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And then there were none?

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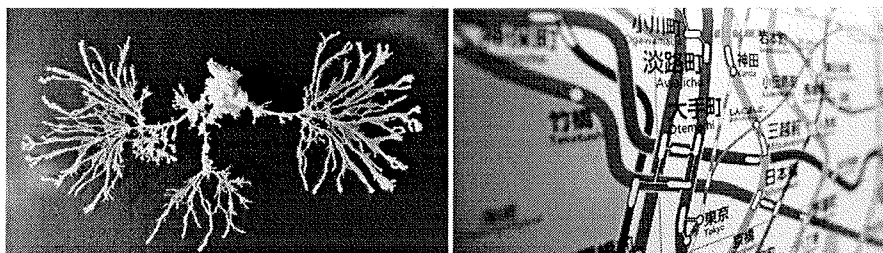
And then there were none?

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Adaptive network formation. The slime mold *Physarum polycephalum* is a single-cell organism that forms a veined network that explores the available space and connects food sources (left). Understanding the formation and behavior of this type of biological adaptive network may inform the development of real-world dynamic technological networks such as mobile communication networks or transportation systems, such as the Tokyo rail system (right).

By rhythmic contraction of its cytoskeleton, cytoplasm is continually pumped through these veins, and this continuous mixing seems to be the reason why all nuclei proceed synchronously through the cell division cycle. The network architecture is highly dynamic. Veins change in thickness, they may form and vanish again, and the plasmodium as a whole can crawl over its substratum, moving over centimeters in a couple of hours. Plasmodia usually do not dissociate. If food sources are spatially separated, such as oat flakes scattered over a wet surface, the plasmodial veins attempt to connect these food sources along the shortest possible pathways, even finding optimized paths through a maze (2). How this optimization is performed in terms of molecular mechanisms remains a challenging question.

Tero *et al.* present a surprisingly simple mathematical model for the development of a network of veins connecting multiple purposefully placed food sources. In their experiment, cities around Tokyo were represented as oat flakes on a wet surface that was inoculated with *Physarum*. Plasmodial veins connected these oat flakes by forming an optimized network closely approaching the purposefully designed Tokyo railway system.

Networks of plasmodial veins form without any central control mechanism that might instruct the organism about the relative position of the oat flakes or tell it how to connect them. The self-optimization algorithm that drives this morphogenesis works equally efficiently for networks with few or many nodes (oak flakes). The absence of central control mechanisms inspired Tero *et al.* to design a corresponding computational model capable of adaptive network design. Using a simple and robust algorithm, the model generates *in silico* networks that closely resemble those formed by the plasmodium. It is essentially based on feedback loops between the thickness of each tube and the cytoplasmic flow through the respective tube, where streaming

rate positively influences tube diameter and thus its transport capacity for cytoplasm. The dynamics and adaptability of the network structure are the direct results of the iteration of these local rules. The described algorithm or similar ones may provide general solutions for developing real-world, fault-tolerant networks without the need of a centralized control system.

In addition to inspiring next-generation engineering solutions, the work of Tero *et al.* offers a new approach to systems biology. It provides a simple mathematical model for a complex biological phenomenon—adaptive plasmodial shape control—involving growth,

morphogenesis, and homeostasis coordinated with maintenance, self-optimization, and self-repair of morphological and functional structures, the molecular and mechanistic bases of which are completely unclear. Even though the mathematical model has no basis in any specific molecular mechanism, it is nonetheless beautifully useful. It quantitatively mimics phenomena that are fundamental to any living system—phenomena that can be neither captured nor quantified by verbal description alone. Because the model has a number of tunable parameters that can be determined by computational fitting of experimental data, it provides objective readouts (e.g., to search for mutants that display quantitative alterations). Are there genes specifically involved in self-optimization, self-organization, or self-repair? Can molecular circuits be identified, and if so, how are they built, how do they function, and how are they linked to other regulatory systems at the single-cell level? Addressing these questions may lead to yet undiscovered fundamental functionalities in living cells and unravel their molecular basis.

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PALEONTOLOGY

And Then There Were None?

Richard G. Roberts¹ and Barry W. Brook²

Direct dating of fossils of the putative last survivors of the Australian megafauna supports claims that they were extinct by 40 thousand years ago and not later.

