The comparison of manual and software based species identification using acoustic recordings of bat vocalizations

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Abstract:

Automated species identification software has become a popular tool in the wildlife field for acoustic recordings of bat vocalization as part of bat management. Since accurately identifying bats is extremely important for bat management due to significant decreases in populations, an efficient identifying method is critical. In this paper, a comparative analysis between an automated bat identification software, SonoBat[™] (SonoBat, Arcata, CA) and the traditional manual identification method using spectrograms generated by the software SCAN'R[™] (Binary Acoustic Technology, Tucson, Arizona) was performed. Four years worth of data was used for this study. Comparison of the two methodologies resulted in no significant difference between the two methods.

Introduction:

Bats generally use echolocation as an orientation system and for locating their prey (Schnitzler and Kalko 2001). They emit signals of high frequency and analyze the returning echoes so that they can detect, characterize, and localize the reflected object (Schnitzler and Kalko 2001). Bats have species-specific signal types that can differ in frequency structure, duration, and sound level (Schnitzler and Kalko 2001). The signal type can vary by the task the bat is performing (Schnitzler and Kalko 2001). A search signal that a bat emits when looking for prey differs from an approach signal when a bat has found its prey (Schnitzler and Kalko 2001). Bats are generally hard to study because of their small size, nocturnal habits, and difficulty to capture (Jennings et al 2008). However, acoustic monitoring has allowed biologists to study the level of use of habitat and their activity (Frick 2013). However, acoustic monitoring cannot be used to determine the abundance of bat species but acoustic recordings allow the identification of bat species by analyzing their echolocation calls.

Brookhaven National Laboratory (BNL) is using two methods to identify bat species. These two methods include the automated identification software, SonoBat[™], and a manual decision tree system using spectrographs generated by the software SCAN'R[™].

SonoBat[™] is an automated species identification software that analyzes and compares high-resolution full spectrum sonograms from bat echolocation calls. Full spectrum data is a digitized representation of the complete acoustic waveform (Szewczak 2010). SonoBat[™] is able to analyze the data by extracting frequency and amplitude contents by sampling overlapping snippets of the waveform (Szewczak 2010). It also makes a representation of the soundscape by passing the signal first through band pass frequency filters and which it repeats this process for each frequency band (Szewczak 2010). A sonogram that is generated from SonoBat[™] displays a high resolution rendering of the time, frequency, amplitude, and multiple frequency content of a signal. SonoBat[™] provides higher resolution and higher quality renderings of the time frequency domain of the calls (Szewczak 2010).

Another method that is currently being used is the manual method decision tree system using spectrographs generated by the software SCAN'R[™]. You're essentially just looking at spectrographs SCAN'R[™] produces and using an identification chart to identify the bat species. SCAN'R[™] created by Binary Acoustic Technology is a snapshot characterization and analysis software (Binary Acoustic Technology 2010). SCAN'R[™] was designed to address two of the primary issues present in bat monitoring projects: 1) handling the high volume of data that is produced by modern Time Expanded (TE) and Full Bandwidth (FB) bat detectors, and 2) converting the recordings into meaningful measurements that can potentially be used to identify individual species and estimate populations (Binary Acoustic Technology 2010). SCAN'R[™] is able to separate actual bat calls and false calls such as insect and other noise sources; SCAN'R[™] separates these files into two lists, a "passed" list and a "failed list". SCAN'R[™] also processes the passed bat calls to isolate each bat vocalization and measures the relevant vocalization parameters.

Using both these methods has led to the question: which method is more accurate when identifying bat species? To address this question, a comparative analysis was performed using data collected from mobile surveys. It was hypothesized that SonoBatTM would have a higher identifying rate, higher rate at differentiating between big brown bat (*Eptesicus fuscus*) and silver-haired bat (*Lasionycteris noctivagans*) and would have a lower unidentified rate than manually identifying using SCAN'RTM.

