Rectification of Twitching bacteria through narrow channels: A numerical simulations study

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Abstract

Bacteria living on surfaces use different types of motility mechanisms to move on the surface in search of food or to form micro-colonies. Twitching is one such form of motility employed by bacteria (e.g. Neisseria gonorrhoeae) in which the polymeric extensions known as type IV pili mediate its movement. Pili extending from cell body adheres to the surface and pulls the bacteria by retraction. The bacterial movement is decided by the two-dimensional “tug-of-war” between the pili attached to the surface. Natural surfaces in which these micro-crawlers dwell are generally spatially inhomogeneous and have varying surface properties. Their motility is known to be affected by the topography of the surfaces. Therefore, it is possible to control bacterial movement by designing structured surfaces which can be potentially utilised for controlling biofilm architecture. In this paper, we numerically investigate the twitching motility in a two-dimensional corrugated channel. We simulate the bacterial movement by two different models: (a) a detailed tug-of-war model which extensively describe the twitching motility of bacteria assisted by pili and (b) a coarse-grained “run-and-tumble” model which depicts the motion of wide-ranging self-propelled particles. The simulation of bacterial motion through asymmetric corrugated channels using the above models show rectification. The bacterial transport depends on the architecture of the channel. In particular, the variation of the particle current with the geometric parameters of the micro-channels show that we can optimise the particle current for specific values of these parameters.

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I. INTRODUCTION

Many bacterial species dwell on surfaces. Each species employ a particular or a combination of different motility mechanisms such as swimming, darting, gliding and twitching to survey the surfaces for food and colonies [1]. Surface-dwelling bacteria such as Neisseria gonorrhoeae cannot actively swim in a liquid medium; instead, they possess a form of surface motility known as “twitching motility” [2, 3]. The motility is mediated by the polymeric extensions emerging from the cell body known as pili and is characterised by intermittent and jerky movement [4, 5]. Pili have various functions, but a class of these pili known as type-IV pili (Tfp) assist in motility over surface [2, 3, 6]. Tfp undergoes cycles of polymerisation and de-polymerisation. The polymerisation results in the generation of new pilus and subsequent elongation, out of which some get attached to the surface. Whereas, depolymerisation leads to retraction and eventual disappearance of a pilus. The retracting attached pilus exerts a force on the cell body and pulls the bacterium along its direction. A single pilus can generate a force exceeding 100 pN [7–9]. The vectorial balance of forces exerted by various Tfp in different directions as in a tug-of-war eventually decides the direction of motion of the bacterium [10–13].

Unlike many other bacterial species, the N. gonorrhoeae cannot sense chemical gradient as the chemotaxis gene is absent in them [14]. Due to the absence of any biases, these “micro-crawlers” essentially executes an unbiased random walk on flat surfaces. In its natural habitat, however, the bacteria encounter surfaces having spatial inhomogeneities and varying surface properties. The topography of the surface influence the motility of the bacteria as recent experimental studies indicate that N. gonorrhoeae can sense the topography of the surfaces and the microscopic structures can guide their movement [15, 16]. Structured surfaces have been designed where the physio-chemical properties control the bacterial movement and potential biofilm architecture [15, 17]. In general, controlling microbial locomotion have potential applications in diverse areas such as diagnostics [18], therapeutic protein synthesis [19] and photosynthetic biofuel production [20–22].

