

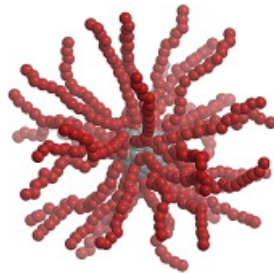
Star polymers provide insight on Rabl-like chromosome conformations

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*Second Annual MIT PRIMES
Conference, May 20, 2012*

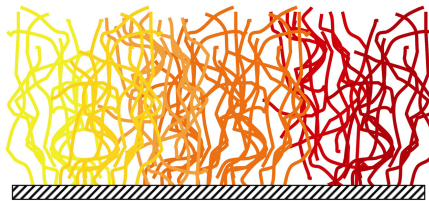
Background

Star polymers: polymers that are bound together at a point



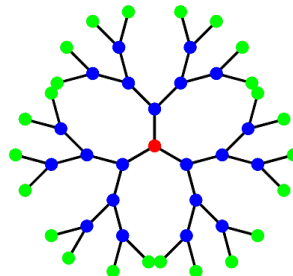
Solomon 2003

Brush polymers: polymers bound to a backbone



Bello 2006

Dendritic polymers: polymers with a repeated branching pattern

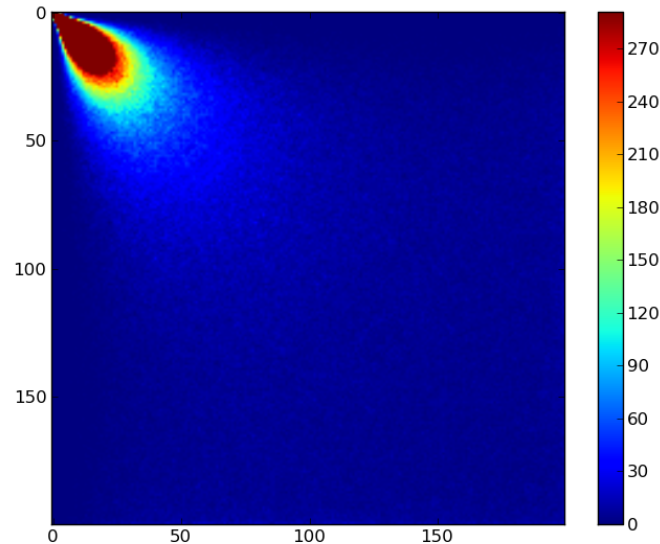


Chow 2012

Background

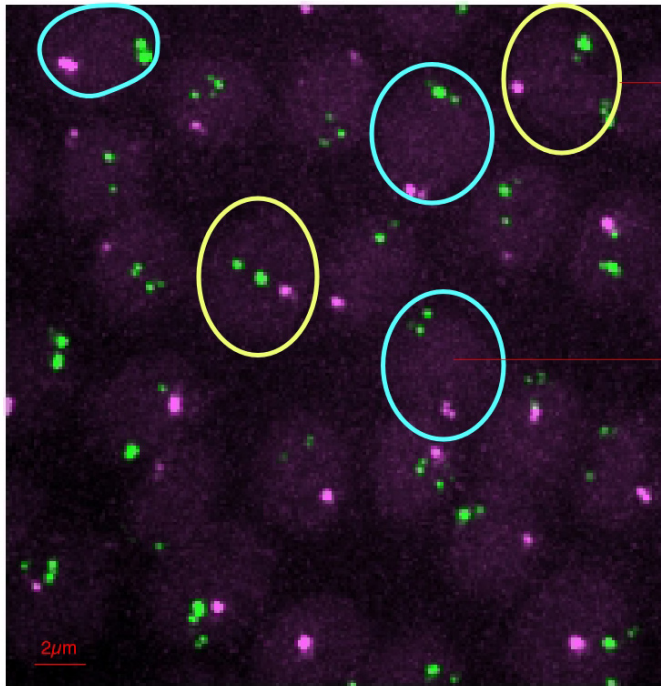
Averaged Contact Map: heat map of all contact points averaged over many states

Heat Map: a graphical representation of values in colors



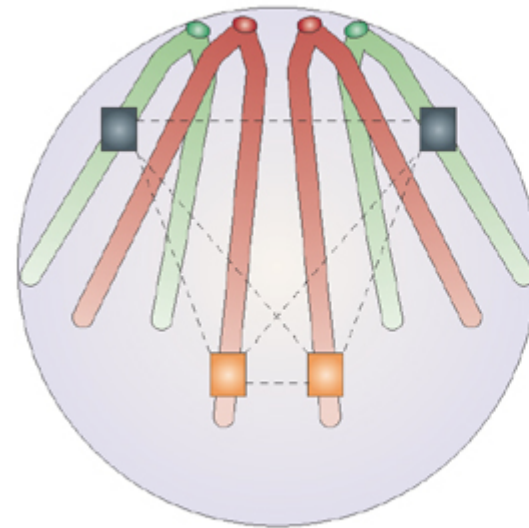
Biological implications for star polymers: Yeast Chromosomes

Rabl Formations in Yeast Cells:



