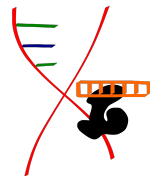


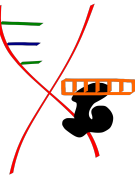
Deep Learning Techniques for the determination of cross-species structural gene expression

Andrew Gritsevskiy
Dr. Gil Alterovitz
Annual MIT PRIMES Conference
May 21, 2017



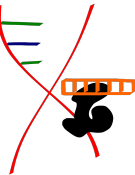
Background

- Next-generation sequencing



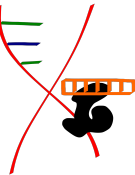
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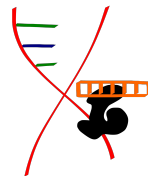
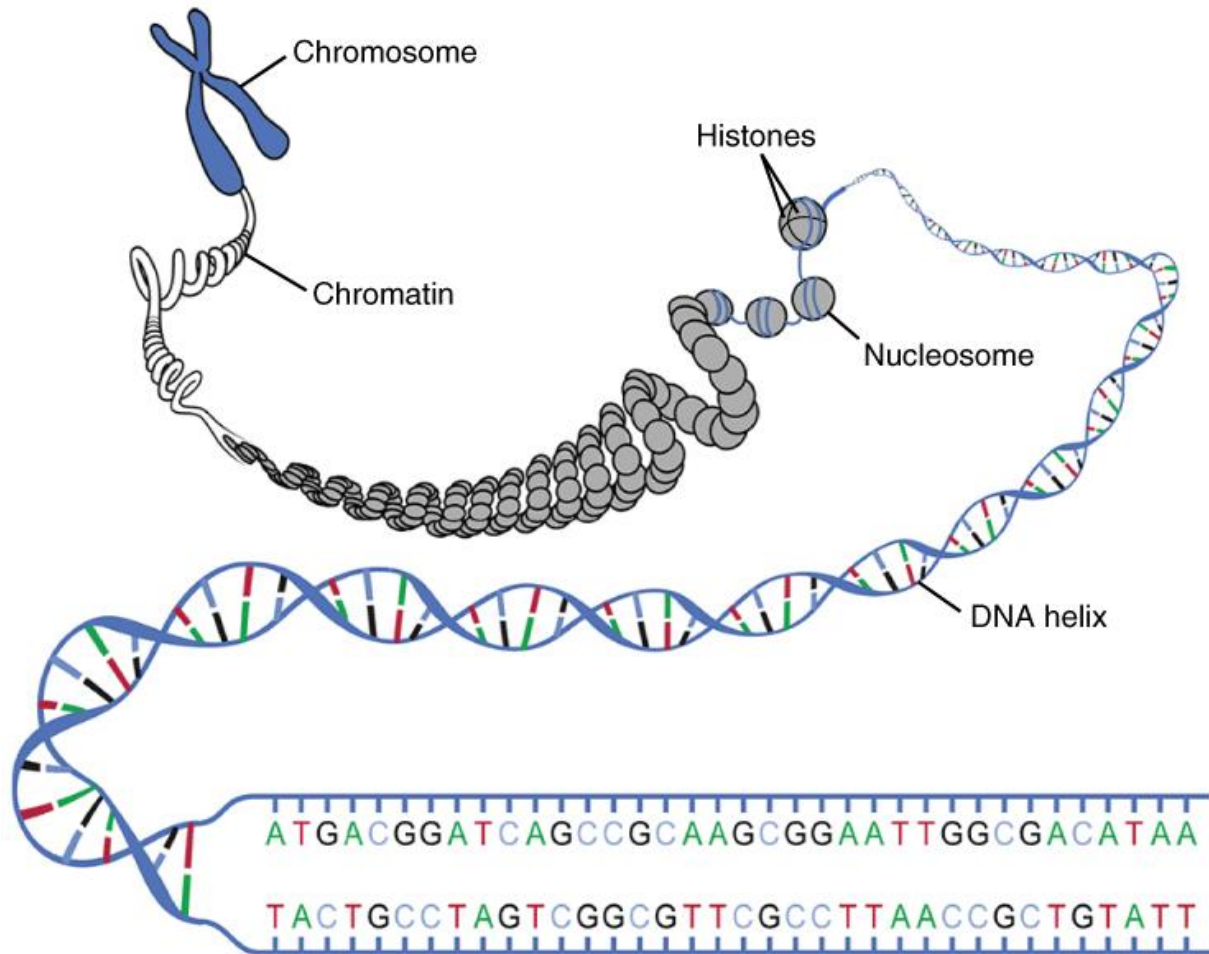
- Next-generation sequencing
 - 3D Structure



