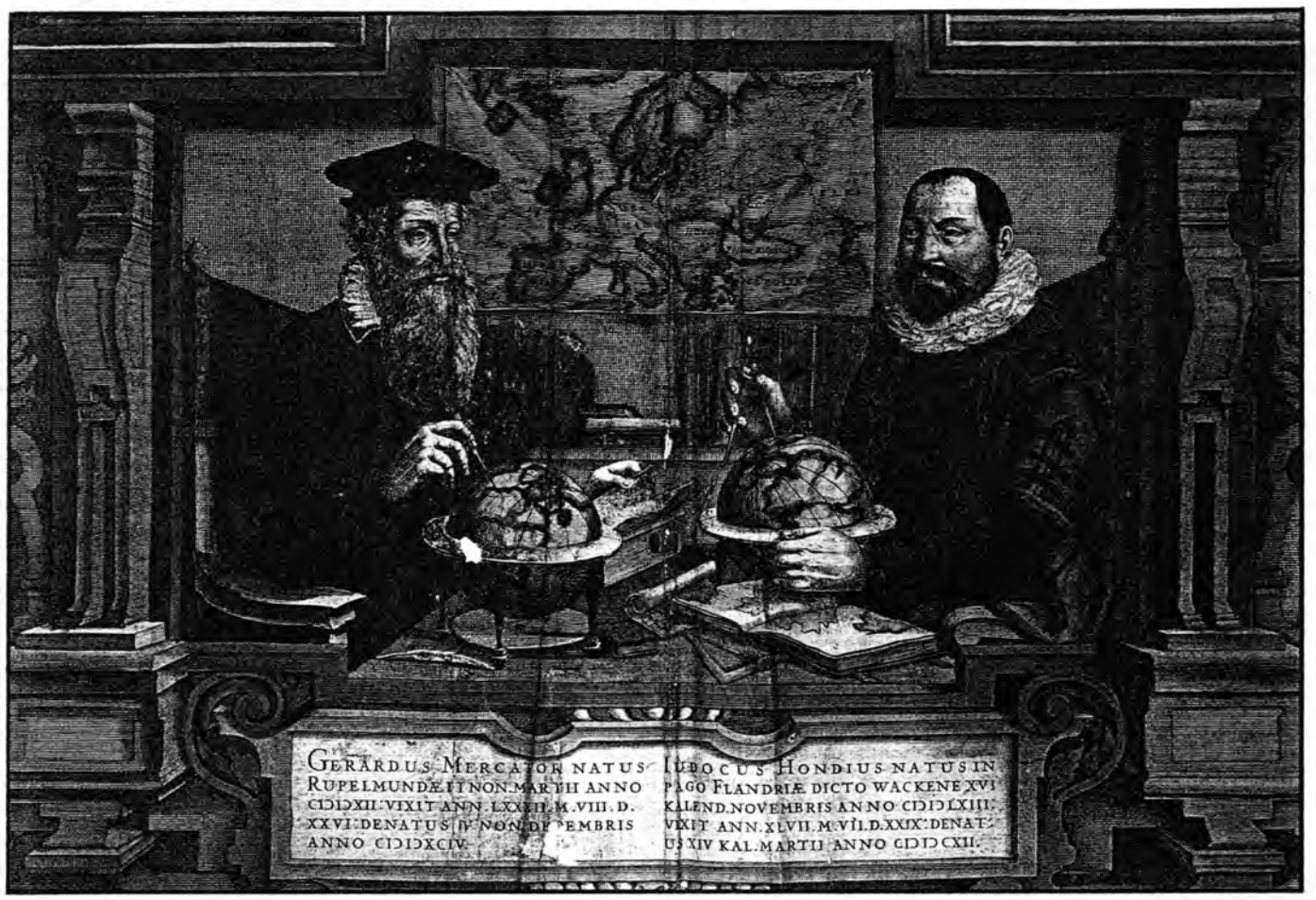


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Antimatter and the Moon

SIR — The recent measurement of the shadow of the Moon in charged cosmic rays with energies in the 10 TeV energy region¹ shows a displacement of 0.15° from the Moon's position; as pointed out previously² the Earth–Moon system acts as an ion spectrometer and can be used to differentiate matter and antimatter in the cosmic radiation. The direction and magnitude of the shift in this Tibetan air-shower experiment is in agreement with the hypothesis that most of the cosmic radiation at this energy is composed of protons (matter). Although the cosmic radiation does show an anomalously high flux of anti-protons at energies of 1–10 GeV (ref. 3), there is no direct experimental evidence of the nature of the cosmic radiation at energies above 20 GeV; in principle all of this high energy component could be antimatter.