The bacterial movement can be controlled and directed by exploiting the so-called active ratchets. They are realised by the self-propelled particles (SPPs) which can be biological (e.g. bacteria) or non-biological (e.g. Janus particles). In these ratchets, the SPPs moving through an asymmetric medium show rectification in their motion and there is a net transport of
particles in a particular direction [23–25]. This asymmetrical or directed response can be accounted to the spatial asymmetry and the temporal asymmetry in the system [26]. The temporal asymmetry is inherent in the motion of SPPs as the presence of self-propelled velocity drives the system out-of-equilibrium. On the other hand, the spatial asymmetry is imposed by spatial inhomogeneities in the medium, which acts as entropic barriers [27]. The rectification in motion has been observed for diverse biological micro-swimmers in various geometries such as Escherichia coli swimming in a chamber with an array of V-shaped funnel barriers [28–30] or U-shaped funnel barriers [31] and E. coli passing through ratcheting micro-channels [32, 33]. To the best of our knowledge, there have been no similar studies of transport of surface motile twitching bacteria in the asymmetric medium. Unlike the micro-swimmers, the hydrodynamic interactions are absent in these systems, and only steric surface interactions could play a role in the rectification process.

In this paper, we numerically investigate the twitching motility of bacteria in narrow two-dimensional (2d) channels having periodic boundaries with broken reflection symmetry. We have implemented the stochastic tug-of-war (TW) model to mimic the twitching motility of N. gonorrhoeae [12]. To characterise the motion, we compute mean squared displacement (MSD) and identify distinct diffusion regimes for different time scales. The bacterium confined in the corrugated channel experience rectification in motion as evident by the non-zero value of mean displacement along the axis of the channel. The particle current which gives a measure of net transport of bacteria is dependent on the ratio of the persistence length and the size of the compartment of the channel. We show that the particle current can be optimised by careful selection of geometric parameters of the channel. We also compare our results with a coarse-grained run-and-tumble (RT) model, which is a generic model used to describe the motion of SPPs [34, 35].

The rest of the paper is organised as follows. In Sec. II, we introduce the two models we have used to simulate the twitching motility of bacteria in the 2d corrugated channels. In Sec. III, we first discuss the geometry of the corrugated channel that we have used in simulation. Next, in the section, we evaluate quantities such as MSD, mean displacement along the $x$ axis and spatial probability density to investigate the rectified motion of a bacterium. In the latter part, we study the dependence of particle current on geometric parameters of the channel for the two models. Finally, in Sec. IV, we conclude by providing a summary and discussion of our results.
II. MODELS FOR TWITCHING MOTILITY

A. Twitching motility using stochastic tug-of-war (TW) model

We simulate the twitching motility of *N. gonorrhoeae* bacteria using the 2d stochastic tug-of-war (TW) model described in Ref. [12]. We model the cell body of the bacterium as a point particle with straight rodlike pili emerging radially from the cell body in random directions. A pilus can be in any one of the elongating, retracting or attached to surface states. The pilus stochastically switches between these states with the rates that are estimated from the experiments. The retraction velocity and the unbinding rate of a pilus depend on the force experienced by the pilus. Whenever there is a disparity in the number of pili in the opposite direction, the pilus on the side with a lesser number of pili will experience greater force than the pili on the opposite side and hence will be more likely to unbind from the surface due to force dependent nature of the unbinding rate. The unbinding of pilus in the weaker side further increases the imbalance causing a sharp escalation of unbinding of pili from the weaker side resulting in a rapid motion in the direction of pili who win the *tug-of-war*. The further rebinding or unbinding of pili, dissolution of pili due to full retraction or creation of new pili, alter the force balance resulting in the change in the direction of motion. This model incorporates directional memory to explain the experimental observations by allowing the pilus bundling and the re-elongation of fully retracted pili with some finite probability. The experiments have reported that the persistence time of the trajectories increases with an increase in the average number of pili [12]. In our simulations, we obtain the trajectories of different persistence length by varying the rate of pilus creation $R_{cr}$, which determines the average number of pili. In a wild type *N. gonorrhoeae* bacterium a persistent length of $1 - 2\mu m$ corresponds to average seven pili [11, 12].