Background

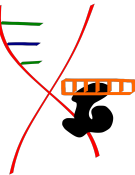
- Next-generation sequencing
 - 3D Structure
 - Methylation





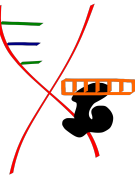
Background

- Next-generation sequencing
 - 3D Structure
 - Methylation
 - DNA modification



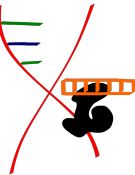
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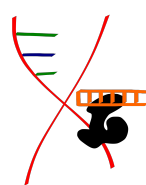
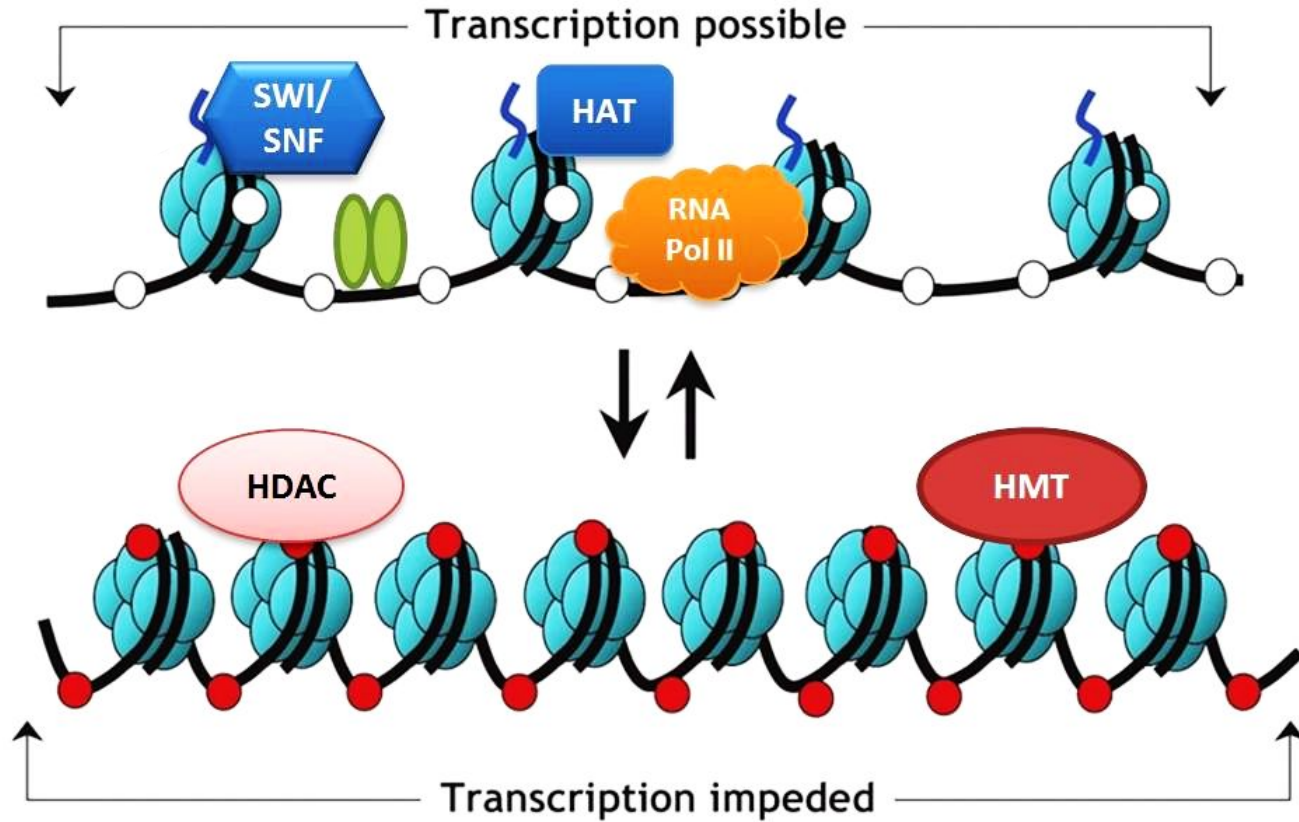
- Next-generation sequencing
 - 3D Structure
 - Methylation
 - DNA modification
 - Histone modification



