



# Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings

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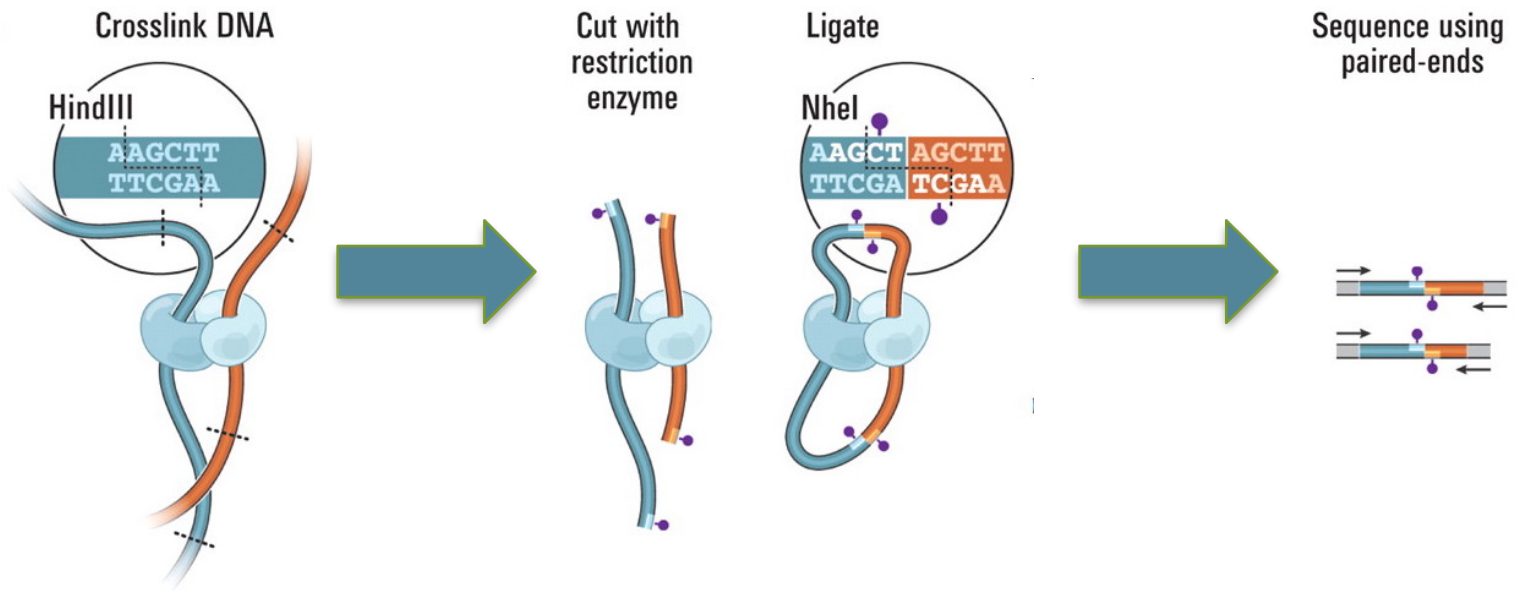
*Nucleic Acids Research*, Volume 45, Issue 7, 20 April 2017, Pages 3663–3673,

<https://doi.org/10.1093/nar/gkx172>

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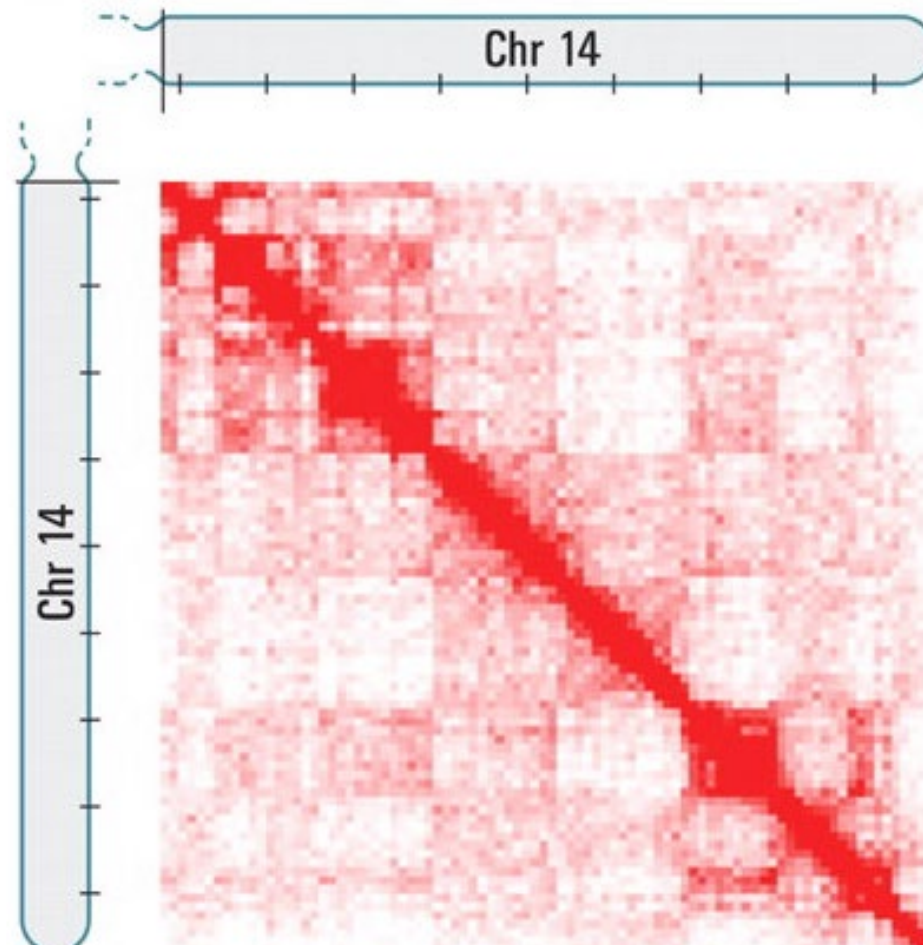
**Presenters:**  
**Natalie Sauerwald & She Zhang**  
**09/14/2017**

