Dr. Giuseppe Negro 6/03/2023 [gnegro2@ed.ac.uk](mailto:giuseppe.settimio.negro@gmail.com)

- Ordering properties in complex fluids and non-equilibrium systems Active fluids (dense suspensions of bacteria, cytoskeletal extracts, Microtubules bundles)
- Hydrodynamic and Statistical mechanics modelling
- High Performance Computing

Dynamical phase transitions in complex fluids and nonequilibrium systems

WP1 Spoke 2 b5 Physics of Complex Systems (UniBa)

- Prof. Giuseppe Gonnella
- Antonio Suma (RTB)
- Antonio Lamura

Lattice Boltzmann Methods MPI

Molecular dynamics simulations with implicit and explicit solvents (LAMMPS+ CustomMulti Particle collision Dyanamics Package)

Phase Field Theories of complex and active fluids Non-equilibrium statistical models for self propelled particles and DNA transcription

Non equilibrium Phase transitions in Active Brownian **Particles**

Topological Phase transitions of Choleric Shells Confined in Shells

Self-Propulsions of active droplets in 3D

Active Turbulence

Polymer models to study transcription and dynamics in Human Chromosomes

PHASE FIELD THEORIES

liquid crystals

Oriental Order **National Smooth Deformations**

Order Parameter Shells via Anchoring in Moderation. Phys. Rev. Rev. 2017. Re Described by a second rank traceless symmetric Tensor

$$
Q_{\alpha\beta} = S \langle \mathbf{n}_{\alpha} \mathbf{n}_{\beta} - \frac{1}{d} \rangle
$$

Landau-De Gennes Theory

Tensor order parameter First order transition for orientational order

Chirality Elastic energy

$$
\mathcal{F}\left[\phi, Q_{\alpha\beta}\right] = \int dV \left[A_0 \left[\frac{1}{2}\left(1 - \frac{\chi(\phi)}{3}\right)Q^2 - \frac{\chi(\phi)}{3}Q^3 + \frac{\chi(\phi)}{4}Q^4\right] + \frac{L}{2}\left[\left(\nabla\cdot Q\right)^2 + \left(\nabla\times Q + 2q_0Q\right)^2\right]\right]
$$

3 Control Parameters

Activity

DYNAMICAL EQUATIONS

 $(\partial_t + \mathbf{v} \cdot \nabla) \mathbf{Q} - \mathbf{S}(\mathbf{W}, \mathbf{Q}) = -\frac{1}{\Gamma}$ Γ **H** $H = -\frac{\delta \mathcal{F}}{S}$ *δ***Q** + **I** 3 *Tr* $\sqrt{2}$ *δ*ℱ *δ***Q**) **Advection relaxation for the tensor order parameter**

Dynamical fields

Numerically solved via a hybrid Lattice Boltzmann Scheme

Advection diffusion for concentration field

$$
\partial_t \phi + \nabla \cdot (\phi \mathbf{v}) = \nabla \cdot \left(M \nabla \frac{\delta \mathcal{F}}{\delta \phi} \right)
$$

•Nematic tensor $\mathcal{Q}_{\alpha\beta}$ • Velocity field **v** • Concentration field ϕ

LATTICE BOLTZMANN MODELS

Based on phase-space discretisation form of the Boltzmann equation

Discretised both in real and velocity space

Mass and momentum density are defined as

$$
\partial_t f + \xi_{\alpha} \partial_{\alpha} f + \frac{F_{\alpha}}{\rho} \partial_{\xi_{\alpha}} f = \Omega(f)
$$

$$
f_i(\overrightarrow{r} + \overrightarrow{\xi}_i \Delta t, t + \Delta t) - f_i(\overrightarrow{r}, t) = \mathcal{C}(f_i, t)
$$

$$
\mathcal{C}(f_i, t) = -\frac{1}{\tau}(f_i - f_i^{eq})
$$

$$
\sum_{i} f_i^{eq} \xi_{i\alpha} = \rho u_{\alpha} \qquad \sum_{i} f_i^{eq} = \rho
$$

$$
\sum_{i} f_i^{eq} \xi_{i\alpha} \xi_{i\beta} = \rho u_{\alpha} u_{\beta} - \sigma_{\alpha\beta}
$$

- The Equilibrium distribution functions are expanded up to a given order in the fluid velocity
- The Navier Stokes equations can be formally derived from the Lattice Boltzmann equation in the long wave length limit through Chapman-Enskog expansion

Review Letters, 128 (2022)

ACTIVE TURBULENCE

Jörn Dunkel, Sebastian Heidenreich, Knut Drescher, Henricus H. Wensink, Markus Bär, and Raymond E. Goldstein

