



Everything, Everywhere, All at Once: Open-source Automation for Situational Awareness in Shared Resource Laboratories

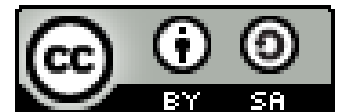
David Rach, Natarajan Ayithan, Xiaoxuan Fan

UMGCCC Flow Cytometry Shared Resource

June 6th, 2026



Slides Here



On a good day at a small SRL



Everything is normal

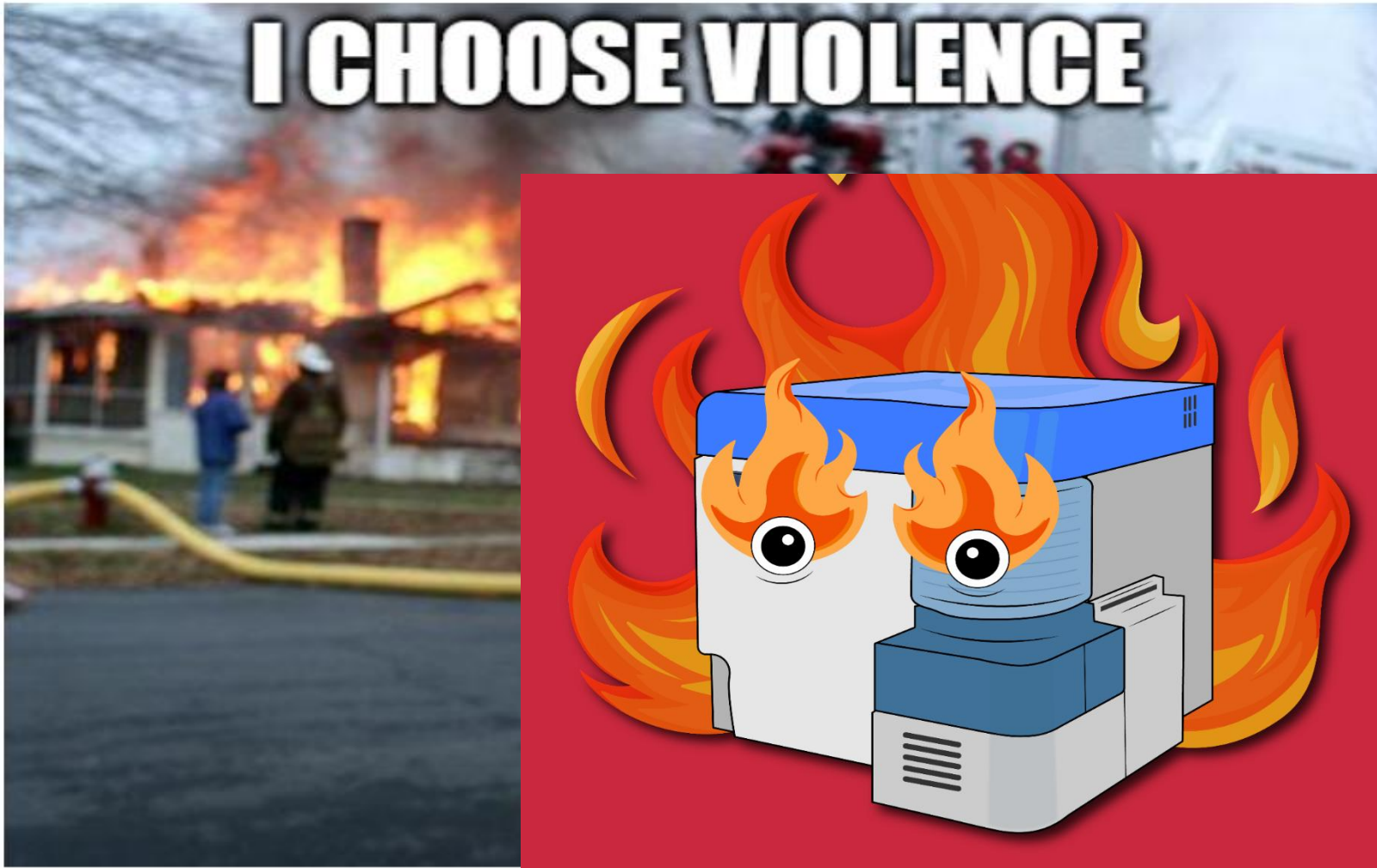
- ❑ Show up
- ❑ Change sheathe and waste
- ❑ Flush out the fluidic lines
- ❑ Run QC

Drink your fourth cup of coffee

- ❑ Cell Sorting
- ❑ Training new users
- ❑ Building panels
- ❑ Deep diving interesting data

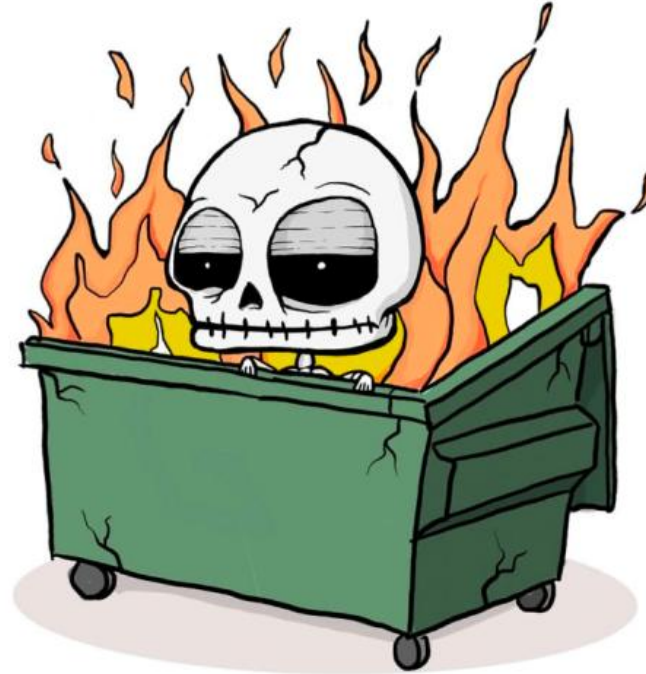
Go home, rinse and repeat

However, on a bad day at a small SRL...



New Goal for the Day: Simply Survive

**MY JOB IS BASICALLY
PUTTING OUT FIRES I DIDN'T START**



WITH TOOLS I DON'T HAVE

NEVER
BEEN
DEADER



Visible and Hidden Costs

Issue was detected, cytometer not in use

- ❑ Staff time
- ❑ Lost Revenue
- ❑ Delayed User Experiments

Issue undetected, cytometer still in use

- ❑ Poor Quality Data
 - ❑ More complex analysis
 - ❑ Need for experiment repeats
- ❖ Reputational Costs



Are you treading water or drowning?



<https://homeschooling2e.com/2021/04/11/treading-water/>



Can we anticipate the waves?



- ❑ Laser/Detector Issues
- ❑ Bleach-damaged QC Beads
- ❑ Debris Accumulation in fluidic lines
- ❑ Degrading tandem dyes
- ❑ Additional autofluorescences

What stories can the data already being acquired daily at our cores tell us?

UMGCCC Flow Cytometry Shared Resource



ISAC RECOGNIZED
Shared Resource Laboratory



Analyzers:

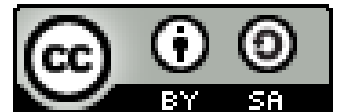
- ❑ 3 Cytex Aurora
- ❑ 1 Amnis FlowSight
- ❑ 1 MacsQuant10
- ❑ 1 BD LSR-II
- ❑ 1 BD Canto



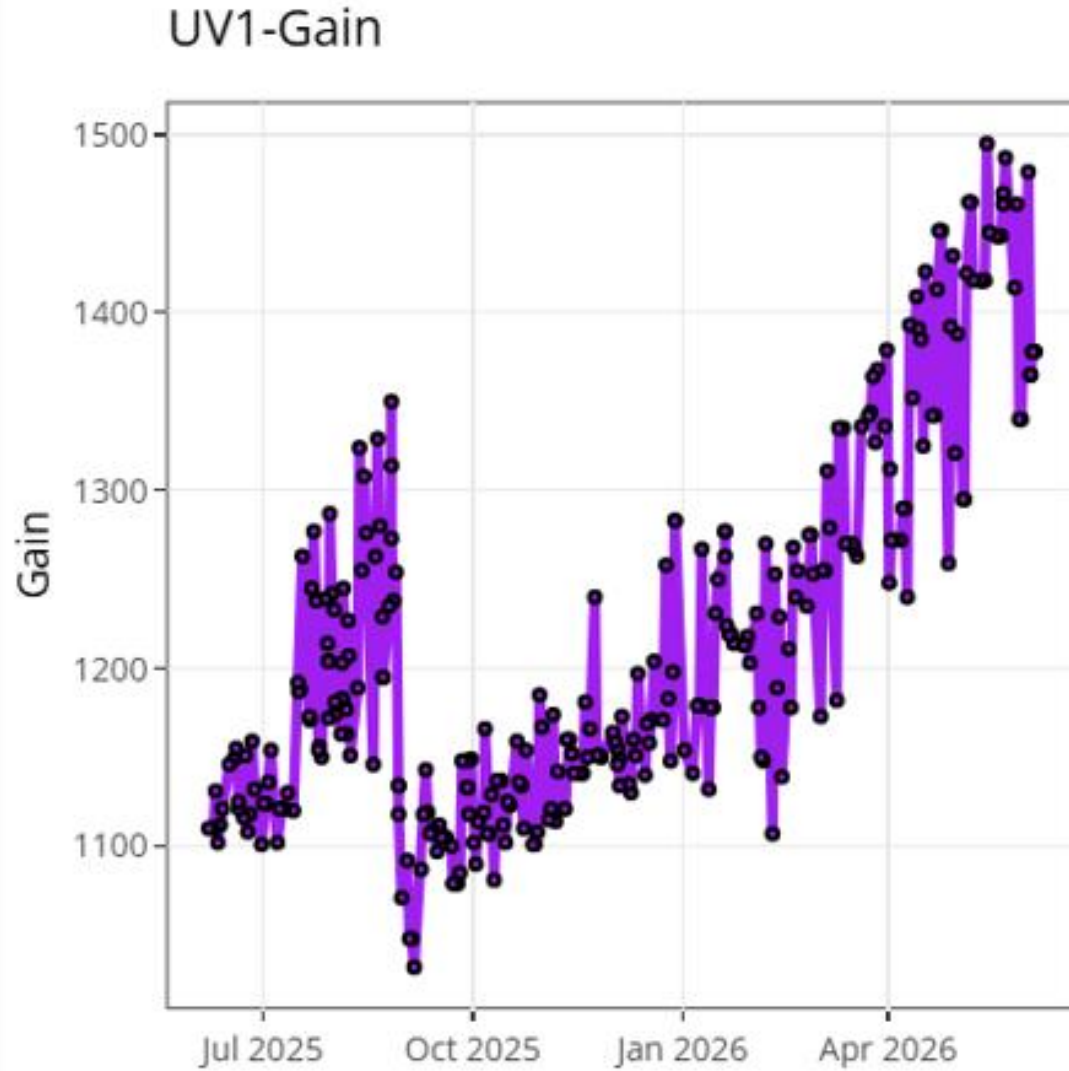
Cell Sorters:

- ❑ 1 Cytex Aurora CS
- ❑ 1 BD Aria II

Flow Cytometry Staff: 3

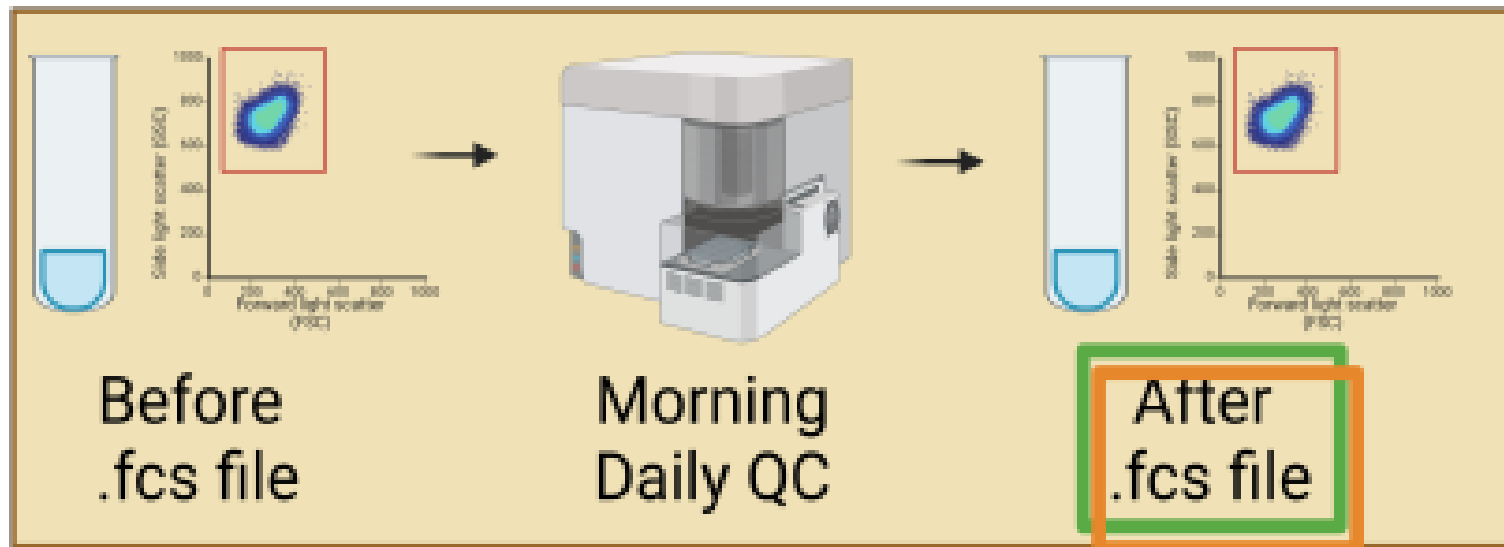


Our Goals



- Develop the tools
- Find bandwidth to leverage them
- Keep expenses minimal
- Share our code

