NIH NLM NCBI National Center for Biotechnology Information

We are happy to partner with
UTSouthwestern
Lydia Hill Department of Bioinformatics
Bioinformatics Core Facility
UNIVERSITY OF DALLAS Biology Department
Biological Sciences & Mathematical Sciences
THE UNIVERSITY OF TEXAS AT DALLAS Departments

NCBI North Texas Workshops

May 11, 12, 13 & 14, 2021

Tuesday, May 11 – 9am-12noon CT

NCBI Resources for Genetic Disease Discovery and Clinical Support

The use of genetic testing in patient care is becoming more common in clinical practice. NCBI has long had resources for biologists to explore what is known about genomes, genes and genetic variations, but has recently developed clinically-focused resources. This module is designed for those involved in clinical practice and/or translational research.

Based on a real-world case study, you will learn how to:

- Find a MedGen record with links to various clinical decision support resources and those which could assist with patient education
- Identify a relevant diagnostic genetic test and examine sample test results
- Based an identified genetic variant, explore the affected gene and gene product with regard to structure and function
- Explain the patient's disease etiology and effectiveness of therapeutic interventions

This module ends with a session where you will be given your own case study to solve.

Register here: http://bit.ly/NorthTexas_GeneticDiseaseDiscoveryRegistration

Wednesday, May 12 – 9am-12noon CT

NCBI Resources for Human Genome Research

This workshop is for those involved in human genome research. It focuses on finding and retrieving genome assemblies and annotation, identifying the best NCBI database for different data types, and visualizing both NCBI and external data in our Genome Data Viewer. Although web-based, this workshop touches on other methods for data retrieval and analysis.

In this workshop you will learn how to:

- Find, view and download genomic sequence and annotation data.
- Differentiate between RefSeq and GenBank records.
- Identify gene-specific information, including orthologs, expression, and genetic variation.
- Visualize both NCBI and external data in our Genome Data Viewer.

Register here: http://bit.ly/NorthTexas_HumanGenomeResourcesRegistration

FOR INVITING US AND WORKING WITH US ON THIS EVENT, WE'D LIKE TO THANK:

University of Texas Southwest Medical Center:
Brandi Cantarel PhD, Venkat Malladi MS & Rebekah Craig MPH

University of Dallas: Inimary Toby PhD

University of Texas at Dallas:
Zhenyu Xuan PhD & Pankaj Choudhary PhD

For questions about any of the workshops or the codeathon,

please contact a partner at your institution

or send an Email to workshops@ncbi.nlm.nih.gov

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Due to their technical nature, the enrollment for each of these two workshops is limited to 50. If you are interested in applying, please fill out the form(s) linked below. We will let you know about your status by May 3rd.

Thursday, May 13 – 9am-12noon CT

Getting Started with NCBI Data in Python

Learn how to tackle bigger biomolecular datasets more reliably with the power of Python programming. This workshop is designed for biologists without programming experience. Our examples will use genomic, transcript, and protein sequence data, but the programming skills will be broadly relevant for all biologists.

In this workshop you will learn how to:

- Use Python programming to download, analyze, and visualize data.
- Use Jupyter to create data analysis 'lab notebooks' that make it easy to reproduce & share your work.
- Find data that is relevant to your project using the new NCBI Datasets resource. Explore metadata to learn about which datasets are available.
- Download sequence data with NCBI Datasets and manipulate it with the BioPython package.

Apply here: http://bit.ly/NorthTexas_NCBIDataandPythonApplication

Friday, May 14 – 9am-12noon CT

An Introduction to NCBI Cloud Computing for Biologists

As DNA sequencing becomes a commonplace tool in biological research, the need for accessible, scalable, and secure computational environments to process this deluge of data is growing. NCBI has partnered with leading cloud computing providers to provide tools and data to this growing industry. This workshop is designed for experimental biologists without cloud computing experience. While not required, it is most useful for researchers who do sequence-based research and who have some familiarity interacting with a Linux command-line.

In this workshop you will learn how to:

- Navigate the AWS cloud console page and understand how to access and use some popular console-based tools.
- Access and mine metadata for information in the NCBI SRA database to select an interesting dataset for further study using the AWS Athena service.
- Retrieve SRA sequence data and perform a sequence alignment analysis using the containerized NCBI tool MagicBLAST.
- Visualize the aligned data against the wealth of information in NCBI databases by uploading it to the NCBI Genome Data Viewer browser application.

Apply here: http://bit.ly/NorthTexas_NCBIDatainCloudApplication