On the assumption that the Universe is baryon symmetric and that higher-energy cosmic rays are of extragalactic origin, Stecker and Wolfendale⁴ have shown that the observed ratio of \bar{p}/p below 20 GeV can be explained; at energies of 10 GeV this ratio is 0.1%, and the prediction is that it rises with energy to as much as 20% above 10 TeV.

The significance of the Moon shadow detection is at the 7.1 σ level (Fig. 1); the displacement of the centroid of the shadow image from the known position of the Moon is (0.16+0.11/–0.09)° to the west and (0.02+0.07/–0.09)° to the south. The calculated shift of the image by the geomagnetic field is estimated to be 0.15° to the west¹ for the mode energy of protons at the zenith angle of the observations.

If the cosmic radiation was composed

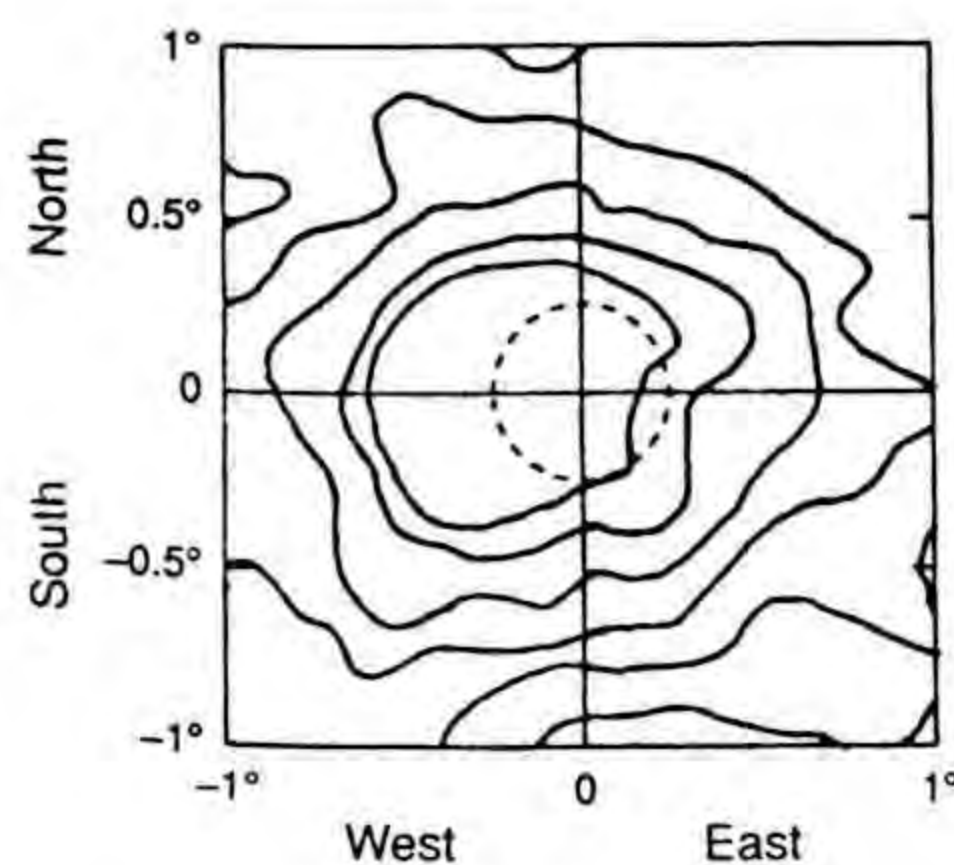


Fig. 1 Distribution of arrival directions of air showers in a box 2° × 2° centred on the position of the Moon as recorded in the Tibet air shower experiment¹.

entirely of antiprotons, the shadow would be displaced to the east by the same amount; a mixed composition would result in an elongated or displaced image. We have simulated the Moon image for various mixtures of matter and antimatter

