

Lab 5 : Polymers

MSE-421 Statistical Mechanics

Contents

Objectives:

1. How does temperature alter the shape of polymers?
 2. Study the coil-globule transition and obtain the crossover temperature
 3. Estimate the Flory exponent and characterize the polymer
-

Deadlines:

- Lab04 (Liquids) : Wednesday, 29 May 2024, 03:00
- Lab05 (Polymers) : Tuesday, 4 June 2024, 03:00

Polymers in everyday life



Polyisoprene



Teflon



Polyester



Polyethylene



Proteins
(myoglobin)

Polymers

Staudinger (1920) : Macromolecular Hypothesis

“Polymers are molecules made of covalently bonded elementary units, called monomers.

Staudinger, H. (1920), Über Polymerisation. Ber. deutsch. Chem. Ges. A/B, 53: 1073-1085 (in German)

(Nobel Prize in Chemistry 1953)

I U P A C	Recommended Term	CC BY SA
polymer		
A substance composed of <u>macromolecules</u> .		
<i>PAC, 1996, 68, 2287. (Glossary of basic terms in polymer science (IUPAC Recommendations 1996)) on page 2289</i>		
More info at: https://doi.org/10.1351/goldbook.P04735		Official IUPAC Definition

<https://en.wikipedia.org/wiki/Polymer>

Flory Theory of a polymer chain

Established by Paul J. Flory (Nobel Prize in Chemistry, 1974)

Paul J. Flory – Nobel Lecture. NobelPrize.org. Nobel Prize Outreach AB 2024. Thu. 23 May 2024.

The theory lies on the assumption that we can consider a real polymer chain as composed of two components:

1. An ideal (no interactions) chain (entropic contribution)
2. A dilute 'gas' of monomers (energetic contribution)

For a real polymer chain, monomer-monomer and monomer-solvent interactions are considered.

Scaling “law”

$$R_g \sim bN^\nu$$

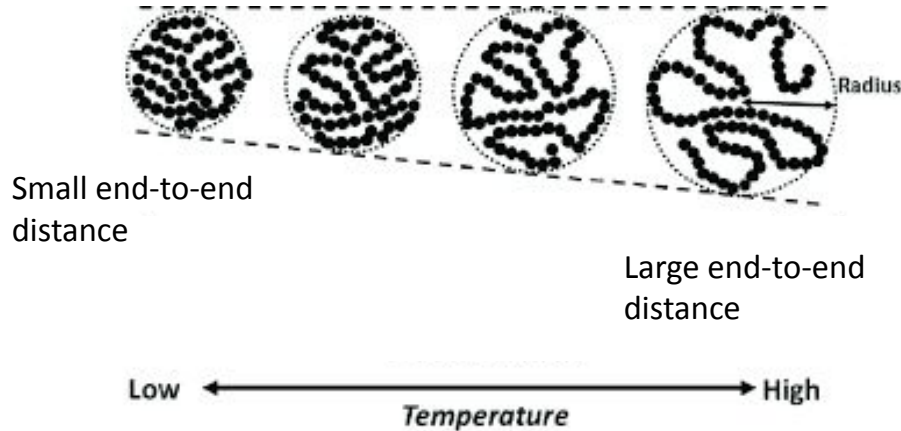
Ideal polymer chain
 $\nu = 1/2$

Coil-globule thermodynamic transition

Of great importance in biology : such transitions are observed in proteins and DNA

J. Chem. Phys. 102, 6595–6602 (1995)

Study the average end-to-end distance as a function of T .



