Assessing the Causes of Late Pleistocene Extinctions on the Continents

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Supporting Online Material

Methods and Definitions

Intensity of the Pleistocene Extinction. The total number of extinct genera is 121 (Table S1) if one counts those that disappeared from at least one continent (versus 97 global extinctions). The extinction preferentially stripped the large mode or tail from mammalian body size distributions in the Americas and Australia (*1*). In North America, the only continent where the Pleistocene extinction has been comprehensively compared to earlier Cenozoic mammalian extinction events (*2*), the Pleistocene event is unusual in intensity and in preferentially affecting large mammals (≥10 kg). Similar analyses have yet to be done for other continents; an underlying assumption of all past studies is that the extinction is unique in these respects worldwide.

Taxonomy. Following past analyses, we focus on genera because species-level taxonomy is less stable. We used ref. (*3*) for a standardized taxonomy.

Radiometric-Age Terminology. When possible, dates for the last 45,000 years are expressed in units of 1000 radiocarbon years before present (ky RCBP). Dates calibrated to calendar years from this interval and dates from before this interval are reported as ky or my (million years) BP.

Human Impacts on Fauna. "Overkill" means that human hunting precipitated extinction by causing death rate to exceed birth rate, with the process taking 1500 years or more (*4*). "Blitzkrieg" is a special case of overkill, in which hunting by humans was so intense that it

caused extinction in less than about 500 years, with extinctions occurring more rapidly along a geographic front (*5*). Both overkill and blitzkrieg are plausible based on hunting behavior of industrialized and non-industrialized humans (*1, 6*), but extrapolating modern human behaviour into the past is problematic. Extinction through habitat alteration, or sitzkrieg (*7*), was proposed as an alternative to blitzkrieg and gradual overkill. The sitzkreig model has been postulated especially for Australia, where human alteration of the landscape by fire has been suggested as a major driver of extinction (*8-10*).

Explanatory Text
Simulations

Table S2 summarizes the simulations that have been developed to test the overkill theory. In general, early simulations that focus on entry of Clovis hunters into North America had mixed results and some exhibited intrinsic dynamical instability. Those that focus on extinction of moas in New Zealand suggest overkill is probable and blitzkrieg may be possible under certain assumptions. Simple optimal foraging models with just 1 or 2 prey items typically do not support overkill, whereas those with more variable prey support overkill under certain circumstances. Early models tailored to examine Aboriginal impacts in parts of Australia, or that examined the effects of prey naiveté on single species, did not support overkill as a general result. The Alroy simulation (*11*), which involves multiple species with realistic geographic ranges and population dynamics, but without selective human foraging, supports overkill under a range of conditions.

The Alroy Simulation. In the Alroy simulation, an error in the parameterization of prey *r* values makes it difficult to assess the reported sensitivity tests (*12*), but a subsequent correction (*13*) reran the best-fit trial with appropriate *r* values, and correctly predicted the fate of 34 of 41 species with final human population densities of ~28 people/100 km^2 getting ~30% of their calories from large animals. The median time to extinction was 895 years, supporting overkill but too slow for blitzkrieg *sensu stricto.*

The chief critiques of this simulation were (i) that it failed to account for the low number of kill-sites in North America, especially the lack of kill-sites for many extinct species (*14, 15*) and (ii) that it over-predicted overkill because it did not allow prey to lose naiveté to human hunters as their numbers diminished (*16*). As discussed in the printed text and in greater detail below, for most species the missing kill-site critique is weak. "Prey-hardening" to the hunting

techniques of predators is hard to quantify, but in simulations of predation on single species, particularly those with fixed, low human densities, inclusion of hardening should certainly decrease the probability of overkill, as demonstrated in ref. (*16*). Ref. (*16*) did not simulate human population densities as high as those in Alroy's revised best fit scenario, and did not examine a multi-species case that allowed prey switching, so it is not surprising that they found overkill less likely. In addition, a recently published sensitivity analysis based on this model commonly yielded size selective overkill that closely matched observations, despite moderate loss of naïveté (*17*). Finally, in the real world, where humans are simultaneously hunting many species with variable intrinsic rates of increase, the only sure-fire hardening method would be flight to depopulated refugia. This may explain why many extinct taxa had their last occurrences in the high Arctic (*18*), or on isolated islands (*19, 20*), or why many surviving slow-breeders are alpine, deep-forest, nocturnal, arboreal or high-latitude (*21*).

