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## THE BEHAVIOUR OF GOLOBOFF'S TREE FITNESS MEASURE $F$

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Running title: TREE FITNESS

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*Abstract*--Goloboff recently introduced a method of character weighting that can be performed concomitantly with tree reconstruction. The basis for this method is his tree fitness measure  $F$ . The behaviour of  $F$  is examined for a number of hypothetical and real data sets. It depends strongly on the value of the concavity constant  $k$ , and does not seem to be predictable. This makes it difficult to make general recommendations about the appropriate value of  $k$  in specific cases. The basis for  $F$ , the number of *extra* steps taken by a character on a tree, does remain valuable as a basis for quality measures of trees, because it is independent of the number of states in the character, unlike the total number of steps and measures based on it such as CI and RC. Although no new measure is developed here, a number of requirements are formulated for an ideal tree quality measure.

## Introduction

Recently, Goloboff (1993a) proposed a new scheme for weighting a set of characters. His main concern about previously proposed schemes (e.g. successive weighting: Farris 1969) was that there are no unambiguous criteria for the weighting procedure and that the resulting trees are not always self-consistent. Thus, the result of successive weighting is dependent on the initial weighting. Self-consistency is the property that a tree implies, under some weighting scheme, weights for the characters that will lead to the same tree when reanalysed. Another way of expressing this is that in the case of character conflict (homoplasy), characters that show the lowest number of homoplasies are favoured over others that have more homoplasy on the tree under consideration. In other words, the tree itself tells us how much confidence to place in each character. Trees in the set resulting from successive weighting are not necessarily self-consistent because the weight of each character is implied by the resulting set of trees, rather than by each tree individually.

Goloboff (1993a) developed a weighting method which weights each character according to the number of extra (homoplasious) steps it takes on a tree. Because the weight of a character depends solely on the number of extra steps it takes on the tree under consideration, it is possible to evaluate each tree without reference to other trees, just as the total number of steps on a tree is independent of the number of steps on other trees. Goloboff's weighting scheme therefore allows character weighting to proceed simultaneously with tree reconstruction. This has the advantage of requiring only a single pass through the data in order to come up with the 'best' trees. Whether these trees are actually self-consistent is a point not addressed by him.

Goloboff's formula for the weight of a character (or *fit*) is:

$$f_i = (k+1)/(s_i - m_i + k + 1), \quad (1)$$

where  $s_i$  is the actual number of steps observed for character  $i$  on a particular tree,  $m_i$  is the minimum number of steps possible for character  $i$  (i.e. the number of states minus 1), and  $k$  is a constant of concavity added in order to influence how severely homoplasious characters are down-weighted. The total fitness  $F$  for a tree equals  $\sum f_i$ . Goloboff notes that "[t]he degree of

concavity that should be preferred ..... remains to be investigated." It is our intention to investigate here some properties of  $f_i$  and of  $F$ , and thus attempt to answer Goloboff's question.

### **Behaviour of $f_i$ and $F$**

From equation (1) it can readily be seen that  $f_i$  depends on the number of extra steps (ES)  $s_i - m_i$ . For ES=0 (i.e. for a perfectly fitting character)  $f_i$  is maximal and equal to 1. As the number of steps increases,  $f_i$  decreases. The weighting function is concave, more precisely a hyperbola. It reaches its lower limit (but  $>0$ ) when ES is maximal. This will always be the case on a completely unresolved tree, but may also occur on (partly) resolved trees. For increasing values of the concavity constant  $k$  the steepness of the hyperbola decreases. For values of  $k$  approaching infinity,  $f_i$  approaches 1; in other words, all characters are weighted equally independent of the value of ES. This behaviour of  $f_i$  is very straightforward and needs no further comment.

The behaviour of  $F$  is less easily predicted. Because  $F = \sum f_i$ , and  $f_i$  for each character depends on the topology of the tree, there is no straightforward relation between  $F$  and, e.g. total number of extra steps. The only thing that can be concluded directly is that as  $k \Rightarrow \infty$ ,  $F$  becomes equal to the number of characters in the data matrix, and thus the lengths of trees under implied weights become equal to their lengths under unweighted parsimony analysis. Thus, for  $k = \infty$  selecting trees with the highest fit becomes equal to selecting the most parsimonious trees under equal weights (MPTs). However, for low values of  $k$  this is not necessarily the case.

We can think of no biological reason for preferring one particular value of  $k$  over any other. A reasonable initial guess would seem to be  $k=0$ , or  $k=\infty$ . The latter is equal to not weighting at all, as shown above, and  $k=0$  may be too strong a weighter, according to Goloboff (1993a). We chose to investigate a number of different hypothetical and real data sets in order to elucidate the behaviour of  $F$  for different values of  $k$ . Because the computer program Pee-Wee, in which Goloboff (1993b) implemented  $F$ , only allows values of  $k$  up to

5 to be used, we calculated  $F$  values for different values of  $k$  and different trees using a spreadsheet program and an APL programming environment. Using hypothetical data sets for limited numbers of taxa allowed us to investigate all possible trees for these data sets. The trees submitted for the hypothetical data sets were unrooted, because the number of character state changes, and thus  $f_i$ , depends only on the topology of the unrooted tree (network).

For a data set in which all characters are congruent, here exemplified for seven taxa (matrix All7, Fig. 1), the behaviour of  $F$  is reasonably regular. The tree that fits the data perfectly (no homoplasy, i.e. no extra steps) receives the highest  $F$  value of 51. This value is equal to the number of characters in the matrix, and is independent of the value of  $k$ . Up to trees with three extra steps the behaviour of  $F$  is regular, decreasing linearly with the number of extra steps. For trees with four extra steps this regularity breaks down: two different  $F$  values are observed. Trees with ES=5 or 6 again all have the same  $F$  value. This behaviour is consistent for all values of  $k$ .

Introducing a single homoplasy (matrix All7\_2, Fig. 2) increases the range of  $\Sigma$ ES values for which  $F$  shows hysteresis. Equally interesting, for  $\Sigma$ ES=4 some trees have a lower value of  $F$  than some trees for which  $\Sigma$ ES=5, at least for  $k=0$ . For  $k=1$ , the best  $F$  value for  $\Sigma$ ES=5 becomes equal to the worst  $F$  value for  $\Sigma$ ES=4. For  $k=2$  and higher, all trees with  $\Sigma$ ES=4 have better  $F$  values than any tree with  $\Sigma$ ES=5.

For matrix All7h11 (Fig. 3), for which the two MPTs have  $\Sigma$ ES=9, similar behaviour is observed, but here some trees for which  $\Sigma$ ES=10 have a better  $F$  than any MPT, at least for  $k=0$ . For  $k=1$  the MPTs have  $F$  values equal to those for some trees with  $\Sigma$ ES=10, while for values of  $k>1$  the trees with the highest  $F$  belong to the set of MPTs.

