

Maddison *et al.*⁴ now point out several pitfalls in this procedure, which indicate general difficulties in building significance tests for genealogical data. First, although the test takes as a null hypothesis that the tree is constructed by the successive addition of African or non-African clades, rejection of this null model does not necessarily support one hypothesis about ancestral location over another. Second, the test takes the structure of the tree as certain, even though it is in fact estimated from the data; this could favour the preferred 'African Eve' hypothesis. Finally, the probability calculations were incorrect, in that they found the chance of seeing *precisely* the observed locations, rather than the chance of seeing that, plus all more extreme patterns. Given these difficulties, Maddison *et al.*⁴ instead used the straightforward criterion of parsimony to infer ancestral location, choosing that which requires fewest migrations. This procedure gave no clear evidence that our common mitochondrial ancestor lived in Africa; some trees suggested an African origin, some did not.

Worry

Human mtDNA sequences, like most such data, have been analysed using methods originally designed for establishing the relations between species. These methods tell us about the ancestry of one gene, but not about the structure of the whole population or about the forces that determine the spread of the gene we observe. A serious worry is that the relatively recent ancestry of human mitochondrial genomes reflects the recent spread of a favourable mutation, and so can tell us nothing about the population as a whole. Such 'selective sweeps' have reduced genetic diversity in regions of low recombination within the nuclear genome¹⁵.

If we take mtDNA to be strictly neutral, the probability of any particular genealogy being produced within a panmictic population of N genes can be written explicitly: at any time, the chance that two lineages will coalesce into one is just $1/N$. So one can use maximum likelihood to estimate the population size, and to test whether changes in the rate of coalescence of lineages reflect significant changes in population size, as in a founder event. Felsenstein has shown that this likelihood approach gives much more information than concentrating on the date of the one common ancestor, or on pairwise measures of sequence divergence⁷. When very many individuals are sampled, one-third of pairwise comparisons will be between lineages separated by the deepest split in the tree, and so will reflect one chance event. Maximum likelihood is more effi-

cient because it gives appropriate weight to all the branching events.

As the number of individuals increases, it becomes progressively harder to resolve the true tree³. But Felsenstein has shown how the likelihood approach extends naturally to give a sum over the set of all plausible trees⁸. Although this takes much more computing time than a search for the optimal tree, some such averaging over trees is essential. The problems with the interpretations of Wilson's group stemmed largely from concentration on one arbitrarily chosen tree — which is of course common practice.

Although Felsenstein only discusses the simple case of a single randomly mating population, it should be possible to extend likelihood methods to include hypotheses about the location of the ancestral population, and rates of gene flow. Slatkin and W. Maddison have already developed cladistic methods for estimating gene flow⁹. Their simulations reveal a consistent relation between the minimum number of migration events estimated by parsimony, and the actual number of migrants in each generation; they show that the tree of Cann *et al.*⁵ gives significant evidence of population subdivision.

Wilson's group pioneered the study of intra-specific variation in DNA sequence: ultimately, such variation must reveal more about the evolutionary processes that have shaped life than will comparisons between species. The controversy over the interpretation of geographical patterns in human mtDNA has shown the need for statistically sound methods of making inferences from genealogies, however, and the question of whether or not genetic data support an African origin either for our mitochondria, or for the human population as a whole, is still open. □

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Light work

THE art of manipulating atoms in beams of light emerges from the realm of the esoteric into the plainly practical with the description of a scheme for directly drawing electronic structures on silicon substrates (M. Prentiss *et al.* *Appl. Phys. Lett.* **60**, 1027–1029; 1992).

Conventional photolithography works by using light to transfer a pattern (that will ultimately become the microcircuit) from a material mask to the silicon substrate. Prentiss *et al.* reverse matters: an atom beam directed at the substrate will have to pass through focused laser beams to be directed into place on the surface. In their experiment, lines a few tenths of a millimetre across are written onto the silicon surface using a beam of sodium atoms and orange laser light. The ultimate prospect, the authors hope, is for direct writing with the resolution of a single wavelength of light.

Dog's dinner

It is one thing to show that oral vaccination of foxes in the wild may stem the tide of rabies in Europe (*Nature* **354**, 520–522; 1992), quite another to find a bait attractive to potential carriers of the disease elsewhere. H. Kharmachi *et al.* now report on their trial, with biomarkers, of the comparative allure of sausage, fishmeal, chicken head and sponge baits to Tunisian dogs (*Vet. Rec.* **130**, 494; 1992). The sponges contained "an attractant of minced meat, eggs, yoghurt, fish and cheese which had been kept for several days at room temperature", but came a poor last in the acceptance stakes at 30%. Chicken heads (98%) were most attractive. Chicken head and vaccine sachet would have to be brought together by hand, however, making the bait time-consuming to prepare.

Bright spark

STARS crushed by black holes may be the source of γ -ray bursters, suggests B. Carter (*Astrophys. J.* **391**, L67–L70; 1992). If, as seems likely in the light of data from the Compton observatory, these flashes of γ -radiation originate outside our Galaxy, they must be exceptionally energetic. For several years Carter has been studying the fate of stars that come too close to black holes, but has assumed that little of the inevitable heating comes out as radiation. What, he asks now, if that energy is converted into γ -rays? The doomed stars are compressed into pancakes and raised to temperatures of 10^9 K. The radiating phase could last a fraction of a second to many tens of seconds, in the range actually seen. Although he says the proposal is speculative, Carter highlights the possibility of identifying what kind of star has been consumed from the way the γ -ray intensity rises and falls.