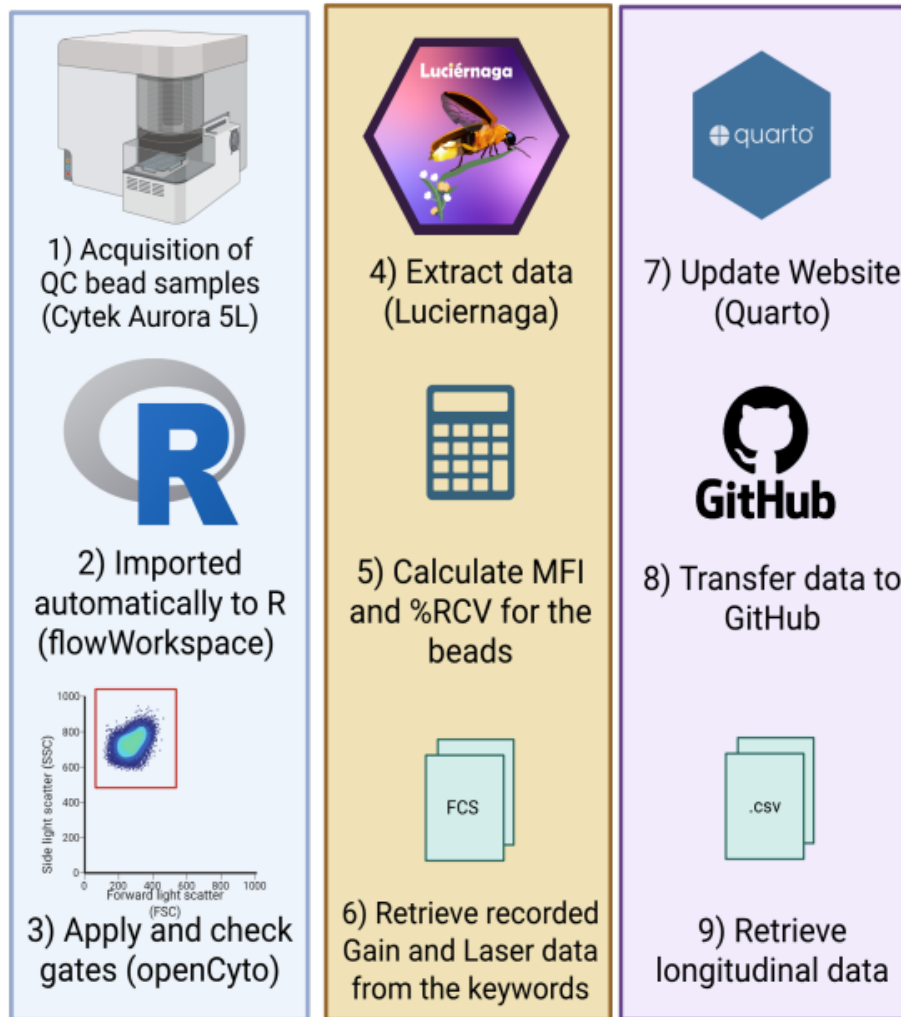
What data is already sitting around?



Before and After QC .fcs files

- For Every Instrument
- Back to 2017

Automated Daily Processing



Behind-the-scenes:

- ❑ Using R (and increasingly Rust) to process the .fcs files
- ❑ Automated transfer to GitHub via Windows Task Scheduler
- ❑ Our Quarto Website gets updated twice daily via a GitHub action

Eclectic Mix of Computation:

- ❑ Existing Instrument Computers
- ❑ Repurposed Windows 10 End-of-Life computers running Linux
- ❑ Small motherboard computers (Raspberry Pi 4b)

Instrument Quality Control Dashboard



Dashboard



How-To

UMGCC FCSS

Home
Levey-Jennings Plots ▾
Historical ▾

Help
Download Data
Other ▾
🔄
🔍

📘 Please see left-sidebar for definitions
✕

Dashboard data last updated on **2026-06-05**

Definitions:

Pass: All gains within 100% baseline and all RCVs <6% for all detectors.

Caution: All gains within 100% baseline, but at least one detector had a RCV above the >6% cutoff. Instrument remains usable but resolution for fluorophores on the failed detector may decrease.

Fail: Either a gain exceeded 100% baseline, or RCVs exceeded >6% for at least one indicator detector. Significant variation and batch effects may occur.

For additional information, navigate to the [Help](#) page.

University of Maryland, Baltimore

Detector	Gain		%RCV	
	Value	Status	Value	Status
FSC	471	Pass	1.57	Pass
SSC	270	Pass	3.63	Pass
SSC-B	129	Pass	3.34	Pass
V1	312	Pass	1.03	Pass
V2	331	Pass	1.18	Pass
V3	407	Pass	1.29	Pass
V4	249	Pass	1.41	Pass
V5	322	Pass	1.41	Pass
V6	282	Pass	1.49	Pass

Instruments

Date	3L	4L	5L	CS
2026-06-05	Pass	NA	NA	Pass
2026-06-04	Pass	NA	Pass	Pass
2026-06-03	Pass	Pass	Pass	Pass
2026-06-02	Pass	Pass	Pass	NA
2026-06-01	Pass	Pass	Pass	Pass
2026-05-29	Pass	Pass	Pass	Pass
2026-05-28	Pass	Pass	Pass	Pass
2026-05-27	Pass	Pass	Pass	NA
2026-05-26	Pass	Pass	Pass	Pass
2026-05-22	Pass	Pass	Pass	NA

Built with [Quarto](#). How? [Find Out](#)



Instrument Quality Control Dashboard



UMGCC FCSS

Home

Levey-Jennings Plots

Historical

Help

Download Data

Other



Please see left-sidebar for definitions

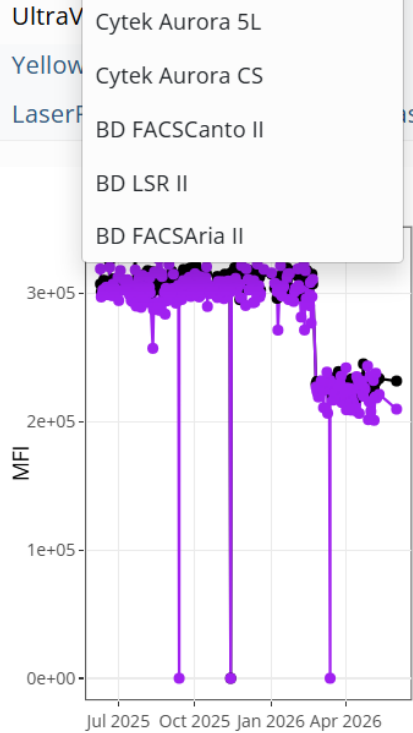
Dashboard data for the **Cytek Aurora 5L** last updated on **2026-06-01**

Note: Cytek QC Bead Lots were switched on 12-06-2024. MFI change on this date was expected.

First Column: MFI Median Fluorescent Intensity (MFI) values for QC beads acquired Before and After QC. Measures stability over time.
Second Column: Gain Gain (Voltage) values set for instrument after QC. Changes over time reflective of laser health.
Third Column: RCV Percentage change of Robust Coefficient Variation (RCV) after QC. Higher values reflect decreased resolution between positive and negative for that detector.

For additional information concerning individual

<https://umgccfcss.github.io/InstrumentQC/Aurora5L.html#>



UV2-A

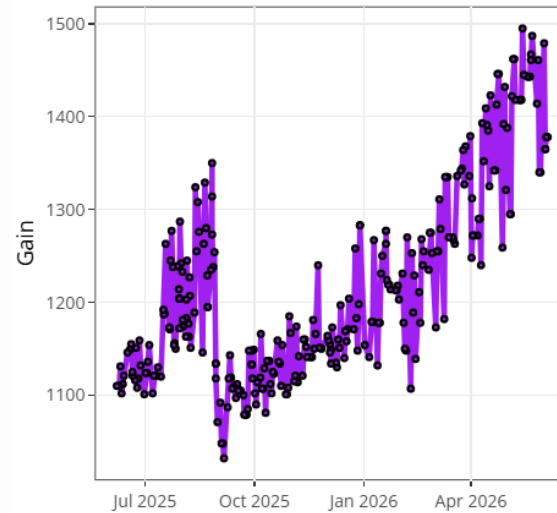


Timepoint
— After
— Before

Timepoint

UltraViolet Violet Blue
YellowGreen Red Scatter
LaserPower LaserDelay LaserScaling

UV1-Gain

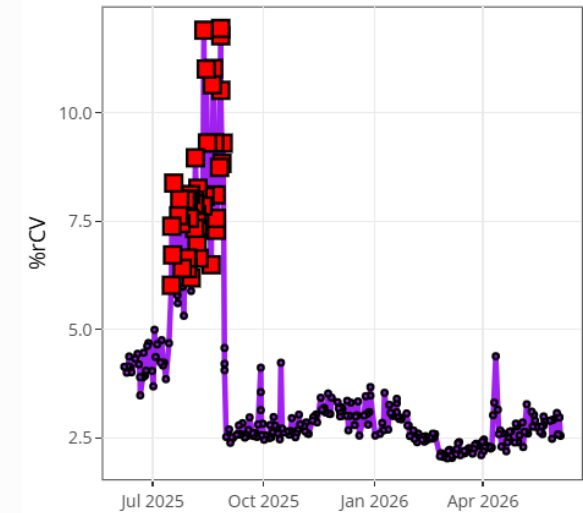


UV2-Gain



UltraViolet Violet Blue
YellowGreen Red Scatter
LaserPower LaserDelay LaserScaling

