Supplemental Figure 1. **Sorting trajectories at static biases for different strains.** Each plot shows n = 180 runs (20 simulations of 9 biological replicates for each strain). Dotted gray line indicates 5 rounds of sorting as a reference. For the J/A strain, biases below 0.5 did not converge.
**Supplemental Figure 2. Number of rounds for different bias schedules.** Schedule A switches from first bias to second bias after a certain number of rounds. Schedule B alternates between first bias and second bias. Schedule C switches from first bias to second bias after a certain probability is recovered. Each cell is the average value across $n = 180$ trials (20 runs on data from 9 technical replicates).
Supplemental Figure 3. Change in number of rounds for different bias schedules compared to using just the first bias. Values are calculated as $(R/R_0 - 1)$ where $R$ is the number of rounds using the schedule and $R_0$ is the number of rounds using the first bias. Red indicates a positive change, i.e. using the schedule increases the number of required rounds. Blue indicates a negative change, i.e. using the schedule decreases the number of required rounds.
Supplemental Figure 4. Trajectories for different bias schedules. Rows correspond to the given first bias for a strain and the different lines correspond to the second bias. Dotted lines indicate the non-schedule trajectory (i.e. maintaining the first bias).