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# Comparing the results of four widely used automated bat identification software programs to identify nine bat species in coastal Western Europe

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**ABSTRACT.** Commercially available automated bat identification software packages are widely used in environmental studies to identify bat species from recordings of bat echolocation calls. Caution is, however, needed if the results are used without further verification, as the programs do not guarantee that the results are correct, and wrong species identifications often happen. Taking automated species identifications for granted might hence lead to erroneous conclusions in environmental studies.

The goal of our study was to objectively assess the performance of four commercially available and commonly used automated identification software programs by processing an identical reference dataset with all four programs. The reference dataset consisted of nine species selected based on their preference for open habitats in Western Europe or because they occur as vagrants at sea and therefore are vulnerable to the development of onshore and offshore wind farms. Offshore areas are being increasingly examined, as recent studies have identified possible conflicts of offshore wind farms and certain bat species.

In our test, we included two automated identification programs that have not yet been tested in other studies, and a reference dataset from a different geographical region (Western-Europe) with a different species composition compared to other studies. Our data hence add to the knowledge base needed for an appropriate assessment of the reliability of analytical software.

In general, BatIdent (77% correct species identifications) and Kaleidoscope (71%) seem to be relatively reliable while the performance of BatExplorer (31%) is relatively poor. SonoChiro correctly identified 65% of the sequences to species level. While the tested programs may be considered valuable tools to detect bat calls from the recordings, a trained bat expert needs to cross-check the automated species identifications to avoid erroneous conclusions. Our test hence affirms the conclusions of previous studies in Northern Europe and the USA.

KEYWORDS. Bats, Chiroptera, echolocation, automated bat identification software.

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## Introduction

Bats (Mammalia, Chiroptera) produce high frequency echolocation calls to collect information about their surroundings (NEUWEILER 1989; KALKO 1995; FENTON & SIMMONS 2014). Echolocation calls vary depending on the task (e.g., orientation, foraging) and the environment (OBRIST 1995).

To identify bat species from their echolocation calls, species-specific characteristics of the individual calls (e.g., frequency range, frequency of maximum energy, duration of the call) and of call sequences (e.g., time interval between consecutive calls) must be recognised (BARATAUD 2015; RUSSO et al. 2018). Overlap in these echolocation characteristics between species often makes species identification problematic (e.g., BARCLAY 1999; OBRIST 1995; RUSSO & VOIGT 2016; RUSSO et al. 2018). Therefore, manual identification requires a high degree of expertise and is highly time consuming. Bats are often studied with acoustic detectors registering echolocation calls (e.g., AHLÉN & BAAGØE 1999; PARSONS & SZEWCZAK 2009) as they allow gathering data on species distribution and abundance in a consistent way, over a longer period of time. Automating the analysis by means of machine learning algorithms (e.g., artificial neural networks, discriminant analysis) has been tested in the past (VAUGHAN et al. 1997; HERR et al. 1997; PARSONS & JONES 2000; RUSSO & JONES 2002) and has the advantage that large datasets can be analysed in a short time span. Commercially available automated bat identification software packages (e.g., SonoChiro, BatIdent, BatExplorer, Kaleidoscope) use a similar approach and are widely used in environmental studies. Caution is, however, needed if the results are used without reevaluation of the species identifications by a bat specialist (RUSSO & VOIGT 2016; RUSSO et al. 2018). Those programs do not guarantee that the results are correct, and wrong species identifications often happen. Taking automated species identifications for granted might hence lead to erroneous conclusions, and hence impact the decision-making process in conservation management and/or in the consenting process of environmental permits for new projects (e.g., wind farm siting).

Recently, the discussion on the prudency needed when using automated identification programs was started by RUSSO & VOIGT (2016) and RYDELL *et al.* (2017). LEMEN *et al.* (2015) further showed that there is low agreement between different automated identification programs when analysing an identical dataset. This study aims to contribute to this discussion by comparing the performance of four widely used automated bat identification software packages.

## Methodology

### **Research strategy**

Making an objective assessment of different automated identification software programs involves testing their performances by processing an identical dataset. This reference dataset can either be a set of unidentified call recordings that are manually processed by an expert, or recordings of specimens with absolute certainty of the species identity. In the current study, we used the latter.

