

Big data can't yet crack big animal extinction mysteries.

Too many of the analyses that aim to establish whether humans or climate change drove past extinctions use poor quality or poorly understood data, insist **Gilbert J. Price** and colleagues.

In March, the last male Northern White Rhinoceros died. The sub-species joins the long list of large land animals that have gone extinct at some point over the past 100,000 years.

The reason for the demise of the Northern White Rhinoceros is undisputed: hunting and land disturbance by people. By contrast, who or what caused the extinctions of Earth's earlier Quaternary megafauna – including mammoths, enormous ground sloths and gigantic kangaroos – continues to be one of the most contested topics in the historical sciences.

Were early humans the dominant driver of the losses as they dispersed from Africa more than 85,000 years ago? Or was it climate change? The latest way to try to settle the debate involves meta-analyses that attempt to link the time of extinctions with shifts in the climate, or to evidence of the first appearance of humans in a particular region. Over the past five years, there has been a marked increase in the number of meta-analyses conducted. Many of them have been published in high-impact journals and they are starting to shape the debate (see graphic).

Understanding why certain groups succumbed while others survived the massive extinctions of the past could provide insights about how modern-day species might survive (or not) climatic and environmental changes, and the resilience of natural ecosystems to increasing anthropogenic impact. But in our view, the 'big data' approach cannot, at this point, get us closer to the answer -- for the simple reason that there aren't enough good-quality data available. An understanding of what drove the extinctions of large animals over the past 100,000 years requires detailed analysis on a species-by-species basis. This means investing effort into finding more fossil specimens, and verifying the ages of those that have already been discovered using improved dating methods. It also means relating such dates to detailed local environmental, climatic and archaeological records.

A typical meta-analytical study involves researchers mining the literature for dates associated with now-extinct megafauna as well as estimates for when humans arrived at a particular region (based on archaeological and other data). In some cases, these records are then combined with global-scale palaeoclimate data, such as those obtained from ice cores collected from the Arctic. Through mapping correlations between events, investigators try to identify the dominant factor driving species losses.

Over the past two decades, most of the meta-analyses that merge continental or global-scale datasets have pointed the finger at modern humans. In fact, some researchers contend that the results are so clear that there is no further need for debate^{1,2}.

For any meta-analysis, however, the reliability of the results is largely governed by the GIGO principle: garbage in, garbage out. In our view, most of these analyses depend on questionable data, making the results hard to interpret at best. Six key problems in particular undermine many of the studies conducted so far.

Outdated geochronological information. Models frequently use outdated geochronological information. For instance, during the 1980s radiocarbon dating of species such as the Eurasian woolly rhinoceros, *Coelodonta antiquitatis*, suggested that it survived well into the Holocene -- perhaps until as recently as 3,600 years ago³. Since then, refinements in the dating method have shown that the rhinos disappeared by about 14,000 years ago³. Some of the most recent ‘big data’ studies^{4,5} still use the erroneous early dates in their analyses.

Contested dates. In other cases, the dates associated with certain species are still contested. For instance, researchers first estimated the age of the elephant-like, *Stegodon trigonocephalus*, not by dating the fossils themselves, but strangely by dating fossils of other animals from deposits over 100 km away⁶. Other investigators have flagged the problems with the ages⁷, but such estimates continue to be fed into meta-analyses⁸.

In some cases, ages are assigned to species that have never even been dated, either directly or indirectly. In a 2016 study⁵, for instance, Australian animals such as the land crocodile *Quinkana* and giant wombat *Ramsayia* were listed among the ‘megafauna’ thought to have existed in the past 100,000 years, even though the fossils of these species have never actually been dated⁹. In fact, over 25 Australian ‘megafaunal’ species lack dates of any kind reflecting the paucity of work in the region.

Insufficient data. Other meta-analyses conflate the last appearance of a species in the fossil record with the time when the animal went extinct⁴. In the rare cases where hundreds of samples have been found, for instance for mammoths and mastodons, a species’ disappearance from the fossil record may well signal its demise. Yet where only a few specimens exist, the last appearance in the fossil record may have little bearing on the timing of the species’ extinction.

A step in the right direction are probabilistic models of extinction times. These incorporate some degree of error associated with the age of specimens, based in part on the quality of the methods used to date them. But again, the robustness of the results depends on the quality of the data fed in. At this point, very few of the species that went extinct over the past 100,000 years are associated with reliable dates¹⁰. (In our view, the cave lion, woolly rhino and woolly mammoth of Eurasia are among the handful of species for which sufficient data exist to enable a modelling approach.)

Problematic proxies. In the absence of fossil bones, some researchers have used proxy data to test megafaunal extinction hypotheses. For instance, the coprophilous fungus, *Sporormiella*, is a common component of the pollen and spore fossil record. Because this fungus occurs on animal dung, an abundance of it in a sediment core is often taken to indicate high numbers of big herbivores. And some investigators assume that a decrease in the appearance of the fungus over time and its eventual disappearance from the fossil record signals the extinction of megafauna¹¹.

