Cytometry in R: A free weekly course for coding beginners

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COMPREHENSIVE CANCER CENTER

ISAC RECOGNIZED
Shared Resource Laboratory

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 exisiting resources are typically geared towards those with intermediate bioinformatics skills, presenting additional barrier to entry.

Starting in Februrary 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

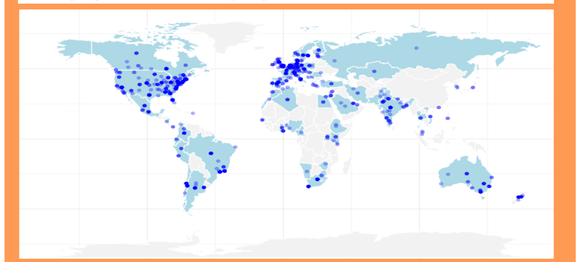
One topic per week, roughly for an hour
Beginners need detailed examples that can be worked through on their own time
Take-home problems can additional enable acquisition independent code troubleshooting skills
Consistency is key, being able take what you learn and apply to your own datasets helps maintain this

Systematically build on prior concepts, enabling tackle more complicated problems as course advances

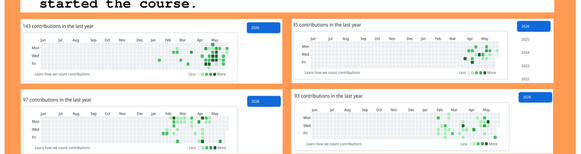
Beyond Cytometry in R, provide a solid R foundation and teach coding best practices and reproducible workflows

Who is currently taking the course?

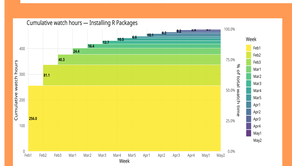
Following course announcement in November, we quickly had over 2000 people worldwide sign up for course emails

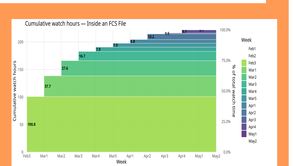


Based on GitHub account creation, and forking of the CytometryInR course repository, over 600 participants have started the course.

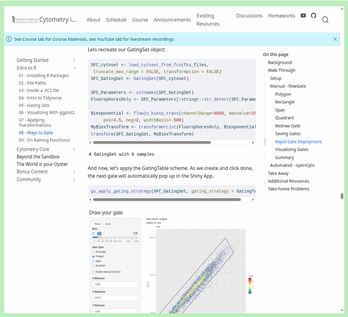


Based on our Google and YouTube analytics, we currently have around 200-300 active weekly participants worldwide. Many are following along at their own pace.





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

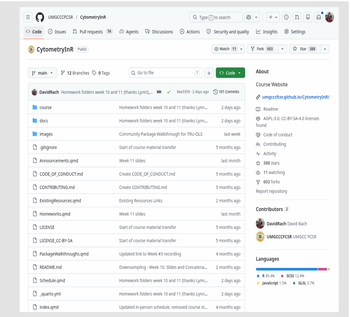
To start course, fork (i.e. copy) the course repository

Bring in new course materials each week by syncing, and pulling to your own computer

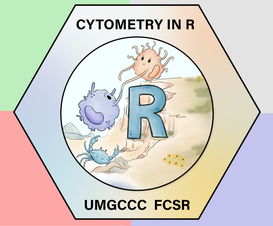
Open Science & Open Source

All Materials: CC BY SA

All Code: AGPL Free as in Freedom

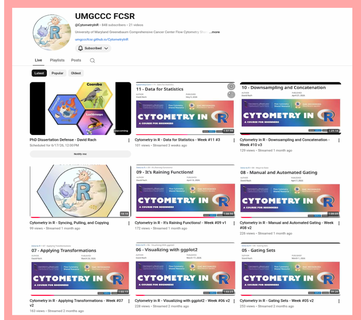


Website



UMGCCC FCSR

Code



Not everyone learns well by just reading a website

Some topics take longer to grasp. Being able to revisit the material is key

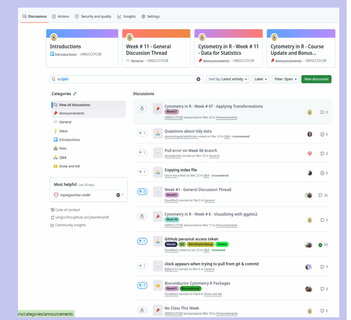
When life gets busy, ability to circle back to where you had left off

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

Previous Course Emails

Take-Home Problems

YouTube

Help

Schedule

Introduction to R

Installing R Packages | File Paths | Inside an .FCS file | Intro to Tidyverse | Gating Sets | Visualizing with ggplot2 | Applying Transformations | Manual & Automated Gating | It's Raining Functions! | Downsampling & Concatenation | Data for Statistics | Spectral Signatures | Similarities & Hotspots | Unmixing in R | Cleaning Algorithms

Cytometry Core

Unsupervised Analysis

Clustering Algorithms | Normalization Algorithms | Dimensionality Visualization | Annotating Unsupervised Clusters

Beyond the Sandbox

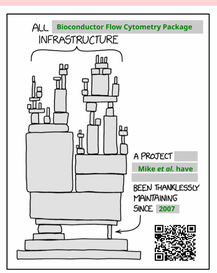
The Art of GitHub Diving | XML Files All The Way Down | Utilizing Bioconductor Packages | Building your First R Package | Everyone gets a Quarto Website | Reproducibility & Replicability | Open Source Licenses

The World's your Oyster

Validating Algorithmic Tools | Databases Repositories | Assembling Web Data | Future Directions

Course Participant Feedback Survey #1

Future Plans



David finally graduates June 17 and gets his free time back!

Wrap up our planed 30-week sequence, and make available resources that entire community will benefit from

Rising tides float all boats. There are 72 Bioconductor (+ ~30 GitHub) cytometry-focused R packages, many under-utilized. What if every one also had a community walk-through?

Y quizás tambien si todavia me queda cafe... Citometria en R

Our core is supported by funds through the Maryland Department of Health's Cigarette Restitution Fund Program - CH-649-CRF and the National Cancer Institute - Cancer Center Support Grant (CCSG) - P30CA134274

Take some stickers and track our progress!

https://github.com/UMGCCCFCSR

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