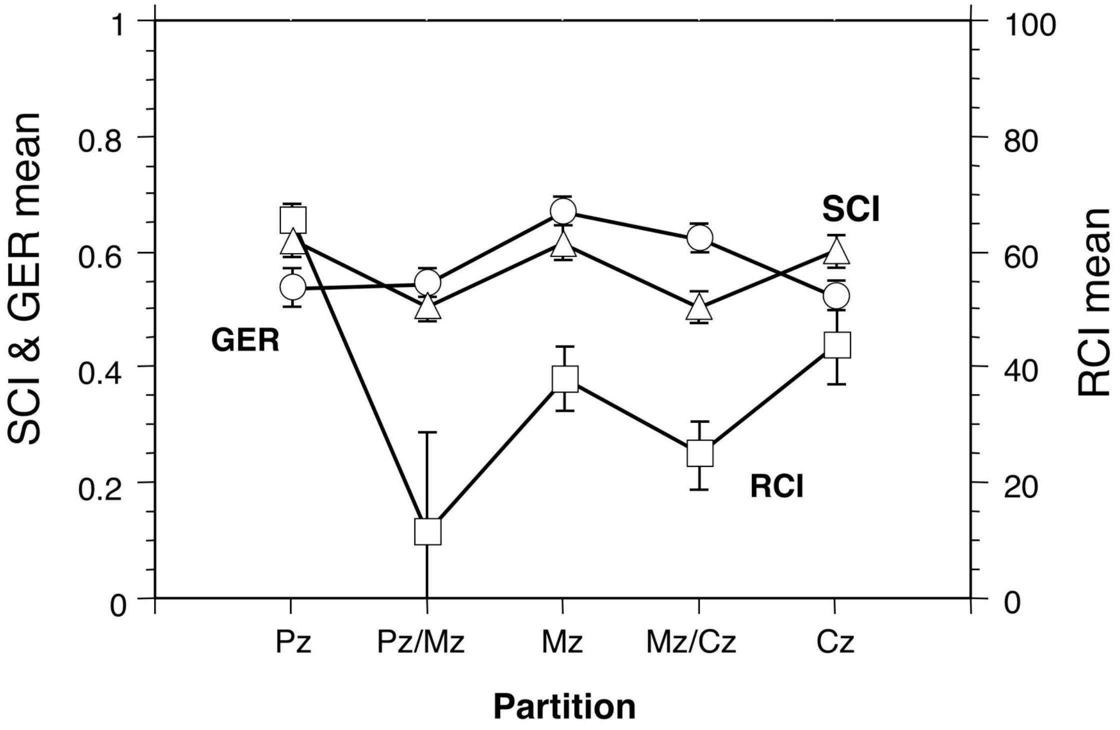


Figure 1. Data from which Benton et al. (2000) concluded that there is no change in fossil record quality through time. This differs slightly from their figure 1 in that all stratigraphic intervals have been treated as being of unitary duration (rather than being dated in My). Patterns are substantially unaltered. Mean scores (±SE) of the Stratigraphic Consistency Index (SCI; triangles), the Relative Completeness Index (RCI; squares) and the Gap Excess Ratio (GER; circles) for five geological time partitions of the data set of 1,000 cladograms. Pz, cladograms with origins solely in the Palaeozoic; Pz/Mz, cladograms with origins spanning the Palaeozoic and Mesozoic; Mz, cladograms with origins solely in the Mesozoic; Mz/Cz, cladograms with origins spanning the Mesozoic and Cenozoic; Cz cladograms with origins solely in the Cenozoic. Cladograms spanning two eras (i.e., Pz/Mz and Mz/Cz) have markedly lower RCI and somewhat lower SCI values than those solely within one era. Cladograms spanning two eras potentially have a longer range of origination dates than those confined within a single era.

