In Search of the Roots of Social Complexity

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Abstract

This is a report on results from research that tested a hypothesis stating the aggregate phenomenon known to social science as clan-level social complexity can be explained computationally using the following theoretic components: human metabolic and bio-reproductive theory, nutrient seeking (foraging) behaviors, evolutionary theory, and a spatial ecology. To test this hypothesis an agent-based model was created wherein each agent had an artificial chromosome containing eleven genes (8-bits per gene) ten of which had independently inheritable, graded, and expressible traits like draught tolerance, temperature sensitivity, a robust metabolism, and improved fecundity in small-group settings, for example. The agents could move freely within a diverse 2D ecology, enjoyed caloric and water metabolic costs, and had human-like 28-day reproductive cycles with gestation and nursing metabolic adjustments. One simulation in particular ran for more than 200 agent generations of 6,421 simulated years. Reported here are results of that simulation, the changes that occurred in three of the eleven genes in the agent population under test as a consequence of artificial evolution, and how "sociality" may have begun to emerge in the population.

In Search of the Roots of Social Complexity

This work is part of on-going research that is attempting to understand the first principles of a complex adaptive system (CAS) known to social science as clan-level social complexity. To do this, an agent-based model (ABM) of human-inspired, self-mobile, reproductive, hunter-gatherer (HG) agents was constructed. Although, issues like the role memory may play in the process have been examined (consider Cioffi-Revilla, Paus, Luke, Olds, & Thomas, 2004), what is of interest to this work is the question of whether or not clan-level social complexity might emerge coincident with clan-level social-network organization and simulated genetic adaptation in a synthetic, spatial ecology.

To test this hypothesis, an ABM was constructed that featured climatologically distinct and spatially adjacent biomes, multiple independent and self-replicating software (agent) objects possessing artificial genetic structure and basic foraging rules, and three types of self-mobile prey and one type of stationary (edible) plant species as HG foraging options.

At simulation start, HG software agents were placed at random locations within the ecology as variously sized small-group cohorts. Placement was without regard to ecological biome or cohort size. Similarly, four prey/food species were also started or placed, respectively, at random locations on the terrain but were keyed to their associable biomes. In general, the ABM was a non-empirical abstraction of five selected ecological and climatological biomes, and several sources of agent nutrients believed to have relevance to the research question.

This is a report associable with the interim state of the foregoing research. That is, this verification test report describes results emanating from the model wherein instead of requiring the agent population to hunt/gather their own supplies of food and water, each group of proximally co-located agents in the simulation received an exogenous, constant, but constrained provision of food and water nutrients. This method of providing each co-located group of agents (defined as a cohort) with a constant nutrient allotment permitted the taking of baseline readings on the effect of environmental supply-side change (implicit carrying capacity effects) on individual agent artificial physiology and genetics. Additionally, this experimental procedure allowed for the evaluation of the underlying evolutionary algorithm functions and the performance of the individual agent non-cognitive behavioral drives over thousands of simulated years without fear of entire populations of agents crashing for unexplainable reasons. For example, in a later section of this report, we will be able to literally see the genes for draught tolerance (gene 1), robust metabolism (gene 2), and fertility scent (gene 6) evolve over time throughout the agent population in clear-cut, graphical, and decisive ways.

Therefore, this report concerns itself with such results from the experiment as described. An edited and detailed software design/description document appears in the Research Methodology section. (Presumably, this section will be of use to those with interest in understanding the experimental method used although it does contain some test results.) The majority if the test results are presented in the Results and Discussion section.

Research Methodology

The general area of research was that of self-organizing complex systems. The specific area of interest was that of systems demonstrating emergent and self-sustaining social behavior. The research method was the construction, operation, and post-operation result analysis of an agent-based computer model. Thus, an ABM was constructed to allow examination of the behavior of computer agents existing at the boundary between individual and emergent clan-level social interaction. The model was constructed using only the following components modeled in computer code: rules representing human metabolic and bio-reproductive theory, rules for non-cognitive nutrient foraging, a simple genetic metaphor (inspired by Goldberg, 1989), an abstract model of terrestrial ecology, and no a priori constructs of social organization. Following in the steps of previous ALife researchers (for example Yager, L. 1994), the ABM constructed represented a set of abstract biomes, situated and discrete (agent) software objects with metabolic, bio-reproductive, foraging behavioral rules, and foragible sources of nutrients. What follows now is an edited version of the software design and description document for the ABM created for this report.

