

The role of motility gradients in proliferating active matter: the case of sibling inhibition in *Pseudomonas aeruginosa* bacteria

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ABSTRACT

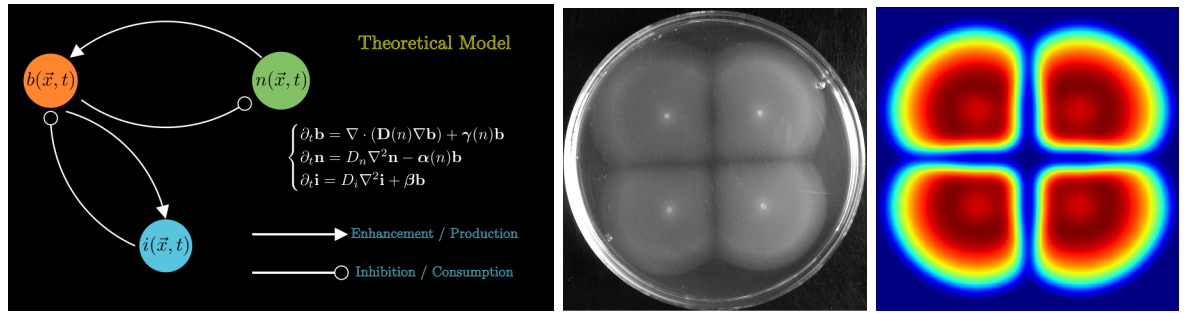


FIGURE 1. **Left:** Schematic representation of the theoretical model; **Center:** Experimental sibling inhibition; **Right:** Simulation of sibling inhibition

The ability of bacteria to swim in liquids or swarm on semi-solid surfaces, gels, porous media, and tissues is essential for colonising new territories, finding nutrients, and avoiding toxins.

Sometimes sibling colonies avoid each other just as they tend to avoid antibiotics thus forming distinct demarcation lines (DLs) between them. Although this phenomenon has been reported in literature, it is far from being understood[1–5]. We address this problem both experimentally and with numerical simulations.

Using a custom-built setup, we demonstrate that DLs are not associated to cell death [1], nor to quorum sensing (QS) signals or gel deformations [3]. We also show how colonies merge at different nutrient concentrations thus confirming the role of nutrient consumption in sibling inhibition. However, an irregular evolution profile that emerges at high nutrient concentrations does not allow the presence of a non-lethal inhibitory factor to be completely ruled out.

We model these collective behaviours with a Fisher-Kolmogorov type model using reaction-diffusion equations $\partial_t \mathbf{b} = \nabla \cdot (\mathbf{D}(n) \nabla \mathbf{b}) + \gamma(n) \mathbf{b}$. In such a model, the diffusion and replication coefficients depend on the local concentration of nutrients $n(x, t)$.

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In doing so, we deal with space- and time-dependent diffusivity $\mathbf{D}(x, t)$ and replication $\gamma(x, t)$. We calibrate this model to experiments in homogeneous environments, thus decoupling motility and proliferation to study separately how they are influenced by nutrient concentration.

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