Automatic bat call analysis with the batcorder-system.

Description of automatic bat call identification procedure and advices for the interpretation and revision of results. - Ulrich Marckmann, Dr. Volker Runkel

Version 1.02 (August 2010)

Analyse

1. Contents

1. Introduction

The batcorder-system represents a new and powerful tool for an automated recording and species determination of bat calls. It enables you to quickly collect and analyse qualitative and quantitative data, thus permitting comparative field studies of bat activity ranges. As a novel system, it requires a solid examination of its techniques and opportunities in comparison with conventional methods.

Contrary to previous acoustic analysing tools, the batcorder-system automatically identifies and measures bat calls, and determines the corresponding bat species by applying advanced statistical methods. Since it is a black-box solution, one may ask for the reliability of the analysis and for a possible revision of the acquired data. With the great amount of data that are automatically collected and analysed, such data revision and interpretation have to be adapted to the specific research issue.

This manual provides assistance for the automated species determination and gives instructions for revising acquired data. We additionally recommend to consider the advises given by the Landesamt für Umwelt Bayern (LfU), which complements this manual and lists determinations keys for Bavarian species (German only):

http://www.ecoobs.de/downloads/Kriterien_Lautzuordnung_10-2009.pdf

1.1. Drawbacks and opportunities associated with acoustic species determination

1.1.1. „*Bats are not birds*“

Most errors in acoustic bat species determination are caused by the intraspecific variability of echolocation calls. The resulting overlap in call parameters inevitably leads to some uncertainty in species determination. Researchers often refer to an article written by Barclay (1999) “Bats are not Birds”, which explicitly describes the dilemma of call analysis: bats do not echolocate in order to broadcast their species belonging but to gather information about their environment and prey. Consequently, a reliable species classification via analyzing echolocation calls is limited and sometimes, under certain circumstances impossible.

Furthermore, the intraspecific call variability complicates a definite description and classification of a “typical call” of a species. Fewest species can be classified distinctively upon simple boundary values and parameters. In most cases, only a sophisticated linkage of several call properties permits a discrimination between similarly calling species. Specific recording conditions also have an influence on call measurements in the automated analysis. Suboptimal records (intense echos, elevated acoustic noise) can lead to incomplete measurements of the signals, thus resulting in doubtful call classifications. Since no analysing method will ever achieve an absolute certainty in species classification, it will always be essential to conduct an error estimation and an interpretation of results.

1.1.2. Classification Rate and Quality

In order to test the quality of a specific classification method, one needs to refer to the rate of correctly classified test calls. The identified rate for the batcorder-system lies at 95%, which is an excellent value compared to values of manual and other automated classification methods cited in the literature (Ahlen 1981; Fenton & Bell 1981; Weid & Helversen 1987; Fenton 1988; Weid 1988; Ahlen 1990; Zingg 1990; Herr et al . 1997; Vaughan et al . 1997; Ahlén & Baagoe 1999; Barclay 1999; O'Farrell & Miller 1999; O'Farrell et al . 1999; Tibbels 1999; Jones et al . 2000; Parsons & Jones 2000; Russo & Jones 2002; Rydell et al . 2002; Obrist et al . 2004). Normally, this high rate cannot be accomplished in the field, because only calls with suitable quality (without disturbances) are used for the training and testing of classification methods.

Even under optimal conditions the remaining five percent account for a certain proportion of unclassified or incorrectly classified calls. However, the batcorder-system is aimed at comparative studies in space and time and this remaining uncertainty is irrelevant for these investigations. Taken a study of a specific species' habitat use: a few incorrectly classified sequences (Type-I Error; false-positive) at locations of little importance to this species are irrelevant to the outcome of the study because there will be hundreds of correctly classified records from locations that are preferentially used by this species.

1.1.3. Manual Check-up

Investigations with manual recording systems (e.g. with time-expansion detectors) usually generate moderate amounts of data. Such comparatively small data sets permit a detailed analysis of each recorded signal. Ideally, the sonogram of each call is examined at the computer and even low quality records can possibly be assigned to a species or group of species.

This is neither possible nor necessarily required in surveys with the batcorder-system (or other passive monitoring systems) because of the huge amount of collected data. Nevertheless, the batcorder-system's analyses can and should be revised, in particular if data are used to generate distribution maps or if they provide the basis for expertise on endangered and protected species in nature conservation. Besides, one has to keep in mind that the batcorder-system "only" provides the data and that it is necessary to interpret these data corresponding to specific research issues.

2. The procedure of automatic call analysis

The automated call analysis (bcAdmin/batIdent) is not quite comparable with the determination by an auditory impression (heterodyne/frequency division detectors) or with manually analysing sonograms of recorded calls at the computer. There are wide differences concerning error sources. In summary these are the characteristics of an automated analysis:

⇨ **unbiased**

Results do not depend on the user's knowledge and ability.

⇨ **verifiable**

Results are verifiable and reproducible at any time. Recorded files can always be re-analysed using other or improved programs.

⇨ **uncritical regarding rare or locally uncommon species**

Contrary to a manual species classification the automated analysis does not interpret results. There is no human factor (e.g. the knowledge of a species' local distribution) that interferes and adulterates findings. Thereby, the risk of circular reasoning is abandoned and thinking patterns like "it can't be because it is not supposed to be" do not occur.

⇨ **judgement of calls/sequences uncoupled from their temporal context**

Since the analysis examines and classifies calls of a sequence separately, single outliers within a sequence are not so easily recognized. Temporal patterns of a sequence (e.g. consecutive recordings) are thus not considered by the automated analysis.

⇨ **limited decision criteria concerning the quality of signals**

Dans la mesure où les signaux d'une séquence sont examinés et déterminés séparément lors de l'analyse, les anomalies que peut comporter une succession de signaux sont plus difficilement identifiées. De même, les informations temporelles des séquences (par exemple succession directe de plusieurs enregistrements) ne sont pas prises en compte par l'analyse automatique.

⇨ **limited decision criteria concerning the quality of signals**

An automated analysis system can decide whether to incorporate detected signals only to a certain extent. Most times a person that manually examines recordings at the computer would immediately realise if signals are incomplete or if signals overlap with other signals. A trained person would also identify echoes, social calls or unknown types of calls. An analysis program does not possess this broad know-how. Although it uses criteria to assess call quality and identify outliers, it cannot cope with all possible situations.

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The results of the automated analysis highly depend on signal quality and on the technical equipment that is used for recording. For an appropriate measurement of parameters, the signals must be above a certain amplitude threshold and a reasonably good signal to noise ratio. Similarly, technical recording characteristics (frequency response, directionality of the microphone, inherent noise, sample rate, and dynamic range) influence the measurement of signal parameters. Therefore, an automated recording system can only achieve optimal results if training calls for the statistical identification procedure were recorded with the same technical equipment.

