

At the root of sociality: Working towards emergent, permanent, social affines

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Abstract

Complexity science often uses generative models to study and explain the emergent behavior of humans, human culture, and human patterns of social organization. In spite of this, little is known about how the lowest levels of human social organization came into being. That is, little is known about how the earliest members of our hominini tribe transitioned from being presumably small-groups of ape-like polygamous/promiscuous individuals (beginning perhaps as early as *Ardipithecus* or *Australopithecus* after the time of the Pan-Homo split in the late Pliocene to early Pleistocene eras) into family units having stable breeding-bonds, extended families, and clans. What were the causal mechanisms (biological, possibly cognitive, social, and environmental, etc.) that were responsible for the conversion? To confound the issue, it is also possible the conversion process itself was a complex system replete with input sensitivities and path dependencies i.e., a nested complex system. These processes and their distinctive social arrangements may be referred to favorably (as one notable anthropologist has called them) as, "the deep structure of society." This essay describes applied research that uses discrete event computer modeling techniques in an attempt to model-then-understand a few of the underlying social, environmental, and biological systems present at the root of human sociality; at the root of social complexity.

Introduction

Within the complexity sciences that are the pillars of Artificial Life, computational social science (CSS) often bases its claim of legitimacy on an ability to describe past, ongoing, and future human events through the use of generative computer models that attempt to explain fundamental and emergent human behavior, human culture, and patterns of human social organization (Axtell, 2002; Cioffi-Revilla, 2007). CSS is an applied science: a co-mingled branch of Computer Science and Social Science that pursues its verification and validity from comparisons made between axiomatic, cross-culturally recognized, "first principles" of human behavior. However in spite of this, the literature reports on scant few computer models that test hypotheses on the most basic structure of human social organization. This was the challenge that motivated the current research thread and it led us to consider several related questions.

For example what were the socio-environmental, biopsychological, and or cognitive drivers that contributed to

the initial emergence of the "household?" How did the causal mechanisms of emergent social complexity interact to precipitate such individual and group-level social behaviors as stable breeding-bonds or reciprocal exogamy? Can statistical models (Gavrilets, 2012) which have no socio-temporal interaction memory or explicit socio-spatial context be a reliable indicator of the causes of human sociality? Or, are explanations devoid of biological representation or rich socio-environmental interaction (Kaulakis, R., 2012) but containing seductive oversimplifications of social intercourse based in abstract organizational logic really be plausible explanatory resources? Clearly, innate primate drives like territoriality constrained by pre-adaptive physiological enablers, environmental and social circumscription, and philopatry/dispersal (Parish, 2000) played a role. Moreover, our species seems to have emerged from the milieu of its clade almost in spite of its roots in mixed polygamy over promiscuity without significant benefit of fossil or proxy evidence (Chapais, 2013). So, what realistic set of causal mechanisms (biological, environmental, cognitive, and social) were responsible for our particular species within the hominini tribe to begin its transition from one of likely polygamy-modulated inter-actor promiscuity (sans incest) to one that today purposefully maintains and ultimately exchanges its social affine resources via highly controlled inter-group mating practices? Without at least a few basic answers to these questions the plausibility of models positing their explanatory power over emergent human social organization (and social complexity) might be called into some degree of suspicion. How can we believe the "household" to be the legitimate, primary unit of generative social organization inquiry if the emergence of the household itself cannot be more fully explained? Moreover, is it reasonable to abide the "household" as the basis-unit of computational social science modeling-making if its first principles, its origins, and its fundamental mechanisms are so poorly understood? This is where our research began.

The research described here is work in progress. The purpose in writing this interim report is to create a baseline image of the progress of the work; to establish in public what are our science, our intent, and our tools. The plan is to first identify and then to computationally investigate several of the necessary and sufficient causes of basic human social organization. Together with the current work and its predecessor experiments we have created a single, contiguously coded model whose results emulate

emergent, self-aggregating (hominid-like) local-groups that are terrain-situated, mobile, and give spirit to autonomous agent-actors as socially and physiologically plausible as possible. We believe that it is only through such a rich software setting and diverse computational artificial life test bed that one can derive a reliable social science product and a plausible explanatory vehicle for the range of topics that call themselves emergent social complexity.

Methods

We know that the hominini, a tribe that includes the species *Homo* and its extinct ancestors, e.g., *Ardipithecus* (Lovejoy, 2009) and *Australopithecus*, split from the main branch of the African primate phyla roughly 5 – 7 million years ago (mya). And, we also know that *Pan*, our closest genetic relative in the hominid phylum, last shared an ancestor with us perhaps 7 – 9 mya. Thus, if we can agree that stable breeding-bonds and reciprocal exogamy currently exists in *Homo* but do not exist in *Pan* and if we further assume that stable breeding-bonds are a necessary prerequisite to human social organization as it exists today, then we may have a way to logically isolate and confront the confound of this particular nested complex system. As it turns out, it can be shown through phylogenetic decomposition (Chapais, 2009) that the social patterning we refer to as “stable breeding-bonds” in *Homo* is actually an emergent homoplastic result and not a case of homologous epigenetic inheritance. This will free us in our subsequent analyses to consider only convergent evolution as the determining cause of the processes in question. However, we will still be forced to ask ourselves what manner of circumscription (Carniero, 1988) is in play and how to best go about modeling the remaining complex system. It is upon this layer of theoretic reasoning that we have begun constructing our most recent computer codes.

