

Training Schedule August 2016

NIH Library

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AUG 1	1-2:30pm	Poster Design and Presentation	C W
AUG 2	1-2pm	From RePORTER to Web of Science and InCites: Bibliometric Analysis	W
	1-3pm	3D Printing Orientation	C
AUG 3	2-3pm	Introduction to the BTRIS Limited Data Set Application	C
AUG 4	9-11am	Machine Learning for Computer Vision with MATLAB	C
	1-3pm	Deep Learning with MATLAB	C
AUG 8	2-3pm	Ethical Writing: Issues in Scientific Publication	C
AUG 10	9am-12pm	Introduction to R: Data Wrangling	C W
	1:30-4pm	Sequence Similarity Search: BLAST-Like Alignment Tool (BLAT)	C
AUG 11	10-11pm	Bibliometrics for Portfolio Analysis	C W
	1-3pm	Modeling Proteins for 3D Printing	C
AUG 16	1-2:30pm	EndNote Web: Using EndNote From Anywhere	C
AUG 18	9:30am-4pm	GeneSpring 13.1	C
AUG 24	1-4pm	Intermediate R: Data Visualization	C W
AUG 25	9:30am-4pm	QIAGEN Ingenuity Variant Analysis (IVA)	C
AUG 30	9:30am-4pm	Partek Flow	C
AUG 31	9:30am-4pm	QIAGEN CLC Genomics Workbench	C

REGISTRATION

Registration is required. Register online at nihlibrary.beta.libcal.com/calendar/nihltraining 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

3D Printing Orientation

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

Bibliometrics for Portfolio Analysis

In this session, you will learn about the opportunities and limitations of bibliometrics for portfolio analysis, the types of questions that bibliometrics can address, and some of the data sources and tools available for performing bibliometric portfolio analysis.

Deep Learning with MATLAB

This session will explore how MATLAB addresses handling large sets of images and retraining existing network architectures. We will highlight the computer vision workflow using Deep Learning with MATLAB including: accessing and managing large sets of images, leveraging the use of pre-trained networks for transfer learning, using standard computer vision techniques to augment the use of deep learning, and speeding up the training process using GPUs.

EndNote Web: Using EndNote from Anywhere

EndNote Web is a web-based research and writing tool and a perfect complement to EndNote and Reference Manager. 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 bibliography.

Ethical Writing: Issues in Scientific Publication

This class introduces authors to the major issues of publication ethics including: identifying and understanding science writing ethical issues, learning how to properly cite the work of other authors, recognizing when copyright permission is necessary, and an introduction to ethical writing resources and organizations.

From RePORTER to Web of Science and InCites: Bibliometric Analysis (Webinar)

This course demonstrates how to move publication data from RePORTER to Web of Science and conduct bibliometric analyses. It also provides an introduction to InCites, a program that can provide fast bibliometric results.

GeneSpring 13.1

GeneSpring 13.1 is 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.

Intermediate R: Data Visualization

This class will introduce participants to using ggplot2 and other R visualization tools with RStudio to create a variety of data visualizations. R's ggplot2 is a data visualization package that implements the Grammar of Graphics, a theoretical framework for building graphs and charts up from their individual components, including data, geometric objects, coordinates, and aesthetic properties.

Introduction to R: Data Wrangling

In this course for non-programmers, participants will learn the basics to get started with R. We will cover key terminology and concepts, and will use RStudio to learn about loading, aggregating, and processing data.

Introduction to the BTRIS Limited Data Set Application

The BTRIS Limited Data Set application allows researchers to access data from across all active and terminated protocols conducted within the NIH intramural program. Access clinical research data from 1976-present across 515,000 subjects to pose hypotheses and generate new research ideas. You must have a BTRIS account for access to identified data https://www.surveymonkey.com/s/Request_Data_Access.

Machine Learning for Computer Vision with MATLAB

This session will discuss and explore how MATLAB addresses common challenges for using machine learning techniques with images and video. The class will cover: importing and managing large sets of images and video, training, evaluating and comparing a range of machine learning models, and automatically extracting discriminative information from images.

Modeling Proteins for 3D Printing

Learn how to create protein models using Chimera and how to prepare them for printing using Meshmixer.

Partek Flow

This two-part, hands-on class covers using Partek Flow for RNA-Seq and DNA-Seq data analysis. Participants will learn how to analyze NGS data, integrate NGS data with microarray data in Partek Flow and overcome common analysis challenges. The first section will be devoted to analysis using a sample dataset. The second section is an open lab where researchers can bring their own data for analysis.

Poster Design and Presentation

This workshop will teach participants skills to clearly and effectively get a message across in a professional research poster presentation. We will discuss best practices for presenting data, principles of visual perception and the psychology of communication, and software and tools to help create appealing presentations and visualizations.

QIAGEN CLC Genomics Workbench

This class covers QIAGEN's CLC Genomics Workbench, which offers customizable solutions for genomics, transcriptomics, epigenomics, and metagenomics. Participants will learn about this application's integrated tools which can be used for the analysis and visualization of data from all major next-generation sequencing platforms.

QIAGEN Ingenuity Variant Analysis (IVA)

Ingenuity Variant Analysis (IVA) combines analytical tools and integrated content to help rapidly identify and prioritize human sequence variants. This workshop will focus on how to upload datasets, efficiently use different filters within variant analysis to identify causal variants, export results, as well as recent IVA updates.

Sequence Similarity Search: BLAST-Like Alignment Tool (BLAT)

This course demonstrates how to use BLAT to map a cDNA/mRNA sequence to a genome to identify exon-intron locations in the genomic sequence, and a protein sequence to a genome to search for gene family members in the genome. It also demonstrates how to visualize the alignment in the UCSC genome browser and compare the results to a similar search done using NCBI's BLAST.