How I selected chr19 from bigwig files

1. Log in to cn45 > navigate to ctoenhake@cn45:/scratch/ctoenhake/data/fg1\_r\_data/blueprint/chip\_bw
2. Download bigwig files from blueprint data portal using wget.
   * <http://dcc.blueprint-epigenome.eu/#/experiments/ERX547983>
   * Used datasets:
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547980.H3K27ac.bwa.GRCh38.20150528.bw
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547983.H3K27me3.bwa.GRCh38.20150528.bw
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547982.H3K9me3.bwa.GRCh38.20150528.bw
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547981.H3K4me1.bwa.GRCh38.20150528.bw
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547984.H3K4me3.bwa.GRCh38.20150528.bw
     + http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C00408/CD14-positive\_CD16-negative\_classical\_monocyte/DNase-Hypersensitivity/NCMLS/C004084E.ERX197157.Dnase.bwa.GRCh38.20150529.bw

wget http://ftp.ebi.ac.uk/pub/databases/blueprint/data/homo\_sapiens/GRCh38/venous\_blood/C000S5/CD14-positive\_CD16-negative\_classical\_monocyte/ChIP-Seq/NCMLS/C000S5H2.ERX547983.H3K27me3.bwa.GRCh38.20150528.bw

1. Download tools to convert bigwig to wig and wig back to bigwig
   * <http://hgdownload.soe.ucsc.edu/admin/exe/linux.x86_64/>
   * Create new directory for tools: /scratch/ctoenhake/tools.
   * Download tools with:

rsync -aP \ rsync://hgdownload.soe.ucsc.edu/genome/admin/exe/linux.x86\_64/bigWigToWig ./

rsync -aP \ rsync://hgdownload.soe.ucsc.edu/genome/admin/exe/linux.x86\_64/wigToBigWig ./

1. Write custom bash script that uses these tools to select chr19 from original .bw file, and convert resulting .wig file back to .bigwig:

ctoenhake@cn45:/scratch/ctoenhake/data/fg1\_r\_data/blueprint/chip\_bw$ cat select\_chr19.sh

#!/bin/bash

# use tools from UCSC to convert bigwig to wig and select chr19 along the way.

# and then convert chr19.wig to bigwig

# use: bash select\_chr19.sh input.bigwig output.bigwig

bwin=${1}

bwout=${2}

echo "Select chr19 and write wig for" ${bwin}

/scratch/ctoenhake/tools/bigWigToWig -chrom=chr19 ${bwin} ${bwin}.chr19.wig

echo "Convert back to bigwig and save as" ${bwout}

/scratch/ctoenhake/tools/wigToBigWig ${bwin}.chr19.wig hg38\_chr19.chromsizes ${bwout}

rm ${bwin}.chr19.wig

1. Use this script on all bigwig files
2. Copy resulting \*.chr19.bw to the web accessible directory that I also used for the trackhubs `/molbiol/mb03-sdb1/mbdata/ctoenhake/edu/fg1\_r\_data/blueprint/chip\_bw`
3. Download file from there to my mac with curl -O [filename] .
4. Upload these files to the learn.proto extdata/week3/
5. Continued in R to select specific window around the TSS of 40% of genes from chromosome 19, see code in prepdata.Rmd.