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Appendix A

Estimates of lifetime reproductive variance

The following has been kindly provided by P. Jarman (pers. comm.). These are estimates of males contribution of genes to an annual cohort of young, which have been based upon 5 years of observations on the males' behaviour.

1. 6 males contribute genes to the young produced in any one year.

2. The alpha male contributes genes to 75% to 80% of an annual cohort.

3. The other males may contribute 4% to 5% each.

4. The alpha male typically holds tenure for one year only.

5. Prior to this year at the top, the alpha male is likely to have achieved matings in the past two years only.

The following has been derived from my observations on female reproduction and the survival of their young.

a) The typical cohort size of young produced in a population was 49.5 if there were 51 adult females.

b) The proportion of young surviving in any one year varied considerably (0.16 to 0.80).

c) The average proportion of young surviving per year was 0.38.

d) 1.5 male young are produced per female young.

I calculated the females' rates of rearing young to weaning from the number of young they reared to weaning over the number of months they were observed. But I subtracted the months for which they were observed rearing a young at the end of the study which was not counted as it had not passed the age of high mortality. I have also added a few months for females for whom observation was commenced when they were already part way through rearing a young. This was done in order to reduce the potential for exaggerating female's success rate. As the typical female was estimated to breed for 8.5 years, I multiplied the females rates of rearing young per month by 100 months.

The 51 females were estimated to rear to weaning on average 3.686 young/100months (SE 2.293). In total 188 young were reared to weaning. If 38% of all young produced were reared to weaning, then the females are estimated to have produced 494 young in total. If the offspring sex ratio is 1.5 sons to daughters, then of 494 young 198 were daughters and 296 sons.

Thus of 198 daughters produced, 75 are likely to survive to weaning. Not all subadult females survived to reproduce. I estimated that about 70% may have bred. Thus if the 53 of these bred with the same variation as estimated from my sample of the female population at Wallaby Creek, then the average daughter in turn produces 0.949 young.

Variance is 3.947.
Standard error is 0.142.
(Range 0 to 10)

I estimated that 494 young would be produced in approximately 10 annual cohorts. This number of cohorts also allows for some annual variation in the number of young reared. This variation is important in estimating variation of male reproductive success. As the percent of a cohort of young which survives to weaning can vary greatly, the lifetime reproductive success of alpha males will also vary greatly between individuals.

Male mating achievements per cohort were used to estimate variation between years in male reproductive success. The γ male becomes the β male the following year and the α male the next. The ϵ becomes the δ male. I have calculated mean and variance for male reproductive success by using the above and estimations of the number of young of an annual cohort who survived and of the consequent esimated number of young per year that

	male rank							
% alpha mates	α	β	γ	δ		ζ	*number of cohort surviving*	*% cohort surviving*
75	*20*	*2*	*1*	*1*	*1*	*1*	*26*	*53*
80	*21*	*1*	*1*	*1*	*1*	*1*	*26*	*53*
75	*5*	*1*	*1*	*0*	*0*	*0*	*7*	*14*
80	*6*	*1*	*0*	*0*	*0*	*0*	*7*	*14*
75	*8*	*1*	*1*	*1*	*0*	*0*	*11*	*22*
80	*9*	*1*	*1*	*0*	*0*	*0*	*11*	*22*
75	*28*	*2*	*2*	*2*	*2*	*1*	*37*	*74*
80	*30*	*2*	*2*	*1*	*1*	*1*	*37*	*74*
75	*10*	*1*	*1*	*1*	*0*	*0*	*13*	*26*
80	*11*	*1*	*1*	*0*	*0*	*0*	*13*	*26*
							total 188	*ave.38*

each of the 6 highest ranking males would father (see the table above) (these estimations are based upon observations from the 4 study years).

The 296 male young produced average 0.635 young produced each.

Variance 12.416

Standard error 0.205.

Range (0 to 33)

Males' estimated lifetime reproductive success is significantly more variable than that for females (F test, df1=295 df2=197, F=3.146 $p < 0.05$). It should be noted that the estimated mean male lifetime reproductive success does not equal that for the female. This difference is a function of more male young than female young being produced (see section 3.7).

Note that the variance is likely to reduce as more sons are produced per daughter, but the same number of males reproduce with the same level of success. However, more of the sons produced are less likely to reproduce. I should also point out that as the distribution of estimated lifetime reproductive success was highly skewed, with most males failing to produce any young who were reared to weaning, the above calculations for variance are somewhat statistically inappropriate. However, they allow a degree of comparison to be made between the sexes. If I use only those males and females who produced at least 1 young which was reared to weaning then the following apply:

males	*number*	*21*
	average	*8.952*
	variance	*104.948*
	standard error	*2.236*
females	*number*	*44*
	average	*4.399*
	variance	*3.751*
	standard error	*0.295*

F test:
df1=20 df2=43 F=27.979
$p < 0.05$

Thus the expected lifetime-reproductive-success estimated for those males and females who produced at least one young who was reared to weaning, was still much greater for males than females.

Appendix B

The timing of females reproduction

The annual frequency distributions of the inter-PEP intervals for 1983 to 1985 are depicted in figs. 93, 94, and 95.

