

TOWARDS EMERGENT SOCIAL COMPLEXITY

by

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Doctor of Philosophy
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DEDICATION

To Lillian and others upon whose shoulders I have stood.

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I publicly acknowledge all of those whose commitments to the professions of education, the arts, engineering, the sciences, and to me personally have made my work and family possible. Their names are legion and my memory poor. If I could be sure that I could name them all, I would try. Instead, knowing my own corruption, I choose to thank them in my heart. I will forever be in their debt.

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LIST OF ABBREVIATIONS

After program start	APS
Agent-based model	ABM
Association of Zoos and Aquariums Ape Taxon Advisory Group	AZA Ape TAG
Bitmap	BMP
Communication(s).....	COM
Communications Device Class	CDC
Complex Adaptive System	CAS
Computational Social Science	CSS
Central Processing Unit	CPU
Digital terrain elevation data	DTED
European Conference on Artificial Life.....	ECAL
Gigahertz.....	GHz
Graphical User Interface	GUI
Heuristic, Algorithmic, Learning	HAL
Hunter-gatherer	HG
Identification	ID
Institute for Electrical and Electronic Engineers	IEEE
Individual-based model	IBM
Integrated Development Environment.....	IDE
Java virtual machine.....	JVM
Last glacial maximum	LGM
Kilometer	km
Millions of years ago	mya
Multi-agent simulation	MAS
Multi-agent system	MAS
Personal Computer	PC
Personal Computer Interface.....	PCI
Random access memory	RAM
Random number generator	RNG
Receiver/Transmitter.....	RXTX
Red, Green, Blue	RGB
Software Design Description	SDD
Thousands of years ago	kya
Universal serial bus	USB
Virtual Machine	VM

ABSTRACT

TOWARDS EMERGENT SOCIAL COMPLEXITY

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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 dissertation describes applied research that used 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.

What will be revealed here is that even beneath the least levels of complex social organization some degree of true, non-reciprocal, non-kin-based social altruism may be necessary before any of the higher levels can emerge. It may be that such “true” altruism is, perhaps, a necessary foundation to the social structures and complex social organizations that are typically believed to derive from stable households and reciprocal exogamy. In the end new work will be suggested that could extend the current work. That work might involve adding specific cognitive features for extra-social behaviors common to the highest-primates. Those behaviors might include territoriality and patrilocality. And, it is hoped that in the future someone will be able to extend the results of the current work and realize through it a fuller computational social science, an instance of a richer artificial sociality, and demonstrate a plausible model explaining the proximal and ultimate bases of reciprocal exogamy, collective intelligence, and complex social organization.

CHAPTER 1. BACKGROUND

This dissertation discloses the results of experiments that took place within a computer simulation. The simulation was a computer program whose name is Clans. The Clans simulation involves the creation of artificial life in the form of hominid-like software agents. The agents have artificial genetics (biomimetic constructs that express themselves as simulated agent physiology and innate behaviors), simple cognitive features (like cognitive dissonance), reactive behaviors (like those related to foraging and group-size preferences), and the agents “live” in mobile, self-organizing cohorts for thousands of simulated years. For example, Clan agents enjoy mother-offspring behavioral modeling (teaching of preferred foods at weaning), herbivorous habituation offset by carnivory (Mitani & Watts, 2005), voluntary foraging and mating, birth, death, migration, and many other features common to higher-primate and hominid life. As a Clans simulation executes, many novel artifacts and results resembling what may appear to some to be self-organized sociality can emerge. This describes Clans research.

The experiments disclosed here used a computer simulation technology called an agent-based model, or an ABM, to explore a constrained set of self-organizing social properties and behaviors believed to exist at the least-organized end of every complex (human) social system. The reason one should care about this work is that it experimentally asks questions about the social antecedents of the household, reciprocal

exogamy, and modern sociality. These are basic life questions whose answer, for the most part, has only been handed down to us over the centuries by myth and religion. This work examines the basis of sociality (ours) computationally, experimentally.

In particular, the social system(s) studied were several populations of detailed, highly-social, initially promiscuous, primate-like software agents that inhabited an explicit, virtual environment. It is believed the experiments created a plausible, artificial social fabric within which the agents were able to autonomously generate adaptive (survival-related), innate, small-group social behaviors. These behaviors are believed to have spontaneously emerged from within the population and included community fission and fusion (Isbell & Young, 1996), voluntary migrations, simulated sexual reproduction resulting in new agent birthing, aging, and death, and semi-permanent breeding-bonds.

1.1 Research Question

The research question asked if it might be possible to bring about emergent and permanent agent breeding-bonds, breeding-pairs, family units, clan-like social structures, or nascent reciprocal exogamy within an otherwise wholly promiscuous, (primate-like) population. Simply put: Might it be possible to cause “household-like” social organization to arise within a population of promiscuous, artificial, primates by endogenous rather than exogenous means?

In order to test the question, a decision was made to use a single (independent) variable experimental protocol. The independent variable chosen was the pro-social trait,

social altruism¹ (defined here as non-reciprocal and non-kin based). This is a trait that in humans is known to be cross-cultural and believed to be phenotypic (at least since Hamilton, 1963). And, because the experimental protocol required that social altruism be added to or removed from every member of the population under test, it was quickly understood this experiment could not be run on living beings. At this point, a system model based on the primates *Pan* and *Homo* was adopted (for computational purposes), a simulated control population of those primates and capable of generating a robust socio-environmental simulation pedigree was instantiated (for experimental purposes), and a commitment made to do the research. After several months of work the final results shown in Section 4.2 were produced. Many of those results compare favorably to the empirical evidence seen in the primates adopted by the system model. This dissertation describes these experiments as they tried to answer the research question. What follows is an explanation of how the model was conceived and constructed.

1.2 System Model

The experiment involved a system of independent agents comprising a population of simulated primates situated in an explicit and forageable, niche habitat. A niche habitat was used in order to allow for tight experimental control of variables and to demand that plausibility exist at every level of the experimental protocol. The experiment explored the complex social system that emerged within the population at its socially least-organized end. The population and their habitat (a virtual environment) were instantiated with as much empirical realism as possible while still maintaining a simplified system

¹ The genetic basis of social altruism and implicitly social alliance is stipulated. The experiment does not test their evolvability or inevitability, only the effect of their presence or absence on a population.

model. The system model involved giving the agents simulated sexually dimorphic biology with features like sex-specific nutrition and water requirements (Portman, 1970; Milton, 1999; Association of Zoos and Aquariums Ape Taxon Advisory Group (AZA Ape TAG), 2010), and primate-based reproductive fertility constraints (Tutin, 1979; Lancaster, 1986). Additionally, each agent enjoyed artificial genetics (an 88-bit chromosome), autonomous terrain mobility, and the capacity to suffer cognitive dissonance (Festinger, 1957) when/if frustrated by unsatisfying foraging options. They demonstrated emergent genetic drift (Wright, 1932) through Baldwinian evolution (Baldwin, 1896) and each one had the need to survive long enough to fulfill its individual obligations to participate in the dynamic maintenance of viable population numbers. Above all else, the agents had to survive enduring periods of simulated time within their habitat through self-selected, artificial sexual reproduction, and natural selection (Darwin, 1859).

1.2.1 Constraints

The greatest single constraining issue confronting (and liberating) the success of the experiment was the fact that very little is actually known about how permanent breeding-pairs, or “households,” came into being during the evolution of our species (Chapais, 2013). Additionally, conflicting with the stated research question was the knowledge that the sharing of food resources among primates is generally unrecognized outside of *Homo* (Jaeggi & Gurven, 2013). And finally, the research question itself implicitly contradicted at least one first-principle belief sometimes associated with cultural anthropology (although typically stated axiomatically) that the most basic structure of human social

organization, the “household,” is the primary social unit from which complex social organization emerges in nomadic societies (Rogers, 2007; Cioffi-Revilla, Rogers & Latek, 2010). These challenges required the adoption of a foundational “temporal perspective” when constructing the system model.

1.2.2 Temporal conjecture

There is a temporal perspective underlying the current work and it is within that temporal framework that the system model and the research question were constructed and studied, respectively. An experimental assumption here is that it was among the earliest hominids, the *Homo*-antecedents like the *Ardipithecines* (Lovejoy, Suwa, Simpson, Matternes & White, 2009) and the *Australopithecines* (Asfaw, 1999) that the behaviors we will study first emerged. Moreover, the behaviors we must consider explicitly involve (sexually) reproductive social activity.

To confound our work, we must also understand that while reproductive activity, as a social behavior, may generate ultimate (proxy or fossil) artifactual evidence, it cannot fully explain the proximal cause of those artifacts or those behaviors. Therefore, since there can be no complete record of the causes or circumstances of the proximal reproductive social behavior of the earliest hominids; the when, how, or why our hominid family transitioned from polygamous *Gorilla* and or promiscuous *Pan* into the societies of *Homo* whose behavior is often characterized by stable breeding-pairs, and more recently, “households” cannot be known deterministically. This may seem somewhat frustrating. But, actually, it liberates us to consider the research question from several

viewpoints simultaneously and to pursue a balanced conjecture involving proxy evidence and time.

For example, we may choose to consider the phylogeny of our species. We may examine our current corporal morphology versus those of our ancestors, our own cognitive capacity versus the implicit cognitive capacity of our ancestors (based on modern tests, post-mortem and fossilized cranial capacity evidence), the occulted estrus of the females in our species versus the visible estrus of those others in the primate line, the tendency of our species to practice indiscriminate patrilocality and or matrilocality in extended family groupings versus a rigorous species-wide either/or philopatry and dispersal as do *Pan*, *Gorilla*, and *Pongo* (orangutan) in the wild. From these perspectives we might conjecture the causal root of the “household” lies somewhere, temporally, within the Homininae sub-family of African primates shown in **Figure 1** specifically located sometime after the *Pan-Homo* split 5 – 7 million years ago. However, that may be just about as exact a time frame as we may deduce. **Figure 1**, inspired by Chapais (2008) but amplified by all of the foregoing concerns, illustrates how the genus of *Homo*, within the African Primate order, is easily differentiable by its physiology and core social behaviors. However, less clear is the path of the social and cognitive character of *Homo* as it emerged within the Hominini tribe manifest through a transition from polygamous/promiscuous behavior into permanent breeding-bonds and breeding-pairs. That is the question that concerns us here. How and why did this happen?

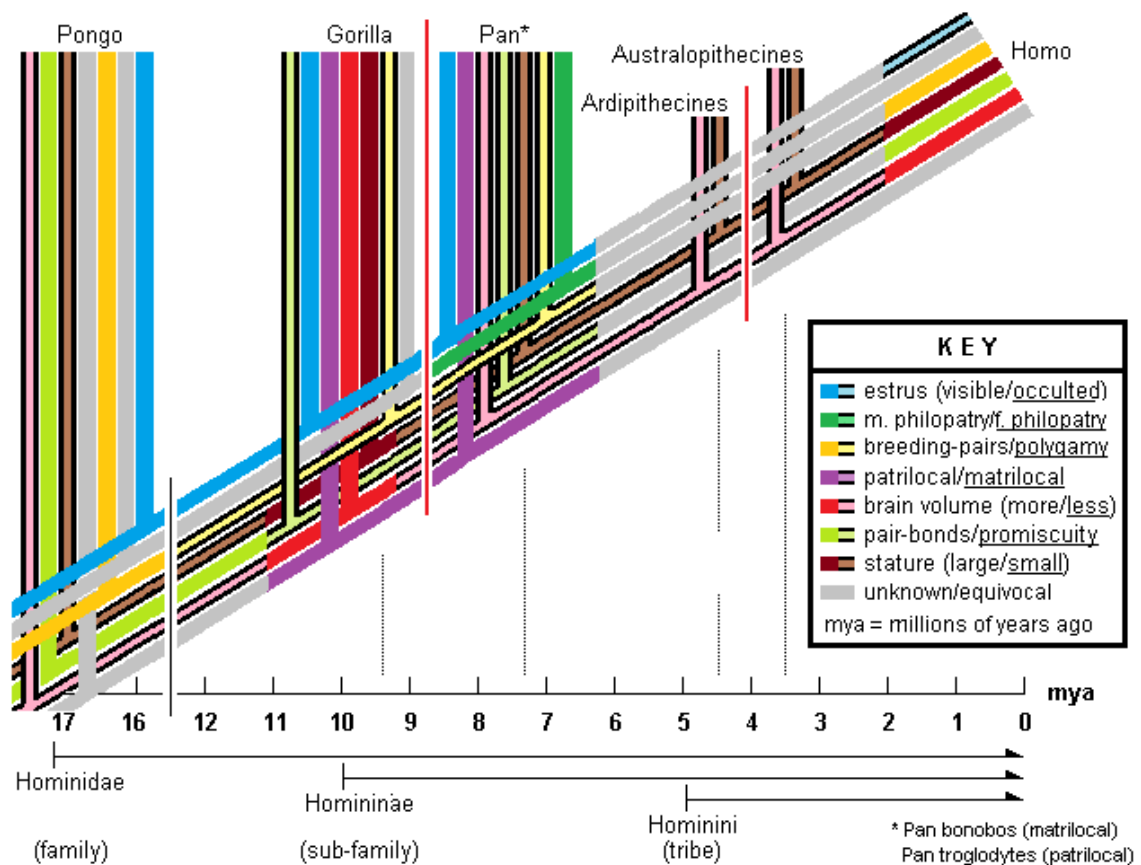


Figure 1 The “Family Tree” of *Homo*.

What this means is that our temporal conjecture cannot deliver a concrete explanation of how or why the “household” itself emerged. Rather, it can only frame our work and the entire set of questions we will ask. Did “households” spring forth fully formed in the species of *Homo ergaster* or *H. sapiens*, while hiding nascent in the genera of the extinct *Ardipithecines*² and or the *Australopithecines*? Did the household” co-evolve with hominid cognitive capacity or was it singularly caused by ecological pressure? Answers to these questions may actually lie outside the scope of our knowing.

² *Ardipithecines* (members of the species *Ardipithecus ramidus*) have sometimes been nicknamed Ardi.

But, our questioning will give us an idea about what must be our system model; about how we might build our software in order to try and answer these questions.

The system model taken for this research involves a pristine niche ecology within which are situated explicit, primate-inspired, social agents as a (hypothetical) hybrid *Pan-Homo* species. Using an artificial (computational) niche ecology permits us the luxury of studying our research question in-silico and with complete control over what cultural confounds will, or as in our case will not, interact with our agents as they evolve, adapt, and survive as a simulated species. Considered another way, the temporal conjecture and this research is grounded upon two symbiotic hypotheses: 1) *a pristine environment is necessary for the identification of the fundamental principles of small-group social behavior*, and 2) *an environment having a sufficient absence of cultural confounds but also one having a sufficient fullness of socio-environmental stimuli is required for a complete understanding of “emergent” sociality*.

1.3 Research Perspective

This research is science performed using simulation technology. These experiments tested a single independent variable hypothesis, made comparisons between a control setting and experimental results, and were constructed using empirical data taken from published literature. More specifically, this was generative Computational Social Science. It grew out of models of the type instantiated by Epstein & Axtell (1996), Kohler, Kresl, Van Wes, Carr, & Wilshusen (2000), and Axtell, et al., (2002) and it was inherently deductive in its approach. This work based its algorithms and conclusions on

computation drawn from empirical or empirically derived parameters (**Appendix A**), objectively substantive relationships, and observable processes (Epstein, 1999).

1.4 Model Complexity

The set of all things *sufficient* to describe, or model, a complex system must include at least those things which are *necessary*. However, without a priori knowledge of the enumeration methods of the former, a systems modeler will always be tempted to include too many (or too few) of the latter. Given the research question explored here and the complex social system it surveyed, this experiment was no exception. Indeed, even the act of conceiving of a system model sufficient to capture the determinant features of the system under study was an incremental and difficult process. It was believed from the outset that to address the research question plausibly, fully, would require the creation of a simulation having independent, socially-aware, biologically-grounded, hominid-like agents situated in an explicit virtual environment. Moreover, it was felt that in order to validate any experimental findings, those same agents would need to exist for an enduring time³ and produce results that could be compared to empirical data from similar species living in the wild. The short-sighted goal was to develop a system model of a complex social organization from which system artifacts like birth rates, infant mortality rates, incest occurrence, breeding-bonds, breeding-pairs, and possibly “households” might emerge as outputs rather than as parameterized inputs as they do in more traditional models of social organization and or social complexity. It is believed the

³ In this dissertation the phrase enduring time, or enduring periods of simulated time, will refer to an experimental definition of simulation time intervals lasting at minimum hundreds, or preferably thousands, of years of simulated days.

short-goal was a measured success. The long-goal however, model validation, may only have occurred in the last demonstrator experiment. In that particular experiment the simulation lasted for over 10,000 years-of-days. And, for most of the simulated interval, the population had a cohort to land-occupation ratio of roughly 60 to 120 hominids over a 64 km² region. The agents in this simulation had to be manually terminated. So, while the set of factors *sufficient* to produce emergent permanent breeding-pairs (or the ‘household’) may remain at arms-length to us, in defense of the model created, great care was taken to evaluate and decide on the inclusion (or exclusion) of each parameter and process believed to be *necessary*. In summary, the Model Complexity sub-section may answer a rhetorical question so often heard by the author: Why is the model and the software so complicated? The answer is simple. It is a tiny model of life, artificial life.

1.5 Motivation

This dissertation is motivated by a desire to better understand small-group social behavior. In particular, its goal is 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 developed for this dissertation, that we can begin to visualize the emergence of the structures most fundamental to complex human social organization. Simulation allows 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 not an exclusive list.

1.6 Research Contribution

The contributions made by the research described here are four-fold: First, this work contributes a finding that emergent small-groups of independent actors having relatively permanent breeding-bonds can emerge out of a cohort of wholly promiscuous individuals when the initial cohort is changed by nothing more than the addition of social altruism. Implicitly, this may suggest the existence of a necessary social “stepping stone” leading to the “household.” Second, this dissertation contributes to the permanent record of science by reporting its own existence and the system model it developed. Third, a contribution of the work was to make plain its own motivations, intent, methods, and results. And finally, fourth, a contribution made by this research is a thorough description of the tools used so that the work can be replicated.

Anyone suggesting that this research is or should be complete would be tacitly admitting a lack of any personal understanding of the complexity of the problem at hand. Indeed, fully answering the question of how (and why) did our “Family Tree” transition from being a cohort of promiscuous/polygamous apes into small-groups having affine relationships is something we cannot do today. Therefore, this research is just one step along a much longer path. We have only just begun to identify, and then to investigate, the *necessary* and *sufficient* causes of the origins of social complexity.

1.7 Organization of the Dissertation

The thesis of this dissertation was prepared and presented as a peer-reviewed essay at the European Conference on Artificial Life (ECAL) in York, United Kingdom, July 20-24,

2015⁴. Thus, the organization of this dissertation is simple: it follows but significantly extends the ECAL essay (the thesis). The reader will find sections named Introduction (Chapter 2), Method (Chapter 3), Results (Chapter 4), Discussion (Chapter 5), and Summary/Conclusion (Chapter 6) each of which track and extend the ECAL thesis essay, respectively. In each of the Chapters, beginning with the Introduction, the first part of each Chapter will be a reprint of the respective section from the peer-reviewed ECAL paper. In some cases the ECAL paper will have been slightly edited in order to fit into the layout of this dissertation. The second part of each Chapter will be new material added for this dissertation. In general, the new material in the second part of each Chapter will add details that enlarge and or enhance the general scope and delivery of the first part of the Chapter. Additionally, there will be a brief introductory section in each Chapter that attempts to introduce and describe what will follow.

This dissertation spans interdisciplinary topics ranging from computation and computational technologies to biology, primatology, ethology, psychology, anthropology, and social science. It reveals its experimental constraints by cross-listing the Constant parameters used in the software (named Clans) within **Table 2** (in **Chapter 3**) onto a topical list of the substantive biological, cognitive, situational, and environmental assumptions underlying the construction of the agents and the synthetic environment they inhabit. The constraints and the assumptions are grounded within the literature resources topically outlined in **Appendix A**. By using material in the **Appendix A**, a reader can

⁴ Rouly, O. (2015). At the root of sociality: Working towards emergent, permanent, social affines. In Andrews, P., Caves, L., Doursat, R., Hickinbotham, S., Polack, F., Stepney, S., Taylor, T. & Timmis, J. (Eds.). *Proceedings of the European Conference on Artificial Life 2015*. pp. 82-89, MIT Press.

follow the citation references into the bibliographic **References** list at the back of the dissertation to discover the research literature that was used to establish the empirical authority, the basis of the system model, and the face validity of the experimental science.

Appendix B contains header-profiles for the report files that are periodically generated by the program during runtime. These header-profiles are not explicitly intended for (user) reading. Rather, they are intended to serve as amplified footnotes describing the schema (a form of data organization template) produced by the operation of the simulation as it records runtime events. By referring to the schema, a user of the simulation may craft stand-alone spreadsheets or other analytic and or graphical illustrations of the simulation output whenever they choose.

CHAPTER 2. INTRODUCTION

The first part of this chapter is a reprint of the same-named section of the peer-reviewed paper presented as a public talk at the European Conference on Artificial Life (ECAL) in York, United Kingdom, July 20-24, 2015. The second part of the chapter (Sections **2.2**) is entirely new material unavailable to the ECAL conference. Included in the latter sections are results of a literature review that hopefully lends support to the implicit claim of novelty made by the paper and this dissertation.

2.1 ECAL Paper

(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, et al., 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 (see Section **2.2**) 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, bio-psychological, 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 which have no socio-temporal interaction memory or explicit socio-spatial context (Gavrilets, 2012) really be reliable indicators of the causes of human sociality? Or, can explanations devoid of biological representation or rich socio-environmental interaction (Kaulakis, 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, de Waal & Haig, 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 the 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.

2.2 Background

This section speaks to the claims of uniqueness and implicit novelty laid out in the previous section (the ECAL paper) where it was bluntly stated that a search of the literature would reveal only “scant few computer models” testing the research questions motivating this dissertation. The format of the ECAL paper could not support an extensive literature review. So, within the next three sub-sections, the results of a literature review are presented. Simply put, this review was unable to find any reference to either a combined body of work or any single experiment that computationally dealt with all of our questions regarding the emergence of most basic structures of human social organization; at least as they are dealt with here. First, there is a table that expands these ideas but in a concise format: this is **Table 1**. Second, it could be said that the research most theoretically similar to our own might be the work of Gavrilets (2012). Although, it could also be argued that the work appears to be computationally incomplete, i.e., it lacks sufficient explicit evidence of a computer-based, individual-based modeling, analytic treatment. Many other works were discovered and are also described in the second section. These too will be compared for their overlap onto the current research. Among those works was that of Epstein & Axtell (1996) and Axtell, et al., (2002). These demonstrated a very high degree of computational overlap in that the authors developed a generative agent-based model to test their hypotheses. However, the authors did not address our research question. Other research will be considered as well. The third section explains the criteria used to test the literature for inclusion or exclusion into the final comparative list.

2.2.1 Table of comparisons

Table 1 Comparisons between this and related works in the literature.

	Epstein & Axtell	Gavrillet	Griffith, et. al	Gros, et. al	Hemelrijk, et. al	Kaulakis, et. al	Suzuki, et. al	Rouly
state memory								
epoch (day or less)								
enduring time								
individual agent-actors								
birth								
weaning								
sexual maturity								
fertility cycles								
death								
autonomous mobility								
philopatry/dispersal								
social interaction								
altruism								
preferential relocation								
kin-based recognition								
social-causality								
sexual dimorphism								
sexual reproduction								
incest rejection								
networks								
culture								
environmental parameters								
terrain height differentiation								
explicit forageables								
water sources								
weather/temperature								
climate/seasons								
cognition								
cognitive features								
Maslow prioritizations								
drive-reduction								
temporal inference/order								
evolution								
artificial genetics								
Darwinian effects								
Baldwinian effects								
genetic drift								

2.2.2 Literature review

Beginning with at least Hamilton (1963; 1964a; and 1964b), many authors have logically extended Darwinian evolutionary theory into the domain of altruism and social behavior. Moreover, the existence of altruism as a shared trait within this experiment is stipulated and is not in question as to its fitness or evolvability. This was not an experiment testing the fitness, evolvability, inevitability, or the utility of social altruism. The works of Wilson (1987) and Wilson, Pollock & Dugatkin (1992) would be more typical of this latter line of theoretic inquiry.

Among recent scientists to consider questions about the transition of higher-primate breeding practices from promiscuity/polygamy to permanent breeding-pairs over evolutionary time has been Chapais (2010; 2013; and 2014). He has proposed a theoretic framework for the emergent social change in hominids: something that he calls the “deep social structure” of mankind (2011). This dissertation has been critically inspired by his work.

