

# Social Interactions in Myxobacterial Swarming

Yilin Wu<sup>1</sup>, Yi Jiang<sup>2</sup>, Dale Kaiser<sup>3</sup>, and Mark Alber<sup>1,\*</sup>

<sup>1</sup>Departments of Physics and Mathematics, and Center for the Study of Biocomplexity, University of Notre Dame, Notre Dame, IN 46556-5670; <sup>2</sup>Theoretical Division, Los Alamos National Laboratory, Los Alamos, NM 87545; and <sup>3</sup>Department of Biochemistry, Stanford University, Stanford, CA 94305

\* Author for correspondence: Mark Alber (malber@nd.edu)

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**Abstract:** Swarming, a collective motion of many thousands of cells, produces colonies that rapidly spread over surfaces. In this paper we introduce a cell-based model to study how interactions between neighboring cells facilitate swarming. We chose to study *Myxococcus xanthus*, a species of myxobacteria, because it swarms rapidly and has well-defined cell-cell interactions, mediated by type IV pili and by slime trails. The aim of this paper is to test whether the cell contact interactions that are inherent in pili-based S motility and slime-based A motility are sufficient to explain the observed expansion of wild type swarms. The simulations yield a constant rate of swarm expansion, which has been observed experimentally. Also the model is able to quantify the contributions of S motility and A motility to swarming. Some pathogenic bacteria spread over infected tissue by swarming. The model described here may shed some light on the colonization process.

## Synopsis

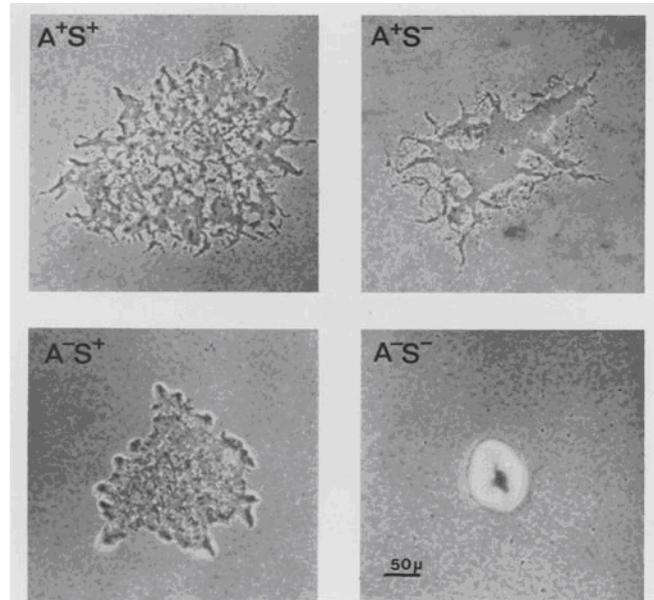
Many bacteria are able to spread rapidly over the surface, using a strategy called swarming. When the cells cover a surface at high density and compete with each other for nutrients, swarming permits them to maintain rapid growth at the swarm edge. Swarming with flagella has been investigated for many years, and much has been learned of its regulation. Nevertheless, its choreography, which is somewhat related to the counter-flow of pedestrians on a city sidewalk, has remained elusive. It is the bacterial equivalent of dancing toward the exit in a crowd of moving bodies that usually are in close contact. *Myxococcus xanthus* expands its swarms at 1.6  $\mu\text{m}/\text{min}$ , about a third the speed of individual cell gliding over the same surface. Each cell has pilus engines at its front end and slime secretion engines at its rear. Using the known mechanics of these engines, and the way they are coordinated, we have developed a cell-based model to study the role of social interactions in bacterial swarming. The model is able to quantify the contributions of motility engines to swarming. It also shows that microscopic social interactions help to form the ordered collective motion observed in swarms.

## Introduction

Bacterial swarming, a coordinated motion of many bacterial cells, facilitates their spread on the surface of a solid medium, like agar [1]. Swarming may have evolved to permit the bacteria in a colony to expand their access to nutrients from the subsurface and to oxygen from above. When the surface is a tissue in a live host, pathogenic bacteria swarm to create a biofilm and to spread the infection. Swarming is observed in cells that are propelled by rotating flagella [2], by the secretion of slime [3], and by retracting type IV pili [4, 5]. Bacterial swarming has been studied quantitatively in the modeling context of self-propelled particle systems [6, 7, 8]. Most models such as those for *Bacillus subtilis* and *Escherichia coli* (see [8] for a review) are based on long-range cellular interactions facilitated by chemical gradient or nutrient level (chemotaxis). However, myxobacteria show no evidence of long-range communicating systems to guide their collective motion; they have only local contact signaling and use social interactions between neighboring cells for swarming [9]. How interactions between cells facilitate swarming is still an open question. Understanding this question might shed light on the self-organizing process in bacteria, when they spread as a biofilm in an infected tissue and when they develop multicellular fruiting bodies. In this paper we describe a new cell-based model and study the effects of social interactions between cells, including the interaction mediated by slime trails and by type IV pili, on swarming. Type IV pili are found at one pole of a wide range of bacteria, including many pathogens that cause plant and animal disease.

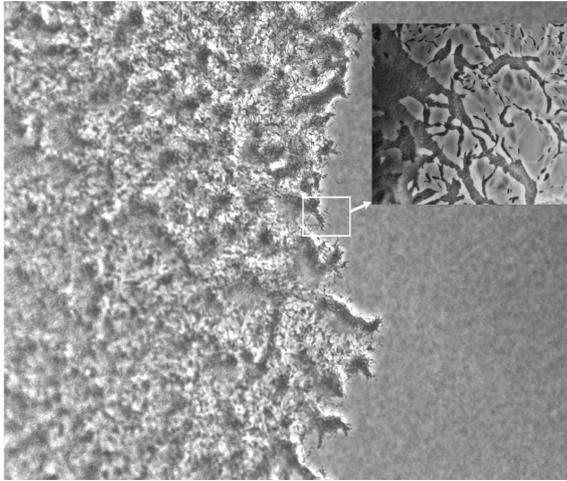
We chose to examine *Myxococcus xanthus*, because it swarms rapidly, has typical type IV pilus engines at the front end of cells, has slime secretion engines at the rear, and coordinates the two engines with each other. It has been studied for more than a century; numerous swarming mutants have been identified and characterized. Myxobacteria are commonly found in cultivated soils, where they feed on other bacteria. On the surface of nutrient agar, they swarm away from a point inoculum, spreading outward at a constant rate for two weeks. Although the bacteria are growing (and in fact they must grow to swarm), 90% of the swarm expansion rate is due to motility and to interactions associated

with motility, as shown by the low spreading rate of non-motile mutants [10, and Figure 1].



**Figure 1.** The cell distribution patterns of young swarms of *Myxococcus xanthus* (DK1622) and its two types of motility mutants photographed after 40 hours incubation (Reproduced from [11]). The letters A and S denote the two motility systems of *M. xanthus* (see text for details). All four strains grow at the same rate in an aerated liquid medium, but their swarms expand at different rates.

Individual *M. xanthus* cells are rod shaped, roughly 5 micron in length and 0.5 micron in width. They have two types of molecular motors that provide the thrust necessary for their gliding movement over a surface [9]. At the leading end of the cell are retractile type IV pili, long and thin hairs responsible for S motility. When a cell is close to a group of other cells, the cell's type IV pili can attach to the fibrils, which cover the surface of the neighboring group of cells like a fisherman's net. After attachment, the pilus retracts, and the retraction force pulls the piliated cell forward, while the group hardly moves. This pilus-mediated interaction produces many asymmetric cell clusters that often have tips that are pointed at one end (arrowhead shaped) and is characteristic of S-motility. Arrowheads can be seen in the A<sup>-</sup>S<sup>+</sup> panel of Figure 1. S motility is found among pathogenic *Neisseria* and *Pseudomonas*, where it is called twitching motility [4, 5].



**Figure 2.** Picture of a rectangular section of a typical, swarm edge of wild type *M. xanthus* strain DK 1622 ( $A^+S^+$ ). Several small peninsulas project outwards from the edge of the swarm. The inset is a higher magnification view of a segment of a typical swarming edge in which single cells and clusters of cells are evident. The inset was taken from a different but similar experiment. Dense clusters of cells (darker shades of gray) are evident in both

pictures.

At the trailing end of myxobacterial cells are several hundred pores, from which slime is secreted. There are roughly 150 pores scattered over the sides of the cell, also secreting slime, that becomes a thin layer, protecting the cell from lysis by cell-wall digestive enzymes being secreted by all the cells [3]. Both the lateral and the polar slimes are thought to be the same polysaccharide that is part of A motility; hereafter simply referred to as slime. Importantly, slime is completely distinct from the fibril polysaccharide that serves S motility [11]. Slime secretion from the rear pushes the cell forward, leaving a trail of slime behind the cell [3, 12] and generating movements called A motility. When a moving cell encounters a slime trail, it tends to turn through the acute angle to follow the slime trail. When an A motile cell collides with the side of another cell, the pushing of the slime engines at the rear causes the cell, which is flexible, to bend. The colliding cell thus reorients parallel to the other cell, producing a side-by-side cluster of cells. Such clusters are transient because the two cells do not adhere and often slide past one another.

