Supplement

Table S1. Logger types used in the different northern fulmar colonies

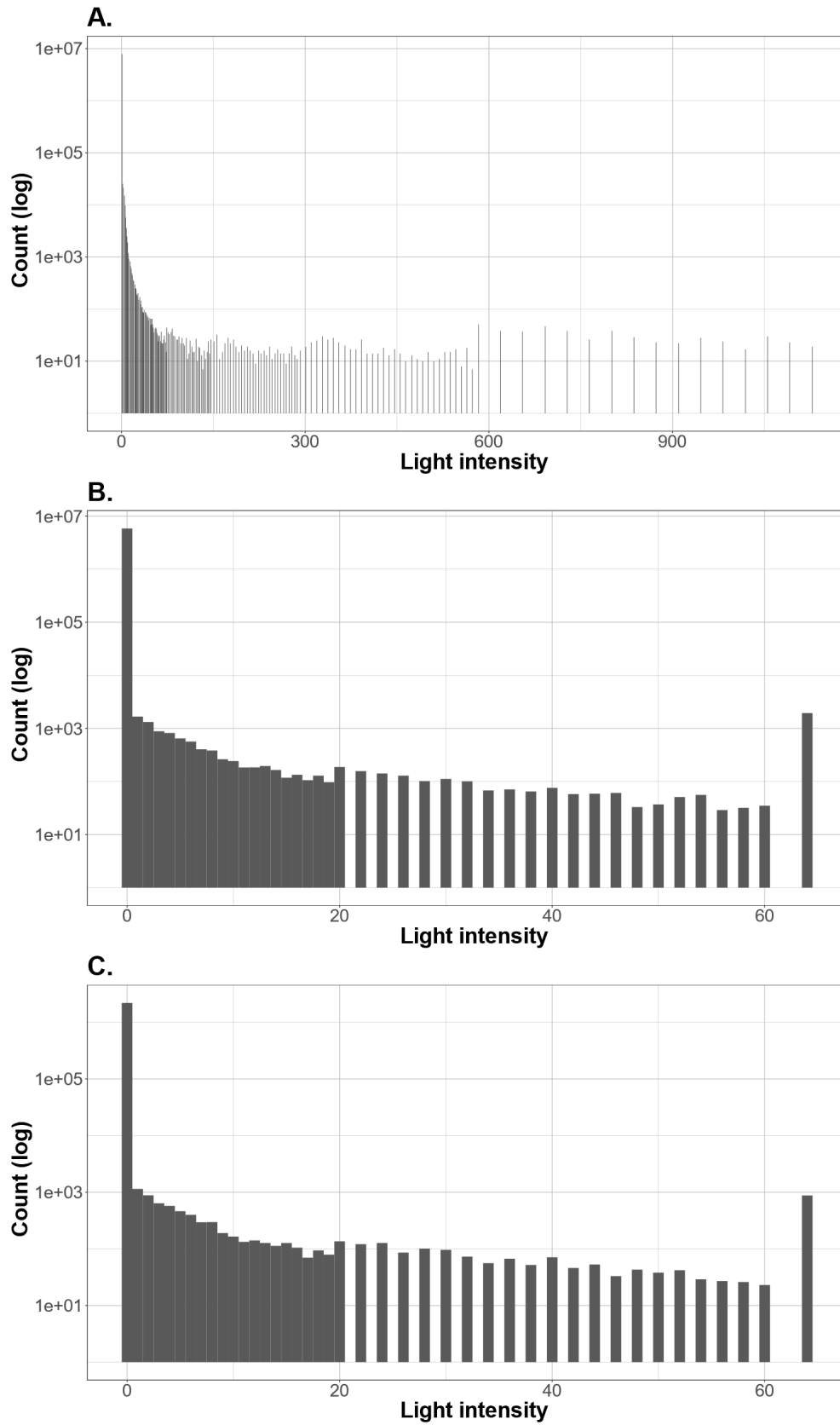|	Alke-fjellet	Bjørn-øya	Breida-fjordur & Reykja-nes	Eyn-hallow	Faroe Islands	Jan Mayen	Jarstei-nen	Langa-nes & Skjál-fandi & Grim-sey	Papey & Hólma-nes	**Total**
Bio-track High	5	6	0	97	0	14	6	15	0	**143**
Bio-track Low	4	39	0	70	7	32	6	43	0	**201**
Mi-grate Tech-nology	14	24	17	72	14	41	9	47	11	**249**
Total	**23**	**69**	**17**	**239**	**21**	**87**	**21**	**105**	**11**	**593**

