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Bears across borders - accounting for temporary migration in genetic capture-recapture.

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Abstract

In this thesis we investigate the bias in the current method of estimating the brown bear population in four regions of Sweden using a simulation study. The method currently used is the genetic capture-recapure with scat samples collected by volunteers. One region is surveyed each year with every fifth year being an off year. The source of bias we are specifically investigating is the one caused by the temporary migration of bears across the region borders. This migration causes bears to possibly be counted for the population in more than one region in addition to bias in the estimation of the parameters used in the genetic capture-recapture models. Combined these cause an on average overestimation of the regions population. An alternative method were we take the positions of the found scat samples into account will also be tried to see if the bias of the standard estimate can be mitigated. The findings of the simulation study suggests that the current method used will on average overestimate the bear population by somewhere inbetween 7 and 17 percent depending on the region. The alternative method was found to mitigate the bias by a relatively large amount, however in the worst case it would still on average overestimate the bear population in one of the Swedish regions by 7 percent. Switching to the alternative method would in theory reduce the bias in the estimation of Swedish brown bear population, however a better method would be extending the search of scat samples to a distance outside of the currently surveyed region. This way a better understanding of the border problem in the Swedish case could be achieved.

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