Capturing dynamic conformational change in proteins during gel network formation

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1. Background

Many biological systems rely on protein unfolding

Mechanical behaviour of individual protein affects greater network [1]

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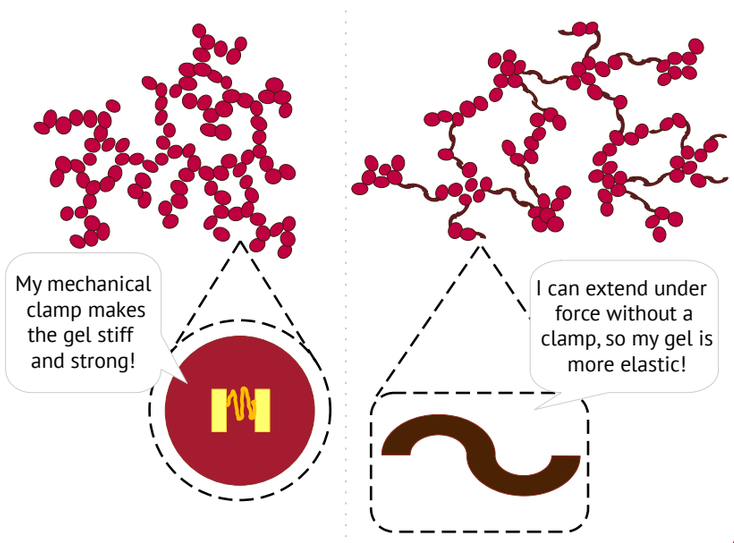
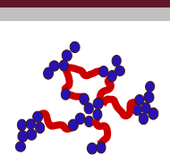
Bulk gel deformation induces protein unfolding

How can we **exploit unfolding** in protein networks?



2. Objectives



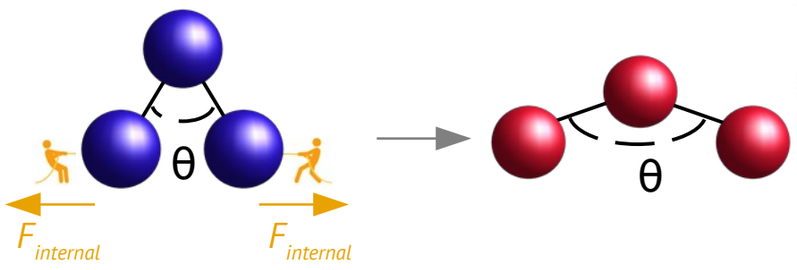
Produce a network-scale model with dynamic unfolding

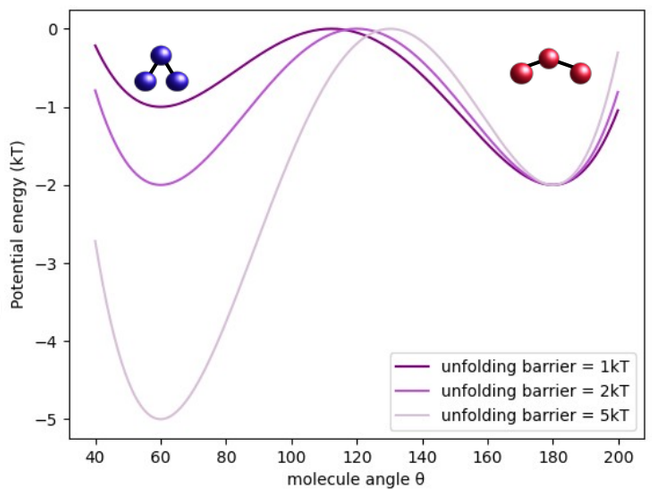
Localise unfolding and force distribution

Characterise mechanical and structural properties

3. Coarse-Grained Model

A protein overcomes an **energy barrier** to go from a folded to an unfolded state