Simulation component overview

An individual-based model was created in Java and was based on a spatially explicit and ecologically grounded metaphor. The model had three components: a set of five geometrically defined biomes, a set of four prey species keyed to the biomes, and human-inspired HG software agents capable of object self-instantiation.

System simulation epoch

An epoch was defined as a complete pass through the simulation wherein all appropriate software modules were executed and the result was a single time-step update of all emulated parameters. The least unit of simulated time was one epoch. In this simulation, an epoch was one day and 365 days were one year. The epoch was used for software component synchronization and developing agent migratory, reproductive, and predatory emulations.

System biomes

These were spatially explicit, non-empirical, geometric divisions (polygons) defined on an n x m grid. The polygonal divisions were surrogates for niche ecologies (biomes). Each biome was an abstract representation of a stereotypic climatologic, faunal, and or floral ecology. The five biomes modeled were Desert, Estuary, Forest, Grassland, and Tundra. Biome Cartesian coordinate boundaries did not overlap although temperatures and prey species movements were distributed across the biomes. See Figures 1 and 2. Drinking water existed in probabilistic quantities in all biomes at all times everywhere. The exceptions were those areas

geometrically near (or within) the Estuary (river or lake) areas. These areas always had abundant water.
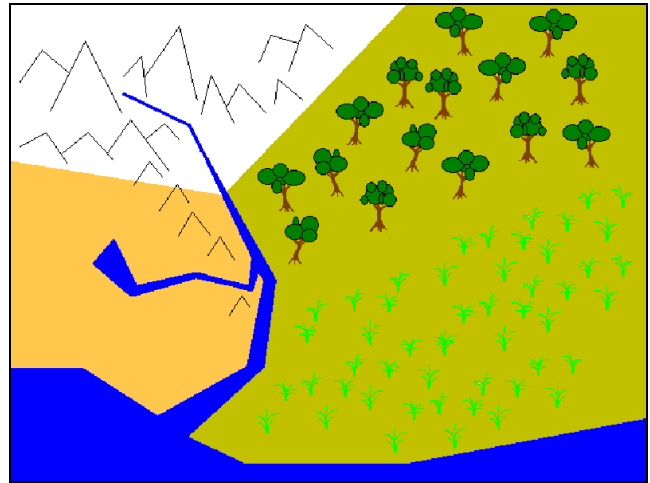

Figure 1 Cartoon-like abstract of five climatologic faunal and floral biomes. These graphically distinct biomes (Tundra, Forest, Grassland, Estuary, & Desert) provided the user with reference to agent location, qualitative insight into agent circumstance, but not empirical quantification. In operation the bison, deer, fish, maize, and HG agents were shown as individual color-coded pixels moving across the terrain interacting with one another.
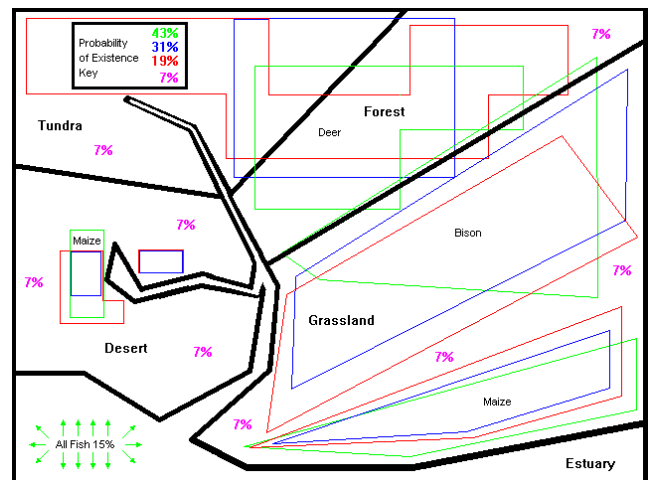

Figure 2 The simulated terrain was 800 x 600 cells in size. Prey/Food items were assigned to their respective biomes within the limits of probabilities similar to those shown in this early requirements graphic. Interlocking polygons used in the simulation were also similar to those shown above.

