

Altruism in the Evolution of Communication

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Abstract

Computer models of evolutionary phenomena often assume that the fitness of an individual can be evaluated in isolation, but effective communication requires that individuals interact. Existing models directly reward speakers for improved behavior on the part of the listeners so that, essentially, effective communication *is* fitness. We present new models in which, even though “speaking truthfully” provides no tangible benefit to the speaker, effective communication nonetheless evolves. A large population is spatially distributed so that “communication range” approximately correlates with “breeding range,” so that most of the time “you’ll be talking to family,” allowing *kin selection* to encourage the emergence of communication. However, the emergence of altruistic communication also creates niches that can be exploited by “information parasites.” The new models display complex and subtle long-term dynamics as the global implications of such social dilemmas are played out.

1 Models of the Evolution of Communication

Although schoolbook treatments often leave the impression that Darwinian evolution is about never-ending competition, a ceaseless struggle for survival by individual creatures in a nasty environment, it doesn’t take much wide-eyed observation of the natural world to see that cooperation among individuals also plays a huge role. Using communication to accomplish tasks is a central example, as many other forms of cooperation presuppose a means of communication.

“Communication” is a very broad concept; here we focus only on evolutionary issues related to sending and receiving *initially arbitrary signals* about a shared environment. Focusing on signals avoids the complexities of syntax and compositional semantics, while initial arbitrariness excludes certain degenerate cases — a sudden change in direction, for example, might be an “incidental communication” to others that a predator is approaching. Though this may actually be the most prevalent means by which information moves between individuals, for present purposes it is uninteresting since such behavior presumably will be selected for even if the individual is alone.

We also wish to eliminate the possibility of “mimetic semantics,” wherein an emitted signal somehow imitates the stimulus it represents, as in the use of a hissing sound to denote a snake. Such signals may be non-trivial from an evolutionary point of view, if they provide no direct value to the signaller. The question of why such signalling would evolve thus arises, and that is indeed the central question we wish to explore. However, although the *motivation for sending* a mimetic signal is non-trivial, the *mechanism for understanding* it is degenerate. Initial arbitrariness forces us to consider the harder problem of evolving both “speaking” and “understanding” abilities *simultaneously*.

There are, principally, two recent simulation models of the evolution of communication (MacLennan, 1991; Werner & Dyer, 1991; see also Hutchins, 1991, for an interesting but less closely related model), and it is useful to compare them briefly with the approach we are taking. MacLennan (1991) considers a population of simple machines, represented genetically (and phenotypically) by truth tables, and creates a shared environment through which the machines can pass initially arbitrary signals. A mostly conventional genetic algorithm (Holland, 1975; Goldberg, 1989) is used to evolve the population, based on a scoring function that measures how effectively communication is being used by the machines. Crucially, for our present purposes, the scoring function is such that the *speaker*, as well as the listener, is rewarded whenever a “match” occurs, meaning that the listener performed an action appropriate to the stimulus the speaker saw. One could imagine a circumstance where “truthful speech” by a speaker and “right action” by a listener causes food to rain down on both. MacLennan observes effective communication evolving in his machines, but other phenomena typically associated with communication do not occur. Lying, for example, is utterly pointless under such conditions: either both parties benefit or neither does.

The model of Werner & Dyer (1991) is different in a number of respects. Unlike MacLennan’s model, there is no explicit scoring function; instead, effective communication allows “males” to find “females” more rapidly and thus increases the reproductive rate of individuals that communicate compared to those that do not. One could imagine this as a sort of “firefly” model, in which females in the grass below signal to males flying above, using basically arbitrary signals for more efficient mate-finding. In principle at least, one could imagine more subtle communication phenomena emerging in