# Hi-C: Measuring Chromosome Structure



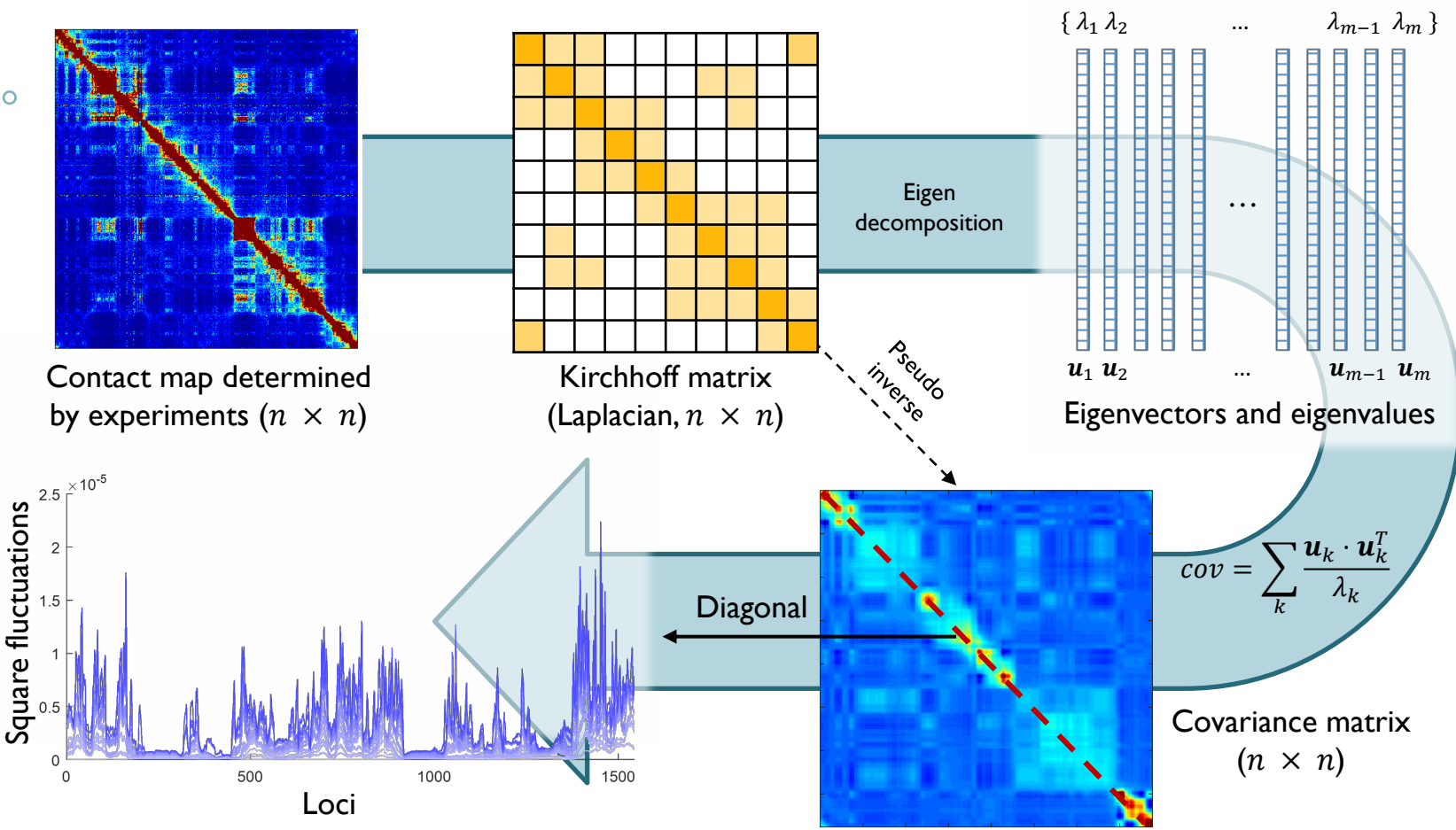
Lieberman-Aiden, Erez, et al. "Comprehensive mapping of long-range interactions reveals folding principles of the human genome." *science* 326.5950 (2009): 289-293.

