## Supplementary materials

**Non-invasive molecular survey of sarcoptic mange in wildlife: diagnostic performance in wolf faecal samples evaluated by multievent capture-recapture models**

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**File S1. Methodological approach for multievent capture-recapture model**

Assuming the initial state vector *IS*, the survival matrix *S*, the transition matrix *T*, the detection matrix *D*, the test matrix *M* and the event matrix *B* [1]. If $\pi$ denotes the proportion of newly marked individuals in the state M+ and 1- $\pi$ in state M-, $\varphi$ the probability that an individual survives from *t* to *t+1*, $\psi$ the probability that it changes state, *p* the detection probability of an individual, *m* the probability that an individual sample is tested for the presence of *S. scabiei* DNA and *b* the probability that it is assigned a given observation:

$S =$

| | M+ | M- | D |
|---|---|---|---|
| M+ | $\Phi$ | 0 | 1- $\Phi$ |
| M- | 0 | $\Phi$ | 1- $\Phi$ |
| D | 0 | 0 | 1 |

$T =$

| | M+ | M- | D |
|---|---|---|---|
| M+ | 1- $\psi$ | $\psi$ | 0 |
| M- | $\psi$ | 1- $\psi$ | 0 |
| D | 0 | 0 | 1 |

*D* =

| | ND | M+ | M- |
|---|---|---|---|
| M+ | 1-*p* | *p* | 0 |
| M- | 1-*p* | 0 | *p* |
| D | 1 | 0 | 0 |

*M* =

| | ND | M+ tested | M- tested | Not tested |
|---|---|---|---|---|
| ND | 1 | 0 | 0 | 0 |
| M+ | 0 | 1- *m* [(a)] | 0 | *m* [(a)] |
| M- | 0 | 0 | 1- *m* [(a)] | *m* [(a)] |

*B* =

| | 0 | 1 | 2 | 3 |
|---|---|---|---|---|
| ND | 1 | 0 | 0 | 0 |
| M+ tested | 0 | 1-*b* | *b* | 0 |
| M- tested | 0 | 1- *b* [(b)] | *b* [(b)] | 0 |
| Not tested | 0 | 0 | 0 | 1 |

Fixed values in the most supported model:

[(a)] $m$=0.247 (the proportion of samples not tested for mange)

[(b)] $b$=0

**References:**


1. Pradel, R. Multievent: an extension of multistate capture-recapture models to uncertain states. *Biometrics* **2005**, *61*, 442–447, doi:10.1111/j.1541-0420.2005.00318.x.

**Table S1. Parametrizations of the most supported model and models with ΔAICc<4.** Differences to the most supported model highlighted in bold.

| | Model parametrization | | | | | nP | Deviance | AICc | ΔAICc |
|---|---|---|---|---|---|---|---|---|---|
| # | **Survival** | **Transition between states** | **Detection** | **Test for mange** | **State assignment** | | | | |
| 1 | Age 1: constant<br>Age 2: constant | Prob. M+ to M- constant<br>Prob. M- to M+ temporal covariate seroprevalence same year | Constant | Prob. not being tested = 0.247 | Prob. M- test positive = 0 | 8 | 1,099.02 | 1,115.46 | 0 |
| 2 | Age 1: constant<br>**Age 2: mange effect** | Prob. M+ to M- constant<br>Prob. M- to M+ temporal covariate seroprevalence same year | Constant | Prob. not being tested = 0.247 | Prob. M- test positive = 0 | 9 | 1,097.84 | 1,116.40 | 0.94 |
| 3 | Age 1: constant<br>**Age 2: mange and sex effect** | Prob. M+ to M- constant<br>Prob. M- to M+ temporal covariate seroprevalence same year | Constant | Prob. not being tested = 0.247 | Prob. M- test positive = 0 | 10 | 1,096.80 | 1,117.48 | 2.02 |
| 4 | Age 1: constant<br>Age 2: constant | Prob. M+ to M- constant<br>Prob. M- to M+ temporal covariate seroprevalence same year | Constant | Prob. not being tested = 0.247 | **No constraints** | 9 | 1,099.02 | 1,117.57 | 2.11 |
| 5 | **Age 1: mange effect**<br>**Age 2: mange effect** | Prob. M+ to M- constant<br>Prob. M- to M+ temporal covariate seroprevalence same year | Constant | Prob. not being tested = 0.247 | Prob. M- test positive = 0 | 10 | 1,097.84 | 1,118.52 | 3.06 |

nP, number of estimable parameters; ΔAICc, difference between the AICc of the current model and that of the most supported model