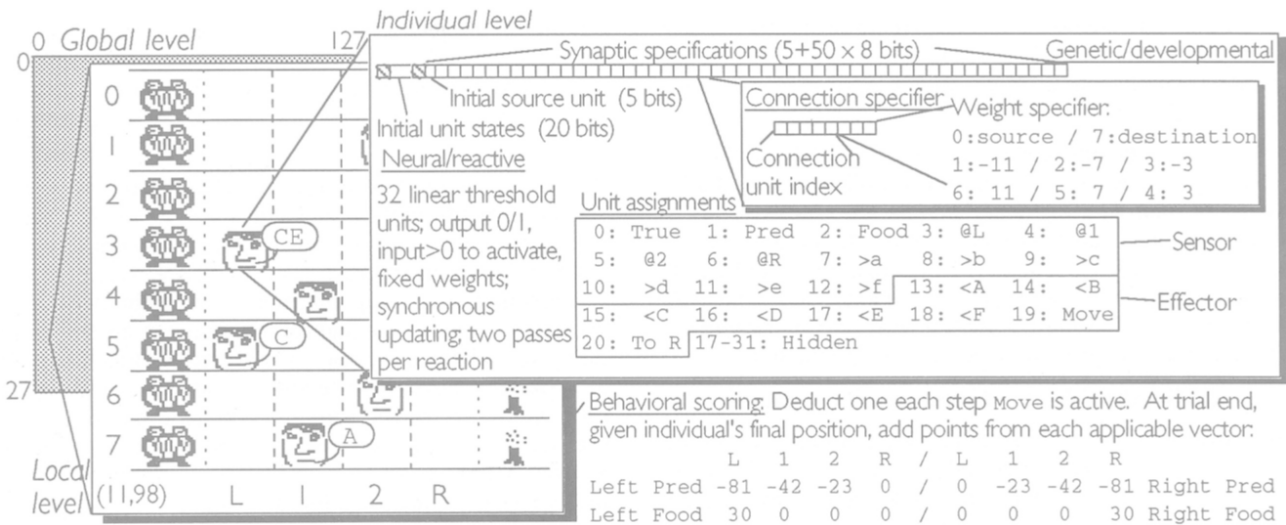


FIGURE 1. Model summary

this model — if, for example, during evolution the initial population divided itself into multiple species, a female of one species might send a misleading signal to a male of another species to impede his search for a suitable mate. Their model does postulate a spatially-distributed population, so one could imagine speciation along “territorial” lines occurring, and they discuss such possibilities. However — perhaps because of the globally-mixing reproduction strategy they employed — neither speciation nor any more complex communication phenomena were observed, so for present purposes the Werner/Dyer model is akin to the MacLennan model, in practice if not in principle, in that communication always turns out to be a win-win proposition for those involved.

2 Model Description: Worlds Within Worlds

Figure 1 sketches the models we explore. There are three organizational levels, which we refer to as *individual*, *local*, and *global*. The individual level captures the representation of genetic information in a *genotype*, the behavioral characteristics of a *body* or *phenotype*, and how a body is developed from a genotype. The local level captures the environment within which a group or *subpopulation* of individuals lives, the mechanism for allowing communication among the individuals of a subpopulation, the process of assigning a behavioral score to each individual in a subpopulation, and a within-subpopulation strategy for birth and death. The global level captures principally migration between subpopulations, although in two of the variations we present below, reproduction and migration are at least partially coupled and therefore reproduction is a global issue as well.

The level are interdependent in various ways; here we start at the local level, then go down to the individual level, and then up to the global level. We try to be as complete about details of the model as we can, not because we believe every detail to be critical — some of them certainly *seem* minor — but to be clear about what we have and have not built into the model “up front”, and because, as experience with computer models of complex systems shows over and over again, it is nearly impossible to be certain *which* details don’t matter.

2.1 Local level: A day in the life

First, we consider the behavior of individuals in a subpopulation, without worrying about how an individual implements any particular behavioral pattern. A subpopulation consists of eight individuals in a partially shared environment. The environment can be envisioned as eight horizontal *tracks* separated by walls that block *vision* but allow (non-localized) *sounds* to pass over. Each track is divided into four locations, labelled L(left), 1, 2, and R(right), and one individual lives in each track. An individual may move left or right along its track, one location per step, and may also *speak* on any or all of six independent audio channels (labelled A–F).

Nasty, flame-throwing predators (Pred) and delicious foods (Food) can appear at either end of the tracks, or both. When an individual is at L or R it will *see* either Pred, Food or nothing depending on what stimulus happens to be at that end; individuals at 1 or 2 see nothing. Also, each individual may *hear* (labelled a–f) the sum of the speech emitted by the subpopulation on the previous step.

A round of behavioral scoring, a *day*, begins by setting the individuals’ scores to zero, and is then followed of 36 independent *trials*. The L and R stimuli are constant and identical across tracks during a trial. The eight individuals are initialized and placed at various *starting* locations in their tracks, and they then *react* for three *steps*. After the trial, each individual’s behavioral score is adjusted as a function of the L and R stimuli, its final location, and how much it attempted to move, as shown in Figure 1.

The 36 trials consist of four repetitions of the nine possible combinations of L and R stimuli. The individuals’ starting locations are randomized except that each individual begins in a different location on each repetition of a stimulus-pair, and exactly two individuals start in each location. This behavioral scoring procedure, though costly in simulation time, has the analytically useful property that unless the individuals of a subpopulation actually are communicating, the resulting individual behavioral scores are completely deterministic. We can compute, for example, that the best score possible in ab-

sence of communication is -12 , and therefore any behavioral score greater than -12 is *proof* that that individual, on that day, definitely benefitted from signals emitted by the rest of its subpopulation.

At the end of the day, depending on the model variation involved, a *local reproduction* may occur. When it does, the following occurs: The eight individuals are ranked based on their behavioral scores. Two *parents* are chosen uniformly at random from the top half of the subpopulation, and an *offspring* is created (details in the next section). Then, one of the eight existing individuals is chosen uniformly at random and *killed*, and the offspring replaces it in the population.

2.2 Individual level: Genes and neurons

The previous section described the sensations and actions that an individual *may* experience and perform; which of them are *actually* used, and in what manner, is determined by the *brain* of the particular individual, which, in turn, is determined by the individual's genes. In the models we present in this paper, no "plasticity" or "adaptation" is involved — the genes completely and permanently determine the "wiring" and cognitive function of the individual.

An individual's brain is a synchronously updated neural network containing a total of 32 linear threshold units (Rumelhart, et al, 1986) assigned as follows: 12 *sensor units*, providing information about food, predators, location, and sound; 8 *effector units* controlling whether to move, which direction to go, and what to say; a *true unit* that always has value 1; and 11 *hidden units* that have no prespecified function.

The genome of an individual defines a wiring diagram and initial conditions for this architecture. A total of 448 bits of genetic information is divided up into three groups: 19 bits for the initial states of the effector and hidden units at the beginning of each trial; 405 bits of *synaptic specification genes* describing up to fifty connections between units; and 24 left-over bits, *pseudo genes* that are never decoded.