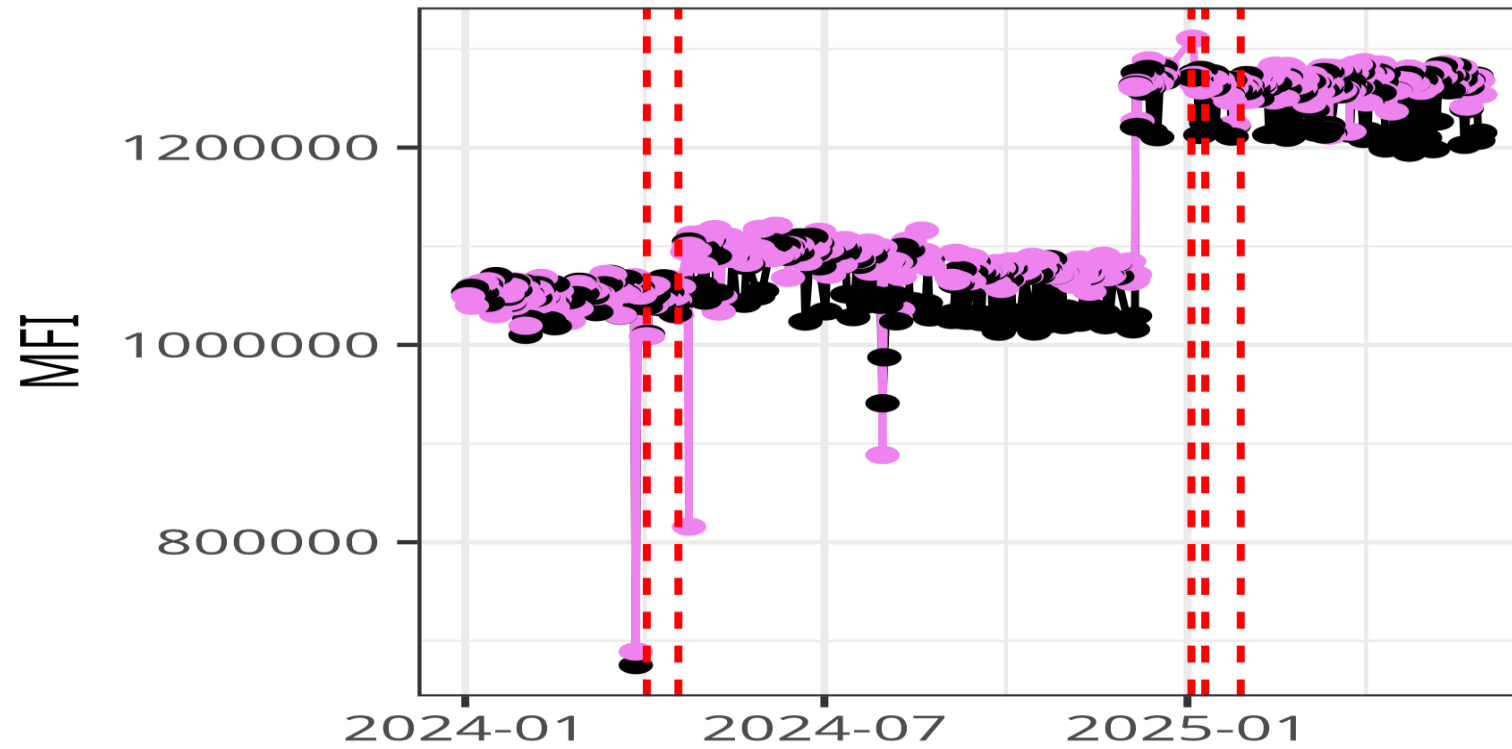
UV1-% rCV



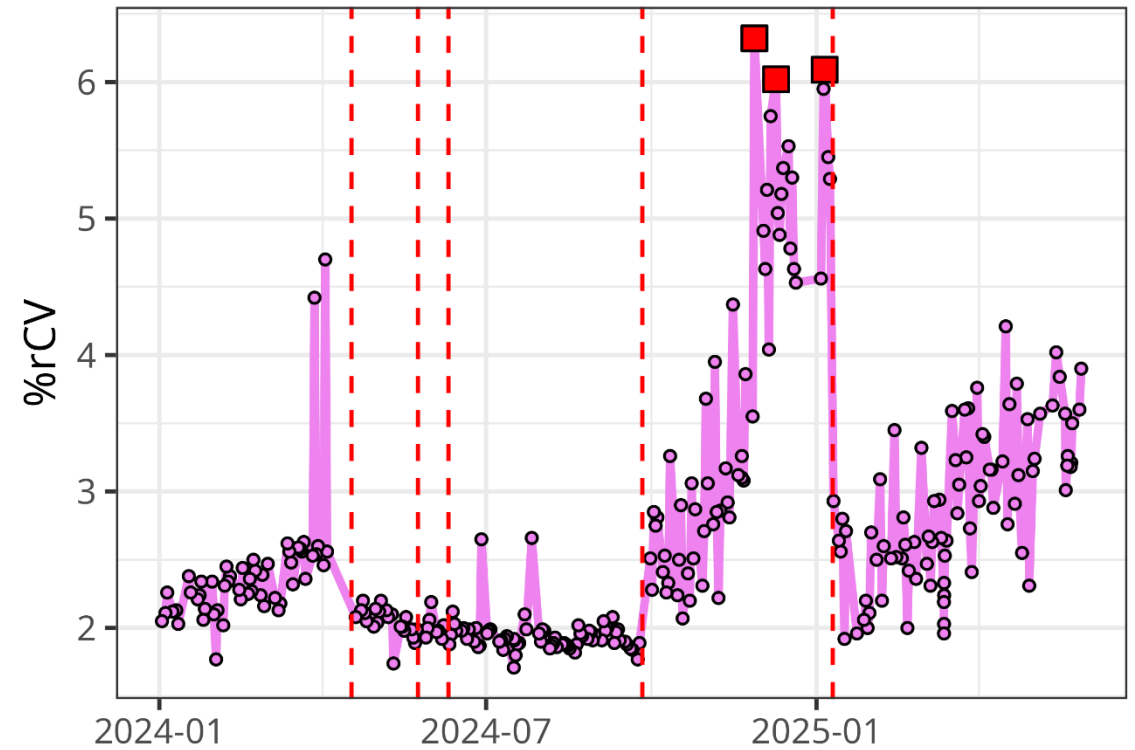
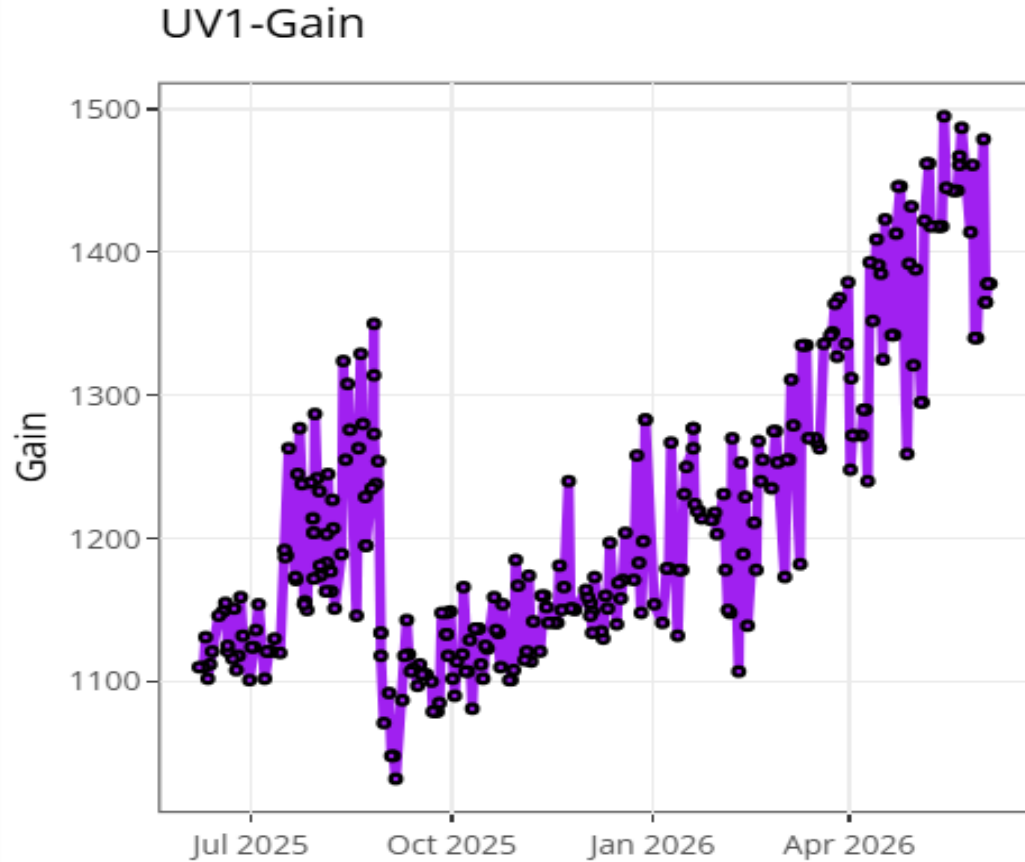
UV2-% rCV



Instrument Stability over Time

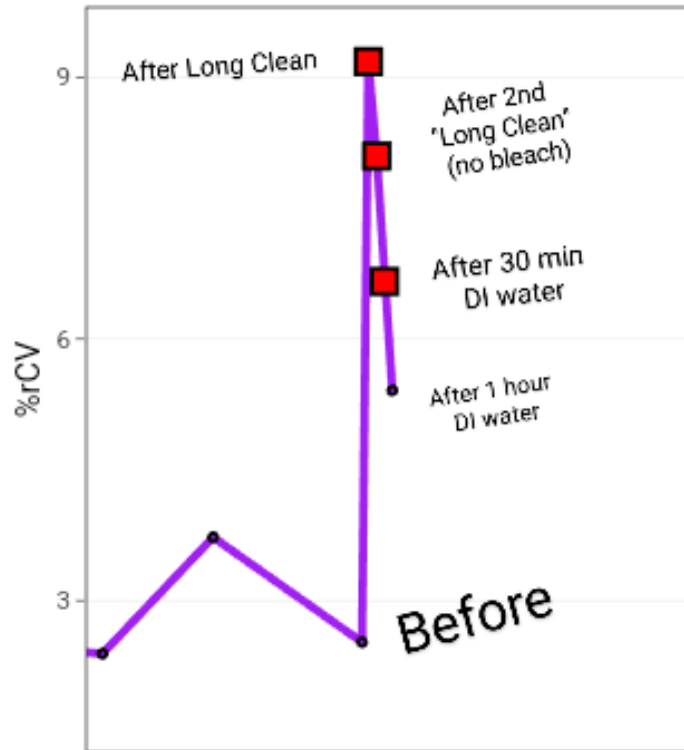


Early warning on Lasers/Detectors



Front row seats to Bleach-Sensitive QC Bead Lots

UV16-% rCV



Data



“Wait, when was QC last run???” Evaluating MFI drift after morning QC and its impact on unmixing.

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 1 Molecular Microbiology and Immunology Graduate Program, University of Maryland School of Medicine, Baltimore, USA
 2 Flow Cytometry Shared Resource, University of Maryland Greenebaum Comprehensive Cancer Center, Baltimore, USA

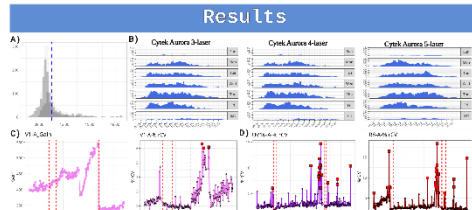
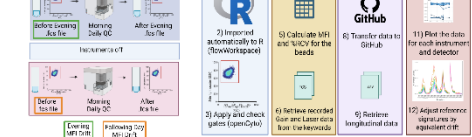
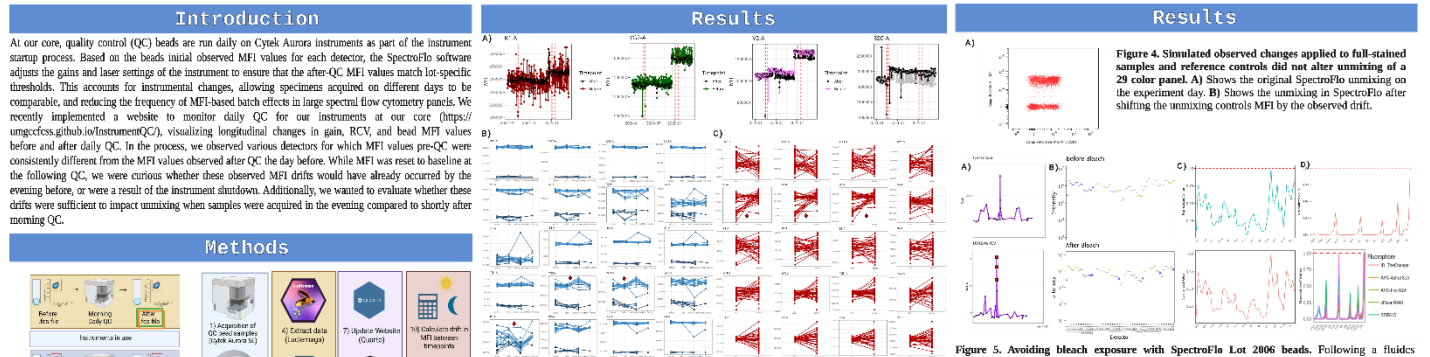


Figure 1. Automated QC processing, tracking and visualization allows for long-term monitoring of instrument performance. A) The histogram depicts when daily QC was performed, as recorded in the .fcs file metadata. B) The histogram plots depict the typical user hours shown by hour and weekday for each instrument, based on total recorded instrumental sit flushes in the Application Log. C) The Levey-Jennings plots depicts change in gain and %RCV representative of a falling laser, with field service engineer visits appearing as red dashed lines. D) The Levey-Jennings shows spikes in %RCV associated with QC beads exposure to bleach.

Figure 2. Drift in MFI can be observed by evening, but are more pronounced the following day. A) Typical MFI drift pattern observed for the Cytek Aurora 5-laser. B) The lineplots depict the MFI measurements of QC beads acquired before and after both morning and evening QC. C) The lineplots depict the recorded MFI measurements of QC beads after morning QC, and before morning QC the following day.

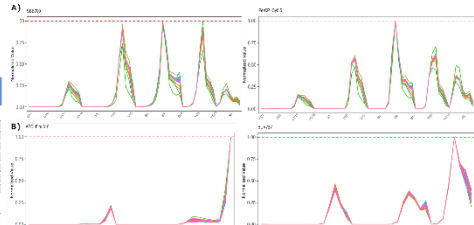


Figure 3. Simulated shifts in reference signatures arising from observed MFI drifts. Evening and morning after MFI drifts were calculated for each instrument for a six-month period, and fluorophore reference signatures were adjusted to account for the observed drift in detector. Line plots with each day a different color. A) shows two examples from the 5L instrument where variation was observed, while B) shows more typical minimal changes.

Acknowledgements
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<https://github.com/UMGCCFCSS> xiaoxuanfan@som.umaryland.edu

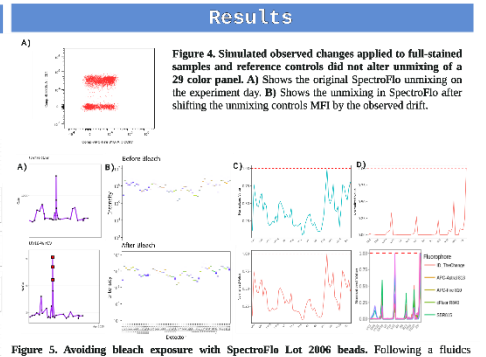


Figure 4. Simulated observed changes applied to full-stained samples and reference controls did not alter unmixing of a 29 color panel. A) Shows the original SpectroFlo unmixing on the experiment day. B) Shows the unmixing in SpectroFlo after shifting the unmixing controls MFI by the observed drift.

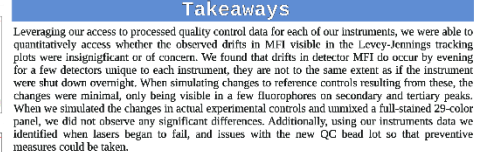


Figure 5. Avoiding bleach exposure with SpectroFlo Lot 2806 beads. Following a fluids shutdown with bleach, fresh QC beads were run. A) Levey-Jennings plots show spike in gain and %RCV. In B) spectrum plots show bead MFI before (top) and after (bottom) bleach exposure. C) lineplots depict grouped normalized signatures from individual cells before and after bleach exposure. In D), the after bleach MFI was subtracted from before bleach bead MFI, and the difference normalized to identify suspected stripped fluorophore.

Takeaways
 Leveraging our access to processed quality control data for each of our instruments, we were able to quantitatively assess whether the observed drifts in MFI visible in the Levey-Jennings tracking plots were insignificant or of concern. We found that drifts in detector MFI do occur by evening for a few detectors unique to each instrument, they are not to the same extent as if the instrument were shut down overnight. When simulating changes to reference controls resulting from these, the changes were minimal, only being visible in a few fluorophores on secondary and tertiary peaks. When we simulated the changes in actual experimental controls and unmixed a full-stained 29-color panel, we did not observe any significant differences. Additionally, using our instrument's data we identified when lasers began to fail, and issues with the new QC bead lot so that preventive measures could be taken.

Data availability
 Would you like to do this your own dataset? The R code used for the analysis and figure generation is available on our GitHub (https://github.com/DavidRach/EveningQC_Cyto2025). The current and historical QC data for all our instruments is available via our website (<https://umgccfcss.github.io/InstrumentQC/Data>).

Interested in setting up an automated QC tracking website for your own instruments? We have a how-to tutorial for those with some coding literacy (https://github.com/DavidRach/InstrumentQC_Install), and for those without, we are actively finishing an R package that will automatically set one up for Cytek and BD instruments with a single click (<https://github.com/DavidRach/CytometryQC>).

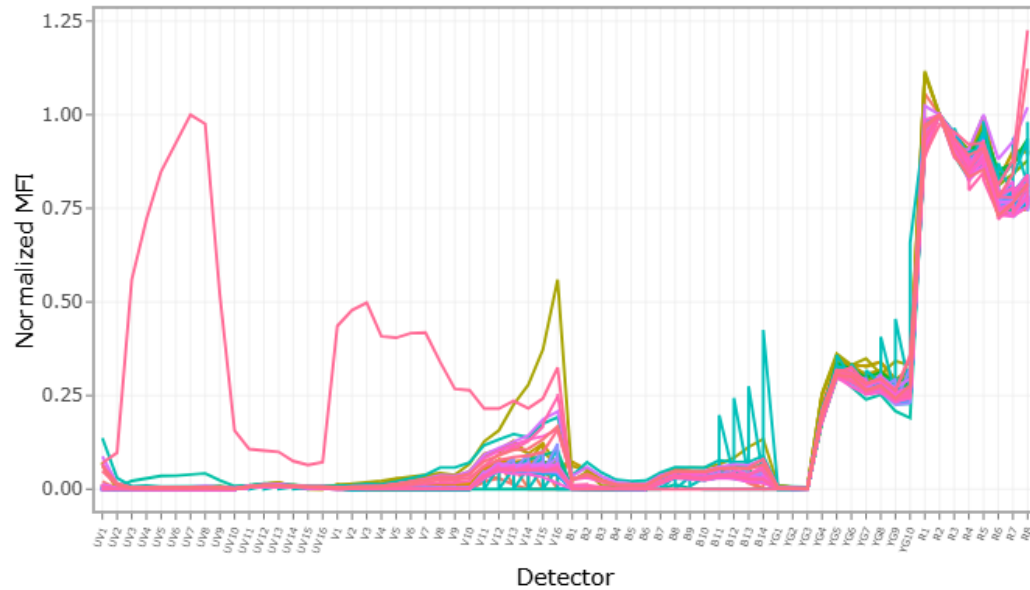
Take some stickers and track our progress!



