for mammal and bird species. It also suggests that $z$ values may be taxon-specific when dealing with continental biotas. 

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Sir — Heywood et al. propose an explanation for the discrepancy between the high extinction rates predicted by theory and the low rates observed in reality. The admission that there is a discrepancy is something of a breakthrough. Theoretical predictions of extinction rates, derived from species–area relations, have previously been presented as if they were verified facts. Indeed, the popular press, environmental organizations and many politicians have taken them to be such; witness the frequently cited ‘fact’ that 50,000 species a year are being driven to extinction, or a statement to the UN commission on sustainable development by US vice-president Al Gore that one-half of all species may be extinct within the lifetime of our grandchildren.

Heywood et al. seek to reconcile the discrepancy by arguing that there is a time-lag of some indeterminate length during which species that are ‘committed’ to extinction persist. An equally parsimonious explanation is that the predictions are simply wrong. In an earlier publication, two of the co-authors of ref. 1 argued that the species–area relation is a poor tool for making predictions: in a mainland situation, it is “nothing more than a self-evident fact: that as one enlarges an area, it comes to eventually encompass the geographical ranges of more species. The danger comes when this is extrapolated backwards, and it is assumed that by reducing the size of a forest, it will lose species according to the same gradient.” Yet that is precisely what was done to obtain the oft-cited, very high extinction-rate figures. Wilson uses the species–area relation $S = k A^z$, and, plugging in an estimate of the rate at which tropical forests are being cleared and using $z = 0.15 - 0.35$, calculates that “if deforestation rates are maintained, then in thirty years at the present rate, one-tenth to one-quarter of the rain-forest species will disappear”.

As Heywood and Stuart pointed out, there are many reasons why the species–area relation may be descriptive without being predictive, especially on a global basis: species are not distributed at random; conservation measures already protect many key habitats (including those critical to 95 per cent of Afrotropical avifauna, for example); some species may be able to adapt to secondary habitats. In an earlier review of the species–area relationship, Connor and McCoy noted that the power relationship $S = k A^z$, first proposed in 1921, tends to exaggerate, producing impossibly high values of species when extrapolated to large areas. The authors’ analysis of 100 sets of species–area data led to doubt that there is any biological significance to the relation whatsoever; they suggested it may be nothing more than a sampling phenomenon, a “correlation... without a functional relationship”. Far from being proof that some consistent biological law was in operation, the fact that the values of $z$ (determined by the slope of a best linear fit of log $S$ versus log $A$) typically fell in the range $0.2 - 0.4$ was, they found, simply characteristic of any regression system with a high $r$-value and a large range in the independent variable relative to that of a monotonic dependent variable.

Heywood et al. take comfort from one quasi-empirical test of the theoretical extinction rates calculated from the species–area curve: A species-by-species analysis of threatened birds tallied 450 that appear doomed to extinction, a mere factor of 3 (as opposed to 100) off from the predicted value of 1,350. Yet Heywood and Stuart noted that hunting, collecting, disease and introduced species (as opposed to loss of habitat area, the presumed driving force in the theoretical predictions) have had “very major effects” on the decline of these particular species, most of which are not associated with tropical forests in any event. It is the loss of tropical forests that drives the very high global extinction-rate predictions, however. And even allowing for the operation of time lags, large losses in tropical forest area have occurred at least in one case without any comparable loss in species. The Atlantic coastal forests of Brazil, which have a higher species diversity than the now-threatened Amazon forests, were reduced by nearly 90 per cent, mostly in the nineteenth century; a recent survey by zoologists could not document a single extinction. On the contrary, several birds and six butterfly species believed 20 years ago to be extinct were rediscovered. According to the species–area relationship, a loss of 50 per cent of species should have occurred. Given such discrepancies, one would appear to be justified in continuing to take the much-cited global extinction rates with a grain of salt.

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We searched the RMSA-1 DNA and protein sequences against the US National Center for Biotechnology Information’s non-redundant nucleotide and protein sequence databases using the BLAST network service. Surprisingly, we found that the 418-codon open reading frame reported in this paper contains two Alu sequences (see figure). The presence of these Alu elements is absolutely unambiguous, whether protein or DNA sequence is used as query in the database search. The first Alu element runs from codons 173 to 278 of the putative RMSA-1 open reading frame, whereas the second begins at codon 364 and extends 112 nucleotides past the translational stop codon. The two Alu elements align with more than 70 per cent nucleotide identity with putatively active Alu elements, both contain characteristic poly(A) tails, and the second Alu element is flanked by a typical target site duplication. Of particular note, all three consensus p34^{cd2} phosphorylation sites identified by Yeo et al. are contained within these Alu regions. Also, the poly-L-lysine sequence reported by the authors as a potential nuclear localization signal is encoded in the poly(A) tail of the first Alu element, which would contribute significantly to a predicted pI of greater than 10, rather than a pI of 6.33, as stated by Yeo et al.

Several issues are raised in the light of our observations. The presence of two translated Alu elements (accounting for 34 per cent of the encoded protein) calls into question whether the cloned cDNA encodes the 47K protein recognized on immunoblots, or whether, for example, it represents the messenger RNA of an expressed pseudogene. In fact, given the co-migration of a crossreacting 47K species on immunoblots of proteins from humans, mice and chickens (and the fact that Alu elements are not present in the last two organisms), it seems unlikely that these Alu elements would be represented in the true 47K product. Furthermore, Yeo et al. used antisense RNA expression of the entire cloned cDNA (which includes both elements and a third Alu element downstream of the open reading frame) for functional studies. Given the very large number of Alu insertions within introns, untranslated regions and possibly, in rare cases, coding sequences of human genes, the results of such experiments are difficult to interpret. Of course, should it be the case that translated Alu elements exist in the functional 47K human protein, this would represent the first report of its kind and would have important evolutionary implications.

In our opinion, this example supports the view that peer review of papers containing DNA or protein sequence data should involve direct evaluation by experts in sequence analysis. This would require direct access of sequence information at the time of review, together with the submitted manuscript, to allow searches to be repeated or performed by a sequence specialist before acceptance for publication.

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YEO ET AL. REPLY — We agree that Alu elements are present in the RMSA-1 cDNA sequence that we reported1. Tugendreich et al. suggest that one possible explanation is that we may have cloned an expressed pseudogene. However, we have reviewed our published and unpublished data and firmly believe this not to be the case. We are currently carrying out confirmatory, direct experiments to establish that the RMSA-1 coding sequence contains Alu elements.