IDP Project Final Presentation

Proliferating Cell Collectives: A Comparison of Hard and Soft Collision Models

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Outline

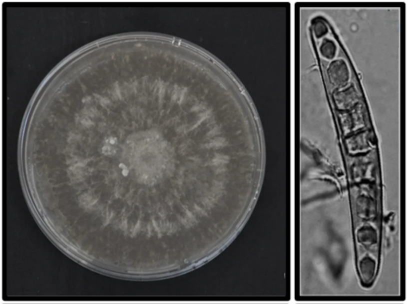
Computational Biology: A Growing Field

Why simulate biological systems?

- Link micro-to macroscopic behavior
- Test hypotheses in silico
- Beautiful visualizations

The computational challenge:

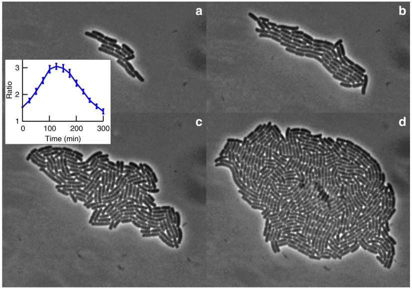
- Large system sizes
- Complex interactions
- Long timescales



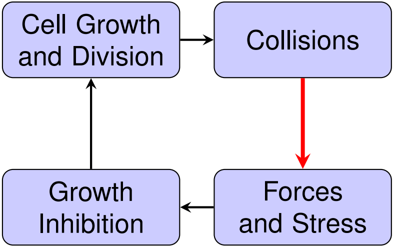
Real fungal colony showing ring patterns [Bankole et al., 2023].

This Work: Comparing Collision Models

- Bacteria that grow, divide and compress each other
- Investigate and compare two collision models

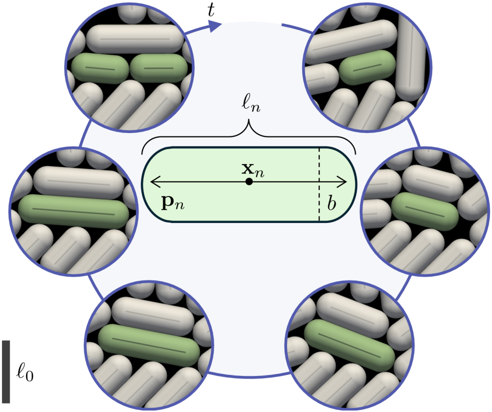


E. coli colony [DellâArciprete et al., 2018]



Outline

Cell Representation: Rigid Spherocylinders

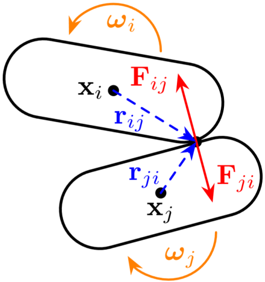


Spherocylindrical cell model [Weady et al., 2024].

Cell Dynamics

Overdamped dynamics:

- Collision cause forces
- Inertia negligible
- Cells ‘swim in honey”



Equations of motion:

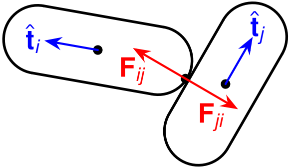
Translation: $$\mathbf{u}_i = \frac{1}{\zeta \ell_i} \sum_{j \neq i} \mathbf{F}_{ij}$$

Rotation: $$\omega_i = \frac{12}{\zeta \ell_i^3} \sum_{j \neq i} \mathbf{r}_{ij} \times \mathbf{F}_{ij}$$

Cell Growth

Stress-dependent growth:

- Exponential growth
- Inhibited by longitudinal stress



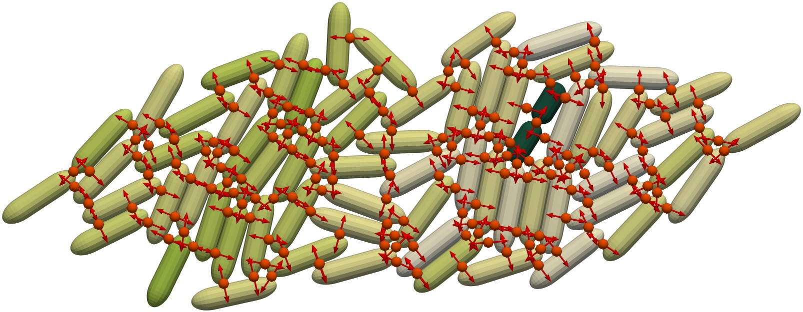
Growth rate:

