Spatial organisation of multiple species of active particles interacting with an interface

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Introduction

- **Dynamic Interface:** The cell membrane is inherently dynamic, fluctuating due to thermal noise and active forces from the cytoskeleton, membrane proteins etc.
- **Reciprocal Coupling:** Active components deform the membrane (inducing curvature) and are simultaneously advected by the resulting shape, creating a feedback loop [2].
- **Limitations of Existing Models:** Minimal models often focus on single-species dynamics, neglecting the complex cocktail of active agents in real cells.
- **Theoretical Interest:** The bead-slider model has been extensively studied with Edwards-Wilkinson (EW) and Kardar-Parisi-Zhang (KPZ) dynamics [5], making it a robust framework for studying active matter on fluctuating interfaces.
- **This Work:** We study the competition between multiple species—specifically "Pushers" (promote valleys) and "Pullers" (promote hills)—whose affinity for curvature is decoupled from their deformation effects, leading to distinct emergent behaviours / patterns.

Motivation: Emergent Structures

We observe rich emergent behaviors when two species interact. These structures motivate our deep dive into the underlying model.

- **(a) Micro-clustering:** Separation into small clusters [1].
- **(b) Mixing:** Strong correlation and homogeneous mixing due to cancellation of activity.
- **(c) Traveling Giant Cluster:** Aggregation & directed motion.
- **(d) Lock-in:** Arrested dynamics, phase separation.

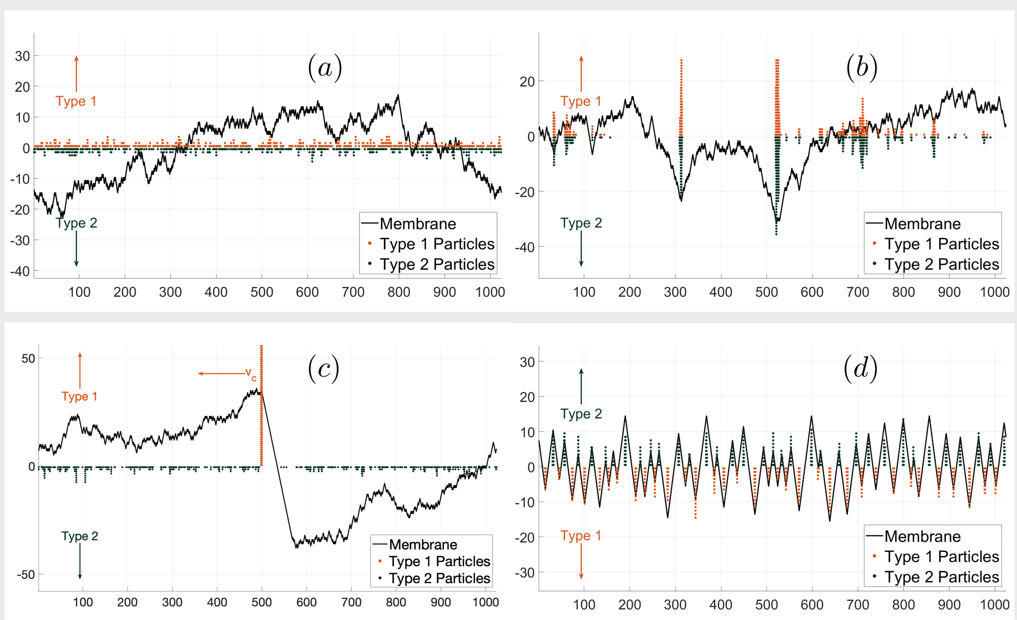

Fig 1: Snapshots of different membrane configurations and particle distributions. (a) $\{+,-,-,+\}$ Micro-clustering: similar to single species. (b) $\{+,+,-,+\}$ Homogeneous mixing: equal distribution. (c) $\{-,-,-,+\}$ Traveling Giant Cluster: Type 1 forms a large cluster chasing a smooth interface. (d) $\{+,+,-,-\}$ Lock-in: Arrested phase separation (extremely slow coarsening).

Model Schematic

1. Interface Dynamics: Sites flip ($\wedge \leftrightarrow \vee$) with rates depending on the number of particles n:

$$p_n^{\pm} = u\frac{e^{\pm n\beta}}{e^{n\beta}+e^{-n\beta}} \tag{1}$$

- $\beta > 0$: Pusher ($\wedge \to \vee$ favored).
- $\beta < 0$: Puller ($\vee \to \wedge$ favored).

2. Particle Dynamics: Hop rates to left/right sites are biased by local slope ∇h:

$$q^{\pm} = q_0\left(1 \pm \frac{\gamma}{2}\nabla h\right) \tag{2}$$

- $\gamma > 0$: Downhill bias (Gravity-like).
- $\gamma < 0$: Uphill bias (Anti-gravity).