# Hi-C: Measuring Chromosome Structure



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# Gaussian Network Model (GNM)



**Data source:**

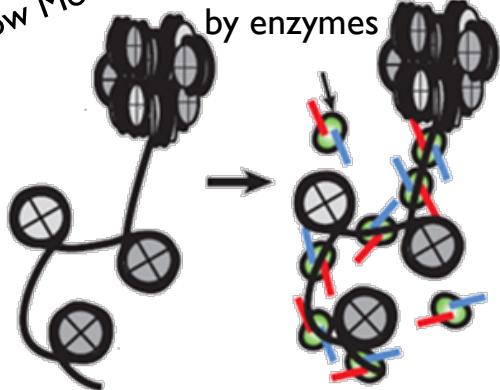
Rao, S. S., ... Aiden, E. L. (2014). A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. *Cell*, 159(7), 1665–1680.

**Cell Type:**

GM12878, human B-lymphocytes.

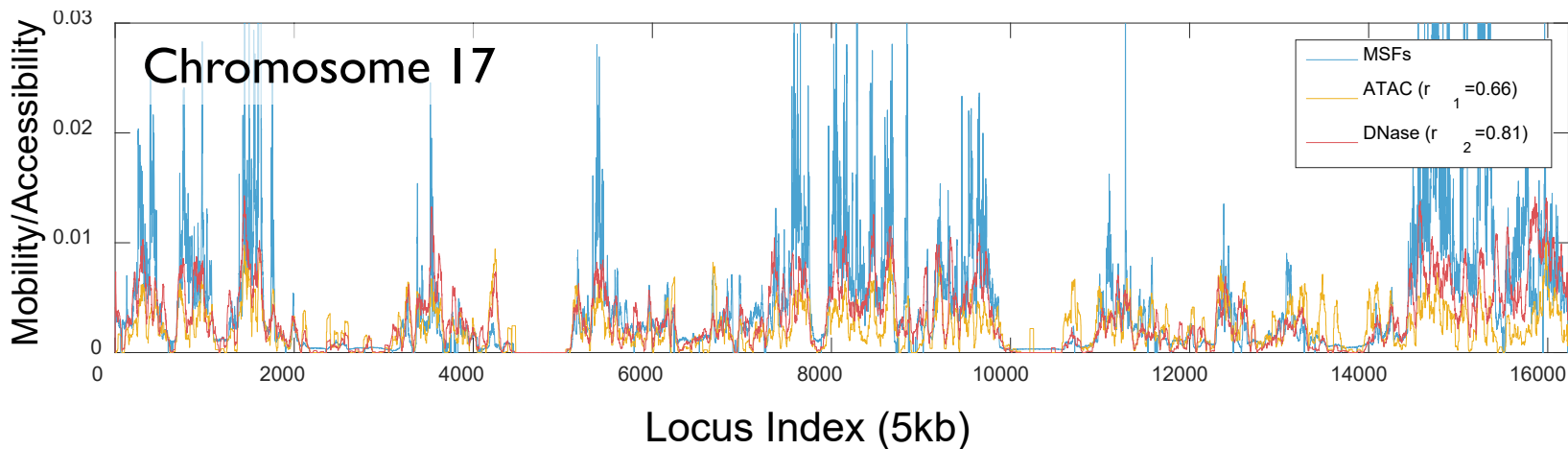
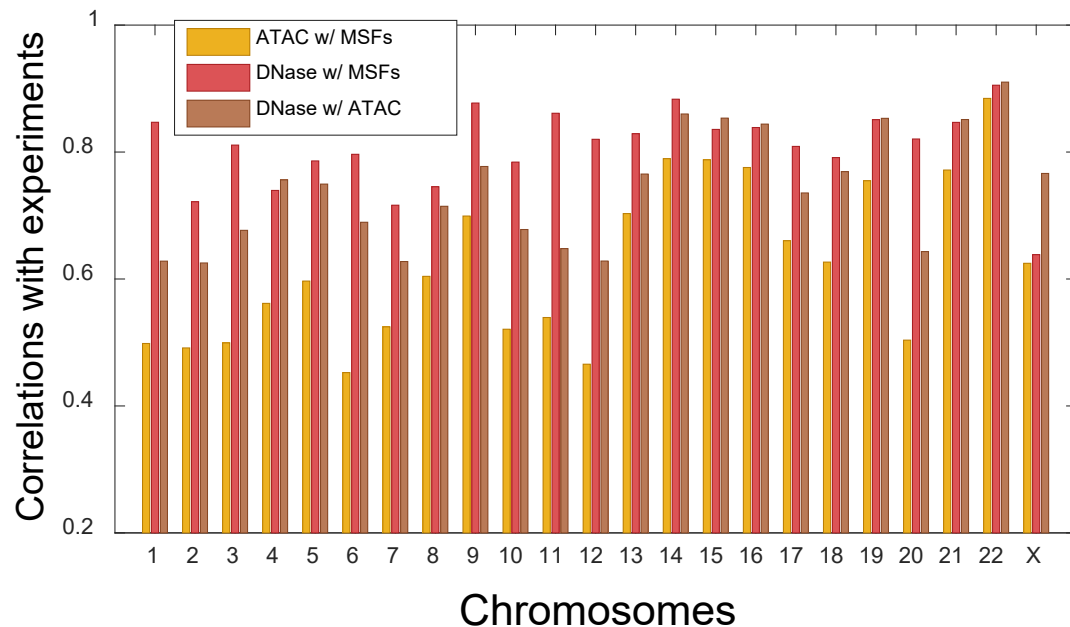
# Square Fluctuations vs. Chromatin Accessibility

