CSCI 4314: Homework 1

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Part 1

Problem 1

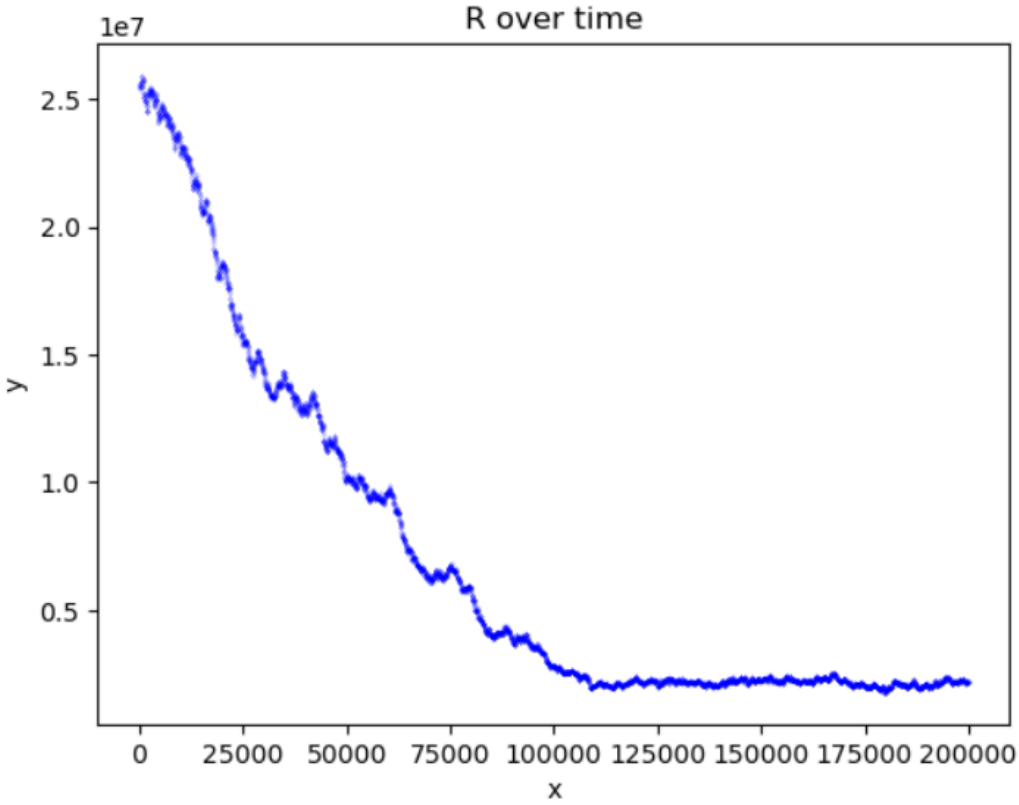

Figure 1: N = 25

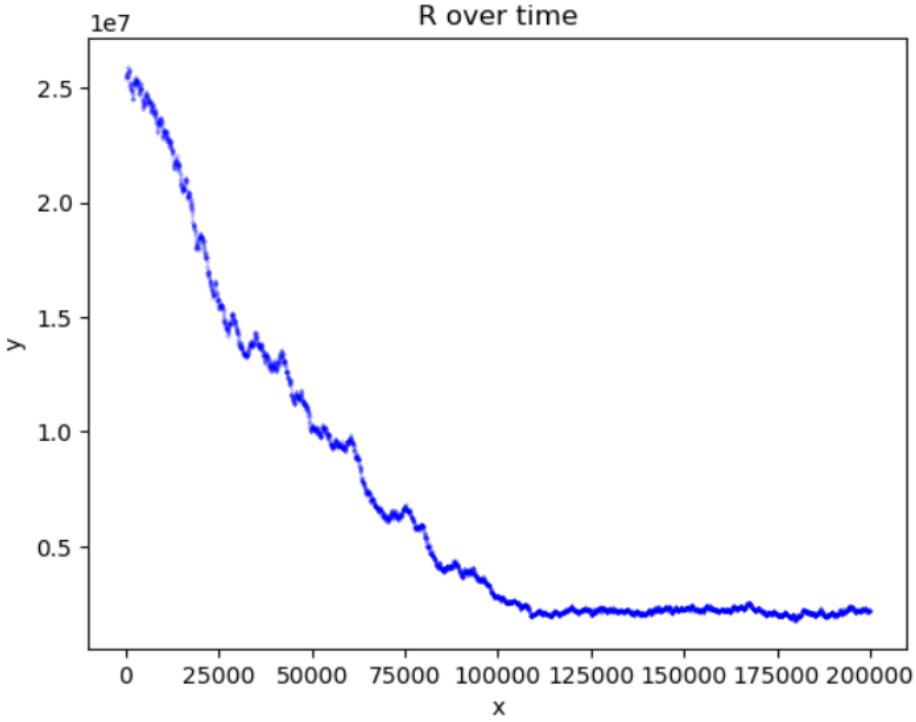

Figure 2: N = 10

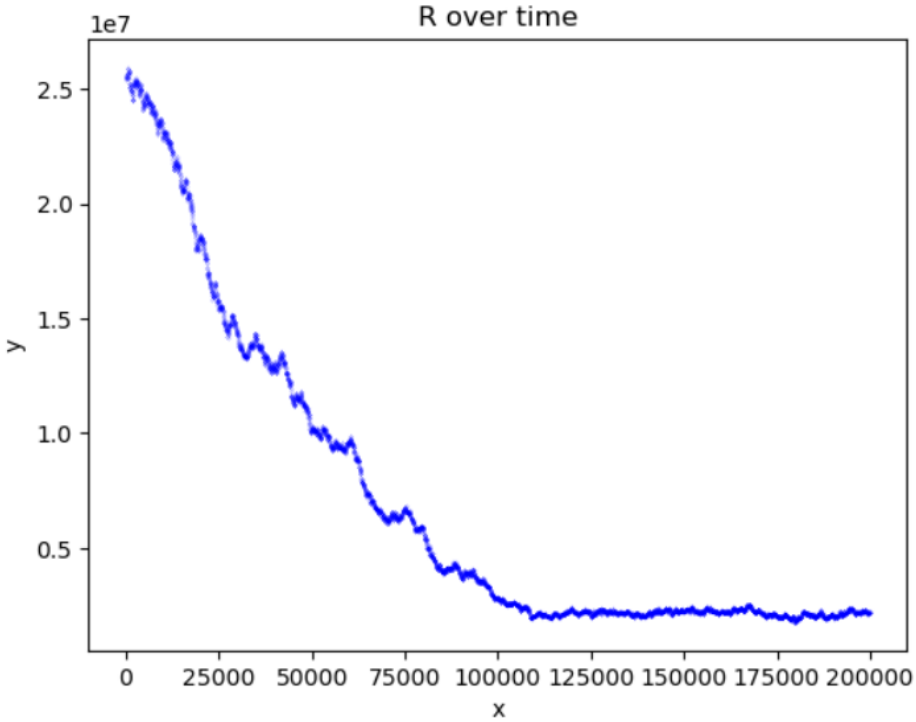

Figure 3: N = 5

Problem 2

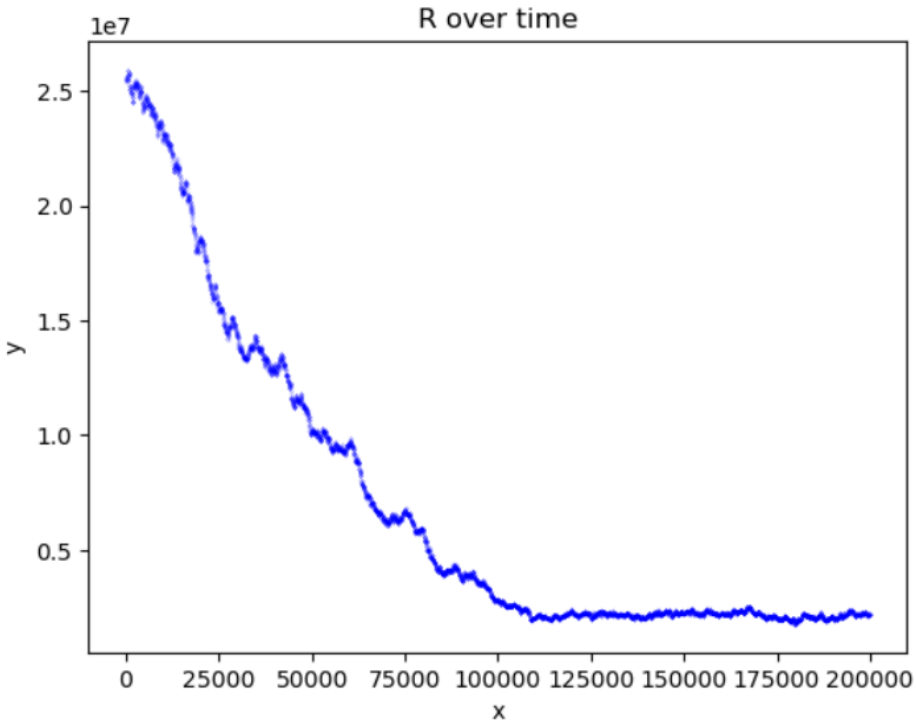

Figure 4: $\epsilon = 1$

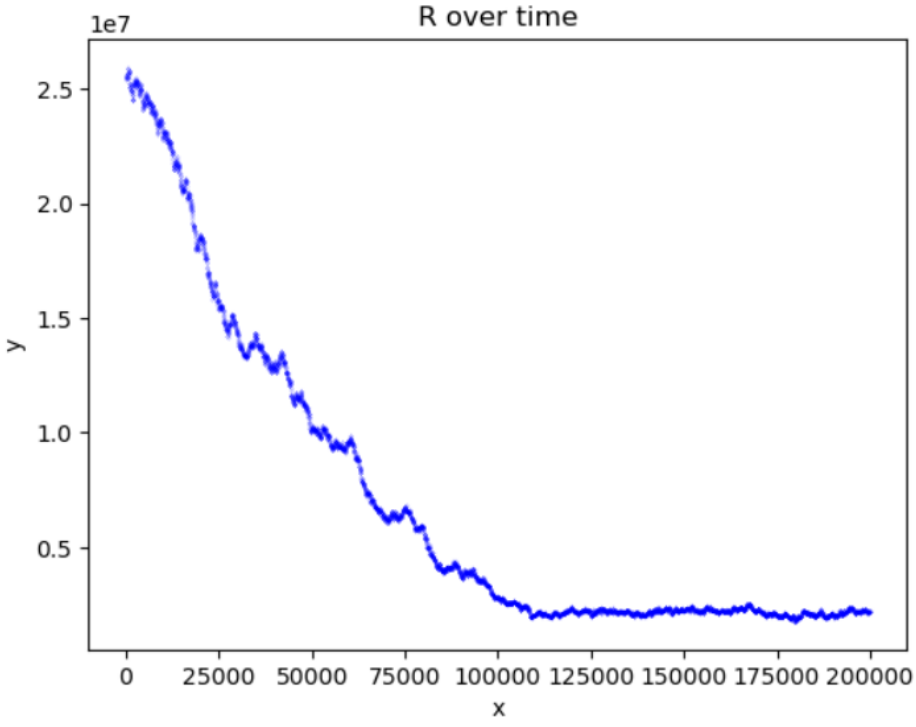

Figure 5: $\epsilon = 0.5$

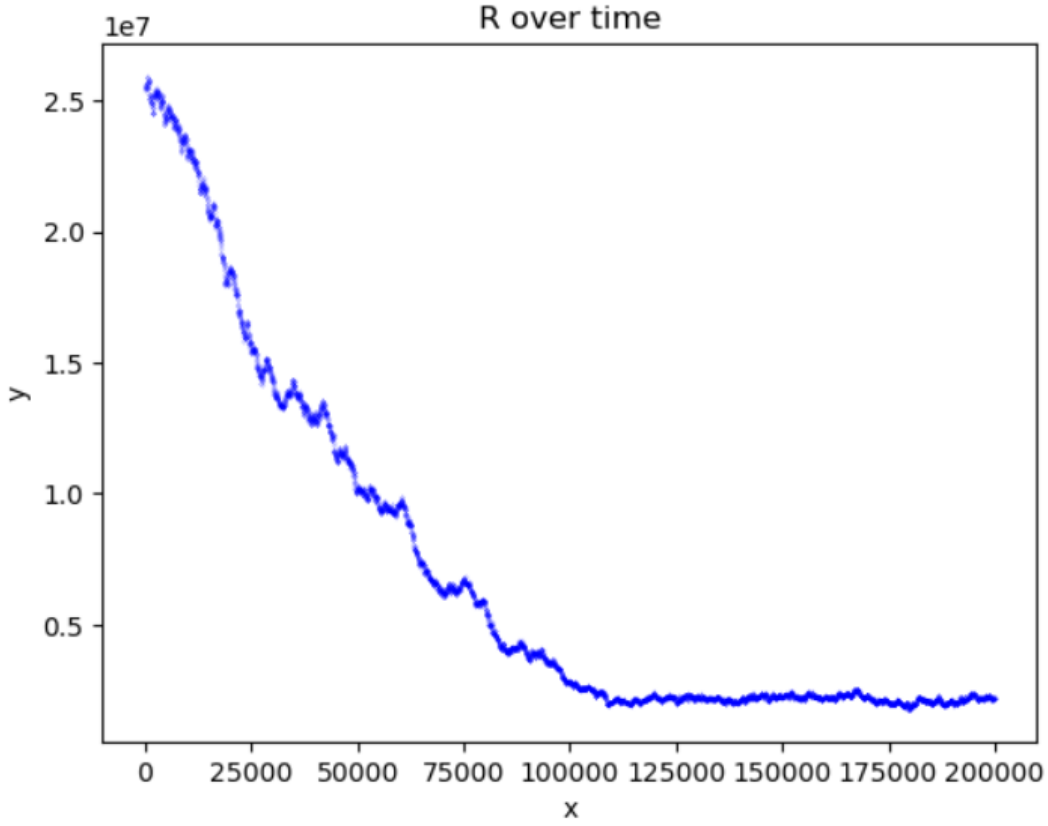

Figure 6: $\epsilon = 0$

Part 2

The paper's main contribution is showing how both principles of biotechnology - sequence summery minimization, and dynamic mathematical modeling - the mathematical theory of