The A and S motility engines, which are located at opposite poles of the rod-shaped cells, have engine-specific social interactions. During movement, a cell's polarity reverses regularly every 10 minutes or so [13, 14], and reversal is required for swarming [15, 16].

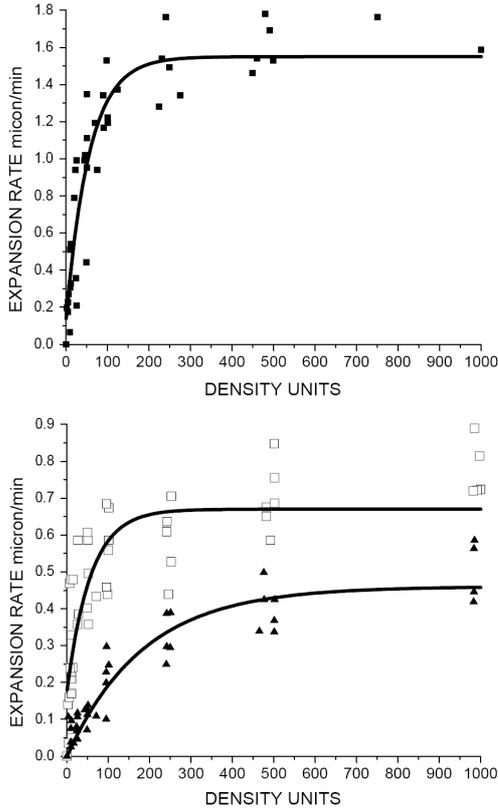
A wild-type cell ( $A^+S^+$ ) expresses both A and S motility.  $A^+S^-$  mutants express only A motility, while those with S motility but no A motility are called  $A^-S^+$  mutants [9].

Because wild type and  $A^+S^-$  mutants are self-propelled by A-motility engines, a comparison can expose the social interactions specific to the type IV pili. In both cases, individual cells are observed to move, stop, and move again, sometimes slightly changing direction and regularly reversing [3]. To investigate the coordinated motion within *M. xanthus* swarms, culture droplets of each mutant were placed on agar plates, and the swarm expansion rates were measured [10]. Figure 2 shows the edge of a typical swarm of wild type ( $A^+S^+$ ) cells. It is observed that swarm expansion rates remain constant until the swarm covers the entire surface available [10]. The expansion rates for various initial cell densities in K-S units<sup>1</sup> were measured and plotted against the cell densities. The fitted functions of expansion rate data for the three cell types are shown as solid lines in Figure 3. To a first approximation, the velocity of individual cells, when they are moving, is the same for  $S^-$  mutants ( $A^+S^-$ ) and wild-type ( $A^+S^+$ ) cells, about 4  $\mu\text{m}/\text{min}$ , but their swarm expansion rates are different [10]. The  $A^+S^-$  mutant swarms with a maximum rate of 0.7  $\mu\text{m}/\text{min}$ . Surprisingly, when S motility cooperates with A motility in wild-type *M. xanthus* ( $A^+S^+$ ), the maximum swarming rate is 1.6  $\mu\text{m}/\text{min}$ , about 2.3-fold larger than that of  $A^+S^-$  or of  $A^-S^+$  ([10], as shown in Figure 3).

Previously we used a lattice-based model to study myxobacterial fruiting body development after starvation [17, 18]. Swarming with sufficient nutrient supply has been studied using a continuous model in the form of partial differential equations (PDE) [19]. The effects of engine mechanics and cell shape have yet to be taken into account. Recently, we introduced a simplified off-lattice stochastic description of swarming [20], and herein add our current understanding of engine mechanics to investigate swarming and the role of social interactions.

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<sup>1</sup> K-S unit, or Klett-Summerson unit, is a measurement of cell density in suspensions [10]. A sample of cell suspension with 100 K-S units has approximately  $4 \times 10^8$  cells/ml. Using the experimental data in [10], we find that 100 K-S units correspond to a close-packing arrangement of cells in a two dimensional area.



**Figure 3.** Fitting curves of spreading rates of wild-type ( $A^+S^+$ ) myxobacteria and motility mutants (reproduced by using data from [10]). The dots are experimental data points. The fitting functions are: for wild-type ( $A^+S^+$ ),  $f(x) = a+b*\exp(-x/c)$ , with  $a = 1.55\pm 0.06$ ,  $b = 1.41\pm 0.10$ ,  $c = 56\pm 10$ ; for  $A^+S^-$  mutant,  $g(x) = a+b*\exp(-x/c)$ , with  $a = 0.67\pm 0.03$ ,  $b = 0.49\pm 0.05$ ,  $c = 57\pm 16$ ; for  $A^-S^+$  mutant,  $h(x) = b*(1 - \exp(-x/c))$ , with  $b = 0.46\pm 0.02$ ,  $c = 184\pm 27$ . The density is in K-S units and the expansion rate is in micron per minute.

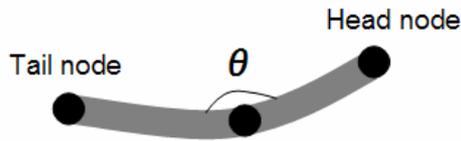
This paper is organized as follows. We start by describing the model of cell behavior and social interactions. Then we present the simulation results, and compare them with the experimental observations. We demonstrate a constant rate of swarm expansion and show that the model accounts for the significant difference in swarming rates between wild-type and  $A^+S^-$  myxobacteria arising from the loss of S motility. We also study in detail the order of collective motion in myxobacterial swarms. A detailed description of the computational model is given in the Methods section.

## Model of cell behavior and social interactions

### The motion of individual cells

In this paper we focus on the collective motion of a large number of cells in a swarm of high cell density, taking only the local, contact-mediated interactions between cells into

account. We represent each cell as a string of  $N$  nodes in two-dimensional space, following our earlier work [20] (Figure 4). The vector pointing in the direction from the tail node to the head node represents the orientation of a cell. We define an energy function (Hamiltonian) for the node configuration of a cell body and use it to constrain the cell length and the cell shape to a certain range. The active motion of an individual cell is then modeled as follows. After the head moves in a particular direction, a Monte Carlo approach [21] is used to reconfigure positions of other nodes in an attempt to minimize the Hamiltonian (see Methods). This allows the cell body to bend and to change its length by random fluctuations, which reflects the experimental observations [22].



**Figure 4.** The cell body of a bent cell is represented by 3 nodes (solid black dots). The cell has a length to width ratio of 10:1.

As mentioned in the introduction, the measured velocities of individual cells vary over a wide range, but the average velocities of  $A^+S^-$  and  $A^+S^+$  cell types are similar. To a first approximation, we take the cell velocity to be constant and the same for wild type  $A^+S^+$  and  $A^+S^-$  cells, with a magnitude of  $4 \mu\text{m}/\text{min}$  [10]. The direction of cell movement is determined dynamically by the model, which takes the interactions between neighboring cells into account.

Frequently cells reverse their motion by 180 degrees. Reversals are regulated by an internal biochemical clock that is not be affected by collisions or other interactions between cells [15, 16]. We model regular reversals of cell motility engines by switching roles of head and tail nodes in accordance with an internal clock (see Methods). The swarming efficiency (the ratio of the swarm expansion rate to the speed of individual cells) of myxobacteria primarily depends on social interactions between neighboring cells. The expansion rate of a swarm without social interactions, would be zero since the cells

would move back and forth equally without any net displacement in the long run. Social interactions help a swarm of reversing cells to spread.

