ChromHMM Report

Title: Determination of combination of histone marks that are characteristic of each of N different Epigenetic types (Manually assigning to each of the N epigenetic types a possible biological function).

Input Directory: Luperjoseph > ChromHMM

Output Directory: MYOUTPUT

Types of Cells Used: The following .bam files were used for the experiment

Number of States**:** 10

Assembly: hg18

- wgEncodeBroadHistoneHmecH3k09me3AlnRep1.bam
- wgEncodeBroadHistoneHmecH3k27acStdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k27me3StdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k36me3StdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k4me1StdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k4me2StdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k4me3StdAlnRep1.bam
- wgEncodeBroadHistoneHmecH3k79me2AlnRep1.bam
- wgEncodeBroadHistoneHmecH3k9acStdAlnRep1.bam
- wgEncodeBroadHistoneHmecH4k20me1StdAlnRep1.bam

**Control:** This control .bam file was used for all experiments

- wgEncodeBroadHistoneHmecControlStdAlnRep1.bam

**Chromosome Used:** Human genome (version hg19)

Algorithm (Softwares) Used:

- ChromHMM for annotaion
- UCSC GenomeBrowser
- Baum-Welsh algorithm
- ChromHMM with BinarizeBam option to convert ChIP-seq profiles (bam files) into a table of 1 and 0 to create bins of the lenght of 200 bp
- ChromHMM with LearnModel option to automatically detect parameters for N various genomic regions with the major histon marks and specific combinations

Results from ChromHMM
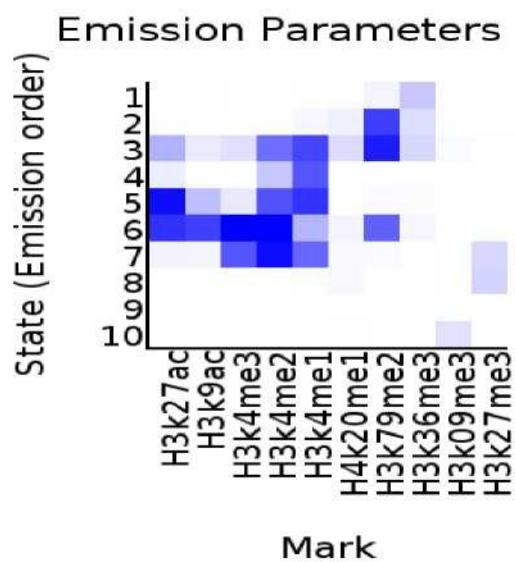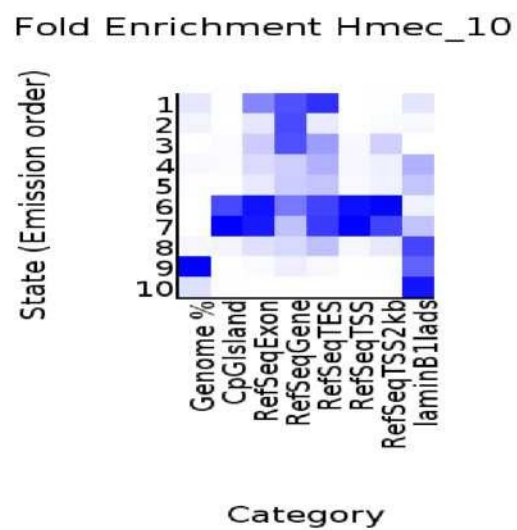
(a)   (b)

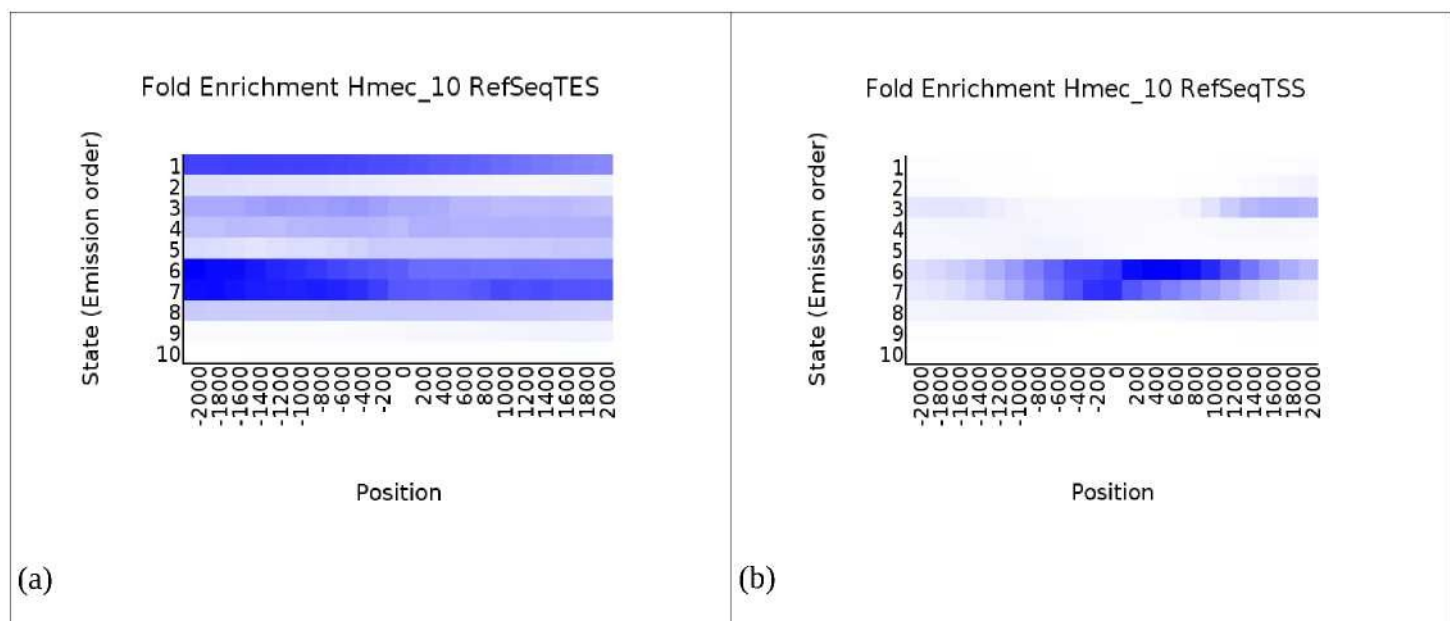Fig.1: (a) Shows emission parameters for Hmec_10 while (b) Shows Fold Enrichment for Hmec_10

