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A Simulation of Anthropogenic Mammoth Extinction

M. Klapman

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1 Introduction

There are multiple hypotheses as to why the Columbian Mammoth (*Mammuthus columbi*) and other megafauna in North America went extinct relatively recently and relatively quickly. The most popular of which are disease, climate change, meteorite strikes, and over hunting by humans [2, 9]. There is evidence to show that a combination of factors contributed to the megafaunal extinction, but "overkill" explores the idea that early humans migrated onto the continent and then hunted the mammoths and other megafauna to extinction. The overkill hypothesis was first proposed by anthropologist Paul Martin in 1973 [8]. Evidence from radiocarbon dating shows that the extinction of megafauna in North America was a geologically very sudden event. Not only was it very sudden, but it lines up well with our current estimations of when humans migrated onto the continent of North America about 13,000 BP (years before present) [8].

Jared Diamond's 1997 *Guns, Germs, and Steel* popular science book was the first time to bring the overkill theory to the general public [4]. Then, paleobiologist John Alroy's work published in 2001 was the first evidence using computer simulations that overkill was the likely cause of the megafaunal extinctions of North America. He found that extinction was inevitable for a large number of species, but matching the true fates (extinction vs survival) of species was only partially accurate; 32 of 41 species fates were correctly determined in the best performing simulation run [1].

In 2015, Frank et al published the paper *Investigating Anthropogenic Mammoth Extinction with Mathematical Models*. This paper attempted to determine extinction dates using a continuous ordinary differential equations model [5]. This model uses differential equations to calculate rates at which humans and mammoths were born, died, and migrated. The goal of their project was to find any stable equilibria, therefore determining whether the populations stabilize either at extinction or at survival. One potential flaw of this model is that it has continuous state variables. This allows the movement of fractions of humans or mammoths throughout the simulation. These fractions, while simply being unrealistic, also lead to erroneous results such as when extinction is not declared due to mammoth population being just a fraction above the extinction criteria.

The exact timeline of when humans first migrated and how they migrated is a heavily debated topic. Throughout this paper, we will be following the assumption that the first humans migrated into North America through Beringia by means of an "ice-free corridor" around 13,000 BP [3, 6, 13]. The earliest Clovis (or early human) artifacts to be found in North America date around 12,000 BP to 11,500 BP [13]. Most megafaunal extinctions in North America were complete by 10,000 BP [7], and there is evidence to suggest that North America was completely settled by humans by 9,000 BP [14]. Using these dates and information, we conservatively assumed that the shortest time frame for human migration would be between 13,000 BP and 12,000 BP, while the longest time frame for human migration would be between 13,000 BP and 9,000 BP. This resulted in a possible range of human migration through North America of between 1000 and 4000 years. These migration time-spans were used to calibrate the migration rates throughout our final simulations.

In this paper, we expand on this research in anthropogenic mammoth extinction by creating a discrete stochastic model. The goal is to create a model that is analogous to the ordinary differential equations (ODE) model in Frank’s paper while reducing computation time and finding more realistic migration rates. Reducing the computation time will allow us to run simulations representing a larger land mass so that we will not have to make the assumption to scale up our predictions linearly.

2 Models

2.1 Single-Patch

The discrete stochastic model that we used was first tested against the previous results of the single-patch ODE model used by Frank [5]. Throughout the entire paper, we used the same parameter names that were used in the ODE paper. The description of the value ranges and units of these parameters are shown in Table 1. We constrict the human and mammoth populations to the carrying capacities K_H and K_M respectively. The parameters r_H and r_M represent the growth rates for each species, while we also put a strong Allee effect, A , on the mammoth population [12, 15]. This Allee effect makes it so that a mammoth population will “pass a point of no return” at the value of A . The mammoth population is not able to recover when it dips below A , so this is used as the extinction criteria. The parameters a_H , a_m , and b account for predation rates between the humans and mammoths.

For the single-patch model, c_H and c_M are used as the migration rate inside and outside of the system. When we move to the metapopulation model, these values change to be a random value to account for terrain differences throughout the grid. Also unique to the single-patch model, N_H and N_M are used to represent the number of humans and mammoths that are outside of the patch we are looking at. Because migration is not allowed from outside of the system in the metapopulation model, these values are not used in our rate calculations.

