IS A BIRD IN HAND REALLY WORTH TWO IN THE BUSH?

MODELS OF TURKEY DOMESTICATION

ON THE COLORADO PLATEAU

By

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MAY 2011
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My mom listened patiently and gave me encouragement when I was homesick or stressed; my dad reveled in countless geeky calls about Java, R, SQL, iPhones and all things tech. I am sustained by the love of my family. I may be at the opposite corner of the U.S., but my heart is with y’all.

Special thanks to my advisor, mentor, and friend Tim Kohler, who has shown unwavering support and dedication to me and all of his graduate students.
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Abstract

by Ronald Kyle Bocinsky, M.A.
Washington State University
May 2011

Chair: Timothy A. Kohler

In this thesis, I explore the relationships between turkeys and humans in the Pueblo Southwest as a means of understanding how human agency directs the process of domestication. The models presented here define potential decisions made by human agents during the process of domestication, and describe how we might expect these decisions to pattern the archaeological record of domestication. I begin by describing the genetic and demographic implications of turkey domestication for turkey flocks, noting that variations in the treatment of turkey—feeding, breeding, and use—should generate distinguishable archaeogenetic signatures. In the second part, I imagine the adoption of turkey domestication as a resilience trap—the ‘Avicultural Trap’—making the Pueblo subsistence system increasingly rigid and narrow while simultaneously allowing explosive population growth. I describe how a feedback loop between turkey, maize yields, and human population growth amplified to the point where the Pueblo subsistence system was unable to respond to climate-induced reduction in agricultural yield. In the final section, I focus on ‘domestication’ as food production and incorporate domestication into the patch-choice model from classic optimal foraging theory. I implement that model in the
Village simulation, and generate further expectations of the spread of the adoption of
domestication. These include the prediction that domestication likely spread outwards from the
most agriculturally productive areas of the landscape, and may have been less enthusiastically
embraced in areas with other available high-quality protein resources.
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Dedication

For my grandfather, Lt Col Samuel Field Smith, III,

the wisest turkey I know.
CHAPTER ONE

INTRODUCTION

The Duckfoot Site (5MT3868; Lightfoot 1994; Lightfoot et al. 1993; Walker 1993)—situated on the periphery of the Montezuma Valley and the Monument-McElmo drainage, in the Northern San Juan (NSJ) region of Southwest Colorado (Figure 1.1)—is a small, 19-room Pueblo I habitation, occupied for some 30 years during the late ninth century A.D. The site organization follows the Northern San Juan pattern (Lipe 2006:266)—a site form ubiquitous throughout the region for well over 600 years—with an above-ground pueblo, four pithouses, and a large midden. Though short lived, Duckfoot saw active growth during much of its occupation, with 3-4 construction episodes over a 30-year period. People there subsisted heavily on maize (Adams 1993:214), storing it in several of the rooms of their above ground pueblo (including in specialized storage rooms; Adams 1993:211-214; Lightfoot 1994:99), and also were successful hunters (Walker 1993:240). Faunal analysis from an excavation of the site has shown a meat diet that relied on artiodactyls and especially lagomorphs for food, skins, and tool manufacture (Walker 1993:252; Table 1.1). People living at the site likely had little trouble meeting their subsistence needs, as evidenced by maize paleoproductivity reconstructions for the region (Kohler 2011c) and dental analyses of individuals recovered from the site (demonstrating dental caries indicative of a high maize diet and little other evidence of malnutrition; Hoffman 1993:291; Lightfoot 1993:299), as well as close access to wild game in the pinyon-juniper woodland that dominates the drainage to the southwest (Lightfoot et al. 1993:6). Only a few turkey remains, representing about 0.5 percent of the faunal assemblage, were found at the site (Badenhorst 2006:Appendix C). The site was abandoned at around A.D. 880, as evidenced by the
cessation of new construction and by the ritual burning of several of the structures (Lightfoot 1993:298).

Figure 1.1. The Central Mesa Verde region of the northern U.S. Southwest. The Village Ecodynamics Project study area is the area of focus for Chapter 5. Map designed by Stefani Crabtree.

A few canyons to the west, and some 300 years later, people at the Green Lizard Site (5MT3901; Driver et al. 1999; Huber 1993; Huber and Lipe 1992) were living in a quite similar setting. The site lies on the west edge of Sand Canyon, just down-canyon from the large community center of Sand Canyon Pueblo, and was probably directly associated with that much larger community, though initiation of occupation at Green Lizard, around A.D. 1175, predates the peak occupation of Sand Canyon by some 75 years (Huber 1993:177). Partial excavation and testing revealed at least two pitstructures where people lived and cooked, and associated above-ground room blocks for living and storage (Munro 1994:15). In many ways, the people of Green
Lizard likely made a living much like those at Duckfoot—farming in the Montezuma Valley and on nearby mesa tops and hunting in the Monument-McElmo drainage—but with one significant difference: people at Green Lizard were heavily dependent on turkey as a meat source (Table 1.1; Badenhorst 2008:Appendix C). Turkey bones represent 55 percent of the faunal assemblage, with the remainder apparently derived from lagomorphs.

**Table 1.1.** Faunal assemblages at the Duckfoot site (5MV3868) and the Green Lizard site (5MV3901). Lag.: *Lagomorpha*. Art.: *Artiodactyla*. Mel.: *Meleagris gallopavo* + other large birds (Badenhorst 2008:Appendix C).

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<th>Estimated Occupation</th>
<th>NISP</th>
<th>Proportion NISP</th>
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<tr>
<td>Duckfoot</td>
<td>850 - 880</td>
<td>1802</td>
<td>326</td>
</tr>
<tr>
<td>Green Lizard</td>
<td>1175 - 1300</td>
<td>596</td>
<td>40</td>
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What could be the cause for this disparity? The environment around these two sites is broadly similar as they are both located in piñon-juniper woodland at similar elevations (~ 7000 feet). Yet this pattern of dependence on hunted resources for most of the region’s occupation, then a rapid and substantial shift to turkey consumption, occurs throughout the NSJ (Badenhorst 2008; Badenhorst and Driver 2009).

One possible cause is population pressure and wild protein resource depletion. By the best estimates, the population in the region in A.D. 1175 was about twice that of the late 800s (Varien et al. 2007:283). Maybe turkey eating was a new cultural tradition, imported as part of a migration of people from the south into the NSJ (Varien et al. 2007:289). Or perhaps there was a shift in agricultural technology, substantially increasing yield and allowing the new-found surplus to be heavily invested in the birds, either through active feeding or passively allowing them to graze in fields. How were these turkey-use strategies adopted by people on the landscape? Was it a ‘catching’ technology, spreading rapidly through the region? Or were there
pockets of hunting refugia, where a transition to turkey keeping was not necessary? Finally, a larger question is whether and how turkey use impacted peoples’ other strategies for living on the landscape, and what role it may have played in their decisions to abandon the landscape at the end of the thirteenth century?

To begin to answer some of these questions, I develop several models of the adoption and impact of turkey domestication. I use the term *model* in its broadest sense: “a fundamental form of human reasoning ... in the analogical sense of a structure intended as isomorphic to some aspect of a physical system” (Nersessian 1999:14-15). “The model is the mode of representation between the phenomena and expression in a language (including mathematics) ... [Models are] the actual forms of reasoning through which concept formation and change take place” (Nersessian 1999:15). Analogical modeling can take many forms, from narrative accounts of historical (and thus causal) processes to mathematical formulations. The modeler-scientist—and Nersessian (1999) stresses that all scientific thought consists initially of cognitive modeling—calls on basic principles and constraints as well as prior knowledge, and uses these as tacit assumptions concerning the behavior of some system. Models are mentally constructed and articulated, their expectations generated and tested, and their assumptions adjusted based on those tests.

Here, I use prior knowledge of the culture-history of the NSJ region and prior research on animal domestication and turkey use to generate expectations for the archaeological record in the region. After introducing some aspects of domestication theory and reviewing pertinent aspects of the culture history of the Pueblo Southwest in this chapter, I describe specific genetic and demographic expectations for various turkey use practices, derived from the study of other
human faunal domesticates (Chapter 2). I then present a historical narrative of the adoption and
effect of widespread investment of maize in turkey (the ‘Avicultural Trap’ model; Chapter 3),
both incorporating current archaeological knowledge and expectations from the genetic model
presented in Chapter 2. This narrative is but one possible scenario for the impact of turkey use in
the Southwest, and serves as a departure point for further research, both in this thesis and
elsewhere. I then present a model of turkey use within an optimal foraging framework (Chapter
4), and suggest that the mere knowledge of the strategy on the landscape—and not necessarily its
direct use—will have an effect on foraging strategy and thus the archaeofaunal record. I then
implement this model within the Village Ecodynamics Project simulation (Kohler 2011a) and
examine the effects of that modification on the demographic and spatial structure of simulated
populations on the NSJ (Chapter 5). I compare the simulation output to archaeological patterns
as a means of model selection (Kohler and van der Leeuw 2007), and I find that simulation runs
that include my optimal foraging model of turkey use better ‘fit’ the archaeological record than
do runs without turkey use. Using this information, I generate a new set of spatial and temporal
predictions for the adoption of turkey use across the region.

Domestication As Process

Although animal and plant domestication have been studied intensively for centuries, there
remains widespread disagreement about how it ought to be defined, and thus how it may be
studied. Throughout our species’ existence, humans have been enjoying the benefits of
mutualistic relationships with plants and animals. While a mutualism in and of itself does not
domestication make, researchers taking an evolutionary perspective have suggested that such
mutualisms are the seeds of domestication (Rindos 1980). However, studies of domestication
easily betray these mutualistic origins, and often have been overshadowed by anthropocentric assumptions. By exploring domestication solely as the result of human agency, or as ‘events’ (Beck et al. 2007), researchers have often denied any role to the animals themselves. Humans are said to have ‘tamed nature’ (this notion is still prevalent in some literature, e.g., Kareiva et al. 2007) or, alternatively, spontaneously innovated the technologies required to domesticate without going through a process of intensification (e.g., Blumler 1992).

Since the work of Charles Darwin, however, other researchers have viewed the domestication relationship from within an evolutionary framework. In *The Variation of Animals and Plants Under Domestication*, his follow-up to *The Origin of Species*, Darwin (1868) wrote that the human innovation behind domestication was the ability to impose ‘artificial’ selective forces upon domesticated animals, thus initiating morphological and behavioral changes within the domesticate. Darwin’s views have seen a renaissance since the 1950s, especially among ecologists and archaeologists who have recognized the potential of tracing the evolutionary impacts of domestication. Domestication is now viewed as a coevolutionary process during which two species entering into a mutualism will undergo evolutionary changes that feed back to enhance aspects of that mutualism (Rindos 1980). Coevolution occurs when interaction between two species positively affects their chances for survival. Domestication is the result of improvements in the survivability of both species (Rindos 1980:752; Zeder et al. 2006). Thus, researchers interested in the origins of domestication now take a far more comprehensive approach to their work. Prevailing theory suggests that observable adaptations will occur in both domesticates and their human counterparts (e.g., McCracken 1971).

It is perhaps the immense variety of examples of human/animal interactions that invokes the
need for a broad coevolutionary model of domestication. A general model for domestication must not exclude contextualizing factors that allow or prohibit the evolution of domestication relationships between species (Flannery 1986). Consideration of these factors will include assessing the environment where a mutualism develops, the various pre-domestication characteristics of each species in the mutualism, and the adaptive responses of each species to the domestication process. The call to consider each of these, in turn, is not new. For instance, David Rindos, in his controversial, but influential review of evolutionary models of domestication and agriculture, viewed domestication as the realization of “evolutionary potentials which may develop whenever an animal consistently feeds upon any set of food plants” (1980:751), or any species of food animal, for that matter. Rindos clearly takes the stand that domestication ought to be viewed as a process, during which a mutualism between humans and an animal species is reinforced via coevolution.

As has been noted elsewhere (Redding 1988:60; Watson 1995), Rindos fails to address the ‘why’ of domestication, focusing solely on the ‘how.’ Rindos assumes the mutualism, and describes how that mutualism might evolve into domestication. Stated differently, this critique suggests that viewing domestication as a process denies the impact of human agency. Critical human decisions might be made before, during, and after the domestication process that direct the process and pattern archaeological evidence reflecting it. In this thesis, I explore a historically and spatially situated example of a mutualism—that between turkey and humans in the Pueblo Southwest—as a means of addressing the agency-driven ‘why’ of domestication. I define potential decisions made by human agents during the process of domestication, and describe how we might expect these decisions to pattern the archaeological record of
domestication. I further explore the impact of human agency on the domestication process in the next section.

**Domestication As Agency**

While domestication may be defined as the coevolutionary process described above, anthropologists are often interested in understanding human decision-making as it relates to domestication (Berry 1969; Bökönyi 1969; Flannery 1986; Wills 1988; Zeder et al. 2006). For some, it is this decision-making that differentiates domestication from other coevolutionary processes. In their recent volume on tracking domestication genetically and archaeologically, Zeder and colleagues (2006) stress that human decisions in the propagation and care of their animal counterparts are the forces directing the process of domestication. A focus on human agency—the human capacity to make willful, thoughtful decisions that impact their social and physical environments (Dornan 2002:309-314)—permeates many definitions of domestication. For Zeder and colleagues (2006), human agency in domestication is exercised as a security enhancement strategy. By keeping an animal local, and investing energy and resources in their upkeep, humans are able to bring stability to their protein resource base.

Wills (1988:32) captured this same sentiment two decades earlier, defining domestication as the “intentional decision to enhance resource security” via the adoption of a cultigen or domesticate. For Wills, cultivation is the agency-driven action; domestication is the process of isolating a cultigen from wild competitors and rendering it unable to reproduce efficiently without human intervention. For Wills, the process of domestication depends less on human agency than does the initial adoption of a domesticate or cultigen. A cultigen does not become a domesticate unless it is isolated and unable to reproduce in the wild.
Bökönyi (1969:219-220) focuses even more on human agency. Domestication is “nothing other than mans’ special interference in the life of certain animal species.” While “capturing animals, keeping them in corrals, and killing them at appropriate times does not amount to domestication,” the additional action of breeding them in captivity shifts the activity to domestication. Bökönyi adopts two levels of domestication, ‘animal keeping’ and ‘animal breeding.’ Animal keeping involves propagation in captivity without direct human intervention other than keeping the domesticate separate from wild populations. Animal breeding is selectively breeding the domesticate for certain traits and the control of both quality and quantity of feeding (Bökönyi 1969:220). The view that selective breeding for certain traits ultimately represents the strongest form of human agency in domestication has existed since Mendel (1996 [1865]) and Darwin (1868) and is at the core of modern genetic studies of domestication (Zeder et al., editors, 2006).

Perhaps the most general definition of domestication proffered in the archaeological literature comes from Flannery (1986:4): “[The] Origins of agriculture involved both human intentionality and a set of ecological and evolutionary principles.” Though he is discussing agriculture specifically, the same factors come into play when considering animal domestication. At stake is not only the willful intent to behave towards an animal in a given way, but the ecological and evolutionary reality enabling the existence of that decision in the first place. For the present study this includes the presence of turkey (captive or wild) on the landscape, and the knowledge required to behave towards them in a given way. If taken, certain decisions will necessarily preclude other options: for instance, multiple generations of controlled and selective breeding might render a domesticate unable to reproduce in the wild, after which a reversion to
uncontrolled breeding becomes infeasible (at least if one wishes to continue to utilize the domestic stock). Even outside the evolutionary or time-dependent interactions between decisions, certain behaviors may be mutually exclusive, such as selecting for a given phenotype while declining to control breeding. While these two decisions could be made simultaneously, needless to say, they would not be very effective.

The models presented here are designed to generate archaeological expectations of the various ways ancestral Pueblo peoples may have been purposefully interacting with turkey. To that end, I do not make the a priori assumption that turkey were domesticated. The first model (Chapter 2) generates demographic and archaeogenetic expectations of turkey populations for a variety of turkey-use practices, only a small subset of which would fit the strictest definitions of domestication given above—i.e., the behaviors reviewed do not all require turkeys to have been “born, raised, and killed at human sites” (Munro 1994:142). The second model (Chapter 3), a historical narrative describing the potential impacts of a widespread decision to stabilize protein resources by feeding maize to turkeys, assumes only that people across the landscape would have had the knowledge and will to use turkey in this way. The final model (Chapter 5), an agent-based simulation implementing an optimal foraging model described in Chapter 4, relaxes the pretext of universal adoption, and explores adoption of turkey investment as being structured by ecological factors such as the availability of hunttable wild game and maize surpluses. Thus it situates the general optimal foraging model in a particular cultural, temporal, and spatial context.

Can we ‘see’ domestication archaeologically? If we take domestication to be a process, as I do, then I argue that the answer is ‘no’, at least not directly. Archaeological data are witnessed by archaeologists not as a continuous stream but as discontinuous points. Archaeologists can only
suggest models of the processes such as domestication, and then assess how well archaeological
data fit into expected patterns derived from those models. Model-based research has attracted
archaeologists at least since Taylor’s ‘Conjunctive Approach’ (1948) and the Binfords’ (1968)
‘New Archaeology.’ Even modern ‘post’-processual archaeology continues this tradition, simply
broadening the types of patterns to be fitted and models to be employed (for example,
contributions in Hodder 2006, editor). The process of model specification, pattern fitting, and
model revision describes all research acting from within the modern, Western scientific paradigm
(Grimm et al. 2005:991). This type of research is at its strongest and most persuasive when
models and their patterned expectations are transparently articulated and documented. The
present study aspires to meet this high calling.

In Chapter 2, I discuss how the impacts of domestication shape our interpretation of turkey
use in the Southwest—with particular attention to archaeologically knowable data—but first, we
need a bit more context. In the following section, I outline the cultural and geographic
environments in which turkey use occurred in the Southwest and I review the current state of
knowledge about turkey domestication.

A Brief Culture History of the Northern San Juan in the U.S. Southwest

The Northern San Juan Basin (henceforth “NSJ”, and sometimes referred to as the Mesa
Verde region; Lipe 2006:312) is a hydrologic area in the U.S. Southwest extending from the San
Juan River in northwestern New Mexico to the confluence of the San Juan and Colorado rivers in
south-central Utah, roughly encompassing the northeastern half of the Four Corners region of the
U.S. The NSJ is bordered to the north by the San Juan and La Plata mountains; the Colorado
River forms its western boundary; the La Plata river, which forms the headwaters of the San Juan
river, bounds the NSJ to the east (Lipe 2006:262; Varien 2010:3). Major landforms within the
NSJ include the Mesa Verde cuesta, Ute Mountain, and the Great Sage Plain. This region is
dominated by woodlands interspersed with arid grasslands, with mesas and cuestas cut by deep
canyons (Adams and Peterson 1999; Badenhorst and Driver 2009:Table 1).

Aboriginal peoples have likely inhabited the U.S. Southwest for more than 10,000 years
(Huckell 1996:320). Earliest known Archaic occupation in the region dates to ca. 9500 B.C. (the
Ventana Complex in southern Arizona; Huckell 1996:327), and later Early Archaic presence has
been well-described for several subregions (Irwin-Williams 1973; MacNeish 1993 [editor];
Sayles and Antevs 1941; Huckell 1996 reviews these studies and others). Less is known about
the Paleoindian (pre-7500 B.C.) and Archaic periods (7500 – 200 B.C.) in the NSJ (Lipe and
Pitblado 1999:95, 105-106, 120; but see Matson 1991 and Huckell 1996:333), due to the
ephemeral nature of Archaic sites and a low site density. What we do know, however, is that
there seems to have been gradual transition from mobile hunting and gathering to a more
permanent annual or seasonal residential system marked by early experimentation with maize
cultivation (Lipe and Pitblado 1999:130).

Ancestral forms of maize began to be cultivated in the western region of Mexico between
7000 and 4000 B.C. (Piperno et al. 2009:5023), and gradually spread northward with human
migration and cultural transmission. The earliest evidence of maize cultivation in the U.S.
Southwest has been dated to approximately 2000 B.C. (Merrill et al. 2009), though widespread
cultivation is not seen until 1000 B.C. (Huckell 1996:344; Lipe 1999:134), and sedentary
agriculture does not become firmly established in the NSJ until after 200 B.C. (Lipe 1999:135).
Beginning with the Late Basketmaker II period (A.D. 1 – A.D. 500), sedentism became
widespread in the western and southern areas of the NSJ, though not in the area just north of Mesa Verde proper (the Central Mesa Verde [CMV] region; Wilshusen 1999:167; Wright 2006). Wright (2006:121) has shown that the CMV region was afflicted with a generally cold climate until around A.D. 600, and was possibly not suited for widespread maize agriculture until this time. By the end of the Basketmaker III period (A.D. 500 – 700), however, maize agriculturalists had colonized the area (Wilshusen 1999:167). By the late sixth century, people throughout the NSJ began to adopt year round sedentism, as indicated by a transition from primarily shallow, circular pit structures to more permanent square or rectangular roofed pithouses with a standard suite of features, including antechambers (Wilshusen 1999:174). People also cultivated beans and squash during this time (Wilshusen 1999:185).

The Pueblo I period (A.D. 700 – 900) marks the onset of substantial population growth throughout the Southwest and in the NSJ (potentially due to immigration; Varien et al. 2007:289). Kohler and colleagues (2008a) describe this population expansion as the ‘Neolithic Demographic Transition’, though they identify some striking differences with its European counterpart, in particular a 2,500-year lag between the earliest cultivation of maize in the Southwest and the onset of rapid population growth. Some researchers suggest that the costs associated with maize agriculture, such as disease and sedentism, may have outweighed its benefits until populations reached a certain threshold, or until potential maize yields reached a high-enough level. Maize agriculturalists in the NSJ practiced ‘dry-farming,’ or rain-watered farming, both on mesa tops and on valley floors (Wilshusen 1999a:230; Lipe and Varien 1999:257). Families lived in circular, subterranean dwellings (generally called ‘kivas’ at sites in the Pueblo II period and later) much like during the Basketmaker periods, but also built above-
ground roomblocks as living and storage facilities (Wilshusen 1999a:200). This architectural site layout—a roomblock with associated kiva and midden commonly referred to as a ‘Unit Pueblo’—was maintained as the traditional residential unit throughout the Pueblo periods (Lipe 2006).

During the Pueblo II period (A.D. 900 – 1100), substantial changes took place throughout the greater Southwest. To the south of the NSJ, the Chaco culture gained ascendancy and was arguably the center of a vast, ritually-powered sphere of influence (Plog 2008:96). Meanwhile, people living in the VEP study area, just north of the Mesa Verde landform, experienced drought and emigrated in significant numbers around A.D. 900 (Varien et al. 2007:289). This emigration was likely amplified by a low-frequency cooling trend in the region, which brought shorter growing seasons and decreased maize yields (Wright 2006:122). With renewed immigration in the late-A.D. 1000s local populations greatly exceeded the Pueblo I peak by the end of the Pueblo II period (Varien et al. 2007:289).

Population growth in the eastern half of the NSJ continued into the Pueblo III period (A.D. 1100 – 1300; Varien et al. 2007:285), and was possibly fueled by the collapse of the Chaco culture and subsequent immigration to the NSJ of people from the south by A.D. 1130 (Lipe 2006; Varien et al. 1997:289). Population density also rose in eastern half of the NSJ, and Pueblo peoples initially continued to aggregate near the most agriculturally productive areas (Lipe 1995:152-153; Varien et al. 2007) and then near the heads of canyons (Glowacki and Ortman 2011). Much larger villages began to form (Lipe 1995:153); many communities were built in defensive locations, and monumental-scale masonry architecture—including towers and defensive walls—are typical of this period (Lipe 1995:154). A large drought and cooling trend,
apparently on the scale of the one 300 years earlier, began to impact the region in the early 1200s (Wright 2006:122; Varien et al. 2007). This resulted in an initial emigration from the region, and further substantial aggregation of remaining populations around water sources (usually springs and seeps at the heads of canyons; Glowacki and Ortman 2011; Varien et al. 2007). There is evidence of violence and warfare (Kuckelman et al. 2000), and numerous sites with evidence of cannibalism (Kuckelman et al. 2002; Turner and Turner 1999). Construction seems to have halted by A.D. 1280, and the entire NSJ was abandoned by A.D. 1300 (Varien 2010:15). The causes of this abandonment remain one of the classic problems of archaeology in the U.S. Southwest (see contributions in Kohler et al., editors, 2010).

**What We Know About Turkey Use**

Turkey use, and eventual domestication, played a central role in prehistoric economies of the American Southwest and Mexico (Munro 1994:143-149). Evidence for turkey keeping (specifically, *Meleagris gallopavo gallopavo*; Crawford 1992:309) appears as early as 200 B.C. in what today is central Mexico, and by A.D. 200 in the U.S. Southwest early Basketmaker peoples were constructing turkey pens and almost certainly using turkey in ritual contexts (Muir and Driver 2002:174). However, turkey does not appear to have commonly been consumed as a food source until the late Pueblo II period, as identified by butchery marks on turkey bones in archaeological assemblages (ca. A.D. 1050; Badenhorst and Driver 2009; Munro 1994:106-115). Muir and Driver (2002), in their multi-scalar survey of faunal assemblages across the Southwest, noted that some turkeys were interred whole or beheaded during earlier periods and that these remains show none of the signals of butchery or food preparation.

Archaeologists have noted that turkey remains during the late-Basketmaker and early-Pueblo
times were scarce relative to other species (Badenhorst and Driver 2009:1838), with a clear shift
during the Pueblo II period when turkey remains became far more prevalent in midden contexts
and show clear evidence of butchery (Muir and Driver 2002:174). As the Pueblo III period
began, turkey use further intensified relative to lagomorphs, and became the dominant protein
source at many sites in the NSJ (Badenhorst 2008:Appendix C). Muir and Driver (2002)
postulate that increased reliance on turkey as a food item, as opposed to a ritual object, coincided
with a severe depletion of more traditional protein resources on the northern Southwestern
landscape. Recent computer simulation of regional Pueblo ecologies have supported this
suggestion by demonstrating rapid artiodactyl depletion coincident with simulated human
population growth, and some researchers posit that turkey use as a protein source enabled
populations in the northern Southwest to continue expanding throughout the twelfth and
thirteenth centuries (Kohler et al. 2008b:150).

Analyses of genetic diversity in modern wild turkey and in archaeological remains have
forced reassessment of some long-held assumptions about turkey use. Since the earliest evidence
for turkey domestication has been from central Mexico, archaeologists assumed that turkey
domestication as a ‘technology’ was imported into the Southwest from the south, along with
already domesticated birds (Rea 1980). It followed that modern wild populations in the
Southwest would be genetically derived from these Central Mexican imports. Other researchers
argued for novel domestication of indigenous wild turkey in the Southwest, presumably from *M.
g. merriami*, the wild sub-species dominant in the region today (Schorger 1966). Since those
arguments were made, a critical phylogeographic study by Mock and colleagues (2002) mapped
the distributions of turkey matrilines across the current wild population of the United States.
They found that the Merriam’s turkey was not a likely descendent of either the Eastern (M. g. *silvestris*) or Gould’s (M. g. *mexicana*) populations, the most likely candidates for the importation hypothesis. Rather, Mock and colleagues (2002:653) found the Merriam’s subspecies more closely related to the Rio Grande subspecies (M. g. *intermedia*).

