### S1 Table. Model Notation

#### Time
- $T$: current generation time
- $G$: maximum generation time
- $t$: intra-generation time
- $n$: maximum intra-generation time

#### Agent associated designators
- $A_a$: agent $a$
- $N_A$: number of agents
- $E_a(t)$: local environment of agent $a$ at time $t$
- $B_a(t)$: biomass of agent $a$ at time $t$
- $L_a(t)$: location of agent $a$ at time $t$

#### Agent movement
- $M(P_a)^a$ specifies if and where to agent $a$ will move at time $t$, as determined by a vector of parameters $P_a$
- $\alpha$: competition-tradeoff parameter (parameter $a$ in Nova code)
- $\delta$: neighbor-discount parameter (parameter $b$ in Nova code)
- $\rho$: movement-threshold parameter (parameter $w$ in Nova code)

#### Agent consumption
- $u$: maximum resource extraction rate
- $h$: the extraction efficiency parameter
- $q$: the competition parameter
- $\kappa$: biomass conversion rate parameter
- $c$: metabolic loss rate parameter
- $r$: resource intrinsic growth rate
- $g$: reservoir parameter
- $s$: saturation parameter

#### Cells
- $C_{ij}$: cell at row $i$ and column $j$ in the array
- $C_k$: cell $k$, where $k = 1, ..., n_i n_j$ is a 1-D renaming of the matrix 2-D array
- $R_k(t)$: resource value of cell $k$ at time $t$
- $N_k(t)$: number of agents remaining in cell $k$ after movement at time $t$
- $J_k^M$: average number of agents per cell in the Moore neighborhood of cell $k$
- $F_k(t)$: resource extraction by an agent in cell $k$ at time $t$