Epstein & Axtell (1996) and Axtell, et al., (2002) are arguably the most influential contributors to the advancement of, and generally in the field of, agent-based modeling for CSS. Their joint and individual seminal works of *Sugarscape* and the Anasazi Paleo-Indian culture replication experiments demonstrate the highest-order of multi-agent social interaction with emergent social, cultural, and autonomous locomotion, simple cognitive components, and evocative questions concerning the practical limits of this simulation genre for experimental social science. Their works succeeded within their scope and mandates. One believes if their tasking had also included a demonstration of more

detailed metabolism, longitudinally emergent social networks, kin-based social relationships, long-term genetic effects, or isopraxis realizations (MacLean, 1975) like altruism or philopatry and dispersal they and their colleagues could have easily conquered the challenges.

Gavrilets (2012) has specifically addressed the issue at hand by offering a non-linear symbolic model describing social forces driven by evolved biology and changing patterns of mate protectionism. This is an evolutionary dynamics model evaluated exclusively using the concurrency of sequential (iterative) computation. The model is rich in plausible social-causality but lacks any environmental parameters, agent heterogeneity, or subjective individual agent memory. Gavrilets cautions us to use heterogeneity in modeling complex social systems so he leaves us wondering why he does not heed his own advice. This work seems to propose that humans developed pair-bonding without benefit of socio-environmental, complex, and socio-personal interaction.

Griffith, Long, & Sept (2010), Janssen, Sept, & Griffith (2005; 2007) produced a set of possibly two models and three reports on experiments exploring questions about *Australopithecus boisei* and *Homo ergaster* foraging behavior. Since these works may be overlapping in code-use and or hypothesis testing, it is difficult to know if there were actually two or more models described by the authors. These works involved detailed agent-based models on an explicit terrain with diverse forageables and fine-grained time-scales (sub-daily units). Their works did not report the effects of Baldwinian evolution or any cognitive features. Their agents also did not reproduce or have artificial genetics. Finally, sociality was not featured in the Griffith and Janssen works. In contrast, sociality

(or at least its emergence) is an artifact of the dependent variables pursued by this thesis model.

The work of Gros, Hovestadt, & Poethke (2008) involved an experiment somewhat similar to the work of this thesis. This discrete-event simulation centered on an individual-based model (IBM) considering the concurrently evolving and evolved consequences of sexual dispersal and incest in relationships between agents. However, unlike this thesis model, the agent population in the Gros, et al., model was fixed and survival of individual agents was not determined by run-time choices made by the agents themselves. Rather, the agents had alleles that expressed for dispersal tendencies and the experiment was run to find out which, if any, dispersal strategy was more successful.

Hemelrijk (1999; 2002a; 2002b; 2002c), Hemelrijk, Wantia, & Gygax (2005), Hemelrijk & Steinhauser (2007), and Hemelrijk, Wantia, & Isler (2008) disclose a set of models and model extensions that are absolutely exquisite. These agent-based and individual-based models⁵ capture terrain, sociality, temporality, state memory, foraging dynamics, sexual and non-sexual competition dynamics within minimally seven reports. However, the works do not claim any underlying artificial genetics or evolved Baldwinian effects. Although it is understood the model might demonstrate simulation time intervals of days to weeks there is no indication the authors made an effort to obtain enduring simulations on the order of thousands of simulated years.

⁵ The difference between an agent-based and individual-based model is somewhat subjective. While the encapsulation of encoded purpose within the software entities that are the agents is similar, an agent model may purpose itself with greater abstract anthropomorphic focus or intent than an individual model. By contrast, then, an individual model may just as easily capture anthropomorphic elements but may also abstract for non-human agency or concentrate on non-human elements. These later models, and also the former, may find useful application in spatial constructions. Both are considered forms of multi-agent systems or models. In the mind of the author the terms can be used “almost” interchangeably.

Kaulakis, et al., (2012) produced a social network model upon which analysis of endogenous features like membership number, organizational configuration, and cognitive processing (characterized) by information transfer were considered. This model reported no environment, no social template, no genetics, no agent mobility, nor enduring time simulation. While output from this work is social in nature and it did use computation to achieve its ends, it is believed that Kaulakis, et al., did not come close to achieving any meaningful comparison with this thesis model.

Suzuki & Arita (2010) constructed a model that explicitly explored the results of niche ecology construction when agents are empowered by Baldwinian choices. The authors tightly constrained their exploration to results on a small grid wherein changes made to the habitat (grid) were either the consequence of sequential processes or parallel processes. Not unsurprisingly, more rapid niche evolution was found to be related to emergent parallel processes. The model does not admit sociality, agent foraging, enduring simulation time, or dynamic sexual reproduction of its own agent population. In fact, the agents in this work operate more like software objects within an object oriented program than actors in a discrete event simulation ABM or IBM.

Wilson (1987) and Wilson, et al., (1992) presents theoretic models that consider the rational cause, effect, and value of altruism as it involves evolved sociality. Wilson (1987) examined the relationships between hypothetical siblings to determine if altruism might evolve in a setting absent a plausible ecology. In a later and comparable model, Wilson, et al., (1992) presented a gridded system with a lottery-based, binary schema used to approximate the ultimate evolutionary value of altruism.

2.2.3 Comparison list criteria

Many reasons exist for evaluating related previous literature. For example: 1) one may want to know what was done before in order to intentionally repeat, or avoid repeating, an experiment, or 2) if similar work was done before then one may want to know if the previous work can advise the current work. Unfortunately, no honest literature search can conclusively prove the non-existence of previous work. This would be a proof of the null hypothesis. However, if an honest effort is made to locate existing literature resources and if those efforts are competent, consistent, and graded against a value-based rubric then, a point of departure for comparison and evaluation of new work can be made. It is upon this basis that **Table 1** was constructed. It could also be noted that each entry in table is not a parameter, *per se*, in the experimental software. Rather, here in the comparative literature section, the entries in the table reflect primary modeling concerns and or model paradigms implicit in the system model (Section 1.2) that could be identified in related literature and that dictated how the experimental software was to be constructed. That said there may actually be instances of the some of the table entries as variables, by name, in the software. For example, epoch is a variable used by name and that represents the count of times (years) the model has completely cycled. But, this is an exception. Consider that evolution, also a table section entry, has two important sub-sections named for implicit paradigms that underlie the temporal conjecture (Section 1.2.2), that were instantiated in the experimental code, and that were understood to require the software instantiate mechanisms simulating artificial evolutionary genetics (Darwinian across generations) and behavior-adaptive genetics (Baldwinian over

evolutionary time). However, neither the word Darwin or Baldwin are variables in the software.

When surveying the existing literature, a few concepts and components believed to be primary modeling concerns and or model paradigms critical to the plausible operation and instantiation of the system model became apparent. These concepts and or components became the corresponding entries in the table. The following paragraphs iterate over those entries by heading and sub-heading. If a model reviewed in the literature had substantial overlap with the work here then, the other work (by author) was listed on the table and its overlapping characteristics noted. If the other work did not overlap the current work then, that work was not included. There was literature evaluated that is not listed on the table.

For example, the works of van der Post and Hogeweg (2004; 2008; 2009) as well as van der Post, Ursem and Hogeweg (2009) were considered but not listed in the table. These works described ABMs of high-quality, with rich explicit and abstract culture transmission. The works were not listed in the table because it was felt they lacked sufficient foundation in the areas of enduring time, artificial genetics, cognition, and small-group interaction.

Other works, like the work of Yager (1994) were considered but were not included. His was an ALife project that was highly abstract and generally ahead of its time. But, it was felt, the work was without sufficient explicit formulation for relevant genetic and biomimetic features similar to those of *Pan* or *Homo* in metabolism and or reproduction to be included based on plausible merit. Yager “grounded” his agents with

a simulated visual sense and achieved unprecedented success in that regard. This was an example of agents foraging, evolving, and reproducing autonomously. However, the work did not demonstrate any psychological formalism and or construct theory. The agents apparently made no use of temporal inference or temporal ordering as they made life changing decisions. The agents did not admit any subjective drives or innate priorities beyond those evolved by their neural networks. For example, Maslow (1943) and Festinger (1957) were not mentioned. There was no mention of social networks, genealogical or otherwise, and was there was no mention of kin-based recognition.

2.2.3.1 State memory

The state memory section attempts to identify the use of formal and or abstract processes a simulation may use to maintain synchrony among its computations, actors, and side-effects. In the current work there are several such processes that serve in the artificial environment and or the simulation of agent-actors within that environment. In the models considered here, state memory also symbolized the implementation of a formal step-iterator like a unit-event, a day, or a cycle indicator. By contrast, an evolutionary dynamics model, like Gavrillets (2012), appears to make exclusive use of concurrency but has no explicit synchronization mechanisms other than the sequential iteration of computation itself. Most critical among variables holding program state may be the master loop counter (referred to here in this research as an epoch). In general, this rubric put a high value on simulations demonstrating enduring simulated periods of time. Thus, this rubric looked for simulations suggesting they could iterate and track accumulated epochs (intervals) numbering or representing thousands of years-of-days.

2.2.3.2 Individual agent-actors

The individual agent-actors section is the most subjective part of the table. This section considered model plausibility derived from abstractions of hominid life and behavior. Birth connoted a simulation that possibly had its agent-actors instantiated dynamically (during runtime) and that may have held a place in state memory. Similarly, death connotes an agent model having a place in state memory for death. Moreover, a dead agent should have experienced birth. This work dealt with simulated mammals.

Weaning is a life phase through which all mammalian life transitions, is pertinent to the context of learned behaviors leading to self-sufficiency in foraging, and was important to the system model instantiated here. Thus, it was added to the table. Fertility, philopatry/dispersal and sexual maturity are all intertwined hallmarks of primate socio-cultural foundation and are believed necessary to drive the basal extents of sociality sought by the experiment. Finally, autonomously initiated mobility is an enabler of (non-philopatric) dispersal, facilitates foraging over seasonally modulated terrain and dwindling food resources, and is ubiquitous among (it seems) all living creatures. Each of these properties contributed to the instantiation and subsequent evaluation of external literature for inclusion/exclusion to the individual agent-actors comparison list.

2.2.3.3 Social interaction

Social interaction is the heading of the next section of the table. This section looked for evidence of either explicit or inferred social interaction in the reviewed literature.

Altruism, an independent variable in the current experiment needed to be mentioned in any experiment (from the literature) if it were considered for addition to the list. So too

did preferential relocation contribute a similar result between the reviewed material and the current work, and for similar experimental reasons. In real primates like *Homo*, *Pan*, and others kin-based recognition lays a framework for social interaction (Maestripieri, 2012), dominance hierarchies (Hemelrijk, et al., 2005; 2008), and family groups (Chapais, 2008). Social-causality is an entry that represented a recognizable agent-on-agent cause and effect relation. Simply, if one agent did something to another agent during a simulation then the agent acted upon would need to react in some way. A reviewed model would need to demonstrate some form of social-causality in order to make it onto the list. Sexual dimorphism is an implicit cause or contributor to behaviors that differentiate between two agents of different sex. Dimorphism may relate to biological differences in subject mass, caloric requirement, or issues of fertility and reproduction. Likewise, sexual reproduction not only facilitates agent births into the next generation but also relies on sexual dimorphism for its basis. Incest rejection is a discriminatory feature of most social systems. In the system model it is implemented according to theory attributed to Westermarck (late in Section 3.3.3.3.7). It is an implicit directive on how social group members interact in primate society. Incest rejection needed to be accounted for if sexual reproduction was the basis for generating new agent-actors. Thus, it appears in the comparisons table. Social networks exist between two or more interacting agents whether that network is explicitly defined or only implicitly recognized by an observer. Once birth occurs from sexual reproduction a genealogical network is implicitly formed and then tracked in this research (Section 3.3.3.3.7). Reviewed literature had to indicate some sufficient degree of consideration of emergent

social networks in order to be listed on the table. Finally, in the current work, culture is an emergent artifact and one that is often correlated with spontaneous migrations of the *Pan-Homo* hybrid. Only the research project of Epstein & Axtell (1996) was thought to sufficiently address the property of culture and thus made it onto the list.

2.2.3.4 Environmental parameters

Within the bounds of what questions this research was designed to consider are those open ended questions searching for the causality for social outcomes in circumscription: climatic, environmental, bio-evolutionary, social, etc. In this section, environmental parameters, the problem space of plausible agent virtual environments in the literature is addressed. In this research the system model and the temporal conjecture both relied on a plausible virtual environment in which to situate the simulated primate agents and thus imply causality. However, the test for the literature was did it imply or explicitly state that it incorporated plausible explicit or abstract terrain height differentiation, explicit forageables, water sources, weather/temperature, or climate/seasons? If it did then, that literature was eligible for inclusion in this section.

2.2.3.5 Cognition

This part of the table is the most imprecise: dealing with implicit stimulus causality and explicit behavioral consequence. Cognition is the next section of the table and it concerns itself with a covert behavior, a process having only notionally identifiable character, may be an implicit precursor of some overt behavior, and has no deterministic component. Any model referenced in the literature that contained evidence of sufficient overlap to the broad goals of this work and modeled cognition as it is defined here was

considered for inclusion in this table section. The Heuristic, Algorithmic, Learning (HAL) section (Section 3.3.3.3.5) of this dissertation addresses the components of those cognition-like properties instantiated in the agent-actors of this research. Beginning with cognitive features (like an ability to recognize and react to a source of drinking water if thirsty) and ending in an innate ability of the agent-actor to infer and or to explicitly order goals temporally (temporal inference/order), the cognition section either qualified or disqualified related/relatable research from the literature for inclusion in the table. Drive reduction, a property of adaptive, intelligent creatures and described in Hull (1943) can be recognized in association with subject, subject environment, antecedent stimulus, subject behavioral response, and stimulus reinforcers. The incorporation of a drive reduction component in the system model of this research is a defining feature. Literature wherein drive reduction could be recognized is noted on the table. Maslow hierarchy prioritizations are cognitive schema providing covert (and subjective) pressure on an agent-actor to temporally order subjective drives for reduction. In particular, Maslow (1943) finds its way into the cognitive behavior scheduler of this research in the following sequential pattern, “fear/panic, water, food, group, dispersal, comfort” (see Appendix A.1.11, “drive order”). Literature that explicitly dealt with Maslow or implicitly prioritized behaviors in a similar way are noted in the list.

2.2.3.6 Evolution

This section identifies external literature that coincides with the current work in the domain of system motivation bias. The bias in this research is that evolutionary processes drive agent social change but that environmental changes in turn drive

evolution. As subjects of these mathematically complex processes, agent-actors are the derivative products of their own artificial genetics situated in a virtual world. In this research, each agent-actor has its own 88-bit chromosome with 11 unique genes. Each gene is assigned a biomimetic function that maps onto the physiological and or behavioral predispositions of the agent-actor. Evolutionary effects, be they Darwinian effects or Baldwinian effects, contribute to the ultimate emergent social order produced by the model and displayed through the behaviors of the individual agent-actors in the simulation. Genetic drift is an emergent outcome of inter-agent intercourse within the virtual environment, modified by Baldwinian choice and Darwinian selection, and enabled by the artificial genetics each agent-actor possesses. Specifically, genetic drift provides a quantifiable measure of social change through biomimetic means. If external literature addressed the foregoing issues in the context of the current work then, that literature made the list.

CHAPTER 3. METHODS

The first two parts of this chapter are an edited reprint of the same-named sections of the peer-reviewed paper presented as a public talk at ECAL in York, United Kingdom, July 20-24, 2015. The third part of the chapter (Section 3.3) is entirely new material unavailable to the ECAL conference and captures an informal Software Design Description (SDD) loosely joining purpose, scope, context, and summary per the Institute for Electrical and Electronic Engineers (IEEE) Systems Design Specification 1016-2009⁶. Simply put, the purpose of the SDD here is to provide an overview of program structure, data flow, variable names, architecture components, modeling paradigms, etc. Only where necessary does the SDD discuss design motivation and then it does so only to the extent believed appropriate to clarify how the adjacent and or distal model sub-components interrelate. The SDD will describe hardware, software, and Constant parameters definitions, will provide abbreviated citations referencing primary sources of Constant parameter authority, and a breakout of the artificial genetic structure of the agent-actors. **Appendix A** and **Appendix B** contain additional materials that may assist the reader should they decide to anticipate model reproduction or “docking” (Axtell, 2000).

⁶ IEEE Standard for Information Technology--Systems Design--Software Design Descriptions. <http://dx.doi.org/10.1109/ieeestd.2009.5167255>

3.1 ECAL Paper

(Methods)

We know that the hominini, a tribe that includes the species *Homo* and its extinct ancestors, e.g., *Ardipithecus* (Lovejoy, et al., 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 (Bower, 2015). 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, 2008) 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, 1970; 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.*

3.1.1 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.

3.1.1.1 Code donor 1

In search of 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. **Figure 2** is a graphic produced using *NetDraw* (Borgatti, 2002). The graphic depicts a typical social network that often emerged within the genetics of the 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 among the agents in the model. What is visualized is a population-inclusive effect called Genetic Drift, or the Sewell-Wright Effect (Wright, 1932). The image graphically articulates the drift that emerged within the chromosomes of the agent population over 4,259 years-of-days using shades of the color yellow. This captures the emergence of the effect within the genetics of the 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 color shift from the center “rings” (first generations) to the outer “rings” (last



Figure 2 The Sewell-Wright Effect emerges in an artificial agent social network.

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.

3.1.1.2 Code donor 2

A prototype, multi-agent system for the study of the Peopling of the Western Hemisphere (Rouly & 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.

3.1.1.3 Code donor 3

Sexually differentiated philopatry and dispersal: A demonstration of the Baldwin effect and genetic drift (Rouly & 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 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 3 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. On the left is an illustration of the initial distribution of a representative gene value in the starting

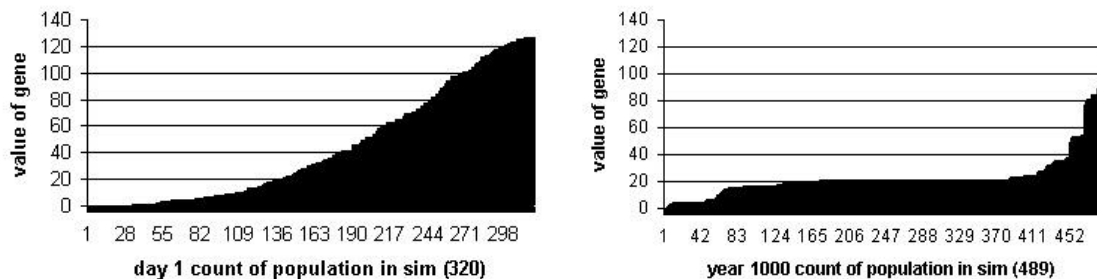


Figure 3 Genetic drift (Sewell-Wright Effect) caused by Baldwinian evolution.

population. The number of agents was 320 on day 1 and the values were initialized as a [folded] 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.

3.2 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 4** 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 per each square kilometer (Section 3.3.3.2). This is aimed directly at improving bandwidth utilization in multi-core processors with large random access memory (RAM) capacity. Together these changes allow topographical maps of spatial environments past,

present, or abstract to be imported for study. Finally, because of 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.

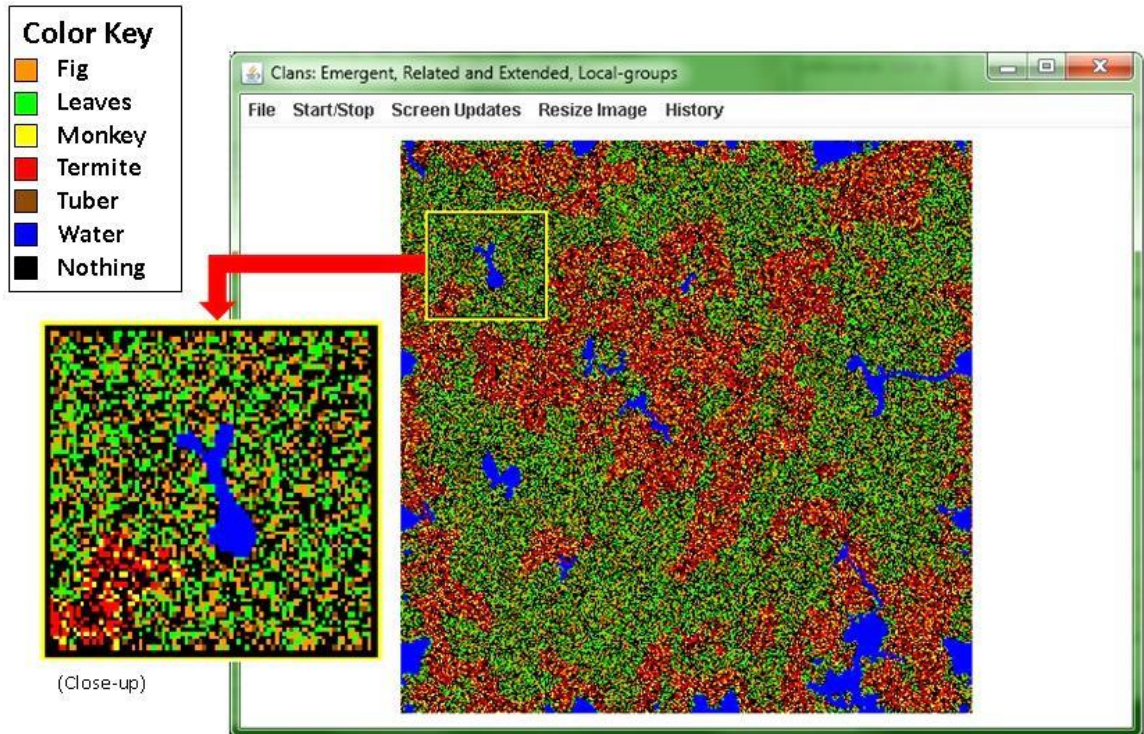


Figure 4 A 4 km X 4 km 2.5-D terrain map showing forageables distribution.

In this screen capture we see current model based on a 4 km X 4 km 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 (Section 3.3.3.2). 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.

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 & 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 Universal Serial Bus (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.”

3.3 Software Design Description Overview

This section (the SDD) describes the Java source code for the program Clans in summary overview. Clans extended previously existing Java resources. And, although Clans was created under Windows and on a PC computational platform, it has demonstrated that it can be transported, compiled, and may operate on other operating systems and other hardware platforms because of its underlying Java Virtual Machine (JVM) technology. Clans and the original, related code-base it extended, is original work. Clans is not built-on, or part of, any simulation framework or modeling environment constructed by anyone other than the author.

This SDD is organized into three sections loosely joining purpose, scope, context, and summary. The first section, Section **3.3.1**, contains a high-level description of the computational technology used to create the Clans simulation program. It will suggest a set of platforms (hardware, software, and entropy requirements) that might be helpful in replicating the experiment. The second section, Section **3.3.2**, illustrates the structural layout of the program in terms of its interrelated source code files and its underlying relationship to the Operating System file sub-system. The final section, Section **3.3.3**, discusses the operation and design of the source code as it relates to the research question and implements the system model.

The goal of this SDD is to introduce the reader to the methodology of the science the Clans simulation experiment undertook to represent. Clans addressed a research question using a system model originating in the domain of the Social Sciences. The subject matter was explicitly socio-environmental and required construction of computer code to create data structures and computational methods that could model the dynamic relationships that exist between higher-primates, their biology, the environmental niche ecologies they occupy, and intimate inter-social relationships that emerge between them.

Thus, as one might expect, any reasonable attempt to try and describe the methodological approach in general, and Clans in particular, will tend toward anthropomorphization. It is anticipated the juxtaposition of terminology between the engineering sciences and the social sciences may be uncomfortable to both the engineer (computational scientist) and the anthropologist (social scientist). Effort has been taken

to disentangle the two disciplines, making them stand side-by-side in the text in many cases, and to make the Clans SDD accessible to every reader.

3.3.1 Platforms for replication scope

Clans was specifically created (extended) using an existing Java code-base for the purpose of testing the hypothesis and research questions described in this dissertation.

When its predecessor forms are accounted for, this research has been in step-wise development for a period of four years. The purpose of this SDD is to aid in experiment replication. Because of this, the following platform technical details are provided.

3.3.1.1 Hardware

Recently, code development has taken place on an Intel Core-2 Quad Q8200 2.33 GHz CPU with NVIDIA-based PCI-X graphics acceleration. This is a consumer-grade device hosted by a Zotac PC motherboard with 4 GB RAM. The simulations reported in this dissertation have taken place on a dual Intel Xeon W5590 3.33 GHz i7 CPU with NVIDIA-based adapter graphics acceleration. This is an industrial-grade workstation with an Intel motherboard and 48 GB RAM.

3.3.1.2 Software

Clans was written in pure Java. It is believed that Java is a high-level, highly-transportable, computer programming language. Currently, the developer of Java is the Oracle Corporation.

3.3.1.2.1 Operating systems

The Operating Systems used during all development work were from Microsoft and included at various times XP, 7, and 8. The source code has also shown itself to be

compatible with the Apple products with minor modifications. (Description of any such modification needed to operate Clans on a platform other than a Windows computer is beyond the scope of this dissertation.) After compiling, Jar execution has been successfully demonstrated on Windows platforms. All simulation products shown in this dissertation came from PC platforms with the Windows family of operating systems using Jar execution.