System simulated terrain

The simulated terrain was made up of a matrix of software objects one cell deep distributed across, and completely

covering, the n x m grid area described in System biomes. At program start and synchronized with the simulation epoch (as appropriate), each cell object had properties that included: the biome name (Desert, Estuary, Forest, Grassland, or Tundra); available water; a graded and real-valued temperature derived from a qualitative assessment of each respective biome; foraging opportunities over prey (Bison, Deer, Fish, or Maize); a set of probabilities associable with the existence of the foraging opportunities each prey species contributed to the biome; variables for recording Deer and Bison sign in recent (epochal) history; and others.

System prey within biomes

Each biome supported at least one prey species. Prey/food species, as software objects, maintained their own records for number of animals in a herd, the location of a herd, school, or field, trajectory of herd motion, etc. Species reproduction was not modeled except for seasonal maize production.

Deer and Bison moved across the inter-biome boundaries of Tundra and Forest, yet were defined independently. Maize could move between Grassland and Desert if transported by female HG agents. Fish movements in the Estuary (all water areas) were defined by rules in prey Fish. [For brevity sake, detailed definition of the prey/food properties and their epochal updating is not discussed here beyond the minimum of what is needed to understand the model. For example, caloric value of the flesh of eaten prey or the duration of edible freshness of each respective species is not discussed but was modeled.]

Prey motion within biomes

Self-mobile prey moved within their respective biomes in straight lines until encountering a map probability boundary or the non-torodial system grid limit. When boundaries were encountered, new (random) directions could be taken at the next epoch. Alternatively, the prey movement could momentarily cease or instantaneously start. Effectively, mobile prey moved like "bouncing balls" sometimes passing through boundaries, other times "bouncing" off, halting or moving under random control but always within the respective biome/prey probability and grid limits.

HG agents

Each HG agent was a software object that modeled a simplified, self-mobile, and reactive predator. Male and female HG agent objects were simulated. The percentage of male to female agents was slightly skewed. The initial number of agents (at program start) was adjustable but set to 256 for the experiment reported here. Those agents instantiated at program start were divided into small groups of 1 to 15 member cohorts that in turn were distributed randomly about the terrain. Agents were free to remain in their cohorts or to self-navigate about the terrain. Cohorts were defined as proximally co-located HG agents that

shared common food, water, and a foraging-related technologies, i.e., water containers and simple tools. The explicit definition of proximally co-located is "in the same terrain cell."

Agent census data (beyond the initial population of 256) was knowable only when an HG agent ceased to exist (experienced simulated death) and exited computer memory. At the time of an agent death, the simulation issued a certificate. A typical example of accumulated annual census data is shown in Figure 3. This record
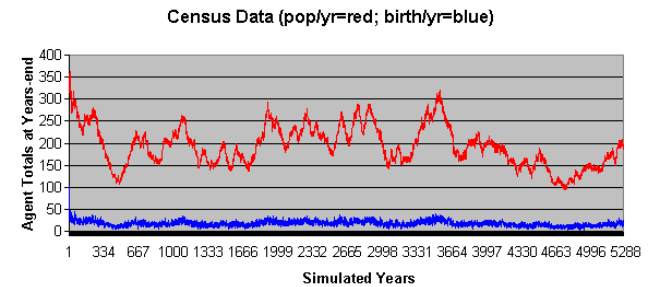

Figure 3 5,288 simulated years after program start, this accumulative census data strip was produced. The red line is the head-count of living HG agents in the simulation (shown per year). Similarly, the blue line is the number of births (also shown per year).

included agent date of birth, date of death, mother ID, father ID, location of birth and death, and several other data. Additionally, the total and momentary counts of agent births, deaths, and agents currently alive were reported on a simulated annual basis.

HG agent migration

HG agents were able to migrate between cells on the terrain grid and between biomes within the simulated ecology in order to locate size-discriminated and size-preferred social groups, in order to find mates, in order to avoid uncomfortable environmental temperatures, or in order to locate prey/food or water. Agent non-cognitive drives reacted to environmental properties, events, and multi-agent "social" situations to produce what might be described as complex migratory and in-place "social" behavior. Agent behavioral and run-time "life" trajectories were highly path dependent (combining stochastically) and demonstrated a high degree input variable sensitivity.