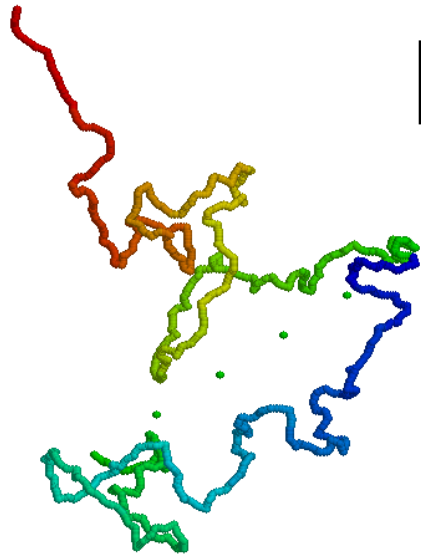
Cell Science 2006

a The Rabl configuration of interphase chromosomes

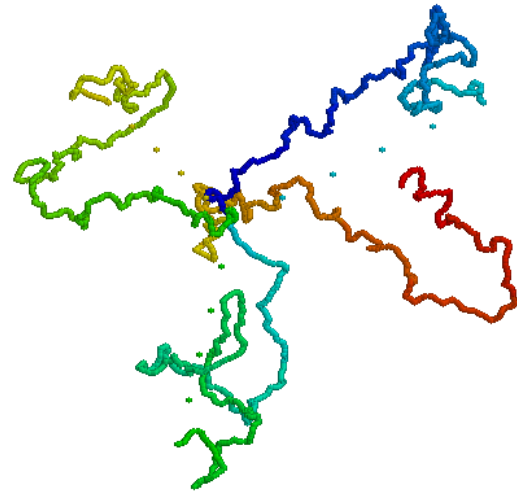


Barzel 2008

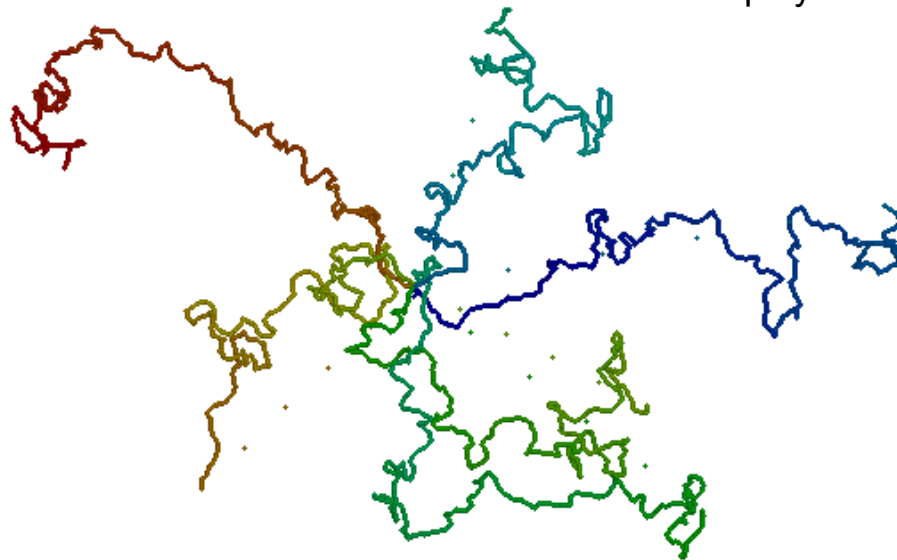
Models



2 polymers



4 polymers



6 polymers

Goal

To study the pattern of interactions between two arms in a star polymer

Method: simulate and create contact maps of star polymers (with various numbers of arms)

My programs

1. Creating the system:

slice a long coiling polymer

rotate and translate slices to origin

tether to origin

2. Simulating star-polymers over long times

use Brownian (Molecular) Dynamics

collect simulation data

3. Analyzing the simulations:

Take in contact maps and output contact probabilities

compare two contact maps

create cross sections

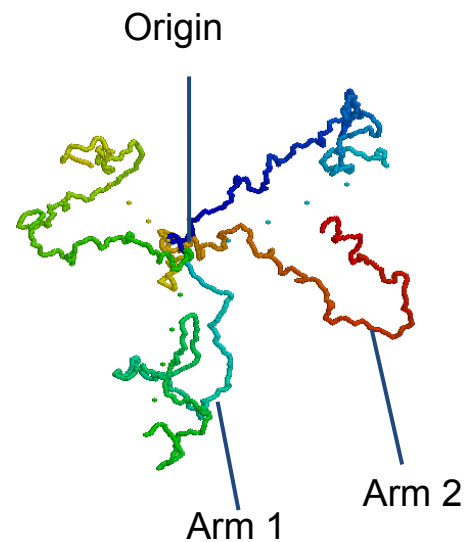
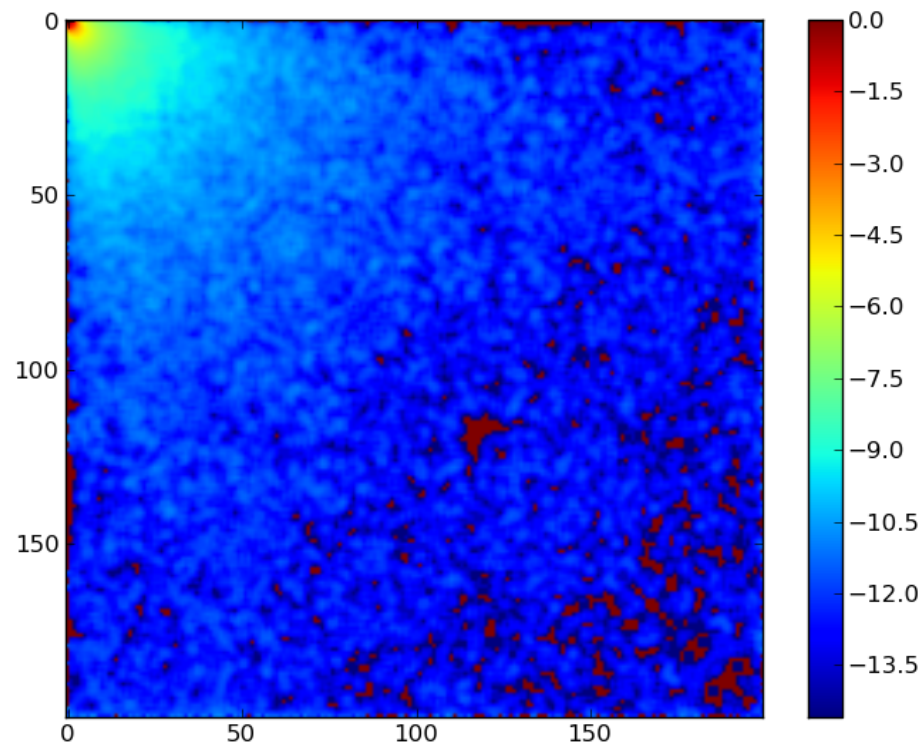
Results

