

Clinical and Research Genomics Assignment #3

From Lecture_07-09 (April 5th): Epigenomes, DNA Modifications, and Chromatin Dynamics

Assignment: Analyze and contextualize data pertaining to chromatin dynamics and epigenetics.

Due Date: 10:00AM April 12th

Epigenome and DNA Modifications

Analyze and Contextualize DNA Methylation data from a RRBS experiment

If you do not already have it installed, install the free statistical program R on your computer:

<http://www.r-project.org/>

You can use the slides on this blog to understand the algorithms that we have discussed in class:

<http://zvfak.blogspot.com/2013/03/epiworkshop-2013-dna-methylation.html>

If you have trouble getting the package for R from the tutorial, you can download it here:

<http://code.google.com/p/methylkit/>

Utilize the tutorial to familiarize yourself with R and the program.

Then, from the test dataset within the package, your assignment is to:

1. Check if there is an indication of PCR bias in the experiment.
 2. Calculate # of differentially methylated cytosines (DMCs)
 3. Annotate the DMCs with genes and discuss implications of that annotation.
 4. Check correlation between samples.
 5. Cluster samples to see if replicates cluster together
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Please hand the assignment on the day of the lecture, or email if you cannot attend.

For any questions, please contact Alexa McIntyre (abm237@cornell.edu), Ebrahim Afshinnekoo (eba2001@med.cornell.edu), Priyanka Vijay (prv2004@med.cornell.edu), or Professors Mason (chm2042@med.cornell.edu), Elemento (ole2001@med.cornell.edu), Leslie (cleslie@cbio.mskcc.org), and Li (shl2018@med.cornell.edu)