# Metaphase chromosome decondensation

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After cells divide, their chromosomes decondense from a compact metaphase arrangement into an interphase state. However, little is known about the process of decondensation. To investigate decondensation, we initialized simulations from the latest polymer model of metaphase chromosome organization and allowed the chromosomes to unfold with different constraints. We studied two models for decondensation: in the first, we preserved the majority of consecutive backbone bonds in the metaphase chromosome, but released a subset of these bonds. We observed domain formation on the heatmap, and the scalings partially matched experimental data. In the second, we introduced crosslinks between regions close in space. In this model, we observed scalings that did not match the experimental data in interphase.
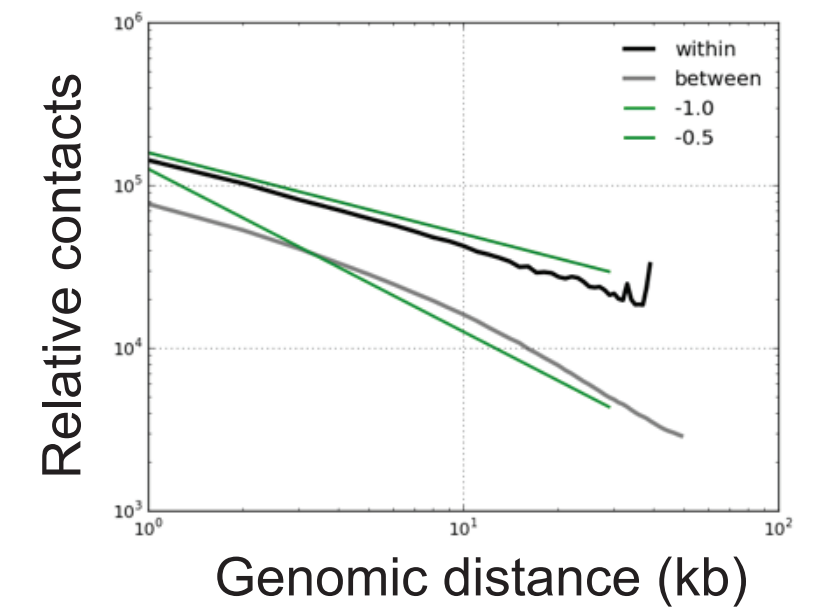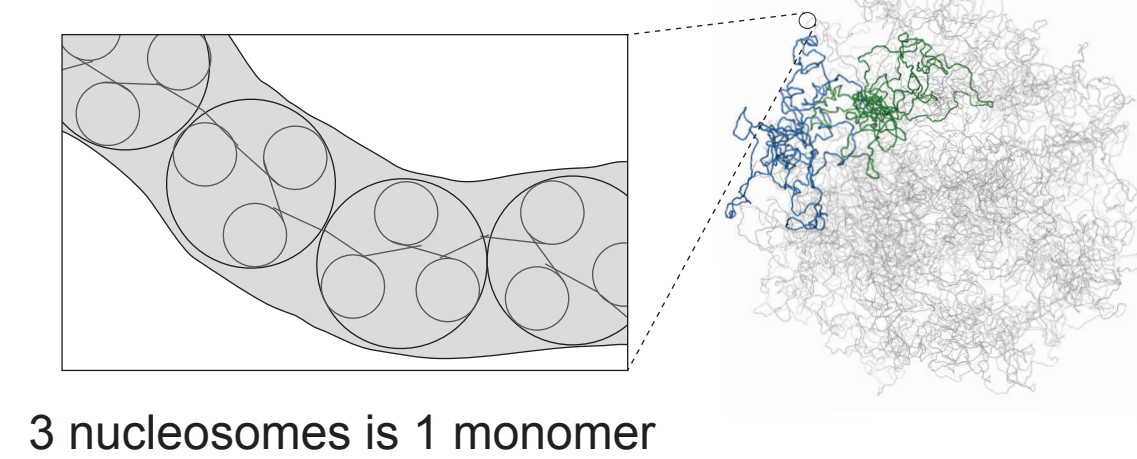
## How do chromosomes decondense from mitosis to interphase?
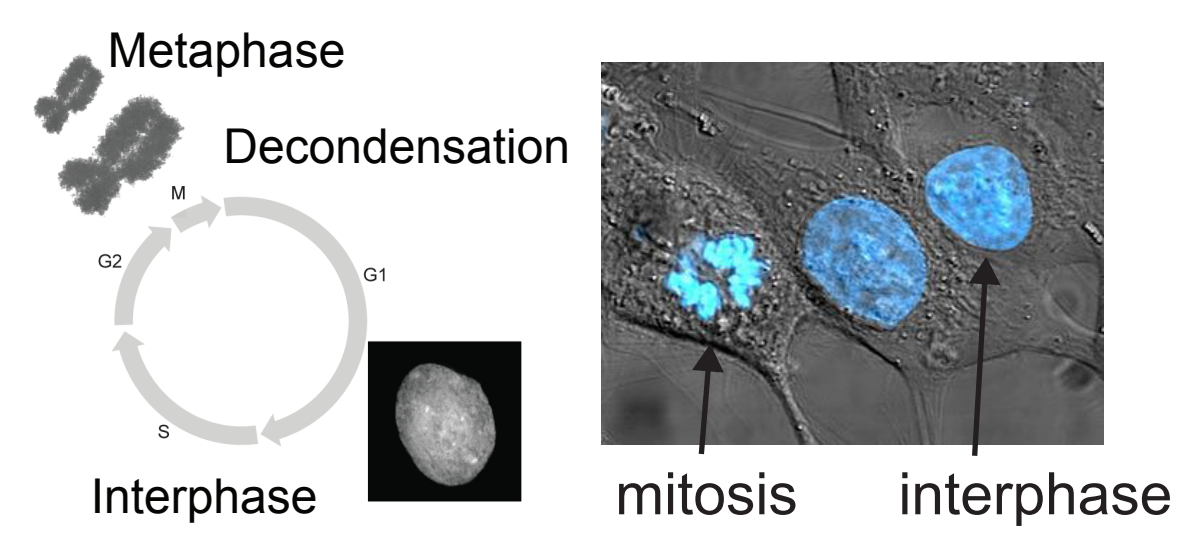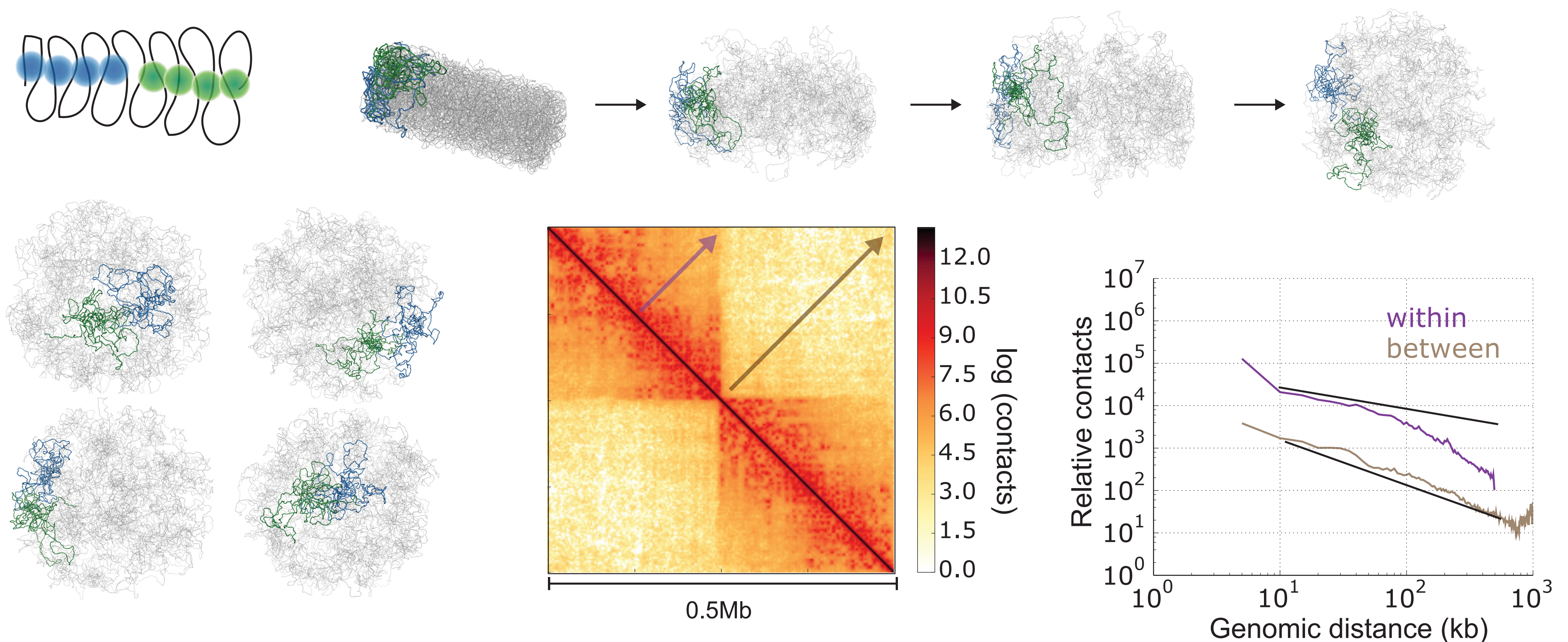