Phys. Rev. Lett. 110, 228102 - Published 28 May 2013

Cascade or not cascade? Energy transfer and elastic effects in active nematics LN Carenza, L Biferale, G Gonnella Europhysics Letters 132 (4), 44003 (2021)

Multiscale control of active emulsion dynamics

LN Carenza, L Biferale, G Gonnella Physical Review Fluids 5 (1), 011302 (2020)

Planned Activity

Multi-Phase models

Typical Runs: 128/256 cores for 48 hours 50 exploratory runs 307200 core hours

Non-equilibrium statistical models for self propelled particles and DNA transcription

•
$$
U(r) = \frac{U_{\text{Mie}}(r) - U_{\text{Mie}}(r_{\min})}{0 \text{ if } r \geq r_{\min}}
$$
 if $r < r_{\min}$

•
$$
\mathbf{F}_{FENE} = -\frac{k(\mathbf{r}_i - \mathbf{r}_j)}{1 - r_{ij}^2 / r_0^2}
$$

$$
m\ddot{\mathbf{r}}_i = -\gamma \dot{\mathbf{r}}_i - \frac{\partial U_{FENE}}{\partial r_{i,i+1}} \hat{\mathbf{r}}_{i,i+1} - \sum_{j \neq i}^{2N} \frac{\partial U}{\partial r_{ij}} \hat{\mathbf{r}}_{ij} + F_{\text{act}} \hat{\mathbf{n}}_i + \sqrt{2D_0} \eta_i ,
$$

$$
m\ddot{\mathbf{r}}_{i+1} = -\gamma \dot{\mathbf{r}}_{i+1} + \frac{\partial U_{FENE}}{\partial r_{i,i+1}} \hat{\mathbf{r}}_{i,i+1} - \sum_{j \neq i+1}^{2N} \frac{\partial U}{\partial r_{i+1,j}} \hat{\mathbf{r}}_{i+1,j} + F_{\text{act}} \hat{\mathbf{n}}_{i+1} + \sqrt{2D_0} \eta_i
$$

 \mathbf{F}_{act}

Contract

ACTIVE PARTICLES

 $\sqrt{2D_0}$ η_{i+1}

Molecular Dynamics Methods

It can be used with multiple CPUs and with a GPU

-
-
-
-
-
-
-

LAMMPS is a classical molecular dynamics code with a focus on materials modeling.

It's an acronym for Large-scale Atomic/Molecular Massively **Parallel Simulator.**

Bead-spring polymer melt with 100-mer chains and FENE bonds: •32,000 atoms for 100 timesteps •reduced density 0.8442 (liquid) •force cutoff of $2^{(1/6)}$ sigma •neighbor skin = 0.4 sigma •neighbors/atom = 5 (within force cutoff) •NVE time integration

Molecular Dynamics Methods

Active self-propelled particles

Active (with repulsion) Passive (with attraction)

- Micro and macro phase separation of $\overline{}$ active systems
- Self-organization and dynamics of $\overline{}$ active clusters
- Phase diagram $\overline{}$

Cugliandolo et al. PRL 119 (26), 268002 2017 Digregorio et al. PRL 121, 098003 2018 Caporusso et al. PRL 125 (17), 178004 2020

Planned Activity

Three control parameters Attraction Activity Density

Attraction, low activity, low density: Gel Phase

Attraction, higher activity, low density: Arrested Phase Separation

Attraction, high activity, high density: Percolating Network

No Attraction, Any value of density and activity

> Typical Runs: 256 cores for 48 hours 30 exploratory runs 368640 core hours

POLYMER MODEL FOR GENE ORGANIZATION AND TRANSCRIPTION

 \blacksquare Neutral

Binding sites (TU)

Binders (TF) Weakly with all others

TFs SWITCH BETWEEN ACTIVE AND INACTIVE STATES Rapid exchange of factors and polymerases between bound and free states seen in photobleaching experiments

C. A. Brackley et al. Nat. Comm. (2021) MD SIMULATION

3Mbp-> 1000 beads (each 30nm in diameter->3Kbp)

TU in a cluster

TU+TF

Ranked Data Simulations

Ranke

Active Stress Tensor

Dissipative/reactive term Non-Equilibrium terms

 $\sigma_{\alpha\beta}^{act} = -\zeta \phi Q_{\alpha\beta} - \bar{\zeta} \epsilon_{\alpha\mu\nu} \partial_{\mu} (\phi Q_{\nu\beta})$

Active Cholesteric Droplet: A novel Motility mode

150000

Molecular Dynamics Methods

Typical Runs: 128 cores for 48 hours 45 exploratory runs 276480 core hours

USE CASES (UNIBA)

Model for lipid bilayers and ion channels

Coarse-grained