Between-Arm Contact Probability in a 4-Arm Star Polymer

Origin

Arm 2

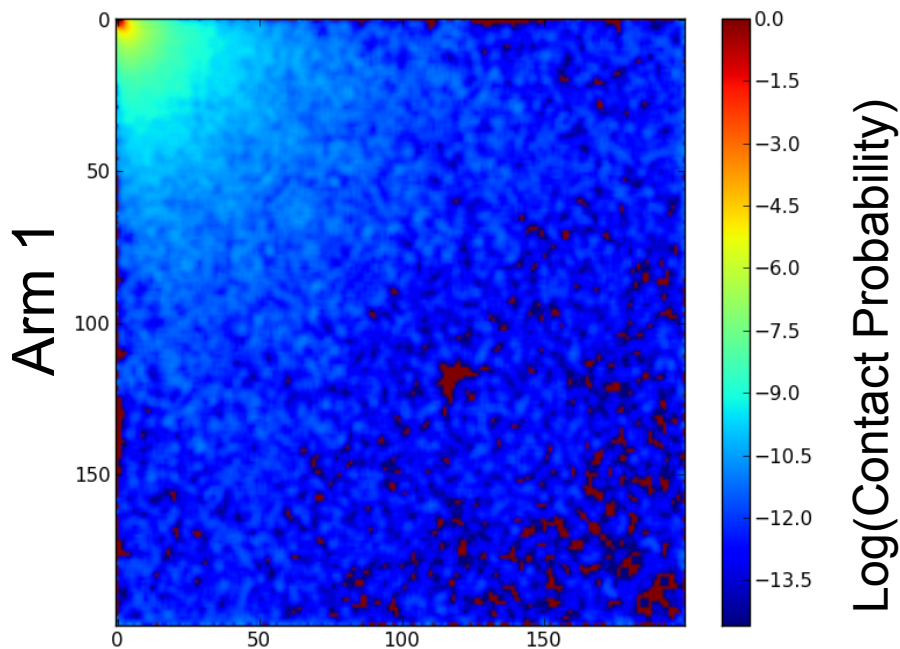
Arm 1



Results: arms in a many-arm star polymer run away parallel to each other

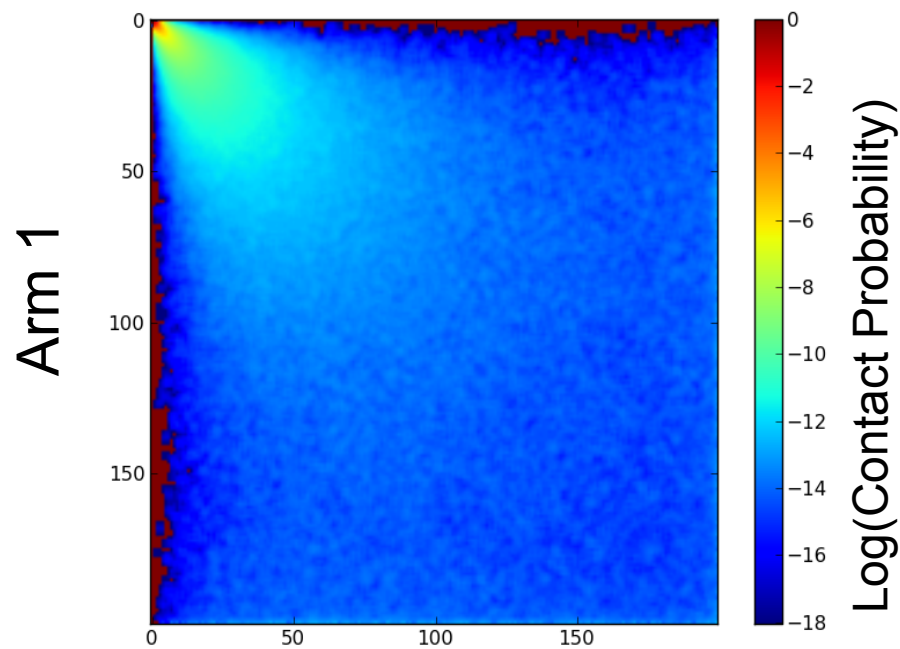
