## Global change

# Glacial pace picks up

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**

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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 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?

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## 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.

They propose a three-way comparison of data: of the expansion rate of the Universe as it changes with distance (from measurements made using type-Ia supernovae, which originally led to the discovery of dark energy[2,3]); with measurements[4] of the temperature fluctuations in the cosmic microwave background (the relic radiation of the Big Bang); and with measurements of the clustering of galaxies on large scales. Studies of the cosmic microwave background (CMB) have provided remarkably precise constraints on most major cosmological parameters, and are in some sense complementary to the limits derived using type-Ia supernovae. To describe the different possibilities for dark energy, an 'equation-of-state' parameter, $w$, is defined. This is the ratio of the pressure to the energy of the material. For the cosmological constant, $w$ is exactly $-1$; any measured difference from this value would signal the need for another explanation. Data from the CMB, in combination with those from supernovae, currently limit $w$ to the range $-1.2 < w < -0.8$, consistent with the value for a cosmological constant[4,5]. (For comparison, $w$ for matter is 0, and for radiation it is 1/3.)

But Kunz et al.[1] point out that allowance should be made for a possible dynamical variation of $w$ over time. The key new ingredient they throw into the mix is a comparison between the observed clustering of matter on large scales across the Universe and the predicted level of such clustering based on observations of the fluctuations of the CMB. It turns out that, because of the way that the dark energy comes to dominate the expansion of the Universe, the CMB temperature fluctuations should change on the largest angular scales (spanning more than about ten degrees across the sky) in a way that is sensitive to the dark-energy equation of state.

Now, from the CMB fluctuations on large scales, the overall scale of the clustering of matter in today's Universe — on the scale of galaxy clusters, millions of light years across — can be predicted: in the case that $w < -1$, the prediction is that clustering would be decreased. Thus, by comparing this prediction with measurements of galaxy clustering from large-scale redshift surveys, it might turn out that the value of $w$ is not $-1$ — and so dark energy does not arise through a cosmological constant. The simplest interpretation of existing data suggests that this is not the case. But Kunz et al. point out that, first, there is a large spread in the data and, second, interpretation of the data is implicitly sensitive to assumptions about the nature of the dark energy. It is still possible that future studies could favour a value of $w$ that is not $-1$.

All of this points to what could be a big problem in cosmology lurking on the horizon. At present, the data are completely con-sistent with a cosmological constant being behind dark energy. Unfortunately, however, there are other possible sources of dark energy — some of which I consider to be the best-motivated alternatives to a cosmological constant — that would produce a value for $w$ of roughly $-1$. Thus, measuring $w = -1$ does not uniquely specify the origin of dark energy. Only if $w$ is not equal to $-1$ would we at least be able to say definitively that the dark energy is not associated with the ground-state quantum-mechanical energy of the vacuum.

Thus, some of us wake up in the middle of the night worrying that the discovery of dark energy may put cosmology on the same footing as particle physics, with all of the data that have come in over the years pointing consistently to exactly the same set of cosmic parameters, but without revealing any smoking-guns that could direct us to a fundamental theoretical rationale for why the data take these values. I have even made a bet with physicists Stephen Hawking and Frank Wilczek that this will happen (then, even if my worst nightmare turns out to be true, I will at least get a few bottles of wine out of the bargain). On the other hand, perhaps the cross-comparison of present and future cosmological observations, along the lines proposed by Kunz et al.[1], will yield some new handle on this slippery problem. In that case, I might lose my bet, but the 'golden age' of cosmology would persist. ∎

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**Cell biology**

# Sight at the end of the tunnel

## Arthur Horwich

A chaperone molecule called trigger factor binds new polypeptide chains as they emerge from the protein-synthesis machinery. Crystal structures suggest that this molecule forms a hydrophobic 'cradle'.

Cells seem to leave nothing to chance, including the final step of information transfer — the folding of a newly made chain of amino acids into a three-dimensional, active, 'native' protein. Specialized proteins called molecular chaperones ensure that the process of folding, determined by the amino-acid sequence of a polypeptide chain, does not go awry[1,2]. On page 590 of this issue, Ferbitz et al.[3] present crystallographic images of a bacterial chaperone called trigger factor. The images provide clues to how this molecule interacts with the newly synthesized polypeptide chain as it emerges from a tunnel in the protein-synthesizing machinery (the ribosome), potentially cradling and protecting segments of the polypeptide.

Chaperones typically assist the folding process by specifically binding to poly-peptides through a feature that is unique to non-native proteins — exposed hydrophobic surfaces. These surfaces become buried in the interior of a protein in its final form. Such hydrophobic regions, left to their own devices, can bind to each other, producing aggregates, which are not only a dead-end for protein function but also potentially toxic to the cell; for example, aggregates are found in several neurodegenerative diseases. Chaperones intervene by binding these exposed surfaces through a hydrophobic site of their own, preventing aggregation and enabling productive folding when the chaperoned protein is released.

The long-awaited structure of the trigger-factor chaperone, presented by Ferbitz et al.[3], reveals an extended arrangement of three domains — a 'crouching dragon' with a head, tail and arms — and a notable hydrophobic surface in the shape of a cradle that is exposed in the hollow between the tail and arms. Excitingly, Ferbitz et al. place this in a functional context by means of a second structure. This structure shows the tail portion of trigger factor in complex with the large subunit of the ribosome, suggesting the position of intact trigger factor as it might interact with the ribosome.

This second structure is a considerable technical achievement, involving astute evolutionary considerations, incisive biochemical analysis and some deft crystallography. The only ribosomal large subunit that has been observed at high resolution by X-ray crystallography is that from the archaeon *Haloarcula marismortui*. The structure of this subunit, presented several years ago[4], provided unprecedented resolution of such features as the reaction centre, where peptide bonds are formed, and the exit tunnel. But archaea lack trigger factor, instead using other molecules to protect nascent chains. The investigators had previously identified[5] the contact site for trigger factor on the ribosome of the bacterium *Escherichia coli*,