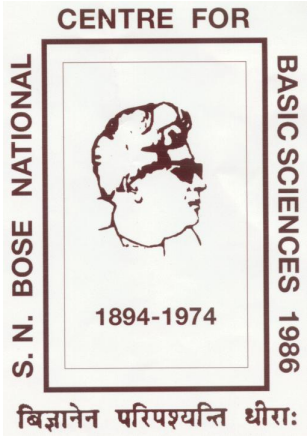
Protein aggregation from Monte Carlo simulation

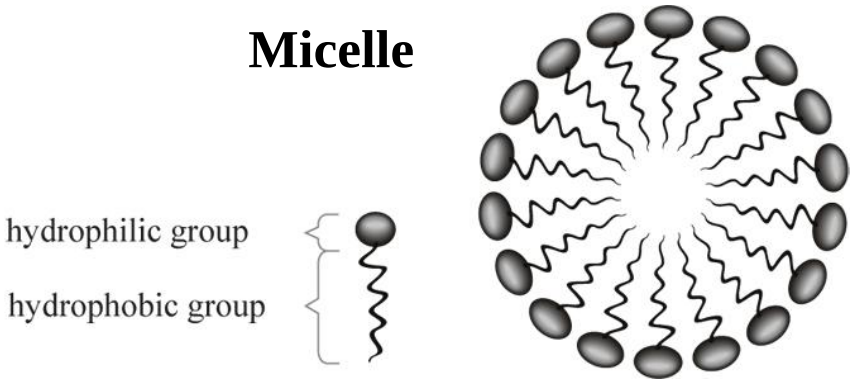
Jaydeb Chakrabarti

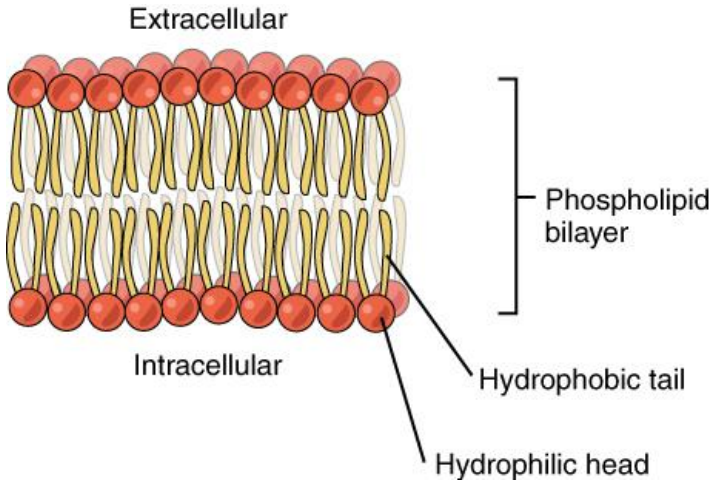


Department of Chemical, Biological & Macromolecular Sciences
S. N. Bose National Centre for Basic Sciences, Sector III, Block JD, Salt lake, Kolkata -700106, India

