Supplemental Information for

Signal percolation within a bacterial community

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Figure S1

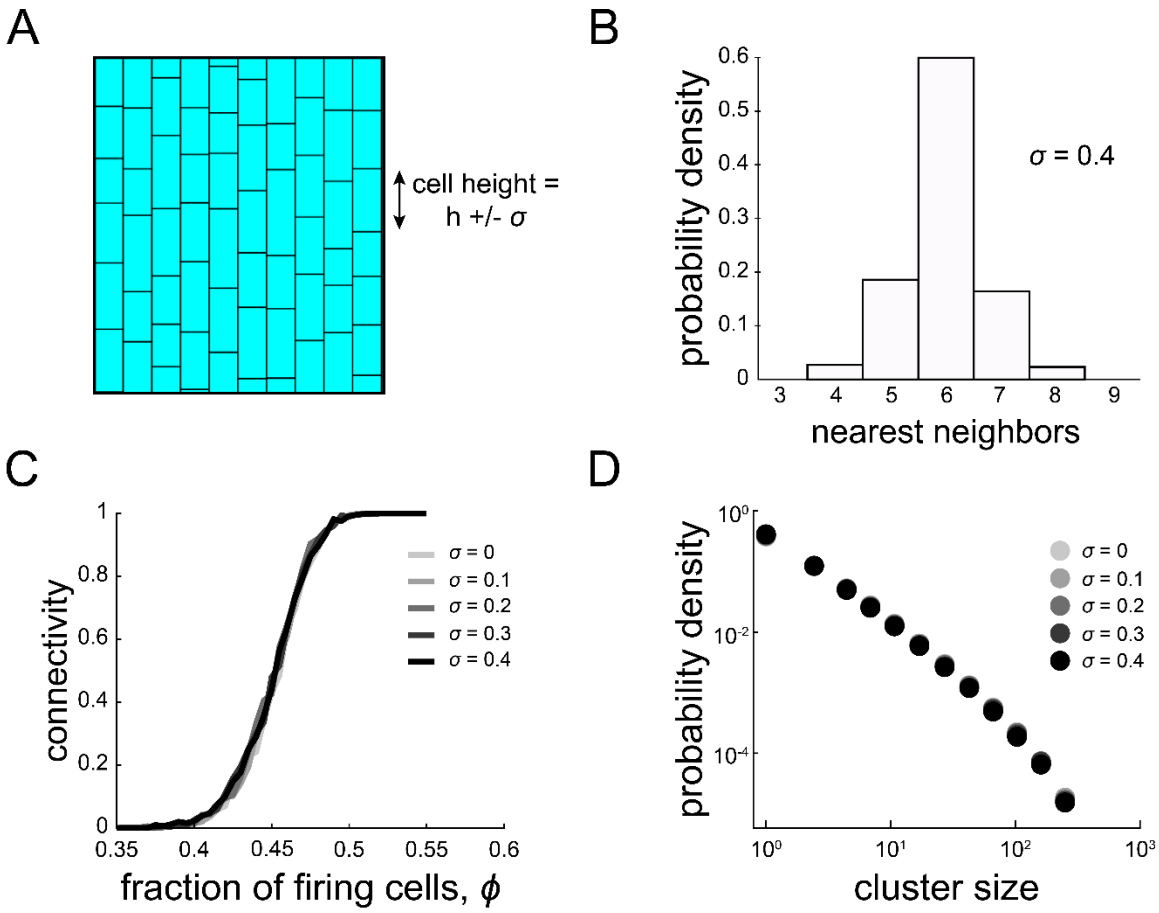

Figure S1. Disordered lattices have the same percolation properties as triangular lattices. Related to Figure 1. (**A**) A disordered lattice may be created by starting with a triangular lattice and adding random noise (σ) to the height of each cell. (**B**) This yields a model biofilm with a distribution of nearest neighbor numbers, as shown in this histogram from a σ = 0.4 biofilm. Some cells have more than 6 nearest neighbors, some fewer. (**C**) These perturbations do not affect the percolation threshold, as shown in this connectivity plot near the threshold value of ϕ_c = 0.45. σ = 0 represents the triangular lattice used in the paper. All curves overlap. (**D**) For different σ values, the cluster size distribution is not significantly changed near the percolation threshold, as shown in this cluster size distribution plot for different σ values.

