

siml68B Evolution of Sociality.

- siml68B is similar to siml67B and siml66, but with modifications to let the subpopulations start from more appropriate launch points. The run simulated subpopulations separately for 5000 cycles under one of the 3 sharing regimes. After 5000 cycles, the resulting state is stored as a 'stable' population under the regime. 3 of each type of subpopulation were jointed together to make the starting population for the simulation.
- siml68B differs from siml67B by zeroing out the mutation load for the starting population.
- 15 groups of 3 types are simulated in parallel. Groups operate according to Maternal, K5, or 50/50 sharing regimes and are independent except for their mutual influence on density; there is no inter-group cooperation or sharing and kin boundaries do not cross group boundaries. Each group only associates with its own kind. Density depends on total consumption of the populations, as was first simulated in siml63.
- starting population. A population of 100000; subpopulations of approx 6666. Each ego is in her own social/matriarchal/kinship group and has an isolated family tree (no common ancestors back 5 generations)
- Ron's new measure of density would be $E/TotC$ where TotC is total of all consumption in the entire population. "This is better because it says that the more energy is extracted from the environment the more difficult it is to extract more [decreasing marginal returns]. Simply counting people in the total population and basing density on that measure gives the same weight to infants and prime age adults, which cannot be correct" (4/11/2007).
- new mortality formulation:
`adjust.hx <- (gene.risk*lethality + epsilon) * sharing.gamma^(e.mortality) ;`
- kinship sharing is based on kinship5.id
- no dispersal
- fission / Using Tim's odd/even split, keeping kin5 together (TMpkin5). All fissioned groups retain their subpopulation membership.
- fusion. Uses Tim's algorithm which splits small groups into two classes and then combines members from each class. Only groups within the same subpopulation are combined with each other.
- kinship ids. There are 4 measures of relatedness which are presented. Tim's measurement (anc), and 3 variants of Carl's (kinship3.id, kinship4.id, kinship5.id) which look backwards 3,4,5 generations in their determination of what constitutes 'kin'. This is presented in the 1st plot of sim.pdf Tim's measure and kin3 almost completely coincide after some initial differences. Going back an extra generation increases the average group size by a bit less than 1. Only kin5 is calculated and used here.
- gamma.kin contributes to gamma.sharing in the K5 and 50/50 group types. The component is calculated (based on kinship5) and its age profile is presented in the final plot.