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~~10. Markov and Hidden Markov Models of Genomic and~~

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~~Protein Features Higher~~

~~order nucleosome structure~~

~~From Human~~
2019 STAT115 Lect14.1

Chromatin Interaction HiC

~~Prof. Daniel Panne:~~

~~Structural insights into~~

~~genome folding by CTCF and~~

~~cohesin~~ How DNA is Packaged

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Predicting High Order

(Advanced) *François Robert :*

\ "Transcription and

chromatin remodeler Chd1

join forces to convey FACT

to genes\ " The Connection

Between MTHFR and DNA Aging

Reprogramming the Human

Genome With Artificial

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Intelligence - Brendan Frey

- NIPS 2017 Genomic

Prediction of Complex Traits

~~MIT Deep Learning Genomics -~~

~~Lecture 10 - Epigenomics~~

~~3Dgenome (Spring20)~~

6.047/6.878 Lecture 1 -

Introduction (Fall 2020) Re-

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Chromatin Interactions
writing the Code of Life:

CRISPR Systems and

Applications of Gene Editing

~~How does DNA fold? The loop~~

~~extrusion model~~ i read the

books that 'predicted

coronavirus' so you don't

have to *Attention for time*

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series forecasting

COVID predictions - Isaac

Godfried **Chromatin, Histones**

and Modifications, Rate My

Science Multi Scale Modeling

of Chromatin and Nucleosomes

~~Nucleosome Assembly in~~

~~Eukaryotes Cardano ADA: What~~

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~~are analyst saying? Price
predictions/history Why~~

~~Medicine Needs Deep Learning~~

~~—Brendan Frey *Breaking Down
the 2020 Presidential*~~

~~*Election By the Margins* Gene~~

~~Function Prediction~~

~~*Epigenetic Epidemiology*~~

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Short Course - Pre-course

*Lecture 1: What Is
Epigenetics?* Toshio

Tsukiyama seminar:

"Regulation of Quiescence
through Chromatin"

~~Nucleosome Remodeling~~

Chromatin structure :

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Nucleosome 2020 STAT115

Lect17.1 Module II Review

Gene Regulation and the Order of the Operon

7. ChIP-seq Analysis; DNA-
protein Interactions

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Chromatin Interactions

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Predicting High-order
Chromatin Interactions from
Human Genomic Sequence using

Deep Neural Networks. Rui
Peng Sunday 3rdDecember,
2017. Background.

Understanding and modeling
high-order chromatin

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organization is a fundamental problem in computational genomics.

Chromosome fold into complex shapes by itself mostly by following rules written in the genomic sequence.

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Predicting High-order

Chromatin Interactions from Human ...

Chromatin interactions play important roles in regulating gene expression. However, the availability of genome-wide chromatin

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interaction data is very limited. Various

computational methods have been developed to predict chromatin interactions. Most of these methods rely on large collections of ChIP-Seq/RNA-Seq/DNase-Seq

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Chromatin Interactions
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datasets and predict only
enhancer-promoter
interactions.

*Predicting chromatin
interactions between open
chromatin ...*

Maximum entropy model

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Chromatin Interactions

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predicts higher-order interactions . Higher-order interactions involving more than two chromatin components have not been well studied except for a few examples , . This limits a systematic evaluation of

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Chromatin Interactions

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these higher-order
predictions, although our
finding that third order
interactions improved
maximum entropy model
coherence score performance
likely indicates third order
interactions well captured

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Chromatin factor cross-talk
represented in the data.

*Global Quantitative Modeling
of Chromatin Factor
Interactions*

three-dimensional genome
organization and high-order

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Chromatin interactions of functional elements remain an under-explored area for deep learning models. To approach this, we develop, to the best of our knowledge, the first deep learning architecture for

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Chromatin EPIs using only
sequence-based features,

*Predicting enhancer-promoter
interaction from genomic ...*

Maximum entropy model
predicts higher-order
interactions. Higher-order

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Chromatin Interactions involving more than two chromatin components have not been well studied except for a few examples , . This limits a systematic evaluation of these higher-order predictions, although our

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finding that third order
interactions improved
maximum entropy model
coherence score performance
likely indicates third order
interactions well captured
chromatin factor cross-talk
represented in the data.

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Predicting High Order Chromatin Interactions

*Global Quantitative Modeling
of Chromatin Factor*

Interactions

features from the genome
sequence and can capture non-
linear dependencies in the
sequence to predict speci?c

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Chromatin Interactions [27].

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functional annotations [27].
However, three-dimensional
genome organization and high-
order chromatin interaction
of functional elements
remain an unexplored area
for deep learning models.

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*Chromatin Enhancer-Promoter
Interaction from Genomic ...*

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As mentioned above, the process of predicting a 3D genomic organization from HR-3C data is known as the 3D-GRP . It should be noted that the 3D-GRP has also

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been referred to as the 3D chromatin structure modeling problem and that these two phrases can be used interchangeably. More formally, the 3D-GRP can be formulated as an optimization ...