Recent mtDNA study of archaeological turkey remains and fecal samples from across the Southwest (Speller et al. 2010) found that turkey remains recovered from archaeological sites in the Southwest were also not descended from the South Mexican varietal (M. g. *gallopavo*). More surprisingly, most archaeological samples from Basketmaker III - Pueblo III contexts exhibited the least-common matriline found among Merriam’s turkeys today, a type that is closely related to both the Rio Grande turkey (M. g. *intermedia*) and the Eastern wild turkey (M. g. *silvestris*). Speller and colleagues (2010) name this the aHap1 matriline. The studies by Mock and colleagues (2002) and Speller and colleagues (2010) call into question not only the prevailing models for domestication in the Southwest, but generally redefine the expected distribution of wild turkey genotypes that existed prior to turkey use and domestication in the region. Widely distributed and available wild breeds seem to have been ubiquitous across the region, demanding entirely different models than the previous ‘origin-and-spread’ scenario. Correct interpretation of the results from these studies requires models allowing for variation in turkey-use practices across the landscape and accounting for interactions between captive and wild birds.

In Chapter 2, I focus on the genetic implications of domestication in order to develop a set of specific genetic expectations for different turkey domestication scenarios in the Southwest. In Chapter 3, I apply these expectations to a historic narrative of turkey domestication derived from data about turkey use in the region and interpreted as a ‘resilience trap’.
CHAPTER TWO
GENETIC IMPACTS OF TURKEY DOMESTICATION

Biological impacts of domestication—on both humans and domesticates—are well documented in the literature, especially for Old World domesticates such as sheep, pigs, and cattle (Albarella et al. 2006; Bradley 2006; Bruford and Townsend 2006; Larson et al. 2007; McCracken 1971; Tchernov and Horwitz 1991; Zeder et al. 2006). However, researchers have often assessed these impacts differently for each species, focusing either on the morphogenetic responses of domesticates and humans, or on broader human behavioral adaptations to encourage the domestication relationship. Morphological traits generally common in Old World domesticates, such as smaller brain size, smaller bodies, and a general decrease in sexual dimorphism, have been thoroughly reviewed by Zeder (2006).\(^1\)

Zeder (2006) reviews various morphogenetic impacts of domestication including earlier onset of sexual maturity, heightened sexual receptivity, and smaller bodies. Zeder (2006) notes that a decrease in body size is one of the most widely noted morphogenetic impacts of domestication. Evidence of this has been produced for many primary domestic species including cattle, pigs, sheep, goats (Tchernov and Horwitz 1991), and turkey (Crawford 1992:311). However, size patterns among domesticates often correlate with other physical and environmental characteristics, such as degree of tameness. Interpretation via size analysis, and other morphogenetic analyses, may be further complicated by differences in particular domestication practices. For instance, domestication of food animals is often characterized by a

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\(^1\) These types of morphological changes can be generally considered paedomorphic—a reversion to a more juvenile form. The process of selecting for paedomorphic characteristics has received greater attention in studies of the behavior of domestic dogs, where humans have artificially selected playfulness, trainability, and other generally youthful traits (Driscoll et al. 2009).
female-biased sex ratio (Albarella et al. 2006:209). Any amount of sexual dimorphism within the domesticate will thus force mean size within the population to appear nearer to that of the female sex. If demographic factors are not accounted for, results of size analysis may be skewed.

Sex ratios within populations of archaeological remains, while not an outcome of coevolution per se, are nevertheless an important source of information on animal use. Arguably, herders will strategically cull their herds (or flocks; say, by emphasizing the slaughter of young, yet fully grown males) in ways different from the choices a hunter will make (who may be more likely to select prey based on size rather than sex; Zeder 2006). Both hunting and culling may be recognized in an archaeological assemblage, so long as sufficient information is known about the practices themselves.

Population-level genetic impacts are also common outcomes of the domestication process. Genetic bottlenecks, or a reduction in net genetic diversity within a population, can arise from founder effects, in which a non-representative portion of the progenitor group becomes the basis for all future genetic diversity among the domesticate, or through the process of artificial selection, as certain traits are selected for (and become fixed) within the domesticated population. Cases of serial bottlenecks are indicative of the expansion of domesticated plants and animals through a region. Domestication centers of origin show more genetic diversity within a domesticated species relative to neighboring regions with that domesticate (Bradley 2006; Bruford and Townsend 2006). This has been used to track the spread of multiple Old World domesticates, such as sheep and cows.

Archaeogenetic analyses of domestication often privilege certain parts of the genome—namely mitochondrial DNA (mtDNA)—due to the relative ease of extraction and sequencing.
Limitations to mtDNA studies should not be forgotten, however. The same aspects that grant mtDNA its analytical power (high copy number, matrilineal inheritance, manageable size, known hypervariable regions, and so on) can encourage its inappropriate or incautious use. Most notably, a study of mtDNA completely fails to consider the genetic contribution of males. Thus, it must not be forgotten that phenotypic sub-species identifiers (such as avian featheration) are likely to not align cleanly (if at all) with mtDNA matrilines, especially in domestication contexts where female breeding opportunities are not greatly controlled.\(^2\) It is therefore crucial that multiple patterns are considered (demographic, archaeogenetic, and phenotypic) when assessing turkey use practices. I consider each of these below, but first I explore parallels between turkey domestication and that of another household domesticate, the pig.

**Of Birds and Bacon: Pig Parallels to Turkey Domestication**

The similarities between the processes of pig (*Sus scrofa*) domestication and what is understood about the turkey are striking, and it might be prudent to see what aspects of pig-use may inform our understanding of turkey use in the Southwest. The wide distribution of domestic pigs and their wild relatives makes simple geographic specification of the origin of pig domestication difficult (Albarella et al. 2006; Larson et al. 2007). Wild boars from multiple lineages were present across most of the Old World prior to domestication, and independent domestications of pigs occurred across the African, European, and Asian continents (Albarella et al. 2006:209). Additionally, pigs and their wild counterparts enjoy a wide range of possible relationships with humans beyond being a protein resource. Pigs are active composters, may play a role in fertilizing fields, and are social, intelligent animals with little natural aversion to being

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\(^2\) This is because nuclear DNA assorts independent of mtDNA.
around humans (Price 1984; Rappaport 1967:20-21). Rappaport (1967) also reports ritual use of pigs among the Tsembaga of New Guinea, noting that domesticated pigs are almost never killed outside of community-wide pig feasting rituals. These rituals most often take place during periods of “physiological stress” (Rappaport 1967:22), such as periods of warfare, illness, injury, or death.

Turkeys likewise have a varied history of interactions with humans, and were almost certainly not constrained to being solely a food resource. Turkey feathers were used widely by ancestral Pueblos, both as ornamentation and woven into turkey feather blankets (Hargrave 1965a:205). Turkeys have also enjoyed ritual significance to people in the Americas, with ethnographic accounts describing use of turkey blood in various ritual contexts, from christening to marriages (Thompson 1938:596), and archaeological contexts (especially Basketmaker III and Pueblo I contexts) having yielded whole or beheaded turkeys interred alone or in association with human burials (Muir and Driver 2002:174).

Many modern pig herders allow their livestock to forage free-range for food, and some actively encourage hybridization with wild populations. Among the Etoro of New Guinea, male pigs are castrated and sows are allowed to wander free-range and mate with wild boars (Rappaport 1967:21; Rosman and Rubel 1989, cited in Albarella et al. 2006:209). Outbreeding—or the practice of allowing females to breed outside of captive stock—is done to maintain the size of the domestic stock. Pigs, like turkey, will tend to be smaller in size once bred in captivity. Turkeys prefer a broad diet and tend to return to a home-site to roost nightly, and so are similarly adapted to be free-ranging. Thus, models explaining the phylogeographic patterns of turkeys in the past need to account for the possibility of hybridization of free-range domestic turkey with
wild turkey populations.

Different pig use-practices result in different sex-linked age-at-death assemblages, and this is likely true for turkey as well, though the effect has not to my knowledge been studied for turkey. For example, modern domesticated male pigs are slaughtered at a relatively young age, upon reaching full size (Albarella et al. 2006:217). This pattern may be similar to the outcome of intensive hunting practices, with full-grown males selectively sought as a way to maximize hunting returns, though these remains will presumably reflect wild age demographics. A zooarchaeological assessment of mortality-curve changes throughout sites with turkey remains in the Southwest is needed in order to ascertain what patterns exist (but see Hargrave [1965] for an example of age-estimation of archaeological turkeys using the clavicle bone). Seasonality of hunting will also impact the composition of assemblages, as seasons correlate with group structure among turkey flocks. During the mating season, toms and hens feed and roost together; for the remainder of the year, however, toms forage and roost alone, while hens and their broods travel together in multi-hen groups (Schorger 1966).³

Archaeogenetic and Demographic Expectations of Turkey Use

I now generate expectations for the archaeological and ecological record of turkey use in the U.S. Southwest, particularly the genetic aspects of these records (Table 2.1). Numerous assumptions are inherent in the expectations given in this table. First, I assume an extra-regional homeland for Southwestern domestic turkey (following one of the possible conclusions of Speller et al. 2010); this implies that the diffusion of aHap1 turkeys (the most common “domestic” mitochondrial haplotype) present in wild populations extended deeply into the

³Turkey ecology is discussed further in Chapter 5.
Southwest. However, the dominance of the matriline in turkey populations would deteriorate with distance from a presumed western-Kansas origin of the domesticate (Speller et al. 2010) either through outbreeding (as detailed below), or as transported turkeys became feral. Second, this model does not account for ecological requirements of different use-strategies. For instance, allowing one’s turkey to feed in the wild (“outfeeding”) requires living near suitable turkey habitats. Similarly, outbreeding would require relatively local wild turkey populations. Either of these requirements may not have been met in certain locations.
Table 2.1. Aspects of turkey use in the American Southwest and their expected genetic and demographic effects on captive and wild populations. This model assumes turkey were imported from the ancestral range of the wild Rio Grande subspecies (*M. g. intermedia*).

<table>
<thead>
<tr>
<th>Use</th>
<th>Archaeogenotypic</th>
<th>Archaeophenotypic</th>
<th>Archaeodemographic</th>
<th>Archaeoisotopic</th>
<th>Neogenotypic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breeding</td>
<td>Outbreeding</td>
<td>Founder effect in female lineage only</td>
<td>Hybridization of feather phenotype; Maintenance of turkey size</td>
<td>Sex-ratio heavily (if not completely) skewed towards females</td>
<td>Probably implies outbreeding</td>
</tr>
<tr>
<td></td>
<td>Inbreeding</td>
<td>Founder effect in male and female lineages</td>
<td>Feather phenotype preserved; Size decreases, unless larger size is artificially selected for</td>
<td>Sex-ratios determined by use</td>
<td>Indeterminate</td>
</tr>
<tr>
<td>Feeding</td>
<td>Outfeeding</td>
<td>May imply outbreeding</td>
<td>Carbon-isotope ratios slightly enriched from natural baseline; nitrogen-isotope values slightly depressed from baseline</td>
<td>May imply outbreeding</td>
<td>Carbon-isotope ratios greatly enriched from natural baseline; nitrogen-isotope values slightly depressed from baseline</td>
</tr>
<tr>
<td></td>
<td>Infeeding</td>
<td>Implies inbreeding</td>
<td>Carbon-isotope ratios greatly enriched from natural baseline; nitrogen-isotope values slightly depressed from baseline</td>
<td>Implies inbreeding</td>
<td>Implies inbreeding</td>
</tr>
<tr>
<td>Use</td>
<td>Feathers</td>
<td>May be either subspecies-dependent (ornamentation) or species-independent (feather blankets)</td>
<td>May either imply inbreeding (ornamentation) or be indeterminate (feather blankets)</td>
<td>May be either female-weighted (feather blankets) or sex-independent (ornamentation)</td>
<td>Indeterminate</td>
</tr>
<tr>
<td></td>
<td>Protein</td>
<td>Presumably sub-species independent; may reflect founding population and/or wild-type</td>
<td>Probably implies outbreeding or artificial selection for size</td>
<td>Sex-ratios heavily skewed towards females as breeding stock; males potentially killed upon maturity</td>
<td>Indeterminate</td>
</tr>
</tbody>
</table>
Turkey breeding practices may be related to turkey plumage preferences and/or turkey size considerations. Outbreeding with local wild birds would not only indicate the lack of importance in the turkey feather coloration phenotype, but might also signal the active maintenance of turkey size (Tchernov and Horwitz 1991). Thus, outbreeding will be accompanied by a founder effect only in the mtDNA and maintenance of limited mtDNA diversity (assuming captive male sterilization), a general maintenance of turkey size, and notable feather coloration hybridization with local turkey populations. Inbreeding, on the other hand, would limit diversity in both mtDNA and nuclear DNA, general size reduction among captive birds, and the preservation of feather coloration and patterning, at least in the absence of willful artificial selection.

The feeding of flocks is an important aspect of domesticate maintenance, and, like breeding, may be accomplished via either outfeeding or infeeding. Outfeeding, or allowing domestic turkey to forage in the wild, may go hand-in-hand with outbreeding. In addition to the morphogenetic effects of outbreeding noted above, outfeeding would be signaled by the maintenance of a natural turkey diet, as reflected in stable carbon-isotope ratios obtained from captive turkey bone. Outfeeding may have had the advantage of not taxing Pueblo food stores, though it would only be viable at sites with appropriate local turkey habitats. Infeeding, or allowing captive turkey to graze on agricultural (i.e., maize) stores, would dramatically raise the stable carbon-isotope ratios in captive turkeys, and the restricted diet breadth would be notable in palynological analyses of turkey feces (e.g., Nott 2010). This feeding strategy does not require proximity to wild turkey habitats, but would require a potentially prohibitive maize surplus, as turkeys would directly compete with humans for calories (see Chapter 5 for details of turkey dietary needs).
Finally, as turkey changes from a mainly ritual use to a protein resource, artificial selection and the demographic effects of flock culling will reflect changing use patterns. Using turkeys for feathers, whether as ornamentation or for blankets, will have little impact on the age of slaughtering, if slaughtering happens under these conditions at all. Adult turkeys molt twice annually (Leopold 1943) and would thus be more valuable alive than dead. Also, turkey size maintenance might be less important in these use contexts, possibly leading to a general decrease in captive turkey size due to the predominance of inbreeding to maintain feather phenotype.\footnote{This assumes that the genes that control for body size are not linked to plumage quality and quantity.} Such an expectation is in line with McKusick’s notion of the ‘Small Indian Domesticate,’ an early breed of turkey used primarily in ritual settings (McKusick 1986). Demographics of turkey being raised as a protein resource will be structured by natural size differentiation between males and females. The males will most likely be killed upon reaching full maturity, while more females will be maintained as breeding stock. People might have killed non-breeding males as soon as they reached a reasonable size for eating. If this were the case, then as food becomes limited, the remains of younger and younger toms (and perhaps hens as well) might end up in middens, as feeding them might have become too costly, and feeding on them all too attractive.

In the next chapter, I develop a narrative model of turkey domestication in the NSJ, specifically incorporating the expectations just derived.
CHAPTER THREE

THE AVICULTURAL TRAP MODEL

Question-based—or model-based—archaeology has a long history in the U.S. Southwest (Martin 1971). Perhaps the abundance of data—stemming from pristine preservation, a thorough historic and contemporary ethnographic record, and the extensive coverage of archaeological survey in the region (Kohler 2011b)—has allowed researchers in the Southwest to generate models with abundant testable predictions, and to bring the record to bear on these in a highly productive way. There has always been healthy feedback between model development and data collection in the Southwest. While models were often initiated by a process of generalizing obvious patterns on the landscape (for example, cultural classification schema such as the Pecos Classification [Kidder 1927]), additional data and nuanced analyses of those data have allowed researchers in the region to expand model development dramatically (Phillips 2009). This has often included the incorporation of quantitative models similar to those proffered in human behavioral ecology. For instance, Phillips (2009) reviews current efforts to formally model the spread of agriculture in the U.S. Southwest, and presents a model incorporating marginal costs of different subsistence strategies.

Until recently, however, archaeologists have shown restraint in—if not measured resistance to—moving beyond linear relationships as models for the patterns they observed.5 While these linear models had the benefit of being highly tractable and eminently testable, some researchers have become dissatisfied with the simplicity of such models—notably pioneers of historical

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5 This statement is perhaps unfair; it is not to say that archaeologists have not recognized the complexity of human-environment interactions in the past. Rather, it might be that we have lacked the tools necessary to build models that can cope with such complexity. This barrier is being rapidly overcome, and thus our models are evolving.
ecology (Crumley 1993)—and have sought more ‘complex-systems’ approaches to organizing and analyzing archaeological data. Many of these approaches, including the agent-based simulation approach discussed later, evolved out of the ecological literature and development of chaos and complexity theory at places like the Santa Fe Institute and Arizona State University (Kohler and van der Leeuw 2007). After Holling’s (1986) formalization of the panarchy concept, Folke (2006), Redman (2003), and others began developing the concept of resilience within complex systems—self-organization of these systems and their ability to withstand external perturbations. The resilience concept is becoming foundational for historical ecology. Sander van der Leeuw and colleagues (2000) have championed a complex-systems approach to resilience, with nested, highly connected systems, and have stressed a multi-scalar approach to studying systemic sustainability. A related body of theory on ‘robust systems’ has been built up by researchers at the Santa Fe Institute and elsewhere (Jen 2005, editor) and applied to Pueblo societies in the northern Southwest to help explain its well-known thirteenth century depopulation (Kohler 2010, 2011a).

Recently, Michele Hegmon and colleagues have sought to operationalize resilience theory in the archaeological record by focusing on episodes of systemic failure in the U.S. Southwest, and by identifying domains of rigidity within those systems (Hegmon et al. 2008). Structural rigidity within a system refers to a winnowing of possible trajectories for that system. Put another way, rigidity is an attribute of a system that suppresses agency of actors within the system by limiting their possible choices. A ‘rigidity trap’ (Holling 2001) occurs when agency is effectively eradicated from a system and the only way the system can respond to perturbations is by large-

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6 See also Campbell et al. (2009:8) for a brief but insightful discussion of the barriers to incorporating Folke’s conceptualization of resilience into historical ecology.
scale systemic change, or transformation. Hegmon and colleagues focus on three iconic episodes of cultural collapse and reorganization in the region—the Hohokam in southern Arizona, the Mimbres in southwest New Mexico, and the Ancestral Pueblo people of the Central Mesa Verde region of southwest Colorado—each of which experienced dramatic and often violent social transformations towards the final periods of occupation in their respective regions. They identify three measures or domains of rigidity accumulation in the study areas: degree of integration, degree of social power/stratification, and degree of technological conformity within each culture. They quantify these (somewhat arbitrarily) along multiple lines of evidence, and compare them to measures of magnitude of change related to systemic collapse and reorganization. They find that, indeed, there is a strong correlation between high rigidity in each of the three domains and the magnitude of transformation.\(^7\) Hegmon and colleagues close by offering multiple theories on why rigidity might build within a system, including cultural attachment to traditions and technologies, and the presence of path dependence or trajectory rigidity within the system.

While Hegmon and her colleagues offer a compelling initial application of resilience theory to the archaeological record, they stop short of fully explaining how rigidity may accumulate within the domains they identify. This may be because of the aforementioned overwhelming abundance of data, as opposed to a lack thereof. Identifying trends over broad areas is difficult at best (Balée 2006); it may be that we (and our computers) can only conceptualize these systems at a given moment in time, or at an extremely broad scale. If we take path dependence to be a mechanism for rigidity buildup in these systems, however, we might not need to observe data

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\(^7\) Hegmon and colleagues use a relative ranking to quantify total degree of transformation, based on measures of the degree of change in different domains, including ceramic style, household organization, architectural style. They also include metrics of physical suffering related to health problems and violence, and the degree of integration in the core areas.
from complex systems during the entirety of the buildup, but rather, we may use computer simulations that enable complex systems to behave in self-organizing ways, where ‘rigidity traps’ or other kinds of path-dependence (Holling 2001) may emerge from the internal dynamics of the model. How the model is specified may thus be taken as an explanation for high-level patterns in the archaeological data. Agent-based simulation (ABS) of socionatural systems provides one mechanism for generating high-level patterns by specifying low-level model behavior and observing the impact of bottom-up processes (Kohler 1999). In ABS, autonomous agents interact with one another in prescribed ways. By giving ‘agency’ to many realms of a system—say, to humans as well as their landscapes—we may create dynamic systems that more closely resemble systems in the past, and that demonstrate cycles of resilience and rigidity over time. Through ABS, we may gain a greater understanding of how those domains interact with one another in complex ways. If we design such ABSs to reflect archaeological systems, we may ‘fit’ patterns in the record to those produced by ABS as a way of testing hypotheses derived from the resilience construct (Grimm et al. 2005; Kohler and van der Leeuw 2007).

**Subsistence Rigidity and the Avicultural Trap**

As mentioned, the VEP study area (Figure 1.1) saw substantial demographic change during the thirteenth-century A.D., including dramatic aggregation around canyon heads followed by complete depopulation by around A.D. 1280 (Duff and Wilshusen 2000; Lipe and Ortman 2000; Varien et al. 2007). Several models employing both ecologically and culturally based accounts have been created in an attempt to explain this massive depopulation. Researchers have long agreed that while regional drought was a principal cause of emigration, sociocultural influences likely directed the trajectory (literally and figuratively) of the migrations (Lipe 1995). Recent
research—including that of the VEP—is beginning to clarify the roles of low-frequency
temperature and precipitation signals proxied by pollen data, and their interaction with high-
frequency variability proxied by tree-rings (Wright 2006, 2010; Kohler 2010). Most researchers
find it necessary to include demographic, social, climatic, and environmental factors in current
explanations for both the initiation and the direction of the regional depopulation.

I now would like to extend and clarify Hegmon and colleagues’ (2008) model mentioned
earlier by providing a scenario—specific to the Central Mesa Verde region—in which expanding
human populations deplete wild protein resources, leading to reliance on an avicultural strategy.
This strategy, in turn, may have driven population aggregation, agricultural intensification, and
the heightened importance of maize in the Pueblo resource-base. The importance of agricultural
yields across multiple subsistence domains (providing both calories and protein) might have
driven increasing rigidity within other domains of Pueblo society, leading to societal collapse. I
intend this to be a somewhat idealized version of historical events, aimed at articulating one
possible way in which turkey use might be implicated in the buildup of structural rigidity in the
NSJ and its eventual abandonment. Put another way, this narrative is a reorganization of present
archaeological knowledge of population history and turkey use in the NSJ, blended with
predictions developed in Chapter 2.

The model is developed chronologically, as follows.

_A.D. 600 – 900: Initial immigration and growth._

Maize agriculturalists move into the region and begin farming in small
(Varien et al. 2007:284), and are initially distributed as small hamlets across the
landscape in a way that accounts for agricultural productivity, water availability, fuel wood access, and the proximity of protein resources. Protein, in the form of deer, hare, and rabbit, is hunted in the area around each site. Deer are an important meat source during this time, relative to lagomorphs (Badenhorst 2008; Badenhorst and Driver 2009). Population grows until the late 800s (Varien et al. 2007:285). The villages that form towards the end of this period begin to impact deer availability (Duff et al. 2010:173), though not to the extent seen later in this area. Turkey are kept at sites in small numbers and are used primarily for feathers and as a ritual resource (Muir and Driver 2002:174; Munro 1994:149). Genetic signature of turkey at sites likely patterned after type of use; if specific feather phenotypes are favored, genetic bottlenecking may occur.

_A.D. 900 –1060: Counterexample ~ Resilient population decline_

A period of dry and cold years around from the late 800s through the mid 900s reduces agricultural productivity across the landscape (Varien et al. 2007:279; Wright 2006). Populations decline regionally, but remain aggregated in the most productive areas given the prevailing short summers (Varien et al. 2007:290). Maize agriculture and deer, rabbit, and hare hunting continue, though there is a shift away from deer towards lagomorphs, perhaps as deer become depleted on the landscape (Duff et al. 2010:173). Turkey continue to be used only or primarily as a ritual resource (Munro 1994:149). Genetic expectations are the same as those from the previous period. Lower agricultural yields may force people to abandon turkey keeping, perhaps leading to more homogeneity in turkey lineages across
space as trade in turkey-based goods (feathers, blankets, and tools) potentially intensifies.

A.D. 1060-1250: Depletion of Deer and the Baiting of the Avicultural Trap

Human populations grow rapidly in the last half of the A.D. 1000s (Varien et al. 2007:285), probably aided by immigration to the NSJ of peoples with Chacoan affiliations from the south (Lipe 2006; Varien et al. 2007:289). Deer populations decline and remains suppressed after this point (Duff et al. 2010:173; Johnson 2006). Households may have ‘chased’ deer across the landscape as deer populations in areas profitable for maize-producing became severely depressed. With continued population growth human populations continue to aggregate into communities (Varien et al. 2007); households become more clustered in areas on the periphery of the remaining areas of relatively high deer productivity. People in areas of high maize productivity may adopt the avicultural strategy as it becomes less calorically expensive to feed and raise turkey than to hunt for other protein. This stimulates a greater dependence on maintaining surpluses of maize, as turkey feed on corn (almost exclusively in some places: Rawlings 2006:166; Rawlings and Driver 2010). Wild turkeys (if available) may have initially been hunted for protein, but their populations, like deer, can be expected to have been rapidly depressed.\(^8\) There could be a shift towards larger phenotypes (McKusick 1986),

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\(^8\) The evidence supporting wild turkey hunting—and especially the eradication of wild populations—is sparse. Local (Duff et al. 2010; Munro 1994) and regional (Badenhorst 2008; Badenhorst and Driver 2009; Muir and Driver 2002) archaeological faunal analyses indicate a trend where as deer become less abundant, turkey become more so. However, lagomorph abundances also increase, as do lagomorph indices (Badenhorst and Driver 2009:1838). This suggests enhanced focus on prey that are lower-ranked than turkey, indicating either that turkey were not abundant on the landscape to begin with, or that turkey populations were swiftly depressed.
which would be reflected genetically. As infeeding intensifies, it will drive genetic separation of captive turkey populations from both wild populations and captive populations in other areas. Human populations continue to increase, yet contract spatially (Varien et al. 2007:290); this in turn requires further agricultural intensification. Hierarchical social structures emerge (Lipe 2002), as reflected by public and private architecture (Glowacki 2006); this may have occurred as high populations obliged cooperation for efficient resource distribution or for competitive advantages vis-à-vis other communities (see Hooper et al. 2010). Intensification of maize production may have precluded spending more time on deer hunting, if these repopulated certain areas during this time, and might encourage specialization in general (Fargher 2009:356). Population peaks at around 30,000 in the VEP study area, driven in part by emigration from less favorable areas to the west and northwest (Glowacki 2006).

_A.D. 1250 – 1280: Transformation and abandonment_

Unfavorable agricultural conditions, which dominate the first half of the 1200s (Wright 2006:122), persist into the late 1250s; although these conditions improve in the late 1260s, that improvement lasts only a few years (Varien et al. 2007:Figure 3). By about A.D. 1270, a combination of emigration from the NSJ (Duff and Wilshusen 2000; Wilshusen 2002:118-119), violence (Kuckelman et al. 2000), and the potential of high mortality rate with low fertility rate (suggested by Varien 2010, but not yet systematically evaluated) has reduced population size in the VEP area to approximately 10,000 people (Varien et al. 2007). Aggregation
around fortified critical water sources, which began in the mid-1100s (Glowacki and Ortman 2011:Table 14.1), intensifies; these may have been restricting resources on the landscape, potentially leading to competition over their control (Kolm and Smith 2011). By this period’s end, communities abandon turkey husbandry due to lack of maize surpluses (Beecham 2006; Kuckelman 2010a, 2010b). Populations potentially revert to deer (Duff et al. 2010:174) and perhaps wild turkey hunting, as well as harvesting wild turkey eggs (Beecham and Durand 2007). I expect the signature of turkey genetics to shift to match locally available wild birds. Depopulation of the western portions of the NSJ likely begins by A.D. 1240, and from the eastern portions by A.D. 1260 (Glowacki 2010). Those who migrated likely went to the northern Rio Grande (Ortman 2010) and elsewhere (Davis 1964; Lekson et al. 2002).