4-arm star polymer

Arm 2



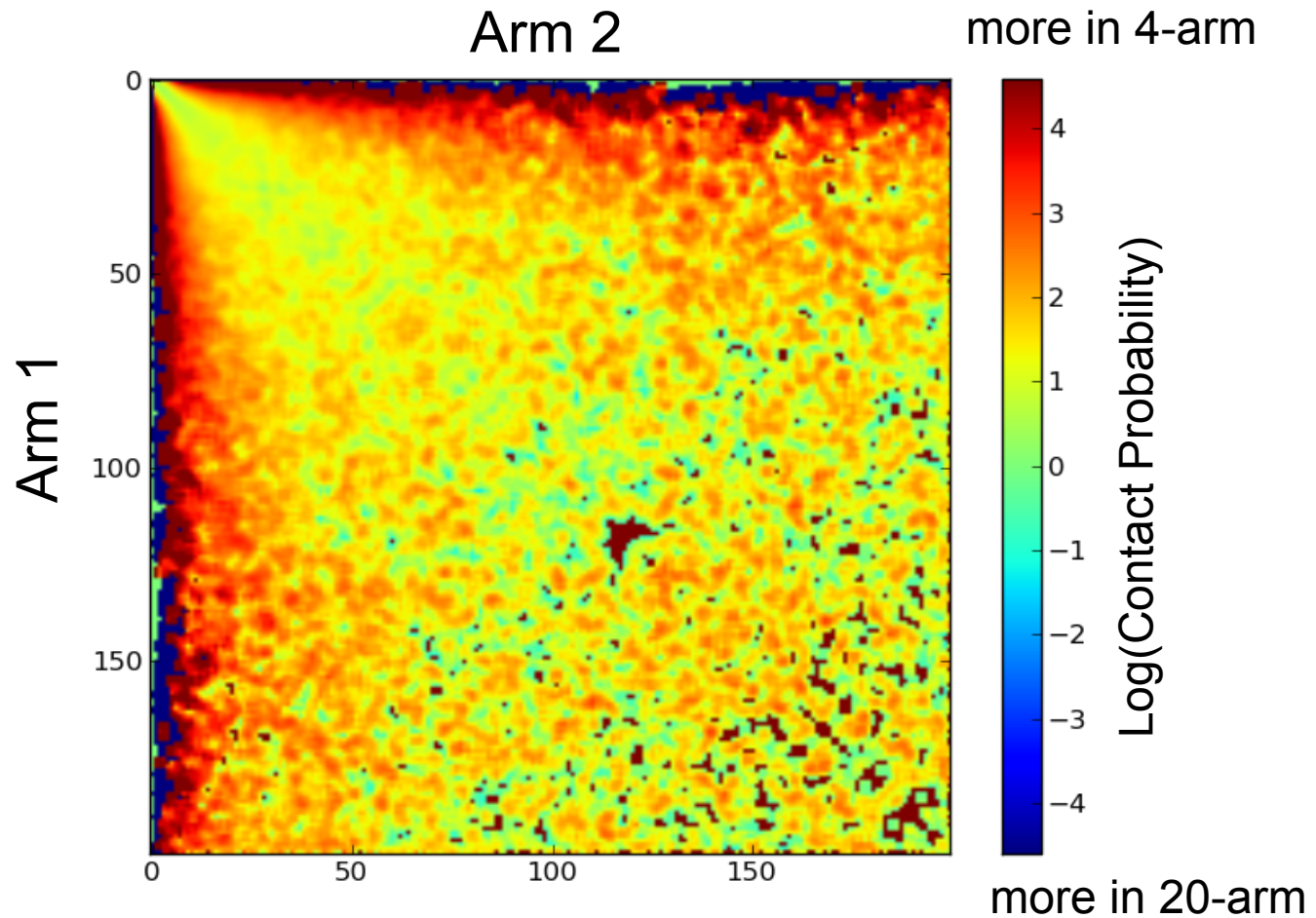
20-arm star polymer

Arm 2



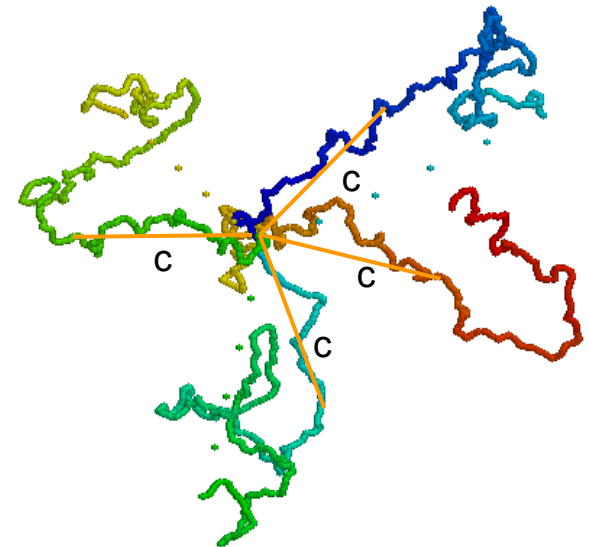
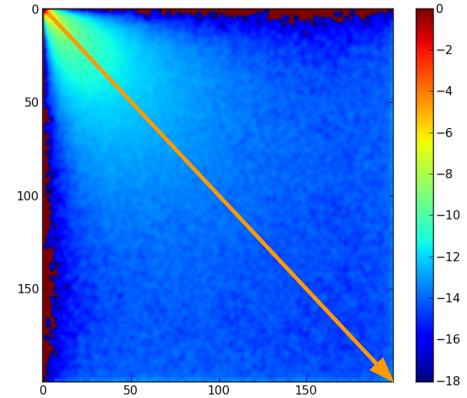
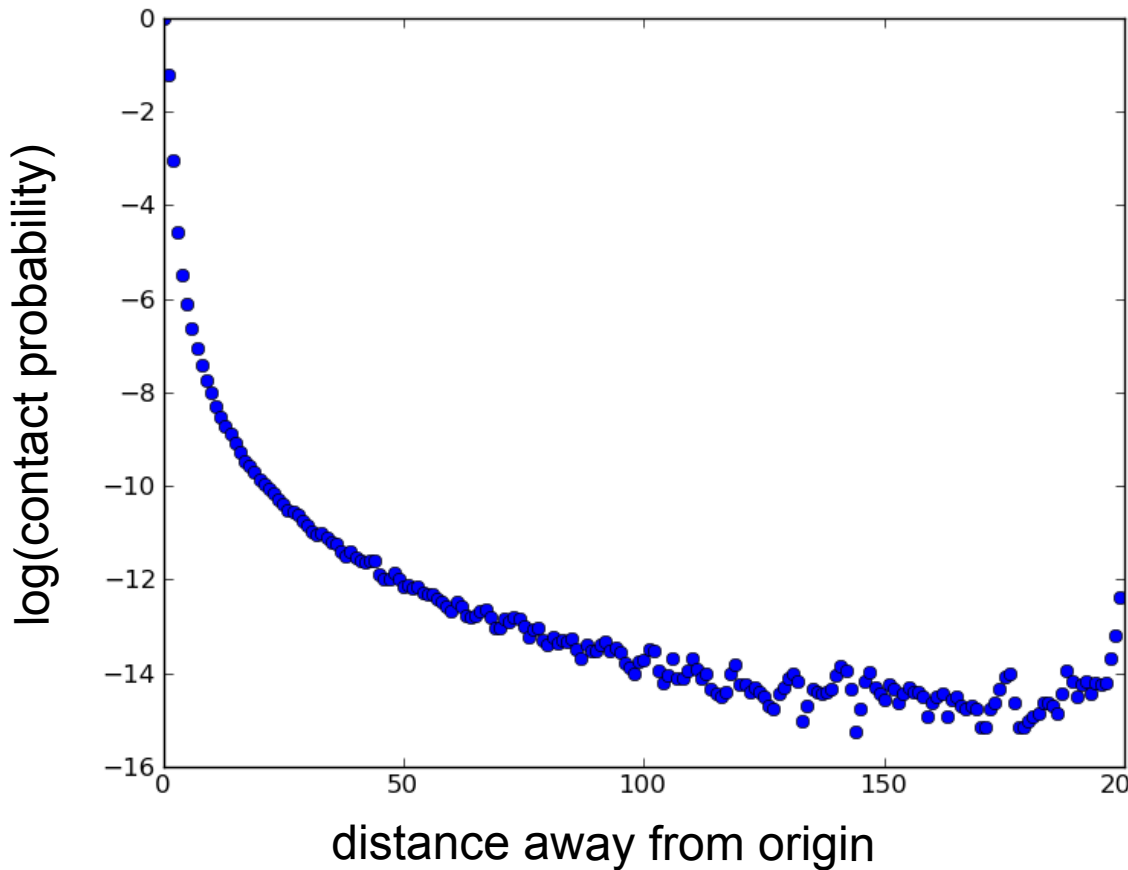
Results