For the real data matrices *Fordia* (Schot 1991; Table 1) and *Arytera* (Turner 1995; Table 2) similar behaviour is observed. *Fordia* represents a data matrix for which there are 111 MPTs of length 165 (CI .47, RI .63) with few unknown data and a reasonably resolved consensus tree. *Arytera* is messier in that there are many unknown entries, but the number of

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<sup>1</sup> Note that in Pee-Wee  $F$  values are multiplied by 10 and are corrected for autapomorphies, thus resulting in a value of 40 for matrix All7. Also, the concavity index in Pee-Wee, set with the command CONC, equals  $k+1$ .

MPTs is much smaller at 17 (length 336, CI .30, RI .59). Due to the number of taxa for these matrices ( $N=19$  and  $N=33$ , respectively) no full evaluation of all tree topologies was possible. Instead, Pee-Wee was used to find all fittest tree topologies for  $k$  values up to 5, using the option mult\*50. In addition, the  $F$  values for the set of MPTs and the best-fitting trees from Pee-Wee were evaluated for  $k$  values up to 49. The results are presented in Tables 3 and 4.

As can be seen in Table 3, for Fordia, among the set of MPTs,  $k$  values up to 19 show the same five trees to be fittest; above  $k=19$ , however, two different trees are fittest (at least up to  $k=10,000$ ). The fittest trees at  $k=0$  have lengths of 172 and 173 on the unweighted data matrix ( $\sum ES=93$  and 94, respectively); at  $k=1$  and  $k=2$  the same tree of length 167 is fittest; at  $k=3$  and  $k=4$  the fittest tree has length 166; and at  $k=5$ , in addition to two MPTs, the same tree as for  $k=3$  or 4 is fittest. However, probably due to shortcuts taken during fitness calculation, the results reported by Pee-Wee are inexact. As can be seen in Table 3, the two trees reported as fittest at  $k=0$  actually differ in fitness by .008 (i.e. within the margin reported by Pee-Wee); also the two MPTs reported as fittest at  $k=5$  actually rank as second and third, respectively, nor do they become the fittest MPTs at any value above  $k=5$ . We can thus not guarantee that trees obtained by Pee-Wee (and reported here) as fittest for  $k=0--5$  are indeed the best-fitting ones.

For Arytera (Table 4) at  $k=0$  there are three fittest trees of length 357 ( $\sum ES=256$ ); at  $k=1--4$  the same tree is selected each time, of length 347; and at  $k=5$  again three trees, this time of length 338, are fittest. None of these trees is in the set of MPTs, however. The fittest MPTs are the same trees for all values of  $k$  (at least up to 10,000). MPTs only become fitter than the fittest trees at  $k=0--5$  for values of  $k>11$  (Table 4). In addition to these trees, 978 non-MPTs with lengths up to 341 were generated using PAUP version 3.1.1 (Swofford 1993). The minimum and maximum  $F$  values were calculated for these trees with  $k$  values up to 49. The results (Fig. 4) show that the MPTs are fittest among this set of trees only for values of  $k>4$ .

## Discussion and conclusions

The behaviour described here seems to indicate that there is a minimal value of  $k$  above which all fittest trees are MPTs. For lower values of  $k$  less parsimonious (under equal weighting) trees may have a better fitness. We offer no proof for this conjecture but in our experiments we have not met a single counterexample. The conflict that arises when faced with a choice between a set of MPTs for a particular unweighted data set and a different set of trees that is fittest according to their  $F$  value seems to disappear when the value of  $k$  is chosen sufficiently high. The borderline case appears to be related to the maximum  $ES_i$  value over the set of MPTs,  $ES^{\text{MPT}}_{i,\text{max}}$ . For matrix All7\_2 the maximum  $ES^{\text{MPT}}_{i,\text{max}}$  value is 1, for matrix All7h11 it is 2. For values of  $k$  below this border value the fittest trees are not necessarily part of the set of MPTs, but may have a higher  $\sum ES$  value; for such values of  $k$ , which particular set of trees is fittest may vary with the value of  $k$ . For Fordia and Arytera the  $ES^{\text{MPT}}_{i,\text{max}}$  equals 7 and 11, respectively. For these matrices also,  $ES^{\text{MPT}}_{i,\text{max}}$  functions as a borderline value for  $k$ , below which not all fittest trees are in the set of MPTs.

Within the set of MPTs, which trees are fittest may also depend on the value of  $k$  (e.g. for Fordia). Getting rid of a step in a very homoplasious character at the expense of acquiring one in a character with good fit will always result in a decrease in  $F$ , because the decrease in  $f_i$  for the better character is larger than the corresponding gain for the worse one regardless of the value of  $k$ . However, gaining extra steps in a good character while losing one each in several slightly more homoplasious ones does not necessarily result in a decrease of  $F$ . Only as  $k \Rightarrow \infty$  will the difference in  $F$  values between equally parsimonious trees become infinitely small, or in other words, will all MPTs become equally fit. This behaviour makes it necessary to investigate whether the MPTs that are selected as fittest remain the same above a certain value of  $k$ . For the Fordia matrix, at  $k > 19$ , different MPTs are chosen than at lower values of  $k$ . This shows that neither  $ES^{\text{MPT}}_{i,\text{max}}$  nor the absolute maximum for  $ES$  over the data matrix, i.e. its value on a completely unresolved polytomy for the taxa,  $ES_{i,\text{max}}$  (10 for Fordia), is the borderline value. Because Pee-Wee allows only values of  $k$  up to 5 to be

evaluated, we could not check whether such a borderline value of  $k$  exists. Such an investigation will have to wait till this constraint is removed from the program.

Goloboff's concern that MPTs may not be self-consistent is unfounded if self-consistency can be equated with maximum fitness according to his formula for  $F$ . At sufficiently high values of  $k$  at least some MPTs are always in the set of fittest trees. Moreover, character weighting presupposes that some characters are phylogenetically more informative than others. Even taking this assumption for granted, it does not follow necessarily that more homoplasious characters are *per se* less reliable as indicators of phylogeny. Rather, in our view homoplasy is in the first place the result of incorrect assumptions of homology and should be treated as such by re-assessing these assumptions in the light of the initial analyses (cf. e.g. Hennig 1966; Bryant 1989). If the possibilities for re-assessment of homology statements (i.e. hypotheses of synapomorphies) have been exhausted, the remaining homoplasy *may* be indicative of the unreliability of the affected characters as markers of phylogeny, but still not necessarily so. In itself, the re-assessment of homology assumptions constitutes reweighting of the characters, but based on biological grounds (observations made on the specimens), till all characters are equally reliable as markers of phylogeny. The only remaining basis for weighting characters then becomes a parsimony argument, namely in order to select those MPTs in which the maximum number of characters are congruent. This can be done by adjusting  $k$  so that a subset of the MPTs is selected, or by applying other measures based on the same line of reasoning (e.g. OCCI [Rodrigo 1992] or average  $r_i$  [Turner 1995]). We can see no foundation for preferring any particular  $k$  value that does not result in a subset of the set of MPTs. The same criticism (that weighting may lead to sets of trees not in the set of MPTs) can be expressed towards successive weighting (cf. Platnick et al. 1991).