Beyond .fcs files, what else can we leverage?



SpectroFlo .Expt Files

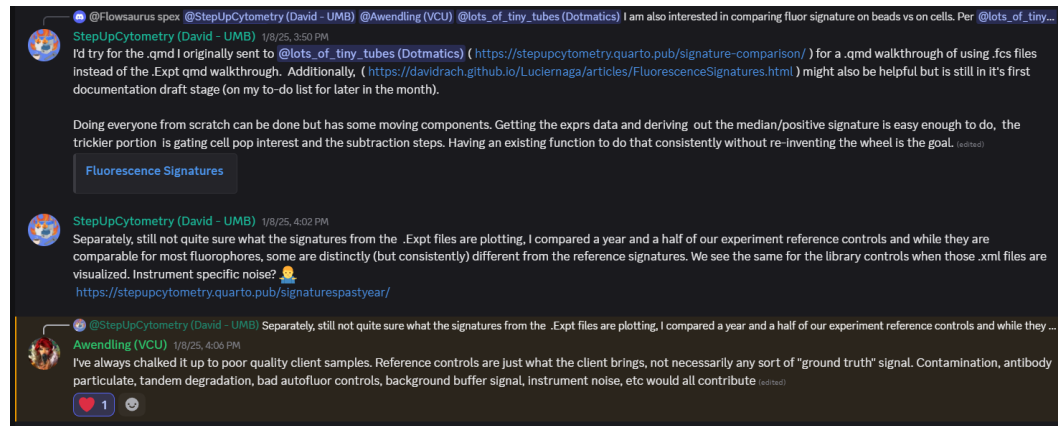


Every .Expt file

- ❑ Read in XML to R
- ❑ Access Experimental Metadata

Useful

- ❑ Fluorophores
- ❑ Markers



SpectroFlo .Expt files

Reference Controls from Expt Files From All Users

PUBLISHED
January 8, 2025

Data Acquisition

After initial acquisition, experiments are exported by users to an external hard-drive for long-term storage. We want to identify all zipped-folders, find the .Expt files, and copy them over to a separate folder for subsequent analysis.

▼ Code

```
library(purrr)

InPath <- file.path("F:")
OutPath <- file.path("C:", "Users", "12692", "Desktop", "Storage")
```

▼ Code

```
AllUsers <- function(InPath, OutPath){

  AllZipFiles <- list.files(path = InPath, pattern = "\\\\.zip$", full.names = TRUE, recursive=TRUE)
  message(length(AllZipFiles), " Zipped Files Found")

  AllZipFiles <- AllZipFiles[!grepl("RECYCLE", AllZipFiles)]

  walk(.x=AllZipFiles, .f=ExptFileLocate, OutPath=OutPath)
}

ExptFileLocate <- function(x, OutPath){
  ZippedFolder <- x
  ZipContents <- unzip(x, list = TRUE)$Name
  ExptFiles <- ZipContents[grepl("\\.Expt$", ZipContents)]

  walk(.x=ExptFiles, .f=ExpFileCopy, ZippedFolder=ZippedFolder, OutPath=OutPath)
}

ExpFileCopy <- function(x, ZippedFolder, OutPath){
  Tempd <- tempdir()
  unzip(ZippedFolder, files = x, exdir = Tempd)
  ExtractedPath <- file.path(Tempd, x)
  file.copy(ExtractedPath, OutPath, overwrite = TRUE)
}
```

▼ Code

```
AllUsers(InPath=InPath, OutPath=OutPath)
```



Code

Gather

- ❑ Identify the Zipped Folders
- ❑ Unzip
- ❑ Copy out the .Expt File
- ❑ Re-zip

Process

- ❑ Parse for Fluorophores
- ❑ Parse for Markers
- ❑ Save outputs by user and experiment

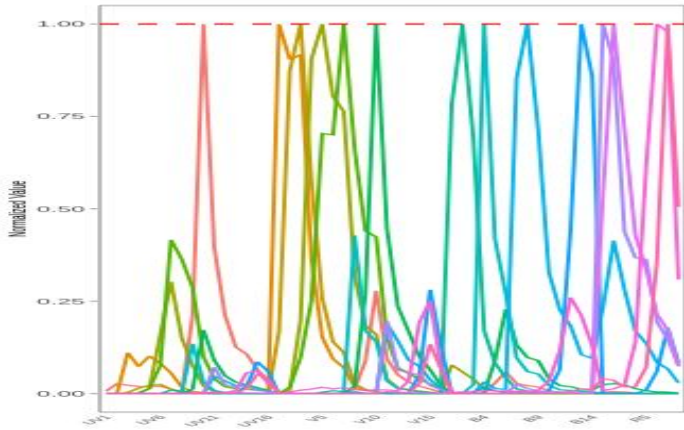


What can we do with that data?



- How many fluorophores in our largest user panel?
- “Does anyone have an anti-human Alexa Fluor 647 CD163 that we can borrow?”

Evaluate User Panels



D	WV	Fluorophore	Antigen	D	Fluorophore	Antigen	D	Fluorophore	Antigen
V1	428								
V2	443								
V3	458								
V4	473								
V5	508	BV480	CD11b	B1					
V6	525		B2	FITC	MHC II				
V7	542	BV510	CD8	B3	Spark Blue 550	CD3			
V8	581	BV570	Ly6C	B4	PE	F4-80			
V9	598			B5					
V10	615	BV605	CD4	B6					
V11	662	BV650	CD317	B7	7-AAD	Viability	R1		
	679			B8	PE-Cy5	CD25	R2		
V12	695			B9	PerCP-Cy5.5	CD11c	R3		
V13	718	BV711	Ly6G	B10		R4	Alexa Fluor 700	CD45	
	738			B11		R5			
V14	750					R6			
	760			B12		R6			
V15	781	BV785	CD127	B13	PE-Cy7	PD-1	R7	APC-Fire 750	LAG-3
V16	812			B14		R8			

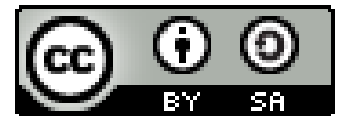
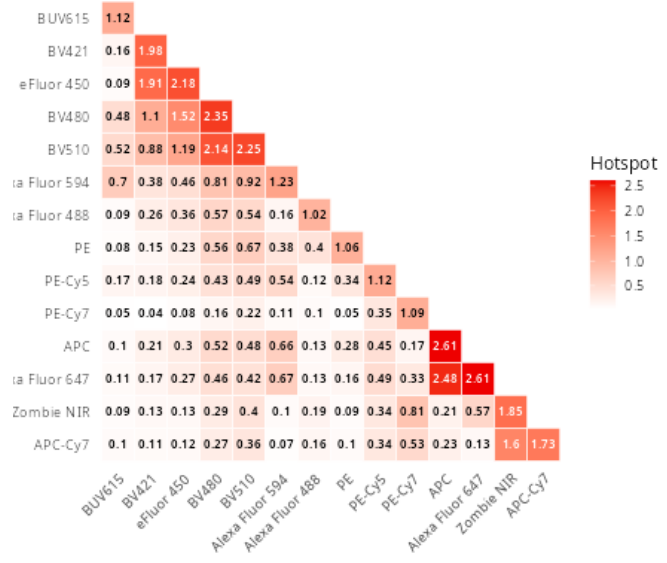
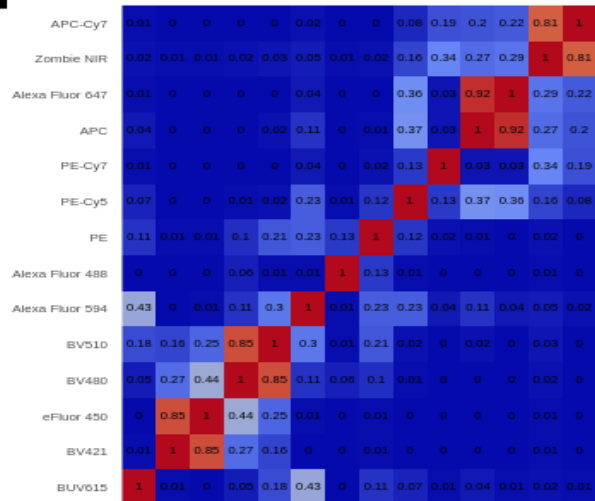
Not all user panels are “good”

Once we have parsed the panels fluorophores

- ❑ Signatures (based on references)
- ❑ Signature Worksheet
- ❑ Cosine Values (Similarity Matrix)
- ❑ Matrix Condition Number (Complexity Index)
- ❑ Collinearity (Unmixing-dependent Spread)



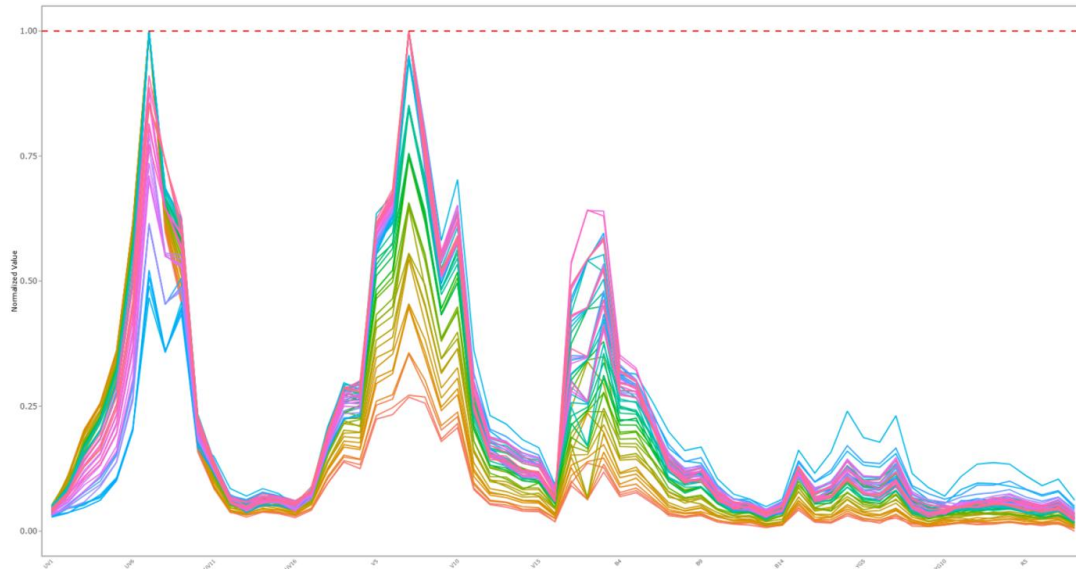
Code



What about the quality of the actual data?



Evaluating Unmixing Controls



1) Acquisition of unmixing controls (Cytek Aurora 5L)




2) Import to R (flowWorkspace)



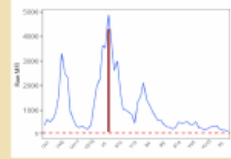
3) Apply and check gates (openCyto)




4) Extract data (Luciérnaga)




5) Identify detector with brightest MFI for individual cells




6) Enumerate total cells for each peak detector, and identify location fluorophore and autofluorescence peak(s)



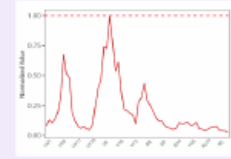
7) Group cells with shared peaks



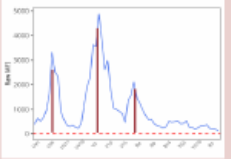
8) Subtract Out Autofluorescence



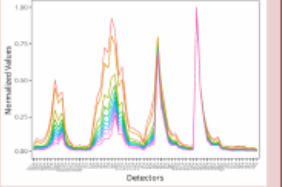
9) Generate normalized signature of individual cells for identified fluorophore detector



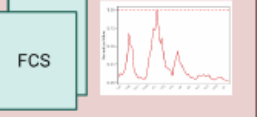
10) Identify all peaks using local maxima



11) Group cells with shared primary peaks and similar heights other peaks



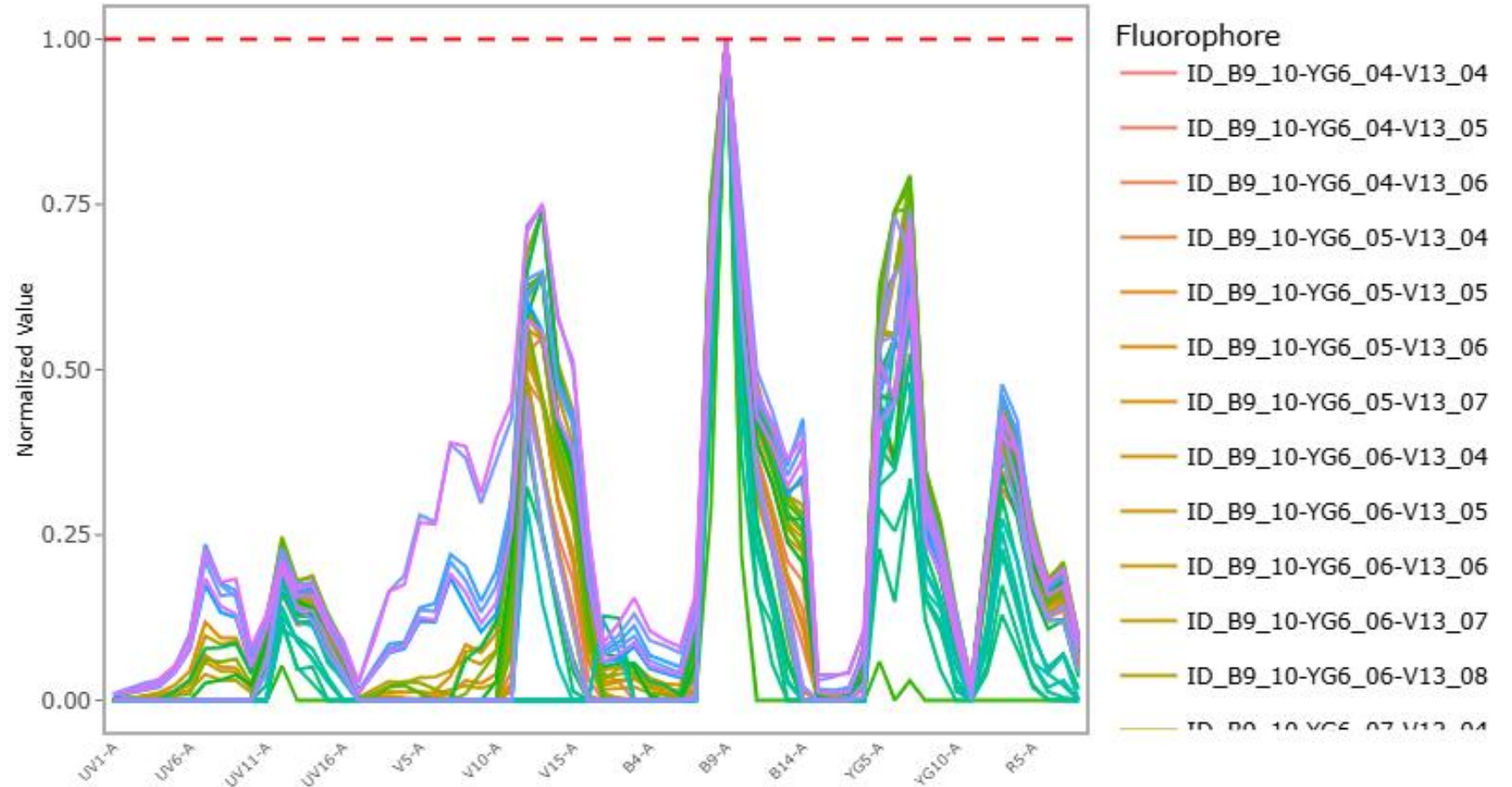
12) Retrieve original data for identified cells and export out new .fcs files containing purified signatures



