

Starch composite Hydrogels for Waste-Water Treatment

DISA- Design Innovation Summer Award

Summer of 2018
May '18 – July '18



Proposed By :

- | | | |
|------|---------------|---------------|
| I. | Rohan Yuttham | (2017ME10605) |
| II. | Arpit Agrawal | (2017ME10566) |
| III. | Aman Kumar | (2017CH10196) |

Under the supervision of:

Dr. Gaurav Goel

Table of Contents

- Abstract
- Excerpt of the work done in the project
- Analysis
- Future Aspects and Conclusion

Abstract

The central goal of the project was to study the interaction between Thermo-plastic starch, water, and clay Nano-particles in a simulated environment.

To achieve this goal, we worked with the software namely,

- Gromacs
- Packmol
- Pymol

The duration of the project was 8 weeks during the month of May to July.

Excerpt of the work done in the project

1. Prepared a correct topology file of Thermo-Plastic Starch(TPS) from available coordinate files of
 - Amylose,
 - Amylopectin, and
 - Sorbitol.

From previous research work done we had the composition of TPS as –

Compounds	#mols
Amylose	90
Amylopectin	42
Sorbitol	4633
Water in Charmm36	$256 \times 13 = 3240$

And we get the weight of TPS= $W_i = 1.34 \times 10^{-21} \text{g}$

2. To accomplish our task, we required to make a hydrogel system with percentage composition(w/w) as-

- a. TPS-10%
- b. Water-90%

3. Now we aimed to prepare the final hydrogel in a cubic box of side length 15 nm equivalent to volume of 3375nm^3 .

We were expecting a density less than 1.1 g/cm^3 and greater than 1 g/cm^3 .

So, we needed to find the **weight of thermos-plastic starch** using the above data.

Calculation:

Assume total weight of system as 'x' gram.

Then, Weight of TPS= 0.1'x' gm

Its density= 1.34 gm/cm^3

Its volume = $(0.1\text{x}/1.34)\text{ cm}^3$

Weight of water= $.9\text{x gm}$

Its density= 1gm/cm^3

Its volume = 0.9x cm^3

So, total volume = 0.975x cm^3

Equating it to $3375 \text{ nm}^3 \Rightarrow \text{Weight of TPS (x)} = W_n = 0.3462 \times 10^{-18} \text{ g}$
Which gives $W_n/W_i = 0.08$

Maintaining this ratio of weights calculated from above data, the new number of moles will be 0.08 times the previous one-

This gives:

Compounds	#mols
Amylopectin	3
Amylose	7
Sorbitol	371
Water	1X256

Total mass (from gromacs) : 445722.081 amu

- 4.** Now we packed these molecules using the software “Packmol”.

The output is a .pdb file.

- 5.** Next ,we prepared a correct topology of TPS.
We used ‘pdb2gmx’ and edited the topol.top file according to our need.

6. Begin with simulations in Gromacs.
7. First step is solvation of the box.
 - i. Command used- `gmx solvate`.
Results:
 - a. Volume- 3375 nm^3
 - b. Density- 1.097 gm/cm^3
8. Secondly, Energy Minimization of the solvated system
The parameters are given in `minim.mdp`^[1].
9. It was followed by NVT and NPT steps. The parameters are given in `nvt.mdp`^[2] and `npt.mdp`^[3] respectively.
10. After completion of the two equilibration phases, the system was well-equilibrated at the desired temperature and pressure.
11.
We are now ready to release the position restraints and run production MD for data collection. The script is given in `md.mdp`^[4].