Chronology

   Eurasia, Alaska, and the Yukon. In Eurasia, warm-adapted megafauna that were abundant during preceding interglacials (straight-tusked elephants, hippos) became extinct between 45 and 20 ky RCBP (*22*). In Alaska and the Yukon, hemionid horses (*23*) and short-faced bears became extinct at ~31 and 21 ky RCBP, respectively. The second pulse of extinctions began near the Younger Dryas (YD) and hit cold-adapted animals. Datable mammoth fossils dropped in abundance across Europe and Alaska after 12 ky RCBP, arguably indicating a decrease in effective population sizes then; however, mammoths survived until 9.7 ky RCBP on the Taimyr Penisula, 3.7 ky RCBP on Wrangell Island, and 7.9 ky RCBP on St. Paul Island (*18, 19, 24*). In western Europe, giant Irish deer dropped in abundance and began to dwarf during the YD (*25*) before disappearing as recently as ~9.2 ky RCBP (*26*). In Alaska, caballoid horses began to dwarf at 25 ky RCBP and became extinct at 12.5 ky RCBP (*23*). The small number of datable fossils seems to indicate a population crash for many species near the Pleistocene-Holocene boundary in Eurasia and Alaska, including both ultimate victims and animals that survived into recent times somewhere in the Holarctic (*18*). In general, warm-adapted species disappeared as Last Glacial Maximum (LGM) glacial conditions developed and cold-adapted species moved north as the LGM ended and climates warmed, just as they had at prior glacial-interglacial transitions (*22*). In some cases, such as the extinction of Irish deer in

Ireland (*25, 27*), or the loss of short-faced bears and both horse species in Alaska and the Yukon (*23, 28*), the disappearances occurred before apparent sign of human contact.

Australia. The Australian extinction and human occupation chronologies are for the most part too old for radiocarbon dating, but dates have been supplied by new, though less precise techniques such as optical luminescence, amino acid racemization, and ^{230}Th/^{234}U dating of sediments (*9, 29*). Many of the fossils are from caves or other complex deposits; thus, accepted dates rely on a stringent set of criteria that includes articulation of remains (*29*), which minimizes the potential of including bones that have been moved from their original sedimentary context. Abundant dates using amino acid racemization, accelerator mass spectrometry (AMS), ^{14}C and thermal ionization mass spectometry (TIMS), and luminescence dates on *Genyornis* eggshells and associated sediment supports extinction of that large bird about 50 ky (*9*). Controversy remains about criteria for accepting dates and about which sites should be considered as providing robust evidence (*30*). Recent work (*30*) suggests that megafauna persisted longer than the reported youngest limit of about 40 ky (*29*). Should younger dates such as those reported for Cuddie Springs prove reliable (*30*), and should it be demonstrated that that local environmental history is decoupled from the regional paleoclimate proxies afforded by South Pacific marine curves, it would weaken the argument that humans were the primary agent of extinction in Australia. In any case the overlap of humans with megafauna for the several thousands of years that now seems likely would refute blitzkrieg in Australia.

Africa. In Africa, only 8 genera of Pleistocene megafauna went extinct; 3 of these were known only from north Africa, and 2 only from south Africa (*31, 32*). Extinction of 5 genera cannot be dated more precisely than the last 100 ky BP; 3 went extinct in the Holocene.

