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:

<table>
<thead>
<tr>
<th>Data Analysis</th>
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<td>The Bioinformatics Core promotes experimental design, advanced computation and informatics analysis of ‘omics’ scale datasets that drives research forward.</td>
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<th>Research Computing</th>
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<td>Maintain and make available high-performance computing hardware and software necessary for todays data-intensive bioinformatic analyses.</td>
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<th>Training</th>
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<td>The Core helps to educate the next generation of bioinformaticians through highly acclaimed training workshops, seminars and through direct participation in research activities.</td>
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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 Feltstykker
- 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/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