Parameter	Units	Description	Value	Reference
K_H	<i>humans</i>	human carrying capacity	10	[7]
K_M	<i>mammoths</i>	mammoth carrying capacity	250	[7]
r_H	$year^{-1}$	human growth rate	$[\ln(1.001), \ln(1.034)]$	[7]
r_M	$year^{-1}$	mammoth growth rate	$[\ln(1.04), \ln(1.05)]$	[10]
A	<i>mammoth</i>	Allee effect critical population size	[5, 8]	[11]
a_H	$year^{-1}$	human predation rate	[1, 10]	[7]
a_M	$\frac{mammoth}{human \cdot year}$	mammoth predation rate	[10, 15]	[7]
b	<i>mammoth</i>	predation saturation constant	[1, 10]	assumed
c_H	$year^{-1}$	human migration rate	[0.005, 0.05]	assumed
c_M	$year^{-1}$	mammoth migration rate	[0.2, 0.5]	assumed
N_H	<i>humans</i>	external human population size	[5, 9]	assumed
N_M	<i>mammoths</i>	external mammoth population size	[3, 5]	assumed

Table 1: A list of parameters and their values for patches representative of a 10 square mile area used in Equations (1) and (2). Each of the entries in the “Value” column given in brackets is a range of viable values determined either from the literature or assumed (“Reference” column).

The differential equations given in the ODE model [5] to describe the dynamics of the human

and mammoth populations are as follows,

$$\frac{dH}{dt} = r_H H \left(1 - \frac{H}{K_H}\right) + \frac{a_H M^2 H}{M^2 + b^2} + c_H H \left(\frac{M}{N_M} - 1\right), \quad (1a)$$

$$\frac{dM}{dt} = r_M M \left(1 - \frac{M}{K_M}\right) \left(\frac{M}{A} - 1\right) - \frac{a_M M^2 H}{M^2 + b^2} + c_M M \left(1 - \frac{H}{N_H}\right) \quad (1b)$$

The terms of these differential equations are used to calculate the weighted probability of each event occurring. The events used in the single-patch model are human birth, human death, mammoth birth, mammoth death, human population increase by hunting, mammoth population decrease by hunting, human migration, and mammoth migration. The human hunting event is a case where the human population grows due to the increase of resources gained from the mammoth. It is treated similarly to a growth term. With using the single-patch, the assumption is made that mammoths and humans are able to migrate in and out of the patch from outside of the model, something that will be changed in the metapopulation model later.

A single simulation using the single-patch model runs as follows. The humans and mammoths both begin at carrying capacity, our conservative assumption. During each realization, one event is randomly selected out of the possible events listed previously. This is done using rates calculated directly from the ordinary differential equations. Whichever event is chosen, the populations of the respective species are changed by either adding one, subtracting one, or there will be no change. This continues until the mammoth population reaches the extinction criteria of the Allee threshold.

In order to show that the stochastic model is analogous to the previous ODE model, we ran simulations using the same set of parameters determined by the latin hypercube sampling that was used in the ODE model.

2.2 Metapopulation

The Metapopulation model design involves forming a square grid of single patches to create the system. As in the single-patch case, the event rates for our stochastic model come directly from the equations in the metapopulation ODE model. All of the same event types are used, except migration is changed to disallow movement in and out of the system. The rates for each event type are dependent on the parameters and the number of humans or mammoths in each patch. For migration, the rates are dependent on the parameters, the number of humans or mammoths in the current patch, and the number of humans or mammoths in the neighboring patches. Neighboring patches are defined to be any patch that shares a common side or corner to the current patch.

For convenience, the differential equations used by Frank for patch (i, j) were

$$\begin{aligned} \frac{dH_{i,j}}{dt} &= r_H H_{i,j} \left(1 - \frac{H_{i,j}}{K_H}\right) + \frac{a_H M_{i,j}^2 H_{i,j}}{M_{i,j}^2 + b^2} \\ &\quad + \sum_{g=-1}^1 \sum_{h=-1}^1 H_{i,j}^{\text{mig}} \end{aligned} \quad (2a)$$

$$\begin{aligned} \frac{dM_{i,j}}{dt} &= r_M M_{i,j} \left(1 - \frac{M_{i,j}}{K_M}\right) \left(\frac{M_{i,j}}{A} - 1\right) \\ &\quad - \frac{a_M M_{i,j}^2 H_{i,j}}{M_{i,j}^2 + b^2} + \sum_{g=-1}^1 \sum_{h=-1}^1 M_{i,j}^{\text{mig}} \end{aligned} \quad (2b)$$

where the terms for migration between neighboring patches, H^{mig} and M^{mig} , were defined according to the rules:

if $M_{i,j} > M_{i+g,j+h}$ then

$$H_{i,j}^{\text{mig}} = c_{i+g,j+h \rightarrow i,j} H_{i+g,j+h} \frac{M_{i,j}}{K_M}, \quad (3a)$$

