Motion of two micro-wedges in a turbulent bacterial bath

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Abstract. The motion of a pair of micro-wedges ("carriers") in a turbulent bacterial bath is explored using computer simulations with explicit modeling of the bacteria and experiments. The orientation of the two micro-wedges is parallel and fixed by an applied magnetic field but the translational coordinates can move freely as induced by the bacterial bath. As a result, two carriers of same orientation move such that their mutual distance decreases. Eventually the two carriers stack on each other with no intervening bacteria exhibiting a stable dynamical mode where the two micro-wedges follow each other with the same velocity. These findings are in qualitative agreement with experiments on two micro-wedges in a bacterial bath. Our results provide insight into understanding the self-assembly of many micro-wedges in an active bath.

1 Introduction

A wide variety of active suspensions\(^{[124]}\) are known to form remarkable spatio-temporal patterns\(^{[56]}\) with the appearance of coherent dynamics structures on scales that are large compared with a single self-propelled unit. Examples range from bacterial suspensions\(^{[89]}\), spermatozoa\(^{[101]}\), human crowds\(^{[12]}\) to suspensions composed out of artificial self-propelled particles\(^{[314,1516,171,8]}\). Such systems have frequently been studied in the last year in bulk focusing on clustering\(^{[1920212223]}\), swarming\(^{[24252627]}\) and complex swirling or turbulence\(^{[2829303132333435]}\). A static confinement has been shown to be able to stabilize these structures\(^{[36]}\), accumulate and guide active particles\(^{[37,58,394041]}\). This effect has been used to rectify the motion of swimmers\(^{[4341454647]}\) and to build sorting\(^{[48495051]}\) as well as trapping devices\(^{[524541]}\). Furthermore the motion of passive but mobile particles submersed in an active fluid has been studied, starting with spherical and curved tracers\(^{[55596061]}\) to long deformable chains\(^{[58]}\). Using asymmetric cogwheels a spontaneous directed rotation\(^{[596061]}\) can be extracted out of an active bath. The translational analog is a directed motion of a single micro-wedge along its cusp induced by the active particles\(^{[5263]}\).

In this paper, we consider micro-wedges as passive carriers and expose them to a turbulent bacterial bath. The case of a single carrier has been explored previously both by computer simulation of appropriate models resolving the individual bacteria and by experiments\(^{[62]}\). For a micro-wedge kept fixed in orientation by an external
Fig. 1: Schematic representation of the system. The self-propelled rods with an aspect ratio $\ell/\lambda$ have a propulsion velocity $v_0$ directed along the main rod axis $\hat{u}$. The single six Yukawa segments are shown by red circles, whereby the larger interaction prefactor of the first segment is indicated by darker color. The Yukawa segments of the wedgelike carriers are shown in blue. The distance between the carriers is given by $d$ and $L$ corresponds to the contour length of each carrier. On average their velocity will be directed along the cusp and are denoted by $v_1$ and $v_2$.

field and moving on a two-dimensional substrate as far as its translational motion is concerned, it was found that turbulence of the bath maximizes the directed carrier speed along its cusp. The responding mechanism was attributed to swirl depletion in the inner wedge area which gives some bacteria which are close to the wedge angle the possibility to push the carrier forward in an efficient way.

Here we consider the case of two micro-wedges with the same fixed orientation and explore by computer simulation and experiments the motion of a carrier pair in two dimensions. This can be understood as a first step towards the hierarchical self-organization of many carriers in a bacterial bath. Here we show in qualitative agreement two carriers of same orientation move such that their mutual distance decreases. Eventually, the two carriers will end up in a state where they stack closely on top of each other such that there are no intervening bacteria left. They exhibit a stable dynamical mode in which the two micro-wedges follow each other with the same speed. The distribution function of the wedge distance averaged over a finite time shows a subtle multiple-peak structure which is compatible with the swirl depletion picture. We obtain our results within the same model successfully applied to the description of a single micro-wedge by calculating the average relative velocity and the distribution of the wedge distances. Our numerical results are in qualitative agreement with experiments on two micro-wedges in a turbulent bacterial bath.

This paper is organized as follows: in Sect. 2 we will explain the used model before we present results for the motion of the micro-carriers obtained by particle resolved simulations in Sect. 3 and experiments in Sect. 4. Finally, we conclude in Sect. 5.

