

Training Schedule **September 2016**

NIH Library

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SEP 7	2-3pm	Excel Tips & Tricks for BTRIS Users	C
SEP 8	9:30am-4pm	Pathway Studio	C
SEP 13	9:30am-4pm	Expression Data Analysis of Microarray and NGS Data in Partek Genomics Suite	C
SEP 15	9:30am-4pm	ChIP-Seq Analysis	C
SEP 20	9:30am-4pm	MetaCore: Enabling Systems Biology Research through Pathway Analysis	C
SEP 22	10-11:30am	EndNote Desktop: Managing Your Search Results	C
	2-3pm	Principles of Effective Data Visualization	C W
SEP 26	1-4pm	Introduction to R: Data Wrangling	C W
SEP 27	1-4pm	Intermediate R: Data Visualization	C W
SEP 28	1-2:30pm	Publication Analysis Using Web of Science and Scopus	W
SEP 29	10-12pm	3D Printing Orientation	C
SEP 30	2-4pm	Introduction to 3D Modeling with SOLIDWORKS	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

Class Descriptions

3D Printing Orientation

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

ChIP-Seq Analysis

An introduction to ChIP sequencing data analysis that prepares participants to independently run basic ChIP-seq analysis for peak calling using a “point and click” approach on a Galaxy platform. This class includes a tutorial demonstrating the use of ChIP-seq analysis workflow.

Excel Tips & Tricks for BTRIS Users

Learn the powerful features and functions in Excel that can help organize and manipulate data in BTRIS. Excel provides the flexibility to sort, search, view, and manipulate discrete and text data. Participants must have a BTRIS user account for access to identified data, available at: https://www.surveymonkey.com/s/Request_Data_Access. For additional information on this session go to <http://btris.nih.gov>.

EndNote Desktop: Managing Your Search Results

Learn how to use EndNote, a reference management tool for finding, downloading, and organizing references in a personal, searchable database. This class will cover how to import references from online databases such as PubMed, search for and edit references, insert references in manuscripts with Microsoft Word’s “Cite While You Write,” create bibliographies, and choose from thousands of journal publishing styles to format references and bibliographies.

Expression Data Analysis of Microarray and NGS Data in Partek Genomics Suite

Attend this training to acquire a working knowledge of Partek Genomics Suite and Partek Pathway, tools that the NIH Library makes available to NIH researchers for microarray data analysis and downstream functional analysis of NGS data.

Intermediate R: Data Visualization

This class will introduce participants to using ggplot2 and other R visualization tools in 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 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. The class covers key terminology and concepts and will use RStudio to learn about loading, aggregating, and processing data.

Introduction to 3D Modeling with SOLIDWORKS

SOLIDWORKS is a powerful modeling tool that can be used to design and create 3D parts and assemblies. This class will demonstrate how to document a model, assemble multi-part models, change interface settings, and how to work with 3D printers.

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MetaCore: Enabling Systems Biology Research through Pathway Analysis

Learn about MetaCore’s molecular database, which contains over a million interactions including over 700,000 compounds and their targets. This class covers how to simplify the generation and prioritization of experimental hypotheses following ‘omics’ or NGS experiments, assess and validate potential therapeutic targets and disease biomarkers, and how to use the analytical tools.

Pathway Studio

Learn to use Pathway Studio Web, an integrated online research solution that combines a large knowledgebase of extracted scientific facts with analytical and visualization tools. This training will focus on pathway building and high-throughput data analysis.

Principles of Effective Data Visualization

This session provides an overview of how data visualizations are constructed, how people tend to understand visual cues like shape and color, and how to use these cues to create visualizations that are both attractive and informative.

Publication Analysis Using Web of Science and Scopus

This is an introduction to methods of assessing individual and organizational publication performance with emphasis on citation analysis. The class will demonstrate methods to explore how bibliographical data might be analyzed and retrieved using Web of Science and Scopus.