if $M_{i+g,j+h} > M_{i,j}$ then

$$H_{i,j}^{\text{mig}} = -c_{i,j \rightarrow i+g,j+h} H_{i,j} \frac{M_{i+g,j+h}}{K_M}, \quad (3b)$$

if $H_{i,j} < H_{i+g,j+h}$ then

$$M_{i,j}^{\text{mig}} = c_{i+g,j+h \rightarrow i,j} M_{i+g,j+h} \frac{H_{i,j}}{K_H}, \quad (3c)$$

if $H_{i,j} > H_{i+g,j+h}$ then

$$M_{i,j}^{\text{mig}} = -c_{i,j \rightarrow i+g,j+h} M_{i,j} \frac{H_{i+g,j+h}}{K_H}. \quad (3d)$$

For our stochastic metapopulation model, the steps for each simulation are as follows:

1. Set the parameters and set the population initial conditions.
2. Create a matrix of random migration rates to account for terrain.
3. Begin looping over number of events.
4. Calculate the rates of each event type for each patch in the grid or each path between patches for migration.
5. Sum the rates of each individual event type, and then sum all total rates.
6. Update the time elapsed.
7. Randomly select an event type.
8. Randomly select a patch or path depending on event type.
9. Modify respective human or mammoth populations accordingly.
10. Repeat until extinction criteria is met, or until a set time is reached without extinction, and output extinction time, runtime, and total number of events.

In step 1, two $n \times n$ empty grids are created each of which represent the mammoth and human populations respectively. The constant parameters and initial conditions are then set. In step 2, to account for migration rates for both populations, a matrix of randomly generated values between 0 and c is created. This matrix is used to represent differences in terrain across the grid. Then, in step 3 the simulation is set to loop over the number of events until the mammoth population has reached global extinction. Global extinction of mammoths is defined to be when the mammoth population in each patch is less than the Allee affect A .

In step 4, within the simulation loop the rates for each event are calculated using the equations from the ODE model. These equations are shown explicitly in Table 2. An $n \times n$ rate matrix is created for each event type to represent that any event could happen in any patch. Migration is slightly different as instead of looking at patches to calculate rates, we look at the paths between patches. Each patch has migration rates for leaving the patch into each surrounding patch.

Mammoth Demography	$r_M M_{i,j,k} \left(1 - \frac{M_{i,j,k}}{K_M}\right) \left(\frac{M_{i,j,k}}{A} - 1\right)$
Human Demography	$r_H H_{i,j,k} \left(1 - \frac{H_{i,j,k}}{K_H}\right)$
Mammoth Hunting	$\frac{a_M M_{i,j,k}^2 H_{i,j,k}}{M_{i,j,k}^2 + b^2}$
Human Hunting	$\frac{a_H M_{i,j,k} H_{i,j,k}}{M_{i,j,k}^2 + b^2}$
Mammoth Migration	If $H_{i,j,k} < H_{i+g,j+h,k}$: $c_{i,j,g,h} M_{i+g,j+h,k} \frac{H_{i,j,k}}{K_H}$ If $H_{i,j,k} > H_{i+g,j+h,k}$: $-c_{i,j,g,h} M_{i,j,k} \frac{H_{i+g,j+h,k}}{K_H}$
Human Migration	If $M_{i,j,k} > M_{i+g,j+h,k}$: $c_{i,j,g,h} H_{i+g,j+h,k} \frac{M_{i,j,k}}{K_M}$ If $M_{i,j,k} < M_{i+g,j+h,k}$: $-c_{i,j,g,h} H_{i,j,k} \frac{M_{i+g,j+h,k}}{K_M}$

Table 2: Equations used to calculate event rates for each patch in the metapopulation model.

The rates for the populations migrating into the patch from the surrounding patches are just the negatives of those rates.

After the rates are calculated for each event type for each population, in step 5 the rates are totaled for each event and then also a grand total of all rates for all events is calculated. Next is step 6 where the time it took for the event to occur is calculated randomly based on this grand total and is added to the total time elapsed. Next, step 7 consists of choosing a random event type. A random number is generated between 0 and the grand total of the rates. This random number is used to select an event at random by going through each event total and adding them together until this running total is greater than the random number. After the event is chosen, the same process is repeated in step 8 but with a new random number generated between 0 and the total of the rates for the event selected. The running total is created by summing the rates in each patch, or in the case of migration each path. Once the running total is greater than the random number, the last patch whose rate was added is the selected patch where the event happened.