This dataset was processed with four of the most commonly used automated species identification programs. The outcome was then compared with the correct identification of the reference data and scored based on the number of correct identifications. With this approach, we could identify for which genera and species the programs are performing well and for which the identification is more problematic.

### **Reference dataset**

For our analysis, we selected nine bat species that typically occur in open habitats in Western Europe or because they occur as vagrants at sea and are therefore often impacted by the development of onshore and offshore wind farms. Offshore areas are being increasingly examined, as recent studies have identified possible conflicts of offshore wind farms and certain bat species (LAGERVELD *et al.* 2014, 2017). The following species were selected: Northern bat *Eptesicus nilssonii*, serotine bat *Eptesicus serotinus*, pond bat *Myotis Dasycneme*, Daubenton's bat *Myotis daubentonii*, Leisler's bat *Nyctalus Leisleri*, common

Methods used to confirm the species identity of the reference recordings included in the test. N is the number of reference recordings of sequences of bat calls per species.

| Species                   | Method   | Ν  |
|---------------------------|--|----|
| Eptesicus nilssonii       | Distribution range (altitude)  | 16 |
| Eptesicus serotinus       | Visual confirmation  | 14 |
| Myotis dasycneme          | Visual confirmation  | 18 |
| Myotis daubentonii        | Visual confirmation  | 18 |
| Nyctalus leisleri         | Capture - release and visual confirmation  | 8  |
| Nyctalus noctula          | Visual confirmation and/or sequence includes social calls or other 100% species-specific calls | 18 |
| Pipistrellus nathusii     | Sequence includes social calls or other 100% species-specific calls                            | 19 |
| Pipistrellus pipistrellus | Capture – release  | 19 |
| Vespertilio murinus       | Sequence includes social calls or other 100% species-specific calls                            | 18 |

noctule Nyctalus noctula, common pipistrelle Pipistrellus pipistrellus, Nathusius' pipistrelle Pipistrellus nathusius and parti-coloured bat Vespertilio murinus.

The reference dataset consisted of 148 recordings of sequences of bat echolocation calls of known species, in open environments. The dataset contains no calls recorded in cluttered environments or social bat calls. Species identity was confirmed in several ways: a) by visual confirmation of the recorded bat, b) by capture and release of specimens (this was only the case for *N. leisleri* and *P. pipistrellus*), c) by making recordings outside the distribution range of other species (e.g., at high altitude to separate *E. serotinus* and *E. nilssonii*) and d) by focusing on social calls or other 100% species-specific calls included in certain recordings (BARATAUD, 2015) (Table 1). Additionally, two bat experts independently re-evaluated and confirmed the species identification of all reference recordings in the dataset based on the specific call characteristics given by BARATAUD (2015) and SKIBA (2009).

We made full-spectrum recordings with ecoObs Batcorders (types 2.0, 3.0 and 3.1; ecoObs GmbH, Germany) in .RAW format (sampling rate: 500 kHz, record quality: 20, threshold amplitude (sensitivity): -27 / -36 dB, post trigger: 400 ms, threshold frequency (sensitivity): 16 kHz). BatIdent can identify both .RAW and .WAV files. The other programs can only identify .WAV files, therefore we converted the .RAW files into .WAV format.

For automated identification of bat calls it is important to prevent the recording of reflecting echoes. Echoes of bat calls are similar to actual bat calls, but the characteristics of echoes are different and, as such, would lead to false identifications (RUNKEL & GERDING 2016). Therefore, we made recordings more than three meters from reflecting surfaces such as the ground surface, trees or water by installing the Batcorder on a rod or tower. The recordings were made in open environments with no foliage, buildings etc. in front of the microphone. An exception was made for *M. dasycneme* and *M. daubentonii*, as these species fly close to the water surface. For these species we installed the microphone of the Batcorder within 2 cm of the water surface to prevent excessive echo recordings. Consequently, our dataset consisted of high quality, independent recordings, optimized for the automated identification of bat calls.