Since our interest is in the study of the twitching motility in the confined narrow channels, the nature of motility near the boundaries play a significant role in the transport properties. We implement the boundary condition on the walks in the TW model in the following manner. When the bacterium is near the boundaries of the channel, the pili cannot attach to the surface beyond the boundary of the channel. So the pili can attach only in a direction which is towards the interior of the channel. It restricts the bacterium to take a step beyond the boundaries and is thus confined by the boundaries of the channel.
B. Twitching motility as \textit{run-and-tumble} (RT) motion

Here we discuss the motivation towards the coarse-grained model of the twitching motility. The motility of \textit{N. gonorrhoeae} have been recorded and analysed in various experimental studies [11, 16, 17]. In these experiments, the bacteria crawling on glass plates were observed under a microscope, and movies tracking their positions were recorded for a duration of a few minutes. A distribution of step lengths $\ell$ was generated by analysing the recorded tracks [11, 36]. The step length distribution $P(\ell)$ was found to follow an exponential distribution given by

\begin{equation}
P(\ell) = \frac{1}{\ell_p} \exp\left(-\frac{\ell}{\ell_p}\right).
\end{equation}

The persistence length $\ell_p$ is the average distance a bacterium travels before taking a turn. The typical value of the average speed $v$ of \textit{N. gonorrhoeae} was reported to be 1.5–2 $\mu$ms$^{-1}$ [15]. A coarse-grained model for bacterial motility can be constructed using experimentally observed features of \textit{N. gonorrhoeae} walks [36]. We model the point particle executing a 2d random walk with step lengths drawn from the exponential distribution of Eq. (1). The particle selects a new direction at each turn from a uniform distribution between $[0, 2\pi)$. We have taken a fixed value of average speed $v = 1.5 \mu$ms$^{-1}$ with the time duration to complete a step of $\ell$ length is given by $\ell/v$. The motility is characterised by straight trajectories with sudden random changes in the direction. The resulting motion is referred to as \textit{run-and-tumble} and is quite ubiquitous in SPPs. In our model, the time duration of the tumbling event is zero, and the change in the direction happens instantaneously at each turn.

Using the above model of bacterial motility, we study the transport of bacteria in a corrugated channel. In our simulations, we impose a form of a boundary condition in which bacterium is reflected towards the interior but in a random direction. So, when the bacterium hits the boundary wall, a new proposed direction is selected randomly from a uniform distribution $[0, 2\pi)$. If the new direction is not towards the interior of the channel, another direction is chosen from the distribution until the proposed direction is towards the interior of the channel. The bacterium instantaneously turns to the new direction and is hence confined by the boundary walls of the channel.
Figure 1: Tracks obtained from simulation of bacterial motility in corrugated channel using (i) TW model for $R_{cr} = 20$ s$^{-1}$ and (ii) RT model for $\ell_p = 1$ µm.

III. SIMULATION METHODS AND RESULTS

We simulate the twitching motility using the two models described in section II. The bacterial motion is confined in a 2d corrugated channel. The channel extends infinitely along $x$ axis and is bounded by a periodic function along $y$ axis (Fig. 1). The boundaries of the asymmetric channel are modelled by a boundary function having broken reflection symmetry which is widely used in literature [37–42]. The boundary function $w(x)$ is given by

$$w(x) = A - B \left[ \sin \left( \frac{2\pi x}{L} \right) + \frac{\Delta}{4} \sin \left( \frac{4\pi x}{L} \right) \right].$$

Here, $L$ is the spatial periodicity along $x$ axis of the channel. The extent of asymmetry in the shape of the channel is determined by the asymmetric parameter $\Delta$. For a symmetric periodic channel, $\Delta = 0$. The channel is biased towards the positive $x$ direction for $\Delta < 0$ and the negative $x$ direction for $\Delta > 0$. In this study, we have primarily done simulation for a channel biased towards the negative $x$ direction. The parameter $A$ controls the slope of the channel boundaries whereas $B$ determines the half-width [43]. The parameters $A$ and $B$ are related to the minimum width $w_{min}$ and the maximum width $w_{max}$ of the channel as

