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Appendix 1

Parameterization of multi-event models using shared and non-shared DNA monitoring data.

Table A1. Model selection results for Norway (NO SHARE design).

Table A2. Model selection results for Sweden (NO SHARE design).

Figure A1. Time and sex-specific detection probability estimates.

Figure A2. Growth rate estimates from den counts and DNA in Norway.

Figure A3. Growth rate estimates from den counts and DNA in Sweden.

Parameterization of multi-event models using shared and non-shared DNA monitoring data

Data-sharing scenario

In the case of an integrated design, all wolverines were potentially observable while alive, irrespective of their transition across the Norway–Sweden border, as a result of the data-sharing between the two monitoring programs. The resulting model structure we comprised seven possible states:

- 1- Alive and highly detectable in Norway
- 2- Alive and lowly detectable in Norway
- 3- Alive and highly detectable in Sweden
- 4- Alive and lowly detectable in Sweden
- 5- Legally harvested in Norway
- 6- Recently dead for other causes
- 7- Dead (absorbing state)

We decomposed the whole process into its four main probabilistic components: initial state probability, probability of performing a geographic transition, survival probability, and event probability. First, we constructed a matrix I to describe the probability for each newly marked individual of being in a given state at first capture:

$$I = [\pi_1 \quad \pi_2 \quad \pi_3 \quad \pi_4 \quad 0 \quad 0 \quad 0]$$

Then, at each session, each individual still present in the population was allowed to perform a transition between Norway and Sweden. This process resulted in the following transition matrix T :

$$T = \begin{bmatrix} 1 - \gamma_{NS} & 0 & \gamma_{NS} & 0 & 0 & 0 & 0 \\ 0 & 1 - \gamma_{NS} & 0 & \gamma_{NS} & 0 & 0 & 0 \\ \gamma_{SN} & 0 & 1 - \gamma_{SN} & 0 & 0 & 0 & 0 \\ 0 & \gamma_{SN} & 0 & 1 - \gamma_{SN} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

where γ_{NS} is the probability to move from Norway to Sweden, and γ_{SN} the probability to move from Sweden to Norway. For the scopes of our analysis, we considered the geographic transition probabilities γ to be not time dependent. Also, we assumed that an individual in a given class of detectability did not change it when moving from one geographical state to the other, meaning that the individual heterogeneity in detection was not country-dependent.

After the transition process, we accounted for survival including the probability for each individual to die for different causes:

$$S_t = \begin{bmatrix} \phi_{1,t} & 0 & 0 & 0 & H_{1,t} & 1 - \phi_{1,t} - H_{1,t} & 0 \\ 0 & \phi_{2,t} & 0 & 0 & H_{2,t} & 1 - \phi_{2,t} - H_{2,t} & 0 \\ 0 & 0 & \phi_{3,t} & 0 & 0 & 1 - \phi_{3,t} & 0 \\ 0 & 0 & 0 & \phi_{4,t} & 0 & 1 - \phi_{4,t} & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

where ϕ is the state and time-dependent survival probability, whereas H is the probability to die by legal harvest. It should be noted that such probability is set to zero for individuals in states three and four (Sweden), as no legal harvest occurred in Sweden during the whole study period.

Finally, we considered four possible detection events: detected in Norway, detected in Sweden, reported as legally shot, and not detected. We then built the following event matrix E :

$$E_t = \begin{bmatrix} p_{1,t} & 0 & 0 & 1 - p_{1,t} \\ p_{2,t} & 0 & 0 & 1 - p_{2,t} \\ 0 & p_{3,t} & 0 & 1 - p_{3,t} \\ 0 & p_{4,t} & 0 & 1 - p_{4,t} \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

where $p_{z,t}$ are the state and time-dependent detection probabilities. Detection probability in state five (dead for legal harvest) was set to one, as all legally shot wolverines were reported to the authorities, whereas states six (recently dead for other causes) and seven (the absorbing state) were parameterized as unobservable.