Transition (theta)
point \rightarrow Ideal chain

Polymer in a solvent and scaling laws

- **Good solvent** : A solvent in which a polymer expands
- **Poor solvent** : A solvent in which the polymer collapses
- **theta solvents** : A solvent in which a polymer acts like an ideal chain

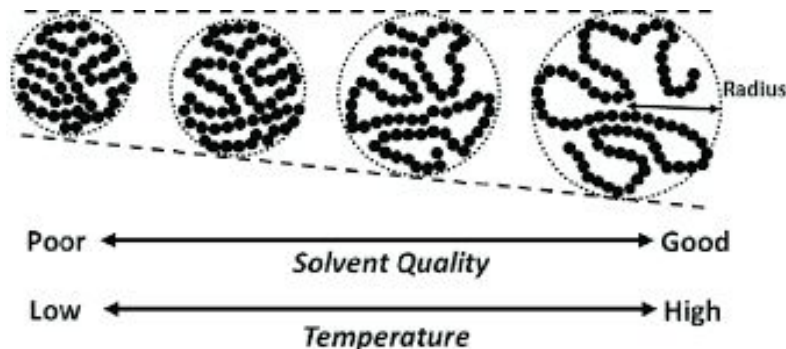
$$R \sim N^{3/5}$$

$$R \sim N^{1/3}$$

$$R \sim N^{1/2}$$

(Random walk)

inter-monomer and
solvent-chain
interactions cancel each
other



$$R = r_N - r_1$$

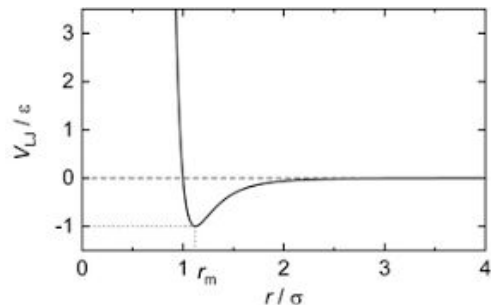
Lab 5

Our physical system:

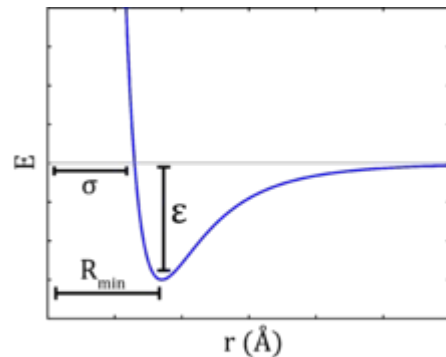
- Single chain in vacuum
- 100 identical monomers
- Monomers are linked by a harmonic potential

$$V_N(\{\mathbf{r}_i\}) = \frac{1}{2}k \sum_j |\mathbf{r}_{j+1} - \mathbf{r}_j|^2$$

- Lennard-Jones interaction between monomers



$$V_{LJ}(r) = 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$



Lab 5

Study the shape of polymer chains for the following temperature values

$$T \in \{0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.4\} \text{ (LJ units)}$$

$$T = \frac{k_B T_{\text{(in K)}}}{\epsilon}$$

Study coil-globule transition and determine crossover temperature.

For a given temperature value $T = 4.4$, extract the Flory exponent.

$$N \in \{75, 100, 150\}$$

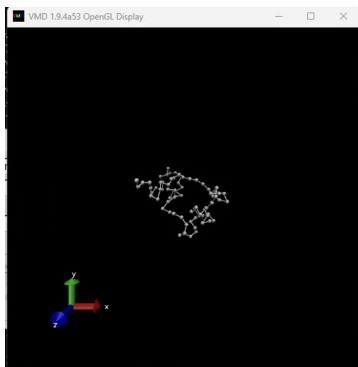
Molecular Dynamics

“MD is the science of simulating motion of a system of particles according to Newton's classical equations of motion”

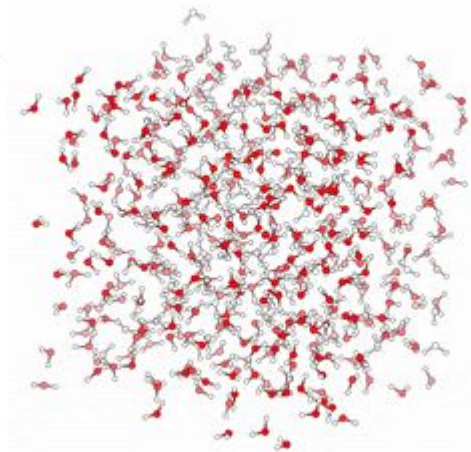
(“[Pursuing Laplace's Vision on Modern Computers](#) | [SpringerLink](#)” by Schlick T.)