Archaeology and Paleontology

Few kill-sites (as defined by stringent standards such as a spearpoint intermingled with fossil bones) are verified in North America, but associations between archaeological remains and megafaunal bones are more common than kill-sites *sensu stricto* (*33*). In Eurasia and Africa humans hunted extinct megafauna long before the extinction event (*34*). Still, ref. (*35*) observes that there are more well-documented proboscidean kill-sites from the latest Pleistocene of North America than there are from all of Africa over the past 100,000 years. This no doubt reflects the extreme rarity of fossil and archaeological site preservation, discovery and analysis. These

differences between Eurasia, Africa, and North America have called overkill models into question, but are largely explainable by the fact that different criteria are used to accept evidence that humans were utilizing megafauna on the different continents. In Australia, there is no evidence for direct human modification of extinct megafauna (*30, 36*), and lithic artifacts and extinct Pleistocene megafauna have been found in stratigraphic association only at Cuddie Springs (*37*). In South America, evidence for utilization of extinct megafauna by humans exists at a few sites (*38, 39*), and artifacts and extinct megafauna are associated at a number of sites (*40*).

      Missing Kill Sites. Previous analyses (*33*) have assessed the ratio of kill-sites to paleontological occurrences by comparing the number of securely-documented kill sites with the total number of Pleistocene fossil sites reported for a given taxon (*41*). Still needed is comparison of the number of kill-sites or archaeological associations with only the number of late Pleistocene occurrences for various taxa (rather than with all Pleistocene occurrences). The FAUNMAP database (*41*), combined with rigorous application of kill-site criteria (*33*), provides one way to estimate this for North America, where much controversy has centered. We assumed that the ratio of Clovis age mammoth kill sites to all late-glacial FAUNMAP mammoth sites approximates the frequency at which kill sites might be preserved, and applied a chi-square test that compares the mammoth kill-site ratio to those for other taxa (Table S3). We discovered that (1) a high proportion of late-glacial mammoth sites (27%) are well-documented kill-sites; (2) *Platygonus* may be represented at fewer kill-sites than would be expected; and (3) most taxa are too rare in the fossil record to say whether or not their frequency of kill sites differs significantly from *Mammuthus*. Using the low *Mammut* ratio as the kill-site standard suggests that no other taxa are known at enough sites for kill sites to be expected, except for *Mammuthus*, which by comparison was hunted exceptionally often. Megafauna sites in minimally acceptable archaeological context exceed 40% of the total late-glacial sites known for *Camelops*, *Capromeryx*, *Equus*, *Hemiauchenia*, and *Mammuthus* (Table S3). "Minimally acceptable archaeological context" means that the sites pass the first cut of the stringent vetting applied by reference (*33*), but do not provide irrefutable evidence that humans were killing or using the animals.

Comparison of similarly standardized data sets for all continents would clarify where the numbers of archaeological associations with extinct megafauna or kill sites was significantly high or low.

Climatic Change and Ecological Effects

Climatic extinction models regard climate as causing unusual late Pleistocene vegetation changes, which in turn affected the fauna. Several glacial-interglacial cycles preceded the last one, but did not cause megafaunal extinction (*22, 42-45*). Thus, any extinction models that rely on climatic change must specify differences between the last glacial-interglacial cycle and previous ones. Also, climate-extinction models must be consistent with what we know about how animals react to unusual climatic changes.

Summary of Relevant Climatic Changes. The Earth began to experience pronounced cycles between glacial and interglacial conditions ~2.5 myr BP (*46*). These cycles were paced by orbitally-driven changes in insolation. Low amplitude cycles with a 41 ky frequency gave way to 100 ky cycles ~1.2 my BP, and the amplitude of the 100 ky cycles became more pronounced ~600 ky BP (Fig. 2A). In each 100 ky cycle, maximum glaciation lasting ~10 ky was generally followed by ~10 ky of maximum interglacial warmth, which then was followed by a long, stepped decline back to full glacial conditions over the next 80 ky.

Glacial/interglacial transitions were accompanied by changes in atmospheric and ocean circulation, sea level, atmospheric composition, seasonality of temperature and precipitation, position of storm tracks, monsoonal activity, vegetation assemblages and many other parameters. The magnitude of response on land varied with latitude, altitude, and distance from the ocean. At the Last Glacial Maximum (LGM), ~18 ky RCBP, temperatures were 2-5°C cooler than today at low altitudes near the equator, and 10-20°C colder at higher latitudes and altitudes (*47*) (Fig. 2B,C).