Self assembly of Amphiphiles

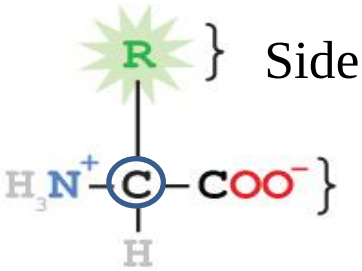
Micelle



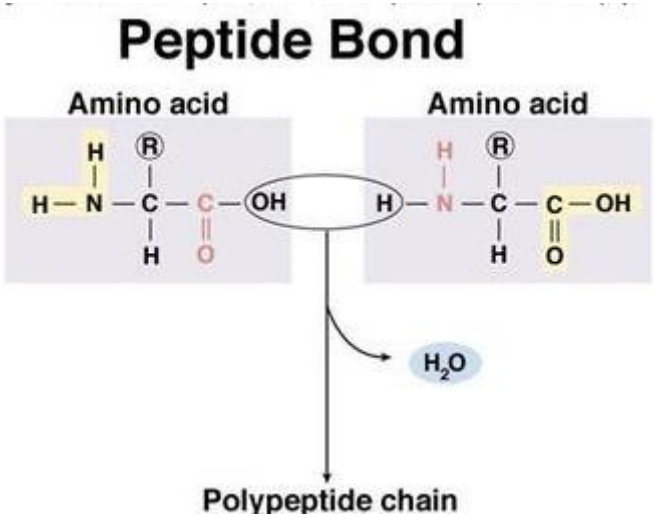


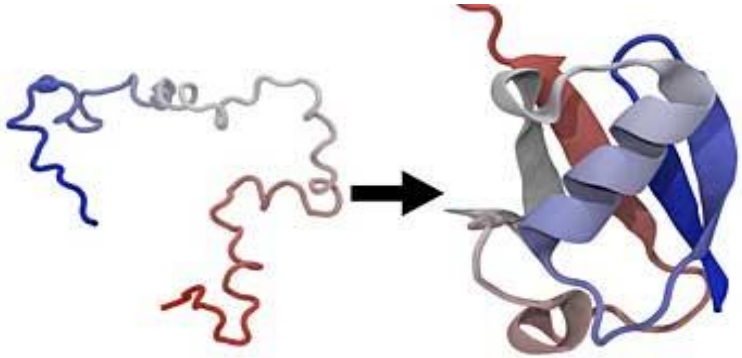
- Scientifically interesting to different fields & technology

