# Estimating the total weight of Scandinavian brown bears Ursus arctos from field-dressed and slaughter weights

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Source: Wildlife Biology, 1(3) : 177-179

Published By: Nordic Board for Wildlife Research

URL: https://doi.org/10.2981/wlb.1995.023

**SHORT COMMUNICATION**

Short communication articles are short scientific entities often dealing with methodological problems or with byproducts of larger research projects. The style is the same as in original articles.

# Estimating the total weight of Scandinavian brown bears *Ursus arctos* from field-dressed and slaughter weights

**Jon E. Swenson, Finn Sandegren, Arne Söderberg & Robert Franzén**

Swenson, J.E., Sandegren, F., Söderberg, A. & Franzén, R. 1995: Estimating the total weight of Scandinavian brown bears *Ursus arctos* from field-dressed and slaughter weights. - Wildl. Biol. 1: 177-179.

Regressions are presented to predict the total weight (TW) in kg of Scandinavian brown bears *Ursus arctos* from field-dressed weights (FW), where TW = 4.01 + 1.16 × FW, and slaughter weights (SW), where TW = 4.63 + 1.49 × SW. Both regressions had high predictive values ($r^2 = 0.97$) and were not significantly affected by sex or genetic lineage of the bears. Formulas to calculate confidence intervals are also presented.

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*Received 12 April 1995, accepted 7 August 1995*

*Associate Editor: Henning Noer*

Body mass is an important biological parameter for wildlife, and is often used by researchers and managers. With adequate weight data, we can determine growth rates, regional variation in growth or adult weights, factors determining body size and reproduction, and variation in life-history strategies of animals (Sæther & Haagenrud 1983, 1985, Sæther 1985, Langvatn & Albon 1986, Langvatn et al. in press). But, it is often difficult to obtain homogeneous data on the weights of a large proportion of hunter-killed large mammals. In North America, biologists commonly use the relationship between chest circumference and body weight of bears to estimate total weights of bears killed by hunters or captured in control actions (see review in Swenson et al. 1987). In Scandinavia, almost all brown bears *Ursus arctos* now killed by hunters or in control efforts are weighed and the weights are reported to the Scandinavian Brown Bear Research Project. However, these carcasses are sometimes weighed whole, sometimes as field-dressed carcasses (internal organs removed), and sometimes after slaughter (skinned, with head and feet removed). Definitions follow Langvatn (1977). In order to maximise the usefulness of these data, we have determined the ability to estimate total weights from both dressed and slaughter weights. As these relationships can be useful for others working with the brown bear in Europe, we report our results in this short communication.

## Methods

A quota system was initiated for bear hunting in Sweden in 1981. In order to be able to stop the hunting when the quota was filled, hunters were required to notify the authorities immediately after killing a bear. Later, samples from and information on all killed bears were also required to be sent to the authorities. The hunters have the

opportunity to report the weight of the bear to the nearest 1 kg as total weight (TW), field-dressed weight (FW, only the internal organs removed), or slaughter weight (SW, internal organs, skin, head and feet removed). In many cases, they have reported two or all three weights. This is the base for our study. We have analysed the relationship between TW and both FW and SW using linear regression analyses. First, however, we tested whether sex or genetic lineage of the bear had any effect on the regression with an analysis of covariance using general linear models procedure (SAS Institute, Inc. 1989). Genetic lineage was tested because bears in Sweden belong to two distinct lineages based on mitrochondrial DNA, with a distinct geographical separation (Taberlet et al. 1995). Model I regressions were run using StatView software (Feldman et al. 1988). Formulas to determine the confidence intervals around TWs estimated from a given FW or SW, using our regressions, are from Sokal & Rohlf (1981: 473-474).

## Results and Discussion

### Field-dressed weights

We received data on both FW and TW for 62 bears. Neither sex (ANCOVA, $F = 0.24$, $P = 0.63$) nor genetic lineage (ANCOVA, $F = 0.27$, $P = 0.61$) affected the regression relationship between these weights. Variation in the FW explained 97% of the variation in TW (Fig. 1), indicating an excellent predictive value of the regression ($r^2 = 0.987$, $df = 61$, $P < 0.0001$). The equation is: $\hat{TW} = 4.01 + 1.16 \times FW$.

