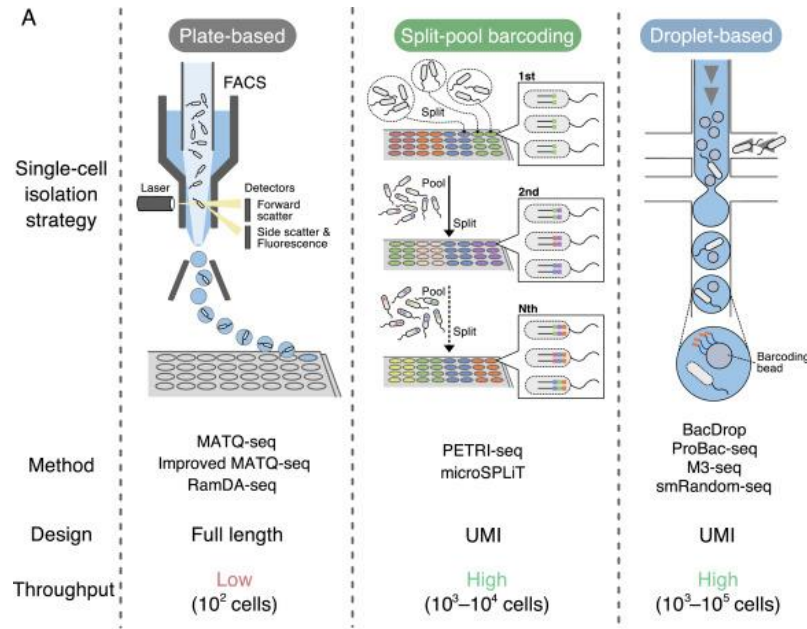
- Calcein Violet is good counterstain allowing for growth
- SYTO9, BactiView Green, Calcein Violet are RNALater fixable

Next steps:

Try sorting with calcein violet

Various methods

Highly reproducible



FACS sorting is vital regardless of method

- remove dead cells + debris
- ensures no bacteria sticking to each other*

*FACS sorter w/ “imager” is recommend to visualize the single cell

B

Method	Year	Features										
		Single-cell sorting strategy			cDNA generation & amplification		rRNA depletion			Single-cell barcoding		
		FACS	Split-pool	Droplet	In situ generation	Random displacement amplification	RNaseH	Cas9	Other (Customized probe)	Split-pool	Droplet	Hybrid
PETRI-seq	2020		*		*							*
MATQ-seq	2020	*										
microSPLIT	2021		*		*						*	
BacDrop	2023			*	*		*				*	*
ProBac-seq	2023			*	*				*		*	
M3-seq	2023			*	*		*				*	*
Improved MATQ-seq	2023	*						*				
smRandom-seq	2023			*	*			*			*	
RamDA-seq	2023	*				*		*				

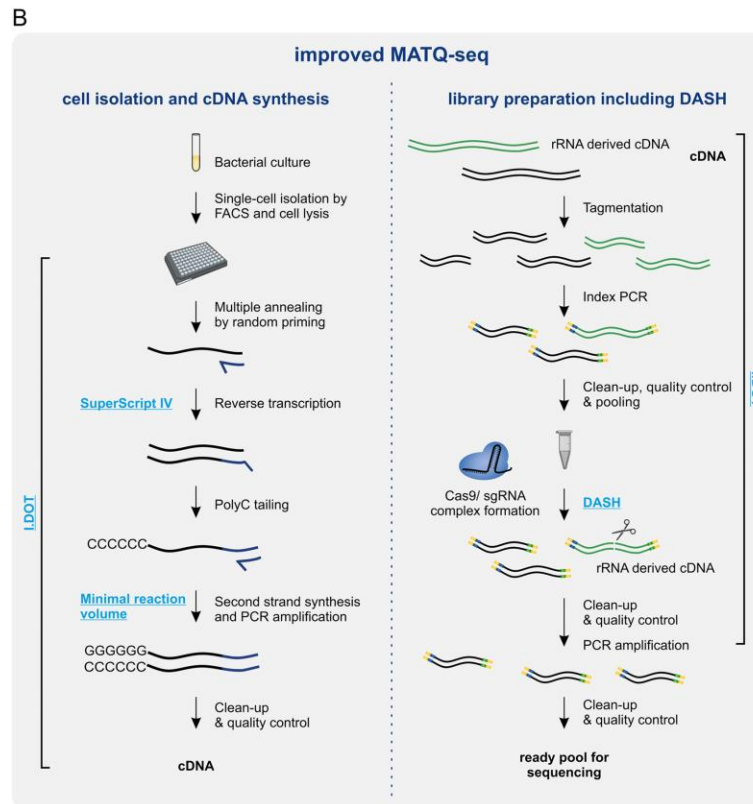
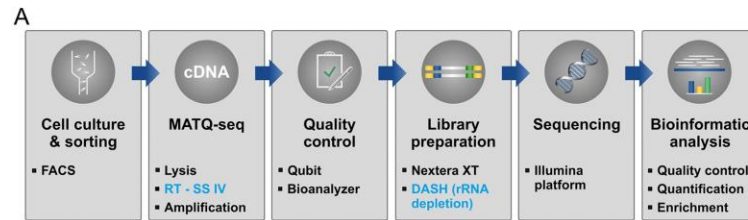
Similar better method coming out soon!
Reproducible

