

To Maa and Baba...

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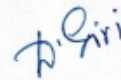
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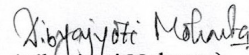
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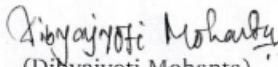
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ABSTRACT

Since the invention of synthetic polymers (e.g., plastic), polymeric materials have brought ease to a great extent in everyday life. Various applications of polymers encourage scientists to study the configurational properties and dynamics of polymers under different physical conditions. The polymer is a long chain molecule with repetitive units called a 'monomer.' The functionality of the monomers (number of reactive ends) classify the structure of the polymer. Polymers from living organisms are known as biopolymers, such as DNA (Deoxyribonucleic Acid), RNA (Ribonucleic Acid), Protein, etc. The cells have a very crowded environment because they are composed of different biomolecules that may occupy a large fraction of the total volume. This leads to the phenomenon called volume exclusion which is caused by the steric repulsion among different molecules. The confinement that arises due to this may influence the stability, dynamics, and function of biomolecules. In the context of polymer physics, confinement reduces a large number of configurations of biopolymers. Hence, there is a reduction in entropy which influences the free energy of the biopolymers. There is another contribution to the free energy arising due to attractive interaction among non-bonded nearest monomers. The polymeric system usually equilibrates at a constant temperature to minimize its free energy. However, change in temperature or solvent quality may lead biopolymer to change its states from coil or swollen to globule or collapsed state. The emphasis of this present thesis is to study the loss in configurational entropy and gain in free energy on different biological processes.

Chapter 1 deals with a brief literature survey on the biopolymers under confinement environments. This includes varying pore shapes in living organisms such as Mycobacterium Smegtatis Porin A (MSPA), Nuclear

Pore Complex (NPC), Viral capsid, etc. We highlight some significant issues associated with the confinement of biopolymers. The second part of this chapter consists of modeling polymers and biopolymers and techniques (Exact Enumeration and Monte Carlo simulation) required to calculate the physical observables in the framework of statistical mechanics.

In Chapter 2, we study the migration of the polymer chain across an entropic trap in quasi-equilibrium condition and explore the effect of solvent gradient present in the entropic trap which acts both parallel and perpendicular to the direction of migration. The Fokker-Planck formalism utilizes the free energy landscape of polymer chain across the channel in presence of entropic trap to calculate the migration time. It is revealed that the migration is fast when the solvent gradient acts along the migration axis (say, x -axis) inside the channel in compare to the channel having entropic trap. We also study for the first time that the entropic trap makes the migration faster at certain value of solvent gradient. We also study the effect of transverse solvent gradient (along y -axis) inside the trap and investigate the structural changes of the polymer during migration through the channel. We observe the non-monotonic dependence of migration time on the solvent gradient.

Chapter 3 deals with force induced unzipping of a dsDNA (double stranded DNA) by applying force on a single strand (while other strand is free) in presence of an attractive surface. Manipulation of force on pulled strand, surface attraction energy and temperature reveal various phases of dsDNA. We report that at low surface attraction dsDNA desorbs as zipped form and melts in bulk at higher temperature. While at high surface attraction dsDNA unzips from the surface itself below melting temperature. Noteworthy finding includes that at moderate surface attraction the desorbed but zipped dsDNA melts with increasing temperature and the free strand gets adsorbed to the surface.

The separation of two strands of dsDNA may be induced either by changing the temperature (DNA melting) or the pH value of the solvent (DNA denaturation). In chapter 4, we study the DNA melting and translo-

cation of a biopolymer (*cis*-side to *trans*-side) across a cone-shaped channel. The shape of MSPA protein pore looks like a cone-shaped channel. Motivated by this, we model the system on a square lattice in such a way that its 3/4 volume corresponds to the *trans*-side, and the remaining 1/4 volume is of *cis*-side. We study the melting profile of dsDNA across the pore, which differentiates two different kinds of solvents. If solvent across the pore remains the same, the dsDNA prefers to stay in the *trans* side for all temperatures due to the large configurational entropy of the dsDNA available on the *trans* side. When the *cis*-side contains poor solvent, we observe that the DNA prefers to stay on the *trans* side with relatively poor solvent.

Chapter 5 deals with the equilibrium properties of a dsDNA confined in a strip. One side of the strip contains a relatively poor solvent compare to another side. This induces a solvent interaction gradient which may be thought of as a temperature gradient. This allows us to model DNA thermophoresis, where DNA migrates from the hot side and gets accumulated near the cold side. We employed a simple lattice model of polymer to show that dsDNA transfers to the cold side in a zipped form at a particular solvent interaction gradient. We have also studied the effect of sequence (AT-rich, GC-rich, AT-GC diblock DNA) under varying solvent interaction gradients. We observed that GC-rich DNA migrated faster to the colder side in comparison to the AT-rich sequence.