2 Model

We model the bacterial bath in two spatial dimensions by $N$ rod-like self-propelled units with an effective body shape asymmetry analogous to Ref. 62. Each rod of
length $\ell$ and width $\lambda$ is discretized into $n = 6$ spherical segments equidistantly positioned along the main rod axis $\mathbf{u} = (\cos \varphi, \sin \varphi)$, see Fig. 1. The according aspect ratio $p = \ell/\lambda = 5$ is chosen in order to model Bacillus subtilis suspensions. A repulsive Yukawa potential is imposed between the segments of different rods [61]. The resulting pair potential of a rod pair $\alpha, \beta$ is given by

$$U_{\alpha\beta} = \sum_{i=1}^{n} \sum_{j=1}^{n} U_{ij} \exp\left[-r_{ij}^{\alpha\beta}/\lambda\right]/r_{ij}^{\alpha\beta},$$

where $\lambda$ is the screening length and $r_{ij}^{\alpha\beta} = |\mathbf{r}_i^{\alpha} - \mathbf{r}_j^{\beta}|$ the distance between segment $i$ of rod $\alpha$ and segment $j$ of rod $\beta$ ($\alpha \neq \beta$). In analogy to our previous work [62,65] we incorporate an effective shape asymmetry to account for the experimental observed swim-off effect of colliding bacteria [69,66]. We increase the interaction prefactor for the first segment with respect to the others of each rod. This quantity is given by $U_0^2/U_j^2 = 3$ ($j = 2 \ldots n$) [62]. Any overlap of particles is prohibited by choosing a large interaction strength $U_j^2 = 2.5F_0\ell$. Here $F_0$ is an effective self-propulsion force directed along the main rod axis and leading to a constant propulsion velocity $v_0$ [67]. We do not resolve details of the actual propulsion mechanism. Hydrodynamic interactions between the swimmers are neglected which is justified at high packing fractions in the absence of any global flow.

Micro-swimmers move in the low Reynolds number regime. The corresponding overdamped equations of motion for the positions $\mathbf{r}_\alpha$ and orientations $\mathbf{u}_\alpha$ are

\begin{align}
\mathbf{f}_T \cdot \partial_t \mathbf{r}_\alpha(t) &= -\nabla_{\mathbf{r}_\alpha} U(t) + F_0 \mathbf{u}_\alpha(t), \\
\mathbf{f}_R \cdot \partial_t \mathbf{u}_\alpha(t) &= -\nabla_{\mathbf{u}_\alpha} U(t),
\end{align}

in terms of the total potential energy $U = (1/2) \sum_{\alpha,\beta(\alpha \neq \beta)} U_{\alpha\beta} + \sum_{\gamma,\alpha} U_{\gamma\alpha}$ with $U_{\gamma\alpha}$ the potential energy of rod $\alpha$ with the carrier $\gamma$. The one-body translational and rotational friction tensors for the rods $\mathbf{f}_T$ and $\mathbf{f}_R$ can be decomposed into parallel $f_\parallel$ and perpendicular $f_\perp$ and rotational $f_R$ contributions which depend solely on the aspect ratio $p = \ell/\lambda$ [68,69].

\begin{align}
\frac{2\pi}{f_\parallel} &= \ln p - 0.207 + 0.980p^{-1} - 0.133p^{-2}, \\
\frac{4\pi}{f_\perp} &= \ln p + 0.839 + 0.185p^{-1} + 0.233p^{-2}, \\
\frac{\pi a^2}{3f_R} &= \ln p - 0.662 + 0.917p^{-1} - 0.050p^{-2}. 
\end{align}

Accordingly, the propulsion velocity is given by $v_0 = F_0/f_\parallel$ and sets the characteristic time unit $\tau = \ell/v_0$.

We model a pair of micro-wedges $\gamma, \delta$ analogous to the swimmers by tiling the wedge contour length $L = 20\ell$ into Yukawa segments and restrict their motion to translation. The wedge angle is kept rectangular. The resulting equation of motion for the carriers is

$$\mathbf{f}_T \cdot \partial_t \mathbf{r}_\gamma(t) = -\nabla_{\mathbf{r}_\gamma} U_\gamma(t),$$

where $\mathbf{f}_T$ corresponds to the hydrodynamic friction coefficient of the micro-wedge, calculated using the software package HYDRO++ [70,71] and $U_\gamma = (1/2) \sum_{\gamma,\delta(\gamma \neq \delta)} U_{\gamma\delta} + \sum_{\gamma,\alpha} U_{\gamma\alpha}$ is the total interaction on a single micro-wedge.