You will not have to implement anything!

→ We will use the software Visual Molecular Dynamics



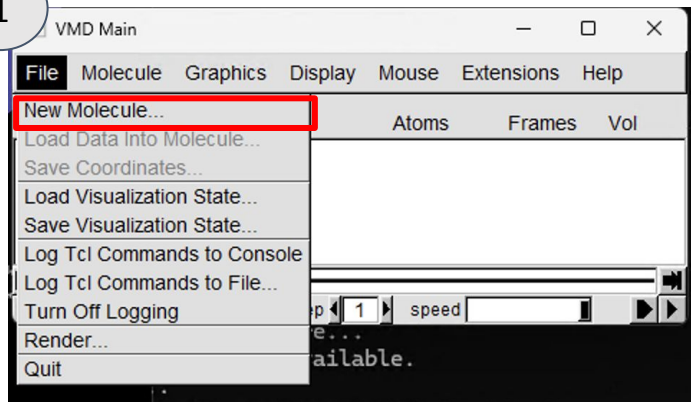
VMD
Visual Molecular Dynamics



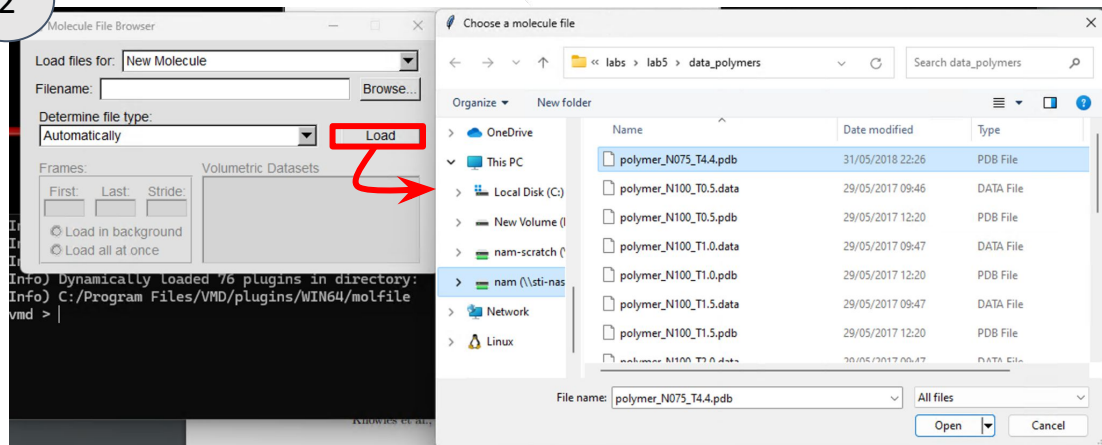
VMD / Load a molecule