Finally in step 9, now that the event type and event location is selected, the final step is to update the population matrices with the changes. If human birth was selected, the human population in the selected patch will increase by 1. If mammoth death was selected, the mammoth population in the selected patch will decrease by 1, and so on. At the end of the loop, the global extinction criteria is checked. If extinction occurs, the loop ends and it returns the extinction time, runtime, and total number of events.

3 Experiments

Before coming up with a new parameter set to test the stochastic model, a couple experiments were needed. Both of these experiments had the ultimate goal of coming up with a more realistic migration rate for each species.

3.1 Migration Rate Comparisons

Throughout this experiment, we used parameter set one from the original latin hypercube sampling (LHS) as shown in Table 3. Though, instead of using the parameters provided for c_H and c_M , we used a more general random number between 0 and 1. Then we used multipliers to explore differences in migration rate magnitudes between the two species. For example, the migration rates for the human population could be a distribution between 0 and 1, and then we would set

a migration multiplier for the mammoths to be 10. So, the mammoth migration rate for any single path would be exactly 10 times the human migration rate for that same path. We used this method to explore how changing magnitudes of migration rates between the species caused the final extinction time to behave.

3.2 Migration Parameter Calibration

The general idea of this experiment was to find how long it would have taken humans to move from the starting location (the top left patch) to the farthest corner of the grid (the bottom right patch). Using the timeline described in the Introduction Section, the goal was to find a range for the migration rates that satisfied the extremes of the time it took humans to migrate across the continent. These extremes are 1000 years and 4000 years as stated in the introduction. For this experiment, parameter set one from the original latin hypercube sample was used. The exiting criteria for these simulations is when there is at least one human in the bottom right patch rather than the mammoths going extinct. This is because we are looking to find a migration rate corresponding to how long it took humans to migrate that far, not necessarily kill off the mammoths.

The method used to determine the new range on the migration parameter was as follows. An estimated guess of a migration rate was selected, 10 simulations of an n -by- n grid as n increased from 1 to 20 were run, and then the predicted human migration time was found using linear regression. This continued as more estimated guesses were made, bringing us closer to the desired human migration times of 1000 years and 4000 years.

4 Results

4.1 Migration Rate Results

The main result from the migration rate comparison was that the mammoth migration rates did not have a significant effect on the extinction time as shown in Figure 4.1. The predicted extinction time was more dependent on the human migration rate. This allowed us to simplify the model by only having a single migration parameter in our final model.

For the migration parameter calibration, simulations were run as described for varying sizes of the migration parameter. The parameter value corresponding to a human migration of 1000 years was found to be 0.002, and the parameter value corresponding to a human migration of 4000 years was found to be 0.00055. For our new latin hypercube sampling, these two values are used as the range on the migration parameter.

4.2 Single Patch Model Comparison

To show that our stochastic single-patch model is analogous to the ODE model, we focused on testing parameter set 8 from Table 3 as this was the only parameter set that led to mammoth extinction in the ODE model. We ran 10,000 simulations of the stochastic model with the initial conditions of 20 mammoths and 10 humans, averaging the species populations at every time step of 0.01 years. Figure 4.2 shows that the stochastic single patch model is analogous to the ODE single patch model, with slightly faster extinction times as expected.

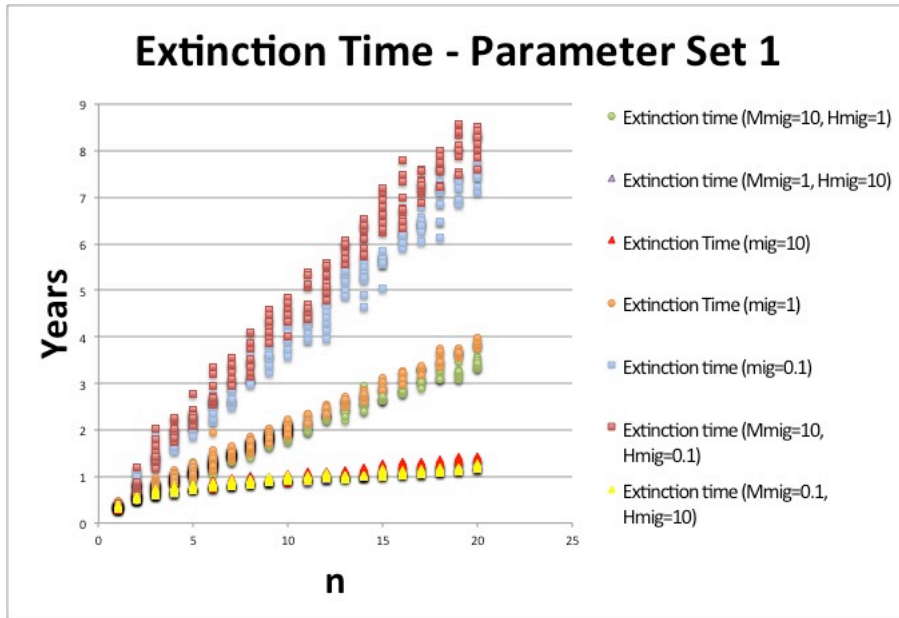


Figure 1: A comparison of extinction times with varying migration rate multipliers.