3.3.1.2.2 Development environment

The Java Integrated Development Environment (IDE) was JGrasp version 2.0.1 Beta 2. The Java compiler was Oracle Java version 1.8.0_20. All verification tests and simulations were run in the Java Runtime Environment 1.8.0_20-b26 with client Virtual Machine (VM) build 25.20-b23 mixed mode.

3.3.1.3 Entropy sources

Clans needs a very large pool of randomly sequenced, non-repeating, integer and real-valued, random numbers in order to produce reliably descriptive output. In order to satisfy this requirement, Clans can be built (compiled) using the factory Java Class Random number generator or alternatively a hardware based entropy (random number) stream provider. The default mode of operation is to use the Java factory Random Class. If default operation using the Java factory Class is preferred then, no changes are needed in the Clans source code. Alternatively, if operation with a hardware based entropy provider is selected then, the Boolean variable “USE_FIXED” in the ModelConstraints file found in the Root folder will need to be changed to: USE_FIXED = false. Superior simulation results may be obtained through the use of an external entropy source. The

use of the TrueRNG⁷ USB hardware random number dongle as a streaming device is highly recommended.

Using the TrueRNG dongle will however, require the user provide and install the USB hardware and a few additional, external software components. If the user chooses to use a TrueRNG dongle then they will need to install at least one Windows USB Communications Device Class (CDC) driver in the Windows driver folders and the libraries of RXTX⁸ within the compile-time and run-time Java folders. Although internal software support for the TrueRNG dongle is already incorporated into the Clans source code, additional external Windows and RXTX software support for Clans TrueRNG hardware entropy generation is outside the scope of this research since it is optional.

3.3.2 Structural layout context

The source code is organized as, and is stored across, twelve packages (or folders) extending into and over a 3-deep hierarchy of Operating System folder levels. Root, the top-level package, contains the Java Class Clans (the same name as the program) and one other Java Class (ModelConstraints) that was previously introduced. **Figure 5** depicts the Clans packages, or operating system folders, as a tree diagram.

When compiling Clans, a compiler must have access to the Clans Class in order to compile and build the Clans program. The Java main method is in the Clans Class.

There is no separate make file provided with Clans in its current form. **Figure 6** shows a Unified Modeling Language block diagram (with structural interconnections) of the

⁷ TrueRNG is a USB hardware device that sources Serial Communications provided entropy. See <http://ubld.it/products/truerng-hardware-random-number-generator/> for more information.

⁸ RXTX - Receiver/Transmitter; is a set of open source Java Classes that can convert a suitably prepared Windows platform into one supporting USB to Serial Communications. See http://rxtx.qbang.org/wiki/index.php/Main_Page for more information.

Classes within the Clans program as they existed on May 5, 2015. Currently, Clans is not under formal configuration management.

```
root\  
root\ecology  
root\ecology\climate  
root\ecology\fauna  
root\ecology\flora  
root\ecology\groups  
root\ecology\terrain  
root\events  
root\gui  
root\hominini  
root\rng  
root\writers
```

Figure 5 Tree diagram of the Java packages holding Clans.

3.3.3 Program operation and design summary

There are twenty-one Java source code (text file) Classes in the Clans program. This section provides a description of some of the operational characteristics and programmatic structures that are the design features of that source code. Roughly speaking, the Classes of Clans can be grouped into 3 areas of specialization; each group having some greater or lesser degree of complimentary functionality within the final simulation product. Those functional areas are: 1) Ecology – a multi-threaded, 2.5-D, raster-based, virtual environment simulating a pristine niche ecology, 2) Social Agents – an autonomous and self-reproducing population of explicit, primate-inspired social agents, and 3) Bindings – a loosely coupled set of social agent-oriented and programmatic source codes that enable the instantiation and simulation of the situated social agents in a virtual environment. We begin with a tabular listing of the all of the Constant parameters used in the May 5, 2015 version of the source code. Then, the section continues with a discussion the three functional areas just named, their operation, and their design features.

3.3.3.1 Constant parameters

Along with the top-level Class (Clans) the ModelConstraints Class resides in the Root folder. ModelConstraints is a Java Interface containing several user-configurable Constant parameters some of which are shared by many of the other Classes in Clans. However, because of its global visibility, ModelConstraints also contains many critical run-time parameters, coded as Fields or Constants that should not be changed by the user. Because of this ambiguous ModelConstraints use-case and for the purposes of

experimental replication, the values of the Constant parameters in ModelConstraints should initially be considered for-reference-only.

Constants parameters are those values in computer program source code that often have easily identifiable symbolic names and typically always have their runtime value held “constant” during the execution of any instantiated version of that code. For example, the number of days in a lunar year is defined by Constant as $YEAR = 364$, the Boolean steering variable used to include (or exclude) a TrueRNG entropy device can be arbitrarily true or false as may suit the user, and the number of calories in 1 pound of loose figs (16 pieces) is defined as $FIG_VALUE = 720.0$ (representing kilo-calories). The use-case for Constant parameters such as these can range from potentially complicated, to simple, and to critically important in any combination. In the case of the first Constant, the number of days in a lunar year, its value is proposed here as an experimental definition and is potentially complicated. The lunar year definition needs visibility throughout the program but has no need to be empirically precise so long as the underlying experimental definition and experimental protocol it implies are accepted by the user. The second example value, a program steering Constant called `USE_FIXED`, is simple. However, like `YEAR`, it requires some global visibility. The last Constant, the caloric value of figs, needs to be empirically precise, does not need wide visibility, but is critically important. The `FIG_VALUE` Constant is a type of parameter that may, depending on the complex execution-path that emerges during simulation, influence the validity of the overall experimental result. So, in this case, it is believed that the

authority responsible for defining FIG_VALUE becomes critically important, should be cited, and a reference to that authority given.

Table 2 shows the Constants used in Clans. The values shown in the table were used in all simulations whose results appear in **Chapter 4**. Over 200 Constant parameters were identified in the May 5, 2015 version of the code. Additional descriptive and parameter value citation authority can be found in **Appendix A Constant Parameter Authority** listed by topic area. Partial citations found here are fully expanded in the **References** section.

Table 2 Constant parameters by Class and assigned value.

ArtificialGenetics (Class 8), (Total 8)
<p> GENE_LENGTH = 8; // hard coded count of characters. GENE_COUNT = 11; // count of genes in chromosome. MALE_SKEW = 0.495; // likelihood a hominid is a male. SEX_BIT = 7; // bit to which assigned. RANDOM_TYPE = 0; // default GENE type is uniform random. GAUSSIAN_TYPE = 1; // value based on Gaussian distribution. </p> <p> See Appendix A A.1.20 Mutation rate (<i>Homo</i>) MUTATION_PROBABILITY = 3; // using 100K equivalent and 0.003%. SEARCH_SPACE = 100000; // accelerated in search space for above. </p>
Biology (Class 25), (Total 33) – 1 of 2
<p> See Appendix A A.1.5 Calorie requirements M_HIGH_CAL_NEED = 2450.0; // oldest male calorie need. M_LOW_CAL_NEED = 950.0; // youngest male calorie need. F_HIGH_CAL_NEED = 1350.0; // oldest female calorie need. F_LOW_CAL_NEED = 850.0; // youngest female calorie need. </p>

See **Appendix A A.1.4** Calories in pound of fat

FAT_AS_CALORIE = 3500.0; // 1 lb. conversion approx. for 3,555

See **Appendix A A.1.34** Water requirement

M_HIGH_WAT_NEED = 0.750; // oldest male gallon need.

M_LOW_WAT_NEED = 0.425; // youngest male gallon need.

F_HIGH_WAT_NEED = 0.700; // oldest female gallon need.

F_LOW_WAT_NEED = 0.400; // youngest female gallon need.

// Weight constraints, in pounds for adults and babies (hybrid *Pan-Homo*)

HEALTH_6YR_M_LBS = 15.0; // healthy 6yr male weight.

HEALTH_40YR_M_LBS = 155.0; // healthy 40yr male weight.

HEALTH_6YR_F_LBS = 12.0; // healthy 6yr female weight.

HEALTH_40YR_F_LBS = 120.0; // health 40yr female weight.

BABY_WEIGHT = 6.0; // healthy baby weight.

See **Appendix A**

A.1.5 Calorie requirements

BABY_CALORIE_LOAD = 275.0; // F-only, gestation & nursing kcal load.

BABY_WATER_LOAD = 0.275; // F-only, gestation & nursing water load.

See **Appendix A A.1.1** Age at menarche

MALE_FERT_AGE = 13; // M-only, minimum age of M fertility.

FEM_FERT_AGE = 15; // F-only, minimum age of F fertility.

FEM_NF_CYC_DAYS = 23; // F-only, nr of days non-fertile.

FEM_F_CYC_DAYS = 5; // F-only, number of days fertile.

GESTATION_END = 252; // F-only, day # at end of pregnancy.

NURSING_END = 1092; // F-only, day # nursing ends (>3yrs).

See **Appendix A A.1.7** Death as result of starvation

DEATH_LBS_PERCENT = 0.650; // death trigger percentage.

CALIB_YEAR = 6.0; // used to determine b in $y = mx + b$ form.

ARBITRARY_ADVANTAGE = 127.0; // 50%, arbitrary advantage of gene.

Clans (Class 5), (Total 38)

REAPER = 0; // symbol for the Reaper Report path in ModelReports.
DAILY = 1; // symbol for the Daily Report path in ModelReports.
DAY = 86400; // 1 day's worth of seconds.
HRS = 3600L; // 1 hour's worth of seconds.
MIN = 60L; // 1 minute's worth of seconds.

Climate (Class 4), (Total 42)

CLIMATE_CHANGE_INTERVAL = YEAR; // count of days before change.

See **Appendix A A.1.29** Temperature requirements (*Pan*)
MIN_TEMP = 55.0; // minimum temperature each cell will get.
RANDOM_TEMP = 10.0; // some cells get up to this much more.
CELL_COUNT = horizontalLimit * verticalLimit; // updates climate.

Ecology (Class 11), (Total 53)

ODD = true; // used to control the placement of forageables.
EVEN = false; // used to control the placement of forageables.
CLIMATE_CHANGE_INTERVAL = YEAR; // count of days before change.

See **Appendix A A.1.3** Calorie counts of forageables
FIG_VALUE = 720.0; // cal. for 1 pound (16 loose fruit) figs.
FISH_VALUE = 150.0; // kcal. for 4 oz., small fish.
LEAVES_VALUE = 625.0; // kcal. for 1 lb. loose leaves.
MONKEY_VALUE = 575.0; // kcal. for 8 oz. meat, small monkey.
TERMITE_VALUE = 700.0; // kcal. for 125 g., loose live termites.
TUBER_VALUE = 776.0; // kcal. for 8 small cassava root.
EMPTY = (byte) 0x00; // symbol for EMPTY.
FULL = (byte) 0x01; // symbol for FULL.

Fauna (Class 6), (Total 59)

```
FAUNA_FORAGABLES =  
{"monkey", "monkey",  
"termite", "termite", "termite", "termite", "termite",  
"none", "none", "none"}; // 3/10ths are null, used to create probabilities.
```

```
See Appendix A A.1.12 Fish foraging by early hominids  
FISH_PROBABILITY = RNG.nextFloat(); // a general probability.  
FISH_PRODUCTIVITY = 1.0F * FISH_PROBABILITY; // specifically.  
STEP = 100; // pixels across the square kilometer.  
TILE_PIXELS = 10000; // nr pixels in a kilometer square.  
TILE_COUNT = (this.horizontalLimit * this.verticalLimit) / TILE_PIXELS;
```

Flora (Class 4), (Total 63)

```
FLORA_FORAGABLES =  
"tuber", "tuber",  
"fig", "fig", "fig", "fig",  
"leaves", "leaves", "leaves", "leaves", "leaves",  
"none", "none", "none"}; // 3/14ths are null, used to create probabilities.  
STEP = 100; // pixels across the square kilometer.  
TILE_PIXELS = 10000; // nr pixels in a kilometer square.  
TILE_COUNT = (this.horizontalLimit * this.verticalLimit) / TILE_PIXELS;
```

```
START_SCREEN_WALLPAPER = "MaelzelEmbossedLogo.gif"; // optional
START_WINDOW_WIDTH = 640; // a VGA video mode screen size.
START_WINDOW_HEIGHT = 480; // a VGA video mode screen size.
IMAGE_ZOOM_SIZE_STEP = 2; // used with Zoom in-out.
IMAGE_DEFAULT_SIZE = 1; // used with Zoom.
IMAGE_ZOOM_MINIMUM = 1; // used with Zoom.
IMAGE_ZOOM_MAXIMUM = 4; // used with Zoom.
DAILY_UPDATE = 1; // map update each day.
WEEKLY_UPDATE = 7; // map update every 7 days.
MONTHLY_UPDATE = 28; // map update every 28 days.
YEARLY_UPDATE = 364; // map update every 364 days.
INITIAL_RATE = DAILY_UPDATE; // the default update rate.
BLACK = new Color( 0, 0, 0).getRGB(); // the RGB black color.
BLUE = new Color( 0, 0, 255).getRGB(); // the RGB blue color.
BROWN = new Color(128, 64, 0).getRGB(); // the RGB brown color.
GRAY_0 = new Color( 32, 32, 32).getRGB(); // an RGB gray color.
GRAY_1 = new Color( 64, 64, 64).getRGB(); // an RGB gray color.
GRAY_2 = new Color( 96, 96, 96).getRGB(); // an RGB gray color.
GRAY_3 = new Color(128, 128, 128).getRGB(); // an RGB gray color.
GRAY_4 = new Color(160, 160, 160).getRGB(); // an RGB gray color.
GRAY_5 = new Color(192, 192, 192).getRGB(); // an RGB gray color.
GRAY_6 = new Color(224, 224, 224).getRGB(); // an RGB gray color.
GREEN = new Color( 0, 255, 0).getRGB(); // the RGB green color.
ORANGE = new Color(255, 128, 0).getRGB(); //the RGB orange color.
PURPLE = new Color(128, 0, 128).getRGB(); //the RGB purple color.
RED = new Color(255, 0, 0).getRGB(); // the RGB red color.
WHITE = new Color(255, 255, 255).getRGB(); // the RGB white color.
YELLOW = new Color(255, 255, 0).getRGB(); //the RGB yellow color.
FILE_HEADER_LENGTH = 54; // Bitmap (BMP) file header length.
H_MAX = bmpWidth; V_MAX = bmpHeight; // get when BMP is read-in.
LAST_CELL = H_MAX * V_MAX; // find size.
WATER_R = 0; // RGB color integer value for pixel.
WATER_G = 0; // ditto.
WATER_B = 255; // ditto.
LO_LAND_R = 34; // RGB color integer value for pixel.
LO_LAND_G = 177; // ditto.
LO_LAND_B = 76; // ditto.
HI_LAND_R = 128; // RGB color integer value for pixel.
HI_LAND_G = 128; // ditto.
HI_LAND_B = 0; // ditto.
```

Groups (Class 0), (Total 104)

N/A

HAL (Class 1), (Total 105)

HIGH_THRESHOLD = 0.90; // least prob. will move for temp change.

Hominid (Class 33), (Total 138) – part 1 of 2

AGE_SKEW = 0.795; // seed-group likelihood age is 15 to 35.

See **Appendix A A.1.21** Old age mortality

AGE_PATHOLOGY = 0.625; // all pathologies by 35-45 avg.

FEM_RECEPTIVITY = 0.750; // F-only, probability mating occurs.

MINIMUM_AGE = 6; // minimum age of an initial setup agent.

TYPICAL_MIN = 15; // typical min age initial setup agent.

MAXIMUM_AGE = 35; // maximum age initial setup agent.

FEMALE_DISPERSAL = true; // F-only, on maturity, walk.

MALE_DISPERSAL = false; // M-only, on maturity, walk.

MIN_DAYS_NO_WATER = 5; // minimum days any hominid can go.

WEIGHT_LOSS_DUE_TO_DISEASE = 0.010; // a scalar loss.

See **Appendix A A.1.18** Maximum number of offspring

LIFETIME_MAX_BIRTHS = 7; // F-only

See **Appendix A A.1.31** Troop / community size (Pan in the wild)

SCALING = 0.00392; // results in 1.00 for 255 bin.

PREFERRED_GROUP_SIZE7 = 7; // and is gene6.

PREFERRED_GROUP_SIZE21 = 21; // same works with gene6.

PREFERRED_GROUP_SIZE35 = 35; // same works with gene6.

ALLIANCE_ADVANTAGE = 0.50; // arbitrary comparative advantage.

ALTRUISM_ADVANTAGE = 0.50; // arbitrary comparative advantage.

FAT_CAL = bio.FAT_AS_CALORIE; // number of calories in a fat pound.

GROUP_SIZE_7_ADVANTAGE = 500.0; // maximum advantage.

GROUP_SIZE_21_ADVANTAGE = 1000.0; // medium advantage.

GROUP_SIZE_35_ADVANTAGE = 2000.0; // minimum advantage.

Hominid (Class 33), (Total 138) – part 2 of 2

See **Appendix A A.1.29** Temperature requirements (*Pan*)
STD_TEMP = 55.0; // standard temperature range 60- 85 F.
UPPER_TOLERANCE = 10.0; // an upper temp tolerance limit.
LOWER_TOLERANCE = 10.0; // a lower temp tolerance limit.
ARBITRARY_ADVANTAGE = 1; // arbitrary advantage of gene.
LOW_END = 7; HIGH_END = 247; // scaled end of gene 0-255 range.
TEMPERTURE_SETPNT_GENE (implicit).

See **Appendix A A.1.25** Philopatry/dispersal
EMIT_FERTIL_SCENT_GENE (implicit).
PHILOPAT_DISPERSE_GENE (implicit).
DRAUGHT_TOLERANCE_GENE (implicit) (logical deduction).
ROBUST_METABOLISM_GENE (implicit) (logical deduction).

HominidKit (Class 8), (Total 146)

SUPPLY_CARRYING_LIMIT = 0.1; // N/A. Not used.
SUPPLY_START_AMOUNT = 0.100; // N/A. Not used.
SUPPLY_DEPLETION_RATE = 0.010; // N/A. Not used.
FLASK_TIME_LIMIT = 14; // N/A. Not used.
MAX_SURVIVAL_TECH = 0.955; // N/A. Not used.
HOMINID_NOT_IMPERILED = 0.0; // N/A. Limiting case. Not used.
HOMINID_PERIL_RATE = 0.01; // N/A. Not used.
INDIV_IS_IMPERILED = 1.0; // N/A. Limiting case. Not used.

LifeExperiences (Class 2), (Total 148)

EMPTY = (byte) 0x00; // symbol for EMPTY.
FULL = (byte) 0x01; // symbol for FULL

USE_FIXED = true; // RNG seed is fixed or random.
CALIB_SEED = 1234567890123456789L; // a fixed seed.
RANDOM_SEED = System.nanoTime(); // fast time seed.
RUN_TIME_DISPLAY = true; // true=normal false=DIAGNOSTIC.
FORAGING_DISPLAY = true; // true=forage false=waterBasin.
TRUE_RNG_PORT = "COM5"; // system specific COM port.
BIN_FOLDER = "root" + File.separator; // utility folder.
DATA_FOLDER = "data" + File.separator; // utility folder.
MAP_FOLDER = "maps" + File.separator; // utility folder.
WATER = 0; // terrestrial feature specific to Sim
LO_LAND = 1; // terrestrial feature specific to Sim.
HI_LAND = 2; // terrestrial feature specific to Sim.
YEAR = 364; // year of days in lunar year of 13 months.
FAT_AS_CALORIE = 3500.0; // 1 lb. conversion approx. for 3,555
DISCRETE_FACTORS_GENE = 0; // gene 0 on chromosome.
DRAUGHT_TOLERANCE_GENE = 1; // gene 1 on chromosome.
ROBUST_METABOLISM_GENE = 2; // gene 2 on chromosome.
SOCIAL_ALTRUISM_GENE = 3; // gene 3 on chromosome.
TERRITORY_DEFENSE_GENE = 4; // gene 4 on chromosome.
PAIR_BND_ALLIANCE_GENE = 5; // gene 5 on chromosome.
EMIT_FERTIL_SCENT_GENE = 6; // gene 6 on chromosome.
PHILOPAT_DISPERSE_GENE = 7; // gene 7 on chromosome.
RESERVED_GENE_8 = 8; // gene 8 on chromosome.
RESERVED_GENE_9 = 9; // gene 9 on chromosome.
TEMPERTURE_SETPNT_GENE = 10; // gene A on chromosome.
MAXIMUM_GROUP_SIZE = 10; // max nr in seed group.
NUMBER_OF_GROUPS = 5; // max nr of hominid groups.
WATER_DAYS = 2; // max allowed consecutive epochs in water.
PREY_ATTITUDE_CHANGE_THRESHOLD = 0364; // 1 year days = 0364.

See **Appendix A A.1.24** Patrols

CHANCE_OF_PREDATION_HI = 0.0000140; // day, 0.50% year.
CHANCE_OF_PREDATION_LO = 0.0000001; // day, 0.04% year.

See **Appendix A A.1.16** Infanticide rate

INFANTICIDE_MORT = 0.000055; // daily, 2.0% annual.

See **Appendix A A.1.9** Disease rate (Pan in the wild)

DISEASE_THRESHOLD = 0.000055; // daily, 2.0% annual.

See **Appendix A A.1.35** Weaning age

RANGE_OF_EARLY_WEANING = 3; // + 0-2 by factory RNG.

MIN_WEANING_AGE = 4; // minimum oldest when weaned. Maximum is 6.

See **Appendix A A.1.33** Water availability, water basins

MIN_WATER = 1.0; // minimum gals of water each basin will get.

RANDOM_WATER = 3.50; // some basins get up to this much more.

RATE_OF_LOWLAND_WATER_BASINS = 0.5; // % cells water basins.

RATE_OF_HIGHLAND_WATER_BASINS = 0.3; // % cells water basins.

FLORA_SUCCESS_BIAS = 0.50; // min seasonal forageable production.

FAUNA_SUCCESS_BIAS = 0.50; // min seasonal forageable production.

INITIAL_PRODUCTIVITY = 99.0; // initial percent production.

FORAGING_COST = 1.0; // percent cost per hominid / per day if foraged.

FORAGING_RCVRY_RATE = 0.50; // percent terrain recovery rate / day.

See **Appendix A A.1.3** Calorie counts of forageables

// equivalent to eating 100% of a 2700 kcal diet composed entirely of tubers.

DAILY_MEALS = 3.48; // "multiplier" best case situation.

AFFECT_WORD_WIDTH = 8; // Java can support up to 30.

GROUPED_DRIVES = 3; // nr of highest priority group.

FEAR_STEP = 2; // n X 10 meter movement distance per day.

WATER_STEP = 15; // n X 10 meter movement distance per day.

FOOD_STEP = 15; // n X 10 meter movement distance per day.

GROUP_STEP = 30; // n X 10 meter movement distance per day.

WATER_START_AMOUNT = 0.7; // water amount to start with.

WATER_CARRYING_LIMIT = 1.0; // only hand-to-mouth (gals).

FOOD_START_AMOUNT = 0.7; // food amount to start with.

FOOD_CARRYING_LIMIT_F = 0.7; // only hand to mouth (lbs.).

FOOD_CARRYING_LIMIT_M = 0.9; // only hand to mouth (lbs.).

ModelReports (Class 15), (Total 219)

```
DAILY_REPORT_TITLE = "DailyReport.txt"; // common report name.
DAILY_REPORT = "DailyStatistics"; // collated report.
REAPER_REPORT_TITLE = "ReaperReport.txt"; // common report name.
REAPER_REPORT = "BoundReaperReport"; // collated report.
SOCIAL_REPORT = "SocialNetworkReport"; // collated report.

VERTICES = "*Vertices "; // a required header.
ARCS = "*Arcs"; // a required header.
MALE = "RGB0000FF"; // this is blue.
FEMALE = "RGBFF0000"; // this is red.
BLACK = "RGB000000"; // this is black.
EDGE = " 1 c " + BLACK; // this black edge has thickness 1.
SPRING = 1; // the defined first day(s) of each season.
SUMMER = 91; // continued.
FALL = 182; // continued.
WINTER = 273; // continued.
```

RGB (Class 4), (Total 223)

```
ALPHA_BASE = 16777216; // used in converting integers to color.
RED_BASE = 65536; // used in converting integers to color.
GREEN_BASE = 256; // used in converting integers to color.
BLUE_BASE = 1; // used in converting integers to color.
```

SeedGroup (Class 2), (Total 225)

```
EMPTY = (byte) 0x00; // symbol for EMPTY.
FULL = (byte) 0x01; // symbol for FULL.
```

Socioecology (Class 3), (Total 228)

```
W_DAYS = 1.00D; // Westermarck-days prohibit incest percent.
GENDER_BIAS = 0.01; // smaller number reflects greater bias.
AGE_MIN = 19; // initial minimum choice for the age of the Alpha.
```

Terrain (Class 3), (Total 231)

```
STEP = 100; // width of a one kilometer tile.  
TILE_PIXELS = 10000; // number of pixels per tile.  
TILE_COUNT = (this.horizontalLimit * this.verticalLimit) /  
              TILE_PIXELS; // # tiles X-Y span of the user map.
```

TrueRNG (Class 7), (Total 238)

```
NR_OF_BYTES = 8; // factory Random uses 6-byte 48-bit seed.  
RESET_LIMIT = 0; // works with resetCounter as its limit.  
COUNTER_MAX_SPIN = 17; // the max resetCounter limit.  
COUNTER_MIN_SPIN = 9; // the min resetCounter limit.  
BITS_PER_BYTE = 8; // 8-bits per byte.  
REQUESTING_APPLICATION = "dummy";  
MS_DELAY = 1000; // delay in millisecond. Used while TrueRNG starts.
```

3.3.3.2 Functional area - ecology

Ecology provides the hominid Social Agent population with an explicit, 2.5-D ecosystem: a virtual habitat. This is the first functional area. It simulates a grid-based spatial terrain with forageable vegetation and prey, water resources, and a simplified, annually varying, weather model simulated by ambient temperature changes. The deterministic limits of terrain water availability and forageables production are set by Constant parameter. Additionally, within this functional area, instances of the Cell Class hold the memory pointers to the hominid social groups whose communities gather, disassemble, and move about on the terrain. The Classes that are associated with this functional area are: Ecology, ModelConstraints, Flora, Fauna, Climate, Terrain, Groups, Cell, and LifeExperiences.

