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Supplemental Information

Semblance of Heterogeneity in Collective Cell Migration

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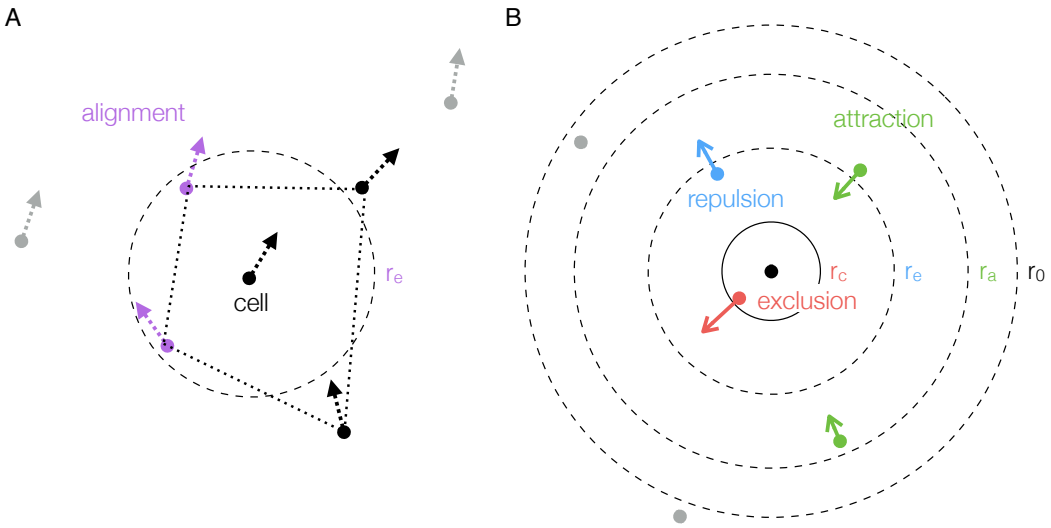


Figure S1: Related to Method details. Schematic of interaction zones in the SPP model. Cells are drawn as dots with their direction of movement shown by dashed arrows (A), and the forces acting on them by solid arrows (B). (A) Alignment: A cell (drawn at the center of the circle) aligns with the direction of movement of neighboring cells within distance r_e (shown in purple). Interactions are restricted to nearest neighbors, which are the vertices of the Voronoi region around the cell, as indicated by the dotted black line (here, cells within r_e are a subset of the nearest neighbours, but this is not generally the case). Non-nearest neighbors shown in grey. (B) Intercellular forces: Cells are attracted or repelled from each other depending on their separation. Within r_e, a repulsive force is exerted upon neighboring cells, shown in blue. At distances greater than r_e, but smaller that r_0, cells are attracted to each other, as shown in green. Thus r_e is the preferred distance between cells. To model volume exclusion, cells exert a strong (approximately infinite) repulsive force upon neighbors within r_c, shown in red. Non-nearest neighbors (shown in grey) do not interact, neither for alignment, nor for attraction-repulsion. Dashed lines mark the various interaction zones around the central cell. This schematic is drawn in two dimensions for simplicity, but applies analogously to the 3D model.

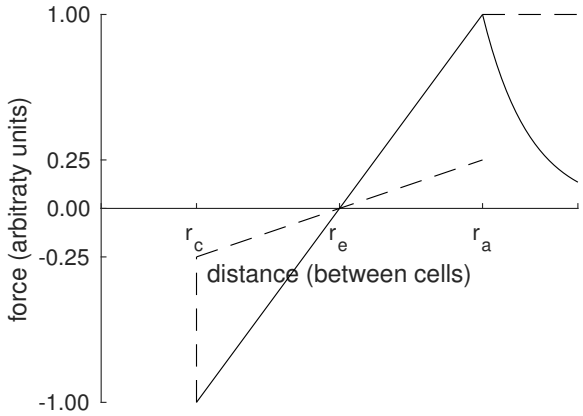


Figure S2: Related to Method details. Intercellular forces, as in Grégoire et al. (2003) (dashed line), and the modified force used here (solid line). Positive forces are attractive, negative sign indicates repulsion. Below r_c, the repulsive force is infinite, so that volume exclusion between cells is enforced (see main text for details).