Growth rate: $\dot{\ell}_i = \frac{\ell_i}{\tau} e^{-\lambda \sigma_i}$

Cell stress: $\sigma_i = \sum_{j \neq i} \frac{1}{2} \left| \hat{\mathbf{t}}_i \cdot \mathbf{F}_{ij} \right|$

Outline

Contact Mechanics



- Models only differ in how they calculate force magnitudes

Two Paradigms

Soft Model

Potential-based

- Local pairwise forces
- Allows overlap
- Simple calculation
- Similar to MD simulations

$$\mathbf{F}_{ij} = k\delta^{3/2}\hat{\mathbf{n}}$$

Hard Model [Weady et al., 2024]

Constraint-based

- Global optimization
- Strict non-overlap
- Complex solver
- Based on Contact Mechanics

$$\mathbf{F}_{ij} = \gamma_{ij}\hat{\mathbf{n}}$$
$$\text{s.t. } \mathbf{0} \leq \boldsymbol{\gamma} \perp \boldsymbol{\Phi} \geq \mathbf{0}$$

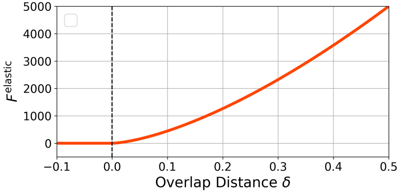
Soft Model: Hertzian Contact

$$\mathbf{F}_{ij} = k_{cc}\sqrt{d}\,\delta^{3/2}\,\hat{\mathbf{n}}$$

Characteristics:

+ Embarrassingly parallel
+ Simple implementation
+ Local calculations

– Numerically stiff
– Tiny timesteps needed
– Allows overlap



Force increases with overlap

Hard Model: Optimization Formulation

Key idea: Ensure no overlap via optimization

- Define gap function:

$$\mathbf{\Phi}_{ij} = \text{"signed distance between cells i and j"}$$

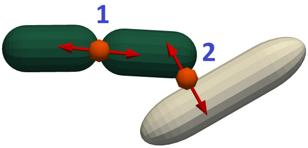
- Express forces based on unknown multipliers γ:

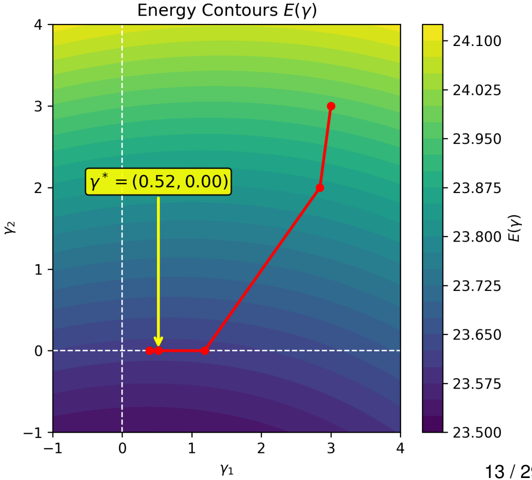
$$\mathcal{F}(\gamma) = \mathcal{D}\gamma$$
$$\boldsymbol{\sigma}(\gamma) = \mathcal{L}\gamma$$

Reformulate as energy minimization:

$$\min_{\gamma \geq \mathbf{0}} E(\gamma) = \min_{\gamma \geq \mathbf{0}} \gamma^\top \mathbf{\Phi}^k + \frac{\Delta t}{2} \gamma^\top \mathcal{D}^\top \mathcal{M}^k \mathcal{D} \gamma + \mathbf{1}^\top \frac{\Delta t}{\lambda} \left(\frac{\ell}{\tau} \odot e^{-\lambda \mathcal{L} \gamma} \right)$$

Hard Model: Solution Characteristics





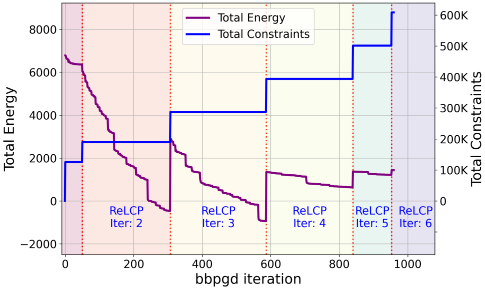
Solution guarantees:

1. Repulsive Forces
2. All overlaps resolved: (Tolerance $\varepsilon = 10^{-3}$)
3. No forces between non-contacting cells

Hard Model: Performance

Characteristics:

