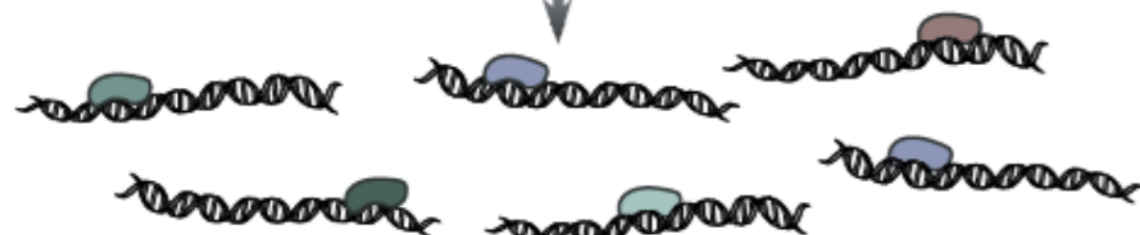# ChIPseq

BCMB bootcamp

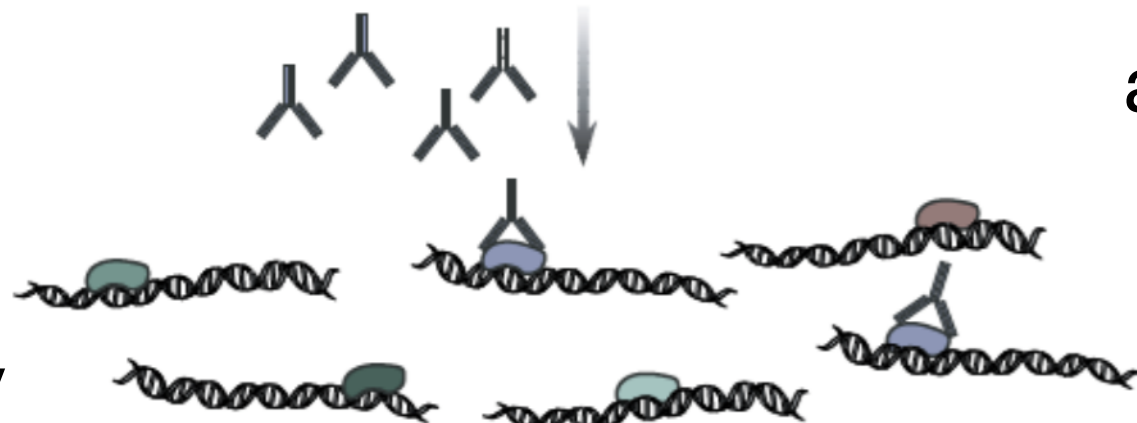# ChIPseq: querying proteins bound to DNA

- every cell in your body has the same DNA but different cell types vary drastically in phenotype

- this is due to epigenetic modifications of the DNA: methylation, bound proteins etc

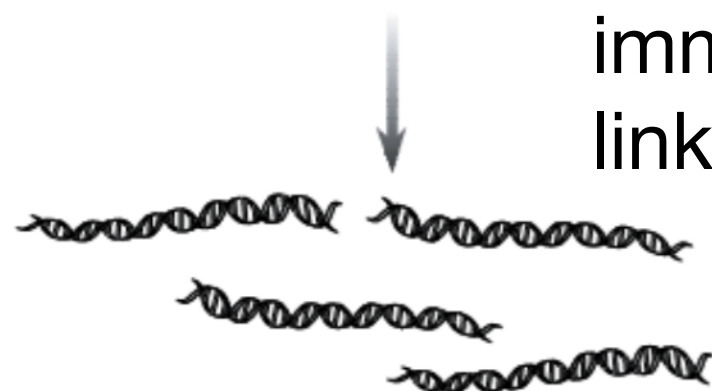- ChIPseq is a way to assess where a given protein is bound across the genome

cross link
sonicate or digest

add antibody

no antibody

immunoprecipitate, reverse cross
links, purify DNA

total input

enriched
sample

sequencing, alignment, peak calling

ChIPseq analysis workflow

- looking for peaks of piled-up reads that indicate a bound protein

- first need to align all the reads to the genome

- then run a peak caller like MACS2 to find peaks in the enriched sample that are not present in the input

- output of peak caller: BED file with coordinates of peaks

- look at reads (bam files) for total input and enriched samples, and peaks (bed file) in IGV (http://software.broadinstitute.org/software/igv/)

p13 | p12.3 | p12.2 | p12.1 | p11.23 | p11.21 | p11.1 | q11.1 | q11.21 | q11.22 | q11.23 | q12 | q13.11 | q13.13

17 kb

48,820 kb | 48,822 kb | 48,824 kb | 48,826 kb | 48,828 kb | 48,830 kb | 48,832 kb

S64_rep1.H3K27_sorted.bam Coverage [0 - 11]

S64_rep1.H3K27_sorted.bam

S64_rep1.input_sorted.bam Coverage [0 - 10.00]

S64_rep1.input_sorted.bam

PREX1

S64_H3K27_summits.bed

HUES64_H3K27_peak_693   HUES64_H3K27_peak_695