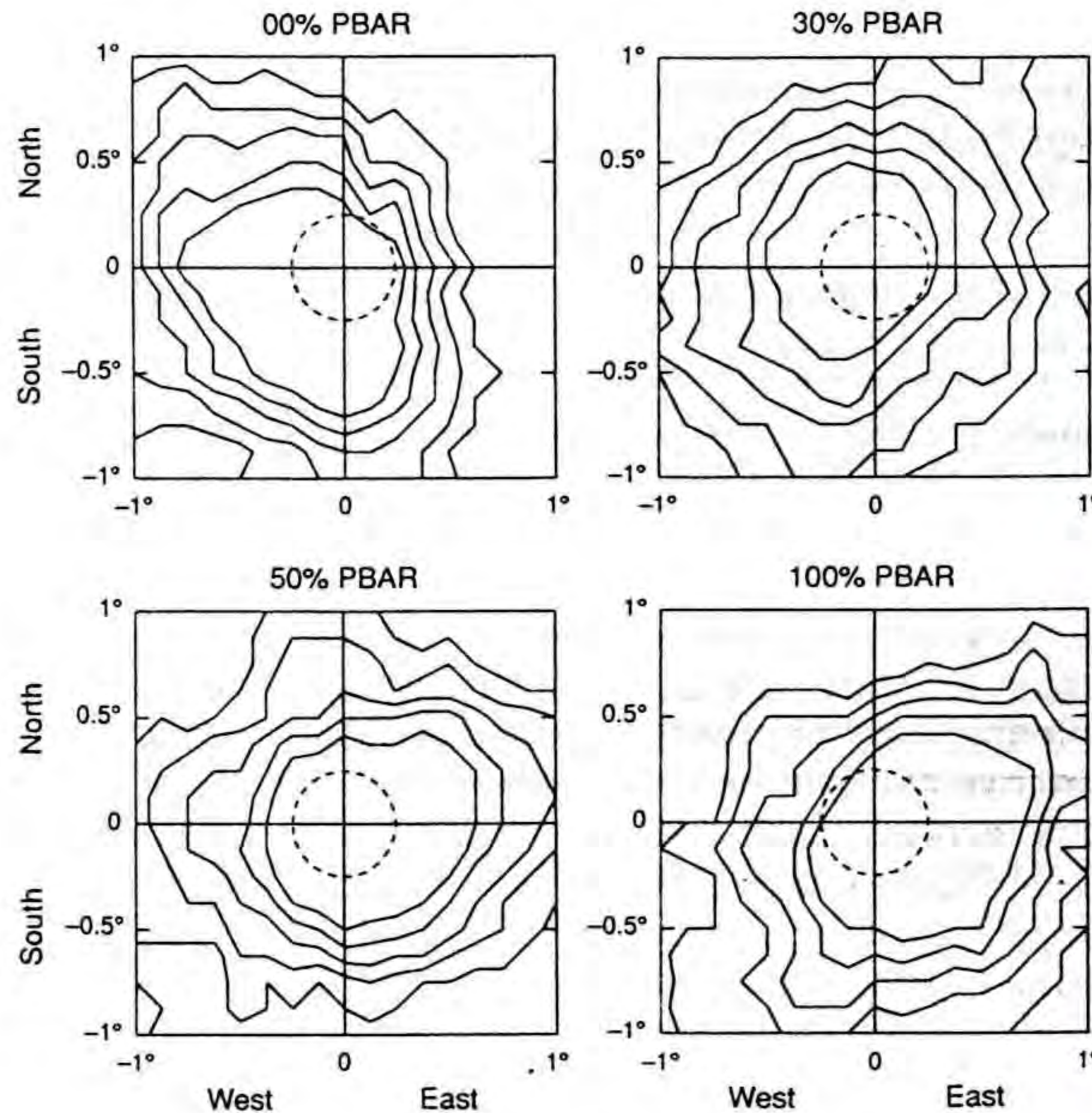


Fig. 2. Simulations of the arrival directions of a similar number of events assuming the composition ($\bar{p}/p+\bar{p}$) is 0, 30, 50 and 100%.

assuming a uniform magnetic field deflection of 30 mrad E^{-1} (TeV) and using a similar analysis procedure to that used in the Tibetan experiment (Fig. 2). The clear displacement of the measured image to the west (matter) and the lack of any significant elongation in the east–west direction agrees with the hypothesis that the bulk of the cosmic radiation at these energies is composed of protons. Although it is difficult to arrive at a quantitative limit without a detailed modelling of the Tibet experiment, a conservative figure (based on a visual comparison of Figs 1 and 2) is that the antimatter component is less than 30%; this limit is not sufficient to challenge the baryon symmetric model⁴ but does show that all the high-energy cosmic rays cannot be antimatter.