Toy Model

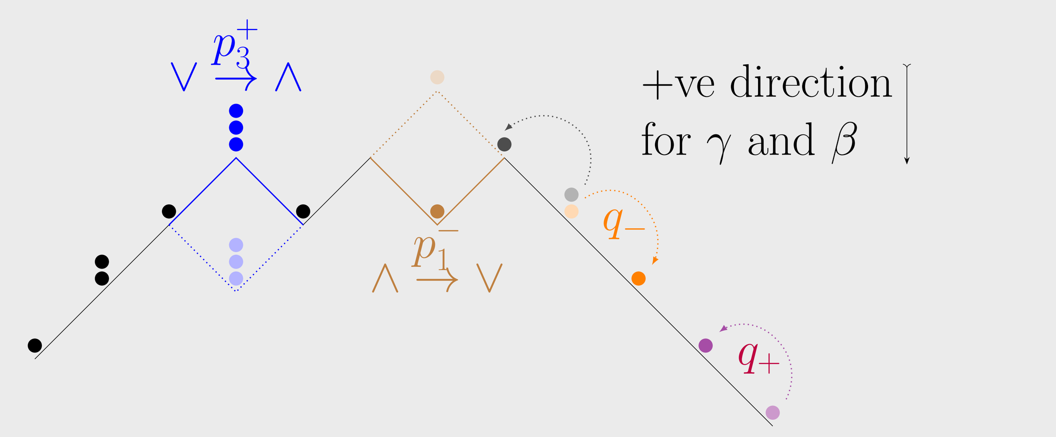

Fig 2: Model Schematic. Interface updates: Valley → Hill (Blue) and Hill → Valley (Brown). Particle motion: Downhill (Orange) and Uphill (Violet). Positive β favors Hill → Valley; Positive γ favors downhill motion.

Single Species Results

Competition between gravity (clustering) and activity (disruption) determines the phase.

Correlation $G(r)$: Active particles show anti-correlation at for some values of β and γ.

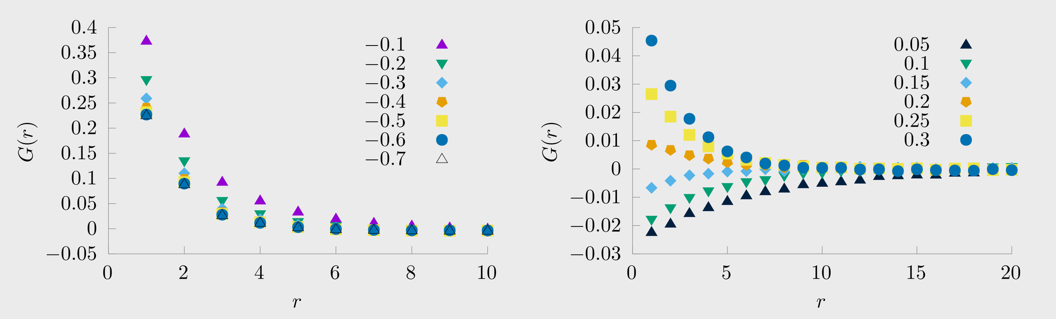

Fig 3: Density Correlations $G(r)$. (Left) Fixed $\gamma = 0.8$: increasing activity $|\beta|$ reduces correlation. (Right) Fixed $\beta = -0.8$: increasing gravity γ enhances clustering.

Phase Diagram:

- **Anti-correlation:** Low γ, high $|\beta|$.
- **Correlation:** High γ.

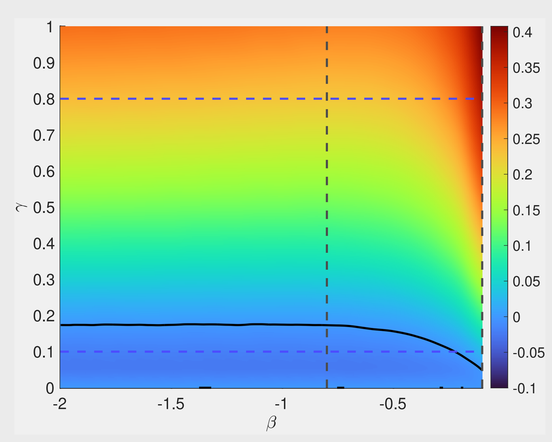

Fig 4: Correlation Phase Diagram ($G(1)$). (a) Positive-correlation (>0) driven by gravity γ. (b) Zero-correlation (solid line) where activity balances gravity. (c) Negative-correlation (<0) dominated by activity breaking up clusters.

Cluster Structure: Active particles show **Exponential decay**, passive show Power Law.