Large amplitude climate oscillations also occurred on a sub-orbital, millennial time scale through full glacial and transitional intervals, and perhaps in some of the interglacial intervals (*48, 49*). Sub-orbital climate variability was strong during the LGM-Holocene transition. In the northern hemisphere, a sudden, sharp cold snap, the Younger Dryas (YD) event, beginning ~11 ky RCBP (~12.9 ky BP) abruptly reversed a warming trend that had been accompanied by widespread deglaciation (Fig. 2C). The YD, which may have been more extreme than earlier

reversals in deglaciation (*50*), ended abruptly at ~10 ky RCBP (~11.6 ky BP), and warm conditions leading to the current interglacial prevailed. While some southern hemisphere climate records show YD cooling, others show a gradual warming (*51*).

Faunal Response to Current Climatic Warming. The response of biota to current, anthropogenically-induced global warming, which may be faster than the end-Pleistocene warming (*52, 53*), does not yet include megafaunal extinction, although simulations suggest substantial extinction may eventually result (*54*). Most documented biotic effects of warming are on taxa of low trophic level and small body size (*55, 56*), but geographic ranges and population density of large ungulates have also been affected (*55, 57-59*). Pronounced range shifts of both small and large mammals have been documented at the late Pleistocene extinction event, and generally are attributed at least partly to climatic influences (*22, 41, 42, 60, 61*).

Faunal Response to Earlier Pleistocene Glacial-Interglacial Transitions. Records of how mammal communities responded to prior Pleistocene glacial-interglacial transitions have long been known from Europe (*22, 42*) and have recently been reported from North America and Australia (*43, 44*). The latter are informative in that humans were absent during the earlier climatic transitions and reveal that diversity patterns, size, trophic, and taxonomic structure changed more from the late Pleistocene to the late Holocene than they had in the previous million years. Where data are sufficient, the climatic changes that precipitated faunal change at these earlier glacial-interglacial transitions, in the absence of humans, seem to have affected lower size and trophic categories (*62*). Such bottom-up changes also characterized the late Pleistocene-Holocene transition, but added to them were the top-down impacts that resulted in megafaunal extinction.

Keystone Species Model. Proboscideans have been proposed as late Pleistocene keystone species, with their removal by either humans or climatic change leading to shifts in vegetation and cascading impacts on other species (*63*).

Co-evolutionary Disequilibrium Model. Co-evolutionary disequilibrium posits that strong niche-partitioning among Pleistocene herbivores was disrupted by an unusually rapid transition to new Holocene biomes. The assumption of resource-partitioning among herbivores is supported by recent isotopic studies of paleodiet (*64, 65*).

Mosaic-Nutrient Model. The mosaic-nutrient model, developed for Beringian biomes, argues that climate changed such that the growing season and local plant diversity decreased, and

plant anti-herbivore defences increased. The model assumes that extinct caecal fermenters needed a greater diversity of forage types than ruminants, and were thus more susceptible to nutritional stress in Holocene biomes. Isotopic data from Texas and Florida do not offer strong support for these assumptions about diet, though they show that the few surviving herbivores (e.g, bison, deer) had very homogeneous diets (*64, 65*).

Table S1. Extinct genera on each continent. Placement within one of the age bins is based on our vetting of the literature to extract the youngest reliably dated occurrence (see footnotes d, e, i). The age assignments are conservative, in that we required a date robust enough to allow a genus to be placed within the bracketing ages of each bin; and (ii) for ages younger than 50 ky, the last records of some genera are dated to shorter intervals within each of the age bins shown in the table.

