Mathematical appendix: modeling mechanochemical coupling in cell polarity maintenance

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1 Maintenance-phase as a steady state

1.1 CDK-1 (RNAi)

By treating embryos with *CDK-1* (RNAi), we can extend maintenance phase and determine whether the myosin and flow profiles we see in wild-type embryos are true steady states. Figs. **??** and **??** show the myosin intensity and pattern of flow over the last eight minutes of the extended maintenance phase. What is strange about this data is that the myosin intensities *never* look like the wild-type. There appears to be more than the expected amount of myosin on the posterior domain. An interesting observation also is that extending maintenance causes the boundary to move to the *right*.

2 Stability of myosin in maintenance phase

To understand the threshold for instability of Eq. (1) in the main text, we first define the cytoplasmic concentration via conservation of total protein

$$M_{\text{cyto}} = \frac{1}{hL}\left(M^{(\text{Tot})}L - \int_0^L M(x)\,dx\right), \tag{M1}$$

where L is the domain length, h is the cytoplasmic thickness, and $M^{(\text{Tot})}$ is the density of myosin on the cortex when all of it is bound. We then scale the equations by appropriate time ($1/k_M^{\text{off}}$), length (L), density ($M^{(\text{Tot})}$), and velocity ($\sigma_0/\sqrt{\eta\gamma}$) scales. Defining the dimensionless (hatted) variables

$$x = \hat{x}L \qquad t = \hat{t}/k_M^{\text{off}} \qquad M = \hat{M}M^{(\text{Tot})} \qquad v = \hat{v}\frac{\sigma_0}{\sqrt{\eta\gamma}}, \tag{M2}$$

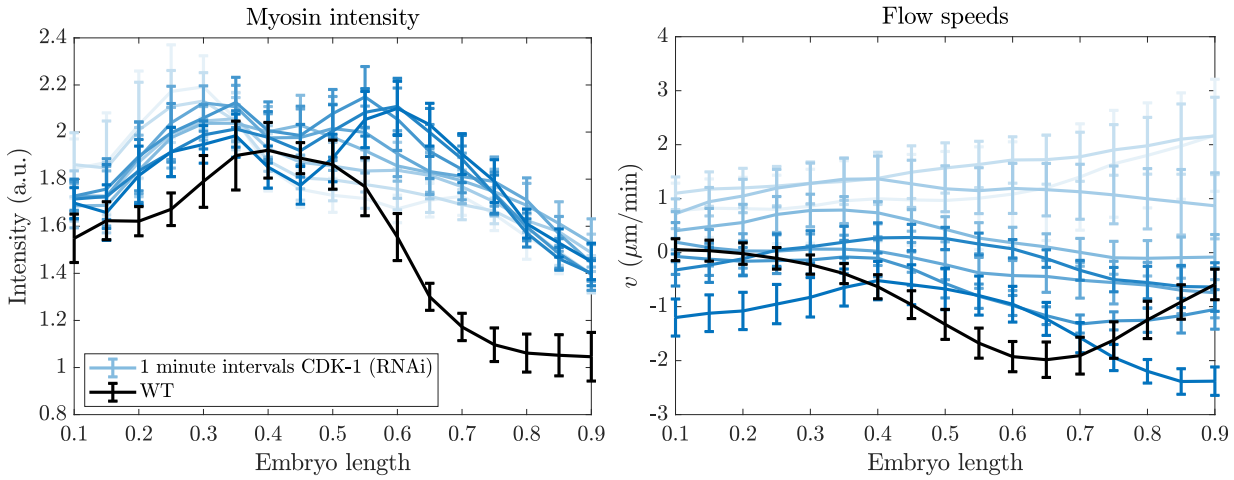

Figure M1: Comparing the end of maintenance phase in *CDK-1* (RNAi) mutants to wild-type embryos. Left panel: myosin intensity profile. Right panel: flow speeds. The blue colored lines show 1-minute intervals of maintenance phase in *CDK-1* (RNAi) embryos, with darker blue denoting later times. The black line shows the profile extracted from the last minute of maintenance phase in wild type embryos [10].

the resulting equations are

$$\partial_{\hat{t}}\hat{M} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{M}\right) = \hat{D}_M\partial_{\hat{x}}^2\hat{M} + \hat{K}_M^{\text{on}}\left(1 - \int_0^1 \hat{M}(x)\,dx\right) - \hat{M} \tag{M3a}$$

$$\hat{v} = \hat{\ell}^2\partial_{\hat{x}}^2\hat{v} + \hat{\ell}\partial_{\hat{x}}\hat{\sigma}_a(\hat{M}) \tag{M3b}$$

and are controlled by the dimensionless parameters

$$\hat{\sigma}_0 = \left(\frac{\sigma_0/\sqrt{\eta\gamma}}{Lk_M^{\text{off}}}\right) \qquad \hat{D}_M = \frac{D_M}{k_M^{\text{off}}L^2} \qquad \hat{K}_M^{\text{on}} = \frac{k_M^{\text{on}}}{hk_M^{\text{off}}} \qquad \hat{\ell} = \frac{\sqrt{\eta/\gamma}}{L}. \tag{M4}$$

Recalling that $1/k_M^{\text{off}}$ is the residence time, these dimensionless parameters can be understood in the following way:

1. $\hat{\sigma}_0$ is the fraction of the domain over which a given myosin molecule is transported while it is bound to the membrane (the residence time $1/k_M^{\text{off}}$ $\times$ the advective velocity $\sigma_0/\sqrt{\eta\gamma}$).