For this reason the batcorder-system is composed of harmonised hard- and software. The batcorder itself is designed to preferably record signals with appropriate quality and sound level. Accordingly, the automated call discovery and measurement of call parameters by the program bcAdmin (Fig. 1) is exactly adjusted to these recordings in its default settings. Furthermore, the statistical method of species determination in the program batIdent (former bcDiscriminator) was trained with call parameters that were generated with analogous settings of the batcorder and bcAdmin. Modified recording- or bcAdmin settings may lead to an increased recording of calls with suboptimal quality which in turn can result in imprecise or wrong species determinations.

The statistical species determination is implemented in batIdent (former bcDiscriminator) (Fig. 2). This open-source program takes the measured data from bcAdmin and thereby assigns calls to species groups or, if possible to a single species. For this, batIdent applies a multi-level method of discrimination called randomForest (Fig. 2 illustrates the tree of analysis).

A special SVM-Algorithm (Support-Vector-Machine) identifies and rejects outliers (unknown and low quality calls) on each level. After all calls of a recording are analysed, up to three species are extracted from the list of classifications of individual calls of a sequence. For this, determined potential species/species groups are arranged according to the frequency of call occurrence and classification confidence. The determination result is calculated if more than 2 calls and a mean probability greater than 60% is achieved. Resulting classification results of up to three determined species are summarised and saved in a file that can be imported to bcAdmin.

By this procedure calls are not necessarily determined to the species level. If for instance a discrimination is doubtful because of an overlap of calls from two species, a species group is given as result of the analysis. Calls or signals that are unknown to the program are labelled as “spec”.

The analysis works even when several species are calling simultaneously because up to three species are extracted per sequence. Additionally, the outlier analysis guarantees that improperly measured or unknown signals, which primarily had been assigned to a species but did not fit into the calling repertoire of this species are excluded from the resulting species list.

2.1. Statistical method and its characteristic values

This chapter describes the informative value of characteristic values of the statistical analysing method. Rates of dissociation in terms of confusion tables and classification confidence expressed as probabilities that are delivered for each analysed call are examined in detail. It is important for the interpretation of results to understand how these values are produced and what significance they have.

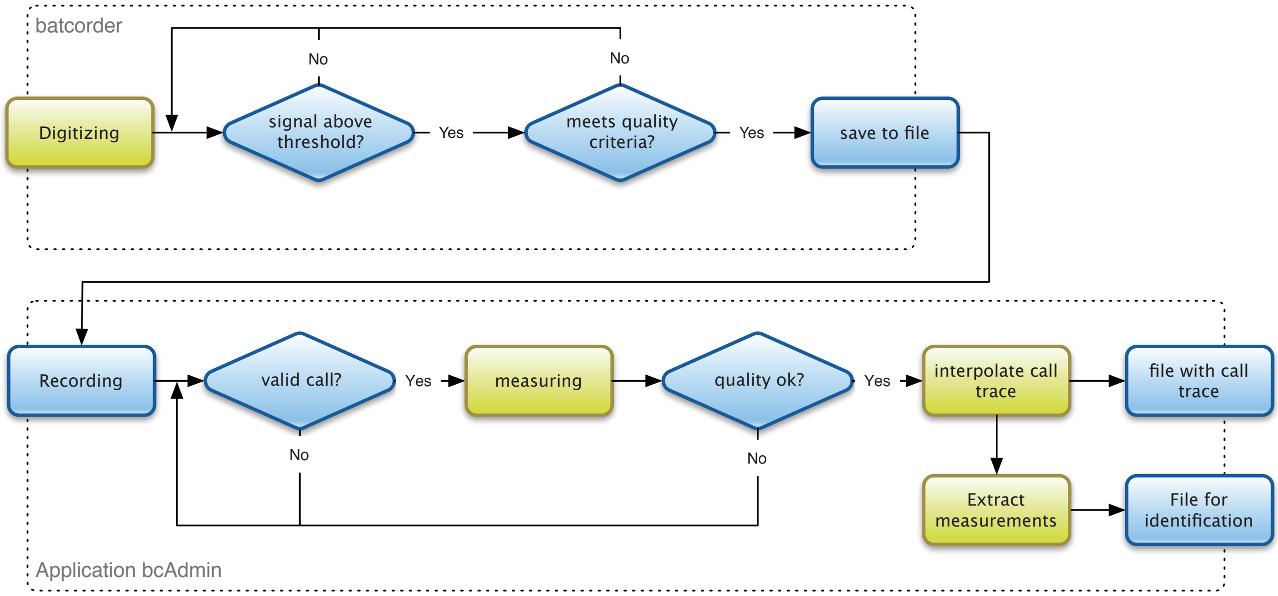

Fig. 1: Steps of analysis of the Batcorder and bcAdmin.

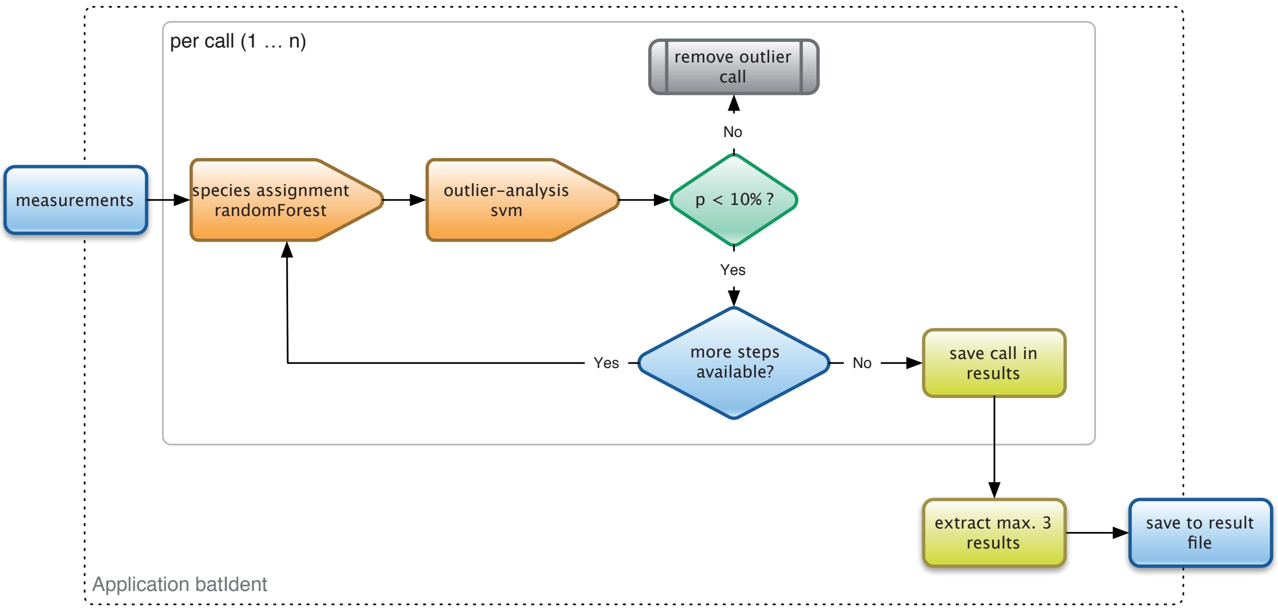

Fig. 2: Steps of analysis of batIdent/bcDiscriminator.