#	TAXON	LAST 100 ky [g]	100- 50 ky	50-13 ky RCBP	13-10 ky RCBP	HOLOCENE[h]	REFERENCE[i]
	AFRICA						
	Mammalia						
	Proboscidea						
	Elephantidae						
1	Elephas	X					(66)
	Perissodactyla						
	Equidae						
2	Hipparion	X					(66)
	Artiodactyla						
	Camelidae						
3	Camelus	X					(66)
	Cervidae						
4	Megaceroides[a]	X					(66)
	Bovidae						
5	Megalotragus					X	(67)
6	Pelorovis					X	(68)
7	Parmularius	X					(66)
8	Bos					X	(3)
	AUSTRALIA						
	Reptilia						
	Varanidae						
9	Megalania			X			(29)
	Meiolanidae						
10	Meiolania			X			(29)
11	Ninjemys	X					(69)
	Crocodylidae						
12	Palimnarchus			X			(29)
13	Quinkana			X			(29)
	Boiidae?						
14	Wonambi		X				(29)
	Aves						
15	Genyornis			X			(29)
	Mammalia						
	Marsupialia						
	Diprotodontidae						
16	Diprotodon[b]			X		?	(29)
17	Euryzygoma	X					(69)
18	Euowenia	X					(69)
19	Nototherium	X					(69)
20	Zygomaturus		X				(29)
	Palorchestidae						

#	Taxon						Ref
21	*Palorchestes*			X			(29)
	Vombatidae						
22	*Phascolomys*	X					(69)
23	*Phascolonus*			X			(29)
24	*Ramsayia*	X					(69)
	Thylacoleonidae						
25	*Thylacoleo*			X			(29)
	Macropodidae						
26	*Protemnodon*			X			(29)
27	*Procoptodon*	X					(69)
28	*Simosthenurus*			X			(29)
29	*Sthenurus*		X				(29)
	EURASIA						
	Mammalia						
	Carnivora						(42)
	Hyaenidae						
30	*Crocuta*				X		(42)
	Proboscidea						(42)
31	*Mammuthus*				X		(42)
32	*Palaeoloxodon*		X				(42)
	Perissodactyla						(42)
	Rhinocerotidae						
33	*Dicerorhinus*			X			(42)
34	*Coelodonta*				X		(42)
	Artiodactyla						(42)
	Hippopotamidae						
35	*Hippopotamus*		X				(42)
	Camelidae						
?	*Camelus*				?		(42)
	Cervidae						
36	*Megaloceros*					X	(26)
	Bovidae						
37	*Spirocerus*			X			(42)
38	*Ovibos*					X	(42)
	NORTH AMERICA[c]						
	Mammalia						
	Xenarthra						
	Glyptodontidae						
39	*Glyptotherium*	X					(70)
	Megalonychidae						
40	*Megalonyx*				X		(42)
	Megatheriidae						
41	*Eremotherium*	X					(70)
42	*Nothrotheriops*				X		(42)
	Mylodontidae						
43	*Glossotherium*			X			(42)
	Pampatheriidae						
44	*Pampatherium*				X		(71)
	Rodentia						
	Castoridae						
45	*Castoroides*				X		(72)

	Hydrochoeridae						
46	*Hydrochaeris*	X					(70)
47	*Neochoerus*	X					(70)
	Carnivora						
	Ursidae						
48	*Arctodus*				X		(42)
49	*Tremarctos*				X		(73)
	Felidae						
50	*Homotherium*			X			(74)
51	*Miracinonyx*				X		(75)
*	*Panthera*				X		(42)
52	*Smilodon*[d]				X	?	(42)
	Proboscidea						
	Elephantidae						
53	*Mammuthus*[d]				X	?	(42)
	Gomphotheriidae						
54	*Cuvieronius*			X			(64)
	Mammutidae						
55	*Mammut*[d]				X	?	(42)
	Perissodactyla						
	Equidae						
56	*Equus*				X		(42)
	Tapiridae						
57	*Tapirus*				X		(76)
	Artiodactyla						
	Tayassuidae						
58	*Mylohyus*				X		(42)
59	*Platygonus*				X		(42)
	Camelidae						
60	*Camelops*				X		(42)
61	*Hemiauchenia*				X		(42)
62	*Paleolama*				X		(42)
	Cervidae						
63	*Bretzia*	X					(70)
64	*Cervalces*				X		(42)
65	*Navahoceros*	X					(70)
66	*Torontoceros*	X					(70)
	Antilocapridae						
67	*Stockoceros*	X					(70)
68	*Tetrameryx*	X					(70)
	Bovidae						
69	*Bootherium*	X					(70)
70	*Euceratherium*					X	(42)
71	*Saiga*	X					(70)
	SOUTH AMERICA[e]						
	Mammalia						
	Xenarthra						
	Dasypodidae						
72	*Eutatus*					X	(77)
73	*Propaopus*					X	(78)
	Glyptodontidae						
74	*Chlamydotherium*					X	(79)

