given in our articles, although as we point out in both articles, and as Self notes, gaps do exist especially with regard to the paucity of recent community-based surveys in the Pacific Region and in some countries of Africa.

Self's comments and the presented data are thus particularly relevant in this context. Indeed, one of the implicit aims of our articles was to elicit responses from those working on filariasis with regard to our estimates and the data on which these are based, since we believe that much pertinent unpublished data may be available with individuals/institutions for many of the under-represented countries in our database. Incidently, although we worked closely with the Filariasis Control Section of the WHO at Geneva while constructing the database, I am surprised that at no time did we come across the data presented by Self. This suggests that much relevant data may also be available locally at the various germane WHO Regional Offices.

Whatever the source, I would strongly urge the relevant individuals/institutions to make such data easily available, either by publication or by some other easily accessible form of public dissemination. However, to be truly useful, these reports will crucially require to be accompanied by details (see above), which would allow some independent assessment of the quality of the data collected (this equally applies to the data presented by Self). Such information will also be essential for proper standardization of the data for comparative purposes[1,2].

We are currently planning to update and map the distribution of filariasis at various levels from global, regional to within-country. Doubtless, new data on infection and/or disease distribution and the effects of or plans for control at any of these levels, such as those likely to be available from Self and others, will greatly enhance the utility of this exercise. I look forward to their publication or availability by other forms in the not too distant future.

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Searching for a Tree That Can be Trusted

In his *Comment* 'Can *Trypanosoma* Trees be Trusted?' Noyes[1] discusses possible reasons for a faster evolution in the Salivarian species compared to the remaining trypanosomes and other trypanosomatids, as it appears in the published rRNA phylogenetic trees[2–5], and also questions the reliability of such trees. This scepticism is well justified.

It is known that unequal rates of sequence evolution in different lineages may result in the 'branch attraction' artefact[6]. Speaking in terms of the trypanosome trees, accelerated rates of evolution in Salivarian trypanosomes would cause the long branches of an outgroup (the cryptobiid *Trypanoplasma borreli*) and *Trypanosoma brucei* to get together to the exclusion of all other species, thus rendering the entire genus *Trypanosoma* paraphyletic[2,5]. A known cure to this problem includes finding species which would 'cut' the long branches[7]. We have recently attempted this kind of analysis[8]. Subdivision of the long branches was done by using several other Salivarian species and a reptile trypanosome, as well as two additional bodonids (*Dimastigella trypaniformis* and *Rhynchobodo* sp.). Additional reduction of the homoplasy (similarity due to reversions or parallelism and not a common origin) was achieved by using only the most conserved sites of the rRNA alignment. Subsequently, we saw a bootstrap support for the monophyly of trypanosomes increasing to 97% and 92% levels for maximum likelihood and maximum parsimony analyses, respectively. This result is in agreement with the protein-based trees[9,10]. However, the best monophyletic trees were not significantly shorter than the trees in which trypanosomes were 'forced' to be paraphyletic. We interpreted these results as evidence for the victory of the monophyletic model, however, the margin is very narrow.

Returning to the question asked by Noyes, we hope that including additional trypanosome sequences and finding closer bodonid outgroup species would result in the trypanosomatid trees finally become more trustable and provide us with a lot of interesting information on 'evolutionary expansion'[11] of these rather successful parasites.

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A Key to Understanding *Trypanosoma* Trees

In a recent *Comment* article in *Parasitology Today*, Noyes has raised some fascinating points concerning the increased evolutionary rate in salivarian trypanosomes[1]. We were disappointed, however, to see that the article uses the 'usual' limited number of sequences to produce a distance tree which continues to promote the idea that the genus is polyphyletic; this, as the most recent comprehensive work by Lukeš *et al.*[2] illustrates, now appears not to be the case. Moreover, as alluded to by Noyes himself, it is apparent that much (if not all) of the confusion concerning the monophyly (or otherwise) of *Trypanosoma* in early studies was due primarily to insufficient suitable taxa and associated phylogenetic artefacts (see, for examples, Refs 3, 4). As Maslov and Simpson[5] and Maslov *et al.*[6] have indicated, the key to understanding the evolution of Kinetoplastida may well lie in studying organisms not included in earlier analyses, such as the trypanosomes of fish, amphibians and reptiles. Similarly, we suggest that the small number of *Schizotrypanum* (two *T. cruzi* species) included, compared with the preponderence of salivarian taxa, may be significant in clustering them artificially with other unrelated taxa due to long branch