Contact Probability Difference Between 4-arm and 20-arm star polymers

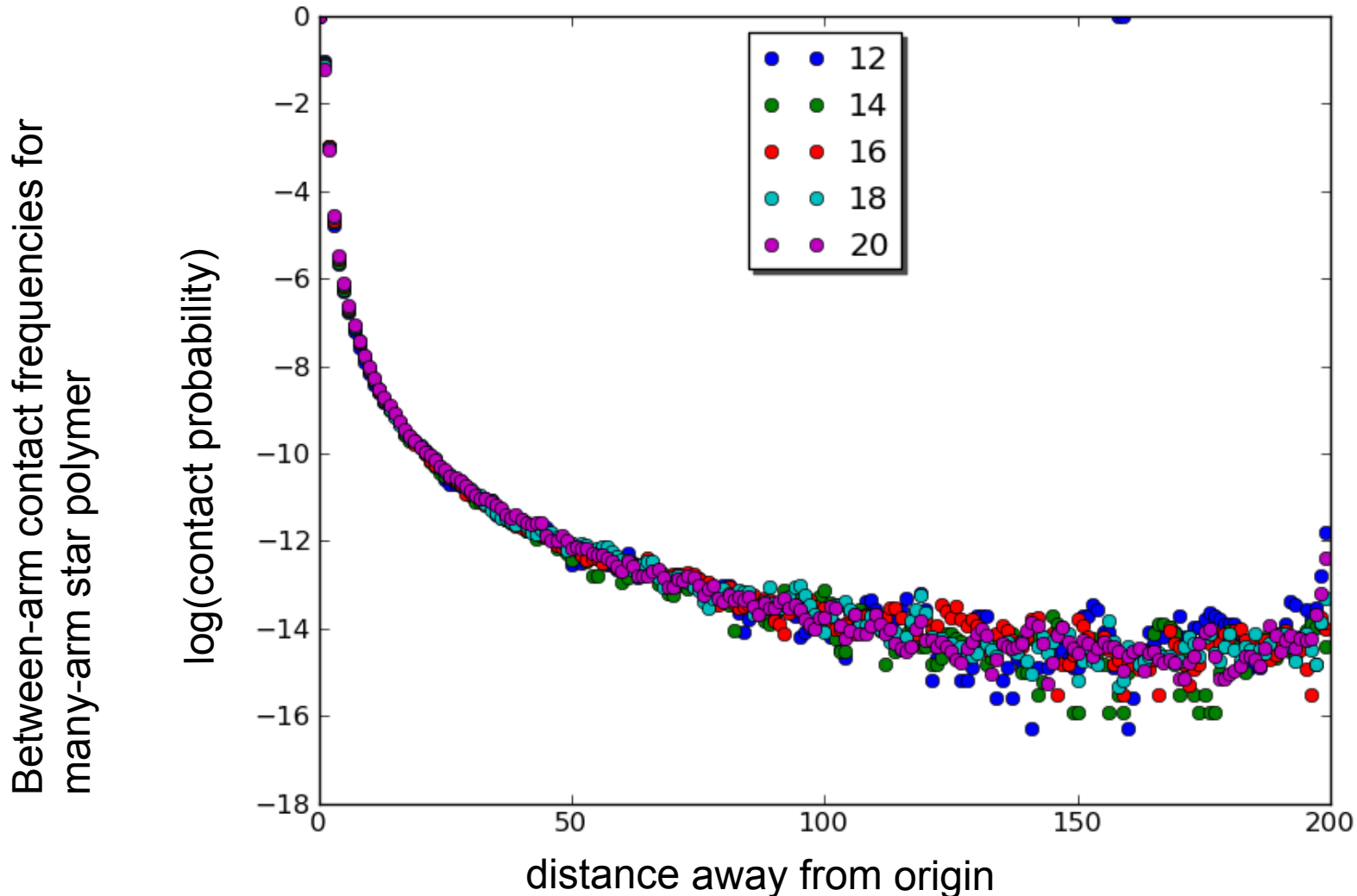


Results: contact probability decays with distance from the origin

Between-arm contact frequencies for 20-arm star polymer

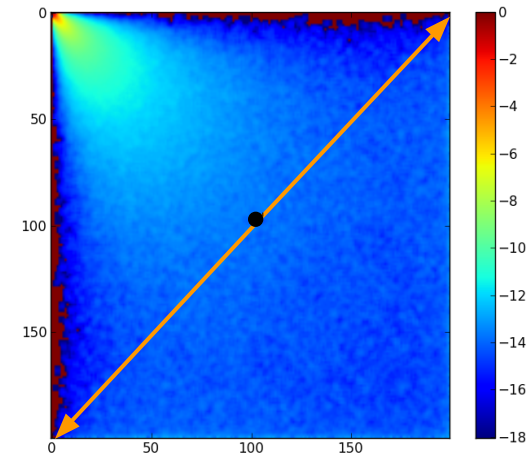