75	*Doedicurus*					X	(80)
76	*Glyptodon*					X	(78)
77	*Heteroglyptodon*	X					(3)^j
78	*Hoplophorus*					X	(78)
79	*Lomaphorus*	X					(70)
80	*Neosclerocalyptus*	X					(70)
81	*Neothoracophorus*	X					(70)
82	*Parapanochthus*	X					(70)
83	*Panochthus*	X					(70)
84	*Plaxhaplous*	X					(70)
85	*Sclerocalyptus*	X					(70)
	Megalonychidae						
86	*Valgipes*	X					(70)
	Megatheriidae						
87	*Eremotherium*					X	(79)
88	*Megatherium*					X	(80)
89	*Nothropus*	X					(70)
90	*Nothrotherium*	X					(70)
91	*Ocnopus*	X					(70)
92	*Perezfontanatherium*	X					(3)^j
	Mylodontidae						
93	*Glossotherium*				X		(81)
94	*Lestodon*	X					(70)
95	*Mylodon*				X		(82)
	Pampatheriidae						
96	*Pampatherium*	X					(70)
	Scelidotheriidae						
97	*Scelidotherium*					X	(79)
	Litopterna						
	Macraucheniidae						
98	*Macrauchenia*	X					(70)
99	*Windhausenia*	X					(70)
	Notoungulata						
	Toxodontidae						
100	*Mixotoxodon*	X					(70)
101	*Toxodon*				X		(83)
	Rodentia						
	Hydrochoeridae						
102	*Neochoerus*					X	(79)
	Octodontidae						
103	*Dicolpomys*	X					(70)
	Carnivora						
	Canidae						
104	*Theriodictis*	X					(70)
	Felidae						
105	*Smilodon*					X	(79)
	Ursidae						
106	*Arctodus*	X					(70)
	Proboscidea						
	Gomphotheriidae						
107	*Cuvieronius*				X		(84)
108	*Haplomastodon*					X	(79)
109	*Notiomastodon*	X					(70)

#	Genus						Ref
110	*Stegomastodon*				X		(85)
	Perissodactyla						
	Equidae						
111	*Equus*					X	(79)
112	*Hippidion*				X		(86)
113	*Onohippidion*	X					(70)
	Artiodactyla						
	Camelidae						
114	*Eulamaops*	X					(70)
115	*Hemiauchenia*				X		(83)
116	*Palaeolama*					X	(78)
	Cervidae						
117	*Agalmaceros*	X					(70)
118	*Antifer*[f]				X		(85)
119	*Charitoceros*	X					(70)
120	*Morenelaphus*	X					(70)
	Tayassuidae						
121	*Platygonus*	X					(70)

* Historic reports, not counted in totals.

? Questionable occurrence, not counted in totals.

[a] *Megaloceros* of ref. (*66*).

[b] Ref. (*29*) reports a disarticulated *Diprotodon sp.* from the Holocene.

[c] North America north of Mexico

[d] Grade 7 dates reported for the Holocene. Grade 8 and 9 dates imply extinction between 13-10 ka. Grades based on the radiocarbon grading scale of ref. (*87*). This scale rates the type of material dated (on a scale of 1-6) and the strength of association (on a scale of 1-3) between the dated material and the fauna within the deposit—the rating for the type of material dated and the strength of association are added together. Wood, charcoal, and amino acids are given a rating of 5 or 6, while shell, terrestrial carbonate, and whole bone are given a score of 1 or 2, for example. A strong association is given a score of 3, medium association is given a 2, and weak association is given a 3. A genus that had amino acids dated will receive a grade of 9 [Type of material (grade 6) + association strong (grade 3)]. Refs. (*87-89*) argue that dates with a grade of 8 or 9 are "good dates" and are the only dates that should be used in analyses of the chronology of the late Pleistocene extinction.