The following sections describe the construction of a specially prepared individual-based model that it is believed: 1) will offer insight into the causal mechanisms implicit at the lower bounds of social organization theory, and 2) has already shown pertinent, preliminary results. Our goals will be: 1) to test our hypotheses in transportable Java code, and 2) to facilitate the replication of our work by others through the free sharing of that code. The research is purposed to demonstrate emergent, stable, breeding-bonds that may lead toward emergent reciprocal exogamy. The motivating hypothesis is: *Reciprocal exogamy emerged because of innate drives for specific territoriality constrained by evolved pre-adaptive physiological “enablers” consequent to bipedal mobility, social altruism and alliance, environmental and social circumscription, and sexually differentiated philopatry.*

Code Donors

The Java instantiation has a general theme that tends more towards inclusive plausibility than exclusive abstraction. The results enjoy at least the following features: tightly coupled artificial evolution (Darwinian and Baldwinian) expressed through simulated agent cognition and artificial

genetics, agent-spatial mobility, 2.5-D simulated terrain with feedback coupled nutrient regrowth carrying capacity, agents with self-adaptive and autonomous learned foraging preferences, agnatic, consanguineal, and uterine kin recognition, mating, disease, malnutrition, infanticide, death by old-age, and single-threaded agent objects bounded by runtime “birth” to “death” encapsulation. In order to abbreviate software development costs, three code donors have been enlisted and severally enlarged from previous works. Features have been added (or removed) to accommodate the specific problems of the current question. Here is an outline of the three code donors used and the names of the respective conference publication titles describing those works. The subsumed donor code features are fully outlined.

A search for the roots of social complexity: Niche adapted agents (Rouly, 2009). This paper and its Java code-base received a poster invitation to the 10th European Conference on Artificial Life held in Budapest, Hungary. This was a spatial agent-based model simulating a niche ecology occupied by fully mobile, sexually dimorphic, and reproductive male/female agents. Each agent had an independent and inheritable artificial chromosome containing eleven genes. The genes were mapped onto graded and expressible biological functions and physiological traits like draught tolerance, temperature sensitivity, robust metabolism, and improved fecundity in small-group settings, as a small example.

- 1. Figure 1** depicts a typical social network that often emerged among the agents in the model. What is visualized is a population-inclusive effect called Genetic Drift (Sewell-Wright Effect, Wright, 1932). The image uses a social network to visually articulate the drift that emerged within the chromosomes of the agent population over 4,259 years-of-days.
- 2. A prototype, multi-agent system for the study of the Peopling of the Western Hemisphere** (Rouly and Crooks, 2010). This applied work extended the previous research code base. The extensions included highly-detailed, agent-terrain spatial interactions, better agent foraging autonomy, and improved socio-spatial mobility. This work was delivered to the 3rd World Congress on Social Simulation in Kassel, Germany. Specific requirements for empirically-derived environment and terrain components built for this Java model demanded that enhancements be made to the code base so as to more fully articulate daily climate, flora, fauna, and water resource updates. The new features included daily and seasonal updates of the ecology through multi-threaded execution that took better advantage of multi-core, multi-processor technologies.
- 3. Sexually differentiated philopatry and dispersal: A demonstration of the Baldwin effect and genetic drift** (Rouly and Kennedy, 2011). This work further extended the code base. Here we refactored previous work in order to introduce two new features. The first feature was the addition of an empirically grounded process of sexually differentiated philopatry and spatial dispersal.

The behavior of spatial dispersal occurs in many primates when they become sexually mature. The second feature involved a new agent behavioral control mechanism that simulated a cognitive (adaptive) process in addition to the existing innate (biogenic-reactive) processes. This

new work demonstrated self-aggregating cohorts (fission and fusion) and increasingly plausible, situated and embodied, hominid-like agent behavior. Finally, the agents in this new experiment were required to make individual foraging choices that de-conflicted their