$$w_{min} = 2(A - B\delta) \quad \text{and} \quad w_{max} = 2(A + B\delta).$$

The $\delta$ is an monotonic increasing function of $\Delta$ for $\Delta > 0$. For a typical value of $\Delta = 1$, $\delta = 1.1$. Simulations are performed for the parameter values $\Delta = 1$, $A = 1$ µm, $B = 0.7$ µm and $L = 5$ µm unless explicitly mentioned otherwise. For these values of the parameters,
$w_{\text{max}} \approx 3.5$ $\mu$m and $w_{\text{min}} \approx 0.46$ $\mu$m. The ensemble averages of all physical quantities denoted by $\langle .. \rangle$ are derived by averaging over $10^4$ trajectories unless mentioned otherwise. In our simulations, the bacterium always starts from a fixed initial position $(x_0, y_0) = (0, 0)$.

Figure 2: (a) MSD $\langle \Delta r^2 \rangle$ as a function of time $t$ for the pili creation rate $R_{cr} = 5, 10, 15, 20$ $s^{-1}$ obtained by simulation of the bacterial motility in the corrugated channel using the TW model. (b) The plot of $\langle \Delta r^2 \rangle$ versus $t$ for $\ell_p = 0.1, 1, 10$ $\mu$m for RT model. Inset: The exponent $\beta$ as a function of $t$. (c) Mean displacement along $x$ axis $\langle \Delta x \rangle$ for the TW model. (d) The plot of $\langle \Delta x \rangle$ versus $t$ for the RT model.

We show prototypical tracks traced by a bacterium having $R_{cr} = 20$ $s^{-1}$ and $\ell_p = 1$ $\mu$m, simulated by TW and RT models, respectively in Fig. 1. The tracks from TW model are detailed and capture the jerky movements of the bacterium. On the other hand, tracks from the RT model lacks the detailed structure and gives a coarse-grained representation of the motility. In both the cases, the movement is directed at short times and random at longer time scales. It is demonstrated by the plot of the mean squared displacement (MSD)
\[ \langle \Delta r(t)^2 \rangle \] as a function of time \( t \) which is depicted in Fig. 2(a)-(b). Here, \( \Delta r(t) = r(t) - r(0) \). The dynamics is characterised by MSD exponent \( \beta \) defined by \( \langle \Delta r(t)^2 \rangle \sim t^\beta \). In Fig. 2(a), we plot \( \langle \Delta r^2(t) \rangle \) calculated from the trajectories of TW model for \( R_{cr} = 5, 10, 15, 20 \text{ s}^{-1} \). In the inset we show the variation of \( \beta \) with \( t \) which is evaluated by using the relation \( \beta(t) = \log_{10}[\langle \Delta r^2(10t) \rangle/\langle \Delta r^2(t) \rangle] \). The \( \beta \approx 2 \) for short time scales indicates ballistic motion. The exponent gradually reduces to \( \beta \approx 1 \) indicating diffusion for intermediate value of \( t \). The motion again approaches superdiffusive regime for large \( t \). In the TW model the motion achieves the steady state after some period of time. In this initial transient state of the motion, \( \beta > 2 \) for very small \( t \). In Fig. 2(b), we depict the plot \( \langle \Delta r^2(t) \rangle \) computed from RT trajectories for \( \ell_p = 0.1, 1, 10 \text{ \textmu m} \). The motion changes from super-diffusive at very short time scales \( (t \lesssim 0.1 \text{ s}) \) to sub-diffusive at intermediate time scales \( (1 \lesssim t \lesssim 100 \text{ s}) \). It again approach super-diffusive regime for longer time scales \( (t \gtrsim 100 \text{ s}) \). Bacterium having \( \ell_p \) comparable to the channel dimension undergoes multiple collision with the asymmetric boundaries leading to super-diffusive behaviour. On the other hand, when \( \ell_p = 0.1 \text{ \textmu m} \), bacterium spends most of the time in the bulk and boundary effects are less dominant resulting in diffusive behaviour at long time scales. We compute mean displacement along \( x \) direction \( \langle \Delta x(t) \rangle \) to ascertain the rectification in bacterial motion where \( \Delta x(t) = x(t) - x(0) \). It is substantiated by the plot of \( \langle \Delta x(t) \rangle \) versus \( t \) in Fig. 2(c)-(d). Notice that \( |\langle \Delta x(t) \rangle| \neq 0 \) for large time scales and it increase with the persistence length in both TW and RT models. The plots are steep for larger values of persistence length which indicates that the particle current have a dependence on the persistence length. We will discuss it in detail in the later part of this section.