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Predicting High Order Chromatin Interactions

Computational methods for predicting 3D genomic ...

The model can also serve as an inference engine for predicting unknown chromatin ... that is capable of capturing higher-order

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Chromatin Interactions

interactions through group
L1-regularization-based ...

*Global Quantitative Modeling
of Chromatin Factor
Interactions*

A recent paper, released as

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preprint in biorxiv, has explored long-range interaction patterns and identified TAD cliques that can predict key features of chromatin organisation. TAD Spatial organisation and packaging of the genome is

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Chromatin Interactions
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vital for gene expression
regulation and can often be
altered in disease.

*TAD cliques predict
chromatin organisation
features*

Recent high-throughput

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Chromatin Interactions From Human
mapping methods such as Hi-C
(Lieberman-Aiden et al.,
2009; Rao et al., 2014) and
ChIA-PET (Fullwood and Ruan,
2009; Tang et al., 2015)
have revealed that higher
order genome organizations
harbor more complex global

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Chromatin interactions than we previously thought. One of the most intriguing examples involves the ...

Predicting CTCF-mediated chromatin loops using CTCF-MP ...

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The predicted interactions are consistent with the experimental long-read ChIA-PET interactions mediated by CTCF and RNAPOL2 for GM12878 cell line. The contribution of sequence information and chromatin state defined by

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epigenomic features to the prediction task is analyzed and reported, when using them separately and combined.

Machine learning polymer models of three-dimensional

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Predicting High Order Chromatin Interactions

Weak interactions in higher-order chromatin organization
Nucleic Acids Res. 2020 May 21;48(9):4614-4626. doi:
10.1093/nar/gkaa261. Authors
Omar L Kantidze 1 , Sergey V
Razin 1 Affiliation 1

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Institute of Gene Biology
Russian Academy of ...

*Weak interactions in higher-
order chromatin organization*

DeepC predicts domain
boundaries at high
resolution, learns the

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Chromatin Interactions
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sequence determinants of
genome folding and predicts
the impact of both large-
scale structural and single
base-pair variations....

*DeepC: predicting 3D genome
folding using megabase-scale*

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If one-body energies u and two-body interactions u_2 are known, Eqs. (2) allow us to construct particle distributions n and n_2 exactly. Conversely, we can use Eqs. (5) to find u

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Chromatin Interactions
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and ? from one- and two-
particle distributions.

However, the two-particle
distribution is not directly
measured in current high-
throughput experiments, in
which chromatin from many
cells is mixed together ...

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Predicting High Order Chromatin Interactions

Statistical mechanics of nucleosome ordering by chromatin ...

PRISMR predicts higher-order chromatin structure from genome-wide chromosome conformation capture (Hi-C)

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data. Using the EPHA4 locus as a model, the effects of pathogenic SVs are predicted in silico and compared to Hi-C data generated from mouse limb buds and patient-derived fibroblasts.

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Polymer physics predicts the effects of structural ...

Recent advances in ligation-free, genome-wide chromatin interaction mapping, such as split-pool recognition of interactions by tag extension (SPRITE) and ChIA-

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Drop, have enabled the identification of simultaneous interactions involving multiple genomic loci within the same nuclei, which are informative to delineate higher-order genome organization and gene

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regulation mechanisms at
single-nucleus resolution.

*MATCHA: Probing Multi-way
Chromatin Interaction with*

...

Direct interactions between
TFs and the transcription

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pre-initiation complex
require genomic proximity to
the transcription start site
(TSS) or higher-order
chromatin looping ,
corresponding with TF-
binding motifs in the
promoter or

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Predicting High Order enhancer/silencer regions respectively [2, 7].

*Predicting expression: the
complementary power of
histone ...*

On the basis of our data, we
thus predict that higher-

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Chromatin Interactions

order assemblies of nucleosomes would experience substantial thermally induced shape fluctuations at physiological temperatures, which argue...

Uncovering the forces

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Chromatin interactions using

DNA . . . From Human

To assess chromatin folding into TADs independently of pairing events, we also analyzed cells showing distinctly unpaired unique chromosomes, labeled with

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the 3-Mb probe (fig. S3E) .
We noticed heterogeneity in
the higher-order arrangement
of these TADs, ranging from
a compact conformation to
rarer unfolded chromosomes
(Fig. 2, F and G). In this
...

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Predicting High Order Chromatin Interactions

TADs are 3D structural units of higher-order chromosome

...

However, no algorithm exists to predict EPI using sequence-level signatures only. In the past year,

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there has been an explosion of deep learning approaches to the related problem of genome annotation [8-13]. However, no deep learning model currently exists to predict the high-order chromatin interactions of

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functional sequences.

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10addc1cfa10fd5e6eda3