HG agent non-cognitive drives

There were four drives reduced by non-cognitive means within each agent: a drive to inhabit a comfortable temperature environment, a drive to be in a social group of some particular size determined by individual agent genetic propensity (literally a single 8-bit gene value), a drive to eat, and a drive to drink. No a priori cognitive mechanisms were emulated in the HG agents. No inherent social structures of kin or clan-level behaviors were

assumed or modeled. The intent was to model selected HG agent drives that were reactive mechanisms inspired by biological and sociological first principles observed across human cultures and across higher primate species.

HG agent genetic basis

Upon instantiation (birth), each HG agent was given its own unique eleven gene (8-bits per gene) chromosome. There were ten inheritable genes embedded in each chromosome with the eleventh 8-bit gene holding a gender bit. Inheritable properties included draught tolerance, temperature sensitivity, a robust metabolism, a tendency toward or against improved fecundity in small-group settings, enhanced or diminished visual acuity, an enhanced or diminished capacity to maintain a continuous long-distance self-movement capability, sensitivity toward plant versus animal protein digestion capability, and three others. In all, there were eleven genes simulated with each "keyed" to some aspect of physiological survival or socio-behavioral complexity in the agent/ecological environment.

At HG object instantiation (birth), integers were encoded in each gene as independent Gaussian distributions expressed as values of 0 to 255, one per gene, in each respectively. The one gene that contained the agent gender definition was mapped as a byte of eight discrete bits. Only the gender bit was active in this gene. See Table 1.

Table 1 Eleven 8-bit genes unique to each HG agent

g0	DISCRETE_FACTORS_GENE (b0 gender)
g1	DRAUGHT_TOLERANCE_GENE
g2	ROBUST_METABOLISM_GENE
g3	ROBUST_UPPER_BODY_GENE
g4	QUICK_TWITCH_MSCL_GENE
g5	LONG_DIST_RUNNING_GENE
g6	EMIT_FERTIL_SCENT_GENE
g7	OLF_DEER_URIN_SNS_GENE
g8	GEN_VISUAL_ACUITY_GENE
g9	PROTEIN_DIGST_TOL_GENE
g10	TEMPERTURE_SETPNT_GENE

HG agent life span and generations

An agent lifespan was defined as the period starting from the date of agent instantiation (birth) until agent exit from computer memory (death). The oldest agent age recorded during the experiment reported here was 43 years. Figure 4 shows data from 4,259 years after program start (APS). A generation was defined as the longest shortest path between all agents in the entire HG agent network taken over all agents ever instantiated into that network. Thus defined, the average value of an agent generation depended on the total number of agents having existed from program run-start to that moment the statistic was calculated. Values ranged from a low of 19 years to a high of 41. For example in the year 2260 APS, a generation was 19.8 years. In the simulated year 1803 APS, it was 26.1 years.
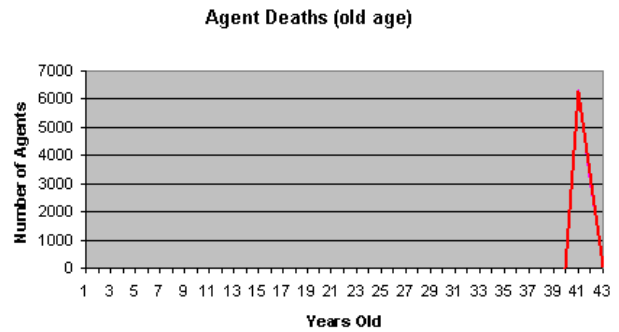

Figure 4 If no other disease pathology, malnutrition, or lack of water killed an agent then old age would.

