**Parameter Optimization**

A derivative-free CMA-ES (pycma v.4.0.0)(cite) was employed to fit eight biophysical parameters of the pescoid fluid-dynamics model (diffusivity, tau\_m, flow, activity, β, γ, r, m\_sensitivity). First, all search dimensions were first mapped to the unit hyper-cube [0,1] so that a single global step size is isotropic across the domain, removing scale differences between coordinates for the covariance-matrix adaptation. Parameters that span several orders of magnitude were log-transformed before scaling and the remaining parameters were scaled linearly. The optimizer was initialized with a global step size of σ0=0.15, a population size of 36, 4,000 maximum evaluations and an internal stagnation criterion of 8 generations. Four restarts were permitted and each seeded with the best solution obtained so far.

The fitness objective function is defined as:

where and are the dynamic EMA-based weights for radius and mesoderm errors, respectively, and denotes the L² norm of the difference between the simulated and experimental trajectories of tissue radius  and mesodermal fraction . We converted generations to minutes and linearly interpolated simulation outputs onto a matching experimental grid (30 minutes). Each channel was standardized by the sample standard deviation of its experimental series to prevent unit-driven dominance by either error. Channel losses were combined with dynamic weights equal to the inverse of an exponential-moving-average (EMA, α=0.1) of their recent values to allow the search to adapt to changes in the relative scale of the two error terms as convergence progresses. Weights were clipped between [0.05, 1.95] to prevent either error term from being assigned an excessively large or small weight due to fluctuations. Simulations yielding non-finite outputs, premature termination, or inconsistent array lengths were penalized to discourage exploration of infeasible regions without creating flat fitness plateaus.