In order to test whether there were more females producing peak young consecutively than expected, I first calculated the expected frequencies of females who would produce only peak young, for females who were observed to produce 5,4,3,2, and 1 young separately. The expected frequencies were determined from the binomial distribution with the probability of a peak young being produced as 0.71 (there were 118 of 167 young who permanently emerged in the peak season). The sum of the observed frequencies of females who produced only peak young was compared to the sum of the expected frequencies with a χ^2 test:

Number of young a female was observed to produce							
	5	*4*	*3*	*2*	*1*	*total*	*females in population*
females observed to produce only peak young:	*0*	*7*	*11*	*3*	*5*	*26*	*54*
females expected to produce only peak young:	*0.54*	*4.8*	*6.1*	*5.0*	*3.6*	*20*	*54*
						$\chi^2 = 2.858$ < 0.1†	

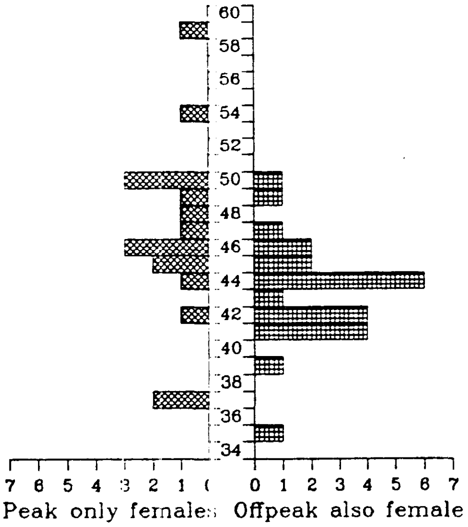


Figure 93: *Frequencies (on x-axis) of inter-PEP intervals (on y-axis, units weeks) during the period April 1983 to March 1984 inclusive. An interval is considered as occurring during the relavent period according to the second PEP date.*

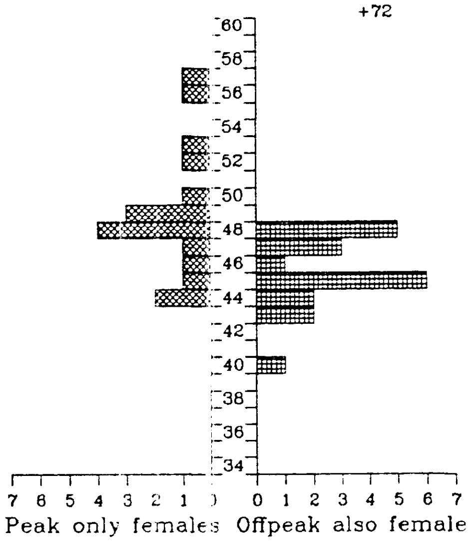


Figure 94: *Frequencies (on x-axis) of inter-PEP intervals (on y-axis, units weeks) during the period April 1984 to March 1985 inclusive. An interval is considered as occurring during the relavent period according to the second PEP date. Extremely long inter-PEP intervals which did not fit on the y-axis are presented separately in numeric form above the relavent x-axis.*

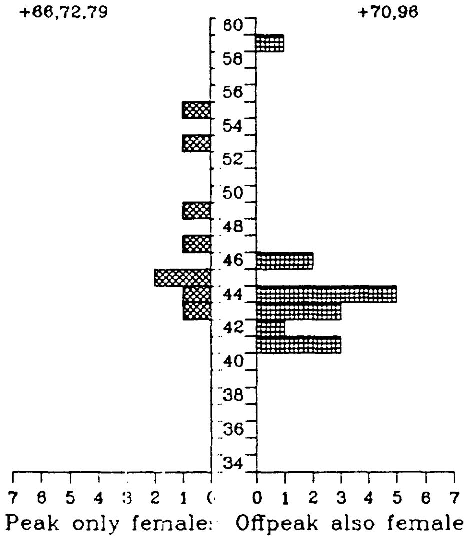


Figure 95: *Frequencies (on x–axis) of inter-PEP intervals (on y–axis, units weeks) during the period April 1985 to March 1986 inclusive. An interval is considered as occurring during the relavent period according to the second PEP date. Extremely long inter-PEP intervals which did not fit on the y-axis are presented separately in numeric form above the relavent x-axis.*

Appendix C

Age of young at disappearance

190 young were known to be produced; the earliest date of identification occurred at about 2 months of age when a mother's pouch bulged distinctly. 11 of these young were lost when their mother disappeared from the study site. I have excluded these 11 young from calculating the rates of disappearance of young at different ages, as I was interested in the 'age' when young were most vulnerable to death rather than when their mothers were most vulnerable; though I acknowledge that there is likely to be some degree of dependancy of when young disappear and their mothers' condition.

As there were 27 cases of inter-PEP intervals which were greater than 48 weeks, it is possible that some might have involved the loss of a neonate between the two permanent emergences. If all cases involved the loss of a neonate, then 27 neonates of a total of 206 were lost.

11% to 23% lost as pouch-young. 42% lost as YAF.

Age of pouch-young lost when mother lost vs when mother not lost

	SPY	pouch-infant
mother lost	8	3
mother survived	5	15

G test G=6.781 *

206 young produced		*217 young*
young lost	*at age*	*young lost when mother lost*
27	*neonates*	*?*
5	*small PY*	*8*
4	*dim. PI*	*1*
4	*small to large PI*	*0*
7	*very large PI*	*2*
159 young reached PEP		
43	*1 month YAF*	
24	*2 month YAF*	
10	*3 month YAF*	
5	*4 month YAF*	
2	*5 month YAF*	
1	*6 month YAF*	
1	*7 month YAF*	
73 young weaned		