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As already mentioned above, the call by call species discrimination is achieved by a statistical method called randomForest (Breimann 2001). To train this procedure, calls were sub-classified to “call types” for each species in order capture the whole intraspecific call variability. Approximately 500 calls per species were incorporated, containing all identified call types in equal parts. Confusion rate and thereby the quality of the analysis was established by a set of test calls with known species belonging and displayed in confusion tables.

The main principle of the procedure is to compare every new call with the training calls and to count how many similar training calls there are within each species. The species with the most corresponding training calls is taken and is displayed after the import to bcAdmin. If for example the procedure finds 60 calls similar to training calls from species A and 40 similar to species B, the call is assigned to species A with a confidence of 60%. In bcAdmin the probability of species determination of a whole sequence is then composed of the mean probabilities of individual calls.

Tab. 1 gives an example on the basis of the confusion rate of individual calls from the Northern and Serotine Bat:

	true			
assignment	*Eptesicus nilssonii*	*Eptesicus serotinus*	n	false-positive
Eptesicus nilssonii	529	66	595	11,02%
Eptesicus serotinus	70	531	601	11,73%
n	599	597	1196	
false-negative	11,69%	11,05%	11,37%	

Tab. 1: Confusion table of a randomForest analysis for individual calls from the Northern and Serotine Bat. True species are shown in columns and species assignments based on the analysis are shown in rows. The proportion of calls of a species that were incorrectly assigned to the other species are called false-negative assignments. The proportion of incorrect assignments in relation to the total amount of calls is called false-positive rate.

Figure 3 illustrates the (hypothetical) distribution of the training calls of two species within a character-/discrimination-space. From both species an equal number of calls are incorporated and the species’ intraspecific call variability is equally covered. There is a distinctive overlap between the two species. The markers show the assignment probabilities for specific call types within the character-space. As explained above, these probabilities result from the amount of calls of a species that resemble the corresponding call and therefore are closely located to them within the character space.

Confusion tables and assignment probabilities are important statistical values and permit a comparison of different discrimination methodologies. Supplement 1 provides a confusion table with our discrimination rates

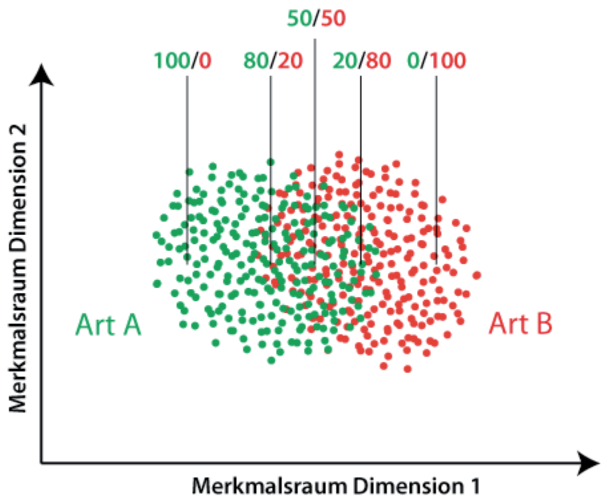

Fig. 3: Distribution of calls from two species in a hypothetical character space with overlapping calling spectra. Numbers give assignment probabilities at distinct locations within the scatterplot.

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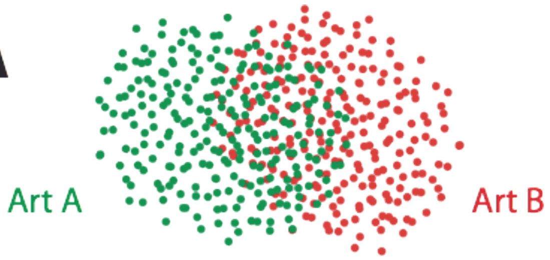
for individual calls. batIdent's sequence-wise summary of results and determination of doubtful calls (at the species group level) are disregarded in this table in order to keep it clearly arranged and and to facilitate the comparison with values of other methods. Confusion tables also provide useful information about the risk of an mix-up between pairs of species, which helps to interpret results in the field. Assignment probabilities are helpful to control the classification of individual doubtful calls and sequences.

However, confusion rates and assignment probabilities are primarily calculated for training and test calls and are not implicitly transferable to recordings in the field.

They are basically influenced by the number of calls belonging to a species, their quality and a weighting of different call types (Fig. 4). If two confusable species with an equal number of calls distributed evenly across their calling spectra are analysed, ninety percent of the calls are correctly assigned to the species and confusion rates match the rates of corresponding training calls (Fig. 4-A). However, if fewer calls of species B are included, the rate of false-negative assignments remains constant but the rate of false-positive assignments of species B increases (Fig. 4-B). This instance becomes clearer, if we imagine a location where only calls of species A occur: statistically 10% of these calls are assigned to species B. Thus, all (100%) assignments to species B for this location are incorrect (false-positive). In another example (Fig. 4-C) an equal number of calls of both species are detected but most calls from species B are located within the overlapping zone. As a result both, false-negative assignments to species B and false-positive assignments to species A increase. In such a case also assignment probabilities are misleading: the probability for calls within the overlapping zone should be 50% for both species because an equal number of training calls were incorporated in the statistical method for this scenario. In our example much more calls from species B are located within the overlapping zone. However, the probability of the occurrence of a calls from species B within the overlapping zone should be at 80%.

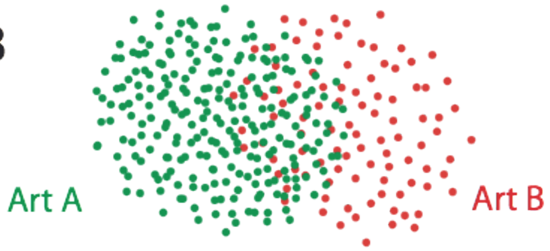
The chance of an ideal case as explained in example 4-A is quite low to occur in the field. Moreover, the quality of recorded calls in the field is often lower than calls we used to train and test the analysing method. Therefore, both confusion rates and assignment probabilities are important hints for the interpretation of discrimination results but are not ubiquitously applicable. Results should particularly be handled with caution if confusable species occur with highly unequal abundances.