Above a certain threshold value of  $k$  the subset of fittest MPTs seems to remain stable. This raises the possibility that this  $k$  value can be used as a basis for an index of the quality of the data set as a whole. Such an index would have at least the desirable properties that unlike CI and RC, it is independent of the number of taxa in the matrix, and independent of variation in the minimum number of steps due to characters with different numbers of states, because

neither influences the number of extra steps. Data sets with different numbers of characters are not directly comparable, however. As the number of characters increases, so will  $F$ .

Possibly, the *fitness index*  $FI_k$ :

$$FI_k = (F - F_{\min}) / (F_{\max} - F_{\min}), \quad (2)$$

(where  $F_{\max}$  is the  $F$  value for a data matrix of equal dimensions but without homoplasy and thus equal to the number of characters in the data matrix, and  $F_{\min}$  is the  $F$  value for a completely unresolved tree on the data matrix under consideration) will be comparable across different data sets, at least for fixed values of  $k$ . As  $k \Rightarrow \infty$ ,  $FI \Rightarrow 1$  for any data matrix, so  $k$  should be set as low as possible in order to obtain maximum resolution. When comparing two data sets, the  $k$  value above which the set of selected MPTs remains stable for both matrices might be chosen as the  $k$  value at which to calculate  $FI$ .

We have shown above that  $F$  is not well-behaved in that (1) different values of  $k$  may result in different sets of fittest trees, and (2) even within the set of MPTs the fittest tree may depend on the value of  $k$ . This behaviour is not completely unexpected, because different weighting schemes (i.e. different values of  $k$ ) are expected to give different results. Our (and Goloboff's) initial question as to the appropriate value of  $k$  could not be answered. There seems to be no foundation for any particular choice. Therefore,  $F$  seems inappropriate as a tool for weighting characters. At best, it may serve as a secondary tool with which to select a subset of the set of MPTs for the unweighted data set. The value of  $k$  above which the selected subset remains stable may serve as an indication of the quality of the data set as a whole. In addition,  $F$  may form an appropriate basis for a general quality measure which can be used to compare different data sets.

Nevertheless, the concept of counting number of extra steps remains valuable in that it is independent of number of states per character, unlike CI and RC. Also, the number of extra steps a character takes on a tree depends solely on the topology of the tree in question, and can be calculated for any optimization scheme. These are valuable properties which make  $ES_i$  a good basis for a quality measure of trees, because it allows trees to be selected or discarded

independently of other trees and therefore requires only a single pass through the data, thus retaining the advantages of implied weighting. An ideal function for implied weighting should also be independent of any buffering constant, unlike  $F$  which is dependent on  $k$ . Other requirements can be formulated that should be met by such a weight function. These are the following:

- (1) The measure must differentiate between trees of different length, preferring the most parsimonious trees. The weight function should have a combination of  $ES_i$  and the total number of (extra) steps for all characters on the tree in the denominator, i.e. it should weight against longer trees.
- (2) It should differentiate between trees of the same length, both within the set of MPTs and within sets of trees with a fixed larger number of extra steps. The weight function should have in its numerator a parameter describing the difference in degree of homoplasy among characters on the same tree.

Thus the general form of a weight function is:

$$W_{\text{tree}} = \sum w_i \quad w_i = g(\text{homoplasy difference}) / h(ES_i, \sum ES), \quad (3)$$

The exact form of functions  $g$  and  $h$  will have to be determined in future research. On the basis of such a weight function, by analogy to equation (2) a general quality measure can be devised, which is independent of the size of the data matrix, and of the kind and relative frequency of different types of characters (binary or multistate).

### **Acknowledgements**

We would like to thank an anonymous referee for pointing out several inconsistencies in the original manuscript and doing suggestions which have considerably improved its quality.

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Note, to be added in proof:

According to Sang (1995), the average unit character consistency (AUCC) can be used to differentiate between MPT's. As such it could be a candidate for a parameter in a (implicit) weight function. However, in our experience AUCC performs only according to specification within the set of MPT's and not among them. In our view the corrected extra length (CEL) may perform better in this respect as it is defined as

$$CEL = ES + 1 - [\sum ri]/n$$

where ES equals the extra steps for the cladogram compared with the theoretical minimum, and  $[\sum ri]/n$  equals the average unit retention index.

Sang, T. 1995. New measurements of distribution of homoplasy and reliability of parsimonious cladograms. *Taxon* 44: 77-82

## Figure captions

Fig 1. Data matrix All7, most parsimonious tree, and diagram of maximum and minimum fitness values vs. ES for all possible different tree topologies at different values of  $k$ .

Fig. 2. Data matrix All7\_2, most parsimonious tree, and diagram of maximum and minimum fitness values vs. ES for all possible different tree topologies at different values of  $k$ .

Fig. 3. Data matrix All7h11, most parsimonious trees, and diagram of maximum and minimum fitness values vs. ES for all possible different tree topologies at different values of  $k$ .

Fig. 4. Minimum and maximum  $F$  values for the 17 MPTs and 978 additional trees up to five steps longer, at different values of  $k$ .

Table 1. Data matrix Fordia (Schot 1991). Characters 13 and 14 ordered, all others unordered.

Table 2. Data matrix Arytera (Turner 1995). All characters unordered.

Table 3.  $F$  values for all 111 MPTs and the best-fitting trees at  $k=0--5$  (according to Pee-Wee; note that the *exact* values differ!) for the Fordia data set, for different values of  $k$ . MPTs are sorted according to fitness at  $k=0$ .  $F$  values for best-fitting trees are shown in **bold**.

Table 4.  $F$  values for all 17 MPTs and the best-fitting trees at  $k=0--5$  for the *Arytera* data set, for different values of  $k$ . MPTs are sorted according to fitness at  $k=0$ .  $F$  values for best-fitting trees are shown in **bold**.

