

Discriminant and graphical analyses of Norwegian Knot biometrics: the sex and race problem revisited

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A number of recent studies have used wader biometrics in the analysis of intraspecific problems such as sex discrimination (Puttick 1981, Harrington & Taylor 1982, Skeel 1982, Maron & Myers 1984). With the lack of between-sex plumage differences in a number of bird species, discriminant analysis has become valuable tool for sex determination (Green 1982, Wood 1987). This paper presents some preliminary analyses of a sample of Knot *Calidris canutus* data provided by recent visits to a migration staging area in north Norway (Davidson & Evans 1986, Davidson *et al.* 1986, Uttley *et al.* 1987).

Methods and results

2,267 Knots were caught with cannon nets in May 1985 and 1986 in Balsfjord, Norway (69°21'N, 19°18'E). A sample was measured in the field and then sacrificed to be used in studies of body condition. Thus they provided a sample of known sex birds. Only adult birds were used in this analysis. Four measurements were taken: (1) wing length, (2) bill length, (3) head and bill length (head length being derived from this), (4) tarsus and toe length. Data were transferred to computer file and analysed using standard software packages (SAS and MINITAB).

A number of body size measurements were made on these Knot but not all were required in a discriminant analysis which calculated a linear combination of the measurements

serving to differentiate the sexes (Chatfield & Collins 1980). A stepwise discriminant analysis was performed on the data (using the method of inclusion and removal at each step) to investigate the best combination of sex predictor variates. The analysis identified wing and bill as the best sex prediction measurements, and the following discriminant function was derived:

$$D = 0.494B + 0.203W - 51.33$$

where D is the discriminant score, B the measured bill length and W the measured wing length.

The main problem with this discriminant function (and hence with the data) is that the probability of misclassification of a bird is 0.24 for females and 0.28 for males. These figures are more readily understood by reference to Figure 1, where measurements of the sexed birds are presented along with the discriminant line (50% probability of misclassification) and the 90% confidence prediction limits*. We can be 90% certain of the sex of an individual Knot if it lies outside the confidence limits on Figure 1.

Data from the Knot found in Balsfjord are providing very strong evidence that they are from the Nearctic population *C. c. islandica* (Davidson *et al.* 1986, Uttley *et al.* 1987).

It is still possible to speculate, however, that there may be some birds from the Siberian population *C. c. canutus* mixed with the Nearctic birds. If this latter hypothesis were correct, then the biometrics of the Balsfjord Knot would exhibit a multimodal size frequency distribution within the sexes of the population. To give a theoretical example, if we expect just one race of birds in the population, then the size frequency distribution of measurements should be as in Figure 2a. However, two races with a sexual dimorphism gives a more complicated picture as in Figure 2b.

This hypothesis can be tested using a simple graphical technique of a theoretical quantile-quantile plot (Chambers *et al.* 1983) (for an explanation of this technique see appendix). Measurements of wing length are presented for this analysis although other measurements give similar results.

Figure 3 presents the simple frequency histograms of male and female Knot wing lengths. Few patterns may be envisaged in these data but we need a technique for comparing the frequency distributions with what might be expected if the data were sampled from a normally dis-

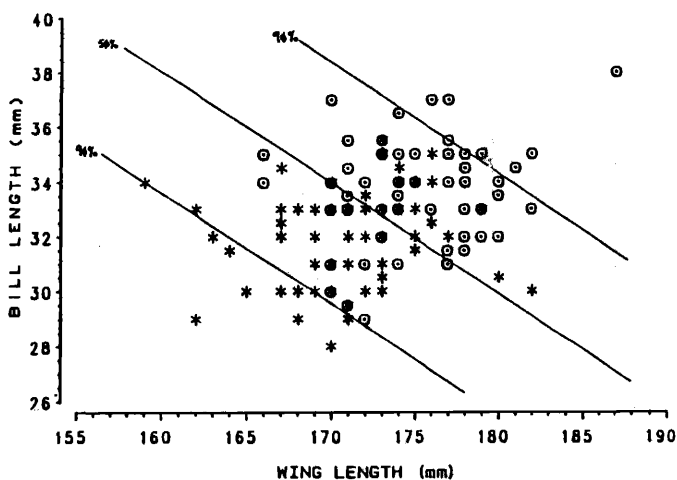


Figure 1. Bill and wing lengths of male (*) and female(O) Knot, with the discriminant line ($0.494B = 51.33 - 0.203W$) labelled 50%. Birds lying outside the 90% confidence prediction limits have a less than 10% chance of being misclassified.

* They approximate to $\pm \log_e (0.90/(1.0-0.90))y$ variate coefficient from discriminant function.



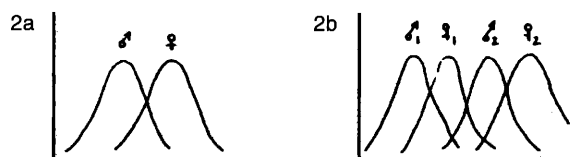


Figure 2. Theoretical size frequency of birds:

- a) one population with sexual dimorphism,
b) two populations with sexual dimorphism.

tributed population. Figures 4 and 5 give such a graphical comparison, where the original data are plotted against the theoretical normal distribution (normal score) for such a sample of data. Any departures from normality in the Knot wing lengths would show up as departures from a straight line in Figures 4 and 5 (Chambers *et al.* 1983). Clearly both male and female Knot wing lengths exhibit little deviation from what would be expected if the data were samples from one population. Therefore we conclude that there is only one "population" of Knots in Balsfjord in May.