The *developmental process* grows a network from a genome, sequentially interpreting the synaptic specifications, operating in either *source mode* or *destination mode*. It begins in source mode. The 405 synaptic specification bits are: a five bit *initial source* group, and fifty *connection specifier* groups of eight bits each. The initial source yields an integer from 0 to 31, denoting a unit to use as the *current unit*. In source mode, new connections are created from the current unit to a unit determined by the next connection specifier; in destination mode, new connections are created to the current unit from a unit determined by the next connection specifier. A connection specifier is a five bit *connection unit* index and a three bit *weight specifier*. Two of the eight values of a weight specifier are *mode shift codes*: value zero means "set the current unit to the connection unit and enter source mode", and value seven means "if the connection unit is a sensor unit, do nothing, otherwise set the current unit to the connection unit and enter destination mode." The other six values of the weight specifier indicate that a specifically-weighted connection is to be grown between the current unit and the connection unit, as indicated in Figure 1.

This scheme for neural development, though devised mostly to conserve computer memory, has the effect that small

changes in the genome can lead to large changes in the resulting phenotype. A single bit flip in the connection unit group of a mode-shifting connection specifier, in particular, can transfer many synapses from one source or destination to another.

At the beginning of each trial, the effector and hidden units are initialized from the initial states genes. On each step, the network *reacts*: first, the sensor unit values are determined from the environment: zero or one for the *Pred*, *Food*, *L*, *1*, *2*, and *R* units, as appropriate, and zero to eight for each of the six hearing ears — the sum of all speech from the previous time step (all zeros are always heard on the first step). Then, an *update pass* over the effector and hidden units is done: For each unit, the weighted sum of its inputs is computed, and if that sum is greater than zero, the unit adopts value one, otherwise it adopts value zero. Two passes over the network are performed each step, making it possible, for example, for a hidden unit to contribute to the decision about what to do now based on the latest environmental input. After both passes are concluded, the effector unit states are read off and executed — attempting to move left or right, or not, as directed, and contributing speech on channels *A..F*, or not.

The only individual level aspect we have not discussed is the way an offspring genotype is derived from two parent genotypes. There is one almost certainly inconsequential detail, and one very likely consequential detail, about how we do this. The basic mechanism we employ is *genetic recombination*, or *crossover*; the specific variation we use is, in the genetic algorithms literature, called *parameterized uniform crossover* (Spears & De Jong, 1991; Ackley, 1987) with a crossing probability of 0.05 per *byte* — and that is the almost certainly inconsequential detail: It is impossible, in this scheme, to cross more than once in a single byte of genotype.

The likely consequential detail is this: In these studies, we use *no* mutation at all. Recombination is the only *genetic operator* we employ. This is out of step with most genetic algorithms research — if anything, the trend in the last decade has been towards higher mutation rates, to combat the "premature convergence" problem that genetic algorithms often display on optimization tasks. One of us has actively championed that trend, in fact, in previous writing (Ackley, 1987). Why do we reverse direction in this case?

As we explored early versions of this model, hoping to see effective communication without "paying off" the speakers, we found ourselves turning the mutation rate lower, and seeing the results becoming more promising. Even a low mutation rate, it seemed, destroyed communicating subpopulations, eating them up from the inside out. With some trepidation, we decided to turn mutation off entirely... and the model behavior became much more interesting. We will return to this issue in Section 4.

2.3 Global level: Reproductive and migratory

Now we have discussed how an individual works, from its genes up to its sensorimotor interface and "cognitive function", and how individuals in subpopulations are evaluated, bred, and slaughtered. Just that much is a complete algorithm, in the sense that one could simulate one such group of eight individuals, and watch what happens. We did just that, during

exploratory simulations — and what happens is not very interesting. The tiny group converges, genetically, in a flash, usually with very poor behavioral scores for the individuals. To make the model really cook, we need to have many such subpopulations evolving at once, and then consider what happens when individuals move between subpopulations. That is what the global level of the model does.

As in some prior work (Ackley & Littman, 1993), we designed the global structure of our model to match the overall characteristics of the fairly large parallel computer we were fortunate to have available. Overall, the world is a square array of 128×128 cells, each of which contains a subpopulation of eight individuals, for an aggregate population size of 131,072. The *neighborhood* of each cell are the eight closest cells on the array; the array overall is configured as a torus. A *quad* of cells is any 2×2 group of adjacent cells.

In the case studies described in the next section, we employ two global level mechanisms, alone and in combination. The first mechanism, *wind*, implements simple migration. *Windy days* occur at regular intervals, with a frequency that varies from case to case. On a windy day, first, all the normal daily events occur. A global wind direction is then chosen uniformly at random from the eight compass directions. In each subpopulation, an individual is then selected uniformly at random, then all the selected individuals migrate to the “downwind” neighbor cell. The immigrant immediately takes up residence in the track vacated by the emigrant.

The second mechanism, *festival*, implements a combination of reproduction and migration. *Festival days*, like windy days, occur at regular intervals with a case-specific frequency. On a festival day, first, the normal behavioral evaluation occurs. Then, instead of performing a local reproduction in each cell, festivals are held in each of 4,096 quads. The 32 individuals from the four cells of a quad are ranked in a single list based on their behavioral scores for that day, and a *quad reproduction* is performed, selecting two parents uniformly at random from the top quarter of the ranking, crossing them as in a local reproduction, killing an individual chosen uniformly at random from all 32, and placing the offspring in the subpopulation the dead individual was part of.