Fig.2: (a) Shows fold enrichment Hmec_10 RefSeqTES while (b) Shows fold enrichment Hmec_10 RefSeqTSS
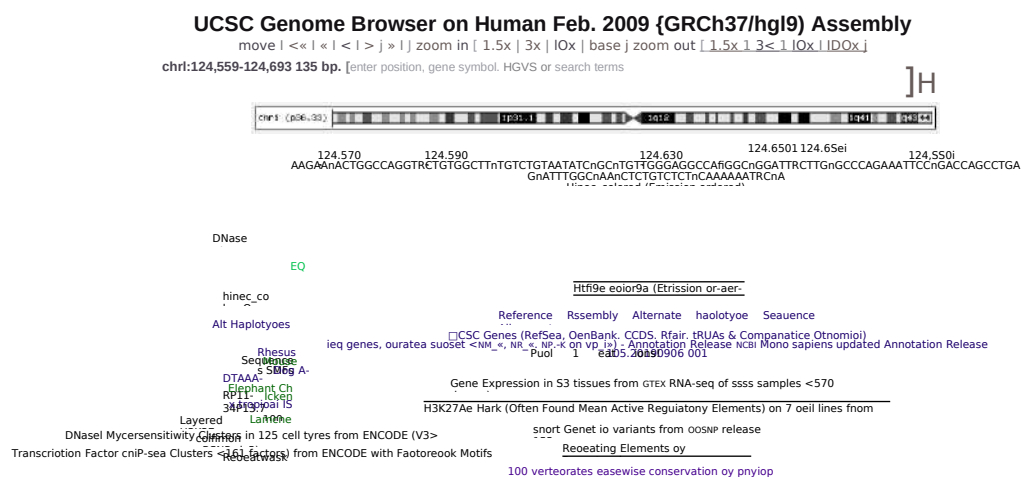
Fig.3: Shows the transition parameters

Table with the Epigenetic States, their Features and Names

Epigenetic State	Features	Name
State 1	Active promoter	H3k36me3
State 2	Weak promoter	H3k79me2
State 3	Inactive/poised promoter	H3k79me2, H3k4me1, H3k4me2
State 4	Strong enhancer	H3k4me1
State 5	Strong enhancer	H3k27ac, H3k4me2, H3k4me1
State 6	Weak/poised enhancer	H3k27ac, H3k9ac, H3k4me3, H3k4me2, H3k79me2
State 7	Weak/poised enhancer	H3k4me3, H3k4me2, H3k4me1
State 8	Insulator	H3k27me3
State 9	Transcriptional transition	-
State 10	Transcriptional enlongation	H3k09me3

Fig.4: Table with Epigenetic States, their Features and Names

Visualization in UCSC GenomeBrowser: Snapshots from UCSC GenomeBrowser with various genomic regions and epigenetic states

Link to my Sessions on Genome Browser:
- http://genome.ucsc.edu/s/Josephluper/Dense.bed%20ChromHMM
- http://genome.ucsc.edu/s/Josephluper/Expanded.bed%20ChromHMM

Fig.5: Shows genomic regions of ChromHMM dense.bed

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AAOAAnACTCOCCAGOTReTCTGCCTTnTOTCTGTAATATenCCnTGTTGOGAOGCCAfiOGCnCOnTTRCTTOnGCCCAGAAATTCCnCACCAOCCTGAOnATTTOGCnAAnCTCTOTCTCTnCAAAAAAT
RenA

-AAACTT--TTTTA-- -AAAOACAA

Fig.6: Shows genomic regions of ChromHMM expanded.bed

Visualization of Chromatin States from ChromHMM and corresponding Histone Marks Links
to panels with profiles of histone modifications using with epigenetic states

•   http://genome.ucsc.edu/s/Josephluper/Histone%20Marks%20in%20CromHMM%20expanded.bed

• http://genome.ucsc.edu/s/Josephluper/Histone%20Marks%20in%20CromHMM%20dense.bed

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List of Commands Used:
cd ChromHMM

• $ java -mx4000M -jar ChromHMM.jar BinarizeBam -b 200 CHROMSIZES/
hg19.txt chip_seq cellmarkfiletable.txt binarizedData

• $ java -mx4000M -jar ChromHMM.jar MakeBrowserFiles -c MYOUTPUT/Colors
MYOUTPUT/Hmec_10_segments.bed Hmec_colored Hmec_colored

• $ java -mx4000M -jar ChromHMM.jar MakeBrowserFiles -c MYOUTPUT/Colors
Hmec_10_segments.bed Hmec_colored Hmec_colored

• $ ln -s ~/bin/ChromHMM/ChromHMM.jar

• $ ln -s ~/bin/ChromHMM/CHROMSIZES

• $ cellmarkfiletable.txt