Supplementary Material 1

Non-spatial capture recapture and spatially explicit capture recapture models for estimating wolf abundance and density in Southern Carpathians, Romania

1.1. Non-spatial capture recapture models

Non-spatial capture recapture models (CMR) are often used to estimate population size for wildlife. These models require at least two sampling events (one capture and one/more recapture events). We used several CMR models, namely Chao's Mh and Darroch models from RCapture package, as well as ECM and TIRM models from the Capwire approach. The CMR modelling was performed on $S1_{sa}$, $S3_{sa}$ and $S3_{la}$.

Model selection based on the Capwire likelihood ratio test found Capwire TIRM to be the best-fitting model (p = 0.011, 0.010 and 0.000 for TIRM vs. ECM for $S1_{sa}$, $S3_{sa}$ and $S3_{la}$ respectively), but in our case this model yielded wide confidence intervals, especially for the male predictions and for the $S1_{sa}$ and $S3_{sa}$, indicating a poor model precision (Table 1). The Capwire ECM model had a poor fit and low precision.

Of the models included in RCapture, the Chao's Mh model performed best with the lowest AIC in 4 out of 9 modelling scenarios, and had dAIC < 2 from the model with the lowes AIC in all other scenarios. Chao's Mh model also had robust performance across the three sampling sessions and its results were more comparable between sessions than the other model results (Table 1). Therefore, this model was selected to estimate the population size within the study area. Darroch's Mh model had a higher AIC and extremely high CIs for $S1_{sa}$, being not comparable across sessions.

We calculated the sex ratio based on the Chao's Mh estimates of abundance.

The minimum sex ratio is given by:

$$\textit{Minimum sex ratio} = CI_{lower} \textit{ of females}/CI_{upper} \textit{ of males}$$

The maximum sex ratio is given by:

$$\textit{Maximum sex ratio} = CI_{upper} \textit{ of females}/CI_{lower} \textit{ of males}$$

Table 1. *Results of wolf abundance estimates (Abund.) obtained through non-spatial capture recapture (CMR) and spatially explicit capture recapture (SECR) modelling approaches. For the CMRs, CI_{lower} and CI_{upper} denote the limits of 95% confidence intervals. Models denoted by asterisk ('*') and bold letters are considered the most robust and the sex ratio calculated based on these models' result. In the case of SECR the abundance estimates must be interpreted for the effective sampling area, which is not comparable to the results of CMR approach. BCI_{lower} and BCI_{upper} denote the limits of 95% Bayesian Credible interval.*

Models	Sex	Season 1 Small area ($S1_{sa}$)			Season 3 Small area ($S3_{sa}$)			Season 3 Large area ($S3_{la}$)		
		Abund.	CI_{lower}	CI_{upper}	Abund.	CI_{lower}	CI_{upper}	Abund.	CI_{lower}	CI_{upper}
CMR models:										
Capwire ECM	All	20	19	22	19	19	19	29	28	30
Capwire ECM	Males	8	8	8	10	10	10	14	14	14
Capwire ECM	Females	13	12	19	9	9	9	15	14	17
Capwire TIRM	All	25	19	33	20	19	23	31	28	36
Capwire TIRM	Males	9	8	20	13	10	18	14	14	15
Capwire TIRM	Females	17	11	29	9	9	10	17	14	24

Mh Chao *	**All**	**25**	**16**	**34**	**21**	**15**	**27**	**31**	**25**	**38**
Mh Chao *	**Males**	**9**	**6**	**13**	**9**	**8**	**10**	**16**	**10**	**21**
Mh Chao *	**Females**	**19**	**14**	**34**	**14**	**4**	**24**	**17**	**12**	**22**
Mh Darroch	All	27	15	39	22	17	26	35	27	43
Mh Darroch	Males	10	5	14	9	8	11	16	12	21
Mh Darroch	Females	20	-2	41	14	5	24	18	10	27

							SECR Effective sampling area		
							Abund.	**BCI_lower**	**BCI_upper**
Bayesian SECR model	All						70	50	90

					SECR prediction downscaled to Season 3 Small area from CMR (S3sa)			**SECR prediction downscaled to Season 3 Large area from CMR (S3la)**		
Bayesian SECR model	All				26	18	33	33	23	42