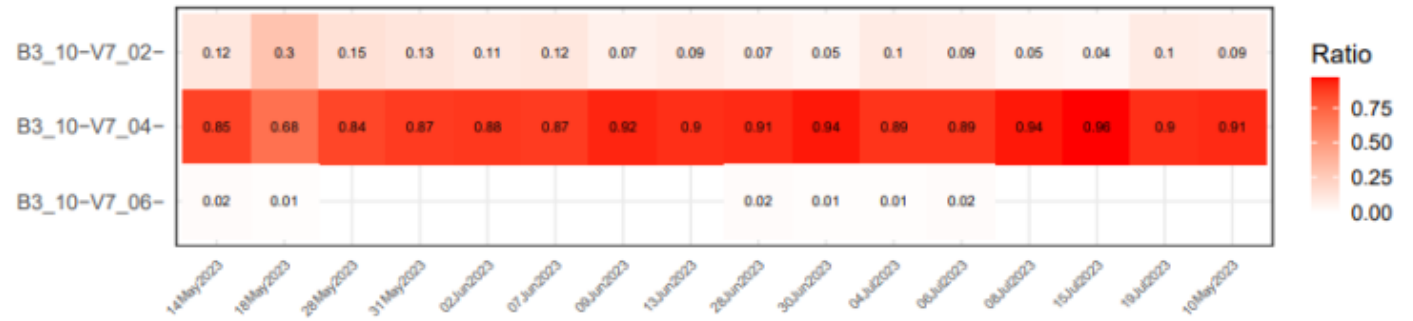
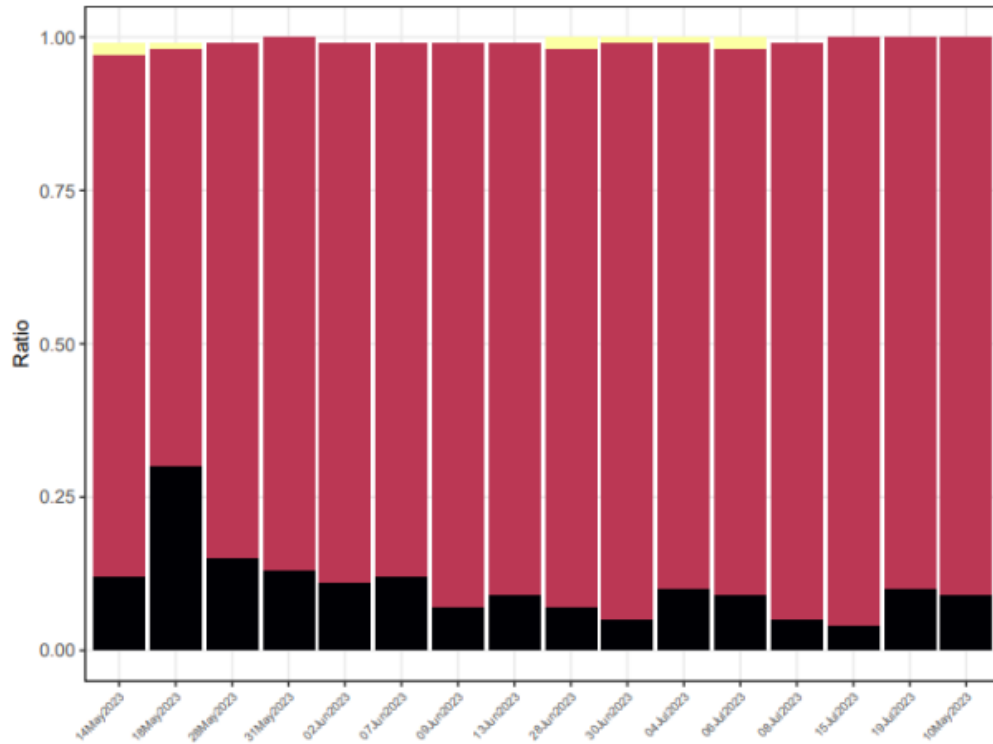
When PerCP-Cy5.5 degrades



Interactive
Plots

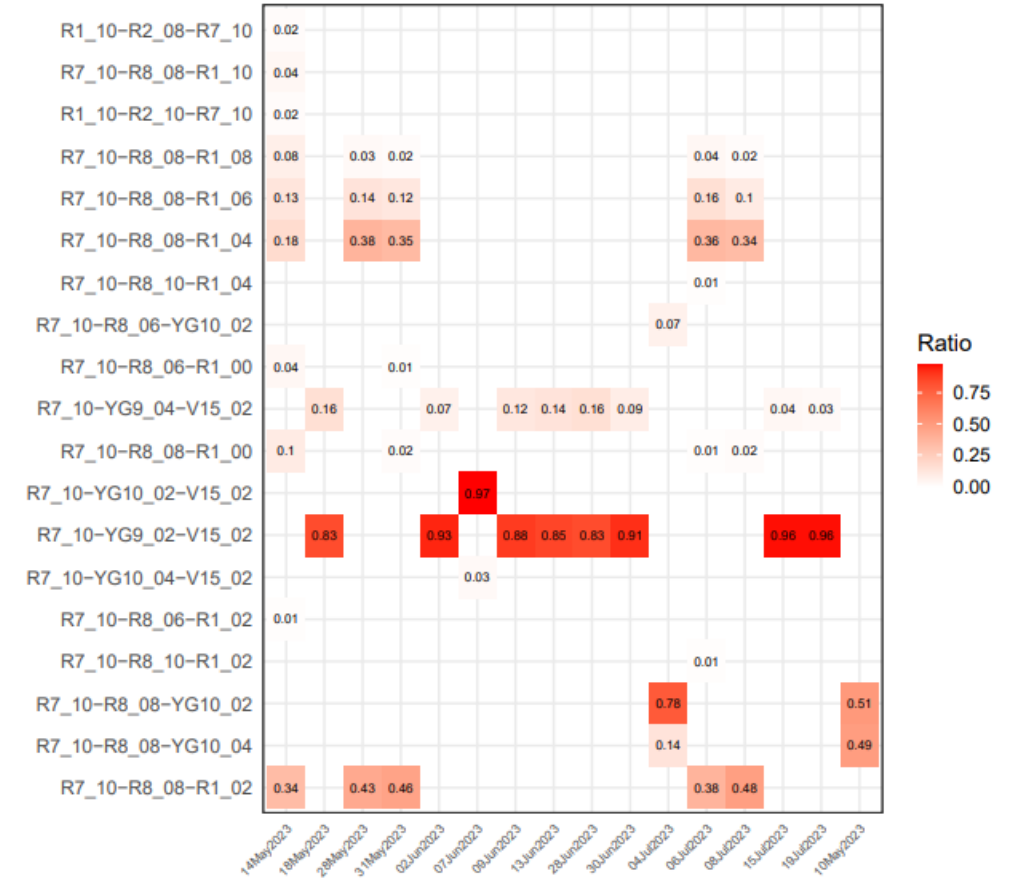
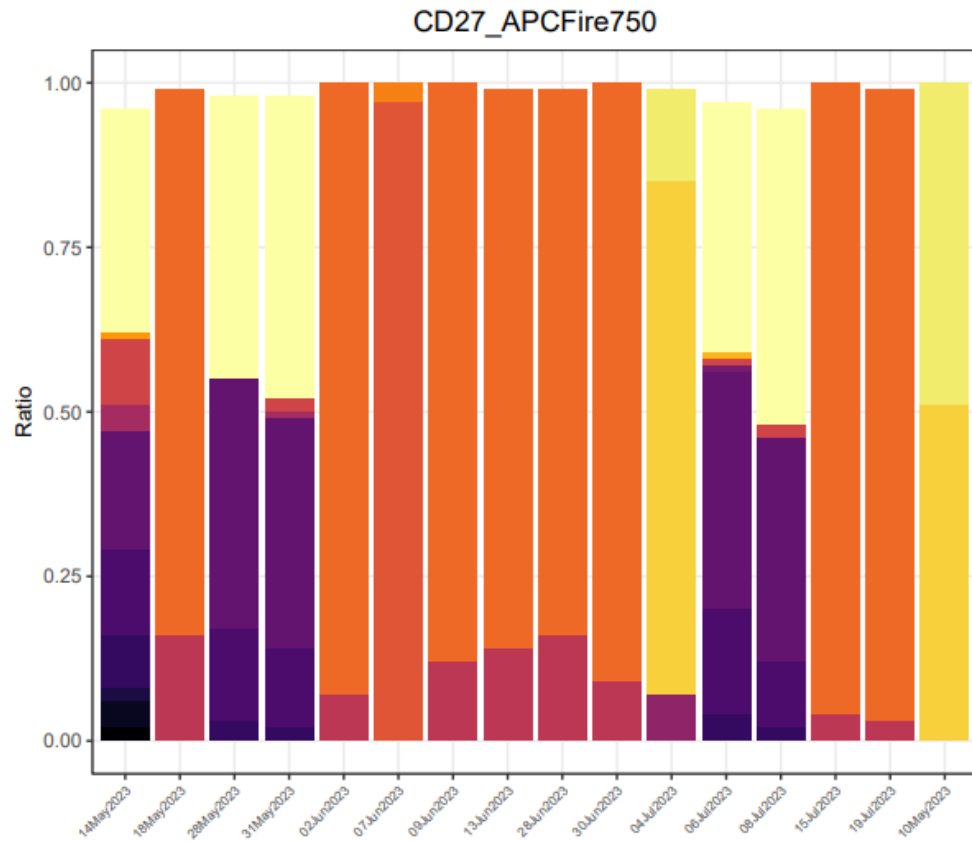


When antibody vials are in good condition



- Few normalized signature variants

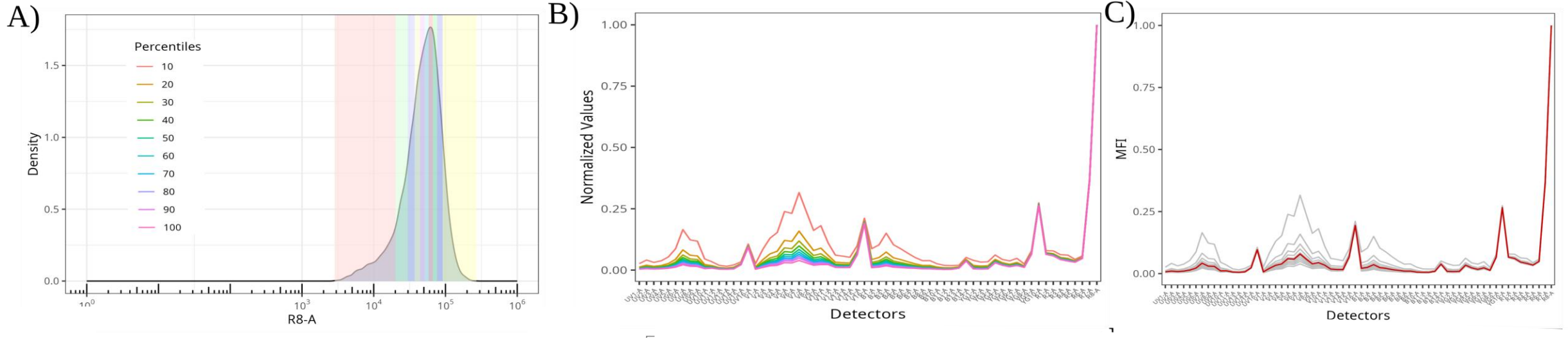
When the tandem starts degrading



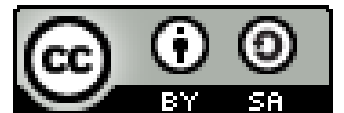
□ Noticeable increase in normalized signature variants