A.

B.

C.

Fig. S1. Frequency distributions of light levels recorded at night for (A) the Migrate Technology group, (B) the Biotrack low group and (C) the Biotrack high group
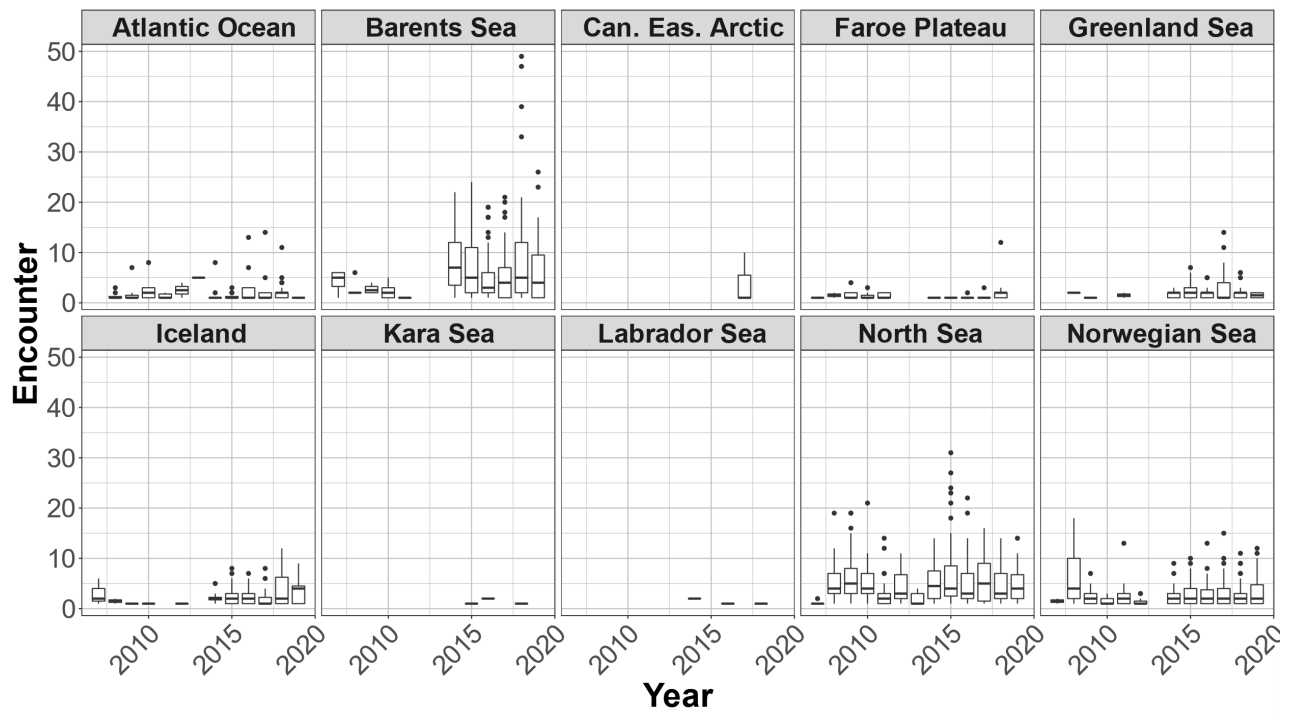
Fig. S2. Yearly variation in the number of encounters between northern fulmars and fishing boats in