Figure S2

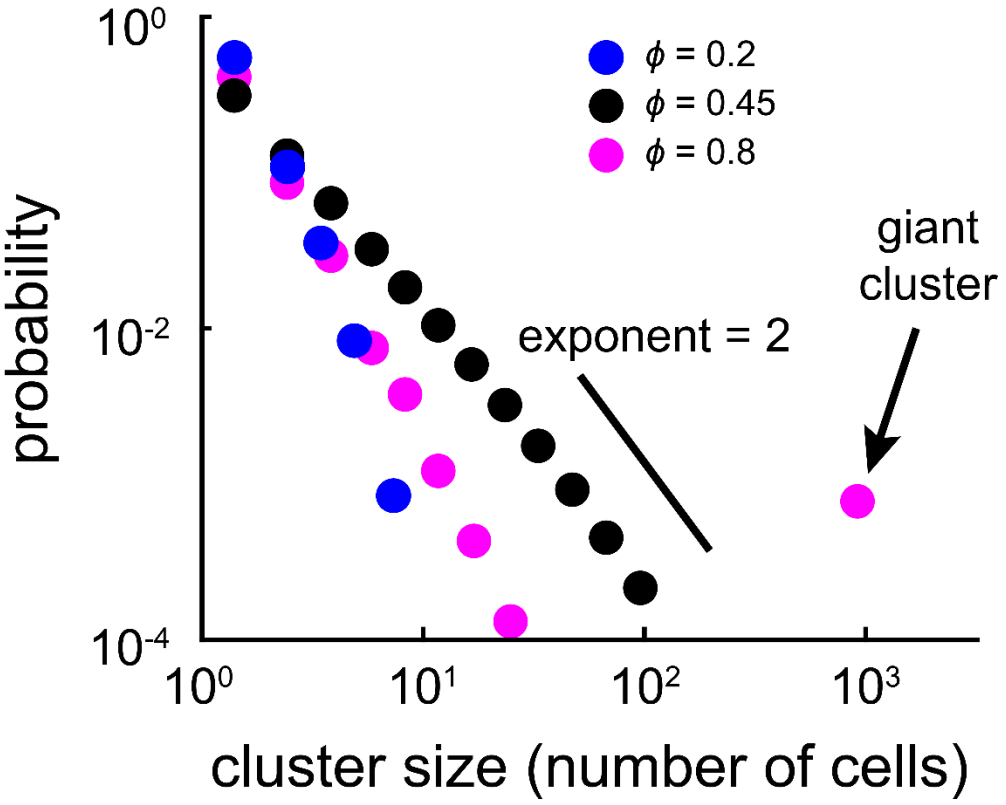

Figure S2. Cluster size distribution in model biofilms changes with fraction of firing cells. Related to Figure 1. Model-generated cluster size distributions for values of ϕ depicted in Figure 1F, G. Only when $\phi = \phi_c$, are clusters distributed according to a power-law (black circles). Above the percolation threshold (magenta circles), a giant cluster develops near the system size.

Figure S3

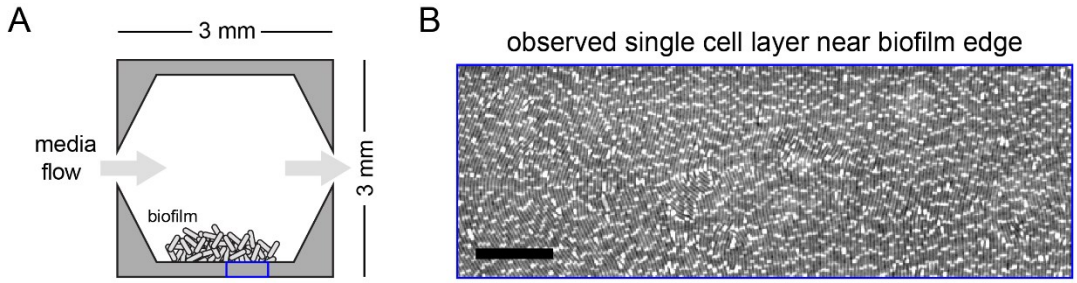

Figure S3. Microfluidic system for single molecule measurements of biofilms. Related to Figure 2. (**A**) Schematic of microfluidic device used in these experiments. Cells are seeded under a strip of PDMS (bottom) and allowed to grow into a biofilm as media flow is controlled. During biofilm growth, the edge region under the PDMS strip is confined to single cell thickness (e.g. blue rectangle), enabling imaging at single-cell resolution, as shown in the phase image in (**B**), Scale bar, 20 μm.