A



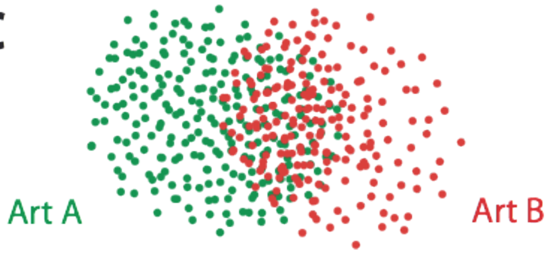
Wahr / Vorhersage	Art A	Art B	falsch-positiv
Art A	450	50	10%
Art B	50	450	10%
n	500	500	
falsch-negativ	10%	10%	

B



Wahr / Vorhersage	Art A	Art B	falsch-positiv
Art A	450	20	4,26%
Art B	50	180	21,74%
n	500	200	
falsch-negativ	10%	10%	

C



Wahr / Vorhersage	Art A	Art B	falsch-positiv
Art A	450	150	25%
Art B	50	350	12,50%
n	500	500	
falsch-negativ	10%	30%	

Fig. 4: different call distributions of two species in a hypothetical character-space and the resulting confusion rates that emerge from applying always the same statistical method of discrimination. A: equal number of calls evenly distributed across the calling variability; B: significantly less calls of species B are included; C: equal number of calls - the majority of calls from species B are located within the overlapping zone.

3. Options for manual revision of analysis results

An examination of species identification results allows in many cases to find and eliminate mistakes. With a reasonable revision of automatically classified sequences advantages of automated and manual species determination are combined and error sources of both techniques are minimised. There are several options to check results concerning plausibility and to re-determine species if necessary.

The extent of a revision depends on the scope of the study (e.g., scientific study vs. rough scanning), on the user's experience, and on the potential occurrence of species at a given study location. It is for instance much easier to proof whether the Barbastelle Bat occurred as compared to the question whether Parti-Coloured Bats and Lesser Noctules occurred simultaneously at a study site.

The following criteria are available to revise and improve results of automated analyses:

⇨ **The complete night**

- Assessment of the whole species spectrum and frequencies of species determinations
- Chronology of call sequences

⇨ **Single call sequences**

- Number of calls and assignment probability
- Completeness / Quality of call measurements
- Call amplitude
- Social calls
- Shape of calls and several measurable parameters

3.1. Assessment of species composition and abundances

With some experience wrong determinations can already be identified by inspecting the species composition and the amount of recordings per species or species group. If there are only a few recordings of a species (especially in relation to the complete amount of recordings) determinations should generally be treated more critically. Neither the automated nor a manual analysis can guarantee absolute reliability. One should always keep in mind that single sequences of a locally abundant species could be incorrectly classified. If the call repertoire of an abundant species considerably overlaps with repertoires of rare species, one should either accomplish a detailed analysis of the relevant sequences or consider the species classification as unreliable and consequently should ignore it.

automatically analysed			true species inventory	
species	sequences	%	species	sequences
Hsav	1	0,8		
Bbar	7	5,8		
Nyctaloid	13	10,8		
Enil	95	79,2	Enil	117
Nlei	1	0,8		
Mkm	2	1,7		
Mbart	1	0,8	Mbart	3
sum	**120**	**100**		

The table shows the automatically analysed species composition of a location. Incorrectly classified sequences are highlighted in red; in fact only the Northern Bat (*Eptesicus nilsso-*

nii) and a unspecified Whiskered Bat (*Myotis brandtii / mystacinus*) called at this location. The occurrence of the Northern Bat can be viewed as a firm result based on the great amount of classified calls. There has been also been classified one sequence as Lesser Noctule (*Nyctalus leisleri*) and one as Savi's Pipistelle (*Hypsugo savii*). Those are very likely misclassifications because these species use quite similar calls like the Northern Bat. After an inspection the sequences classified as Barbastelle Bat (*Barbastella barbastellus*) were quickly revealed as echo fractions of Northern Bat calls. Even though only a few sequences were recorded, the *Myotis*-classifications

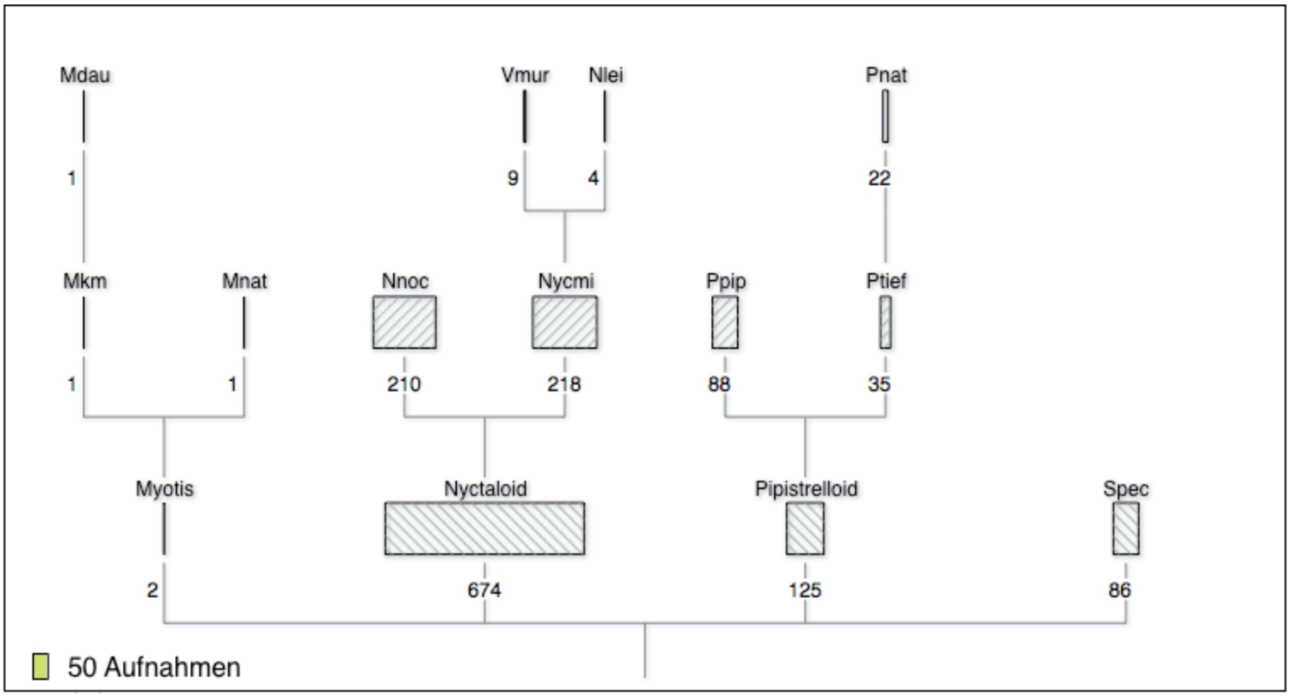
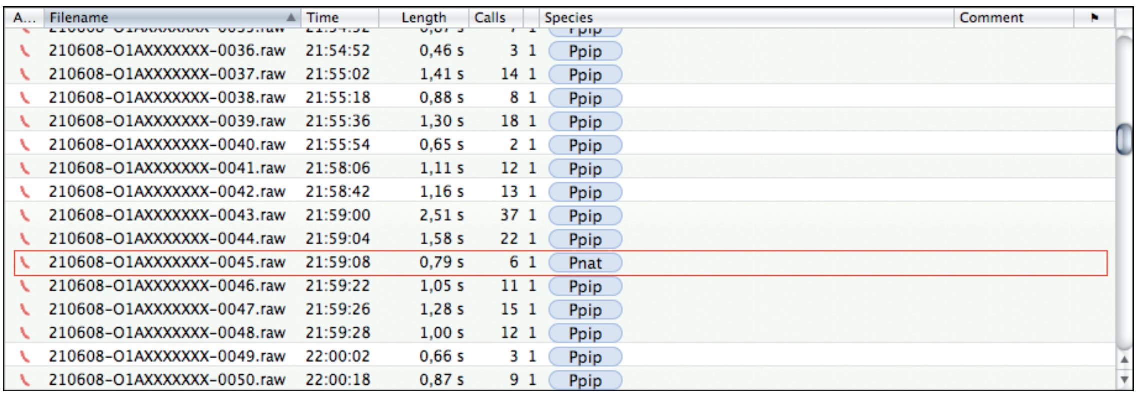