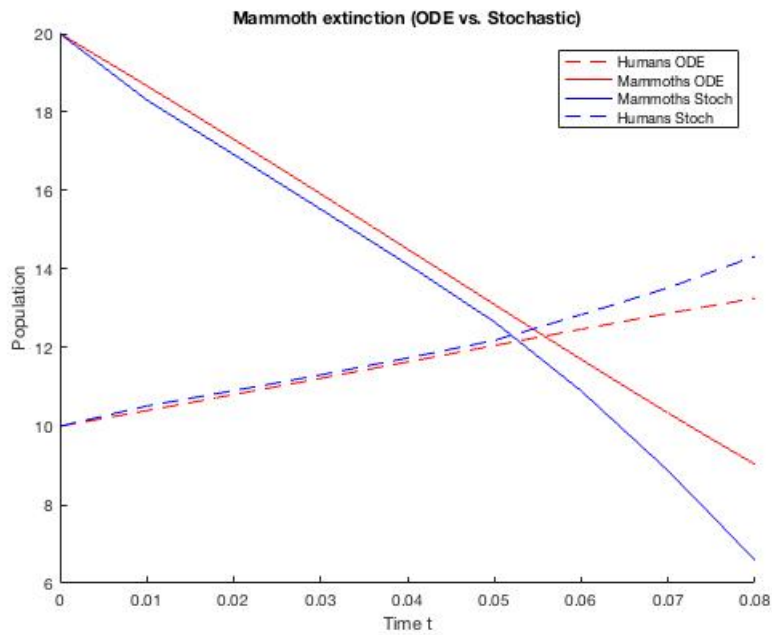


Figure 2: A comparison of extinction time between the stochastic and ODE models using parameter set 8 from Table 3. The stochastic model consisted of the average species populations at every time step of 0.01 years of 10,000 simulations.

4.3 Metapopulation Model Comparison

To show that our stochastic metapopulation model is analogous to the ODE model, we used the same parameter sets determined by the latin hypercube sampling used for the ODE model which are provided in Table 3 below. For each parameter set, 50 simulations were run on a 100-patch grid. Extinction times, runtimes, and the number of events taken place were recorded. As shown by Figure 4.3, the data from the stochastic model lines up with the ODE model, though shifted down slightly.

Set	r_H	r_M	A	a_H	a_M	b	c_H	c_M	N_H	N_M
1	0.0237	0.0395	5.5509	8.0611	13.5954	9.4623	0.0404	0.2594	7.2730	3.0496
2	0.0101	0.0471	7.8002	2.4568	12.1257	5.1982	0.0229	0.2023	5.8742	3.3543
3	0.0294	0.0404	5.6317	7.1550	12.9399	3.4307	0.0487	0.3604	6.2844	3.5872
4	0.0030	0.0439	6.0450	9.3177	13.2375	1.4927	0.0126	0.4420	5.0591	3.6465
5	0.0072	0.0481	7.4892	8.3160	10.3371	8.7196	0.0291	0.4951	8.7977	4.4658
6	0.0182	0.0416	7.0539	1.5843	11.7268	2.4764	0.0232	0.3824	8.3457	4.2570
7	0.0127	0.0457	7.1140	3.0830	14.8006	5.8975	0.0413	0.2662	7.4196	3.8716
8	0.0205	0.0468	6.6377	4.3353	14.2925	6.6317	0.0074	0.4227	6.8224	4.1162
9	0.0321	0.0423	6.2961	5.9224	10.9096	4.2181	0.0354	0.3068	5.7760	4.9218
10	0.0152	0.0448	5.2890	4.7508	11.3723	7.8136	0.0151	0.3423	7.8533	4.6368

Table 3: **Original Parameter Sets:** Ten different parameter sets created from a latin hypercube sampling of the parameter ranges given in Table 1. These parameter sets were used to run simulations for the single patch model. Additionally, they were the ten sets of parameters used for simulations of the metapopulation model. The last four columns were not used for the metapopulation model, as those parameters were defined differently.

