

MOLECULAR DYNAMICS SIMULATION

Why Simulation?

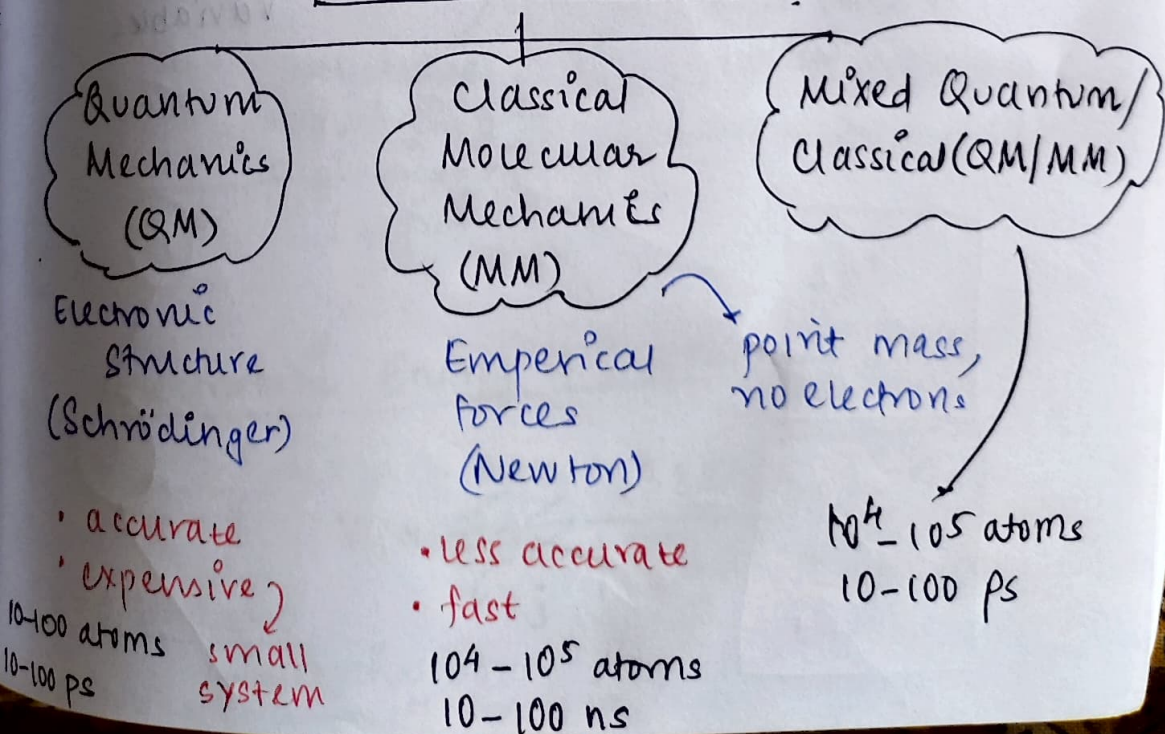
- replace expt.
- provoke expt.
- explain expt.
- aid in establishing intellectual property.

Molecular Modeling?

descripⁿ of the atomic & molecular interⁿ that govern microscopic & macroscopic behaviors of physical systems.

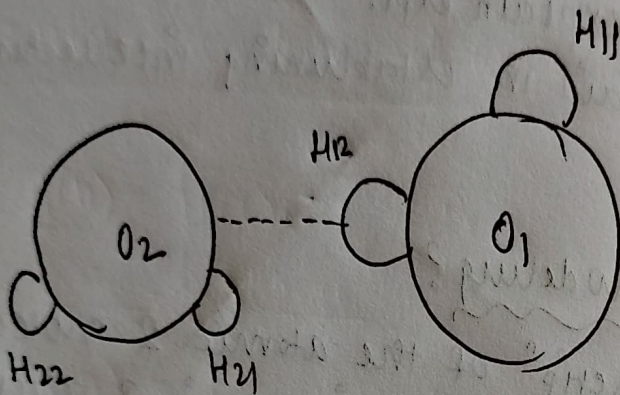
↓
relation / connection b/w the macroscopic world and the microscopic world provided by the theory of statistical mechanics.

Computational Tools



Proteins → performs functions in the order of milisee.

