

# 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](mailto:helpdesk@genomecenter.ucdavis.edu)
- Bioinformatics related questions, including but not limited to  
bioinformatic methods questions, software use, data questions  
[Bioinformatics.core@ucdavis.edu](mailto: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/Diana)

## 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: 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: Variants with R (Matt)**

**Closing**