the different wintering areas
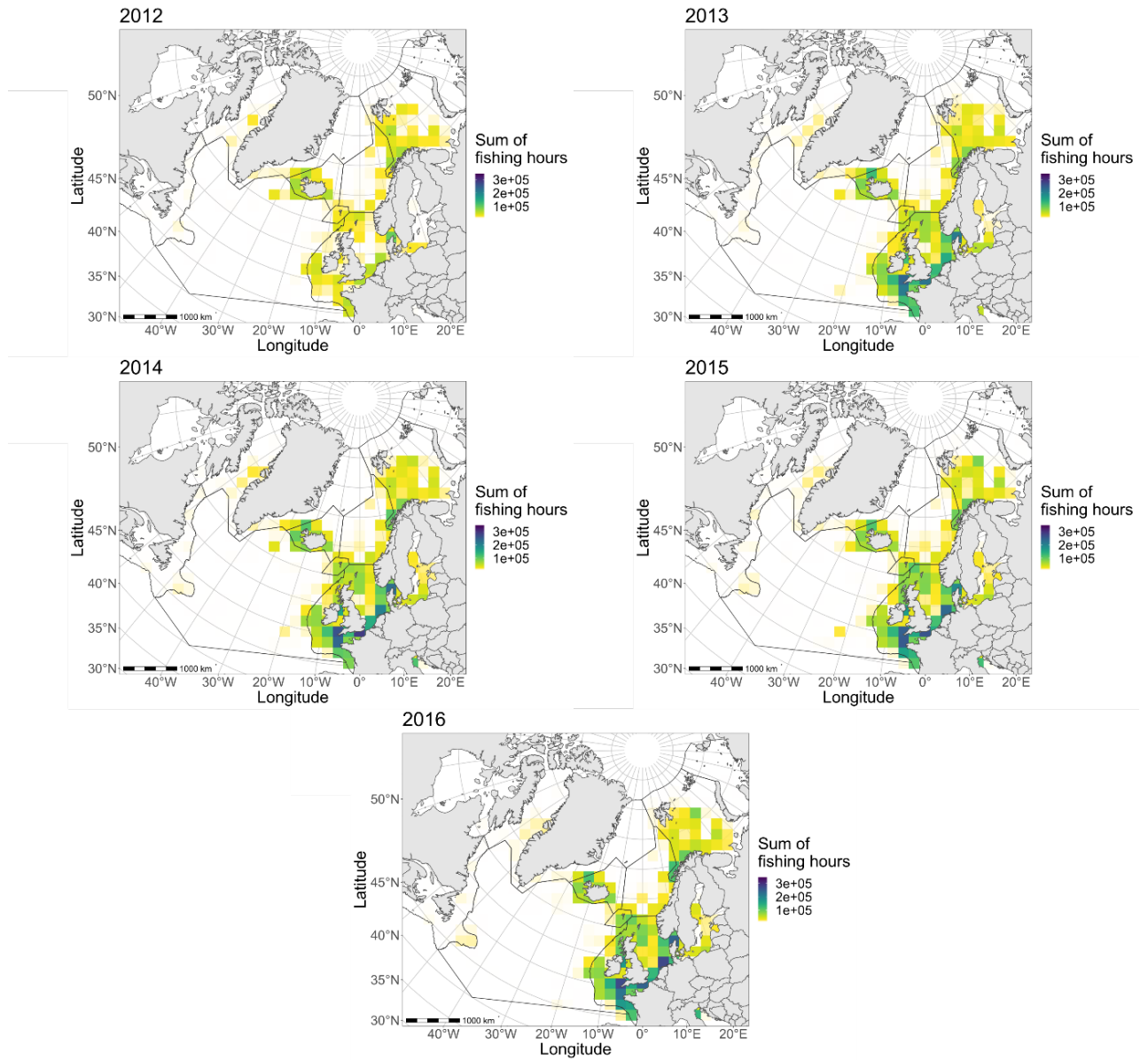
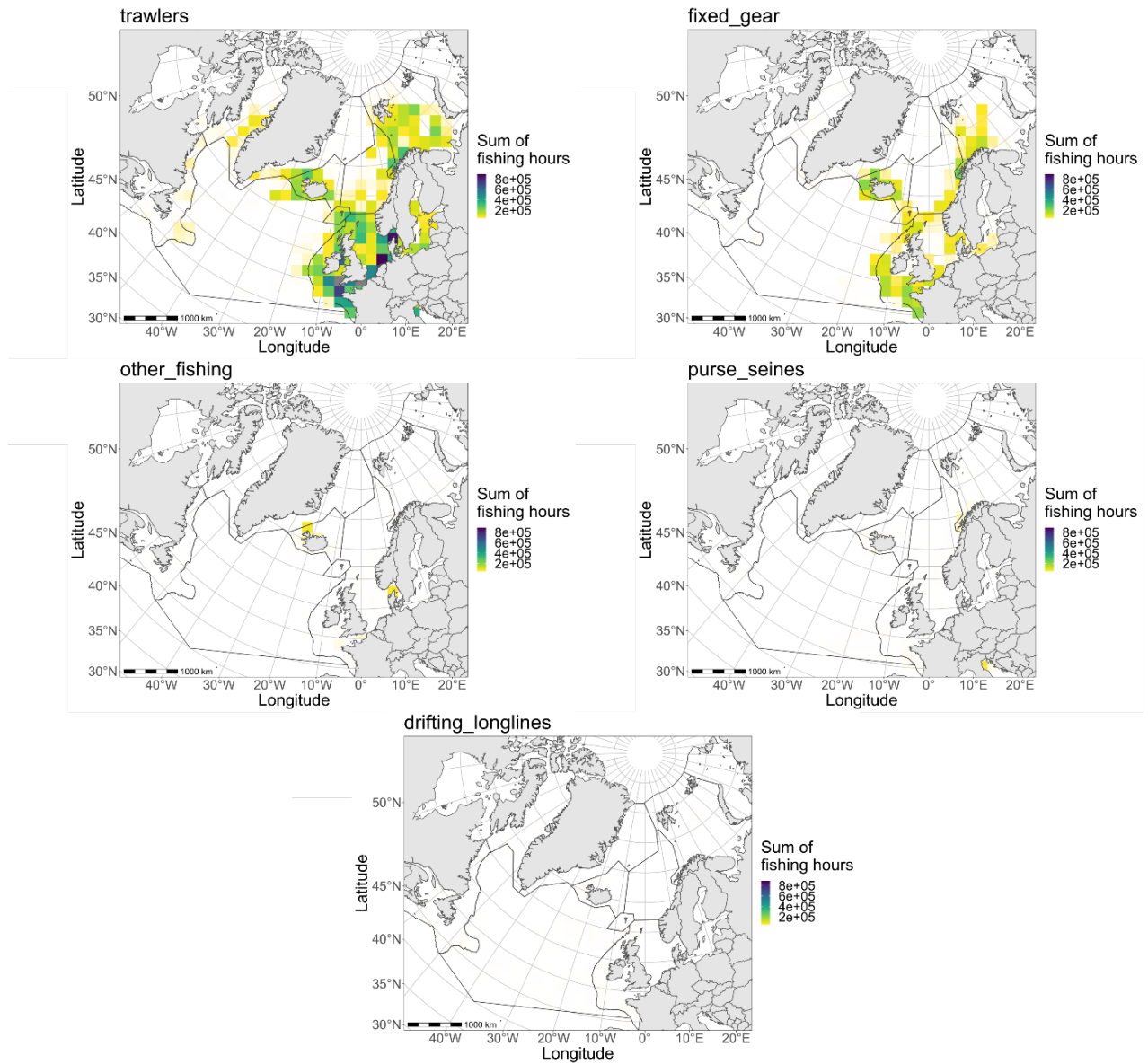Fig. S3. Interannual variation of fishing effort