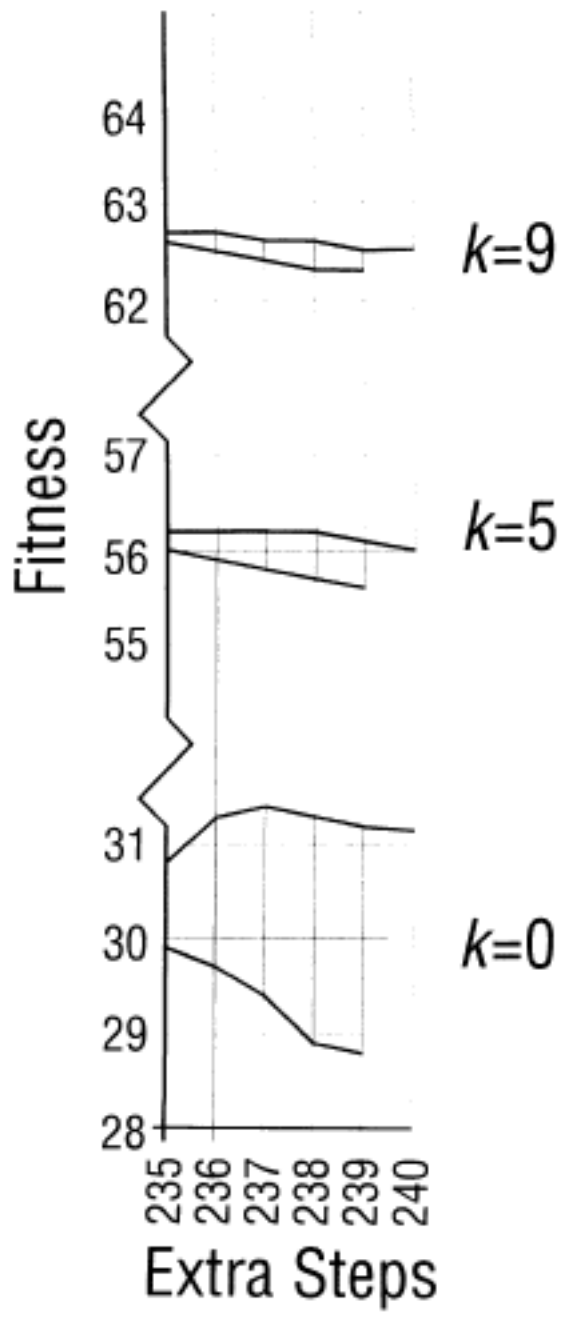


Fig. 4

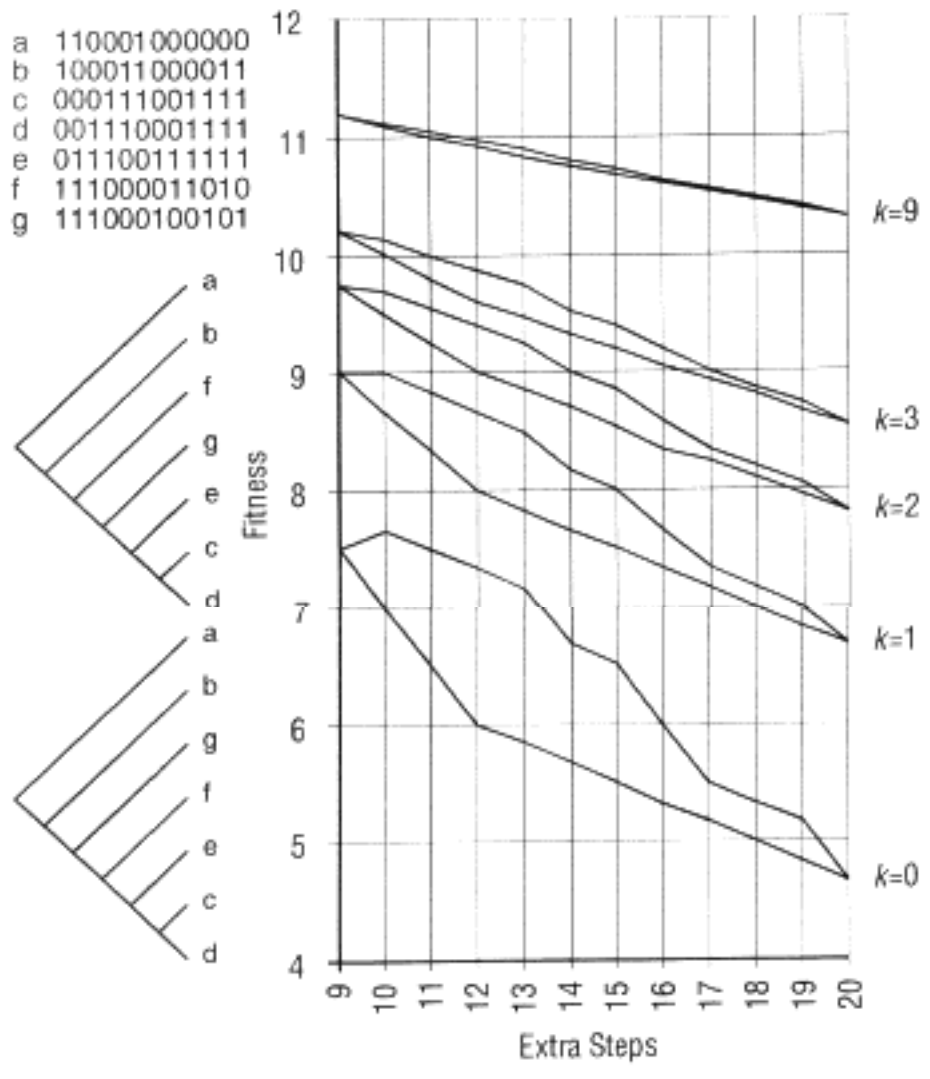


Fig. 3.

a 10000  
 b 00001  
 c 00011  
 d 00111  
 e 01111  
 f 11111  
 g 11111

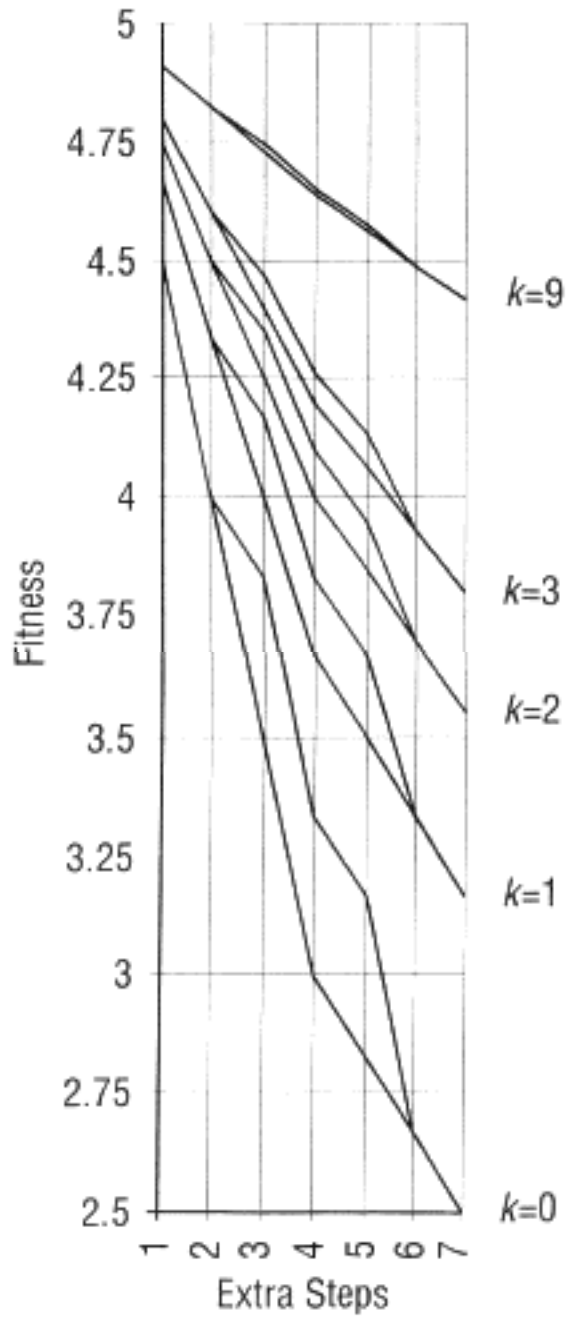
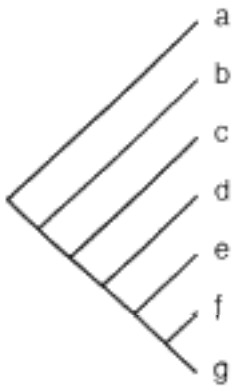


