3.2.2 DNA: Genetic analyses to determine population size or density

Objective

Determines the effective population size by genetics (individuals or pellets).

Measure estimated

Effective population size (Ne).

Applicability

All ungulates.

Methodology

Several conceptually different types of Ne can be distinguished, but the most used is the number of individuals in a population who contribute offspring to the next generation (Ridley 2004). The estimates of Ne tend to provide a lower number than an actual population size.

Determining the Ne (local) by genetics is possible if appropriate sampling and corrections based on population dynamics parameters are applied. Nonetheless, this approach is time demanding and relatively expensive (Luikart et al. 2010).

Nowadays, this method is also applied associated to SCR methods.

Genotyping of faecal pellets has been used to assess population parameters of wild ungulates (e.g., Blåhed et al. 2019; Ebert et al. 2009, Ebert et al. 2010; Ebert et al. 2012a 2012b; Goode et al. 2014; Morden et al. 2011; Poole et al. 2011). Genetic analyses could also be done from hair traps, which has been used for instance in roe deer (Fickel et al. 2012), but they do not always work well (e.g., Ebert et al. 2010). Pellets can be collected and genetically analysed for individual genotyping, providing an indirect way to count and identify individuals in each population (Broquet et al. 2007).

Although costs for DNA analyses have been decreasing in the last years, analyses of multiple samples (as requested to apply mark-recapture approaches) are time-consuming and expensive, and therefore, this method not commonly used in ungulates.
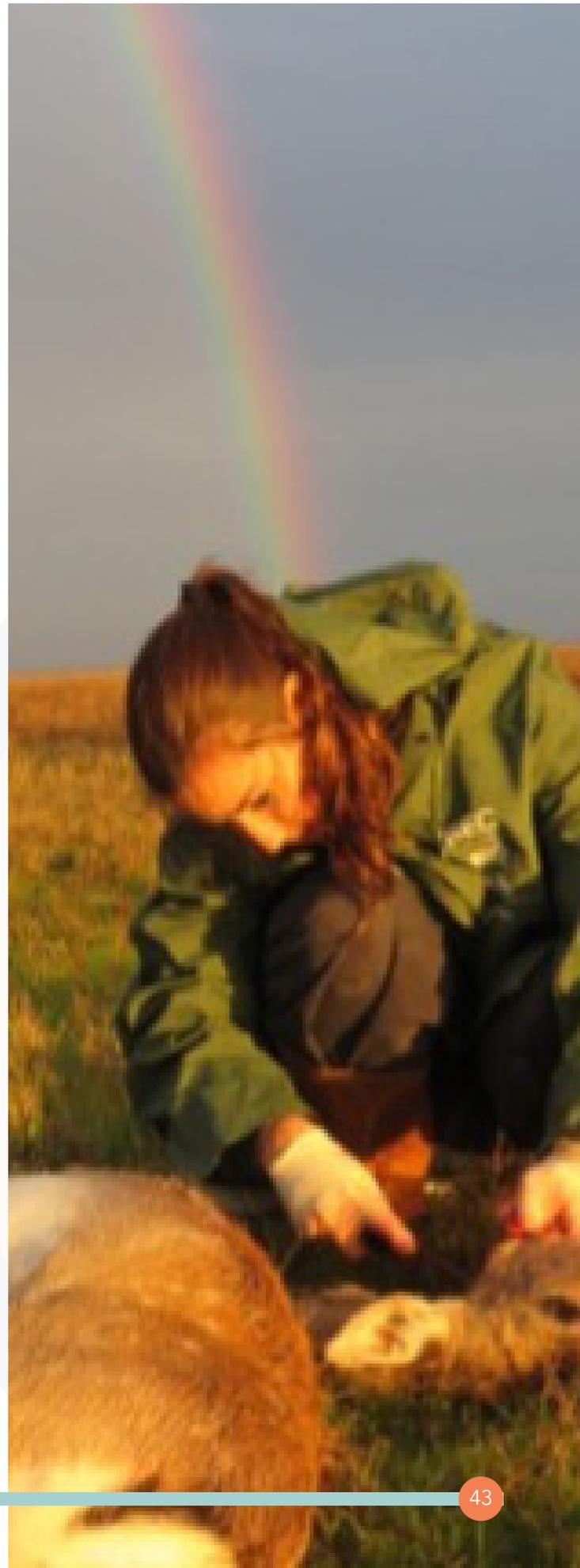
Evaluation

· Pro: high accuracy.
· Con: mainly in winter, high effort, expensive, need for assumptions, hardly applicable in low densities, still needs to be combine with other sampling techniques in most cases.
· Accuracy: high.
· Habitat: all, performs well in forest areas.

Recommendations to improve comparability and accuracy:

These techniques have the molecular modelling part (modelling of marking and recapture has been already discussed before). The following is regarding the molecular side:

• Make robust designs for DNA sampling; avoiding biases in the collection of data associated with the behaviour of animals or habitat selection.
• Assesses the probability of capture locally to consider the necessary effort.
• Standardize and test laboratory protocols.
• Collect information on hunted (sampled) animals.
• Make a good selection of quality samples.
• Optimize the use of genetic markers (within and between laboratories) .