Two details conclude the description of the global level, and of the model overall: First, on successive festival days, the *phase* of the assembled quads is shifted, so that after four festivals, any given cell will have interacted with all eight of its

neighbors. Second, in the case where it is possible to have *windy festival days*, the festival occurs first, and then the wind blows.

3 Case studies: Results and Observations

As the previous section should have made clear, although our model is but a pale shadow of even a small natural world ecology, it is a significant computational challenge. Despite efficient programming, the running time for each simulation reported here is measured in multiples of weeks. As a result — like many natural world experimenters, but unlike most artificial life researchers — we have not had the luxury of running many repetitions of each model variation to assess noise sensitivities. This is significantly less worrisome than it would be in a smaller model — for example, since we have over sixteen thousand subpopulations being simulated in parallel, random variations in the initial subpopulations tend to average out *spatially* in the early stages of a single run — but nonetheless, fair warning should be given.

We have focused on longitudinal empirical explorations, performing an extended simulation of each of three global strategies: wind-only, wind+festival, and festival-only. The festival-only strategy was so successful that we invested in a second run, varying only the pseudo-random number seed. Although the runs were unique in many details, the qualitative phenomena we discuss below appeared both times.

3.1 Case 1: Wind-only

In the first variation we used wind migration, with every fifth day being windy. We ended up letting it run for 13,110 simulated days before deciding we had seen most of the phenomena it was going to display. Some overall statistics are summarized in Figure 2. The upper curve represents the highest average behavioral score for a subpopulation and the lower, dotted curve displays the average of all behavioral scores over the entire array. The individual dots are average behavioral scores for randomly-selected subpopulations to help show the spread in the population. The average steadily grows and ends up just shy of the -12 mark. The mode subpopulation is -56 from around day 1000 to almost day 3000. From then on, the -12's dominate the array — the sample dots fuse into a line.

As we watched that data coming in, at first we were excited, when the maximum behavioral scores jumped to 42 — communication was definitely beginning to happen! — and then

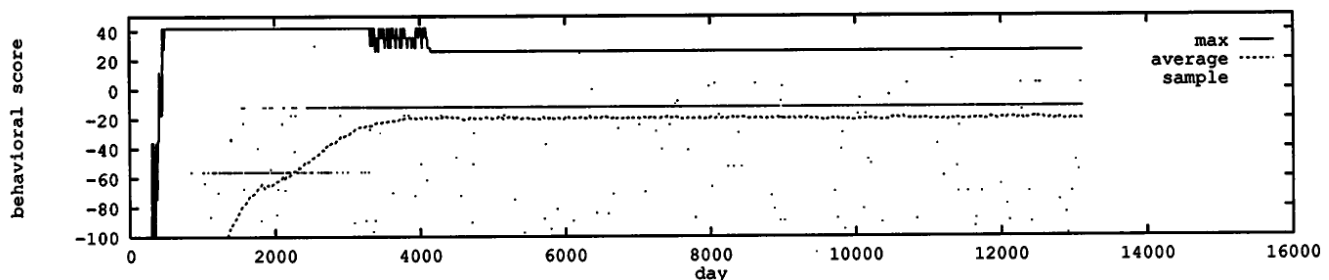


FIGURE 2. Behavioral scores versus time: Case 1 — Wind-only

we were disappointed when they fell back to 26, since it was “heading the wrong way” and we knew from first principles there were communication strategies that could score far higher than 42.

Our understanding was aided by watching “movies” of the spatial dynamics, based on data files written by the simulator. Plate 2 consists of six *frames* taken from the wind-only simulation. Each frame contains 128x128 pixels, one for each subpopulation, each assigned a color on the basis of the average of the behavioral scores in the corresponding subpopulation on a given day. The mapping from behavioral score to solid and horizontally striped colors, shown at the bottom of each plate, was chosen only to highlight score differences, and it is repeated beneath each of the frames along with a compressed histogram of the number of subpopulations versus subpopulation-average behavioral score.

We made movies for each of the model variations, and all shared distinctive features, supporting the idea that many of the effects are repeatable and depend more on the overall structure of the model and less on noise effects specific to a particular case. The following discussion of the initial part of the wind run can serve as an introduction to early features shared by all the cases.

We refer to an organism type by the score it obtains in a subpopulation of “clones,” since that is deterministic. A creature described as, say, a “26,” may receive a completely different score in a mixed population.

The nature of the neural architecture and the developmental process is such that, for a randomly generated genotype, by the far the most probable resulting behavior pattern is never to move at all. Such individuals receive behavioral scores of -696 and are so common at day 0 (Plate 2a) that subpopulations made up entirely of such stiffies are the most common shade of grey in the first frame. These sessiles are soon rooted out by more active strategies, which have spread and taken over small patches of the array by day 430 (Plate 2b).

By day 1620 (Plate 2c), more improvements have been discovered and spread to the majority of the array. The most popular organisms at this time score -56 and appear dark green. The -56's combine a default strategy of running to one end of the track with an overriding strategy of running the other way if a predator is seen. The medium green subpopulations visible in the same picture consist of -12's, which implement

the same strategy as the -56's except that they default to whichever end is nearer at the start of each trial. As mentioned in Figure 2.1, this is actually the best a non-communicating individual can do.

By day 3800 (Plate 2d), these self-reliant creatures dominate the array, forming the global “cellular” structures typical of these simulations. The borders between regions usually have lower behavioral scores resulting from crosses between incompatible organisms. (Some properties of such *mixing zones* are discussed in Ackley & Littman, 1994).

