# Appendix 1. Mark recapture models used for estimating brown bear regional population size.

Regional population size estimates for a brown bear population in Southern Carpathians, Romania. We used several mark-recapture modelling approaches (hereafter CMR): we used the generalized linear model approach with the information-theoretic model selection (Burnham & Anderson, 2002), as applied in program MARK (White & Burnham, 1999); we used the Chao's Mh and Darroch models (Chao, 1987), which are robust to capture heterogeneity, and used the R package RCapture (Baillargeon & Rivest, 2009) to fit these models. We also used the Capwire approach (Miller, Joyce & Waits, 2005) with the R-package Capwire (Pennell *et al.*, 2013); All the models we used assume a demographically closed population. Since sampling was designed to be relatively short and before reproduction, during the autumn hyperphagia period, we assumed that the sampled population should behave as demographically closed. We used the Pradel model with recruitment and survival parametrization in program MARK to check this assumption. We removed the autocorrelated samples from the CMR analysis. If two or more samples of the same animal were found on the same day less than 0.5 km apart, they were considered statistically non-independent and only one of these samples was retained for the analysis.

**MARK analysis & closure test:** we considered MARK for analysis of our data because of its well-developed model selection procedures and flexibility to include additional information about individuals, or groups of individuals, directly in the models. For analysis in MARK we organized the samples into sampling intervals, taking care that each detected animal would have between 15% and 30% probability of being detected within a certain interval. At the upper and lower part of this range, we ended up with 8 or 6 intervals, respectively. Both datasets were analysed, but the 6-interval data seemed to have better properties (denser data, higher capture probability in each interval, less heterogeneity) and its results are being reported. Goodness-of-fit test with the median c-hat method showed good fit of the model (estimated c-hat = 1.038, ideal fit is c-hat = 1). MARK has a very well-defined model selection procedure that allows for hypothesis testing using an information-theoretic approach. This makes it useful for testing various assumptions about the dataset, and the results can be used to better formulate and interpret other modelling approaches. We generated an a-priori set of 11 plausible models using the Huggins modelling approach. The selected models included capture heterogeneity and sex (modelling capture probability differently for males and females). This makes sense considering the high sampling bias, particularly at rub trees.

Population closure test with the Pradel model (with recruitment and survival parameterization) supported the assumption of population closure since model that fixed survival at 1 and recruitment at 0 was selected as the best model, and was considerably better than the model where these two parameters were estimated from the data (dAIC = 3.99). Estimated from the data, survival for both sexes was estimated as >0.99, and recruitment <0.01, further supporting the closure assumption.

**Capwire and Rcapture analysis**: Both approaches use continuous sampling data, which fits better to how we actually collected samples in the field. Because of this, we could expect these models to have narrower confidence intervals than MARK models (they should use the data more efficiently). For Capwire, we used likelihood-ratio test to select between two innate rates model (PART and TIRM). The Capwire model selection preferred the model that included heterogeneity of capture (TIRM). Since both the direct genotyping results and MARK analysis indicated different capture probability for each sex, and Capwire

doesn't allow including groups directly in the model, we ran the models for each sex separately and added both results to obtain the total number of animals. We took the similar approach with the Rcapture analysis.

**Models selected for local population and density modelling:** Within the same sampling session all models returned similar regional population size estimates but differed in terms of their CI's. The estimates dropped from 2017 to 2018 mostly because of the lower success of detecting females in the population. While the MARK approach requires discrete sampling sessions, this was not how we collected the samples in our study. MhChao and Darroch had a poor performance with highest CI's (Table 1). Thus, we decided to interpret Capwire TIRM models (table cells highlighted in light grey in Table 1 below) and use these model estimates for further modelling of local population size and density estimates. Given the high difference in females' detectability and estimates from 2017 to 2018, and because female estimates drive the total population size, we extrapolated the Capwire TIRM 2018 predictions for females and for all individuals from the 2018 estimates for males and by keeping the same sex ratio as in 2017 (sex ratio derived from CMR; Table 1). This extrapolation is highlighted in dark grey boxes and include all calculations in Table 1 below. Note that calculation of CI accounts the uncertainty of sex ratio calculation by using an average sex ratio, as well as a minimum and a maximum. We did so as the interpolation has to account for the entire uncertainty of the sex ratio - meaning the entire uncertainty of the 2017 abundance estimates for males and for females - and this should be included not to overestimate precision of the result. The conservative approach here is to use the upper and lower limits on abundance estimates to estimate the upper and lower limits of the sex ratio estimate, and to use these in the estimates of the CI for 2018 females' estimates. Check the formulas in the box below with Cid and Ciu standing for lower and upper confidence intervals limits.

