

# User Training

## Training Update: March 16, 2020

As part of Harvard Medical School's response to COVID-19, HMS Research Computing is now working remotely.

All training classes will be held online until further notice, via Zoom meetings.

## Fall 2020 (Part 2) Registration is now open!

**Important Notice:** After registration, you should receive an confirmation email from the Harvard Training Portal with a Zoom link. If you do not have your email address on file in the Training Portal, such messages cannot be sent to you. Please contact us for the Zoom meeting details if you did not get a confirmation email.

**You must have a Harvard University ID (HUID) to be able to register for a class. This is required to access the Harvard Training Portal.**

Those members of the HMS community who do not have HUIDs - such as employees at affiliate hospitals, or collaborators from other institutions - may self-register for one as a "Person of Interest" with their faculty member's sponsorship. The form may take several days to process, so we encourage non-HUID users to fill out this form ASAP in preparation for upcoming training:

<http://iam.harvard.edu/files/iam/files/authorized-identity-request-form.pdf>

(please read through the form for submission details)

Class	Date	Time	Room	Seats	Material	Registration ( <b>Only click here to register!</b> )
R/Biostatistics Part I	11/6/2020	1-3p	Virtual	48	<a href="#">R Biostatistics Files</a>	<a href="#">link</a>
R/Biostatistics Part II	11/13/2020	1-3p	Virtual	48	<a href="#">R Biostatistics Files</a>	
R/Biostatistics Part III	11/20/2020	1-3p	Virtual	48	<a href="#">R Biostatistics Files</a>	

### R/Biostatistics

R/Biostatistics is a multi-part course covering the basics of RNA-seq analysis with R. This biostatistics course covers standard supervised approaches and functional enrichment analyses of a breast cancer RNA-seq dataset. Topics include edgeR for differential analysis, GOSeq for functional enrichment analyses, and KEGG pathway analysis. Deep learning applications will be discussed. High-throughput data visualization techniques are emphasized. Each class includes a lecture and R practicum, and registration is for all courses. Laptops are encouraged.

## Fall 2020 (Part 1) Registration is open!

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Class	Date	Time	Location	Seats	Training Materials	Registration ( <b>Only click here to register!</b> )
Intro to O2	Wednesday, September 16, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to Python	Wednesday, September 23, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
No class	Wednesday, September 30, 2020					
Intro to R/Bioconductor	Wednesday, October 7, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>

Intro to Matlab	Wednesday, October 14, 2020	3-5p	Virtual	50	<a href="#">User Training github</a>	<a href="#">link</a>
Intermediate O2	Wednesday, October 21, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to O2	Wednesday, October 28, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to Git/Github	Wednesday, November 4, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to Parallel Computing	Thursday, November 12, 2020	3-5p	Virtual	50	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to Python	Wednesday, November 18, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to O2	Wednesday, November 25, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to Python	Wednesday, December 2, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>
Intro to R/Bioconductor	Wednesday, December 9, 2020	3-5p	Virtual	30	<a href="#">User Training github</a>	<a href="#">link</a>

## Intro to O2

O2 for New Users addresses the needs of users who have very little linux experience, and are just getting started with HPC. More time will be devoted to covering linux basics, and the concepts of schedulers and jobs, and data management best practices. The lecture portion of this class is one hour, the second hour will be spent clinic-style with HMS RC staff to address workflow-specific questions and help convert commands to O2 SLURM syntax.

## Intro to Python

Python is a popular scripting language for scientific computing and available across all computer platforms. The course will introduce you to some of the basics of the Python language as well as some of the nuances involved with its use specific to the O2 environment. The goal is to provide users with a foundational level of familiarity. Topics covered include basic data types and declaration, flow control (if/else), loops, a brief introduction to constructing a script, and a briefer introduction to modules. The course will be taught on O2, but general concepts are easily translatable to desktop and local installations.

## Intro to R/Bioconductor

Intro to using R and Bioconductor. R is a powerful, open-source, highly adaptable statistical language useful for crunching numbers to datasets like those produced by next-gen sequencing. This class covers R basics and learning to think like/understand R. Users will learn how to set up personal R libraries on O2, and use O2 R for its high memory allocations and parallelization. Topics include how to install packages, learn about variables, data types. data manipulation, flow control, and functions, perform simple statistical tests, and create a variety of plots. Laptops are encouraged.

[Class Files Here](#)

## Intro to MATLAB

Matlab has become the "language of science" in the past few decades. It is simple to use, yet powerful enough to be productive on large computing infrastructures. If you need: 1) Fast prototyping of research ideas; or 2) avoid spending too much time in coding instead of doing real science by taking advantage of Matlab's built-in functions; 3) User friendly graphical interface and educational documentation; 4) Simplicity of code; 5) Easy access to GPU computing power; 6) Easy plotting and presentation of data; you will find this introduction course useful. This course will introduce the basics of the MATLAB coding language with O2-scalability and data presentation.

## Intro to Parallel Computing

This is a short introduction to Parallel Computing that will include an overview of the basic concepts of parallel programming: from running your job in an embarrassingly parallel way to writing simple shared and distributed memory parallelization codes in different languages. The seminar will cover several examples of actual parallel codes however it will not have any "hands on" components. A basic programming experience (of any language, no parallelization) is preferred in order to better follow the topics presented during the seminar.

## Intermediate O2

Intermediate O2 is for current O2 users who would like to brush up on their bash skills, learn more advanced file transfer techniques, and unleash

some of the powerful features of the SLURM scheduler.

## **Intro to Git and GitHub**

This course introduces Git and GitHub and covers topics including: Getting Started with Git for version control, Using GitHub Desktop effectively, Collaborating with others on GitHub, and Utilizing GitHub Flow for better workflow. No previous exposure is assumed. We hope attendees will leave the class with the knowledge and tools necessary to start integrating Git into their workflows and excited to begin collaborating on GitHub.

## **Additional computational trainings are available through other groups:**

- [Training from the Harvard Chan Bioinformatics Core](#)
- [Training from the Data Management Working Group](#)
- [Training from the SBGrid Consortium](#)
- [Training from BioGrids](#)

Please reach out directly to the above groups if you are interested in attending their trainings.