### Data-processing with the different software programs

We selected four commercially available and commonly used automated bat identification software programs to analyse the reference dataset: BatIdent 1.5 (EcoObs GmbH), BatExplorer 1.11.4 (Elekon

AG, Switzerland), SonoChiro 4.0 (Biotope, France) and Kaleidoscope Pro 4.5.4 (Wildlife Acoustics Inc., U.S.A.). BatIdent works in combination with the program bcAdmin (EcoObs GmbH). bcAdmin searches for bat calls in recordings, and takes measures of all found calls. These are then used by BatIdent for the species (group) identification of the calls (ECOOBS 2014).

The programs were operated with the default settings. For Batident, these were a minimum average probability of species extraction of 0.6; and a minimum call count for species extraction of 3. For SonoChiro, the region was set to 'North, temperate'; the time expansion was x1; the minimum call duration equalled 0.5 ms; and sensitivity 7. For Kaleidoscope, signal of interest was 8–120 kHz for 2–500 ms with a maximum inter-syllable gap of 500ms; and a minimum of 2 pulses; for the classifier, the setting was bats of Europe 4.3.0 and a sensitivity of 'balanced (0)'. For BatExplorer, we used a crest factor of 6.0; a lower frequency limit of 15kHz; an upper frequency limit of 150 kHz; hysteresis of 0.95; intensity tolerance of 0.20; minimum call length of 1.0 ms, with a minimum call intensity of 10% and a frequency tolerance of 7kHz.

Only the programs SonoChiro and Kaleidoscope have the possibility to adjust the sensitivity. The programs were run with default settings, which is 7 for SonoChiro and 'balanced (0)' for Kaleidoscope. For those two programs we also ran the analysis with the least and most sensitive settings, being 1 and 10 for SonoChiro and 'more accurate (+1)' and 'more sensitive (-1)' for Kaleidoscope. The manuals of Kaleidoscope and SonoChiro do not provide more information on how these sensitivity settings could change the results.

The output of the four programs shows some differences. Each program renders an identification for every recording. BatExplorer suggests up to four alternative species, each with a probability. It is up to the user to select the correct species. BatIdent and SonoChiro also provide a likelihood of correct identification for each identification. Kaleidoscope gives a species name and in most cases one or even two alternative possibilities. SonoChiro outputs a species (sometimes with one or more alternative results) and a species-group (ENVsp = *Eptesicus, Nyctalus* and *Vespertilio* sp.; Myosp. = *Myotis* sp.; Plesp. = *Plecotus* sp.; Pip50 = *P. pipistrellus* and *P. pygmaeus*; Pip35 = *P. kuhlii, P. nathusii* and *Hypsugo savii*; BIOTOPE 2013). This can be useful for bat species with similar echolocation characteristics: the species identification might be wrong but the correct species-group might be given. BatIdent provides both a group identification (Pipistrelloid (= Pipistrellus, Miniopterus and Hypsugo); Nyctaloid (= *Nyctalus, Vespertilio, Eptesicus, Tadarida* and *Vespertilio*); Nycmi (= *N. leisleri, E. serotinus* and *V. murinus*); ECOOBS 2013) and a species identification. If BatIdent is unable to identify the recording to species level, only a group identification is given instead.

### Performance comparison of the software

We presented the results of all software programs as percentage of correctly identified species-groups and species to allow direct comparisons of the software performance. Alternative species, as suggested by BatExplorer, Kaleidoscope and SonoChiro were not taken into account as these could not be used in an objective comparison of the four programs.

Additionally, we investigated if the false identifications by the programs were random for all species or if certain species are more prone to misidentifications for the programs as compared to others.

Lastly, we compared the results of this study with the results of Rydell *et al.* (2017) for the three species (*E. nilssonii*, *M. dasycneme*, *M. daubentonii*) and the two programs (Kaleidoscope and SonoChiro) under consideration in both studies.

In comparison with other studies (LEMEN *et al.* 2015; RYDELL *et al.* 2017), we included two additional automated identification programs that had not yet been tested, and our reference data were collected in a different geographical region (Western-Europe) with a different species composition. Hence, our data significantly contribute to the validation of commonly used bat identification software.