Fig. 2.

a 00000  
 b 00001  
 c 00011  
 d 00111  
 e 01111  
 f 11111  
 g 11111

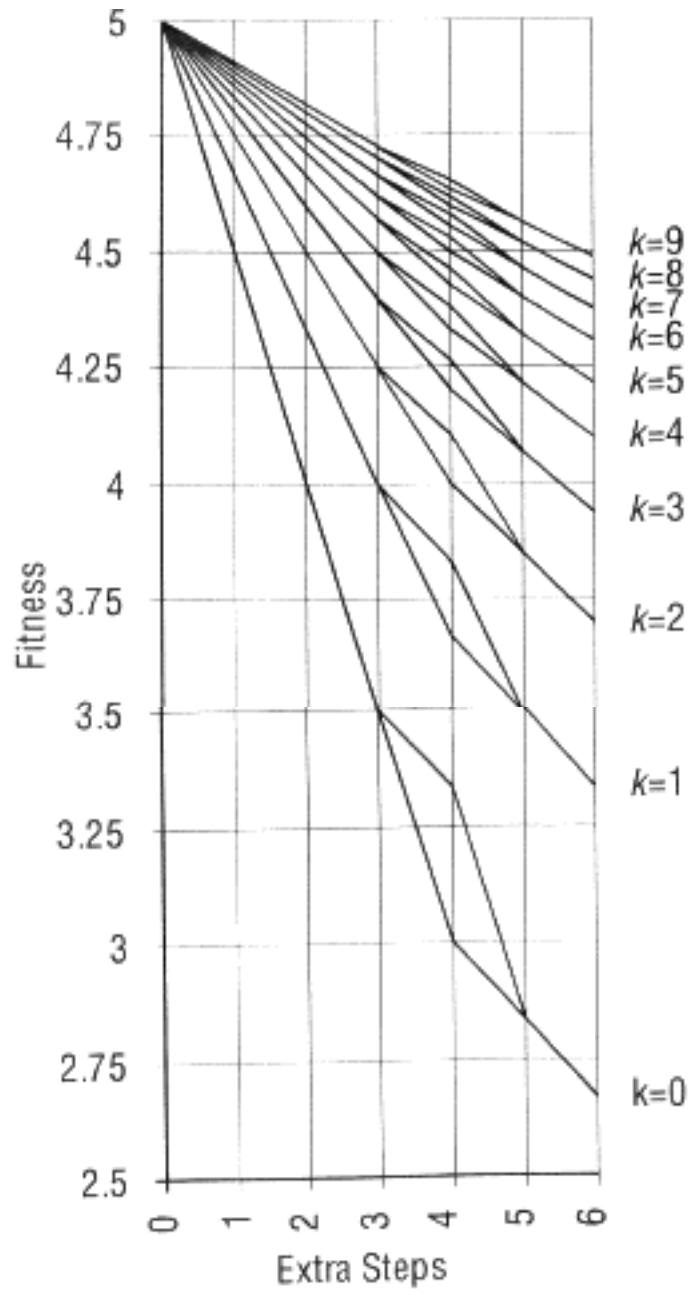
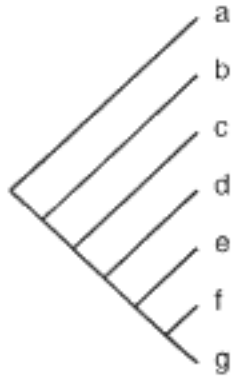


Fig. 1.

**Table 1**

Species	Character number
	000000000 111111111 222222222 333333333 44444 0123456789 0123456789 0123456789 0123456789 01234
<i>Millettia pulchra</i>	1111311231 5451112111 1111321211 1111411114 12111
<i>Fordia albiflora</i>	1111123122 5321114322 121232223? 1233422111 11133
<i>F. brachybotrys</i>	1212123221 3432115221 3121121111 2124212113 12122
<i>F. bracteolata</i>	1111123112 4321111112 121232223? 1233422111 21133
<i>F. cauliflora</i>	1221412221 2433212321 3121111112 2112411113 12133
<i>F. incredibilis</i>	122223222 432322322 2211211231 1213422112 11133
<i>F. johorensis</i>	1121221132 1113214321 3121121132 2131212111 11233
<i>F. lanceolata</i>	1221213111 1332212121 3121121112 2133111111 11211
<i>F. leptobotrys</i>	1121223112 5321214322 221122123? 1233112111 11122
<i>F. ngii</i>	1111123122 5322212122 2211221131 2232212111 13133
<i>F. nivea</i>	1121223122 5322212122 2211211131 1232212111 13133
<i>F. ophirensis</i>	1221321231 2321212221 31211?11?? 2132311113 13133
<i>F. pauciflora</i>	1221211232 4223312121 3121121122 2133121122 11133
<i>F. rheophytica</i>	1112223221 3532212121 3121121111 2112411214 12111
<i>F. splendidissima</i>	1212222221 3642212121 3121121111 2124411213 12112
<i>F. stipularis</i>	122223211 3442212121 31211?11?? 2112411113 12113
<i>F. unifoliolata</i>	2111123112 1111214122 121231223? 1232422112 11133
<i>F. spec. a</i>	1221223222 4323224422 2211121131 1212422112 11133
<i>F. spec. b</i>	2111114231 3533212121 3121121111 2134211113 12111