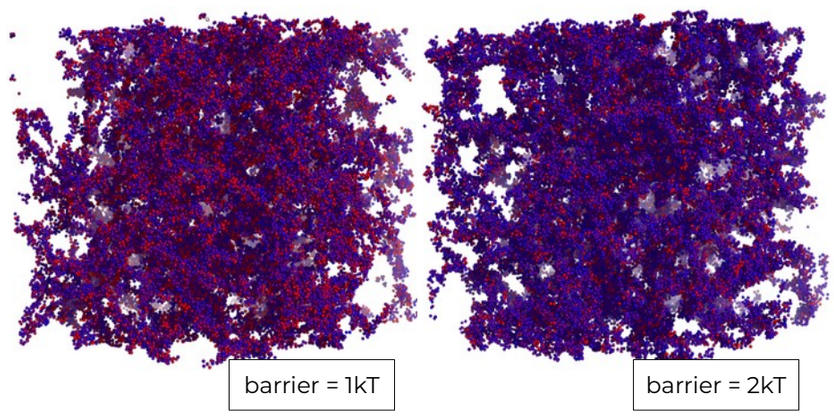


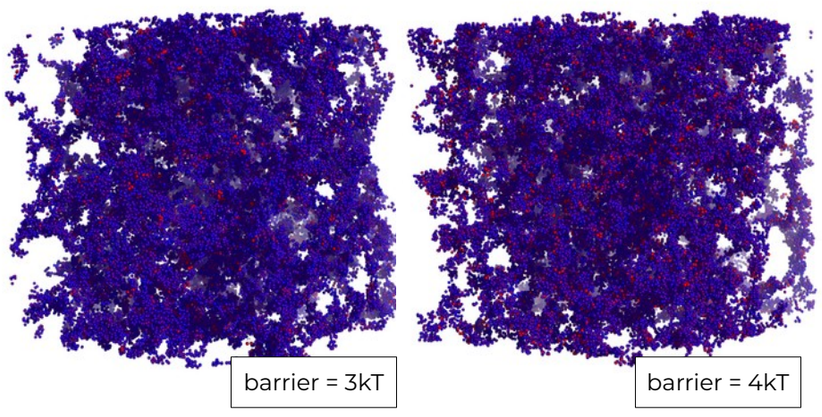


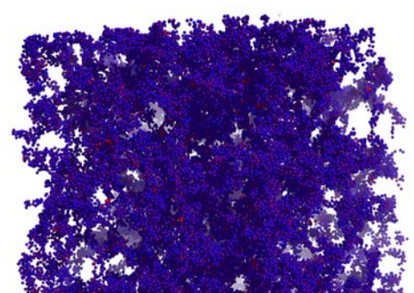
This energy barrier is part of a **double-well** potential that describes which state is preferred

- Truncated repulsive LJ potential
- Molecular dynamics with Brownian motion
- Performed using LAMMPS

