

# 8.592 Project Proposal

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## Title

Polymer folding through quorum-sensing active compartments

## Abstract

Chromatins exhibit spatially segregating domains of varying transcriptional activity: euchromatic compartments (A) are active and resides in the nuclear interior, while heterochromatic compartments (B) are silent and resides at the nuclear periphery [4]. It has been proposed that this compartmentalization arises due to pairwise interactions between the different domains [2]: attractive interactions between heterochromatic regions are important while strong interactions between euchromatic regions are ruled out. Recently, Goychuk and Kannan [3] demonstrated an alternative mechanism for compartmentalization, showing that correlated, nonuniform active noises can reproduce the structural patterns of chromatins. These active processes are present in the nucleus as enzymes consume ATP to exert mechanical forces or perform nonequilibrium reactions.

In this project, I plan to investigate whether a combination of activity and interactions can exhibit the chromatin folding structures. Specifically, I will look at models of polymers with euchromatic and heterochromatic regions with uniform activity, but regions interact via quorum sensing only with other regions of the same type. I will first focus on the case with strong heterochromatic slowing down quorum sensing and no euchromatic quorum sensing, in accordance with [2]. I will write code in Julia, building on Sunghan's code in 8.08, to perform simulations of this system with either Euler-Maruyama or stochastic Runge-Kutta method. I will attempt analytical calculations of properties of this model, and/or compare the results of this model with data published in [3].

One direction I'm interested in (which might be too ambitious for this project) is how activity might lead to robust memory recall [1]. For example, the chromatin might have multiple preferred configurations which might be achieved via nonuniform quorum sensing interactions. Would the activity then help the chromatin find a preferred configuration if it does not start super close

to that configuration? I'm curious how biologically relevant this is, or is it just a contrived scenario I thought of.

## References

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- [3] Andriy Goychuk, Deepti Kannan, Arup K Chakraborty, and Mehran Kardar. Polymer folding through active processes recreates features of genome organization. *Proceedings of the National Academy of Sciences*, 120(20):e2221726120, 2023.
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