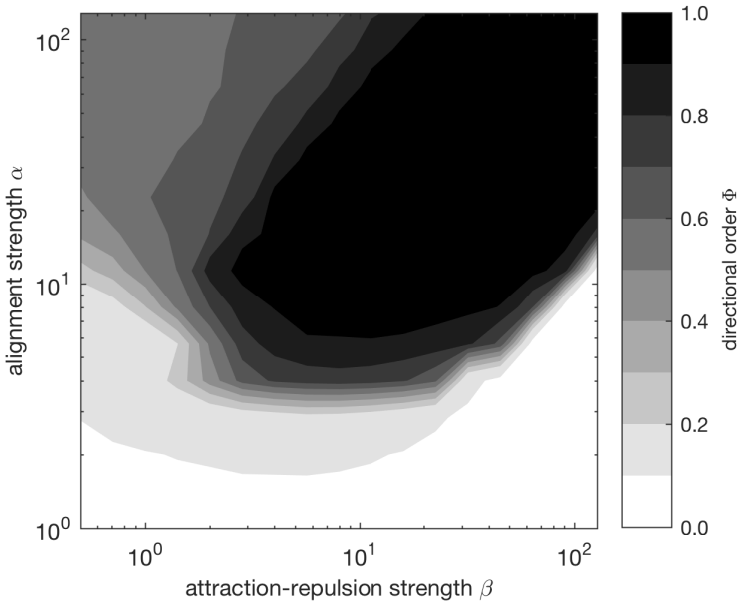
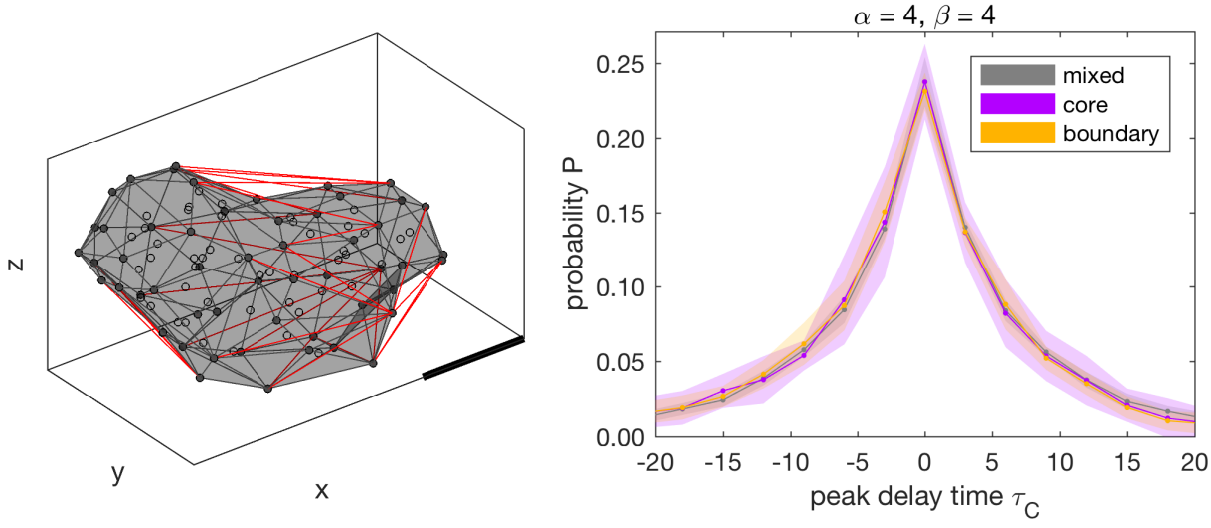


Figure S3: Related to Fig. 1 and Quantification and statistical analysis. Global model behaviour, characterised by the phase diagram of the order parameter Φ, which is the overall alignment of cells ($N = 100$), averaged over 500 time-steps (after discarding the first 500 time-steps). Parameters were sampled on a log-spaced grid with 17 points in β and 15 points in α. For each parameter combination, the order parameter shown is an average over 10 simulations, with the same random number generator seed used for each run of every parameter combination.



(A) (B)

Figure S4: Related to Fig. 2. Apparent heterogeneity is not restricted to boundaries of the population. (A) Cells at the boundary are identified through a modified Delaunay triangulation: From a Delaunay triangulation of all cell positions (circles), we remove any edges (red lines) longer than the interaction distance, r_0. The boundary of the remaining triangulation (grey surface) identifies the boundary cells (filled circles). (B) Peak-delay distributions for boundary, core, and mixed cells. As cells change their relative positions over time, we classify cells as 'boundary' or 'core' if they spend $> 90\%$ or $< 10\%$ of time-points, respectively, at the boundary. Cells in neither category are classified as 'mixed'. Points show the average for each bin over 10 simulations, shaded area shows the standard deviation.