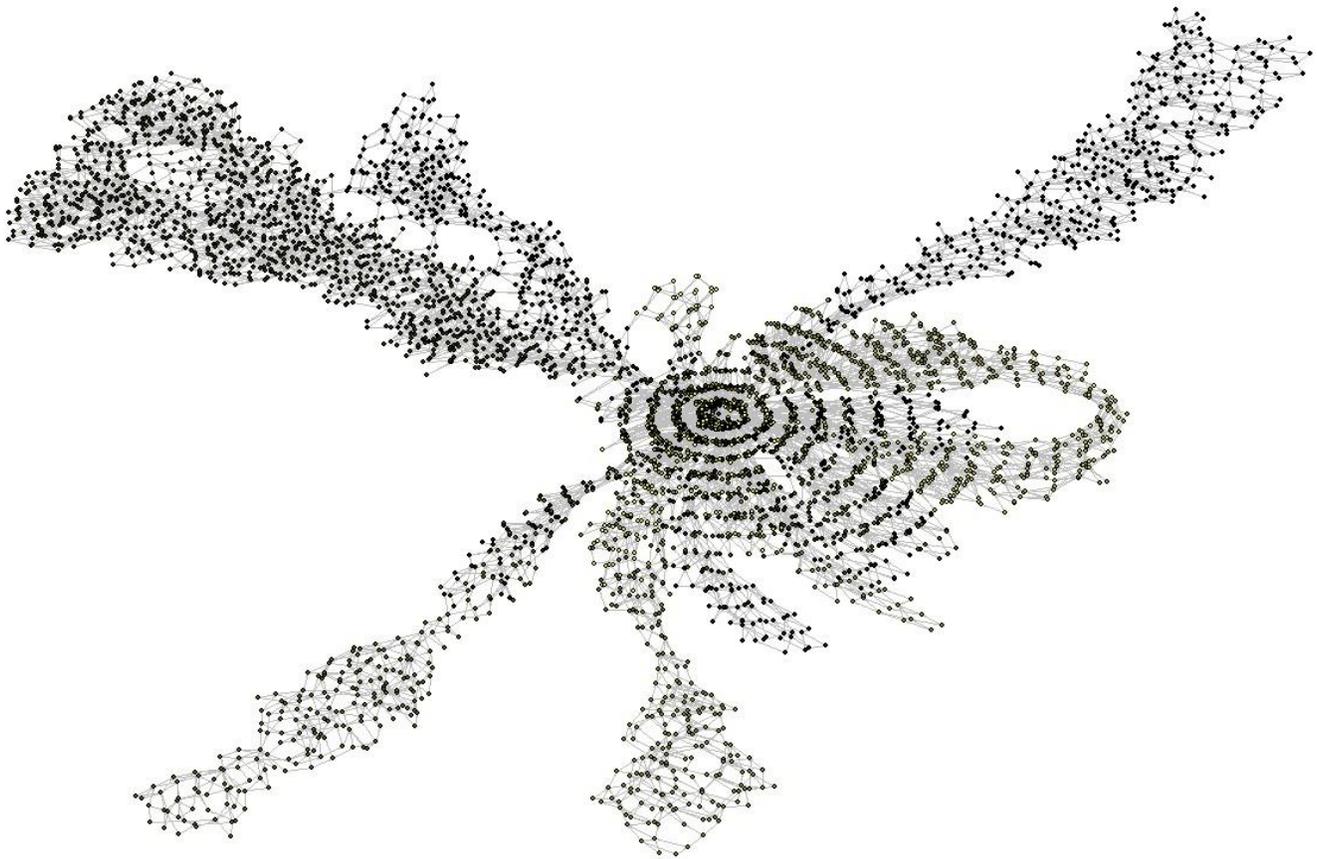


Figure 1 This illustration captures the emergence of the Sewell-Wright Effect within the genetics of an artificial agent social network. The temporal-spatial progress of the emergent process appears as a pattern of expanding “tree rings” among the interconnected network nodes. The radial arms are spatially separated cohorts of promiscuously “mating” agents. The “evolution” of genetic content is shown as a subtle color shift from the center “rings” (first generations) to the outer “rings” (last generations). Bridging connections between radial arms are the “mating” activities that occurred between otherwise spatially separated agent groups, or cohorts, as time passed and the cohorts became more and more spatially distant. Longer radial arms represent more adaptive genetic results in a particular part of the niche ecology.

mother/infant taught eating practices with terrain food-choice availability in real-time. By isolating a few independent variables in what had by now become a rich and stable software test bed, agent perceptual conflicts arising during foraging allowed us to observe the results of simulated cognitive dissonance. As the process of dissonance resolution executed within each individual agent an emergent, quantifiable, species-changing genetic result was observed but in abbreviated evolutionary timescales. **Figure 2** revisits the emergent genetic drift produced by the previous baseline code but in the context of this new experiment. Here we see a quantifiable result:

the skewed distribution of genetic values after Baldwinian evolution.

The Current Code

Logical extensions made for the current research have required new code to be written. Consequently, the donor code has been significantly refactored and nominally three new Java classes named TrueRNG, Socioecology, and Groups, were created. Additionally, genes for social altruism and alliance were added for independent variable comparison testing. Great care was taken not to

introduce, or tolerate, regression errors in the code donor base-classes.

The software can now dynamically accommodate maps of any size so long as the incoming graphic is based on square kilometer increments. As the map is read-in, any number of colors appearing on the map can be tagged and used as "land features" within the model. This can and does include 2.5-D relief features. Once incoming "land features" are recognized, the distribution of a plausible set of calorie providing forageables can be placed on the

terrain. **Figure 3** shows one such distribution of forageables. During the execution of the simulation "land features" like climate, flora, fauna, and water resources, etc., are updated (per epoch) in separately executing threads for each square kilometer. This is aimed directly at improving bandwidth utilization in multi-core processors with large RAM capacity. Together these changes allow topographical maps of spatial environments past, present, or abstract to be imported for study. Finally, because of