2. $\hat{D}_M$ is the maximum fraction of the domain a molecule diffuses before it unbinds (in the extreme case when the gradient in the domain is $1/L$, the diffusive velocity is D_M/L).

3. $\hat{K}_M^{\text{on}}$ sets the uniform steady state of the model by $\hat{M}_0 = \hat{K}_M^{\text{on}}/\left(1 + \hat{K}_M^{\text{on}}\right)$.

4. $\hat{\ell}$ is the ratio of the hydrodynamic lengthscale (the lengthscale on which fluid flows can "grab" neighboring molecules) to the domain length.

Parameter	Description	Value	Units	Ref	Notes
L	Domain length	134.6	μm	[2]	radii 27×15 μm ellipse
D_M	Myosin diffusivity	0.05	$\mu\text{m}^2/\text{s}$	[3]	
$\hat{K}_M^{\text{on}}$	Myosin attachment rate	0.4			Fit to get 30% bound myosin
k_M^{off}	Myosin detachment rate	0.12	1/s	[3]	
η	Cytoskeletal fluid viscosity	0.1	Pa·s		$100 \times$ water
γ	Myosin drag coefficient	5×10^{-4}	$\text{Pa·s}/\mu\text{m}^2$		$\ell = \sqrt{\eta/\gamma} = 14\,\mu$m [7]
σ_0	Stress coefficient and form	0.0071	Pa		Fit in Sec. 2.1.1
$\hat{\sigma}_a(\hat{M})$	Stress function of myosin	$\hat{M}$			Fit in Sec. 2.1.1

Table 1: Parameter values for myosin model. Parameters listed with a citation are lifted directly from the corresponding study. See Section 2.1 for a discussion of the fitting procedure for the other parameters.

Prior to performing linear stability analysis, we need to first determine the function σ_a and the other parameters.

2.1 Parameter estimation

Table 1 lists the parameters for the myosin model. According to [2], the *C. elegans* embryo has a roughly ellipsoidal shape, with half-axis lengths $27 \times 15 \times 15$ μm. The in-membrane diffusivity of myosin, as well as the detachment rate, have both been measured in [3]. For the attachment rate, it was estimated in [3, Fig. S3m] that roughly 30% of myosin is bound to the cortex in wild-type embryos. Recalling that the uniform steady state is $\hat{M}_0 = \hat{K}_M^{\text{on}} / \left(1 + \hat{K}_M^{\text{on}}\right)$, this gives $\hat{K}_M^{\text{on}} = 0.43$. The total amount of myosin scales out of the equations.

For the fluid parameters, we assume that the viscosity of the cytoskeletal fluid on the cortex is 100 times water, which gives 0.1 Pa·s. The "hydrodynamic length scale" of $\ell = \sqrt{\eta/\gamma} = 14$ μm, measured in [7, 9], then gives the myosin drag coefficient γ. But more important than either of these is the stress as a function of myosin concentration. We fit this from the wild-type data of [10] in the next section.

2.1.1 Inferring flow profile from experiments

Because we can measure the cortical velocity and myosin intensity, we can actually infer the function $\sigma_a(M)$ in dimensional units from the experimental data [10]. We in particular isolate the myosin intensity and flow speed during late maintenance phase in wild type embroys [10, Fig. 1B(bottom)],

