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# Simulating Liquid Crystals

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**T**he specificity of DNA base-pair interactions gives considerable functional control in the design of anisotropic nano-particles, enabling the formation of liquid crystal phases. This project aims to study the liquid phase behaviour of such non-conventional liquid crystal molecules, with a particular focus on the novel ‘nunchuck’ structure - two rigid rods connected via a flexible linker. The Eiser Group have previously considered intra-molecular interaction potentials at the single-nucleotide level for a single DNA nanoparticle, and I am now implementing these potentials in larger, more coarse-grained models of multiple nanoparticles, through open-source software LAMMPS (Large-scale Atomic/Molecular Massively Parallel Simulator). Such systems are expected to form smectic (layered) phases at high volume fractions. THIS WILL BE EDITED AT THE END

## 1 Introduction

What are we studying? (brief) - introduce nunchuck particles (but not implementation) Why are we interested? Applications of this!

Outline of report

## 2 Background

### 2.1 Liquid Crystals

Include known phases etc - de gennes textbook gives useful milestone references

### 2.2 Onsager Theory

Introduce theoretical predictions to be validated later Mathematical derivations may be provided in appendices

### 2.3 Order Parameter

The degree of order in a liquid crystal phase is characterised by an order parameter, chosen such that it is non zero in the ordered phase but vanishes in the isotropic phase. A familiar example of this is the magnetisation  $M$  of a ferromagnet; when raised above a critical temperature, the magnetisation vanishes as the ferromagnet undergoes a phase transition. While the choice of order parameter for the nematic phase transition is less intuitive than this, it relies on the formation of genuine long-range

orientational order. We may therefore define the angle ( $\theta$ ) between each molecule's axis and the system director, and traditionally let the order parameter  $S$  be given by:

$$S_n = \langle P_2(\cos(\theta)) \rangle = \left\langle \frac{3}{2} \cos^2(\theta) - \frac{1}{2} \right\rangle \quad (1)$$

where  $P_2$  simply denotes the second Legendre polynomial [1]. While  $\langle \cos^2(\theta) \rangle$  would function alone as the order parameter, this has the useful property of giving unity for a perfectly aligned system, and zero for a completely random system. Further motivation for this choice is provided in Appendix B.1.

Similarly we will find it helpful to define a smectic order parameter, to characterise the formation of one-dimensional long-range positional order. Intuitively, we expect a non-zero Fourier component of the normalised density along the director, and so we may write:

$$S_s = \frac{1}{N} \left| \sum_{j=1}^N \exp^{ik_z z_j} \right| \quad (2)$$

where the  $z$  axis lies along the director, and thus normal to the smectic layers [2]. Here  $k_z = 2\pi/\lambda_z$ , for a layer periodicity of  $\lambda_z$ , and  $z_j$  is the  $z$  coordinate of the centre of mass of the  $j$ th molecule.

## 2.4 Previous Computational Work

## 3 Methods

As introduced in Section 2.4, all molecular dynamics simulations were completed in LAMMPS. LAMMPS (Large-scale Atomic/Molecular Massively Parallel Simulator) is a medium coarse-grained, classical molecular dynamics code developed to replicate solid-state materials and soft matter mesoscopic systems [3, 4].