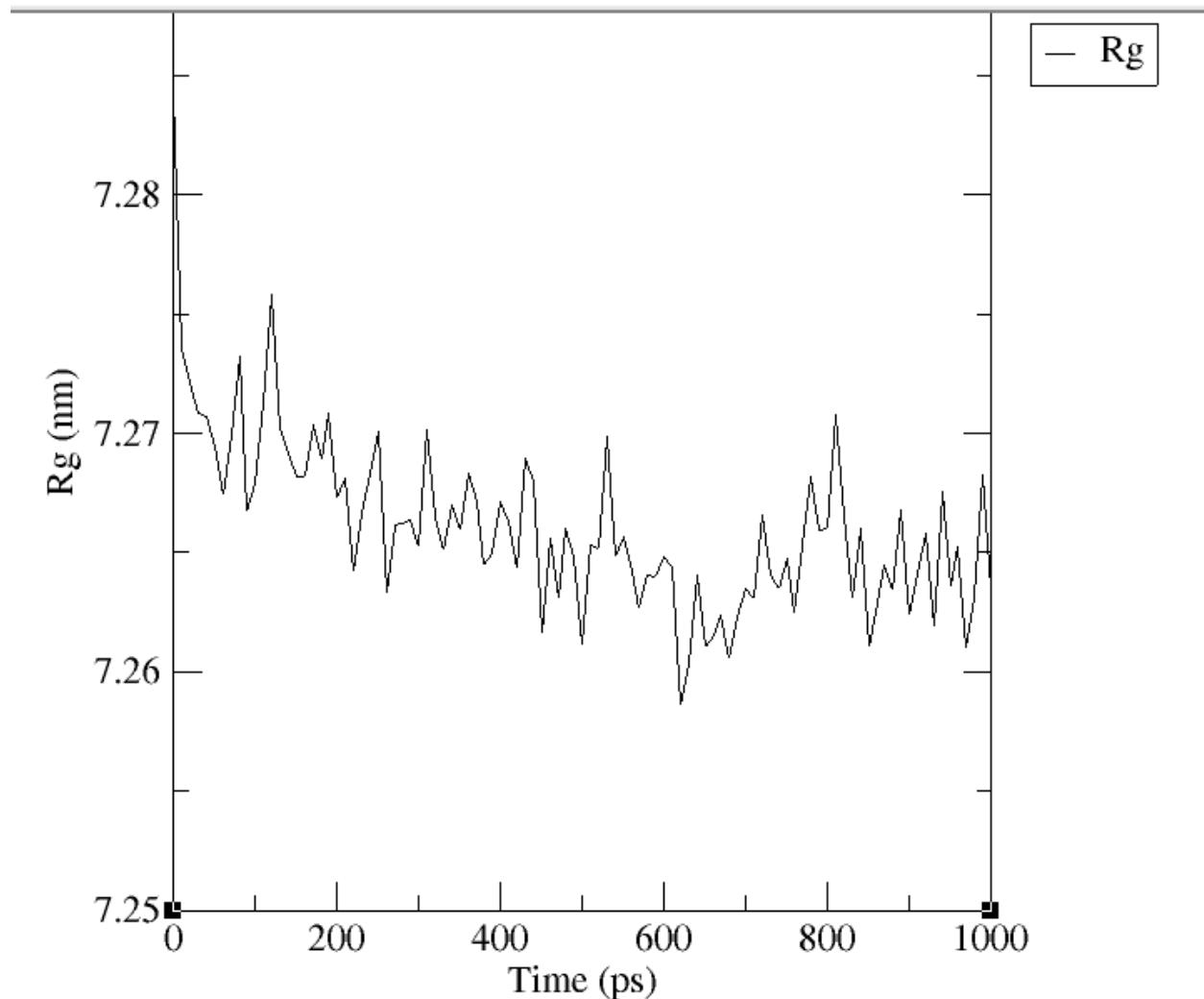
Finally we got a `md_0_1.gro` file and other associated files with it.

Note: that the temperature, pressure, simulation time and other parameters are stored in the `.mdp` script. The parameters were decided based on discussions with seniors.