In all three cases we've explored, patches of communicating individuals do arise and expand. Some examples are visible in Plates 2c – 2f as yellow/orange (26's) and light green (4's) patches. Under the wind model, however, these communicating subpopulations are ephemeral. Before growing large, they are squeezed out by -12's that have discovered ways to mislead and deceive them. As we observed the wind model dynamics, we realized we “could have predicted it”: After each windy day, at least potentially, “you'll be talking with strangers”, so kin altruism has a hard time stabilizing, and cheaters have an easy time invading.

From that perspective we were impressed that, from day 4150 until we killed the run, the 26's manage to stave off extinction without ever controlling more than a handful of subpopulations at a time. They seem to survive because they “trust their ears” only in limited circumstances: Most of the time they follow the optimal non-communicating strategy of the -12's, and rely on signalling only to avoid fleeing from one predator to the other in the dangerous Left Pred/Right Pred trials. Given the “anything goes” nature of wind, the emergence of such “cautious communicators” was a satisfying result.

3.2 Case 2: Festivals and wind

Despite the persistence of the cautious communicators in the wind run, they never manage to hold a significant portion of the array for very long. We devised festival reproduction to increase the cohesion of groups in the hope that cautious communicators might be able to stabilize and more trusting communicators might appear.

Festival reproduction is in a sense a score-sensitive migration mechanism since only individuals with behavioral scores in the top quarter of their quad are given opportunities to reproduce into neighboring subpopulations. We expected that us-

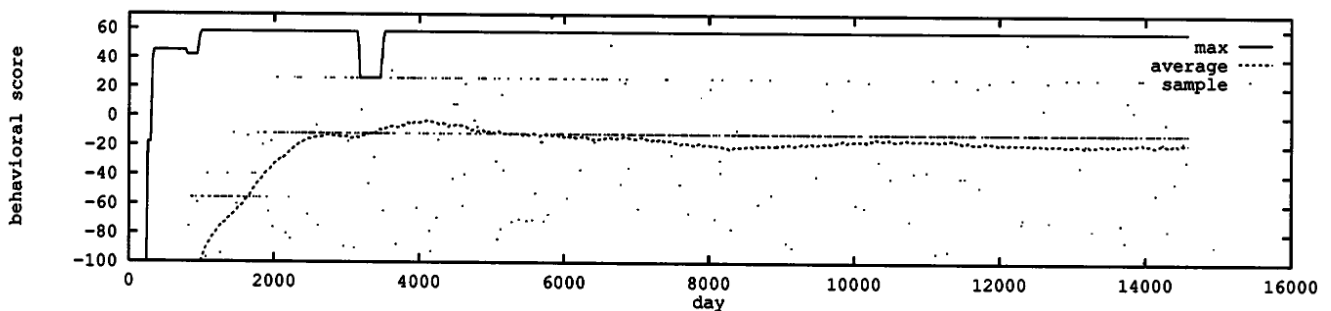


FIGURE 3. Behavioral summaries versus time: Case 2—Wind+festival

ing more festivals than wind would allow for greater stability of high scoring subpopulations, and greater resistance to intruders from other subpopulations.

We ran the simulator with festival reproduction every other day and wind migration every 10th day for a span of 14,580 days. Our predications were only partially borne out, as can be seen in Figure 3 and Plate 3. In the figure, notice that the cautiously communicating 26's are populous enough to be clearly visible in the random samples. Furthermore, for a brief time between day 3000 and day 5000, the population average actually exceeds -12: The average subpopulation was communicating.

Plate 3 tells the story of ongoing battles between cooperating communicators and competing individualists. By day 2000 (Plate 3a) a large cast of characters is onstage: dark green -56's, a rogue's gallery of green -12's, a vigorous species of yellow/orange 26's, and a colony of orange/red 58's. Over the next several hundred days, the 26's spread over the -12 species east and west of them, even as embedded species of -12 eats them up from the inside. By day 3440 (Plate 3b), the 26's hold substantial territory, but have been chopped completely in two by the (no-longer-embedded) -12's. Also, a group of light green 4's can be seen overrunning a patch of -12's (right of center). By day 4020 (Plate 3c) those 4's have been taken over by orange/red 58's, while marauding -12's continue to pressure the (now-reconnected) 26's.

The balance of power shifts over a few thousand days (Plates 3d and 3e) and by day 8400, few communicating species remain. A reemergence of 58's around day 11,000 (Plate 3f) is soon quashed by disruptive breeds of -12's. Communicators spread farther and faster in the wind+festival model than in wind-only but they are still unstable.

3.3 Case 3: Strictly festival

Wind migration tends to favor disruptive species, allowing them to infect and parasitize communicating species. By permitting migration by festival reproduction only, we hoped to

shift the balance still further towards group-cohesion. We ran the simulator using festival reproduction every two days for 99,980 days. A second run of 26,400 days yielded similar results. Only the longer run is reported here.

Figure 4 shows the behavioral summaries for the run. The global population average behavioral score exceeds -12 around day 5000, continues to rise through most of the run and reaches almost 100 — though that sharp decline in the average behavioral scores in the mid-20000's demands investigation.

Plate 4 illustrates some of the history of this run. Early on (day 2000, Plate 4a), the array is dominated by growing -12's (green) and dwindling -56's (dark green) but two large communicating populations (both orange/red) have appeared. On the left is a species of 59's, on the right, 58's.