Agent lifespan was truncated by an exponential decay function as shown in the accumulated totals chart in Figure 4. However, far more typically, agents died in infancy or due to starvation, or under dehydration conditions. Figures 5a, 5b, and 5c show data on each of these respectively accumulated totals (as percentages) up to year 4,259 APS.
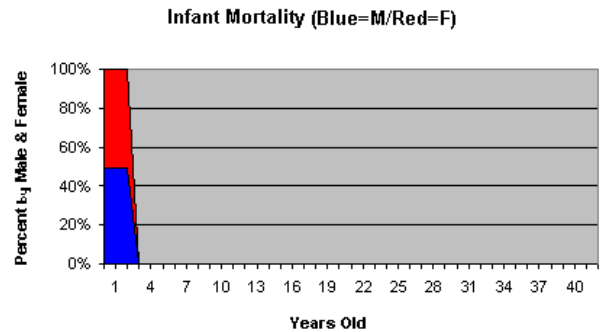

Figure 5a Undifferentiated for cause of death, during infancy infant mortality claimed lives with unbiased gender equality.
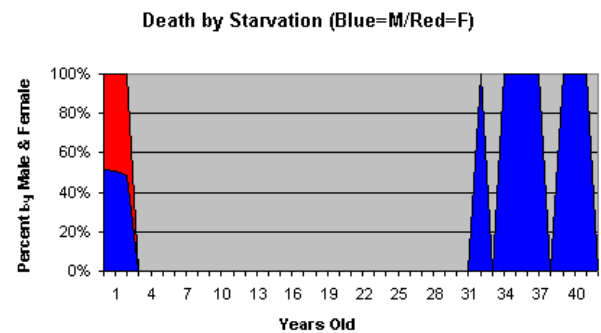

Figure 5b However, over the entire 4,259-year period and in spite of plentiful resources, males appear to have suffered from starvation more often than did females. Infants too often died due to their mothers premature deaths (likely from her dehydration). Surrogate (wet) nursing was not modeled.
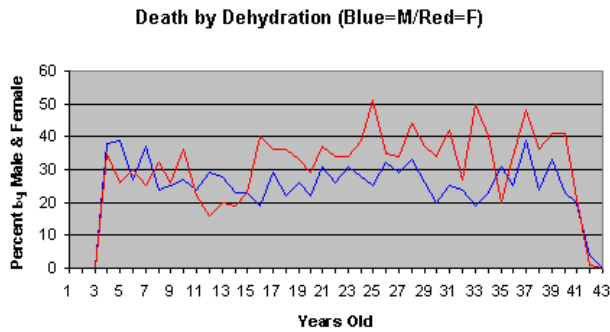
Figure 5c By far the most significant source of mortality, simulated water constraints weighed on the HG population as the single greatest determinant of terrain carrying capacity. The accumulated toll of deaths from dehydration shows a subtle (but important) detail in the red line of female water intake. Females became fertile at age 15 in the simulation. Notice the sudden increase in water related deaths for females after they (ostensibly) began to gestate and nurse when (if) they became pregnant.

Since agent food and water requirements were supplanted exogenously, agent internal drives to forage were "turned off." Thus, it was possible to stress the agents to the point of death by using the complex interaction of simulated metabolic biology and artificial genetics. Figure 5c is an example of that in action. Each cohort received a simulated 25 pounds of food calories per day but only 9.9 gallons of simulated water. Thus, before the cohort population was sufficiently large that gene 6 (a fecundity and group-size related gene) could begin to drive agents to relocate to other less populated areas, the constrained water supply, i.e., the terrain carrying capacity for water, would begin to stress the agents. Typically, such mortal stress was first and more devastatingly felt by the pregnant and nursing female population as shown above.

Additionally, catastrophic cohort loss (death of all proximally co-located agents) was possible in the simulation as was individual agent disease death. There was no record of the former in the annual records. Such an occurrence existed in the simulation to allow for the possibility of a cohort loosing a life-dependent technology, for example, or a fast adding natural calamity. The later cause of death (death by disease) however, manifest itself as an accelerated chronic wasting syndrome and was thus recorded on the death certificate as starvation even though the cause could have been an unnamed pathology that resulted in the same fatal syndrome.

HG biology: nutrition

From age 0 to 3 years all agent water and caloric nutritional requirements were satisfied by the mother of the agent. If the mother died during this period then, the 0 to 3 year old infant object died too. Surrogate (wet) nursing was not modeled.

At age three infants, both male and female, were reclassified as juveniles and started taking their nutrition and water from the cohort common supply. The taking of nutrition continued to be the responsibility of each individual agent until their death with the added requirement that agents were responsible for taking part in whatever foraging took place in the terrain cell currently occupied and thereby directly contributing to the cohort common supply. Details of this activity will be reported in a subsequent report.

