

# MOLECULAR DYNAMICS SIMULATION

## Why Simulation?

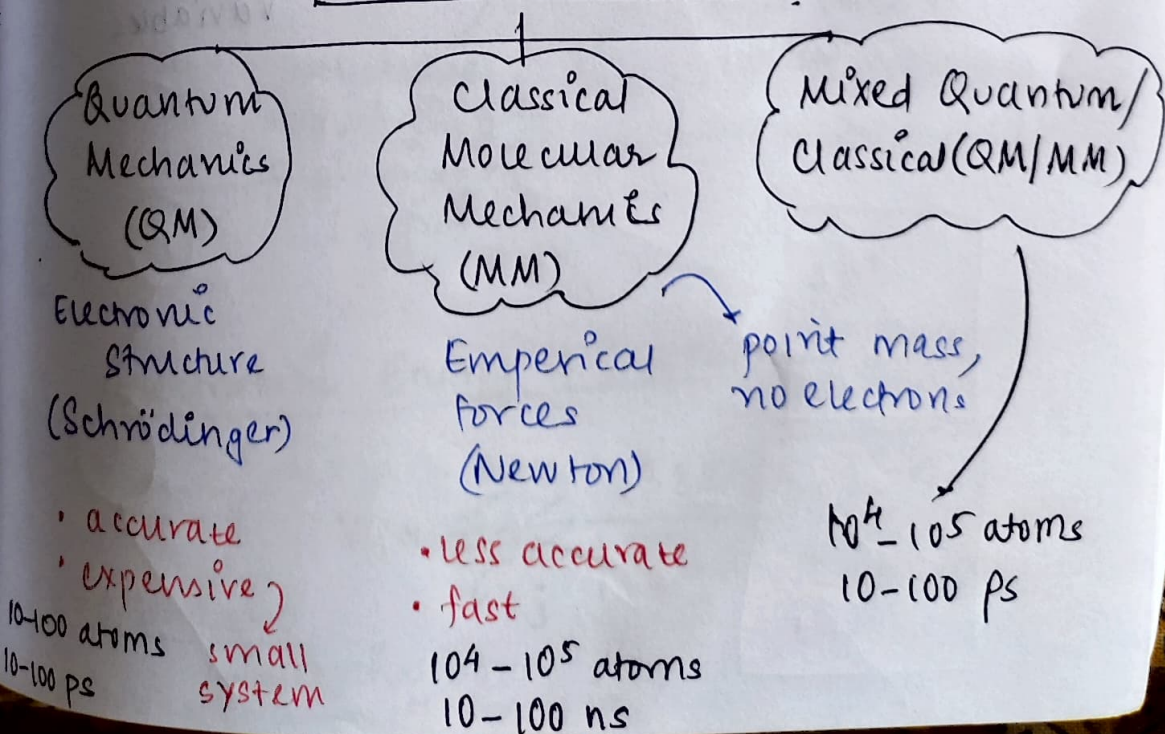
- replace expt.
- provoke expt.
- explain expt.
- aid in establishing intellectual property.

## Molecular Modeling?

descrip<sup>n</sup> of the atomic & molecular inter<sup>n</sup> that govern microscopic & macroscopic behaviors of physical systems.

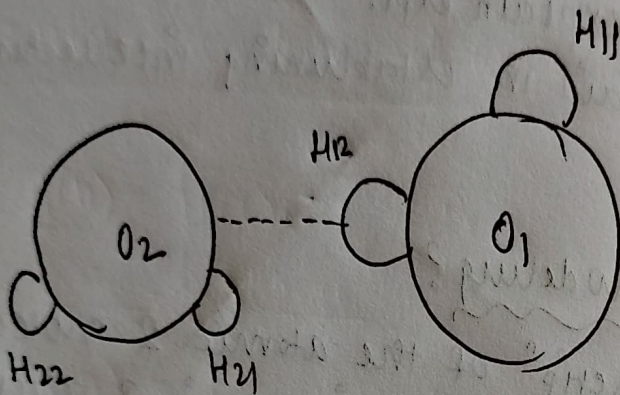
↓  
relation / connection b/w the macroscopic world and the microscopic world provided by the theory of statistical mechanics.

