A minimal physical model captures the shapes of crawling cells

E. Tjhung1,*, A. Tiribocchi1,*, D. Marenduzzo1 & M.E. Cates1

Cell motility in higher organisms (eukaryotes) is crucial to biological functions ranging from wound healing to immune response, and also implicated in diseases such as cancer. For cells crawling on hard surfaces, significant insights into motility have been gained from experiments replicating such motion in vitro. Such experiments show that crawling uses a combination of actin treadmilling (polymerization), which pushes the front of a cell forward, and myosin-induced stress (contractility), which retracts the rear. Here we present a simplified physical model of a crawling cell, consisting of a droplet of active polar fluid with contractility throughout, but treadmilling connected to a thin layer near the supporting wall. The model shows a variety of shapes and/or motility regimes, some closely resembling cases seen experimentally. Our work strongly supports the view that cellular motility exploits autonomous physical mechanisms whose operation does not need continuous regulatory effort.
How do living cells move around within their environment, whether in vitro (for example, on a glass slide) or in vivo (for example, within a tissue)? Is their motion sustained by continuous action of the cell complex biochemical networks, or do these issues instructions to a physically autonomous engine of motility? Experiments that replicate cellular motility with simplified in vitro systems have gone some way towards answering these questions 1–4.

Cellular self-propulsion in 3D gels or tissues might involve either ‘grabbing’ of the extracellular matrix or ‘swimming’ via actomyosin flow in the cell interior 5–7. However, as 3D motility is hard to study experimentally, detailed mechanisms remain largely speculative. Much better understood is a case we address here: cells moving on a 2D solid substrate.

The crawling motion of such cells combines two processes 2. One is actin polymerization, in which monomers add to one end of an actin filament and leave from the other. Given a net polarization of the actin network, this ‘treadmilling’ pushes the leading edge of the cell forward. The second process is the ‘walking’ of myosin motors along filaments. This creates a contractile stress that, alongside interfacial tension and/or membrane elasticity, opposes cellular elongation. Contractility thus assists retraction of the rear part of a crawling cell (which includes the nucleus). Also implicated in crawling are assemblies of intracellular membrane proteins called focal adhesions, which enhance mechanical connectivity between actomyosin and the solid substrate. These increase the effective wall friction and improve crawling efficiency (just as a child can crawl more easily on a pile carpet than a polished floor). Focal adhesions also signal alterations to the balance between treadmilling and contractility 9,10.

Notably though, significant motility is maintained even in laser-ablated or reconstituted cell fragments that lack most or all of the cell regulatory machinery 11.

Our goal here is to set up a minimal model of crawling motility, to see how fully the observed behaviour can be understood using physics alone. To achieve this goal, we intentionally rely on a very simplified description of complex biochemical and biophysical processes such as F-actin polymerization and actomyosin contractility. We also employ only an elementary description of the cell membrane, as well as of its coupling to the interior and exterior of the cell. The advantages of such an approach is that there are arguably as few free parameters as possible within the model, and this allows us to isolate the key physical elements of cell crawling (and/or spreading) at surfaces. In other words, we can directly answer the question posed above: can cellular motility be seen as a physics-based machinery, which is coupled to, and controlled by, a complicated underlying biochemical network, but is nevertheless able to function independently? The alternative is that the biochemical detail is fundamental, and no aspects of it can be disregarded, even for a basic understanding of motility. This is an important question, both to understand the basic mechanism of cell motility and to inform subsequent biomimetic work intending to replicate cellular behaviour with synthetic components. In this respect, our simulation model can be viewed as the in silico analogue of in vitro experiments with cell extracts and cell fragments 11.

The drawback inherent within our approach is that, from the beginning, some of the important biological detail is lost. One can argue that, if experimental observations are reproduced by the minimal framework, this detail may be inessential to the fundamental biophysics of motility, and this by itself is very useful information. Nevertheless, to check the picture and to prove the previous statement unambiguously, one should eventually insert back realistic details one by one, and explicitly compare the results obtained with those of the fully simplified, minimal model. We initiate this last approach here as well, for a few cell biological features that our baseline model does not capture well. These include the allowance for a relatively high membrane viscosity, and, for wall slip, or equivalently, retrograde flow 13; see Supplementary Note 1–3 for details of these checks.