Sex ratio based on Mh Chao model		2.11	1.07	5.66	1.55	0.4	3	1.06	0.57	2.2

1.2. Spatially explicit capture recapture model and its results

1.2.1. Model presentation

Modeling procedure is based on López-Bao et al. (2018) and Royle et al. (2013). The spatially explicit capture recapture (SECR) models are used to estimate the abundance or density of animals in space within an effective sampling area. The effective sampling area is a buffer around the detector grid to minimize the detection probability of animals outside the study area. These types of models typically require two input data: 1) a dataset which describe the location of detectors and the detector level covariates (Figure S1), and 2) a dataset about detections of each individual at each detector (e.g., a N-by-M matrix where N is the number of individuals and M is the number of detectors).

The Bayesian Hierarchical Markov Chain Monte Carlo model approach uses a spatial point process, i.e., randomly samples' activity centers (coordinates) from the space and links the distance of locations to each detector via a detection function. We used half-normal detection function:

$$\lambda_{ij} = \lambda_0 exp(\frac{-d^2_{ij}}{2\sigma^2})$$

where λ_0 is the baseline encounter probability, d_{ij} is the distance between the i individual's activity center and j detector while σ is the Gaussian scale parameter of the distance.

Detector level covariates, in our case the sampling effort (Figure S1) was linked to each observation:

$$\log(\lambda_{0j}) = \alpha_0 + \alpha_1 \times E_j$$

where E_j is the detector level sampling effort.

Finally, the number of times an individual occurs at a given detector is described by a Poisson distribution whose expected value is the λ_{ij} value shown above:

$$y_{ij} \sim \text{Poisson}(\lambda_{ij}).$$

We ran three MCMC chains with 1000 burn-in steps and 50,000 iterations with thinning rate 5, resulting in 30,000 outputs. For checking the convergence of MCMC parameters we used the Gelman-Rubin statistic R-hat (Gelman & Rubin, 1992), where all values were below 1.1 thus indicating a good convergence. The goodness-of-fit of models were tested threefold using Bayesian p-values described in Royle et al. (2013): i). individual encounter frequencies per detector, ii). individual encounter frequencies aggregated for each individual; and iii) detector frequencies aggregated for each detector. The Bayesian p-value is calculated by the proportion of points above the 1:1 equality line. P-value between 0.05 and 0.95 indicates good fit, while 0.5 indicates perfect fit (Figure S2).

After the preliminary studies we used the Nimble code developed by López-Bao et al. (2018). Nimble is a powerful tool to implement Bayesian hierarchical models and to run them. The Nimble code is written inside R statistical environment, compiled to a C++ code which ensures fast running.
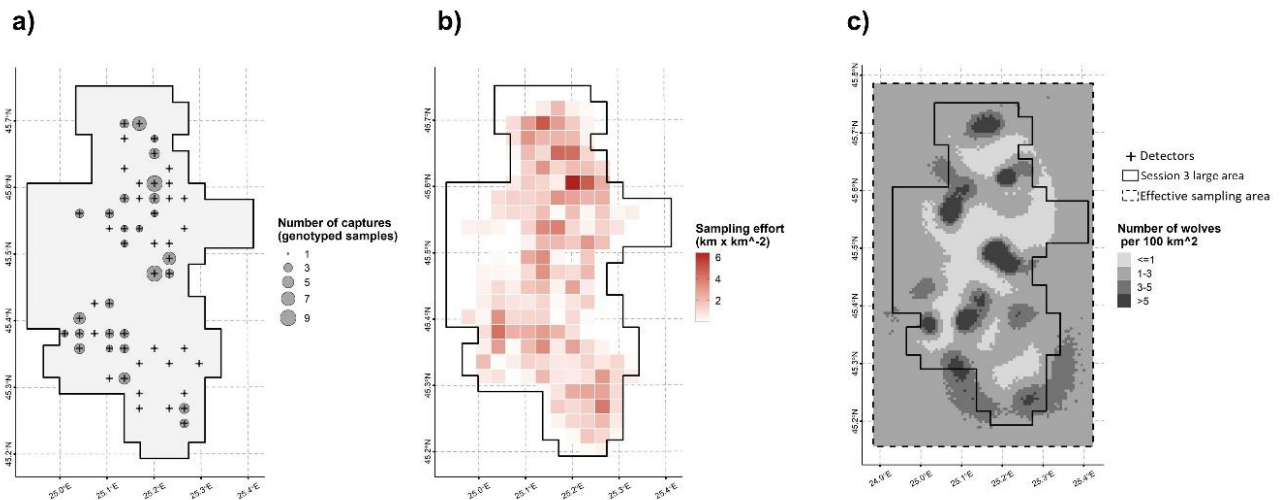