## Computational Tools



Proteins → performs functions in the order of microsec.

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$(x_{O1}, y_{O1}, z_{O1})$

$(x_{O2}, y_{O2}, z_{O2})$

$(x_{H11}, y_{H11}, z_{H11})$

$(x_{H22}, y_{H22}, z_{H22})$

$3N$   
variables

Monte Carlo →  $3N - 6$   
variables

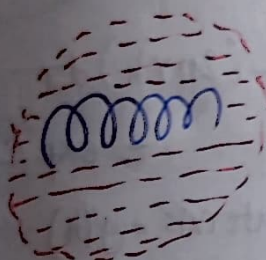


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solvation  $\rightarrow$  water

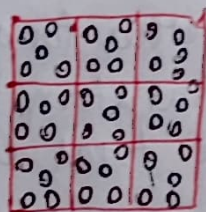
stochastic boundary cond<sup>n</sup>

region of interest is solvated in a water sphere at 1 atm



Explicit Solvent Model

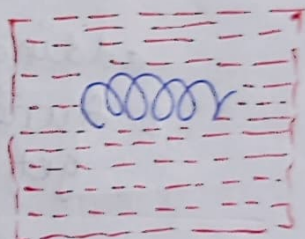
periodic repeats of system of interest



each box has uniform no. of atoms

otherwise applic<sup>n</sup> of laws of physics becomes impossible

the algorithm takes care of that



Periodic Boundary conditions

fully solvated central cell is simulated, in the environment produced by the repetition of the cell in all dim.

Electrostatic Energy of Crystal

$a, b, c \in [0, n]$

$$V = \sum_i \sum_j \frac{332 q_i q_j}{|\vec{r}_{ij} + a\vec{a} + b\vec{b} + c\vec{c}|}$$

$a=0, b=0, c=0$

original box

$a=1, b=0, c=0 \rightarrow$  1st box in x dim.

Periodic repeats of coordn.

$$(x_i + La, y_i, z_i), (x_i + 2La, y_i, z_i) + \dots + (x_i + NLa, y_i, z_i) \\ (x_i + La, y_i + La, z_i), x_i + \dots$$

Fourier Transform<sup>n</sup> of Gaussian Charge Distrib<sup>n</sup>

$$g(h) = \int_{-\infty}^{\infty} \rho(x) e^{-2\pi i x h} dx$$

for each atomic charge:

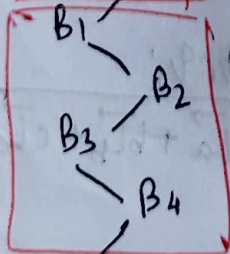
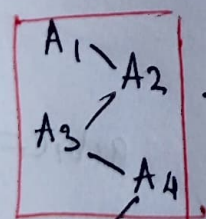
$$g''(h) = \int_{-\infty}^{\infty} \exp(-kx^2) \exp(-i2\pi x h) dx \\ = \exp(-ah^2)$$

adding together for all atoms =  $g''(h)$   
& Fourier transform<sup>n</sup> again to  
get the total energy.

# Coarse Grain Models:

All-atom model  
16 (CH<sub>2</sub> or CH<sub>3</sub> atoms)

centre of mass  
(A<sub>1</sub>-A<sub>4</sub>)



centre of mass  
(B<sub>1</sub>-B<sub>4</sub>)