Fig. 5: bcAdmin's classification tree for selected recording nights (from v. 2.0 on).

are trustful because *Myotis*-species can hardly be confused with Northern Bat calls. bcAdmin (from v 2.0 on) includes a classification tree of selected recording nights, which facilitates a revision as explained above (Fig. 5).

3.2. Chronology of sequences

The automated analysis does not comprise the temporal context of sequences. Several sequences of similar calls recorded in close succession clearly indicate an individual bat calling within the microphone's range, e.g. while hunting for prey. Be careful if these sequences are assigned to different species or species groups (especially if these



A...	Filename	Time	Length	Calls		Species	Comment
	210608-O1AXXXXXXX-0036.raw	21:54:52	0,46 s	3	1	Ppip	
	210608-O1AXXXXXXX-0037.raw	21:55:02	1,41 s	14	1	Ppip	
	210608-O1AXXXXXXX-0038.raw	21:55:18	0,88 s	8	1	Ppip	
	210608-O1AXXXXXXX-0039.raw	21:55:36	1,30 s	18	1	Ppip	
	210608-O1AXXXXXXX-0040.raw	21:55:54	0,65 s	2	1	Ppip	
	210608-O1AXXXXXXX-0041.raw	21:58:06	1,11 s	12	1	Ppip	
	210608-O1AXXXXXXX-0042.raw	21:58:42	1,16 s	13	1	Ppip	
	210608-O1AXXXXXXX-0043.raw	21:59:00	2,51 s	37	1	Ppip	
	210608-O1AXXXXXXX-0044.raw	21:59:04	1,58 s	22	1	Ppip	
	210608-O1AXXXXXXX-0045.raw	21:59:08	0,79 s	6	1	Pnat	
	210608-O1AXXXXXXX-0046.raw	21:59:22	1,05 s	11	1	Ppip	
	210608-O1AXXXXXXX-0047.raw	21:59:26	1,28 s	15	1	Ppip	
	210608-O1AXXXXXXX-0048.raw	21:59:28	1,00 s	12	1	Ppip	
	210608-O1AXXXXXXX-0049.raw	22:00:02	0,66 s	3	1	Ppip	
	210608-O1AXXXXXXX-0050.raw	22:00:18	0,87 s	9	1	Ppip	

Fig. 6: A bcAdmin recording table shows a doubtful Nathusius Pipistrelle-classification (Pnat) within a block of Common Pipistrelles (Ppip).

sequences “came” from confusable species) because there could be incorrect classifications (Fig. 6). However, it can be interpreted as an affirmation of classification results if sequences of confusable species occur clearly separated in time.

3.3. Closer inspection of individual sequences

You should consider a closer inspection of sequences if species relevant to nature conservation or locally uncommon species were determined, or if only a few sequences of a species were recorded, or if the chronology of recordings indicate misclassifications. In most cases a check-up of all sequences is not possible due to its enormous time consuming effort; besides it is normally not necessary.

Following criteria are available for a revision of individual sequences:

- number of calls and probabilities
- correct and complete measurement of calls?
- call amplitudes
- are social calls included?
- shape of calls and other measurable parameters

3.3.1. Number of calls and assignment probabilities

bcAdmin’s list of sequences gives number of calls and assignment probabilities next to species determinations that can be consulted for the revision of doubtful sequences. For an explanation of the statistical methodology of species determination please refer to chapter 2.1.

The amount of recorded calls and their assignment probability basically determines the reliability of species determinations (Fig. 7). It is unlikely that a few outliers within a sequence of many calls adulterate the classification of the whole sequence. If however that sequence consisted of only a few calls, outliers can have a significant impact on the whole sequence and this may lead to an incorrect species determination.

Although batIdent/bcDiscriminator already includes the number of calls in its calculations, there is no universal rule of how many calls and which assignment probabilities are needed to deliver correct species determinations. Since sequences with calls of the Common Pipistrelle are almost always classified with 90%, lesser assignment probabilities have to be considered critically. Species calls of the Genus Myotis and Nyctalus hardly ever reach such high probabilities. A Daubenton’s sequence (Myotis daubentonii) with a probability of 80% is a secure result (ca. 1% false-positive classifications).

Calculated probabilities do not necessarily equal mean rates of correct call classifications. Assignment probabilities merely describe how the analysed call is ranked according to the training calls. A value smaller than 100% indicates that the call is located in the overlapping zone of at least two species. bcDiscriminator assumes that species with this calling type are equal in abundance and that their call repertoire has the same composition as the training calls. A good example to illustrate this problem is the pair of species consisting of the Alcathoe’s Bat (Myotis alcathoe) and the Common Pipistrelle (Pipistrellus pipistrellus):

Especially in or along dense vegetation the Common Pipistrelle tends to call with quite short and steep calling types, which are similar to calls of the Alcathoe’s Bat. If both would occur simultaneously and if both would call with their complete call repertoire, batIdent would misclassify only 1% of all calls. A sequence with 98% assignment

	filename	time	length	Calls	Species 1	Prob.	S
☑	100708-I3XXXXXXXX-0046.raw	23:45:28	0,46s	1	Mkm	77%	
☑	100708-I3XXXXXXXX-0047.raw	23:45:28	0,46s	1	Mkm	71%	
☑	100708-K1XXXXXXXX-0043.raw	23:38:22	1,40s	12	Mbart	79%	
☑	100708-K1XXXXXXXX-0044.raw	23:38:46	2,05s	21	Mbart	90%	
☑	100708-K1XXXXXXXX-0045.raw	23:39:06	2,66s	18	Mbart	87%	

Figure 7: The list extracted from bcAdmin shows a positive corelation of call number and identification probability. The first two sequences, both containing only a single call, were identified on group level Mkm at a lower probability only. For example the fourth sequence with 21 calls gets identified as *Myotis mystacinus/brandti* at a much higher assignment probability.

probability would have been classified correctly in 98 of 100 cases on average. However, if only the Common Pipistrelle would occur and fly close to dense vegetation, the rate of misclassifications would increase. In this scenario an Alcathoe's-sequence with 98% assignment probability would always be misclassified.