3.3.3.2.1 Multi-threading

Once each simulated day (i.e., each simulation epoch) the ecosystem is aged. In this way, Flora and Fauna are fully processed every day while the Climate (environmental temperature) and Terrain (large bodies of water) are processed only once a year. Overall, aging is a process that uses a multi-threaded algorithm that is dynamically configured for runtime during user start-up time terrain map loading. The number of threads that will be invoked over the entire habitat map during the aging process is proportionate to the number of square kilometers depicted on the terrain map the user has chosen to provide. Additional information about the internal aspects of the loading of a terrain map is available in Section 3.3.3.4.1. In general, this entire mechanism is hidden from the user during operation but is explained here for obvious reasons.

The ecosystem aging process starts with a single master thread spawned on a daily (per epoch) external call from within the Clans master control loop. (More detail on the master loop appears in Section 3.3.3.4.2). The current thread, in turn, spawns four large multi-threaded sub-task thread pools. The four subordinate sub-task thread pools then enumerate over Climate, Terrain, Flora, and Fauna each, respectively. As each thread pool associated with a respective sub-task begins to fire, individual aging (updating) routines subdivide the entire habitat into 1 square kilometer increments and process the respective environmental sub-task as a pool of 1 square kilometer focused threads. Terrain is responsible for updating some of the water reservoir quantities via a quantity-refresh process. Climate handles processes that change the environment temperature via probability re-assignment. Flora simulates a seasonal (sinusoid

modulated), discrete, linear regrowth function for part of the edible forageables in the environment, and Fauna simulates changes in the availability of the remainder of the edibles (prey species) via direct probability re-assignment. When all sub-tasks are complete, control is passed back to the Clans master control loop.

3.3.3.2.2 Cell

Instances of the Cell Class represent the least spatial increment of the Ecology data structure and the terrain grid in general. A grid cell simulates a 10 X 10 meter terrain unit: this is the least unit. These are raster-organized cells in a "virtual habitat" within and upon which the entire simulation takes place. An instance of Cell contains properties like elevation, the name of the Biome it hosts, the temperature of the cell, water by quantity (if the cell has any water), a baseline quantity of water (if it has water), a foraging option (figs, roots, termites, etc.) associated with the cell, the probability that attempting to consume that forageable will result in foraging success, and a maximum limit on seasonally fluctuating foraging productivity probability.

3.3.3.2.3 Terrain

The Terrain Class is closely associated with the terrain grid and is partially responsible for program control of water reservoirs; sharing some its responsibilities with the Classes Flora and Fauna. More will be said about the division of water-related tasking in a moment.

There are two types of water reservoirs. The first type of reservoir is a body of water (and there can be many) provided by the user and depicted on the terrain map loaded at program start (see Section **3.3.3.4.1**). The other reservoir type are small,

randomly dispersed pools holding anywhere from a few quarts of water to several gallons. The first reservoir type can be thought of, nominally, as a standing body of water and the latter type as a water basin. The distribution of water basins on the terrain is set by Constant in ModelConstraints.

Changes leading to the depletion of water container content levels are directly proportionate to the amount of water visiting hominid agents may take (drink) from a particular reservoir during the current epoch (day). In a complimentary fashion, the water reservoir content levels are refreshed (refilled) by program control during the ecosystem updating and aging processes. Water basins are refilled daily according to their respective biomes and elevations in the 2.5-D virtual environment.

Currently, the simulation only has three, 2.5-D elevation levels representing a lowland biome, a highland biome, and a water base-level. Thus, a compromise was taken. The water basins in the lowland biome are refilled through the threaded daily processes of the Flora Class when the forageables of Flora are refreshed. And, the water basins in the highland biome are similarly refilled in the threaded daily processes of the Fauna Class when the edible prey species of Fauna are refreshed. Finally, standing bodies of water provided by user habitat maps are refilled yearly.

Distributing reservoir refilling activity in this way was indeed a compromise made to save master control loop time. It could easily be modified to have all water reservoirs updated in the Terrain class simultaneously, each according to its need, if this added some benefit.

3.3.3.2.4 Flora and fauna

The Flora and Fauna Classes are almost symmetrical twins operating in the 2.5-D Ecology. That is, the multi-threading mechanisms in both Classes are identical but their detailed forageables updating schema are slightly different. The forageables updating scheme in Flora involves a modulating sinusoidal function that simulates a seasonal vegetation production oscillation set at 1 cycle per year. In Fauna, the updating scheme for prey forageables is entirely probabilistic.

Additionally, the Flora and Fauna Classes are surrogate representatives of two different niche ecologies, or biomes, which can apply differentiated foraging stressors on the Social Agent population. Flora is an abstract lowland biome and Fauna a highland ecology. Flora maintains a list of edible hominid foods like figs, roots, and leaves. Fauna, on the other hand, provides edible forageable from a list of foods like fish⁹, termite, and Red Colobus monkey. All of these foods can be consumed by the hominid Social Agents as a product of individual agent choice, acquired and conforming habits, and forageables availability.

Flora forageables availability, or more technically the carrying capacity of a terrain cell in the lowland biome, is a complex emergent result driven by non-deterministic agent foraging activity and simulated vegetation regrowth. Hominid “over-foraging” can diminish or even completely destroy (kill) the productive capacity of a Flora grid cell. However, left unharvested cells hosting Flora forageables will return to their maximum through a Constant parameter-based, discrete, linear regrowth function.

⁹ Fish are found in all large bodies of water but never in water basins. Large bodies of water are experimentally defined to exist at lowest (simulated vertical) level in the 2.5-D space.

(Assuming the cell was not completely over-harvested to begin with, of course.) Fauna prey (like termites and Red Colobus monkey) is always available probabilistically.

3.3.3.2.5 Groups

Although Groups is technically a component within the functional data structures of Ecology, it is a translation device that allows external objects access to the hominid social cohorts that occupy the terrain grid at any given moment. The code in Groups provides external modules access to counters, and statistical and accessor methods associated with the terrain grid cohort array lists. A cohort is a Java ArrayList holding an n-sized group of agents in one 10 X 10 meter grid cell.

3.3.3.2.6 Life experiences

LifeExperiences is a Class in the events package. It provides translation and interaction services between the functional areas of Clans. Although the Social Agents exist in (are associated with) n-sized cohorts within the Ecology area, Social Agent behaviors within and between cohorts are the result of the (autonomously computed) voluntary choices of the hominid Social Agents coordinated through the methods of LifeExperiences.

LifeExperiences helps the hominids realize a quasi-concurrency of interaction between themselves and their environment. LifeExperiences provides a computational mechanism that functionally straddles, and figuratively flattens, the logical division between the functional areas of Ecology and Social Agents.

The computational mechanisms supplied by LifeExperiences are a compromise. They are a stand-in for more advanced Virtual World simulation technologies built on authoritative server architectures. A Virtual World technology is a malleable simulation

technology that supports the concurrent emulation of emergent individual and small-group interactions in situated, socio-environmental settings. Unfortunately, when Clans was being extended for this project, time constraints did not allow for its transition to a Virtual World simulator. This is a situation that could be rectified in a subsequent revision and or extension to Clans.

3.3.3.3 Functional area – social agents

Social Agents emulates individual, hominid-inspired, software agents. This is the second functional area. The agents are crafted to operate within the context of the Ecology (Section 3.3.3.2) and to appear to be spatially-situated, mobile, adaptive, virtual entities with constrained, autonomous (computational), decision-making capabilities. As the agents interact collectively, they generate what can metaphorically be said to resemble social behaviors that lead to a primitive form of emergent social organization. The agents have artificial genetic structures, simplified biology simulating sexual dimorphism, and abstract cognitive features (psycho-social/and spatial) that steer their individual, long-term, existential outcomes. The code in this functional area is responsible for generating and maintaining agent artificial genetics, simulating sexually dimorphic biology, enabling cognitive feature synthesis, providing agents with access to optional kit, and for developing data structures that give the agents latent socio-ethological character. Classes associated with Social Agents are ModelConstraints, ArtificialGenetics, Biology, HAL, Hominid, HominidKit, SeedGroup, Socioecology, and LifeExperiences.

3.3.3.3.1 Seed group

It is the responsibility of SeedGroup to start the initial Social Agent population in an instantiation of the Clans simulation and to place those (one or more) hominid-inspired agents into the Ecology described in Section 3.3.3.2. The ModelConstraints Class provides SeedGroup with Constant parameters specifying the number and size of the initial hominid cohorts but the spatial placement of the cohorts within the habitat Ecology is entirely random.

The agents are drawn from source code taken from the Hominid Class and constructed piece-wise from across the several Classes that make up the Social Agent functional area. The Hominid Class contributes a master framework for the social, cognitive, and innate (survival) behaviors of each agent. ModelConstraints provides genetic definitions and pertinent quantitative constraints to the ArtificialGenetics and Biology Classes. Based on the cross-product interaction of the ArtificialGenetics, Biology, and HAL Classes hominid agents emerge ready for placement in a suitable habitat with intact artificial genetics, assigned sex, sexually differentiated behavioral ethology, and water and food requirements. HAL gives each agent a set of abstract cognitive features with which to manipulate its world. Socioecology, another Class in the Social Agent area, gives each agent a social memory and the basic components necessary to begin to differentiate among its kin, its in-group, and its out-group affiliations. Finally, the LifeExperiences Class becomes the enabler of each agent providing a wide variety of emulated life experiences ranging from self-directed foraging behaviors, social encounters and mating pursuits, terrain mobility, and the death by catastrophe or

drowning. After SeedGroup has formed the initial population of hominids, it returns them as one or more communities of one or more individuals to the Clans main method for further simulation.

3.3.3.3.2 Artificial genetics

Each hominid Social Agent is instantiated with a single, 88-bit, artificial chromosome.

The chromosome is subdivided into eleven, 8-bit bytes called genes. Each gene expresses one or more innate traits. In the May 5, 2015 version of the code, eight of the genes were fully coded and active, three were inactive, and two of the inactive genes were reserved for future use. **Figure 7** shows the genes as functional traits mapped onto an artificial chromosome.

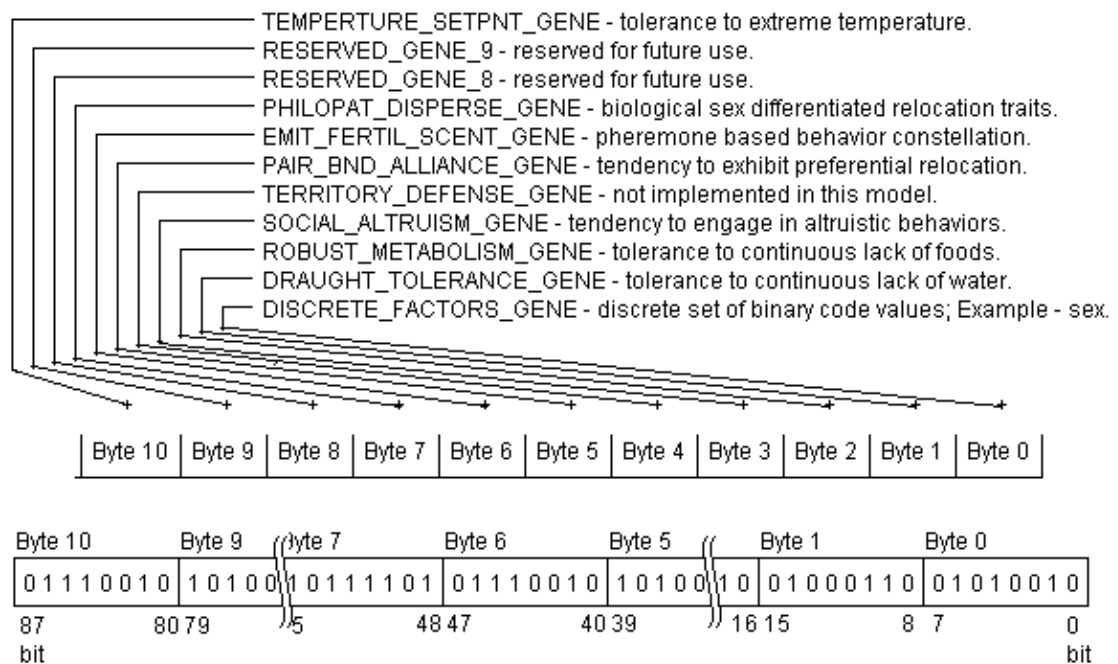


Figure 7 Mapping traits onto an artificial hominid chromosome.

As shown in the figure, of the eight active genes in the current chromosome, seven of them correspond to individual genes encoded as 8-bit integer values. These genes express across all eight of the bits (alleles) within each byte. However, one of the eight active bytes was encoded as a unary-mapped set of 8 discrete, Boolean-valued bits (alleles). Currently, only one of the bits in that byte is used and it is coded for the sex of the agent. This mechanism extends the computational techniques of simple genetic algorithms, including those of mutation and cross-over described in Goldberg (1989), but in a manner that assigns an explicit role for each gene to play in shaping agent physiology and behavior. **Table 3** describes the simulated hominid chromosome in more detail.

Table 3 Description of simulated hominid genetic material.

DISCRETE_FACTORS_GENE

- SEX_BIT (7)

This bit specifies the biological sex of the bearer. This genetic trait is phenotypic.

- OTHER_NAMED (6)
- OTHER_NAMED (5)
- OTHER_NAMED (4)
- OTHER_NAMED (3)
- OTHER_NAMED (2)
- OTHER_NAMED (1)
- OTHER_NAMED (0)

These bits are reserved.

DRAUGHT_TOLERANCE_GENE

This gene influences the capacity of the bearer to survive draught, i.e., the ability to survive with lesser amounts of drinking water. DRAUGHT_TOLERANCE is expressed in both sexes.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

The bearer's actual momentary drinking water requirements are annually adjusted based on the value in the gene and proportioned to bearer sex and age. The final genetic advantage of DRAUGHT_TOLERANCE is related to the integer value encoded in the gene and one of three, calculated, sum and product equations. Currently, there are three integer ranges overlapping the 0 – 255 span. The ranges are 0 - 98, 99 - 198, and 199 to 255, inclusive. Gene base values found to be within these ranges cause bearer drinking water requirements to be calculated by one of three separate, arbitrary, water requirements settings equations. This genetic trait is phenotypic.

ROBUST_METABOLISM_GENE

This gene influences the capacity of the bearer to survive extreme weight loss, i.e., to survive otherwise withering weight loss due to disease and or malnutrition.

ROBUST_METABOLISM expresses for both sexes (genders).

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

The bearer's ultimate mortality weight is based in part on the base value of the gene and some calculation. The genetic advantage ranges from 0.0 to about 5.1 pounds of additional, survivable weight loss taken arbitrarily from within a range of 35-50% of survivable total body mass loss projected by forensic practitioner for humans. A system standard mortality weight of 1.00 – 0.35 or 0.65 (65% per **Appendix A**) of standard bearer body mass set by sex and age is always available to the bearer. The bearer of this gene may enjoy a slight advantage. This genetic trait is phenotypic.

SOCIAL_ALTRUISM_GENE

This gene controls the tendency of the bearer to engage in the "gifting" of excess food resources. The gene expresses differentially in males and females.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

Larger values of the gene lead the bearer to engage in the "gifting" of excess self-held food resources. This genetic trait is phenotypic.

- **Expression in Males**

"Gifting" may occur when the benefactor is an adult and the beneficiary is an adult female.

- **Expression in Females**

"Gifting" may occur when the benefactor is an adult and the beneficiary is the youngest, weaned offspring of the benefactor.

TERRITORY_DEFENSE_GENE

This gene influences the likelihood the bearer will engage in behaviors to protect increasingly larger territory. (Reserved in May 5, 2015 version and not implemented.)

PAIR_BND_ALLIANCE_GENE

This gene is responsible for the tendency of the bearer to engage in socio-preferential movements. The gene is expressed similarly in males and females. However, the age and sex of the bearer does differentiate bearer behavior especially during the year a female bearer becomes sexually mature. Juvenile female bearers, in the year they become sexually mature, will selectively choose random dispersal instead of preferential relocation to be with a benefactor.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

Larger values of the gene lead the bearer to demonstrate the behavior of "selective co-location." "Selective co-location" is defined as that condition that occurs when the bearer of the gene preferentially selects to relocate into a spatial cohort containing some other. In particular, the other is one's benefactor. This genetic trait is phenotypic.

EMIT_FERTIL_SCENT_GENE

This gene differentially influences its bearer according to the sex of the bearer. It expresses with regard to behaviors undertaken in groups of various sizes.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

This genetic trait is phenotypic.

- **Expression in Females (Only)**

This gene influences the probability that a fertile, non-pregnant, non-nursing, sexually mature female will engage in mating behavior during estrus. Its purpose is to emulate the effect of a female sex pheromone whose likelihood of successful mating influence is directly proportionate to the size (numeric magnitude) of the cohort wherein the female is physically located. EMIT_FERTIL_SCENT relies on the ability of the female to recognize the number of individuals in her local small-group. The resultant influence is graded against four numeric group size ranges which are 0, 1 - 7, 8 - 21, and 22 or more. A monotonically increasing likelihood of female presentation will occur in smaller numbered groups but not in larger.

- **Expression in Males and Females**

This gene expresses as an implicit violation of an unconscious social comfort zone. It relies on the ability of the bearer to recognize the number of individuals in the cohort under consideration. The bearer of this gene, whether male or female, experiences a monotonically increasing likelihood of discomfort when situated in larger social groups.

PHILOPAT_DISPERSAL_GENE

This gene influences the characteristic of the bearer to engage in spatial dispersal (leaving the natal community) versus philopatry (staying near or within the natal community or spatial area) in the year the bearer becomes sexually mature. This gene can express in males, females, both, or neither depending on system experimental settings.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

Only the integer value of PHILOPAT_DISPERSAL, the subject sex (gender), and the system experimental settings are involved. This genetic trait is phenotypic.

AGNATIC_MEM_STRCT_GENE

This gene influences the capacity of the bearer to recognize kinship through paternal lineage. (Reserved in May 5, 2015 version and not implemented.)

RESERVED

(This gene was reserved in the May 5, 2015 version and not implemented.)

TEMPERTURE_SETPNT_GENE

This gene influences the bearer to seek spatial relocation in order to avoid contact with a subjective, uncomfortable thermal environment. The absolute value of TEMPERATURE_SETPNT is a genetic trait that can be associated with innate temperature sensitivity.

The pedigree of this gene determines its value. In all cases the value is defined to be an integer on the interval 0 - 255, inclusive. If the bearer was formed as a product of in situ mating then the value is the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. If the bearer was formed at program initialization then the value of this gene is set by random Gaussian distribution over the interval.

This genetic trait is phenotypic.

If a hominid is created by SeedGroup then the genetic pedigree of its chromosome is the result of a random Gaussian process. For SeedGroup hominids, ArtificialGenetics creates chromosomes with gene and allele values taken from a Gaussian distribution of all possible allele values. However, if a hominid is the product of an in situ mating¹⁰ then the genetic pedigree of that hominid (the offspring product of the mating) will be the explicit consequence of genetic cross-over between, and artificial mutation of, the chromosomes of the mated hominid parents. Moreover, the algorithms within the ArtificialGenetics Class provide gene and allele manipulation methods with processes that can emulate naturally occurring genetic mutations at a rate slightly higher than that

¹⁰ In situ mating is experimentally defined as the circumstantial cross-breeding of two sexually mature hominid objects (male and female agents).

of *Homo*. The rate is accelerated in order to permit a more rapid visualization of genetic changes as they occur in the population but on shorter, simulation-bounded time scales.

3.3.3.3.3 Biology

The Biology Class provides the agents with important characteristics specifying individual qualities of optimal weight, hunger and calorie requirements, fertility cycles, thirst, and much more. These individualized qualities are computed as a preferential backdrop before any agent socio-environmental behaviors and their consequences can occur. Then, based on nuanced, individual biology a hominid can experience social and or physiological changes like hunger, satiety, pregnancy, death, weight loss or gain, etc., when interacting with its cohort.

There are several Constant parameters within the Biology Class that are used to set and to calculate juvenile and adult hominid nutrition requirements for caloric and water needs. Using these Constants the conditions and extents of ideal hominid weight and momentary caloric and water requirements are computed as linear results differentiated only by age and sex. Juvenile male and female results are used directly as are adult male results used directly. Adult female nutritional and water requirements are additively incremented based on positive (increased) gestation and nursing adjustments for water and food (calorie) consumption. In the case of infants, the limits of these too are set by Constant in Biology. Infant nutritional and water requirements are always associated with and directly loaded upon the associable inventories of the mother.

The forgoing physiological constraints and results are available from within the Biology Class by accessor. Once a year, on the birthday of the individual hominid, these

several nutritional requirements are recomputed. The results remain in force until the next year but are changed by females when they begin a new pregnancy or end a lactation interval. Additionally, on their birthday, every hominid is given a new random number seed for use in all of their activities and computations. This feature is a complimentary function of the LifeExperiences Class in cooperation with the TrueRNG Class.

3.3.3.3.4 Hominid

Hominid is the foundation Class within the Social Agents functional area. An instance of Hominid is a hominid. Hominids are used in this research as the primary theoretic and experimental species addressing the Temporal Conjecture (Section 1.2.2). A hominid agent can be instantiated under any of four Class constructors. These span a functional range from default (a memory pointer), to Adam and Eve (used by SeedGroup as the parenting agents for each of the first generation hominids), SeedGroup (the actual first generation hominids themselves but not Adam and Eve), and offspring (any hominid product of the in situ mating of two sexually mature agents). Hominid binds together as sub-classes the capabilities of ArtificialGenetics, Biology, HAL, HominidKit, LifeExperiences, and Socioecology to produce an individual Social Agent.

A hominid agent is an encapsulated object. This property facilitates individual hominids being gathered together as a population of hominids. Organized as a population, individual births (instantiations) and deaths (removals from computer memory) of agents becomes an easy to maintain process soon to be discussed in Bindings, Section 3.3.3.4. A hominid can be instantiated (born) and removed from computer memory (die) as a consequence of simulated death by old age, dehydration,

hunger, disease, predation, infant abandonment, infanticide, or catastrophe. Typically, an agent will die of old age at around forty years of age if no other pathology or environmental factor is encountered. When it is instantiated (birthed) an agent will have a 49.5% chance of being male (else female). If the hominid agent is formed at program start, it will be created by the Class SeedGroup. In this case it could be instantiated as a juvenile or an adult: infants are never started by SeedGroup. Creation by SeedGroup does convey a greater likelihood that the agent instantiated will be between the ages of 15 and 35. And, if the agent is female it will not be pregnant.

Figure 8 is a flowchart that schematically illustrates the activities loop that is undertaken during one simulated day in the “life” of a hominid. Notice the entry point “Start.” This is where the Clans main method (Section 3.3.3.4.2) enters into the loop. In the figure one sees a day in the “life” of a hominid social agent. Arbitrary life phases (divisions) are A=adult, J=juvenile, B=baby, and N=needs reassignment (at death) are tested and then drop-thru as the properties of the respective agent are recognized. A hominid has four life phases: infant, juvenile, adult, and dead. With the exception of a hominid population started by the SeedGroup Class, hominid life begins (is instantiated after) after a successful in situ mating, a maternal carry-to-term interval (252 days = 36 weeks * 7 days), and birth. If an in situ mating results in the instantiation of a new agent object (a birth), the infant (a hominid object) will be instantiated (born) and placed into the same terrain grid cell as its female parent (mother object). The infant will then accompany its mother everywhere until it is weaned. The father (male object) of the offspring need not be alive or present at instantiation (birth).