This narrative builds on many aspects of the archaeological record (transition towards turkey as protein circa A.D. 1050; aggregation in the most agriculturally productive areas in twelfth and thirteenth centuries A.D., usually far from protein resources; final fortification in cliff-dwellings or canyon-head settlements, situated around critical water sources; and dramatic regional abandonment circa A.D. 1280); but questions remain. Paleoproductionity reconstructions—with associated estimates of human and turkey carrying capacity—will continue to enable us to quantify the degree to which people had to abandon potentially productive hunting grounds for agricultural areas better suited to support themselves and the turkey they ate. Eggshell analysis (Beecham and Durand 2007), in conjunction with zooarchaeological evidence already collected, will indicate how people across the landscape differed in their degree of commitment to
aviculture over time. Ancient and modern DNA studies (Mock et al. 2002; Speller et al. 2010) will contribute to our understanding about how turkey use practices varied across the landscape before and after aviculture was adopted, as well as while it was being intensified (Zeder et al. 2006).

One final note: throughout this model I have defined turkey use as ‘controlled breeding’. This definition does not, however, capture the complexity of the turkey/human relationship, as described in the Chapter 1. Domestication, under this definition, is an especially intensive stage of an evolving mutualism between humans and an animal species. The intensity of a mutualism may be measured by the degree of codependence two species have on each other (Zeder et al. 2006). It may be the case that humans developed a closely linked (and thus highly rigid) mutualism with a specific subspecies of turkey, *M. g. intermedia*, during the millennia of turkey use in the region. Such a codependence with a single subspecies might explain the demonstrated dominance of a probable *M. g. intermedia*-derived matriline of *M. g. merriami* in the archaeological record (Speller et al. 2010) and perplexing dearth of the domestic matriline in wild modern populations regionally (Mock et al. 2002). We can therefore postulate that people either transported their turkey with them when abandoning the northern Southwest, butchered all of their turkey before leaving, or left domestic turkey behind who were ill adapted to feral living, especially in poor turkey habitats. Rigidity impacts all parts of a system, and it may be the case that domestic mutualisms are by definition particularly rigid systems, especially when unified under a common means of subsistence, as with the case of human and turkeys subsisting on maize agriculture and sparse water sources.
CHAPTER FOUR

AN OPTIMAL FORAGING MODEL OF AUXILIARY RESOURCE PROCUREMENT

In addition to informing models of biological change, such as the genetic implications of turkey domestication enumerated Chapter 2, evolutionary theory has enjoyed a foundational role in the development of behavioral optimization models (MacArthur and Pianka 1966; Shoener 1971; Winterhalder and Smith 2000). These models—which gained prominence in the ecology literature but have since been widely employed with human systems (generally in the field of human behavioral ecology; Winterhalder and Smith 2000)—hinge on the assumption that, given variation in a particular fitness-relevant behavior, the optimal form of that behavior will exist as the modal trait within a population. Such models need not depend on assumptions of static environs or even static behavioral phenotypes (though these assumptions have often been made), but can instead allow for behavioral plasticity. Optimization models are designed to ask the question: What is the optimal means of achieving a given end in a particular situation? Once that has been answered, one may ask: How does observed behavior of a population or individual diverge from that optimal expectation, and what are the causes and fitness implications of that diversion?

In many ways, the VEP simulation described in Chapter 5 is an optimization model on a grand scale; VEP researchers seek to model the optimal behaviors of individuals living and competing on a landscape, and to assess how peoples’ behaviors in the past deviate from those expectations. The implicit assumption is that any deviation is the product of non-economic decisions (or at least non-optimal economic decisions) made by these people. These may be
socially-mediated (and, in turn, socially-mediating) decisions about where to live, what to hunt, what to produce, and so on.

Several models have been articulated that seek to define optimal behavior when acquiring critical resources on a landscape. Under the umbrella of optimal foraging theory (OFT; Schoener 1971), these models predict the behavior of a forager seeking to maximize returns for a given resource usually measured in calories by searching, pursuing, capturing, processing, and consuming resources. Like all optimization models, OFT models are used to generate expectations of animal behavior, and their predictions have been upheld in many studies of both animal and human behavior (Lupo 2007; Smith 1983).

In this chapter, I briefly describe two of the most basic models from OFT—the fine-grained prey-choice model and the patch-choice model—and discuss their central assumptions and notable critiques. I reference particular examples of ethnographic applications of OFT; archaeological applications have been thoroughly reviewed elsewhere (see Lupo 2007). I then explore alternative means of resource acquisition, noting that humans have many means of gaining critical resources, including not only solo hunting and gathering, but also socially mediated resource acquisition, such as cooperation in foraging, domestication, specialization, and exchange. I argue that each of these methods of resource acquisition can be explicitly included in an OFT framework, because each carries associated ‘search’ and ‘handling’ costs which may be defined and quantified. Bringing such ‘auxiliary’ means of resource acquisition into the OFT framework allows us to develop models for the emergence of these different strategies. Relatively higher-cost strategies will be used only if the return of all lower-cost strategies drops below a critical threshold. Several requirements of such a model emerge,
including multi-currency investment and, for exchange, a capacity to specialize in a given strategy. Keegan (1986) developed a similar extension to OFT for horticulture, and found OFT models to be appropriate for analyzing subsistence change. Finally, I briefly outline the archaeological implications of including alternative foraging in classical OFT models, focusing in particular on the interpretation of archaeofaunal assemblages.

**Optimal Foraging Theory in Ecology and Anthropology**

OFT models have existed in the ecology literature since the mid-sixties, but gained prominence with the works of Charnov (1973) and Schoener (1971). Schoener (1971) describes the procedure for finding an optimal behavior as follows: 1) choose a currency, 2) choose the cost-benefit functions, and 3) solve for the optimum. Although this schema might seem simple in the abstract, it has spurred nearly half a century of debate. Selecting cost-benefit functions for a particular resource requires making a series of often-controversial assumptions. OFT models by definition require the assumption that there be real and explicit fitness benefits to behaving in an optimal way. This assumption often requires that increases in fitness be correlated—generally linearly—with increases in the currency of choice. What is more, it was quickly noted that optimal behavior is heavily mediated by the structure of resources on a landscape, the historical effect of resource depletion, as well as the amount of competition encountered by a forager on that landscape (Charnov 1976; Grayson 2001).

The original and simplest OFT model is the ‘fine-grained’ prey-choice model (Schoener 1971; Smith 1983). This model imagines a landscape with a uniform distribution of various resources available at proportions relative to one another. These resources are ranked by value
measured in a particular currency (e.g., calories) and an associated handling time, which includes searching for, processing, and consuming the resource. Relative rank occurs such that,

$$ r_i = \frac{v_i}{h_i} $$

where $r_i$ is the relative rank of resource $i$, $v_i$ is the resource’s value, and $h_i$ is the handling time of the resource (Smith 1983). Handling time is defined as the time spent pursuing, capturing, processing, and consuming an item; note that time can be cast in terms of energetic requirements for each of these activities, thus simplifying the value. In addition to handling time, search time aggregates according to the probability of finding a given resource during any unit of time, based on the random-encounter assumption (Smith 1983). Foragers search for all prey items simultaneously, and once an item has been located, make a decision whether to consume it, accruing the handling costs and forgoing the search for any other prey item during the handling time. Smith (1983) points out that the intersection of the cost curves for search and handling costs, respectively, defines the maximum return rate of foraging. As number of different prey types increases, handling costs increase due to the inclusion of lower-return types, while search costs decrease due to the higher probability of locating acceptable items. Formally, any prey type $j$ is in the optimal set if and only if,

$$ \frac{v_j}{h_j} > \frac{\sum (\lambda_i \cdot v_i)}{\sum (\lambda_i \cdot h_i) + 1} $$

where $\lambda_i$ is the encounter rate for prey type $i$, and the rest of the variables are as defined above (Smith 1983).
Smith (1983) describes several testable predictions arising from the fine-grained prey-choice model. Notably, increasing availability of higher-ranked prey should result in a more specialized diet; when availability of high-ranked prey decreases, the opposite is true. Also, whether a prey type is included in the optimal diet is purely a function of the costs associated with higher-ranked types, and particularly their handling efficiencies. Finally, the inclusion of a prey type is independent of its availability. If a type is included in the optimal diet, it will be taken if encountered.

The fine-grained prey-choice model includes several assumptions: a homogenous distribution of resources, zero variance in handling costs within a prey type, and, in most implementations, a static encounter probability for each prey type (Pyke et al. 1977). The model may be rendered more realistic by relaxing one or more of these assumptions. For example, the patch-choice model (Charnov 1973, 1976) imagines a landscape where prey types are dispersed heterogeneously; the encounter rate for each prey type can then be allowed to vary from patch to patch. This raises two new problems for foragers: which patch to forage in, and how long to spend in each patch (Charnov 1976). Patches are assumed to suffer from diminishing returns: the productivity of a patch declines with use. The patch-choice model is derived and fully explained by Charnov (1976). Following Smith (1983), I summarize it graphically in Figure 4.1.

Charnov (1976) proposed the Marginal Value Theorem (MVT) as a joint solution to the two problems encountered by foragers on patchy landscapes. The MVT states that, given a forager with multiple patches to choose from, each patch will have its own return curve (potentially, though not necessarily associated with the operation of fine-grained prey-choice processes within that patch); patches are ranked by their average return rates. For any given set of patches, which
may define the foraging area of a predator, there exists an average return rate of that set. The optimal solution to how long a forager ought to stay in each patch is then the length of foraging time it takes for the marginal return rate of the patch (the derivative, or momentary slope, of the curve of net return by time) to drop to this average return rate for all patches. A graphical model is presented in Figure 4.1.

![Figure 4.1. The marginal value theorem of patch-choice.](image)

The MVT imagines a forager with the opportunity to forage in several discrete patches (A-F), each with its own diminishing return curve from foraging, defined as net gain ($N_T$) per unit time ($T$). For the entire set of patches, there exists a mean return rate ($\bar{R}$) over the foraging period; patches whose return curves pass above this mean will be utilized (black curves), while those that don’t will not be (grey curve). The amount of time spent in each patch is the amount of time hunting in a patch before the marginal return rate (the first derivative of the return curve) equals $\bar{R}$. These times are shown by the dropped dotted lines ($T_A - T_E$). Adapted from Smith (1983).
The MVT has many interesting features. Notably, only patches with initial marginal returns greater than the average return rate will be used, and a higher average return rate decreases the amount of time spent in any one patch (Charnov 1973, 1976; Smith 1983). Travel time between patches is an obvious factor in whether a patch is utilized; these are considered in my discussion of central-place models below.

Various extensions to the fine-grained prey-choice model and the patch-choice model have been suggested, and I briefly discuss three of particular interest: models that minimize the probability of starvation, models that optimize in currencies other than calories, and models where foraging trips are taken from a 'home-base.' McNamara and Houston (1987) suggest a refinement to the fine-grained prey-choice model where, instead of merely attempting to maximize their caloric intake, foragers adopt a strategy to minimize starvation over a given time period. As opposed to classical theory, which does not consider energetic storage or time constraints on foraging, the authors model a situation where foragers decide to take an item only if it increases their storage amounts (which the authors do not limit, but which may be limited), and where a storage amount of zero represents the death of the forager. Using dynamic programming, they show that the optimal solution is for a forager to take any prey item that yields positive net energy. This solution is based on an alternative interpretation of forager fitness: instead of fitness increasing linearly (or even non-linearly) with caloric gain, it is a function of survival time. Individuals who live longer have more opportunities for reproduction.

A second survival-based model they explore requires a forager to obtain enough energy storage to survive an amount of time with no foraging, such as animals that are diurnal or nocturnal, or animals that hibernate (McNamara and Houston 1987). They find that in this
situation, the optimal strategy correlates with storage amount and time left for foraging. Namely, as the time left for foraging approaches zero, less profitable items are no longer taken. The decisions of the forager become dominated by the need to survive the foraging hiatus as opposed to avoiding the lethal boundary. This is due to the fact that time keeps ticking while prey are being handled; non-continuous foragers must avoid lower-ranked prey, lest they waste all of their time handling non-profitable prey types.

The second survival-based model is particularly relevant for human hunting and gathering. Foraging in human groups, especially outside of the tropics, is often seasonal. For many groups, winter and early spring are times of hunger when human populations are heavily dependent on stored resources (Speth and Spielmann 1983). We should expect shifts in foraging strategy as these periods approach. Such a signal should be especially visible in archaeological assemblages created by residentially mobile hunter-gatherers, because assemblages made later on in the foraging cycle would show greater preference for higher-ranked (generally larger) game.

From their conception, OFT models have been designed with the flexibility of operating on any currency deemed appropriate, though over the history of their application, energy (in the form of calories) has been the overwhelming nutrient of concern (Pyke et al. 1977). This is true both for models concerned with gathering predominately floral resources, as well as for models of hunting. One benefit of sticking with energy is that both costs and returns may be cast in a single currency; search and handling times can be converted to caloric costs, thus rendering simple caloric returns to foraging. Caloric conformity also allows for broad comparison between foraging decisions between groups and within groups. For instance, extensive ethnographic research has noted dramatic differences in foraging returns of men versus women in small-scale
societies; these data consistently use caloric returns, and have been variously interpreted as due
to cooperation between mating pairs via a sexual division of labor, conflicting reproductive
strategies, or specializing in social versus somatic capital (Bird 1999; Hawkes and O’Connell
1992; Hawkes et al. 1997). Some of these studies have shown that differing behavioral strategies
may not be explained simply as optimization on different currencies. For instance, among the
Meriam of the Torres Strait, women collect shellfish and other low-ranked prey at low tide, while
men choose to spear fish on the reef; women routinely enjoy double the caloric return rate of
their male partners, and men have a high risk of returning empty-handed (Bird 1999). Bird notes
that in this example, "cooperative nutrient complementarity fails as an explanation for the sexual
division of labor," (1999:68) because the resources being gathered have similar nutrient profiles.
What Bird and others fail to address, however, is whether men and women might be operating on
different, yet complementary, foraging models. In the case of the Meriam, women might be
operating on a short-term survival model, while males are able to focus on long-term, storable
resources. By cooperating, males and females may be subverting time-based trade-offs and
emulating the choices of a continuous forager, even in the face of critical daily nutrient
requirements.

Optimization on alternative currencies—namely protein or edible meat weight—may be
appropriate when considering hunting by sedentary agriculturalists. The hunting behavior of
agriculturalists is often a net-negative contribution to overall caloric returns in comparison to the
cultivated resource. Hunters, and the people they feed, specifically seek meat, perhaps for
particular nutrients or fats, but more likely to satisfy culinary tastes or social needs (Le Gros
Clark 1968, cited in Allen and Ng 2003:38). In these cases, tracking calories derived from prey,
which can vary non-linearly with meat weight, is an inappropriate currency choice, and will generate foraging patterns substantially different from protein or weight-based models.

A final extension I would like to discuss concerns foraging patterns that originate from a 'home-base,' or central-place models (Grayson 2001; Orians and Pearson 1979). In these models, search and handling costs are a function of the distance from a home-base to where a resource is procured. Travel time to the patch will directly affect the baseline returns from that patch, as will hauling costs of resources to and from that patch, should the resource not be consumed in situ. Central-place models are special cases of the marginal value theorem, in that they too seek to optimize patch choice and foraging time within patches. Without going into details, certain expectations have been generated by central-place models; namely, foraging time increases at further sites, as foragers attempt to make the most out of costly foraging trips. Also, the additional costs associated with distant foraging can promote greater diet breadth (Grayson 2001).

Extensions to classic OFT models such as these have led to a robust set of expectations for resource use by increasing, spatially structured and constrained populations. Grayson summarizes these thus:

We can, as a result, expect that increasing predation pressure by human hunters will result in the decline in abundances of higher return, and thus usually larger, prey species on the landscape and in the diet. Likewise, we can expect that the abundances of lower return, and thus usually smaller, prey species will increase in the diet. We can also expect that, at times, greater numbers of species will be incorporated into the diet—that is, that "diet breadth" will expand—and that those species that are taken may be more intensively utilized. We can expect the people involved to respond to this situation by increasing the distances they travel across the landscape or by relocating if possible. We may also expect technological innovation by human agents directed towards increased extractive efficiency (Grayson 2001:7).
In the next section, I add to this list by arguing that we may in certain cases expect the adoption of alternative resource procurement strategies that may become optimal once resources are sufficiently depleted. Namely, domestication and exchange, which generally carry low return rates relative to hunting, may be treated as alternative ‘patches’ for foraging, or more accurately as forces that alter the optimal marginal return rate of a foraging patch.

**Folding Alternate Procurement Strategies into an OFT Framework**

Hunting and gathering arguably provide the highest returns to humans as they attempt to meet their needs in low-population settings. When resources are abundant, we only need to account for search and handling costs of a resource; while these costs may vary between resource types, the costs associated with ‘alternative’ procurement strategies are almost always higher. For example, the active cultivation of a plant resource may require selection of good candidate seeds or young plants, active winnowing, clearing a plot of competing species, guarding against other predators, and decreased ability to take advantage of other foraging opportunities. While many of these processes may be rendered more efficient with artificial selection (for example, the processing of many cultivated grasses), the net effect is still costly when compared to costs of foraging on resource-abundant landscapes. What is more, these costs may intensify as cultivation is attempted in environments outside of the domesticate's wild habitat. A similar argument may be made for domesticated animals; significant investment must be made in birthing, raising, housing, protecting, and feeding faunal domesticates before their size (and thus potential returns) is maximized. Hunting wild animals requires none of these investments, and is dramatically cheaper so long as high-ranked prey are available. Exchanged resources may be less dramatically
costly, but obtaining them will always be more expensive than the original procurement due to additional transportation, curation, and 'price mark-ups' by exchange partners.

What is interesting about these alternative strategies for protein procurement is that their cost-curves may differ greatly from that of standard foraging. Whereas returns in a foraging patch follow diminishing marginal returns with time (and thus energy) investment (Charnov 1976), a strategy like domestication may have the reverse relationship, where investments in infrastructure (such as pens or fences) or management (such as shepherding) allow for very low additional cost per animal kept. Other costs, such as nutritional requirements of domesticates, are somewhat linear.

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9 Rosenberg (1982) calls this ‘learning by using’. Arthur (1989) extends this idea by describing how technologies compete for adoption and may in some cases result in increasing not decreasing returns.
Figure 4.2. The marginal value theorem of patch-choice with an alternative strategy. Here, an alternative strategy gives a higher return rate ($R^*$) than the mean rate from all possible patches ($\bar{R}$). This creates new minimum marginal return rates and foraging times for each patch ($T_{A^*} - T_{C^*}$), and restricts the number of patches utilized (red curves). All other symbols as in Figure 4.1. Adapted from Smith (1983).

Here, I model a flat return rate (or a constant marginal return, as opposed to one that changes due to either diminishing or increasing returns) for an alternative procurement strategy in the patch-choice model using logic congruent to the marginal-value theorem (Figure 4.2). Imagine a strategy with a given return rate $R^*$. If $R^* < \bar{R}$ —where, as before, $\bar{R}$ represents the average return across patches—the alternative strategy should never be used, and the duration of foraging in each patch will depend on $\bar{R}$. If, however, $R^* > \bar{R}$, foraging in each patch should only occur until the marginal return rate for that patch becomes equal to $R^*$. If resource needs are not met by foraging under these constraints, the alternate strategy ought to be taken up for the remainder
of the forager's needs. Likewise, foraging on a fine-grained, homogenous landscape should only occur so long as the marginal rate of return does not fall below $R^*$. 

This model generates several expectations for foraging patterns. First, we can expect that the existence of an alternative resource procurement strategy will only impact foraging patterns if its returns exceed the mean returns of all patches in the foraging area, or the mean returns of all harvested species in a fine-grained area. The former is obvious; in the latter, we can expect diet breadth to increase due to resource depletion only while average returns for all harvested resources exceed that of the alternate strategy. Thus, alternate strategies have the effect of setting an upper limit on diet-breadth in a given foraging environment. Second, when $R^*$ is greater than mean patch returns, foraging times in all patches will decrease, number of patches utilized will decrease, and marginal returns for any given patch will never fall below $R^*$. Finally, as competition for resources increases on a landscape, maximum return rates for any given patch may decline to the point where a complete commitment to the alternate strategy becomes the optimal choice.

**A Brief Comment on Animal Domestication and Archaeology**

The model described above seeks to outline the optimal behavior of a single forager using a particular portion of a landscape. Just as the size and makeup of foraging ranges may be expected to differ across a landscape, costs for a particular alternate strategy, such as animal domestication, may also vary relative to the local environment. For instance, for a social, locally roosting animal such as turkey, the amount of locally available wild turkey habitat can significantly reduce the cost burden of domestication, raising returns on domestication and in turn impacting foraging strategies. Also, the mere availability of domestication as an option will
have these effects on foraging strategy by reducing patch foraging time as well as diet breadth. This generates two patterns which deserve exploration, particularly in the archaeofaunal record. First, the arrival of an alternate strategy in an area will impact faunal assemblages recovered there, even assemblages that lack remains of the domesticate. A reduction in diet breadth will occur prior to the physical arrival of a domesticate in an assemblage, potentially counteracting the standard expectation of increased diet-breadth coincident with resource depletion. This will occur on both a fine-grained landscape (where animals whose return rates fall below that of the alternate strategy will not be utilized) and on a patchy landscape (where low return areas of the environment will not be utilized). Second, these signals will be amplified in areas of the landscape providing naturally lower costs of keeping domesticates; these areas will not only adopt the domestication strategy earlier, but they will show even more restricted diet breadth prior to adoption of the domestication strategy. Assuming the model outlined above in association with knowledge of the availability of wild faunal resources and their associated handling costs for a given area, it should be possible to inductively estimate the local costs of domestication strictly based on faunal indices. Knowing the local costs of domestication would help researchers differentiate between the various domestication strategies outlined in Chapter 2. Such a study is beyond the scope of this thesis, however.
CHAPTER FIVE

APPLYING THE MODEL TO VILLAGE

I now turn to the Village Ecodynamics Project (VEP) simulation (Kohler 2011a; Kohler et al. 2008b) and impose on it a simplified version of the OFT model presented in the last chapter. I begin with a review of the structure of the Village simulation, and a discussion of how agents hunt in the simulation. I then discuss my implementation of turkey domestication as an alternate protein resource on the landscape. The model as presented above and implemented below does not address the origins of domestication, but only the adoption of an already established strategy. I implement domestication within the hunting structure already in place in the Village simulation. The hunting algorithm, which I describe below, does not align with any particular model from classic OFT described in Chapter 4. While this inhibits my ability to make conclusions specific to widely known OFT models, using the current hunting algorithm enables me to compare model output to previously published VEP simulation output (Johnson 2006; Bocinsky et al. 2011). I discuss the results of a small sweep of simulation runs designed to test the effects of adding domestication.

Protein Subsistence In The Village World

One goal of the VEP is to generate a complex agent-based computer simulation of human population and ecosystemic dynamics in a portion of the northern U.S. Southwest (Varien et al. 2007). In the simulation, an initial number of independent agents are seeded on a landscape resembling—with reasonable fidelity—a portion of the central Mesa Verde region in southwestern Colorado. The agents, which represent households, are able to grow maize, hunt, exchange maize and protein, gather wood and water, procreate, die, and fission to form new
households.

The region in which the model is set enjoys one of the most thoroughly analyzed and high-resolution archaeological records in the world. The simulation output can therefore be compared to the archaeological record, both spatially (in terms of distribution of sites on the landscape) and demographically (in terms of numbers of households), while varying a number of model parameters. By doing this, VEP researchers hope to identify causal processes—both social and natural—for changes in population size and distribution (Kohler et al. 2007), including the famous depopulation of the entire region in the late 1200s.

The VEP study area encompasses an 1816 km$^2$ area of southwestern Colorado modeled as 45,400 200 x 200 meter cells (see Figures 5.7-5.9 as examples). Floral and faunal resources are managed in the simulation by each simulated cell. Each cell is populated with vegetation based on its modal soil type, and then populated with deer, rabbit, and hare based on those species’ preferred browse (i.e., the animals’ diet). Cell resource regrowth occurs annually, after fuelwood and protein have been harvested by the human agents, and other plant resources have been eaten by the resident animals.

The model landscape provides sources of protein in the form of three non-domesticated herbivore populations—mule deer (*Odocoileus hemionus*), black-tailed jackrabbits (*Lepus californicus*), and desert cottontails (*Sylvilagus audobonii*)—that vary in size spatially and temporally. They ‘grow’ on a model landscape that contains 139 soil complexes, each of which supports some combination of 93 native vegetation species. Animal population sizes depend in part on how much of their preferred browse is available within local plant communities. Browse production in turn is controlled by the action of a climatic signal on a soil of a specific category.
The VEP climate signal and soil productivity estimates build upon pioneering work by Van West (1994), who used modern weather and agricultural productivity data, soil surveys, and tree-ring measurements, as well as Palmer Drought Severity Indices (PDSI)—a measure of soil moisture retention—to estimate annual potential maize productivity across different elevations and soil depths. She extended these estimations back to A.D. 900. VEP researchers refined Van West’s methods, and retrodicted the predictions to A.D. 600 (Kohler 2010, 2011b). Tree-ring records provide VEP researchers with high-frequency temperature and precipitation signals over the simulation period (A.D. 600-1300, which is in turn split into 14 modeling periods; Table 5.1). Another critical climate signal is provided by palynological analysis. Aaron Wright (2006) reconstructed low-frequency (>25 years, or a human generation) climate change, and found evidence for several significant cooling events in the 800s-900s and the 1200s (Kohler 2010:111-113); however, this signal is not yet included in our productivity estimates. Thus, during these periods of below-average temperatures, our estimates of simulated productivity are likely higher than the actual agricultural potentials. We calculate the net primary productivity for each modeled species of plant; each plant’s productivity in a given soil is weighted by the proportion of its contribution to that soil relative to other species modeled (Kohler et al. 2007).
Human hunting has a dramatic impact on faunal populations in the simulation. Perhaps the most striking pattern we see is how quickly agents manage to significantly deplete the simulated deer population, usually bringing deer populations down to about 2000 deer by A.D. 1000 (Bocinsky et al. 2011). At this stocking level deer hunting is difficult, as the low density of deer on the landscape entails high search costs. These high costs in turn keep simulated human populations relatively low. Simulated human populations generally level off and fall below levels estimated by the archaeological record at about the same time as deer become depleted (Bocinsky et al. 2011).\(^\text{10}\) This is partially the product of not allowing for more nuanced protein procurement strategies in the simulation, such as the domestication of turkey. Turkey remains show up in the zooarchaeological record throughout the occupational sequence of the NSJ, and become dominant as a protein source in the mid-A.D. 1000s (Badenhorst and Driver 2009:1838). Modified turkey index values, which measure turkey and large bird abundance relative to lagomorphs, are higher than 0.5 in 64 percent of Pueblo III assemblages in the NSJ (Badenhorst

\(^{10}\) This account is somewhat simplified; in fact we can vary the extent of the effect that protein depletion has on human population size via a parameter called “protein_penalty” (see Table 5.2) and we can likewise vary the amount of protein sought by each person in each household, which affects rates of game depression.
and Driver 2009:Table 8). I expect turkey-keeping to allow human population to continue its upward trajectory while maize production continues to remain favorable.

