Human evolution

Pedigrees for all humanity

Jotun Hein

Simulations based on a model of human population history and geography find that an individual that is the genealogical ancestor of all living humans existed just a few thousand years ago.

Writing on page 562 of this issue, Rohde, Olson and Chang[1] address a simple but fascinating question: how far back in time must we go to find an individual who was the ancestor of all present-day humans? After a little consideration, the existence of such an individual (the 'universal ancestor' or, as the authors put it, our 'most recent common ancestor') should not surprise: I have two parents, four grandparents, and the growth in the population of my ancestors is close to exponential as I trace them back in time. This is true for anybody's ancestors, and there must soon be an overlap between the ancestors of two or more randomly chosen individuals (Fig. 1).

In simplified models, which assume random mating, the average number of generations back to a universal common ancestor has been estimated[2–4] to be around $\log_2 n$, where n is the population size. So if, for instance, the present-day population were to consist of 1,000 people, the average number of generations back to the universal ancestor would be $\log_2(1{,}000)$ — about 10 generations. For populations of size 10^6, or the present human population of size 6×10^9, it would be 20 or 33 generations, corresponding to 500 or a bit more than 800 years, respectively (assuming a generation time of 25 years). This is surprisingly recent.

And an even more surprising conclusion from such models is that, only a little farther back in time, a large fraction of the population will be the ancestors of everybody alive today. The remaining individuals back then will be the ancestors of no one. As Rohde *et al.*[1] describe it, "When genealogical ancestry is traced back beyond the [universal ancestor], more and more people in earlier generations become ancestors of the [whole] present-day population". At a certain point in history (the 'identical ancestors' point), people can be divided into two groups: either they are common ancestors of all present-day humans, or their lineages have died out. Being the ancestor of only some living humans is not an option. At this point, Rohde *et al.* say, "everyone alive now had exactly the same ancestors". In the simplest model, the fraction of 'ancestors-of-all' is about 80%, and in most estimates so far, the time back to the 'identical ancestors' point is a bit less than twice the number of generations back to the first universal ancestor.

These estimates are not only astonishing, however; they are also unrealistically low, because of the simplicity of the underlying models. Key missing factors are geography (which influences population structure) and history (which affects population growth), and these are the ingredients that Rohde *et al.* have taken seriously to arrive at more credible estimates of the time back to the universal and identical ancestors.

The authors carried out simulations based on several scenarios, incorporating different degrees of population growth and different degrees of isolation of subpopulations, with occasional migration linking these subpopulations. The authors' first model is relatively simple and includes up to ten large subpopulations, which exchange just one pair of migrants per generation. In one set of estimates based on this model, the mean time back to the universal ancestor is 2,300 years (76 generations, assuming a generation time of a bit less than 30 years) and to the identical ancestors it is 5,000 years (169 generations) — the time of Aristotle and the first pyramids, respectively. The latter date is especially startling: had you entered any village on Earth in around 3,000 BC, the first person you would have met would probably have been your ancestor! A considerably more detailed model, which describes population density within continents, the opening of ports and more, does not change these estimates much.

The main weakness in the models comes from migration. As the authors point out, if one region is totally isolated (something that they do not simulate), with no migrants connecting it to other subpopulations, then the universal ancestor must logically have lived before the period of isolation began. Only after that period ends would the dates for the universal ancestor become less distant. Because of the effects of isolation, had we been living in 1700, say, and tried to work out when our universal and identical ancestors lived, the answers would have been further back in time than the answers we obtain now. Tasmania, for instance, was conceivably completely isolated at the time, and probably had been for millennia; this would therefore have pushed back the dates for universal and identical ancestry. So uncertainties about population structure introduce uncertainty into the proposed dates.