Figure S1. Panel a) Map of the study area with the number of genotyped samples collected at each detector (black crosses). Panel b) Sampling effort on the study area: the density of transect length (km x km-2). Panel c) The estimated wolf density within the effective sampling area (bordered with dashed lines; black crosses denote the detectors).

1.2.2. Model performance and result

All the model parameter estimates (Table S2) were considered good based on R-hat statistics; all R-hat values were <= 1.1. The Bayesian p-values were between 0.05 and 0.95 indicating a good fit of the model (Figure S2).
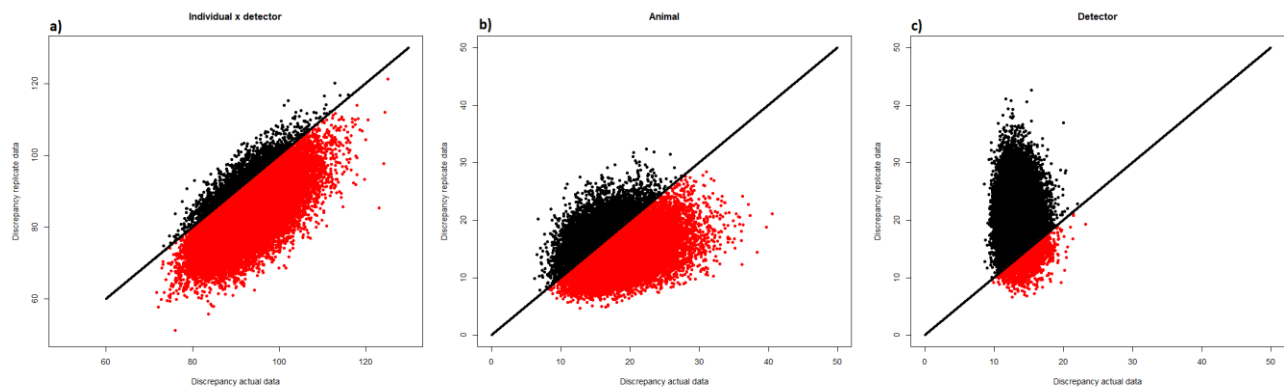
Figure S2. Discrepancy measures for SCR-Poisson Model used for SECR. Panel a) individual encounter frequencies per detector (p-value = 0.07); panel b) individual encounter frequencies aggregated for each individual (p-value = 0.24); panel c) detector frequencies aggregated for each detector (p-value = 0.93).

The Gaussian scale parameter (σ) had a posterior mean 0.332 (×104 meters). This means that in the case when an individual's activity center is 3320 meters from the detector gives a detection probability of 0.6 without taking into account the sampling effort dependent baseline encounter probability. The SECR model estimated the wolf abundance at 70 individuals (95% Bayesian Credible Interval; BCI = 50-90; Table S1) on the effective sampling area. The estimated mean density of wolves was 2.35 individuals / 100 km^2 (95%BCI = 1.68-3.03). Downscaling the abundance estimates from the SECR effective sampling area to the sampling area of CMR showed comparable wolf abundances in S3$_{sa}$ and S3$_{la}$ as well as good overlap in the confidence intervals (Table 1).

Table S2. Posterior mean estimates of the SECR model parameters to estimate wolf density. Alpha1 (α1) and alpha2 (α2) are the model parameters of the sampling effort covariate, psi (ψ) is the parameter of data augmentation and sigma (σ) is the Gaussian scale parameter of the half-normal detection probability function.

Parameters	Mean	SD	Lower BCI bound (2.5%)	Upper BCI bound (97.5%)
Density ($\hat{D}$)	2.35	0.36	1.68	3.03
alpha1 (α1)	-0.009	0.238	-0.472	0.46
alpha2 (α2)	0.18	0.071	0.042	0.318
psi (ψ)	0.305	0.055	0.201	0.413
sigma (σ)	0.332	0.026	0.285	0.384

References

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