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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

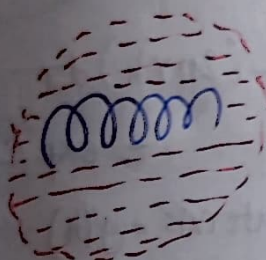
Monte Carlo → $3N-6$
variables

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solvation \rightarrow water

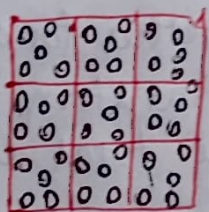
stochastic boundary condⁿ

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



Explicit Solvent Model

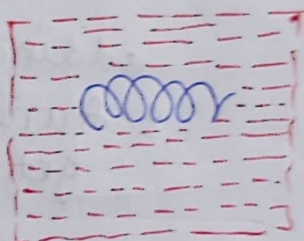
periodic repeats of system of interest



each box has uniform no. of atoms

otherwise applicⁿ of laws of physics becomes impossible

the algorithm takes care of that



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

Electrostatic Energy of Crystal

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

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

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

\hookrightarrow 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 Transformⁿ of Gaussian Charge Distribⁿ

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

for each atomic charge:

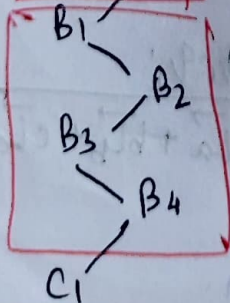
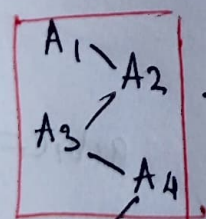
$$g''(h) = \int_{-\infty}^{\infty} \exp(-kx^2) \exp(-i2\pi x h) dx = \exp(-ah^2)$$

adding together for all atoms = $g''(h)$
& Fourier transformⁿ again to
get the total energy.

Coarse Grain Models:

All-atom model
16 (CH₂ or CH₃ atoms)

centre of mass
(A₁-A₄)



centre of mass
(B₁-B₄)

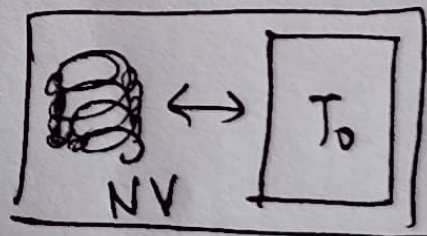
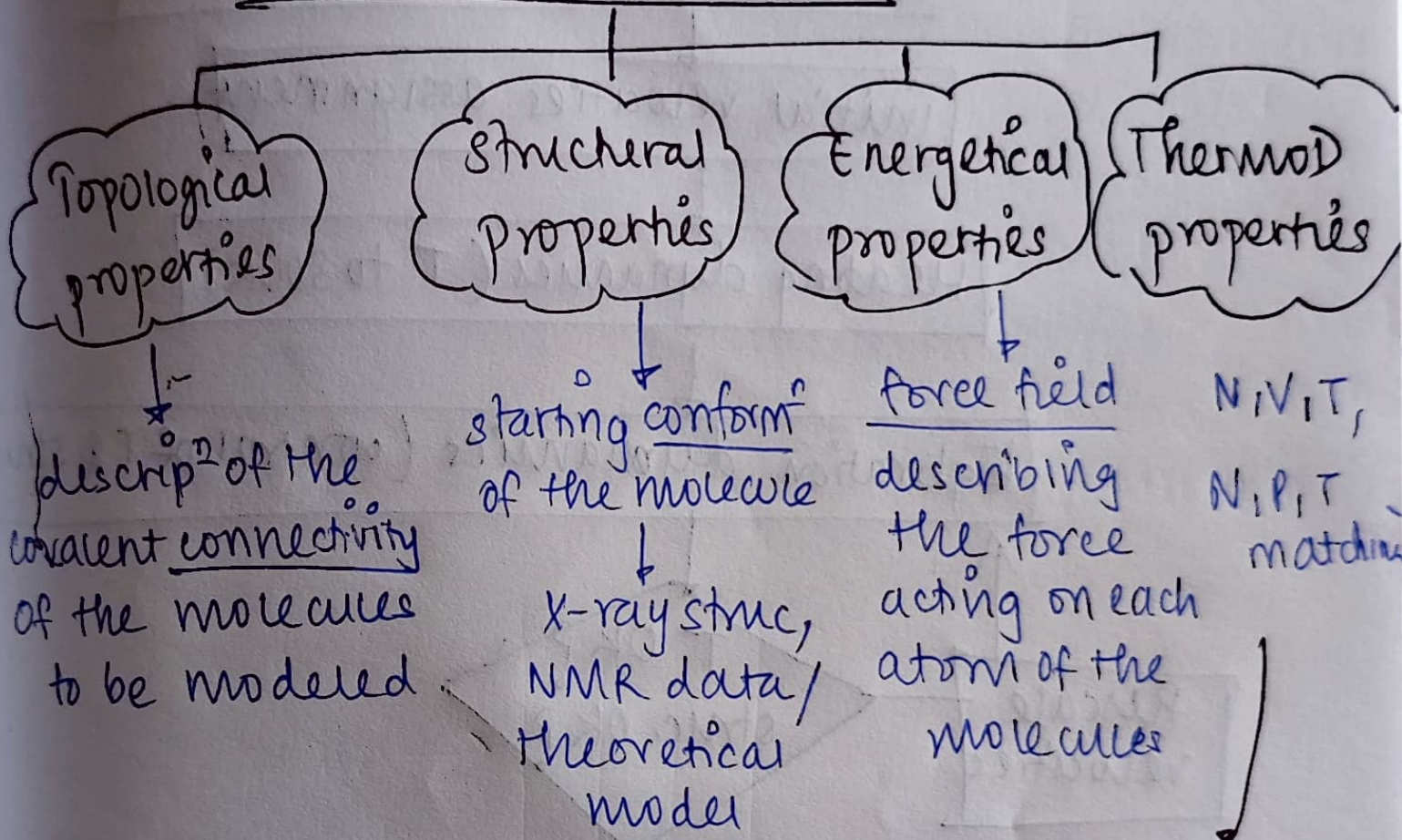
A

