Lab 7: Exploratory analysis of ChIP-seq data

This lab will repeat some tasks performed at previous lab. We will look at some ChIP-seq data and do simple joint analysis of ChIP- and RNA-seq data.

Data used in this lab can be obtained from the class website. The zip file contains two ChIP-seq datasets for Cmyc and Pol2 binding, and one RNA-seq data. All data are for K562 cell line. We will show that (1) Cmyc and Pol2 bindings are highly correlated, that is, both proteins tend to bind at similar location, and (2) gene expression is correlated with Cmyc and Pol2 bindings. Follow the R script on the website to perform the analyses.

Note that because most of the popular peak calling software run on command line and the installation of those software could be tricky, so we will skip the peak calling practice. If you have software (MACS, CisGenome, etc.) installed and would like to practice peak calling, please consult the instructor for datasets.