Discussion and conclusions

A discriminant analysis of the biometric data from this population does not give a clear distinction between the sexes. Despite the substantial overlap in the size of male and female Knot, the extremes can be sexed, using the derived discriminant function, from measurements taken in the field.

Simple univariate plots of the distribution of measured wing lengths of Norwegian Knot provide further evidence for the hypothesis proposed by Davidson *et al.* (1986) and Uttley *et al.* (1987), that only the race *Calidris canutus islandica* is present in Balsfjord, North Norway in May.

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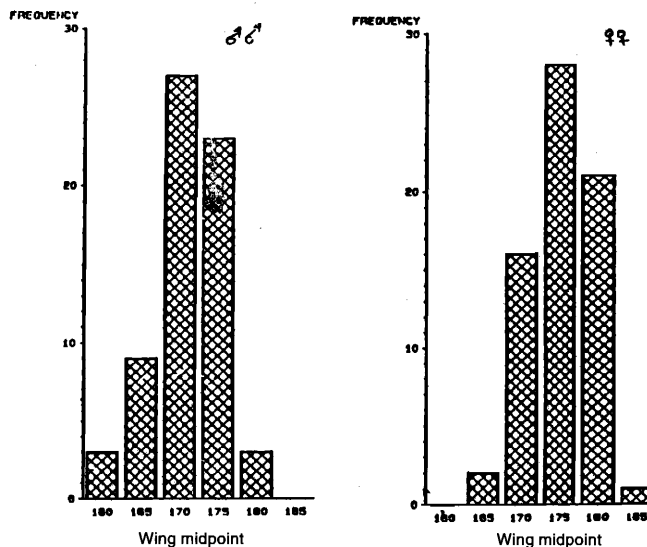


Figure 3. Frequency histograms of male and female Knot wing lengths.

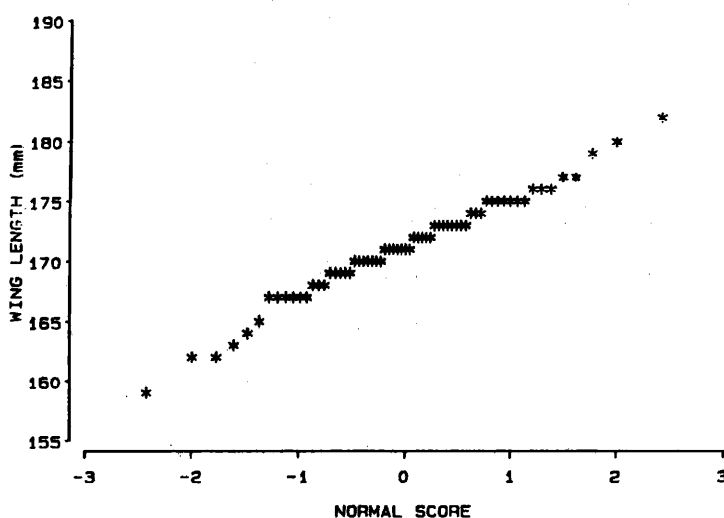


Figure 4. Wing length of male Knot plotted against the theoretical normal distribution.

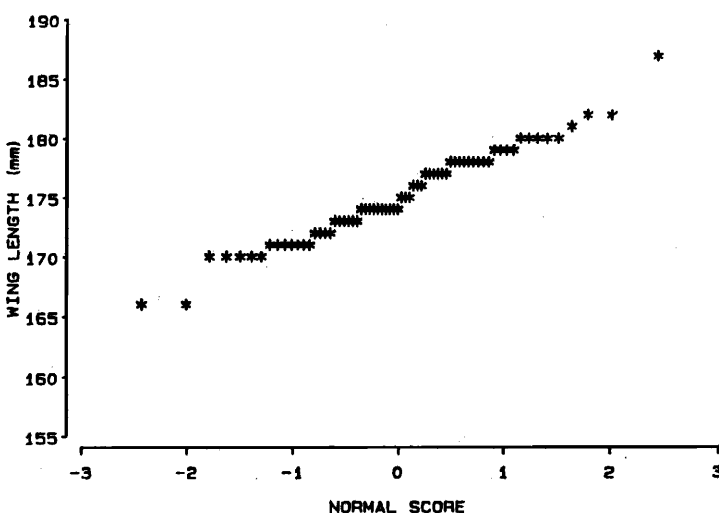


Figure 5. Wing length of female Knot plotted against the theoretical normal distribution.



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Appendix

The concept of a quantile is closely connected with the familiar concept of percentile. We define the 0.65 quantile of a set of data to be a number on the scale of the data that divides it into a fraction of 0.65 of the observation below and a fraction of 0.35 above. The median of the data is therefore 0.5 quantile. An effective method for making comparisons of the distributions of two data sets is to plot the quantiles of each distribution against the other. In this paper I have been interested in comparing the frequency distribution of Knot wing lengths against the normal distribution. Therefore I have plotted a theoretical quantile–quantile plot, with the empirical quantiles of wing length plotted against the corresponding quantiles of a normal distribution (sometimes called a normal probability plot). When the quantiles in the data closely match the theoretical quantiles, the points on a quantile–quantile plot will fall near the line $y = x$.