## Results

The reference recordings were all analysed by the four programs. Five of the 148 recordings were erroneously classified as noise by SonoChiro, and three by Kaleidoscope. The differences in performance of the software packages in our test are large. The two programs that make an identification to species-group level, BatIdent and SonoChiro, did so correctly in 88% and 85% of the cases (Table 2), respectively. In 25 of the 148 recordings (i.e., 16.9%), BatIdent made an identification to the species-group level only. This was especially the case for recordings of *E. serotinus* and *N. leisleri, N. noctula* and *V. murinus*.

When rating the correct number of species-identifications in this test, BatIdent scored the best (77%), followed by Kaleidoscope (71%), SonoChiro (65%) and BatExplorer (31%) (Table 2). In this score, the species-group identifications of BatIdent were considered as a false result, even if the species in the recording is part of the outputted species-group. For five of the nine species we tested, BatIdent scored higher than 90%. This is the case for two species with Kaleidoscope and SonoChiro, but none with BatExplorer (Table 2).

Kaleidoscope is the program with the lowest number of false identifications at species level (10.7%), which can be explained by the higher number of cases where this program provides no identification at all (18%). For the other programs, this rate of 'NoIDs' is much lower. With BatIdent (22.7%), SonoChiro (34.7%) and BatExplorer (66.7%), the number of false identifications was considerably higher. Adjusting the Kaleidoscope sensitivity setting to 'more sensitive' significantly increases the percentage of correct species identifications to 80.7%. With the 'more sensitive' setting, 14 species were correctly identified, which had all been all classified as 'NoID' with both the 'balanced' and 'more accurate' settings. The performance of Kaleidoscope with the 'more accurate' setting is similar to the performance with the 'balanced' (default) setting, resulting in 70.7% and 71.3%, respectively, of correct species identifications.

Changes in the sensitivity setting of SonoChiro also slightly impacted the performance of the program. With the most sensitive setting (i.e., 10), the performance, with 66.7% correct species identifications, is slightly better than the performance with the default (i.e., 7) and most conservative settings (i.e., 1), which scored 65.3% and 62.7%, respectively.

Most false identifications, with all programs, can be attributed to the nyctaloid species *E. serotinus*, *N. leisleri* and *V. murinus* (Table 3). *Nyctalus leisleri* and *V. murinus* are also relatively often confused with *Plecotus auritus*. *M. dasycneme* also shows a high frequency of false results, especially with BatExplorer, which confuses *M. dasycneme* with *P. auritus* and *N. leisleri*. *For P. nathusii*, most mistakes with all programs were made within the genus *Pipistrellus*.

Although the geographical region of our test is different from the study by RYDELL *et al.* (2017, 2018), Western and Northern Europe respectively, the performances of Kaleidoscope and SonoChiro at the species level are very similar (Table 4).

## Discussion

### Program reliability of species identifications

The differences in performance of the software packages tested in this study are large. In general, it can be concluded that the identifications to species-group level made by BatIdent and SonoChiro are reliable. Both programs succeed in classifying the recordings in the correct genus or multi-genera group (BatIdent: 88.0%, SonoChiro: 85.3%). However, when it comes to identifications at species level, the number of correctly classified recordings is much lower. Compared to the other two programs, BatIdent and Kaleidoscope still score relatively highly (77.3 and 71.3%, respectively). Although the geographical region of this study is different from the study by RYDELL *et al.* (2017), Western and Northern Europe respectively, the performances of Kaleidoscope and SonoChiro at species level in both tests is very similar (see Table 4). Changing the sensitivity settings significantly improved the performance of

Overview of the performance of the four tested programs presented as the percentage of reference files that were correctly or falsely identified. BatIdent and SonoChiro identified the recordings at species-group and at species level, BatExplorer and Kaleidoscope only at species level. 'NoID' percentage is the number of samples where the programs did not provide an identification of the species(-group) in the recording. Species abbreviations: Enil = Eptesicus nilssonii, Eser = Eptesicus serotinus, Mdas = Myotis dasycneme, Mdau = Myotis daubentonii, Nlei = Nyctalus leisleri, Nnoc = Nyctalus noctula, Pnat = *Pipistrellus nathusii*, Ppip = *Pipistrellus pipistrellus*, Vmur = *Vespertilio murinus*.