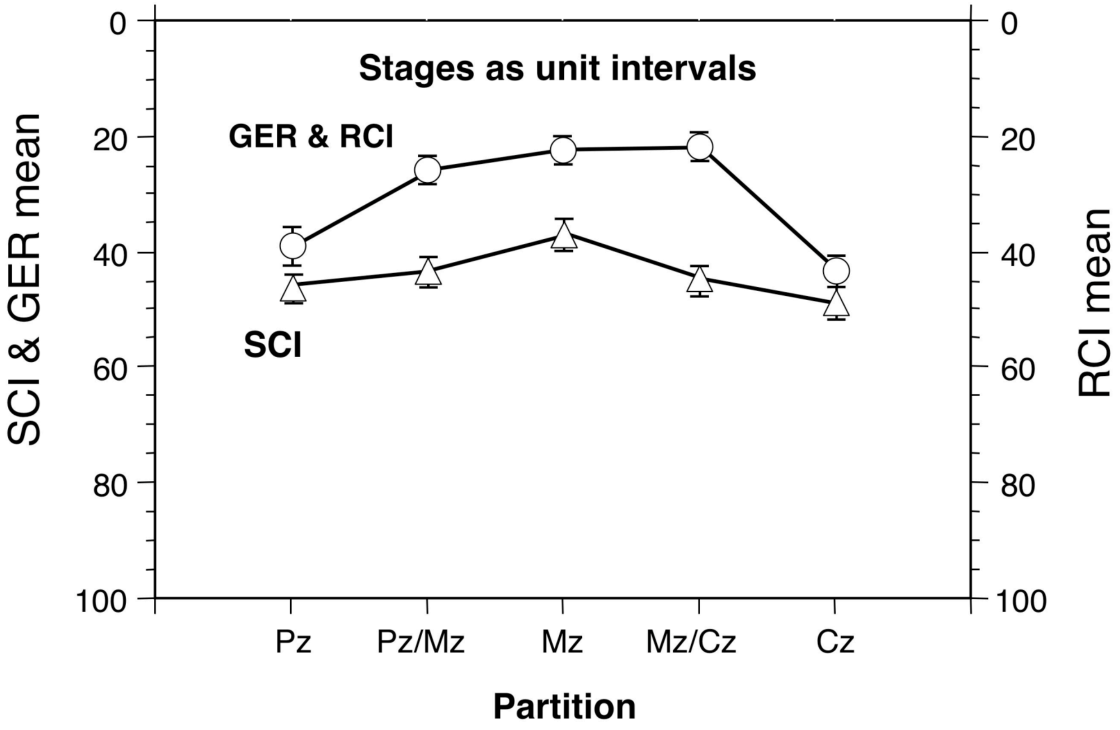
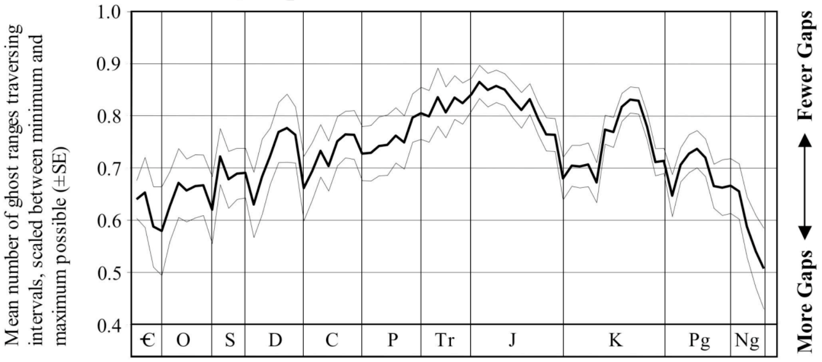
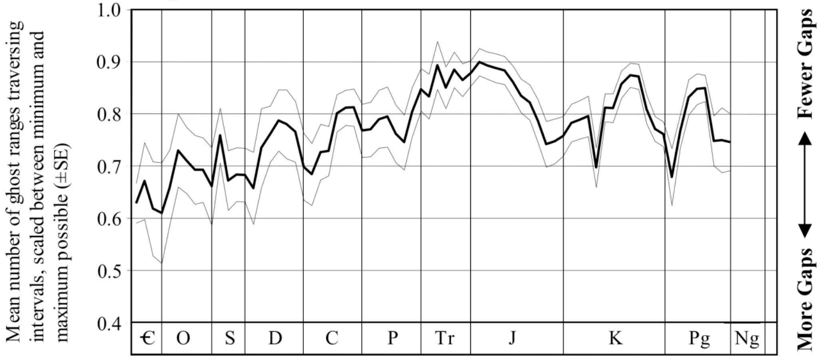