Figure S4

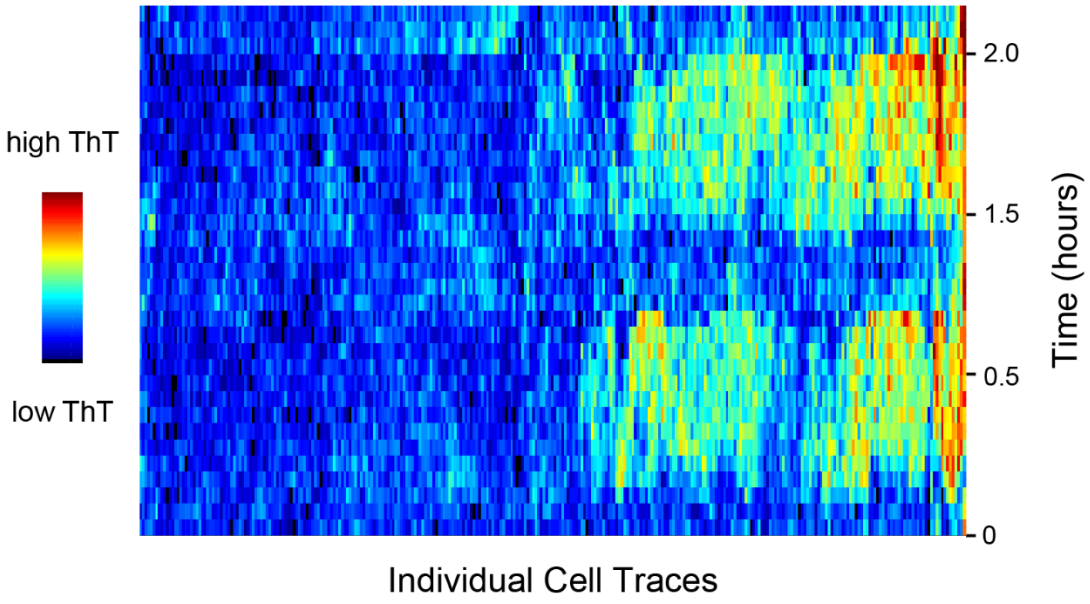

Figure S4. Cells generally do not switch signaling state between pulses. Related to Figure 2. A heatmap of 320 single cell ThT traces from two consecutive pulses in a wild-type biofilm. Each column is a ThT trace from one cell with time increasing along the vertical axis. The traces are organized with hierarchical clustering. The heatmap illustrates that the cells maintain their firing state. Cells that fire on the first pulse have a much higher probability of firing on the second pulse than those that do not and vice versa.