Close Chromatin  
(Low Mobility)

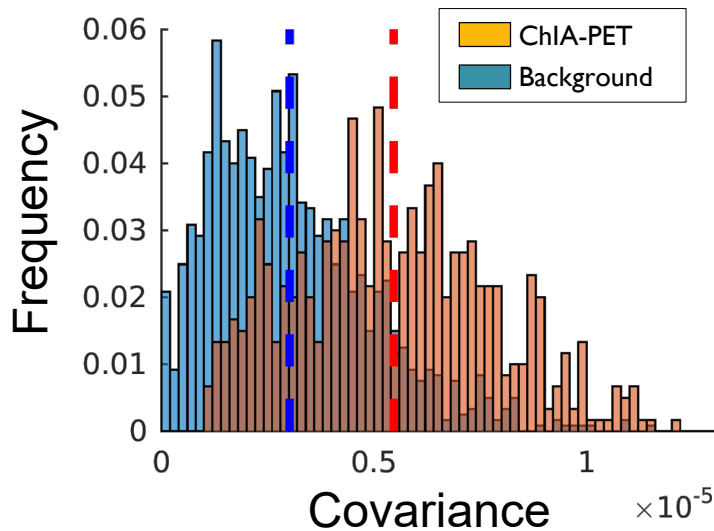
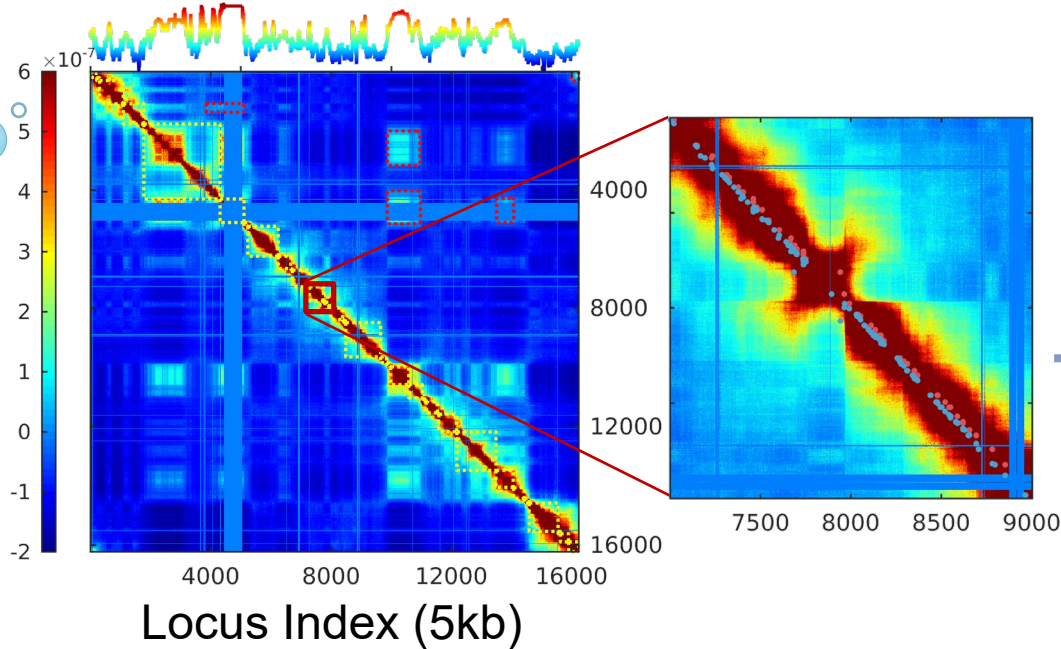