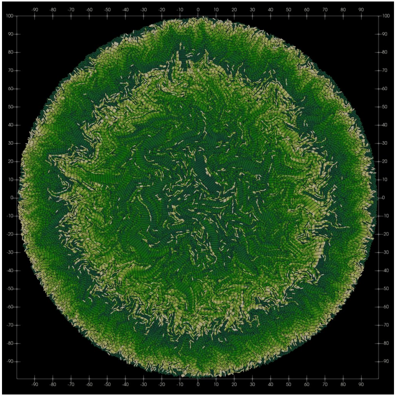
+ Fewer numerical stiffness
+ Larger timesteps possible
+ Strict non-overlap
– High per-step cost
– Complex implementation
– Global synchronization
– Requires multiple passes



Outline

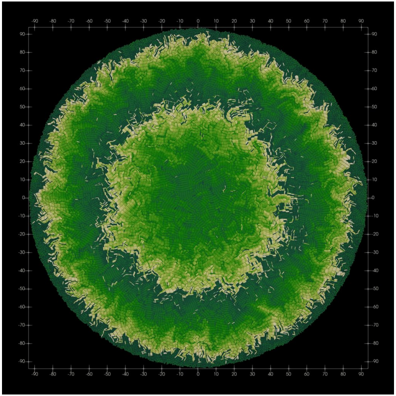
Concentric Ring Formation

Hard Model



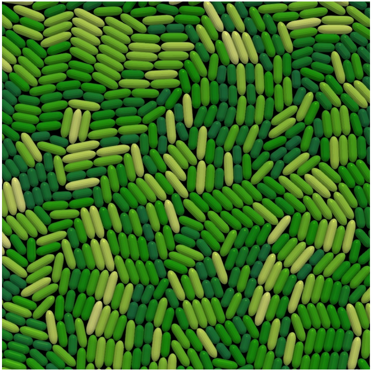
View video

Soft Model

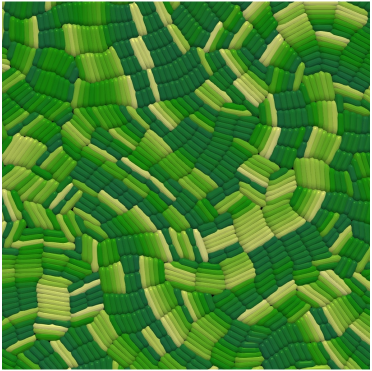


View video

Critical Difference: Packing Density

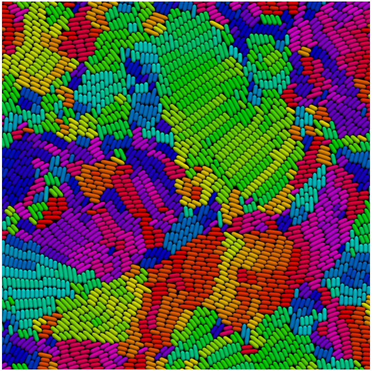


Hard Model

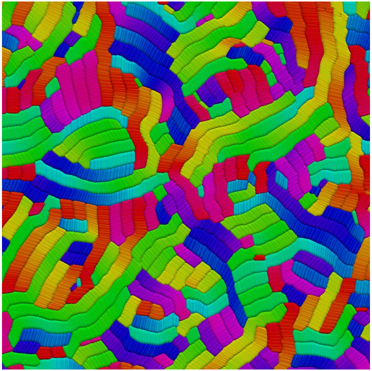


Soft Model

Critical Difference: Microdomain Structure



Hard: realistic patches



Soft: elongated bundles

Outline

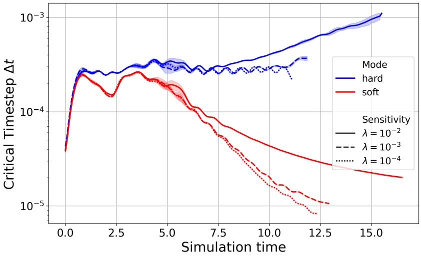
Courant-Friedrichs-Lewy (CFL) Condition

Adaptive timestepping:

$$\Delta t = \frac{0.5\,\varepsilon}{u_m}$$

where $u_m =$ median velocity,

$\varepsilon =$ overlap tolerance



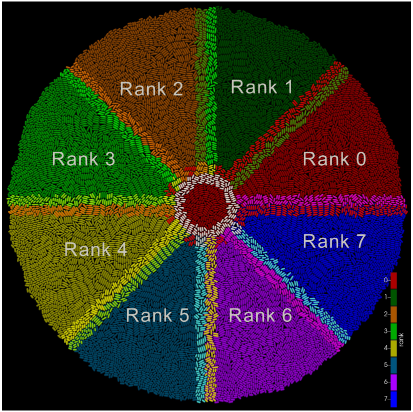
Key observations:

- Hard: stable at $\Delta t \sim 3 \cdot 10^{-4}$
- Soft: drops to $\Delta t \sim 10^{-5}$
- $30\times$ larger timesteps!

