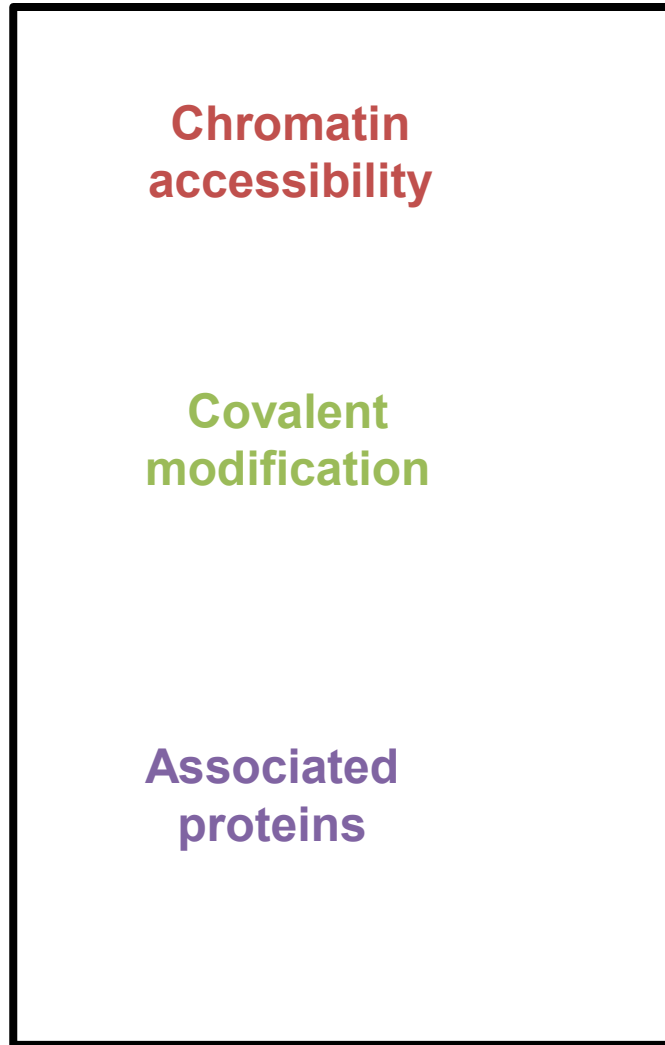


One genome



Many epigenomes

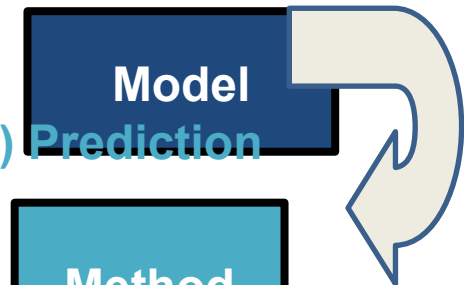


Machine learning

1) Learning



2) Prediction



One example: Segway

Accessibility

AACCGATT

DNase-seq
FAIRE-seq

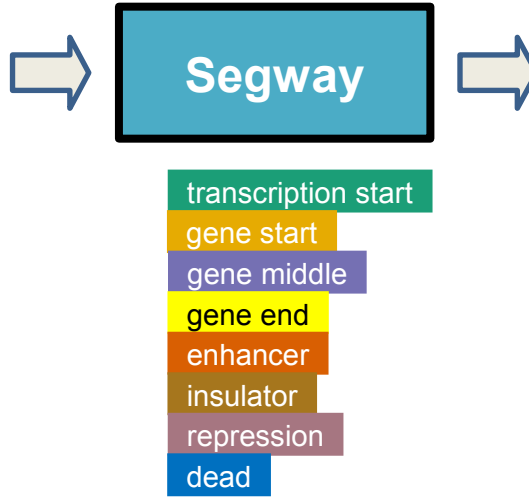
Associated proteins

AACCGATT

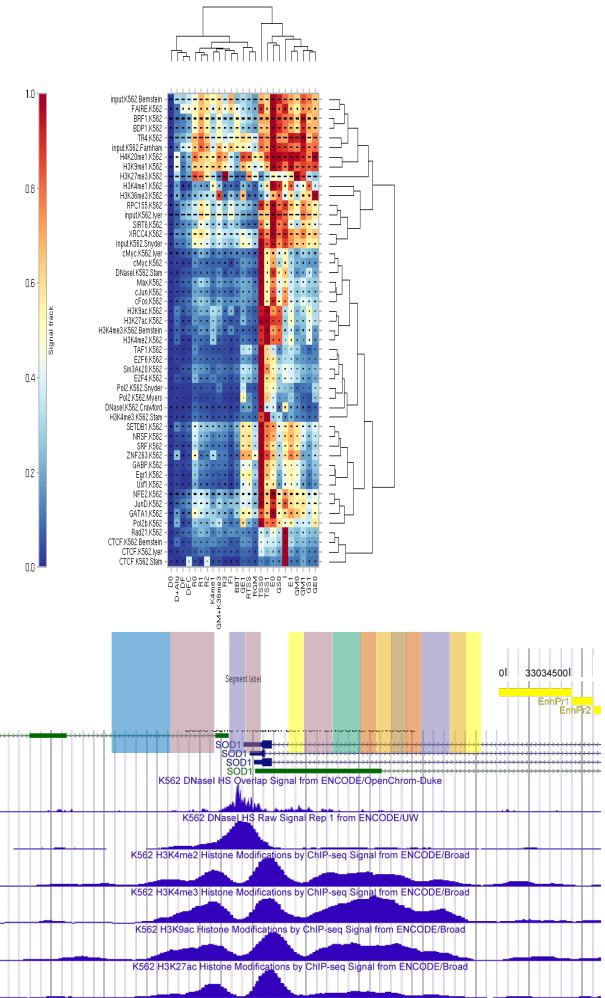
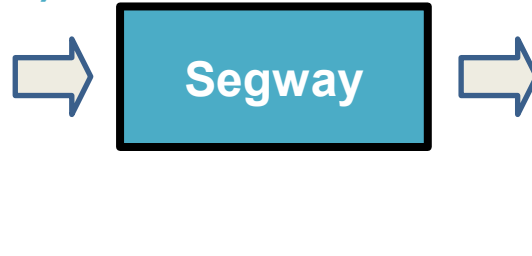
ChIP-seq

- histone modifications
- transcription factors

1) Learning



2) Prediction



Hoffman MM *et al.* 2012. *Nat Methods* 9:473.

Hoffman MM *et al.* 2013. *Nucleic Acids Res* 41:827.

Many examples: your science

Do you use any of the following kinds of functional genomics data?

Chromatin accessibility



DNase-seq
FAIRE-seq
ATAC-seq

Covalent modification



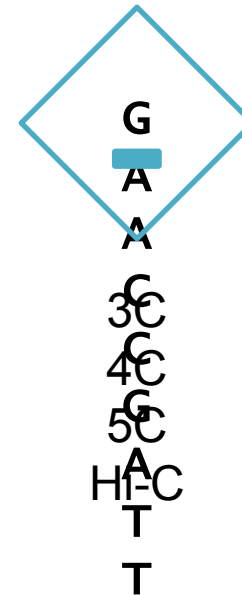
bisulfite seq
methyl-seq
oxBS-seq
redBS-seq

Associated proteins



ChIP-seq
ChIP-exo
PB-seq
DamID

3D conformation



Gene expression



RNA-seq
CAGE-seq
GRO-seq

Machine learning: our methods

We could work together.

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