The genealogical questions addressed by Rohde *et al.* are distinct from questions about the history of our genetic material. In models that trace genetic material back in time, any given nucleotide position in our genomes can eventually be found in a single individual and on a single chromosome. Thus, being in the *pedigree* of all of humanity

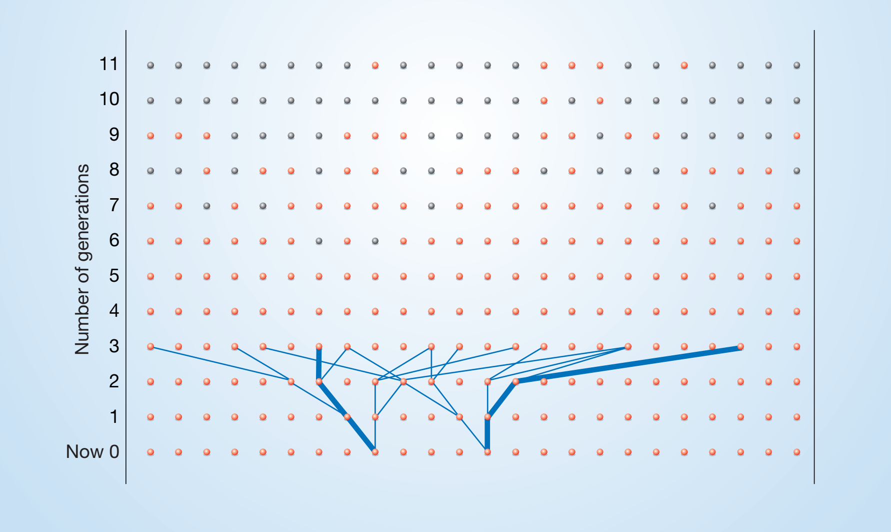
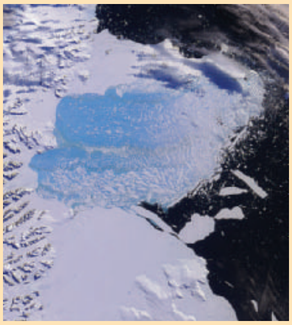


Figure 1 **Searching for our universal common ancestor. The figure shows how the number of ancestors of two people alive today builds up in a manner that is close to exponential. Because the human population has a finite size, however, we do not need to go back many generations before we find an ancestor that is common to both people. The same applies in searching for the ancestor of all living humans (universal ancestors are represented as grey balls). In simplified models, the expected time back to this universal ancestor is $\log_2 n$, where n is the population size. If we were to trace not both parents of each individual, but only one random parent for each (thick lines), we would in effect be tracing the history of gene variants (alleles). In standard models, the number of generations back to the common ancestor of a particular allele will be of the order $2n$, which is much longer ago. If we trace the history of genomes, not genes, recombination would complicate matters; this genetic 'shuffling' ensures that each child does not inherit exactly the same genomic information as its siblings, and means that the genealogical relationship of different genome segments can be different.**

Global change

Glacial pace picks up



NASA/GSFC/LARC/JPL, MISR TEAM

When a huge chunk of Antarctic ice shelf broke up in 2002, it provided dramatic pictures (see right) for the world's press and a control experiment for researchers. The ice shelf, Larsen B, is a floating extension of the ice of the Antarctic peninsula. The collapse of a substantial part of it — more than 3,000 km^2 — was attributed to increasing temperatures and released shoals of icebergs into the Weddell Sea. But a southerly remnant remained in place, enabling ideas to be tested about how ice shelves might affect glacier flow from the continental interior.

Two groups now report their results of satellite-tracking glacier behaviour in the region (E. Rignot *et al.* and T. A. Scambos *et al. Geophys. Res. Lett.* 10.1029/2004GL020697; 10.1029/2004GL020670). They found that five glaciers flowing into the area formerly buttressed by the ice shelf all accelerated at various times, whereas two farther south, which ran into the remnant ice shelf, did not. Speed of glacier flow is also reflected in their thickness: higher flow rates stretch and thin the ice, in these cases yielding estimated rates of thinning of tens of metres per year.

The main implication is that ice shelves act as a restraint on glacier flow. This conclusion was by no means obvious. Earlier, theoretical studies gave conflicting results; and there are also possible confounding factors, such as water, produced by seasonal melting of surface ice, acting as a lubricant at the glacier base.

A prospect for the future — and a worrying one as far as larger ice shelves and glaciers are concerned — is that a feedback system could kick in, accelerating glacier melting and producing significant rises in sea level. **Tim Lincoln**

---

does not imply that an individual makes a significant *genetic* contribution to the present population. In fact, that individual might have contributed nothing. This distinction is also illustrated by 'mitochondrial Eve' — the woman who purportedly lived hundreds of thousands of years ago and carried mitochondrial genes that are ancestral to all present mitochondrial genes. In Fig. 1 you would reach this Eve by tracing only female lineages backwards (rather than both lineages).