Open regions  
can be accessed  
by enzymes

Open Chromatin  
(High Mobility)

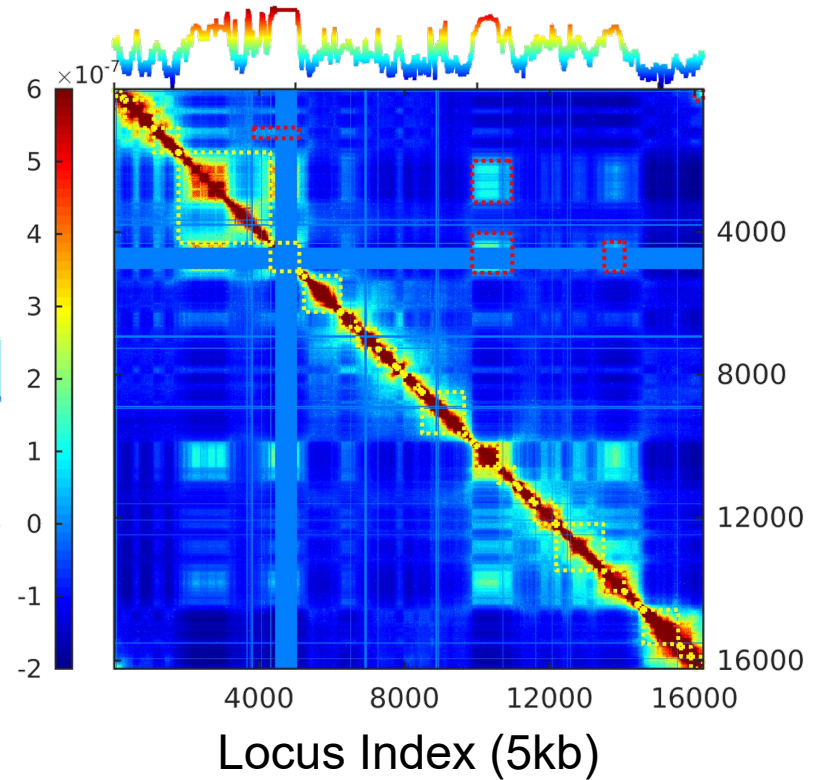
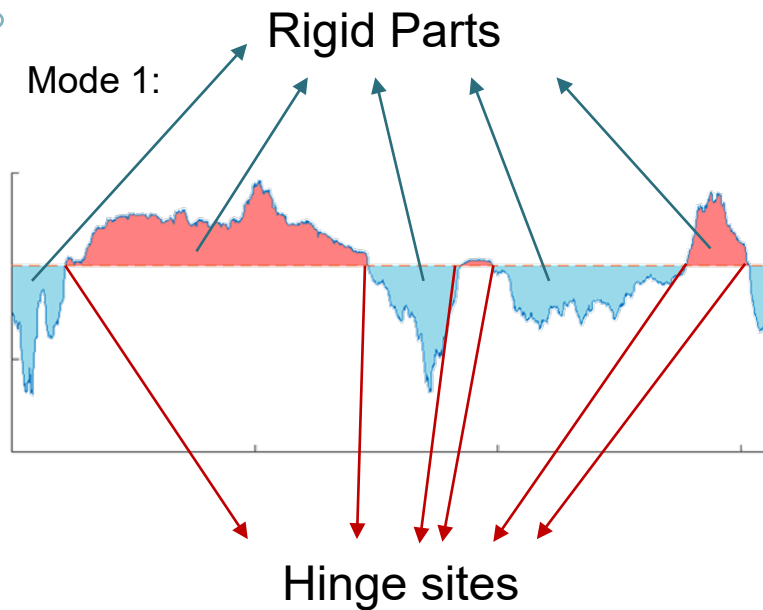


# Dynamical Coupling Supported By ChIA-PET Measurement



“Long range” (~100 kbp) interactions identified by ChIA-PET were found to possess higher covariance in movement calculated by GNM than background pairs.