B

VMD - Visualization

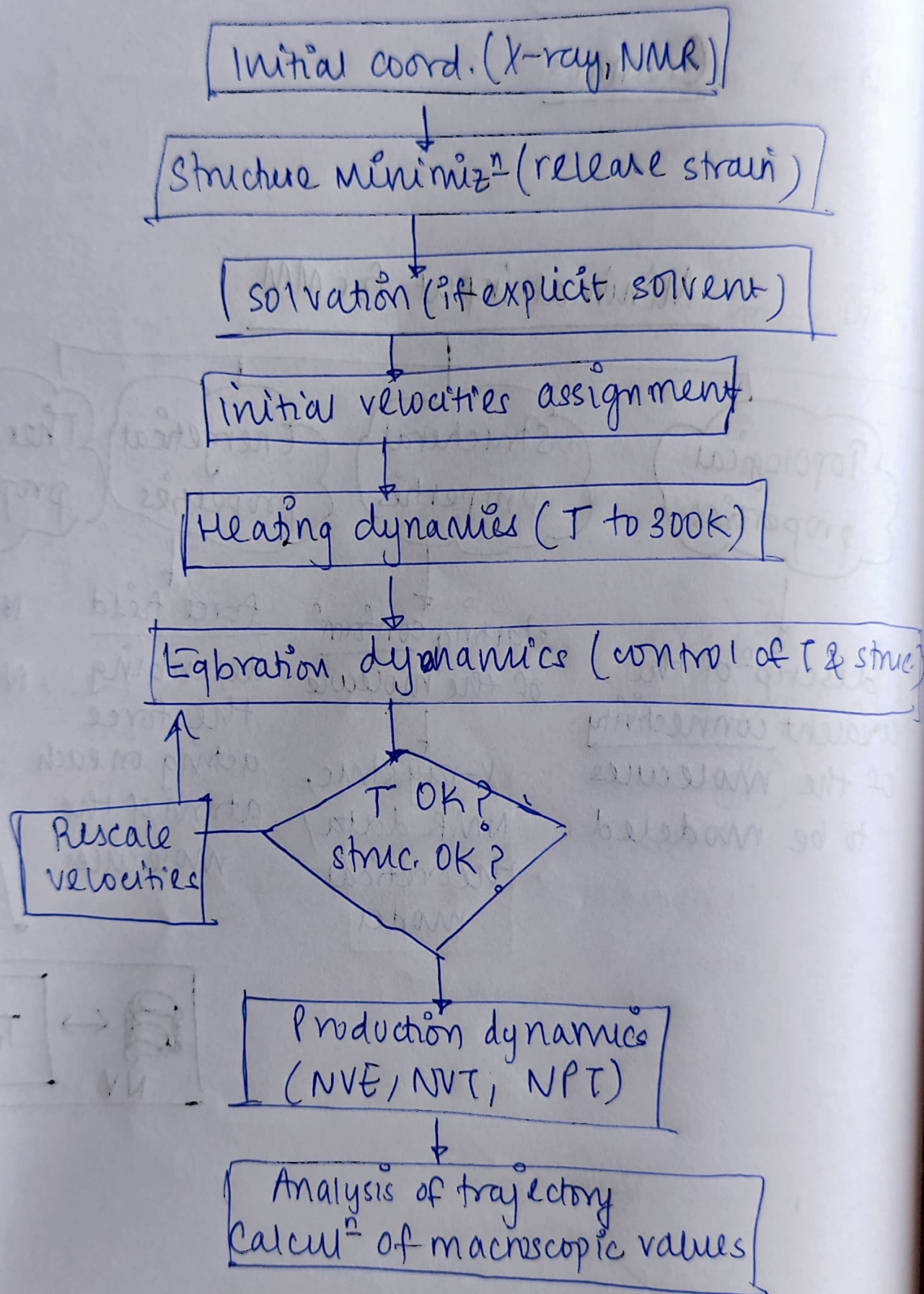
Gromacs

Minimal input for MM

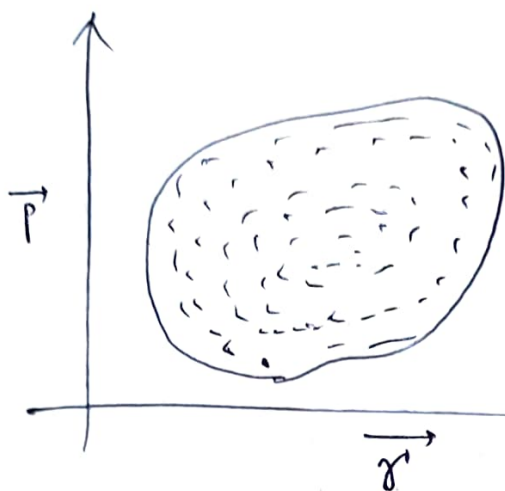


MD flowchart

Q111



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→ depends on the MD simul²

↓

so we do replicates

↓

at least 3

↓

if two are identical

statistically significant ←

rare event ←