Analysis

- Radius of Gyration

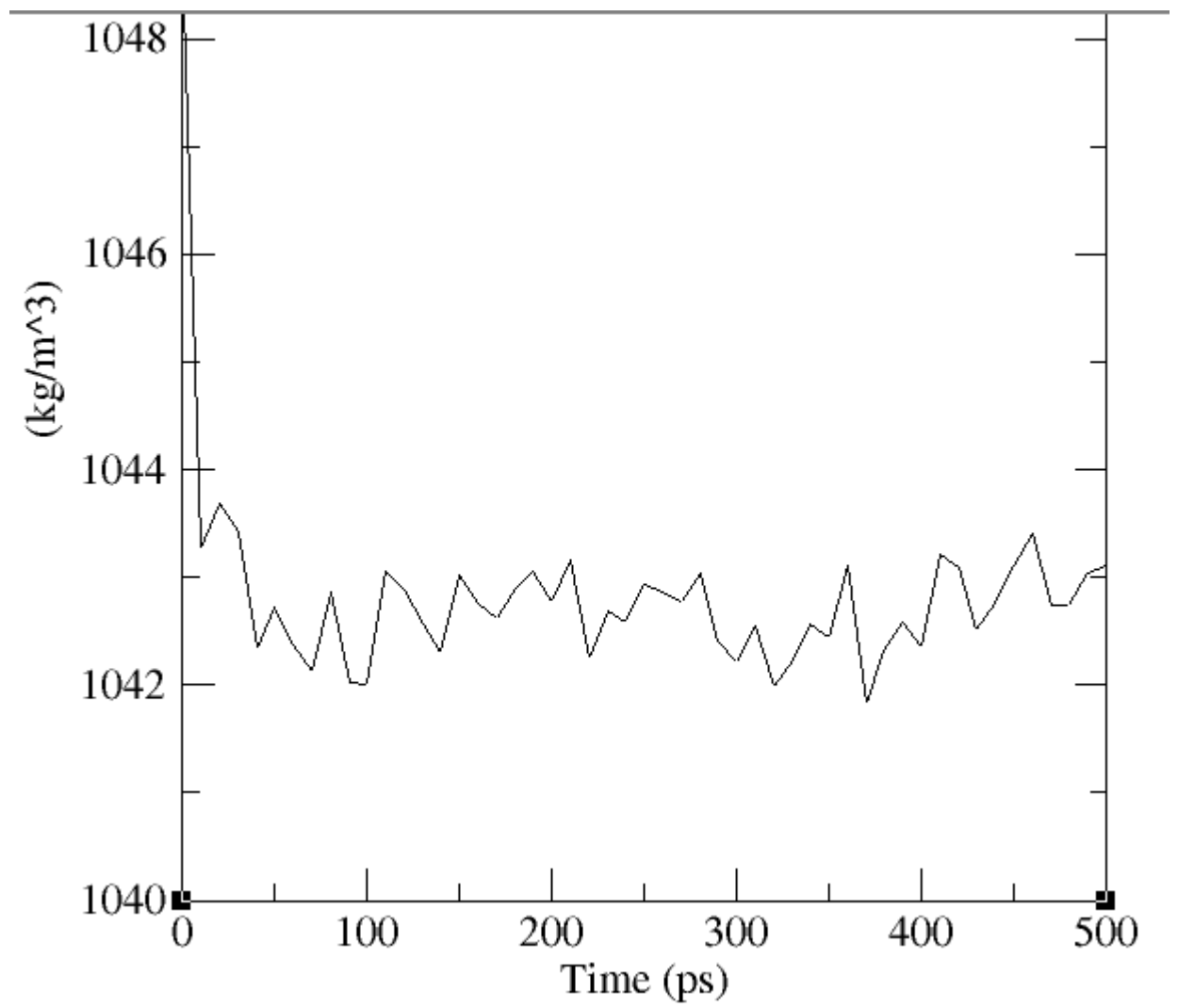
The R_g is plotted against time as



* The radius of gyration of a protein is a measure of its compactness. If a protein is stably folded, it will likely maintain a relatively steady value of R_g . If a protein unfolds, its R_g will change over time.