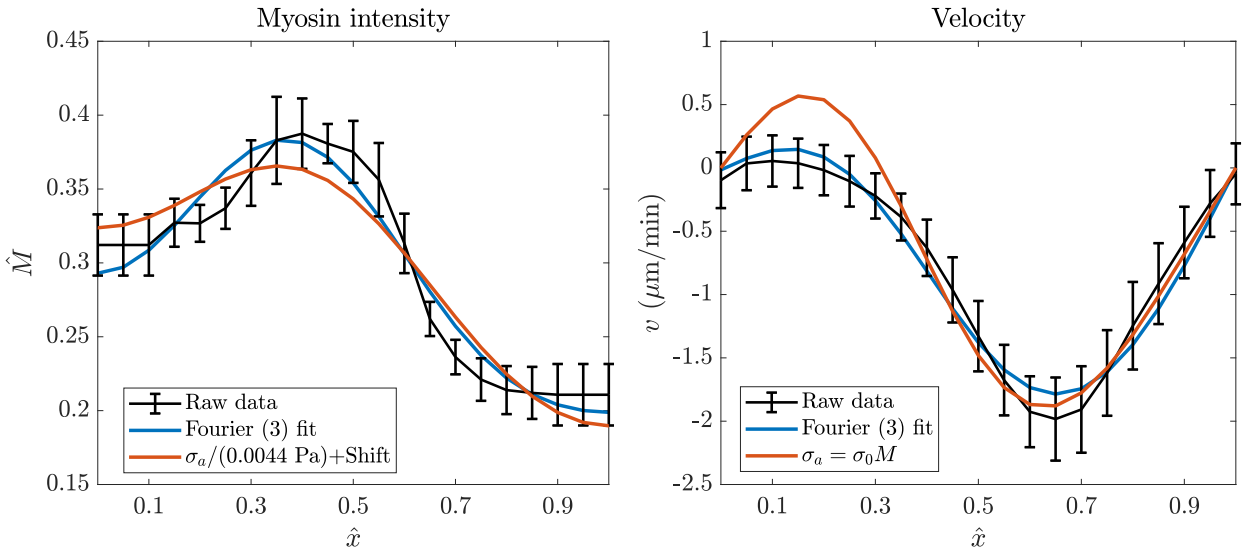

Figure M2: Extracting the active stress from the velocity profile. Left: the experimental data for myosin intensity (black with the outer 10% of the embryo on each side adjusted to be constant) and Fourier fit (blue), compared to the fitted stress (red). Right: velocity in μm/min (black) and Fourier fit (blue), compared to the velocity obtained when $\sigma_a = \sigma_0 M$.

plotting the results in black in Fig. M2. For the myosin intensity, we normalize so that the mean amount of bound myosin is 0.3 [3, Fig. S3], and adjust for the sensitivity of our measurements near the embryo edges by setting the myosin intensity at the outer 10% of the embryo to be constant and equal to that measured at the 10% boundary. We then periodically extend this data so that we fill the whole circumference (2 embryo lengths), and fit with a 3-term (4 terms including the constant) Fourier series.

To extract the stress profile from the smoothed velocity and myosin intensity, we consider a hybrid dimensional form of the velocity equation ((1b) in main text)

$$\gamma v - \frac{\eta}{L^2}\partial_{\hat{x}}^2 v = \frac{1}{L}\partial_{\hat{x}}\sigma_a(M).$$

Let the Fourier series representation for $v(\hat{x}) = \sum_k \tilde{v}(k)\exp(2\pi i k\hat{x})$, and likewise for $\hat{\sigma}_a$. Then, in Fourier space, the solution for σ_a is given by

$$\sigma_a(k) = \frac{\gamma + \eta/L^2\,(2\pi k)^2}{2\pi i k/L}\tilde{v}(k). \tag{M5}$$

The $k = 0$ mode is undefined because σ_a only appears differentiated; thus stress is only available up to an arbitrary constant.

We insert the parameters from Table 1 into (M5), then rescale the resulting stress by $\sigma_0 = 4.4 \times 10^{-3}$ Pa plus an arbitrary constant, so that it aligns with the myosin intensity we determined

experimentally. The left panel of Fig. M2 demonstrates that we can set

$$\hat{\sigma}_a = \hat{M} \tag{M6}$$

as a good approximation to the (dimensionless) stress. Using $\sigma_0 = 4.4\times10^{-3}$ Pa and the parameters in Table 1, the dimensionless parameter $\hat{\sigma}_0$ defined in (M4) is therefore equal to

$$\hat{\sigma}_0 = \left(\frac{\sigma_0/\sqrt{\eta\gamma}}{Lk_M^{\text{off}}}\right) \approx 0.04, \tag{M7}$$

which will control the stability analysis in the next section.

Prior to doing this, we make the observation that inserting the wild-type stress $\sigma_a = \sigma_0 M$ into the velocity equation gives the velocity profile shown in red in the right panel of Fig. M2. In the posterior, we obtain a velocity profile which perfectly matches the data. In the anterior, on the other hand, there is a clear mismatch where the model predicts more contractility (flows into the myosin peak) than the data show. This demonstrates that there are additional agents inhibiting contractility in the anterior. We will address the source of this ambiguity in Section 4.

2.2 Linear stability analysis

Now that all the parameters are known, we can perform linear stability analysis to see if the system could spontaneously polarize. The uniform steady state is $\hat{M}_0 = \hat{K}_M^{\text{on}}/\left(1+\hat{K}_M^{\text{on}}\right)$. We consider a perturbation around that state $\hat{M} = \hat{M}_0 + \delta\hat{M}$, where $\delta\hat{M} = \delta\hat{M}_0 e^{\lambda(k)\hat{t}+2\pi ik\hat{x}}$. Plugging this into (M3b), we get the velocity [1, Eq. (11)]

$$\hat{v} = \frac{2\pi ik\hat{\ell}\hat{\sigma}_a'(\hat{M}_0)}{1+\left(2\pi k\hat{\ell}\right)^2}\hat{\delta}M. \tag{M8}$$

Substituting this velocity into (M3a), and considering only the first order terms, we get the following equation for the eigenvalues

$$\lambda(k) = \frac{4\pi^2k^2\hat{\ell}\hat{M}_0\hat{\sigma}_0\hat{\sigma}_a'(\hat{M}_0)}{1+4\pi^2k^2\hat{\ell}^2} - \hat{D}_M 4\pi^2k^2 - 1 \tag{M9}$$