## **Social interactions between neighboring myxobacterial cells**

### **Social interactions between cells**

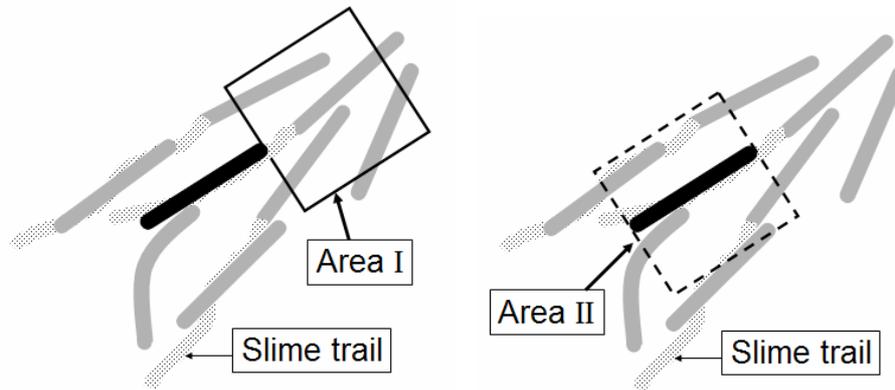
Ideally, interactions between all the more than  $10^7$  cells in a swarm would be considered, but that is not possible. Instead, we try to identify for each cell a neighborhood within which a majority of its interactions are expected to be found. Social interactions arise in S-motility when the type IV pili of one cell attach to the fibrils that surround other cells. Social interactions arise in A-motility from the tendency of a cell to follow the trail of slime left by another cell, and from collisions between cells that cause a moving cell to stop and its engines to stall, or that cause a cell to change its direction. Using the experimental data of Figure 3, an area of interaction for each cell type,  $A^+S^-$ ,  $A^-S^+$ , or  $A^+S^+$ , was defined as the statistically averaged area around a cell within which most of its social interactions occur. The interaction areas were taken to be proportional to the inverse of parameters in the exponential term of the formula obtained when an exponential curve was fitted to the experimental data in Figure 3. Fitting functions are specified in the legend to Figure 3. Each curve represents the observed swarm expansion rate as a function of the initial cell density of the culture. The interaction area for wild-type cells was found to be smaller than the sum of the interaction areas of the  $A^+S^-$  and  $A^-S^+$  mutants. We suggest that this unanticipated finding results when both engines are working because the two engines on a wild-type cell are not statistically independent but are constrained by the structure of a cell to propel it in the same direction.

Pilus-mediated interactions depend on the dynamics of pilus retraction [23] and on the spatial distribution of the fibrils to which the pilus tips have attached [24, 25]. Although these factors are mechanically complex and not yet understood in detail, the interaction has straight-forward effects. Pilus retraction provides a driving force for cell movement

that happens to be large, several times larger than the force developed by muscle actomyosin. And, because the force is almost never directed along the cell's long axis, the force tends to re-orient the direction of gliding. Because we are confined by the approximation that isolated cells move with constant speed, we need only consider the reorienting effect of pilus retraction. No effect on cell speed is considered, except that it drops to zero when one cell collides with another. Inasmuch as the fibrils tend to bundle groups of cells, as will be described below, the large size of the cell cluster prevents a significant reorientation of the bundle; only the cell whose pili have attached is reoriented. We model the reorientation effect of pilus-mediated interactions as driving the local alignment of cells (see Area I of Figure 5 and Methods). Although we represent the interaction area by a rectangle, a circle, or some irregular domain could have been employed. The important quality of an interaction domain is its area. That area is proportional to the probability that a cell has an interaction. Swarms of wild-type cells cover a larger area than those of  $A^+S^-$  or  $A^-S^+$  mutants, which is evident in Figure 1. Moreover, the peninsulas are more dense with cells that are well aligned side by side, as evident in Figure 9, below. Both effects illustrate reorientation due to pilus-retraction. Cell clusters tend to be narrow in the case of an  $A^+S^-$  mutant and wide in the case of wild-type bacteria.

A-motility engines at the rear of the cell push it forward in the direction of their long axis. A-motility also produces slime trails, and cells tend to follow them due to the adhesion of newly secreted slime to the older slime in the trail. The resulting alignment of the slime polysaccharide chains also reorients the direction of gliding. Slime trails are represented in the model by the paths that were taken by the last cells to have passed through Area II (Figure 5). Further details are given in the slime orientation field described in the Methods. Rod-shaped A-motile cells, which are pushing at their tail ends, tend to form parallel arrays if they collide or come into close contact with each other. These effects are illustrated in Area II of Figure 5 and are elaborated in Methods. Alignment results from inelastic collisions between cells that change their orientations. More generally, alignment in regions of high cell density arises spontaneously from the physical clustering of self-propelled rods [26].

For wild-type cells, we first model A and S motility, individually. Then, we combine them under the approximation that isolated cells move at a constant rate, as described above. The persistent active motion is taken to be led by the head of the cell, no matter which engines are functioning. Finally, we model the re-orientation due to pilus retraction and to the alignment of A-motile cells with their neighbors, or with the slime field.



**Figure 5.** Diagram showing the two types of social interactions for a cell (black). Although the pilus length varies with extension, retraction and breakage, most pili are of order of one cell length [27]. Area I represents pilus-cell interaction area. Its sides are taken as the average pilus length. If either the head or the tail of another cell falls within this area, it can be contacted by pili from the black cell. Area II is the corresponding interaction area for A motility. A bent gray cell in direct contact with a dark cell illustrates the bending and alignment due to collisions between cells. Slime trail following is illustrated by trails (light grey shaded area) inside of the Area II. An artificially low cell density has been used in Figure 5 to clarify the several interactions. In reality, many cells are adjacent to each other within the interaction area.

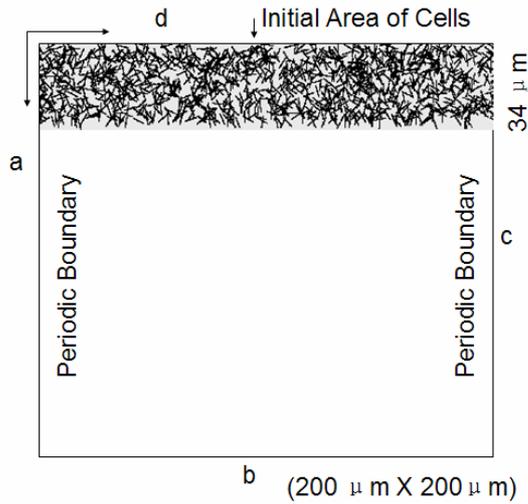
## Results

### Swarm expansion

To test the consistency of the model, we simulated the motion of cells near the edge of the swarm, and studied the expansion of the swarm. Although *M. xanthus* swarms consist of many millions of cells, the radial symmetry of a swarm, makes it possible to consider a

small rectangular sector of the swarm (Figure 2). A rectangular area of 200 microns by 200 microns (Figure 6) was convenient.

To compare the simulation with experimental measurements (shown in Figure 3), we considered that growth in the center of the swarm was driving a net radial outflow of cells from their center [15], and that the swarm was expanding at a constant rate. A constant cell density near the swarm edge was observed experimentally as the edge moved out [10]. Skipping the early transient phases, we start the simulation after the steady state has been reached. Although cells in the initial area are oriented in all directions, the orientations are radially symmetric. Both conditions apply to the Initial Area of Cells in Figure 6.



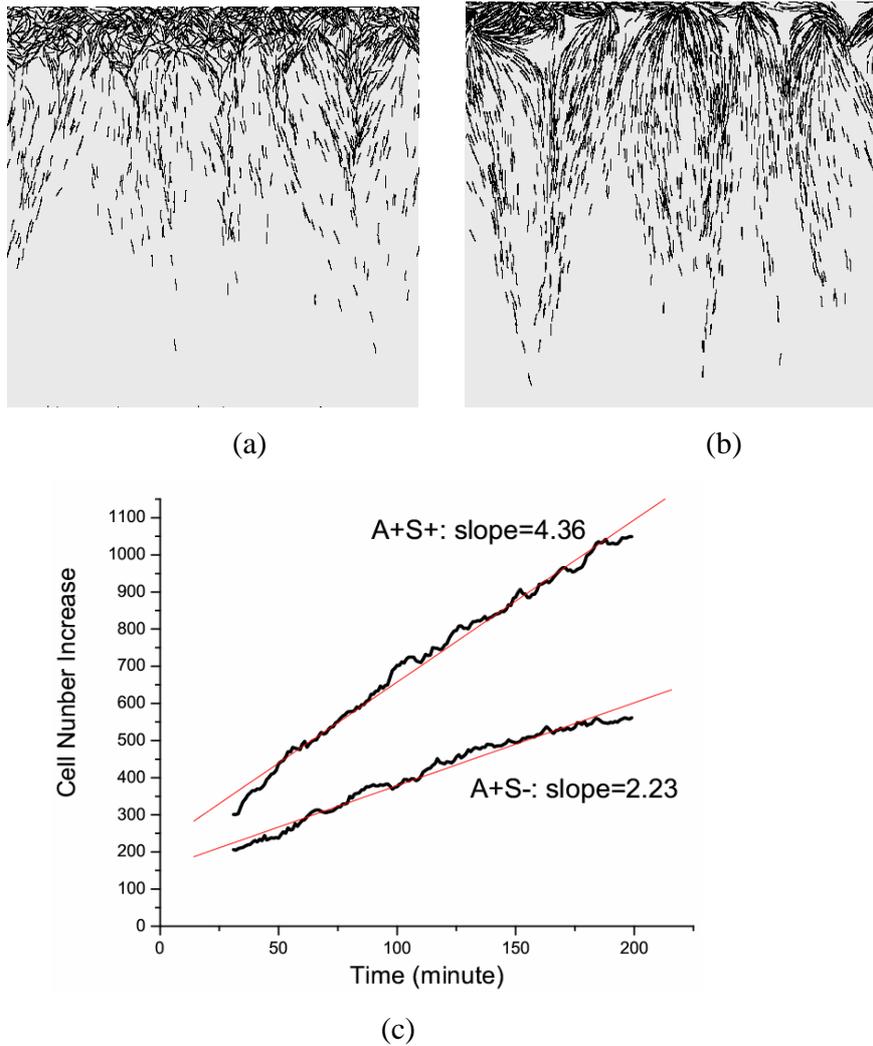
**Figure 6.** The simulation domain. Periodic boundary conditions are used at sides a and c, while reflection boundary condition is imposed at side d (see Methods). Cells at a density of 50 K-S units are shown randomly distributed in the initial area. Their initial orientations are chosen in accordance with the distribution function described in Methods, equation (12).