Annually, the caloric and water requirements of each individual agent were recalculated in general and in addition at the beginning of reproductive gestation and the end of infant nursing for females in specific. Two simple probabilistic linear relations were used to set body weight and water requirements for all agents based on gender and age. That is, one was used for males and the other for females, respectively. All subsequent agent food and water utilizations were based on this calculation. During gestation and nursing, female requirements for food and water were adjusted upward.

HG biology: reproduction

At program start, agent ages were randomly distributed between 15 and 35 years, all agents were sexually mature, and none was pregnant. During program execution, female agents could become pregnant and give birth (instantiate) up to eight simulated offspring from the time of their individual puberty (onset of simulated menses tracking) until their death.

In female agents, a human-like reproductive cycle of 28 days was modeled. The reproductive cycle had five days of fertility followed by a 23-day non-fertile interval. There was a genetic tendency (based on the value of gene 6 in the female) for female agents to present as receptive to potential mating more frequently if their cohort had less than 7 members (regardless of actual cohort gender makeup). The likelihood of increased mating presentation stepped downward for cohorts with greater numbers.

Males also had this gene and expressed their phenocopy behaviors as a preference for relocating into cohorts with seven or fewer members (inspired by Hill & Dunbar, 2002). If selected for mating by a presenting female, a male agent would have (at minimum) their chromosome copied into the female object for later cross-over use in simulated birthing post-gestation. Conception was a certainty if mating occurred. Simulated genetic mutation completed the Genetic Algorithm.

Immediately after conception, a female agent began to gestate. After a 252 day gestation period (9 months), a female agent could give birth to an offspring (causing the system to instantiate a separate infant object) if the mother herself survived the 252 day interval. Females nursed their offspring for a 1095-day period (3 years) after giving birth. After nursing and weaning her offspring (assuming the offspring survived), a female was able to repeat the mating, gestating, nursing cycle when her first fertility interval returned. If her offspring died during the 3-year nursing

period, she could also repeat the mating-birthing cycle when her first fertility interval returned. As previously stated, in this way a female could birth (instantiate infant objects) up to eight times in her lifetime. During the 3-year nursing interval, females produced no new offspring in a manner similar to that of other, related higher primates (e.g., E. Lonsdorf, personal communication April 16, 2009). Male agents were not required to be alive or present at the time of the birth of their offspring.

Results and Discussion

The software has been run several dozen times, often continuously for several real-time days. This report describes one occasion when the code ran for a period of 6,421 simulated years or about three real-time days. On that occasion and during those simulated years, all of the initial 256 cohorts either died-out or self-relocated (spatially) to form one extended colony in the Grassland biome. That colony of agents self-organized into "genetically strongly-related and spatially adapted small-group cohorts." This was an important first step toward supporting the hypothesis. The several social-network graphics that follow will help support and illustrate this claim. The colony just mentioned flourished until it was voluntarily extinguished at 6,421 simulated years. When the simulation ended, it had instantiated an estimated 200 generations of HG agents calculated using intervals of about 32 years per agent per generation.

What follows is an inspection of genes one, two, and six as they were expressed within the HG population from simulation start to the simulated year 4,259 APS. It can be seen in the graphics that follows that a web of artificial life (a complex adaptive system) emerged as the rules of cohort mechanics, biological drives, and a spatial ecology interacted.

Genetic component results

Each HG agent had eleven genes. For this report, three genes are reviewed at two different times in the simulation lifespan. It is easy to see how the genetic metaphor provided a powerful aggregating mechanism that stimulated socio-spatial order to emerge among the agents using the nutrient provisioning paradigm discussed earlier. A final review of the behavior of the agents with the other seven genes is forthcoming in a separate report when completely self-responsible foraging will be enforced.

