

Supporting Information

Ward et al. 10.1073/pnas.0710344105

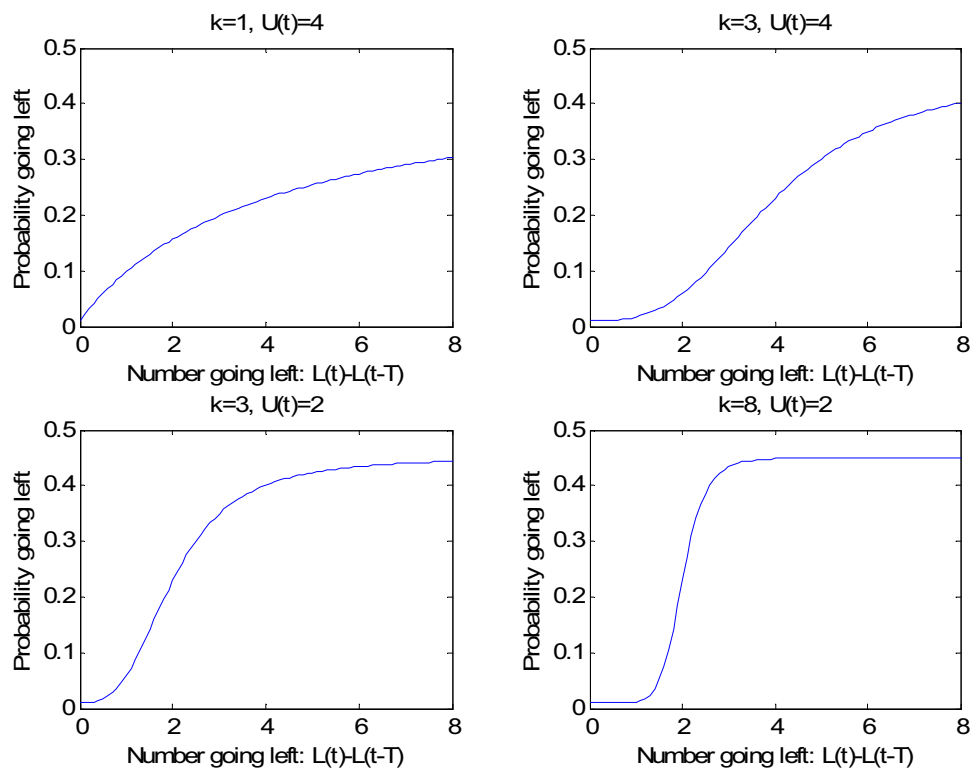


Fig. S1. Example plots of Eq. 1. Here, we set $l = 0.01$, $m = 0.45$, $R(t) - R(t - T) = 0$ and vary values of k , the threshold steepness, and $U(t)$ the group size.

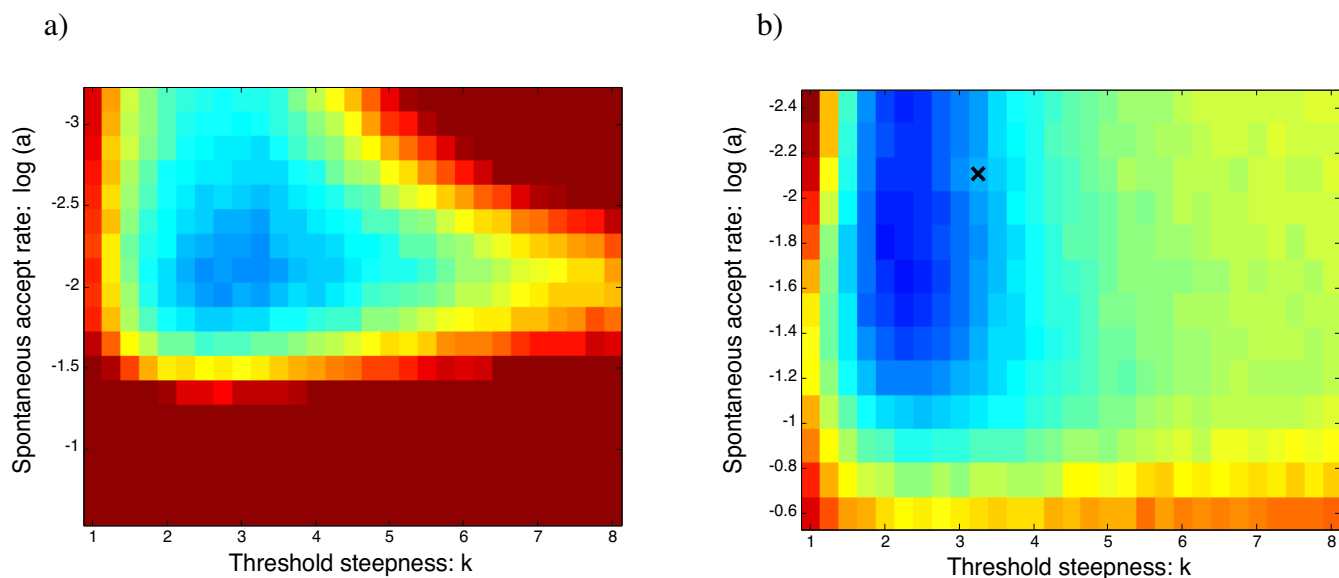


Fig. S2. Goodness of fit of model to data in the absence (a) and presence (b) of a predator. Goodness of fit was measured as the sum of squares of difference between data and model over all experimental treatments. In particular, for each treatment and group size, we calculated the sum of squares (expected; - observed)² where i denotes the histogram boxes for the proportion of fish going right 0-20, 20-40, ..., 80-100. The sum of squares was summed across all treatments and group sizes to give the overall fit of the model for a particular parameter combination. The density plots show the sum of squares for different parameter combinations. Blue indicates small values of sum of squares for a particular set of parameter values (good fit) and red a large value (poor fit). (a) Predator absent: $T = 40$ and the best fit for spontaneous acceptance rate and threshold steepness parameter were $a = 0.0078$ and $k = 3.2$. (b) Predator present: $T = 4$ and the best fit in this case was $a = 0.0110$ and $k = 2.25$. As a reference point, the black cross indicates the best fit for the parameters in the case of no predator.