|                  |                                  |                                  | BatIdent                |                         |             | B                       | BatExplorer             | L           | Ka                      | Kaleidoscope            | )e          |                                  | S                                | SonoChiro               | 0                       |             |
|------------------|----------------------------------|----------------------------------|-------------------------|-------------------------|-------------|-------------------------|-------------------------|-------------|-------------------------|-------------------------|-------------|----------------------------------|----------------------------------|-------------------------|-------------------------|-------------|
| Species          | Right<br>species<br>group<br>(%) | Wrong<br>species<br>group<br>(%) | Right<br>species<br>(%) | Wrong<br>species<br>(%) | NoID<br>(%) | Right<br>species<br>(%) | Wrong<br>species<br>(%) | NoID<br>(%) | Right<br>species<br>(%) | Wrong<br>species<br>(%) | NoID<br>(%) | Right<br>species<br>group<br>(%) | Wrong<br>species<br>group<br>(%) | Right<br>species<br>(%) | Wrong<br>species<br>(%) | NoID<br>(%) |
| Enil<br>(n=16)   | 93.8                             | 6.2                              | 93.8                    | 6.3                     | 0.0         | 37.5                    | 62.5                    | 0.0         | 75.0                    | 0.0                     | 25.0        | 100.0                            | 0.0                              | 93.8                    | 6.3                     | 0.0         |
| Eser<br>(n=14)   | 78.6                             | 21.4                             | 14.3                    | 85.7                    | 0.0         | 0.0                     | 100.0                   | 0.0         | 85.7                    | 7.1                     | 7.1         | 92.9                             | 7.1                              | 85.7                    | 14.3                    | 0.0         |
| Mdas<br>(n=18)   | 94.4                             | 5.6                              | 94.4                    | 5.6                     | 0.0         | 0.0                     | 100.0                   | 0.0         | 100.0                   | 0.0                     | 0.0         | 83.3                             | 16.7                             | 77.8                    | 22.2                    | 0.0         |
| Mdau<br>(n=18)   | 94.4                             | 5.6                              | 94.4                    | 5.6                     | 0.0         | 72.2                    | 27.8                    | 0.0         | 88.9                    | 0.0                     | 11.1        | 100.0                            | 0.0                              | 61.1                    | 38.9                    | 0.0         |
| Nlei<br>(n=8)    | 75.0                             | 25.0                             | 12.5                    | 87.5                    | 0.0         | 25.0                    | 50.0                    | 25.0        | 0.0                     | 50.0                    | 50.0        | 87.5                             | 12.5                             | 25.0                    | 75.0                    | 0.0         |
| Nnoc<br>(n=18)   | 77.8                             | 22.2                             | 77.8                    | 22.2                    | 0.0         | 38.9                    | 55.6                    | 5.6         | 77.8                    | 11.1                    | 11.1        | 77.8                             | 22.2                             | 66.7                    | 33.3                    | 0.0         |
| Pnat<br>(n=19)   | 100.0                            | 0.0                              | 100.0                   | 0.0                     | 0.0         | 31.6                    | 68.4                    | 0.0         | 68.4                    | 10.5                    | 21.1        | 52.6                             | 47.4                             | 42.1                    | 57.9                    | 0.0         |
| Ppip<br>(n=19)   | 100.0                            | 0.0                              | 100.0                   | 0.0                     | 0.0         | 47.4                    | 52.6                    | 0.0         | 100.0                   | 0.0                     | 0.0         | 100.0                            | 0.0                              | 100.0                   | 0.0                     | 0.0         |
| Vmur<br>(n=18)   | 77.8                             | 22.2                             | 66.7                    | 33.3                    | 0.0         | 22.2                    | 77.8                    | 0.0         | 16.7                    | 27.8                    | 55.6        | 88.9                             | 11.1                             | 27.8                    | 72.2                    | 0.0         |
| Total<br>(n=148) | 88.0                             | 12.0                             | 77.3                    | 22.7                    | 0.0         | 31.3                    | 66.7                    | 2.0         | 71.3                    | 10.7                    | 18.0        | 85.3                             | 14.7                             | 65.3                    | 34.7                    | 0.0         |