Appendix D

Cluster results of distance between home range centres

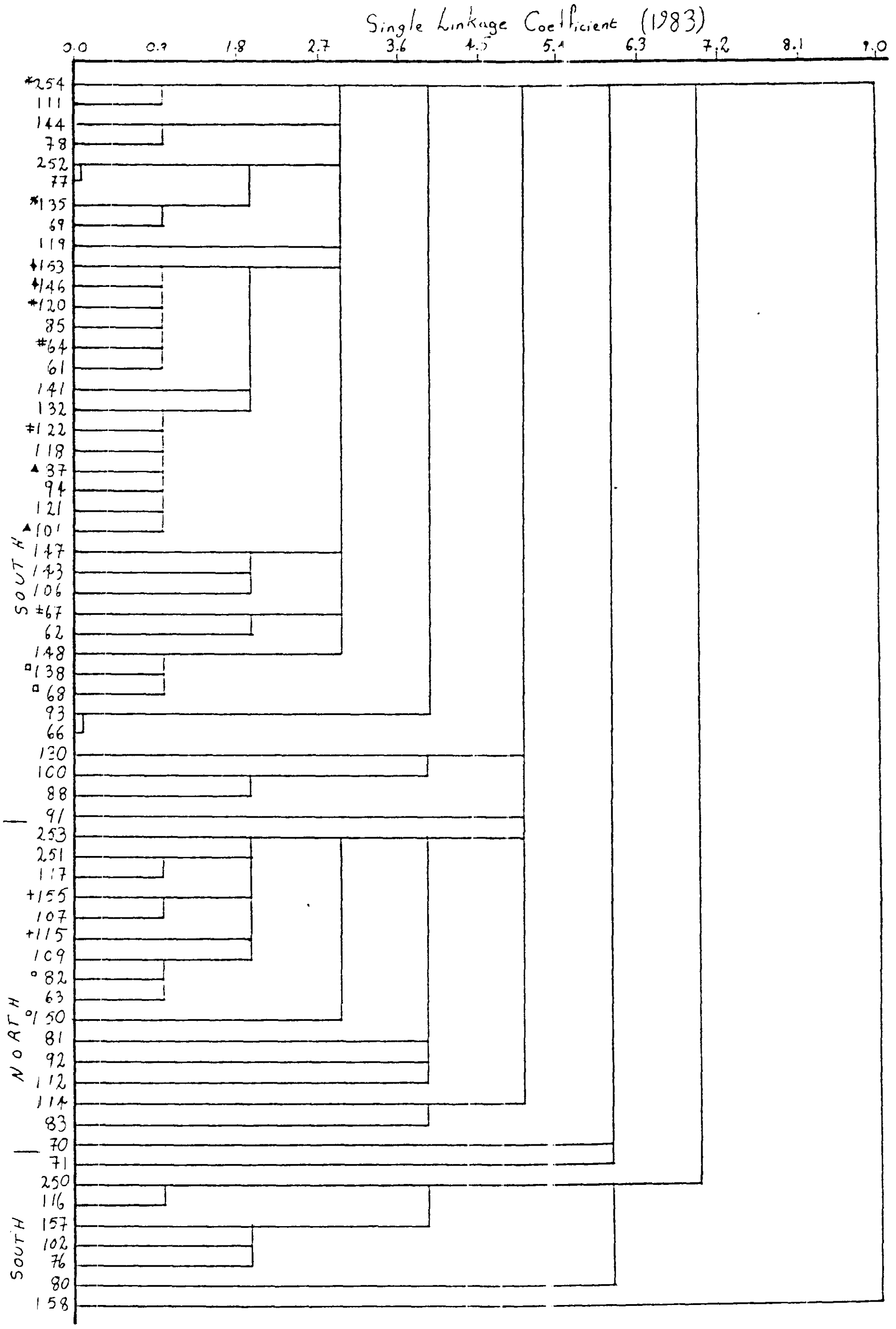
In order to describe the spatial location of females' home ranges relative to each other I conducted cluster analyses of the distance between all pairs of females' annual home range centres. Data from 1983 and 1984 were used. Both single and average linkage clustering algorithms were used. I did this to determine which clusters were consistently present and thus probably biologically significant, rather than an artefact of a particular algorithm (see Sokal, 1977).

The dendrograms resulting from these analyses are presented below. Females are identified by an individual number on the X-axis. The females who are grouped into clusters at the base of the dendrogram are inferred to have home range centres much closer to each other than to those females to whom they are linked at the top of the dendrogram.

Mother-daughter pairs are indicated by similar symbols placed next to their identity numbers.

When referring to the females according to the distance between their home range centres I employ the term neighbours.