Denoting cell density as  $p(r, \theta)$  and the radial density as  $P(r)$ , due to the symmetry and the steady state we have:

$$P(r) \equiv \int_0^{2\pi} p(r, \theta) r d\theta \approx \text{Constant} \quad (1)$$

This shows that the cell number flux across the lower boundary of the initial area (or the increase rate of total cell number in the whole simulation domain) is linearly correlated with the colony expansion rate in Figure 3. We calculate the cell number flux rather than expansion rate directly. Therefore, we do not have to increase the simulation domain or

the total number of simulated cells. Further details of the simulation setup, implementation of the algorithm, and the choices of parameters are described in Methods and Table 1. Simulations show formation of long clusters (peninsulas) in both  $A^+S^+$  and  $A^+S^-$  cases (see Figure 7 (a) and (b)), which was observed experimentally [10].



**Figure 7.** (a) and (b) are pictures of the edges of the  $A^+S^-$  and wild-type ( $A^+S^+$ ) swarms respectively, after 200 minutes of simulation. (c) shows linear increase in the number of cells in the simulation domain with time. The red lines are best fits of simulation data with slopes indicated in the plot.

Simulations were performed for cell densities ranging from 2 to 200 K-S units, and linear increase of cell number was observed in all cases (for example see in Figure 7 (c)). This

implies that the cell number flux is almost constant during the whole swarming process for a given initial cell density, in full agreement with experiments [10]. Figure 7 corresponds to an initial density of 50 K-S units, which is a near saturation density for the rate curves of Figure 3.

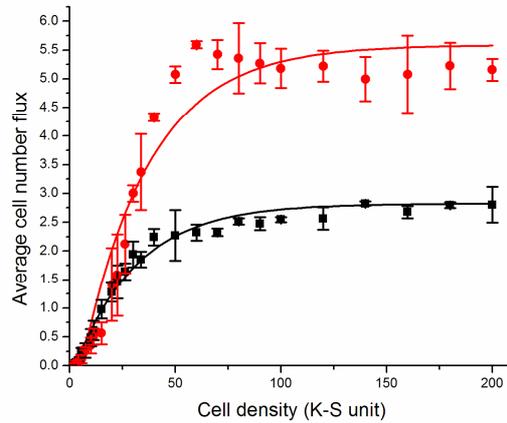
### **Comparison of $A^+S^+$ and $A^+S^-$ swarm rates**

We have calculated linear fits for the cell number increase data at various cell densities, and taken the slopes to be the average cell number fluxes, as shown in Figure 7.c. The results for both  $A^+S^+$  and  $A^+S^-$  cells are plotted against cell density in Figure 8 (a). We found that the cell number flux of the wild-type ( $A^+S^+$ ) is greater than that of the  $A^+S^-$  mutant at all cell densities. At densities higher than 50 K-S units, the cell number flux for  $A^+S^+$  is 2-fold larger than the  $A^+S^-$ .

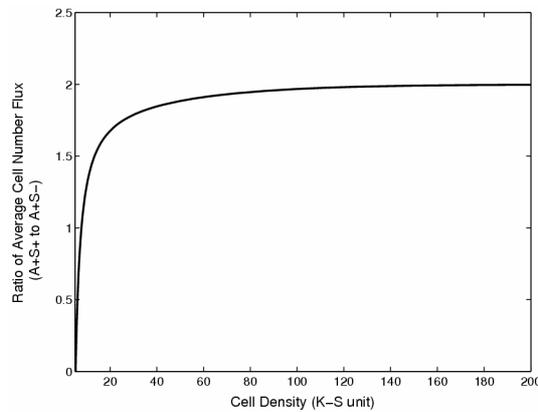
To see this effect more clearly, we fit the average cell number flux data into the first order exponential decay function, which is similar to the function used in Figure 3 from [10]. The fitting functions for wild-type  $A^+S^+$  cells and  $A^+S^-$  mutants are found to be  $f(x)=5.6-6.6*\exp(-x/32.1)$  and  $g(x)=2.8-3.1*\exp(-x/29.4)$  respectively. The ratio of these two fitting functions is plotted against cell densities in Figure 8 (b). It is equivalent to the ratio of colony expansion rates since the cell number flux is linearly correlated with the expansion rate. The ratio first increases and then saturates around 2 for cell densities higher than 50 K-S units. Experimental data shows that the  $A^+S^+$  rates are 2 to 2.5-fold larger at cell densities higher than 50 K-S units (Figure 3). Therefore, our result shows a significant difference in swarming rates between wild-type and  $A^+S^-$ , arising from the contribution of S motility that agrees with experiment.

Collision occurs in the model, whenever the head of one cell overlaps the area occupied by another cell. At this point, the moving cell stops; it is not permitted to glide on top of the other cell. As a consequence, at high cell densities the movement of individual cells is reduced. In reality cells do glide over each other. Reduction becomes significant above 100 K-S units, because at 100 K-S unit the average area occupied by an individual cell is

close to the area of a cell body (i.e., the area is closely packed with cells). In practice, due to the tendency of cells to cluster, cell movement is reduced beginning at concentrations of 60 K-S units. This effect explains the decrease in cell flux observed at higher cell densities ( $>60$  K-S units) for the wild-type in Figure 8 (a). The decrease results in a smaller value of maximum ratio (about 2 fold, see Figure 8 (b)) than experimental data (about 2 to 2.5 fold).



(a)

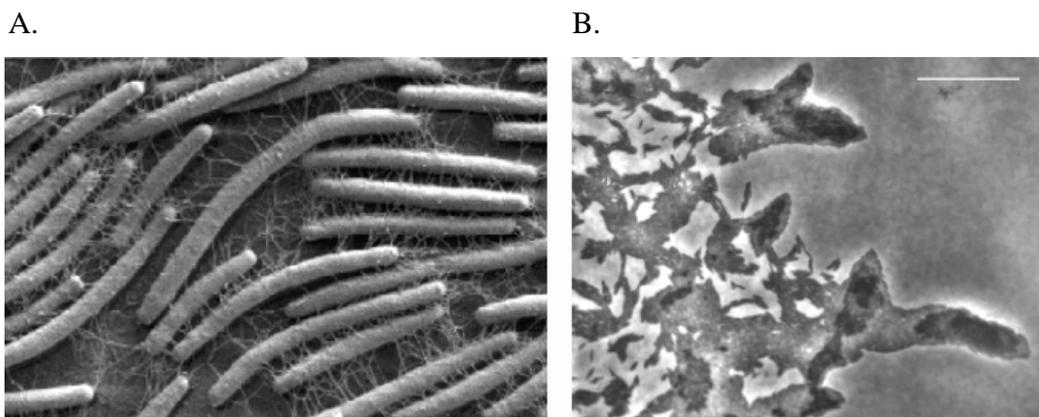


(b)

**Figure 8.** (a) The average cell number flux data from 3 simulation runs with error bars indicating standard deviation. The red dots and black squares indicate results for wild-type cells and  $A^+S^-$  mutants respectively. (b) Plot of the ratio of fitting functions  $f(x)/g(x)$  against cell density.

## The swarming of $A^-S^+$ mutants

Comparing the three curves of Figure 3 shows clearly that  $S$  motility contributes to the swarming of wild-type ( $A^+S^+$ ) cells. Figure 3 also shows that  $A^-S^+$  swarms expand without help from  $A$  motility, although the rate of expansion is less than  $1/3$  the wild-type at every cell density. With these data in mind, a puzzle takes shape: how are pili able to support expansion of an  $A^-S^+$  swarm when there should be no fibrils, to which the type IV pili might attach, beyond the edge of the swarm? The surface ahead of the swarm edge never had cells upon it. Must the belief that pili attach to fibrils before they can retract be abandoned? This section describes an attempt to solve the puzzle by examining the evidence that pili bind fibrils specifically, by offering a mechanism whereby specific binding and retraction can bring about the expansion of an  $A^-S^+$  swarm, and by testing the mechanism proposed.