Table 2

Species	Character number
	000000000 111111111 222222222 333333333 444444444 555555555 666666666 777777777 0123456789 0123456789 0123456789 0123456789 0123456789 0123456789 0123456789 0123456789
<i>Cupaniopsis anacardioides</i>	1232131312 1211222141 121211211? 11113??1? 1111222121 112211311 1??1????2 2??21211
<i>Mischocarpus sundaicus</i>	42221331?1 222222232 11121?2?1? 1112311112 ?221122112 1222222111 122112?111 221131211
<i>M. pentapetalus</i>	12321331?1 123222223? 121221111? 11123221?3 3221122112 1112211111 122222?112 21??21211
<i>M. pyriformis</i>	12321331?1 ??3112212? 1212?11111 1112?221?3 3221122112 1222222111 122212?111 11??31211
<i>M. anodontus</i>	1122133311 123112222? 12121?1?1? 1112211112 ?221121112 1212121311 122122?111 12??11211
<i>M. exangulatus</i>	52221311?1 113122213? 1112111111 12122?21? 2221121212 1122112311 122111?111 121232211
<i>Arytera arcuata</i>	4121113322 ?11112213? 1?1121211? 111?12111 2111221211 1??1111112 1112211221 1?222?111
<i>A. bifoliolata</i>	1112112211 121112223? 2?12?11111 1111331121 11122121?1 ?22122231? 1112?111?2 ?121?1?1?
<i>A. brackenridgei</i>	4231113322 ?1212212? 1?1121211? 1111?1?111 1111221111 1221122?? ?112?11?1? ?1211111
<i>A. bullata</i>	123223331?1 322222132 1312122211 1122233111 311122?121 1111113111 121222?122 211221?21
<i>A. chariacea</i>	1122133312 ?11112222? 2212111122 1112?11221 3111222111 2221122?22 211??11221 12223?111
<i>A. collina</i>	1112133312 1?11122121 12122?1124 1112?11211 3111222111 ?112?11112 211221122? ?22233111
<i>A. densiflora</i>	2112?1?1?? 123221122? 222211121? 22?????21 1112????21 ?221122211 111221?22? 1221211?2
<i>A. dicyvoneura</i>	31121?2211 3?2122233? 1212111111 111233?121 ?112111121 1221111311 111111?121 12112211?
<i>A. distylis</i>	1112112311 1222122231 1212111?11 1112?2?121 1112212121 1221222311 111221?221 122?2?111
<i>A. divaricata</i>	1232231211 123221123? 2?22?11?11 1112?2?121 1111212121 1221122311 1112??221 122111112
<i>A. foveolata</i>	22322311?? 123121123? 3212111112 2111122121 11112121?1 1221122211 111221?22? ?22211111
<i>A. gracilipes</i>	4231113312 3212122132 1?11112111 1111?12111 111122??11 1221122111 111?21?122 212222111
<i>A. lautereriana</i>	12223331?1 ?222122132 3?1?112211 1222231111 3111221121 ?221222311 121112?112 2112??1?1
<i>A. lepidota</i>	4231113312 3212212131 1?1?112111 1111212111 1111221211 112111?311 111221?1?2 212222111
<i>A. lineosquamulata</i>	2122??1?1? 1232211231 2222111?14 1??????23 1112?2121 1221122211 111221?222 1?11111?2
<i>A. litoralis</i>	1?3221?23? 222211111? 111????121 ?111212121 1221122211 111?1???? ?2??11112
<i>A. macrobotrys</i>	12323331?1 ?22222122 1?12122111 11?2222111 311122?121 1221121311 121?1???? 211211?21
<i>A. microphylla</i>	111211231? 1212122231 3?121????31 111?231122 ?1122121?1 1222222?11 111221?222 1?1?111?
<i>A. miniata</i>	112221121? 123222112? 2?12111111 111223?12? 2111212121 1221122212 2112212222 ?211?11?
<i>A. morobeana</i>	2112?112?? 1232211232 221211111? 21?????21 1112?2121 1221122211 111221?222 1122111?2
<i>A. multijuga</i>	2232?31??2 1132221132 2?12211111 12?????11 211?2?1221 1111211121 121221?122 1112211?1
<i>A. musca</i>	11222?1212 123221123? 2212111111 221222?123 1111212121 1121122211 1112?1?222 212232112
<i>A. nekorensis</i>	1112133312 3211122122 1212221124 11122??121 3111221121 2222222122 2??21?222 2222331?1
<i>A. neoebudensis</i>	122213331? ?11212222? 121221112? 121221?221 3111222111 12211?1?22 22?2211?22 ?22222111
<i>A. novaebritanniae</i>	12222?1211 112121113? 1?12111112 1112312221 1111212121 1221122?11 111221?22? 222211112
<i>A. pauciflora</i>	1112211212 123221123? 1212111211 2211?2?121 ?111212121 2221122?11 111121?222 212211111
<i>A. pseudofoveolata</i>	21121???? 1232211131 2212111114 11?????23 211?2?121 1221122211 1112?1?222 ?111111?2

Table 3

Tree	ES	k																
			0	1	2	3	4	5	6	7	8	9	14	19	24	49		
1	86	21,75833333	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,26005606	41,94930608	43,38440819	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,26005606	41,94930608	43,38440819	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,26005606	41,94930608	43,38440819	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,26005606	41,94930608	43,38440819	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,26005606	41,94930608	43,38440819	27,16031746	30,41428571	32,62395382	34,23412698	35,46435231	36,43712121	<b>37,22672883</b>	<b>37,88108142</b>	<b>38,43255764</b>	<b>38,90387668</b>						
40,25908856	41,94904294	43,38436867	27,12698413	30,39285714	32,60966811	34,22420635	35,45720946	36,43181818	37,22268842	37,87793457	38,43006014	38,90186203						
40,25550088	41,94729831	43,38379357	27,09285714	30,36904762	32,59206349	34,21049784	35,4461039	36,42255245	37,21478521	37,87107892	38,4240343	38,89650937						
40,24692245	41,94322831	43,38252588	27,07380952	30,34404762	32,56666667	34,18668831	35,42445887	36,403108	37,1973804	37,85549451	38,41004829	38,8839178						
40,24692245	41,94322831	43,38252588	27,07380952	30,34404762	32,56666667	34,18668831	35,42445887	36,403108	37,1973804	37,85549451	38,41004829	38,8839178						
40,24692245	41,94322831	43,38252588	27,07380952	30,34404762	32,56666667	34,18668831	35,42445887	36,403108	37,1973804	37,85549451	38,41004829	38,8839178						
40,24692245	41,94322831	43,38252588	27,07380952	30,34404762	32,56666667	34,18668831	35,42445887	36,403108	37,1973804	37,85549451	38,41004829	38,8839178						
40,24692245	41,94322831	43,38252588	27,07380952	30,34404762	32,56666667	34,18668831	35,42445887	36,403108	37,1973804	37,85549451	38,41004829	38,8839178						
40,24954264	41,94470978	43,38306145	27,07460317	30,34642857	32,56998557	34,19047619	35,42842158	36,40707071	37,2012432	37,8592033	38,41357662	38,8872558						
40,24316305	41,9413744	43,38192463	27,06190476	30,33214286	32,55555556	34,1765873	35,41536797	36,39494949	37,19005439	37,8489011	38,4040959	38,87852564						
40,24316305	41,9413744	43,38192463	27,06190476	30,33214286	32,55555556	34,1765873	35,41536797	36,39494949	37,19005439	37,8489011	38,4040959	38,87852564						
40,24316305	41,9413744	43,38192463	27,06190476	30,33214286	32,55555556	34,1765873	35,41536797	36,39494949	37,19005439	37,8489011	38,4040959	38,87852564						
40,24316305	41,9413744	43,38192463	27,06190476	30,33214286	32,55555556	34,1765873	35,41536797	36,39494949	37,19005439	37,8489011	38,4040959	38,87852564						
40,24316305	41,9413744	43,38192463	27,06190476	30,33214286	32,55555556	34,1765873	35,41536797	36,39494949	37,19005439	37,8489011	38,4040959	38,87852564						
40,23737653	41,93889516	43,38121866	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
20	86	21,60952381	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
40,23737653	41,93889516	43,38121866	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
40,23737653	41,93889516	43,38121866	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
40,24595496	41,94296516	43,38248635	27,04047619	30,32261905	32,55238095	34,17676768	35,41731602	36,39780497	37,19333999	37,85234765	38,40755078	38,88190315						
40,24595496	41,94296516	43,38248635	27,04047619	30,32261905	32,55238095	34,17676768	35,41731602	36,39780497	37,19333999	37,85234765	38,40755078	38,88190315						
40,23737653	41,93889516	43,38121866	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
40,23737653	41,93889516	43,38121866	27,02142857	30,29761905	32,52698413	34,15295815	35,395671	36,37836053	37,17593518	37,83676324	38,39356477	38,86931157						
40,23361713	41,93704125	43,38061741	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,23361713	41,93704125	43,38061741	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,23361713	41,93704125	43,38061741	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,24219556	41,94111125	43,3818851	27,02857143	30,31071429	32,54126984	34,16666667	35,40822511	36,38964646	37,18601399	37,84575425	38,4015984	38,87651099						
30	86	21,60952381	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,23361713	41,93704125	43,38061741	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,23361713	41,93704125	43,38061741	27,00952381	30,28571429	32,51587302	34,14285714	35,38658009	36,37020202	37,16860917	37,83016983	38,38761239	38,86391941						
40,24219556	41,94111125	43,3818851	27,02857143	30,31071429	32,54126984	34,16666667	35,40822511	36,38964646	37,18601399	37,84575425	38,4015984	38,87651099						
40,23640904	41,93863201	43,38117913	26,98809524	30,27619048	32,51269841	34,14303752	35,38852814	36,3730575	37,17189477	37,83361638	38,39106727	38,86729692						
40,23640904	41,93863201	43,38117913	26,98809524	30,27619048	32,51269841	34,14303752	35,38852814	36,3730575	37,17189477	37,83361638	38,39106727	38,86729692						
40,23264964	41,9367781	43,38057788	26,97619048	30,26428571	32,5015873	34,13293651	35,37943723	36,36489899	37,16456876	37,82702298	38,38511489	38,86190476						