if not

Autodock →

whichever interaction has ↓ energy

→ good structure

Structure minimizⁿ

↙

↘

reach a global minimum

→ energy

when we minimize

→

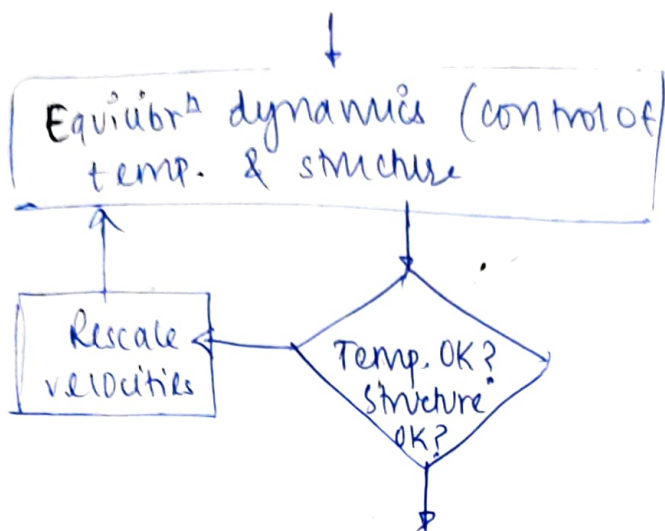
we have to define a force field

- ⇒ Accelerⁿ = 0 ⇒ const. velocity
- ⇒ Atoms are under const. force
- ⇒ Accelerate & velocity ↑
- ⇒ at one point, can burst