Figure 2. Mean percentage of randomised range reassignments (500 iterations) yielding indices of congruence as good as or better than those from the original data (±SE). Data from Benton et al. (2000) with abbreviations as above. All whole-cladogram indices of congruence are potentially biased by differences in tree size (number of taxa) duration (number of stratigraphic intervals) balance (pectinate or otherwise) and the distribution of range data. In Figure 1 (above) those trees with origins spanning two eras had lower mean congruence scores for the RCI and SCI than those trees with all origins confined to a single era. Huelsenbeck (1994) and Wills (1999) proposed the use of stratigraphic range randomisation tests to minimize the effects of most of these sources of bias. The percentage of randomized range reassignments with indices as good or better than those from the original data offers a superior measure of congruence than the raw indices. Randomized GER and RCI values are identical, since only the sum of ghost ranges (MIG) is altered by permuting the range assignments over the cladogram. The GER has a distinctly convex profile through time, with the poorest congruence (and hence greatest gappiness) in those cladograms with origination dates confined to the Palaeozoic and Mesozoic. The SCI has a shallower convex profile, and is a less sensitive metric overall (Wills 1999).

(a) All trees, Gap Index



(b) All trees, omitting lineages originating in the Recent Gap Index



(c) All trees, omitting lineages persisting to the Recent Gap Index

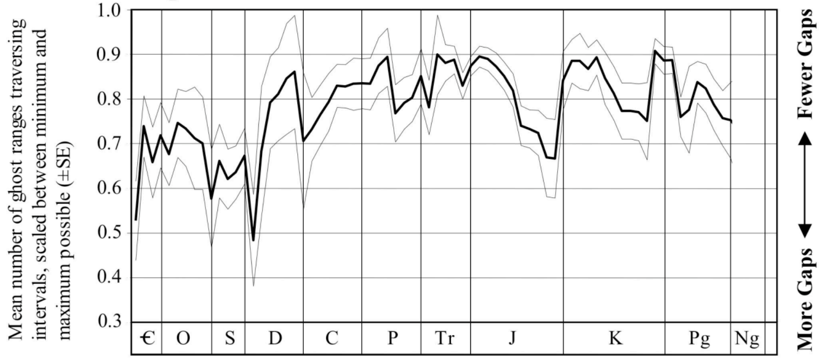


Figure 3. Data from 1,000 cladograms, encompassing all taxa. Data are filtered to exclude those cladograms where the range of possible gap values is less than 8 for a given interval (rather than 6 as in the main body of the manuscript). (*a*) Mean GI ±SE. (*b*) As in "*a*", but weeding out ghost ranges subtended between one or more taxa not known as fossils. (*c*) As in "*a*", but weeding out ghost ranges subtended between one or more taxa persisting to the Recent.

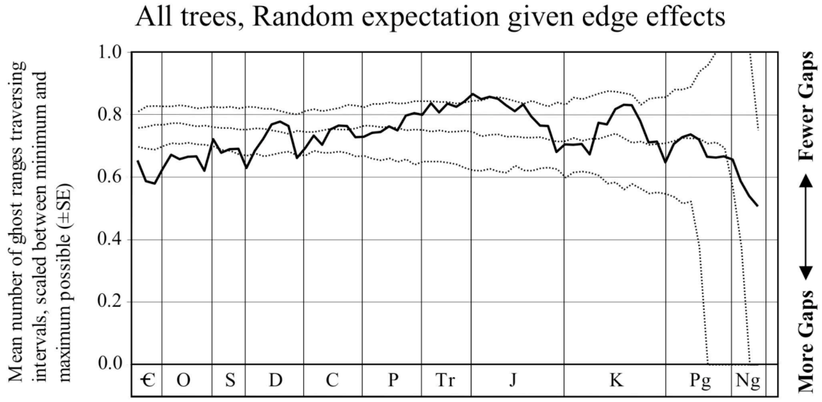


Figure 4. Is the pattern of GI through time significantly different from that expected for randomly dated cladograms with the same properties as our sample? Data were filtered to exclude those cladograms where the range of possible gap values was less than 8 for a given interval. All 1,000 trees were randomly redated in absolute age, while retaining the relative ages of their constituent lineages. 200 Monte Carlo simulations were run to yield 95% confidence intervals above and below the median (dotted lines). Observed pattern of GI as solid line.