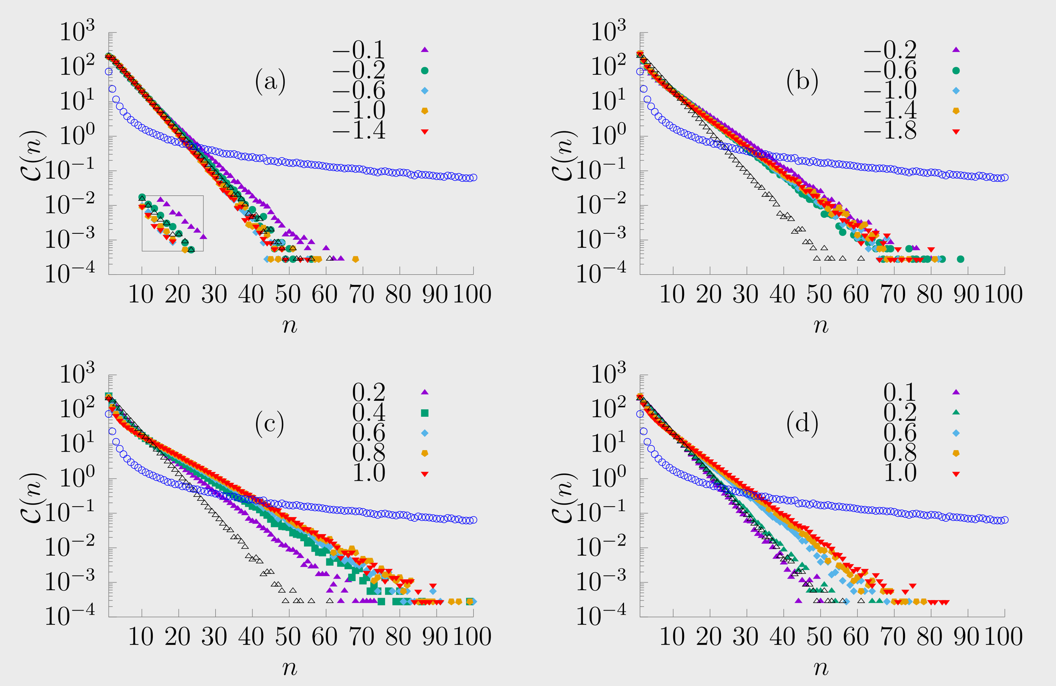

Fig 5: Cluster Size Distribution $\mathcal{C}(n)$. (a,b) Varying β at fixed $\gamma = 0.1, 0.8$. (c,d) Varying γ at fixed $\beta = -0.1, -0.8$. Active systems show exponential decay $\sim e^{-n/n^*}$, while passive cases ($\beta = 0$) show power-law decay $\sim n^{-1.5}$.

Two Species: System Configurations

We analyze 4 distinct combinations of activity (β) and gravity (γ) for two species. The system is denoted by the order $\{\beta_1, \gamma_1, \beta_2, \gamma_2\}$: Given $\beta = \pm 2$, $\gamma = \pm 1$, there are 4 possible configurations:

$$\{+,-,-,+\}\ \{+,+,-,+\}$$
$$\{-,-,-,+\}\ \{+,+,-,-\}$$

Two Species Results

Cluster Distributions: Distinct decay behaviors for different phases. Type 1 in Phase (c) shows a power-law tail (Giant Cluster).