We further investigate the directed transport in the asymmetric channels by calculating the spatial probability density \( \rho(r) \) from the bacterial trajectories obtained from simulations for the time duration \( t = 10^6 \text{ s} \). In Fig. 3(a)-(b), we plot the colour maps of \( \rho(r) \) for \( R_{cr} = 10, 20 \text{ s}^{-1} \) for the TW Model. The arrows in Fig. 3 show the direction of the average velocity \( \nabla(r) \) at a given position in the compartment. We observe from the \( \rho(r) \) profile that the bacterium tend to spend more time near the boundaries for larger \( R_{cr} \). This was also observed experimentally when bacteria were allowed to interact with 3D obstacles [16]. Similarly, the colour maps of \( \rho(r) \) computed by RT model tracks for \( \ell_p = 0.1, 1 \text{ \textmu m} \) are plotted in Fig. 3(c)-(d). We note that for \( \ell_p = 0.1 \text{ \textmu m} \) bacteria remain in the interior of the channel and encounters the boundary rarely which explains the random orientation of
Figure 3: The color map of spatial probability density $\rho(r)$ of the bacterium in the compartment of the corrugated channel. The top row shows the plots of $\rho(r)$ for (a) $R_{cr} = 10 \text{ s}^{-1}$ and (b) $R_{cr} = 20 \text{ s}^{-1}$ obtained by using TW model to simulate the bacterial motility. The arrows depict the direction of the average velocity of the bacterium $\mathbf{v}(r)$ in the compartment. The bottom row depicts the corresponding plots for RT model for (c) $\ell_p = 0.1 \mu\text{m}$ and (d) $\ell_p = 10 \mu\text{m}$.

An essential quantity that quantifies the particle transport across the channel is the particle current. Since the geometry of our system is a quasi one-dimensionsal (1d) along the $x$ axis, the particle current $J_x$ can be considered to be due to motion along the $x$ axis alone and is defined by

$$J_x = -\lim_{t \to \infty} \frac{\langle \Delta x(t) \rangle}{t}.$$  

We have taken a negative sign in our definition of $J_x$ as our channel is biased toward negative $x$ direction. In all our simulations, we have calculated the $J_x$ at time $t = 10^3 \text{ s}$. This time is sufficient time to reach a steady state such that $J_x$ is stabilised. The particle current depends on the nature of the walks, which in the case of twitching motility are characterised
by their persistence length. In the TW model, the persistence length is directly proportional to the pili creation rate $R_{cr}$ whereas in the RT model, $\ell_p$ determines the persistence of the walks. In Fig. 4(a), we plot the variation of $J_x$ with $R_{cr}$ and found it to increase with the increase in $R_{cr}$. It is understandable since as $R_{cr}$ increase, the average number of pili increase, which in turn leads to an increase in persistence length. For a large persistence length, the bacterium encounters the boundary walls more resulting in increasing $J_x$. In Fig. 4(b), we have chosen a large variation of $\ell_p$. We notice that $J_x \simeq 0$ for small values of $\ell_p$ ($\ell_p \lesssim 0.5 \, \mu$m) as bacterium rarely experience the asymmetric boundaries. The $J_x$ increases rapidly in the intermediate region where the $\ell_p$ is comparable to the dimension of the compartment $0.5 \lesssim \ell_p \lesssim 10 \, \mu$m. The current then becomes independent of $\ell_p$ and saturates for larger values of $\ell_p$ ($\ell_p \gtrsim 100 \, \mu$m). It indicates that the particle current has a strong dependence on the ratio of the value of the geometric parameters of the channel to the value of the persistence length, which we investigate in detail in the following segment.