### 3.1 Simulation Molecules

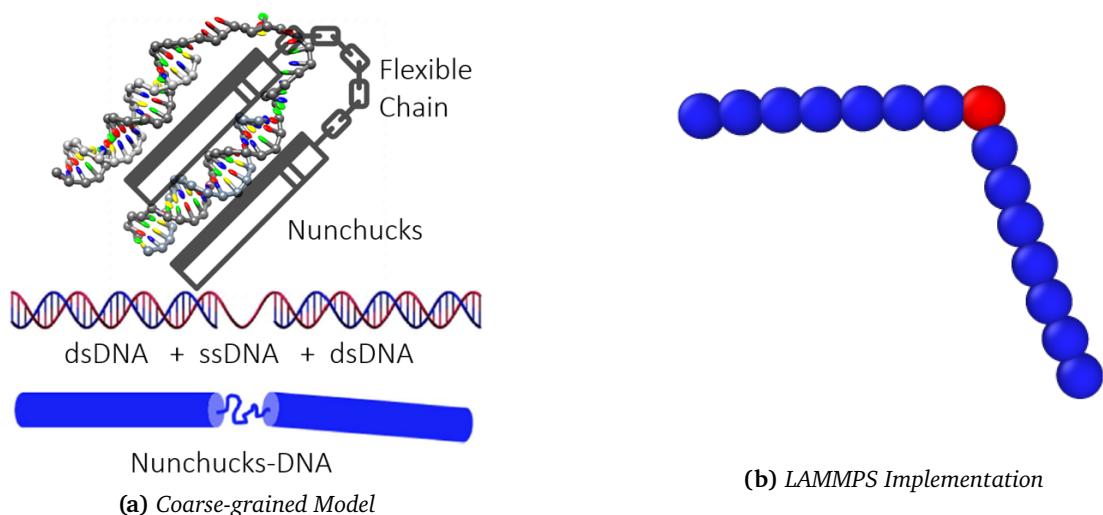
As introduced in Section X, we are considering 'nunchuck' molecules formed of two rigid rods connected by a flexible linker, as depicted in Figure 1a. However, as the interaction potential of an anisotropic particle is rather complex, it is computationally simpler to consider each molecule as a system of connected spheres, each with a separate isotropic interaction potential (detailed further in Section 3.3).

This is visualised in Figure 1b, for rigid rods of aspect ratio 7. The ss-DNA is represented by a further sphere in the centre of the molecule, coloured differently in red to highlight its differing mechanical properties. It has a modified bond angle, so the molecule is bent around this element, and reduced bond rigidity so the particle may also stretch about this point.

A system of natural units was used in simulations, and replicated in our results here. Based on the Lennard-Jones potential, the cut-off length and characteristic energy are both set to unity. The simulation timescale is then fixed by the choice of these values, and the mass of the simulation body.

The physical values for a system may be considered for a specific system (in this case strands of ds-DNA) through scaling via the relevant mass, length scale and energy scale of this system. However the dimensionless simulations presented here may be generalised to any similarly-shaped mesogens; we would expect other systems to display the same behaviour over an appropriate timescale determined by their material properties [5].

For the nunchuck particles considered, a length scale of 2 nm is used (corresponding to the width of ds-DNA, and hence the diameter of a simulation sphere) [6]. It is worth noting that the persistence length of DNA is around 50 nm [7], so the approximation of perfect rigidity is valid for all rods considered here (maximum length 30 nm). Using the standard value of 0.33 nm [8] for the average length of a base pair, each sphere corresponds to a sequence of six base pairs. This gives the mass of each sphere as  $6.5 \times 10^{-24}$  kg, based on an average formula mass per base pair of 650 Da [9]).



**Figure 1:** Depiction analogy between the DNA mesogen and the nunchucks. Note the appearance of the flexible ss-DNA linker between the rigid ds-DNA rods, and the implementation within LAMMPS on the right. The central red sphere, representing the ss-DNA, is given modified bond properties to replicate the nunchuck's flexibility. Figure (a) created by Jiaming Yu (Eiser Group, Cambridge).

We may also define the characteristic energy scale; this is formally the depth of the potential well in the full Lennard-Jones potential, but the thermal energy serves as a common approximation [10] in agreement with experimental data [11]. Using these values, we find that the characteristic timescale for this system is 79 ps. In this context, the simulation timestep would be 0.4 ps, and typical simulation of  $20 \times 10^6$  steps had a total duration of 7.9  $\mu$ s. For 1000 particles, this took approximately 8 hours to run on a standard laptop CPU.

### 3.2 Simulation Structure

All simulations in this report were conducted a system of 1000 particles, with a time step of  $0.005\tau$ , (where  $\tau$  is the characteristic time), unless otherwise stated. The system was initially configured in a dilute, isotropic state; a non-trivial process for large numbers of mesogens as molecules must be placed randomly without overlap, to prevent any initial order affecting the formation of ordered phases. I am grateful to Iria Pantazi for writing a python script to automate this process for dilute rigid rod systems, and a generalised version of this is available in the supplementary material. Alternatively, simulations were also initiated from a perfectly ordered square crystalline phase, with all molecules aligned along a common axis. The choice of this axis is arbitrary, as the system is invariant under global rotation [12], but is taken to be directed along the y-axis for clarity. Care was taken to ensure molecules did not overlap, and the system was stable in this ordered phase.