No data-sharing scenario

When simulating two isolated monitoring programs and no data sharing between Norway and Sweden, a separate analysis was performed for each of the two countries. In this case, sex possible states were included in parameterization, as the use of two classes of heterogeneity in detection for the unobservable state made no sense. They are listed for the case of analyzing Norwegian data:

- 1- Alive and highly detectable in Norway
- 2- Alive and lowly detectable in Norway
- 3- Alive in Sweden
- 4- Legally harvested in Norway
- 5- Recently dead for other causes

6- Dead (absorbing state)

The initial state, transition, survival, and event matrices looked as follow:

$$T = \begin{bmatrix} 1 - \gamma_{NS} & 0 & \gamma_{NS} & 0 & 0 & 0 \\ 0 & 1 - \gamma_{NS} & \gamma_{NS} & 0 & 0 & 0 \\ \gamma_{SNh} & \gamma_{SNI} & 1 - \gamma_{SNh} - \gamma_{SNI} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$$S_t = \begin{bmatrix} \phi_{1,t} & 0 & 0 & H_{1,t} & 1 - \phi_{1,t} - H_{1,t} & 0 \\ 0 & \phi_{2,t} & 0 & H_{2,t} & 1 - \phi_{2,t} - H_{2,t} & 0 \\ 0 & 0 & \phi_{3,t} & 0 & 1 - \phi_{3,t} & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$$E_t = \begin{bmatrix} p_{1,t} & 0 & 1 - p_{1,t} \\ p_{2,t} & 0 & 1 - p_{2,t} \\ 0 & 0 & 1 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix}$$

Table A1. Model selection for the analysis of wolverine population size in southern Norway 2002–2013. The analysis is based on the temporary-emigration design including only Norwegian data: $\pi 1$ is a model with one class of heterogeneity; t is a country-specific time effect; effort is the total number of km driven inside each home range; border dist. is the distance between each individual’s sampling center and the national border.

Model N.	Survival	Harvest rate	Transition	Detection	k	deviance	QAIC	DQAIC
1	$\pi 1 + \text{sex}$	sex	border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	22	2457.565	2501.565	0
2	$\pi 1 + \text{sex} + \text{time}$	sex + time	border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	42	2421.228	2505.228	3.663
3	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	43	2420.520	2506.520	4.955
4	$\pi 1 + \text{sex}$	sex	border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	25	2456.585	2506.585	5.020
5	$\pi 1 + \text{time}$	time	border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	40	2427.319	2507.319	5.754
6	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort} + \text{dendist}$	44	2420.452	2508.452	6.887
7	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{sex} + \text{time} + \text{effort} + \text{dendist}$	47	2418.326	2512.326	10.761
8	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{sex} + \text{effort}$	33	2462.070	2528.070	26.505
9	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{sex} + \text{time}$	42	2446.184	2530.184	28.619
10	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex+border dist.	$\pi 1 + \text{time} + \text{effort}$	42	2452.577	2536.577	35.012
11	$\pi 1 + \text{sex} + \text{time}$	sex + time	sex	$\pi 1 + \text{sex} + \text{time} + \text{effort}$	42	2464.180	2548.180	46.615

Table A2. Model selection for the analysis of wolverine population size in southern Sweden 2002–2013. The analysis is based on the temporary-emigration design including only Swedish DNA data: $\pi 1$ is a model with one class of heterogeneity; t is a time effect; effort is the total number of km driven inside each individual’s home range; border dist. is the distance between each individual’s sampling center and the national border.

