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.

More details will be posted here soon, and we will notify enrollees with more details on how to use Zoom to attend class.

Spring 2020 Part I Registrations are open!

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)

MathWorks Spring Seminar Series at Harvard Medical School

April 14, 1 - 3pm, TMEC Rm. 128 REGISTER HERE

Creating, Sharing and Deploying Your Custom MATLAB Applications
Please join us for a complimentary seminar to explore some of the different ways you can share your custom MATLAB code as desktop, web and enterprise applications. Topics include:

Creating custom MATLAB apps without having to be a professional software developer
Packaging your applications so that they can be run by MATLAB users, or by others who do not have MATLAB
Generating components from your MATLAB algorithms, so that they can be called from programs written in other software languages

May 12, 1 - 3pm, TMEC Rm. 128 REGISTER HERE
Optimizing and Accelerating MATLAB Code
In this session, we will demonstrate simple ways to improve and optimize your code that can boost execution speed by orders of magnitude. We will also address common pitfalls in writing MATLAB code, explore the use of the MATLAB Profiler to find bottlenecks, and introduce the use of Parallel Computing Toolbox and MATLAB Parallel Server to solve computationally and data-intensive problems on GPUs, multicore computers and clusters. Topics include:

Understanding vectorization and best coding practices in MATLAB
Addressing bottlenecks in your programs
Incorporating compiled languages, such as C, into your MATLAB applications
Utilizing additional hardware, including multicore processors and GPUs, to improve performance
Scaling up to a computer cluster, grid environment or cloud

June 16, 1- 3pm, TMEC Rm. 128 REGISTER HERE
Demystifying deep learning: A practical approach in MATLAB
Are you new to deep learning and want to learn how to use it in your work? Deep learning can achieve state-of-the-art accuracy in many humanlike tasks such as naming objects in a scene or recognizing optimal paths in an environment. The main tasks are to assemble large data sets, create a neural network, to train, visualize, and evaluate different models, using specialized hardware - often requiring unique programming knowledge. These tasks are frequently even more challenging because of the complex theory behind them. In this seminar, we'll demonstrate new MATLAB features that simplify these tasks and eliminate the low-level programming. In doing so, we'll decipher practical knowledge of the domain of deep learning. We'll build and train neural networks that recognize handwriting, classify food in a scene, and figure out the drivable area in a city environment.

Along the way, you'll see MATLAB features that make it easy to:
• Manage extremely large sets of images
• Visualize networks and gain insight into the black box nature of deep networks
• Perform classification and pixel-level semantic segmentation on images
• Import training data sets from networks such as GoogLeNet and ResNet
• Import and use pre-trained models from TensorFlow and Caffe
- Speed up network training with parallel computing on a cluster
- Automate manual effort required to label ground truth
- Automatically convert a model to CUDA to run on GPUs

**Image Processing and Computer Vision in MATLAB**

**February 11, 1pm – 3pm, TMEC Rm. 128**

This seminar will be particularly valuable for anyone interested in using MATLAB to process, visualize, and quantify imagery. Rather than focus on extracting information from a few homogenous images, we will introduce a typical real-world challenge, and discuss approaches to managing and exploring collections of widely heterogeneous images. We will also describe approaches to implementing deep learning networks in MATLAB, and will compare and contract those approaches with more computer vision and machine learning techniques.

In this presentation, we will:

* Explore and manage a range of real-world image sets
* Solve challenging image processing problems with user interfaces
* Classify images by content using machine learning techniques
* Detect, recognize, and track objects and faces in images

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<tr>
<td>R/Biostatistics Part I</td>
<td>4/3/2020</td>
<td>1-3p</td>
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**R/Biostatistics description:**

The HMS Research Computing R Biostatistics course is a three class, advanced instructional course covering the basics of RNA-seq analysis with Bioconductor and the R statistical programming language. Bioconductor provides tools for the analysis and comprehension of all types of high-throughput genomic data. Students should have a beginner's level of proficiency in R programming and an understanding of basic statistical principles before registering for the course.

The course covers standard supervised statistical approaches for the comprehensive analysis of a published Cancer Genome Atlas (TCGA) human breast cancer RNA-seq dataset. Topics include edgeR differential gene expression analysis and GOSeq functional enrichment analysis of gene ontology terms. Data visualization techniques are emphasized, and each two-hour class includes a lecture and R practicum. The third two-hour class includes a lecture on deep learning in the biomedical sciences. Course registration includes all 3 classes. Comprehensively commented R scripts are provided to the student (R Biostatistics Files), as the objective of the course is to learn common biostatistical methods used for RNA-Seq analysis. Students are strongly encouraged to use personal laptops for the course.

To be prepared for the classes, students are encouraged to download and install the latest versions of R and RStudio prior to the first class. R - [https://cran.r-project.org/](https://cran.r-project.org/)

RStudio - [https://rstudio.com/products/rstudio/download/#download](https://rstudio.com/products/rstudio/download/#download)

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<td>2/5/2020</td>
<td>3-5p</td>
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<td>User Training github</td>
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## 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.

## 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 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.

## 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.

## Intro to Perl

Perl is an open source programming language that's flexible, available for nearly all platforms, and is easy to learn. It is well suited for data munging, and processing biological data. Topics covered include variables (scalars, arrays and hashes), numerical and string functions, loops and conditions, regular expressions, and reading and writing files. A brief introduction will be given for subroutines and BioPerl. The class will be focused on running Perl on the O2 cluster, though the fundamentals are applicable for using Perl installations elsewhere.

## 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.