All simulations are conducted within an oblong box defined by the Cartesian axes, with periodic boundary conditions used to eliminate surface effects and replicate conditions in the bulk phase [13]. The aspect ratio of this box may be varied, to support phase formation in anisotropic systems, as discussed in Section X. An isenthalpic ensemble was used (where pressure is fixed) to vary the size of the simulation region, allowing sampling of different volume fractions from the same initial configuration. The microcanonical ensemble, where both the system volume and energy are conserved, was then used to allow the system to reach thermodynamic equilibrium. Time integration was evaluated using the Nose-Hoover thermostat [14, 15] natively implemented in LAMMPS [16].

A typical simulation consists of multiple stages, alternating between these two ensembles to sample the system properties at a range of volume fractions. Approximately  $2 \times 10^4$  steps are simulated when varying the simulation volume (depending on the resolution of volume fraction sampling), followed by  $2 \times 10^6$  to allow the system to reach equilibrium in each stage. The output of thermodynamic variables,

as well as particle positions, at the end of each stage allows for subsequent calculation of the order parameter at equilibrium. This data was also retrieved at regular intervals during each simulation stage, to track the time evolution of the system.

To ensure stability of the system, a Langevin thermostat [17] was also used throughout, and energy conservation was verified over a range of timescales. The damping for all thermostats is equal to the characteristic timescale of the simulation (i.e. unity in natural units).

### 3.3 Intermolecular Potential

A shifted, cut-off Lennard-Jones potential was chosen to represent pair-wise interactions between molecules. While the Lennard-Jones potential [18, 19] has long been the natural choice for molecular dynamics simulations [20], its infinite range introduces computational complexity as interactions between all pairs of particles must be considered. It is therefore increasingly common to use a cut-off version, whereby the potential is set to zero beyond a ‘cut-off’ radius, and here we chose to neglect the entire attractive tail. As well as simplifying the calculations required, this also allows our results to be generalised to any mesogens without attractive inter-molecular forces (that typically favour ordered-phase formation), as any phase transitions observed here must be purely entropically driven. This is commonly known as a soft-core model, where particle overlap is suppressed via this repulsive potential rather than any excluded volume interactions, and is computationally much less demanding [21, 22].

However, this cut-off may cause unphysical behaviour if the potential does not tend to zero smoothly at this point. This is remedied by the addition of a constant term, described in the full form of the pair-wise potential  $U_{ij}$  in (3):

$$U_{ij} = 4\epsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right] + \epsilon \quad r_{ij} < r_c = 2^{1/6}\sigma \quad (3)$$

Here  $\sigma$  and  $\epsilon$  are the relevant length and energy scales of the system, formally corresponding to the particle separation at which the  $U_{ij} = 0$ , and the depth of the potential well. It is worth noting that the effects of this truncation and shift on the overall thermodynamic quantities are well documented [23, 24], and changes in lyotropic properties are negligible in 3D bulk liquids with a conserved particle number [25].

### 3.4 Analysis

The visualisation freeware Ovito [26] has been employed to animate the molecule motion over the simulation period, and was used to generate all molecular images presented here. Thermodynamic variables, such as internal energy and pressure, were extracted to track the system’s progress towards equilibrium, and verify its stability.

The volume fraction and nematic order parameter were computed for comparison with Onsager’s theorem, as detailed in Section X. Calculation of the order parameter is complicated by the absence of an imposed director (ie if no electric field is applied), and we use the approach taken by Eppenga and Frenkel [27] which is reproduced in Appendix B.2.

Further analysis included the calculation of the smectic order parameter, and pair-wise orientational correlation coefficient, detailed in Section X. All scripts for data extraction and analysis were written by the author, *and can be found in the supplementary material?*.

## 4 Rigid Rod Simulations

Used to benchmark sys etc and demonstrate techniques to identify phase transitions

## 5 Nunchuck Simulations

## 6 Conclusion

Summarise key results from above, and emphasise their importance. Also give limitations of results obtained, and suggest direction for further work.