Figure S5

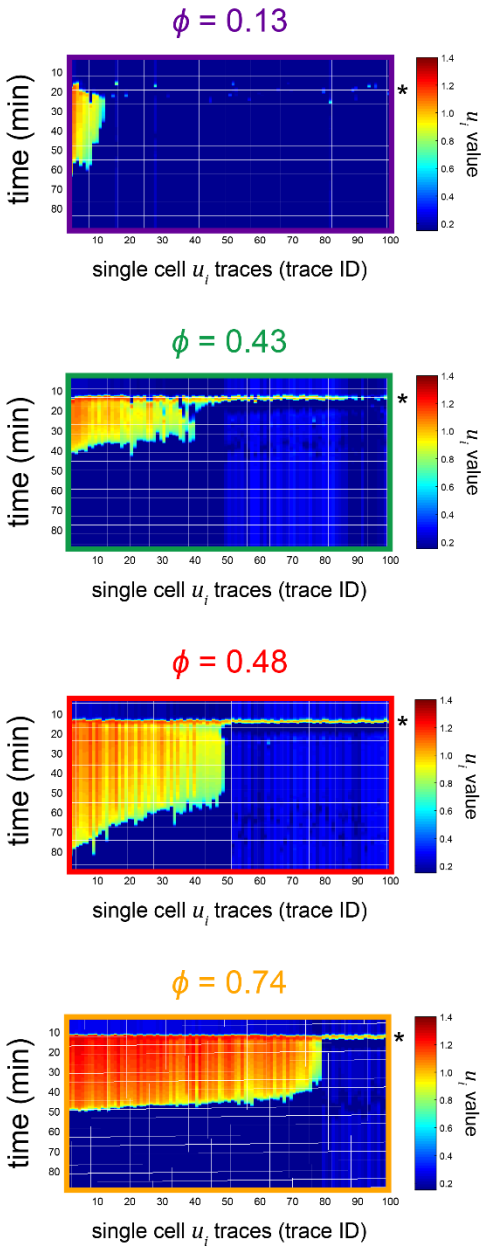

Figure S5. The model predicts heterogeneous single-cell time traces. Related to Figure 3 and Figure 4. Heatmaps displaying time traces from the model for 100 randomly chosen cells from biofilms with parameters matched to those of the four experimental strains (see STAR Methods for details). For each heatmap, a single column is that trace from one cell and time moves from top to bottom. The time point of excitation for each heatmap is marked with an asterisk. Compare to the experimental heatmaps from Figure 4C of the main text.

Figure S6

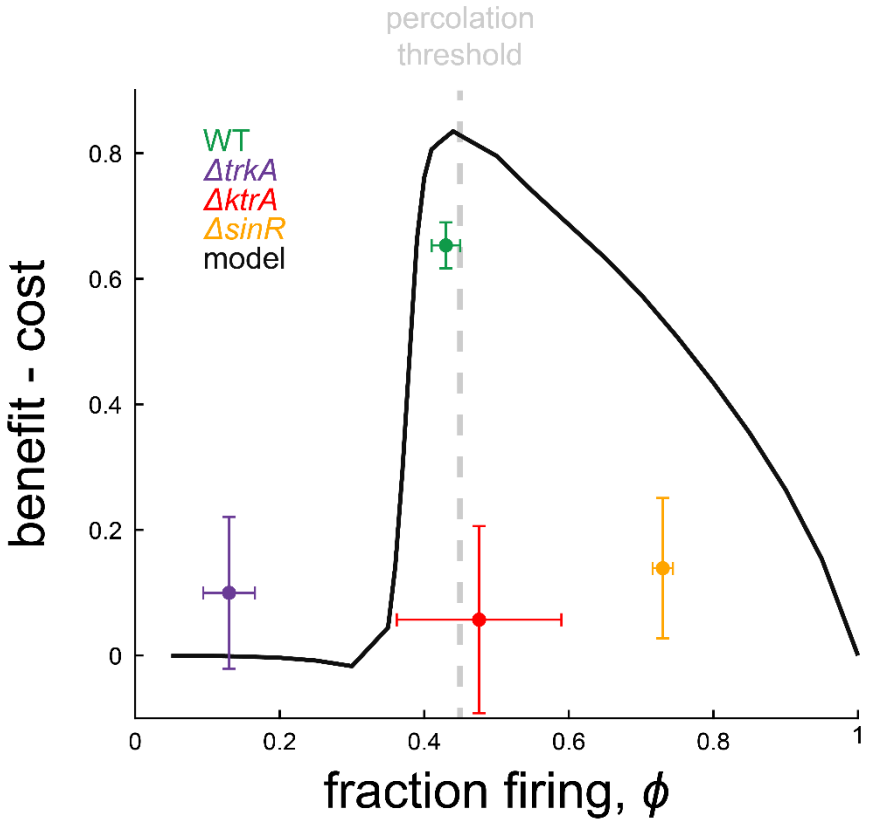

Figure S6. Benefit minus cost yields a peak near the percolation threshold. Related to Figure 6. Benefit minus cost is plotted as a function of fraction of firing cells for experimental data (colored points) and the model with wild-type parameter values (black line). Because benefit is a number between 0 and 1 and cost unbounded, we normalize cost by dividing it by the highest pulse time value measured. The curve bends down at higher ϕ values because the pulse time from the model slightly increases with ϕ for the same τ value (see STAR Methods). As with benefit divided by cost, this function exhibits a peak near the percolation threshold.