**Implementing Turkey Domestication**

Here I discuss how I implemented the adoption of turkey domestication within the Village framework. This allows me to examine the implications of domestication for population size, site location, and degree of household aggregation. Turkey domestication as modeled is crucial to three activities in which agents engage: protein procurement, household relocation, and access to water. I will first describe each of these aspects of my implementation at a general level (see Appendix A for specifics). Before discussing the results of this implementation, I outline a few key simplifying assumptions of the model before discussing the results of this implementation. Aspects of turkey ecology, diet, and demography are detailed throughout the model description (see Schorger 1966 for a complete treatment).

Hunting in the Village simulation currently implements a two-tiered prey-choice model, with deer the most highly ranked prey and lagomorphs lower-ranked (low-level details of the hunting algorithm are documented in Appendix A; see also Cowan et al. 2011). Agents first begin hunting deer in their home cell, then spiral away from that cell searching for deer in each subsequent cell. For instance, an agent will search the eight cells immediately surrounding their home cell, before proceeding to the next sixteen cells (radius 2). Once a simulated hunter reaches a distance of 20 cells (4 km) from his home cell in his search for deer he will begin looking for lagomorphs in his home cell. From then on, each cell searched for deer at a distance $d$ from the home cell will be joined with a search for lagomorphs at a distance $d$ minus 20.

Agents accrue costs for searching, hunting, and transporting prey. An agent does not have
complete knowledge of all animals present in a cell, but has a probabilistic knowledge of their numbers falling randomly in the 30 – 75 percent range. If animals are found in a cell, agents accrue a cost for searching that cell (pursuit time), and butchering and transporting the meat back to their home cell (processing and handling costs). Agents in runs without turkey domestication continue hunting until they run out of territory or time (defined as the total hours an agent may work per year minus the hours spent in the previous year on non-hunting activities), or meet their protein needs.

**Table 5.2. Key parameter settings employed in this sweep.**

<table>
<thead>
<tr>
<th>Parameter Name</th>
<th>Value(s)</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOMESTICATION</td>
<td>true, false</td>
<td>“True” makes domestication available as an option.</td>
</tr>
<tr>
<td>TURKEY_WATER</td>
<td>true, false</td>
<td>Toggles whether agents are responsible for providing water to turkeys. If true, amount of water an agent collects will be incremented by the water needs of its turkey flock.</td>
</tr>
<tr>
<td>TURKEY_MAIZE_PER</td>
<td>0.5, 0.7</td>
<td>Proportion of turkey diet expected to come from maize.</td>
</tr>
<tr>
<td>HUNT_SRADIUS</td>
<td>20, 40</td>
<td>Radius for hunting (in cells; 20 cells = 4 km).</td>
</tr>
<tr>
<td>PROTEIN_NEED</td>
<td>5, 15</td>
<td>Target meat consumption in grams/person/day.</td>
</tr>
<tr>
<td>PROTEIN_PENALTY</td>
<td>1</td>
<td>Penalty for protein deficiency. When [0], no protein penalty; when [1], removal of STATE_GOOD bonus if agent is in a good state.</td>
</tr>
<tr>
<td>SPEED_MOVE</td>
<td>FALSE</td>
<td>Faster hunting search algorithm. Instead of hunting at every possible move location, this algorithm creates a single hunting potential for all 25 cells in a 5 cell square.</td>
</tr>
<tr>
<td>SOIL_DEGRADE</td>
<td>1</td>
<td>Mild degradation, to 70 percent of potential.</td>
</tr>
<tr>
<td>HARVEST_ADJUST_FACTOR</td>
<td>0.75</td>
<td>Acts as a divisor to maize harvest. Hence, a values of 0.75 boosts production by 33 percent over the baseline.</td>
</tr>
<tr>
<td>NEED_MEAT</td>
<td>0</td>
<td>Agents may move to locations without huntable protein resources.</td>
</tr>
<tr>
<td>STATE_GOOD</td>
<td>0.1</td>
<td>When agent state is good, birthrate is incremented by 10 percent, and deathrate is decremented by 10 percent; when state is bad, the opposite occurs.</td>
</tr>
<tr>
<td>H2O_TYPE</td>
<td>3</td>
<td>Allows agents to get water from rivers and springs only.</td>
</tr>
</tbody>
</table>

*Note. All other parameters set to values of runs reported in the VEP I final report (Kohler 2011a).*
When domestication is implemented (as fully described in Appendix A; see Tables 5.1 and 5.2 for descriptions of parameters mentioned here), agents implement the same hunting routine described above, but also constantly calculate their net caloric costs from hunting. The maximum caloric cost of hunting is defined as the cost that carries the minimum protein return-rate above that which is expected if getting protein by other means (i.e., from domestication). Stated differently, agents will hunt until their return rate from hunting falls below that of turkey-keeping. Hunting return rates are recalculated at the end of hunting in each cell and are calculated to account for the possibility that an agent’s return rate from hunting might become better after hunting in the next cell by calculating the best return rate an agent could receive if it were to meet its needs at the time of calculation. The maximum caloric cost is calculated thus, using terms defined in Tables 5.1 and 5.2:

\[
\text{maximum hunt calories} = \frac{\text{household protein need} \cdot \text{BASE}_\text{CAL}_\text{TURKEY} \cdot \text{TURKEY}_\text{MAIZE}_\text{PER} \cdot \text{PROTEIN}_\text{PER}_\text{TURKEY}}
\]

Two things may occur during this revised hunting algorithm: either all of the agent’s needs are met from hunting, or the agent switches over to the domestication strategy. Once the agent switches to the domestication strategy all remaining protein needs of the agent are tallied, the number of adult turkeys required to fulfill these needs is calculated, and agents receive that amount of protein in exchange for the maize required to feed all of those turkeys for a year. Agents are not allowed to entirely deplete their maize storage in order to keep turkey; the amount of maize they invest is limited by only allowing agents to use maize surpluses over the amount of maize their household required in the previous year. If the agent’s protein needs remain unfulfilled (e.g., if they cannot raise enough turkey due to lack of maize surplus), the agent will
attempt to get protein through exchange with other agents (Kobti 2011).

In the Village simulation, protein is a critical resource driving household relocation. If an agent is unable to meet its needs in its current location, it will attempt to move to a better location within a 20-cell radius. The agent estimates its caloric cost of living in all cells in its move radius, and will move to the cell with the lowest cost of living. Costs that get calculated include agricultural costs, and the costs of acquiring protein, water, and fuel wood. Agents calculate ‘imaginary’ hunting costs in a way congruent with the actual hunting algorithm; they perform an imaginary hunt radiating out from each potential home cell, continuously calculate their protein return rate, and ‘switch’ to domestication if their costs rise too high. This has the effect of leveling the playing field for potential sites that have high agricultural productivity but low protein availability, in that those sites no longer appear very poor, while maintaining a preference for sites with available protein (see Appendix A for documented code).

While there most certainly were many additional costs associated with keeping and potentially breeding turkey beyond merely feeding them, only one other cost is implemented here. In this implementation, agents are required to provide a year’s worth of water for each of their turkeys; this requirement is a parameter in the simulation in order to systematically assess its impact. When the parameter TURKEY_WATER is set to true, agents not only have to spend calories meeting this requirement, but account for turkeys’ water needs when relocating the household (via greater household water need accounting for imaginary turkeys). As we shall see in the discussion, though, these watering costs have very little effect on agent success.

Assumptions of the Turkey Use Model

Any model attempting to explain processes in the real world necessarily makes simplifying
assumptions; this is done both to improve tractability of models of highly complex systems (such as the Village simulation), and to estimate values that have not yet been empirically verified.

This implementation of turkey domestication contains simplifying assumptions of both types. The model vastly oversimplifies the situation in the Southwest and creates a strictly economic model of turkey domestication. Here, I describe and defend key simplifying assumptions in the parameter settings, how turkey are acquired, and how turkey are killed. I also address a potential critique of this implementation, i.e., that the same results could be reached through simply increasing maize needs for all agents, and reducing or eliminating protein needs.

<table>
<thead>
<tr>
<th>Parameter Name</th>
<th>Value(s)</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>BASE_CAL_TURKEY</td>
<td>292000</td>
<td>Annual turkey caloric need, in kilocalories. This is based on numerous assumptions, since the diet of wild turkeys is not well documented. I take the average daily dietary need of turkey to be 8 oz of food (Hurst 1992; Lyle 2004). Using the MAIZE_KG_CAL conversion factor of 3560 kcal/kg I arrive at a daily caloric need of turkey of ~ 800 Cal maize.</td>
</tr>
<tr>
<td>TURKEY_WATER_NEED</td>
<td>0.454</td>
<td>Amount of water, in kg, per day needed by a single turkey. This is calculated at 2x the amount of food, by weight, needed per day. Turkey water consumption appears to be very poorly recorded. This number comes from a professional turkey hatchery (<a href="http://www.millerhatcheries.com/Information/Turkeys/turkey_rearing.htm">www.millerhatcheries.com/Information/Turkeys/turkey_rearing.htm</a>)</td>
</tr>
</tbody>
</table>

Key parameter settings used in the implementation discussed here are given in Tables 5.2 and 5.3. Parameters selected to be constants match those of the best-fit run completed for the final VEP I volume, Run 230 (Kohler et al. 2011); HUNT_SRADIUS [20, 40] and PROTEIN_NEED [5,15] are swept over. The only other difference is that agents are able to get water from rivers and springs only, as opposed to runs where agents can get water from more ephemeral sources as

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11 To sweep over a set of parameters means to perform runs of a simulation using every possible combination of the various predefined parameter values.
well. This creates a slightly more restricted water resource distribution in order to accentuate the impact of having to water turkeys.

A primary parameter assumption is the percentage of turkey diet expected to come from human-provided maize resources (TURKEY_MAIZE_PER); here, I sweep over two values, 50 and 70. In actuality, proportion of maize in turkey diet can be expected to have been far more variable. Turkeys are local foragers, and habitually return to a single spot to roost. It is therefore probable that, given access to the appropriate turkey habitat, Pueblo turkey farmers might have ‘put their birds to pasture.’ People living far from natural turkey foraging patches, however—such as those living on the Great Sage Plain—would have had to provide proportionally more food to their birds. Thus, a more satisfactory implementation of turkey domestication would allow for turkey foraging where possible. This implementation is not that complex; in any given run, all agents are expected to provide the same proportion of maize to their turkeys. The higher percentage (70) was chosen to mirror maize requirements of the agents in the Village simulation; turkey kept at late Pueblo III sites in the Northern San Juan have been found to have been consuming a maize diet similar to that of their keepers (Rawlings and Driver 2010:2439). Indeed, Rawlings and Driver (2010:2440) conclude that turkey were likely not allowed to forage for themselves, due to the low amounts of animal (insect) protein and exceptionally high amounts of maize when compared to other other fauna.

Static parameters in this implementation include the average amount of protein available in an adult turkey, the base annual caloric need for turkey, and the base daily water need of turkey. The U.S. Department of Agriculture estimates 30 g protein in 100 g wild turkey meat, or 1238 g protein in a 13-lb turkey (www.nal.usda.gov). I take all turkeys to be 13 lbs, the mean of adult
hens and gobblers. Although these figures are derived from modern wild turkey breeds, there is little evidence that ancient breeds deviated significantly from this norm. However, McKusick (1986) consistently differentiates between the ‘Small Indian Domesticate’ and the ‘Large Indian Domesticate’ in archaeological contexts in the Southwest. McKusick believes that the larger was bred for eating. These two breeds do significantly differ in size, yet weight estimates of the birds have not, to my knowledge, been proffered. McKusick’s distinction is an important consideration, however, as a larger or smaller bird will yield different return rates for keeping turkey. Although I only deal with one size in this analysis, it would be prudent to test the model’s sensitivity to other bird sizes.

The base caloric and water needs of an adult wild turkey are far more elusive. Wild turkeys have an impressive diet breadth making it hard to estimate daily caloric intake or expenditure. Turkey diet varies by age, sex, season, and availability of food (Hurst 1992). Wild turkey crops (part of the avian digestive system) are highly expandable, however, and can store 8 to 16 ounces of food (Hurst 1992). Schorger (1966:200) notes that when three-quarters of a turkey’s diet is comprised of acorns, half a pound of acorns per bird per day is sufficient. In contrast, modern domestic turkeys are only fed 0.03 lbs, or 13.6 g, of high-nutrient food. Here, I take daily food needs to be 8 ounces. This number is within the range reported by Schorger and others, and is aligned with an estimate used in an unpublished model of turkey domestication requirements at Sand Canyon Pueblo in southwestern Colorado (Lyle 2004). Eight ounces of food converts to a daily caloric need of approximately 800 Cal, using the conversion factor for maize of 3560 kcal/kg. Although I assume all turkeys’ needs come from maize in this conversion, this assumption is tempered by the TURKEY_MAIZE_PER parameter.
The water need of turkey is an even more elusive quantity in the wildlife management literature. While turkeys certainly need drinking water, the amount they require depends on the water content of their food, the season (including temperature and humidity), and behavior. Here, I implement a daily water intake of 0.454 kg of water per day per bird, which is double their dry food intake. This is in line with modern turkey domestication practices where turkeys are fed dry meal (http://www.millerhatcheries.com/Information/Turkeys/turkey_rearing.htm). All of these parameters, which I argue are sufficient for the present cause, are easily adjusted in the simulation code via a parameter class.

A critical simplifying assumption of this implementation is the costless and instantaneous (and, thus, effortless!) acquisition of turkey by agents in the simulation. If agents determine that they would be better off keeping turkey, they are able to keep them. A more satisfying implementation might place ‘wild’ turkeys on the landscape, at differing densities depending on the habitat, and allow agents to either hunt or capture them for initial domestication, or to trade with their neighbors for already domestic turkey. As I stated in the introduction, however, this model is interested in testing the economic feasibility of using turkey to convert maize to protein, and to ascertain whether such a conversion improves the fidelity of the simulation to the archaeological record. While acquisition costs might have been substantial, they are not considered here. There are really two assumptions at play here: 1) Turkey were domesticated, or at least held at some sites, by the Pueblo I period, and 2) This made obtaining turkey quite a low-cost activity. As I reported in the introduction, evidence supporting the first assumption is substantial. By Basketmaker III at the latest, Pueblo peoples had the technology necessary to house turkey, and were already using them for ritual purposes. This may not have been too
considerable a feat in any case. Turkeys are naturally social, inquisitive, noisy, messy birds, and have very little instinctual fear of humans. Field workers in the Wetherill Mesa Archaeological Project relate the sometimes-daunting and often-hilarious task of dealing with flocks of wild turkeys, noting that they moved into residential areas of the park, preferring the human-built environment over the ‘natural’ one (Pinkley 1965). Pinkley asserts that the birds were such a nuisance, and so destructive, that Ancestral Pueblos met with the same avian army would be practically required to domesticate them:

The birds, once established, could not be driven off. Arrogant, cantankerous bullies, they were in the villages to stay. There was nothing left for the Indians to do but to corral them at night and herd them during the day. They had to be kept out of the fields and away from choice stands of grasses and other plants, out of the fine berry patches and away from the heaviest nut crops and, lastly, out of the villages most of the time, if the women were to prepare meals in peace and the living areas were to be kept even partially free of manure. Knowing how these birds take full advantage of man, how impossible it is to discourage their depredations, how rapidly they can drive people to distraction, I marvel how the Indians did not systematically kill them off before they realized to what use their feathers and later their flesh and bones could be put. My sympathies lie with the Indians; they were truly exploited [Pinkley 1965:72].

While Pinkley’s narrative may have been written tongue-in-cheek, there is certainly some truth to it. Unless wild birds were behaviorally very different two millennia ago, it was likely the maintenance, and not the acquisition, of turkey that was the most costly.

A third simplifying assumption I make is that this implementation requires agents to provide a full year’s-worth of food for each of their birds. Agents consume their annual protein needs, and any remaining protein goes into storage, where it is subject to a degradation adjustment. This assumption is mirrored by that already implemented for hunting; people only attempt to obtain protein once a year, during the summer. This is done for both computational expediency and tractability. The realistic assumption is, of course, that hunting, and the killing and butchering of
domestic turkey, would have been a year-round, or at least multi-season activity. Over the
duration of a household, these activities are expected to average out annually. A larger problem is
the lack of consideration of poult care and other aspects of turkey breeding. Including this may
be a fruitful extension of this model, though it is not one I undertake here.

Finally, one might appropriately ask the question, “If you are just allowing agents to convert
maize to protein, why not get rid of the protein requirement altogether and just raise the maize
requirements?” My interest is in the transition from hunting to domestication, both when it
occurs and on what parts of the landscape. Exploring this transition requires agents to have the
ability to switch between these two strategies as each becomes beneficial. It is far less expensive,
when wild game is readily available, for agents (and, presumably, for people in the past) to
acquire protein through hunting. That agents in less protein-rich areas of the landscape, or on the
landscape as a whole should deer become depleted, have the option to switch to a less costly
alternative to hunting (and back, should local conditions improve) is the central design element
in the model. Under various parameter combinations, this model generates testable expectations
for the archaeological record, including the distribution of faunal remains, and the differential
timing of turkey consumption across the landscape. While the comparisons discussed in the next
section only seek to test this model using coarse demographic variables, it is designed to be
tested against a diverse set of archaeological patterns.

**Results and Discussion: When Does it Pay to Invest in Turkey?**

The VEP simulation was designed from the outset to produce output that could be compared
with various aspects of the archaeological record—specifically, population size and distribution.
We adhere to what Grimm and Railsback (2005) term Pattern-Oriented Modeling: designing and
implementing models precisely to be compared with observed patterns in the system being modeled. If for example we wish to generate a simulation of the spread of a viral infection through a population, we might consider system-level patterns such as the rate of infection among different segments of the population, which in turn might be a function of the density of the population and degree of interaction between individuals. We might also be interested in individual-level patterns: How does infection differentially impact individuals, and how does that affect their interaction with others? Are there certain behaviors that reduce virulence, such as avoiding others or washing your hands? Each of these patterns of systemic and individual behavior are patterns that can be reasonably described, but that by themselves are probably inadequate at describing the system as a whole. Models may be designed that produce patterns visible in the reference system, which thus allow the model to be tested against observations along multiple lines of evidence. Grimm and Railsback (2005: 41) note “[a] combination of several seemingly ‘weak’ patterns can be more powerful for [developing] good model designs.” They go on to argue for the incorporation of patterns from multiple scales—systemic, individual, and intermediate—in order to generate robust models.

Archaeologists deal in patterns. Although our strongest patterns often occur in the aggregate (site location, population size, assemblage composition, and so on), we have become very adept at identifying patterns of even individual activity. Where we have often failed, however, is in linking these patterns, especially across multiple scales (cf. Muir and Driver 2002). Pattern-oriented modeling using agent-based simulation is just the tool to help us overcome these challenges. Agent-based simulation is at its core based on the principle that higher-level patterns emerge from the complex interactions among patterned individuals. This is one way in which
Model-based Archaeology (Kohler and van der Leeuw 2007) can be pursued. The task of the modeling archaeologist is to generate models that reproduce archaeologically knowable patterns and assess the relative goodness-of-fit between the simulated and archaeological patterns.

Analysis of output from the VEP simulation has focused on the goodness-of-fit along two system-scale patterns across time: population size and site location (Varien et al. 2007; Kohler et al. 2011). Additional correlations have occasionally been noted, as for the case of the temporal correlation between deer depletion in the simulation and the transition to turkey as a protein resource in the archaeological record (Bocinsky et al. 2011). In this analysis, I broaden the scope of patterns that may be compared between the virtual and observed records, while generally remaining at a systems-level scale of analysis. I begin by looking at demographic impacts of turkey domestication in the simulation, and assess goodness-of-fit using both population size and rate of change. I then look at the impacts of domestication on spatial distribution, and compute a corrected measure of correlation between simulated and real site locations across time. I also estimate the degree to which different parameters are contributing to high correlation. Finally, I briefly touch on the location and adoption rate of turkey domestication under various parameter settings, and compare these to recent archaeological data from the Colorado Plateau.
**Table 5.4.** Runs reported in this sweep, with figure key.

<table>
<thead>
<tr>
<th>Run</th>
<th>DOMESTICATION</th>
<th>HUNT_RADIUS</th>
<th>PROTEIN_NEED</th>
<th>TURKEY_WATER</th>
<th>TURKEY_MAIZE_PER</th>
<th>Style in Figures</th>
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**Demographic impacts**

Two data streams output from the Village simulation are of specific interest here: population size and ‘site’ (household) distribution. The population trajectories for each of the 20 runs reported here are shown in Figure 5.1 (see Table 5.4 for parameter settings). All dates are A.D. The grey boxes represent high, medium, and low population estimates for each of the 14 modeling periods (I prefer the middle approximation; see Varien et al. 2007 for a description of how these estimates were constructed). The runs lacking domestication (1, 2, 3, and 4) clearly display high and low trajectories, primarily corresponding to the hunting radius, and secondarily to the protein need. Populations in runs with the smaller radius (runs 1 and 2) are able to maintain a long, steady growth before depleting their resources in the 1100s; agents in runs with the larger search radius (runs 3 and 4) deplete non-local fauna rapidly (by 900) and decline.
slightly through the rest of the simulation.

Figure 5.1. Simulated versus estimated populations. Population estimates follow those presented in Varien et al. (2007). Run parameters given in Table 5.4.
Runs where agents are able to keep turkey should hunting become too costly show a variety of trajectories previously unrecorded for the Village simulation. Domestication runs with large search radii and high protein need (runs 11, 12, 19, and 20; the gold runs in Figure 5.1) peak very early (by 850), and decline throughout the remainder of the simulation. In these runs, hunted protein gets depleted very rapidly (and remains depleted) and keeping enough turkey to meet the high protein need is unsustainable, especially in light of declining agricultural productivity in the region during the late 800s (Varien et al. 2007). Curiously, these are the first runs reported for the Village simulation that match the declining post-Pueblo I population estimates into the mid-900s. This might suggest that local Pueblo I peoples had some mechanism for supplementing their protein by increasing investment in agriculture, though not necessarily turkey domestication. The more rapid population slide during the late 800s (than that in runs 3 and 4) reflects this greater dependence on agriculture, and greater costs for continuing to try to hunt at the larger radius, even though there is no deer to be found. Agents in domestication runs with low hunting radii and high protein need (runs 7, 8, 15, and 16; the red runs in Figure 5.1) are slightly more successful; because of their small search radius, their hunting costs are significantly lower than those of the gold runs. This consistent upward trajectory is also a novel signal for the village simulation, enabled by domestication. Agents in domestication runs with a low hunting radius and low protein need (runs 5, 6, 13, and 14; the blue runs in Figure 5.1) are highly successful, and their population trajectories are only slightly lower than those of the same parameters without domestication. Agents maintain a balance between domestication and hunting throughout the simulation, leading to not-as-dramatic increases during good years, but also not-as-precipitous declines during bad ones. Domestication runs with a large hunt radius but small
protein need (runs 9, 10, 17, and 18; the green runs in Figure 5.1) are the most difficult to interpret, as this is the only group of runs that dramatically splits due to the amount of maize agents are required to feed turkey. When this amount is at a high level, the agent population declines dramatically after 900. In runs with a lower maize investment in turkey, populations are able to persist at high levels. This pattern is probably due to the lower return rate on investment in turkey when the cost of domestication is high, as well as the larger search radius. Agents with higher domestication costs are slower to switch to domestication when hunting becomes difficult. Agents in the lower domestication investment runs deplete deer just as quickly, but they are able to switch over to domestication if their hunting costs get too high.

One pattern we can address with these population data concerns how closely the runs track the population estimates. Figure 5.2 and Table 5.5 give the absolute deviation from estimated populations for each of the 14 modeling periods. I averaged across the populations from each year in a given period of a run, then took the absolute difference between this value and the middle population estimate from Varien et al. (2007). In Table 5.5, best-fit runs—runs that have the lowest absolute deviation from the estimates—are given in bold for each period. Those runs are also listed in Table 5.6, along with their parameter values.
Figure 5.2. Absolute population deviation from estimated. Runs with values closer to zero (top, as presented) are best-fitting. Run parameters given in Table 5.4.
| Period | Run 1 | Run 2 | Run 3 | Run 4 | Run 5 | Run 6 | Run 7 | Run 8 | Run 9 | Run 10 | Run 11 | Run 12 | Run 13 | Run 14 | Run 15 | Run 16 | Run 17 | Run 18 | Run 19 | Run 20 |
|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 6      | 18    | 25    | 35    | 38    | 41    | 39    | 25    | 38    | 27    | 12    | 38    | 40    | 26    | 19    | 32    | 38    | 26    | 11    | 39    |
| 7      | 513   | 467   | 401   | 454   | 407   | 306   | 289   | 454   | 503   | 459   | 451   | 454   | 530   | 441   | 367   | 448   | 541   | 546   | 436   |
| 8      | 520   | 503   | 319   | 195   | 417   | 333   | 129   | 39    | 432   | 511   | 345   | 332   | 464   | 508   | 290   | 141   | 502   | 594   | 461   | 275   |
| 9      | 698   | 792   | 381   | 301   | 609   | 471   | 114   | 9     | 681   | 676   | 106   | 8     | 591   | 641   | 177   | 14    | 682   | 739   | 67    | 22    |
| 10     | 1830  | 1926  | 1274  | 1047  | 1637  | 1471  | 893   | 730   | 1760  | 1471  | 503   | 425   | 1626  | 1646  | 909   | 707   | 1677  | 1510  | 457   | 440   |
| 11     | 2381  | 2371  | 1309  | 992   | 2131  | 2015  | 926   | 780   | 2269  | 1200  | 325   | 300   | 2024  | 2058  | 1032  | 843   | 2138  | 1187  | 336   | 239   |
| 12     | 2697  | 2438  | 842   | 597   | 2267  | 2204  | 690   | 470   | 2448  | 733   | 167   | 152   | 2097  | 2241  | 795   | 649   | 2349  | 659   | 72    | 234   |
| 13     | 3141  | 2733  | 599   | 464   | 2417  | 2274  | 769   | 466   | 2612  | 605   | 264   | 247   | 2291  | 2448  | 757   | 711   | 2469  | 514   | 223   | 321   |
| 14     | 2914  | 2331  | 239   | 258   | 1991  | 1891  | 303   | 83    | 2140  | 189   | 1005  | 1035  | 1948  | 2165  | 82    | 142   | 2026  | 340   | 975   | 1044  |
| 15     | 2686  | 1761  | 799   | 845   | 1654  | 1489  | 28    | 416   | 1743  | 773   | 1590  | 1611  | 1711  | 1850  | 374   | 362   | 1770  | 938   | 1541  | 1610  |
| 16     | 2093  | 1189  | 904   | 992   | 1371  | 1224  | 106   | 458   | 1274  | 870   | 1731  | 1755  | 1391  | 1541  | 503   | 434   | 1444  | 1014  | 1708  | 1755  |
| 17     | 1656  | 807   | 1161  | 1226  | 1083  | 781   | 208   | 632   | 975   | 1140  | 1918  | 2001  | 1112  | 1182  | 728   | 557   | 1189  | 1180  | 1943  | 2029  |
| 18     | 323   | 207   | 2034  | 2128  | 93    | 190   | 887   | 1314  | 41    | 2040  | 2739  | 2828  | 194   | 53    | 1524  | 1200  | 1917  | 2782  | 2840  |
| 19     | 2204  | 1917  | 137   | 88    | 2177  | 1941  | 1490  | 994   | 2044  | 161   | 564   | 605   | 2343  | 1983  | 757   | 1181  | 1932  | 329   | 570   | 614   |
Two trends are immediately noticeable from Figure 5.2 and Table 5.6: 1) Gold runs have low deviation from estimates through period 13, and red runs thereafter (until period 18), and 2) the best-fit runs are almost always runs with domestication. The first pattern can be described as a shift from a large hunting radius to a lower one around year 1060. The gold runs track the Pueblo I population dynamics very closely, while the red runs capture the population increases until the very last periods of occupation. None consistently perform well throughout the simulation.