Proteins



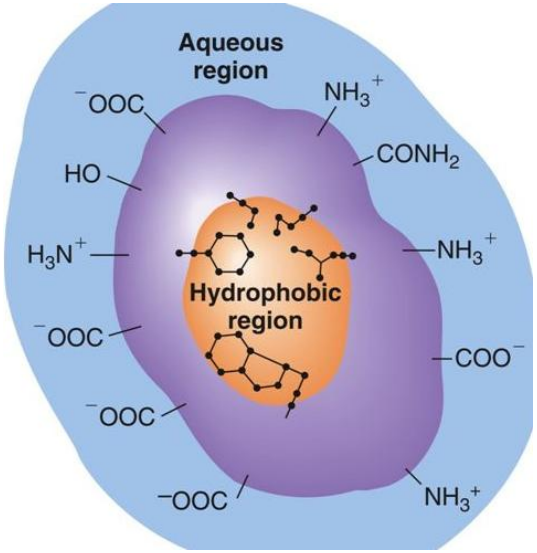
Residue



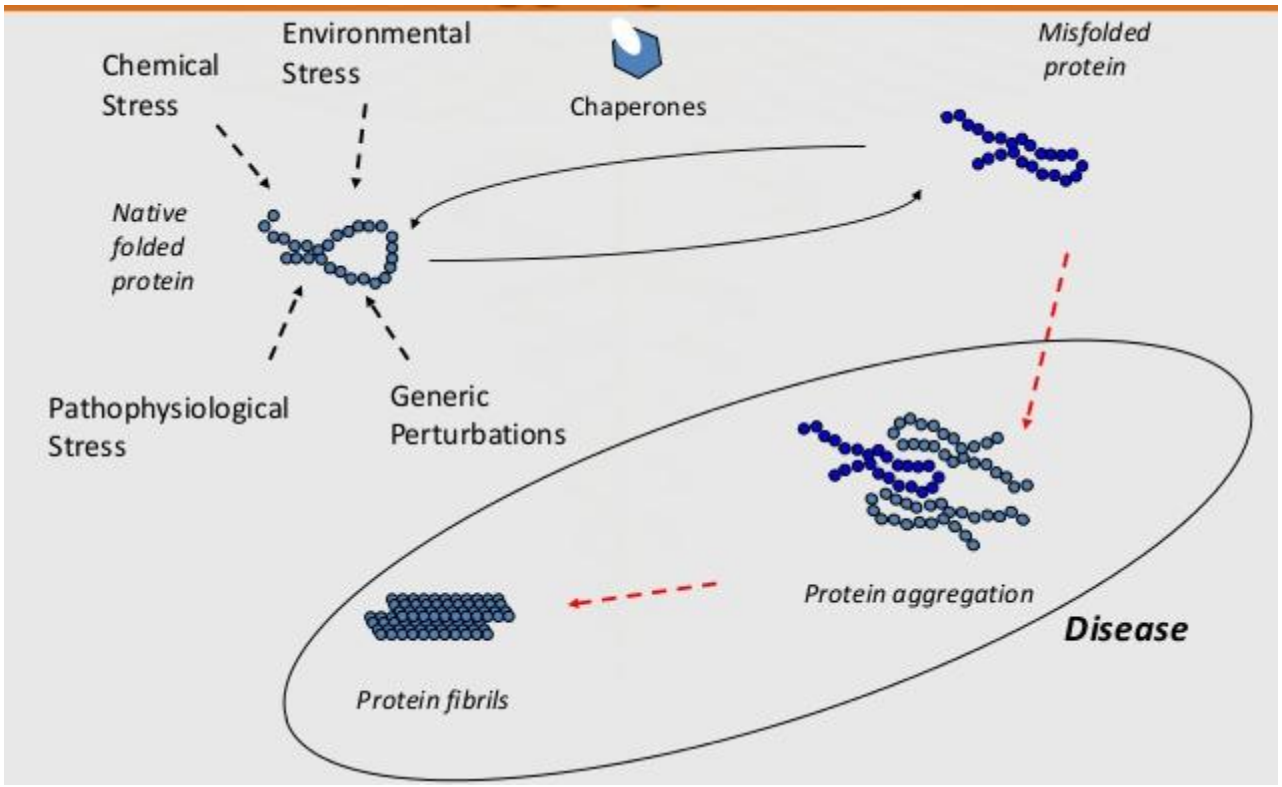


Unfolded

Folded conformation



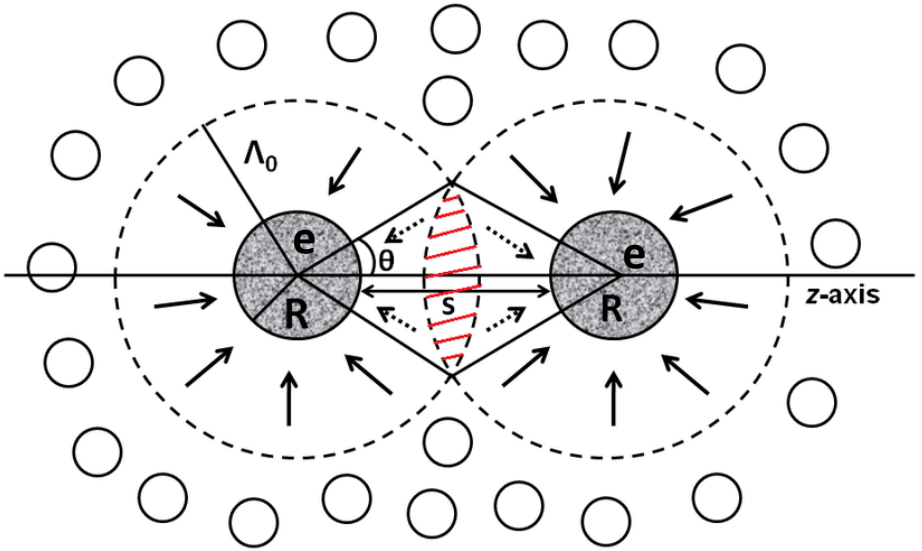
Protein aggregation



- Peptide amphiphiles: Biomedical application
- Above a critical aggregation concentration: neurodegenerative disorder

Model System

- Surface of a spherical particle repelling solvents, charge at centre
- Electrostatic interaction of screened Coulomb type: DLVO potential