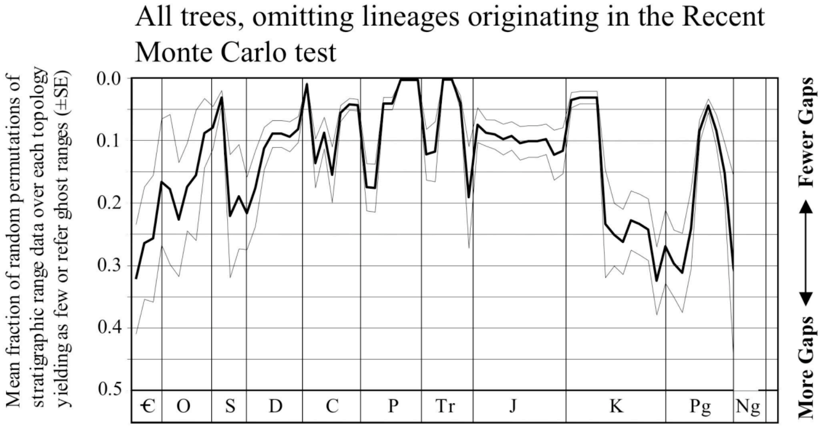
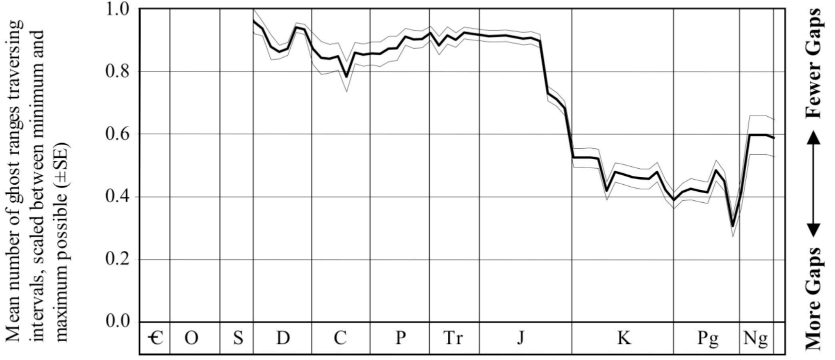
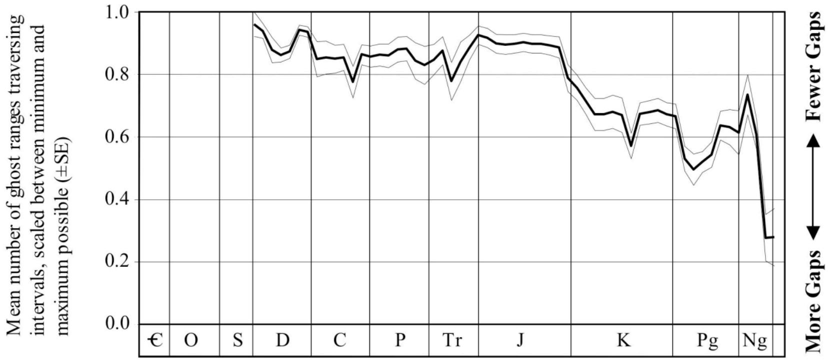


Figure 5. Monte Carlo test, randomizing the assignment of stratigraphic range data over each topology 400 times (see Wills 1999). Data were filtered to exclude those intervals and cladograms where the range of possible gap values was less than 8 for a given interval, and also to exclude the contribution of lineages persisting to the Recent. The fraction of randomized trees with a GI as high as or higher than the original shows a similar convex pattern to the GI.