Not only was the data analogous to the ODE model, but the average simulation time for each parameter set was significantly smaller. While the ODE model averaged 12.6 minutes for a 100-patch grid simulation, the stochastic model averaged just 56.4 seconds.

4.4 Runtime Analysis

The next goal of the metapopulation stochastic model was to find the order as the size of the grid increased. We would like to predict how long larger simulations will take without making the assumption that the simulations will scale linearly. Figure 4.4 shows a graph of the average runtime of 10 simulations of an $n \times n$ grid of parameter set 1 as n increases from 1 to 20. As seen in Figure 4.4, the runtime for our model was best fit as a cubic polynomial in n , with $R^2 = 0.98732$.

4.5 Final Simulation Results

After making sure that our model was analogous to the previous model used [5], we conducted another latin hypercube sampling, creating ten new parameter sets utilizing the new range on the migration parameter. The predicted extinction times are shown in Figure 4.5. Seven of the ten parameter sets show mammoth extinction times in the range of 1,000 and 2,500 years. However, parameter sets 2, 4, and 5 all show rather large and unrealistic extinction times and variances.

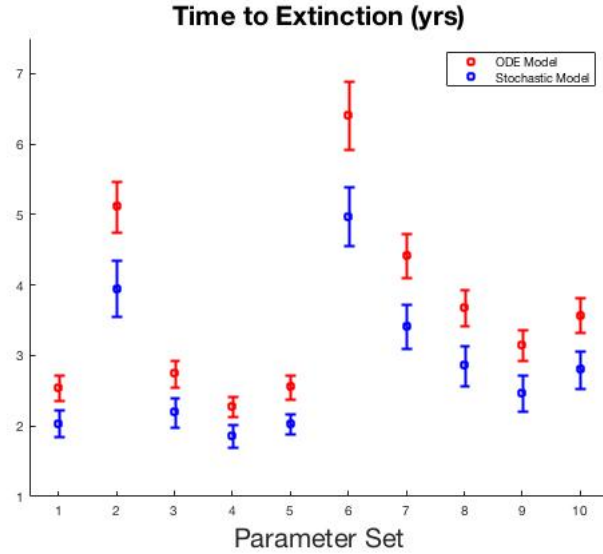


Figure 3: A comparison of average mammoth global extinction times in a 100-patch simulation between the ODE model and the stochastic model. The horizontal axis represents the 10 parameter sets. Each point is an average of 50 realizations with error bars representing \pm two standard deviations.

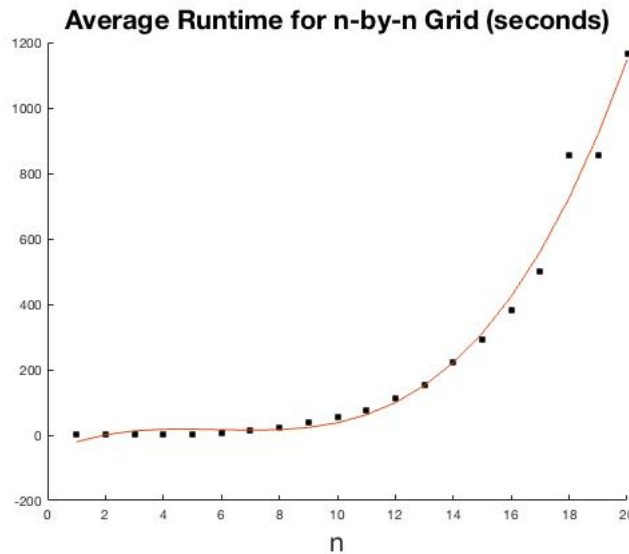


Figure 4: Average runtime (in seconds) of 10 realizations of parameter set 1 vs n , the length of the $n \times n$ spatial grid. The best fit cubic curve is displayed, with $R^2 = 0.98732$

4.6 Parameter Significance

Because three of the ten predicted extinction times were in an unrealistic range, we performed power regression analysis comparing the values of each parameter to the predicted extinction time and then compared the R^2 value of each parameter, as shown in Table 4. The two parameters