Background

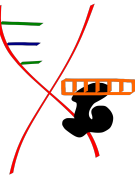
- Next-generation sequencing
 - 3D Structure
 - Methylation
 - DNA modification
 - Histone modification
 - Other epigenetic factors





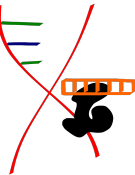
Background

- Next-generation sequencing
 - 3D Structure
 - Methylation
 - DNA modification
 - Histone modification
 - Other epigenetic factors



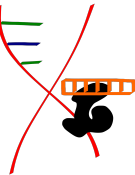
Motivation

- Relate structure to function



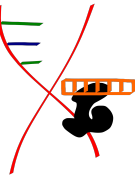
Motivation

- Relate structure to function
- Improve understanding of epigenetics



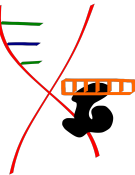
Motivation

- Relate structure to function
- Improve understanding of epigenetics
- Binding factors



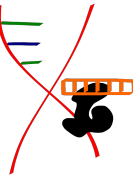
Motivation

- Relate structure to function
- Improve understanding of epigenetics
- Binding factors
- Applications of high-level methods to other fields



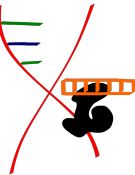
Methods

- Given two nearby structures in the genome, figure out how they interact



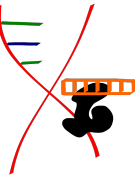
Methods

- Given two nearby structures in the genome, figure out how they interact
 - Convolutional neural network



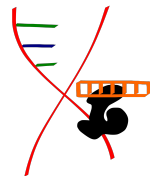
Methods

- Given two nearby structures in the genome, figure out how they interact
 - Convolutional neural network
 - AlexNet (Krizhevsky et al.)



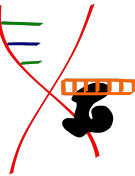
Methods

- Given two nearby structures in the genome, figure out how they interact
 - Convolutional neural network
 - AlexNet (Krizhevsky et al.)
 - Custom extensions (smaller pixel size, sparsity, wide first-layer convolutions)



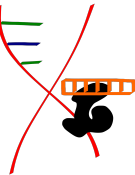
Methods

- Find out how genome structures affect gene expression



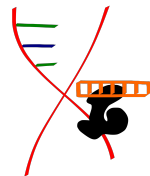
Methods

- Find out how genome structures affect gene expression
 - Convolutional neural network



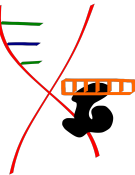
Methods

- Find out how genome structures affect gene expression
 - Convolutional neural network
 - One-shot learning



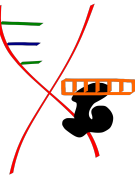
Methods

- See how the function of genomic structures varies across species



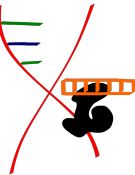
Methods

- See how the function of genomic structures varies across species
 - Currently only human and mouse available



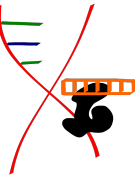
Results

- 3D genome interactions predicted with low probability



Future work

- Improve genome interaction modeling
- Find specific structural motifs related to gene expression
- Find the “common ancestors” of epigenetic structure



Acknowledgements

Many thanks to:

- Dr. Gil Alterovitz
- MIT PRIMES
- Everyone in Dr. Alterovitz's lab
- My parents

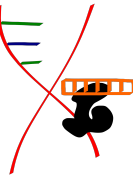


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