**Figure 9.** Panel A. A scanning EM image of the network of fibrils that covers the cell surfaces and the space between them, from [32]. Slime is not evident in this image; it appears as part of the cell's surface seen beneath the fibrils. Panel B. Phase contrast image of the cell distribution at the edge of a young  $A^-S^+$  swarm that is expanding to the right. Older  $A^-S^+$  swarms stop expanding when their edge becomes smooth and many layers deep. The white scale bar is  $50\mu\text{m}$  long.

Evidence for specific binding includes the observation that  $A^-S^+$  cells move only when they are within a pilus length of another cell [10, 28]. Figure 9A shows that fibrils are present in profusion, and that they envelop clusters of adjacent cells. Although only half of the fibril mass is polysaccharide (the other half is protein [24]), several experiments

have revealed that removing the protein has no effect on pilus binding [24, 25, 29, 30, 31]. Evidently, *M. xanthus* pili bind fibril polysaccharide.

Therefore, side-by-side clusters of *M. xanthus* cells, like the peninsulas in Figure 9B, are viewed as a bundle that is enveloped by an elastic fisherman's net formed by association of polysaccharide fibrils that the cells have secreted. Bundling of cells by fibrils offers an explanation for the pointed shape, which A-S+ peninsulas tend to have. The points aim away from the swarm center (Figure 9B and [10, 35]), and in the general direction of swarm expansion. The shape and orientation of the peninsula tips suggest that cells at the tip of peninsula have been pushed into their position at the tip. Consider a cell within the body of the peninsula that happens to be moving toward the tip of the peninsula. This cell will have projected its pilus forward and attached it to the fibril network on cells ahead of it and closer to the tip. Retraction of that pilus could pull the cell forward and upward to add a new layer of cells to the peninsula. Indeed, most peninsulas have a second (or third) layer near their tips, which are evident in Figure 9B. On other occasions, retraction would pull the piliated cell right up to the end of a cell in the bottom layer that lies just ahead of our piliated cell. Recalling the description of A motility in the Introduction, each cell is also covered by the slime polysaccharide, which protects them from autolysis. Since the network of fibrils that envelops cells of a peninsula bundles them, both the elasticity of the fibrils and the cohesion between the slime on adjacent cells would tend to prevent their separation, by wedging action of the rounded end of the pushing cell, from cells to their left and right in the tip of the peninsula. Consequently, complete retraction of the pilus would cause the moving cell to push the cell in the peninsula that is immediately ahead of it. The pushed cell might slide forward while adhering through its slime covering to the cells on either side. Localized sliding would be reflected in a sharpening of the tip contour to a point, as observed (Figure 9B).

The hypothesis of pushing by S-motile cells was tested by analysis of 7 time-lapse movies of the advancing edges of A<sup>-</sup>S<sup>+</sup> swarms, each movie of 1 to 3 hours duration. Figure 9B is a single frame from one of the movies. In that frame numerous single cells and many peninsulas of various sizes are evident. Several observations relevant to A<sup>-</sup>S<sup>+</sup>

swarming could be made from the movies (Key and Kaiser, unpublished). First, almost all of the many thousands of cell movements were found within clusters of 10 or more cells. No isolated cell moved significantly, unless the cell was within pilus-striking distance of another cell. This shows that the cells are moving with S motility alone. Second, although the peninsulas either elongated or moved forward, the translocation rate was much less than the rate of individual cell movement in the same field. A lower rate correlates the peninsula's advance to its being pushed from behind, because the hypothesis has the pushed cell sliding past its neighbors in the peninsula. The sliding friction would decrease the rate of advance. Finally, the movies show many examples of individual cells, which appear to be moving more or less randomly, behind an arrowhead or a peninsula. Individual cells advancing toward the rear edge of the peninsula could have pushed it. A quantitative analysis of cell movement in the movies will be published separately, but this qualitative analysis supports pushing.

### **Social interactions result in higher order of collective motion**

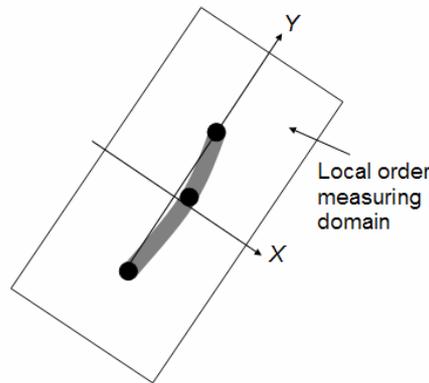
In previous sections we have shown that our model for social interactions is consistent with experimental results at the level of individual cells. In this section we investigate how microscopic social interactions facilitate swarming at population level. We demonstrate that social interactions lead to an increase in the order of collective motion, which is strongly correlated with swarming efficiency. We start by introducing an order parameter to characterize collective motion of bacteria in swarms with complex clustering patterns.

After analyzing experimental data and taking into account regular reversals of myxobacteria cells, we define the most ordered state as follows: all cells move side by side in close contact with each other in the same or opposite direction. The collective motion is considered purely non-ordered when either one of the following criteria is satisfied: (1) the orientations of neighboring cells of any given cell are random (or uniformly distributed); (2) any pair of cells is well separated so that cells are not in direct contact.

Vicsek et al. [34] used the average velocity as a global order parameter for analyzing the motion of self-propelled particles. However, myxobacteria cells reverse regularly and two opposite directions should be considered as being equivalent to each other. There are always cells moving in the direction opposite to the net motion of the whole cluster in most cell clusters in experimental movies. Also, as shown in the inset of Figure 2, the swarming pattern often exhibits localized clusters of aligned cells with different orientations of motion and one would need to take local order into account when measuring global order of motion. Therefore, the average velocity is not the best way of measuring the nematic order in myxobacteria swarms.

We first define two local measuring components to describe the local orientational order and positional order of a given cell, denoted as  $\Psi$  and  $P$  respectively. For a given cell  $k$  ( $k=1,2,\dots,M$ ,  $M$  is the total cell number) we choose the rectangular domain (of area  $S_0$ ) illustrated in Figure 10 as the local measuring domain (one cell length by two cell lengths), centered at the center of mass of a cell. We then measure the total area  $S$  occupied by neighboring cells within the local measuring domain and define the local positional order as the following:

$$P_k = \begin{cases} S_k / S_0, & \text{if } S_k < (S_0 / 2) \\ 1, & \text{if } S_k \geq (S_0 / 2) \end{cases} \quad (2)$$



**Figure 10.** Local measuring domain

We record the orientations  $\theta_j$ , with  $j=1,2,\dots,n$  of the neighboring cells with either head node or tail node inside the local measuring domain, in a way used in equation (11) in Methods. Then the angles between these orientations and X-axis in Figure 10  $\tilde{\theta}_j$ , with  $j=1,2,\dots,n$ , and  $\tilde{\theta}_j \in [0,\pi]$  are calculated. If cell  $k$  has no neighbors ( $j=0$ ), we define  $\Psi$  as 0. Otherwise, the local orientation order function is defined as follows:

$$\Psi_k = \frac{\Phi_k - \Phi_0}{1 - \Phi_0}, \quad (3)$$

$$\text{with } \Phi_k = \frac{1}{(n-1)n/2} \sum_{\substack{l \neq m, \\ l,m=1,\dots,n}} \exp\left(-\left|e^{i2\tilde{\theta}_l} - e^{i2\tilde{\theta}_m}\right|\right), \quad (4)$$

$$\text{and } \Phi_0 = \frac{1}{(n-1)n/2} \sum_{\substack{l \neq m, \\ l,m=1,\dots,n}} \exp\left(-\left|e^{i2\pi l/n} - e^{i2\pi m/n}\right|\right) \quad (5)$$

$\Phi_k$  determines how ordered the distribution of  $\tilde{\theta}_j$ 's is. The most ordered state corresponds to the case when all  $\tilde{\theta}_j$ 's are equal and  $\Phi_k$  has a maximum value of 1.  $\Phi_k$  is rescaled to the range of  $[0, 1]$ . Therefore, in the case of uniform (random) distribution of  $\tilde{\theta}_j$  the local orientational order function  $\Psi_k$  equals to 0. In the most ordered state all  $\tilde{\theta}_j$ 's are equal and  $\Psi_k$  is equal to 1.