(a) Families, Gap Index



(b) Families, omitting lineages originating in the Recent Gap Index



(c) Families, omitting lineages persisting to the Recent Gap Index

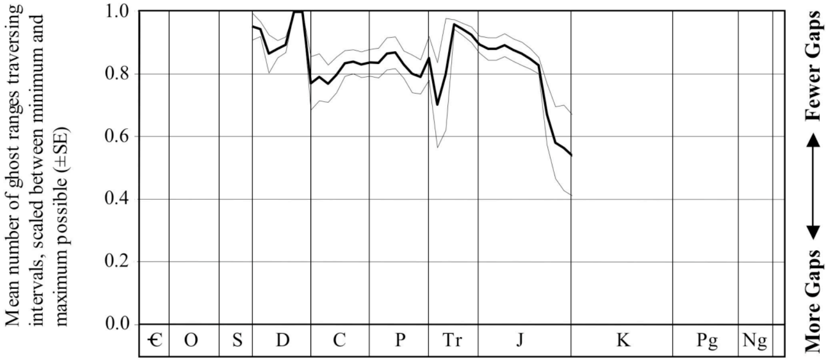
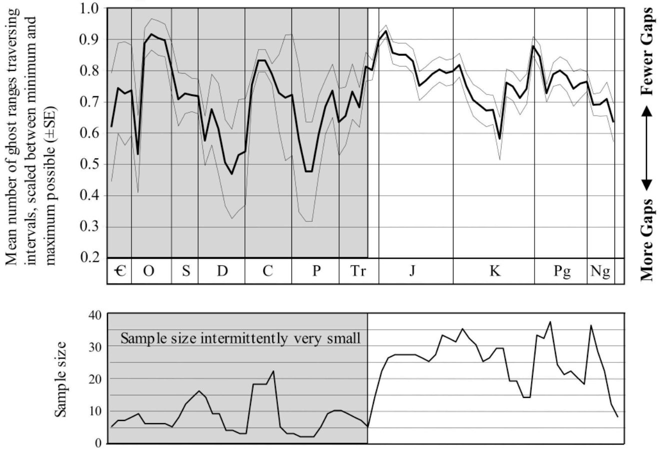
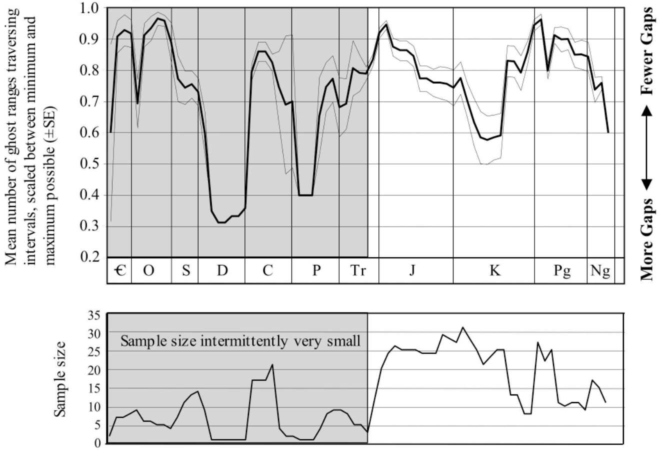


Figure 6. How common are ghost ranges in trees containing taxa predominantly at the family level (*n* = 344)? Data are filtered to exclude those cladograms where the range of possible gap values is less than 6 for a given interval. (*a*) Mean Gap Index. (*b*) As in "*a*", but weeding out ghost ranges subtended between one or more taxa not known as fossils. (*c*) As in "*a*", but weeding out ghost ranges subtended between one or more lineages persisting to the Recent.

(a) Trees comprising taxa below the level of family
Gap Index



(b) Trees comprising taxa below the level of family, omitting lineages persisting to the Recent
Gap Index