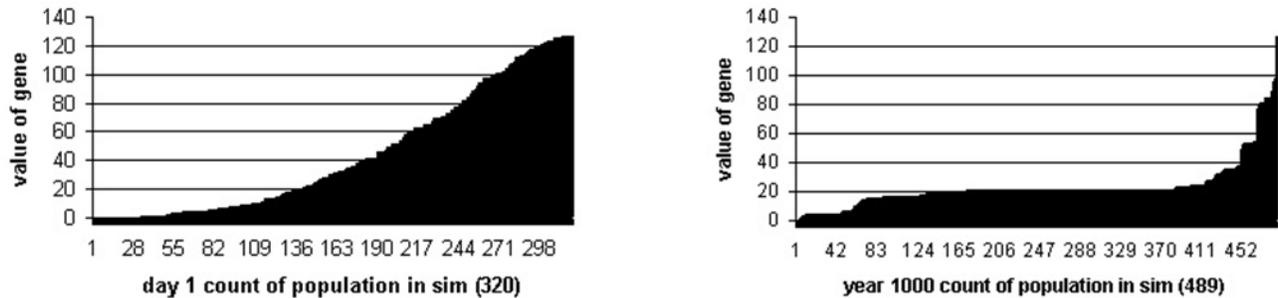


Figure 2 On the left is an illustration of the initial distribution of a representative gene value in the starting population. The number of agents was 320 on day 1 and the values were initialized as a Gaussian distribution. On the right is the skewed result of the same gene in the surviving population (many generations later) in year 1000. The distribution is clearly skewed to the right. The population had grown to 489 agent members.

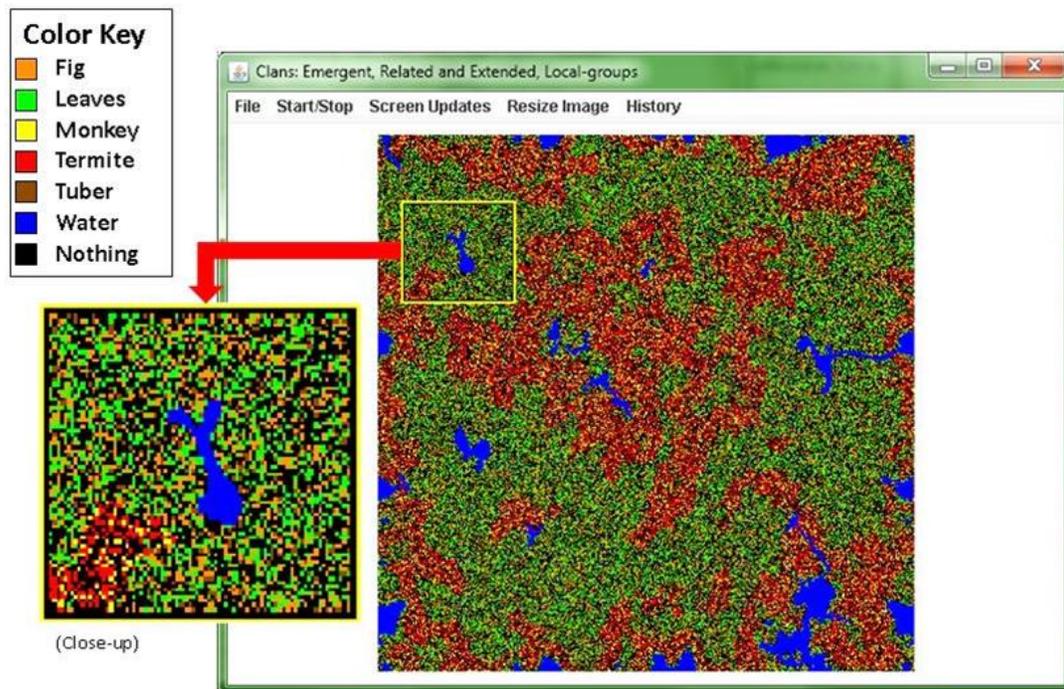


Figure 3 This is a screen capture of the current model based on a 4km X 4km 2.5-D terrain map, or habitat. The key to the left identifies the value of each of the pixels in the map. Each pixel – and the behavior of the hominid agents in the simulation – is based on the assumption that a pixel is a 10m X 10m area. The forageables Fig, Leaves, Monkey, etc., are grouped by 2.5-D relief height. The color of each pixel represents and provides an agent-harvestable calorie or water volume, respectively. The "greenish" areas are lowlands and the "reddish" areas are highlands. Water, in "blue," is the lowest terrain height.

the refactoring, the Ecology related classes of Climate, Flora, Fauna, Terrain, and now Groups, each are in contact with the agent cohorts during multi-threaded execution. This was an important achievement adding plausibility and efficiency by way of quasi-concurrency. The Groups code provides external modules access to statistical and accessor methods addressing the terrain cohort array lists.

Now that the Ecology classes are multi-threaded their combined daily (one epoch) maintenance loops take less real-time to execute. So much was the improvement that forageables can now be dynamically (feed-back) controlled by hominid foraging. It is entirely possible for a hungry horde of hominids to wipe out an entire terrain cell's productive capacity or to drain one of the randomly placed small water basins on a daily basis. Or, to the opposite, allow a terrain cell to recover if sufficient time has passed and the cell forageables are unharvested. This feature is new to the research thread but was inspired by similar work done in the Sugarscape series (Epstein and Axtell, 1996).