By day 5600 (Plate 4b), species of -12's have taken over the entire array except for the two orange/red areas and a third light red patch of 62's that is just beginning to be conquered by a species of 142's (pink) — then the most successful communicators discovered.

As time passes, the 58's and 59's expand, and cautiously communicating 4's (light green) slowly replace the background species of -12's. At day 20,700 (Plate 4c), a group of striped orange 42's is growing from the base of the 142 patch, and the 58's and 59's have just met up. In direct competition, the 59's dominate the 58's and overrun their positions in the array. The leading edge of the 59 invasion wave is visible in the frame.

The increased genetic diversity resulting from the flood of 59's mingling with a new set of genes results in several breakthroughs which hone the 59's into individuals scoring 71 (dark red). At day 24,340 (Plate 4d), the new species can be seen sweeping back across the territory of the former 59's. At the same time, however, another new breed has started to spread. Individuals of this breed score an abysmal -175 when cultured in isolation yet they displace the new 71's very

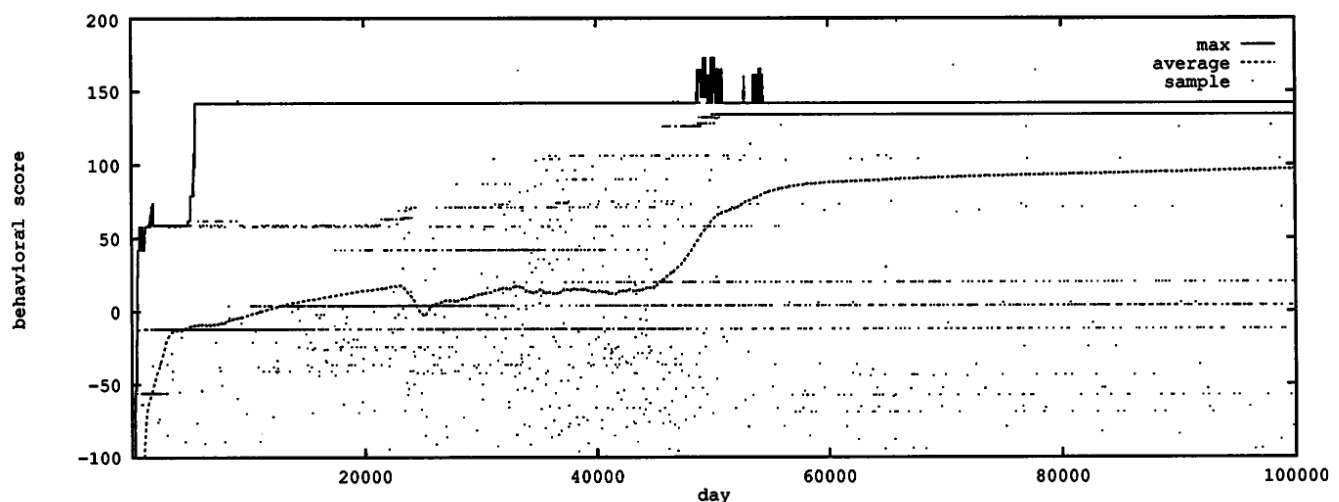


FIGURE 4. Behavioral summaries versus time: Case 3—Strictly festival

rapidly. The -175's decimate the 59/71's only to be eliminated themselves by opportunistic -56's and then -12's. By day 48,780, Plate 4e, only traces remain of the orange/red populations.

That is the sequence of events that caused the temporary crash in the global average, and it highlights a basic difference between this world and the function optimizations performed by conventional genetic algorithms. The fitness scores in a GA form a total order — any pair of individuals always stand in the same relationship to each other: more, less, or equally “fit.” With subpopulation-dependent behavioral scoring, there is no such simple dominance. In this particular simulation, for example, the 71's are “more fit” than the surrounding -12's since they slowly displace them. The -175's are “more fit” than the 71's since they destroy the 71's in direct contact (see the next section) but, completing the circle, the -12's are “more fit” than the -175's and tend to replace them in the population.

By day 48,780 (Plate 4e), the after-effects of the 58-59 collision have mostly died down. The pink 142's still hold nearly the same area of the array and a sequence of species has arisen from the ashes of the earlier conflagrations. These consist of 126's, 128's, 132's and 134's, and appears as various shades of pink spreading up towards the 142's. Over the next 50,000 days (Plate 4f), the dark pink 134's conquer most of the world. Successful communication dominates.

3.4 Analysis: War and Pestilence

The stories and pictures in the previous sections suggest the complexity of the evolution of communication in our simulations, but such global stories only describe *what* happened. To understand *why* things happened we must delve into the local and individual levels of the model.

Similar to Ray (1991), we use *culturing* to analyze interaction effects between various species at the local level. We take a sample of two evolved genotypes, call them A and B, from the simulator's data files. Using the local level of the simulator, we find behavioral scores for a subpopulation of 8 A's. Because of the way the evaluation procedure is designed, an individual cultured with clones will always receive the same behavioral score.

The score tells us how a completely converged subpopulation of A's would do “in the wild.” We also evaluate a population of 8 B's, and then do 50 evaluations for each of the 7 possible combinations of *i* A's and 8-*i* B's. The results show how the scores of A's and B's change when in contact with members of the other species. (Note that they tell us nothing about the result of *mating* A's and B's.) We plot the results for both species as a function of the number of A's, with 95% confidence intervals if there is any variation.