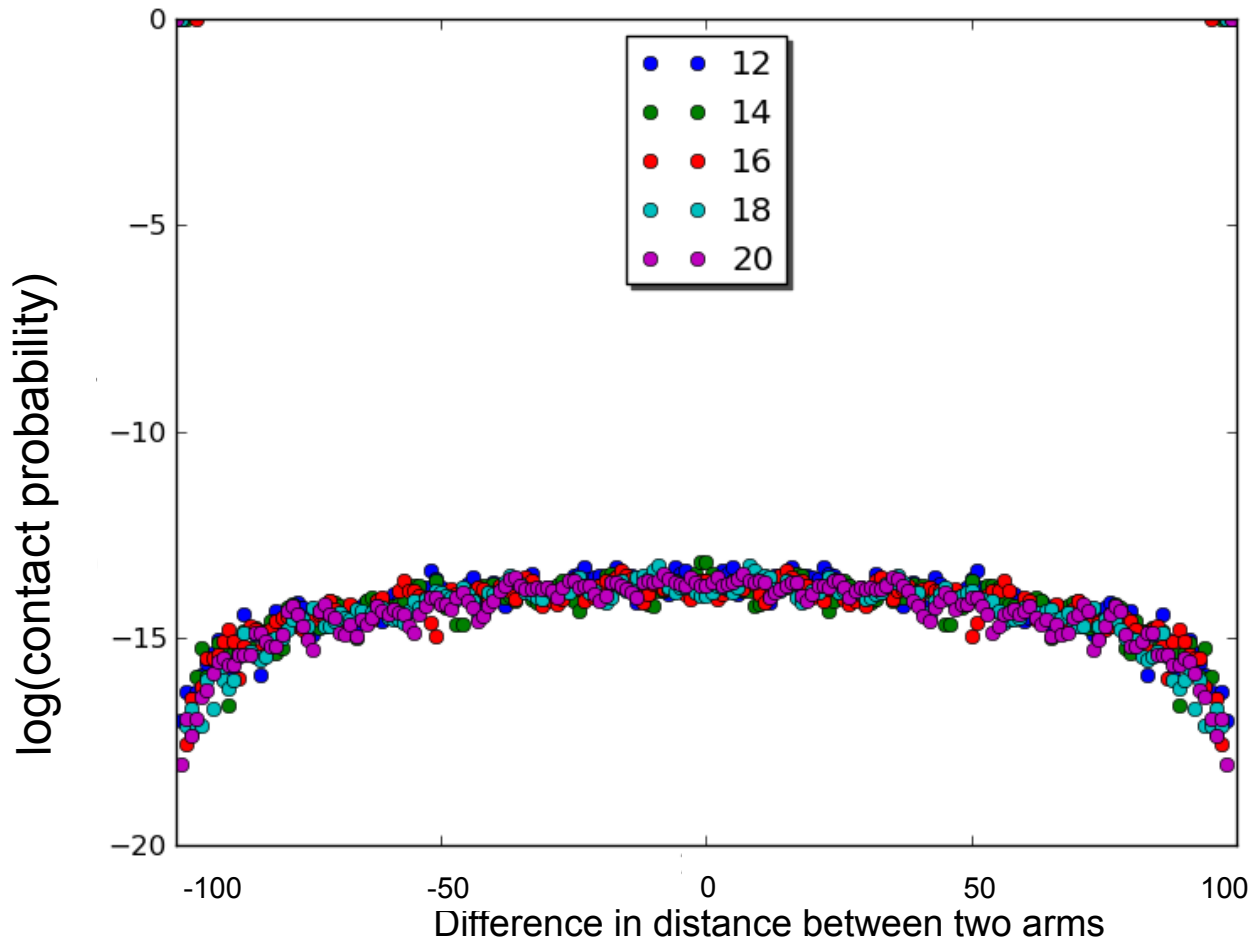


Results: decay of contact probability from origin is remarkably similar for different numbers of arms



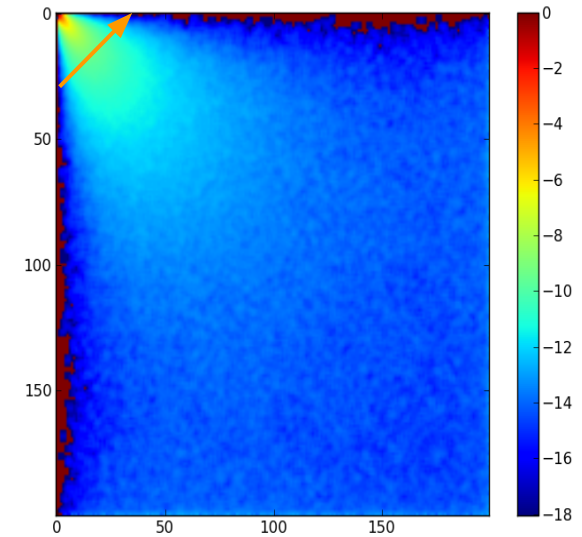
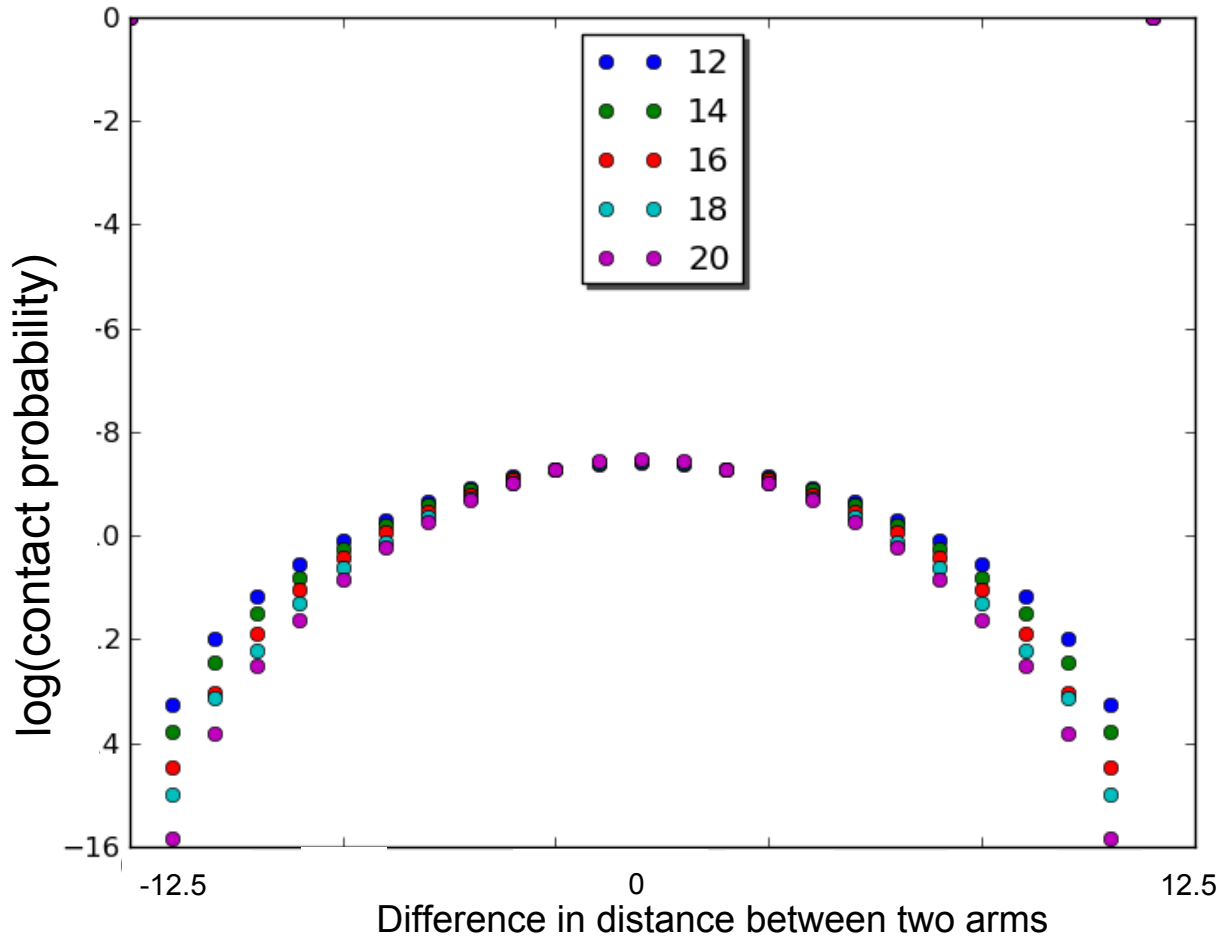
Results: contact probability is similar for arms away from the origin