Gene 1: Draught tolerance. This gene was expressed equally across male and female agents. The Gene 1 phenotype endowed an agent with a metabolic advantage during periods of environmental water shortages. Figures 6a & 6b show their distribution and value within the population at two different times: 148 and 4,259 APS.
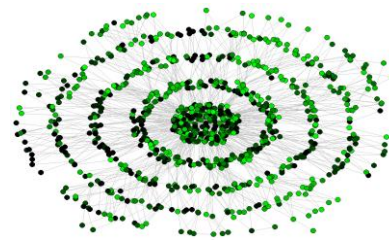

Figure 6a Gene 1 was involved with agent metabolic tolerance to intervals of water shortage. While the concentric circles (a "tree ring" effect) are an artifact produced by the NetDraw (Borgatti, 2002) rendering engine, they also show the individual generations of HG agents emanating from a common ancestor. This graphic depicts the entire HG "family tree" in the year 148 APS. Only agents over 3 years old are shown. Each ball is an HG agent. The gray edges are isMother or isFather social-network features. Agents are gender non-differentiated. The shades of green correspond to the gene values, i.e., dark values are nearer to zero and brighter colors are nearer to 255. Brighter colors were more desirable.
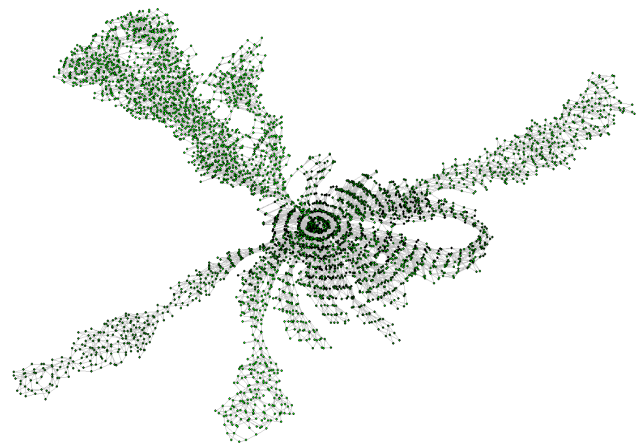

Figure 6b This graphic shows the extent to which gene 1 "evolved" and had spread within the population by the year 4,259 APS. The radial arms emerging from the core were spatially independent cohorts. The "tree ring" effect emanating from the center outward remained evident. Over time, only the "green" adapted extension in the upper left corner of the graph survived on the terrain as a contiguous cohort until simulation end. Gene 1 values converged toward 255 in the surviving cohorts.

Gene 2: Robust metabolism. This gene expressed itself equally across male and female agents. Gene 2 gave a metabolic advantage to agents undergoing an interval of starvation related to environmental food shortages. Figures 7a & 7b show their distribution and value within the population at two different times.
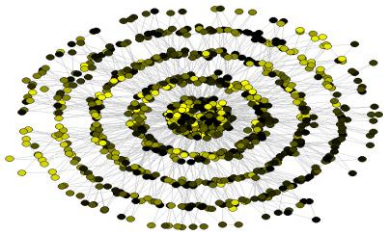
Figure 7a An image of the entire HG "family tree" taken in the 148th year APS shows gene 2 in color codes. At agent birth (instantiation), each gene in the agent chromosome was assigned a unique, Gaussian distributed integer in the range of 0 to 255. This was true for all genes. Here, as with gene 1, the shades of color correspond to those integer values. Values nearer to 255 are brighter yellow. Those darker colors are nearer to zero and proved to be more adaptive.

Figure 7b This graphic shows the extent to which the gene 2 "evolved" and spread within the population by the year 4,259 APS. Over time, only the "dark" extension in the upper left corner survived in the ecology to reach voluntary extinction. The gene 2 values converged toward zero in the surviving cohorts.

Gene 6: Fertility scent. This gene was inspired by recent discoveries in human reproductive science (Gangestad, Thornhill, & Garver-Apgar, 2005) and social-network size (Hill, 2002). Although it expressed itself differently in males and females, this gene had a similar purpose: to control cohort size. In males and females, this gene drove the agent to prefer the company of small-groups over larger ones. That is, more intimate groups. It could be decisive if the agent was relocating and other drives had been reduced. This was demonstrated clearly in the simulation. In females however, it also acted to increase the probability of mating presentation if the current cohort had fewer than seven members. It offered a diminished

incentive in larger groups. Figures 8a and 8b depict this gene in the HG population under test.
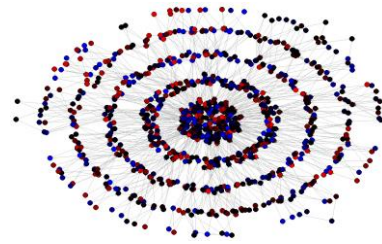

