

Quick Introduction and Introduction to the UC Davis Bioinformatics Core

The **mission** of the Bioinformatics Core facility is to facilitate outstanding omics- scale research through these activities:

Data Analysis

The Bioinformatics Core promotes experimental design, advanced computation and informatics analysis of 'omics' scale datasets that drives research forward.

Research Computing

Maintain and make available high-performance computing hardware and software necessary for todays data-intensive bioinformatic analyses.

Training

The Core helps to educate the next generation of bioinformaticians through highly acclaimed training workshops, seminars and through direct participation in research activities.

UC Davis Bioinformatics Core in the Genome Center

Core Facility Manager

Dr. Matthew Settles

Faculty Advisor

Dr. Ian Korf

Data Analysis Group

Genomics Bioinformatics

Dr. Joseph Fass
Dr. Monica Britton
Nikhil Joshi

Proteomics Bioinformatics

Metabolomics Bioinformatics

Dr. Jessie Li

Biostatistics

Dr. Blythe Durbin-Johnson

Undergraduate Assistants

Research Computing Group

System Administration

Michael Casper Lewis
Richard Feltstykke

Database/Web Programming

Adam Schaal

Undergraduate Assistant

Contacts

- Website: <http://bioinformatics.ucdavis.edu/>
- Computing Issues, including but not limited to
User account questions, equipment failure/malfunction, software install,
software failures (not related to use)
helpdesk@genomecenter.ucdavis.edu
- Bioinformatics related questions, including but not limited to
bioinformatic methods questions, software use, data questions
Bioinformatics.core@ucdavis.edu
- Mailing lists: <http://bioinformatics.ucdavis.edu/contact-us/>

Goals

- End to End understanding of variant analysis
- Experimental design
 - Cost estimation
 - Technologies
 - workflow
- To work through a complete experiment, starting from raw data to completion, including making a few figures.
- Additional topics are discussed (GWAS, Genome Assembly, etc.) to better understand related topics.
- Goal is 30-40% lecture/discussion 60-70% hands-on

Workshop Info

- Internet
 - If your home institution is on eduroam, you should be on already
 - <http://itcatalog.ucdavis.edu/service/eduroam>
 - UCD Guest Wireless
 - <http://itcatalog.ucdavis.edu/service/wireless-guest-access>
- Schedule is loose, we will try and have short breaks often, lunch is ~12-1pm

Workshop Info

- Workshop materials posted on github
 - <https://ucdavis-bioinformatics-training.github.io/2017-August-Variant-Analysis-Workshop/>
- Course will be conducted on our server and cluster
 - ganesh.genomecenter.ucdavis.edu
 - Cluster usage will be under a workshop reservation
- Everyone should have received username/password combo in their email this morning

Schedule

Monday August 21st

Introduction, followed by eclipse viewing

Morning Hands on: Intro to Command Line (Joe)

OR Morning Hands on: “Advanced” Command Line (Nik)

Afternoon Talk: “What is Bioinformatics?” (Matt)

Afternoon Hands on: Running Jobs on the Cluster (Nik)

Afternoon Talk: “Intro to Sequencing” (Matt)

Tuesday August 22nd

Morning Talk/Hands on: Files and File types for Genomes/Annotation [Fasta, fastq, gtf/gff, sam/bam, vcf] (Joe)

Morning Talk: “Experimental Design and Cost Estimation” (Matt)

Afternoon Talk/Hands On: quality check with fastqc, trimming for adapters (scythe), and ReadQScore (sickle) and (Monica)

Afternoon Talk: “Philosophy of Preprocessing” (Matt)

Schedule

Wednesday August 23rd

Morning Talk/Hands on: Alignment (Joe)

Morning Talk: “Genome Assembly and Annotation” (Matt)

Afternoon Talk/Hands on: Talkercise: Variant Discovery Including GATK and Freebayes (Nik)

Thursday August 24th

Morning Talk/Hands on: Variant effect annotation: snpEffect (Monica)

Morning Talk/Hands On: Filtering SNPs (Nik)

Afternoon Talk/Hands On: SNP/CNV (Nik)

Afternoon Talk: “GWAS” Analysis (Matt)

Friday August 25th

Morning Hands on: Intro to R (Blythe)

Morning Talk: “Advanced Sequencing and Wet Lab Topics Related to Variation” (Lutz)

Afternoon Hands on: Exercises: Variants with R (Matt)

Closing