Appendix S1 - Species acoustic identification

All recordings from both bat detector and mobile devices were analysed manually using BatSound (https://batsound.com). Acoustic analysis of the entire dataset was conducted by one of the authors (F.G.), and to ensure accuracy, a blind check of 20% of recordings was carried out by an external expert operator (E.P.), who confirmed the identifications. In particular, a random selection of at least 20% of recordings for each species was checked, with a minimum of 50 recordings per species where possible. For species whose total number of recordings was less than or equal to 50, all recordings were checked.

Species acoustic identification was performed following methods described by Barataud (2020), Russ (2021), and Middleton et al. (2022). Only signals entirely or almost entirely falling in the frequency range recordable by mobile devices were considered.

Tadarida teniotis and *Nyctalus* species were identified in most cases from echolocation sequences, among which the most characteristic were those composed of quasi-constant frequency (QCF) signals (i.e., signals with a bandwidth BW < 5 kHz). For *Nyctalus* species, a distinctive feature was the alternation of signals with slightly different frequency at maximum energy (FME), which allowed them to be distinguished from echolocation sequences of *Eptesicus*, *Tadarida* and *Vespertilio* species (Barataud 2020). To distinguish among the three *Nyctalus* species occurring in Europe based on their echolocation sequences, we adopted the following criteria:

- *N. leisleri*: sequences composed of signals with BW ≤ 3 kHz and end frequency EF > 21.5;
- *N. noctula*: sequences composed of signals with BW ≤ 3 kHz and EF between 17.5 and 19.5 kHz;
- *N. lasiopterus*: sequences composed of signals with BW ≤ 3 kHz and EF between 14.0 and 17.0 kHz.

Sequences composed of signals with intermediate acoustic parameters were classified as undetermined. Echolocation sequences with no FME alternation characteristic of the *Nyctalus* genus, and with an EF below 14 kHz, were attributed to *T. teniotis*.

In some cases, characteristic social calls of *Nyctalus* species (Pfalzer 2002; Middleton et al. 2022) aided in confirming their identification. Particularly, we considered type C.d1 (male advertisement calls), D1 and D2 social calls of *N. leisleri* and *N. noctula*, as their shapes and frequency ranges are well documented in literature (Middleton et al. 2022).

Hypsugo savii and *Pipistrellus* species were identified based on their social calls since echolocation calls are above the range recordable by mobile devices (end frequencies EFs between 30-60 kHz depending on the species considered; Barataud 2020). Nardone et al. (2017) described in detail the social call repertoire of *H. savii*, therefore this work was used as a reference for this species. Particularly, type D calls were found to fall within the range detectable by mobile devices.

Type D social calls were also used to differentiate between *Pipistrellus* species (Pfalzer 2002; Jahelková et al. 2008; Piskorski & Sachanowicz 2021; Middleton et al. 2022). For *P. kuhlii*, *P. pipistrellus* and *P. pygmaeus*, these are short sequences (< 100 ms) of multiple components (usually 2-5). Differentiation among these three species is possible based on FME, taken as an average across the whole sequence, and EF of the lowest call within the sequence (Middleton et al. 2022). However, variability in these parameters is known to occur, leading to some overlap. Based on parameters provided by Middleton et al. (2022), we used the following criteria to differentiate among the three species:

- *P. kuhlii*: average FME < 15.5 kHz and EF of the lowest call < 14.0 kHz;
- *P. pipistrellus*: average FME between 16.0 and 19.0 kHz, and EF of the lowest call between 15.0 and 18.5 kHz;
- *P. pygmaeus*: average FME > 21.5 kHz and EF of the lowest call > 20 kHz.

Sequences with intermediate acoustic parameters were classified as undetermined. Type D social calls of *P. nathusii* are more complex and very characteristic (Jahelková et al. 2008; Middleton et al. 2022). Part *a* (or motif *a*) of these complex calls consists in a short sequence (50-150 ms) of multiple components (usually > 5 and up to 15) with increasing FME, which falls entirely or almost entirely within the mobile device detectability range (Jahelková et al. 2008; Russ 2021).

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