It is currently difficult to determine by statistical tests, which of the resulting clusters of a cluster analysis are biologically significantly distinct entities (Sokal, 1977). However, the average and single linkage analyses conducted on both the 1983 and 1984 data separately, tend to define two 'sets' of females. These two 'sets' of females will be called the North and South females (see dendrgrams).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1.8
2.7
3.6
4.5
5.4
6.3
7.2
8.1
9.0
*254
111
144
78
252
77
*135
69
119
+153
+146
*120
85
#64
61
141
132
#122
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▲37
94
121
▲101
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±67
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93
66
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253
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117
+155
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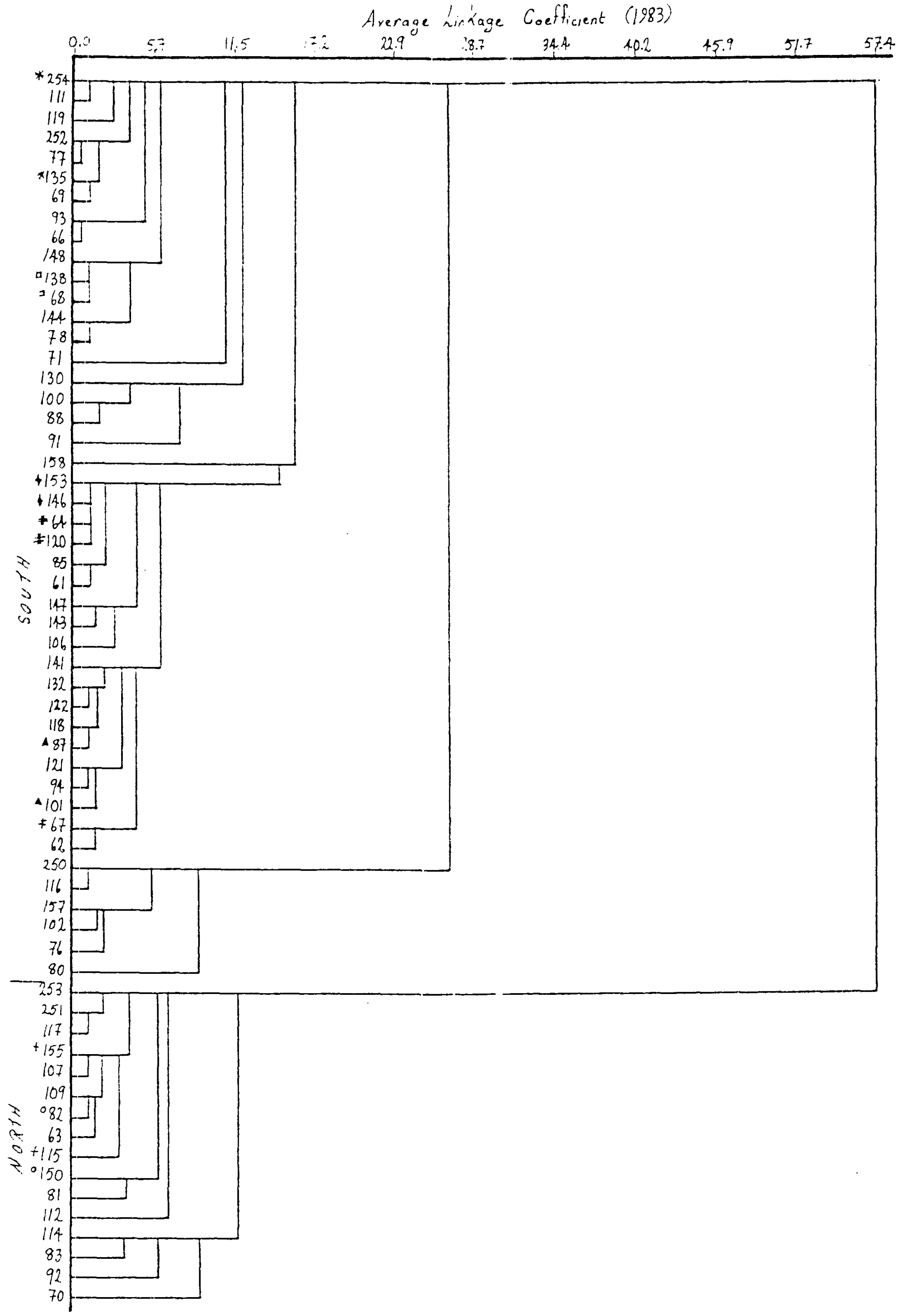
NORTH
SOUTH


