Computational Genomics
An Advanced level Immersion Course for Investigators at UAB

May 6th-9th, 2019 from 9:00-12:30pm

$50 - Faculty, $25 - Post Doc and Fellows, $10 - Students/Staff

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

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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.
# Schedule:

<table>
<thead>
<tr>
<th>Time</th>
<th>Monday, May 6</th>
<th>Tuesday, May 7</th>
<th>Wednesday, May 8</th>
<th>Thursday, May 9</th>
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<tr>
<td>9:00 – 10:00</td>
<td>Introduction to UNIX/LINUX and Virtual Machine for Data Analysis&lt;br&gt;Dr. David Crossman&lt;br&gt;9:00-10:45</td>
<td>Whole Genome Sequencing: Aligning Raw Reads&lt;br&gt;Dr. David Crossman</td>
<td>Whole Genome Sequencing: Identifying causal variants using various databases&lt;br&gt;Dr. David Crossman</td>
<td>Transcriptome: Pathway Analysis of Significant Genes&lt;br&gt;Dr. David Crossman</td>
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<td>10:15 – 11:15</td>
<td>Accessing and Submitting Jobs on UAB’s Compute Cluster, Cheaha&lt;br&gt;Dr. David Crossman</td>
<td>Whole Genome Sequencing: Preparing aligned reads with GATK&lt;br&gt;Dr. David Crossman</td>
<td>Transcriptome: Aligning Raw Reads&lt;br&gt;Dr. David Crossman</td>
<td>Epigenetics: Aligning Raw Reads for ChIP/ATAC-Seq&lt;br&gt;Dr. David Crossman</td>
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<td>11:30 – 12:30</td>
<td>Dr. David Crossman&lt;br&gt;11:00-12:30</td>
<td>Whole Genome Sequencing: Calling Variants with GATK&lt;br&gt;Dr. David Crossman</td>
<td>Transcriptome: Estimating transcript abundances and differential expression&lt;br&gt;Dr. David Crossman</td>
<td>Epigenetics: Calling/Annotating ChIP/ATAC-Seq peaks&lt;br&gt;Dr. David Crossman</td>
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For further information please contact Shaila Handattu at hande@uab.edu.