At energy thresholds of 1 TeV the offset is as much as 1.5°. More precise measurements of the moon shadow and hence of the \bar{p}/p ratio in the 1–10 TeV region will soon be forthcoming from the

ARTEMIS² and CLUE⁵ experiments using the atmospheric Cherenkov technique in the ultraviolet.

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Ancient rituals in Gabon

SIR — During a palaeontological survey of caves in Gabon, West Africa, in 1992, we discovered evidence of past human presence in Paouan cave, near Lastoursville¹, well beyond the limit of light penetration. A sondage in the sediments comprising the floor of a vast chamber revealed the presence of archaeological levels which contained abundant stone tools and charcoal. We examined samples of charcoal by microscope to determine the plant species present, and analysed others by the ¹⁴C method to obtain evidence of the ages of the layers. The earlier of the two levels is 5,570 ± 70 years before present, the later is 4,000 ± 70 years before present.

The stone tools from the lower level consist of hammer stones, flakes, cores, blades and rarer triangular points worked in black to grey jasper and milky quartz. The assemblage as a whole resembles the Tschitoléan industry which is widespread in Zaire, Congo and Gabon². Both types of raw material consist of water-worn pebbles introduced into the dolomite cave by humans.

Among more than 80 charcoal fragments identified, only four species of plant are represented, which indicates that the choice of plants carried into the cave was highly selective, considering that the forest surrounding the cave is extremely diverse (more than 1,000 woody plant species grow in Gabon). The four plant species found in archaeological context in Paouan cave are well known to local inhabitants, all of them having magical-ritual properties. The tree *Pterocarpus tinctorius* yields a red powder used to colour the body, especially during ceremonies such as initiation rites. *Copaifera* resin (copal) is used to manufacture torches, the tree itself considered as the 'king of trees' by many people of the African tropical forest. *Combretum* yields extremely hard wood often used to make batons and clubs, the wood being said to impart "aggressive" qualities to the holder. Finally, the liana *Strophanthus* is used

1. Amenomori, M. et al. *Proc. 23rd Int. Cosmic Ray Conf.* **4**, 351–354 (Calgary, 1993).
2. Urban, M. et al. *Nucl. Phys. (Proc. Suppl.)* **14B**, 223–236 (1990).
3. Stephens, S. A. & Golden, R. L. *Space Sci. Rev.* **46**, 31 (1987).
4. Stecker, F. W. & Wolfendale, A. W. *Nature* **309**, 37–38 (1984).
5. Appollinari, G. et al. *Nucl. Inst. Meth.* **A263**, 255 (1988).

by many African tribes as a source of arrow poison and as a tonic during periods of violent exercise such as iron smelting or prolonged ceremonies.

The highly restricted diversity of plant species carried into Paouan cave, allied to their known properties and modern uses by tropical African tribes, indicate that we may have discovered a place in which magical-ritual practices were carried out around 5,600 years ago. The presence of worked stone and *Strophanthus* charcoal suggests that poison arrows were manufactured in the cave. Poison-arrow manufacture by many African tribes is carried out with elaborate ritual in secret places, such as caves, rock shelters or forest thickets, from which women are excluded. The choice of *Copaifera* resin as the preferred torch-making material, and of *P. tinctorius* accords with the view that Paouan cave was used for magical-ritual purposes.

It seems that by 5,600 years ago, some of the tribes of tropical Africa had mastered the art and phytochemistry of poison-arrow manufacture, and that they had developed elaborate rituals around this activity.

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1. Delorme, G. *Spelunca* 4, 151-160 (1979).
2. Van Noten, F. (ed.) in *The Archaeology of Central Africa* 27-40 (Academische, Gruz, 1982).

Parsimony or statistics?

SIR — In the light of Stewart's Review article¹ on parsimony, I would like to comment on the use of this technique with molecular sequence data. Phylogenetic inference, no matter which method is applied, hinges on the tenet that the method used takes into account the mode of evolution of the molecule analysed. To infer phylogenies from DNA sequence data, there must be a mathematical description of the evolutionary process — a stochastic model.