[e] It is difficult to assign radiocarbon grades (see footnote d) for many of the dates presented in the literature; however, based on the type of material dated very few, if any, of the South American dates reported in the literature would receive a grade of 8 or 9 as defined in ref. (*87*). The South American dates, especially for purported Holocene megafaunal extinctions, need detailed evaluation before they can be considered robust.

[f] *Paraceros* of ref. (*70*).

[g] 100,000-10,000 years ago in Africa, Eurasia, and North America. Late Pleistocene of Australia. Lujanian Land Mammal Age of South America.

[h] <10,000 radiocarbon years.

[i] We utilized review articles and do not cite other articles that give similar dates for the respective taxa; those citations are available in the review articles listed in our References and Notes section.

[j] Ref. (*3*) cites ref. (*90*) as the source for this genus occurring in the Lujanian of South America.

Table S2. Summary of simulations designed to test the overkill model. "# of prey" refers to how many species of prey the simulation involved, and "Coupled Dynamics" refers to whether changes human population numbers are linked to changes in prey density (yes) or fixed (no).

Study by:	#. of prey	Coupled Dynamics?	Do the results support overkill?
Budyko (*91*): evaluates impact of human population growth on Eurasian mammoths	1*	Yes, with exponential human population growth	Yes, but exponential population growth makes extinction inevitable.
Mosiman & Martin (*5*): studies first entry of Clovis hunters into conterminous USA	1*	Yes, with logistic human population growth and a fixed carrying capacity	Yes, with blitzkrieg under certain assumptions. Model fails stability tests so extinction inevitable under most conditions.
Whittington & Dyke (*4*): a sensitivity test of Mosiman & Martin (*5*) model under a wide range of parameter values	1*	Yes, with logistic human population growth and a fixed carrying capacity	Yes, with blitzkrieg under limited conditions and gradual overkill under a wide set assumptions. Model fails stability tests so extinction inevitable under most scenarios.
Belovsky (*92*): an optimal-foraging model for North America with sophisticated treatments of environmental controls on primary production, animal digestion, energetics, and foraging	2 hunted vs. gathered food	Yes, with human population growth determined by an energetic model	No. Assumes a relatively high *r* for prey that may reduce extinctions. Predicts megafaunal extinction in areas of high available primary production, because human population growth is subsidized by gathered food. Megafauna survive in areas of low production (i.e., tundra, forest). Yields general result that extinction results not from megafaunal specialization but rather from population growth of omnivores.
Winterhalder et al. (*93*) optimal foraging model of population dynamics of hunter-gatherers and prey (varied reproductive and nutrient traits); not "place-based"	1 to 2	Yes, with human population growth determined by an energetic model	No. Human populations stabilize or crash after wild oscillations if too much time is spent hunting. Prey persist in either scenario. Yields general result that predators in very simple systems are unlikely to drive prey to extinction; the reverse is more likely.
Anderson (*94*): models moa predation in New Zealand	1*	No, exponential growth at plausible rate	Yes, for blitzkrieg, but claims there are too few moa remains. No consideration of taphonomic impacts on this claim.