Even species classifications with assignment probabilities of 100% cannot be considered as absolutely secure determinations. For the training of batIdent only calls of good quality were used. If calls recorded in the field are not measured completely, resulting fractions can resemble calls of other species. Those can lead to misclassifications even though they were ranked with high assignment probabilities. And even though the statistical method scans outliers (calls that do not occur within the known call repertoire of a species), some incorrectly measured signals can be mixed up with regular calling types.

This frequently happens when isolated end sections of *Myotis*-calls are measured. Concerning their length and frequency these fractions often resemble calls of the Barbastelle Bat (*Barbastella barbastellus*). In this case, calls can incorrectly be determined as calls of the Barbastelle Bat although its calls are usually unmistakable.

If you are interested in call-wise assignment probabilities (as opposed to sequence-wise probabilities), the summarised results of bcAdmin are not sufficient. Particularly if

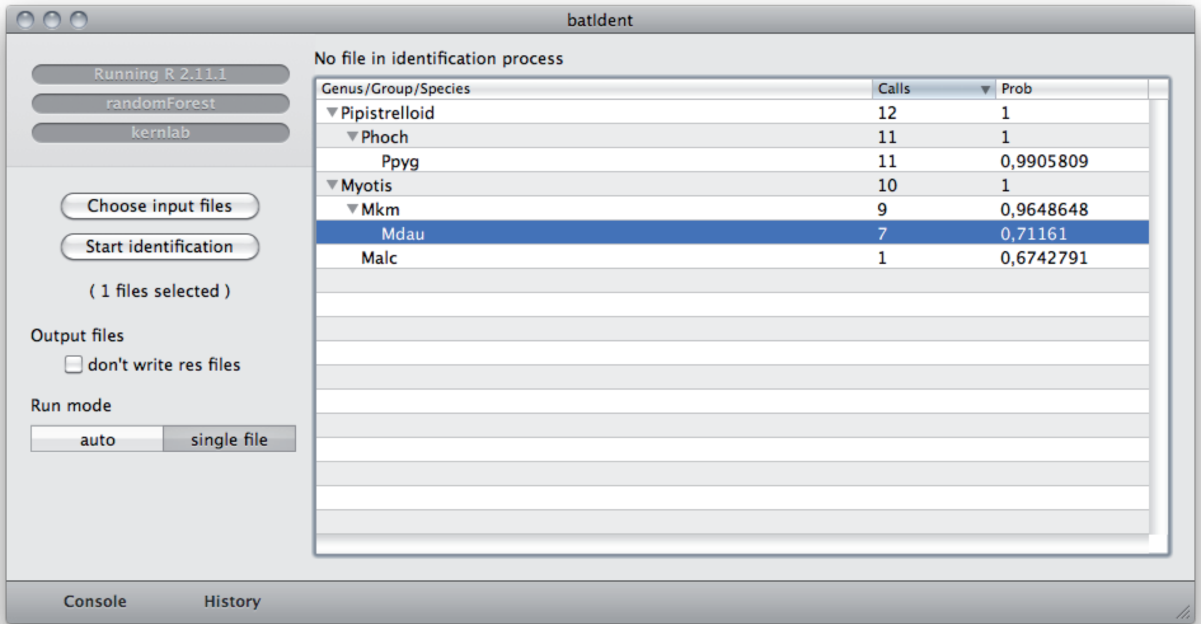


Figure 8: Analysis results of a file displayed in batIdent

several species are found within a recording, these summaries do not provide the information of which calls refer to which species. Therefore you can examine files with batIdent (single file mode) in more detail. Figure 8 shows analysis results of a record-

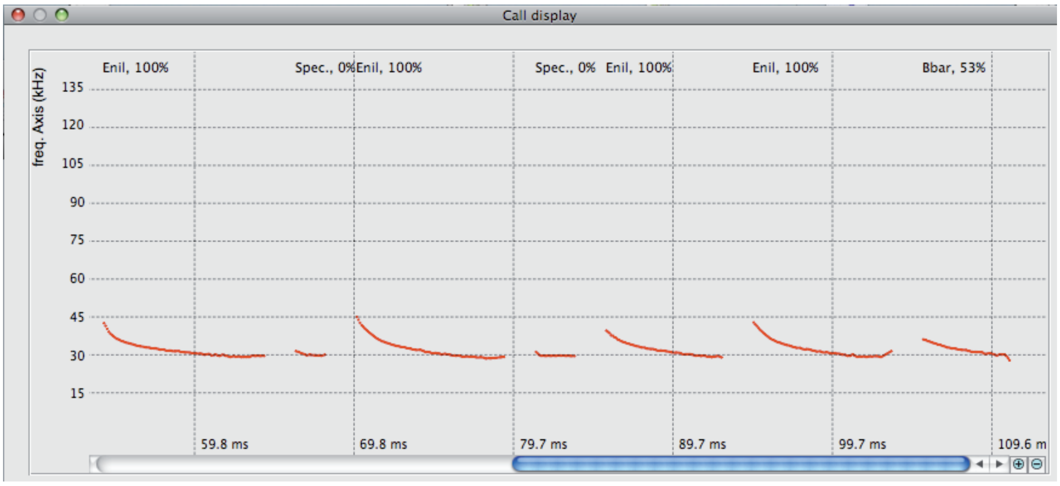


Fig. 9: Assignment probabilities in the Call Display of bcAdmin. Some echoes were measured and simply classified as “Spec”. One call fraction was assigned to the Barbastelle Bat (Bbar) with a low probability. All other calls were properly measured and determined as calls from the Northern Bat (Enil), from which these calls in fact came from (the display of call results is available in version 1.15 and 2.0 respectively).