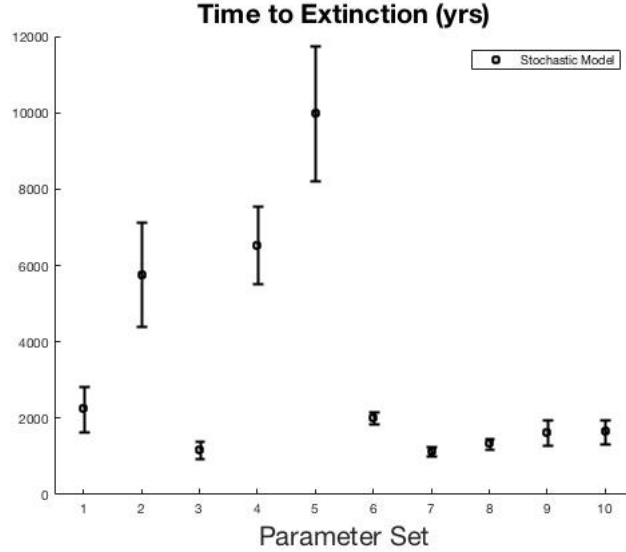


Figure 5: The predicted mammoth global extinction times for a 544-patch grid representing the entire continental United States. The horizontal axis represents the 10 parameter sets. Each point is a predicted extinction time based on a linear regression of simulated extinction times for a single parameter set as the size of the n -by- n grid grew from 2-by-2 to 20-by-20. The bars in this case represent a 95% prediction interval, calculated using SAS

that show some significance are the migration parameter, and the human hunting parameter. This makes sense as how fast the humans move and how much the human population gains from hunting should be good indicators of how quickly the mammoth population goes to extinction. The graphs of the parameters c and a_H are provided in Figure 4.6 and Figure 4.6 respectively.

Parameter	R^2
r_H	0.23
r_M	0.003
A	0.11
a_H	0.70
a_M	0.01
b	0.09
c	0.73

Table 4: This table contains a list of the R^2 values of power regression analyses between each parameter and the predicted extinction times from Figure 4.5

5 Discussion

There are a few improvements that can still be made on this model in regards to studying the extinction of the Columbian mammoth. A few ideas that we had that did not work were having a separate migration parameter for each species in the metapopulation model and also the possibility of an independent migration term.

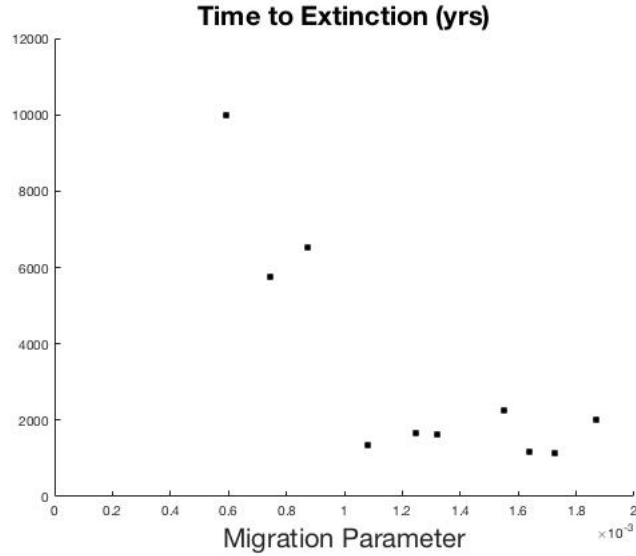


Figure 6: The migration parameter, c , graphed against the predicted extinction time for each parameter set.

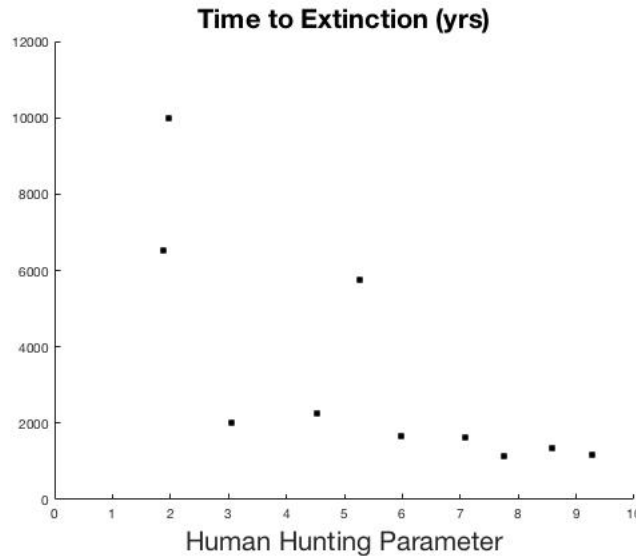


Figure 7: The human hunting parameter, a_H , graphed against the predicted extinction time for each parameter set.