## Interphase Hi-C features



Polymer model



3 nucleosomes is 1 monomer
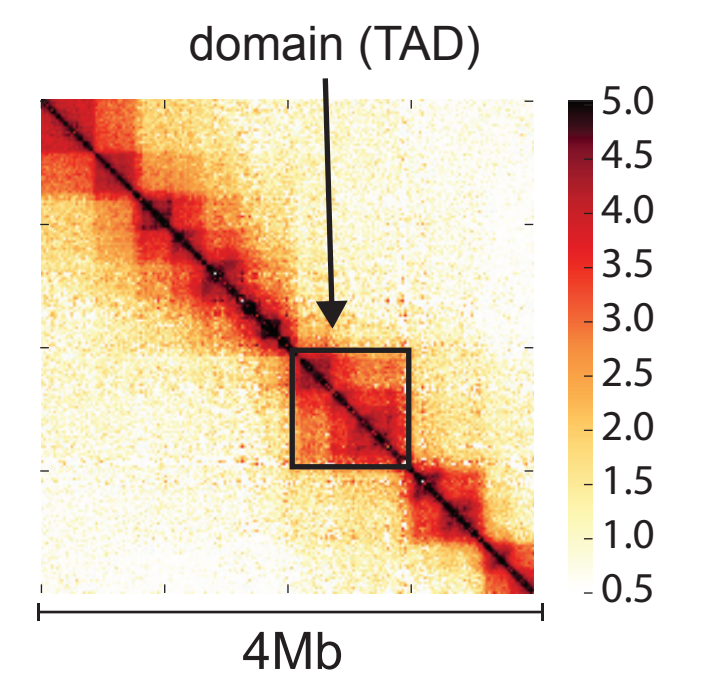
## Model 1: Core monomer bonds form domains (TADs) on heatmaps, and partially recreate experimental scalings from Hi-C

### Domain size: 500kb



## Model 2: Crosslinks between monomers close in space do not recreate experimental scaling for interphase cells as obtained by Hi-C.



Conformation with crosslinks is linearly ordered