Residual Autofluorescence peaks in Single-Color Signatures

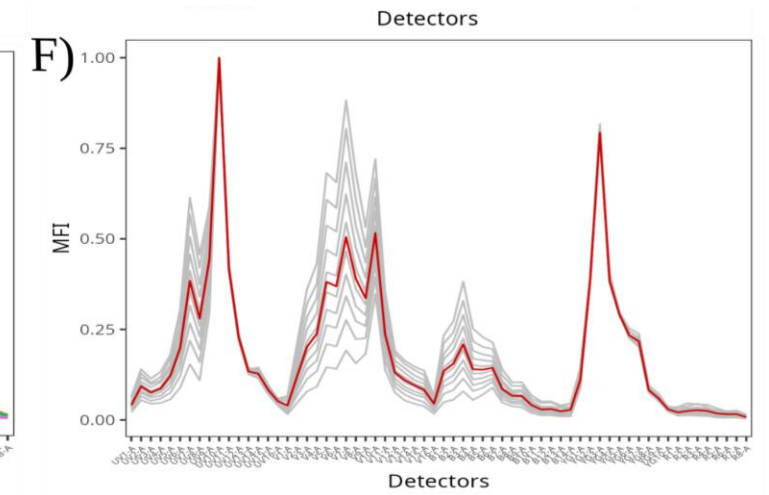
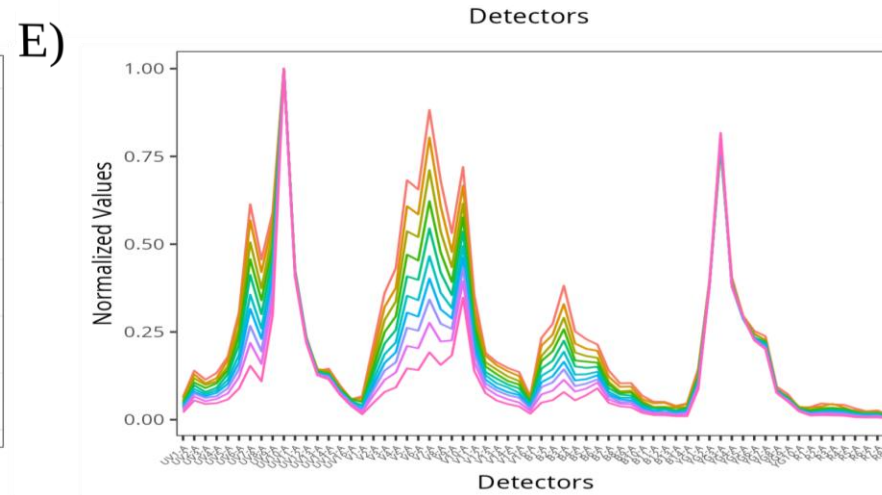
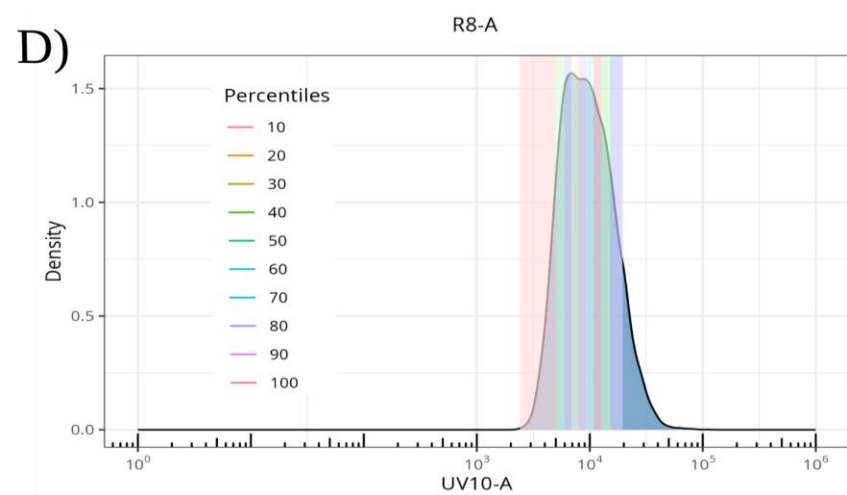


For cell controls with a **moderate density antigen** on **bright fluorophores**, we see that any residual autofluorescence contributes minimally to the overall isolated single-color signature when gated according to best practices

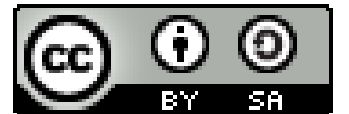




Residual Autofluorescence peaks in Single-Color Signatures



For cell controls with a **moderate density antigen** on **dim fluorophores**, we see substantial residual autofluorescence contributions to the isolated single-color normalized signatures even when gated according to best practices

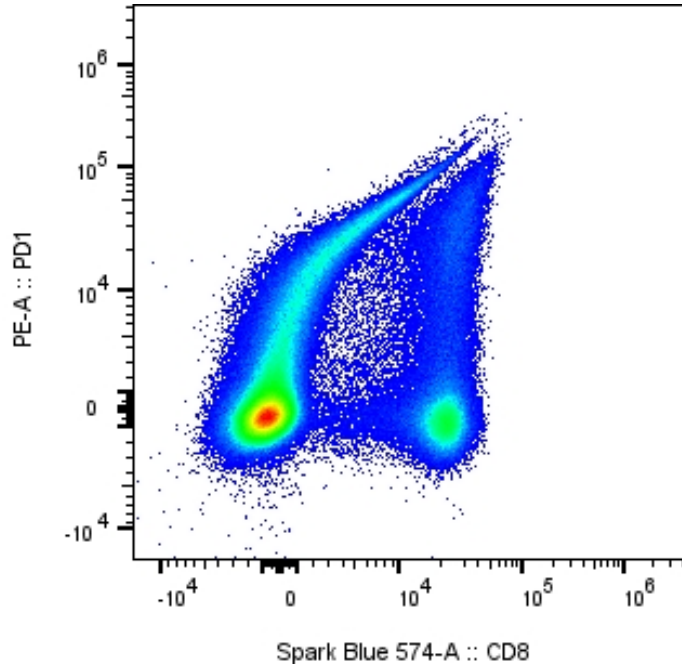




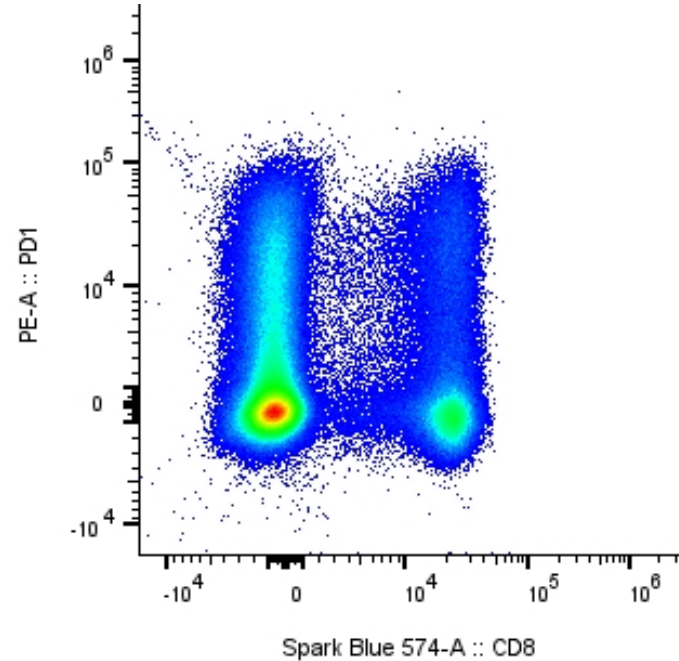
Residual Autofluorescence peaks in Single-Color Signatures



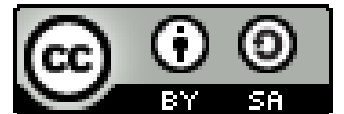
**PE signature with
residual AF**



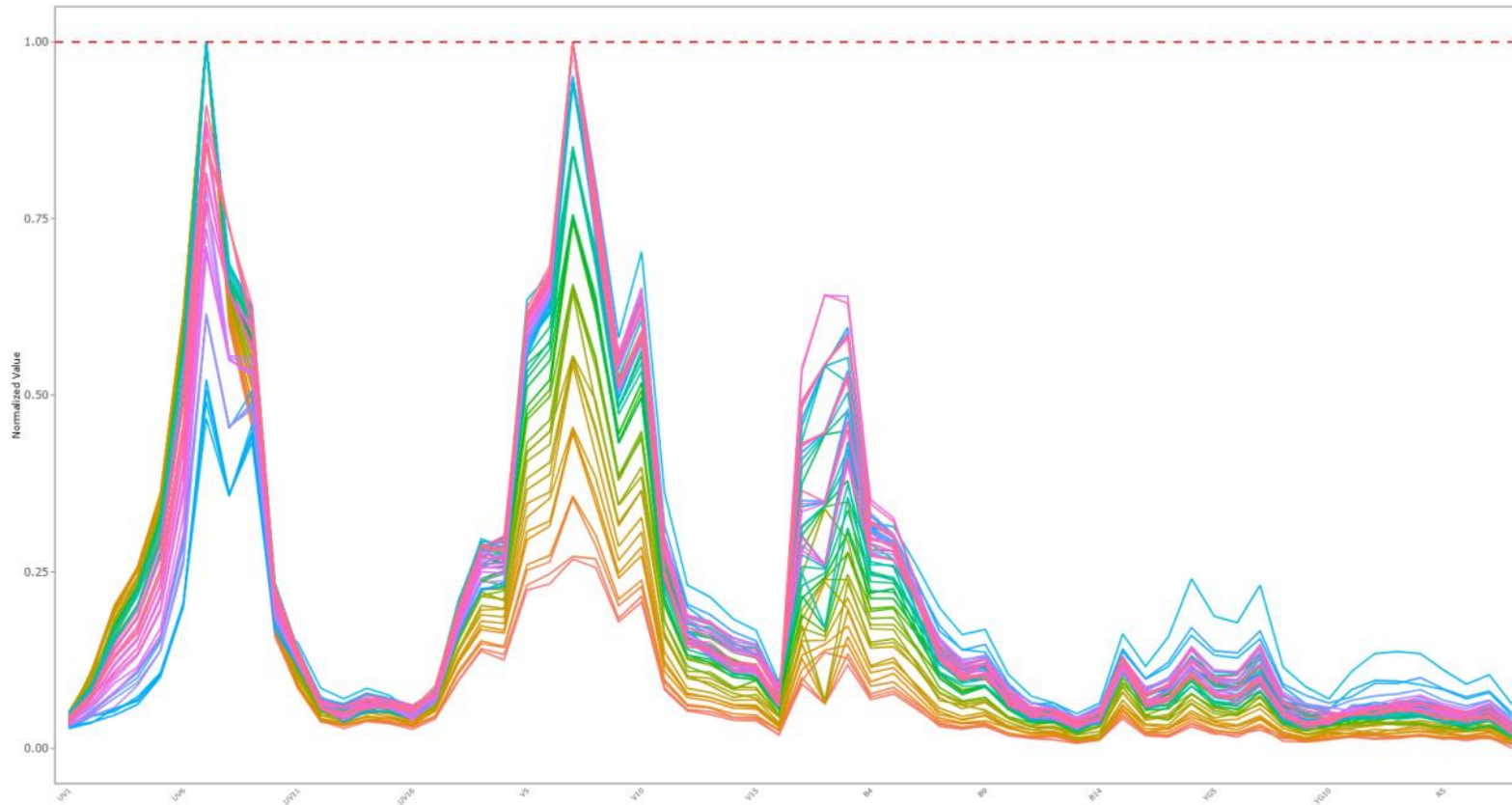
**PE signature without
residual AF**



This residual autofluorescence contribution results in unmixing errors,
and the panel unmixing significantly improved when switched out for bead controls

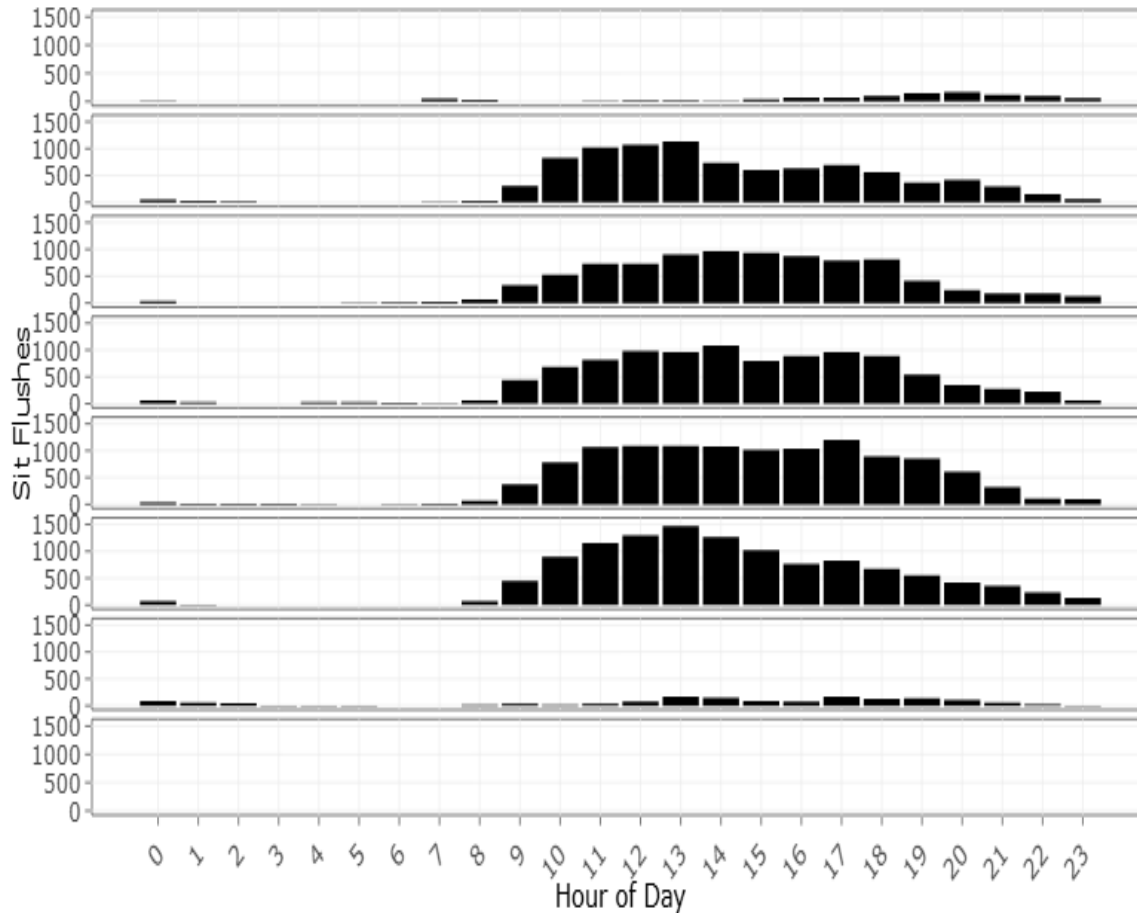


Autofluorescence



- Same process to isolate autofluorescence variants
- Isolate cells with same normalized signature for use in unmixing

Application Log



- Every time a sit-flush occurs, its recorded
- Plotted over time, shows weekly usage patterns for instruments
- Including “off-schedule” usage

- Were clean flow cells and fluidic shut-downs performed?
- What software issues occurring?
- How many hours has each laser been left on?

“Is anyone on after-me?”