Between-arm contact frequencies at a combined distance of 200 from the origin



Results: contact probability varies more with more arms in regions close to the origin

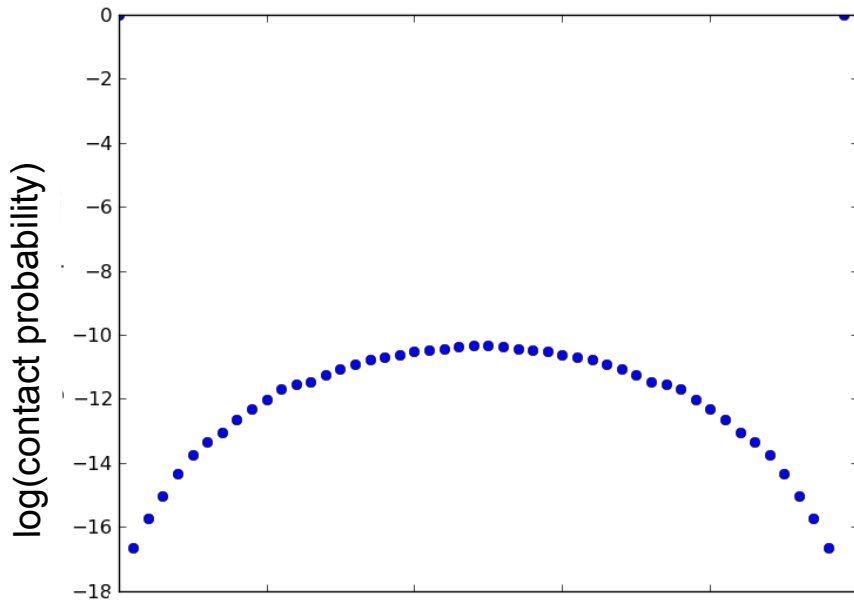
Between-arm contact frequencies at a combined distance of 25 from the origin



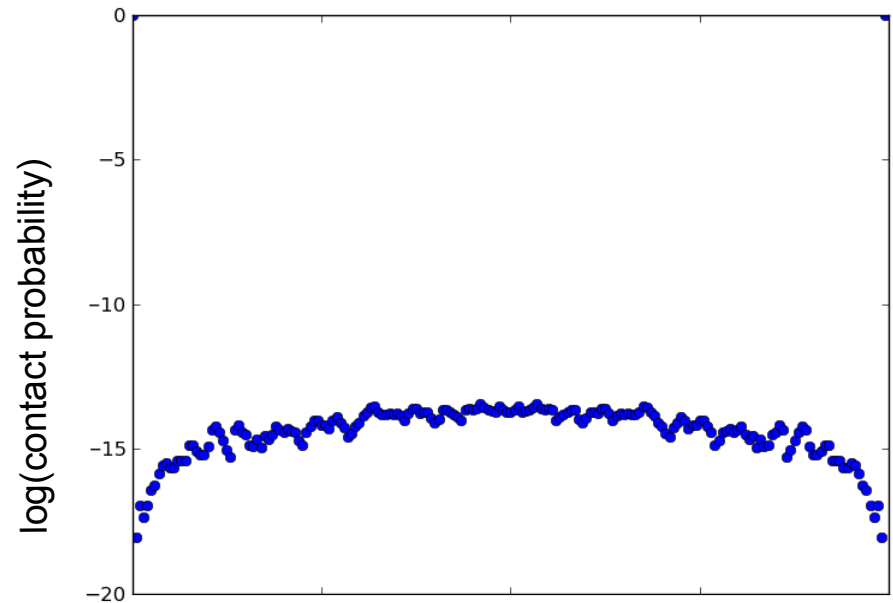
Results: contact probabilities vary more closer to origin

Difference in between-arm contact frequencies at a combined distance of 50 and 200 from the origin