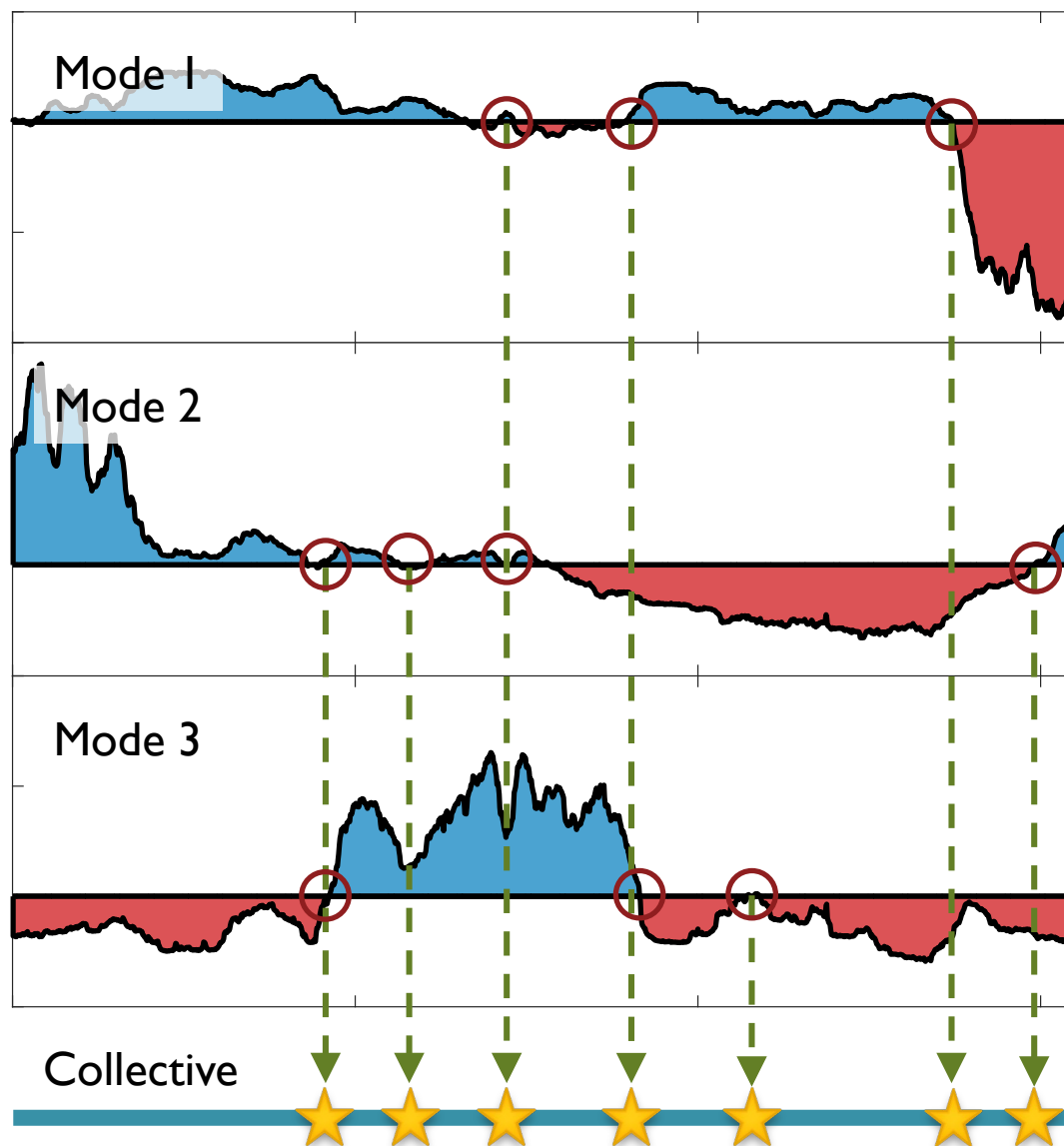
# Structural Domains Identified by GNM modes



Collective GNM domains can be identified by combining hinge sites from different modes

 GNM Domains

# Structural Domains Identified by GNM modes





# Known Structural Domains

## Compartments

multi-megabase-sized regions  
corresponding to genomic features

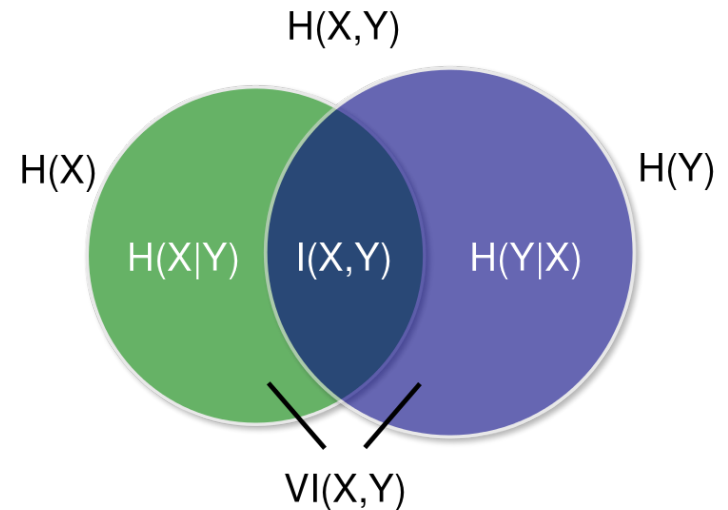
## Topologically associating domains (TADs)