Yet *Sporormiella* lives on the excrement of a vast range of both big and small animals, including mammals and birds, herbivores and even some carnivores¹². Its abundance is also affected by other factors such as the climate and hydrology. In any case, the levels of *Sporormiella* in a pollen core can’t provide information about which species was present at any one time, its abundance and so on.

Insufficient scrutiny. Lastly, long lists of extinct species (frequently just names and numbers in supplementary materials) may not receive the level of detailed scrutiny needed. This has

led to some unfortunate errors. The authors of at least two studies^{5,13} have argued, for instance, that *Homo sapiens* caused the demise of giant wombat-like marsupials such as *Euryzygoma* and *Eowenia*. These were extinct for millions of years before *Homo sapiens* even appeared; they are known only from the Pliocene, a period that occurred 5.3 to 2.6 million years ago. Another recent contribution¹⁴ suggested that the genus *Macropus* went extinct from Australia some 40 thousand years ago. In fact *Macropus* is alive and kicking: it includes Australia's extant kangaroos.

A better way

Megafauna are commonly defined as Quaternary terrestrial vertebrates weighing 44 kg or more in mass -- approximately 100 pounds. This is a nice, round but essentially arbitrary cut-off. Also, in some cases, 'megafauna' are not so mega. For instance, they may include extinct terrestrial vertebrates that are larger than their extant cousins but that weigh considerably less than 44kg. An extinct cousin of the modern-day Australian echidna, *Megalibgwilia ramsayi*, is considered to be megafauna even though it weighed only around 15kg when it existed at least until around 100,000 years ago.

Since megafauna are so biologically and ecologically diverse, with several species separated from each other by hundreds of millions of years of evolution, we should not expect them to have responded in the same way to changes in their environments -- whether driven by humans or the climate.

We believe that while data from the fossil record are still scant, an understanding of what drove the extinctions of large animals over the past 100,000 years requires detailed analysis on a species-by-species basis. This means trying to find new fossils and verifying the estimated age of specimens previously found -- for instance through repeated sampling, or by dating museum specimens using improved techniques. It also means taking into account all the local palaeoenvironmental information that is available to develop a detailed understanding of the palaeoecology of each species and their ecosystems.

To reconstruct the diet of the animal, researchers can use stable isotope analyses of tooth enamel; pollen cores could indicate the local vegetation at the time; the geochemistry of certain formations nearby such as stalagmites might give clues about the local climate; changes in the nature of the sediment laid down in a nearby creek bed, or in the deposition of sand dunes, might hint at local landscape changes; and so on. Indeed, broad global palaeotemperature records are likely to be a crude guide to climatic and environmental changes at local scales.

For each species, investigators should also strive to develop a clearer understanding of the human populations that lived alongside, and the nature of their interactions. This could be obtained by analysing DNA samples extracted from ancient human remains, or by studying middens, ancient dumps for domestic waste.

A recent study elegantly combined new dating with chemical analyses of the teeth of the cave bear, *Ursus spelaeus*, to show that its diet remained unchanged up until its last appearance in Europe¹⁵. Cut marks on bones revealed that some of these animals were prey to humans. Other approaches have used ecomorphology (the study of the relationship between the morphology of an animal and its ecology) to show that the extinct eastern African antelope *Damaliscus hypsodon* inhabited open, dry grasslands, and that its demise tracked the loss of those habitats¹⁶. Similarly, innovative investigations of the coprolites (fossil dung) of New

Zealand's flightless moas have revealed the complexity of their biotic and ecologic interactions in their environment prior to their human-driven extinction¹⁷.

Megafaunal fossils can now be dated with much greater efficiency and precision -- including animals that existed several hundreds of thousands of years ago. This is thanks to various advances in direct dating approaches such as combined U-series / electron-spin resonance dating. Other emerging techniques, such as the extraction and analysis of ancient DNA, can shed light on changes to the population size of now-extinct species, and allude to what may have caused their demise. Several studies have used such approaches to demonstrate that populations of taxa, from giant Irish elk to woolly rhinos, plummeted many thousands of years prior to their ultimate extinction, apparently because of deteriorating local climates and habitat changes^{18,19}.

Some may counter that we're averse to change and simply finding another reason to be alarmed about the demise of the field sciences in a digital world²⁰. But our argument is not with modelling *per se*. With good data, models could provide crucial insights about large-scale changes and the broad nature of the interactions between humans and other big animals as humans dispersed from Africa. Yet more data, of better-quality, can be obtained only through fieldwork and more rigorous analysis of fossil materials.

Gilbert J. Price is a Senior Lecturer in palaeontology at The University of Queensland, Queensland, Australia.

e-mail: g.price1@uq.edu.au

Julien Louys is an Australian Research Council Future Fellow at Griffith University, Queensland, Australia.

e-mail: j.louys@griffith.edu.au

J. Tyler Faith is a Curator of Archaeology and Assistant Professor of Anthropology at the University of Utah, Utah, USA.

e-mail: jfaith@nhmu.utah.edu

Eline Lorenzen is a Curator and Associate Professor at the Natural History Museum of Denmark, København, Denmark.

e-mail: elinelorenzen@snm.ku.dk

Michael C. Westaway is a Senior Research Fellow at Griffith University, Queensland, Australia.

e-mail: m.westaway@griffith.edu.au

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