Using the parameters in Table 1, we have the following values for the dimensionless groups

$$\hat{D}_M = 2.3\times10^{-5} \qquad \hat{M}_0 \approx 0.3 \qquad \hat{\sigma}_a' = 1 \qquad \hat{\ell} \approx 0.07. \tag{M10}$$

Substituting these parameters into the dispersion relation (M11) gives the eigenvalues $\lambda(k)$ shown in Fig. M3 as a function of wavelength k and dimensionless flow speed $\hat{\sigma}_0$. We observe strong flow

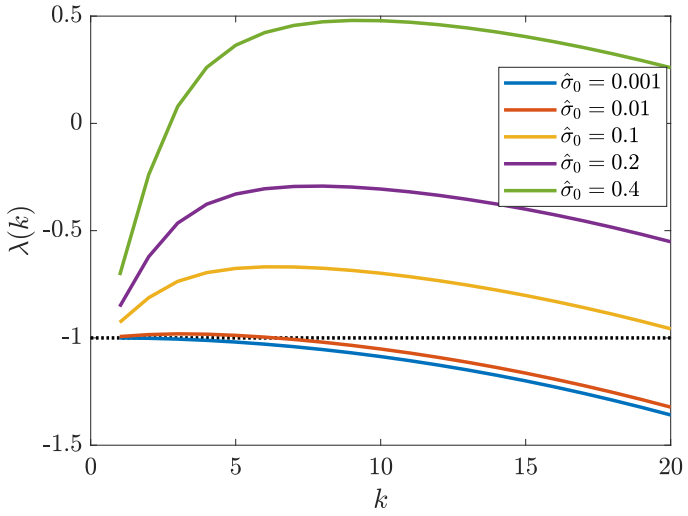

Figure M3: Stability analysis for myosin model (M3). We consider perturbations of size proportional to $e^{\lambda(k)\hat{t}+2\pi ik\hat{x}}$, then solve the linearized form of (M3) to obtain $\lambda(k)$ in (M11). Positive (negatve) eigenvalues indicate instability (stability) of the steady state.

coupling required for instability; with $\hat{\sigma}_0 = 0.2$ (flow transports myosins around 20% of the cell before they come off), the dynamics remain stable. Our estimate $\hat{\sigma}_0 \approx 0.04$ clearly demonstrates that myosin cannot self-polarize in the zygote.

Importantly, the large value of $\hat{\sigma}_0$ needed for instability is a consequence of the -1 in the dispersion relation (M11), which comes from the unbinding kinetics. Thus, unbinding makes it *harder* to destabilize the uniform steady state. Indeed, without the -1, the instability occurs at $\hat{\sigma}_0 \approx 10^{-3}$, which is pretty weak coupling to the flow (and weaker coupling than we observe experimentally). When we account for unbinding, diffusion becomes so small as to be irrelevant, as for the $k = 1$ mode the coefficient in (M11) is $\hat{D}_M 4\pi^2 \approx 10^{-3}$. Thus, the real balance here (to generate the instability) is not between advection and diffusion, but between advection and *unbinding*.

When we neglect diffusion in (M11), the largest eigenvalues occur when k is largest, so we an effectively take a limit as $k \to \infty$ to obtain

$$\lambda(k) = \frac{\hat{M}_0 \hat{\sigma}_0 \hat{\sigma}_a'}{\hat{\ell}^2} - 1 = \frac{\hat{M}_0 \left(\sigma_0/\sqrt{\eta\gamma}\right)}{\ell k_M^{\text{off}}} - 1 \tag{M11}$$

Recognizing $\sigma_0/\sqrt{\eta\gamma}$ as the velocity scale v, the condition $\lambda(k) > 0$ becomes equivalent to $v/k_M^{\text{off}} > \ell/\hat{M}_0$. The main text discusses the most extreme case when $\hat{M}_0 = 1$ (all myosin bound to the membrane).

3 Maintenance phase biochemistry model

We now turn to parameter fitting on the biochemistry model (2) in the main text. To fit missing parameters, we repeat the non-dimensionalization procedure we used for the myosin equation in Section 2 and in [5] for the PAR-3 equations. We scale lengths by L, time by k_A^{dp} (the typical time a molecule of PAR-3 spends on the membrane), and concentrations by the maximum when all protein is bound ($X^{(\mathrm{Tot})}$ for protein X). The resulting dimensionless equations are

$$\partial_{\hat{t}}\hat{A}_1 = \hat{D}_A\partial_{\hat{x}}^2 A_1 + \hat{K}_A^{\mathrm{on}}\left(1+\hat{K}_A^{\mathrm{f}}\hat{F}_A(\hat{A})\right)\left(1-\int_0^1 \hat{A}(x)\,d\hat{x}\right) - \hat{K}_A^{\mathrm{off}}\hat{A}_1 \tag{M12a}$$

$$+ 2\hat{A}_2 - 2\hat{K}_A^{\mathrm{p}}(\hat{P})\hat{A}_1{}^2 + \sum_{n=3}^{N}\left(\hat{A}_n - \hat{K}_A^{\mathrm{p}}(\hat{P})\hat{A}_1\hat{A}_{n-1}\right) \tag{M12b}$$