Open VMD + load a molecule (.pdb extension) from data_polymers/

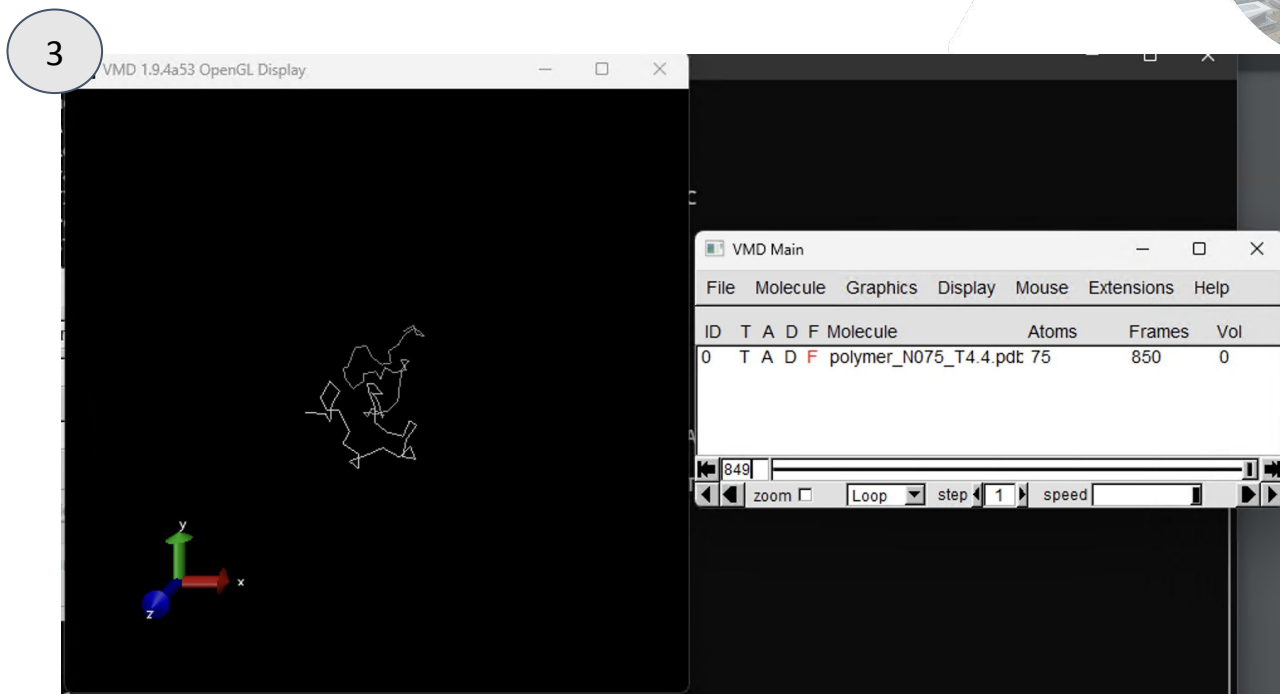
1



2



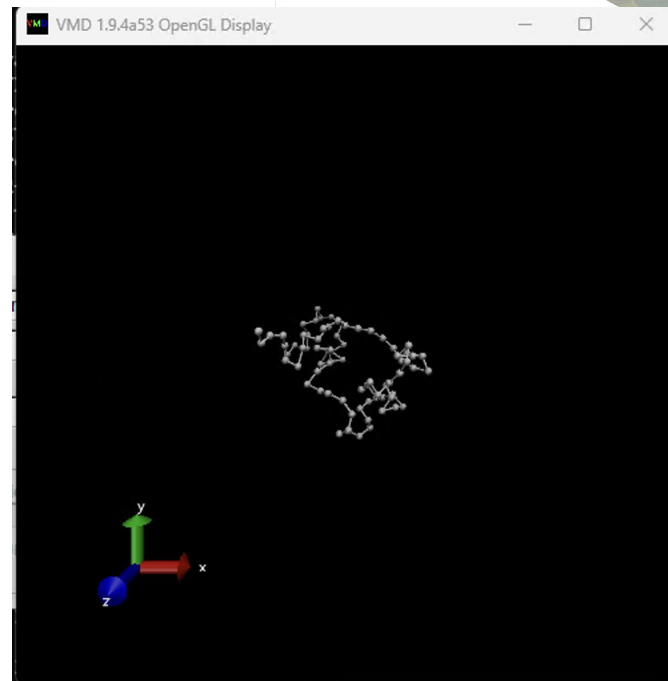
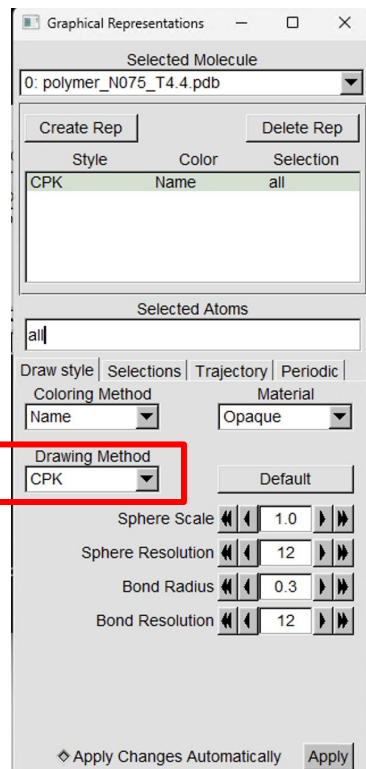
VMD / Load a molecule