In chapter 6, we summarize the overall results of the thesis and comment on the future perspective of our studies.

Acknowledgements

It was a dream for me to have a Ph.D. degree in Physics, and today while I am writing this acknowledgment part, it feels like I am getting closer to that dream. I am privileged to have this space to mention those who have played a role in the completion of the thesis.

First and foremost, I want to express my sincere gratitude towards my supervisor Prof. Debaprasad Giri. During the course of study, he has always stood by and motivated me to explore more in the subject field and simulation studies. Especially in the early days of my Ph.D., when I struggled to find the right way, he advised me to work hard and keep patience. I can not thank him enough for the critical reading and checking of the thesis. The amount of liberty I had while working with him can not be expressed in words.

I want to express my heartfelt gratitude towards my collaborator, Prof. Sanjay Kumar, Department of Physics, B.H.U. I am privileged to be a part of his lab. He is always up for a discussion, and I have learned uncountable things about polymer physics during those interactions. His insights on analyzing a research problem have motivated me a lot during this journey. I am really grateful to him for reviewing the manuscript of the thesis.

I thank RPEC members Dr. Shradha Mishra and Dr. Indrajit Sinha for their constant encouragement and insightful advices during the course of study.

I want to convey my regard to Prof. Sandip Chatterjee, Head, Department of Physics, IIT (BHU) for his support. I thank all the faculties who have taught me during coursework. Especially, I wish to congratulate Prasun Da for many eating outings and the trek to the Himalayas. Those brought much relief during this journey.

I am indebted to the computational resources that I got in Sanjay Sir's lab. Computational facility of Paramshivay supercomputer in IIT (BHU)

is duly acknowledged. I am also thankful to the office staffs of Physics Department, IIT (BHU).

I would like to take this space to thank Prof. V. Balakrishnan's lecture videos which helped me to understand statistical mechanics. His lectures have had a significant influence on carrying my research in the field of statistical physics.

The ups and downs during the years of Ph.D. were memorable. I must thank all my labmates and friends in campus who helped me to complete this journey. At first, I want to thank my seniors, Dr. Amit Raj Singh, Dr. Sesh Nath, Dr. Atul Bharadwaj, Dr. Manoj Jaiswal, Dr. R. K. Singh, Dr. Sadhana Singh, for many discussions about and beyond the research field. I want to thank current lab members Anurag, Ankit, Keerti, Mamta, Manish, Sumitra Di, Dr. Suresh Kumar, Dr. Swarnalata Singh, Dr. Vimal Kishore for their constant support. Special mention to our small group of Mamta, Manish, Sadhana Di, and me for countless dinner parties after a long workday. I am also grateful to 'Dhiraj ki chai' (tea shop) for serving us tea in any odd times which was an integral part of everyday routine. I want to thank friends on campus, Rakesh, Pavan, Bishnu, Ankur, Akher Da, Suresh, Asish, Vinod, Gautam, Vivek, and Nayan Da. My heartfelt wishes to Rakesh and Chinmoy for their excellent company during the early days of my Ph.D. I am also fortunate to have met a Bengali group of friends on BHU campus, Surajit Da, Debraj Da, Topo Da, Kamalika Di, Moumita Di, and Kumkum Di. I want to thank friends of my B.Sc and M.Sc days in Calcutta University, Argha, Soumen, Soumya, Ripon, Raghav, Yeasin, Soumee, Sangita, Pabitra, Soumitra, Dhawal, and Munmun who have encouraged me to take this journey.

Words are not enough to thank friends back at home for always being supportive of my choices in life. Kajal and Dhiman are both the pillars of the little achievements that I have received to date. I am also thankful to Rupamoy Da, Sudip Da, Laki Da, Sujit Da, Prabir, Subir, Proloy, Saikat, Anand, Rajib, Bagha, Antu, and Ashim.

I want to thank my family, who I owe so much, and to whom I dedicate

this thesis. My inspiration, Maa and Baba, have always kept me on track by motivating me to look on the bright side of every aspect of life. Their constant encouragement in every little step of my education made me challenge myself to do better in this journey. Lastly, I want to thank my wife Samima Sabnam for her support, encouragement, love, and caring. I express my heartfelt appreciation towards her for believing in me and motivating me during the hard times of my Ph.D.

Date:24/11/2021

Place: Varanasi

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