Figure 8a The red balls represent female agents and the blue ones males. This graphic was made in the 148th year APS. As with the foregoing graphs, the edges between the balls (nodes) were parental links. Gene values closer to zero produced darker blue and darker red balls. Genes whose integer values were closer to the number 255 produced brighter colors, respectively.
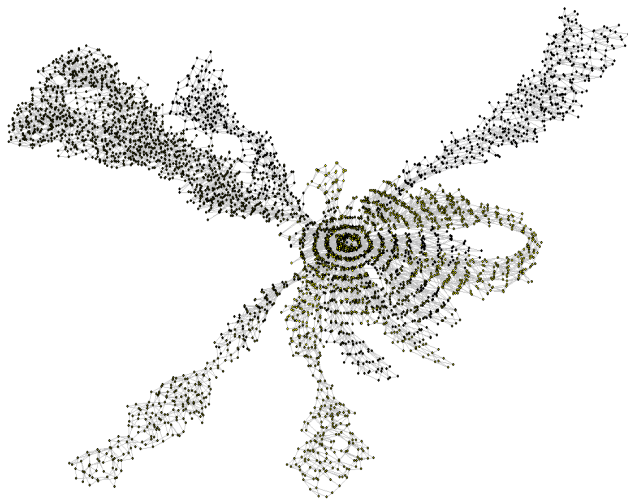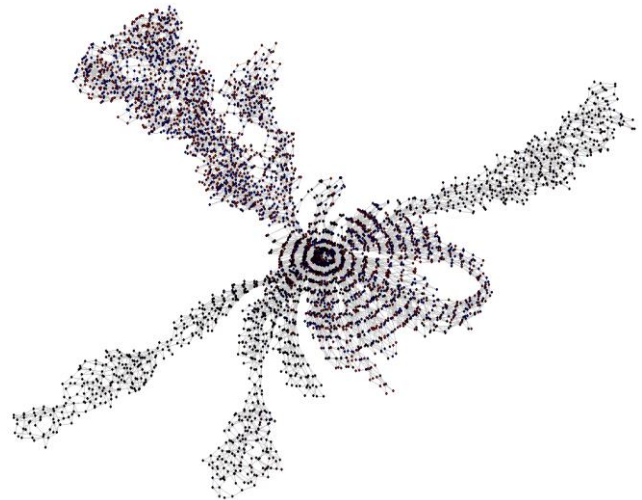

Figure 8b This graphic shows gene 6 as it "evolved" within the population and as it appeared in the simulated year 4,259 APS. Eventually, only the brighter red/blue extension of agents in the upper left corner would survive as a group of colonies in the Grassland biome. Gene 6 values converged toward the integer 255 in both male and female agents.

Conclusion

This report described a specific ABM, a particular simulation made with that ABM, and qualitative results pertinent to complex systems theory in the domain of small-group social dynamics generated by that ABM. While a final report on the research is forthcoming, this verification test, produced interim results that are consistent with the hypothesis.

To be clear, this work exploited only critical model metabolic, bio-reproductive, and artificial genetic sub-

system operations capable of HG agent spatial self-relocation. This report did not attempt to evaluate or describe the performance of any particular non-cognitive or cognitive foraging control scheme. All agent metabolic processes involving food and water were satisfied by constant, distributed, but constrained nutrition provisioning.

By using only the following components: human bio-reproductive rules, non-cognitive nutrition taking, artificial evolution, an abstract spatial ecology, and no a priori constructs of social organization this experiment accomplished two things. Firstly, the complex adaptive systems model under test created an instance of the most fundamental social-network, the "family tree." However, this was expected given the software design: the isMother and isFather relation was necessary to create agent offspring.

Secondly, and of greater importance, the model generated permanent genetic change in the agent population. Although steered only by agent spatial/environmental interaction, artificial genetics, and simple non-cognitive and biologically inspired drives there were apparent changes in social complexity that emerged from this model. That is, without any explicit model rules ordaining clan-like grouping to occur, the experiment generated "genetically strongly-related and spatially adapted small-group cohorts." And, this appears to support the hypothesis.

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