$$\partial_{\hat{t}}\hat{A}_n = \hat{K}_A^{\mathrm{p}}(\hat{P})\hat{A}_1(\hat{A}_{n-1}-\hat{A}_n) - (\hat{A}_n - \hat{A}_{n+1}) \qquad N > n \geq 2 \tag{M12c}$$

$$\partial_t\hat{A}_N = \hat{K}_A^{\mathrm{p}}(\hat{P})\hat{A}_1\hat{A}_{N-1} - \hat{A}_N, \tag{M12d}$$

for PAR-3, which are exactly those we used in [5], except that now the net polymerization rate $\hat{K}_{\mathrm{AP}}^{\mathrm{p}}$ is a function of P. To account for the inhibition of PAR-3 cluster growth by PAR-1 (P), we increase the effective depolymerization rate by setting

$$\hat{K}_{\mathrm{AP}}^{\mathrm{p}}(\hat{P}) = \frac{k_A^{\mathrm{p}}A^{(\mathrm{Tot})}}{k_A^{\mathrm{dp}}\left(1+\hat{R}_{\mathrm{PA}}\hat{P}\right)} := \frac{\hat{K}_A^{\mathrm{p}}}{1+\hat{R}_{\mathrm{PA}}\hat{P}} \tag{M12e}$$

where $\hat{R}_{\mathrm{PA}} = r_{\mathrm{PA}}P^{(\mathrm{Tot})}/k_A^{\mathrm{dp}}$ describes the rate at which pPARs inhibit cluster accumulation relative to the normal rate of depolymerization k_A^{dp}. When $\hat{R}_{\mathrm{PA}} = 0$, we recover the dimensionless grouping $\hat{K}_A^{\mathrm{p}}$ used in [5]. Thus, all of the dimensionless parameters in the PAR-3 equations,

$$\hat{D}_A = \frac{D_A}{L^2k_A^{\mathrm{dp}}}, \quad \hat{K}_A^{\mathrm{on}} = \frac{k_A^{\mathrm{on}}}{k_A^{\mathrm{dp}}h}, \quad \hat{K}_A^{\mathrm{f}} = \frac{k_A^{+}A^{(\mathrm{Tot})}}{k_A^{\mathrm{on}}}, \quad \hat{K}_A^{\mathrm{off}} = \frac{k^{\mathrm{off}}}{k_A^{\mathrm{dp}}} \qquad \hat{K}_A^{\mathrm{p}} = \frac{k_A^{\mathrm{p}}A^{(\mathrm{Tot})}}{k_A^{\mathrm{dp}}},$$

with the exception of $\hat{R}_{\mathrm{PA}}$, are known from [5]. We do not repeat their values here.

The dimensionless forms of the equations for CDC-42, PAR-6/PKC-3, and pPARs are

$$\partial_{\hat{t}}\hat{C} = \hat{D}_C\partial_{\hat{x}}^2\hat{C} + \hat{K}_C^{\mathrm{on}}\left(1-\int_0^1\hat{C}(\hat{x})\,d\hat{x}\right) - \hat{K}_C^{\mathrm{off}}\left(1+\hat{R}_{\mathrm{PC}}\hat{P}\right)\hat{C} \tag{M12f}$$

$$\partial_{\hat{t}}\hat{K} = \hat{D}_K\partial_{\hat{x}}^2\hat{K} + \hat{R}_{\mathrm{ACK}}\hat{C}\delta_{\hat{A}>\hat{A}_0}\left(1-\int_0^1\hat{K}(\hat{x})\,d\hat{x}\right) - \hat{K}_K^{\mathrm{off}}\hat{K} \tag{M12g}$$

$$\partial_{\hat{t}}\hat{P} = \hat{D}_P\partial_{\hat{x}}^2\hat{P} + \hat{K}_P^{\mathrm{on}}\left(1-\int_0^1\hat{P}(\hat{x})\,d\hat{x}\right) - \hat{K}_P^{\mathrm{off}}\left(1+\hat{R}_{\mathrm{KP}}\hat{K}\right)\hat{P}. \tag{M12h}$$

Parameter	Description	Value	Units	Ref	Notes
D_P	pPAR diffusivity	0.15	$\mu\text{m}^2/\text{s}$	[2]	
D_K	PAR-6 diffusivity	0.1	$\mu\text{m}^2/\text{s}$	[8]	
D_C	CDC-42 diffusivity	0.1	$\mu\text{m}^2/\text{s}$		Same as PAR-6
k_P^{off}	pPAR detachment rate	7.3×10^{-3}	1/s	[2]	
k_K^{off}	PAR-6 detachment rate	0.01	1/s	[8]	
k_C^{off}	CDC-42 detachment rate	0.01	1/s		Same as PAR-6
$\hat{K}_P^{\text{on}}$	PAR-2 attachment rate	0.09			$P \approx 1$ in enrichment zone
$\hat{R}_{\text{KP}}$	K inhibiting P	50			Strong inhibition
$\hat{R}_{\text{PC}}$	P inhibiting C	(M15)		[10]	CDC/CHIN-1 relationship (Fig. A5)
$\hat{K}_C^{\text{on}}$	CDC-42 attachment rate	0.07			20% bound with inhibition
$\hat{A}_0$	PAR-3 threshold for PAR-6	0.06		[10]	10% anterior level
$\hat{R}_{\text{ACK}}$	A and C creating K	0.1			20% bound K
$\hat{R}_{\text{PA}}$	P inhibiting A	2			α on posterior in wild-type

Table 2: Additional parameter values for the biochemistry model.

