Model simulates chemotaxis with clusters of eukaryotic cells

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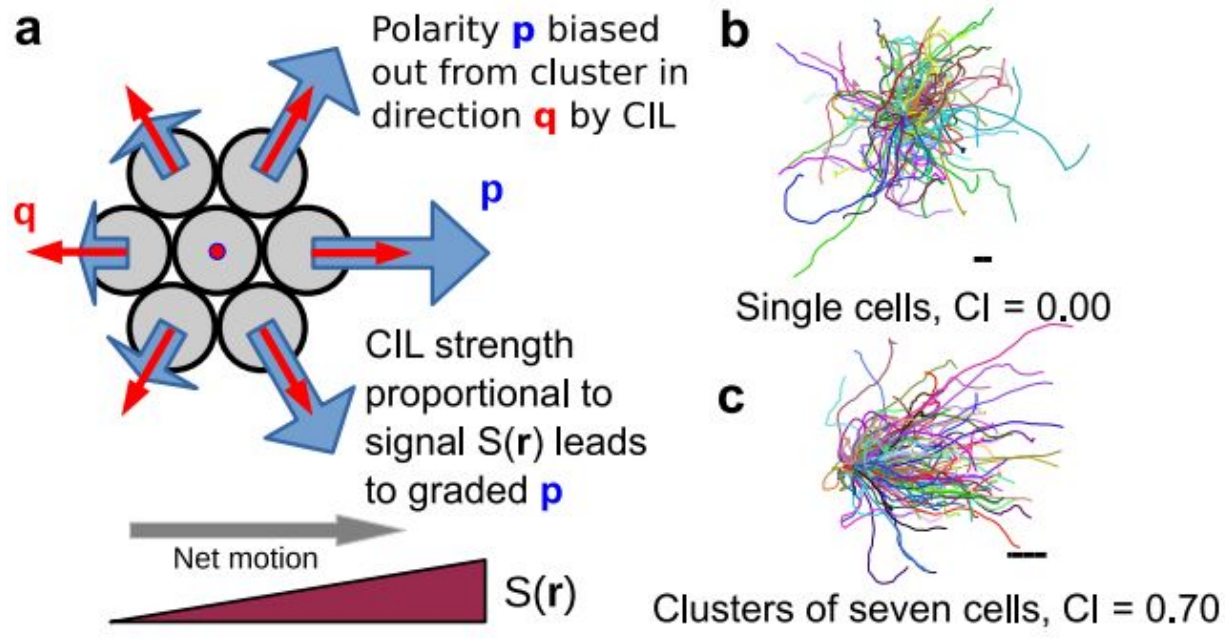

Signal-dependent contact inhibition of locomotion creates directed motion. Credit: arXiv:1506.06698 [physics.bio-ph]

(Phys.org)—A small team of researchers with the University of California and Rice University has created a model of chemotaxis that shows how individual cells may work together to respond to a chemical-concentration gradient. In their paper published in *Physical Review Letters*, the team explains what went into creating the model, how it works and why they believe it closely approximates real live cell

chemotaxis.

Chemotaxis is an action that occurs with cells where they move towards increasing concentrations of a chemoattractant—for food, or to get to a place they know they are supposed to be, to build organs or tissue, for example. Sometimes chemotaxis occurs with individual cells, but other times it occurs in groups when individual cells work together to allow them to move to a desired destination. How cells work together to do so, however, has not been understood—in this new effort, the researchers have built a computer model that suggests one possibility.

To build their model, the researchers began with what has already been learned through observation and experimentation—when cells get close together, for example, they react by trying to move farther away—tests have shown that cells also tend to move away from one another more quickly as chemical concentrations increase. The researchers set proportional variables to represent such actions. They also focused on both rigid and non-rigid clusters (where cells are stuck together and are attempting to pull apart or do actually pull apart). For rigid clusters, the researchers noted that general directional movement would be in the direction of the cell that was attempting to move away from the other the hardest. For non-rigid clusters, they noted that the cells still tended to move in the direction of the cell that pulled away the hardest, but they did so slower than with rigid-clusters. Adding such information allowed for the creation of cell movement simulations, that when compared to real world cell movement, coincided, suggesting the model was correctly identifying the means by which chemotaxis works when more than one cell is involved.

The researchers suggest that the model could be further validated by additional testing with real world cells—by analyzing how they respond under different conditions, for example, and comparing that with what the model shows.

More information: Brian A. Camley et al. Emergent Collective Chemotaxis without Single-Cell Gradient Sensing, *Physical Review Letters* (2016). DOI: 10.1103/PhysRevLett.116.098101 . On *Arxiv*: arxiv.org/abs/1506.06698

ABSTRACT

Many eukaryotic cells chemotax, sensing and following chemical gradients. However, experiments show that even under conditions when single cells cannot chemotax, small clusters may still follow a gradient. This behavior is observed in neural crest cells, in lymphocytes, and during border cell migration in Drosophila, but its origin remains puzzling. Here, we propose a new mechanism underlying this "collective guidance," and study a model based on this mechanism both analytically and computationally. Our approach posits that contact inhibition of locomotion, where cells polarize away from cell-cell contact, is regulated by the chemoattractant. Individual cells must measure the mean attractant value, but need not measure its gradient, to give rise to directional motility for a cell cluster. We present analytic formulas for how the cluster velocity and chemotactic index depend on the number and organization of cells in the cluster. The presence of strong orientation effects provides a simple test for our theory of collective guidance.