Model N.	Survival	Transition	Detection	k	deviance	QAIC	Δ QAIC
1	$\pi 1 + \text{sex}$.	$\pi 1 + \text{sex} + \text{time}$	17	945.321	979.321	0
2	$\pi 1 + \text{sex}$	border.dist	$\pi 1 + \text{sex} + \text{time}$	18	945.109	981.109	1.788
3	$\pi 1$.	$\pi 1 + \text{sex} + \text{time}$	16	950.301	982.301	2.980
4	$\pi 1 + \text{sex} + \text{time}$.	$\pi 1 + \text{sex} + \text{time}$	27	935.068	989.068	9.746
5	$\pi 1 + \text{sex} + \text{time}$	borderdist	$\pi 1 + \text{sex} + \text{time}$	28	934.800	990.800	11.477
6	$\pi 1 + \text{sex} + \text{time}$.	$\pi 1 + \text{sex} + \text{time}$	29	933.491	991.491	12.170
7	$\pi 1 + \text{sex} + \text{time}$	sex	$\pi 1 + \text{sex} + \text{time}$	29	934.778	992.778	13.45
8	$\pi 1 + \text{sex} + \text{time}$.	$\pi 1 + \text{sex} + \text{time}$	29	934.935	992.93	13.614
9	$\pi 1 + \text{sex} + \text{time}$.	$\pi 1 + \text{sex}$	17	960.024	994.024	14.708
10	$\pi 1 + \text{sex} + \text{time}$	sex + border dist.	$\pi 1 + \text{sex} + \text{time}$	30	934.365	994.365	15.049
11	$\pi 1 + \text{sex} + \text{time}$.	$\pi 1 + \text{sex}$	26	942.535	994.535	15.213