(c) Trees comprising taxa above the level of family
Gap Index

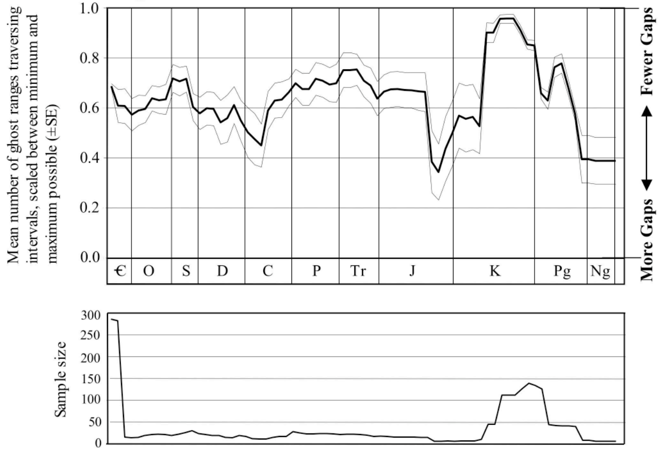
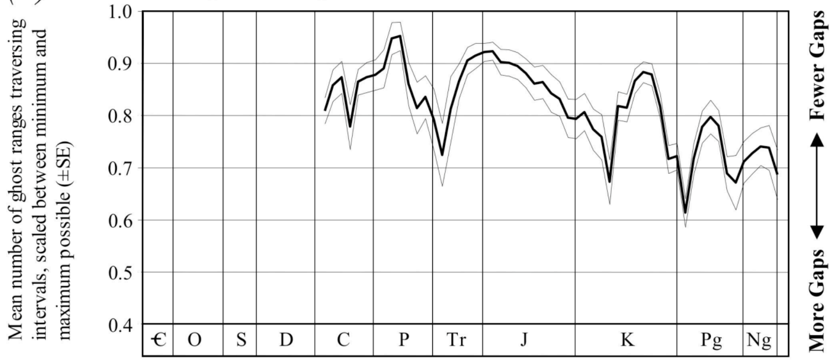
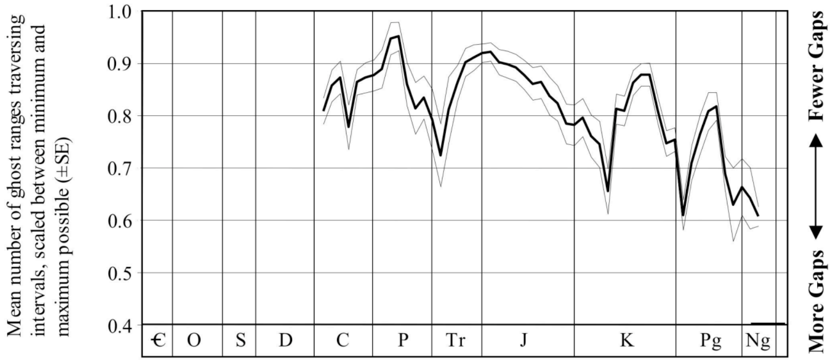


Figure 7. Pattern of GI through time for alternative taxonomic partitions of the data. Data are filtered to exclude those cladograms where the range of possible gap values is less than 6 for a given interval (a) Trees comprising taxa predominantly below the family level. (b) Trees comprising taxa predominantly below the family level, omitting lineages persisting to the Recent. (c) Trees comprising taxa predominantly above the family level. Sample sizes in grey shaded regions are frequently prohibitively small.

(a) Tetrapoda, Gap Index



(b) Tetrapoda, omitting lineages originating in the Recent Gap Index



(c) Tetrapoda, omitting lineages persisting to the Recent Gap Index

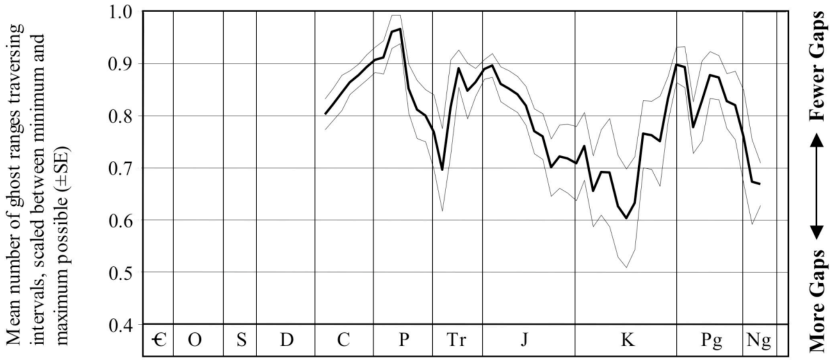


Figure 8. How common are ghost ranges in trees of tetrapods ($n = 512$)? Data are filtered to exclude those cladograms where the range of possible gap values is less than 6 for a given interval. (*a*) Mean Gap Index. (*b*) As in "*a*", but weeding out ghost ranges subtended between one or more taxa not known as fossils. (c) As in "*a*", but weeding out ghost ranges subtended between one or more lineages persisting to the Recent.