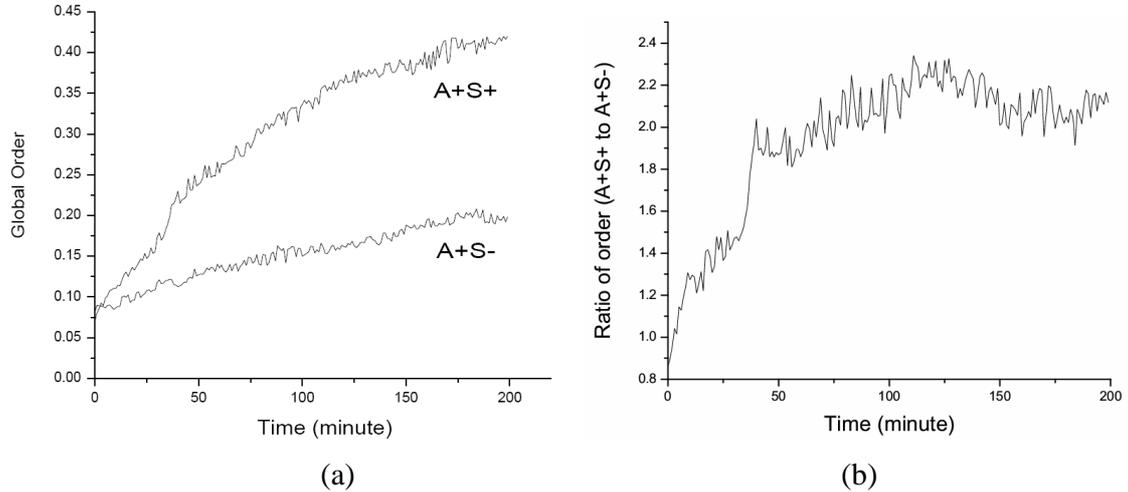
Finally, we combine both the local orientational order and positional order components from equations (3~5) to define the global order parameter for the collective motion of myxobacteria:

$$\Omega = \frac{1}{M} \sum_k^M \Psi_k \cdot P_k \quad (6)$$

where  $M$  is the total number of cells.

The order parameter  $\Omega$  has been specifically designed for myxobacterial swarming. Figure 11 shows values of  $\Omega$  for the simulation of swarming near colony edge with initial cell density 50 K-S units. We find that the order of collective motion in both A<sup>+</sup>S<sup>+</sup>

and  $A^+S^-$  swarms steadily increase and that  $A^+S^+$  cells achieve a much higher (about 2-fold) order than  $A^+S^-$  cells.



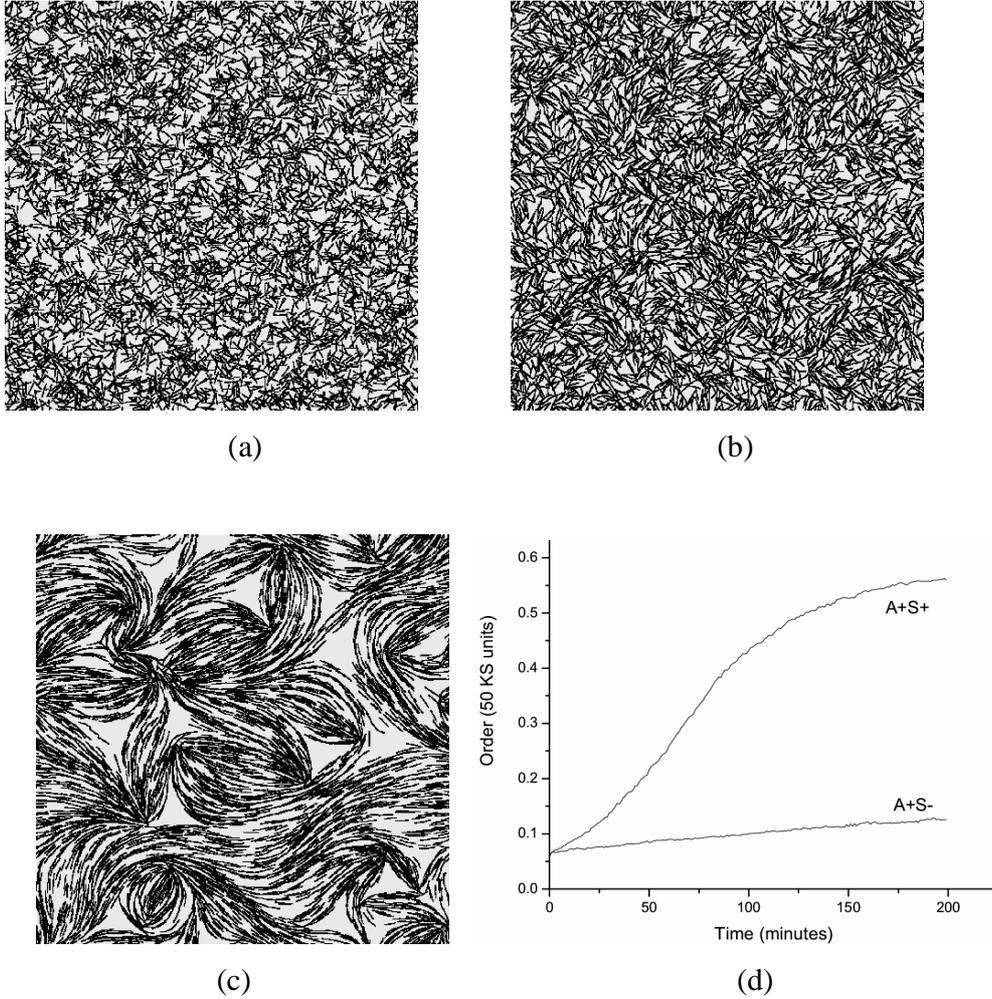
**Figure 11.** (a) Plots of the order parameter  $\Omega$  for the simulation of swarming near colony edge with initial cell density of 50 K-S units. (b) Plot of the ratio of global order parameters for  $A^+S^+$  and  $A^+S^-$  swarms.

Further, we look at the order of cellular motion in the inner area of myxobacteria colony. In Figure 12 (a) cells are randomly distributed in a square area of size 167 microns by 167 microns with a density of 50 K-S units. All boundary conditions are periodic. This is different from the previous simulations for cells near the colony edge, because we do not assume any more a pre-organized orientation distribution of cells.

Figures 12 (b) and (c) are the simulation pictures after 3 hours for  $A^+S^-$  mutant and wild-type ( $A^+S^+$ ) swarms respectively. We see that the pattern of  $A^+S^-$  mutant exhibits lower order, while wild-type ( $A^+S^+$ ) cells form large clusters oriented in various directions. Plots of the parameter  $\Omega$  are presented in Figure 12 (d). Again we see that the order of motion in both  $A^+S^+$  and  $A^+S^-$  cases increase with time, while  $A^+S^+$  cells achieve a much higher order than  $A^+S^-$  cells.

Therefore, we demonstrate that social interactions lead to an increase in the order of collective motion. Type IV pilus-mediated interactions increase the order much greater

than social interactions associated with A-motility. This is consistent with the experimental findings by Pelling et al [35], who observed higher order patterns within wild-type ( $A^+S^+$ ) swarms in comparison with motility mutant swarms.



**Figure 12.** Simulations of cell motion deep inside the swarming colony. (a) Initial random distribution of cells in a square area of size 167 microns by 167 microns at the density of 50 K-S units with periodic boundary conditions. (b)  $A^+S^-$  mutant swarm after 3 hours of evolution. (c) wild-type ( $A^+S^+$ ) swarm after 3 hours of evolution. (d) Plot of the global order parameter  $\Omega$  for the simulations of wild-type ( $A^+S^+$ ) and  $A^+S^-$  mutant swarms.

Comparison of Figure 11(b) with the ratio of cell number fluxes (Figure 8.b) indicates that the order of collective motion strongly correlates with the swarming efficiency. We suggest that higher order of motion results in greater swarming rates as observed in wild-

type myxobacteria experiments. It explains the origin of the significant difference in swarming rates between wild-type and  $A^+S^-$  myxobacteria arising from the coupling of S and motilities.

## Discussion

We have developed an off-lattice cell-based computational model to study the role of social interactions in bacterial swarming. The model is stochastic and it is based on detailed description of the bacterial motility engines and their regulation. The model demonstrates how social interactions facilitate bacterial swarming, and provides an explanation to the significant difference in swarming rates between wild-type and  $A^+S^-$  mutants arising from the effects of S motility. Our simulations indicate that the order of collective motion strongly correlates with the swarming efficiency, which provides a connection between microscopic social interactions and population-level swarming behavior.

The model is two-dimensional and provides a very good approximation for the bacterial behavior near the edge of the swarming population. However, in experiments at higher densities cells were observed to glide on top of each other, resulting in multiple cell layers just behind the edge of the swarm. As discussed in Results section, the two-dimensional nature of our model causes slight decrease in cell number flux at higher cell densities ( $>60$  K-S units) for wild-type myxobacteria (Figure 8.a), and results in a smaller value of maximum ratio (about 2 fold, see Figure 8.b) than experimental data (about 2 to 2.5 fold). A three-dimensional extension of the model will avoid such affects, and allow us to study cell clustering inside of a swarm as well as during fruiting body development under starvation [17, 18].