These equations reveal the following dimensionless groups

$$\hat{R}_{\text{PC}} = \frac{r_{\text{PC}} P^{(\text{Tot})}}{k_C^{\text{off}}}, \quad \hat{R}_{\text{ACK}} = \frac{r_{\text{ACK}} C^{(\text{Tot})}}{k_A^{\text{dp}} h}, \quad \hat{R}_{\text{KP}} = \frac{r_{\text{KP}} K^{(\text{Tot})}}{k_P^{\text{off}}} \tag{M13a}$$

$$\hat{K}_P^{\text{on}} = \frac{k_P^{\text{on}}}{k_A^{\text{dp}} h}, \quad \hat{K}_C^{\text{on}} = \frac{k_C^{\text{on}}}{k_A^{\text{dp}} h}, \quad \hat{A}_0 = \frac{A_0}{A^{(\text{Tot})}} \tag{M13b}$$

$$\hat{D}_P = \frac{D_P}{L^2 k_A^{\text{dp}}}, \quad \hat{D}_C = \frac{D_C}{L^2 k_A^{\text{dp}}}, \quad \hat{D}_K = \frac{D_K}{L^2 k_A^{\text{dp}}}, \quad \hat{K}_P^{\text{off}} = \frac{k_P^{\text{off}}}{k_A^{\text{dp}}}, \quad \hat{K}_K^{\text{off}} = \frac{k_K^{\text{off}}}{k_A^{\text{dp}}}, \quad \hat{K}_C^{\text{off}} = \frac{k_C^{\text{off}}}{k_A^{\text{dp}}} \tag{M13c}$$

Among these, the parameters in (M13c) are all known from literature, and have been reported in the top half of Table 2. This leaves the six parameters in (M13a) and (M13b), which we determine sequentially from the following set of experimental observations:

1. In embryos without myosin flows, roughly 25–30% of the available PAR-2 is bound at steady state [3, Fig. S3]. Because the PAR-2 domain is only 25–30% of the embryo, the concentration of P in its enrichment zone must be near 1. We find that $\hat{K}_P^{\text{on}} = 0.09$ reproduces this result (in dimensional units $k_P^{\text{on}} = 0.13$ μm/s [3]).

2. In embryos without myosin flows, the level of PAR-2 at the anterior is no more than 5% of the posterior level [3, Fig. 2c]. This sets $\hat{R}_{\text{KP}} \gg 1$. We use $\hat{R}_{\text{KP}} = 50$ for strong inhibition.

3. The parameter $\hat{R}_{\text{PC}}$ is available from the data in [10]. To obtain it, we solve (M12f) at steady

state to obtain

$$\hat{C} = \frac{1}{1 + \frac{h k_c^{\text{off}}}{k_C^{\text{on}}} + \frac{\hat{R}_{\text{PC}} k_C^{\text{off}} h}{k_C^{\text{on}}} \hat{P}}. \tag{M14}$$

If we rewrite this in a system of units where $\hat{C} = 1$ when $\hat{P} = 0$, we obtain

$$\tilde{C} = \frac{1 + \frac{h k_c^{\text{off}}}{k_C^{\text{on}}}}{1 + \frac{h k_c^{\text{off}}}{k_C^{\text{on}}} + \frac{\hat{R}_{\text{PC}} k_C^{\text{off}} h}{k_C^{\text{on}}} \hat{P}}$$

Now according to [10], $\tilde{C} \approx 1/(1 + 13.3\hat{P})$, which implies that

$$13.3 = \frac{\hat{R}_{\text{PC}} k_C^{\text{off}} h}{k_C^{\text{on}} \left(1 + \frac{h k_c^{\text{off}}}{k_C^{\text{on}}}\right)} = \frac{\hat{R}_{\text{PC}} k_C^{\text{off}} h}{k_C^{\text{on}} + h k_c^{\text{off}}} \rightarrow \hat{R}_{\text{PC}} = 13.3 \left(1 + \frac{k_C^{\text{on}}}{k_C^{\text{off}} h}\right). \tag{M15}$$

4. In [3, Fig. S3i], it is reported that roughly 25% of PAR-6 is bound in wild-type embryos. Assuming that CDC-42 has a similar set of properties, we can assume 25% of the protein is bound. Setting $\hat{K}_C^{\text{on}} = 0.07$ and combining with the inhibition strength (M15) gives about 20% bound CDC-42 at steady state (in dimensional units $k_C^{\text{on}} = 0.1$ μm/s).