As an example, we used this tool to examine the evolution of the -12's. Figure 5 shows the result of culturing two different species of -12's, an “archaic” breed from near the beginning of the festival run and a more “modern” one from close to the end. Though both species score -12 when cultured with clones, and also in silence (determined in a separate experiment), the archaic -12's obtain terrible behavioral scores in the presence of even one modern.

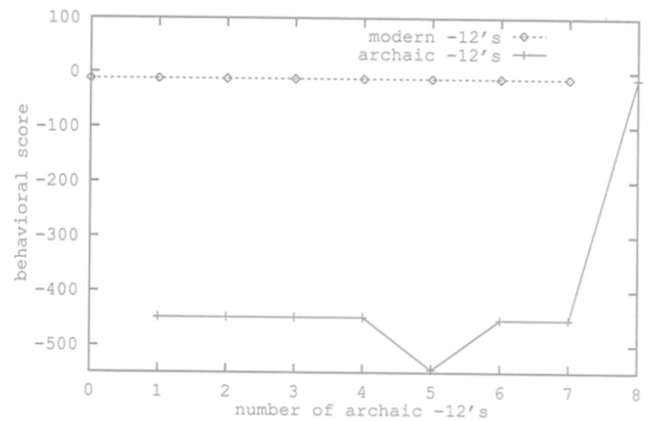


FIGURE 5. Archaic -12's versus modern -12's

The keys to success for the modern -12's are two abilities: On the one hand they are broad-spectrum noise generators, and on the other hand they are themselves resistant to ambient noise. They are “ether warriors”: They jam the signals of communicating groups, and confuse organisms that are sensitive to the ether, even if they don't signal themselves. An examination of the neural networks of these two species shows this clearly. The archaic -12's are sensitive to sounds on several channels and speak on F. The modern -12's have no “ears” at all and they are “wired for speech” on all channels (although only CDEF seem to occur in practice for this breed). They pollute the ether — tending to lower the score of communicators in the subpopulation — without affecting their own scores at all. Such “scorched ether” strategies are very common in the wind and wind+festival studies.

Under the festival-only model, it is generally not possible for one disruptive individual to enter and exterminate a high-scoring subpopulation without first understanding its signals. Thus, instabilities in this variation are of more subtle types. The fall of the 59/71's to the -175's is an excellent example of the takeovers that occur. The -175's are perfectly adapted not only to parasitize the 71's, but to wipe them out entirely. As seen in Figure 6, a single -175 in a population of 71's ex-

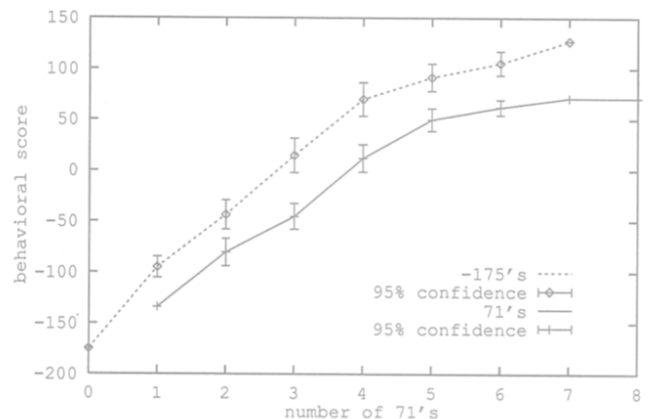


FIGURE 6. Altruistic 71's versus parasitic -175's

plots the signals generated by the 71's to obtain a superior behavioral score. The -175's are then preferentially reproduced — there tend to be more -175's and fewer 71's. Al-

though both species then score worse than they did when there were more 71's, in every possible combination, the -175's score higher. The 71's in the subpopulation are soon exterminated.

There is a second critical factor in the -175 epidemic discernible in Figure 6. Recall that in this simulation, the only way to migrate is to win at festivals. For taking over a single cell, all that is necessary is that the attacker score better than the defender in the cell: An invader to a group of 71's, for example, could take it over by scoring 50 if it could confuse the 71's into scoring 40's. In such a case, though, the invader would never win in festivals with adjacent uninfected groups of 71's. It would be stuck. In Figure 6, by contrast, we see that the canny -175's obtain scores that win festivals against neighboring 71's even when they've taken over fully half a cell, providing plenty of time to infect neighboring subpopulations before the inevitable crash.

An examination of the genomes reveals that the -175's are closely related to the 71's they wipe out, sharing 97.8% of genes. A naive notion of kin selection might predict increasing altruism with increasing levels of genetic overlap, but clearly this need not be. On the contrary, by sharing genes with the 71's, the -175's are in a good position to understand their signals and thereby exploit them.

4 Discussion: Mutation and Migration

We have demonstrated that effective communication based on the exchange of initially arbitrary signals can evolve and stabilize even when it provides no benefit to the individual speaker. We believe that the principal feature of our model that makes this possible is the *partial* alignment of communication and reproduction domains. To the degree they are the same, the potential beneficiaries of a speech act will tend to be close genetic kin to the speaker, and then the "kin selection" or "kin altruism" arguments from evolutionary theory (Hamilton, 1964, and many since) apply and one may hope to see the emergence of altruism. On the other hand, unless communication and reproduction domains are at least sometimes different, subpopulations will tend to converge, and the search for improved forms will be slowed. The case studies presented in the previous section only hint at the scope of the phenomena we have observed; here, we close with brief discussions of two issues that the models raise.