Winteralder & Lu (*95*): optimal foraging model of population dynamics of hunter-gatherers and prey (varied reproductive and nutrient traits); not "place-based" but results used to discuss conservation in Amazonia and Pleistocene overkill	Up to 4	Yes, with human growth determined by energetic model	Overkill in many cases for slow-breeding taxa, particularly if subsidized by a fast-breeding species. Slow breeders are not vulnerable to large game specialists.
Choquenot & Bowman (*96*): models Aboriginal impacts in a hypothetical tract of north Australian *Eucalyptus* savanna on single prey (varied reproductive traits)	1*	No, varied human densities	Mostly no. Varied hunting efficiency and human densities. Counter-intuitively found smaller megafauna would have been more readily exterminated than larger megafauna, a result dictated by using relatively low human densities and typical levels of hunting efficiency. Overkill would require higher human densities.
Holdaway & Jacomb (*97*): models moa predation in New Zealand	1*	No, exponential growth at plausible rate	Yes, consistent with blitzkrieg, predicts extinction of 11 species of moas in < 100 years.
Alroy (*11*): focused on first entry of Clovis hunters into conterminous USA	41	Yes	Overkill under many conditions; slightly too slow for blitzkrieg *sensu stricto* but still less than 1000 years to extinction of most species. Correctly predicts fates of ~73% of the species.
Brook & Bowman (*16*): evaluation of some aspects of Alroy simulation (*11*) with a focus on understanding effects of prey naiveté	1*	No, varied human densities	Mostly no. Results are dependent on assumptions about prey naiveté / human hunting efficiency. Not directly comparable to ref (*11*) because it used lower human densities and simulated predation on a single prey.
Brook & Bowman (*17*): sensitivity analysis of the model used in ref *16*, and comparison of results to size selectivity of extinction at a global level. Varied prey and human population dynamics, prey naiveté, hunting success, and habitat quality	1*	No, logistic growth to equilbrium density	Yes. Overkill under many combinations of parameters, with a best fit to body size data for moderate levels of predation, some loss of naivete, and moderate declines in habitat quality. Median time to extinction between 700 and 800 years.

*While these models treat only 1 prey explicitly, they implicitly assume that humans switch to secondary food sources when this prey become locally extinct.

Table S3. Clovis-age archaeological occurrences, kill-sites, and late-glacial (15.5-9.5 ky RCBP) paleontological occurrences of some extinct megafauna documented in the FAUNMAP database (*74*).

Taxon	A[a] Kill	B[b] Arch.	C[c] FAUN. All	D[d] FAUN. LG	A:C[e] P	A:D[f] P	B:C[e] P	B:D[f] P
Arctodus	0	1	37	8	0.25	0.63 [0.15]	0.41	0.86 [0.20]
Camelops	1	10	139	15	0.09	0.50 [0.17]	0.72	**0.0004** [0.46]
Capromeryx	0	3	25	1	0.35	0.86 [0.61]	0.31	**0.0001** [0.08]
Equus	2	13	440	17	*0.04*	0.15 [0.30]	*0.03*	**<0.0001** [0.30]
Glossotherium	0	1	48	8	0.19	0.63 [0.15]	0.27	0.86 [0.20]
Hemiauchenia	0	3	54	5	0.17	0.70 [0.25]	0.86	**0.02** [0.75]
Pampitherium	0	1	22	3	0.38	0.77 [0.37]	0.76	0.31 [0.78]
Mammut	2	7	211	68	0.07	[*0.001*]	0.15	[*0.001*]
Mammuthus	12	21	337	45		**0.001**		**0.001**
Megalonyx	0	1	53	4	0.17	0.73 [0.31]	0.22	0.44 [0.58]
Platygonus	0	4	88	16	0.08	0.49 [*0.05*]	0.57	0.19 [0.31]
Smilodon	0	1	35	3	0.27	0.77 [0.37]	0.44	0.31 [0.78]
Tapirus	0	1	56	6	0.16	0.67 [0.21]	0.20	0.67 [0.33]

[a] Sites with robust evidence for human predation (*33*)

[b] Sites with minimally acceptable evidence for association between Clovis-age people and extinct megafauna (*33*)

[c] All sites in the FAUNMAP database (*33*) in which the genus is reported, from 40 ky RCBP through Holocene age assignment in the database.

[d] All late-glacial (LG) age (15.5-9.5 ky RCBP) sites with the genus contained in the on-line FAUNMAP database (http://museum.state.il.us/research/faunmap), except *Tapirus*, which is from reference (*41*).

[e] Chi-square probability that the indicated ratio for the genus is the same as the respective ratio for *Mammuthus*; **bold** indicates significantly more archaeological association than expected relative to the reference genus, *italics* indicate less archaeological association than expected.

[f] Chi-square probability that the indicated ratio for the genus is the same as the respective ratio for *Mammut* or [*Mammuthus*]; **bold** indicates significantly more archaeological association than expected relative to the reference genus, *italics* indicate less archaeological association than expected.

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