In our minimal model, we represent a cell or cell extract as a droplet of active polar fluid (actomyosin) immersed in a second fluid and confined by interfacial tension 14. (The latter is similar to, but simpler than, the fixed area constraint imposed by the outer membrane of a real cell.) As in real cells, actin treadmilling is confined both to the leading edge of the cell and within a finite thickness $\lambda$ from the substrate. Our droplet interacts with a solid wall through a controllable friction, represented by a partial-slip boundary condition. In contrast to most previous computer models for cell motility 7,14–21, we treat cells as 3D objects. Previous 2D models often incorporated a number of important biological details, such as variable adhesion with the substrate 15 or the dynamics of signalling proteins 16. A difference with our framework, besides the general philosophy highlighted above, is that these 2D models typically view the cell from above and cannot resolve the flow within the cell, or the presence or absence of slip at the boundary, whereas our model can resolve these features. Importantly, our 3D framework also allows us to directly address the factors influencing the lamellipodium shape, which is the most commonly observed morphology in crawling cells. We are aware of one previous 3D study 22, which recreated the motion of flat cell fragments. Ref. 22 differs from our approach in its aims, as it focuses on a specific type of cell motility, rather than attempting to describe morphological transitions between non-motile and motile cells or between different kinds of motility, as we do here.

Results

Crawling dynamics in quasi-2D. To begin, we consider a quasi-2D geometry describing a thin slice through a crawling droplet (Fig. 1a). At the wall, we assume parallel anchoring of actin polarization (represented by black arrows in the figure), and also a no-slip boundary condition on fluid flow as expected when focal adhesions are plentiful (the effect of a small slip is considered below). In these quasi-2D simulations, actin polarization (hence treadmilling) is confined both to the leading edge of the cell and within a finite thickness $\lambda$ from the substrate. This is to model real cells where actin filaments are present, and polarized, mainly in a cortex towards the exterior 23.

Importantly, no qualitative differences in the results are observed if we choose instead a simpler representation of treadmilling, where this is no longer localized at the leading edge, but still confined within a thickness $\lambda$ from the substrate, see Supplementary Fig. 1. At the droplet’s interface with the surrounding fluid, we impose outward normal anchoring of variable strength $\beta$. The equations of motion are as previously published 24 and detailed in the Methods section.

Figure 1a shows two snapshots of such a quasi-2D droplet in steady state. On increasing the treadmilling rate $\omega_0$, we observe progression from a droplet that moves along the wall with only modest distortion to one that extends a thin protrusion at its leading edge (also see Supplementary Movies 1 and 2). In both regimes the droplet moves with a speed close to $\omega_0$. Figure 1b plots the steady-state wall contact area against $\omega_0$, in the case of no-slip boundary conditions ($s = 0$, red/plusses curve) and partial-slip ($s = 0.02$, $s = 0.04$, $s = 0.06$, green/crosses, blue/asterisks and purple/squares curves, respectively). The parameter $s$ controls the amount of slip of the fluid at the solid wall, and is defined such that $s = 0$ corresponds to no-slip while $s = 1$ corresponds to full-slip (see Supplementary Note 1 for its mathematical definition). The parameter $s$ is thus inversely related to the density of focal adhesions between the substrate and
the cell. In both cases, with or without wall slip, the contact area increases sharply near a critical value \( w_c(s) \), suggestive of a dynamical transition or sharp crossover between two regimes. This transition becomes sharper as the amount of slip on the substrate augments (green/crosses curve), and discontinuous at critical \( w_c \) for higher values of \( s \) (blue/asterisks and purple/squares curves). The strong hysteresis of the last curve confirms its discontinuous nature. Note that in these quasi-2D simulations, arrows here represent actin polarization, which points in the same direction as actin treadmilling. In addition, actin polarization is localized at the leading edge of the droplet to model a crawling eukaryotic cell (also see Supplementary Movies 1 and 2). If the treadmilling rate \( w_c \) is large enough, a thin protrusion form, whose steady-state size (area per unit transverse length) is plotted versus \( w_c \) in (b) (red/plus curve), for the case of no-slip boundary condition between the droplet and the substrate. From (b), we can identify the critical treadmilling rate \( w_c \) above which a thin layer of protrusion is observed in a crawling cell. This transition becomes sharper as the amount of slip at the substrate increases (green/cross) and discontinuous/first order for higher values of \( s \) (blue/asterisk and purple/square curves). The hysteresis loop corroborates its discontinuous character. (c) A plot of the crawling speed as a function of the slip parameter \( s \) (while the treadmilling rate is fixed at \( w_c = 0.002 \)). This controls the discontinuity in fluid velocity at the solid wall, and is defined such that \( s = 0 \) corresponds to no-slip while \( s = 1 \) corresponds to full-slip. An increase of \( s \) causes a decrease of the velocity of the cell. This is because the slip velocity at the surface is in the opposite direction to that of the actin polymerization. Again, we observe a discontinuity at \( s = s_c \) marking a dynamical phase transition from a round-shaped crawling cell \((s > s_c)\) to a protruded shape \((s < s_c)\).