An entirely new addition to the work is the use of a diode-noise-based TrueRNG® random number generator. This is a hardware device (a USB dongle). It has shown itself, in empirical tests, to be able to typically produce no more than one or two integer repetitions in a 64-bit sequence of over 1 billion uniform random number generation attempts. While this is far from perfect, it is several orders of magnitude better than the factory Java class running the same test. In the research described

here the device is used as an entropy source and a generator of random number seeds for the hominid agents once a year on their individual birthdays. The result of adding this TrueRNG® to the research has been to “flatten” the stochastic and often sudden excursions associable with population crash and or explosion. The “downside” is that each run is an entirely unique random/stochastic proof of the validity of the system model but is, by itself, only quantifiable by stochastic repetition.

The Socioecology class is entirely new and supports many significant and novel inter-hominid socializing activities and in-group/out-group recognition results. A challenge of this research is that the experimental definition strictly allows us to only “precipitate” the emergence of stable breeding-bonds and the follow-on occurrence of agnatic memory and exchange-capable affine relations given an initially promiscuous hominid agent base – but not directly cause the related behaviors of polygamous organization or monogamous pair-bonding. In fact, there is explicit negative value attached to hard-coding any of the normal inter-social identifiers and or social behaviors associable with the “household.”

Results

We report here intermediate (in-progress) results. **Figure 4** is a screen capture taken from one model (simulation) run.

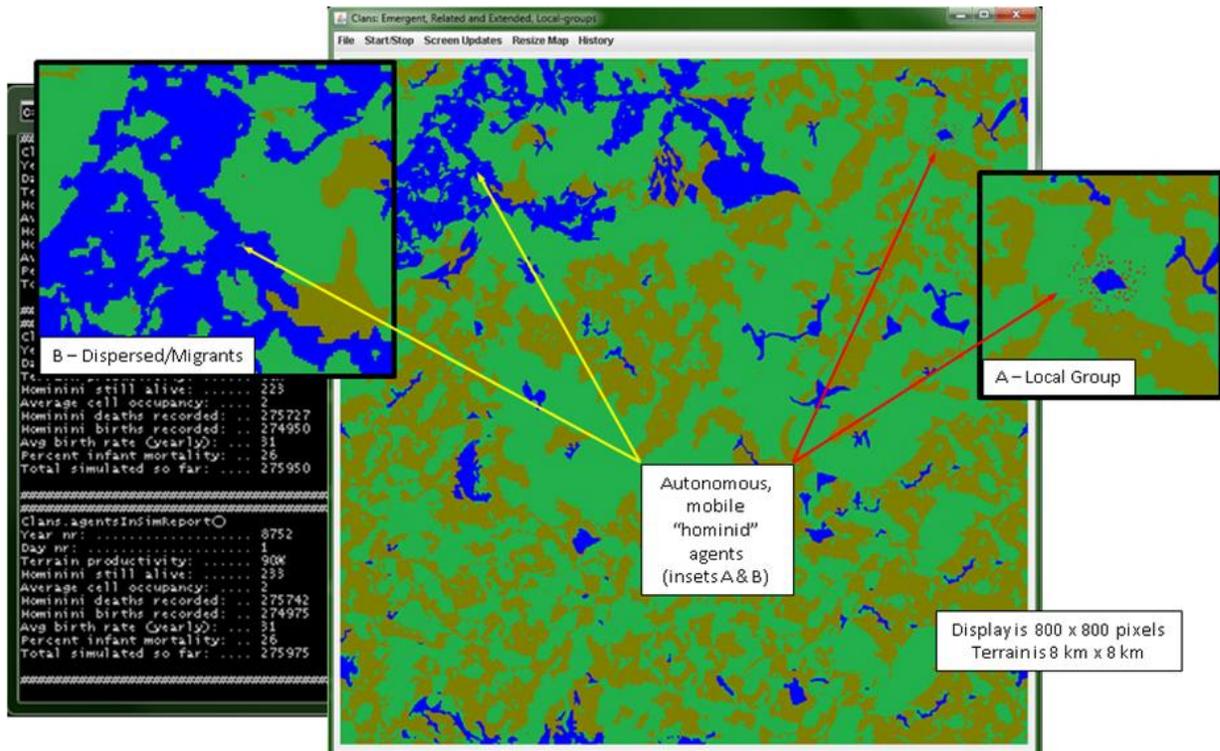


Figure 4 The console display here is showing the results for the simulated year 8,752 after program start. The total count of agents simulated over hundreds of generations was 275,975 with 275,742 deaths recorded. When this screen was captured 233 agents remained. The red pixels near the bodies of large standing water (in the insets) are promiscuous hominid agents.

The simulation epoch is one day and a simulated year is 364 days. In the screen capture, the simulation has been running for 8,752 years-of-days (or 3,185,729 epochs). In the console window to the left of the terrain image there is scrolling output. The output displays a series of cumulative sums taken each year over all previous years. On the map the hominids are visible as “red” pixels. The main local group is near the perimeter (shoreline) of a large stationary body of (blue) water in the upper-right corner of the habitat. This habitat is 800 X 800 pixels square. Each pixel along with the agent behaviors are scaled to 10m X 10m. Thus, the entire habitat is a torus grid 8km X 8km in size and represents 64 simulated square kilometers.