densely self-interacting, finer resolution  
chromatin groups

# Structural Domains Identified by GNM modes

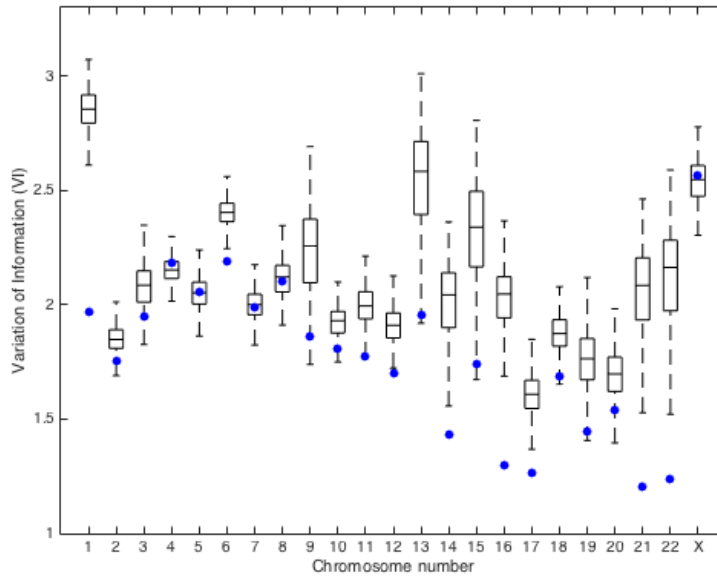
To compare domain sets: Variation of Information