We do not observe the saturation of current for the TW model as the range of variation in $R_{cr}$ is small. We can not simulate the trajectories with extreme values of persistence length in the TW model due to parameter constraint. The range of $R_{cr}$ in Fig 4(a) corresponds to intermediate values of persistence length for which current increase with the persistence length $\ell_p$ as seen in Fig. 4(b).

In various applications, it is desirable to maximize the particle current. This could be achieved by taking the appropriate values of geometric parameters of the channel. We study
the variation of the particle current $J_x$ with the geometric parameters such as the periodicity $L$, the asymmetric parameter $\Delta$, the minimum width $w_{\text{min}}$ and the maximum width $w_{\text{max}}$ of the channel. In the following results, the variation of $J_x$ with the parameter of interest is studied keeping all other parameters fixed. The simulations are performed for $L = 5 \ \mu\text{m}$, $\Delta = 1$, $w_{\text{min}} \approx 0.46 \ \mu\text{m}$ and $w_{\text{max}} \approx 3.5 \ \mu\text{m}$. We first show the dependence of the $J_x$ on the geometric parameters for TW model of motility for $R_{cr} = 10, 15, 20 \ \text{s}^{-1}$ in Fig. 5. In Fig. 5(a), we plot the variation of $J_x$ with the periodicity $L$. For very small values of $L$, the channel is approximately straight, making the current zero. As $L$ increases, the bacterium experiences the boundary less often resulting in a decrease in the current. Therefore we observe distinct peaks in the $J_x$ for the given range of $L$ denoting that there is an optimal value of $L$, independent of the value of $R_{cr}$, for which the current is maximum. However, the current seems to again increase with larger value of periodicity. This warrants further investigation and interpretation in the future. The variation with $\Delta$ in Fig. 5(b) indicates
that the current increases with the asymmetry in the shape of the channel with $J_x = 0$ for a symmetric periodic channel ($\Delta = 0$). In Fig. 5(c), we plot the $J_x$ versus $w_{\text{min}}$ of the channel with fixed values of all other parameters. We note that as $w_{\text{min}}$ increase, the boundaries become flatter resulting in decrease in $J_x$. The variation in $J_x$ versus $w_{\text{max}}$ is shown in Fig. 5(d). The channel is relatively flat for low values of $w_{\text{max}}$ ($w_{\text{max}} \simeq w_{\text{min}}$). As $w_{\text{max}}$ increase the channel become more corrugated resulting in increase in $J_x$. However, for large $w_{\text{max}}$, the bacterium spends most of the time in one compartment resulting in fewer number of trajectories passing from one compartment to another resulting in decrease in $J_x$.

Figure 6: The dependence of the particle current $J_x$ evaluated for the bacterium undergoing RT motility with $\ell_p = 0.1, 1$ and 10 $\mu$m on the channel parameters: (a) periodicity $L$, (b) asymmetric parameter $\Delta$, (c) minimum width $w_{\text{min}}$ and (c) maximum width $w_{\text{max}}$.