The number of false identifications at the species level with different programs. N = number of reference recordings per species. Species abbreviations: Enil = *Eptesicus nilssonii*, Eser = *Eptesicus serotinus*, Hsav = Hypsugo savii, Mdas = *Myotis dasycneme*, Mdau = *Myotis daubentonii*, Nlei = *Nyctalus leisleri*, Nnoc = *Nyctalus noctula*, Pnat = *Pipistrellus nathusii*, Ppip = *Pipistrellus pipistrellus*, Vmur = *Vespertilio murinus*, *Paur* = *Plecotus auritus*, *Pmac* = *Plecotus macrobullaris*, *Pkuh* = *Pipistrellus kuhli*, Mbech = Myotis bechsteini, Mcap = Myotis capaccinii, Mschrei = *Miniopterus schreibersii*, Mmyo = *Myotis myotis*, Nlas = *Nyctalus lasiopterus*, Nycmi = *N. leisleri* + *E. serotinus* + *V. murinus*.

| Reference species       | Misclassified as | BatIdent | BatExplorer | Kaleidoscope | SonoChiro |
|-------------------------|------------------|----------|-------------|--------------|-----------|
| Enil (n=16)             | pipistrelloid    | 1        |             |              |           |
|                         | Ppip             |          | 9           |              |           |
|                         | Nlei             |          | 1           |              |           |
|                         | noise            |          |             |              | 1         |
|                         | NoID             |          |             | 4            |           |
| Eser (n=14)             | nyctaloid        | 8        |             |              |           |
|                         | Enil             | 3        | 8           |              |           |
|                         | Nycmi            | 1        |             |              |           |
|                         | Nlei             |          | 2           |              |           |
|                         | Nnoc             |          | 3           |              | 2         |
|                         | Ppip             |          | 1           |              |           |
|                         | NoID             |          |             | 2            |           |
| Mdas (n=18)             | Vmur             |          | 1           | 1            |           |
|                         | Paur             |          | 8           |              |           |
|                         | Pnat             |          | 1           |              |           |
|                         | Pkuh             |          |             |              | 3         |
|                         | Hsav             | 1        |             |              |           |
|                         | Nnoc             |          | 2           |              |           |
|                         | Nlei             |          | 6           |              |           |
|                         | Mbech            |          |             |              | 1         |
| Mdau (n=18)             | Mbech            | 1        |             |              | 7         |
|                         | Pkuh             |          | 1           |              |           |
|                         | Mcap             |          | 2           |              |           |
|                         | Paur             |          | 2           |              |           |
|                         | NoID             |          |             | 2            |           |
| Nlei (n=8)              | Nycmi            | 2        |             |              |           |
|                         | Vmur             | 2        |             | 3            | 1         |
|                         | nyctaloid        | 3        |             | -            |           |
|                         | Paur             | -        | 3           |              | 1         |
|                         | Nnoc             |          | 1           |              |           |
|                         | Mbech            |          | -           |              |           |
|                         | Eser             |          |             |              | 4         |
|                         | NoID             |          | 2           | 4            | •         |
|                         | Noise            |          | -           | 1            |           |
| Nnoc (n=18)             | pipistrelloid    | 4        |             | 1            |           |
| 1,110 <b>0</b> (11,110) | Nlas             |          | 8           |              |           |
|                         | Nlei             |          | 2           |              |           |
|                         | Vmur             |          | 2           | 1            |           |
|                         | Eser             |          |             | 1            | 2         |
|                         | NoID             |          | 1           | 2            | 4         |
|                         | Noise            |          | 1           | <u> </u>     | 4         |

| Pnat (n=19) | Ppip          |   | 13 |    | 9 |
|-------------|---------------|---|----|----|---|
|             | Pkuh          |   |    | 2  | 2 |
|             | NoID          |   |    | 4  |   |
| Ppip (n=19) | Pkuh          |   | 1  |    |   |
|             | Paur          |   | 7  |    |   |
|             | Pmac          |   | 1  |    |   |
|             | Nlei          |   | 1  |    |   |
| Vmur (n=18) | pipistrelloid | 4 |    |    |   |
|             | Nycmi         | 2 |    |    |   |
|             | Nlei          |   | 3  | 3  | 7 |
|             | Paur          |   | 3  |    | 1 |
|             | Enil          |   | 5  |    |   |
|             | Eser          |   | 1  |    | 2 |
|             | Nlas          |   | 1  |    |   |
|             | Mmyo          |   | 1  | 1  |   |
|             | Nnoc          |   |    |    | 2 |
|             | NoID          |   |    | 10 |   |
|             | Noise         |   |    | 1  | 1 |

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Kaleidoscope. The performance of SonoChiro was only slightly impacted by changes in the sensitivity setting. The other two tested programs have no adjustable sensitivity setting.