At program start in the run shown in the screen capture, there were 1,000 groups of 1 agent seeded onto the habitat terrain. Placement of those seed-groups (referred to as cohorts) was random. The seed population was composed of mixed sex individuals ranging in age from 6 to 35 years. The majority of the agents were between 15 and 35 years of age. None of the females were pregnant or nursing at program start. In the run shown and within a few generations, seed group numbers had dropped to several hundred and many “small” local-groups (cohorts) had coalesced around many widely scattered bodies of water. Within a few hundred years, the cohort in the upper right corner of the Figure emerged as the only local-group remaining. After over 8,000 years-of-days, agent spatial choices had clearly become the stochastic product of autonomous decision making paired with the spontaneous interactions of breeding members within their forageable (niche) environments.

During this particular simulation (or run) the population of simulated hominids ranged in number from a low of near 100 individuals to a high of a few hundred (after initialization). Sadly, the entire colony in this particular run expired just over one hundred years (8,863 actual date) after this image was taken. Preliminary post-mortem analysis suggests the collapse was associated with events surrounding momentary colony membership spatial dispersal, a random shift in new offspring sex-ratios, and a seasonal swing in environmental carrying capacity.

As stated earlier, this is an intermediate report containing progress and observations of model performance. Yet, as described in the preceding paragraph, the experiment has already delivered relevant patterns of interaction between our base-line, promiscuous hominid-like agents, their environment, and their breeding groups. While we are not presenting final quantitative or qualitative conclusions here, regarding the motivating hypothesis, our accumulating social networks, genetic analyses, and socio-environmental results are suggesting that perhaps with the addition of genetics-based social altruism and alliance alone we have begun to see promiscuity changing into polygamy and possibly semi-permanent breeding-bonds. That said, our data is simple and is comprised of longitudinal and statistical results. Consider: Every epoch (day) recently deceased members of the population are expunged from the simulation. When the agents are removed a complete “death certificate” is made for each individual. That “death certificate” contains running data like agent ID, date and location of simulated birth, death, age at weaning, biological mother and father IDs, agent actual weight, caloric and water requirements, preferred prey, cause of death, and several more data points including a complete sample of the genetic material of the

agent. Although it is currently only used for diagnostic testing and software development verification, a complete listing of each of the siblings belonging to the agent and the birth order of those siblings, assuming there were any, can be “listed.” Along with this, a listing of all cohort acquaintances and their respective daily interaction accounts can also be produced.

Discussion

While the overall research thread is extensive, it profits greatly from the described, incremental improvements within and over its predecessor donor codes. It relies heavily on those donor codes described in the Methods section. However, given space constraints, more about the donor codes cannot be discussed. The important new Socioecology class needs our final attention.

Introduced in the Methods section, Socioecology is new code to this research thread. It endows each individual hominid with a dynamic, random access, “social group-memory” capability and several logical operators over that memory. It operates such that as a hominid agent encounters others the self can compare the identity of self and the identities of the others, storing the IDs of the others, and thus later having the capacity to recognize the other agents throughout the lifetime of self. Moreover, each day (epoch) self and other occupy the same spatial cohort (a single 10m X 10m terrain cell) a discrete counter is incremented for the specific other. That counter is available to all logical social operators in the class. Additionally, three important new social functions in the class were created; they are uterine kin recognition, Westermarck recognition, and consanguineal kin recognition.

Uterine Kin

Building on these new inter-agent checks, the Socioecology class has code supporting explicit knowledge of matrilineal family constellations. For example, all primates appear to be able to differentiate some of their dyadic behaviors based on uterine kinship. Thus, the new code can directly store and manipulate others that include siblings, mother, children (if self is female), and logical relations like birth-order. For example, dominance hierarchies are often associated with birth-order (Sapolsky, 2005). Methods also exist to permit agnatic and consanguineal kin identification when those instances occur. The time invested in creating these new kinship identification methods has already paid dividends in the context of incest avoidance (Rodseth, 1991). Previously, interpersonal methods inherited from the donor code-base could only remember one other/father/son/daughter relationship at a time. Thus, while first generation incest was forbidden by rule (and it was very effective) it was also possible within a sufficiently large mating group that incest could occur over a longer period of time between consanguineal kin. Although consanguineal incest is theoretically still allowed to happen, at least when it happens now, there is a console message sent to the operator and a statistic taken for the event. Finally, however, because every hominid knows its mother and its siblings and the mother knows all of her children, incest avoidance based on uterine kin recognition (a necessary

component of any society having patrilocal residence like Pan) is controlled in the new code.

Westermarck Recognition

The code also contains a Westermarck (1921) function based on the hypothesis that "familiarity" may implicitly contribute to incest avoidance. This heuristic suggests that primate sexual relations are forbidden based (effectively) on the number of days self has been in contact with other. In the Socioecology code this is calculated as an average number of days self has been in the proximity of other and a threshold value comparison taken. The Boolean function fires if the number of contact days with other meets a nominal threshold for avoidance. Together with uterine kin recognition and rejection, Westermarck keeps incest rates well below 0.1% over several generations of mating occurrences without benefit of any other explicit incest avoidance rules.

Consanguineal Kin

In promiscuous breeding troops (like those of Pan), any sufficiently old biological father of any troop offspring may not be cognitively certain of his own paternity in the context of any living constellation of infants, juveniles, or younger adults. This appears also true, by reflection, from the viewpoint of younger male and female troop members onto any older extant male. However, the younger members may, by virtue of their individual memory of continuous social interactions, i.e., by virtue of the Westermarck function, be able to make informed inferences regarding the bio-social relationship between self and the older other. If this hypothesis continues proving itself valid in testing, it will facilitate several simple coding mechanisms for generating bi-laterally emergent agnatic relationship recognition. This is a primary goal of the research thread and a latent function within the Socioecology class.

