Online NCBI Bioinformatics Workshops
Sept. 22nd, 23rd, 29th and 30th

The Maine INBRE Bioinformatics Core and Maine Genomics Research Collaborative is co-hosting a series of these four online NCBI Workshops:
1. An Update on NCBI BLAST and Other Sequence Analysis Tools – Tues., Sept. 22nd from 2-5pm.
2. NCBI Resources for Animal and Plant Genomics Research – Wed., Sept. 23rd from 2-5pm.
3. NCBI Resources for Pathogen (Bacteria & Virus) Genomics Research – Tues., Sept. 29th from 2-5pm.
4. NCBI Resources for Gene Expression and Genetic Variation Research – Tues., Sept. 30th from 2-5pm.

These workshops will be given by NCBI Staff who include Drs. Wayne Madden, Peter Cooper, and Rena Morris.

You may register for any or all of the free workshops. Links to register for each of the workshops are listed in the workshop descriptions below. These workshops are jointly hosted by Maine INBRE and Colorado State University.

If you have any questions, please contact Benjamin King (benjamin.l.king@maine.edu) at the University of Maine.

AN UPDATE ON NCBI BLAST AND OTHER SEQUENCE ANALYSIS TOOLS
DATE: Tuesday, September 22, 2020
TIME: 2pm to 5pm
REGISTRATION LINK: https://attendee.gotowebinar.com/register/3795363914158734095
(After registering, you will receive a confirmation email containing information about joining the workshop.)

This workshop highlights new displays and features and introduces best practices for use of NCBI BLAST services. You will learn when and how to use important but often misunderstood aspects of the BLAST programs, specialized services, and databases. You will explore other important sequence analysis services, including Primer BLAST, an oligonucleotide primer designer and specificity checker, and COBALT, a multiple protein sequence alignment tool. Finally, you will see brief demonstrations of standalone BLAST and related tools, including SRA-Toolkit BLAST and Magic-BLAST.

Specifically, you will learn to:
- Select the correct NCBI alignment tool for your task
- Choose the best BLAST database for your search goal
- Understand and use the new BLAST results page, output formats and statistics
- Display BLAST results in genomic context using graphical displays

- Analyze nucleotide primers: design, check the specificity, and display primer alignments
- Assess the taxonomic distribution of your BLAST matches and use the TreeViewer display to visualize relationships
- Use standalone BLAST, Magic-BLAST and SRA-BLAST to search local databases and remote database on the NCBI server

NCBI RESOURCES FOR ANIMAL AND PLANT GENOMICS RESEARCH
DATE: Wednesday, September 23, 2020
TIME: 2pm-5pm
REGISTRATION LINK: https://attendee.gotowebinar.com/register/669748125019533583
(After registering, you will receive a confirmation email containing information about joining the workshop.)

This workshop focuses on NCBI's web-based resources for accessing and analyzing genome assemblies and annotation data, with an emphasis on non-human organisms. You will learn which databases at NCBI best meet your needs, including Genome, Assembly, BioProject, Taxonomy, Gene, and SRA. We will also briefly discuss NCBI's analysis and stand-alone tools, such as the Genome Data Viewer (GDV), SRA Toolkit and Magic-BLAST.

In this workshop you will learn how to:
- Find, view and download the latest genome assembly data
- Access and download annotation data for genes, transcripts and proteins
- Find gene-specific information, including genomic context, orthologs and literature
- Use GDV to visualize both NCBI and external data (Track Hubs or your own data)

NCBI RESOURCES FOR PATHOGEN (BACTERIA & VIRUS) GENOMICS RESEARCH
DATE: Tuesday, September 29, 2020
TIME: 2pm-5pm
REGISTRATION LINK: https://attendee.gotowebinar.com/register/4688857849215238159
(After registering, you will receive a confirmation email containing information about joining the workshop.)

In this workshop, you will learn to use NCBI resources to search, access, and analyze animal and plant pathogen (bacteria and virus) data from individual isolates and metagenomes. You will explore some general resources for all organisms, as well as some newly developed resources for bacteria and viruses. In addition, you will briefly see how to access and analyze data using standalone tools, such as the SRA Toolkit and Magic-BLAST.

Specifically, you will learn to:
- Find, browse, and download genome-, gene-, protein- and sequence read-level data for individual bacterial and viral pathogens and metagenomes
- Access and display precomputed genome analyses and perform your own analyses of assembled and unassembled genomic data to identify organisms and genes
- Find sequences, variants, antibiotic resistance genes using BLAST services, including SRA-BLAST
- Explore the new and developing NCBI Virus and Pathogen Detection Project resources

NCBI RESOURCES FOR GENE EXPRESSION AND GENETIC VARIATION RESEARCH
DATE: Wednesday, September 30, 2020
TIME: 2pm-5pm
REGISTRATION LINK: https://attendee.gotowebinar.com/register/5495016476165741839
(After registering, you will receive a confirmation email containing information about joining the workshop.)

This workshop focuses on NCBI's web-based resources for accessing gene expression and genetic variation data for non-human organisms. You will learn about NCBI's gene expression databases, including Gene, GEO, and SRA. You will learn how you can leverage SRA data for your gene expression and genetic variation analyses. We will also briefly discuss NCBI's analysis and stand-alone tools, such as GEO2R, the Genome Data Viewer (GDV), SRA Toolkit and Magic-BLAST.

In this workshop you will learn how to:
• Find gene-specific expression data in Gene and GEO databases
• Find and explore experimental study information in the GEO database
• Access and analyze SRA data
• Use GDV as a variant analysis tool