Crawling dynamics in 3D. The quasi-2D simulations in Fig. 1 give intriguing hints to the physics of lamellipodial protrusions, which are the pancake-like structures often seen at the leading edge of crawling cells. However, the structure of such cells is fully three-dimensional, and the lamellipodium is only one of several morphologies attained by live cells, whether crawling or stationary, when attached to a solid support. We have therefore performed full 3D simulations of a slight variation of the same minimal model as we used in 2D. With respect to the 2D case, in the 3D case the effect of actomyosin contractility is much stronger, so we present results only with it switched on from the beginning. Unlike actin treadmilling, actomyosin contractility is known to show highest activity deep inside the cell, close to the cell nucleus, rather than at the cell periphery^{23}. To simplify the model in 3D, actin polarization (and thus contractility) is therefore now assumed to be uniform throughout the droplet. In addition, actin polymerization is no longer confined to the leading edge of the cell, but we retain a spatially varying treadmilling rate, \( w_0 \rightarrow w(z) = w_0 \exp(-z/\lambda) \), to confine actin treadmilling close to the substrate. The use of this simplified model, where the active droplet is homogeneously polarized, is motivated by our finding above that the localization of actin polymerization is not essential to observe the morphological transition between non-motile and motile cells in Fig. 1 (see Supplementary Fig. 1).

As we shall see, our minimal 3D model supports the formation of various dynamical cell shapes, some with surprisingly direct experimental counterparts. Figure 2 shows a selection of these steady-state morphologies, together with a direct comparison with experimental morphologies taken from the literature.
Figure 2 | Spreading and crawling cell morphologies. In this figure, spreading and crawling cell morphologies observed in past experiments (left column) and obtained in the current 3D simulations (middle and right column, giving, respectively, top and side view) are shown. Panels a–c show a static cell with a fried-egg shape; the left column panel was originally published in ref. 25. Other frames show moving cells with protrusions resembling, respectively, a lamellipodium (d–f, the left column panel was originally published in ref. 27), a phagocytotic cup (g–i, left column panel taken from ref. 30 with permission), and a pseudopod (j–l, left column panel taken from ref. 32 with permission). Parameters for the 3D modelling (in simulation units; see Supplementary Table 1) are: (a–c) \( w_0 = 0.035; \xi = -0.001; \beta = 0.02; \) (d–f) \( w_0 = 0.04; \xi = -0.0015; \beta = 0.001; \) (g–i) \( w_0 = 0.04; \xi = 0; \beta = 0.001; \) (j–l) \( w_0 = 0.04; \xi = -0.00015; \beta = 0.001. \)

Figure 2a–c shows a droplet subject to strong normal anchoring of the polarity (large \( \beta \)). This boundary condition, which might model the promoted nucleation of outwardly polarized actin by Arp2/3 complexes close to the outer membrane, enforces radial polarization with an ‘aster’ defect at the centre. Treadmilling then causes the droplet to spread, but not to move. In steady state it adopts a symmetric ‘fried egg’ whose shape resembles that of an inactive platelet or a stationary keratocyte. (We speculate that adding boundary pinning of the cell perimeter, and/or radial modulation of the treadmilling strength \( w_0 \), might create shapes more closely resembling mesenchymal stem cells.)

Figure 2d–l shows steady-state cell shapes for (rightwards) crawling cells; the morphology is selected by a combination of treadmilling parameter \( w_0 \), contractility \( -\xi \) and anchoring strength \( \beta \). Figure 2d–f (see also Supplementary Movie 3) arises when all three effects compete; this closely resembles a motile keratocyte (see for example refs 2,27). The pronounced lamellipodium at the leading edge stems from a balance between contractility-induced splay of the polarity field and its soft anchoring at the leading edge. The prediction of this familiar dynamical structure from such minimal physical ingredients is a major finding of this paper (In contrast, the overhang at the cell rear is a detail, and can be eliminated if actin polarization or treadmilling rate \( w(x,y,z) \) is set to zero at the back of the cell, as done for example, in Fig. 1a.)