The research has only in the last few months begun to produce results. From the Code Donors we inherited a base of situated, stable, sexually dimorphic male and female agents. These were agents that had previously enjoyed self-directed foraging and sexually dimorphic philopatric/dispersive behaviors, cognitive features, artificial genetics and biology, and all of the rest. To them we added social altruism and alliance, and an increased capacity for highly-social interaction. Given the foregoing, we look forward to soon being able to report emergent patterns of abstract, implicit kinship and social networks showing a history of permanent breeding-pairs within the populations that inhabit the model.

Summary

This article has disclosed an ongoing computer-based experiment. The experiment uses a computer simulation technique called agent-based modeling (ABM) as the basis of its work. For the last few years this research has led to the identification and accumulation of a set of self-organizing social properties, hominid-inspired behaviors, pristine environments, and physiological enablers believed to exist at the least-organized end of every complex (human) social system. This is the specialized domain of the work.

In particular, the work deals with highly-social populations of explicit, initially promiscuous, primate-like software agents inhabiting 2.5-D virtual environments. We have seen our historical experiments creating plausible, artificial, and vibrant social fabrics within and between situated agents who themselves autonomously demonstrated survival-related and innate small-group social behaviors. In the previous works named in the Code Donors part of the Methods section, we gave testimony and reference to peer-reviewed evidence that our evolving code base has developed agent populations generating spontaneous and emergent social behaviors ranging from community fission and fusion, to voluntary migrations, simulated sexual reproduction, new agent birthing, aging, and death, and now (most recently) what may be semi-permanent breeding-bonds that resemble emergent polygamy from within a wholly promiscuous population.

It is believed that what is contributed by the work reported here is important for two reasons. First, the system model that we adopted for instantiation is inherently detailed and expansive: much as is the subject under study, i.e., natural-life. Metaphorically: This is not research that attempts to sneak a slice or a bit of pie but rather it is an attempt to create a whole pie. This is generative Computational Social Science. It builds on the genre of models instantiated by Epstein and Axtell (1997), Kohler, et. al, (2000), Axtell, et. al (2002), and others and it is inherently deductive in its approach. This work bases its algorithms and conclusions on computations drawn from empirical or empirically derived parameters, objectively substantive relationships, and observable processes (Epstein, 1999). In recent years we have developed better computers and more advanced software engineering techniques. So now the question must be asked, should we not be building and studying more models of similarly complicated and broad-ranging natural-life systems? And, second but more importantly, the simulation about which we report here explores the roots of our own complex, human social structure; at its least-organized end. This is a subject that is known today only by speculation and religion. That alone should be challenge enough for us to harness our technologies and make every attempt to better understand the dynamics of emergent, small-group social behavior.

Our goal was the discovery of new factors contributing to the socio-environmental, bio-psychological, cognitive, and singularly social development of our species. It may be that it is only through explicit simulations, like those disclosed here, that we can visualize the emergence of the structures most fundamental to complex human social organization. Simulations like these allow us to ask "what if" questions; questions that are otherwise unethical, impractical, too expensive, and too time consuming to be tractable by any other means. And, this is of course not an exclusive list.

Our task was to attempt to bring about emergent and permanent agent breeding-bonds, breeding-pairs, family units, clan-like social structures, or nascent reciprocal exogamy within an otherwise detailed, wholly promiscuous (primate-like) population. By step-wise iteration we have found that it appears that if social altruism and alliance (expressed as the voluntary sharing of food resources coupled with post-benefit preferential relocation) were sexually differentiated traits available to every member of a test population then, we may have taken the first steps towards our goal. Said more simply, by adding a single

independent variable (adding gene-based traits for altruism and alliance) we have moved an explicit, promiscuous population incrementally toward polygamy, semi-permanent breeding pairs, and or both. Clearly, this is an experiment that tends more towards inclusive plausibility than exclusive abstraction and lingering doubt. Primates, after all, are very complex social beings.

Conclusion

As is the case with many complex systems models, model initialization can be difficult due to input parameter sensitivity. This model is no different. It has been said that complex systems models experience a “settling period” when they first begin to run (personal conversation with R. Axtell in Fairfax, Virginia, 2015). This occurs as agent schema and parameters are filled with actual runtime versus initialized values. As was noted previously, the use of the TrueRNG® dongle does appear to help smooth population growth dynamics in this latter regard and this is a good thing. But, to complicate matters, we also have implicit constraints associable with our hominid prototype that demand our populations have and keep membership numbers small relative to any habitat size under study.

Considering all of the foregoing and conditions associable with minimized genetic diversity, issues known to plague the prototype species have become issues within our model too. For example, our agents can suffer from problems associated with localized over-grazing if their habitat is too small or their numbers grow to large before troop fission. That said, in an extension to this work we may yet add territorial patrols (Mitani, 1979) to the behavioral ecology of the simulated hominid population (Wrangham, 1975). Of course, we will need a larger artificial habitat. But, in the near term, we can report that with only the addition of genetics-based altruism and social alliance, we have already seen incremental progress towards our goal of emergent, permanent, social affines.