Not reproducible

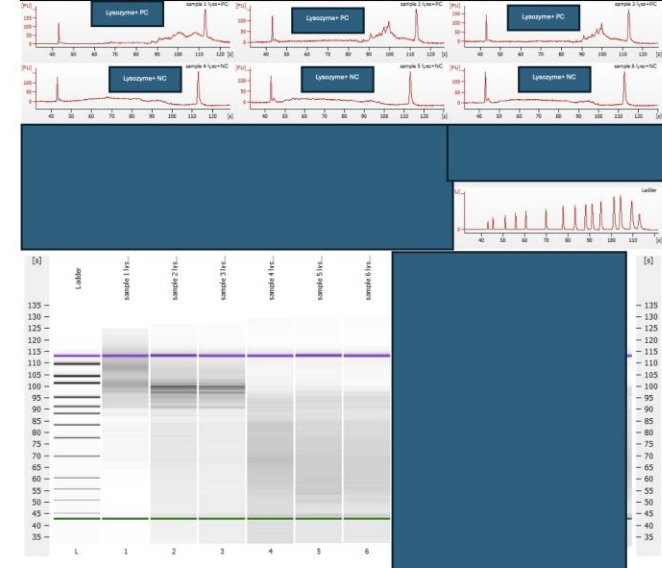
Reproducible

Most methods are similar-
just depends if in well or within cell

Nishimura 2025



Sample 1: RNA+ Lysozyme + 16.2 ng/ul	Sample 2: RNA+ Lysozyme + 9.64 ng/ul	Sample 3: RNA+ Lysozyme + 11.6 ng/ul	Sample 4: NC Lysozyme + 3.76 ng/ul	Sample 5: NC Lysozyme + 2.04 ng/ul	Sample 6: NC Lysozyme + 2.64 ng/ul
Sample 7: RNA+ Lysozyme - 24.4 ng/ul	Sample 8: RNA+ Lysozyme - 23.2 ng/ul	Sample 9: RNA+ Lysozyme - 22.0 ng/ul	Sample 10: NC Lysozyme - 3.86 ng/ul	Sample 11: NC Lysozyme - 2.80 ng/ul	Sample 12: NC Lysozyme - 2.04 ng/ul