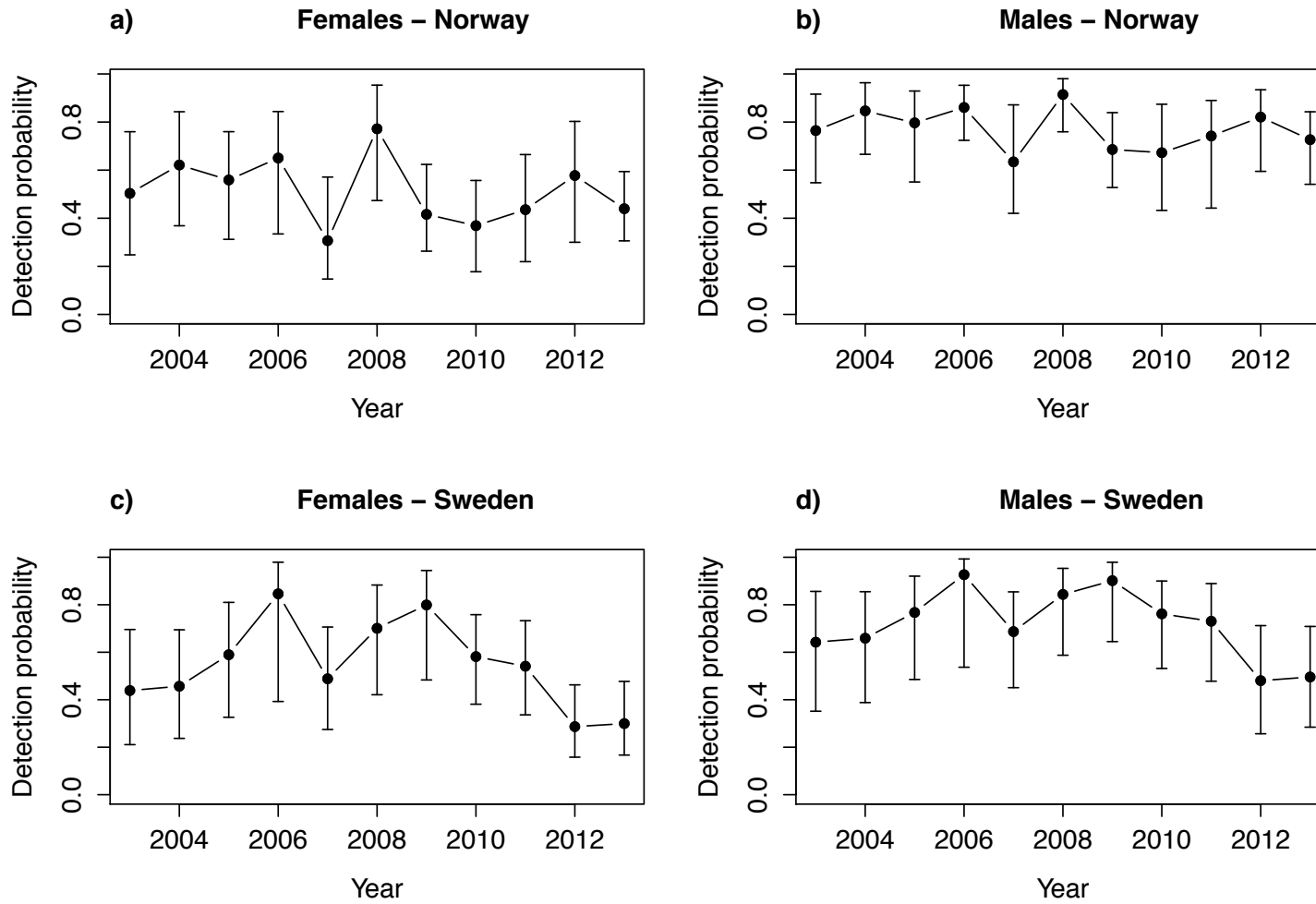


Figure A1. Detection probability estimates for female (a, c) and male (b, d) wolverines in southern Scandinavia between 2003–2012, based on non-invasive genetic sampling and capture–recapture modeling (model 1 in Table 1). Estimates are shown separately for Norway (a, b) and Sweden (c, d).