We did not quantitatively study the motion of mutants with impaired A motility ( $A^-S^+$  mutants) in this paper. As discussed in Results section,  $A^-S^+$  cells only have persistent active motion when they are within a pilus length of other cells so that the type IV pili

can attach to the fibril materials on the surfaces of other cells [33]. Wild-type and  $A^+S^-$  mutant both have A-motility that can produce persistent active motion. The only difference between wild-type and  $A^+S^-$  mutant is the effects of S motility, so it is more convenient to take wild-type and  $A^+S^-$  mutant as the modeling systems. By comparing their movements, we could investigate the role of pilus-cell interactions during swarming, which was one of our aims. In Results we have presented a qualitative analysis of  $A^-S^+$  swarming, which demonstrated that the pushing of cells near the swarming edge can explain the expansion of  $A^-S^+$  swarms. Preliminary simulations with the pushing mechanism show qualitative agreement with experiment in terms of peninsula shape and cell ordering (data not shown). Quantitative modeling of  $A^-S^+$  swarming dynamics will require more knowledge of the distribution and mechanical properties of the fibril.

When studying the effects of social interactions, we have related the swarming efficiency with the order of collective motion. This may provide a novel perspective on quantifying the condition of bacterial swarming. Further experimental investigation of this concept will rely on advances in microscope and image processing of microphotographs. Such experiments require very-high-resolution imaging that can cover large areas of a live bacterial colony [36]. We defined an appropriate order parameter, which characterizes the combined local orientational and positional order. Not limited to the case of myxobacteria swarming, the order parameter provides a quantitative measurement of collective motion in nematic biological systems where local interactions play a dominant role.

We have shown that social interactions mediated by type IV pili, when coupled with active motion, have an alignment effect on neighboring cells and significantly facilitate swarming. Many pathogenic bacteria swarm within infected tissues and have type IV pili as virulence factors. It is likely that the ascent of *Proteus mirabilis* up the urinary tract is a result of growth and swarming with flagella [37]. Similarly the spreading of *Neisseria* in infected tissue is related to swarming with type IV pili since those pili are necessary for virulence [38]. The bacterial swarming model described in the paper may therefore shed light on the colonization and infection process of pathogens.

## Methods

### Modeling the cell body

In the model each cell is represented by a flexible string of nodes (Figure 4) consisting of (N-1) segments, each of length  $r$ . There are (N-2) angles  $\theta_i$  between neighboring segments. For each cell we define the following energy function (Hamiltonian):

$$H = \sum_{i=0}^{N-1} K_b (r_i - r_0)^2 + \sum_{i=0}^{N-2} K_\theta \theta_i^2 \quad (7)$$

The first term in equation (7) is the stretching energy determined by the cells' length. The second term is a bending energy.  $K_b$  and  $K_\theta$  are stretching and bending dimensionless coefficients, analogous to the spring constants in Hooke's Law. They determine the extent to which the segment length and angles can change in the presence of fluctuations, respectively. They are the same for all segments and angles.  $r_0$  is the target length of a segment. In our simulations we choose the number of nodes  $N=3$  (Figure 4), so that  $r_0$  is 2.5 microns (half cell length).  $K_b$  and  $K_\theta$  are set at 5 and 2, based on experimental observation that cells do not change their length a lot but can bend rather easily.

### Modeling cell movement and social interactions

Let's denote the dark cell in the center of Figure 5 as cell  $k$ . In the absence of cell-cell collisions, the velocity direction of cell  $k$  is determined by three contributions: A-motility direction, orientation from slime trail and orientation from type IV pili.

**A motility direction.** The cells secrete slime (polysaccharide) from their tail end, which expands as it leaves the cell body and pushes the cell directly forward [12]. We model this motility by trying to orient the cell along its long axis, which is the tail-to-head direction. Corresponding term in formulae below is denoted as  $\vec{A}_k$ . Small deviations from

the direction of long axis are observed [10]. This is modeled using a Monte Carlo reconfiguration algorithm.

**Orientation from slime trail.** When a moving cell encounters a slime trail, it tends to turn through an acute angle to follow the trail. We define a two-dimensional slime-orientation vector field  $slime(\vec{r})$  which records the slime trail orientation as a vector assigned to each position  $\vec{r}$ . This vector coincides with orientation of a cell that passed through  $\vec{r}$  most recently. We make a simplifying assumption of all orientation vectors having unit length. Once a slime trail is laid down at position  $\vec{r}$ , it will be cleared after the slime aging time  $T_s$ .

**Orientation from type IV pili.** As discussed earlier in section “Model of cell behavior and social interactions”, type IV pilus-mediated interactions are assumed to align neighboring cells. For a particular cell  $k$ , we average the orientations of its neighboring cells within the pilus-cell interacting area (Figure 5, Area I), and define this averaged direction as the contribution of pilus-mediated interactions to the head velocity direction of cell  $k$ . This term is denoted as  $\vec{S}_k$ .

**Cell velocity direction.** When there are no collisions between cell  $k$  and its neighbors, the direction of its head velocity (denoted as  $\vec{V}_k(\vec{r}_{k0})$ ) is determined by the sum of A-motility direction, orientation from slime trail and orientation from type IV pili:

$$\vec{V}_k(\vec{r}_{k0}) = C \cdot \frac{\alpha \cdot \vec{A}_k + \beta \cdot slime(\vec{r}_k) + \gamma \cdot \vec{S}_k}{|\alpha \cdot \vec{A}_k + \beta \cdot slime(\vec{r}_k) + \gamma \cdot \vec{S}_k|}; \quad (8)$$

$$\vec{A}_k = \frac{(\vec{r}_{k0} - \vec{r}_{k(N-1)})}{|(\vec{r}_{k0} - \vec{r}_{k(N-1)})|}; \quad (9, \text{A-motility direction})$$

$$\vec{S}_k = n \cdot \frac{\langle \cos \theta_j \rangle \vec{e}_x + \langle \sin \theta_j \rangle \vec{e}_y}{|\langle \cos \theta_j \rangle \vec{e}_x + \langle \sin \theta_j \rangle \vec{e}_y|} \quad (10, \text{Orientation from type IV pili})$$

In equation (8)  $C$  is a constant cell speed (4 microns/minute);  $\alpha$ ,  $\beta$  and  $\gamma$  are parameters representing the relative strength of each motility term. Denominators are used in all equations for normalization. The experiments suggest that the forces generated from A and S motility are nearly the same, approximately 150 pN [9, 12]. For an  $A^+S^+$  cell we choose  $\alpha=\gamma=1.0$  and for an  $A^+S^-$  mutant we choose  $\alpha=1.0$  and  $\gamma=0$ . The strength of slime orientation effect is set as  $\beta=0.5$ . Note that the slime-orientation vector field  $slime(\vec{r})$  is recorded in a discrete two-dimensional lattice, each lattice site having a slime-orientation vector. Slime trails interact with the newly secreted slime, not with the head of a cell. We analyze slime-orientation vectors at the lattice sites covered by the front half of a cell body, and take the direction, which occurs most frequently, as slime-orientation direction to be followed by the cell. It is denoted as  $slime(\vec{r}_k)$  in equation (8).

Equation (9) determines cell orientation, which is the direction from the tail node ( $\vec{r}_{k(N-1)}$ ) to the head node ( $\vec{r}_{k0}$ ) and which is considered as the A-motility direction. In the equation (10)  $n$  denotes the total number of neighboring cells of the cell  $k$ . We multiply the expression by the factor of  $n$  because we think that type IV pili have a stronger effect on the direction of motion of the head node (pili are located at the head of a cell) and that this effect depends on the number of neighboring cells. Terms  $\cos \theta_j$  and  $\sin \theta_j$  are the  $x$  and  $y$  components of the orientation vector  $\vec{A}_j$  of the  $j$ -th neighboring cell. These vector components are then averaged ( $\langle \cos \theta_j \rangle$  and  $\langle \sin \theta_j \rangle$ ) and are taken as the  $x$  and  $y$  components of the average direction.  $\vec{e}_x$  and  $\vec{e}_y$  denote unit vectors along  $x$  and  $y$  axis. We model the alignment in such a way that cells orient with their neighbors to the acute angle. That is, if the dot product of the tail-to-head directions of cell  $k$  and its  $j$ -th neighbor cell is negative, we choose opposite direction to  $\vec{A}_j$  as its orientation. Therefore, we have:

$$\begin{aligned} \text{If } \vec{A}_k \cdot \vec{A}_j < 0, \quad \cos \theta_j &= -(\vec{A}_j)_x, \quad \sin \theta_j = -(\vec{A}_j)_y; \\ \text{If } \vec{A}_k \cdot \vec{A}_j \geq 0, \quad \cos \theta_j &= (\vec{A}_j)_x, \quad \sin \theta_j = (\vec{A}_j)_y. \end{aligned} \quad (11)$$

This approach is different from that taken by Vicsek et al [34]. The alignment is determined through acute angles because we use cell orientations instead of velocity directions.