50

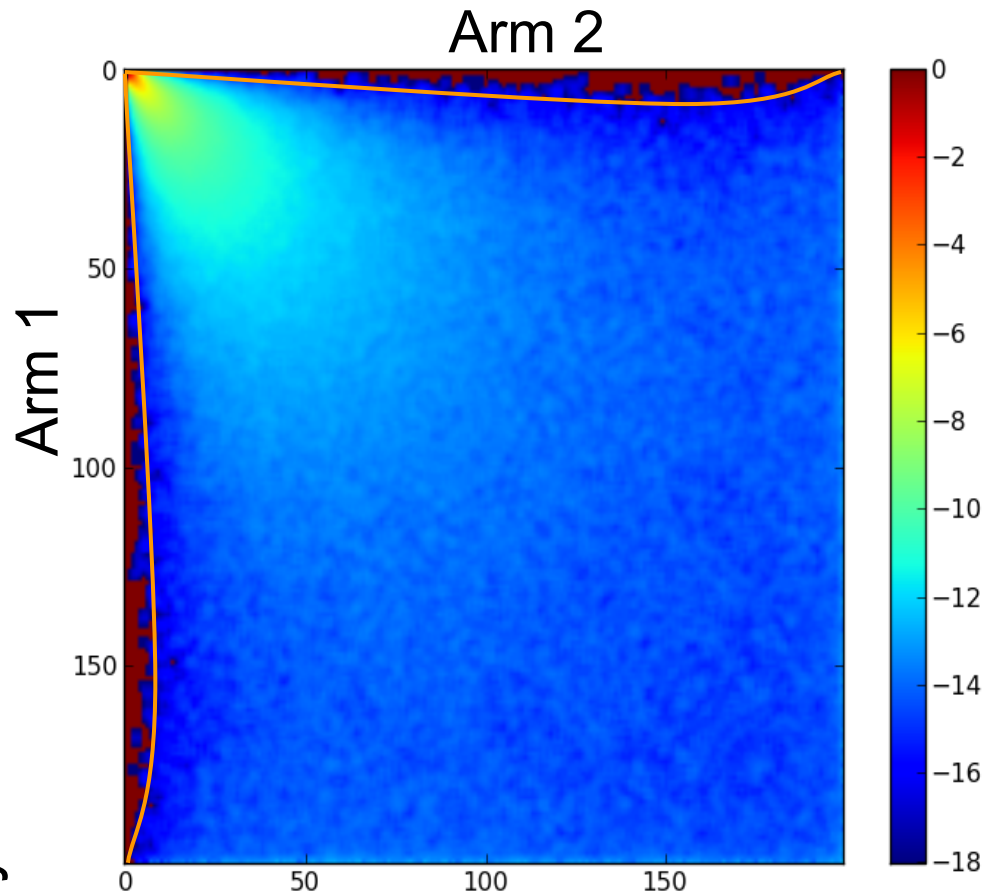


200

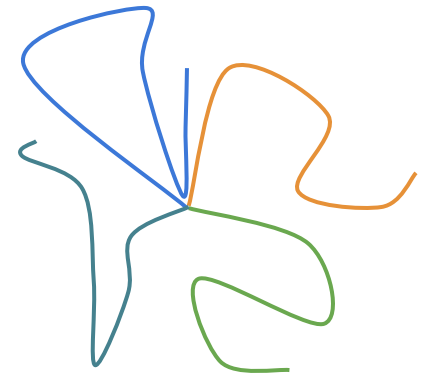


Results: End of polymer tends to loop back to origin more easily than middle of polymer

Contact Probability of a 20 Polymer System



Contact between middle and origin



Contact between end and origin



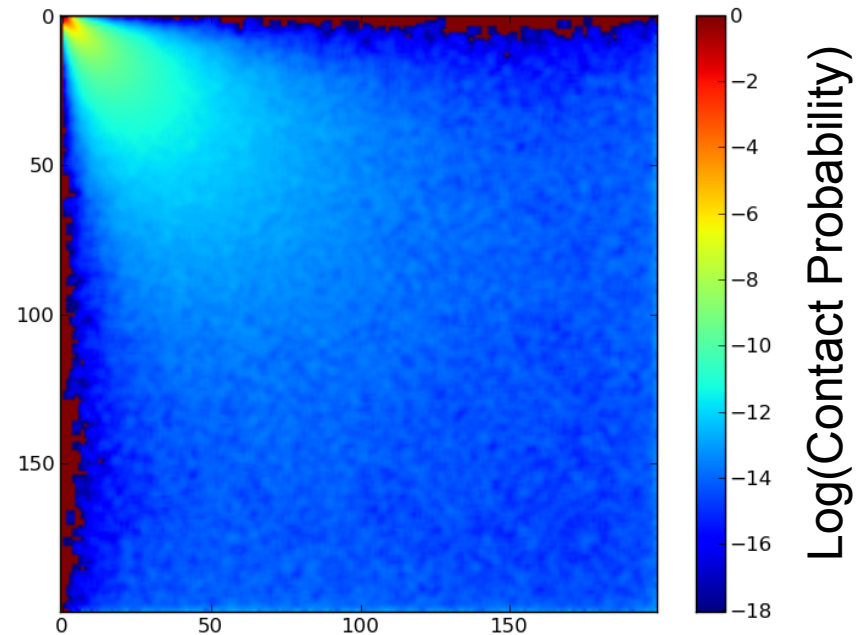
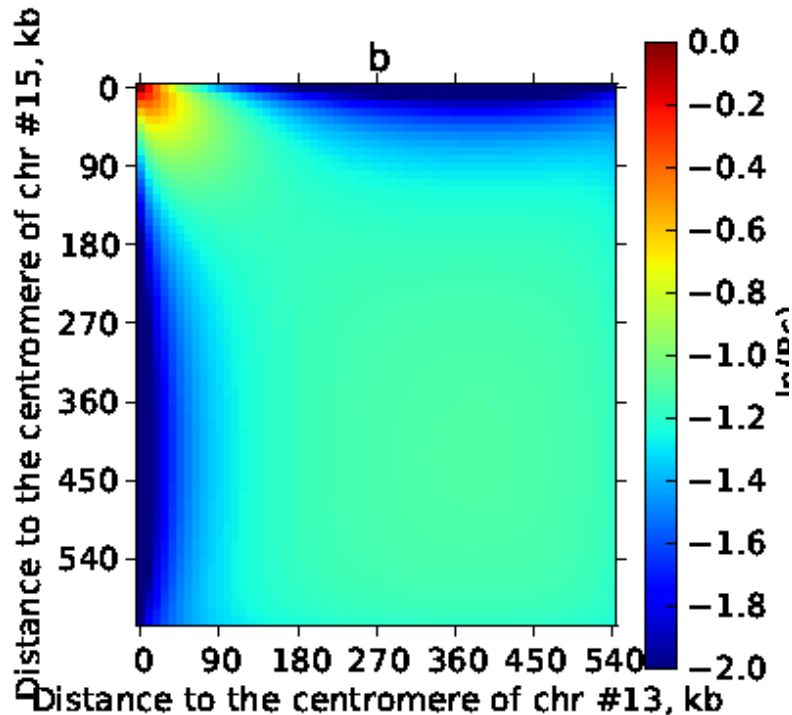
Results show similarities with theoretical models

Theoretical Contact Map

My Simulation

32-arm Star Polymer

20-arm Star Polymer



Acknowledgements

Thanks to the following...

- The MIT PRIMES Program
- Mentors: Max Imakaev, Geoff Fudenberg
- Professor Leonid Mirny