The cell shape in Fig. 2g–i arises in the absence of contractility: the splay is induced by the anchoring and the structure corresponds to an indented structure possibly reminiscent of the ‘phagocytic cup’, which forms when a cell needs to engulf a solid particle. (Such cups are typically not planar but have been reported for crawling as well as free cells.) Finally, Fig. 2j–l shows a droplet where treadmilling is dominant: the anchoring is zero and the contractility is much weaker than in Fig. 2d–f. Importantly, without those contributions the cell shape no longer shows the keratocyte-like lamellipodium morphology. Instead, the leading-edge forms a pointed protrusion, qualitatively resembling a ‘pseudopod’, as often reported in ameoboid cell motion both on surfaces and in 3D geometries.

Phase diagram. The results shown in Fig. 2 were obtained by varying the treadmilling parameter \( w_0 \), the contractile activity \( -\xi \), and also the anchoring \( \beta \), which controls the orientation of the polarization at the cell boundary. Although a systematic study of the phase diagram in this multi-dimensional parameter space is extremely demanding computationally, and hence outside the scope of the current work, we observe (see Fig. 3) that similar morphologies can also be obtained by keeping the value of \( w_0 \) constant, varying \( \beta \) and adjusting \( \xi \) to be as large as possible avoiding at the same time droplet breakup (which occurs when \( \xi \) is too large; see also ref. 33 where a distinct but related study of contractility-driven breakup 2D active droplets is presented).

For very small values of \( \beta \), a finger-like structure (the ‘pseudopodium’ in Fig. 2) is dominant, while fan-shaped geometries (such as the ‘lamellipodium’ in Fig. 2) emerge when \( \beta \) is larger, due to the higher splay distortion of the actin filaments arising at the leading edge of the cell. For very strong...
anchoring, the lamellipodium morphology becomes unstable, and the cell attains a fried-egg shape, which is non-motile. Experiments (see for example, ref. 27) have studied how cell shape is affected by adhesion to the substrate. In our model an increase in the adhesion would affect both the treadmilling and the anchoring, decreasing the first and increasing the second. Interestingly, our simulations suggest that lamellipodia are found for intermediate values of the anchoring strength and are disfavoured when treadmilling decreases, qualitatively confirming what has been experimentally observed by Barnhart et al.27

Evolution of polarization and velocity fields. Besides the concentration field whose structure is shown in Fig. 2, our model also tracks the evolution of the polarization and intracellular flow fields, \( P \) and \( u \), respectively.

In Fig. 4 we show the polarization field close to the substrate (left column) and the flow field (right column) corresponding to the 3D steady-state morphologies reported in Fig. 2. The polarization field shows a transition between the aster corresponding to the ‘fried-egg’ state (Fig. 4a) and polarized uniform (Fig. 4d) and splayed (Fig. 4b,c) pattern; these are qualitatively in broad agreement with the experimental data for keratocytes.

Figure 3 | Phase diagram. 3D steady-state shapes for (a) \( \beta = 0, \zeta = -0.00015, w_0 = 0.04 \); (b) \( \beta = 0.001, \zeta = -0.0001, w_0 = 0.04 \); (c) \( \beta = 0.001, \zeta = -0.0015, w_0 = 0.04 \); (d) \( \beta = 0.02, \zeta = -0.001, w_0 = 0.04 \). Red arrows indicate the direction of the polarization in the cytoplasmic projections (psedudopod (a), phagocytic cup (b), lamellipodium (c) and fried-egg crown (d)). Notice that \( w_0 \) is constant; while \( \zeta \) varies (both \( \zeta \) and \( \beta \) affect droplet elasticity, increasing \( \zeta \) for small \( \beta \) leads to further instabilities such as droplet breakup, which are not relevant for the current work).