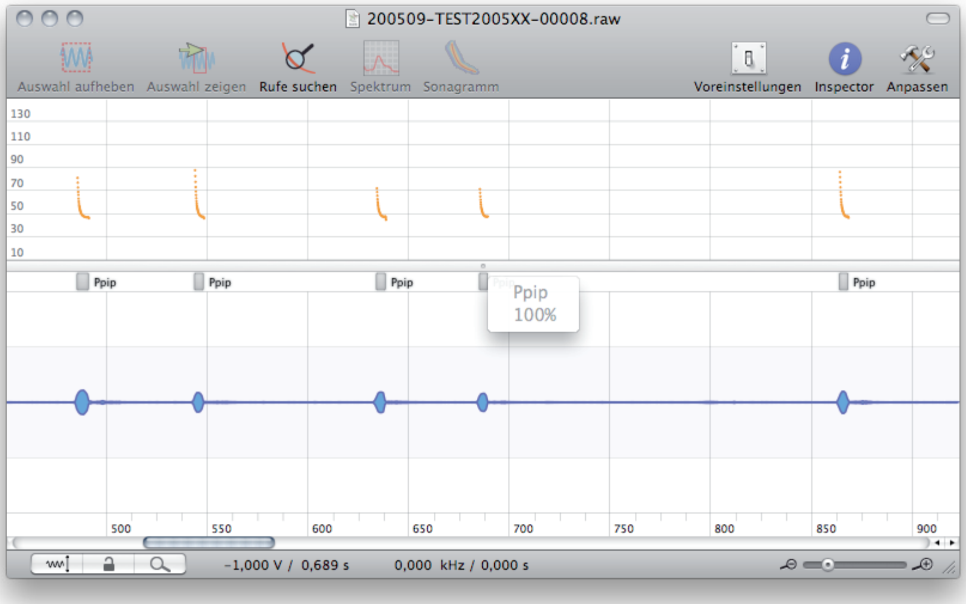


Fig. 10: Call-wise illustration of analysis results in bcAnalyze (available from version 1.07. on). Results are shown above calls if activated in the preferences. You can achieve more detailed information by right clicking on the grey boxes.

ing file in batIdent: the right side of the window provides a decision tree, which depicts single analysis steps with its call numbers and assignment probabilities.

bcAdmin and bcAnalyze show species assignments directly above calls in the Call View Window and in the oscillogram respectively (Fig. 9 and 10).

In summary: given probabilities constitute an important and meaningful tool for the interpretation of results. However, these values must not be viewed as absolute criteria for the examination of single calls although misclassification can quickly be found with some experience.

3.3.2. Are calls measured correctly and completely?

In bcAdmin you can display and quickly go through calls of a sequence in a frequency-time diagram (call display). Incorrectly measured calls which might lead to wrong determinations stand out clearly in most cases (see also Fig. 9, 11, and 12).

There are several factors that can lead to faulty measurements like echoes (Fig. 11) and background noise. An echo that overlaps with a call can be measured as a complete call which often happens with constant-frequency calls. Intense echoes of frequency-modulated calls often cause incomplete measurements. Echoes following calls without delay (e.g., Daubenton's Bats closely above water; Fig. 14) produce oscillating amplitudes (interferences). Gaps in calls cause incomplete measurements because the algorithm only skips short gaps but aborts measurements when gaps are too large. Short call fractions are usually not suitable for a classification and are thus named "Spec." (unidentifiable species). Sometimes such fractions resemble calls of other species (e.g., the Barbastelle Bat),

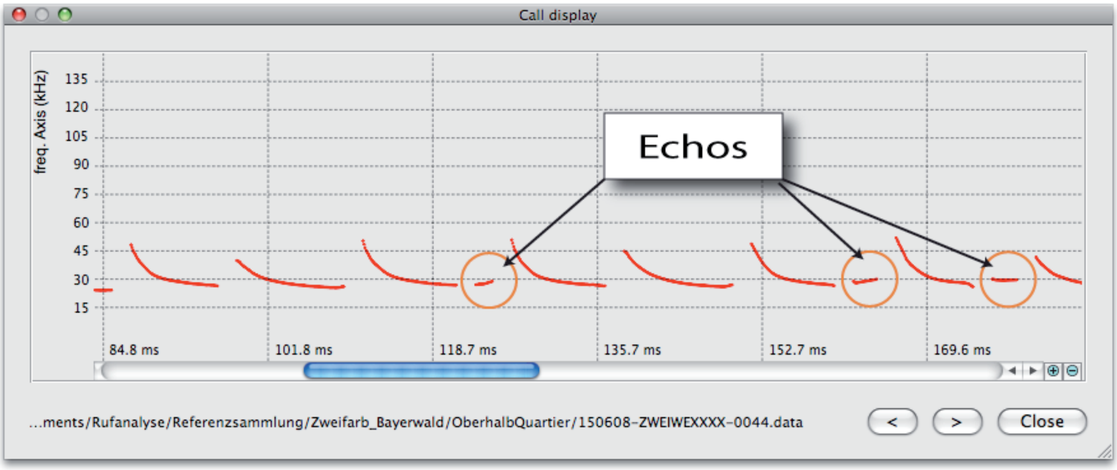


Fig. 11: Example of measured echoes: in this case no corruption of the sequence determination occurred because a sufficient number of calls were measured properly.

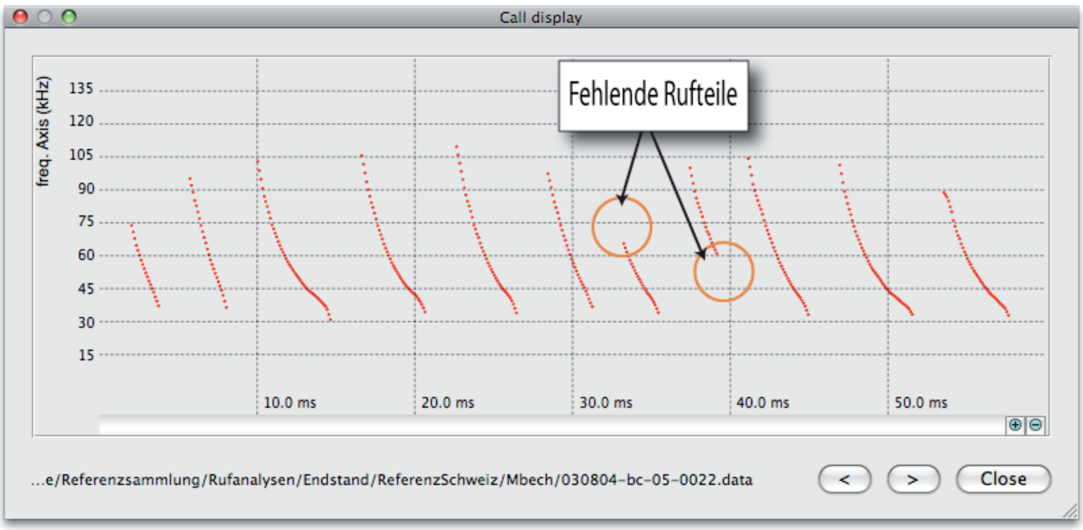


Fig. 12: Example of lacking call beginnings and endings: again this did not influence the determination result significantly because a sufficient number of calls were measured properly.

which can lead to misclassifications. An incomplete signal measurement can also arise from muted calls. In such cases typically the beginning or the end of the call is lacking (Fig. 12).