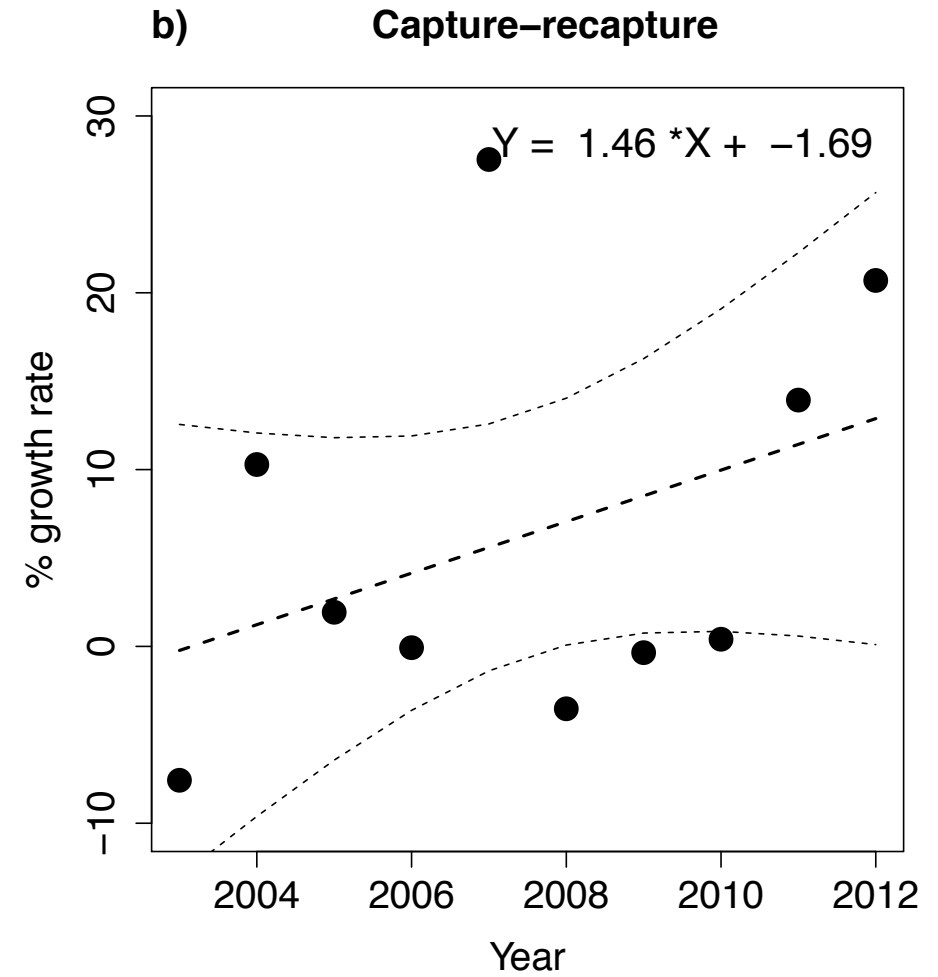
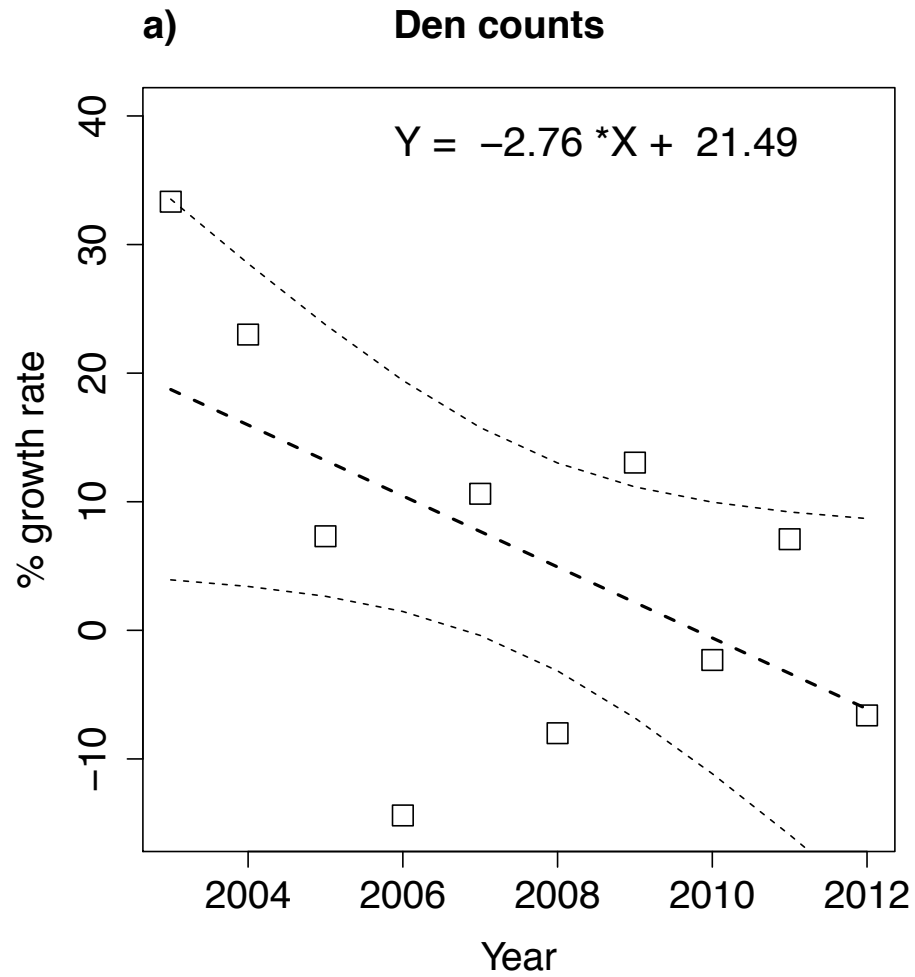


Figure A2. Annual estimates of population growth rate in southern Norway (2003–2012) derived from den counts (a) and DNA-based capture–recapture modeling (b).