Figure 4 | Polarization and velocity fields. This figure shows the section of the polarization field inside the droplet very close to the substrate (left column) and the velocity field (right column) for (a,b) ‘fried egg’ morphology, (c,d) lamellipodium, (e,f) phagocytic cup, (g,h) pseudopodium, respectively.
presented in ref. 25, where it was established that motility requires symmetry breaking of the actin fibre orientation field, from an aster like conformation as in our ‘fried-egg’ morphology (Fig. 4a) to an asymmetric conformation in a lamellipodium, where the barbed ends of actin fibres are approximately normal to the cell membrane at the leading edge (as in our simulations in Fig. 4c).

Coming to the flow field, we first note that u (plotted in Fig. 4) should be thought of as an intracellular solvent flow inside the cell, which has not been measured often in experiments (an exception is ref. 34 which is discussed in the Supplementary Note 2). This intracellular flow is quite distinct from the flow of F-actin, which is usually tracked in cell biology experiments, and which is commonly referred to as ‘retrograde flow’13. F-actin flows inwards within the cell, from the leading edge to the bulk. The velocity field for the ‘fried-egg’ cell is characterized by a quadrupolar velocity profile (in a fully 3D view), more intense close to the surface of the droplet where the curvature is higher than near the substrate (see Fig. 4a). The flow in the vicinity of the membrane is not unlike that droplet where the curvature is higher than near the substrate (see profile (in a fully 3D view), more intense close to the surface of the cell moving in 3D inside matrigel (panel a, from ref. 7; for simplicity in the bulk), and for a cell moving in 3D inside matrigel (panel b, from ref. 5, with permission).

**Discussion**

In conclusion, we present a minimal physical model of cell crawling, based on an active fluid droplet, attached to a solid wall and immersed in a second fluid. Key ingredients in the model are actin treadmilling (confined to a thin layer of depth l close to the substrate), actomyosin contractility (throughout the droplet), full anchoring of the actin polarity parallel to the wall and its partial anchoring normal to the fluid–fluid interface. Hydrodynamic fluid flow is properly treated throughout. We showed that on increasing the treadmilling rate, such a droplet undergoes a nonequilibrium morphological transition to form a protrusion layer whose thickness is set by l (Fig. 6). Variation of the treadmilling, contractility and anchoring parameters leads in 3D to a striking series of cell morphologies, resembling structures seen in real eukaryotic cells including both lamellipodia and pseudopods. We also find regimes where oscillatory modulations of shape and motility arise. Our results show that surprisingly many of the observed features of motile and spreading cells (though of course not all of them) can emerge from relatively simple physical ingredients. This suggests that some aspects of cellular motility might fruitfully be thought of as driven by a physics-based ‘motility engine’ whose function, although controlled by the cell’s complex biochemical feedback networks, does not directly depend on these for its basic operational principles. It...
Underlying free energy

The free energy of the droplet can be expressed as

\[ F[\phi, \varepsilon] = \int d^3r \left[ \frac{k}{2} \phi^2 + \frac{\beta}{2} \varepsilon^2 + \frac{\gamma}{4} \varepsilon^4 \right] \]

where \( k \) is the elastic constant, \( \beta \) is the active stress coefficient, and \( \gamma \) is the shear viscosity coefficient.

Equations of motion

The Navier-Stokes equations for the incompressible fluid can be written as

\[ \nabla \cdot v = 0 \]

\[ \rho \left( \frac{\partial v}{\partial t} + v \cdot \nabla v \right) = -\nabla P + \frac{\partial F}{\partial \varepsilon} + \frac{\partial F}{\partial \phi} \]

where \( P \) is the pressure, \( \rho \) is the density, and \( v \) is the velocity field.

Methods

Basic idea of the model

We briefly outline here the hydrodynamic model used in this work. A droplet of cellular matter sitting on a solid substrate is considered to be a droplet of actomyosin network. The polarization field, where \( \phi \) is a positive (for stability) constant and \( \varepsilon \) is the elastic constant (in the one-elastic constant approximation) that describes the energetic cost due to elastic deformation in a liquid-crystalline environment. The surface tension \( \gamma \) will depend on \( \alpha \) and the elastic constant \( \kappa \). The droplet interface, the values of the concentration and the polarization fields vary smoothly from \( \phi = \phi_{\text{sat}} \) and \( \varepsilon = 0 \) to \( \phi = 0 \) and \( \varepsilon = 0 \). In general, the width of the diffuse interface also depends on the same parameters. In our simulations, the interfacial width is typically much smaller than the size of the droplet. Finally, the last term \( \beta \varepsilon \cdot \nabla \phi \) takes into account the anchoring of the droplet to the solid surface (so that for \( \beta > 0 \) the polar field \( \varepsilon \) preferentially points perpendicularly outwards at the droplet perimeter, while for \( \beta < 0 \) it points perpendicularly inwards).