Giant marsupials, reptiles, and flightless birds once inhabited Australia (see the first figure). But 23 of the 24 genera of these megafauna disappeared in the late Pleistocene (~125 to ~12 thousand years ago). Most Australian megafauna appear to have survived until 51 to 40 thousand years ago, with human impact by hunting or vegetation change proposed as the extinction drivers (1–4). Yet, one site has stood out as an anomaly: Cuddie Springs in interior New South Wales. Persistent claims have been made that this site contains megafauna fossils associated with stone tools in sediments deposited

40 to 30 thousand years ago (5–7), thus indicating prolonged overlap between people and megafauna. These claims have been challenged (2, 8) based on concerns about possible reworking of fossils from older deposits. To resolve this conundrum, Grün *et al.* (9) have now directly dated the fossils themselves. The results provide no evidence for the late survival of megafauna at the site.

Cuddie Springs is an ephemeral lake in the Australian semiarid zone. Fossils were originally discovered when digging wells for water. Many more have since been exhumed from the claypan, including the remains of the giant bird *Genyornis newtoni*, the threeton *Diprotodon optatum* (the largest marsupial ever to roam Australia), and a range of supersized kangaroos. The fossils found in the same sedimentary layers as stone tools (stratigraphic unit SU6; see the second fig-

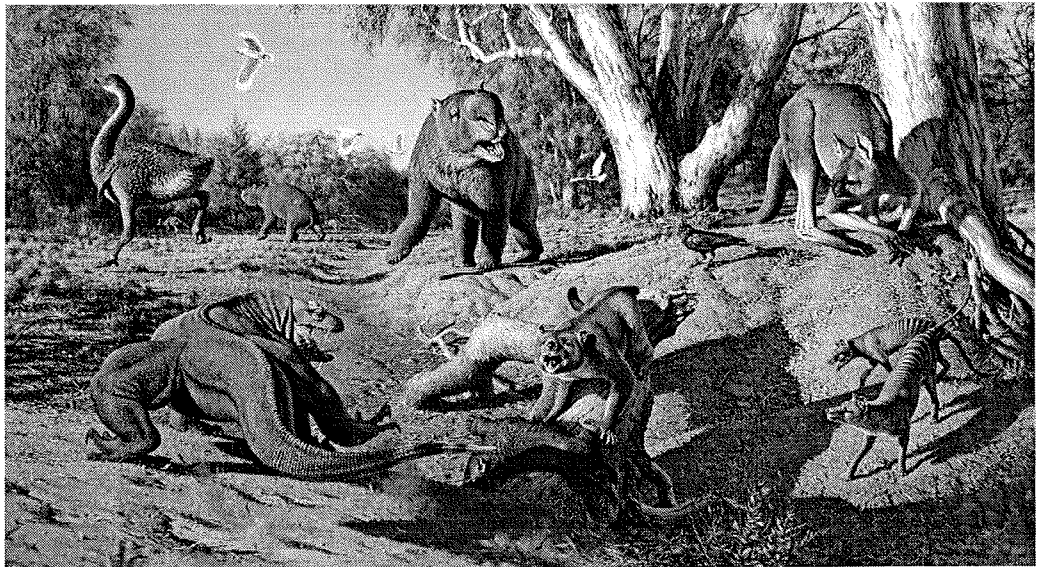
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ure) have attracted most recent attention. The lack of preserved collagen has prevented these fossils from being dated directly by radiocarbon methods (8). Instead, their antiquity has been inferred from radiocarbon dating of charcoal fragments and from optical dating of quartz grains found alongside the bones and stones. The ages range from 40 to 30 thousand years ago, but show no pattern of increasing age with depth. Optical dating of individual sand grains revealed that some were incorporated in the past 12,000 years, indicating recent intrusion of sediment into SU6 (2). Immediately below the lowest artifacts, but separated in time by several tens of millennia, is a geological discontinuity, which represents a former land surface.

Sidestepping the question of whether the fossils are associated with the dated charcoal and sediment grains, Grün *et al.* (9) directly date the teeth of several species of extant and extinct fauna with electron spin resonance (ESR) and uranium-series methods. Both methods are sensitive to the postdepositional history of uranium uptake by the dental tissues, but to varying extents. Minimum ages can be determined by assuming that all the uranium was absorbed soon after burial; tighter constraints can be made for teeth with sufficient uranium by modeling its uptake to obtain combined uranium-series/ESR ages.