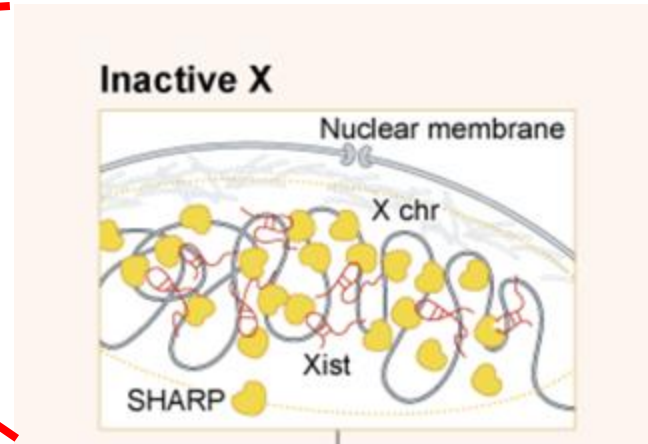
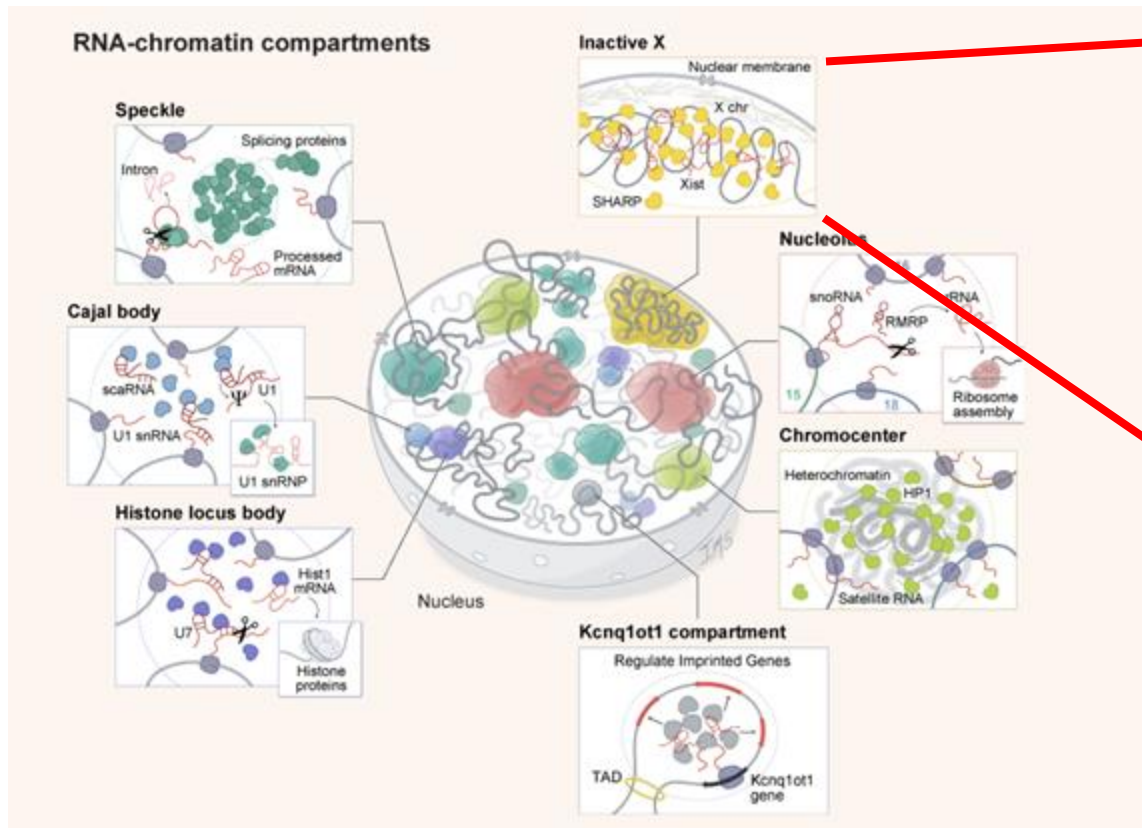


Vera – success @ Caltech. cDNA(no DASH). NC are low, PC are within range w/ expected peak shape. Critical to do in PCR/clean hood.