References

- Axtell, R. L., Epstein, J. M., Dean, J. S., Gumerman, G. J., Swedlund, A. C., Harburger, J., & Parker, M. (2002). "Population growth and collapse in a multiagent model of the Kayenta Anasazi in Long House Valley." *Proceedings of the National Academy of Sciences of the United States of America*, 99(Suppl 3), 7275-7279.
- Carneiro, R. L. (1988). The circumscription theory. *American Behavioral Scientist*, 31(4), 497-511.
- Chapais, B. (2009). *Primeval kinship: How pair-bonding gave birth to human society*. Harvard University Press.
- Chapais, B. (2010). The deep structure of human society: primate origins and evolution. In *Mind the gap* (pp. 19-51). Springer Berlin Heidelberg.
- Chapais, B. (2013). Monogamy, strongly bonded groups, and the evolution of human social structure. *Evolutionary Anthropology: Issues, News, and Reviews*, 22(2), 52-65.
- Cioffi-Revilla, C., Luke, S., Parker, D. C., Rogers, J. D., Fitzhugh, W. W., Honeychurch, W., Fröhlich, B., De Priest, P., & Amartuvshin, C. (2007, January). Agent-based modeling simulation of social adaptation and long-term change in Inner Asia. In *Advancing Social Simulation: The First World Congress* (pp. 189-200). Springer Japan.
- Epstein, J. (1999). Agent - based computational models and generative social science. *Complexity*, 4(5), 41-60. doi:10.1002/(sici)1099-0526(199905/06)4:5<41::aid-cplx9>3.3.co;2-6
- Epstein, J., & Axtell, R. (1996). *Growing artificial societies: social science from the bottom up*. Brookings Institution Press.
- Epstein, J. M., & Axtell, R. (1997). Artificial societies and generative social science. *Artificial Life and Robotics*, 1(1), 33-34.
- Gavrilets, S. (2012). Human origins and the transition from promiscuity to pair-bonding. *Proceedings of the National Academy of Sciences*, 109(25), 9923-9928.
- Kaulakis, R., Zhao, C., Morgan, J. H., Hiam, J. W., Sanford, J. P., & Ritter, F. E. (2012). Defining factors of interest for large-scale socio-cognitive simulations. In *Proceedings of ICCM-2012-Eleventh International Conference on Cognitive Modeling* (pp. 117-122).
- Kohler, T. A., Kresl, J., Van Wes, Q., Carr, E., Wilshusen, R. H.: Be There Then: A Modeling Approach to Settlement Determinants and Spatial Efficiency Among Late Ancestral Pueblo Populations of the Mesa Verde Region, U.S. Southwest. In Kohler, T. A., Gumerman, G. J. (eds.): *Dynamics in Human and Primate Societies: Agent-Based Modeling of Social and Spatial Processes*. Oxford University Press, Oxford UK (2000) 145–178.
- Lovejoy, C. O., Suwa, G., Simpson, S. W., Matternes, J. H., & White, T. D. (2009). The great divides: *Ardipithecus ramidus* reveals the postcrania of our last common ancestors with African apes. *Science*, 326(5949), 73-106.
- Mitani, J. C., & Rodman, P. S. (1979). Territoriality: the relation of ranging pattern and home range size to defendability, with an analysis of territoriality among primate species. *Behavioral Ecology and Sociobiology*, 5(3), 241-251.
- Parish, A. R., de Waal, F., & Haig, D. (2000). The other “closest living relative”: How bonobos (*Pan paniscus*) challenge traditional assumptions about females, dominance, intra- and intersexual interactions, and hominid evolution. *Annals of the New York Academy of Sciences*, 907(1), 97-113.
- Rodseth, L., Wrangham, R. W., Harrigan, A. M., Smuts, B. B., Dare, R., Fox, R., King, B., & Wolpoff, M. H. (1991). The human community as a primate society [and comments]. *Current Anthropology*, 221-254.
- Rouly, O. C. & Crooks, A. (2010). A prototype, multi-agent system for the study of the Peopling of the Western Hemisphere. *3rd World Congress on Social Simulation*, 2010. Kassel, Deutschland. 6th-9th September 2010.
- Rouly, O. C. & Kennedy, W. G. (2011). Sexually differentiated philopatry and dispersal: A demonstration of the Baldwin effect and genetic drift. *Computational Social Science Society of America Annual Conference, 2011*. Santa Fe, New Mexico, USA. October 9-12, 2011.
- Rouly, O. C. (2009). *In Search of the Roots of Social Complexity*. George Mason University. Unpublished manuscript.
- Sapolsky, R. M. (2005). The influence of social hierarchy on primate health. *Science*, 308(5722), 648-652.
- Thompson, M. E. (2013). Reproductive ecology of female chimpanzees. *American journal of primatology*, 75(3), 222-237.
- Westermarck, E. (1921). *The history of human marriage* (Vol. 2). Macmillan.
- Wrangham, R. W. (1975). *Behavioural ecology of chimpanzees in Gombe National Park, Tanzania*. Ph. D. thesis, Univ. of Cambridge.
- Wright, S. (1932). The roles of mutation, inbreeding, crossbreeding and selection in evolution. *Proceedings of the 6th International Congress on Genetics*, 1, pp. 356–366.