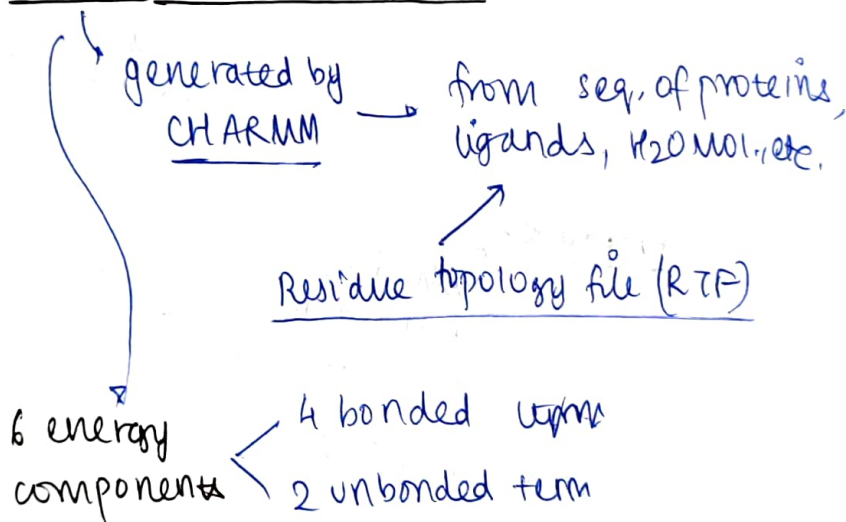
$T \propto (v)^2$

Most proteins: $T = \text{room-temp}$

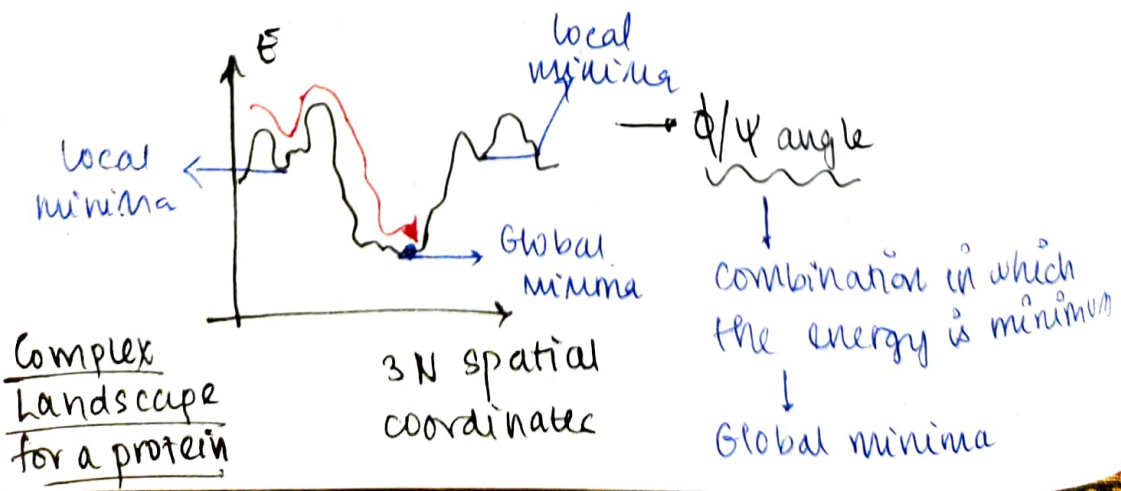
Thermostat



The Protein Structure file (PSF),



Energy landscape



crystal structure we get \rightarrow not minimum energy

How do we go to the minimum E:

\hookrightarrow iterations of small-small steps

\downarrow
small-small variations in ϕ/ψ angle

\downarrow
calculate energy at each step & check whether minimum

Minimization

\hookrightarrow by differentiating the P.F. function

$$\frac{\partial E}{\partial x_i} = 0 \Rightarrow \frac{\partial^2 E}{\partial x_i^2} > 0$$

~~$E_{pot} = \dots$~~

Taylor series expansion

$$f(x+h) = f(x) + h \frac{d}{dx} f(x) + \frac{h^2}{2!} \frac{d^2}{dx^2} f(x) + \frac{h^3}{3!} \frac{d^3}{dx^3} f(x) + \dots$$

Locating Minimum Energy, near a given point:
 $E(x) \rightarrow$ should be differentiable at x

$$E(x+h) = E(x) + h E'(x) + \frac{h^2}{2!} E''(x) + \dots$$

a small
step in
1 dim.

✓ Energy is minimum at
a nearby point:

$$\frac{dE(x+h)}{dx} = 0$$

$$\frac{dE}{dx}(x) + \frac{h}{1!} \frac{d^2E}{dx^2} + \frac{h^2}{2!} \frac{d^3E}{dx^3} + \dots = 0$$

*we can neglect this
as h is small*

$$\frac{dE(x)}{dx} = -h \frac{d^2E(x)}{dx^2}$$

$$h = - \frac{(dE/dx)}{(d^2E/dx^2)}$$

→ step
size

✓ Modified Newton Raphson

✓ Steepest Descent:

$$h = -\lambda \frac{dE}{dx}$$

*Learning
Parameter*