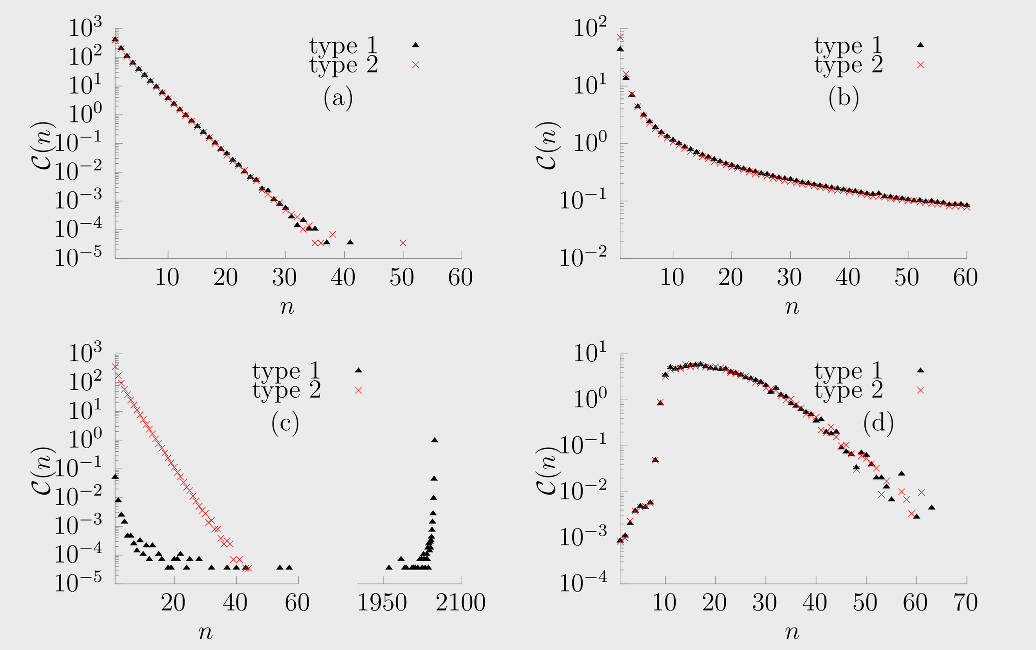

Fig 6: Cluster Distributions for Two Species. Notation $\{\beta_1, \gamma_1, \beta_2, \gamma_2\}$. (a) $\{+,-,-,+\}$ & (b) $\{+,+,-,+\}$: Both species show exponential decay, similar to single species. (c) $\{-,-,-,+\}$: Type 1 (red) exhibits a power-law tail (Giant Cluster), while Type 2 (blue) shows exponential decay. (d) $\{+,+,-,-\}$: Lock-in phase shows distinct distributions.

Dynamics & Ordering Analysis:

- **Giant Cluster Speed:** Type 2 increase speed.
- **Cross-Correlation:** $G_{1,2}(r)$ indicates mixing (positive) or micro-separation (negative) between species.
- **Very Slow Coarsening:** $\tau_{cc} \sim e^{L}$.

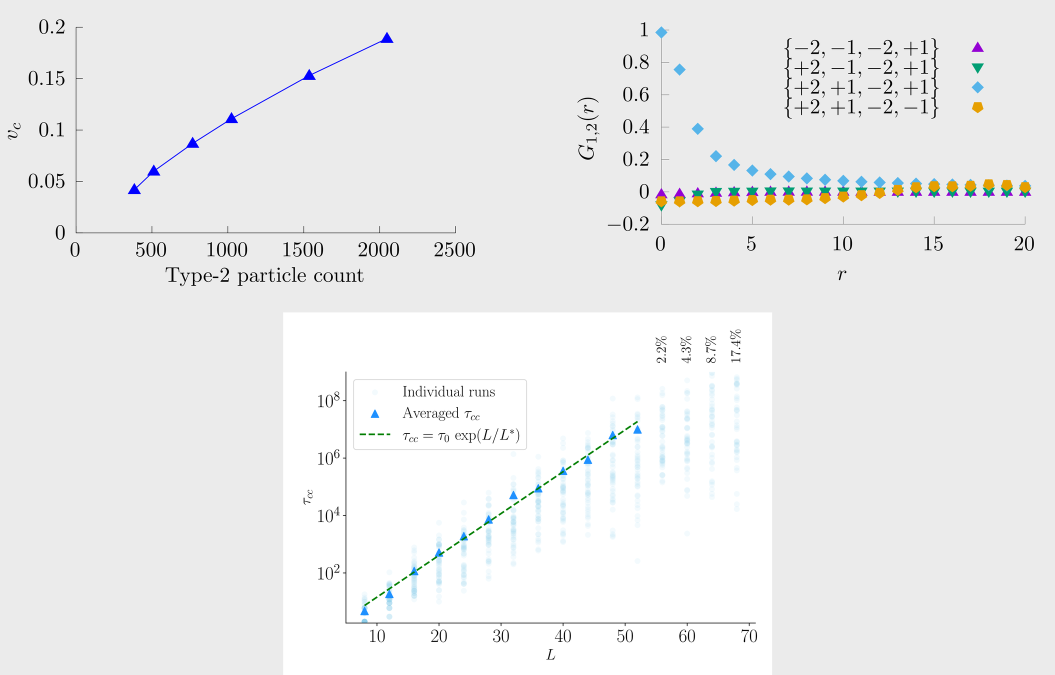

Fig 7: Dynamics & Ordering. (Left) Giant Cluster Speed. (Middle) Cross-Correaltions. (Right) Lock-in Timescales.

Discussion

Comparison to LH Model:

- **Lock-in Phase:** Resembles the Strong Phase Separation (SPS) in the Light-Heavy (LH) model [3] but arises as a *prolonged transient* state due to slow coarsening.
- **Giant Cluster:** Similar to phases of LH model, but exhibits distinct *coherent motion* driven by asymmetry.

Relation to CMAM: The giant cluster dynamics resemble Conserved Mass Aggregation Models (CMAM) [4], where aggregates move and merge. However, here the cluster leaves a *smooth interface trail* that guides its motion, unlike diffusive clusters in CMAM.

Dual Control: The reciprocal coupling allows simultaneous tuning of the **Interface** (roughness) and the **Particles** (mixing vs. demixing), offering a strategy for designing active surfaces.

Biological Relevance: Parallel to cellular dynamics where cytoskeleton and proteins cooperate to generate organized structures.

References

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