

Population densities and home range of the vulnerable Pyrenean brook newt in its core aquatic habitat

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Supplementary material

Text S1. Methodology followed to assess bias in estimated population parameters when using photo-identification for the individual identification of the Pyrenean brook newt.

Context

When studying wildlife population dynamics, false negative errors (i.e., failure to identify a recaptured individual) and false positive errors (i.e., incorrect matching of two different individuals) can differently affect inferences about demographic parameters (Royle and Link, 2006; Miller et al., 2011). Using natural markings, Stevick et al. (2011) showed that false negative errors positively bias abundance estimates, as one recaptured individual not recognized leads to an additional individual in the estimation of total abundance. False positive errors result in large biases when estimating demographic parameters, as they lead to over-estimation of individual capture probability (Schwarz and Stobo, 1999), due to wrongly assigning recaptures to known individuals. Renet (2019) reported a 3% over-estimation of population size of the cryptic salamander *Hydromantes strinatii*, with a false rejection rate (i.e., false negative error; FRR) of 0.04% using Wild-ID software. In Dalibard et al. (2021), we reported a FRR of 0.07% and a false acceptance rate (i.e., false positive error; FAR) of 0.04% using AmphIdent for the photo-identification of Pyrenean brook newt. The bias generated by these errors rates on the estimation of the demographic parameters had not been assessed yet. Below, we describe our methodology and present our main results.

Methods

To assess the bias on the estimation of population density (D), individual detection probability (g_0) and spatial scale of detection (σ) induced by photo-identification, 100 CMR datasets were simulated to which we applied the FRR and FAR obtained in Dalibard et al. (2021) (see above). The CMR datasets were built assuming a population of 3463

individuals, five occasions of sampling with an individual detection probability of 0.09 and a spatial scale of detection of 10m. Those assumptions were based on the estimates provided by the best fitted SECR closed capture model, adapted for linear habitat, in Fougax in 2018.

For each row of the CMR datasets (i.e., individual capture), false rejection and false acceptance errors were simulated successively, following a Bernoulli distribution with a probability of 0.07 and 0.04, respectively. When an error was simulated for an individual capture, the CMR dataset was modified accordingly to account for this error. A new individual with a new identification number was added for a rejection error whereas the identification number of the individual captured was replaced by the identification number of an individual captured during a previous occasion for an acceptance error. We assumed that an acceptance error could not occur (1) between individuals of different sexes because sexual dimorphism is strong in the Pyrenean brook newt, and (2) between two individuals already known (i.e., captured during previous occasions), as Dalibard et al. (2021) highlighted a slight FAR (i.e., 0.01) between known individuals (named FAR2 in Dalibard et al., 2021).

From the real (i.e. true) and modified (i.e. observed) CMR datasets, SECR closed capture models were fitted. Mean (\pm SD) estimated parameters (i.e., D , g_0 and σ) for true and observed datasets were compared to assess bias generated by photo-identification.

CMR datasets were simulated using the package *SECRlinear* (Efford, 2017) in R (R Core Team, 2018) and models were fitted with the function `secr.fit`.

Results and discussion

Mean bias (\pm SD) between true and observed estimated parameters, after 100 repetitions, was 13% for the density (0.135 ± 0.037) and g_0 (-0.125 ± 0.032) (over- and underestimation, respectively), and negligible for σ ($<1\%$) (table S1).

Table S1. Minimum, maximum and mean of true and observed estimated parameters accross the 100 repetitions. D = density, g_0 = individual detection probability and σ = spatial scale of detection.

	D		g_0		σ	
	True	Observed	True	Observed	True	Observed
Min	2801	3243	0.072	0.063	8.48	8.36
Max	3974	4738	0.11	0.095	11.58	11.65
Mean	3501	3971	0.089	0.078	10	10.01

These results indicate that using AmphIdent to identify individually each Pyrenean brook newt leads to an overestimation of population density of 13% and decreases individual detection probability by 13%. The negligible bias detected for the estimation of the spatial scale of detection indicates that there is no spatial incidence of identifications errors. Hence, identification errors should not cause significant movements of individuals, which in turn could bias estimates of home-range size. Estimates of home-range are likely to be robust. The 13% overestimation of population density we found here is four times higher than the one found by Renet et al. (2019) for the identification of *Hydromantes strinatii* using a very similar approach but another identification software. It is however twenty times lower than the overestimation of

population size reported by Morrison et al. (2016) for the Wyoming toad (*Anaxyrus baxteri*).