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A second means of testing goodness-of-fit with demographic data is by assessing how trends in the population estimates are matched by the simulated runs. These runs of the simulation represent time series, and are thus historically contingent. Conditions in the simulation may not favor a particular run at certain points (by ‘favor,’ I mean generate simulated populations similar to those in the record), then switch to be more favorable to that run later on. This can happen since, in the simulations, agents have static decision-making algorithms; peoples’ actions in the past were of course dynamic. Here, I first calculate the point-slope between successive period-midpoints of the intermediate estimated population values, and compare those to slopes in the
simulated runs. For example, the midpoint of period 6 is the year 667, and the midpoint of period 7 is 762. To get the estimated slope, I take the intermediate population estimate at year 662, and subtract it from the intermediate estimate for year 762; I then divide this by the intermediate period length of 95 years. I call years 667-762 period 6.5. For the simulated runs, I calculate a linear regression over households by year for each intermediate period. I then take the absolute deviation of the simulated slope from the estimated slope for each intermediate period. These deviations are given in Figure 5.3 and Table 5.7, and the best-fit-runs are described in Table 5.8.
Figure 5.3. Absolute slope deviation from estimated.
Runs with values closer to zero (top, as presented) are best-fitting. Simulated slopes represent a linear regression over households by year for each period. Run parameters given in Table 5.4.
### Table 5.7. Cross-tabulated slope deviations from estimates, by period.

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Several patterns in these slope deviations are immediately obvious (Table 5.8). Runs with the smaller radius for hunting dominate the list of best-fit runs, as do runs where turkey domestication is enabled. These two factors likely build off each-other. In runs where the hunting radius is lower (and particularly where protein need is high), agents more readily switch to domestication; this in turn makes more of their subsistence dependent on agricultural yields and thus shifts in maize productivity. A similar feedback process may have occurred in the Pueblo past, as I argued in Chapter 3.

Table 5.8. Best-fit runs from slope deviation analysis.

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Some general observations may be gleaned from these demographic patterns. Domestication generally improves demographic goodness-of-fit between the simulated runs and the observed data. This is likely caused by increased sensitivity to climate signals due to the greater dependence on maize upon the adoption of turkey use. In runs without domestication, once protein sources have been significantly depleted agent populations cease to readily respond to fluctuations in faunal availability, and most agents will suffer a reproductive penalty regardless of climate fluctuations; in runs with domestication, these protein penalties are avoided, and populations respond directly to maize productivity changes. However, none of the runs capture
the significant population decline at the end of occupation in the region, even though some runs
capture population declines elsewhere. Also notable is the negative relationship between the
other parameters controlling protein procurement (HUNT_SRADIUS and PROTEIN_NEED)
and the trajectories of domestication runs. These deserve further testing over a broader range of
parameter values, such as intermediate hunting radii and protein needs, to see if these yield
intermediate patterns.

Distribution impacts

This analysis closely emulates an analysis for the broader VEP dataset undertaken by Kohler
and colleagues (2011), using techniques described elsewhere. First, I calculate the Pearson
product-moment correlation coefficient between simulated site locations in each run and the
observed site locations for the region by period. This calculation treats each run as an
‘observation,’ with each cell on the landscape considered a ‘variable.’ Because observed site
locations are highly local, and because people in the past may have been acting in such a way
that they only seek to meet their needs (satisficing, as opposed to maximizing their returns), I use
a slightly smoothed observed dataset (Kohler et al. 2011); this is done using a uniform smoothing
within a 3-by-3 cell window, which accounts for some variation in site location. Areas of the
landscape which lack sites and for which there has been no systematic survey are omitted from
the analysis.

Such an analysis is inherently subject to one known bias; if a run has more agents, it has a
somewhat higher probability that some of those agents will be located in cells with known sites.
To correct for this, I compute a null run by averaging over the correlations between 100
randomized replicates of each run and the observed data (this is done by literally shuffling the
cells). I then subtract this null average from the simulated correlation to arrive at the corrected correlation coefficients for each period, by run. Figure 5.4 and Table 5.9 give the corrected correlation coefficients for each run, and Table 5.10 presents the best-fit run per period, and its parameter values.
Figure 5.4. Corrected correlation coefficients between real and simulated site locations. Thickest lines indicate best-fit runs; intermediate thickness indicates second-best fit. Notice that non-domestication runs (black) perform best only prior to period 12. Run parameters given in Table 5.4.
Table 5.9. Cross-tabulated spatial correlation coefficients, by period.

| Period | Run 1 | Run 2 | Run 3 | Run 4 | Run 5 | Run 6 | Run 7 | Run 8 | Run 9 | Run 10 | Run 11 | Run 12 | Run 13 | Run 14 | Run 15 | Run 16 | Run 17 | Run 18 | Run 19 | Run 20 |
|--------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 6      | -0.007 | -0.004 | -0.003 | -0.012 | -0.006 | -0.007 | 0.000  | -0.007 | -0.006 | 0.004  | 0.003  | -0.026 | -0.006 | -0.009 | -0.016 | -0.019 | -0.006 | **0.004** | -0.001 | -0.015 |
| 7      | -0.007 | -0.003 | -0.016 | 0.014  | 0.007  | 0.004  | 0.004  | -0.003 | 0.003  | **0.052** | 0.028  | 0.000  | 0.027  | -0.013 | 0.004  | -0.001 | -0.013 | 0.047  | 0.008  | 0.016  |
| 8      | 0.023  | 0.018  | 0.029  | 0.018  | 0.004  | 0.026  | 0.025  | 0.018  | **0.031** | 0.014  | -0.005 | -0.005 | 0.016  | 0.014  | 0.028  | 0.006  | 0.012  | 0.004  | 0.005  | 0.017  |
| 9      | 0.023  | 0.030  | **0.043** | 0.008  | 0.015  | 0.019  | 0.001  | 0.009  | 0.024  | 0.008  | 0.018  | 0.005  | -0.002 | 0.004  | 0.008  | 0.003  | 0.011  | -0.002 | 0.006  | 0.009  |
| 10     | **0.043** | 0.029  | 0.026  | 0.014  | 0.022  | 0.012  | -0.001 | 0.006  | 0.039  | 0.010  | 0.019  | 0.022  | 0.026  | 0.023  | 0.026  | 0.013  | 0.005  | 0.011  | 0.014  | 0.025  |
| 11     | 0.029  | 0.035  | 0.030  | 0.055  | **0.055** | 0.028  | -0.006 | -0.012 | -0.001 | 0.023  | 0.013  | 0.048  | 0.005  | 0.042  | 0.045  | 0.001  | 0.024  | 0.021  | -0.004 | 0.024  |
| 12     | **0.102** | 0.065  | 0.052  | 0.039  | 0.055  | 0.069  | 0.034  | 0.020  | 0.045  | 0.026  | -0.005 | -0.001 | 0.064  | 0.049  | 0.049  | 0.019  | 0.053  | 0.050  | 0.000  | 0.002  |
| 13     | 0.073  | 0.054  | 0.013  | 0.011  | **0.089** | 0.047  | 0.025  | 0.023  | 0.070  | 0.021  | -0.013 | -0.001 | 0.029  | 0.072  | 0.023  | 0.067  | 0.087  | 0.029  | -0.015 | -0.001 |
| 14     | 0.060  | 0.030  | 0.043  | -0.007 | 0.089  | 0.035  | 0.020  | 0.012  | 0.059  | 0.006  | 0.004  | -0.000 | 0.106  | 0.043  | 0.005  | **0.112** | 0.101 | 0.029  | -0.004 | -0.007 |
| 15     | 0.068  | 0.038  | 0.013  | 0.002  | 0.064  | 0.059  | -0.003 | -0.006 | 0.081  | -0.007 | -0.000 | -0.003 | 0.068  | 0.045  | 0.003  | 0.033  | 0.054  | 0.003  | -0.005 | -0.001 |
| 16     | 0.023  | 0.058  | 0.004  | -0.006 | 0.058  | 0.047  | 0.008  | 0.001  | 0.033  | 0.006  | 0.008  | 0.005  | 0.051  | **0.084** | 0.005  | 0.019  | 0.038  | 0.013  | 0.001  | -0.002 |
| 17     | 0.043  | 0.032  | -0.007 | -0.006 | 0.061  | 0.031  | 0.011  | 0.017  | 0.016  | -0.000 | -0.001 | 0.005  | 0.039  | **0.077** | 0.012  | 0.010  | 0.024  | 0.007  | 0.001  | -0.007 |
| 18     | 0.021  | 0.010  | 0.000  | -0.008 | 0.018  | -0.003 | 0.007  | -0.007 | -0.004 | -0.007 | 0.013  | -0.006 | 0.014  | **0.049** | -0.003 | -0.002 | -0.005 | -0.008 | 0.000  | -0.006 |
| 19     | 0.016  | -0.001 | -0.009 | -0.008 | 0.004  | -0.006 | -0.002 | 0.000  | -0.008 | 0.001  | -0.014 | -0.001 | -0.008 | -0.001  | -0.018 | -0.012 | 0.001  | -0.005 | -0.006 |
One of the most striking trends in the patterns observable in this spatial analysis is the transition from a generally good fit among runs without domestication prior to period 12 to the dominance of domestication in goodness-of-fit during later periods. As in the slope deviation analysis, many of the best runs are characterized by the smaller hunt radius value, but unlike the other analyses, spatial correlation suggests a better fit between the observed data and runs with the lower protein need. I take this to be suggestive that protein resources generally did not weigh highly into peoples’ decisions on where to live. This somewhat contradicts findings by Kohler and colleagues (2011), who find that higher values for protein need, and especially the imposition of a mandate for the availability of protein when relocating, improve fit substantially. While I do not implement that mandate (NEED_MEAT=1) here, I do note that our analyses differ substantially, in that the analysis of the larger dataset did not include a correction for population size when assessing importance of various parameters.

Another interesting observation is that during the periods of good fit between non-domestication runs and the observed site location (periods 9-12), historic populations were emigrating from the landscape, and populations remained low through these periods (Varien et al. 2007:289). Households also disaggregate on the landscape, beginning in the late 800s, as evidenced by lower numbers of households in community centers (Varien et al. 2007:285). That these periods correlate with a modeled lack of domestication is interesting in that it suggests domestication practices thrive within higher-density populations, and in fact may only be sustainable when high amounts of labor are being dedicated to both maize agriculture and turkey keeping. Of course, the game-depression effects of high density populations may also make a strategy such as turkey domestication more attractive.
We can better gauge the relative importance of each parameter setting in generating a spatial goodness-of-fit by describing the relationship between each parameter and the corrected correlation coefficients by period. To do so, I use multiple linear regression between parameters and corrected correlation coefficients. Each corrected correlation coefficient acts as an observation (yielding 280 observations, one for each combination of the 14 periods and 20 runs), which is associated with a parameter set. Next, I fit an unweighted generalized linear model with a gaussian error distribution to the dataset, treating the corrected correlation coefficients as the response variable, and the parameters as the linear predictors. I discard the two parameters that are only associated with domestication, for these will have no relationship with correlations for the non-domestication runs. This produces regression coefficients for each parameter that describe the direction and strength of the relationship between that parameter and the corrected correlation coefficients. Figure 5.5 presents each parameter’s contribution to the corrected site location correlation. Positive values indicate the importance of the upper or boolean ‘true’ parameter state (for instance, HUNT_SRADIUS[40] or DOMESTICATION[true]); negative

<table>
<thead>
<tr>
<th>Period</th>
<th>Best Fit Run</th>
<th>DOMESTICATION</th>
<th>HUNT_SRADIUS</th>
<th>PROTEIN_NEED</th>
<th>TURKEY_WATER</th>
<th>TURKEY_MAIZE_PER</th>
</tr>
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<td>40</td>
<td>5</td>
<td>FALSE</td>
<td>0.7</td>
</tr>
<tr>
<td>8</td>
<td>9</td>
<td>TRUE</td>
<td>40</td>
<td>5</td>
<td>FALSE</td>
<td>0.5</td>
</tr>
<tr>
<td>9</td>
<td>3</td>
<td>FALSE</td>
<td>40</td>
<td>5</td>
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<td>-</td>
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<tr>
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</tr>
<tr>
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<td>20</td>
<td>5</td>
<td>-</td>
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<tr>
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<td>5</td>
<td>TRUE</td>
<td>20</td>
<td>5</td>
<td>FALSE</td>
<td>0.5</td>
</tr>
<tr>
<td>14</td>
<td>16</td>
<td>TRUE</td>
<td>20</td>
<td>15</td>
<td>TRUE</td>
<td>0.7</td>
</tr>
<tr>
<td>15</td>
<td>9</td>
<td>TRUE</td>
<td>40</td>
<td>5</td>
<td>FALSE</td>
<td>0.5</td>
</tr>
<tr>
<td>16</td>
<td>14</td>
<td>TRUE</td>
<td>20</td>
<td>5</td>
<td>TRUE</td>
<td>0.7</td>
</tr>
<tr>
<td>17</td>
<td>14</td>
<td>TRUE</td>
<td>20</td>
<td>5</td>
<td>TRUE</td>
<td>0.7</td>
</tr>
<tr>
<td>18</td>
<td>14</td>
<td>TRUE</td>
<td>20</td>
<td>5</td>
<td>TRUE</td>
<td>0.7</td>
</tr>
<tr>
<td>19</td>
<td>16</td>
<td>TRUE</td>
<td>20</td>
<td>15</td>
<td>TRUE</td>
<td>0.7</td>
</tr>
</tbody>
</table>
values indicate the strength of the lower or boolean ‘false’ values. Table 5.11 gives the numeric regression coefficients, and their significance values. Note that due to small sample size, many of the regression coefficients are not significant. Kohler and colleagues (2011) performed repeated runs using identical parameter settings but different random number seeds to test the sensitivity of the simulations to random variation, and found that these runs produced highly similar results. Thus, while replicating these runs over several random number seeds would likely increase their statistical significance, their relative trends can be expected to remain similar to the runs reported here.

### Table 5.11. Parameter contribution to site location correlation, with significance values. Values with $p<0.05$ given in bold.

<table>
<thead>
<tr>
<th>Period</th>
<th>DOMESTICATION</th>
<th>PROTEIN NEED</th>
<th>HUNT_SRADIUS</th>
</tr>
</thead>
<tbody>
<tr>
<td>6</td>
<td>-0.003</td>
<td>-0.007</td>
<td>0.002</td>
</tr>
<tr>
<td></td>
<td>0.462</td>
<td>0.124</td>
<td>0.678</td>
</tr>
<tr>
<td>7</td>
<td>0.011</td>
<td>0.002</td>
<td>0.015</td>
</tr>
<tr>
<td></td>
<td>0.341</td>
<td>0.817</td>
<td>0.207</td>
</tr>
<tr>
<td>8</td>
<td>-0.008</td>
<td>-0.002</td>
<td>0.001</td>
</tr>
<tr>
<td></td>
<td>0.071</td>
<td>0.606</td>
<td>0.771</td>
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<tr>
<td>9</td>
<td>-0.016</td>
<td>-0.003</td>
<td>0.001</td>
</tr>
<tr>
<td></td>
<td>0.068</td>
<td>0.655</td>
<td>0.938</td>
</tr>
<tr>
<td>10</td>
<td>-0.007</td>
<td>-0.004</td>
<td>-0.006</td>
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<tr>
<td></td>
<td>0.227</td>
<td>0.458</td>
<td>0.298</td>
</tr>
<tr>
<td>11</td>
<td>-0.011</td>
<td>-0.001</td>
<td>0.004</td>
</tr>
<tr>
<td></td>
<td>0.279</td>
<td>0.878</td>
<td>0.649</td>
</tr>
<tr>
<td>12</td>
<td>-0.024</td>
<td>-0.023</td>
<td>-0.016</td>
</tr>
<tr>
<td></td>
<td>0.026</td>
<td>0.031</td>
<td>0.081</td>
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<tr>
<td>13</td>
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<td>-0.010</td>
<td><strong>-0.038</strong></td>
</tr>
<tr>
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<td>0.485</td>
<td>0.066</td>
<td>0.001</td>
</tr>
<tr>
<td>14</td>
<td>0.009</td>
<td>-0.008</td>
<td>-0.033</td>
</tr>
<tr>
<td></td>
<td>0.647</td>
<td>0.676</td>
<td>0.142</td>
</tr>
<tr>
<td>15</td>
<td>-0.007</td>
<td>-0.010</td>
<td><strong>-0.030</strong></td>
</tr>
<tr>
<td></td>
<td>0.120</td>
<td>0.053</td>
<td>0.001</td>
</tr>
<tr>
<td>16</td>
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<td>-0.010</td>
<td>-0.031</td>
</tr>
<tr>
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<td>0.662</td>
<td>0.485</td>
<td>0.069</td>
</tr>
<tr>
<td>17</td>
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<td>-0.016</td>
<td><strong>-0.031</strong></td>
</tr>
<tr>
<td></td>
<td>0.656</td>
<td>0.155</td>
<td>0.028</td>
</tr>
<tr>
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<td>-0.018</td>
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<tr>
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<td>0.873</td>
<td>0.161</td>
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<tr>
<td>19</td>
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<td>-0.001</td>
<td>-0.009</td>
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<td>0.633</td>
<td>0.867</td>
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</table>
Figure 5.5. Parameter contribution to site location correlation, as given by regression coefficients. Positive values represent importance of upper parameter states (boolean “true”); negative values represent lower states. Significance values given in Table 5.11.
Prior to period 11, most parameters display a weak relationship with high correlation between the real and simulated site distributions, though periods 8-11 show a preference against domestication with a stronger preference in period 12. From periods 13-17, however, well-fit runs have a strong tendency towards domestication, a small hunting radius, and low protein need. The patterns for protein need and especially hunting radius are perhaps more illustrative than that of domestication. These parameters account for a significant amount of the variation in site distribution after period 13. Both have an inverse relationship with site distribution correlation. This perhaps indicates that hunted protein became less important to ancestral Pueblos during the second population boom in the region, beginning around A.D. 1050. The weak positive relationship between domestication and site distribution correlation after period 13 suggests a shift away from hunted protein towards domestic resources. That all three parameters approach zero during the last period suggests protein considerations contributed very little to where people chose to live towards the end of regional occupation. This agrees with Kuckelman’s (2010a, 2010b) finding that the inhabitants of Sand Canyon Pueblo shifted towards a more diverse diet (and away from turkey) during the final years of occupation there.

*Dietary impacts*

A final pattern I consider is the timing and location of widespread turkey keeping for protein. Research has suggested that high levels of turkey consumption did not occur in the Northern San Juan until the late eleventh century (Badenhorst and Driver 2009; Kuckelman 2010a; Muir and Driver 2002; Rawlings and Driver 2010), but rapidly grew compared to lagomorphs and artiodactyls in the faunal diet of people in the region. I assess the simulated timing of turkey protein consumption by graphing the average amount of protein from turkey grown by

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households in the simulation (Figure 5.6), then discuss the simulated timing of domestication on different parts of the landscape under various parameters settings (Figures 5.7 - 5.9).
Figure 5.6. Average proportion of protein from domestication.
Black lines are interpolated splines of runs presented, with the line pattern matching the runs for each color-cluster. Rate and timing of domestication is highly determined by hunting behavior. Run parameters given in Table 5.4.
The rate and timing of the adoption of turkey use in the Village simulation is heavily dependent on hunting behavior (Figure 5.6). The lower value for hunting radius readily generates local inability to meet household protein need, and thus forces agents to switch to the domestication strategy in these regions. Predictably, agents with higher protein need readily deplete these local protein resources, and populations in those runs (in red in Figure 5.6) more rapidly move towards domestication. Agents in all of the small-hunting-radius runs begin keeping turkey almost at simulation outset, and exhibit high percentages of turkey use (70 - 90 percent) by year 900. Populations in runs with the larger search radius have far lower domestication rates. In these runs, even small amounts of domestication do not begin to occur until the mid-1000s, and even then, average amounts of domestication do not rise above 10 percent, with the exception of extremely local spikes. Neither of these trends very accurately replicates the patterns noted in faunal assemblages in the region. The adoption of widespread turkey use is too early in the small hunting radius runs, and too late in the large search radius. There is a need to formally test a range of values for hunting radius between the two extremes noted here in order to see if one captures the timing of turkey use intensification more accurately.

Aggregate statistics, such as those presented in Figure 5.6 and most of the other analyses undertaken here, may betray the fact that agent actions vary widely in the simulation; in particular, agents act optimally in reference to their local physical and social landscape. Because this landscape varies spatially, so do agent actions. Turkey keeping is favored in areas with low natural deer productivity but high human populations due to high potential agricultural yield. We may thus profitably assess the location and spread of domestication practices across the Village.

12 This may be indirect, as hunting behavior also influences agent population size, which can drive deer depletion and thus invite turkey use.
landscape. I first offer a qualitative analysis of the spread of domestication in three runs (runs 1, 7, and 14), then suggest that estimates for the timing of domestication in the central Mesa Verde region have been biased because the estimates were based on sites with relatively good access to ‘huntable’ protein resources, where use of turkey as a protein resource would have been most delayed. I hypothesize that sites in the central Great Sage Plain will show significantly earlier evidence for intensified use of turkey.

Images of all of the runs presented here were taken at years 700, 800, 1000, and 1250. The images of years 700 and 1250 present real (white) and simulated (blue to red) households overlaying real-time maize paleoproductivity estimates for each of the cells on the landscape. Blue households are getting 100 percent of their protein from hunting; red households get 100 percent of their protein from domestication; and the range of purples in-between account for mixed proportions. Images taken in years 800 and 1000 show the same households overlaying simulated deer density; deer exist on a coarser landscape, and brighter cells represent higher densities of deer. In all runs, agents are randomly seeded across the landscape at year 600.

Run 1 (Figure 5.7) is an example of a run with no turkey domestication, but a high population due to relatively inexpensive hunting and low protein need. Simulated agents deplete deer rather early on, but are able to continue subsisting in the north-eastern half of the VEP study area on lagomorphs. Although there is an initial simulated population in the Dolores River area, this area becomes more sparsely populated quite early, probably due to lack of faunal resources once deer are depleted in combination with highly variable maize production that is greatly

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13 It is difficult to visually assess the goodness-of-fit from such images because such assessments only take place within the block-surveyed areas or for isolated locations outside of those which happen to have recorded sites. Still, these images allow us to describe how simulated sites are patterned on the landscape.
reduced in cold years. By the twelfth and thirteenth centuries, simulated agents most densely populate the core of the Great Sage Plain, centered in the middle of the study area (see red ellipse in Figure 5.7). Interestingly, agents only sparsely populate the southern half of the Plain by the end of the simulation. This may be because the deep canyons of the northern part of the Plain provide refuge for deer and other huntable protein resources.

Figure 5.7. Household locations in Run 1. Domestication: false; Hunting radius: 20; Protein need: 5. White dots are the recorded site locations. Colored dots are simulated households; blue indicates a household gets all its protein from hunting, while red indicates a household gets all its protein from turkey. The red ellipse highlights high-density agent populations in the middle of the study area.
Run 7 (Figure 5.8) is a domestication run that produced intermediate populations, but which provides the best fit for populations during the twelfth and thirteenth centuries. Simulated agents in this run quickly decimate deer populations, but are able to shift to a domestication strategy. This strategy first appears in the most densely populated areas of the landscape, and in areas with the highest maize productivity. Simulated populations are most dense in the core of the Great Sage Plain (see red ellipse), but (as of year 1000) much less so on the southwestern edge of the Plain, where most surveyed sites exist. Also notable is the distinct shift of the simulated households to the southern part of the Plain. This shift is likely a function of soil degradation; populations seem to shift from north to south or vice-versa as high population density depletes soil productivity (see Figures 5.7, 5.8, and 5.9).
Figure 5.8. **Household locations in run 7.** Domestication: true; Hunting radius: 20; Protein need: 15; Turkey water: false; Turkey-maize-per: 50 percent. White dots are the recorded site locations. Colored dots are simulated households; blue indicates a household gets all its protein from hunting, while red indicates a household gets all its protein from turkey. The red ellipse highlights high-density agent populations in the southern half of the Great Sage Plain.

Run 14 (Figure 5.9) displays an even clearer signature of the development of a core of domestication in the Great Sage Plain (see red ellipse), with hunting predominant on its periphery. This development occurs in the early years of wild protein depletion, but even at the end of the simulation, households on the western edge of the Plain are somewhat more likely to be hunting for their protein. I want to emphasize that this process begins in the center of the Sage Plain and radiates out. This pattern is not inherent to the design of the simulation, but emerges
out of the interaction between high simulated populations, high estimated maize productivity, and rapid simulated deer depletion in the center of the Sage Plain. Throughout the simulation, areas of high proportions of turkey use are interspersed with households that get all of their meat from hunting; these are likely the agents that hunt ‘first’ in the simulation, and thus deplete local wild protein that may have regenerated during the off-season. In areas on the periphery, privileged access to protein resources may have been socially mediated, contributing to starkly differing faunal assemblages at ecologically similar sites, as Muir and Driver (2002:186) demonstrate when comparing Sand Canyon Pueblo to contemporary nearby sites.

![Figure 5.9. Household locations in run 14. Domestication: true; Hunting radius: 20; Protein need: 5; Turkey water: true; Turkey-maize-per: 70]
percent. White dots are the recorded site locations. Colored dots are simulated households; blue indicates a household gets all its protein from hunting, while red indicates a household gets all its protein from turkey. The red ellipse highlights high-density agent populations in the southern half of the Great Sage Plain, where turkey use is first adopted in the simulation.

In contrast to the southwestern half of the study area, as well as the area around the Dolores River, very little block survey has been possible in this core area due to early modern farming settlement and lack of public land (Varien et al. 2007: Figure 1). Furthermore, many of the larger sites used in zooarchaeological analysis (Badenhorst and Driver 2009; Muir and Driver 2002; Rawlings and Driver 2010) are located along the periphery of the Plain, rather than in its core. This analysis generates a general expectation that turkey use will intensify in a pattern that radiates out from the core agricultural areas. Thus, analyses (Badenhorst and Driver 2009; Muir and Driver 2002; Duff et al. 2010) that have focused on peripheral sites may be presenting an erroneously late signal for intensified turkey use, especially when assemblages from these sites are taken in aggregate. Though a re-analysis of the archaeofaunal data for the region is beyond the scope of this thesis, the hypothesized pattern of a core-to-periphery transition to turkey domestication is likely to show up in the currently available archaeofaunal record.
CHAPTER SIX

CONCLUSION

In this thesis, I set out to explore the relationships between turkeys and humans in the Pueblo Southwest specifically as a means of understanding how human agency directs the process of domestication. The models presented define potential decisions made by human agents during the process of domestication, and describe how these decisions can be expected to pattern the archaeological record of domestication. I will briefly summarize these several models here—focusing on expectations of archaeological patterns—before describing future directions for research.