Fig. S4. Relative importance of the different vessel types in the Global Fishing Watch dataset
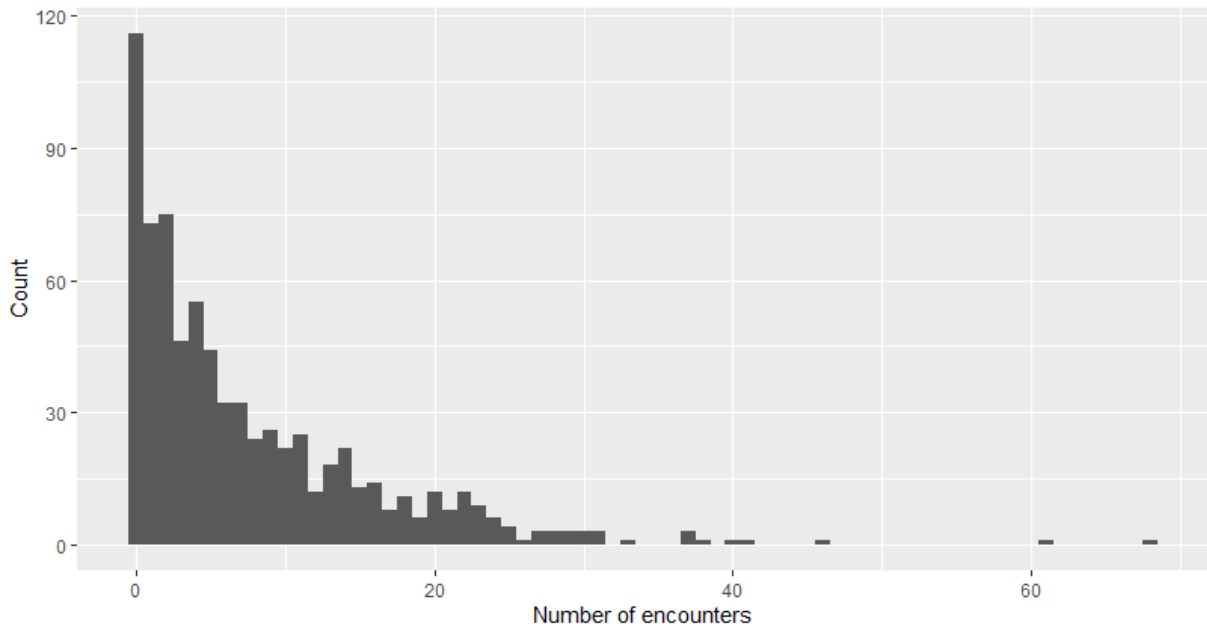
Fig. S5. Frequency distribution of the number of encounters between northern fulmars and fishing boats per track (n = 751)
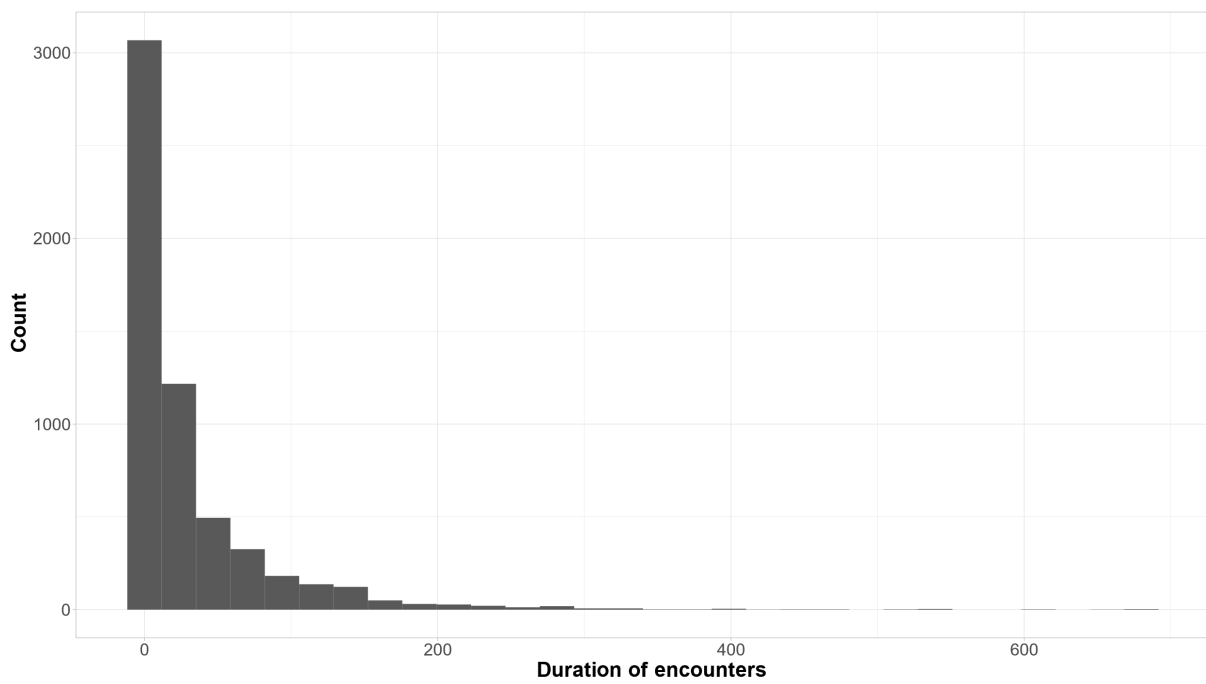