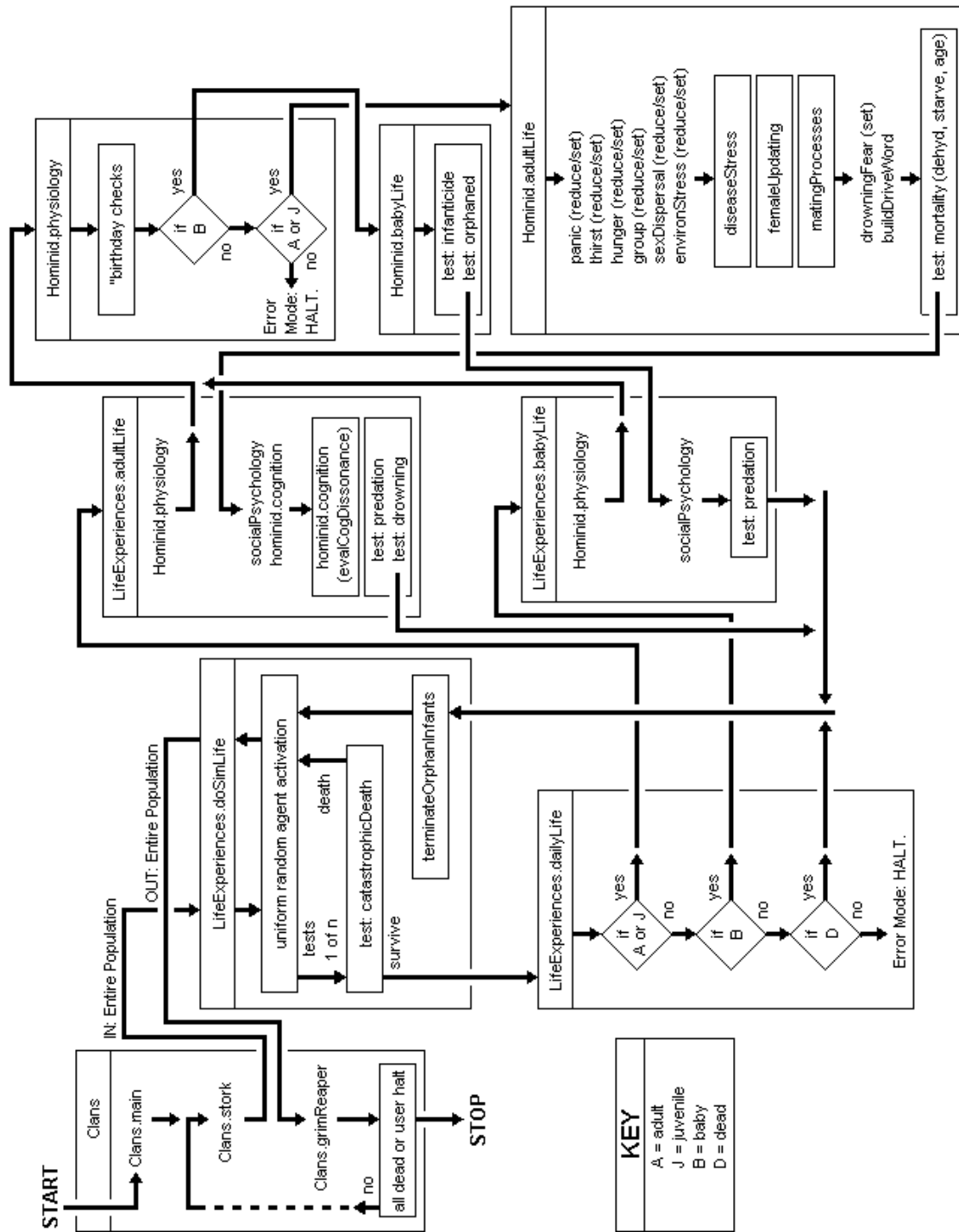


Figure 8 A day in the “life” of a hominid social agent.

Infant hominid existence is tightly-coupled to the existence and behavior of the mother until the infant is weaned. Infants draw all of their nutritional (and water) resources from their mothers and travel exclusively between cell cohorts with their mothers until weaning. Infant weaning occurs on the birthday of the infant, randomly, in their 4th, 5th, or 6th year (**Appendix A**). In fact, if the mother of an infant (one who is not yet weaned) dies then, the infant will die. Wet-nursing is not simulated. After weaning, a hominid becomes a juvenile and must assume responsibility to feed and water itself. Juveniles, like adults, can relocate anywhere in the habitat they choose (or can compute) in order to satisfy their subjective (programmed) needs.

When a juvenile hominid becomes sexually mature it becomes an adult. The transition from juvenile to adult occurs differentially for males and females but it is in the early mid-teen years for both sexes. Adult female agents have 28-day fertility cycles and are receptive 5 of those days. Females, once sexually mature, remain fertile for the remainder of their lives (Lacreuse, 2008). Simulated sexual reproduction can only occur between adult males and females, only when a female is receptive, and only when the mating partners are in the same cohort, i.e., the same grid cell. Incest is suppressed by the function of the Westermarck effect. The Westermarck effect is a socio-cognitive result that does not prohibit incest but rather appears to contribute to its social suppression. The function is described again in Section **3.3.3.3.7**, Socioecology.

Pregnancy and nursing (in females) suppresses additional pregnancies until the current, youngest offspring is weaned. Mating and pregnancy occur until the end of life in the hybrid species modeled. After becoming sexually mature, female hominids

disperse. Dispersal is an innate behavior in higher-primates, as it is in many species (Poethke, Pfenning, & Hovestadt, 2007), and is characterized by the individual attempting to leave their proximal, natal community.

In summary, the successful production of viable hominid offspring is the centerpiece among the emergent artifacts that have arisen from Clans and the system model. Built upon the Hominid foundation stone one sees several emergent effects arising from the code. One sees, for example, individuals making emergent choices of breeding partner(s), emergent average rates of infant mortality and incest per capita, emergent relative and voluntary permanence of breeding partner choice, and emergent temporal endurance of communities of hominids. These are all evidence of the system model at work and critically on the right path. The Hominid Class is the basis of these achievements.

3.3.3.3.5 HAL

The HAL Class provides a finite set of complex, overt, behavioral schema responsive to the needs-based drive reduction engine employed as the animating source of the current hominid ethology. This version of the HAL engine is premised on the notion that hominid objects can not only sense but can perceive causal sensations and that those perceptions have been paired (a priori) with a simulated, innate, drive reducing response. The ethology employed here is similar to the explanations of schema proposed by Tinbergen (1951) for when a stimulus trigger sets off a fixed-action-pattern response in an infrahuman species. Although, it must be admitted, the HAL Class does employ some degree of indirect cognitive complexity. The overall goal of the HAL Class was to

emulate of a set of complex, overt, drive reducing behaviors without claiming it is providing any machine intelligence to the hominid agents. That said, the agents in these simulations emulated at least a few cognitive features typical in *Homo*; seeming to exist in *Pan* (Fouts, 1997), and by logical deduction may have been present in the extinct hominid species *Ardipithecus* and *Australopithecus*. Configured in this way, HAL facilitates hominid agent action taking (responses) within the constraints of a weighted prioritization scheme all while using “computationally light-weight” algorithms to achieve a minimally “cognitive” architecture.

A few of the behaviors provided by HAL include the following: The first behavior involves navigating to, and approaching upon, a body of water. This drive-reducing behavior helps a hominid navigate to the edge of a pool of water in order to get a drink and to reduce a need-based drive for water (mentioned again below as the separable drive it is).

Another involves the resolution of a cognitive dissonance that forms when a cognitive apprehension between some stimulus one and some attitudinally counter-biased stimulus two presents an uncomfortable “cognitive” realization that stimulus one was equally capable of reducing the drive as stimulus two, but was hitherto unrecognized or unaccepted. In this case the drive-reducing mechanism involves a latent circumstance that can occur after a female hominid transfers to her offspring, at weaning, a food (or forageable) preference. If that male or female offspring later, as a juvenile or as an adult, is unable to obtain the preferred food to which it has accustomed itself but can

nonetheless reduce the basal drive for sustenance with some other food or prey species then, a condition of cognitive dissonance may develop.

Yet another function of HAL is to adjudicate over the size of distal cohorts and to seek group affiliations of a preferred size. Hill & Dunbar (2003) provide the authority for agent decision making regarding preferred groups sizes based on innate drives. Thus, implicitly, biologically grounded and need-based drives for self to gather in small-groups of predictable size should exist. This is a function within HAL and it implements a genetic impetus and drive, and facilitates the navigation of self toward groups of preferential size.

The HAL Class implements several additional drive-reducing mechanisms as cognitive features. They are listed here simply: It provides a preferential relocation or alliance schema to bring self to the location of a beneficent other. It provides a drive to disperse, or relocate spatially, in the year self becomes sexually mature. It provides a drive-reducing mechanism to relocate self away from a fear-producing stimulus. It provides a raw, need-based drive to reduce hunger and one to reduce thirst. And, finally, it provides a drive-reducing mechanism to move self away from an uncomfortable environment (simulated by elevated or reduced ambient temperature).

While many of these are innate, genetic, and biological forms some do have a combined bio-psychological basis. However, in every case, HAL implements them as light-weight computational processes that serve only to animate the hominid in its niche ecology. Outside of some limited cognitive features, HAL is a reactive component.

3.3.3.3.6 Hominid kit

The HominidKit Class is an artifact of the Clans legacy code-base. In Clans, HominidKit serves to assemble, store, and enable hominid utilization of foraged resources.

Effectively, HominidKit is the emulation of hand to mouth drinking and eating in the prototype hominid species.

3.3.3.3.7 Socioecology

Socioecology supports the kin-based sociality that emerges with the hominid population of Clans. Here each hominid keeps the memories of its kin and its knowledge of itself among them. It is here that a hominid can store its memories of mother, father, siblings, children (if self is a female) and the birth order of those children, and a recollection of other hominids with which the self has shared a cohort. Since the Clans system model does not allow for explicit agnatic memory, no unique recollection of in situ mating partners is kept. Thus, when semi-permanent breeding-bonds and breeding-pairs emerge it is not due to a recollection of a previous mate of either sex. Said another way, Socioecology enables uterine kin recognition but does not enable the explicit recognition of a previous mating partner of either sex.

Besides supporting the formidable result of uterine kin recognition (Murdock, 1965; and Chapais, 2008), Socioecology also contains a method that emulates the Westermarck (1921) effect. It does so by answering the question: Has other been in the acquaintanceship of self, and in such close proximity to self, such that, disregarding any pre-existing sexual relationship between self and other, mating between self and other would otherwise be proscribed.

More than anything else, Socioecology is a library of relationships and methods to interrogate those relationships for their contribution to kin, in-group, or out-group recognition. This Class is a particularly extensible body of code and it is one of the more recent additions to the Clans simulation research code-base.

3.3.3.3.8 Life experiences

LifeExperiences is a Class in the events package that provides translation and interaction services to all of the functional areas of Clans. Although there is no named code explicitly implementing these several functional areas within Clans, the concept of “functional areas” remains a useful aid to illustrate the internal operations of the Clans program.

For example, hominids are part of the Social Agents area. However, Social Agents are simulated as though they exist within the Ecology area. It is LifeExperiences that helps the hominid objects coordinate their activities in their virtual world. Bindings is the functional area of Clans responsible for maintaining the simulation master control loop. The master control loop is responsible for sending the Social Agent hominids into the environment of Ecology on what appears to be a “daily,” cyclical basis. But in actuality, it is LifeExperiences that takes the population passed to it by the master control loop, prepares a new uniform random activation list over the existing hominid population once every epoch (day), and then submits that list one hominid at a time into its “life” in the Ecology. Again, LifeExperiences provides translation and interaction services throughout all of the functional areas of Clans.

3.3.3.4 Functional area – bindings

The components in the Bindings area are a broad-functioning set of Java assemblies concerned with bringing together the entire Clans program. This is the third and last of the three functional areas. These Classes provide simulation, visualizations, and user interface capability, report writing functions, random number generation, inter-agent social life and life events, top-level binding-codes necessary to provide social agent birthing (new encapsulated agent object instantiation) and death (removal of expired encapsulated social agent objects from computer memory), and operating system entry and exit points into and onto the Clans program overall. The Classes associated with this area are: Clans, ModelConstraints, Graphical User Interface (GUI), Red-Green-Blue (RGB), TrueRNG, ModelReports, and LifeExperiences.

3.3.3.4.1 Clans – initialization

The Class Clans contains the central Java method, main. Main calls the simulation into existence, it directs the instantiation of the Ecology, it directs the simulated birthing (and later death) of a population of Social Agents, and it is the exit point for return to the Operating System. However, the first task of main is to direct the external setup of a GUI as a windowed frame. The GUI is an event-driven interface that is started to give the user control of the simulation during setup and runtime. After the GUI is instantiated, the program waits for the user to select a map of the terrain habitat to be loaded. Once the terrain map is loaded, the final setup of the simulation can begin. Main passes control to the master control loop.

3.3.3.4.2 Clans – master control loop

The simulation master control loop exists in 3-parts. The first part creates a simulation of a single day in the Ecology with all living Social Agents interacting. The second part involves reporting instantaneous data describing the state of the simulation through the GUI and or through ModelReports. The third part of the master control loop handles accumulated disk data and prepares it for disk saves. The loop repeats until either all of the Social Agent population has died or the user chooses to halt the simulation.

It is important to understand how the first part of the simulation control loop operates. In step-wise progression around the loop: 1) increment the current day; 2) call the local method (theStork) and instantiate all new Social Agents ready to be born and adding them to the population, 3) call the external method (doSimLife) and simulate a single day in the “lives” of the population, 4) call the local method (theGrimReaper) and to remove all dead agents from the population, and finally 5) call the external method (ageEcoSystem) and simulate the aging of the habitat Ecology.

3.3.3.4.3 GUI and RGB

The GUI Class and its support class RGB provide Clans with a windowed frame, a point-and-click user interface, and associable display-related components. After Clans starts, the options available through the GUI are to load a habitat map or to exit. If the user chooses to load a map, the GUI Class will load the map file. As the map file loads routines, the GUI Class has methods that interpret the colors on the map as proxies for habitat elevation and cues as to what and where environmental features should be added to the simulation. Once loaded, the user can choose to enlarge or reduce the map, choose

to keep and display a history of where the hominids move on the map, or to select one of four screen refresh rates. Additionally, once the map has finished loading, the user may choose to start a simulation in either of two modes: single step or continuous run. After a simulation has started to run, the user may stop its operation and then choose to restart, stop, single-step, or prepare a statistics output package.

Currently, only a 24-bit color formatted bitmap (BMP) can be used as a habitat map. The GUI Class will accommodate maps of any size so long as the incoming graphic is configured in 1 square kilometer increments and has an implicit resolution of ten meters per pixel. (That is, only maps having X and Y dimensions in increments of one hundred by one hundred pixels in size are acceptable.) As the map is read-in, the pixel colors on the (map) image are identified and interpreted as encodings for 2.5-D "land features" like height data, cues for intended forageables distribution, water source placements, etc. These "land features" are then incorporated into the terrain of the simulation being constructed. If there was a processing error then appropriate messages are sent to the console and processing will likely halt. If the foregoing steps were successful a display map is constructed according to user intent and installed within the GUI window frame. Then, main enters the master simulation control loop described earlier.

3.3.3.4.4 TrueRNG

The use of the TrueRNG (random number generator) dongle is optional. If it is used, Clans contains software to read and incorporate the random, serial, binary bit-stream coming from the device into the simulation. The TrueRNG Class provides the interface

software that processes that serial stream coming from the device. The TrueRNG Class assembles the stream into a small, constantly-refreshed and agitated, 64-bit pool of random, binary digits. Considered sequentially, the digits are intentionally incoherent and hopefully random. Thus, the digit stream coming from the TrueRNG dongle is sometimes referred to as an entropy source. However, once inside the TrueRNG Class, the pool of digits must be configured as coherent atomic types and made available to the simulation on an as-need basis as integers and real-valued random numbers.

The TrueRNG device is a USB hardware dongle. It operates like a legacy communications COM port and thus requires external Operating System support (Windows CDC drivers). Once signals from the USB device are available to Java, Java requires the libraries of RXTX (receive and transmit) to be available for its compile-time and runtime needs. Additional information about Windows and RXTX software support for Clans TrueRNG hardware entropy generation is outside the scope of this SDD.

Initially, a stream of unprocessed binary digits arrives from the dongle and is fed into the 64-bit pool. At this point, the TrueRNG Class enters a loop that continuously watches the dongle for new data. Whenever the dongle buffer containing new bits from the dongle becomes full (has all bits assigned), a signal flag is set. Concurrent with the arrival of a new stream of dongle binary digits, the existing bits in the pool are being agitated by random shifting action within their own data structure. The agitation mechanism aperiodically shuffles the pool and similarly has its own counters replaced in random order. Now, whenever a new random value is requested by external accessor, regardless whatever random configuration the pool may have, the momentary 64-bit

image of the pool is returned. The signal flag is checked; if the flag is set a fresh load of dongle bits is dumped into the pool and the flag is reset. If the flag is not set the pool continues to be agitated randomly. The process continues until program end.

3.3.3.4.5 Model reports

ModelReports is a utility Class. Its purpose is to create, and then write to disk, several reports describing the status of the simulation. It can be started from the GUI by selecting PrepStats under the File menu option. The reports generated are: 1) BoundReaperReport, 2) DeathAnnals, 3) SocialNetworkReport.dat, 4) SocialNetworkReport.net, 5) DailyStatistics, 6) DeathHistory, and 7)YearlyStats. The schema for these reports appears in **Appendix B**. Their respective outputs are fields of comma delimited text and are they are expected to be used as input to a user supplied spreadsheet program.

3.3.3.4.6 Life experiences

LifeExperiences is a Class in the events package that operates within the Bindings functional area. LifeExperiences provides two functions to Clans; the first being a statistical function that controls and tracks the runtime occurrences of incest in the population and the other a starting point for all simulation activity in Clans.

Beyond keeping a running sum of the incidence of incest, LifeExperiences serves as the target object of a memory pointer originating in the Clans Class and extending into the LifeExperiences Class that binds together Clans with LifeExperiences in order to simulate an explicit Ecology and its population of situated Social Agents. From within the master control loop of Clans, an external call to doSimLife in LifeExperiences sets the once-daily (once per simulation epoch) rotation of the entire extant hominid

population (Social Agents) into a simulation of the events of living (executing) in the simulated environment of the ecosystem (Ecology).

When doSimLife in LifeExperiences begins to execute, the first thing it does is to calculate and to assign a new activation order number to each individual agent. This is done new, once each epoch. Assigning each agent a new place in a uniformly randomized list of “next to run” objects, helps ensure unintended sequential, and social and environmental interaction artifacts are minimized when the Social Agents are inserted into the Ecology. Then, as each hominid object is about to be inserted into the Ecology, the object is checked for a statistical probability that it will survive a random, and extremely rare, death-by-catastrophe (marking the hominid for removal from computer memory) test. If the hominid survives the impromptu test, it will be inserted into the ecosystem and “live” (execute) for one day (one epoch). However, as the hominid is about to exit the ecosystem and before it is returned to the population, it is checked for the possibility that it was actually an infant (object). If the hominid was an infant and if its mother (object) is dead then, the “orphaned” infant object must also die (be removed from memory).

Each Social Agent is tested in these ways and may be allowed to execute in the ecosystem Ecology and or be removed from the population. When the entire population of hominid objects has been cycled through the Ecology one time, program flow control and the system memory pointers to the ecosystem and population are released back to the control of the master control loop in Clans. Finally, within Clans (and the master control loop) execution continues as has been discussed.

CHAPTER 4. RESULTS

The first part of this chapter is a reprint of the same-named section of the peer-reviewed paper presented as a public talk at ECAL in York, United Kingdom, July 20-24, 2015.

The second part of the chapter (Section 4.2) is entirely new material unavailable to the ECAL conference. Included in the latter section are results of the simulation experiment that is the basis of this dissertation.

4.1 ECAL Paper

(Results)

We report here intermediate (in-progress) results. **Figure 9** is a screen capture taken from one model (simulation) run. 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 8 km X 8 km in size and represents 64 simulated square kilometers.

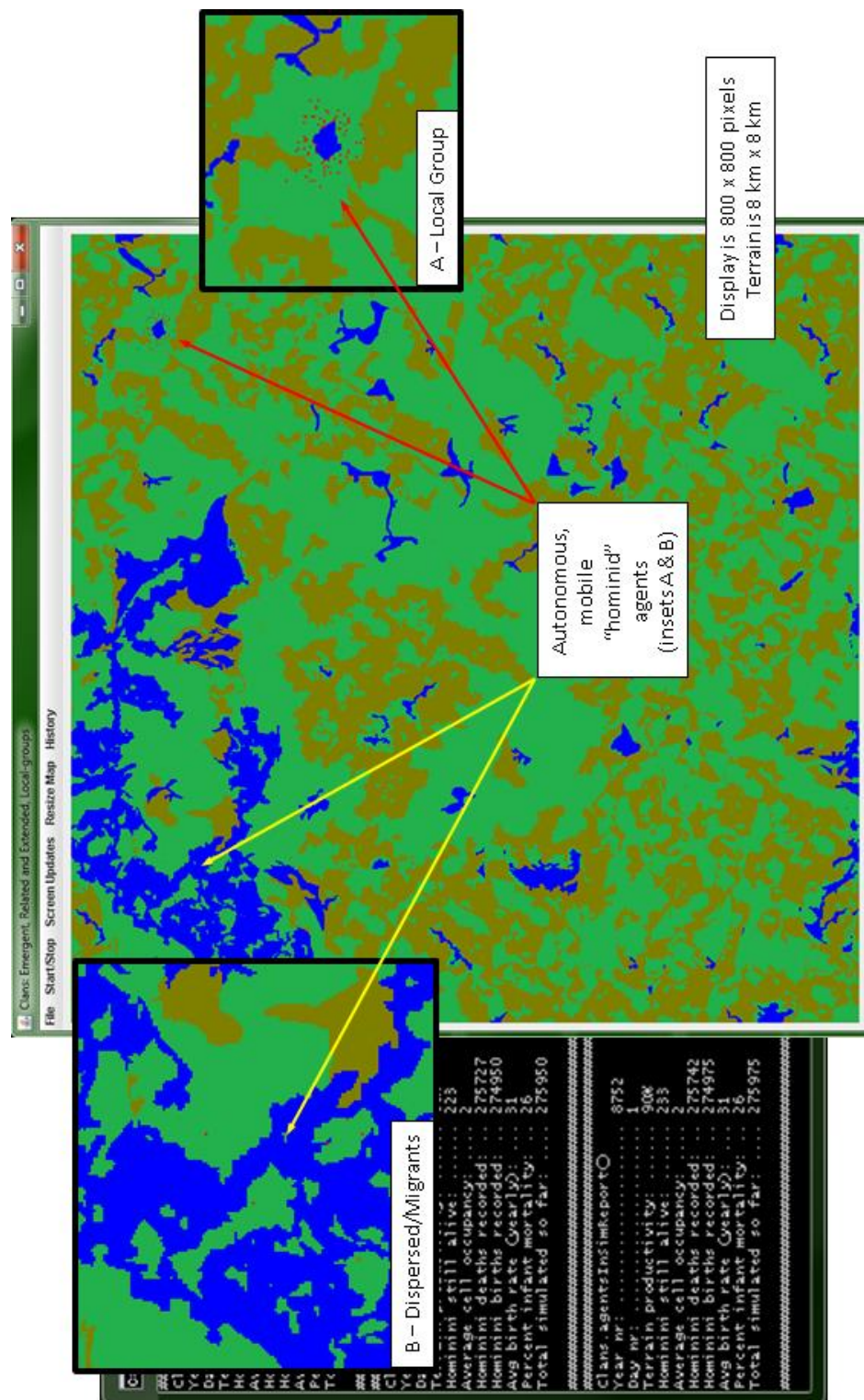


Figure 9 Promiscuous agents at 8,752 simulated years-of-days.

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 interim 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 (identification), 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.

4.2 Final Results

Here we report final (completed) experimental results. This work leveraged a multi-part hypothesis and developed an incremental experimental protocol relying on proof-by-construction. The protocol encouraged continuous re-evaluation of experimental results and allowed for the early termination of the experiment if or when evidence appeared.

Shown here are experimental results believed penultimate to emergent permanent breeding-bonds among hominid-like software agents. In particular, the results will show that non-reciprocal / non-kin based social altruism may be a necessary part of some larger set of individual social behaviors that lead to reciprocal exogamy. This work investigated social organization at its least-organized end.

4.2.1 Presentation of experimental results

These results come from a set of independent variable experiments wherein social altruism was added to, or completely withheld from, every member of eighteen (18) separate simulated populations. The artificial populations under test were genetically closely-related. The experimental schedule called for one group of three (3) populations to serve as reference (or control), another group of fourteen (14) populations to serve as a set of highly constrained experimental cohorts and one (1) last population to serve as a “type” demonstrator. **Table 4** is a schedule of the experiments running over 1000 years.