Table 3--contd.

Tree	ES	k														
			0	1	2	3	4	5	6	7	8	9	14	19	24	49
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23860202	41,94011616	86	21,27619048	26,87380952	30,22261905	32,48571429	34,12914863	35,38160173	36,3700272	37,17111777	37,83416583	38,39239927	38,86908263			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,23002359	41,93604616	86	21,27619048	26,8547619	30,19761905	32,46031746	34,10533911	35,35995671	36,35058275	37,15371295	37,81858142	38,37841325	38,85649106			
40,22626419	41,93419224	80	21,26666667	26,84285714	30,18571429	32,44920635	34,0952381	35,3508658	36,34242424	37,14638695	37,81198801	38,37246087	38,8510989			
40,23720146	41,93968947	86	21,25238095	26,85238095	30,20595238	32,47301587	34,11940837	35,37402597	36,36404429	37,16632257	37,83026973	38,38919414	38,86641618			
40,23720146	41,93968947	86	21,25238095	26,85238095	30,20595238	32,47301587	34,11940837	35,37402597	36,36404429	37,16632257	37,83026973	38,38919414	38,86641618			
40,23344206	41,93783555	86	21,24285714	26,84047619	30,19404762	32,46190476	34,10930736	35,36493506	36,35588578	37,15899656	37,82367632	38,38324176	38,86102402			
40,23344206	41,93783555	86	21,24285714	26,84047619	30,19404762	32,46190476	34,10930736	35,36493506	36,35588578	37,15899656	37,82367632	38,38324176	38,86102402			
40,23606225	41,93931703	86	21,24166667	26,84126984	30,19642857	32,46522367	34,11309524	35,36889777	36,35984848	37,16285936	37,82738511	38,38677009	38,86436203			
40,23606225	41,93931703	86	21,24166667	26,84126984	30,19642857	32,46522367	34,11309524	35,36889777	36,35984848	37,16285936	37,82738511	38,38677009	38,86436203			
40,2290561	41,93578301	86	21,22619048	26,82142857	30,17619048	32,44603175	34,09541847	35,35281385	36,34527972	37,14967255	37,81543457	38,37591575	38,85447641			
40,2290561	41,93578301	86	21,22619048	26,82142857	30,17619048	32,44603175	34,09541847	35,35281385	36,34527972	37,14967255	37,81543457	38,37591575	38,85447641			
40,22389614	41,9335024	86	21,19285714	26,78809524	30,14761905	32,42222222	34,0755772	35,33614719	36,33113831	37,13755134	37,80494505	38,36675824	38,8464178			
40,23247457	41,93757241	86	21,19285714	26,80714286	30,17261905	32,44761905	34,09938672	35,35779221	36,35058275	37,15495615	37,82052947	38,38074426	38,85900937			
40,23247457	41,93757241	86	21,19285714	26,80714286	30,17261905	32,44761905	34,09938672	35,35779221	36,35058275	37,15495615	37,82052947	38,38074426	38,85900937			
40,22389614	41,9335024	86	21,19285714	26,78809524	30,14761905	32,42222222	34,0755772	35,33614719	36,33113831	37,13755134	37,80494505	38,36675824	38,8464178			
40,23247457	41,93757241	86	21,19285714	26,80714286	30,17261905	32,44761905	34,09938672	35,35779221	36,35058275	37,15495615	37,82052947	38,38074426	38,85900937			
40,23247457	41,93757241	86	21,19285714	26,80714286	30,17261905	32,44761905	34,09938672	35,35779221	36,35058275	37,15495615	37,82052947	38,38074426	38,85900937			
40,22013674	41,93164849	86	21,18333333	26,77619048	30,13571429	32,41111111	34,06547619	35,32705628	36,3229798	37,12822533	37,79835165	38,36080586	38,84102564			
40,21951017	41,93144986	86	21,17619048	26,76904762	30,1297619	32,40634921	34,06168831	35,32402597	36,32053225	37,12822733	37,7967033	38,35943223	38,83987018			
40,22731461	41,9352918	86	21,15952381	26,77380952	30,14404762	32,42380952	34,07954545	35,34112554	36,33644134	37,14283494	37,81003996	38,37158675	38,85095076			
40,21497678	41,92936789	86	21,15	26,74285714	30,10714286	32,38730159	34,04563492	35,31038961	36,30883838	37,11810412	37,78786214	38,35164835	38,83296703			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	100	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			
40,22292865	41,93323926	86	21,14285714	26,7547619	30,12619048	32,40793651	34,06565657	35,32900433	36,32583528	37,13351093	37,8017982	38,36426074	38,84440315			

Table 3--contd.