Average Linkage Coefficient (1983)
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17.2
22.9
28.7
34.4
40.2
45.9
51.7
57.4
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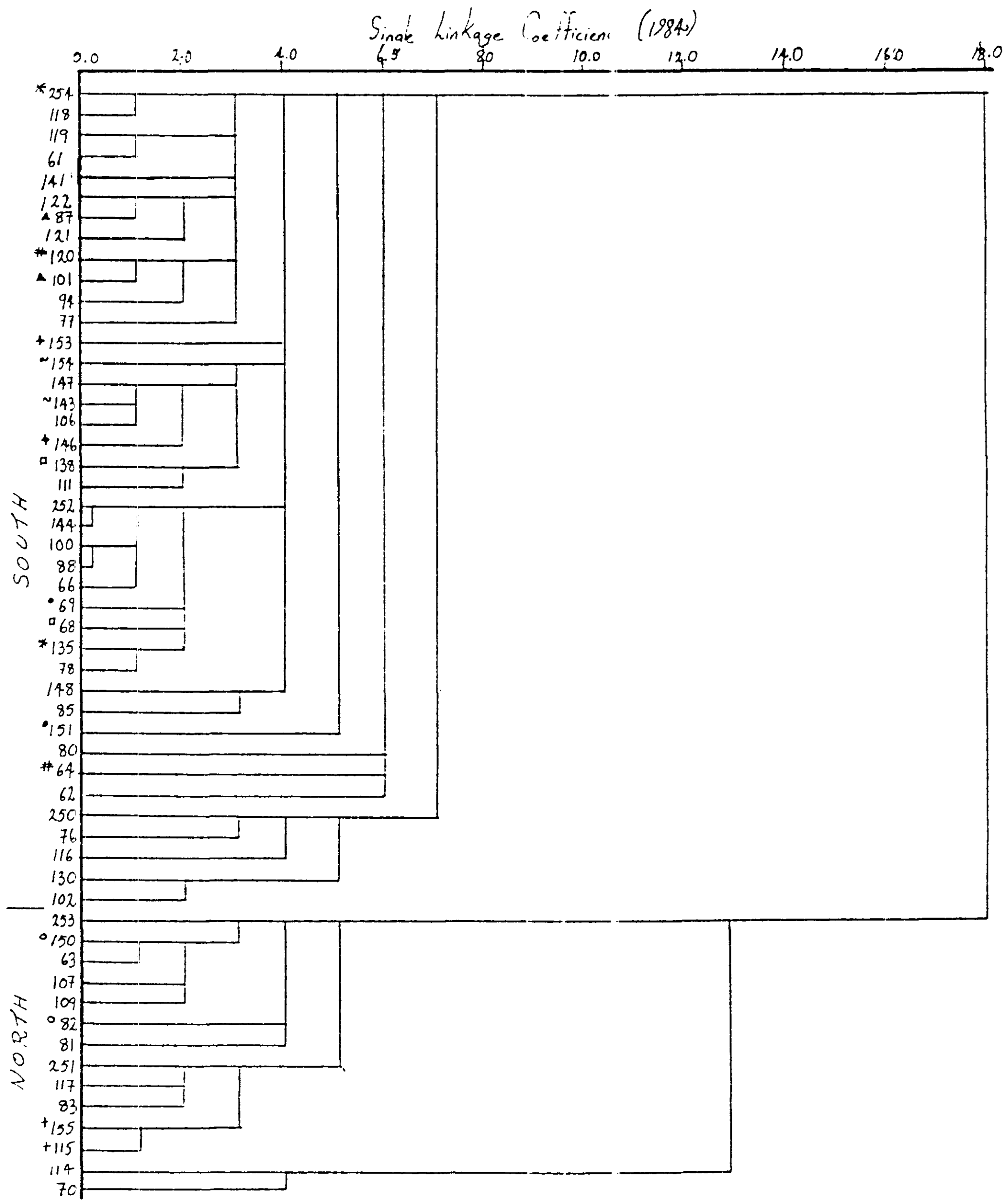
Single Linkage Coefficient (1984)
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2.0
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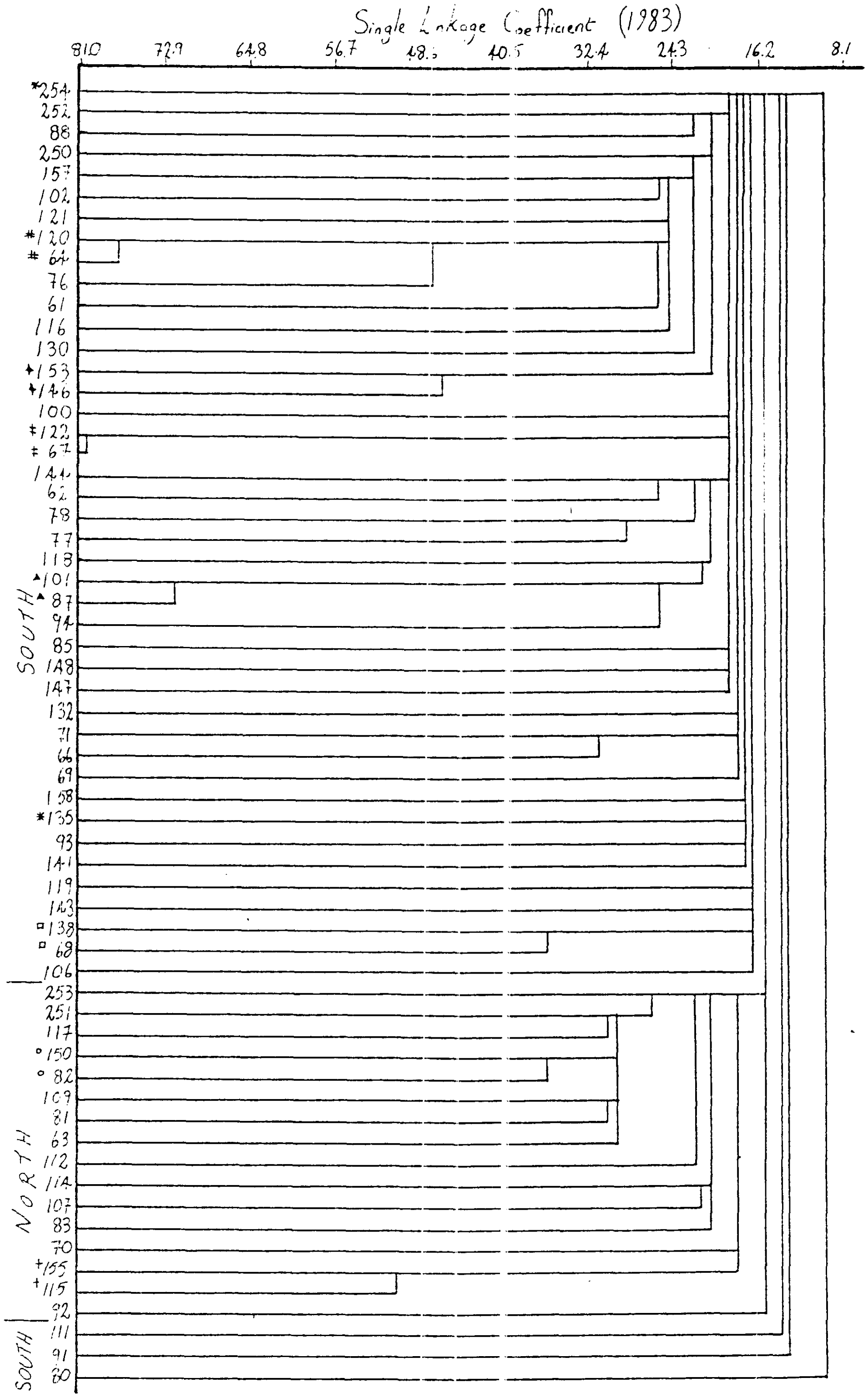
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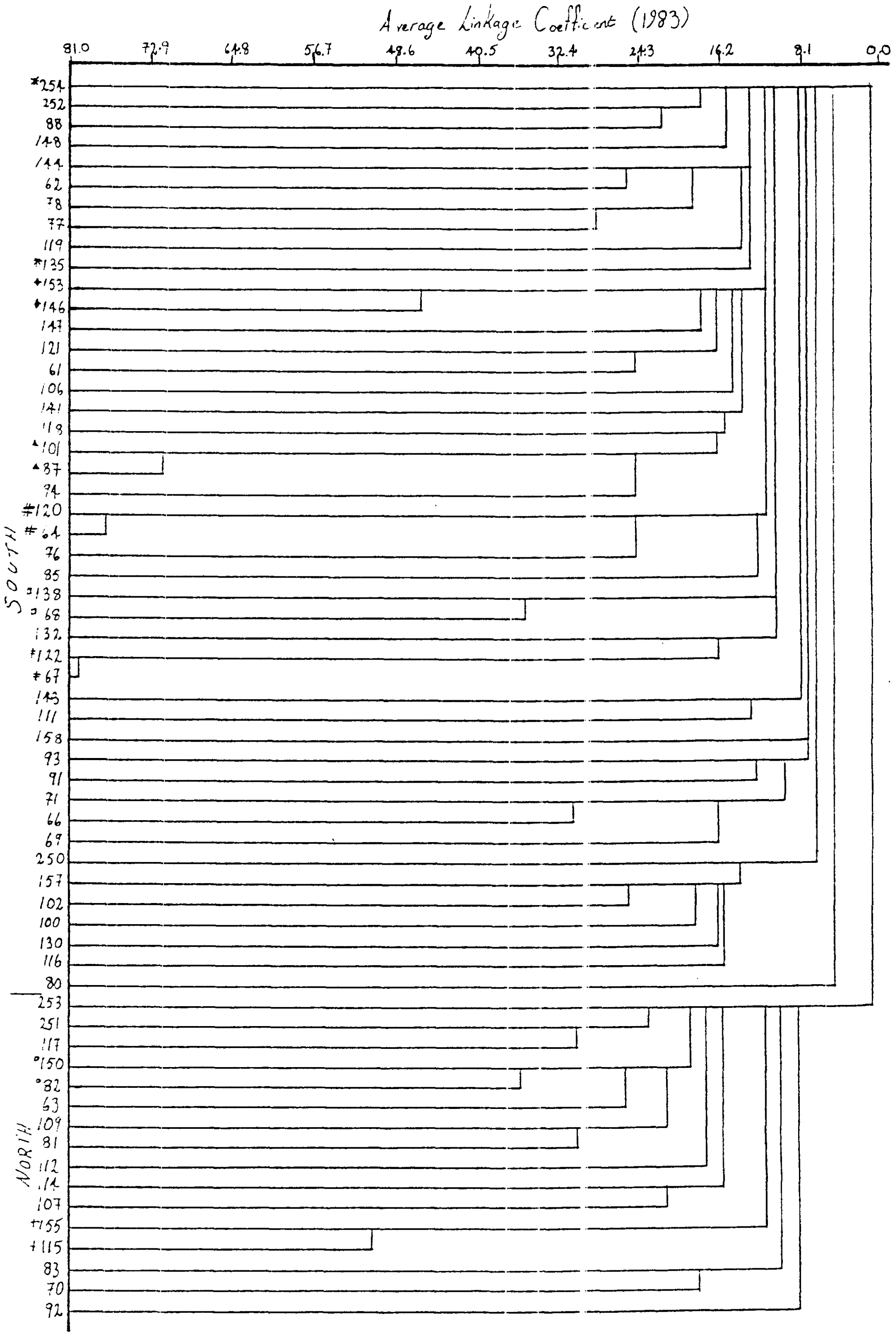
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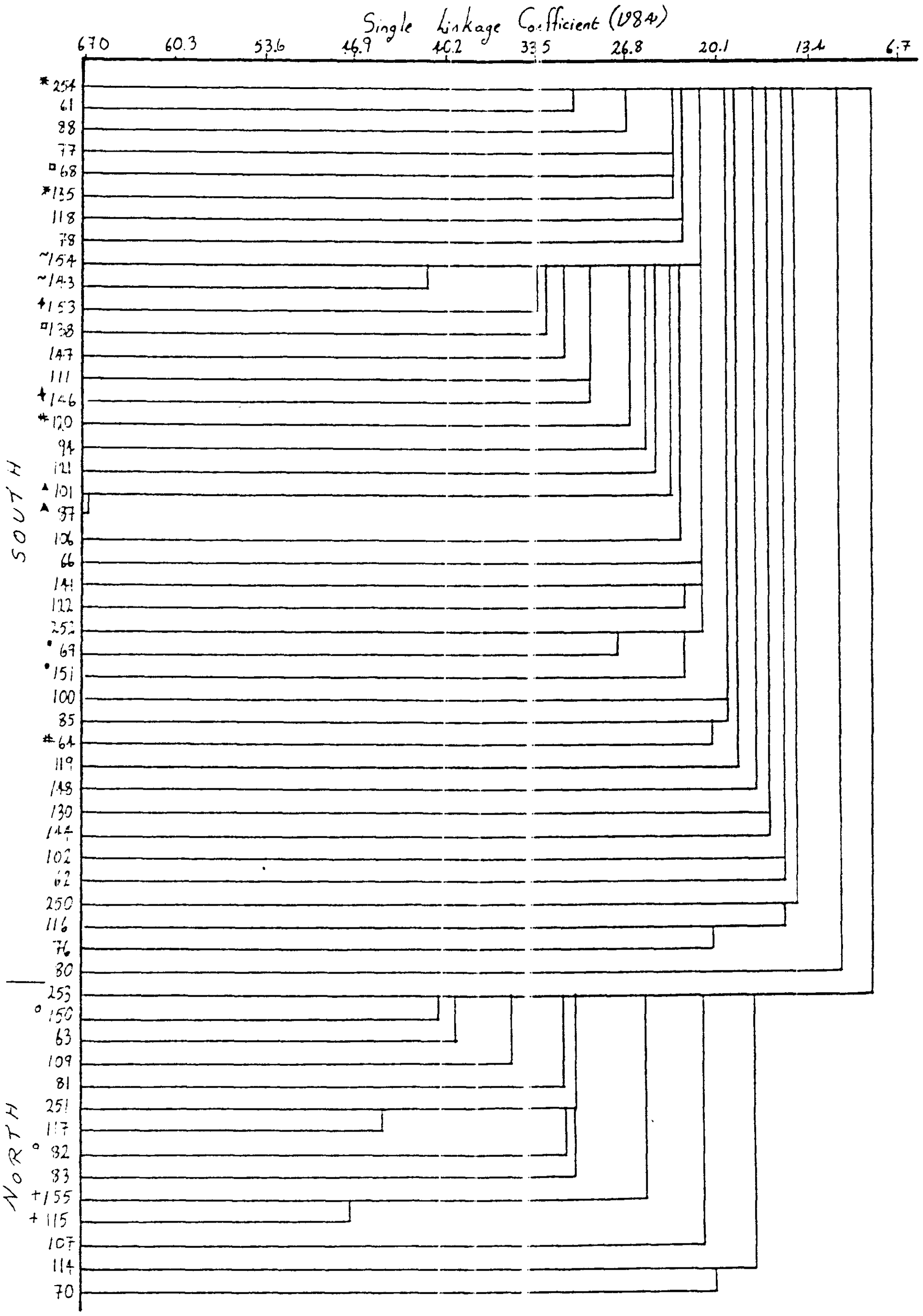