It is guaranteed that in all of the experiments agent simulated life-events (“births,” “deaths,” “mating,” movement, and forageables choices, lifespans, etc.) and all socio-spatial community outcomes were the emergent results of the interplay between the agent objects, their autonomously selected rules of behavior, their environments, the state of the independent (altruist gene) variable they enjoyed, a random number source producing high-entropy¹¹, and either an initial population laydown of 1,000 singleton agents randomly distributed across 64 km² of simulated terrain or 2 groups of 100 agents started at the same two locations within a 16 km² habitat for each of fourteen (14) experiments.

¹¹ All simulations and results were driven by a TrueRNG random number generator: an electronic device.

The potential confound associated with habitat size difference was resolved by reducing initial population density proportionately. The 64 km² simulations were started with 1000 agents and the 16 km² simulations with 200 agents; more than 25% less.

Table 4 Schedule of experiments.

Number	Group Type	Initial Layout	Duration of Simulated Run	Figure
1	Non-Altruists (Control Reference)	1000 X 1	3,572 years	-
2	Non-Altruists (Control Reference)	1000 X 1	4,525 years	-
3	Non-Altruists (Control Reference)	1000 X 1	8,863 years	Figure 9
4	Experimental - Altruists	100 X 2	1,166 years	Figures 26-32
5	Experimental - Altruists	100 X 2	1,199 years	Figures 26-32
6	Experimental - Altruists	100 X 2	1,223 years	Figures 26-32
7	Experimental - Altruists	100 X 2	1,254 years	Figures 26-32
8	Experimental - Altruists	100 X 2	1,278 years	Figures 26-32
9	Experimental - Altruists	100 X 2	1,302 years	Figures 26-32
10	Experimental - Altruists	100 X 2	1,418 years	Figures 26-32
11	Experimental - Altruists	100 X 2	1,571 years	Figures 26-32
12	Experimental - Altruists	100 X 2	1,694 years	Figures 26-32
13	Experimental - Altruists	100 X 2	1,720 years	Figures 26-32
14	Experimental - Altruists	100 X 2	2,240 years	Figures 26-32
15	Experimental - Altruists	100 X 2	2,375 years	Figures 26-32
16	Experimental - Altruists	100 X 2	4,483 years	Figures 26-32
17	Experimental - Altruists	100 X 2	4,683 years	Figures 26-32
18	Altruists (Demonstrator)	1000 X 1	10,027 years	Figure 10, 35 & 36

The hominid agents in the reference (control) experiments were known to be (at least) inherently *promiscuous* and, through explicitly coded rules in the software, lacked the capacity to express phenocopy altruism. Thus, they are referred to here as promiscuous. In the latter experiments the (experimental) agents were at least potentially *altruistic*. Thus, they are referred to here as altruists. Additionally, there were many more experiments (simulations) run than the 18 listed in the table. Only those simulations whose life-span produced an enduring result exceeding 1,000 years are presented.

The non-altruist (promiscuous) populations had their gene-based trait for altruism explicitly disabled. The longest-lived population of this type survived 8,863 years-of-days. Similarly, each population in the altruists group was also long-lived. This population type had survival results ranging from 1,166 to 10,027 years-of-days and enjoyed explicit biological description and emergent social opportunities identical to the non-altruist group. The essential difference between the two groups was the latter group (the altruists) had their capacity to express the gene-based trait for altruism explicitly enabled. The provider of experimental stochasticism in all experiments was an electronic source of true random numbers that drove every associable socio-spatial interaction and resulting outcome. As we will see, quantitative and qualitative results from the two population types were indeed different. For example, we will see differences associated with population “birth” and “death” rates, causes of “death,” and many other associable properties typical of each respective group.

We have already seen an image of a control (reference) experiment in operation while it was inhabited by autonomous, mobile “hominid” agents. That simulation ultimately ran for 8,863 years-of-days. A screen capture of that experiment (a picture of the experimental habitat taken from overhead) and some of the agents inhabiting the simulated habitat was introduced earlier as **Figure 9**. For a direct comparison between that (promiscuous) experiment and a similarly started (altruistic) demonstrator population **Figure 10** is provided. Both of these simulations were started with 1000 individual agents randomly distributed about the habitat and both show the agents in self-organized communities thousands of years into their respective experiments.

We must also repeat the message that the two longest running simulations were started with random placements of 1,000 singleton agents and not the formal 100 X 2 configuration. It is believed the significant difference between these two “starting condition” branches of the experiment was the introduction of the genetic trait for altruism. In the fourteen experimental altruist simulations, all of the agents in each respective case were started from one of two identical locations, not random locations. It turned out this highly-constrained 100 X 2 startup-configuration not only enabled rigorous experimental comparison and reliably predictive outcomes but it also exacted an equivalently high cost on the agents. Let us examine this cost as our first experimental result.

4.2.1.1 The cost of promiscuity

In the case of this research and in particular in association with the protocol requiring an agent population to start from one of two locations in the simulated habit,

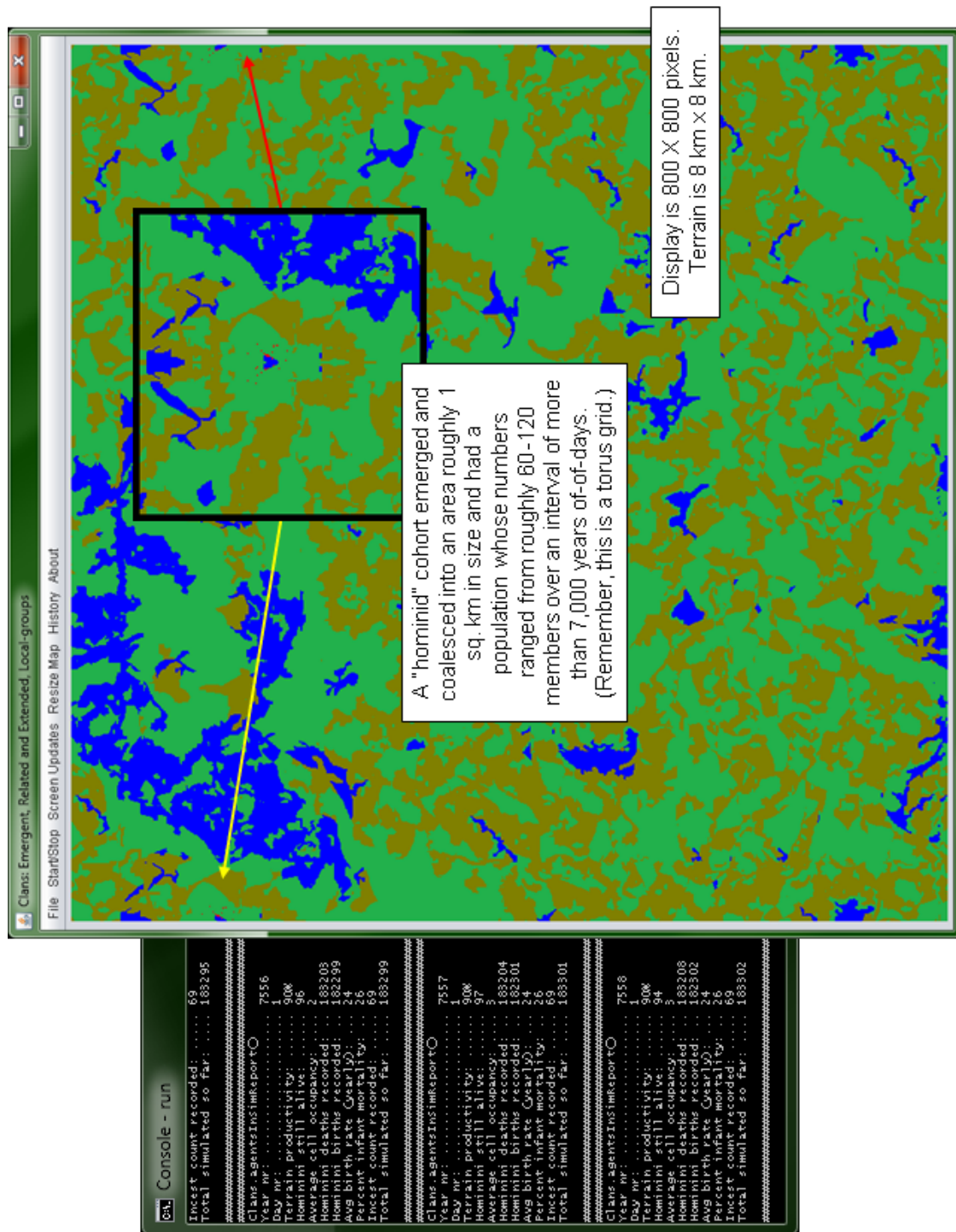


Figure 10 Demonstrator altruists at 7,558 simulated years-of-days.

promiscuous agents were shown to be at a disadvantage. The promiscuous (non-altruist) agents never demonstrated they could survive an experiment started in the 100 X 2 configuration; even after dozens of attempts. After almost a week of repeated trials, all ending in only a few hundred years-of-days, it was understood that the robust fecundity demonstrated by the altruists was beyond the capacity of the non-altruists (the promiscuous hominids). It was decided that the non-altruist (promiscuous) populations should be started in a 1000 X 1 configuration because no simulation of this group type could survive with *enduring time* when started from a 100 X 2 configuration.

Consider the following: During start-up the food preference of the seed-group members (Section 3.3.3.3.1) was inherited from the Terrain Cell (Section 3.3.3.2.2) into which the new cohort and its agents were instantiated. Also beginning at start-up, male and female juvenile and adult agents would instantly begin to forage for their preferred food; the same food. While everyone was foraging, the pregnant females in the cohort would exercise their responsibility to transfer their personal food preferences onto their maturing infants during weaning (Section 3.3.3.3.5). Since every hominid in the cohort would initially attempt to forage for the same food, their simultaneous efforts must have put a tremendous strain on the local ecosystem and depressed its productivity at least in the short run (Section 3.3.3.4.1). Moreover, the gestational term of the female hominids was slightly shorter than the interval of cognitive dissonance associated with the notion of holding on to the cognitive image of a preferred food. This would mean the seed-group members would initially pass on their own static foraging culture into the first generation of new hominids born into the environment.

It appears the 100 X 2 startup configuration caused a cascade of complex, interrelated foraging and reproductive issues that would result in the extinction of this experimental hominid group type. However, since the only difference between the promiscuous groups and the altruistic groups was the former was not genetically endowed with an innate tendency to share limited food resources *altruistically*, the promiscuous populations appeared to have been doomed and the altruists flourished.

4.2.1.2 Promiscuous hominids (altruism disabled)

The promiscuous population (the control group) had no means of expressing the phenocopy behavior of altruism. **Figure 11** is a graph of the number of promiscuous hominids “alive” in the longest running control (reference) simulation year by year.

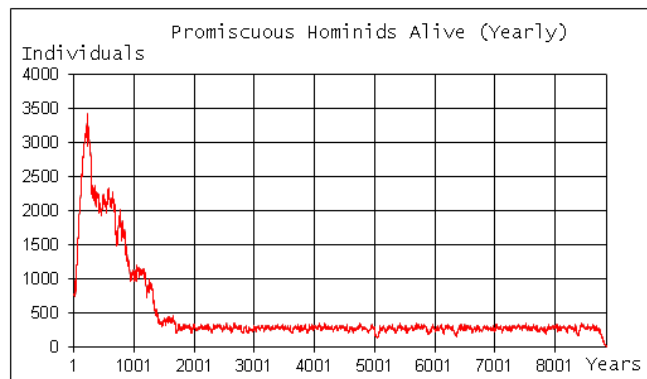


Figure 11 Promiscuous hominids survive over 8,863 years-of-days.

In **Figure 12** we see the count of promiscuous hominid births spiking in the control then slowly descended to a rate approximating roughly 25 - 30 newborns per year. The spike was a consequence of an excess number of initially poorly adapted individuals dying.

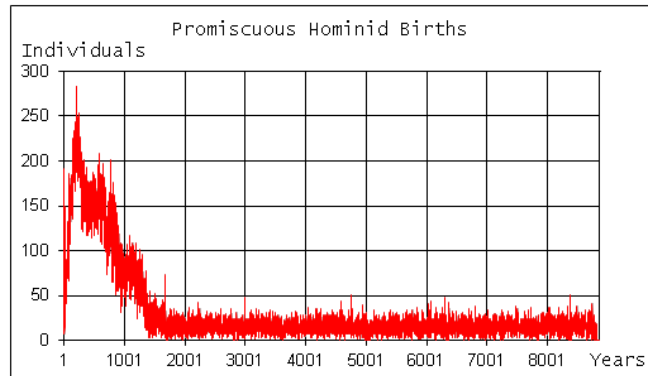


Figure 12 Count of promiscuous hominid births.

There was no apparent indication of model-induced periodicity (a pejorative artifact) in any of the promiscuous hominid signals. Moreover, all of the signals fell into “noisy” equilibrium for over 6,000 simulated years.

Similarly, **Figure 13** shows us how the quantity of promiscuous hominid deaths per year dropped suddenly in the first year as agents looking for forageable resources failed and then rebounded as newborns entered the population. As soon as stable cohorts started to form, over the first 1,500 years, the deaths per year fell to an annual rate near 26 individuals. During the first 1,000 years or so, several cohorts fused (coalesced) to form a single cohort. After that interval sexual dispersal, foraging, ecological choices, and individual group size preferences led to incidences of fission, repeated fusion (Lehmann & Boesch, 2004), and the migratory behaviors characteristic of all the control and experimental populations.

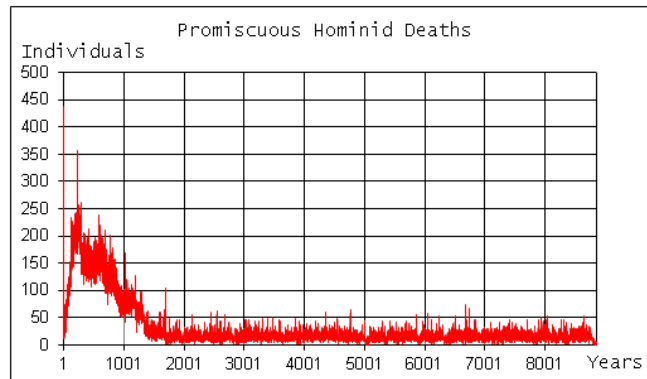


Figure 13 Count of promiscuous hominid deaths.

The final distribution of agent (simulated biological) sex during the entire 8,863 year run is shown in **Figure 14** as a histogram of males versus females. The final distribution is approximately 50/50 with a slight numeric advantage going to the females. This was controlled by probabilistic Constant (0.495 male versus 0.505 female) but was subject to momentary, random fluctuation. Future work will likely see this change and a gene for biological sex-choice-tendency be added that expresses only in male agents. For

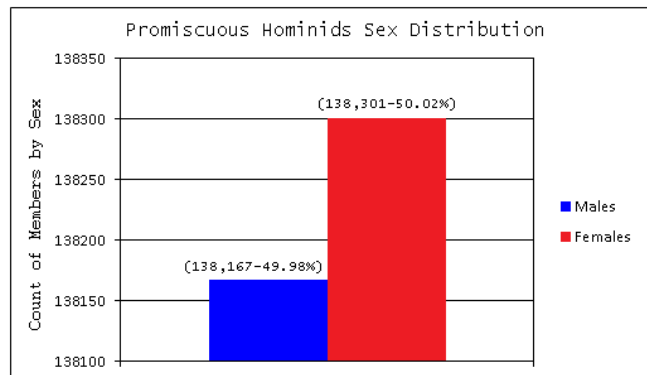


Figure 14 Distribution of sex in promiscuous hominids.

these experiments, both promiscuous and altruistic sex was probabilistically assigned.

Shown in **Figure 15** are the numbers of agent deaths by year and sex. Death according to sex was not well differentiated in the data. Data is depicted here as an overlapping graph.

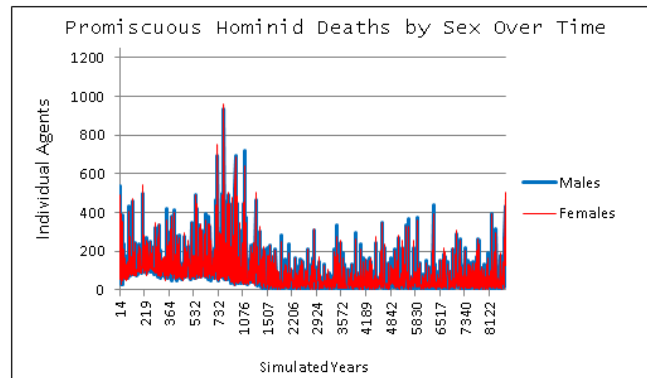


Figure 15 Promiscuous death counts by year and sex.

In spite of the results shown in **Figure 15**, the issue of how and why agents died in the simulation is actually very important. **Figure 16** shows a histogram communicating how, over the entire 8,863 year simulation interval, the cause of death experienced by hominids (of both sexes) were primarily death by starvation first and death by dehydration second. In truth, since disease precipitates a condition of withering to some greater or lesser degree, death by starvation encapsulated both morbidities. Catastrophe, a catchall for very rare fatal conditions, and death by drowning were not observed at all during the simulated control population. Orphan death was the third highest morbidity.

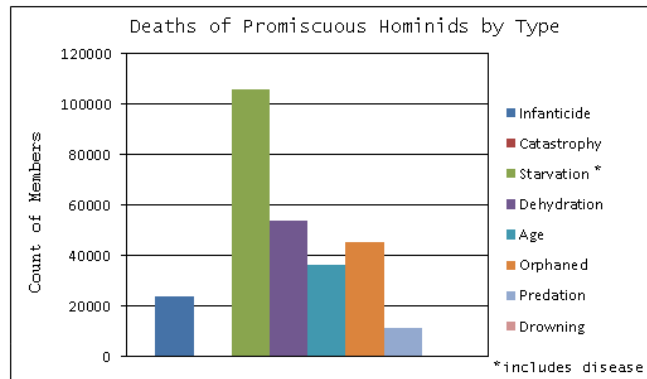


Figure 16 Promiscuous deaths totals by cause and type.

As with the great apes and *Homo* today infant mortality, infanticide, and other causes of premature death in the species of the temporal conjecture examined by this dissertation are causes for concern. Thus, in the overlapping graph shown next, the numeric rate of new births recorded per year is shown in contrast to the percentage rate of infant mortality. Within the control and experimental populations infant mortality rates were identified and counted as the death of a pre-weaned infant. It was not differentiated by its possible causes: orphaning (a state associable with a pre-weaned infant losing its primary source of nourishment, i.e., its mother died) or infanticide. Both of those causal factors were tracked separately in **Figure 16**. Emergent infant mortality and infant birth rates are shown in overlay in **Figure 17**.

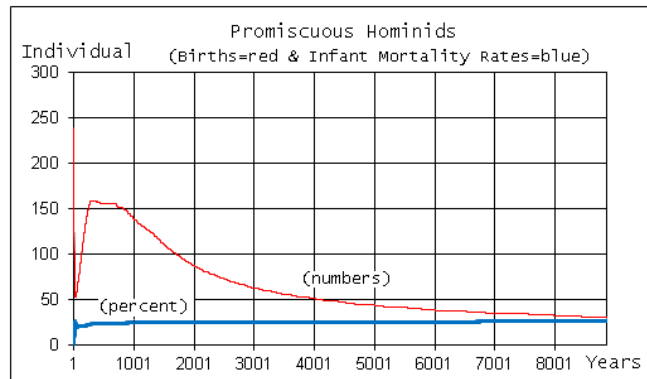


Figure 17 Promiscuous infant mortality and birth rates.

Finally, although control agents could not express the phenotypic “gifting,” a behavior associable with the altruism gene, the gene was in fact passed between agents during simulated biological reproduction. That is, during simulated mating, all parental genetic material was available to an offspring during conception and it became subject to rule-based modification by cross-over and mutation. However, according to the hypothesis, agents in the control group could not experience any causal-coupling between the value of the gene held by an agent and the incidence of repeated matings, i.e., emergent, permanent breeding-bonds, observable in the population. Logically, this provides a verification step with regards to system model instantiation and potentially adds support to the claims made by this dissertation. Stated simply, there should be no causal-coupling between agent genes in the promiscuous population and repetitive matings. **Figure 18** shows the critical Java-coded “switch” that either included or excluded the phenotypic processing of the altruism gene in a social context.

Note: *The potential for a gene-based trait for alliance was always processed.*

However, it was not always acted upon. Its activation was logically contingent upon an agent receiving an altruistic “gift.” Without a “gift” there could (logically) be no “giver” with whom a recipient could seek to relocate. Thus, alliance (or preferential relocation) would be effectively nulled except for those cases (those experimental cases) where USE_ALTRUISM was set TRUE by Constant. Only in the experimental cases were agents empowered to preferentially seek to relocate (or to align with their “benefactor”) after receiving a “gift.” For these USE_ALTRUISM was set TRUE.

```
public void socialPsychology (Hominid self, Ecology ecoSys, int h, int v,
                             int epoch)
{
    ArrayList <Hominid> localGroup = ecoSys.getCohort (h, v);
    self.kin.updateGroup (localGroup);          // inform oneself of one's cohort.

    if (USE_ALTRUISM)
    {
        self.altruism (ecoSys);                // if benefactor, engage in social gifting.
    }

    self.alliance (ecoSys, epoch);              // if beneficiary, engage in relocation.
    // doPatrol add code here.
} // End method.
```

Figure 18 Altruism and alliance gene steering code example.

4.2.1.3 Altruistic hominids (altruism enabled)

There were fourteen constrained configuration, highly-controlled experiments ranging in length from 1,166 to 4,683 simulated years-of-days. By contrast with the promiscuous population (the control group), the altruistic populations (the experimental

groups) did have a means to express the phenocopy behavior of altruism. The longest running altruist experiment was selected to represent the experimental populations here. **Figure 19** shows the number of hominids “alive” in that 4,683 years-of-day simulation, year over year.

In **Figure 20** we see the count of altruistic hominid births initially experiencing noisy bursts of activity then descending into a rate of roughly 40 - 60 newborns per year.

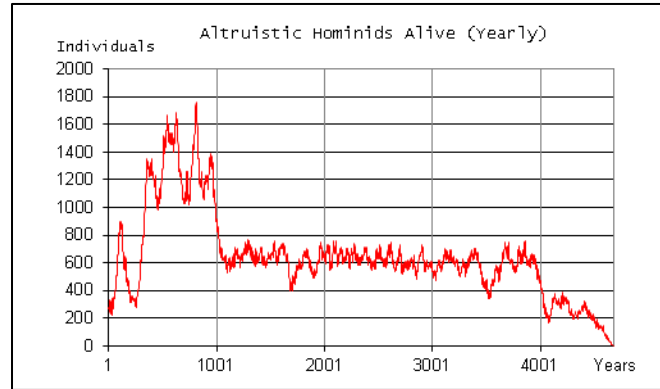


Figure 19 Altruistic hominids survive over 4,683 years-of-days.

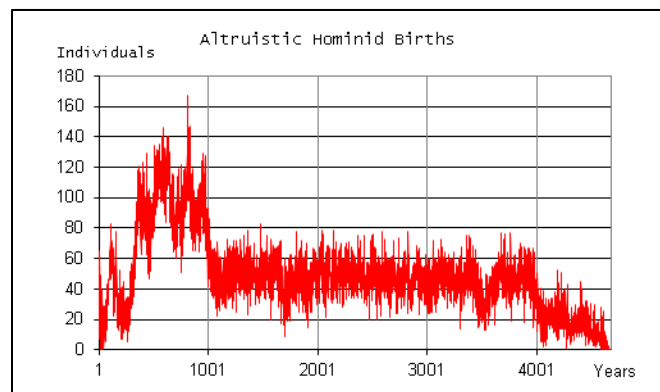


Figure 20 Count of altruistic hominid births.

As in the control experiment, there was no apparent indication of model-induced periodicity in any of the altruist hominid signals. Moreover, the signals fell into a “noisy” equilibrium for over 3,000 simulated years. **Figure 21** shows hominid deaths.

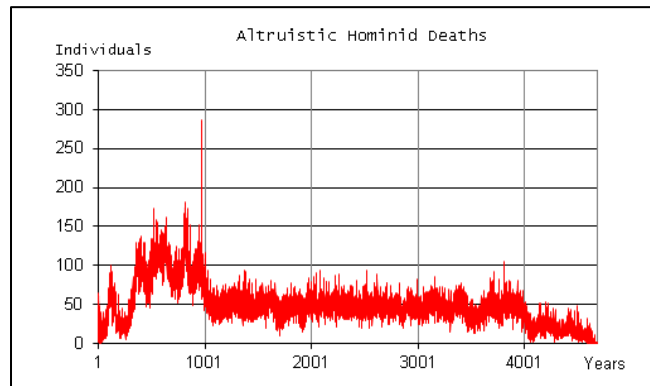


Figure 21 Count of altruist hominid deaths.

A distribution of altruist agent (simulated biological) sex during the entire 4,683 year run is shown in **Figure 22**. The result was within expected, probabilistic bounds.