Next, we report the results for the dependence of $J_x$ on different parameters using the RT model of motility for $\ell_p = 0.1, 1, 10 \mu$m. In Fig. 6(a), we observe that there is an optimum value of periodicity $L$ for which the current is maximum as also seen in the case of the TW model. The current $J_x$ as a function of asymmetric parameter $\Delta$ is shown in Fig. 6(b). The
\[ J_x \simeq 0 \text{ for } \Delta = 0 \] which corresponds to a periodic channel with reflection symmetry. As \( \Delta \) increase, the shape of the channel becomes more and more asymmetric, leading to increasing \( J_x \). Recall that \( \delta(\Delta) \) is an monotonically increasing function for \( \Delta > 0 \) with \( \delta(\Delta) = \delta(-\Delta) \). Therefore, from Eq. 3, we note that as \( |\Delta| \) increase, \( w_{\text{max}} \) increases whereas \( w_{\text{min}} \) decreases resulting in the reduction of current for large \( |\Delta| \). In Fig. 6(c), we plot the variation in current as a function of minimum width \( w_{\text{min}} \). The current is less for small values of \( w_{\text{min}} \) as only a small number of bacterial trajectories can pass from one compartment to another for small \( w_{\text{min}} \). The current increase with increase in \( w_{\text{min}} \). However, as \( w_{\text{min}} \) increases the channel becomes straighter and the effect of the channel shape reduces, resulting in a decrease in current. The current also seems to have a second maxima for \( \ell_p = 10 \mu \text{m} \). This merit further examination and analysis in future. In Fig. 6(d), we show the variation of \( J_x \) with \( w_{\text{max}} \). As discussed in the previous paragraph for the case of TW model, there exists a value of \( w_{\text{max}} \) for which \( J_x \) is maximum. We observe that the dependence of the particle current on the channel parameters are different in the two models of twitching motility. This deviation could be due to the difference in the motility near the channel boundaries in the TW and RT models. Also, we could simulate only for a small range of persistence length in the TW model due to parameter constraints. We could not observe the effects of extreme values of persistence length as done in the RT model.

IV. CONCLUSION

In this work, we study the twitching motility in a 2d asymmetric corrugated channel using the stochastic TW model and the RT model. The TW model quantitatively describes the motility of \( N. \text{gonorrhoeae} \) resulting from the 2d tug-of-war between Tfp. On the other hand, the RT model is a coarse-grained model constructed by analysing the experimental trajectories of the bacteria. It is a ubiquitous model to describe the motion of SPPs. We simulated the bacterial motion in the corrugated channel having boundaries with broken reflection symmetry. Due to the confinement of bacteria in the narrow channels, the motility shows anomalous diffusion at different time scales. We obtain a non-zero finite value of the mean displacement along the \( x \) axis at long time scales which signify that the bacterial motion gets rectified and there is a net transport of bacteria in one direction. The particle current depends on the relative value of the persistence length to the dimensions of the
compartment of the channel. The bacteria having the persistence length comparable to the compartment size undergo multiple collision with the boundaries of the channel resulting in a finite particle current along the channel. We computed the particle current for a range of geometric parameters. Our simulations reveal that we can optimise the particle current by a suitable selection of the size and the shape of the compartments of the corrugated channel for a given value of persistence length. We observe the deviations in the features of the motility for the two models. We have simulated the motility using TW model for a narrow range of persistence length, which is dictated by the experimental observations. The extreme values of persistence length taken in the RW model cannot be replicated for the TW model due to parameter constraints on the TW model. We can simulate the bacterial motility using TW model only for an intermediate value of persistence length. In this range, the general features of the motility from the TW model can be nearly mapped to those from the RT model, except for a few deviations. We presume that these variations could be attributed to the differences in the conditions imposed on the walks near the boundaries for the two models. However, in both models we see enhanced persistence as compared with the motility in absence of the asymmetric channel as seen in some recent studies [25]. Finally, we would like to state that these ratchet effect can also be studied experimentally by creating corrugated channels by microprinting on a substrate and observing the twitching motility under a microscope [15, 44]. We hope that such experiments could further investigate the observations made in our numerical study. We also note that the motility of twitching bacteria in presence of obstacles may further enhance the persistence, work in this direction is currently underway.

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