Tree	ES	k	0	1	2	3	4	5	6	7	8	9	14	19	24	49
			86	21,13333333	26,72380952	30,08928571	32,37142857	34,03174603	35,2982684	36,29823232	37,10878011	37,77962038	38,34432234	38,82641941	40,21059082	41,92731534
86	21,10952381	26,72142857	30,09761905	32,38412698	34,0458153	35,31233766	36,31169386	37,12138972	37,79130869	38,35510323	38,83634454	40,21776869	41,93095865	43,37904159		
86	21,09285714	26,70238095	30,0797619	32,36825397	34,03192641	35,30021645	36,3010878	37,11206571	37,78306693	38,34777722	38,82979692	40,21338272	41,92890611	43,37840631		
86	21,09285714	26,70238095	30,0797619	32,36825397	34,03192641	35,30021645	36,3010878	37,11206571	37,78306693	38,34777722	38,82979692	40,21338272	41,92890611	43,37840631		
86	21,09285714	26,70238095	30,0797619	32,36825397	34,03192641	35,30021645	36,3010878	37,11206571	37,78306693	38,34777722	38,82979692	40,21338272	41,92890611	43,37840631		
111	86	21,09285714	26,70238095	30,0797619	32,36825397	34,03192641	35,30021645	36,3010878	37,11206571	37,78306693	38,34777722	38,82979692	40,21338272	41,92890611	43,37840631	
k=0	93	<b>22,43452381</b>	27,21031746	30,22619048	32,33347763	33,8989899	35,11197136	36,08139083	36,87492507	37,53702547	38,09818368	38,58005638	39,97827624	41,74399679	43,26494601	
k=0	94	22,42619048	27,19444444	30,2047619	32,30822511	33,87121212	35,08260073	36,0510878	36,84415584	37,50611888	38,06737135	38,54950083	39,9495681	41,72064909	43,2498831	
k=1	88	22,17738095	<b>27,37460317</b>	<b>30,52738095</b>	32,67950938	34,254329	35,46175491	36,41934732	37,1986458	37,84591658	38,39251435	38,86049433	40,2116538	41,90526855	43,35471349	
k=2	88	22,17738095	<b>27,37460317</b>	<b>30,52738095</b>	32,67950938	34,254329	35,46175491	36,41934732	37,1986458	37,84591658	38,39251435	38,86049433	40,2116538	41,90526855	43,35471349	
k=3	87	22,15119048	27,35793651	30,52261905	<b>32,68427128</b>	<b>34,26605339</b>	<b>35,47842158</b>	<b>36,43947164</b>	37,22115662	37,87004246	38,4176975	38,88632928	40,23782216	41,92781712	43,36964004	
k=4	87	22,15119048	27,35793651	30,52261905	<b>32,68427128</b>	<b>34,26605339</b>	<b>35,47842158</b>	<b>36,43947164</b>	37,22115662	37,87004246	38,4176975	38,88632928	40,23782216	41,92781712	43,36964004	
k=5	87	22,15119048	27,35793651	30,52261905	<b>32,68427128</b>	<b>34,26605339</b>	<b>35,47842158</b>	<b>36,43947164</b>	37,22115662	37,87004246	38,4176975	38,88632928	40,23782216	41,92781712	43,36964004	
k=5	86	21,70833333	27,12698413	30,39285714	32,60966811	34,22420635	35,45720946	36,43181818	37,22268842	37,87793457	38,43006014	38,90186203	40,25908856	41,94904294	43,38436867	
k=5	86	21,65952381	27,09285714	30,36904762	32,59206349	34,21049784	35,4461039	36,42255245	37,21478521	37,87107892	38,4240343	38,89650937	40,25550088	41,94729831	43,38379357	

Table 4

Tree	ES	k												
		0	1	5	9	10	11	12	13	14	19	24	49	
1	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
<b>74,69353308</b>	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
2	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
<b>74,69353308</b>	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
3	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
<b>74,69353308</b>	235	30,80952381	40,03737374	56,15719281	62,66630325	63,74403774	64,68653988	<b>65,51804802</b>	<b>66,25727666</b>	<b>66,91891912</b>	<b>69,40401746</b>	<b>71,03768699</b>		
4	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
74,69161124	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
5	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
74,69161124	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
6	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
74,69161124	235	30,66071429	39,91753247	56,11015651	62,6412964	63,72206421	64,66707039	65,50067124	66,24166779	66,90481803	69,39493926	71,03134607		
7	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
74,69089662	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
8	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
74,69089662	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
9	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
74,69089662	235	30,37738095	39,78419913	56,08158508	62,62864238	63,71125835	64,65772973	65,49251298	66,23447825	66,89843258	69,3910808	71,02876021		
10	235	30,24642857	39,66911977	56,03388278	62,6043554	63,69017363	64,63926729	65,47622225	66,22000456	66,88549331	69,38311839	71,02338961		
74,6894159	235	30,24642857	39,66911977	56,03388278	62,6043554	63,69017363	64,63926729	65,47622225	66,22000456	66,88549331	69,38311839	71,02338961		
11	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
74,69288851	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
12	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
74,69288851	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
13	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
74,69288851	235	30,23492063	39,68975469	56,07407592	62,63419647	63,71764952	64,6645834	65,49958028	66,24159352	66,905486	69,39715765	71,03372016		
14	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
74,69171765	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
15	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
74,69171765	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
16	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
74,69171765	235	30,21944444	39,66991342	56,05799201	62,62334213	63,7077639	64,65555348	65,49130714	66,23399118	66,89847985	69,39231435	71,03018614		
17	235	29,8297619	39,43578644	55,97435897	62,57754887	63,66727986	64,61948707	65,45896035	66,20480848	66,87201292	69,37502504	71,01799686		
74,68795029	256	<b>32,88134921</b>	40,99292929	55,87023503	62,16986839	63,23185731	64,16533494	64,99265918	65,73121705	66,39474919	68,90885642	70,58151136		
k=0	256	<b>32,88134921</b>	40,99292929	55,87023503	62,16986839	63,23185731	64,16533494	64,99265918	65,73121705	66,39474919	68,90885642	70,58151136		
74,38771674	256	<b>32,88134921</b>	40,99292929	55,87023503	62,16986839	63,23185731	64,16533494	64,99265918	65,73121705	66,39474919	68,90885642	70,58151136		
k=0	256	<b>32,88134921</b>	40,99292929	55,87023503	62,16986839	63,23185731	64,16533494	64,99265918	65,73121705	66,39474919	68,90885642	70,58151136		
74,38771674	256	<b>32,88134921</b>	40,99292929	55,87023503	62,16986839	63,23185731	64,16533494	64,99265918	65,73121705	66,39474919	68,90885642	70,58151136		
k=1	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
74,53904661	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
k=2	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
74,53904661	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
k=3	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
74,53904661	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
k=4	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
74,53904661	246	32,78495671	<b>41,15634921</b>	56,22425075	62,51306292	63,56789594	64,49375006	65,31324985	66,04395503	66,69971813	69,17797581	70,82079756		
k=5	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		
74,66934517	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		
k=5	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		
74,66934517	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		
k=5	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		
74,66934517	237	31,41944444	40,43816739	<b>56,25639361</b>	<b>62,6869256</b>	<b>63,75489454</b>	<b>64,68968745</b>	65,51505831	66,24936785	66,90704656	69,38111749	71,01102993		