Summary: Models of Turkey Domestication on the Colorado Plateau

I began by describing the genetic and demographic implications of turkey domestication for turkey flocks, noting that variations in the treatment of turkey—feeding, breeding, and use—should generate distinguishable archaeogenetic and archaeodemographic signatures (Table 2.1). There are three major categories of domestication practice: breeding practices, feeding practices, and how the domesticate is used. Outbreeding, or the hybridization of domestic stock with wild or feral birds, will result in female-biased founder effect, archaeophenotypic hybridization, female-skewed sex ratios, and a modern genetic record that roughly matches the archaeogenetic one. Inbreeding predicts a founder effect in both male and female lineages, preservation of phenotypic traits, and a neogenetic record that diverges from the archaeogenetic one. Feeding practices mainly affect the isotopic signatures of the birds. Outfeeding—allowing your stock to forage on the landscape—will result in archaeoisotopic carbon and nitrogen values roughly equivalent to the neoisotopic wild baseline for turkey. If the turkey are infed, carbon-isotope
values will be greatly enriched, and nitrogen-isotope values slightly depressed from this baseline. Finally, the actual use of turkey greatly affects the expectations we may have for the archaeological record. Archaeogenotypic, archaeophenotypic, and archaeodemographic signatures of turkey that are used predominantly for feathers will vary with use (ornamentation vs. blankets); the genotypic signature of turkey used for protein will be neutral, while we can expect larger turkey phenotypes to be selected for, as well as a heavy female-skewed sex ratio, especially among mature birds.

Fully laying out these expectations demonstrates that taking any one pattern alone—such as ancient turkey mtDNA or archaeodemographic patterning—is insufficient to define turkey use practices. Multiple patterns are needed in order to qualify turkey use and build a preponderance of evidence for eventual domestication, however defined. This section also illustrated how the identification of archaeological turkey as “domesticated” versus “not domesticated” fails as a useful distinction, given the broad variety of potential relationships between humans and turkey. Instead, taking domestication as human agency allows us to focus on human interactions with turkey and the patterns they produce in the archaeological record.

In the second part, I imagined the adoption of turkey domestication as a resilience trap—the ‘Avicultural Trap’—making the Pueblo subsistence system increasingly rigid and narrow while simultaneously allowing explosive population growth. I describe how a feedback loop between turkey, maize yields, and human population growth amplified to the point where the Pueblo subsistence system was unable to respond to climate-induced reduction in agricultural yield. As Pueblo peoples moved onto the NSJ landscape at the end of the Basketmaker III period, they quickly colonized the best agricultural land—forming relatively large communities around this
land—and continued hunting deer for a majority of their protein through the PI period. When the climate became unfavorable at the end of that period, and agricultural productivity suffered, these communities disaggregated. While human populations dipped in the VEP area, people continued to flourish elsewhere in the NSJ. The more favorable climate of the early-to-mid-PII ushered in a new wave of population growth—supplemented by immigration from the south—and increased aggregation. Populations quickly came to deplete wild faunal resources, and began keeping turkey locally for protein instead of hunting. This allowed their populations to continue growing through the mid-PIII. As this happened, people gradually abandoned the areas of the highest abundance of wild protein in favor of higher agricultural yields elsewhere. When these yields again began declining due to unfavorable climate fluctuations, populations in the richest areas were too high to be sustained. Social unrest resulted, and complete abandonment followed.

This narrative does not generate archaeological expectations on its own—though I do lay out what those expectations would be—but instead illustrates a key aspect of domestication as both agency and process. Agentful decisions by the Pueblo people (to convert maize into protein via keeping turkey) may have led to a buildup of rigidity within their subsistence system, eventually stripping them of their agency as they attempted to maintain their way of life. They simply could not have acted any other way (in terms of protein procurement) and maintain their population and residential structure. We might therefore be able to define a new subset of rigidity traps such as the avicultural trap—traps which are initiated and driven by sequential or widespread conformity in agentful decision making. Many examples of ‘tragedies of the commons’ (Hardin 1968) are just this type of trap: positive short-term decisions made independently and in unison by large numbers of rational actors have potentially negative long-term consequences.
In the final section, I focus on ‘domestication’ as food production and incorporate domestication into the patch-choice model from classic optimal foraging theory. Chapter 4 presented a model based on optimal foraging theory explaining how people might have initially begun to transition to using turkey as an auxiliary protein resource. In the model, any alternative resource procurement strategy will have its own ‘search’ and ‘handling’ costs, and the marginal rate of return from that strategy may thus be compared to those of foraged resources. If an individual can achieve higher return rates from the alternative strategy, the foraging strategy will be abandoned. Results from this model predict a reduction in diet-breadth, a reduction in patch-breadth, and a general shift towards higher abundances of high-ranked items relative to other foraged goods, even as high-ranked items are depleted in the environment. For the case of a faunal domesticate, we can expect this transition—a reversal of those expectations from classical OFT—to occur more quickly in social or physical environments where the costs of domestication are minimized.

The application of this model to the Village Ecodynamics Project simulation—detailed in Chapter 5—demonstrated that the availability of turkey domestication not only improves the fit of that simulation on several metrics, especially of course during the turkey-intensive second population cycle, but also predicts where and when domestication would have first been adopted. To the extent that the OFT-based model used reflects reality, we can expect that keeping turkey for protein would have been first adopted in the core of the Montezuma valley—probably in its southern half—and would have spread gradually to the north and west. This is important for interpretations of the archaeological record (Badenhorst 2008; Badenhorst and Driver 2009)
which have generally focused on this latter area to document the timing of turkey adoption. We can expect that—and test whether—intensive use of turkey began earlier elsewhere.

Future Directions

There are several ways the agent-based implementation discussed in Chapter 5 might be improved in future research. First, while the hunting algorithm in the Village simulation approximates the patch-choice model of classic OFT, it is inadequate. A more thorough implementation might treat each cell as a patch, and have agents thus select patches to forage in based on the marginal value theorem. Foraging within patches should follow the fine-grained prey-choice model. Additionally, travel costs ought to factor into patch-choice (they do not currently), which would be a general implementation of a central-place foraging algorithm.

Having these hunting algorithms more closely match the formal models will more closely align our simulation results with a productive body of literature.

The way in which turkeys are acquired is an obvious starting point for improving the realism of my implementation of turkey domestication. Recall that, in my model, turkey simply are available when needed, as if there were gobbler-with-a-golden-egg at every site. A more realistic implementation would either grow turkey in the wild and allow agents to capture them, or allow agents to specialize in the supply of turkey. Either method adds initial startup costs to raising turkey flocks. Additional startup costs might be the construction of turkey pens and the allocation of labor. Whether these added costs would be sufficient to postpone turkey domestication on the simulated landscape to the extent that the virtual and archaeological records better align remains to be seen. Cultural and status factors might also be involved via taboos against turkey consumption or via a high social value placed on hunted meat.
Once turkey is kept by agents, a more realistic implementation would allow for the internal husbandry of turkey, thus perhaps alleviating the supply problem just mentioned. Furthermore, both the acquisition of turkey and the ensuing husbandry rate, if combined with the relatively simple tracking of turkey lineages, could allow for more accurate models of how genetic change tracks different husbandry practices across space. Areas with higher human populations most dependent on turkey might be expected to have higher husbandry rates in their flocks and perhaps less outbreeding, simultaneously accentuating the effects of bottlenecking (reduction) and population growth (promotion) of genetic diversity. We can expect that on the periphery of the area of intensive turkey domestication these effects would be less pronounced.

Finally, the Village simulation can and should be more generally used to construct virtual archaeological landscapes; an effort should be made to generate data (beyond the current demographic and site location data) that conforms more closely to archaeologically knowable patterns. Of direct relevance to this thesis, data could be quite easily output that spatially situates faunal assemblages associated with simulated households, and allows the user to see how these virtual faunal assemblages are patterned across the landscape, and compare these patterns with spatially situated faunal data from the archaeological record. Data such as these—the red-to-blue color gradient of agent turkey use in Figures 5.7, 5.8, and 5.9 are simplistic examples—will do a better job of addressing the variation in the archaeological record than the aggregate statistics and analytical predictions we currently employ.

The models I have presented here demonstrate that turkey use likely had a substantial impact on peoples’ subsistence strategies; these strategies—centered around a heavy, almost complete dependence on maize—have come to define the northern Pueblo system. That these strategies are
intimately intertwined with physical and social habitats is undeniable. Turkey are thus an important part of the Pueblo story, and these models will assist archaeologists in telling that story.
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APPENDIX A.1

Domestication Code: The DomesticationParameters Class
package com.mesaverde.domestication;

/**
 * Turkey domestication parameters.<p>
 * This class handles the constants for turkey domestication. Certain parameters, such as
 * {@code TURKEY_MAIZE_PER} and {@code TURKEY_WATER} may be controlled through the Repast
 * GUI, or through a parameter file.<p>
 * Domestication itself is toggled in the {@link com.mesaverde.village.Village Village} class.<p>
 * @author R. Kyle Bocinsky <bocinsky@wsu.edu>
 * @version $Date: 2010/11/22 $
 * @since 1.0
 */

public class DomesticationParameters {

    /**
     * Amount of edible meat per average sized turkey, in grams (13 lbs, 4128 grams of meat).
     * U.S. Department of Agriculture [www.nal.usda.gov].
     */
    public static final int PROTEIN_PER_TURKEY = 1238;

    /**
     * Annual turkey caloric need.
     * This is based on numerous assumptions, for the dietary need of wild turkeys
     * is not well documented. Firstly, I take the average dietary need of turkey
     * to be 8oz of food. Using the MAIZE_KG_CAL conversion factor of 3560 kcal/kg,
     * I arrive at a daily caloric need of turkey of ~ 800 Cal, assuming all calories
     * came from maize. This assumption is tempered by the TURKEY_MAIZE_PER adjustment.
     */
    public static final int BASE_CAL_TURKEY = 292000;

    /**
     * This equation calculates the return rate for keeping turkey, which is a constant
     * in the current (11/22/2010) model. We assume turkey are fed for a complete year, and
     * that they receive
     * TURKEY_MAIZE_PER of their caloric needs from maize. This value is in grams/Cal
     * expended,
     * and is used as the cutoff point where agents will switch to a domestication strategy.
     */
    public static final double TURKEY_MAIZE_PER = 0.7;

    /**
     * Whether or not to require agents to provide water for their turkey.
     */
public static final boolean TURKEY_WATER = true;

/**
 * Amount of water, in kg, per day needed by a single turkey. This is calculated at 2x
 * the amount of food, by weight, needed per day. Actual turkey water consumption appears to
 * be very poorly recorded. This number comes from a professional turkey hatchery.
 * http://www.millerhatcheries.com/Information/Turkeys/turkey_rearing.htm
 */
public static final double TURKEY_WATER_NEED = 0.454;
APPENDIX A.2

Domestication Code: The StrictEconomicModel Class
package com.mesaverde.domestication;

import com.mesaverde.village.Agent;
import com.mesaverde.village.Village;

/**
 * The base economic strategy for turkey domestication.<p>
 * This class calculates the number of turkey needed by a household, and forces the
 * household to track the number of turkeys they keep.<p>
 * The {@link #execute() execute} method controls these actions.<p>
 * Domestication itself is toggled in the {@link com.mesaverde.village.Village Village} class.<p>
 * @author R. Kyle Bocinsky <bocinsky@wsu.edu>
 * @version $Date: 2010/11/22 $
 * @since 1.0
 */

public class StrictEconomicModel extends DomesticationStrategy {
    public StrictEconomicModel(Agent agent) {
        super(agent);
    }

    /**
     * A method for controlling turkey domestication. This method is fed {code hh_protein_need}
     * as a parameter, calculates the number of turkeys needed to fulfill that need, and
     * compares that with the maximum number of turkeys allows so as not to deplete maize
     * stores beyond a critical threshold (the amount of maize utilized in the past year). The agent
     * will choose to domesticate the lesser of these two turkey amounts.<p>
     * @see com.mesaverde.domestication.DomesticationStrategy#execute(long)
     * @return {code turkeyCal} calories spent on turkey keeping.
     */
    @Override
    public int execute(long hh_protein_need) {
        boolean domestication = agent.getSwarm().isDomestication();
        double turkey_maize_per = agent.getSwarm().getTurkey_maize_per();

        /**
         * Ensure that this is the strategy that ought to be taken.
         */
        if (DomesticationParameters.DOMESTICATION_STRATEGY !=
            DomesticationParameters.STRICT_ECONOMIC_MODEL || hh_protein_need <= 0 || !domestication) {
            return 0;
        }
        System.out.printf("Domestication Strategy is the Strict Economic Model \n");
        int numTurkey = 0;
        int turkeyNeeded = 0;
        int maxTurkey = 0;
        int turkeyCal = 0;
        /**
* Reset annual number of turkey kept by the household.
* /
agent.turkey_kept = 0;

/**
 * Calculate household turkey need.
 */
turkeyNeeded = (int) (hh_protein_need/DomesticationParameters.PROTEIN_PER_TURKEY);
// System.out.printf("turkeyNeeded: %d\n", turkeyNeeded);

/**
 * Calculate maximum turkey able to be kept by household.
 */
maxTurkey = (int) (((agent.getMaizeStorage() * Village.MAIZE_KG_CAL) -
(agent.EXP_cal_need * Village.MAIZE_PER)) / (DomesticationParameters.BASE_CAL_TURKEY *
turkey_maize_per));
// System.out.printf("maxTurkey: %d\n", maxTurkey);

/**
 * Choose lower of the two values.
 */
if (maxTurkey > 0) {
   if (turkeyNeeded < maxTurkey) {
      numTurkey = turkeyNeeded;
   } else {
      numTurkey = maxTurkey;
   }
}

/**
 * Report the number of calories spent domesticating.
 */
turkeyCal += (int)(numTurkey * DomesticationParameters.BASE_CAL_TURKEY *
turkey_maize_per);

c_domestication += (int)(numTurkey * DomesticationParameters.BASE_CAL_TURKEY *
turkey_maize_per);

/**
 * Increment the number of turkeys kept, so we know.
 */
agent.turkey_kept += numTurkey;

/**
 * Increment protein storage by turkeys kept. Agents are charged a years-worth of
turkey feeding.
 */
agent.setCurrentProteinStorage(agent.getCurrentProteinStorage() + (numTurkey *
DomesticationParameters.PROTEIN_PER_TURKEY));

return turkeyCal;
}
APPENDIX A.3

Domestication Code: The DomesticationHuntingStrategy Class
package com.mesaverde.hunting;

import com.mesaverde.domestication.DomesticationParameters;
import com.mesaverde.village.Agent;
import com.mesaverde.village.Cell;
import com.mesaverde.village.Village;

/**
 * The base hunting strategy including turkey domestication.
 * This class emulates the {@link com.mesaverde.hunting.AlternateHuntingStrategy
 * AlternateHuntingStrategy} written by Jason Cowan, but continuously calculates the agent's return rates from hunting, and
 * abandons hunting once those return rates drop below
 * {@link com.mesaverde.domestication.DomesticationParameters#TURKEY_RR TURKEY_RR}.<p>
 * The {@link #execute() execute} method controls these actions.<p>
 * The {@link #searchHuntatX() searchHuntatX} method allows for domestication to be accounted
 * for during household relocation.<p>
 * Domestication itself is toggled in the {@link com.mesaverde.village.Village Village} class.<p>
 * @author R. Kyle Bocinsky &lt;bocinsky@wsu.edu&gt;
 * @version $Date: 2010/11/22 $
 * @since 1.0
 */

public class DomesticationHuntingStrategy extends HuntingStrategy {

    public DomesticationHuntingStrategy(Agent agent) {
        super(agent);
    }

    /**
     * This alternative hunting routine is designed to allow the cost of
     * hunting to be tracked
     * and forced on the agents. To do this, hunting has been broken up into
     * several different
     * phases. First the agent looks for a cell to hunt in. This is done in
     * a outwardly
     * radiating pattern from the cells location. Next the agent attempts to
     * find animals in the cell.
     * If animals are found, the agent will then hunt deer in the cell. Once
     * the known deer are depleted,
     * the agent will continue to look in new cells for additional deer. If
     * the agent moves beyond 5 km (a
     * variable number from its location) it will go back over hunted cells
     * and start hunting the hares and
     * rabbits in them.
     */
    @SuppressWarnings("unused")
    @Override
    public int execute(long hh_protein_need, int hunt_radius) {
        if (hh_protein_need <= 0 || hunt_radius == 0 || !Village.HUNTING) {
            return 0;
        }
    }
}
int i;
int hunt_cal = 0;
Cell c;
int dx, dy, dw;
int hunts = 0;
int tot_deer;
int known_deer;
int killed_deer;
int tot_hares;
int known_hares;
int killed_hares;
int tot_rabbits;
int known_rabbits;
int killed_rabbits;
int numhunts;
int cont_hunting = 1;
hunters = 0;
double max_hours = 0.0;
double max_hunt_cal;
double hunting_time;
double deer_fix = 0.0;
C_hunt = 0;

double deer_time = 0.0;
double hare_time = 0.0;
double rabbit_time = 0.0;

agent.deer_hunted = 0; // tracks total animals hunted by agent
agent.hare_hunted = 0;
agent.rabbit_hunted = 0;

hunters = agent.getWorkerSize();

// now determine how many hours can be spent hunting
// the max that any agent can work in a year is set at
// 14 hours per day per individual in household over 7 years of age
max_hours = hunters * 14 * 365;

// now subtract last years non hunting hours from this amount
// to determine time that can be spent hunting
hunting_time = max_hours - agent.nonhunt_hrs;

/**
 * @code max_hunt_cal] is the maximum amount of energy an agent can spend hunting before its
 * net protein return rate drops below that needed to meet all of its need from turkey.
 */
max_hunt_cal = (hh_protein_need * DomesticationParameters.BASE_CAL_TURKEY * agent.getSwarm().getTurkey_maize_per()) / DomesticationParameters.PROTEIN_PER_TURKEY;

// Search for potential cell
if (agent.getCurrentProteinStorage() < hh_protein_need) {
    do {
        dx = 0;
        dy = 0;
        dw = 0;

        int[] res = searchNeighborhoodHuntDX(dx, dy, dw, 0, hunts);
dx = res[0];
dy = res[1];
dw = res[2];
hunts = res[3];

if (agent.Hsearchradius <= hunt_radius) {
    // acquire cell found
    c = (Cell) agent.getWorld().getObjectAt(
        Village.wrapX(dx, agent.getX(), agent.getWorldX()),
        Village.wrapY(dy, agent.getY(), agent.getWorldY()));

    // if dw = 0 then deer found, 1 = lagomorphs found
    if (dw == 0) {
        // Determine number of deer able to be hunted
        tot_deer = (int) c.getAnimalTracker().getAmount(Deer.class);
        double dpercent_found = Village.uniformDblRand(0.3, 0.75);
        known_deer = (int) (tot_deer * dpercent_found);
        deer_fix = tot_deer * dpercent_found;

        if (deer_fix > .50 && known_deer < 1) {
            known_deer = 1;
        }
    }

    // Charge the agent for one trip back and forth, in calories and man-hours.
    hunt_cal += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0);
    C_hunt += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0) / Village.WORK_CAL_MAN;
    deer_time += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0) / Village.WORK_CAL_MAN;

    if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
        known_deer = 0;
        cont_hunting = 0;
    }
}

killed_deer = 0;
numhunts = 0;

// Hunt Deer

if (known_deer != 0) {
    do {
        // dpercent_kill is the difficulty number needed
        // to successfully kill a deer
        // dpercent_chance is the number compared to
data difficulty
        double dpercent_kill = Village.uniformDblRand(0.3, 0.75);
        double dpercent_chance = Village.uniformDblRand(0.0, 1.0);
        numhunts++;

        if (dpercent_chance > dpercent_kill) {
            // deer killed
            killed_deer++;
            agent.deer_hunted++;
            known_deer--;
        }
    }
}
agent.setCurrentProteinStorage(agent.getCurrentProteinStorage() + Village.PROTEIN_PER_DEER);
if (agent.getCurrentProteinStorage() > hh_protein_need) {
    known_deer = 0;
}

if (known_deer == 0) {
    // set new deer pops in deercell and cell
    if (c == null) {
        System.out.printf("c is null!");
    } else {
        c.setHuntedDeer(killed_deer);
        // accrue costs of hunting
        hunt_cal += 5 * numhunts;
        C_hunt += 5 * numhunts;
        deer_time += 5 * numhunts;
    }
    if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
        cont_hunting = 0;
    }
    // add costs for retrieval
    double trips = killed_deer * 36
    / Village.CARRY_CAPACITY;
    hunt_cal += agent.calcTravelCal(
        agent.Hsearchradius, 0, trips);
    C_hunt += agent.calcTravelCal(
        agent.Hsearchradius, 0, trips)
    / Village.WORK_CAL_MAN;
    deer_time += agent.calcTravelCal(
        agent.Hsearchradius, 0, trips)
    / Village.WORK_CAL_MAN;
    if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
        cont_hunting = 0;
    }
}
while (known_deer != 0);
}
else {
    // Hunting lagomorphs is different than deer hunting.
    // Instead of acquiring one animal
    // at a time a single hunt will bring in
    // Village.HLAG_HUNT (= 2 hare) or Village.RLAG_HUNT (=5
    // rabbit, Village.h)
    // animals. This means that a cell
    // will not be hunted if there are less than
    // Village.LAG_HUNT rabbits or hares in the cell.
    // Additionally the cost of acquiring these animals is
    // higher.
    if (hunters >= Village.HUNTERS) {
        // Determine number of hares able to be hunted
    }
}
tot_hares = c.getAnimalTracker().getIntAmount(Hare.class);
double hpercent_found = Village.uniformDblRand(0.3, 0.75);
known_hares = (int)(tot_hares * hpercent_found);
if (known_hares < Village.HLAG_HUNT / 2) {
    known_hares = 0;
}

double travelCalc = agent.calcTravelCal(
    agent.Hsearchradius, 0, 1.0);
hunt_cal += travelCalc;
C_hunt += travelCalc / Village.WORK_CAL_MAN;
hare_time += travelCalc / Village.WORK_CAL_MAN;
if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
    known_hares = 0;
    cont_hunting = 0;
}
killed_hares = 0;
numhunts = 0;
if (known_hares > Village.HLAG_HUNT) {
    do {
        // dpercent_kill is the difficulty number
        // needed to successfully hunt
        // dpercent_chance is the number compared to
        // difficulty
        double dpercent_kill = Village.uniformDblRand(0.3, 0.75);
double dpercent_chance = Village.uniformDblRand(0.0, 1.0);
        numhunts++;
        if (dpercent_chance > dpercent_kill) {
            killed_hares += Village.HLAG_HUNT;
            agent.hare_hunted += Village.HLAG_HUNT;
            known_hares -= Village.HLAG_HUNT;
            agent.setCurrentProteinStorage(agent
                .getCurrentProteinStorage() + (Village.PROTEIN_PER_HARE * Village.HLAG_HUNT));
            if (agent.getCurrentProteinStorage() > hh_protein_need) {
                known_hares = 0;
            }
        }
    }
}
if (known_hares < Village.HLAG_HUNT) {
    // set new hare pops cell
    c.getAnimalTracker().huntAnimals(Hare.class, killed_hares);
    // accrue costs of hunting
hunt_cal += 0.5 * numhunts * Village.WORK_CAL_MAN;
C_hunt += 0.5 * numhunts;

hare_time += 0.5 * numhunts;

if (Village.HUNTERS > 1) {
    hunt_cal += 0.5 * numhunts * Village.WORK_CAL_WOM;
    C_hunt += 0.5 * numhunts;
    hare_time += 0.5 * numhunts;
    for (i = 0; i < Village.HUNTERS - 2; i++) {
        hunt_cal += 0.5 * numhunts * Village.WORK_CAL_KID;
        C_hunt += 0.5 * numhunts;
        hare_time += 0.5 * numhunts;
    }
}

// add costs for retrieval
float trips = killed_hares * Village.HARE_WEIGHT / Village.CARRY_CAPACITY;
hunt_cal += agent.calcTravelCal(
    agent.Hsearchradius, 0, trips);
C_hunt += agent.calcTravelCal(
    agent.Hsearchradius, 0, trips) / Village.WORK_CAL_MAN;

hare_time += agent.calcTravelCal(
    agent.Hsearchradius, 0, trips) / Village.WORK_CAL_MAN;

if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
    cont_hunting = 0;
}
} while (known_hares > Village.HLAG_HUNT);

if (agent.getCurrentProteinStorage() < hh_protein_need && C_hunt < hunting_time && hunt_cal < max_hunt_cal) {
    // Determine number of rabbits able to be hunted
tot_rabbits = c.getAnimalTracker().getIntAmount(Rabbit.class);
double rpercent_found = Village.uniformDblRand(0.3, 0.75);
known_rabbits = (int) (tot_rabbits * rpercent_found);
if (known_rabbits < Village.RLAG_HUNT / 2) {
    known_rabbits = 0;
}
}
killed_rabbits = 0;
umhunts = 0;
if (known_rabbits > Village.RLAG_HUNT) {
    do {
        // rpercent_kill is the difficulty
        // number needed to successfully hunt
// rpercent_chance is the number
// compared to difficulty
double rpercent_kill = Village
  .uniformDblRand(0.3, 0.75);
double rpercent_chance = Village
  .uniformDblRand(0.0, 1.0);

numhunts++;

if (rpercent_chance > rpercent_kill) {
  // rabbits killed
  killed_rabbits += Village.RLAG_HUNT;
  agent.rabbit_hunted += Village.RLAG_HUNT;
  known_rabbits -= Village.RLAG_HUNT;

  agent
    .setCurrentProteinStorage(agent
      .getCurrentProteinStorage()
      + (Village.PROTEIN_PER_RABBIT * Village.RLAG_HUNT));
  if (agent.getCurrentProteinStorage() > hh_protein_need) {
    known_rabbits = 0;
  }
}

if (known_rabbits < Village.RLAG_HUNT) {
  // set new rabbit pops cell
  c.getAnimalTracker().huntAnimals(Rabbit.class, killed_rabbits);
  // accumulate costs of hunting
  hunt_cal += 0.5 * numhunts
  * Village.WORK_CAL_MAN;
  C_hunt += 0.5 * numhunts;
  rabbit_time += 0.5 * numhunts;

  if (Village.HUNTERS > 1) {
    hunt_cal += 0.5 * numhunts
    * Village.WORK_CAL_WOM;
    C_hunt += 0.5 * numhunts;
    rabbit_time += 0.5 * numhunts;

    for (i = 0; i < Village.HUNTERS - 2; i++) {
      hunt_cal += 0.5
        * numhunts
        * Village.WORK_CAL_KID;
      C_hunt += 0.5 * numhunts;
      rabbit_time += 0.5 * numhunts;
    }
  }
}

// add costs for retrieval
float trips = killed_rabbits
  * Village.RABBIT_WEIGHT
  / Village.CARRY_CAPACITY;
  hunt_cal += agent.calcTravelCal(trips

