P.32 The role of confinement and interaction range on polarisation and alignment of stiff chains and networks

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Confining a stiff polymer chain to a compartment or pore influences the orientation of the bonds and density distribution of chain segments within the confining region. We utilise a formulation of the chain in terms of a monomer ensemble [1-3] to model the additional effect of an interaction between polymer segments at the mean-field level. In particular, we show how the interaction alters the effective stiffness as well as the spatial profile of the location of segments. We analyse the respective roles of the interaction range and the confinement length scale to identify different types of behaviour for confinement. Our analytical results contrast confinement between parallel plates and restriction to spherical or circular pores. In additional to the analytical arguments we present results from simple molecular dynamics simulations of similar systems. The theoretical methods are also expanded to a formalism of a reversible, tree-like network. In this case variation of the confinement parameter permits a direct measure of elastic properties of such a finite and confined network. Aspects of these results are potentially applicable to some of the networks and chains found at cellular and sub-celluar levels.

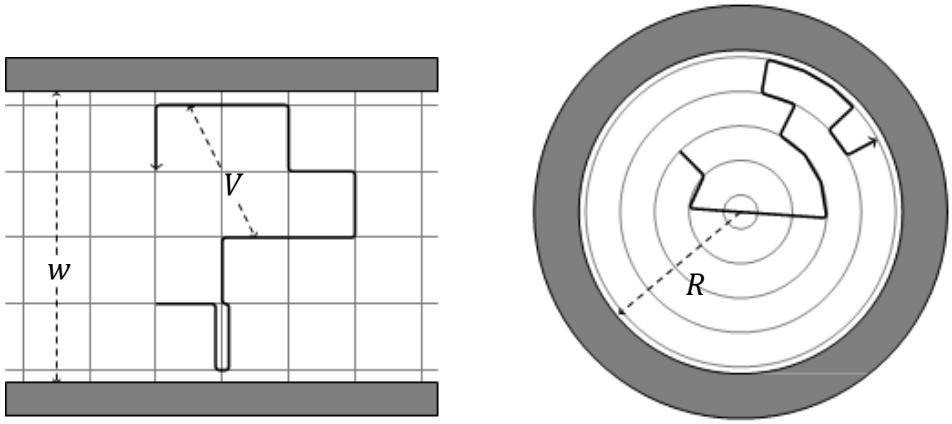

FIG. 1: On the left-hand side we show a sketch of a stiff, lattice-based chain confined between two parallel plates. We wish to determine the polarisation density in dependence of the interaction potential energy V between the bonds and the separation of the plates w. Spherical confinement is the second restricting geometry. We model the chain in a set of shells to derive the orientation profile in this region of radius R.

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