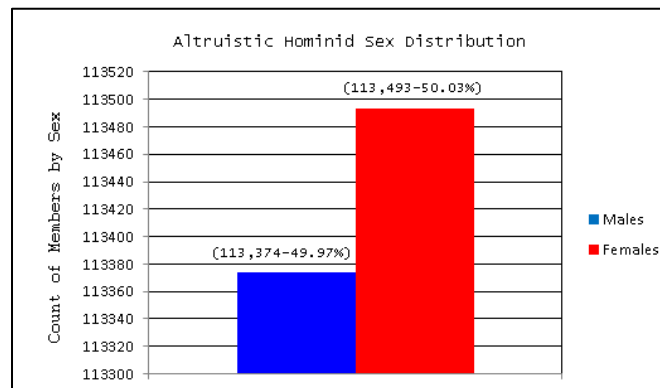


Figure 22 Distribution of sex in altruistic hominids.

Shown in **Figure 23** are the numbers of agent deaths by year and sex. Here, as in the control experiments, death according to sex was not well differentiated. Data is depicted as an overlapping graph.

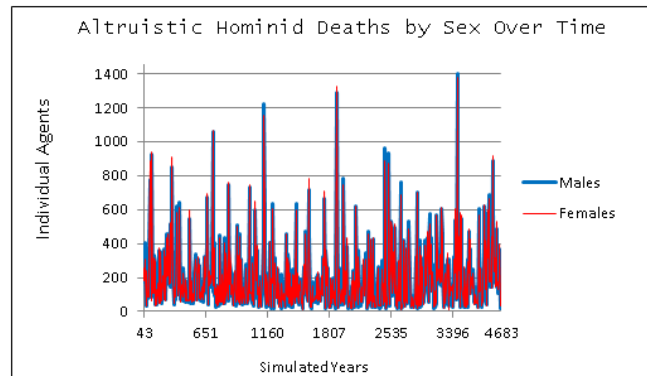


Figure 23 Altruist death counts by year and sex.

Figure 24 shows a histogram communicating how, over the entire 4,683 year simulation interval, the cause of death experienced by hominids (of both sexes) were primarily death by starvation first and death by orphaning second. These are stunning results when compared to those of the control group in **Figure 16**. These results are the first to show us quantitative evidence of a difference between the control and experimental groups. The difference between death by starvation and death from thirst changed from a 2:1 ratio (in the control group) to more than 6:1 (in this typical experimental group). *Clearly, the effect of giving away food reserves, altruistically, has a very real survival cost.* Finally, deaths by catastrophe and or drowning were not evident in this experimental sample.

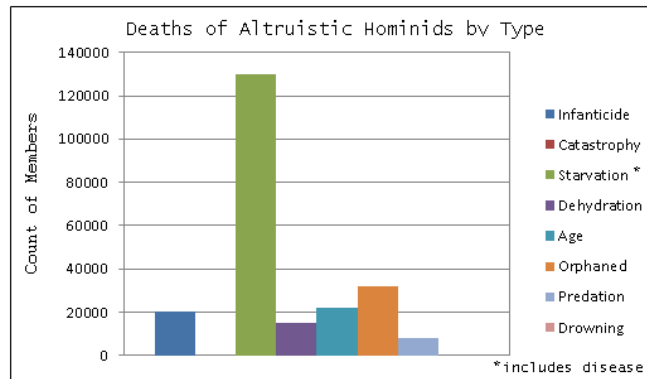


Figure 24 Altruist death totals by cause and type.

Infant mortality and infant birth rates are shown in overlay in **Figure 25**.

Although quantitatively different than the control population the trend and function is similar. However, notice the increased reproductive capacity of the altruistic population.

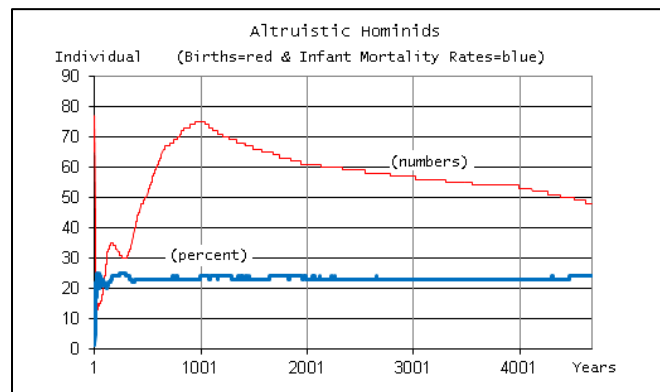


Figure 25 Altruist infant mortality and birth rates.

Here we see a second quantitative difference between the control and experimental groups even if though it may potentially be attributable to issues associable with

environmental circumscription. Compared with an average birth rate of 31 for the control group (read the console report in **Figure 9**) we see an average birth rate for the 4,683 year experiment to be nearly doubled. Thus, the results suggest it is possible to experience a strong increase in birth rate under certain environmental conditions. *Altruistic foraging behaviors within a community of hominid-like agents may facilitate a comparatively greater rate of offspring production than might occur in a similar non-altruistic community if environmental conditions are favorable.*

Up to now, we have contrasted the population of the control experiment with the longest lived (4,683 year) experimental population. From here on we consider the entire set of experimental results as a group. We are looking for population-wide indicators of overt socio-behavioral change occurring contemporaneously with objective changes in basal genetics. Foremost we want to know if a gene-based trait for altruism, perhaps working in tandem with a gene-based trait for alliance, can be correlated with population mating behavior. Simply put, we want to know if our promiscuous control population will demonstrate polygamy and or monogamy simply as a consequence of changes in the independent variable. We now experimentally define the occasion of the bonds between breeding couples to be “permanent” if they co-produce four or more offspring during the female lifetime. Note: Female lifetime offspring production is seven or less per Tutin, 1979, p. 31, with a, “... maximum of five or six offspring who survive to weaning ...” Graphs shown in **Figure 26**, **Figure 27**, and **Figure 28** show alliance in relation to permanent breeding-bonds. These graphs appear to suggest that alliance, if it is gene-based, may be recessive. *If this is an accurate assessment of the condition of the*

prototype then, this is a remarkable result. The reason for this supposition is that only in the case where neither parent has the gene for alliance was it that significant population-wide incidence of semi-permanent bonding emerged. Again, this is only speculative, but an interesting finding none-the-less. More likely is it however, that alliance is a cognitive feature involving the choice of the mated partners to remain in affine relation. A mechanism to test this is not implemented currently but could be in later software.

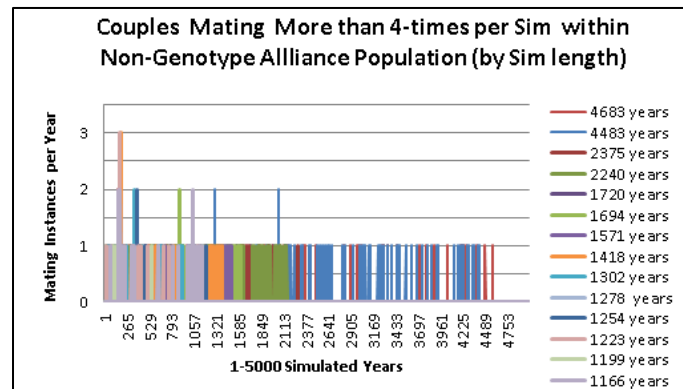


Figure 26 Alliance mating (neither parent has the gene).

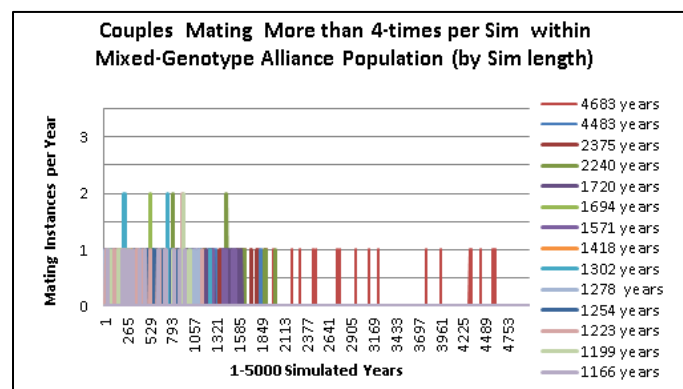


Figure 27 Alliance mating (either parent has the gene).

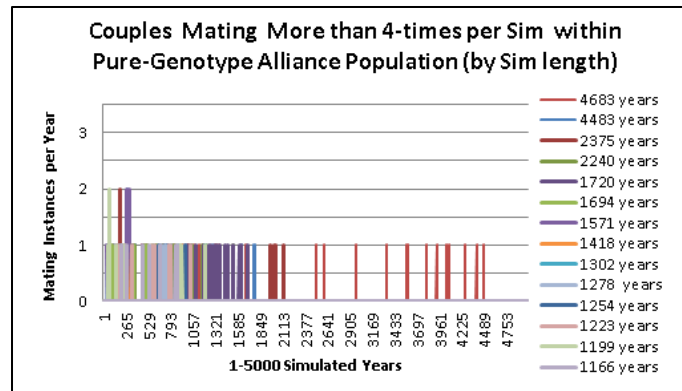


Figure 28 Alliance mating (both parents have the gene).

Next, graphs in **Figure 29**, **Figure 30**, and **Figure 31** reveal that given an enduring period of time, altruism will become pervasive and dominant regardless of the gene value of an individual parent. *Over time, if altruism is an available gene-based trait, it will overtake the population and become dominant.*

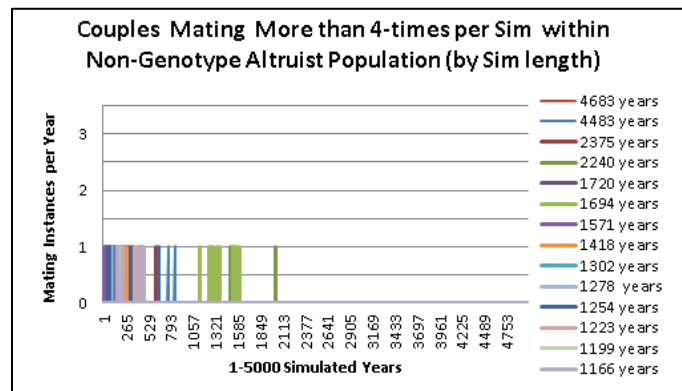


Figure 29 Altruist mating (neither parent has the gene).

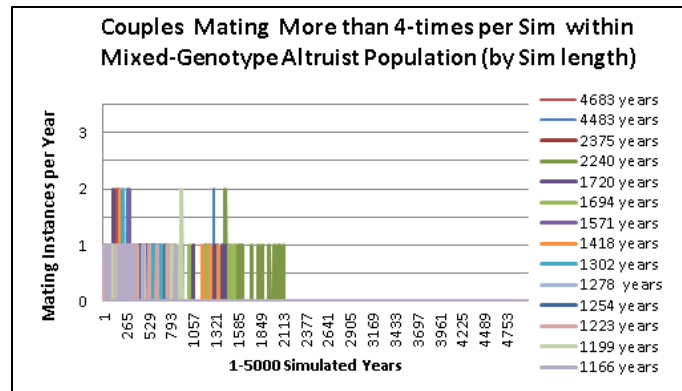


Figure 30 Altruist mating (either parent has the gene).

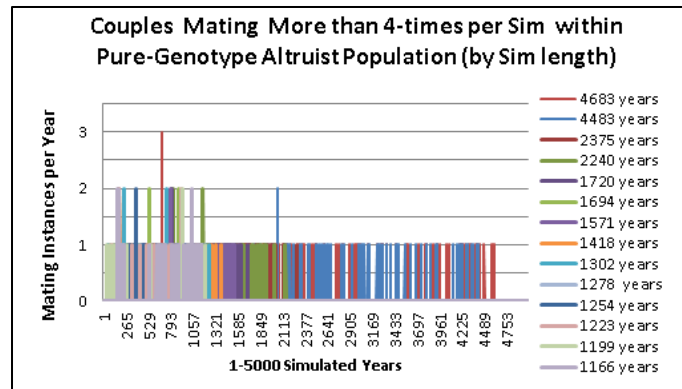


Figure 31 Altruist mating (both parents have the gene).

In **Figure 32**, where both parents were phenocopy altruists and mated four or more times, not only were there many simulations in which two couples mated four or more times but there were at least three couples mating four or more times in the 4,683 year experiment. *In summation, it appears that longer-lived populations enjoying a trait for altruism may eventually find it become phenotypic.* In fact, during the first 1,000 years of those experimental populations described here, the linear tendency for couples mating four or more times actually increased slightly across all average mating instances.

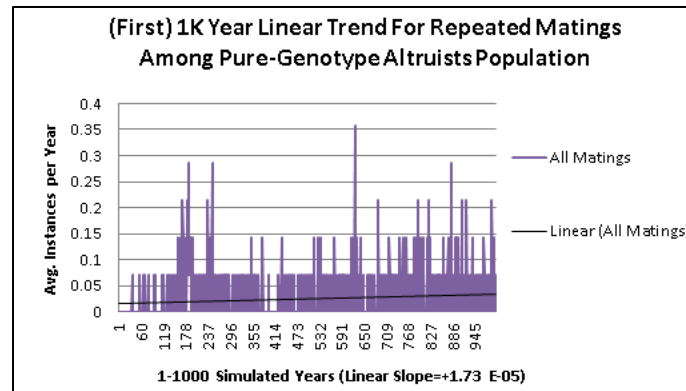


Figure 32 Linear tendency of altruism to perfuse across populations.

CHAPTER 5. DISCUSSION

The first part of this chapter is a reprint of the same-named section of the peer-reviewed paper presented as a public talk at ECAL in York, United Kingdom, July 20-24, 2015.

The second part of the chapter (Section 5.2) is entirely new material unavailable to the ECAL conference. Included in the latter are post-experimental discussion of the results presented in the previous chapter, several technical observations, and claims.

5.1 ECAL Paper

(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.

5.1.1 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, Wrangham, Harrigan & Smuts, 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.

5.1.2 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.

5.1.3 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.

5.2 Post-Experimental Discussion

It needs to be stated clearly that this work has not demonstrated monogamy or achieved the socially complex behaviors of reciprocal exogamy. However, the research was able to show that social altruism in association with preferential relocation (both expressed as adaptive traits) can produce and sustain permanent breeding-bonds within a population of promiscuous hominid-like software agents. Moreover, the experiment produced enduring, long-term simulations containing plausible, highly-social, hominid-like interaction. **Figure 33** and **Figure 34** are depictions of but two genealogical networks produced by the work. Red nodes are female agents, blue males, and edges kinship lines. These graphs were produced by the Pajek software (Batagelj & Mrvar, 2015).

The experimental hypothesis asserted that 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 would lead to the emergence of reciprocal exogamy. It now appears that a sufficient set of causal factors possibly leading up to a requisite set of pre-conditions needed for reciprocal exogamy, i.e., the inculcated practice of breeding partner exchange, may have been identified without the addition of behaviors related to

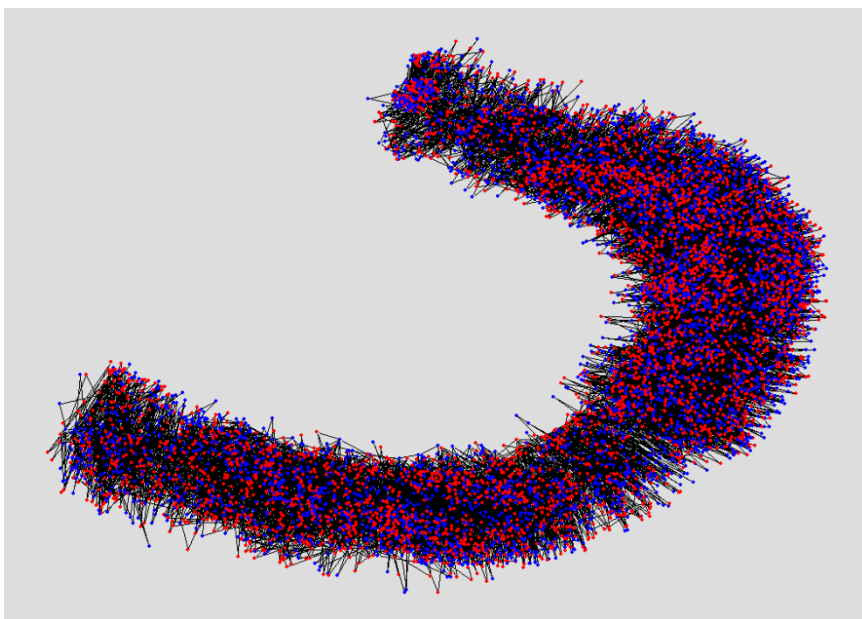


Figure 33 Single-troop genealogical social network, approx. 700 years.

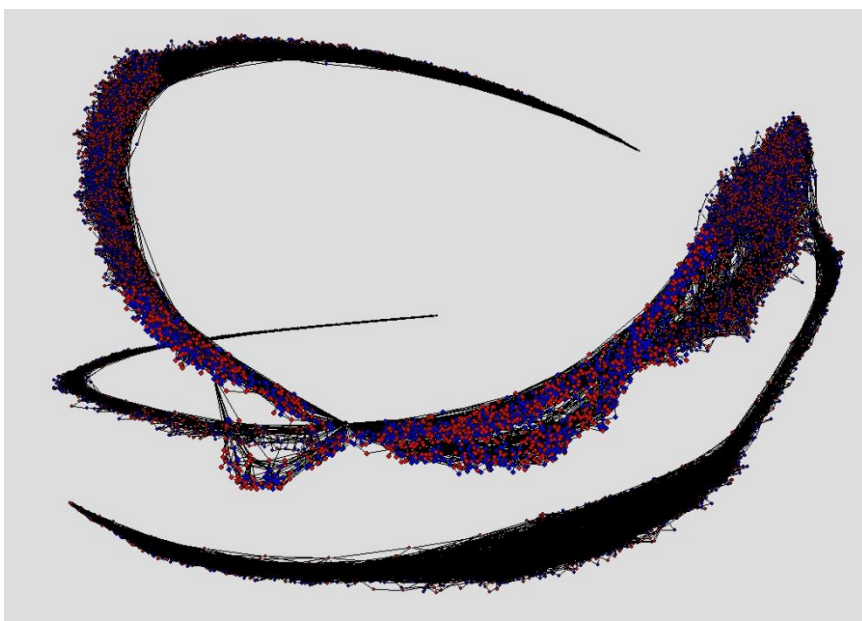


Figure 34 Multi-troop genealogical social network, approx. 2,400 years.

spatial territoriality. *Simply, this experiment suggests that new work building upon the current work and concentrated on exploring the additive effects of conspecific patrilocality and territoriality based in patrol behavior can be planned for a later time and will likely be successful.*

The current experiments demonstrated that with a gene-based trait for social altruism a promiscuous hominid-like population having spatial mobility, a gene-based trait for alliance, pressed by circumscription, and innate drives for sexually differentiated philopatric dispersal will adapt in the direction of social change and social affines. In the experiments here, the transition was grounded first in promiscuity and did, over time, demonstrate polygamy as undifferentiated polyandry and or polygyny. Furthermore, it appears the transition ultimately produced occasions of intense, semi-permanent breeding-bonds in individuals at the rate of four or more matings per pair per lifetime. In summary, the results of the experiment appear to suggest that only a subset of the propositions voiced in the original hypothesis may be necessary. Thus, what is claimed is that it seems that moving a promiscuous population along an incremental, social trajectory in the direction of emergent, social affines and reciprocal exogamy using purely socio-environmental influences and gene-based traits is entirely feasible in-silico. Given what is now known, it is suggested that further research be undertaken to obtain a yet closer approximation of reciprocal exogamy using this work as a model and following the path articulated in the original hypothesis.

5.2.1 Reality checks

This research only used a theoretic framework and empirical evidence to build a spatial agent-based model. More particularly it used an explicit, individual-based model that was a micro-simulation of primitive, hominid-like software agents in order to study human social organization at its least-organized end. The work was constructed around a system model associated with a time period and temporal conjecture emanating from within the phylogenetic chaos of primate evolution at the time of the *Pan-Homo* split somewhere between 5 and 7 mya. It is referred to here as chaos since the proxy evidence left to us in the archeological and geological strata contains no soft-tissue remains or explicit recordings of the proximal, pertinent and daily, social intercourse the primates of the period enjoyed. Finally, the theoretic framework employed by this work has allowed for simplified observation of what resembles evolved survival results from altruistic sharing and socio-environmental circumscription among the agents inhabiting the simulations.

The hominid-like agents in this work were created to crudely capture pertinent aspects of the higher primates: *Pongo*, *Gorilla*, *Pan*, *Ardipithecus*, *Australopithecus*, and *Homo* with a semi-fine focus on a hypothetical *Pan-Homo* hybrid. Additionally, this research used a single independent variable protocol to examine how self-sacrificing altruism based on foraged resource “gifting” might influence emergent sociality. Altruism in *Pan*, our nearest living phylogenetic relative, has for decades been all but completely denied by primatologists arguing in favor of ultimate (evolutionary) over proximal (motivational) causalities (de Wall, 2008; de Wall & Suchak, 2010). This may

be due to assessment methodology failure more than species trait. While empathetic altruism may exist (Warneken, 2006); it has historically been difficult to instrumentally assess the behavior accurately. Thus, a position consistent with the negative was assumed here. Clearly *Pan* has behaviors that resemble reciprocal altruism, or quid pro quo exchange, but self-sacrificing “gifting” is not usually reported as ubiquitous group-behavior. It is unclear if *Gorilla* too is altruistic in either sense nor is the behavior in *Pongo* well defined (Kim, Martinez, Choe, Lee & Tomonaga, 2015) in the same context. Simply, pure self-sacrificing altruism is not a trait strongly associated with any of the species phylogenetically nearest to us in our family tree. Where our extinct relatives *Ardipithecus* and *Australopithecus* are concerned, one can only speculate as to their patterns of small-group social behavior based purely on proxy evidence. However, on the other hand, *Homo* does demonstrate the behaviors of altruism and alliance. Thus, the question of the ubiquity of altruism and its adaptive function phylogenetically is neither farfetched nor trivial. Rather it is believed by the author to be, and has been investigated by this work as, an imperative precursor of our modern sociality; literally, a precursor to the “household.”

It was observed during the course of the experiments that the relative size of the ponds and the watering holes frequented by the hominid agents may have had some influence on the size of the troops sustained by the simulations. For example, environmental circumscription (characterized by constrained biome-based forageability and drinking water availability) encouraged larger sustained troop sizes over enduring periods when those troops were associated with larger watering holes and the longer

associated shorelines they provided. Clearly, the carrying capacity of the biomes and the forageable lands surrounding the watering holes were in dynamic balance as the agents foraged. But, the overall equilibrating effect was to drive the dynamic system toward some self-sustaining population mass arbitrated by the size of the water source, the number of agents, and the available forageable land near the pond. However, this result should not be a surprise to anyone as it is a summary notion witnessed by the Tragedy of the Commons (Hardin, 1968), rests on the Malthusian argument (Malthus, 1798) of population covariance occurring in relation to the availability of subsistence resources, and is common sense.

An instantaneous accounting of all active (simulated “living”) agents in the habitat was periodically recorded by Clans. When several individual agents collocated spatially it was easy to discern them visually. Similarly, when agents wandered away from a cohort their departures could be detected. However, because of software limitations, only whole habitat census numbers were reported. Smaller, aggregate assemblies (like wanders) could be observed but not counted separately. Thus, what we know about the hominid agents comes from census data taken over all the agents in a simulation. We cannot know census numbers of the sub-groups even though we can infer and differentiate their spatial (or social) migration and dispersal patterns. Numerically, all agents in a simulation were counted as being part of the same community. Since the (100 X 2 laydown) experimental habitats covered 16 km² and the (1000 X 1 laydown) reference control and altruist demonstrator habitats covered 64 km², the density and size of an artificial community was easy to calculate.

Typically, after a simulation had run for a little over a thousand years, one or more dominant troops would establish themselves. From this point onward population numbers would settle upon some relatively stable range of values typically between approximately 60 and 300 individuals in the 64 km² reference and demonstrator experiments and 300 – 600 in the constrained 16 km² altruist experiments. (Note: this latter total was often distributed across 2 or 3 troops in the experimental habitat but because of the aforementioned limitations of the software could not be subdivided to provide numeric evidence.) Empirical, real-world census data for extant communities of *Pan* in Africa typically report membership numbers in excess of 50 (Sugiyama, 1968) across distributed spatial aggregations. More detailed censuses have reported troops with numbers and density-of-membership tallies of 150 members in 35 km², according to Watts, et al., (2002). In the 8,863 years-of-days control reference experiment (shown in **Figure 9**) slightly more than 200 individuals¹² resided in the 64 km² habitat on average. **Figure 11** is a graph showing the year over year number of Agents in the Simulation. Experimental populations initialized as 100 X 2 groups produced final population numbers ranging between 300 and 600 (**Figure 19**) but were typically distributed across the habitat as two or three independent troops as already stated. As a whole, these experimental groups were too large for their 16 km² space but they still flourished. When the larger habitat was seeded with 1000 X 1 agents it worked best and produced the more realistic results. Future work is strongly advised to remember this result: *a larger habitat*

¹² Scaling the ratio by two results in a sociospatially unviable but numerically valid ratio of 300 in 70 km².

initially occupied by many self-organizing agents may produce better and more reliable results over enduring time.