From an evolutionary computation point of view, perhaps the most striking aspect of these studies is that they make no use of mutation. As mentioned earlier, we were pushed to this design decision, against our own preconceptions, simply because it worked better — but what makes this case different?

In the majority of the evolutionary computation models in the literature, individuals are evaluated in isolation from each other. Consequently, the effects of a mutation are, initially, limited to only one individual. In our models — and in any co-evolutionary system in which relatively small groups of individuals can interact during the process of selection — the picture is quite different. Individuals in such systems will evolve towards *dependence* on the typical behavior patterns of the group they are part of whenever it provides an advantage. A mutation in one individual can have a much more dis-

ruptive effect, impacting other individuals immediately, in the same generation.

In his paradigm-creating book on genetic algorithms, Holland (1976) argued that crossover is more important than mutation as a genetic operator, and offered mathematical arguments for the hypothesis that the *reason* it is so important is because it improves the efficiency of an evolutionary search for highly-fit individuals. Although his arguments were insightful and elegant, in the nearly two decades of ensuing research, convincing empirical demonstrations in which crossover is more important than mutation have remained elusive; so much so that Holland has recently returned to this question, collaborating on a paper entitled "When will a genetic algorithm outperform hill-climbing?" (Mitchell, Forrest, & Holland, 1994, to appear).

Studying the evolution of communication, we are lead to propose a slightly different hypothesis: Crossover is a critical genetic operator, but not necessarily or even principally because it improves search in highly diverse populations. We suggest that the reason crossover is so important is because it amounts to a *convergence-sensitive variable mutation rate*. With a single mechanism, one can on the one hand generate radical new combinations when no particular strategy is dominant, as evidenced by a diverse genetic pool, while on the other hand preserve all the genetic structures that are "proven winners," as evidenced by their fixation in the population.

Note that to the degree that a system can be viewed as an isolated-individual optimization problem, with a "fitness function" that is stable over evolutionary time, Holland's account and ours are largely complementary takes on the same idea — "effective generation of new structures when diverse" versus "effective preservation of old structures when converged." In such systems his account is preferable because it makes non-trivial claims about why crossover's particular approach to new structure generation is desirable, whereas on the flip side there's basically only one possible strategy for old structure preservation.

However, to the degree that a system is best viewed as a co-evolving organization of relatively converged populations, where the behavioral score of assigned to a genome can change even if the genome remains constant, the situation is different. Clever search techniques that generate novel candidates by extracting information from behavioral scores efficiently are of less value, because the information necessary for success changes. On the other hand, the high-fidelity reproduction of individuals in converged groups has much higher value, because the group members can work together to improve all their behavioral scores if everybody cooperates. As we saw in Section 3, cheaters need not be strangers, so even "rare" changes due to mutation can have disastrous large-scale effects. We suspect many natural systems — and many human and artificial systems as well — are less like diverse population, static optimization problems, and more like co-evolutionary processes involving relatively converged populations. In such cases, crossover may outrank mutation, not because it searches effectively, but because it preserves selectively.

Still, even if this account of the roles of mutation and crossover is accurate, that wouldn't imply that the mutation rate

should optimally be reduced all the way to zero, as we did in the studies reported here. The uniformity of color over large areas in the Plates, for example, suggests that there are many converged subpopulations in which no search at all is taking place (although, as the lone pixel visible in the middle of the pink patch in Plate 4d indicates, even deep in apparently converged regions there are some usually-silent variant alleles that occasionally are revealed via crossover.) The preliminary studies that prompted us to turn mutation off were all based on wind migration. In the festival model, by contrast, perhaps a small amount of mutation could enhance the search process without disastrous global consequences, and this is a possibility we are pursuing.

More generally, these studies suggest that intra-population genetic operators may be less important than inter-population migratory mechanisms in determining the qualitative behavior of distributed population models with subpopulation-dependent behavioral scoring. As a comparison between the wind+festival and strictly-festival studies shows, simple score-insensitive migration — even if relatively infrequent — can have a dramatic impact on the dynamics of the system.

There is a sense in which score-sensitive migration mechanisms such as the festival are fundamentally questionable. Consider ourselves as humans: As members of a communicating species we are products both of our genetic heritage and the communities within which we reside. Though we carry our genotypes with us when we (or our offspring) migrate, the communities we depended upon are left behind. For the artificial creatures in the festival model, although the participating individuals compete on the basis of their behavioral scores, those scores were obtained back in the individuals' "home" cells, not in the context of the whole quad. Such a score may be wholly unrepresentative of how that genotype would perform in another cell (even in absence of any genetic modifications). Using individual behavioral scores to determine who shall cross a score-dependent border is, in a significant way, an unprincipled use of the data.

To the degree that neighboring subpopulations differ from each other, a festival is comparing apples and oranges. As the genocide of the altruistic 75's at the hands of the grossly incompetent -175's showed, sometimes it can go wrong with disastrous consequences for certain species. But — barring degenerate "group selection" mechanisms, wherein entire subpopulations compete, reproduce, and displace each other as units — what choice is there? We didn't even bother with parallel simulations of the no-migration case, since the sequential simulator showed us that completely isolated subpopulations converge rapidly to usually awful scores. Using wind amounts to refusing even to attempt to compare apples and oranges. Despite its perplexing theoretical motivation, the success of the festival mechanism suggests that it is a game worth playing.

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