**Collision-resolving algorithm.** When the head node of cell  $k$  collides with the body of cell  $j$ , this collision is resolved as follows:

1. Calculate distances between the head node of cell  $k$  and two end nodes of cell  $j$ ;
2. If one of these distances is less than a cell width, choose at random a new direction such that dot product of new direction of cell  $k$  and orientation of cell  $j$  is positive, and move;
3. Else take the average direction of both cells  $k$  and  $j$  as the new direction and stall until next time step. (The same method is used in the above alignment algorithm of type IV pilus-mediated interactions.)

**Reversal of gliding direction.** Each myxobacterial cell reverses its gliding direction every 10 minutes or so. (Reversal periods of myxobacteria follow a distribution with an average of about 10 minutes.) For simplicity, we choose the reversal periods in accordance with binomial distribution from 5 minutes to 15 minutes [39]. Each cell is assigned an inner reversal clock and a “counter”. The initial values of the clock “counter” are assigned at random. At each time step of a simulation, the value of “counter” increases by a unit of time. Cell reverses when the value of its “counter” reaches the value of the reversal period and the “counter” is reset to zero.

## **Simulation of swarming near the colony edge**

**Simulation setup.** The simulation domain is chosen in the form a rectangle 200 microns by 200 microns (Figure 6). In simulations a unit of length is equal to 1/6 micron and one time step is equal to 1/5 minute so that the initial cell length (5 microns) is equal to 30 units of length and cell width (0.5 micron) is 3 units. As mentioned in the text, we

approximate that myxobacteria move at the constant speed of 4 microns per minute so that in the simulations a cell moves a distance of 5 units each time step.

Initially cells are distributed within the “Initial Area of Cells” (see Figure 6). Cell centers are distributed at random, but cell orientations are distributed around the radial direction in accordance with the normalized distribution function  $f(x)$  with a peak at  $(\pi/2)$ :

$$f(x) = (\pi/2)^{-3} \sqrt{x(\pi-x)} \quad (12)$$

From experimental observations it follows that a steady rate of swarm expansion is reached only when most cells behind the swarm edge orient themselves outwards along the radial direction. Ideally, one would need to choose the initial orientation distribution  $f(x)$  according to the experimental data measured at the beginning of the steady swarming. However, due to the lack of such data, we select the initial orientation distribution function  $f(x)$  in such a form that most cells initially point outwards from the swarming edge. Cell growth and division are included in our model as maintaining the average density in the simulation domain near the edge.

**Algorithm implementation.** At each time step we implement the following sequence of operations for each cell:

- (1) Check the “counter” of inner reversal clock and decide whether to reverse polarity of the cell or not. Then calculate the velocity direction of the head node according to the model for motility systems. If no collision occurs, move the head node at a distance of 5 units; otherwise use the collision-resolving algorithm to resolve the collision.
- (2) Apply Monte Carlo algorithm to re-configure the positions of other nodes of the cell. Use procedure used in [20]. After moving the head node to a new position, repeat the following operations for (integer part of  $2.5N$ ) number of steps ( $N$  is the number of nodes per cell):
  - (i). Choose node  $i$  at random and move it in the direction from node  $i$  to node  $(i-1)$  at a distance of 5 unit lengths;

(ii). Calculate the energy change  $\Delta E$  due to the relative position change of the nodes. Use Metropolis algorithm [21] to determine the acceptance probability for the positional change of a node:

$$P(\Delta E) = \begin{cases} 1, & \text{if } \Delta E \leq 0; \\ e^{-\Delta E/kT}, & \text{if } \Delta E > 0 \end{cases} \quad (13)$$

(3) Record slime-orientation vectors in the end of individual cell movement at all positions passed through by the cell.

After all cells move, calculate the cell number flux through the boundary into the free space and add the same number of cells into the initial area to keep the cell number in the “Initial Area of Cells” constant. Table 1 provides values of modeling parameters.

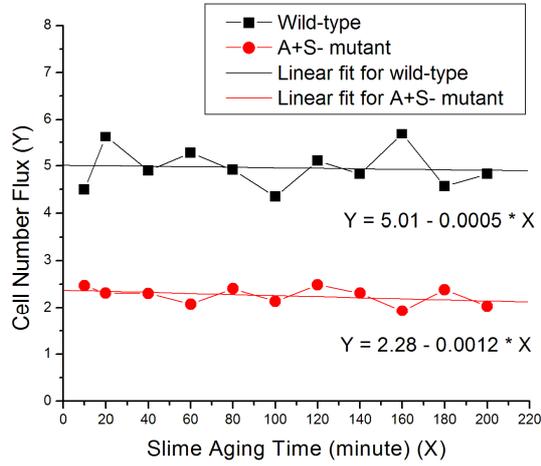
## Appendix

### Parameter ranges for the model of slime trail and slime guidance

Our model depends on two parameters characterizing properties of the slime trail: the slime aging time  $T_s$  and the relative strength of slime guidance. In this section we describe simulation results for different ranges of these parameters to test the robustness of the model.

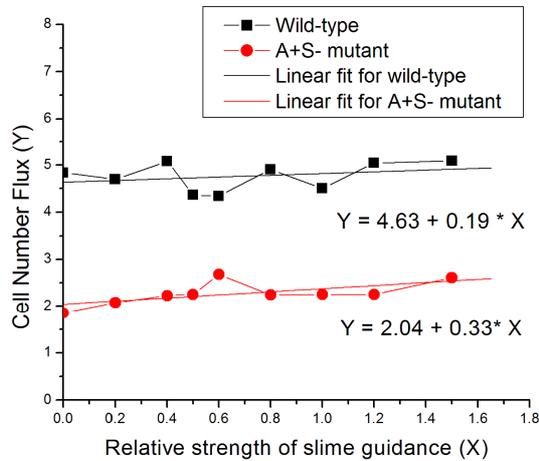
The slime aging time ( $T_s$ ) is defined as the lifetime of a slime trail during which it has the ability to guide the motion of a bacteria. We used a value of 20 minutes in our simulations. In the following figure (Figure 13), we simulate the swarming of wild-type and  $A^+S^-$  mutant at the density of 50 KS unit (the same simulation setup as in Figure 7), and varied  $T_s$  from 10 minutes to 200 minutes (the whole time span of the swarming simulations). We make linear fits for the data points and find that the value of  $T_s$  has little effect on simulation results (the cell number flux). This is because slime guidance is

primarily a local effect, and slime trails will be washed out by other cell's slime at short times when the cell density is high. Therefore, the parameter  $T_s$  is quite robust for the results in Figure 8(b), which is the main validation of our model.



**Figure 13.** The dependence of cell number flux on the slime aging time.

The relative strength of slime guidance is modeled by the parameter  $\beta$  in equation (8). We used a value of 0.5 in the simulations (see Methods). Here we varied  $\beta$  from 0 to 1.5, and calculate the cell number flux in swarms of wild-type and  $A^+S^-$  mutant type at the density of 50 KS unit (the same simulation setup as in Figure 7). The simulation data is plotted in Figure 14 along with the linear fits. We find that as the slime guidance effect gets stronger, the cell number flux increases. It increases slightly faster in case of  $A^+S^-$  mutants than in case of wild-type cells, with the slopes being 0.33 and 0.19 for  $A^+S^-$  mutant and wild-type cells respectively. This result suggests that as the effect of slime guidance gets stronger, the local alignment of cells and the order of collective motion are both increased. However, this does not affect the results in Figure 8(b) much, since the increase of cell number flux in case of  $A^+S^-$  mutants is only slightly faster than that in case of wild-type cells. The ratio of two fitting functions remains bigger than 2-fold till  $\beta=18.5$ . This demonstrates robustness of our model with respect to the relative slime strength (see Figure 8(b)).



**Figure 14.** The dependence of cell number flux on the relative slime strength.

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**Author contributions.** DK formulated biological questions and provided experimental data. MA, YW and YJ designed the off-lattice stochastic model. YW performed simulations and, with MA, YJ and DK, interpreted the results. YW, MA, YJ and DK wrote the paper.

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**Competing interests.** The authors declare that no competing interests exist.

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Parameter description	Parameter values	Notes
Target length of cell body	30 unit lengths	Actual cell length is about 5 microns
Number of nodes per cell	$N = 3$	
Cell width	3 unit lengths	Actual cell width is about 0.5 micron
Stretching and bending coefficients	$K_b = 5$ $K_\theta = 2$	Equation (7), Dimensionless
Boltzmann constant times temperature	$kT = 2$	Equation (13), Dimensionless
Relative strength of motility terms	$a = 1.0, \beta = 0.5, \gamma = 1.0$ ( $A^+S^+$ ) or 0 ( $A^+S^-$ )	Equation (8)
Magnitude of head velocity	$C=5.0$ unit lengths	Equation (8)
Slime aging time	$T_s = 20$ minutes (100 simulation time steps)	

**Table 1.** Parameter values used in the simulations.