VMD / How to make beads visible

From Graphics -> Representations

Choose
CPK in
Drawing
Method

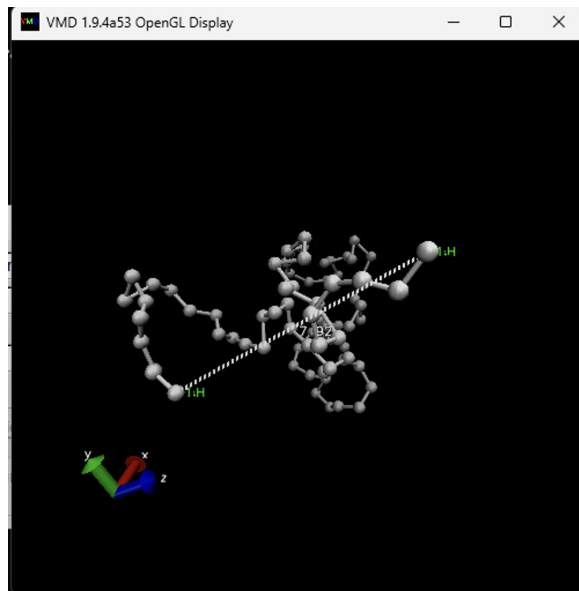


VMD / How to choose end-to-end distance

Use Mouse -> Scale Mode to zoom in

Use Mouse -> Rotate Mode to rotate the structure

Use Mouse -> Label -> Bonds to choose end points of a bond



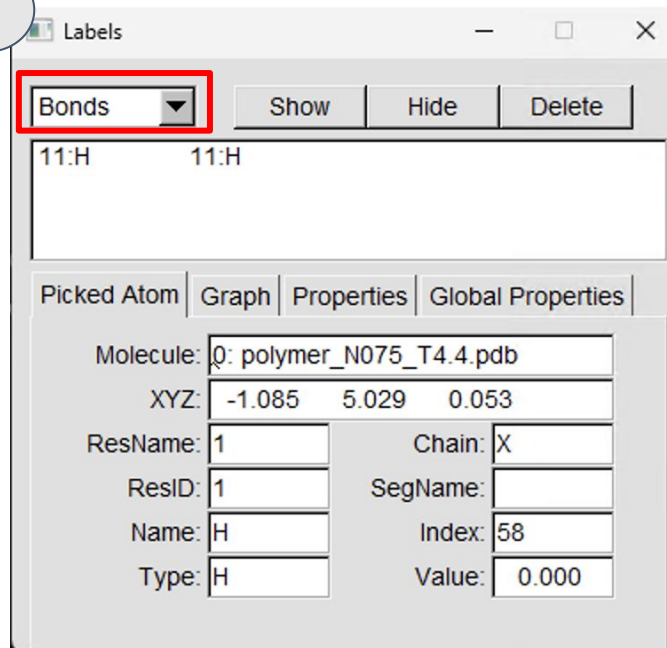
For our polymer,
we can define the
end-to-end
distance

VMD / Time evolution of end-to-end distance

Use Graphics -> Labels

Choose Bonds here

1



2