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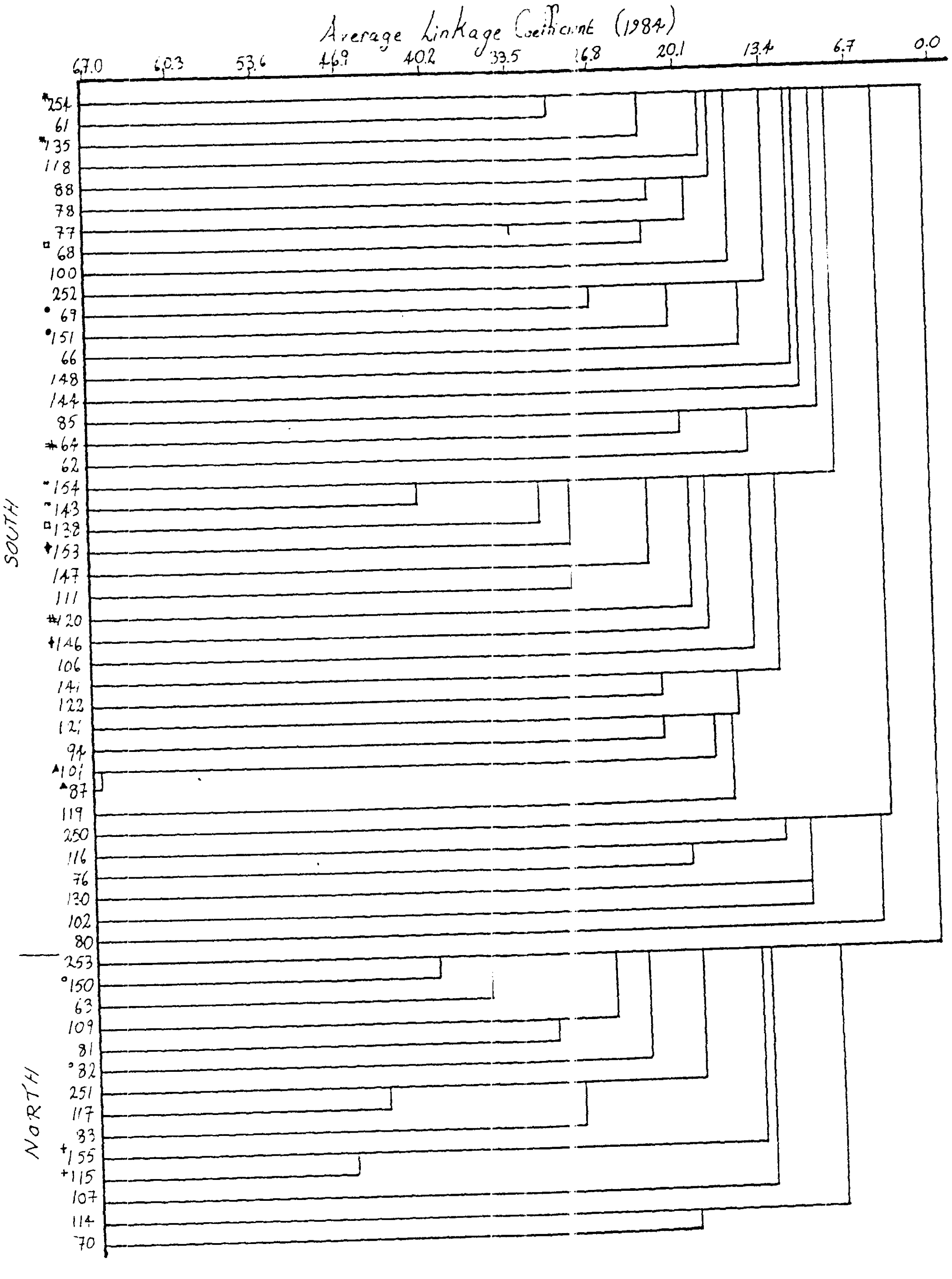
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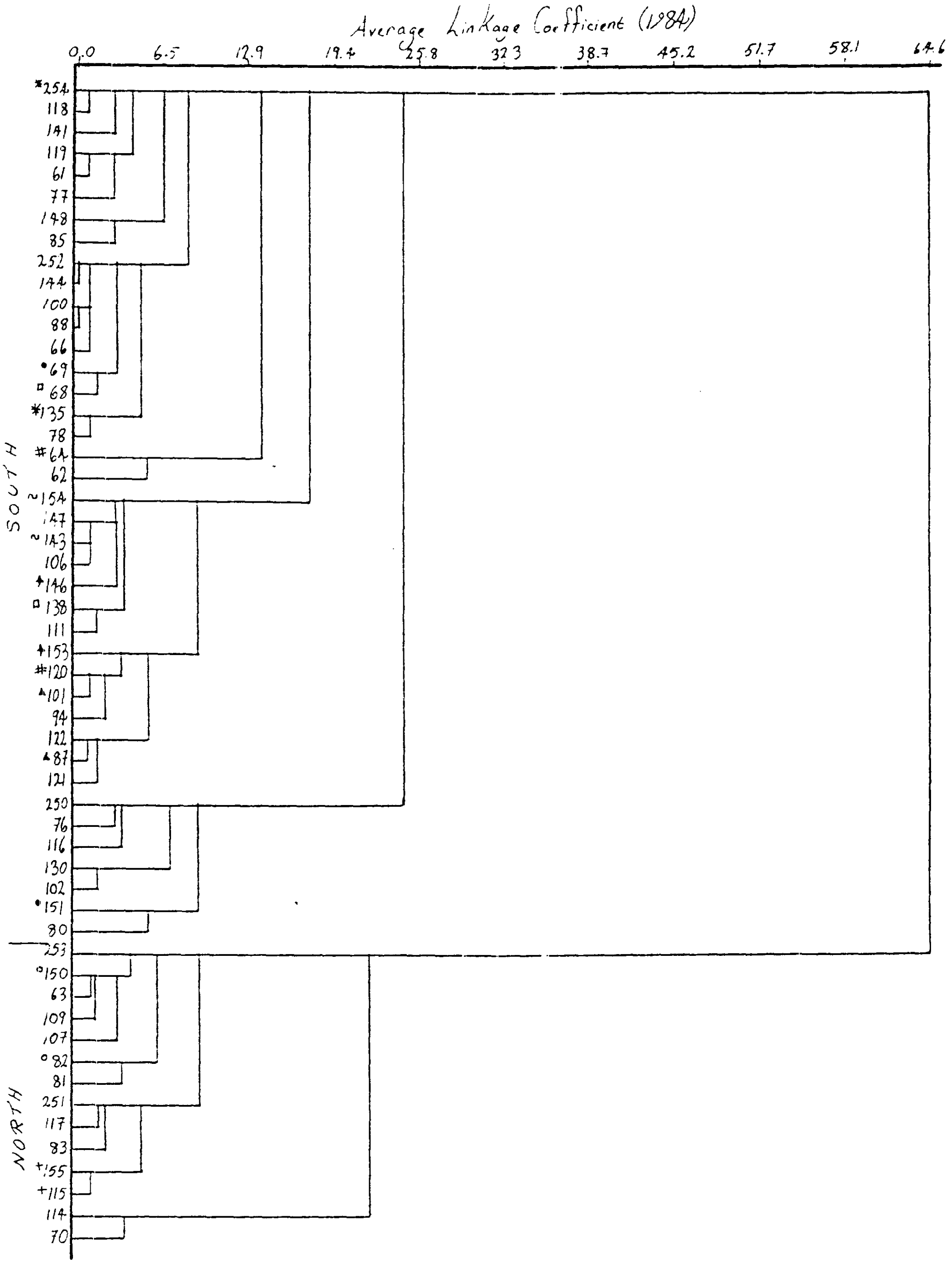
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Appendix E

Cluster results of inter-female association

In order to describe inter-female association preferences, I conducted cluster analyses on female association index values. An association index value was calculated for all pairs of females using Sorenson's index (Pielou, 1977). The index is:

$$100 \times \left(\begin{array}{c} 2 \times (sightingsofA\ with\ B) \\ over \\ ((sightingsofA) + (sightingsofB)) \end{array} \right)$$

A female was considered to be sighted *with* another female, if she was found in the same subgroup.

I conducted both single and average linkage cluster analyses on the data (for my reasons see appendix D). The dendrograms resulting from these analyses are presented below. Females are identified by an individual number on the X-axis. The females who are grouped into clusters at the base of the dendrogram are inferred to have been found relatively frequently in the same subgroup. Females who are linked to each other closer to the top of the dendrogram (i.e. with small association index values) are inferred to have been found infrequently in the same subgroup.

Mother-daughter pairs are indicated by similar symbols placed next to their identity numbers.

When discussing the association relationships of females I refer to the females as associates.

The resulting dendrograms have divided the females into the same two clusters or 'sets' defined from the cluster analyses of distances between females' home range centres.