We use a rectangular simulation domain with $L_y = 3L/\sqrt{2}$, an aspect ratio $L_x/L_y = 3$ and an area $A = L_x L_y$ and periodic boundary conditions. The total number of rods is given by $N = A\phi/\lambda\ell$, where $\phi$ is the dimensionless packing fraction,
Fig. 2: (a) Probability distribution of the carrier distance $d$ measured in swimmer lengths $\ell$ obtained from simulations (magenta) and predictions due to the achieved transport efficiencies of the carriers. (b) Difference of the transport efficiencies $\Delta v = v_2 - v_1$ of the single carriers. Negative values mean that the right carrier is catching up, see Fig. 1. Vertical lines indicate the location of the local maxima in the probability distribution $P(d/\ell)$.

which will be fixed to $\phi = 0.5$. Results are obtained for simulations with randomly chosen starting distances $d$ and statistics are being gathered over a time interval $t = 1000\tau$, using a time step $\Delta t = 10^{-3}\tau$. By measuring the mean displacement along the $x$-direction within a single time step, the individual velocities $v_\gamma$ are determined by $v_\gamma = (x_\gamma(t + \Delta t) - x_\gamma(t)) / \Delta t$, with $\gamma = 1, 2$. The obtained results and the resulting transport efficiencies for the carriers depend weakly on the packing fraction within the turbulent regime of the bacterial bath [65].

3 Simulation results

In the following we consider two cases. Firstly, we confine the motion of the two wedges under the constraint that they both have the same $y$-coordinate and their orientation is fixed while their $x$-coordinates can respond freely to the bacterial bath. Secondly, we only fixed their orientation but relax the constraint in the $y$-direction.
In our experiment the alignment constraints were imposed by the applied magnetic field.

For the first case, Figure 2(a) shows the probability distribution $P(d/\ell)$ for the distance between two micro-wedges, using the reduced distance $d/\ell$ between the carriers, measured along the cusp of the carriers, see again Fig. 1. The distribution reveals four characteristic peaks at distances $d_1 = 1\ell$, $d_2 = 6\ell$, $d_3 = 23\ell$ and $d_4 = 50\ell$ and will be explained step by step in the following.

It is interesting to correlate the peak positions with the behavior of the transport speed difference $\Delta v = v_2 - v_1$ as a function of the carrier distance $d$, see Fig. 2(b). In the absence of velocity fluctuations, a peak in $P(d/\ell)$ is expected either when the transport speed difference vanishes or when the modulus of the speed difference exhibits a local minimum. In case of a vanishing relative speed at $d = d_0$, the sign of the slope $\frac{\partial \Delta v}{\partial d}|_{d=d_0}$ determines the stability of the stationary situation at $d = d_0$: it is stable if $\frac{\partial \Delta v}{\partial d}|_{d=d_0} < 0$ and unstable if $\frac{\partial \Delta v}{\partial d}|_{d=d_0} > 0$. For a stable situation and in the absence of velocity fluctuations, the particle would be stuck at the distances where the velocity is vanishing resulting in a divergence of the distribution function $P(d/\ell)$ at these distances.

In Fig. 2(b) we observe indeed two zeroes at about $d_1 = 1\ell$ and about $d = 28\ell$ which compare with the peaks at $d_1 = 1\ell$ and $d_3 = 23\ell$. Moreover two minima in the speed difference occur at $d_2 = 6\ell$ and $d_4 = 50\ell$ which clearly correlates with the second and fourth peak in $P(d/\ell)$. However, for the actual height of the peak velocity fluctuations are significant which smear out the "ideal" divergence. These are defined as $\sqrt{\left\langle (\Delta v/v_0)^2 \right\rangle}$ and shown in Fig. 2(a) as well and reveal a non-Brownian behavior.

In detail, the first peak at $d_1 = 1\ell$ where the two wedges stick together corresponds indeed to a stable situation. When compressing the wedges more to an even smaller distance than $d_1 = 1\ell$, the repulsive bead forces acting between the different wedges pushes them back, while expanding the mutual wedge distance is inhibited by the osmotic pressure acting on the nearly touching wedges by the surrounding bacteria. The latter effect is similar to the strong equilibrium depletion interaction between parallel rods suspended in passive spheres [72,73]. In our simulations, we observed that once the wedges are sticking together at these small distances they are irreversibly bound during the time scale of the simulations such that we conclude that this is the final state of the system. Accordingly, this first peak will grow if the data are averaged over a longer simulation time when started from a randomly chosen distance.
The occurrence of the next three peaks in $P(d/ℓ)$ is more subtle. In order to obtain a simple geometric picture for the second peak at $d_2 = 6ℓ$, we consider the density distribution of the bacteria around a single wedge in the frame of the moving wedge which is plotted in Fig. 3(a). This density field reveals an accumulation layer of thickness of about $a = 4ℓ$ around the wedge, see Fig. 3(b), and a circular depletion zone of particles inside the wedge. This depletion zone possesses a typical radius $R = 7.5ℓ$ which coincides with the typical swirl size of the bulk bacterial suspension in the absence of any wedge. In fact, the basic idea in understanding the depletion zone is that a typical swirl swipes out particles from the inner wedge.