  * Village.WORK_CAL_MAN;
  C_hunt += agent.calcTravelCal(trips
  * Village.WORK_CAL_WOM;
  C_hunt += agent.calcTravelCal(trips
  * Village.WORK_CAL_KID);
agent.Hsearchradius, 0, trips);
C_hunt += agent.calcTravelCal(
    agent.Hsearchradius, 0, trips)
    / Village.WORK_CAL_MAN;

rabbit_time += agent.calcTravelCal(
    agent.Hsearchradius, 0, trips)
    / Village.WORK_CAL_MAN;

if (C_hunt > hunting_time || hunt_cal >= max_hunt_cal) {
    cont_hunting = 0;
} while (known_rabbits > Village.RLAG_HUNT);
}
}
}
}
}
}
else {
    cont_hunting = 0;
}

if (agent.getCurrentProteinStorage() > hh_protein_need) {
    cont_hunting = 0;
}
if (agent.Hsearchradius == hunt_radius) {
    // if no meat found within hunt radius km then stop hunting
    // can cause birth penalties
    cont_hunting = 0;
} while (cont_hunting != 0);
}

if (C_hunt > 0) {
    agent.hunting_return_rate = 0;
}

if (deer_time > 0) {
    agent.deer_return_rate = 0;
    agent.deer_return_rate += (agent.deer_hunted * Village.PROTEIN_PER_DEER) /
                            (deer_time*Village.WORK_CAL_MAN);
    agent.hunting_return_rate += (agent.deer_hunted * Village.PROTEIN_PER_DEER)/hunt_cal;
}

if (hare_time > 0) {
    agent.hare_return_rate = 0;
    agent.hare_return_rate += (agent.hare_hunted * Village.PROTEIN_PER_HARE) /
                            (hare_time*Village.WORK_CAL_MAN);
    agent.hunting_return_rate += (agent.hare_hunted * Village.PROTEIN_PER_HARE)/hunt_cal;
}

if (rabbit_time > 0) {
    agent.rabbit_return_rate = 0;
    agent.rabbit_return_rate += (agent.rabbit_hunted * Village.PROTEIN_PER_RABBIT) /
                            (rabbit_time*Village.WORK_CAL_MAN);
    agent.hunting_return_rate += (agent.rabbit_hunted * Village.PROTEIN_PER_RABBIT)/hunt_cal;
}
return hunt_cal;
}

/**
 * @SuppressWarnings("unused")
 * @Override
 * public int searchHuntatX(int dx, int dy) {
 *     long hh_protein_need = 0; // grams needed for hh to survive
 *     int protein_cal = 0; //Numbers of Calories used for hunting
 *     int i_protein_storage;
 *     //This alternative hunting routine is designed to allow the cost of hunting to be tracked
 *     //and forced on the agents. To do this, hunting has been broken up into several different
 *     //phases. First the agent looks for a cell to hunt in. This is done in a outwardly
 *     //radiating pattern from the cells location. Next the agent attempts to find animals in the
 *     //cell. //If animals are found, the agent will then hunt deer in the cell. Once the known deer are
 *     //depleted,
 *     //the agent will continue to look in new cells for additional deer. If the agent moves beyond 3
 *     //km (a
 *     //variable number) from its location it will go back over hunted cells and start hunting the
 *     //hares and
 *     //rabbits in them.
 *     Cell c;
 *     int initx, inity;
 *     int dw;
 *     int hunts = 0;
 *     int tot_deer;
 *     int known_deer;
 *     int killed_deer;
 *     int numhunts;
 *     int cont_hunting = 1;
 *     int tot_hares;
 *     int known_hares;
 *     int killed_hares;
 *     int tot_rabbits;
 *     int known_rabbits;
 *     int killed_rabbits;
 *     int hunters = 0;
 *     int i;
 *     double dpercent_found;
 *     double dpercent_kill;
 *     double dpercent_chance;
 *     double trips;
 *     double hpercent_found;
 *     double hpercent_kill;
 *     double hpercent_chance;
 *     double rpercent_found;
 *     double rpercent_kill;
 *     double rpercent_chance;
 *     double max_hunt_cal;
 *     double deer_fix = 0.0;
 *     //calculate protein need for hh to survive. Now, agents only search for the amount of protein
 *     //they acquired from hunting in the last
 */
// year. This effectively raises the rank of cells with less access to protein resources, presumably ones with higher maize productivity.

hh_protein_need = (long)(agent.getSwarm().getP_need() * agent.getFamilySize() * 365);
max_hunt_cal = (hh_protein_need * DomesticationParameters.BASE_CAL_TURKEY * agent.getSwarm().getTurkey_maize_per()) / DomesticationParameters.PROTEIN_PER_TURKEY;

// System.out.printf("family size: %d\n", agent.getFamilySize());
// System.out.printf("max_hunt_cal: %f\n", max_hunt_cal);

i_protein_storage = 0;
agent.hunt_test_penalty = 0;

if (hh_protein_need <= 0 || agent.getSwarm().getHunting_radius() == 0 || !Village.HUNTING) {
    return 0;
}

initx = dx;
inity = dy;
do {
    dx = initx;
dy = inity;
dw = 0;

    int res[] = searchNeighborhoodHuntDX(dx, dy, dw, 1, hunts);
dx = res[0];
dy = res[1];
dw = res[2];
hunts = res[3];

    if (agent.Hsearchradius <= agent.getSwarm().getHunting_radius()) {
        // Accuire cell found
        c = (Cell) agent.getWorld().getObjectAt(Village.wrapX(dx, agent.getX(), agent.getWorldX()), Village.wrapY(dy, agent.getY(), agent.getWorldY()));

        if (dw == 0) {
            // Determine number of deer able to be hunted
            tot_deer = (int) c.getAnimalTracker().getAmount(Deer.class);
dpercent_found = Village.uniformDblRand(0.3, 0.75);
known_deer = (int) (tot_deer * dpercent_found);
deer_fix = tot_deer * dpercent_found;
if (deer_fix > .50 && known_deer < 1) {
    known_deer = 1;
}

protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0);
if (protein_cal >= max_hunt_cal) {
    cont_hunting = 0;
    known_deer = 0;
}
killed_deer = 0;
numhunts = 0;

// Hunt
if (known_deer != 0) {
do {
   // dpercent_kill is the difficulty number needed to successfully kill a deer
   // dpercent_chance is the number compared to difficulty
   dpercent_kill = Village.uniformDblRand(0.3, 0.75);
   dpercent_chance = Village.uniformDblRand(0.0, 1.0);
   numhunts++;
   if (dpercent_chance > dpercent_kill) {
       // deer killed
       killed_deer++;
       known_deer--;
       i_protein_storage += Village.PROTEIN_PER_DEER;
       if (i_protein_storage > hh_protein_need) {
           known_deer = 0;
       }
   }
}
if (known_deer == 0) {
   // accrue costs of hunting
   protein_cal += 5 * numhunts * Village.WORK_CAL_MAN;
   // add costs for retrieval
   trips = (killed_deer * 36) / Village.CARRY_CAPACITY;
   protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, trips);
   if (protein_cal >= max_hunt_cal) {
       cont_hunting = 0;
   }
} while (known_deer != 0);
} else {
   // Hunting lagomorphs and turkeys is different than deer hunting. Instead of accruing
   one animal
   // at a time a single hunt will bring in Village.LAG_HUNT (= 10) animals. This means that a cell
   // will not be hunted if there are less than Village.LAG_HUNT rabbits or hares in the cell.
   // Additionally the cost of acquiring these animals is higher. Hunting Lagomorphs
   // will require Village.LAG_HUNTERS (3) members of the family to be over the age of 7, and costs
   // accrued for Village.LAG_HUNTERS people in the hunt.
   if (hunters >= Village.HUNTERS) {
      // Determine number of hares able to be hunted
      tot_hares = c.getAnimalTracker().getIntAmount(Hare.class);
      hpercent_found = Village.uniformDblRand(0.3, 0.75);
      known_hares = (int)(tot_hares * hpercent_found);
      if (known_hares < (Village.HLAG_HUNT / 2)) {
         known_hares = 0;
      }
   }
protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0);
killed_hares = 0;
numhunts = 0;
if (protein_cal >= max_hunt_cal) {
    cont_hunting = 0;
    known_hares = 0;
}

if (known_hares > Village.HLAG_HUNT) {
    do {
        //dpercent_kill is the difficulty number needed to successfully hunting
        //dpercent_chance is the number compared to difficulty
        hpercent_kill = Village.uniformDblRand(0.3, 0.75);
        hpercent_chance = Village.uniformDblRand(0.0, 1.0);

        numhunts++;
        if (hpercent_chance > hpercent_kill) {
            //hares killed
            killed_hares += Village.HLAG_HUNT;
            known_hares -= Village.HLAG_HUNT;
            i_protein_storage += (Village.PROTEIN_PER_HARE * Village.HLAG_HUNT);
            if (i_protein_storage > hh_protein_need) {
                known_hares = 0;
            }
        }
    }
    if (known_hares < Village.HLAG_HUNT) {
        //accrue costs of hunting
        protein_cal += 0.5 * numhunts * Village.WORK_CAL_MAN;
        if (Village.HUNTERS > 1) {
            protein_cal += 0.5 * numhunts * Village.WORK_CAL_WOM;
            for (i = 0; i < (Village.HUNTERS - 2); i++) {
                protein_cal += 0.5 * numhunts * Village.WORK_CAL_KID;
            }
        }
    }

    //add costs for retrieval
    trips = (killed_hares * Village.HARE_WEIGHT) / Village.CARRY_CAPACITY;
    protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, trips);
    if (protein_cal >= max_hunt_cal) {
        cont_hunting = 0;
    }
}
}

//Determine number of rabbits able to be hunted
tot_rabbits = c.getAnimalTracker().getIntAmount(Rabbit.class);
rpercent_found = Village.uniformDblRand(0.3, 0.75);
known_rabbits = (int) (tot_rabbits * rpercent_found);
if (known_rabbits < (Village.RLAG_HUNT / 2)) {
    known_rabbits = 0;
} /*else if (known_rabbits < (Village.RLAG_HUNT + 1)) {
    known_rabbits = (Village.RLAG_HUNT + 1);
}*/

protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, 1.0);
killed_rabbits = 0;
numhunts = 0;
if (protein_cal >= max_hunt_cal) {
    cont_hunting = 0;
    known_rabbits = 0;
}

if (known_rabbits > Village.RLAG_HUNT) {
    do {
        //rpercent_kill is the difficulty number needed to successfully hunting
        //rpercent_chance is the number compared to difficulty
        rpercent_kill = Village.uniformDblRand(0.3, 0.75);
        rpercent_chance = Village.uniformDblRand(0.0, 1.0);
        numhunts++;
        if (rpercent_chance > rpercent_kill) {
            //rabbits killed
            killed_rabbits += Village.RLAG_HUNT;
            known_rabbits -= Village.RLAG_HUNT;
            i蛋白存储 += (Village.PROTEIN_PER_RABBIT * Village.RLAG_HUNT);
            if (i蛋白存储 > hh蛋白需) {
                known_rabbits = 0;
            }
        }
    } while (known_rabbits > Village.RLAG_HUNT);
}

if (known_rabbits < Village.RLAG_HUNT) {
    //accrue costs of hunting
    protein_cal += 0.5 * numhunts * Village.WORK_CAL_MAN;
    if (Village.HUNTERS > 1) {
        protein_cal += 0.5 * numhunts * Village.WORK_CAL_WOM;
        for (i = 0; i < (Village.HUNTERS - 2); i++) {
            protein_cal += 0.5 * numhunts * Village.WORK_CAL_KID;
        }
    }
}

//add costs for retrieval
trips = (killed_rabbits * Village.RABBIT_WEIGHT) / Village.CARRY_CAPACITY;
protein_cal += agent.calcTravelCal(agent.Hsearchradius, 0, trips);
if (protein_cal >= max_hunt_cal) {
    cont_hunting = 0;
}
} while (known_rabbits > Village.RLAG_HUNT);
else {
    cont_hunting = 0;
}

if (i_protein_storage > hh_protein_need) {
    cont_hunting = 0;
}
}

while (cont_hunting != 0);

//        System.out.printf("hh_protein_need: %d
", hh_protein_need);
//        System.out.printf("Protein From Hunting: %d
", i_protein_storage);

if (hh_protein_need - i_protein_storage > 0) {
    hh_protein_need -= i_protein_storage;

    int numTurkey = 0;
    numTurkey = (int)Math.ceil((double)hh_protein_need / DomesticationParameters.PROTEIN_PER_TURKEY);

    //        System.out.printf("numTurkey: %d
", numTurkey);

    agent.setI_turkey_kept(numTurkey);

    //        System.out.printf("protein from turkey: %d
", (int)(numTurkey * Parameters.PROTEIN_PER_TURKEY));

    protein_cal += (int)(numTurkey * DomesticationParameters.BASE_CAL_TURKEY * agent.getSwarm().getTurkey_maize_per());
}

return (protein_cal);
}
APPENDIX B.1

R Code: VEP Agent and System Stats Analysis
## Data crunching script for the Village Ecodynamics Project.
## Written by R. Kyle Bocinsky on 09-27-2010 using Tim Kohler's SAS scripts as a template.

## Required libraries.
library(reshape)

## Create output directory
dir.create("SummaryData")

## Specify the range or list of numbered runs to be crunched.
runs.range <- 1:20
runs.list <- c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20)

## This first section takes the agent statistics output from each run, drops unwanted variables, 
## aggregates it by taking the mean of variable values across all agents per year (excluding NA 
## values), and outputs a concatenated CSV file (merged_agg_agent_stats.csv) of data from all 
## runs.
## U.S.E.R MU.S.T SPECIFY WHETHER TO LOOP OVER runs.range OR runs.list!!!
## Runs must have numerical tag. Adjust the read command as needed.
for (i in runs.range){
  agentStats <- read.delim(paste('RawData/agent_stats_run_', i, '.out', sep=''))
  agentStats$remarriage_count <- NULL
  agentStats$dad <- NULL
  agentStats$k1 <- NULL
  agentStats$k2 <- NULL
  agentStats$k3 <- NULL
  agentStats$k4 <- NULL
  agentStats$k5 <- NULL
  agentStats$k6 <- NULL
  agentStats$k7 <- NULL
  agentStats$k8 <- NULL
  agentStats$CalVillage._HH_Yr <- NULL
  agentStats$Maize_Given_Phil <- NULL
  agentStats$M_Received_GRN <- NULL
  agentStats$M_Request_GRN <- NULL
  agentStats$M_exchange_GRN <- NULL
  agentStats$M_Wasted_GRN <- NULL
  agentStats$Num_Exchange_GRN <- NULL
  agentStats$M_Received_BRN <- NULL
  agentStats$M_Request_BRN <- NULL
  agentStats$M_exchange_BRN <- NULL
  agentStats$M_Wasted_BRN <- NULL
  agentStats$Num_Exchange_BRN <- NULL
  agentStats$Paid_Back_BRN <- NULL
  agentStats$agent <- NULL
  agentStats$x <- NULL
  agentStats$y <- NULL
  agentStats$Run <- i
  agentStats[agentStats==999] <- NA
  attach(agentStats)
  aggAgentStats <- aggregate(agentStats, by=list(Year), FUN=mean, na.rm=TRUE)
  detach(agentStats)
  rm(agentStats)
  if(i==1){
    mergedAgentStats <- aggAgentStats
  } else {
    mergedAgentStats <- rbind(mergedAgentStats, aggAgentStats)
  }
}
mergedAgentStats <- rbind(mergedAgentStats, aggAgentStats)
}
rm(aggAgentStats)
}

mergedAgentStats$Group.1 <- NULL
write.csv(mergedAgentStats, file = "SummaryData/merged_agg_agent_stats.csv")

## This next section is similar to the first, except it concatenates the system-wide statistics.
## We also create a file that is a simple list of runs and their parameters.
## U.S.E.R M.U.S.T SPECIFY WHETHER TO LOOP OVER runs.range OR runs.list!!!
## This is saved as a CSV file (merged_system_stats.csv).
for (i in runs.range){
  systemStats <- read.delim(paste("RawData/system_stats_run_", i, ".data", sep=""))
  if(i==1){
    mergedSystemStats <- systemStats
  } else{
    mergedSystemStats <- rbind(mergedSystemStats, systemStats)
  }
  rm(systemStats)
}
write.csv(mergedSystemStats, file = "SummaryData/merged_system_stats.csv")

mergedSystemStats$Year <- mergedSystemStats$Deer <- mergedSystemStats$Hare <- mergedSystemStats$Rabbit <- mergedSystemStats$Standing_Crop <- mergedSystemStats$Deadwood <- mergedSystemStats$Agents <- NULL
mergedSystemStats <- unique(mergedSystemStats)
write.csv(mergedSystemStats, file = "SummaryData/runParameters.csv")

## Finally, we merge the agent and system statistics.
## This is saved as a CSV file (agent_system_stats.csv).
agentStats <- read.csv("SummaryData/merged_agg_agent_stats.csv")
systemStats <- read.csv("SummaryData/merged_system_stats.csv")
agentSystemStats <- merge(agentStats, systemStats, by=c("Run", "Year"))
agentSystemStats$X.x <- NULL
agentSystemStats <- rename(agentSystemStats, c(Deer.x="Deer_Hunted", Rabbit.x="Rabbit_Hunted", Hare.x="Hare_Hunted", Deer.y="Deer", Hare.y="Hare", Rabbit.y="Rabbit"))
write.csv(agentSystemStats, file = "SummaryData/agent_system_stats.csv")

## And, just for fun, here is a quick script for creating and outputting the standard
## "Populations vs. Estimates" graph.
## This is saved as a PDF file (agent_system_stats.csv).
popEstimates <- read.csv("http://village.anth.wsu.edu/local/pop_estimates.csv")
systemStats <- read.csv("SummaryData/merged_system_stats.csv")
runParams$X <- runParams$Year <- runParams$Hare <- runParams$Deer <- runParams$Rabbit <- runParams$Standing_Crop <- runParams$Deadwood <- runParams$Agents <- NULL
runParams <- unique(runParams)
colTypes <- colors()[c(24,24,24,24,130,130,34,34,518,518,518,76,76,130,130,34,34,518,518,518,130)]
lineTypes <- c(1,3,4,5,1,3,1,3,1,3,1,3,4,5,4,5,4,5,4,5)
runKey <- list(lines = list(runs.range, lty=lineTypes, lwd=1.5, col=colTypes, space="bottom"),
text = list(as.character(runs.range)), columns = 5, cex=.7, space="bottom", title = "")
library(lattice)
library(latticeExtra)
png(file="SummaryData/pop_vs_estimate.png", height=6, width=8, units="in", res=600)
xyplot(Pop_Max ~ Year, data=popEstimates, type = "h", col=colors()[200], xlab=list("Years A.D.", cex=1, fontfamily="Helvetica"), ylab=list("Population in Households", cex=1, fontfamily="Helvetica"), ylim=c(0,5200), xlim=c(600,1300), scales=list(x=list(tick.number=14), y=list(tick.number=9), fontfamily="Helvetica", tck=c(1,0)), key = runKey) +
xyplot(Households ~ Year, data=popEstimates, type = "h", col=colors()[225]) +
xyplot(Pop_Min ~ Year, data=popEstimates, type = "h", col=colors()[250]) +
xyplot(Agents ~ Year, groups=Run, data=systemStats, type="l", lty=lineTypes, lwd=1.5, col.line=colTypes)
dev.off()
APPENDIX B.2

R Code: VEP Spatial Correlation Analysis
## Data crunching script for the Village Ecodynamics Project.
## Written by R. Kyle Bocinsky on 09-27-2010 using Tim Kohler's SAS scripts as a template.

## Required libraries.
library(reshape)

## Create output directory
dir.create("SummaryData")

## Specify the range or list of numbered runs to be crunched.
runs.range <- 1:20
runs.list <- c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20)

## This first section takes the household location output from each period of each run, makes
## them into a single vector, appends the run and period numbers, and outputs a both concatenated CSV
## file for each run (HHLocations_*_.csv), and a file with data from all runs
## (allHHLocations.csv).
## U.S.E.R MU.S.T SPECIFY WHETHER TO LOOP OVER runs.range OR runs.list!!!
## Runs must have numerical tag. Adjust the read command as needed.
for (i in runs.range){
    for (j in 6:19){
        system(paste("tr -d '\r\n' < ", paste('RawData/H_Yrs_P', j, '_', i, '.txt', sep=''),
        " > ", paste('RawData/H_Yrs_P', j, '_', i, '_flat.txt', sep=''))
        hhlocations <- read.table(paste('RawData/H_Yrs_P', j, '_', i, '_flat.txt', sep=''))
        hhlocations$Run <- i
        hhlocations$Period <- j
        if(j==6){
            mergedHHLocations <- hhlocations
        } else {
            mergedHHLocations <- rbind(mergedHHLocations, hhlocations)
        }
        rm(hhlocations)
    }
    if(i==1){
        allHHLocations <- mergedHHLocations
    } else {
        allHHLocations <- rbind(allHHLocations, mergedHHLocations)
    }
    write.csv(mergedHHLocations, file = paste('SummaryData/HHLocations_', i, '.csv', sep=''))
    rm(mergedHHLocations)
}

## This next section gets the observed and smoothed household locations, and
## appends them to the simulated locations.
## This is saved as a CSV file (allHHLocationsSim&Obs.csv).
allHHLocations <- read.csv("SummaryData/allHHLocationsSim.csv")
obsHHLocations <- read.csv("ObservedHH/HHLocations_Observed.csv")
allHHLocations$X <- NULL
obsHHLocations$X <- NULL
colnames(obsHHLocations) <- colnames(allHHLocations)
allHHLocations <- rbind(allHHLocations, obsHHLocations)
write.csv(allHHLocations, file = "SummaryData/allHHLocationsSim&Obs.csv")
## Finally, we calculate pairwise correlations coefficients between the three observed datasets and the runs, for each period. This is saved as a CSV file (allHHLocationsCorXTableSim.csv).

event <- read.csv("SummaryData/allHHLocationsSim&Obs.csv")
event$X <- NULL
for(j in 6:19){
  periodRuns <- subset(event, Period==j)
  periodRuns$Period <- NULL
  rownames(periodRuns) <- periodRuns$Run
  periodRuns$Run <- NULL
  periodRuns <- t(periodRuns)
  cor <- data.frame(cor(periodRuns, use="complete.obs"))
  cor$real_hyr <- cor$real_hyr_U.S. <- cor$real_hyr_KS <- NULL
  cor$Period <- j
  cor <- cor["real_hyr_U.S.",]
  if(j==6){
    corrs <- cor
  }
  if(j>6){
    corrs <- rbind(corrs, cor)
  }
  rm(cor)
  rm(periodRuns)
}
rownames(corrs) <- corrs$Period
write.csv(corrs, file = "SummaryData/allHHLocationsCorXTableSim.csv")
rm(event)
rm(corrs)

## Here, we generate estimates of the baseline correlation expected if a given number of households are on the landscape. This is done by "shuffling" the vector of cells for a given run and period, recalculating the correlation, and iterating this "n" numbers of times to get an average baseline. This adheres to the SIM1 method reported on the in VEP final report. This takes about 7 minutes to run on 20 runs. This is saved as a CSV file (allHHLocationsCorXTableRand.csv).
n <- 100
allHHLocations <- read.csv("SummaryData/allHHLocationsSim&Obs.csv")
event$X <- NULL
date()
for(j in 6:19){
  periodRuns <- subset(event, Period==j)
  periodRuns$Period <- NULL
  rownames(periodRuns) <- periodRuns$Run
  periodRuns$Run <- NULL
  periodRuns <- as.matrix(periodRuns)
  for(k in 1:n){
    periodRun <- periodRuns
    for(i in runs.range){
      periodRun[i,] <- sample(periodRun[i,])
    }
    periodRuns <- periodRun
    periodRun <- t(periodRun)
cor <- data.frame(cor(periodRun, use="complete.obs"))
cor$real_hyr <- cor$real_hyr_U.S. <- cor$real_hyr_KS <- NULL
cor$Period <- j
cor <- cor["real_hyr_U.S.",]
if(k==1){
  means <- cor
}
if(k>1){
  means <- rbind(means, cor)
}
mean <- t(data.frame(sapply(means, mean, na.rm=TRUE)))
if(j==6){
  corrs <- mean
}
if(j>6){
corrs <- rbind(corrs, mean)
}
rm(cor)
rm(periodRuns)

date()
corrs <- data.frame(corrs)
rownames(corrs) <- corrs$Period
write.csv(corrs, file = "SummaryData/allHHLocationsCorXTableRand.csv")
rm(corrs)

## Now, we can calculate the corrected correlation coefficients for each randomization.
## This comes to be cor(corrected) = cor(sim)-cor(Rand*).
## This is saved as a CSV file (allHHLocationsCorXTableSim.csv).
sim <- read.csv("SummaryData/allHHLocationsCorXTableSim.csv")
rand <- read.csv("SummaryData/allHHLocationsCorXTableRand.csv")
sim$X <- rand$X <- NULL
corrs <- sim-rand
rownames(corrs) <- corrs$Period <- rand$Period
write.csv(corrs, file = "SummaryData/allHHLocationsCorXTable.csv")
rm(corrs)

## This script converts the cross-tabulated correlations into something that may be easily
## graphed.
## This is saved as a CSV file (allHHLocationsCor.csv).
corrs <- read.csv("SummaryData/allHHLocationsCorXTable.csv")
corrs$X <- NULL
for (i in runs.range){
  for(j in 1:14){
    run <- i
    period <- corrs$Period[j]
cor <- corrs[j,i]
count <- c(run,period,cor)
    if(i==1 & j==1){
      counts <- count
    }
    if(i>1 | j>1){
      counts <- rbind(counts, count)
    }
  }
}
colnames(counts) <- c("Run","Period","Correlation")

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# Now, we calculate parameter weightings through a multiple linear regression.

