tree corresponds to a length for the central branch that is not significantly different from zero. But, they used a central branch length of 3.8 per cent in their simulations, longer even that that of their archaebacterial model tree (1.5 per cent), thereby biasing the results towards their conclusions.

Gouy and Li argue that they have compensated for the faster evolution of large subunit sequences by visually selecting conservative positions to be analysed. But an independent augmented distance analysis[9] of the "most conserved domains" at the 3' end of the large subunit sequence (48 sequences were used compared with the 9 used by Gouy and Li) supports the eocyte tree. Furthermore, Gouy and Li find (see below) that when the most slowly evolving eubacterial large subunit sequences are used (*Anacyctis nidulans*, *Bacillus subtilis*, *Micrococcus luteus*), evolutionary parsimony supports the halobacterial tree (at the 5 per cent level) and not the archaebacterial one. Clearly, analysis of the rapidly evolving large subunit sequences is subject to uncertainties of alignment and sequence selection.

It seems clear that Gouy and Li's large subunit analyses, confounded by high rates of evolution, are doubtful. On the other hand, Gouy and Li have confirmed the findings of my earlier analysis of small subunits[1], that is, that evolutionary parsimony supports the eocyte tree, and parsimony and distance matrix support the archaebacterial one. Given their flawed simulations, and the large body of data supporting evolutionary parsimony as the preferred method of analysis, I favour the eocyte tree.

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GOUY AND LI REPLY—Two lines of evidence indicate that the evolutionary parsimony method is not suitable for analysing ribosomal RNA sequence data. First, the results obtained from different data sets are strongly incongruent. For the 22 small-subunit (SSU) and 22 large-subunit (LSU) ribosomal RNA sequences we used (only 9 species were presented[2] because of space limitation), the former strongly supported the eocyte tree whereas the latter strongly supported the archaebacterial tree. Lake argues that LSU sequences are not suitable because they display, on the whole, a greater sequence divergence than SSU sequences. But for the regions we used, the rates in the LSU and SSU sequences are not very different (ref. 2, Fig. 1c). For the LSU data the χ^2 values for the archaebacterial, the eocyte and the halobacterial trees are 34.4, 0.8 and 4.1, respectively. This leads to the question: if the eocyte tree is the true tree, why have all the signals supporting this tree disappeared (the χ^2 value is only 0.8)?

Contrary to Lake's claim above that when the most slowly evolving eubacterial LSU sequences are used, the evolutionary parsimony method supports the eocyte tree, our application of this method to the same sequences with a different alignment supports the halobacterial tree. The evolutionary parsimony method, therefore, gives radically different results depending on the alignment used (Lake's alignment is probably not restricted to structurally conserved regions) and on the choice of species.

Lake[1] used 984 sites from each of 17 SSU sequences and obtained a probability of 2×10^{-6} for supporting the eocyte tree. It is doubtful that one can attain such a high resolution with such a limited amount of data. In our analysis[2] of 1,658 sites from only 8 LSU sequences, we obtained a probability of 5×10^{-6} for supporting the archaebacterial tree. The two results[1,2] are thus diametrically opposite to each other. For this reason we have serious doubts about the usefulness of the evolutionary parsimony method in dealing with the universal tree question, and in general we have reservations about the accuracy of the probability obtained from this method when more than four species are involved.

Lake also argues for the suitability of the SSU data, but our empirical test of the evolutionary parsimony method on the SSU sequences from humans, *Drosophila*, rice and *Physarum* erroneously grouped humans and rice in one clade. The reliability of this method for dealing with cases of deeper divergence is questionable.

By contrast, the neighbour-joining and maximum parsimony methods give completely congruent results in support of the archaebacterial tree, whether the SSU and LSU data are used separately or jointly. The evolutionary parsimony method performs poorly probably because it assumes equal rates of transversional substitutions.

In our computer simulation[2], we used 900 nucleotides because that was the length of the SSU sequences used. Regardless of whether the archaebacterial or the eocyte tree is used as a model both neighbour-joining and maximum parsimony methods are superior to evolution-

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ary parsimony; as we noted[2], the branch lengths of the eocyte tree were estimated by Lake's method. The superiority of neighbour-joining to evolutionary parsimony was supported by a more extensive simulation[10], including the case of large variation in rates among nucleotide sites.

The analysis by Bachelline and Michot[9] of partial sequences would be less reliable than our analysis of full length sequences. Finally, we note that the archaebacterial tree is also supported by RNA polymerase sequence data[11].

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Blur into focus

SIR—Morgan and Benton[1] suggest that the human visual system does not have a general motion deblurring mechanism[2], because the threshold for discriminating the spacing between two bars is degraded significantly by image motion. However, image motion has only modest effects when compared with static spatial blur. For a pair of lines in motion, the interval discrimination threshold, ΔT_i, only doubles for an 8-fold change in image velocity (V), corresponding to $\Delta T_i \propto V^{0.3}$ over the range from 0.75 deg s^{-1} to 6 deg s^{-1}. By contrast, Levi and Klein[3] report that interval discrimination thresholds are directly proportional to static spatial blur (B) when the blur width is comparable to, or larger than, the spatial interval. Also, in a related psychophysical task, Watt and Morgan[4] report that thresholds for discrimination of the extent of static spatial blur increase even more steeply ($\Delta T_b \propto B^{1.5}$). These observations suggest a marked difference in the effects of static blur versus motion blur, and they argue against the simple notion that discrimination thresholds are proportional to motion blur, which in turn is proportional to image velocity. Clearly, the issue deserves a more direct test, in which the effects of motion blur and static blur are compared on the same observers using otherwise identical stimuli and psychophysical tasks.

Without some form of deblurring process, the visual system would face major difficulties in accurately analysing moving images. For the high velocity condition (6 deg s^{-1}) in the Morgan and Benton task, the image traverses about 50 cones during the 100 ms estimated for the normal temporal integration period[5]. This introduces spatial blur and also reduces the intensity of the signal reaching each photoreceptor, thereby degrading its