tiling, can combine to produce self-assembling DNA crystals. In particular, it shows how these self-assembling DNA bio-algorithms can create 2D periodic lattice nanostructures. The essential principle of intermolecular interactions between the sticky ends of branched B-form DNA was exploited to design a process using the mathematical theory of tiling, using Wang tiles, to create a process capable of molecular self-assembly. The sticky ends, which use Watson-crick complementary base pairing, are used to tack together the different antiparallel DNA double-crossover units to produce a woven sheet of material that is able to be manipulated. One of the major strengths of the paper is the attention to detail in describing all of the different fields of knowledge and terminology, creating a very reader centered presentation. The authors do a great job of defining terms and processes of both the mathematical profession along with the biological. One shortcoming of the paper was the lack of reporting on the potential failings of the denaturing polyacrylamide gel electrophoresis (SDS-PAGE) run. I found it interesting that when they couldn't determine the full extent of polymerization they did not do follow up runs to discount the possibilities of poor separation of the protein targets. This is one of the most common issues associated with western blotting techniques (or any other general lab mistake). Another questionable decision made by the paper was the choice to use the old school heuristic approach of sequence summery minimization and not adding on the idea of Mismatch distance that lessons the chance of unwanted intermolecular interactions. As this research continues onto the future it would be interesting to see the 2D DNA structures advance into the creation of the 3D realm; wherein the DNA lattice work has the ability to create the scaffolds for the crystallization of macromolecules like carbohydrates.

Appendix: Code

My Homework 1 Code on GitHub (https://github.com/slowHands7/CSCI4314/blob/main/hw1.py)