Agilent CrossLab | iLab Operations Software | Search... | Go | David Rach | Help | Sign Out

Flow Cytometry Core (FCC) > View Schedule

Aurora-5 Confirm Usage

Week (7 Days) | Sun, 15 Mar - Sat, 21 Mar 2026
Eastern Time (US & Canada) | Calendar Details

	Sun, 15 Mar	Mon, 16 Mar	Tue, 17 Mar	Wed, 18 Mar	Thu, 19 Mar	Fri, 20 Mar	Sat, 21 Mar
12:00 AM	Unassisted Usage	Unassisted Usage	Unassisted Usage	Unassisted Usage	Unassisted Usage	Unassisted Usage	Unassisted Usage
01:00 AM							
02:00 AM							
03:00 AM							
04:00 AM							
05:00 AM							
06:00 AM							
07:00 AM							
08:00 AM						08:30 AM - 10:00 Sara Mangesh Kolhatkar	
09:00 AM	Unassisted Usage / Assisted Usage	Unassisted Usage / Assisted Usage	Unassisted Usage / Assisted Usage	10:00 AM - 01:00 Zhongcheng Mei	09:30 AM - 10:00 Winter Okoth	10:00 AM - 12:00 Adedola Adebamowo	10:00 AM - 12:00 Zhongcheng Mei
10:00 AM				Unassisted Usage / Price: \$95/hr (All Customers)	11:00 AM - 01:30 Katrina Gorga	Unassisted Usage / Price: \$95/hr (All Customers)	
11:00 AM					Unassisted Usage / Price: \$95/hr (All Customers)	12:00 PM - 05:00 Aisha Hegab Souquette	
12:00 PM						Unassisted Usage / Price: \$95/hr (All Customers)	
01:00 PM					01:30 PM - 05:30 Degui Geng		
02:00 PM				02:00 PM - 06:00 Adedola Adebamowo	Unassisted Usage / Price: \$95/hr (All Customers)		
03:00 PM				Unassisted Usage / Price: \$95/hr (All Customers)			
04:00 PM							
05:00 PM						05:00 PM - 07:00 Adedola Adebamowo	
06:00 PM				06:00 PM - 07:00 Adedola	06:00 PM - 07:00 Winter Okoth	Unassisted Usage / Price: \$95/hr (All Customers)	
07:00 PM	Unassisted Usage	Unassisted Usage	Unassisted Usage		07:00 PM - 10:45 Unavailable 4-laser swap	07:00 PM - 08:30 Farah Ammar	
08:00 PM						Unassisted Usage / Price: \$95/hr (All Customers)	
09:00 PM							
10:00 PM							
11:00 PM							

@Aizan (CRO) Is the tracking automated or requires manual input into, say, spreadsheet?

StepUpCytometry (David - UMB) 9/24/25, 10:07 AM
iLab retrieved historical .csv files for the above.

I am setting up a monitor yo display real time schedule for each instruments that scrapes the reservation pages every 15 minutes for the to be automated.

However, my authorization cookies keep expiring and the scrape obviously fails, so some work still required on the automation front.

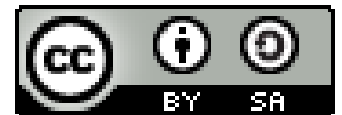
1

rachael sheridan (VAI) 9/24/25, 10:24 AM
If you figure that out, let me know! IT keeps telling me I can't have anything like that and it's iLab's fault... I don't believe them

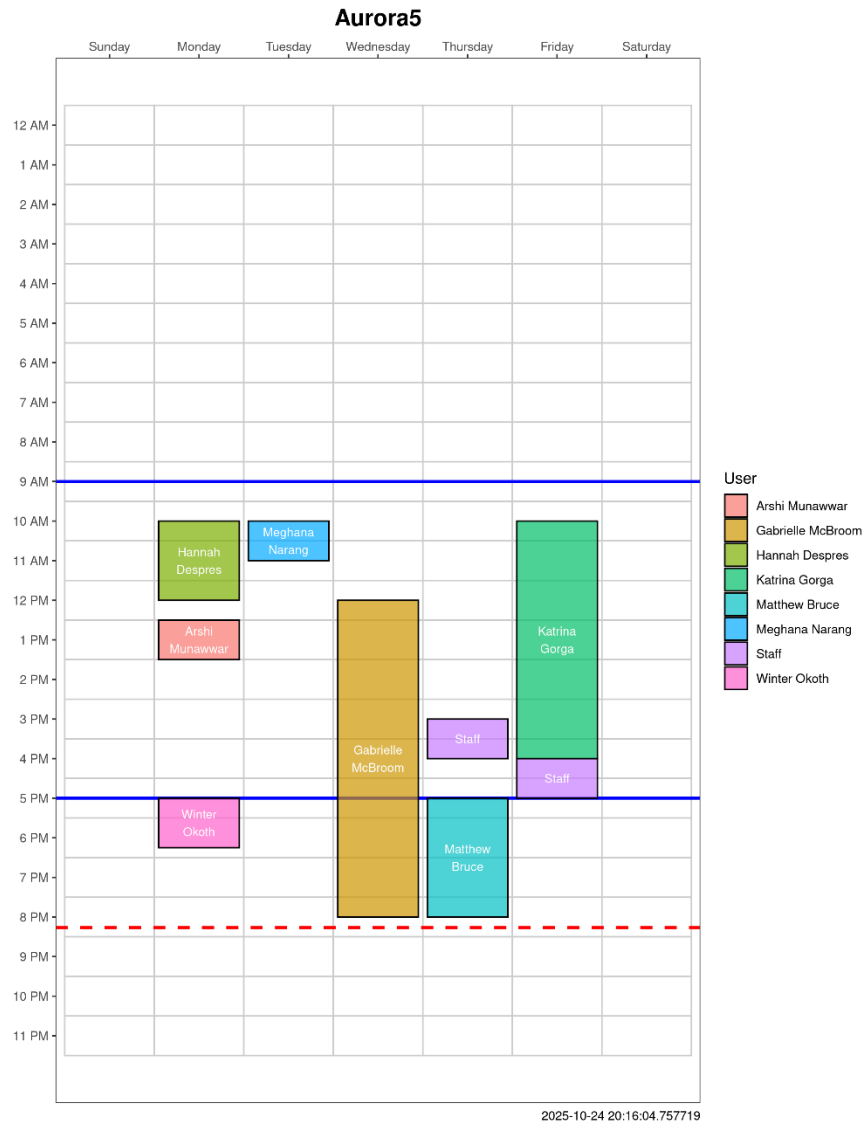
1

Laura Prickett (AstraZeneca) meow 9/24/25, 10:52 AM
I need that for outlook calendars but everything we have is so locked down

100 1

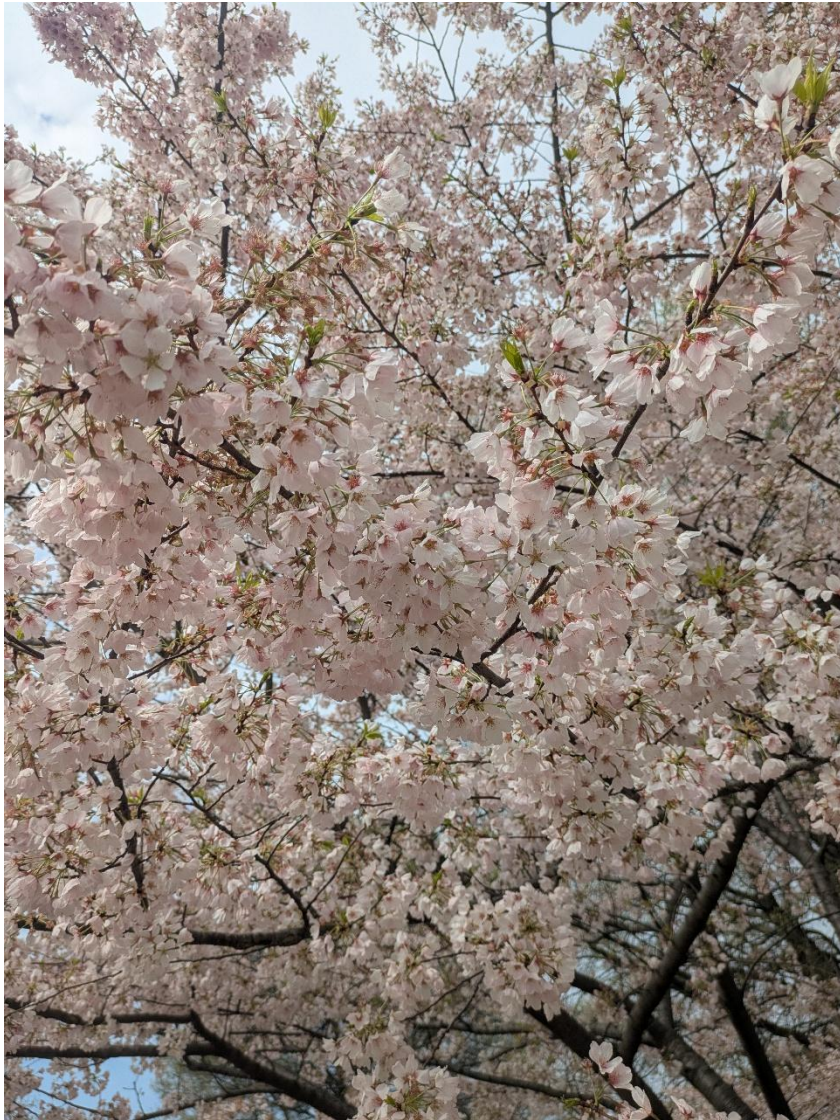


Updating Schedule to Display Monitor



- Displayed on a monitor to a Raspberry Pi 4b
- Cycles continuously through all the instrument schedules
- Refreshes every 15 minutes
- Sends booking data to GitHub
- Currently working on identifying late evening cancellations and sending emails to power down the instrument

What have we learned?



- ❑ Small steps, sequentially implemented, have improved our awareness over time.
- ❑ With most instruments, useful information can be retrieved from unlikely sources
- ❑ Repurposing existing open-source software infrastructure speeds things up
- ❑ Set up for generalization requires additional planning

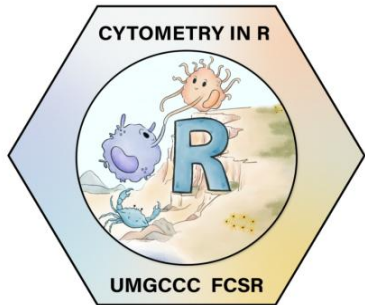
Learn R at your own pace



Cytometry in R: A free weekly course for coding beginners

David Rach^{1,2}, Natarajan Ayithan², Xiaoxuan Fan²

¹ Molecular Microbiology and Immunology Graduate Program, University of Maryland School of Medicine, Baltimore, USA
² Flow Cytometry Shared Resource, University of Maryland Greenebaum Comprehensive Cancer Center, Baltimore, USA



Website

Rationale

With the emergence of spectral flow cytometry, we can quickly profile 20+60 markers for millions of cells in minutes. Consequently, analysis of our datasets is increasingly complex. Semi-supervised & Unsupervised Analytical methods are being developed in response, many often implemented as R packages.

While many flow cytometrists express an interest in learning R, they often don't know where to start. The limited existing resources are typically geared towards those with intermediate bioinformatics skills, presenting additional barriers to entry.

Starting in February 2026, we have been offering a free weekly Cytometry in R course, primarily aimed at those with prior flow cytometry knowledge, but no-to-limited prior experience with programming language R.

Our teaching approach

One topic per week, roughly for an hour
 Beginners need detailed examples that can be worked through on their own time
 Take-home problems can additional enable acquisition independent code troubleshooting skills
 Consistency is key, being able take what you learn and apply to your own datasets helps maintain this
 Systematically build on prior concepts, enabling tackle more complicated problems as course advances
 Beyond Cytometry in R, provide a solid R foundation and teach coding best practices and reproducible workflows

Who is currently taking the course?

Following course announcement in November, we quickly had over 2000 people worldwide sign up for course emails

Based on GitHub account creation, and forking of the CytometryinR course repository, over 600 participants have started the course.

Based on our Google and YouTube analytics, we currently have around 200-300 active weekly participants worldwide. Many are following along at their own pace.

Website

A free bioinformatics course for those with prior flow cytometry experience, but no-to-little coding experience

Our course website is created with Quarto, and hosted on GitHub pages. Contains explanations, code, code outputs and screenshots. Each week has its own page. Extensive use of cross references to both internal and external resources. Search Bar for when we forget where it was covered. Teaching R from a Biologist perspective. Easily editable and expandable for community contributions.

Code is available via our course GitHub repository. We provide actual data needed to run the code. Course participants create a free a GitHub account. To start course, fork (i.e. copy) the course repository. Bring in new course materials each week by syncing, and pulling to your own computer. Open Science & Open Source. All Materials: All Code.

Website **Code**

YouTube

Not everyone learns well by just reading a website. Some topics take longer to grasp. Being able to revisit the material is key. When life gets busy, ability to circle back to where you had left off. We offer 3 YouTube livestreams per week:
 - Tuesday 10:00pm EST (GMT-4)
 - Wednesday 3:30pm EST (GMT-4)
 - Thursday 10:00am EST (GMT-4)

Recordings available immediately after on YouTube. Best of the livestream recordings is added to the course playlist.

Virtual and need help? We have you covered. Our GitHub Discussions page serves as a community forum. Have an installation issue? Need extra clarification? Want to show off your plots? Create a post! Added benefit that anyone taking the course in the future can benefit from the same answers.

YouTube **Help**

Schedule

Introduction to R **Cytometry Core**

Installing R Packages, File Paths, Inside an .RFS File, Intro to Tidyverse, Getting Sets, Visualizing ggplot2, Applying, Manual & Automated Getting, It's a Functions! Connection, Resampling Data for Statistics, Spectral Signatures, Similarities & Hotspots, Using R in R, Cleaning Algorithms

Unsupervised Analysis **Beyond the Sandbox** **The World's your Oyster**

Clustering Algorithms, Normalization Algorithms, Connectivity Visualization, Annotating Neighboring Clusters, The Art of R Shiny, R Shiny Files, Utilizing R Shiny Packages, Building R Shiny Packages, Europe gets reproducibility, Open Source Licenses, Validating Algorithms, Database Reproducibility, Annotating Metadata, Future Directions

Course Participant Feedback Survey #1

What have we done well?
 Where to improve?

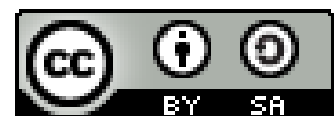
Future Plans

David finally graduates June 17 and gets his free time back! Wrap up our planned 30-week sequence, and make available resources that entire community will benefit from. Rising tides float all boats. There are 12 Bioconductor (+~30 GitHub) cytometry-focused R packages, many under-utilized. What if every one also had a community walk-through? Y quizás también así todavía me queda café... Citometria en R

Our core is supported by funds through the Maryland Department of Health's Cigarette Restitution Fund Program - CR4F-CR and the National Cancer Institute - Cancer Center Support Grant (CCSG) - P30CA14746

Take some stickers and track our progress!