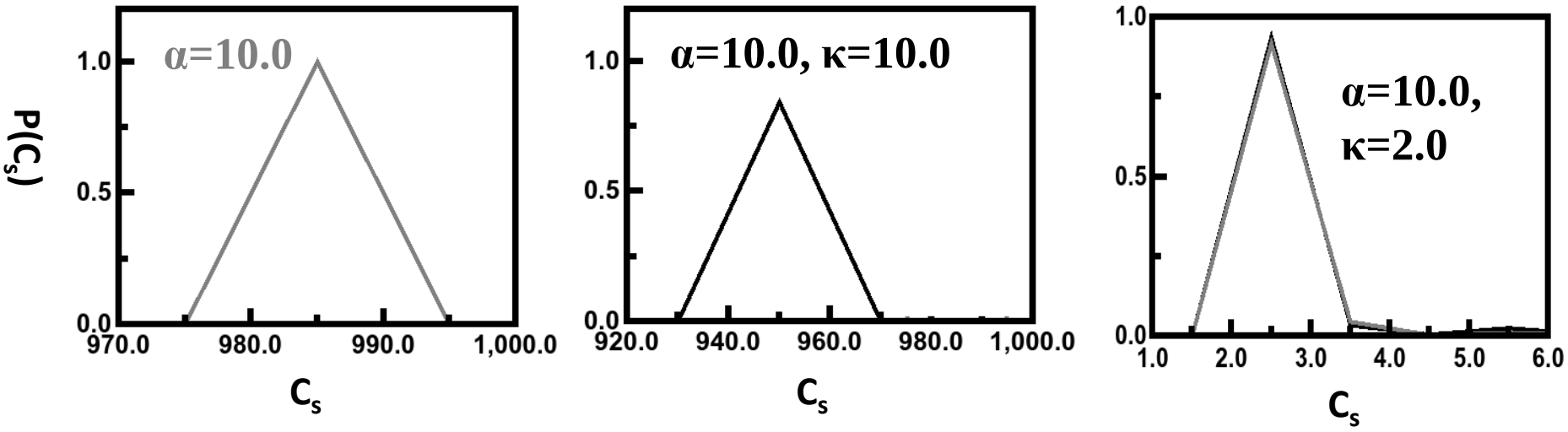
- Repulsion between solvent and solvophobic molecules: attraction between two such solutes

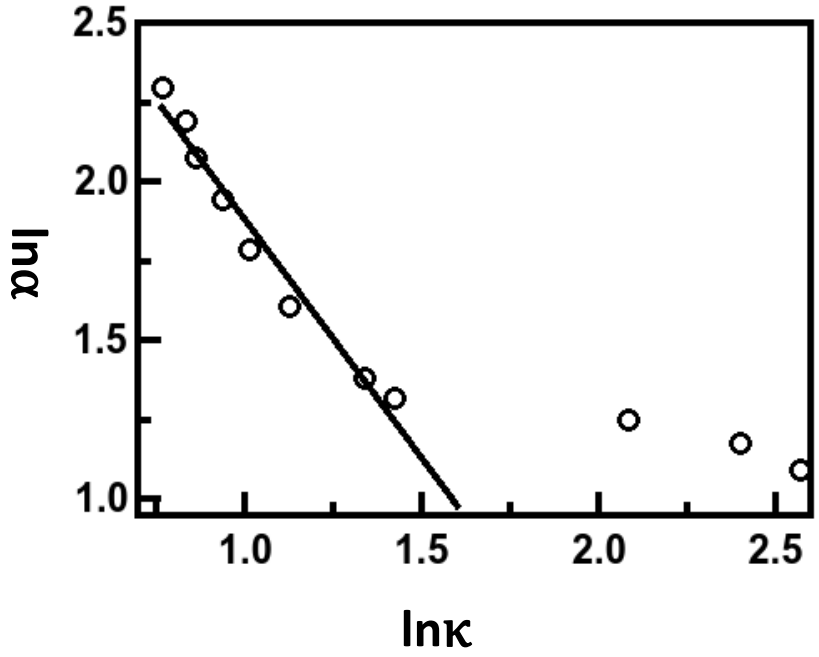
$$V_A(s) = \alpha[s(1 - (\Lambda_0/R)^2) - s^2/2R]$$

$$\alpha = 8\pi\gamma\Lambda_0$$

γ: surface tension

Monte-Carlo:Cluster size





- Aggregation beyond a particular value of κ for a fixed α: κ_{th}

$$\alpha \sim \kappa_{th}^{-1.5}$$

Mean field analysis

$$c(q) = c_{electro}(q) + c_{hydro}(q)$$

$$c(r) \approx -\beta u(r)$$

$$\longrightarrow \quad c(q) \approx C_0 + C_2 q^2 \qquad C_2 = (p/\kappa^4 - \alpha g)$$

$$\Longrightarrow \quad \alpha \sim \kappa^{-4.0}$$

Conclusion

- Aggregation is driven by strong hydrophobic strength
- Electrostatic interaction governs stability of finite size clusters
- Useful for designing nano-bio applications

THANK YOU