5. Let's assume $\hat{C} = 0.25$; then we want to set $\hat{R}_{\text{ACK}}$ to obtain about 25% bound PAR-6 (when there is sufficient PAR-3) as well. Plugging this into the steady state version of (M12g), we obtain

$$\hat{R}_{\text{ACK}}(0.25)(0.75) - (0.0625)(0.25) = 0 \rightarrow \hat{R}_{\text{ACK}} = 0.08 \approx 0.1.$$

6. In embryos depleted of PAR-1 and CHIN-1, the level of PAR-3 at the anterior is roughly 10% of the posterior, and PAR-6 can load onto the membrane everywhere. We therefore set $\hat{A}_0 = 0.06$, since we've already tuned the PAR-3 parameters so that the polarized state has $\hat{A} \approx 0.6$ on the anterior and $\hat{A} \approx 0.06$ on the posterior [5].

7. If $\hat{P} \approx 1$ in the posterior, the parameter $\hat{R}_{\text{PA}}$ can be used to match the distribution of PAR-3 oligomer sizes on the posterior in wild type embryos. As demonstrated in [5], the distribution of oligomer sizes is roughly exponential with exponent $\alpha = \hat{K}_{\text{AP}}^{\text{p}}(\hat{P})\hat{A}_1$. In the absence of PAR-1, $\alpha = 0.42$ on the posterior, giving $(1-\alpha)^2 \approx 30\%$ in monomer form [6]. Setting $\hat{R}_{\text{PA}} = 2$ and substituting $\hat{P} = 1$ in (M12e) gives $\alpha = 0.14$ (85% in monomer form), which is what we use here.

The fitting procedure and values of these seven unknown parameters are summarized Table 2. I have some more stuff about PAR-3 and the other proteins, but not appropriate for this paper.

4 Coupling contractility to biochemistry

We obtain the dimensionless equations which couple biochemistry and contractility via a straightforward combination of (M3) and (M12), advecting all proteins with the myosin flow field [4], and making CDC-42 a promoter of myosin. We also neglect myosin diffusion, since we previously found it to make a negligible contribution to the dynamics, and because bound myosin does not diffuse in the cortex. The resulting equations are

$$\partial_{\hat{t}}\hat{A}_1 + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{A}_1\right) = \hat{D}_A\partial_{\hat{x}}^2 A_1 + \hat{K}_A^{\rm on}\left(1+\hat{K}_A^{\rm f}\hat{F}_A(\hat{A})\right)\left(1-\int_0^1 \hat{A}(x)\,d\hat{x}\right) - \hat{K}_A^{\rm off}\hat{A}_1 \tag{M16a}$$
$$+ 2\hat{A}_2 - 2\hat{K}_{\rm AP}^{\rm p}{\hat{A}_1}^2 + \sum_{n=3}^{N}\left(\hat{A}_n - \hat{K}_{\rm AP}^{\rm p}\hat{A}_1\hat{A}_{n-1}\right)$$
$$\partial_{\hat{t}}\hat{A}_n + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{A}_n\right) = \hat{K}_{\rm AP}^{\rm p}\hat{A}_1(\hat{A}_{n-1}-\hat{A}_n) - (\hat{A}_n - \hat{A}_{n+1}) \qquad N > n \geq 2 \tag{M16b}$$
$$\partial_{\hat{t}}\hat{A}_N + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{A}_N\right) = \hat{K}_{\rm AP}^{\rm p}\hat{A}_1\hat{A}_{N-1} - \hat{A}_N \tag{M16c}$$
$$\partial_{\hat{t}}\hat{C} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{C}\right) = \hat{D}_C\partial_{\hat{x}}^2\hat{C} + \hat{K}_C^{\rm on}\left(1-\int_0^1 \hat{C}(\hat{x})\,d\hat{x}\right) - \hat{K}_C^{\rm off}\left(1+\hat{R}_{\rm PC}\hat{P}\right)\hat{C} \tag{M16d}$$
$$\partial_{\hat{t}}\hat{K} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{K}\right) = \hat{D}_K\partial_{\hat{x}}^2\hat{K} + \hat{R}_{\rm ACK}\hat{C}\delta_{\hat{A}>\hat{A}_0}\left(1-\int_0^1 \hat{K}(\hat{x})\,d\hat{x}\right) - \hat{K}_K^{\rm off}\hat{K} \tag{M16e}$$
$$\partial_{\hat{t}}\hat{P} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{P}\right) = \hat{D}_P\partial_{\hat{x}}^2\hat{P} + \hat{K}_P^{\rm on}\left(1-\int_0^1 \hat{P}(\hat{x})\,d\hat{x}\right) - \hat{K}_P^{\rm off}\left(1+\hat{R}_{\rm KP}\hat{K}\right)\hat{P} \tag{M16f}$$
$$\partial_{\hat{t}}\hat{M} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{M}\right) = \hat{K}_M^{\rm on}\left(1+\hat{R}_{\rm CM}\hat{C}\right)\left(1-\int_0^1 \hat{M}(x)\,dx\right) - \hat{K}_M^{\rm off}\hat{M} \tag{M16g}$$
$$\hat{v} = \hat{\ell}^2\partial_{\hat{x}}^2 v + \hat{\ell}\partial_{\hat{x}}\hat{\sigma}_a(\hat{M}) \tag{M16h}$$
$$\hat{R}_{\rm CM} = \frac{r_{\rm CM}C^{(\rm Tot)}}{k_M^{\rm on}},\ \hat{K}_M^{\rm on} = \frac{k_M^{\rm on}}{hk_A^{\rm dp}},\ \hat{K}_M^{\rm off} = \frac{k_M^{\rm off}}{k_A^{\rm dp}},\ \hat{\sigma}_0 = \frac{\sigma_0/\sqrt{\eta\gamma}}{Lk_A^{\rm dp}},\ \hat{\ell} = \frac{\sqrt{\eta/\gamma}}{L}. \tag{M16i}$$