<https://github.com/UMGCCFCR> flowcore@som.umaryland.edu



Acknowledgements



UMGCCC FCSR

Dr. Xiaoxuan Fan
Dr. Natarajan Ayithan
Mikayla Trainor

University of Maryland School of Medicine

Dr. Cristiana Cairo
Dr. Kirsten E. Lyke

PIN:

Daniela Franco

Molecular Microbiology Immunology Graduate Program

Dr. Eileen Barry
Dr. Heather Ezelle
Bess Tracey



Cytometry Discord

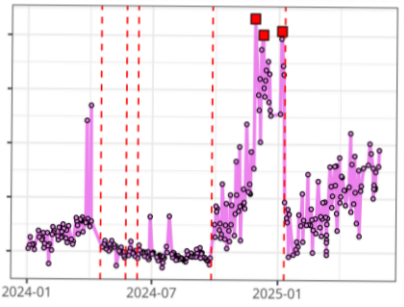
This publication was supported by funds through Maryland Department of Health's Cigarette Restitution Fund Program – CH-649-CRF and the National Cancer Institute – Cancer Center Support Grant (CCSG) – P30CA134274.d Service

 <https://github.com/DavidRach>

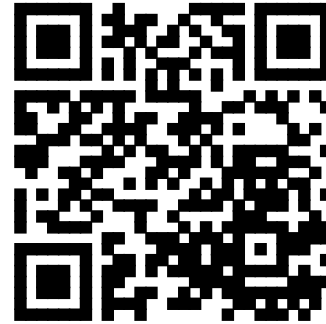
 @davidrach.bsky.social



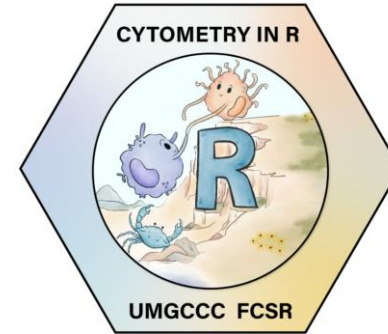
Questions?



UMGCCC FCSR
InstrumentQC dashboard



Luciernaga



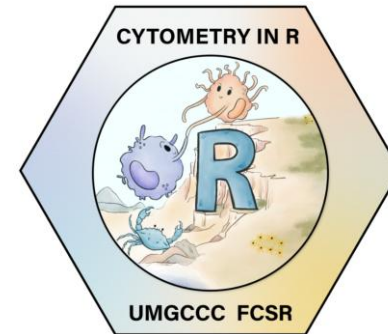
Website - CytometryInR



InstrumentQC How-To



Coereba



YouTube @CytometryInR



- Graduate Next Week
- All coding side-projects will then resume post-defense

IT'S BEEN A LONG TIME COMING

DOCTORAL DISSERTATION DEFENSE
DAVID THOMAS RACH

*"CHARACTERIZATION OF CORD BLOOD
INNATE-LIKE T CELL RESPONSES IN NEONATES BORN TO
HEALTHY WOMEN AND WOMEN LIVING WITH HIV"*

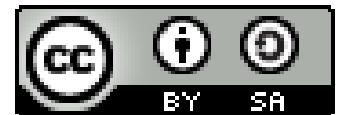
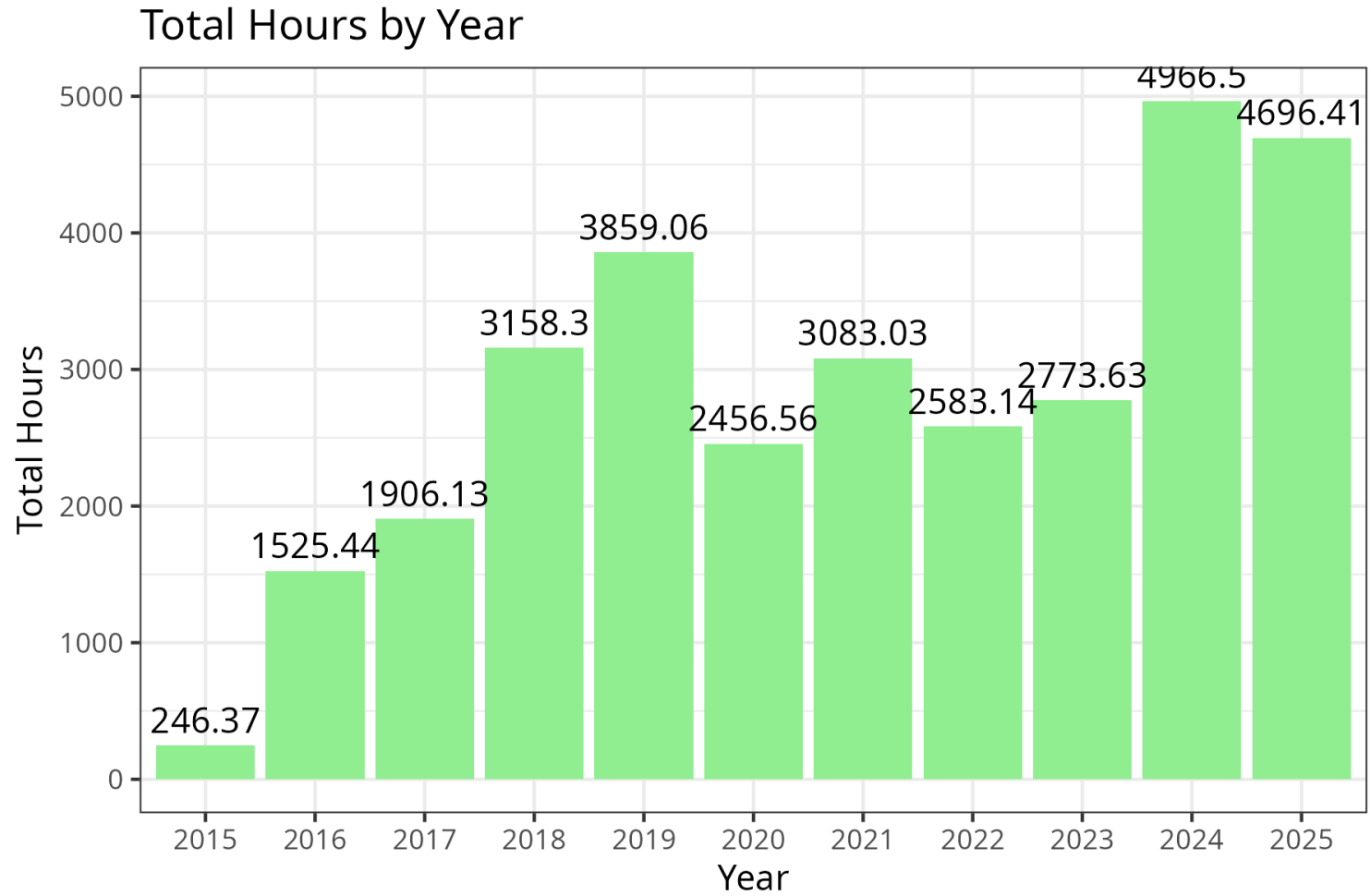
COMMITTEE CHAIRS
DRS. CRISTIANA CAIRO & KIRSTEN E. LYKE

WEDNESDAY, JUNE 17, 2026
12:00 PM — 1:00 PM EST (GMT-4)

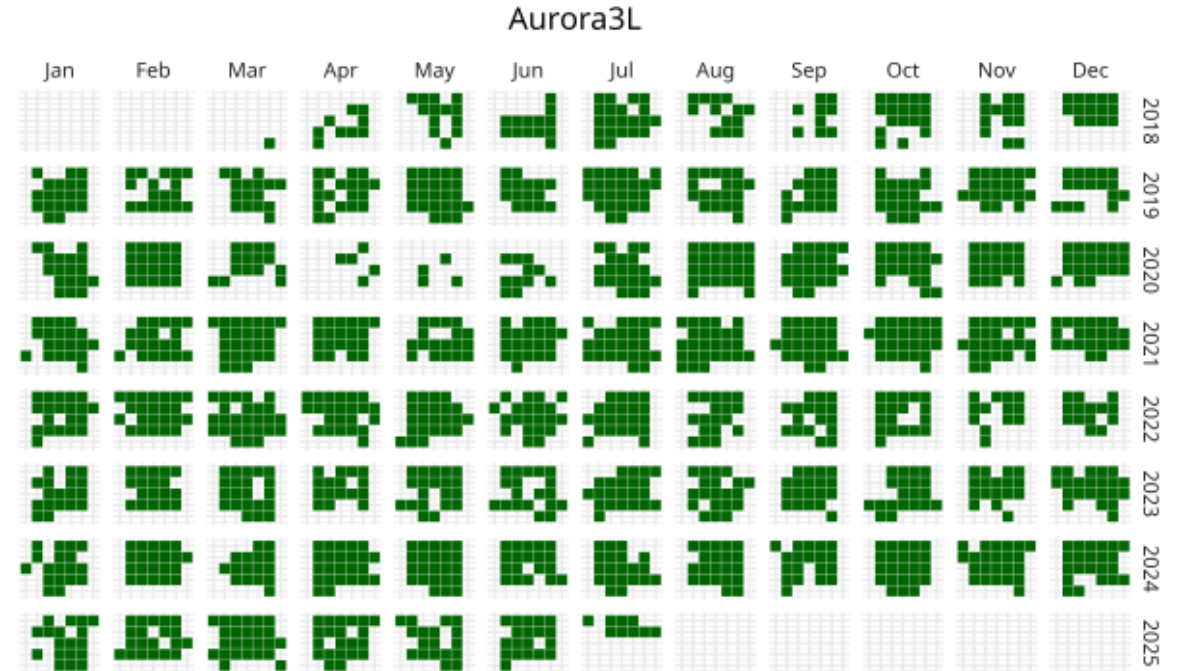


<https://www.youtube.com/@CytometryInR>
<https://github.com/DavidRach>

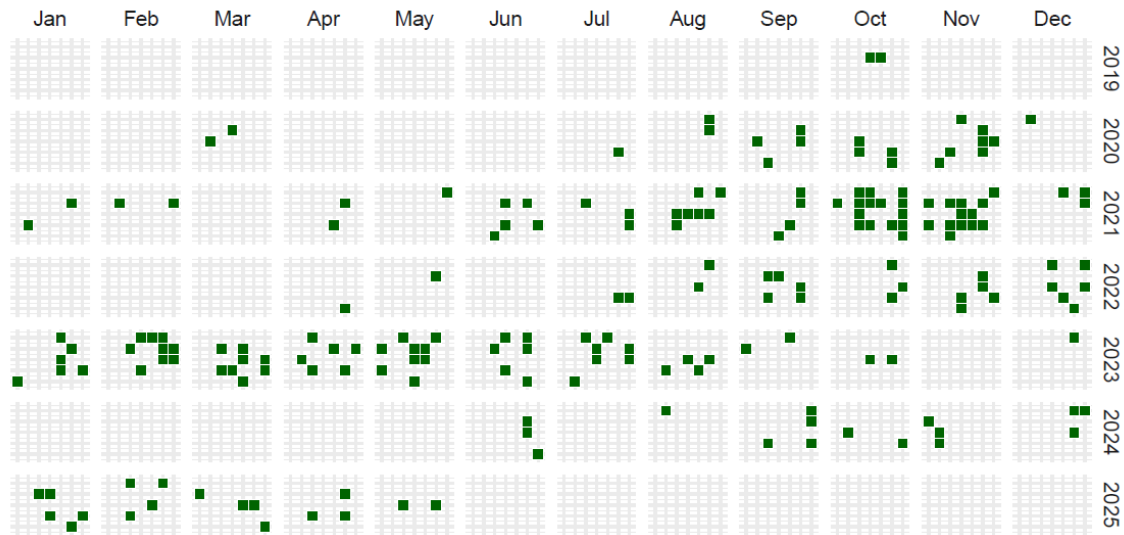
Metrics from iLab



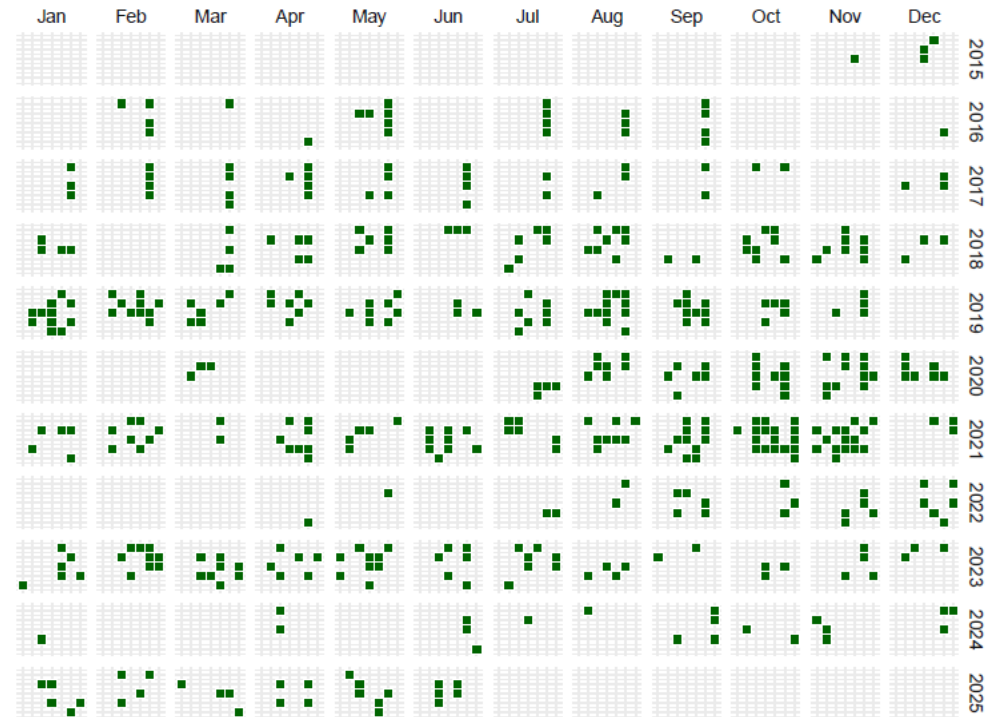
Instrument Use over Time



When did individual users or labs use the instruments?



David Rach



Cairo Lab