Materials and Methods:

12 mobile surveys were performed throughout Suffolk County, Long Island, NY. These routes were pre-selected based on previous years bat activity levels. After a mobile survey was completed, the files were processed through SCAN'R[™]. The files identified were based upon the visual inspections of frequency and shape of calls. The files that had at least five calls were placed into the positive file list. The positive files were then run through SonoBat[™] and manually identified through SCAN'R[™] using a decision tree system and Humboldt State University bat lab's, "Echolocation Call Characteristics of Eastern US Bats" table. Files that could not be identified were labeled "unknown". After both identification methods were complete the data was then imported into Excel for organization, and comparative analysis. These steps were used for each mobile survey.

To compare the identification methods, a mass Excel file was created using all data collected from 2011 through 2014. The Excel file was created to compare three main categories; number positively identified, number unidentified, and the ability to identify between big brown bat (*Eptesicus fuscus*) and silver-haired bat (*Lasionycteris noctivagans*) using both SonoBat[™] and SCAN'R[™]. The average was calculated for each category for each year. The averages were then compiled into the statistic software, JMP, using the statistical test, ANOVA, to test for differences between the two methods.

Results:

There were a total of 1,022 files that were qualitatively identified to species. A total of 10 bat species were identified. SonoBat[™] identified a total of 533 files and the manual method identified a total of 682 files (Table 1). SonoBat[™] could not identify 490 files and the manual method could not identify 337 files (Table 1). SonoBat[™] was able to identify 345 files from either big brown bat or silver haired bat and the manual method was able to identify 303 files (Table 1). SonoBat[™] identified 51% of the files, while the manual method identified 68% (Table 2). SonoBat[™] was unable to identify 49% of the files and the manual method was unable to identify 33% (Table 2). SonoBat[™] was able to identify 34% of the files between big brown bat and silver-haired bat and the manual method identified 30% (Table 2).

Discussion:

The average number of positively identified calls using SonoBat[™] was 0.508 (51%) and with SCAN'R[™] was 0.682 (68%). The p-value was 0.0838; therefore there was no significant difference among SonoBat[™] and SCAN'R[™] when it comes to the number identified (figure 1). The average number of times either method was able to differentiate between big brown bat and silver-haired bat using SonoBat[™] and SCAN'R[™] was; 0.325 (33%) and 0.321 (32%), respectively. The p-value was 0.9828; suggesting there was no significant difference between the two methods (figure 2). The averages for the amount unidentified using SonoBat[™] and SCAN'R[™] were; 0.491 (49%) and 0.316 (32%). The p-value was 0.0783; therefore there was no significant difference between each other (figure 3).

Even though SonoBat[™] and the manual method have proven to have the same capabilities, through personal experience, SonoBat[™] had an advantage over the manual method, which was its time efficiency. SonoBat[™] is capable of analyzing large number of files within a reasonable time, while the manual method took at least two hours to identify around 80 files, because you have to look at several calls within each file to better identify the bat species.

Although there is no significant difference between the two methods, there is still a possibility that each file is mistakenly identified. It is extremely important that species are identified correctly because some bat species populations are being threatened by the, White-Nose Syndrome fungus (*Pseudogymnoascus destructans*), so it is suggested that each file is double-checked using both methods simultaneously.

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Appendix:

Total Files Identified	ID'd Using Sonobat	ID'd Using Scan'R	UnID'd Sonobat	UnID'd Scan'R	ID'd between EPFU/LANO- Sonobat	ID'd between EPFU/LANO- Scan'R
2014	110	158	100	53	52	39
2013	155	231	138	60	89	146
2012	191	153	132	167	146	0
2011	77	140	120	57	58	118
All Years	533	682	490	337	345	303

Table 1: The total number of files identified/unidentified by each category.

Table 2: The percentage of files identified/unidentified by each category.

Total Files	ID'd Using Sonobat	ID'd Using <i>Scan'R</i>	UnID'd Sonobat	UnID'd <i>Scan'R</i>	ID'd between EPFU/LANO-	ID'd between EPFU/LANO-
Identified					Sonobat	Scan'R
	52%	67%	48%	33%	34%	30%



Figure 1: Identified using SonoBat and SCAN'R



Figure 2: Identified between big brown bat and silver-haired bat



Figure 3: Unidentified using SonoBat and SCAN'R