To calculate the (1-α) confidence limits around a TW estimated from FW, we used the following equation:

$$CL_{(1-\alpha)} = \hat{TW}_i \pm t_{\alpha[60]} \times S_{\hat{TW}i}$$

where $CL_{(1-\alpha)}$ = the (1-α) confidence limits
$\hat{TW}_i$ = the estimated total weight
$t_{\alpha[60]}$ = the t value for a desired α and 60 degrees of freedom
$S_{\hat{TW}i}$ = the standard error of $\hat{TW}_i$

The standard error of $\hat{TW}_i$ is calculated using the equation:

$$S_{\hat{TW}i} = \sqrt{90.52\left[\frac{1}{62} + \frac{(\hat{FW}_i - 96.6)^2}{150561.8}\right]}$$

### Slaughter weights

We received data on both SW and TW for 69 bears. Also in this case, neither sex (ANCOVA, $F = 0.00$, $P = 0.96$) nor genetic lineage (ANCOVA, $F = 0.16$, $P = 0.69$) affected the regression relationship between these weights. Variation in SW also explained 97% of the variation in TW (Fig. 2), indicating an excellent predictive value also for this regression ($r^2 = 0.985$, $df = 68$, $P < 0.0001$). The equation is: $\hat{TW} = 4.63 + 1.49 \times SW$.

To calculate the (1-α) confidence limits around a TW estimated from SW, we used the following equation:

$$CL_{(1-\alpha)} = \hat{TW}_i \pm t_{\alpha[60]} \times S_{\hat{TW}i}$$

where $CL_{(1-\alpha)}$ = the (1-α) confidence limits
$\hat{TW}_i$ = the estimated total weight
$t_{\alpha[60]}$ = the t value for a desired α and 60 degrees of freedom
$S_{\hat{TW}i}$ = the standard error of $\hat{TW}_i$

The standard error of $\hat{TW}_i$ is calculated using the equation:

$$S_{\hat{TW}i} = \sqrt{108.43\left[\frac{1}{69} + \frac{(\hat{SW}_i - 73.8)^2}{105191.4}\right]}$$

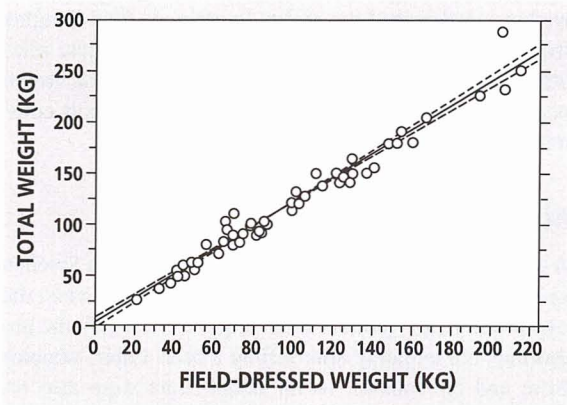


Figure 1. Relationship between field-dressed and total weights, with 95% confidence intervals, of brown bears killed during the autumn hunting season in Sweden.

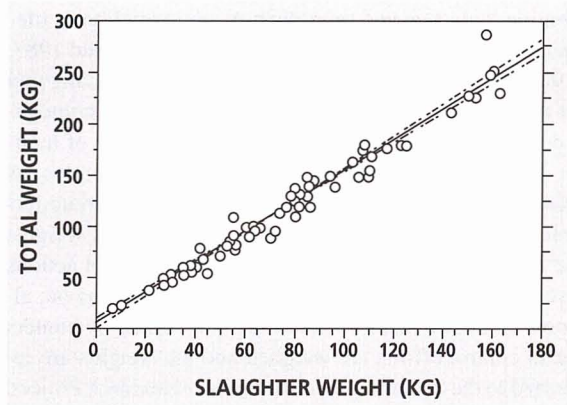


Figure 2. Relationship between slaughter and total weights, with 95% confidence intervals, of brown bears killed during the autumn hunting season in Sweden.

The regressions reported here show a high predictive ability. By using these, we have been able to obtain estimates of the total weights of 473 brown bears killed in Sweden since 1981, even though the actual total weights were only reported for 105 of these bears. The usefulness is enhanced by the finding that neither sex nor mtDNA lineage significantly affected the regression.

We recognise that we underestimated variance in our predictive models by using Model I regressions, because it assumes no error in measurement of the X variables. However, we have not estimated this error and consider the regressions presented to be adequate to predict total weights of Scandinavian brown bears. Sokal & Rohlf (1981) concluded that the Model I design is generally applied when the regression line is fitted mainly for purposes of prediction.

*Acknowledgements* - We would like to thank the hunters that made the extra effort to take several weights of their bears as they slaughtered them. This is a report from the Scandinavian Brown Bear Research Project, which has been financed primarily by the Swedish Environmental Protection Agency, Swedish Hunters' Association, Norwegian Institute for Nature Research, Norwegian Directorate for Nature Management, and World Wildlife Fund, Sweden. We also thank Jonas Lemel and Henning Noer for statistical advice and Rolf Langvatn for comments.

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