*Table 1. Results of regional population size estimates of brown bears obtained through different mark-recapture modelling approaches.*

| Model | Sex | Abundance | Cid | Ciu | AIC |
|---|---|---|---|---|---|
| Capwire PART | All 2017 | 361 | 373 | 428 | |
| Capwire PART | Females 2017 | 202 | 201 | 254 | |
| Capwire PART | Males 2017 | 171 | 180 | 207 | |
| Capwire PART | All 2018 | 228 | 250 | 284 | |
| Capwire PART | Females 2018 | 129 | 123 | 218 | |
| Capwire PART | Males 2018 | 127 | 123 | 175 | |
| Capwire TIRM | All 2017 | 312 | 303 | 398 | |
| Capwire TIRM | Females 2017 | 185 | 170 | 250 | |
| Capwire TIRM | Males 2017 | 149 | 135 | 168 | |
| Capwire TIRM | All 2018 | 221 | 208 | 282 | |
| Capwire TIRM | Females 2018 | 112 | 95 | 171 | |
| Capwire TIRM | Males 2018 | 121 | 112 | 143 | |
| Capwire TIRM | All 2018 *(extrapolated based on 2017 sex ratio)* | 271 | 225* | 408* | |
| Capwire TIRM | Females 2018 *(extrapolated based on 2017 sex ratio)* | 150 | 113* | 265* | |

**Sex ratio estimated in 2017 (CMR)**
185 / 149 = **1.24**
**Sex ratio min**
$Cid_F$ / $Ciu_M$ = 170 / 168 = **1.01**
**Sex ratio max**
$Ciu_F$ / $Cid_M$ = 250 / 135 = **1.85**

| Method | Group Year | | | | |
|---|---|---|---|---|---|
| Capwire TIRM | Males 2018 | 121 | 112 | 143 | |
| Darroch | All 2017 | 308 | 265 | 351 | 60.82 |
| Darroch | Females 2017 | 203 | 122 | 283 | 33.25 |
| Darroch | Males 2017 | 142 | 120 | 163 | 57.50 |
| Darroch | All 2018 | 206 | 174 | 238 | 59.59 |
| Darroch | Females 2018 | 153 | 35 | 272 | 26.94 |
| Darroch | Males 2018 | 115 | 95 | 134 | 52.56 |
| MARK Mh*g 6int | All 2017 | 305 | 227 | 498 | |
| MARK Mh*g 6int | Females 2017 | 169 | 115 | 311 | |
| MARK Mh*g 6int | Males 2017 | 136 | 112 | 187 | |
| MARK Mh*g 6int | All 2018 | 219 | 170 | 326 | |
| MARK Mh*g 6int | Females 2018 | 99 | 73 | 153 | |
| MARK Mh*g 6int | Males 2018 | 120 | 97 | 173 | |
| MhChao | All 2017 | 294 | 252 | 337 | 60.44 |
| MhChao | Females 2017 | 162 | 122 | 202 | 32.49 |
| MhChao | Males 2017 | 143 | 112 | 175 | 61.73 |
| MhChao | All 2018 | 259 | 176 | 341 | 54.49 |
| MhChao | Females 2018 | 133 | 54 | 213 | 24.33 |
| MhChao | Males 2018 | 135 | 89 | 182 | 51.91 |

**References**

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