Of special interest however, was the near perfect result demonstrated by the altruist demonstrator experiment. This simulation was introduced at year 7,558 in **Figure 10**. In particular this experiment: 1) was manually ended after 10,027 years-of-days, 2) was started with 1000 X 1 random agent positions across a 64 km² space, and 3) had a population with an active gene for altruism. The initial population fused and settled into a single, numerically plausible community whose equilibrated numbers ranged from 60-120 individuals over a period of 8,000 years. These numbers included migrants and dispersed females, and compare favorably with actual living troop sizes (Appendix A) for wild *Pan* in Africa (Watts, 2002; Williams, 2008). **Figure 35** and **Figure 36** demonstrate pertinent census data for the altruist demonstrator experiment.

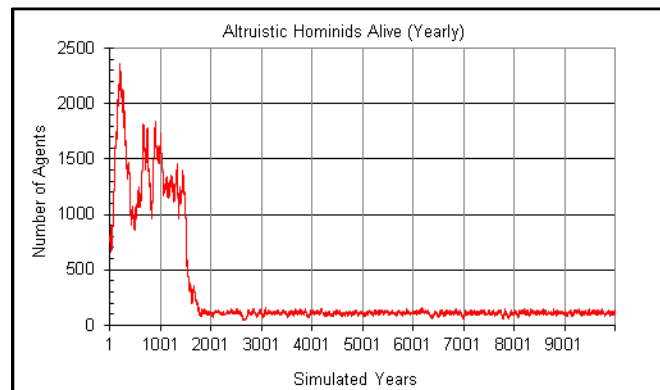


Figure 35 Altruist demonstrators survive over 10,000 years-of-days.

The initial spike and ring in the demonstration Agents Alive signal was common among all of the experiments in this research series. During this early period of time communities were getting established and significant random (and purposive) between-group migrations and foraging sorties were being undertaken. There is a good chance many of the migrants were females in driven dispersal. If so, these may have encountered another cohort, stayed there, and contributed to its gene pool and ultimate success.

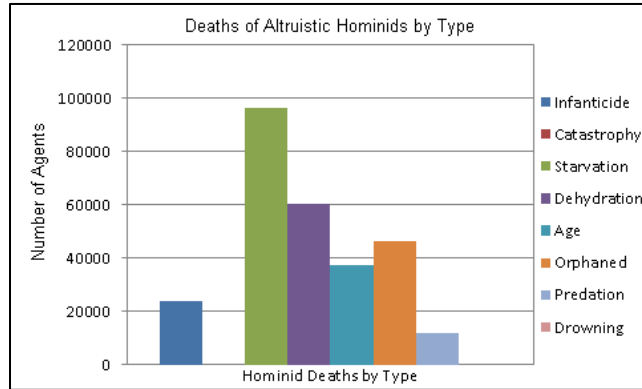


Figure 36 Altruist demonstrator death totals by cause and type.

This result from the Altruist demonstrator is noteworthy for its encoded messages. Given these were altruist agents the high ratio of death by orphaning in this histogram is communicating two things about the female members of the troop. First, they were highly stressed. Often these females were dying before they could complete their responsibility to wean their maturing infants. Compare the result here with those in **Figure 24**, the experimental altruists. The proportionate numbers of deaths by orphaning are roughly 100% higher here than in the longest running experimental setting and is

actually very comparable to the promiscuous result in **Figure 16**. Second, in contrast to their stress, these females were very productive (offspring reproduction). One might surmise that preferential relocation to a benefiting mate might facilitate more advantageous breeding opportunities. Clearly, in the constrained 100 X 2 experiments, altruists (males and females) flourished while their promiscuous peers died out. Overall, even though the demonstrator group was struggling to survive, as witnessed by the large number of deaths by dehydration (likely caused by females under the added stress of nursing); they were still a vital population when they were euthanized for this report at 10,027 years.

5.2.2 Altruism – bipedalism and the hands of Ardi

Clearly, altruism figures prominently in this work and deserves extended treatment. This sub-section offers that treatment and is divided into three topic areas. The first will explain the reason why altruism was introduced into this research; its function and role. The second area will outline the theoretic foundation and the historical framework that underlie that function and role. Then, based in the theoretic foundation and historical framework, a third area will describe the experimental constructs used to simulate altruistic “gifting” in the research. Finally, as we will soon learn, it may be that pro-social altruism rests in the hands of Ardi; a nickname given to the *Ardipithecus ramidus*.

5.2.2.1 Why altruism

During the development of the current research code changes were made to the donor code terrain modules in order to make the carrying capacity of the simulated environment more realistic. These changes enabled the daily regrowth of forageables and the daily

refilling of small water basins practical (see Section **3.3.3.2.1**). Under the new code whenever agents (male and female) foraged, their continuous presence in a location would deplete terrain forageables and would burden the supply of fresh water (depleting the daily-refilled water basin drinking water supplies). Effectively, this constrained the foraging success of the second or later agent arriving at a location. However, as it would turn out it also had an indirect impact on agent intent and ability to form successful long-term affine and social alliances.

On the agent side of things, in the donor codes, there had always been a differentiation made between male and female nutrition and water needs, and the additional amounts of both required by gestating and nursing females. However, the capacity for male and female agents to “hand-carry” food and or water supplies from one day into the next was fixed and undifferentiated by sex. It turned out sexually undifferentiated “hand-carrying” of foraged resources in conjunction with more realistic terrain carrying capacity was a problem. The solution was to address the social altruism called out in the hypothesis stated in the last paragraph of Section **3.1**.

Here is what happened. While the new terrain modules created a more plausible, realistic, and dynamic environment with respect to harvesting nutrients (food and water) from the terrain, when male and female agents tried to forage their sexually undifferentiated “hand-carry” capacities led to an imbalance in how much each sex could find to eat and drink if they were unfortunate enough to be the second or later agent to arrive at a location. Agents arriving late and hoping to forage, or agents with plans to make small-group associations, would only be able to forage based on the instantaneous

and possibly highly-depleted resource levels remaining. If they did arrive late then they might fail to gather adequate nutrition, could subsequently not be able to carry any excess resources into the next day, and then might experience a cascade of related problems. Over time it became obvious the cohorts were disbanding and expiring from hunger, thirst, and lack of mating resource availability.

Often this series of events emerged as an observable cascade. But while observing these events a remarkable hypothesis put forward by Owen Lovejoy in *Science* (Lovejoy, 2009) regarding the evolved changes of the hands and wrists of *Ardipithecus* came to mind. What Lovejoy had surmised from his study of the skeleton of *Ardipithecus* was that through natural selection *Ardipithecus* had transitioned from "knuckle walking" to bipedalism sometime during or after its separation from *Pan*. This physiological transition, he surmised, had freed up the hands of *Ardipithecus* for other tasks like perhaps carrying foraged nutrients (2009, p. 76e4 - 76e6). Borrowing his insight, changes were incorporated into the code. Those changes involved differentiating between the "hand-carry" capacities of the male and female hominid agents. Both sexes might carry similar amounts initially but, when a female was pregnant or nursing, her capacities could now be differentiated from the males. When these changes were introduced into the code and refinements made to the associated parameters, the simulated cohorts started surviving for longer and longer intervals. Adding these simple changes to the code not only made the simulation more plausible but it made the experiments more reliable. Moreover, these additions not only provided support for the motivating research hypothesis but they rested upon a pre-adaptive physiological

“enabler” as Chapais (2008) had suggested. The evolutionary changes seen in extinct hominid hands (described by Lovejoy, 2009) seemed to be among those pre-adaptive physiological “enablers” predicted by Chapais and had an effect on the simulations.

5.2.2.2 Theoretic foundation

Altruism describes those actions undertaken by self to increase the welfare of other even if those actions may be costly to self. Since the mid-1900's many authors including Fisher (1930), Hamilton (1964), Williams (1966), and Dawkins (1976) carefully considered altruism and amplified the basic concerns that Darwin (1871) first described. Even today the problem remains one of simultaneously comprehending the pervasiveness of social altruism and explaining/predicting its counter-intuitive organic operation. Some like Barczyk & Kredler (2014) and Nowak (2006) have attempted to apply mathematical formality to the phenomena in order to understand its processes. Others have approached the problem as a study in economic sociality (Gintis, Bowles, Boyd & Fehr, 2003; Nowak & Sigmund, 2005, and Simon, 1993). Alternatively, since altruistic “gifting” is a species-common behavior, the terminology put forward by MacLean (1975) in the mid-1970's allows one to simply say the behaviors are an example of isopraxis. It seems altruism may just be innate in *Homo*, may be a precursor to complex social organization, and is a pro-social behavior whose perfusion within the hominid cohort we cannot yet fully explain.

5.2.2.3 Experimental constructs

In this research, artificial genetics (Section 3.3.3.3.2) served as the media for the experimental constructs used to explore simple altruistic behavior. A gene for altruism

was assigned to each artificial hominid within their individual chromosomes. The value of that gene controlled the tendency of its bearer to engage in the "gifting" of excess food resources. The gene expressed differentially in males and females. If the bearer was the product of in situ mating (was "born" during the simulation) then the value of the gene was determined to be the genetic cross-over between, and the artificial mutation of, the chromosomes of the mated hominid parents. Altruistic "gifting" was a phenotypic, genetic trait and involved those same (excess) hand-carried food reserves that were just described as being especially costly to individual and cohort survival. Excess food was defined as any foods on-hand beyond that immediately needed by the "gifting" hominid.

For males, the expression of the gene involved the "gifting" of excess food and would occur when the benefactor was an adult male collocated with an adult female beneficiary. In the male case, this was an explicitly non-quid pro quo "gift" from the male to the female and was the altruistic act. Moreover, male "gifting" was non-kin based, i.e., the decision to "gift" did not consider uterine-kin association.

For females, the behavior involved the "gifting" of excess food and it occurred when the adult female benefactor was collocated with one of her offspring. This behavior explicitly took into account the birth order of the beneficiary and was a non-quid pro quo "gift" from the female to her offspring. Female "gifting" behavior was coded to be reactive and to execute without artificial cognition. It resembled an innate isopraxis behavior and supported inclusive fitness implicitly. Because female to offspring "gifting" took place in the experiments reactively (that is without proactive

cognition and or volition) there might be reason to argue the interaction was not even altruistic in its traditional sense (McCullough, 2013 and in correspondence 2015).

5.2.3 Claims

This work makes six claims based on its experiments. They are: 1) *altruistic foraging behaviors within a community of hominid-like agents may facilitate a comparatively greater rate of offspring production than might occur in a similar non-altruistic community if all other forms of circumscription are otherwise equivalent*, 2) *the effect of giving away food reserves, altruistically, exacts a survival cost on the giver*, 3) *over time, if altruism is an available gene-based trait, it will overtake a population and become dominant*, and by corollary 4) *longer-lived populations enjoying a trait for altruism may eventually find that it becomes phenotypic*. Finally, the data suggests that: 5) *a gene-based alliance tendency is at most a recessive phenotype*, and by contrast 6) *it may be that preferential relocation for affine purposes is actually a cognitive feature, or strategy*.

5.2.4 Observation and theory

Often, migrations were observed in the simulated populations. Migrations almost always began when a troop began to forage across-biomes. When migrations began, it appeared the hominids had begun to develop a more advanced synthetic “culture.” More specifically, they had formed a “culture” based on food preference taught through mother-infant transmission, passed between generations, impacting daily life at the survival level, and articulated across and between circumscriptive environmental biomes. As an emergent cultural artifact, migration not only facilitated troop movements between

watering holes in search of more fully available food stuffs but also gave a cohort a greater diversity of foraging resources from which to derive its group-level survival subsistence.

Finally, this work was based on a generative agent-based model of a complex social system. It appears that there may be three domains of practice wherein and whereupon generative agent-based models are most useful or most usefully built. Those domains of practice are: 1) models of historical systems that either existed or are believed to have existed, but because of their antiquity cannot be revisited for study by some other means, 2) models of "long-lived" systems that, for reasons of test subject controllability cannot be studied, and by extension 3) models of systems whose study involves unethical, illegal, unsafe, or unlikely environmental settings or exogenous stimuli.

5.2.5 Future work

New work derived from the current should always be incremental in order to allow for a return to iterative control and reference experiments. Although, a singular long-term goal might involve developing a purely synthetic population of artificial hominids existing entirely within a Virtual World, embodied as Virtual Agents, and complete with individual cognitive engines capable of emulating emotion and self-organizing autonomous learning, a more modest short-term goal would involve adding patrilocality to the current agents, enlarging the habitat to perhaps one hundred square kilometers, giving the males a drive for boundary patrols and territoriality (**Appendix A**), adding violent death within territorial conflict (Mitani & Watts, 2005), and freeing the population sex determination processes to more closely resemble those of living primates.

Beyond these few ideas for new work there are so many others that their enumeration here would require more time and patience than that possessed by either the reader or the author.

CHAPTER 6. SUMMARY/CONCLUSION

This chapter is an edited reprint of the same-named sections of the peer-reviewed paper presented as a public talk at ECAL in York, United Kingdom, July 20-24, 2015.

6.1 ECAL Paper

(Summary)

This dissertation has disclosed the results of a computer-based experiment. The experiment used a computer simulation technique called agent-based modeling 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 dealt 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, 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. After all, we are Primates and primates 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 was 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 too large before troop fission. That said, in an extension to this work we may yet add territorial patrols (Mitani & Rodman, 1979) to the behavioral ecology of the simulated hominid population (Wrangham, 1975; 1980). Of course, we will need a larger artificial habitat. But, for the moment, we can report that with only the addition of genetics-based altruism and social alliance, we have seen incremental progress towards our goal of emergent social complexity.

6.2 Coda

So ends this essay as it began: This dissertation discloses the results of an experiment that took place within a computer simulation. The experiment used a computer simulation technology called an agent-based model, or an ABM, to explore a constrained set of self-

organizing social properties and behaviors believed to exist at the least-organized end of every complex (human) social system.

APPENDIX A CONSTANT PARAMETER AUTHORITY

A.1 Overview

Within the May 5, 2015 version of the Clans code there were over 200 Constant parameters. The following citation authorities support the named/referenced functions:

A.1.1 Age at menarche in years

Notes: 8-9 *Pan*; 12-15 *Homo*

Ref: Lancaster, (1986).

A.1.2 Birth rate (in the wild)

Notes: 0.15 - 0.20 births per year for *Pan*

Ref: Thompson, et al., (2007)

A.1.3 Calorie counts of forageables

Notes: Figs	720 kcal. for 1 pound (16 loose fruit)
Leaves	625 kcal. for X vol., # lbs. loose leaves
Tuber (cassava root)	776 kcal. for 8 small loose roots
Monkey, Red Colobus	575 kcal. for 8 oz. meat, small monkey
Termite	700 kcal. for 125 g. loose live termites
Fish	150 kcal. for 4 oz. small fish

Ref: Book, Dell Purse. (1968).

Additional sources: diet tables, food packages, online search.

A.1.4 Calories in pound of fat

Notes: 3500, 1 lb. conversion approximation for 3,555

Ref: Book, Dell Purse. (1968).

A.1.5 Calorie requirements

Notes: $((2.2 * \text{lb.}) ^{0.75} * 100) = \text{kcal / day}$
Calculated
Male young juvenile;
AZA; 15 lb. -> 421 kcal
Male old age
AZA; 155 lb. -> 2431 kcal
Female young juvenile;
AZA; 12 lb. -> 356 kcal
Female old age
AZA; 120 lb. -> 2007 kcal
Female pregnant or lactating additional 125-150 kcal/kg;
Ref: AZA Ape TAG. (2010).
Gurven et al., (2005).
Milton, (1999).
Portman, (1970).
Prentice, (2005).

A.1.6 Comfort/Discomfort as drive (alliance/temperature)

Notes: positive affective correlation; approach and avoid
Ref: Berridge and Kringelbach, (2008).
Cabanac, (1971).
Craig, (2003)

A.1.7 Death as result of starvation

Notes: positive correlation; approx. at 65% mass loss
Ref: Burkhard, (2005).
Madea, (2005).

A.1.8 Death as result of thirst

Notes: positive correlation; approx. at 10% mass loss
Ref: Gleick, (1996).

A.1.9 Disease rate (*Pan* in the wild)

Notes: average of 48% per year in a 50 member community over 50 years for *Pan* in Kasekela community Gombe National Park, 38-60 members

Ref: Williams, et al., (2008).

A.1.10 Dominance hierarchies

Notes: dominance hierarchies play a critical role in primate social structures

Ref: Chapais, (2008).

Himelryjk, (2005; 2008).

Maestripieri, (2012).

A.1.11 Drive order

Notes: fear/panic, water, food, group, dispersal, comfort

Ref: Maslow, (1943).

A.1.12 Fish foraging by early hominids

Notes: paleo-record

Ref: Braun, et al., (2010).

A.1.13 Genetic basis for altruism

Notes: logical deduction

Ref: Alexander, (1974).

Hamilton, (1963).

Hamilton, (1964).

Lehmann et al., (2006).

A.1.14 Hunting behavior (carnivory)

Notes: evidence of

Ref: Watts, et al., (2002).

A.1.15 Incest rate (*Pan* in the wild)

Notes: “not a single case” referencing Murdock (1965, 119)
mentions “rare,” several authors, and introduces Westermarck
Ref: Chapais, (2008, p. 60).

A.1.16 Infanticide rate

Notes: Ngogo, Kibale National Park, observed 2 year old infant, 2.2 per year
Ref: Watts, Sherrow and Mitani, (2002).

A.1.17 Likelihood mating will produce offspring (*Pan*)

Notes: 16 conceptions between 1966 and 1975 (9 years); incomplete
Ref: Tutin, (1979).

A.1.18 Maximum number of offspring

Notes: 5 - 6 who survive weaning, 7 or fewer births per lifetime
Ref: Tutin, (1979, p. 31).

A.1.19 Migration patterns (*Pan* in the wild)

Notes: males do sometimes migrate, usually females disperse
Ref: Sugiyama, (1999).

A.1.20 Mutation rate (*Homo*)

Notes: $\sim 2.5 \times 10^{-8}$ mutations per nucleotide site or 175 mutations per diploid genome per generation
Ref: Nachman, et al., (2000, p 297).

A.1.21 Old age mortality

Notes: 35 – 45 years on average (in the wild)
Ref: Hill, et al., (2001)

A.1.22 Olfactory implications for sexual and social behavior

Notes: in *Homo* male/female olfactory cues can steer attraction

Ref: Thornhill, et al., (2003).

A.1.23 Ovulation implications for sexual and social behavior

Notes: fertility with olfactory and visual stimuli evoke reproductive behavior

Ref: Gangestad, et al., (2005).

A.1.24 Patrols

Notes: evidence for patrols and related facilitator of violent conflict

Ref: Mitani, et al., (1979).

Mitani, et al., (2005).

A.1.25 Philopatry/dispersal

Notes: *Pan* – (male patrilocality female dispersal)

Ref: Parish, A., et al., (2000).

Praschnik-Buchman, (2000).

Sterck, et al., (1997).

A.1.26 Predation rate

Notes: ranges Williams “none seen” to Boesch 0.30 to 0.60 / year / cohort

Ref: Williams, et al., (2008).

Boesch, (1991, p. 230).

A.1.27 Preferred social network size

Notes: cliques 5; sympathy groups 12; bands 35; cognitive groups 150

Ref: Dunbar, (1998).

Hill, et al., (2003, p. 63).

Bickart, et al., (2011).

A.1.28 Suppression of fertility during nursing

Notes: A. (*Pan*) "...during the later stages of this period not all mothers were necessarily producing milk, we refer to these females as 'lactating' for brevity and because most of our analyses concern the early period of amenorrhea."

B. (*Pan*) "A long period of postpartum amenorrhea is typically followed by several months of nonconceptive cycling, leading to an average birth interval of 5–6 years ..."

C. (*Homo*) humans postpartum have lower "...levels of the reproductive hormones estradiol and progesterone, leading to lower likelihoods of ovulation, fertilization, or implantation."

Ref: A. Thompson, et al., (2012, p. 3).

B/C. Thompson, (2013, p. 224).

Thomson, et al., (1975).

A.1.29 Temperature requirements (*Pan*)

Notes: 60° – 85° F

Ref: AZA Ape TAG. (2010).

A.1.30 Termite foraging by early hominids

Notes: evidence exists of termite foraging

Ref: Backwell, et al., (2001).

Lonsdorf, (2005).

A.1.31 Troop / community size (*Pan* in the wild)

Notes: "More than 50 individuals ... regional population..." (per Sugiyama)

Ngogo, Kibale National Park, 150 members, 35 km² (per Watts)

Kasekela, Gombe National Park, 38-60 members (per Williams)

Ref: Sugiyama, (1968, p. 225).

Watts, et al., (2002).

Williams, et al., (2008).

A.1.32 Vegetation regrowth productivity

Notes: linear regrowth with seasonality, approximation

Ref: Turchin, et al., (2001).

A.1.33 Water availability, water basins

Notes: "... seen digging holes ... to reach the underground water..."

Ref: Boesch, (2002, p. 2).

A.1.34 Water requirements (*Homo*)

Notes: Range is approx. 2 – 5 liters (0.5 – 1.25 gallons / day)

Male young juvenile;

0.37 gallon.

Male old age

0.75 gallon.

Female young juvenile;

0.35 gallon.

Female old age

0.65 gallon.

Female pregnant or lactating

0.85 gallon.

Ref: Gleick, (1996).

A.1.35 Weaning age

Notes: range from 4 years 4 months to 7 years 6 months.

Ref: Tutin, (1979, p. 31).

A.1.36 Weight of infant (*Pan*)

Notes: 2kg (4.4 lb.) average; infants 2-6 kg

Ref: Portman, (1970).

Davenport, et al., (1961).

APPENDIX B SCHEMA: MODELREPORTS

B.1 Overview

What follows are the formatting schema for the ModelReports output files.

B.1.1 BoundReaperSchema.txt

0	RNG_SEED
1	epoch
2	BirthDate
3	DeathDate
4	Chromosome gene 0
5	Chromosome gene 1
6	Chromosome gene 2
7	Chromosome gene 3
8	Chromosome gene 4
9	Chromosome gene 5
10	Chromosome gene 6
11	Chromosome gene 7
12	Chromosome gene 8
13	Chromosome gene 9
14	Chromosome gene 10
15	AgentID
16	MotherID
17	FatherID
18	BirthLoc X
19	BirthLoc Y
20	DeathLoc X
21	DeathLoc Y
22	Age
23	Sex
24	PregnancyStatus
25	CurrentWeight
26	CaloricRequirement
27	WaterRequirement
28	Alpha
29	PreferredPrey

30 CauseOfDeath

B.1.2 DailyReportSchema.txt

0	Sequential Date
1	Year
2	Date in current year
3	Percent productivity of terrain
4	Agents alive in Sim
5	Average size of cohort
6	Agents now dead
7	Total count of births
8	Average birth rate
9	Percent infant mortality
10	Total simulated so far

B.1.3 DailyStatisticsSchema.txt

0	Sequential Date
1	Year
2	Date in current year
3	Percent productivity of terrain
4	Agents alive in Sim
5	Average size of cohort
6	Agents now dead
7	Total count of births
8	Average birth rate
9	Percent infant mortality
10	Total simulated so far

B.1.4 DeathAnnalsSchema.txt

0	End of Year Date
1	Male deaths recorded in current year
2	Female deaths recorded in current year

B.1.5 DeathHistorySchema.txt

0	Sequential Date
1	Sex (m=1, f=0)

- 2 Age
- 3 Died by: infant mortality (boolean)
- 4 Died by: catastrophe (boolean)
- 5 Died by: starvation (boolean)
- 6 Died by: dehydration (boolean)
- 7 Died by: age (boolean)
- 8 Died by: orphaned (boolean)
- 9 Died by: predation (boolean)
- 10 Died by: drowning (boolean)

B.1.6 SocialNetworksSchema.txt

- 0 Self
- 1 Mother
- 2 Father

B.1.7 YearlyStatsSchema.txt

- 0 End of Year Date
- 1 Agents alive in Sim
- 2 Deaths recorded in current year
- 3 Total deaths recorded so far
- 4 Births recorded in current year
- 5 Total births recorded so far
- 6 Currently, annual birth rate
- 7 Currently, infant mortality rate

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BIOGRAPHY

Ovi Chris Rouly was born and raised in the southern and southwestern United States, respectively. His working career has spanned the fields of professional opera, hardware and software research, development, and engineering, science, and academia. He has an Associates of Applied Science degree in Electronic Technology, separate Bachelor of Science degrees in Psychology and Computer Science, and a Master of Science in Electrical Engineering.

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Mr. Rouly is married and has two children. He currently resides in McLean, Virginia.