Even if population densities were overestimated by about 13%, they remain within the 95% confidence interval. Thus, we do believe that error rates estimated for the Pyrenean brook newt are acceptable and should not affect greatly the estimation of parameters derived from SERC models.

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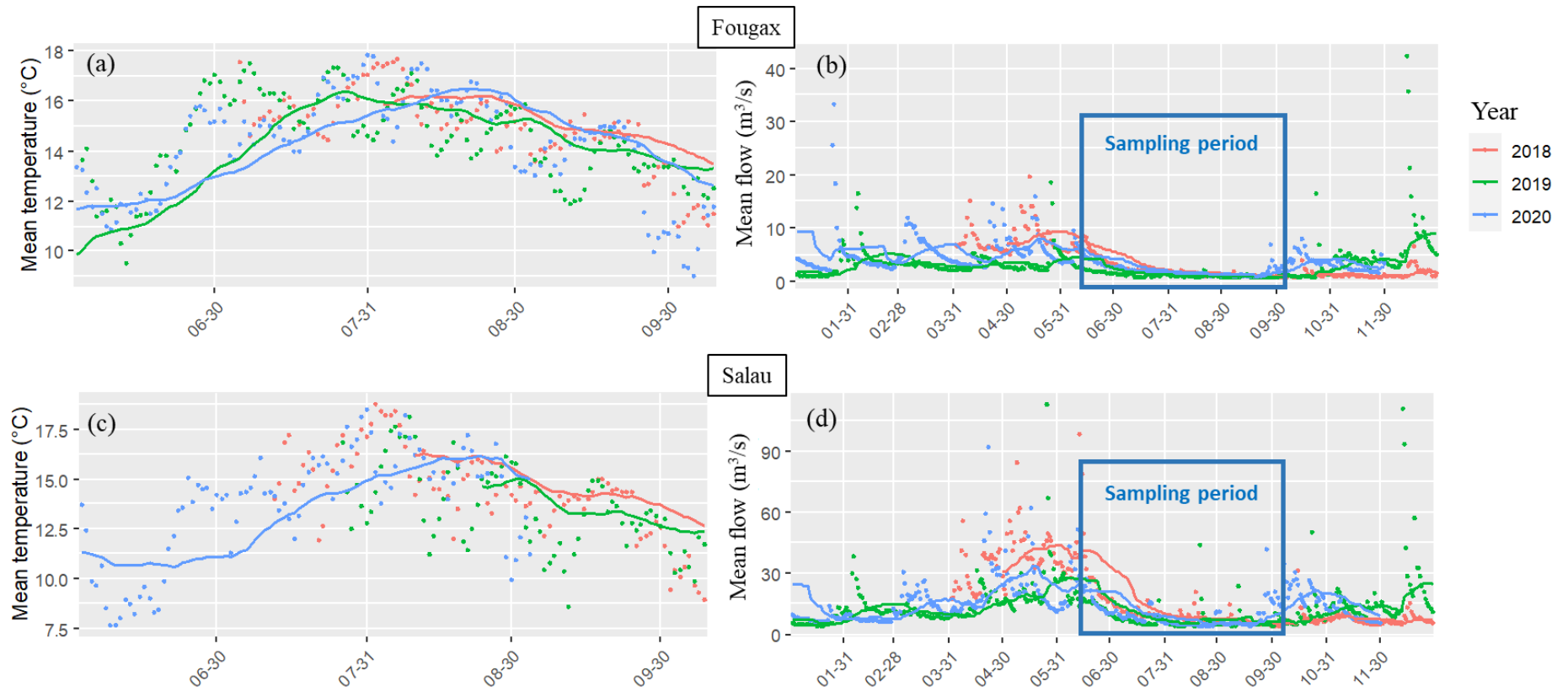


Figure S1. Measured *in situ* water temperature and flow at gauging stations closest to Fougax (Grand-Hers station in Belestia) and Salau (Salat station in Soueix), in 2018 (red), 2019 (green) and 2020 (blue). Dots display mean daily temperature and flow values while lines display running mean over the last 30 days. Temperature values are shown for the sampling period only while flow values are shown over the whole study period (sampling period is delineated by a blue box).