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## Appendix A Onsager Theory

## Appendix B Nematic Order Parameter

### B.1 Theoretical Outline

Here I endeavour to outline the motivation for the nematic order parameter used throughout this report, based on the work of Eppenga and Frenkel [27, 28]. The nematic phase may be differentiated from the isotropic phase by the formation of cylindrical symmetry, as opposed to the spherical symmetry of the isotropic phase. The deviation from spherical symmetry may be quantified through a set of order parameters  $f(\theta, \phi)$  [29]. when considering the axially symmetric nematic phase, independent of  $\phi$ ,  $f(\theta, \phi)$  may be generally expressed in the basis of all even Legendre polynomials  $P_{2l}$ :

$$f(\theta) = \sum_{l=0}^{\infty} a_{2l} P_{2l}(\cos(\theta)) \quad (4)$$

where  $\theta$  is the angle between the molecular orientation and the axis of symmetry of the system. Note that odd-ordered terms are neglected for nonpolar molecules, as the director may point in either of two antiparallel directions and so all odd Legendre polynomials average to zero [30].

In an isotropic phase,  $a_{2l}$  vanishes for all  $l > 0$ , so all angular dependence vanishes. More generally, quantities  $\langle P_{2l}(\cos(\theta)) \rangle$  may be used at the order parameter of the system, with the second order term being referred to as the nematic order parameter. Averaging over a population of  $N$  molecules, we can therefore write the nematic order parameter  $S_n$  as:

$$S_n = \frac{1}{N} \left\langle \sum_{i=1}^N \left( \frac{3}{2} \cos^2(\theta_i) - \frac{1}{2} \right) \right\rangle \quad (5)$$

### B.2 Calculation

The method given above in Appendix B.1 relies on knowledge of the system-wide nematic director (ie the axis of symmetry of the cylindrical phase), to define  $\theta_i$ . However, this is not always possible in physical systems where such a unique direction is not externally imposed.

Instead, as detailed by Frenkel et al. [31], we maximise the expression:

$$S'_n(\hat{\mathbf{n}}') = \frac{1}{N} \left[ \sum_{i=1}^N \left( \frac{3}{2} (\hat{\mathbf{n}}' \cdot \hat{\mathbf{u}}_i)^2 - \frac{1}{2} \right) \right] \quad (6)$$

where  $\hat{\mathbf{u}}_i$  denotes the orientation of the individual molecular axes in the laboratory frame. This may be written further as:

$$S'_n = \frac{1}{N} \langle \hat{\mathbf{n}}' \cdot \mathbf{Q} \cdot \hat{\mathbf{n}}' \rangle, \quad \text{where } \mathbf{Q}_i = \frac{3}{2} \hat{\mathbf{u}}_i \hat{\mathbf{u}}_i - \frac{1}{2} \mathbf{I} \quad (7)$$

The tensor order parameter  $\langle \mathbf{Q} \rangle$  is a traceless symmetric 2nd-rank tensor, with three eigenvalues  $\lambda_+$ ,  $\lambda_0$ ,  $\lambda_-$  [27]. We typically take the largest eigenvalue ( $\lambda_+$ ) as the nematic order parameter, a good approximation in large  $N$  limit. In practice, we actually calculate the eigenvalues of the related tensor  $\mathbf{M}$ :

$$\mathbf{M} = \frac{1}{N} \sum_{i=1}^N \hat{\mathbf{u}}_i \hat{\mathbf{u}}_i \quad (8)$$

as this shares eigenvectors with  $\mathbf{Q}$ , and has eigenvectors  $\mu_n$  related to  $\lambda_n$  by:  $\mu_n = 2/3\lambda_n + 1/3$ .

It is worth noting  $\lambda_+$  is bound above zero, and so does not reach zero in the isotropic phase as would be expected. It is common to use  $S = -2\lambda_0$  when considering such disordered systems, as this

fluctuates about an average much closer to zero [32]. I have not done so in the results presented here, to give continuity in the order parameter over the transition (where the focus on this report lies), however this has meant that the average order parameter in the isotropic phase is slightly above zero.

## **Appendix C   Code?**