CRI SEMINAR
Bioinformatics Workshop Series:
Bioinformatics Bulk RNA-seq Pipeline Hands-on Training Workshop
Speaker: Qiaoshan Lin, PhD
Tuesday, February 25th 1:00pm – 3:00pm CST.
Donnelley (BSLC) Meeting Room #313
REGISTER HERE: **https://mycri.cri.uchicago.edu/educations/trainings/75/register/**

Bioinformatics workshop learning series, hosted by CRI, bioinformatics core. This hands-on training workshop will guide you through the CRI Bioinformatics Core's bulk RNA-seq analysis pipeline, focusing on both the implementation of nextflow for RNA-seq data analysis and performing differential expression analysis using our developed pipeline. Whether you are just getting started or want to refine your skills, this session will provide practical insights and workflows for working with bulk RNA-seq data.

Pre-requisite:
- Familiarity with the basic shell commands in Linux, shell scripts, and R.
- Randi Access: if you don't have access to Randi (the CRI's computing cluster), please request it during registration to ensure you're set up to work with the tools during the workshop.

Learning Objectives:
- 1. Introduction to Bioinformatics Core's bulk RNA-seq analysis pipeline;
- 2. Hands-on training for nextflow implementation for bulk RNA-seq analysis starting from raw sequencing data;
- 3. Hands on training for downstream DE analysis with our developed pipeline.

This seminar will take place at Donnelley (BSLC) meeting room #313. 924 E 57th, Chicago, IL. also, via Zoom. Registration is required for all attendees, whether you plan to attend in person or via Zoom. Registration closes at 12pm on Monday, February 24th. Zoom details will be emailed to registrants one day before the session. Please note that due to limited capacity, registration may close early if capacity is reached. Participation is open to University of Chicago, UCM, and Pritzker School of Medicine faculty, staff, and students.

About the speaker: Dr. Qiaoshan Lin is a bioinformatician, she received her Ph.D. in Ecology and Evolutionary Biology from the University of Connecticut. Prior to joining the CRI Bioinformatics Core in 2022, she studied developmental genetics in Monkeyflowers combining wet and dry approaches. Her bioinformatics experience includes de novo genome assembly, genome annotation, comparative genomics, variant analysis, and workflow development. She is also skilled in RNAseq and small RNAseq data analysis.

About the series: Since 2012, the Center for Research Informatics has offered free training sessions for the University of Chicago community in informatics research tools and techniques. Topics include REDCap, clinical data, bioinformatics analysis, data visualization, high performance computing, grant preparation, and more. To hear about upcoming seminars, sign up for our email list at http://cri.uchicago.edu/seminar-series

Questions? Contact Janaya Lee at janayalee@bsd.uchicago.edu