$$VI(X; Y) = H(X) + H(Y) - 2I(X, Y)$$

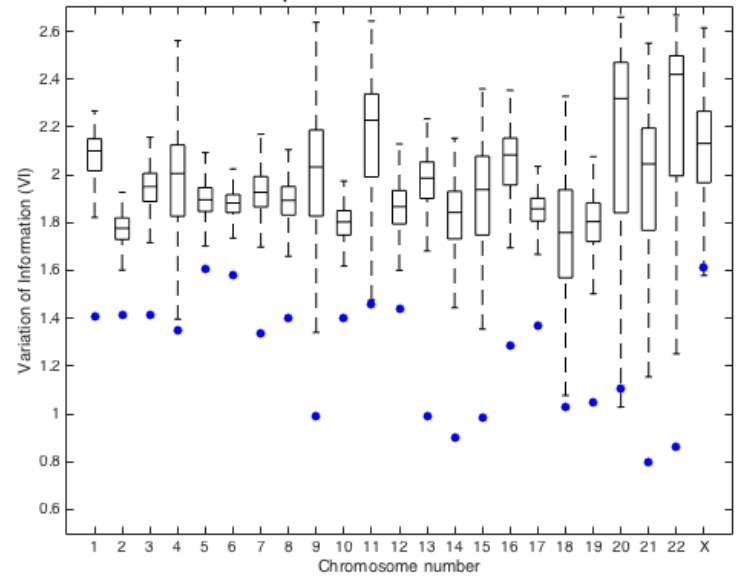


Lower VI = more similar

# GNM Domains (mostly) Correlate to Both



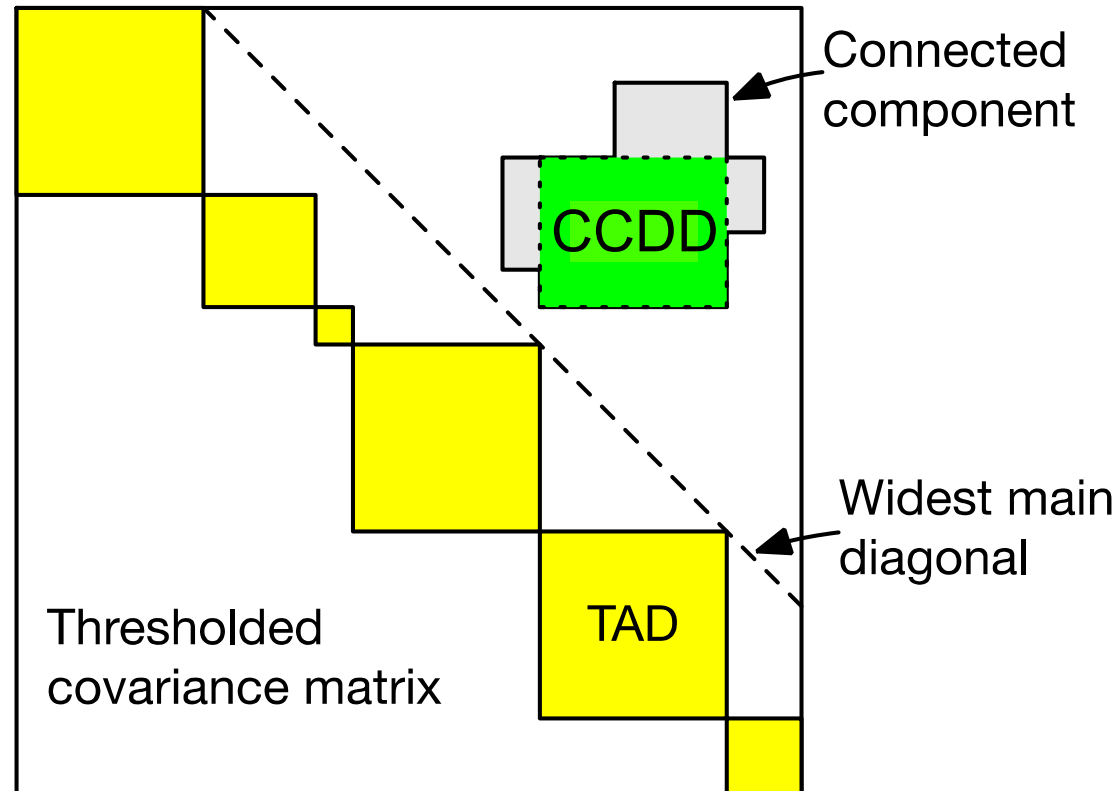
Compartments



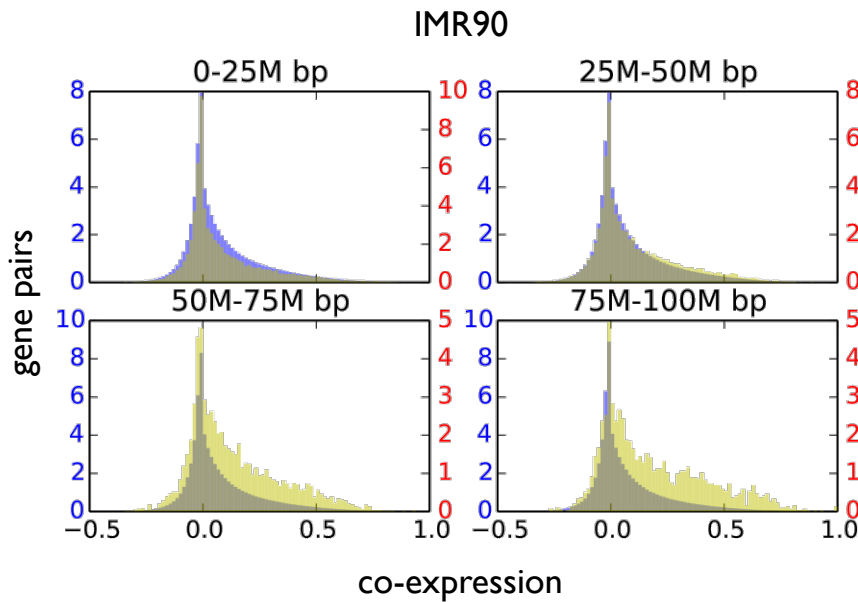
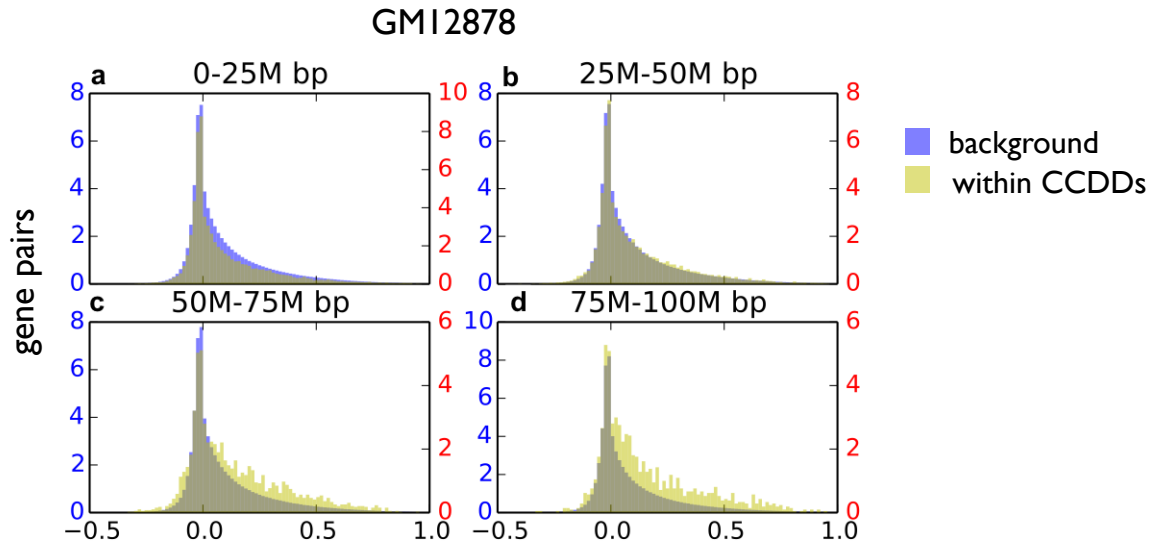
TADs

- GNM domains
- Randomly shuffled domains

# Cross-Correlated Distal Domains (CCDDs)



# Long range interactions



Gene pairs in distant off-diagonal regions have significantly higher co-expression than expected