## PHD <- TRUE

```r
runParameters <- read.csv("SummaryData/runParameters.csv")
correlations <- read.csv("SummaryData/allHHLocationsCor.csv")
runParameters$X <- correlations$X <- NULL

correlations <- merge(correlations, runParameters, by = "Run")
correlations$DOMESTICATION <- ifelse(correlations$DOMESTICATION == "true", c(1), c(0))
correlations$TURKEY_WATER <- ifelse(correlations$TURKEY_WATER == "true", c(1), c(0))

if(PHD){
correlations <- subset(correlations, correlations$DOMESTICATION==0 | (correlations$TURKEY_WATER == 1 & correlations$TURKEY_MAIZE_PER == 0.7))
}

for( i in 6:19){
corrs <- subset(correlations, correlations$Period == i)
attach(corrs)
p_need <- factor(PROTEIN_NEED, levels=c(5,15), ordered=TRUE)
hunt_radius <- factor(HUNT_SRADIUS, levels=c(20,40), ordered=TRUE)
domestication <- factor(DOMESTICATION, levels=c(0,1), ordered=TRUE)
if(!PHD){
turkey_water <- factor(TURKEY_WATER, levels=c(0,1), ordered=TRUE)
turkey_maize_per <- factor(TURKEY_MAIZE_PER, levels=c(0,0.0,0.5,0.7), ordered=TRUE)
}

glm <- glm(Correlation ~ p_need+hunt_radius+domestication+turkey_water+turkey_maize_per)
}
```

else {

```r
summary(glm)
anova(glm)
glm.c <- as.data.frame(t(as.data.frame(coefficients(glm))))
glm.c$Period <- i
glm.c$turkey_maize_per.Q <- NULL
rownames(glm.c) <- i
if(i==6){
corrs.coefs <- glm.c
}
if(i>6){
corrs.coefs <- rbind(corrs.coefs, glm.c)
}
```

if(PHD){
write.csv(corrs.coefs, file = "SummaryData/allHHLocationsGLM_PHD.csv")
}
else { 
write.csv(corrs.coefs, file = "SummaryData/allHHLocationsGLM.csv")
}
```

if(PHD){
corrs.coefs <- read.csv("SummaryData/allHHLocationsGLM_PHD.csv")
}
else {
corrs.coefs <- read.csv("SummaryData/allHHLocationsGLM.csv")
}
## This is saved as a PNG file (Correlations.png).

## graph of correlation coefficients.

corr.coefs = NULL

colTypes = colors()[c(24, 130, 34, 518, 76)]

key.labels = c("PROTEIN_NEED", "HUNT_SRADIUS", "DOMESTICATION", "TURKEY_WATER", "TURKEY_MAIZE_PER")

if(PHD){
  this.key <- list(lines = list(lwd=1.5, col=colTypes[1:3], space="bottom"), text = list(key.labels[1:3]), columns = 3, cex=0.7, space="bottom", title = "", between.columns=0.5)
} else {
  this.key <- list(lines = list(lwd=1.5, col=colTypes, space="bottom"), text = list(key.labels), columns = 3, cex=0.7, space="bottom", title = "", between.columns=0.5)
}

## Here, we plot the parameter loadings by period.

attach(corr.coefs)

if(PHD){
  png(file="SummaryData/ParameterLoadingsPHD.png", height=6, width=8, units="in", res=600)
} else {
  png(file="SummaryData/ParameterLoadingsAll.png", height=6, width=8, units="in", res=600)
}

if(PHD){
  xyplot(p_need.L~Period, type="l", col=colTypes[1], lwd=1.5, xlab=list("Period", cex=1, fontfamily="Helvetica"), ylab=list("Regression Coefficient", cex=1, fontfamily="Helvetica"), scales=list(x=list(tick.number=14), y=list(tick.number=8), fontfamily="Helvetica", tck=c(1,0)), ylim=c(-0.04, 0.02), xlim=c(5,20), key=this.key)+
  xyplot(hunt_radius.L~Period, type="l", lwd=1.5, col=colTypes[2])+
  xyplot(domestication.L~Period, type="l", lwd=1.5, col=colTypes[3])
} else {
  xyplot(p_need.L~Period, type="l", col=colTypes[1], lwd=1.5, xlab=list("Period", cex=1, fontfamily="Helvetica"), ylab=list("Regression Coefficient", cex=1, fontfamily="Helvetica"), scales=list(x=list(tick.number=14), y=list(tick.number=8), fontfamily="Helvetica", tck=c(1,0)), ylim=c(-0.03, 0.02), xlim=c(5,20), key=this.key)+
  xyplot(hunt_radius.L~Period, type="l", lwd=1.5, col=colTypes[2])+
  xyplot(domestication.L~Period, type="l", lwd=1.5, col=colTypes[3])+
  xyplot(turkey_water.L~Period, type="l", lwd=1.5, col=colTypes[4])+
  xyplot(turkey_maize.per.L~Period, type="l", lwd=1.5, col=colTypes[5])
}

dev.off()

## Here is a quick script for creating and outputting the standard
## graph of correlation coefficients.
## This is saved as a PNG file (Correlations.png).

popEstimates <- read.csv("http://village.anth.wsu.edu/local/pop_estimates.csv")
corr <- read.csv("SummaryData/allHHLocationsCor.csv")
corrSx <- NULL

colTypes = colors()[c(24, 24, 24, 130, 34, 34, 518, 76, 76, 130, 130, 34, 34, 518, 76, 76, 130, 130, 34, 34, 518, 76, 76)]
lineTypes = c(1,3,4,5,1,3,1,3,1,3,4,5,4,5,4,5,4)
lineWeights = c(2.5,1.5,2.5,1.5,2.5,1.5,0.5,0.5,2.5,2.5,0.5,0.5,1.5,2.5,0.5,2.5,1.5,1.5,0.5,0.5)
runKey <- list(lines = list(runs.range, lty=lineTypes, lwd=lineWeights, col=colTypes, space="bottom"), text = list(as.character(runs.range)), columns = 5, cex=0.7, space="bottom", title = "")
library(lattice)
library(latticeExtra)

png(file="SummaryData/Correlations.png", height=6, width=8, units="in", res=600)

xyplot(Correlation ~ Period, data=corr, groups=Run, xlab=list("Period", cex=1, fontfamily="Helvetica"), ylab=list("Corrected Correlation", cex=1, fontfamily="Helvetica"), scales=list(x=list(tick.number=14), y=list(tick.number=6), fontfamily="Helvetica", tck=c(1,0)), type="l", lty=lineTypes, lwd=lineWeights, col.line=colTypes, key=runKey)
dev.off()
APPENDIX B.3

R Code: VEP Demographic Correlation Analysis
## Data crunching script for the Village Ecodynamics Project.
## Written by R. Kyle Bocinsky on 09-27-2010 using Tim Kohler's SAS scripts as a template.

## Required libraries.
library(reshape)

## Create output directory
dir.create("SummaryData")

## Specify the range or list of numbered runs to be crunched.
runs.range <- 1:20
runs.list <- c(110,115,120,121,122,123,124,125,130,135,140)

## This first section takes the agent statistics output from each run, drops unwanted variables,
## aggregates it by taking the mean of variable values across all agents per year (excluding NA
## values), and outputs a concatenated CSV file (merged_agg_agent_stats.csv) of data from all
## runs.
## U.S.E.R MU.S.T SPECIFY WHETHER TO LOOP OVER runs.range OR runs.list!!!
## Runs must have numerical tag. Adjust the read command as needed.
for (i in runs.list) {
  agentStats <- read.delim(paste('RawData/agent_stats_run_', i, '.out', sep=''))
  runParams <- read.csv("SummaryData/runParameters.csv")
  runParams$X <- NULL
  agentStats$proteinGotten <- (agentStats$Domestication_Protein + agentStats$Hunting_Protein +
                            agentStats$grnNetwork.getPro_received + agentStats$brnNetwork.getPro_received)
  agentStats$proteinNeeded <- ((agentStats$family_size+agentStats$Deaths-agentStats$Births)*
                               runParams[i,2]*365)
  agentStats$prop_protein_gotten_from_domestication <- ((agentStats$Domestication_Protein)/
                                         (agentStats$proteinGotten))
  agentStats$prop_protein_need_from_domestication <- ((agentStats$Domestication_Protein)/
                                              (agentStats$proteinNeeded))
  agentStats$prop_protein_gotten_from_hunting <- ((agentStats$Hunting_Protein)/
                                           (agentStats$proteinGotten))
  agentStats$prop_protein_need_from_hunting <- ((agentStats$Hunting_Protein)/
                                              (agentStats$proteinNeeded))
  agentStats$Plots <- agentStats$H_plots+agentStats$A_plots
  agentStats$remarriage_count <- NULL
  agentStats$dad <- NULL
  agentStats$kid1 <- NULL
  agentStats$kid2 <- NULL
  agentStats$kid3 <- NULL
  agentStats$kid4 <- NULL
  agentStats$kid5 <- NULL
  agentStats$kid6 <- NULL
  agentStats$kid7 <- NULL
  agentStats$kid8 <- NULL
  agentStats$CalVillage._HH_Yr <- NULL
  agentStats$Maize_Given_Phil <- NULL
  agentStats$M_Received_GRN <- NULL
  agentStats$M_Request_GRN <- NULL
  agentStats$M_exchange_GRN <- NULL
  agentStats$M_Wasted_GRN <- NULL
  agentStats$Num_Exchange_GRN <- NULL
  agentStats$M_Received_BRN <- NULL
  agentStats$M_Request_BRN <- NULL
  agentStats$M_exchange_BRN <- NULL
  agentStats$M_Wasted_BRN <- NULL
  agentStats$Num_Exchange_BRN <- NULL
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agentStats$ Paid_Back_BRN <- NULL
agentStats$ Num_Paybacks_BRN <- NULL
agentStats$ agent <- NULL
agentStats$ family_size <- NULL
agentStats$ Deaths <- NULL
agentStats$ Births <- NULL
agentStats$ Fuel_distance <- NULL
agentStats$ Water_distance <- NULL
agentStats$ H_plots <- NULL
agentStats$ A_plots <- NULL
agentStats$ M_Harvest <- NULL
agentStats$ Hrs_per_wrkr_per_day <- NULL
agentStats$ Water_Cal <- NULL
agentStats$ Hunt_Cal <- NULL
agentStats$ Deer <- NULL
agentStats$ Hare <- NULL
agentStats$ Rabbit <- NULL
agentStats$ Turkey_kept <- NULL
agentStats$ Last_move <- NULL
agentStats$ current_protein_storage <- NULL
agentStats$ max_store <- NULL
agentStats$ Deer_Return_Rate <- NULL
agentStats$ Hare_Return_Rate <- NULL
agentStats$ Rabbit_Return_Rate <- NULL
agentStats$ Combined_Return_Rate <- NULL
agentStats$ CalVillage._HH_Yr <- NULL
agentStats$ P_Deficient <- NULL
agentStats$ Protein_Given_Phil <- NULL
agentStats$ grnNetwork.getPro_received <- NULL
agentStats$ grnNetwork.getProteinExchangeRequests <- NULL
agentStats$ grnNetwork.getProteinRequests <- NULL
agentStats$ grnNetwork.getProteinExchanged <- NULL
agentStats$ grnNetwork.getProteinWasted <- NULL
agentStats$ brnNetwork.getPro_received <- NULL
agentStats$ brnNetwork.getProteinExchangeRequests <- NULL
agentStats$ brnNetwork.getProteinRequests <- NULL
agentStats$ brnNetwork.getProteinExchanged <- NULL
agentStats$ brnNetwork.getProteinPaidBack <- NULL
agentStats$ brnNetwork.getPro_num_paybacks <- NULL
agentStats$x <- NULL
agentStats$y <- NULL
agentStats$Run <- i
agentStats[agentStats==999] <- NA
attach(agentStats)
aggAgentStats <- aggregate(agentStats, by=list(Year), FUN=mean, na.rm=TRUE)
detach(agentStats)
rm(agentStats)
if(i==110){
    mergedAgentStats <- aggAgentStats
}
if(i>110){
    mergedAgentStats <- rbind(mergedAgentStats, aggAgentStats)
}
rm(aggAgentStats)
## This script creates demographic goodness of fit tests.

```r
dev.off
```

```r
fontfamily
```

```r
lineTypes <- c(1,3,1,3,1,3,1,3,4,5,4,5,4,5,4,5)
```

```r
colTypes <- colors()[c(130,130,34,34,518,518,76,76,130,130,34,34,518,518,76,76)]
```

```r
runs.range <- 5:20
```

```r
stats <- subset(stats, stats$Run >= 5)
```

```r
## “Populations vs. Estimates” graph.
```

```r
write.csv(mergedAgentStats, file = "SummaryData/merged_agg_agent_stats_domestication_100.csv")
```

```r
## This is saved as a CSV file (merged_system_stats.csv).
```

```r
for (i in runs.list) {
    systemStats <- read.delim(paste('RawData/system_stats_run_', i, '.data', sep=''))
    if(i==110) {
        mergedSystemStats <- systemStats
    }
    if(i>110) {
        mergedSystemStats <- rbind(mergedSystemStats, systemStats)
    }
    rm(systemStats)
}
```

```r
write.csv(mergedSystemStats, file = "SummaryData/merged_system_stats_domestication_100.csv")
```

```r
mergedAgentStats$Group.1 <- NULL
```

```r
write.csv(mergedAgentStats, file = "SummaryData/merged_agg_agent_stats_domestication_100.csv")
```

```r
## Finally, we merge the agent and system statistics.
```

```r
agentStats <- read.csv("SummaryData/merged_agg_agent_statsDomestication_100.csv")
```

```r
systemStats <- read.csv("SummaryData/merged_system_statsDomestication_100.csv")
```

```r
agentSystemStats <- merge(agentStats, systemStats, by=c("Run", "Year"))
```

```r
agentSystemStats$X.x <- NULL
```

```r
agentSystemStats <- rename(agentSystemStats, c(Deer.x="Deer_Hunted", Rabbit.x="Rabbit_Hunted", Hare.x="Hare_Hunted", Deer.y="Deer", Hare.y="Hare", Rabbit.y="Rabbit"))
```

```r
write.csv(agentSystemStats, file = "SummaryData/agent_system_statsDomestication_100.csv")
```

```r
## And, just for fun, here is a quick script for creating and outputting the standard
## “Populations vs. Estimates” graph.
```

```r
agentSystemStats <- read.csv("SummaryData/agent_system_statsDomestication_100.csv")
```

```r
stats <- agentSystemStats[order(agentSystemStats$Run, agentSystemStats$Year),]
```

```r
#stats <- subset(stats, stats$Run >= 5)
```

```r
#runs.range <- 5:20
```

```r #colTypes <- colors() [c(130,130,34,34,518,518,76,76,130,130,34,34,518,518,76,76)]
```

```r #lineTypes <- c(1,3,1,3,1,3,1,3,4,5,4,5,4,5,4,5)
```

```r
colTypes <- colors()[c(24,130,34,518,76,84)]
```

```r
lineTypes <- c(1,1,1,1,1)
```

```r
runKey <- list(lines = list(runs.list, lty=lineTypes, lwd=1.5, col=colTypes, space="bottom"),
```

```r
text = list(as.character(runs.list)), columns = 7, cex=.7, space="bottom", title = "")
```

```r
library(lattice)
```

```r
library(latticeExtra)
```

```r
png(file="SummaryData/DomesticationProportion_100.png", height=6, width=8, units="in", res=600)
```

```r
xyplot(prop.protein_gotten_from_domestication ~ Year, stats, groups=Run, type="l", lty=lineTypes, lwd=1.5, col.line=colTypes, xlab=list("Years A.D.", cex=1, fontfamily="Helvetica"), ylab=list("Average Proportion of Protein Derived from Turkey", cex=1, fontfamily="Helvetica"), ylim=c(0,1), xlim=c(600,1300), scales=list(x=list(tick.number=14), y=list(tick.number=9), fontfamily="Helvetica", tck=c(1,0)), key = runKey)+
```

```r
glayer(panel.smoother(..., se=FALSE, n=700, lwd=2.0))
```

```r
dev.off()
```

```r
## This script creates demographic goodness of fit tests.
```
library(lattice)
library(latticeExtra)
colTypes <- colors(c(24, 24, 24, 24, 130, 130, 34, 34, 518, 518, 76, 76, 130, 130, 34, 34, 518, 518, 76, 76))
lineTypes <- c(1, 3, 4, 5, 1, 3, 1, 3, 1, 3, 1, 3, 4, 5, 4, 5, 4, 5, 4, 5, 4, 5)
runKey <- list(lines = list(runs.range, lty=lineTypes, lwd=1.5, col=colTypes, space="bottom"),
text = list(as.character(runs.range)), columns = 5, cex=.7, space="bottom", title = "")
popEstimates <- read.csv("http://village.anth.wsu.edu/local/pop_estimates.csv")
systemStats <- read.csv("SummaryData/merged_system_stats.csv")
pops <- merge(systemStats, popEstimates, by=col(c("Year")))
pops$X <- pops$Share <- pops$Deer <- pops$Rabbit <- pops$Standing_Crop <- pops$Deadwood <- NULL
attach(pops)
pops$Period[Year <= 725] <- 6
pops$Period[Year > 725 & Year <= 800] <- 7
pops$Period[Year > 800 & Year <= 840] <- 8
pops$Period[Year > 840 & Year <= 880] <- 9
pops$Period[Year > 880 & Year <= 920] <- 10
pops$Period[Year > 920 & Year <= 980] <- 11
pops$Period[Year > 980 & Year <= 1020] <- 12
pops$Period[Year > 1020 & Year <= 1060] <- 13
pops$Period[Year > 1060 & Year <= 1100] <- 14
pops$Period[Year > 1100 & Year <= 1140] <- 15
pops$Period[Year > 1140 & Year <= 1180] <- 16
pops$Period[Year > 1180 & Year <= 1220] <- 17
pops$Period[Year > 1220 & Year <= 1260] <- 18
pops$Period[Year > 1260 & Year <= 1300] <- 19
pops$Households[Year == 600] <- pops$Households[Year == 601]
pops$Pop_MIN[Year == 600] <- pops$Pop_MIN[Year == 601]
pops$Pop_MAX[Year == 600] <- pops$Pop_MAX[Year == 601]
pops$Year <- NULL
pops <- aggregate(. ~ Period + Run, pops, mean)
pops$Households <- pops$Households-pops$Agents
pops$HouseholdsABS <- abs(pops$Households)
pops$Pop_MIN <- pops$Pop_MIN-pops$Agents
pops$Pop_MINABS <- abs(pops$Pop_MIN)
pops$Pop_MAX <- pops$Pop_MAX-pops$Agents
pops$Pop_MAXABS <- abs(pops$Pop_MAX)
for(i in runs.range){
  devs <- subset(pops, Run==i)[c("Period","HouseholdsABS")]
  row.names(devs) <- devs$Period
  devs$Period <- NULL
  devs <- t(devs)
  row.names(devs) <- i
  if(i==1){
    devs.all <- devs
  }
  if(i>1){
    devs.all <- rbind(devs.all, devs)
  }
  rm(devs)
}
devs.all <- t(devs.all)
write.csv(devs.all,file="SummaryData/deviations.csv")

png(file="SummaryData/PopulationDeviations.png", height=6, width=8, units="in", res=600)
xyplot(HouseholdsABS ~ Period, groups=Run, data=pops, type="l", lty=lineTypes, lwd=1.5, col.line=colTypes, xlab=list("Period", cex=1, fontfamily="Helvetica"), ylab=list("Absolute Deviation from Population Estimate", cex=1, fontfamily="Helvetica"), ylim=c(3500, -200), xlim=c(5, 20), scales=list(x=list(tick.number=14), y=list(tick.number=9), fontfamily="Helvetica"), tck=c(1, 0), key = runKey)

dev.off()

### Slope Study

library(lattice)
library(latticeExtra)

colTypes <- colors() \[c(24, 24, 24, 24, 130, 130, 34, 34, 518, 518, 76, 76, 130, 130, 34, 34, 518, 518, 76, 76)\]

lineTypes <- c(1, 3, 4, 5, 1, 3, 1, 3, 1, 3, 1, 3, 4, 5, 4, 5, 4, 5, 4, 5)

runKey <- list(lines = list(runs.range, lty=lineTypes, lwd=1.5, col=colTypes, space="bottom"),
              text = list(as.character(runs.range), cex=5, space="bottom", title=""))

popEstimates <- read.csv("http://village.anth.wsu.edu/local/pop_estimates.csv")

systemStats <- read.csv("SummaryData/merged_system_stats.csv")

pops <- merge(systemStats, popEstimates, by=c("Year"))

colTypes[pops$Run, pops$Year] <- colors()

pops$X <- pops$Share <- pops$Deer <- pops$Rabbit <- pops$Standing_Crop <- pops$Deadwood <- NULL

pops$Period[pops$Year > 667 & pops$Year <= 762] <- 1

pops$Period[pops$Year > 762 & pops$Year <= 820] <- 2

pops$Period[pops$Year > 820 & pops$Year <= 860] <- 3

pops$Period[pops$Year > 860 & pops$Year <= 900] <- 4

pops$Period[pops$Year > 900 & pops$Year <= 950] <- 5

pops$Period[pops$Year > 950 & pops$Year <= 1000] <- 6

pops$Period[pops$Year > 1000 & pops$Year <= 1040] <- 7

pops$Period[pops$Year > 1040 & pops$Year <= 1080] <- 8

pops$Period[pops$Year > 1080 & pops$Year <= 1120] <- 9

pops$Period[pops$Year > 1120 & pops$Year <= 1160] <- 10

pops$Period[pops$Year > 1160 & pops$Year <= 1200] <- 11

pops$Period[pops$Year > 1200 & pops$Year <= 1240] <- 12

pops$Period[pops$Year > 1240 & pops$Year <= 1280] <- 13

pops$Households[Year == 600] <- pops$Households[Year == 601]

pops$Pop_High[Year == 600] <- pops$Pop_High[Year == 601]

pops$Pop_High[Year == 600] <- pops$Pop_High[Year == 601]

pops$PROTEIN_NEED <- pops$HUNTED_RADIUS <- pops$DOMESTICATION <- pops$STURKEY_WATER <- pops$TURKEY_MAIZE_PER <- NULL

for(i in runs.range){
  for(j in 1:13){
    dev <- subset(pops, Run==i & Period==j)
    slopes <- as.data.frame(i)
    slopes$run <- i
    slopes$period <- j + 5.5
    slopes$sim <- coefficients(lm(Agents-Year, data=devs))[2]
    slopes$observed <- (devs$Households[length(devs$Households)]-devs$Households[1])/length(devs$Households)
    if(i==1 & j==1){
      slopes.all <- slopes
    }else{
      slopes.all <- rbind(slopes.all, slopes)
    }
    rm(devs)
    rm(slopes)
  }
}

slopes.all$fit <- abs(slopes.all$sim-slopes.all$observed)

slopes.all$i <- NULL
write.csv(slopes.all, file="SummaryData/Slopes.csv")
for(i in runs.range){
    devs <- subset(slopes.all, slopes.all$run==i)[c("period","fit")]
    row.names(devs) <- devs$period
    devs$period <- NULL
    devs <- t(devs)
    row.names(devs) <- i
    if(i==1){
        devs.all <- devs
    }
    if(i>1){
        devs.all <- rbind(devs.all, devs)
    }
    rm(devs)
}
devs.all <- t(devs.all)
write.csv(devs.all, file="SummaryData/SlopesX.csv")

slopes.all <- read.csv("SummaryData/Slopes.csv")
png(file="SummaryData/SlopeDeviations.png", height=6, width=8, units="in", res=600)
xyplot(fit ~ period, groups=run, data=slopes.all, type="l", lty=lineTypes, lwd=1.5,
col.line=colTypes, xlab=list("Period", cex=1, fontfamily="Helvetica"), ylab=list("Absolute Deviation from Slope Estimate", cex=1, fontfamily="Helvetica"), ylim=c(45,-2), xlim=c(5,20),
scales=list(x=list(tick.number=14), y=list(tick.number=9), fontfamily="Helvetica", tck=c(1,0)),
key = runKey)
dev.off()
APPENDIX C

R Code: The Marginal Value Theorem of Patch Choice with an Alternative Strategy
```r
png(file="OFT.png", height=6, width=8, units="in", res=600)
quartz(width=8, height=6)

m <- 0.09
mStar <- 0.165
star=TRUE
x<-seq( 0, 10, length = 1000)
r <- m*x
rStar <- mStar*x

a <- c(6/6,6/5,6/4,6/3,6/2,6/1)
d <- 0.75
y <- dy <- dyStar <- matrix(nrow=6, ncol=1000)
mx <- mStar <- list(seq( 1, 2.8, length = 1000),seq( 0.6, 2.2, length = 1000),seq( 0.2, 1.4, length = 1000),seq( 0, 5, length = 1000),seq(0, 5, length = 1000))
t <- ty <- tStar <- tyStar<- c(0,0,0,0,0)

par(family="Helvetica", mar=c(1,1,1,1))

for(i in 1:6)
  y[i,] <- (1-exp(-x/3))/a[i]
t[i] <- -3*log(3*a[i]*m)
ty[i] <- (1-(3*a[i]*m))/a[i]
mx[[i]] <- seq(max(t[i]-sqrt((d^2)/(1-m^2))),0),max(t[i]+sqrt((d^2)/(1-m^2))),0), length=1000)
dy[i,] <- (m*mx[[i]])+(3*m*log(3*a[i]*m)+(1/a[i])-(3*m)
tStar[i] <- -3*log(3*a[i]*mStar)
tyStar[i] <- (1-(3*a[i]*mStar))/a[i]
mxStar[[i]] <- seq(max(tStar[i]-sqrt((d^2)/(1-mStar^2))),0),max(tStar[i]+sqrt((d^2)/(1-mStar^2))),0), length=1000)
dyStar[i,] <- (mStar*mxStar[[i]])+(3*mStar*log(3*a[i]*mStar)+(1/a[i])-(3*mStar)
}

for(i in 1:6)
  if(i==1)
    if(!star){
      if((1/(3*a[i]))>m){
        plot(y[i,] ~ x, type="l", col="black", axes=FALSE, xlab="", ylab="")
      }else{
        plot(y[i,] ~ x, type="l", col="darkgrey", axes=FALSE, xlab="", ylab="")
      }
    }else{
      if((1/(3*a[i]))>mStar & tStar[i]>0.1){
        plot(y[i,] ~ x, type="l", col="red", axes=FALSE, xlab="", ylab="")
      }else if((1/(3*a[i]))>m){
        plot(y[i,] ~ x, type="l", col="black", axes=FALSE, xlab="", ylab="")
      }
    }
    axis(1, labels=FALSE, lwd.tick=0, pos=0)
    axis(2, labels=FALSE, lwd.tick=0, pos=0)
mtext("T", side=1, at=9.95, padj=-1.5)
text(-.18,0.985,expression(N[T]))
    lines(r ~ x, col="black")
    text(min((1/m),9.8),min(0.975, (10*m)+.01),"R")
```
if (star){
    lines(rStar ~ x, col="red")
    text(min((1/mStar)+.1, 10),min(0.975, 10*mStar),"R*", col="red")
}
else{
    if(!star){
        if(1/(3*a[i])>m){
            lines(y[i,] ~ x, col="black")
        }else{
            lines(y[i,] ~ x, col="darkgrey")
        }
    }else{
        if(1/(3*a[i])>m & mStar & tStar[i]>0.1){
            lines(y[i,] ~ x, col="red")
        }else if(1/(3*a[i])>m){
            lines(y[i,] ~ x, col="black")
        }else{
            lines(y[i,] ~ x, col="darkgrey")
        }
    }
}
if(1/(3*a[i])>m){
    lines(dy[i,] ~ mx[[i]], col="black", lty=2)
    segments(t[i],ty[i],t[i],0, lty=3)
}
if(mStar>m & & star){
    lines(dyStar[i,] ~ mxStar[[i]], col="red", lty=2)
    if(tStar[i]>0.1) segments(tStar[i],tyStar[i],tStar[i],0, lty=3, col="red")
}
}
for(i in 1:6){
    text(10.1,(1/a[i])*0.965), LETTERS[i])
}
if(1/(3*a[1])>m){
    text((t[1]), -0.025, expression(T[A]))
}
if(1/(3*a[2])>m){
    text((t[2]), -0.025, expression(T[B]))
}
if(1/(3*a[3])>m){
    text((t[3]), -0.025, expression(T[C]))
}
if(1/(3*a[4])>m){
    text((t[4]), -0.025, expression(T[D]))
}
if(1/(3*a[5])>m){
    text((t[5]), -0.025, expression(T[E]))
}
if(1/(3*a[6])>m){
    text((t[6]), -0.025, expression(T[F]))
}
if(mStar>m & & star){
    if(1/(3*a[1])>mStar & tStar[1]>0.1){
text(tStar[1], -0.025, expression(T["A*"]), col="red")
}

if((1/(3*a[2]))>mStar & tStar[2]>0.1){
text(tStar[2], -0.025, expression(T["B*"]), col="red")
}

if((1/(3*a[3]))>mStar & tStar[3]>0.1){
text(tStar[3], -0.025, expression(T["C*"]), col="red")
}

if((1/(3*a[4]))>mStar & tStar[4]>0.1){
text(tStar[4], -0.025, expression(T["D*"]), col="red")
}

if((1/(3*a[5]))>mStar & tStar[5]>0.1){
text(tStar[5], -0.025, expression(T["E*"]), col="red")
}

if((1/(3*a[6]))>mStar & tStar[6]>0.1){
text(tStar[6], -0.025, expression(T["F*"]), col="red")
}

dev.off()}