PrimeFlow RNA

Amy Chow, Ph.D.
Guttman Lab

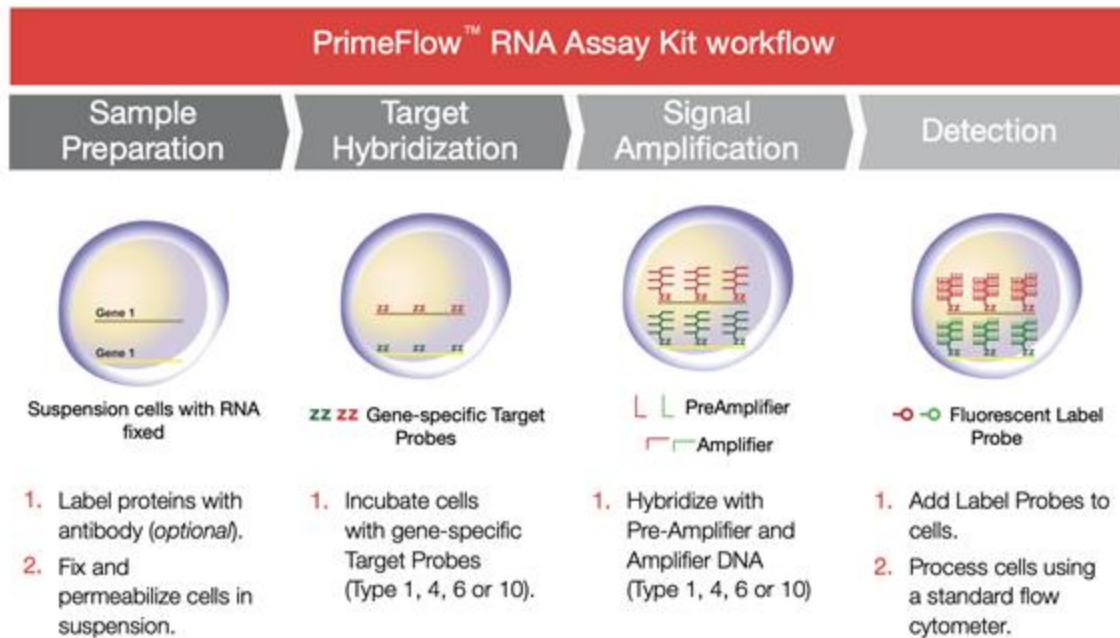
Guttman lab research focus



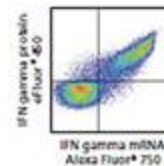
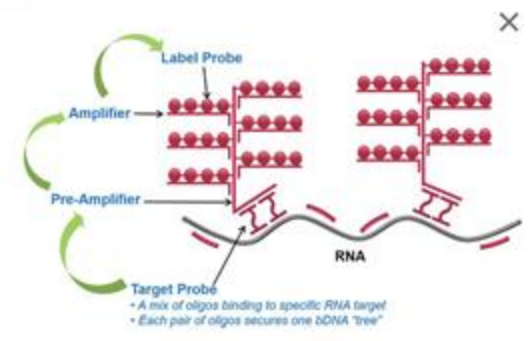
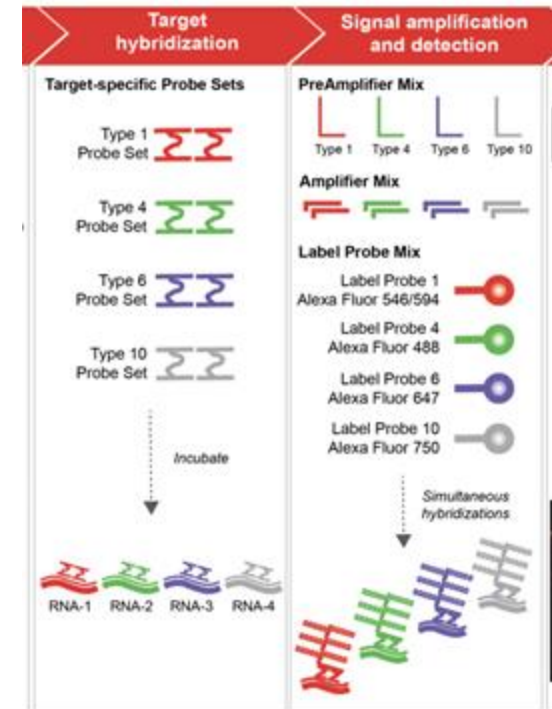
Understanding the role of ncRNAs in organizing chromatin architecture and the impacts on gene expression

<https://guttmanlab.caltech.edu/research/>

PrimeFlow RNA principle

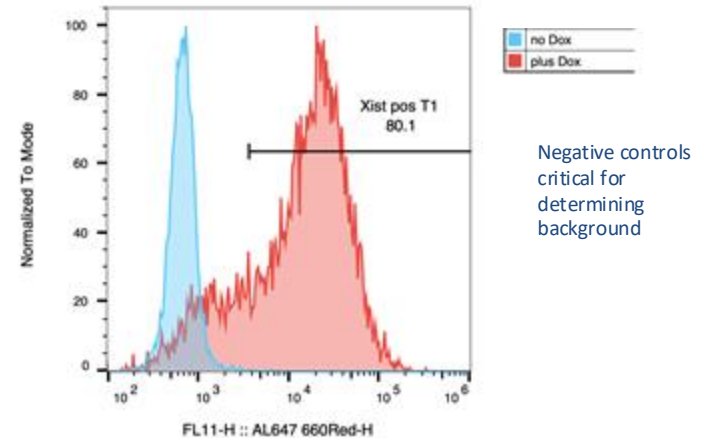


<https://www.thermofisher.com/us/en/home/life-science/gene-expression-analysis-genotyping/quantigene-rna-assays.html>
<https://www.thermofisher.com/us/en/home/life-science/cell-analysis/cellular-imaging/in-situ-hybridization-ish/rna-fish/viewrna-assays.html>
https://documents.thermofisher.com/TFS-Assets/LSG/manuals/MAN0019788_PrimeFlowRNAAssay_UG.pdf



Our results and future plans

CRISPRi screen to find regulators such as Rex1



	Xist on stable?	Yes	No
	Xist off stable?	Yes	Yes



Please give us your Feedback!

Feedback survey →

Future needs questions:

Spectral instruments?

Imaging instruments?

Booking sorting directly?

Other needs/questions?



Please scan the QR code to rate your experience with the Facility and give us some feedback.