Using this multifaceted strategy, Grün *et al.* found that none of the dated megafauna in SU6 were younger than 50 thousand years; even the remains of extant taxa were older than 40 thousand years (see the second figure). SU6 also contained three teeth that dated to the middle Pleistocene (~780 to ~125 thousand years ago). Clearly, at least some of the megafauna teeth in SU6 are derived from older deposits, possibly due to well-digging or lateral displacement.

While making these measurements, Grün *et al.* also discovered a flaw in a geochemical argument used previously to support the hypothesis that the Cuddie fossils have not been redeposited (5). This interpretation was based on the similarity in the rare earth element chemistry of the bones and surrounding sediments. From their profiling of uranium and thorium concentrations in bone, Grün *et al.* conclude that the rare earth element signatures do not reflect the



Past Australian megafauna. Animals that once called Australia home include (clockwise from top left) *Genyornis*; *Diprotodon*; *Procoptodon* (the largest-ever kangaroo); the thylacine (which survived in Tasmania until 1936); *Thylacoleo* (the biggest marsupial carnivore); and the giant lizard, *Megalania*.

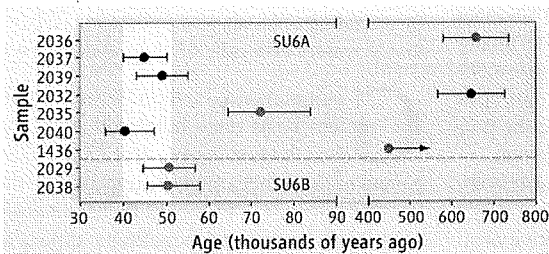
composition of the bone itself. Instead, these signatures mirror the geochemistry of the surface coatings and dirt trapped in cracks and pores, which could have formed long after the bones had been eroded from the sedimentary layers that originally contained them, and redeposited in SU6.

This re-dating of the Cuddie Springs fossils (9) brings the site into agreement with the 51- to 40-thousand-year extinction interval that captures the last survivors elsewhere in Australia (1–4, 10, 11). Claims for sites containing younger megafauna—such as Nomb Rockshelter, Seton Rockshelter, and Cloggs

Cave (6, 7)—should be considered suspect, pending dating using modern methods, preferably on the fossils themselves, as applied elsewhere (1, 4, 10, 11). Reliable ages for redeposited remains can be determined only by direct dating.

So what brought down the Australian megafauna? Given that people arrived in Australia sometime between 60 and 45 thousand years ago, human impact was likely the decisive factor. Humans may have caused the demise of the megafauna in two main ways: hunting—possibly of juveniles at rates as low as one kill per person per decade, termed “imperceptible overkill” (12)—and habitat disturbance, most likely by burning vegetation (3). Vegetation change seems to have accompanied the downfall of *Genyornis* in central Australia (1, 3), but not necessarily elsewhere (4, 13). Climate change—specifically increased aridity—may have reinforced the human impact, but the Australian megafauna were well adapted to dry conditions (13), having survived repeated droughts before succumbing during a period of comparatively benign climate (2, 4, 11, 14).

Recent findings on the North America megafauna may have implications for the earlier Australian extinctions. Using spores of a dung fungus



Teeth as timekeepers. Grün *et al.* dated fossil teeth from Cuddie Springs using electron spin resonance (ESR), uranium-series, and combined uranium-series/ESR. The resulting ages should conservatively be viewed as minimum ages, because they are calculated by assuming uptake of uranium soon after the tooth was buried; if uranium uptake happened later, the calculated ages would be older. The figure shows the ages of the teeth found in sedimentary layer SU6, in which stone tools have also been found. Teeth of extinct megafauna are shown in red. None of the teeth are younger than the 51- to 40-thousand-year extinction window (pale green) that brackets the last-known megafauna occurrences elsewhere in Australia (2). Three teeth are older than 450 thousand years; they are likely sourced from the deposits underlying SU6, which contain many teeth of this age (9). Data from (9).

to track megafauna abundance, Gill *et al.* (15) showed that herbivore populations collapsed shortly before the onset of vegetation change and increased fire. The same chain of events may have occurred earlier in Australia, but over a time span too fine to be resolved by current dating methods. Recovery of ancient DNA from sediments has also revealed that mammoths and horses survived much later in North America than indicated by the fossil record, owing to the improbability of finding and dating fossils of the last survivors, especially in dwindling populations (16). Application of these types of approaches in Australia

may further refine the timing of the events leading up to extinction and provide sharper insights into the likely drivers of this ecological catastrophe.