Universal common ancestry (in the pedigree sense) and genetic common ancestry thus occur on different timescales. The former is proportional to $\log_2 n$, and if you were to double the current population size, the expected time back to the universal ancestor would move back by only one generation in the simple model. But the time back to the genetic common ancestor is typically proportional to the population size, and so doubling the population size would double the time back to that kind of ancestor. The fact that the number of ancestors in a pedigree increases exponentially, whereas the number of genetic ancestors increases much more slowly, has the consequence that not many generations ago (about six), members of our pedigree existed that did not contribute to us genetically. So being somebody's great-great-great-great grandparent is no guarantee of genetic relatedness. To properly understand genetic ancestry, we need the concept of the ancestral recombination graph[5,6] — a generalization of traditional phylogeny that traces genetic material back in time in the presence of genetic recombination.

The increased ease of obtaining genome-sequence data from individuals, and the number of large-scale projects cataloguing variation in the human population, will increase our ability to test hypotheses about human history. Combining pedigree and genetic ancestry will become more and more important, both for data analysis and in exploring properties of population models[7]. Many interesting questions lie ahead. For instance, how much genetic material (if any) did the universal ancestor pass on to the present population? What about that for a non-universal ancestor from the same time? In the idealized models, how far back would one have to go to find a single couple who are the lone ancestors of everybody? And how much could be known about humanity's pedigree if we knew the genome of everybody? ■

Jotun Hein is in the Department of Statistics, University of Oxford, 1 South Parks Road, Oxford OX1 3TG, UK.
e-mail: hein@stats.ox.ac.uk

1. Rohde, D. L. T., Olson, S. & Chang, J. T. *Nature* **431,** 562–566 (2004).
2. Kammerle, K. *J. Appl. Prob.* **27,** 880–885 (1989).
3. Chang, J. *Adv. Appl. Prob.* **31,** 1002–1026 (1999).
4. Derrida, B., Manrubia, S. C. & Zanette, D. H. *J. Theor. Biol.* **203,** 303–315 (2000).
5. Griffiths, R. C. *Theor. Popul. Biol.* **19,** 169–186 (1981).
6. Hudson, R. R. *Theor. Popul. Biol.* **23,** 183–201 (1983).
7. Hein, J. J., Schierup, M. H. & Wiuf, C. H. *Gene Genealogies, Variation and Evolution* (Oxford Univ. Press, 2004).

Cosmology

What is dark energy?

Lawrence M. Krauss

It seems that the rate of expansion of the Universe is accelerating, driven by the so-called dark energy. Is Einstein's cosmological constant behind it? There might be a way to find out.

The nature of the 'dark energy' that is causing the apparent accelerated expansion of the Universe is, without doubt, the biggest mystery in physics and astronomy. Although it was astrophysical observations of the acceleration that led to the discovery of dark energy, there are precious few tests that can be performed to work out what dark energy is — whether it is simply the rebirth of Einstein's cosmological constant, or whether it might stem from something even weirder. All the evidence so far is consistent with the existence of a cosmological constant, which, in modern language, is understood to be the quantum-mechanical energy associated with otherwise empty space. In *Physical Review D*, Kunz *et al.*[1] suggest, however, that by comparing data on a range of astrophysical phenomena, it might be possible to rule out a cosmological constant as the origin of dark energy.

Dark energy is perplexing. Physical theory currently has no explanation of why the energy of empty space should be precisely zero (quantum-mechanical effects combined with relativity in fact predict quite the opposite). But it also gives no explanation of why that energy should not instead be so huge that it would dwarf all of the energy in anything else (making galaxy formation impossible). Yet arguments based on a host of different cosmological observations — even before the direct observation of the accelerated expansion — implied that the energy in empty space could not be more than three to four times greater than the energy contained in the matter and radiation of the Universe. To decide on what physics might be associated with dark energy, we have to rely on experiments and observations. No laboratory experiment we can imagine would be sensitive enough to do the job, so we are left with astrophysical probes. Which is where Kunz *et al.*[1] come in.