Equations of motion

The velocity field \( v(r, t) \) obeys the continuity and the Navier-Stokes equations, which in the incompressible limit are

\[ \nabla \cdot v = 0 \]

\[ \rho \left( \frac{\partial v}{\partial t} + v \cdot \nabla v \right) = -\nabla P + \frac{\partial F}{\partial \varepsilon} + \frac{\partial F}{\partial \phi} \]

where \( P \) is the isotropic pressure and \( \sigma_{\text{active}} + \sigma_{\text{passive}} \) is the total stress, given by the sum of active and passive contributions.

Underlying free energy

Following the phenomenological approach used in refs 7,38, we first introduce a free-energy functional that controls the equilibrium physics of a polar liquid-crystalline passive droplet

\[ F[\phi, \varepsilon] = \int d^3r \left[ \frac{k}{2} \phi^2 + \frac{\beta}{2} \varepsilon^2 + \frac{\gamma}{4} \varepsilon^4 \right] \]

The first two terms of equation (1) control bulk and interfacial properties of the droplet. In particular, \( k > 0 \) determines the droplet interfacial tension and \( \beta > 0 \) is a phenomenological constant. The bulk term is chosen to stabilize a droplet phase \( \phi > \phi_{\text{sat}} \) immersed in a second fluid \( \phi = 0 \) and \( \phi_{\text{sat}} = \phi_{\text{sat}}/2 \). The parameter \( \beta \) controls a second order transition from isotropic \( \langle \varepsilon \rangle = 0 \) to polar phase \( \langle \varepsilon \rangle > 0 \) inside the droplet as the value of \( \gamma \) changes from 0 to 1.
\[ \zeta < 0 \] oblate ones. We have set it positive, as in ref. 7. In addition \( \zeta \) controls whether particles are flow aligning in shear flow \((\zeta > 1)\), hence creating a stable response, or flow tumbling \((\zeta < 1)\), which gives an unstable response. Here we assume \( \zeta > 1 \).

Note that the elastic stress also depends on the molecular field \( h \), defined as \( \partial \phi / \partial q \). The surface tension term takes into account interfacial contribution between the passive and the active phase, and is given by

\[ \gamma_{\text{interface}} = \left(1 - \frac{\partial \phi}{\partial q}\right) \frac{1}{1 + \frac{\partial \phi}{\partial q}} \frac{\partial \phi}{\partial q} \frac{\partial \phi}{\partial q} \]  

This term is borrowed from binary fluids\(^{41}\), with \( f \) being the free-energy density. The dynamics of the concentration of active material \( \phi(r, t) \) is governed by a convective-diffusion equation

\[ \frac{\partial \phi}{\partial t} + \nabla \cdot (\phi (v + w_0) \mathbf{P}) = \nabla \left( \nabla^2 \phi \right) \]  

where \( M \) is a thermodynamic mobility parameter, related to the diffusion constant \( D_0 \) (see equation (1)). \( \partial \phi / \partial q \) is the chemical potential of the system and \( w_0 \) is the self-advective parameter. This \( w_0 \) can be interpreted as the speed, relative to the bulk fluid velocity \( \mathbf{w}(r, t) \), at which each filament is self-propelled along its own tangent. Thus \( w_0 \) is also proportional to the rate of actin treadmilling. In our 3D minimal model, the treadmilling rate is a spatially varying function that is large close to the substrate: \( w_0 - w(\mathbf{r}) = w_0 - \exp(-\sqrt{\mathbf{r}^2}) \) where \( \mathbf{r} \) is the lengthscale for protrusion thickness.

The last ingredient to complete the description of the physics of the system is an evolution equation for the polarization field \( \mathbf{P}(r, t) \). This is given by

\[ \frac{\partial \mathbf{P}}{\partial t} + (v + w_0) \frac{\partial \mathbf{P}}{\partial t} = - \frac{\partial}{\partial \mathbf{r}} \cdot \mathbf{P} + \frac{\partial}{\partial \mathbf{r}} \mathbf{P} \cdot \mathbf{r} = 1 \partial \mathbf{r} \]  

where \( \mathbf{I} \) is the rotational viscosity and \( \mathbf{r} \) is the antisymmetric part of the velocity gradient tensor. The system is thus taken care of by a standard Lattice Boltzmann approach. This numerical predictor-corrector algorithm while the integration of the Navier-Stokes equation is already successfully tested in other systems, such as binary fluids\(^4\), liquid crystals\(^{44}\).

