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
Background

- Next-generation sequencing
  - 3D Structure
Background

- Next-generation sequencing
  - 3D Structure
  - Methylation
On Structural Gene Expression
Background

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

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

- Next-generation sequencing
  - 3D Structure
  - Methylation
    - DNA modification
    - Histone modification
    - Other epigenetic factors
On Structural Gene Expression

Andrew Gritsevskiy (Mentor: Dr. Gil Alterovitz)
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
Image credits

DNA Macromolecule image: By OpenStax [CC BY 4.0 (http://creativecommons.org/licenses/by/4.0)], via Wikimedia Commons

Histone modification image: By Dyndna [CC BY 4.0 (http://creativecommons.org/licenses/by/3.0)], via Wikipedia