Figure 4 displays the density field around two carriers under the constraint that they are at the distances where the four peaks in $P(d/ℓ)$ occur. Figure 4(a) corresponds to the first peak at $d_1 = 1ℓ$ where the two sticking wedges can hardly be distinguished and the overlapping surrounding accumulation layer responsible for the depletion attraction is clearly visible. Figure 4(b) shows the distance $d_2 = 6ℓ$ where the second peak and a speed minimum occurs. Here two stacked wedges can make use of the depletion zone causing strong interpenetration. This mutual attraction is reduced when the mutual surrounding accumulation layers of bacteria around the wedges start to overlap. This occurs roughly at a distance of $2a = 8ℓ$ which is close to the position of the second peak at $d_2 = 6ℓ$.

At a distance $d_3 = 23ℓ$ the density field is shown in Fig. 4(c). Geometrically, as also visualized in Fig. 4(c), this distance matches a swirl diameter augmented by a doubled layer size $2R + 2a = 23ℓ$ and represents the unstable situation where the accumulation layer of the right wedge just starts to touch the inner swirl in the left wedge. Finally, the fourth peak is located at $d_4 = 50ℓ$. However, in this distance regime, the variation in the relative wedge speed and the amplitude of the fourth peak are tiny.

We now analyze the second case relaxing the constraint in the $y$-direction. The probability distribution $P(Δy/ℓ)$ to find the second carrier in the perpendicular direction $Δy$ is shown in Fig. 5. Obviously, this distribution is even in $Δy$ due to the reflection symmetry. For large inter-carrier distances $d$ the probability is almost uni-
formly distributed implying that motion of two wedges is basically uncorrelated, see the data for \( d = 40\ell \) in Fig. 5. As \( d \) shrinks, a triple-peaked distribution \( P(\Delta y/\ell) \) emerges, see the data for \( d = 15\ell \) in Fig. 5 for which the positions of the two wedges are also explicitly indicated. The two side peaks indicate an optimal motion where the apex of the right wedge just experiences the outer range of the depletion zone, see Fig. 3(b). Finally, at closer distance the motion of the right wedge is confined within the aperture of the left one resulting in a localized distribution function \( P(\Delta y/\ell) \). Again, the observed fine structure supports the general swirl depletion picture put forward in Ref. [62].

4 Experiment

We have performed a series of experiments to support our theoretical findings. The micro-wedges were fabricated by photolithography from a mixture of photoresist and nickel particles. Nickel particles conglomerate into long chains in the course of spin coating of the mixture on a silicon wafer. After the exposure, developing, and etching, the wedgelike carriers containing small nickel particles were transferred to water by ultrasonication. Due to magnetization of the particles, the orientation of the fabricated wedges can be controlled by the external magnetic field. Two orthogonal pairs of large Helmholtz coils were used to control the orientation of the carriers. The
Fig. 6: (a) Illustration of attraction and repulsion of wedge-like carriers in a turbulent bacterial bath. The orientation of the wedges is controlled by the applied uniform magnetic field. (b) Distance between carriers of parallel (red circles) and anti-parallel orientation (black squares) as a function of time.

uniform field created by these coils does not affect the positions or horizontal motions of the wedges, but only control their orientation. The dynamics of the wedges in the bacterial suspension was captured by Olympus IX71 microscope and digital monochrome camera (Procilica GX 1660). We observed convergence of carriers of the same orientation and repulsion in the case of the opposite orientations, see Fig. 6 consistent with our simulation results. We emphasise two differences between experiment and numerical simulations: First of all, while the motion of the carriers is confined in two dimensions, the motion of bacteria is three-dimensional. As a result, we also observed large (compared to simulations) fluctuations in the positions of the carriers due to an enhanced bacterial activity. Second, at very small wedge separation ($d < 10\mu m$) there is an additional dipole-dipole interaction induced by the inherent magnetic dipole moment.

5 Conclusions

In line with the fascinating topic of how many passive objects self-organize in an active bath, we have considered here the case of two micro-wedges in a turbulent bacterial bath. We find an efficient stacking of the two wedges leaving no bacteria between them. This state is a stable dynamical mode where the two micro-wedges are following each other with the same speed. There is more subtle behavior in the relative wedge motion which is compatible with the geometric swirl depletion picture put forward in Ref. [62]. Our findings provide a first step towards the general case of many carriers which are therefore expected to form columnar stacks with a large persistence length reminiscent to the columnar phase of stacked bowl-shaped colloidal particles [74].

For the future study, it would be interesting to investigate other particle shapes such as $L$, $C$ shapes [75][76] where stacking is also expected. However, there are also shapes where stacking is frustrated (like for $T$-shaped carriers) which are expected to form loosely-packed gels [77]. Moreover, a microscopic theory for active depletion [78]
is highly desirable to make predictions for the carrier motions which could be based on kinetic \cite{79} or dynamical density functional theory \cite{38,80}.

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