To solve these equations we use a 3D hybrid lattice Boltzmann algorithm already successfully tested in other systems, such as binary fluids\(^{41}\), liquid crystals\(^{44}\) and active matter\(^\text{\textsuperscript{4}}\). It is solved in equations (8) and (9) via a finite difference predictor-corrector algorithm while the integration of the Navier-Stokes equation is taken care of by a standard Lattice Boltzmann approach. This numerical approach is necessary due to the couplings between velocity field and polarization field in equation (9) and velocity field and concentration in equation (8).

**References**

1. Alberts, B. et al. Molecular Biology of the Cell, 4th edn (Garland Science, 2002).
2. Bray, D. Cell Movements: From Molecules to Motility, 2nd edn (Garland Science, 2000).
3. Köhler, S., Schaller, V. & Bausch, A. R. Structure formation in active networks. Nat. Mater. 10, 462–468 (2011).
4. Loisel, T., Boujemaa-Patrou, P., Pantaloni, D. & Carlier, M.-F. Reconstitution of actin-based movement using pure proteins. Nature 401, 613–616 (1999).
5. Poincloux, R. et al. Contractility of the cell rear drives invasion of breast tumor cells. J. Cell Biol. 160, 407–418 (2003).
6. Hawkins, R. J., Poincloux, R., Benichou, O., Piel, M. & Voituriez, R. The role of the actin-myosin II system in fish epidermal keratocytes: mechanism of cell body translocation. J. Cell Biol. 139, 397–415 (1997).
7. Kure, K., Joanny, J.-F., Julicher, F., Prost, J. & Sekimoto, K. Asters, vortices and rotating spirals in active gels of polar filaments. Phys. Rev. Lett. 92, 078101 (2004).
8. Karmakar, P. et al. Actin-myosin network reorganization breaks symmetry at the cell rear to spontaneously initiate polarized cell motility. J. Cell Biol. 178, 1207–1221 (2007).
9. Barry, F. P. & Murphy, J. M. Mesenchymal stem cells: clinical applications and biological characterization. Clin. Dev. Immunol. 2004, 568–584 (2004).
10. Barnhart, E. L., Lee, K. C., Keren, K., Mogilner, A. & Theriot, J. A. An adhesion-dependent switch between mechanisms that determine cell motility. Proc. Natl Acad. Sci. USA 91, 545–553 (2011).
11. Herant, M., Heinrich, V. & Dembo, M. Mechanics of neutrophil phagocytosis: experiments and quantitative models. J. Cell Sci. 119, 1903–1916 (2006).
12. Tuxworth, R. I. et al. A role for myosin VII in dynamic cell adhesion. Curr. Biol. 11, 318–329 (2001).
13. Mercante, V., Charrite, S. J., Bennett, N., Ryckewaert, J.-F. & Letournier, F. Selective membrane exclusion in phagocytic and macroinocytic cups. J. Cell Sci. 119, 4079–4087 (2006).
14. Friedl, P., Bergmann, S. & Brocker, E. A. Amoeboid leukocyte crawling through extracellular matrix: lessons from the Dictostelium paradigm of cell movement. J. Leukoc. Biol. 70, 491–509 (2001).
15. Zhang, H. et al. Phosphorylation of the myosin light chain regulatory light chain plays a role in motility and polarity during Dictyostelium chemotaxis. J. Cell Sci. 115, 1733–1747 (2002).
16. Giomi, L. & De Simone, A. Spontaneous division and motility in active nematic droplets. Phys. Rev. Lett. 112, 147802 (2014).
Additional information
Supplementary Information accompanies this paper at http://www.nature.com/naturecommunications

Competing financial interests: The authors declare no competing financial interests.

Reprints and permission information is available online at http://npg.nature.com/reprintsandpermissions/

How to cite this article: Tjhung, E. et al. A minimal physical model captures the shapes of crawling cells. Nat. Commun. 6:5420 doi: 10.1038/ncomms6420 (2015).