We found when altering the range on the migration constant for the metapopulation model that in general, a change in the human migration rate relative to the mammoths was more significant to the predicted extinction time than a change in the mammoth migration rate relative to the humans. One possible explanation of this is the conservative nature of our initial condition assumptions and how that is manifested in the simulation. For the migration events, a mammoth will only move to a patch if there are less humans in the new patch than the current patch. This accounts for the mammoths moving away from their main predator. As the humans are starting in the upper left

hand corner of the grid and moving with a wave-line formation throughout the rest of the grid, the least amount of humans in an adjacent patch will almost always be to the right and down from the current patch. But, because our initial condition is that mammoths are at carrying capacity in every cell, the mammoth in our current cell will not have a positive rate of moving to the patch with less humans as this would put the mammoth population over carrying capacity. The combination of these two factors result in a situation without much mammoth migration.

One idea we had to make the model more realistic was to have migration terms for both humans and mammoths that are independent of the other species. This independent migration rate would account for migration due to other factors besides the hunting of mammoths such as climate changes due to seasonality, the following of other prey besides mammoths, or just general inhabitability of a region. Once again, because of the conservative nature of our assumptions, we decided that this was not possible. The mammoth carrying capacity initial condition would still prevent migration from happening throughout most of the area.

Frank *et al* had estimated that the Columbian mammoth would go extinct between 6,800 and 19,000 years after humans appeared in North America [5]. The predicted range of the Columbian mammoth extinction time of our simulation is an improvement over that given by Frank et al. With the same conservative assumptions, a discrete individual and stochastic structure to the model, and a new migration parameter calibrated to match anthropological evidence of human migration, we had 7 of 10 our parameter sets from the LHS result in a predicted extinction time of around 1000 to 2,500 years, which is consistent with the overkill hypothesis which necessitates extinction within 3000 years of human arrival. Thus, we conclude that the overkill hypothesis is not only possible, but a probable explanation for the extinction of the Columbian mammoth.

References

- [1] J. Alroy. A multispecies overkill simulation of the end-pleistocene megafaunal mass extinction. *SCIENCE*, 292:1893–1896, 2001.
- [2] Anthony D Barnosky, Paul L Koch, Robert S Feranec, Scott L Wing, and Alan B Shabel. Assessing the causes of late pleistocene extinctions on the continents. *science*, 306(5693):70–75, 2004.
- [3] Sandro L Bonatto and Francisco M Salzano. A single and early migration for the peopling of the americas supported by mitochondrial dna sequence data. *Proceedings of the National Academy of Sciences*, 94(5):1866–1871, 1997.
- [4] J. M. Diamond. *Guns, Germs, and Steel: The Fates of Human Societies*. W. W. Norton & Company, 1999.
- [5] Michael Frank, Anneliese Slaton, Teresa Tinta, and Alex Capaldi. Investigating anthropogenic mammoth extinction with mathematical models. *Spora: A Journal of Biomathematics*, 1(1):3, 2015.
- [6] Lionel E Jackson Jr and Alejandra Duk-Rodkin. Quaternary geology of the ice-free corridor: glacial controls on the peopling of the new world. *Prehistoric mongoloid dispersals*, pages 214–27, 1996.
- [7] P. S. Martin. The discovery of America. *SCIENCE*, 179:969–974, 1973.

- [8] P. S. Martin. *Twilight of the Mammoths: Ice Age Extinctions and the Rewilding of America*. University of California Press, 1 edition, 2007.
- [9] David Nogués-Bravo, Jesús Rodríguez, Joaquín Hortal, Persaram Batra, and Miguel B Araújo. Climate change, humans, and the extinction of the woolly mammoth. *PLoS Biol*, 6(4):e79, 2008.
- [10] R. M. Nowak. *Walker's Mammals of the World*. John Hopkins Univ. Press, 6th edition, 1999.
- [11] S. Nyakaana, E. L. Abe, P. Arctander, and H. R. Siegismund. DNA evidence for elephant social behaviour breakdown in Queen Elizabeth National Park, Uganda. *Animal Conservation*, 4(3):231–237, August 2001.
- [12] Philip A Stephens and William J Sutherland. Consequences of the allee effect for behaviour, ecology and conservation. *Trends in ecology & evolution*, 14(10):401–405, 1999.
- [13] EJ Szathmary. mtDNA and the peopling of the Americas. *American journal of human genetics*, 53(4):793, 1993.
- [14] Spencer Wells and Mark Read. *The journey of man: A genetic odyssey*. Princeton University Press, 2002.
- [15] Shu-Rong Zhou, Ya-Feng Liu, and Gang Wang. The stability of predator–prey systems subject to the allee effects. *Theoretical Population Biology*, 67(1):23–31, 2005.