Parallel Architecture

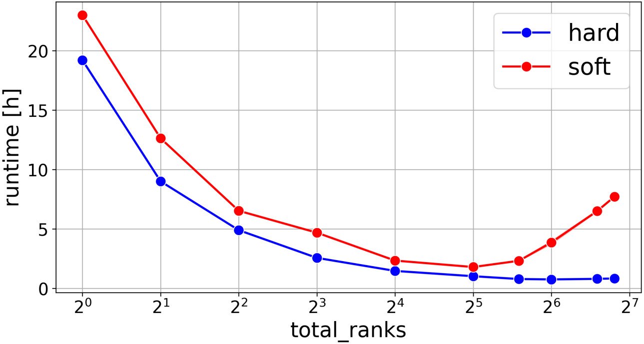
Implementation:

- MPI + PETSc framework
- Distributed vectors/matrices
- Angular sector decomposition
- Ghost particle exchange



Domain decomposition with 8 MPI ranks

Strong Scaling: Runtime to reach $R = 100$



- Hard model is always faster!
- Huge communication overhead (Especially for small Δt)

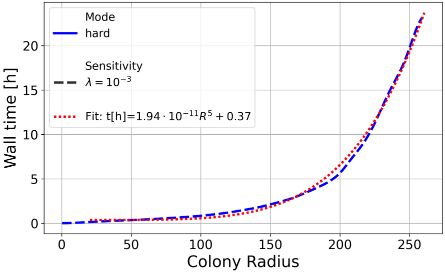
Maximum Colony Size (24h budget, 112 cores)

Hard Model:

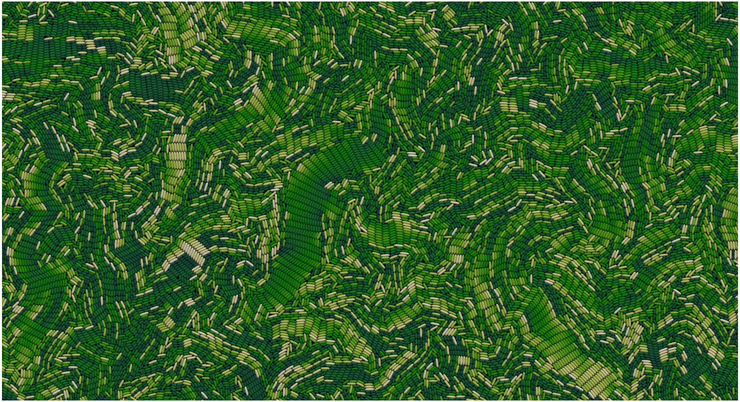
- $R_{\max} = 260$
- 301,116 cells
- Maintains accuracy

Scaling:

- $T[h] \propto R^5 \propto N^{2.5}$
- $\mathcal{O}(N)$ BBPGD iterations per step
- Costly (sparse) matrix-vector products



Largest Colony (R = 260, 301k cells)



View Full Image

Outline

When to use each Model?

Hard Model

Use when:

- Exploring large Colonies
- Cell-scale phenomena matter
- High accuracy required

Advantages:

- Faster simulations
- Physical accuracy

Disadvantages:

- Complex implementation

Soft Model

Use when:

- Exploring small Colonies
- Only macroscopic effects matter
- Artefacts acceptable

Advantages:

- Simple implementation
- Can model 'squishy' bacteria

Disadvantages:

- Slow simulations
- Limited accuracy

Outline

Future Work

1. **Hard Model Solver Improvements**
   - Leverage PETSc GPU support
   - Warm-start BBPGD with previous solution

2. **Model Extensions**
   - Consider overlap, in adaptive timestepping.
   - Consider alternatives to prevent overlap

3. **More Applications**
   - Other cell shapes (soft bodies?)
   - More complex models (Nutrient fields?, Outside forces?)
   - Utilize 3D capabilities

Thank you for your attention!

Questions?

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Code:
https://github.com/manuellerchner/MicrobeGrowthSim-IDP

Supplementary materials:
https://home.cit.tum.de/~ler/bacteria/

References I

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