

Training Schedule **October 2016**

NIH Library

nihlibrary.nih.gov

OCT 4	9-11:30am	Getting Started with MATLAB	C
	1-3pm	Parallel Computing with MATLAB	C
OCT 5	9-11am	Connecting MATLAB to Hardware	C
OCT 6	9:30am-4pm	GeneSpring 14.5 Training Class	C
OCT 11-14	8am-12pm	Software Carpentry (four-day workshop)	C
OCT 11	1-2pm	EndNote Web: Using EndNote from Anywhere	W
	1-2pm	PubMed: Understanding the Basics	W
OCT 13	12-1pm	Advanced PubMed	W
	2-3pm	BTRIS Basics for Clinical Researchers – Retrieving and Reporting Data for Active Protocols	C
OCT 17	10am-12pm	3D Printing Orientation	C
OCT 19	1-2:30pm	Percentile Ranking of Your Publication using Web of Science and Essential Science Indicators	W
OCT 20	9:30am-4pm	Exome Sequencing Analysis	C
OCT 27	10-11:30am	Systematic Reviews: The Basics	C

REGISTRATION

Registration is required. Register online at nihlibrary.beta.libcal.com/calendar/nihtraining or by phone at (301) 496-1080

COURSE DESCRIPTIONS

Full course descriptions with links to course hand-outs, related resources and web tutorials are available online.

ACCOMMODATIONS

Sign language interpreters and other reasonable accommodations can be provided. If you require such accommodations contact the NIH Library Information Desk at (301) 496-1080 five business days in advance. TDD users/callers please call the above number through the Federal Relay Service at 1 (800) 877-8339.

LOCATION

Classes are held in the NIH Library Training Room located in the NIH Library, Clinical Center/Building 10. Webinars are held online.

C
classroom

W
webinar

HANDS ON • FREE • REGISTRATION REQUIRED • NIH/HHS STAFF ONLY • See class descriptions on reverse

Class Descriptions

NIH Library

3D Printing Orientation

Learn how to operate the Makerbot Replicator 2 and Stratasys uPrint 3D printers. Also covered: 3D model preparation and how to avoid common printing problems. Users are required to attend this orientation before 3D printing at the NIH Library.

Advanced PubMed (Webinar)

Learn the advanced features of PubMed to get more precise search results. The featured PubMed search tips and tricks include: using the MeSH vocabulary, creating improved search strategies, filtering your results, exporting citations to bibliographic management software, and saving your searches and bibliographies.

BTRIS Basics for Clinical Researchers – Retrieving and Reporting Data for Active Protocols

Learn how to use the Biomedical Translational Research Information System (BTRIS) to streamline the task of gathering and reporting active protocol data. BTRIS staff will demonstrate how to run queries in BTRIS and guide attendees through running reports for their protocols. You must have a BTRIS account for access to identified data. If you do not have an account please complete this form: https://www.surveymonkey.com/s/Request_Data_Access.

Connecting MATLAB to Hardware

This workshop will demonstrate how to use MATLAB to acquire real-world test signals from data acquisition hardware. We will automate a complete test process with MATLAB by connecting to hardware, performing a custom analysis, and sharing the results. You will learn how easy it is to use MATLAB as a single environment for data acquisition and analysis.

EndNote Web: Using EndNote from Anywhere (Webinar)

EndNote Web is a web-based research and writing tool that serves as a perfect complement to the EndNote and Reference Manager software programs. Add, transfer, or import your references to EndNote Web and access your account via any web browser. Use “Cite While You Write” from EndNote Web to format your in-text citations and bibliographies.

Exome Sequencing Analysis

This class covers whole-exome sequencing data analysis and variant calling. The session will include an introduction to the Linux operating system and demonstrate how to run the cutting-edge analysis programs such as FASTQC, GATK, Bed tools, Picard and Variant Effect Predictor (VEP).

GeneSpring 14.5 Training Class

In this class, learn about GeneSpring 14.5, a data visualization and statistical analysis tool used by biologists for research and drug discovery. It analyzes data from Microarrays, qPCR, NGS, and Mass Spectrometry. The tool enables a user to examine probes across data types, array platforms, and organisms that map to the same biological entity.

Getting Started with MATLAB

This MATLAB workshop will cover importing data from Excel and other databases, creating variables, editing bad data points, and visualizing data to gain scientific insight. Also presented: automating manual plotting routines, creating and editing re-usable functions, and publishing results via HTML and Word.

Parallel Computing with MATLAB

In this session participants will learn how to solve computationally intensive problems using multicore processors, GPUs, and computer clusters. You will be introduced to high-level programming constructs that allow you to parallelize MATLAB applications and run them on multiple processors.

Percentile Ranking of Your Publication using Web of Science and Essential Science Indicators (Webinar)

This class presents an introduction to the methods of calculating the percentile ranks of publications using Essential Science Indicators and Web of Science.

PubMed: Understanding the Basics (Webinar)

This class provides an overview of PubMed’s content, tools and features. The steps to conduct a successful search and access full-text journal content will be presented, along with suggestions on how to make your PubMed searching experience more productive.

Software Carpentry (four-day workshop)

This workshop will cover basic concepts and tools for scientific computing including: basics of structured programming in Python, version control using Git, automating tasks using the UNIX shell, and an introduction to high performance computing at NIH using BioWulf.

Systematic Reviews: The Basics

This class will provide an overview of the systematic review process. Participants will also learn how to identify web-based registries, tools, and archives to assist in protocol registration, data management, and analysis.