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Quant Bio

Week 6

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Command line functions

Install cooltools

conda create -n hic cooltools cooler matplotlib numpy bedtools ucsc-bigWigToBedGraph jupyter

conda activate hic

unzip downloaded files

command: tar xzf 3Dgenome\_encode.tar.gz

Adjust methanation score

Command: awk 'BEGIN{OFS="\t"}{$5=($3-$2)\*$4; print $1,$2,$3,$4,$5}' K562\_hg19\_H3K27me3\_chr3.bg > K562\_hg19\_H3K27me3\_chr3\_norm.bg

Divide the sum of the methylation score by the gene body

Command: awk 'BEGIN{OFS="\t"}{$7=$7 / ($3-$2); print $1,$2,$3,$4,$5,$6,$7}' K562\_hg19\_FPKM\_chr3\_map.bed > K562\_hg19\_FPKM\_chr3\_mapnorm.bed

Determine which genes are in which compartment, and their methylation level.

Command: bedtools map -a K562\_hg19\_FPKM\_chr3\_mapnorm.bed -b K562\_hg19\_H3K27me3\_chr3\_norm.bg -c 5 -F 0.5 -o sum > methyl\_comp