Fig. S6. Frequency distribution of the duration of encounters between northern Fulmars and fishing boats in minutes (n = 5750)

Text S1. Using the Bout Ending Criterion to regroup light peak detections in encounters

We assessed whether 2 light detections belonged to the same encounter by using the Bout Ending Criterion method (BEC) in the DiveMove R package (Luque & Guinet 2007). This method has been developed to analyze diving data and group successive dives into bouts, defined as a succession of dives preceded and followed by a longer resting period. We adapted the method to calculate the amount of time in which 2 light peaks could be considered as belonging to the same encounter. Firstly, we calculated in every track the time between 2 consecutive detections. We did not consider isolated detection in our calculation (i.e. detections that are separated by 1 d or more from the previous detection). The histogram of duration between detections can be described using 2 processes operating on different time scales. At the small scale, light detections belonging to the same encounter are separated by brief and similar intervals. Detections separated by longer intervals represent different encounter events (or bouts). These 2 processes follow a random Poisson distribution, and BEC is used to find the time interval separating the 2 processes. Using the bouts.mle() function, we estimated this BEC, which is calculated with the maximum of likelihood approach as :

$$BEC = \frac{1}{\lambda_f - \lambda_s} log \frac{p\lambda_f}{(1-p)\lambda_s} \tag{S1}$$

With λ representing the probability of an event occurring in the fast (small scale, λ_f) or slow process (large scale, λ_s) per unit of time. *p* is a mixing parameter showing the proportion of fast to slow process events in the sample. The initial value of λ is obtained using the broken stick method (Sibly et al. 1990). We calculated this BEC for each logger group: 117.04 min for the Migrate Technology group, 107.42 min for the Biotrack low group and 141.8 min for the Biotrack high group.

Literature Cited

Sibly RM, Nott HMR, Fletcher DJ (1990) Splitting behaviour into bouts. Anim Behav 39:63–69
https://doi.org/10.1016/S0003-3472(05)80726-2

Luque S, Guinet C (2007) A maximum likelihood approach for identifying dive bouts improves accuracy, precision and objectivity. Behaviour 144:1315–1332
https://doi.org/10.1163/156853907782418213