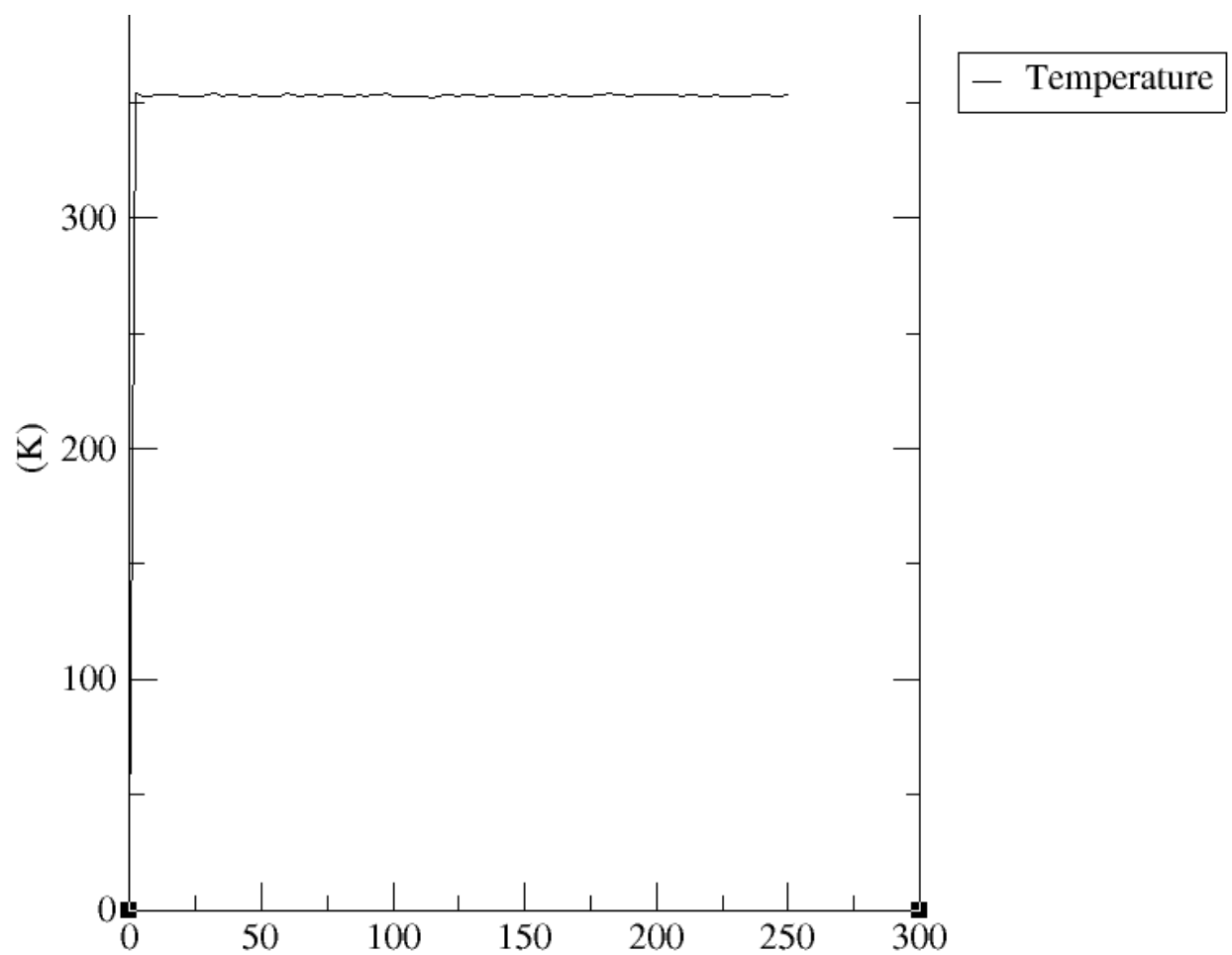
- Density

The density is plotted against time as



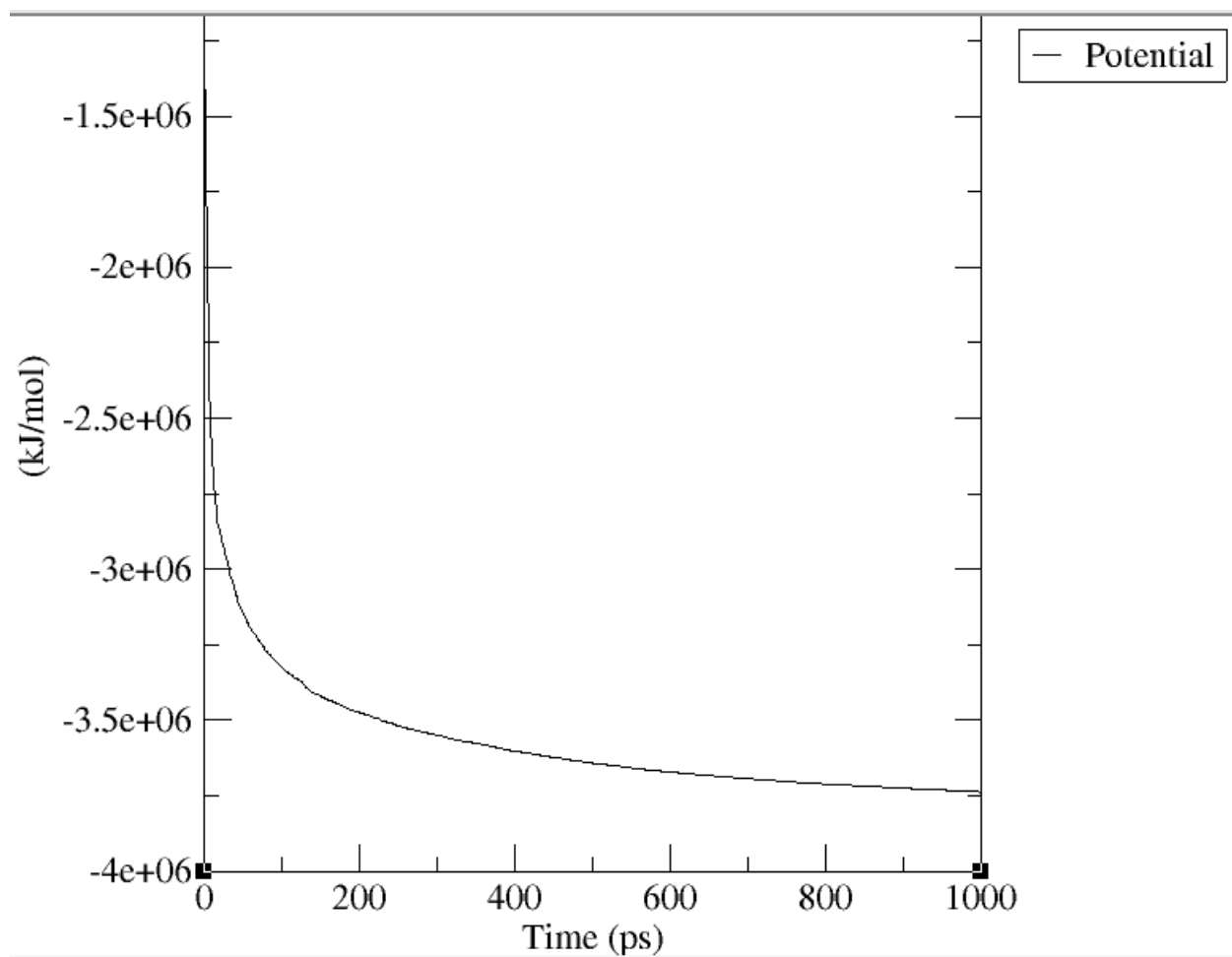
- Temperature

The temperature is plotted against time as



- Potential

The potential is plotted against time as



- The box size being small, some chains might have been incomplete due to finite chain length.
- So, we did new simulation with a cubical box having side length 23nm.

By calculating no of chains from the method mentioned above, required no of chains are:

compounds	#chains
amylose	21
amylopectin	10
sorbitol	1066

- After this the box was solvated with water molecule and performed the energy minimization ,nvt, npt simulations in the similar way.
- This system was much more feasible than the 15nm system due to optimized parameters.

*The files of the above system are also attached.

Future aspects and conclusion

- The equilibrated system of the hydrogel prepared can be used as an adsorbent when simulated with clay nanoparticles with the clay nanoparticles and heavy metals behaving as adsorbates.
- The surface of clay MMT can adsorb certain heavy metal particles on its surface.