Such models have been incorporated into statistical methods of phylogenetic inference, such as maximum likelihood^{2,3} or corrections of pairwise distances⁴. Methods with general models have wide applicability, allowing analysis of sequences that have undergone few or many substitutions, that evolve by a transition

bias, whose positions evolve at different rates, or whose base composition is biased. By contrast, parsimony's implicit stochastic model is highly restrictive. For example, it requires that each nucleotide position has a negligible probability of having changed more than once⁵. It generally is not known *a priori* if evolution generated one's data in accord with this rule. Parsimony has furthermore been shown to be statistically inconsistent (to arrive at the wrong answer at statistical significance) in a wide range of relatively realistic schemes⁶⁻⁸. Parsimony may have its limited set of applications, but for the average phylogeneticist it is not the method of choice.

Further, Stewart states that "[Distance] methods ignore the possibility that apparent overall similarity and true evolutionary relationship are not necessarily the same thing." This statement is incorrect. When properly applied, certain distance methods are powerful methods of phylogenetic inference that make less restrictive assumptions about the evolutionary process than does parsimony. The neighbour-joining method⁹, for example, with properly corrected pairwise distances, is a reliable method of phylogenetic inference even in the absence of a molecular clock⁸.

For nonspecialists, the following may serve as a brief statistical guide for conducting or evaluating phylogenetic sequence analyses. (1) Are the assumptions of the method used met by the mode of evolution of the molecule analysed? Does the method's explicit or implicit stochastic model take account of biased base composition, of different rates of transitions and transversions, or of variations among sites in the rate of evolution, for example? If an analysis was done with parsimony, is its use explicitly justified? (2) Were enough data collected to allow evaluation of multiple internal nodes (those nodes that determine the exact branching pattern of the tree)? (3) Are the conclusions based on significance obtained with a statistical method of phylogenetic inference, such as maximum likelihood, neighbour-joining with properly corrected distances, or invariant analysis? Application of statistical methods of phylogenetic inference avoids many of the pitfalls of parsimony, but has all of its powers.

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STEWART REPLIES — The purpose of my invited Review¹ was to discuss the powers and pitfalls of parsimony analysis in modern molecular evolutionary biology, not to review the numerous methods of phylogenetic inference. For this purpose, it was important to emphasize the key con-

cept — which is not always intuitive — that overall similarity scores do not necessarily reflect the evolutionary relationship of the taxa which they were made. For the sake of explaining this concept (and realizing I might anger some advocates of distance methods), I contrasted similarity analysis with parsimony in a simple manner, explaining the unique power of parsimony and how to detect false similarities. Although I did not discuss other methods that attempt to build true phylogenetic trees from molecular data^{10,11}, such as maximum likelihood^{2,3}, invariant analysis, and distance methods using matrices adjusted for superimposed substitutions^{4,10,11} (so-called "statistical" methods), I do not advocate parsimony to the exclusion of these methods. Indeed, some types of molecular data, such as DNA hybridization and immunological distances, are analysed only by distance methods. I would again refer the interested reader to the excellent review articles^{10,12,13} mentioned in my review for a more thorough discussion of the various methods of phylogenetic inference.

I also highly recommend a recent study by Huelsenbeck and Hillis¹⁴, in which distance, invariants and parsimony methods were compared regarding their abilities to find the correct four-taxon tree. (Maximum likelihood was not included in this study because of its computational expense.) This study is worthy because the 16 methods were extensively examined under several models of DNA evolution, including ones that conform to and ones that violate the assumptions of the methods. Parsimony methods were generally found to be poor at inferring the true phylogeny, so long as the true phylogeny does not suffer from the following conditions: that of having very short internal lineage separation clusters, each cluster having one lineage that is quite long relative to its sister lineage. Because few phylogenetically informative events will occur along the central lineage, homoplastic substitutions on the long lineages tend to group taxa erroneously during parsimony tree building⁶. This well-characterized phenomenon is termed the "Felsenstein zone"¹⁴ in phylogenetic inference. An important observation that Huelsenbeck and Hillis¹⁴ make is that all distance methods can fail to find the correct tree in the Felsenstein zone, and many find the wrong tree with certainty. We fully understand why parsimony can fail under these and some other conditions^{1,8}, but we are only beginning to understand when and why distance methods can find correct trees^{8,14}.

Another noteworthy point illustrated in ref. 14 is that with highly divergent sequences corrected distances become uninformative; distance methods cannot be