The last equation (M16i) defines the key *new* dimensionless parameters relating to myosin. These differ from (M4) because we can only non-dimensionalize time by one quantity, and we choose here to stick with the depolymerization time $1/k_A^{\rm dp}$. Table 1 gives the dimensional quantities σ_0 and $k_M^{\rm off}$, from which we obtain $\hat{\sigma}_0$ and $\hat{K}_M^{\rm off}$. This leaves two parameters which control the myosin profile: the basal rate $k_M^{\rm on}$, and the amount that CDC-42 promotes myosin, $\hat{R}_{\rm CM}$. In wild-type embryos, we estimate the minimum amount of bound myosin (in the absence of CDC-42) as 0.2. This sets $k_M^{\rm on}$ via $k_M^{\rm on}/(k_M^{\rm on}+k_M^{\rm off}h) \approx 0.2$, giving $k_M^{\rm on} = 0.3$ μm/s. The parameter $\hat{R}_{\rm CM}$ is then chosen to match the initial speed of maintenance phase rescue (flow speed 2 μm/min)

Parameter	Description	Value	Units	Ref	Notes
D_R	Branched actin diffusivity	0.05	$\mu\text{m}^2/\text{s}$		Same as myosin
k_R^{off}	Branched actin unbinding rate	0.12	$1/\text{s}$		Same as myosin
$\hat{R}_{\text{CM}}$	C promoting M	3		[11, Fig. 7D]	Fit initial rescue speed
$\hat{C}_R$	Threshold CDC-42 level for branched actin	0.2			Between A and P levels
$\hat{R}_{\text{CR}}$	CDC-42 producing branched actin rate	1			Arbitrary
$\hat{R}_{\text{RM}}$	Branched actin inhibiting myosin rate	15			Fit boundary position

Table 3: Additional parameters for coupled model (M16) with branched actin additions in (M17).

4.1 Incorporating branched actin

We encode these properties in the system of equations by modifying the myosin equation in (M16) and adding an additional equation for branched actin, which we represent by R,

$$\begin{aligned}
\partial_{\hat{t}}\hat{M} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{M}\right) &= \hat{D}_M\partial_{\hat{x}}^2\hat{M} + \hat{K}_M^{\text{on}}\left(1+\hat{R}_{\text{CM}}\hat{C}\right)\left(1-\int_0^1 \hat{M}(x)\,dx\right) - \hat{K}_M^{\text{off}}\left(1+\hat{R}_{\text{RM}}\hat{R}\right)\hat{M} \\
\partial_{\hat{t}}\hat{R} + \hat{\sigma}_0\partial_{\hat{x}}\left(\hat{v}\hat{R}\right) &= \hat{D}_R\partial_{\hat{x}}^2\hat{R} + \hat{R}_{\text{CR}}\left(\hat{C}-\hat{C}_R\right)\delta_{\hat{C}>\hat{C}_R}\left(1-\int_0^1 \hat{R}(x)\,dx\right) - \hat{K}_R^{\text{off}}\hat{R}
\end{aligned} \tag{M17}$$

Here branched actin is produced above a threshold level $\hat{C}_R$ of CDC-42, as indicated by the δ-function. Once produced, branched actin inhibits myosin. We assume for the moment that branched actin has the same diffusivity (0.05 $\mu\text{m}^2/\text{s}$) and unbinding rate (0.12/s) as myosin.

4.1.1 Additional parameters

There are four new parameters in this model that are unknown:

- $\hat{R}_{\text{CM}}$, which is the rate at which CDC-42 produces myosin. As mentioned in the last section, the value $\hat{R}_{\text{CM}} = 3$ gives a good match to the initial speeds of maintenance phase rescue reported in [11, Fig. 7D], which presumably do not yet have interference from branched actin.
- The threshold $\hat{C}_R$ is set by examining the steady state in Fig. **??** without branched actin. There we see that, at late times, CDC-42 goes from about 0.05 in the posterior to 0.45 in the anterior. To block contractility, we set $\hat{C}_R = 0.2$.
- The rate at which CDC-42 produces branched actin sets the amount of bound branched actin. This amount is arbitrary, since what matters is not the amount of branched actin but the total amount of myosin inhibition. We therefore set $\hat{R}_{\text{CR}} = 1$.

- We set the rate at which branched actin blocks myosin $\hat{R}_{\mathrm{RM}} = 10$, which is the parameter we use to control the dynamics, to reproduce the boundary position in wild type embryos.

The parameters are summarized in Table 3.

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