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GEOCHEMISTRY

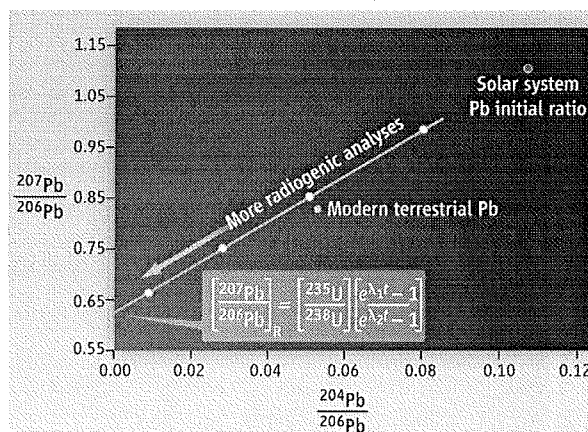
Adjusting the Solar System's Absolute Clock

J. N. Connelly

Meteorites and their components provide the only means to study the circumstances and processes that gave rise to our solar system. But the task of unraveling our origins is by no means straightforward. A single undifferentiated meteorite—a chondrite—typically contains matrix and inclusions formed over a wide range of conditions and time before eventually being accreted into a single body. Understanding this complex assemblage, especially over the critical first 10 million years, allows the formulation of models of the spatially and temporally evolving thermochemical conditions that gave rise to the solar system. Geochronology—the determination of ages of events recorded by meteorites—provides the requisite temporal information. Although advances have been made over the past decade in this field, on page 449 of this issue, Brennecka *et al.* (1) present data suggesting that a basic assumption for the use of the U-Pb chronometer in geochronology, the golden spike for deep time, may be incorrect.

Two types of chronometers are used to measure the ages of ancient meteorites. So-called relative chronometers are based on the rapid decay [half-lives <10 million years (My)] of now extinct, short-lived radioisotopes that were created either just before or during the formation of the solar system. These relative chronometers, such as ^{41}Ca - ^{41}K , ^{26}Al - ^{26}Mg , ^{53}Mn - ^{53}Cr , ^{60}Fe - ^{60}Ni , and ^{182}Hf - ^{182}W , require that the initial abundances of the parent radioisotope are known and that it was homogeneously distributed throughout the solar system. The short half-lives of these extinct nuclides have the potential to provide the most precise age estimates for the first 10 My. But the recent discovery of large-scale isotopic variability of nucleosynthetic origin for elements of contrasting volatility among different meteorite groups (2) casts doubts on the assumption of homogeneous distribution of short-lived radioisotopes.

Absolute chronometers are based on long-lived radioisotopes so that the present-day parent-daughter ratio in a sample provides an



Setting a date. In the inverse Pb-Pb diagram, the radiogenic $^{207}\text{Pb}/^{206}\text{Pb}$ ratio $[(^{207}\text{Pb}/^{206}\text{Pb})_R]$ can be calculated by projecting a line through data points with variable mixtures of radiogenic Pb and initial Pb to the y intercept, where the initial Pb is theoretically zero. This variability is created by strategically analyzing related fragments, minerals, or acid leachates with variable U/Pb ratios. (Subscript R refers to radiogenic; λ_1 and λ_2 represent the decay constants of ^{235}U and ^{238}U , respectively; and t represents time.)

age in years before present with no assumptions necessary regarding the initial inventory of the parent radioisotope or its homogeneous distribution. Of the absolute chronometers, only the U-Pb system has half-lives and systematics suitable for resolving events in the first 10 My of the solar system. In addition to its high resolution, the U-Pb system is unique in a second way. Two isotopes of U, ^{235}U and ^{238}U , break down spontaneously at different rates (half-lives of 0.704 and 4.47 billion years) to produce ^{207}Pb and ^{206}Pb , respectively.

If it is accepted (and it has been) that the $^{238}\text{U}/^{235}\text{U}$ of all objects is 137.88, then one may calculate an absolute age knowing only the ratio of radioactively produced ^{207}Pb and ^{206}Pb (see the figure). This so-called Pb-Pb method is advantageous, if not necessary, because late alteration and/or laboratory treatment to remove ubiquitous contaminant terrestrial Pb typically alters the U/Pb ratio so that the measured parent-daughter

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