Computational Genomics

An Advanced level Immersion Course for Investigators at UAB

May 15th-18th, 2017 from 8:30-12:30pm

$50- Faculty, $25-Post Doc and Fellows, $10 –Students/Staff
Continental Breakfast served daily

Location: Finley Conference Center
720 20th St. S, Birmingham, AL 35233

Register Here

This course will provide the end user with a better knowledge of how to analyze their Genomics data using various Linux (command line) based analytical tools. Hands-on activities include analyzing whole genome for causal variants, transcriptome for gene expression, and epigenetics for calling peaks in ChIP/ATAC-Seq.

Learning Objectives:

1. Learn how to use Linux/Unix command line tools to analyze Next Generation Sequencing (NGS) data (whole genome/exome, transcriptome, epigenome).
2. Identify causal variants from whole genome/exome NGS data using Broad's Genome Analysis Toolkit (GATK) Best Practices guidelines.
3. Identify significant genes being regulated in transcriptome studies.
4. Call and annotate peaks from ChIP-Seq and ATAC-Seq studies.

Heflin Center for Genomic Sciences   CCTS

Schedule:

	Monday, May 15*	Tuesday, May 16	Wednesday, May 17	Thursday, May 18
8:30-9:00	Breakfast	Breakfast	Breakfast	Breakfast
9:00-10:00	Overview **Dr. Bruce Korf** **9:00-9:15**	Whole Genome Sequencing: Aligning Raw Reads **Dr. David Crossman**	Whole Genome Sequencing: Identifying causal variants using various databases **Dr. David Crossman**	Transcriptome: Pathway Analysis of Significant Genes **Dr. David Crossman**
10:15-11:15	Introduction to UNIX/LINUX and Virtual Machine for Data Analysis **Dr. David Crossman** **9:15-10:45**	Whole Genome Sequencing: Preparing aligned reads with GATK **Dr. David Crossman**	Transcriptome: Aligning Raw Reads **Dr. David Crossman**	Epigenetics: Aligning Raw Reads for ChIP/ATAC-Seq **Dr. David Crossman**
11:30-12:30	Accessing and Submitting Jobs on UAB's Compute Cluster, Cheaha **Dr. David Crossman** **11:00-12:30**	Whole Genome Sequencing: Calling Variants with GATK **Dr. David Crossman**	Transcriptome: Estimating transcript abundances and differential expression **Dr. David Crossman**	Epigenetics: Calling/Annotating ChIP/ATAC-Seq peaks **Dr. David Crossman**

*Please note the change in timings

For further information please contact Shaila Handattu at hande@uab.edu