Overlap in call characteristics makes it indeed difficult and sometimes impossible, even for experts, to distinguish species by their echolocation calls (BARATAUD 2015). This is, for instance, the case for the mid-frequency nyctaloid species *E. serotinus*, *N. leisleri* and *V. murinus*. Consequently, false identifications are expected to prevail in this species group, and this was also demonstrated in this study. The best performing program, BatIdent, managed to correctly identify only one out of eight *N. leisleri* call sequence recordings but still correctly identified the species-group in five other recordings. Identifications at the species-group level are therefore in some cases the only possible correct result.

Our results further demonstrate that false identifications also happen between species that have completely different call characteristics, e.g., *N. leisleri* and *V. murinus* being confused with *P. auritus*. Our own observations suggest that this might be caused by non-species-specific calls used by *N. leisleri* and *V. murinus* when approaching prey, which sometimes resemble the characteristics of the species-specific calls of *P. auritus*.

Finally, echoes of bat calls can be problematic for an automated identification of bats (RUNKEL & GERDING 2016). In nine examples in the current study, BatIdent identified a *Nyctalus* sp. as a *Pipistrellus* sp. This might be caused by the fact that the calls of *Nyctalus* sp. are often followed by a soft, flat echo, which is being misinterpreted by BatIdent as the social call of *Pipistrellus* sp. Presumably, the identification of social calls is not yet fully included in BatIdent and the program classifies most social calls as a *Pipistrellus* sp. call.

### Application of automated identification software programs in research

Automated identification software programs are valuable tools for bat researchers as they result in considerable time gain during the processing of data. Our own experience taught us that they are helpful to separate noise from datasets in high clutter environments, and as such provide the researchers with a full set of bat calls extracted from a given recording. Also, some easy-to-recognize species (e.g., *P. pipistrellus*, which was successfully identified by three of the four tested programs) can be effectively identified, offering researchers the opportunity to easily focus on other species of interest in large

Performance (% of correct species identifications) of the programs Kaleidoscope and SonoChiro for the species included in RYDELL *et al.* (2017, 2018) and in this study.

| Performance (%)     | Kaleide               | oscope                | Sono                   | Chiro                 |
|---------------------|-----------------------|-----------------------|------------------------|-----------------------|
|                     | BRABANT <i>et al.</i> | RYDELL <i>et al</i> . | BRABANT <i>et al</i> . | RYDELL <i>et al</i> . |
| Eptesicus nilssonii | 75.0                  | 85.0                  | 93.8                   | 91.5                  |
| Myotis daubentonii  | 88.9                  | 88.2                  | 61.1                   | 57.8                  |
| Vespertilio murinus | 16.7                  | 16.0                  | 27.8                   | 20.0                  |

datasets. In general, these tools thus make manual identification of bat recordings more feasible. Similar applications of these programs were already suggested by RYDELL *et al.* (2017), RUSSO & VOIGT (2016) and LEMEN *et al.* (2015). However, this and other validation studies (LEMEN *et al.* 2015; RYDELL *et al.* 2017) illustrate that the species-identifications made by current software packages are not reliable enough to use alone and should always be re-evaluated by a bat expert. We would like to emphasize that the reference dataset in our test consists of high-quality recordings only. Consequently, the performance of the software packages for identifying species might be even less reliable in other situations (e.g., social interactions; multiple specimens or species at the same time).

We therefore strongly support the plea for prudence with the use of these automated identification software packages in environmental and scientific studies, as was made by RUSSO & VOIGT (2016) and RYDELL *et al.* (2017): none of the programs should be used unsupervised, and species identifications need to be checked by a trained bat expert, to avoid erroneous conclusions in environmental studies and mistakes in management decisions.

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