A

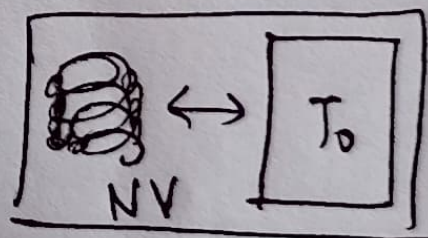
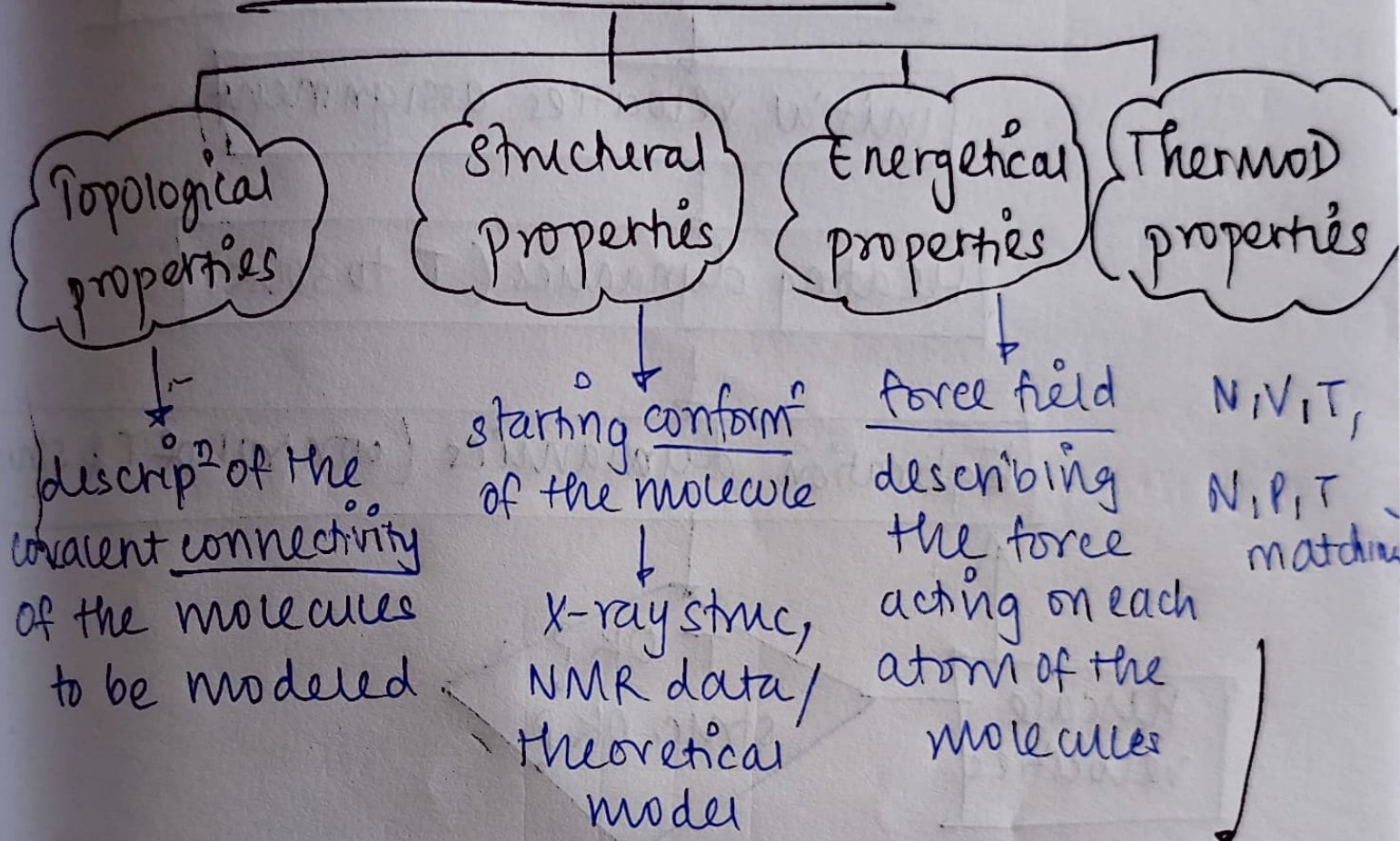
B



VMD - Visualization

Gromacs

Minimal input for MM





# MD flowchart

Q11