4. Network Formation



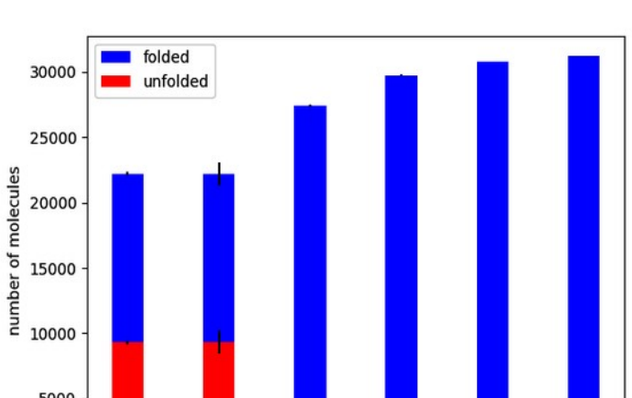




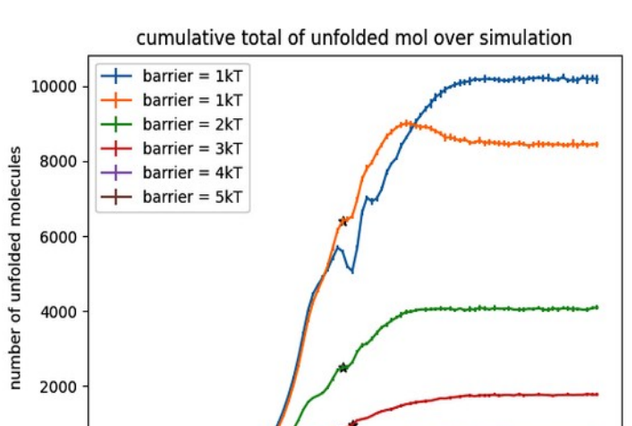
V_f = 7%
31000 molecules

Blue = folded
Red = unfolded

5. Results

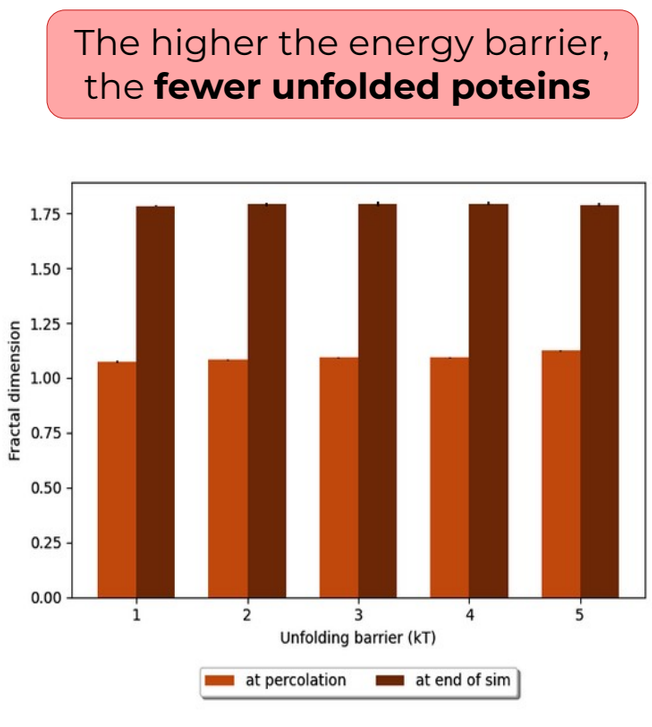


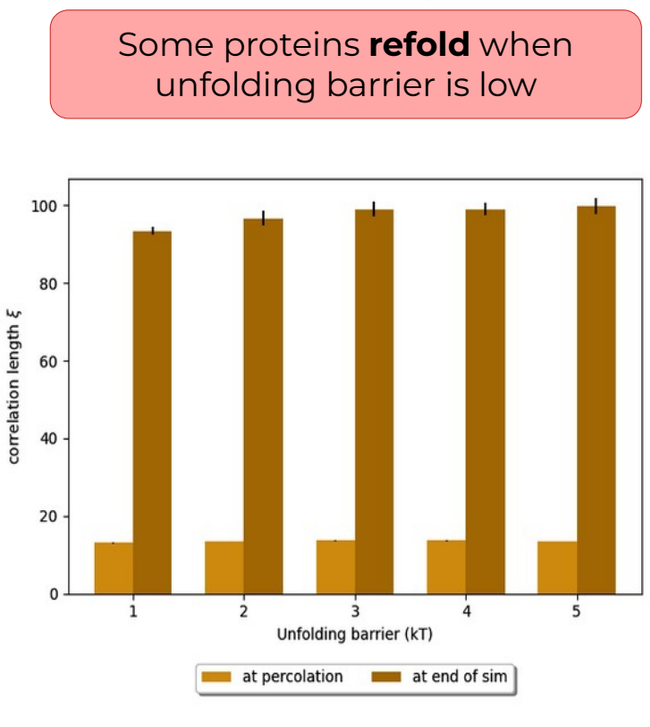
The higher the energy barrier, the **fewer unfolded poteins**



Some proteins **refold** when unfolding barrier is low

If the energy barrier is lower, proteins prefer to remain in an **"intermediate unfolded state"**





Structure is **minimally affected** by energy barrier

6. Next Steps

Characterise structural features in depth

Perform shearing simulations for mechanical properties

1. Hughes et al. ACS Nano 15 (7), 11296-11308. 2021.

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