



Capstone 2: Adult and Disease Epigenetic Map

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Analysis Goals

- ► Uniform data processing, finalize QC
- Differential modification analysis between cell types and brain regions
- ► Role of cell type composition in epigenetic variation
- Genetic regulation of histone modification
 - ► integrate with GWAS and eQTL summary statistics
- ► Interpret the effect of non-coding variation



Number of Samples Per Study

Number of samples



Number of Samples Per Brain Region

Number of samples









ATACseq Statistics

Number of samples



Create a consensus peak for H3K4me3

Merge all the narrow peaks

Consensus Peaks



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Keep all the peaks where at least in one Study, 10% of individuals show significant coverage (cpm>1)















Genetics-only approach

histone QTL



Neural network functional prediction

histone QTL



Convolutional neural network (CNN) prediction



Neural network functional prediction



Functional scores from ATAC-seq





peak166976: 7:117,458,272-117,458,826



peak65926: 16:75,299,578-75,301,561



100

50

0.30 0.25 0.20 0.15 0.10 0.05 0.00

> A C G





____ loss _____ gain

GGATCGTGTGGTGGCCAGGGCGTCTGACCTTGGCTCTCACCCGGAGGCCATCCAGG

GTGGCCG

150