These interfering factors are ignored by the discrimination algorithm to some extent, but with more improperly measured calls more incorrect call classifications occur. Several misclassified calls amongst regular calls within a recording file can lead to a misleading determination of a “second species”. It is therefore advisable to check recordings with several species determinations.

Those error source are mostly visibly to the user in the call display of bcAdmin. However, for a closer analysis it might be necessary to examine the oscillogram and sonogram. Such an in-depth revision of measured calls is feasible in bcAnalyze.

3.3.3. Sound level of calls

Measurement quality increases with the sound volume of calls. Particular call beginnings of frequency modulated calls (e.g., calls of the Genus *Myotis*) are quiet and

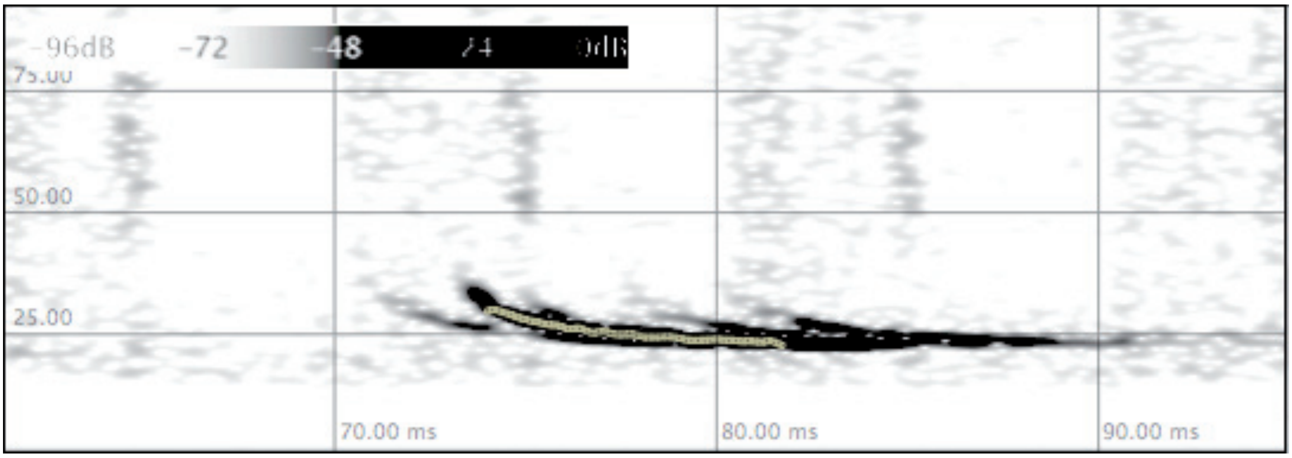


Fig. 13: Example of a sonogram: the call could not be measured completely due to overlapping echoes. White points within the call show the measured section.

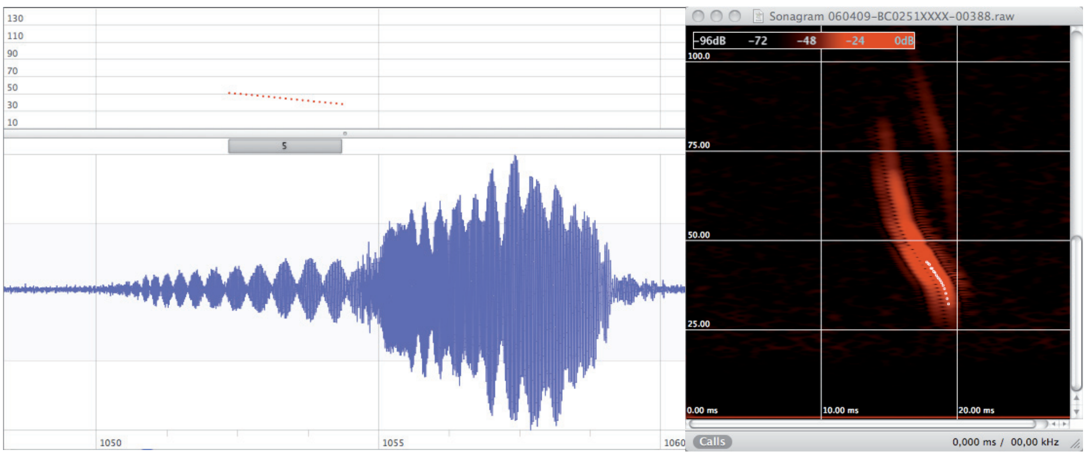


Fig. 14: Call oscillogram and sonogram of a Daubenton’s Bat hunting above water. Oscillating amplitudes (beating waves) resulting from a pronounced overlapping echo are visible in the oscillogram. The sonogram unveils that the call is almost completely coalesced with its own echo. bcAdmin only identified a short part of the complete call. This fragment is shown above the oscillogram and marked by white points in the sonogram.

are not detected in recordings with a low recording level. This can lead to an alteration of measurements such as starting frequency and call duration. The determination of a sequence becomes equivocal if the sequence consists of only a few and quiet calls.

A control of the sound level is possible in bcAnalyze's oscillogram view.

3.3.4. Social calls

A program for automated determination can only utilise calls for which it has been trained for. Calls that were not part of training calls are problematic for the program's algorithm. For the training a substantial range of echolocation calls but almost no social calls were incorporated (except for the genus *Pipistrellus* in batIdent). Apart from specific locations (roosts) and certain times of the year (mating season) social calls are barely recorded in the field.

Bats emit different types of social calls regarding their complexity: there are plain social calls with only a single element but also complex social calls composed of several units. The former can be measured easily unless they are not masked by echoes. The latter however are hard to measure automatically because they consist of an iteration and combination of different call elements. The statistical analysis is also more complicated because other parameters (especially chronological features) have to be considered. Structures made of several syllables are easy to recognise manually but can hardly be extracted automatically. Social calls that are clearly separated in time are even more difficult to handle because they are recognised as single calls.

Moreover, some social calls greatly vary within species and other social calls are used in a similar way by many species (e.g., trills). All these factors impede an automated determination so that a manual revision becomes necessary. For this, especially the temporal aspect (chronology of recordings) is helpful. Social calls can be assigned to species if they lie in between sequences of temporally connected recordings which are correctly determined by the measurement of echolocation calls.

However, great numbers of social calls are rarely recorded in investigations. Dr. Volker Runkel conducted a comprehensive two-year study with automated species analyses for his Ph.D. thesis: for example in August 75% of all recordings of Soprano Pipistrelle's (*Pipistrellus pygmaeus*) were social calls. In all the other months often much less than 25%, down to nearly 0% of all recordings were social calls. Species determinations were possible in most instances because the recordings contained enough clear echolocation calls. For *Myotis* species less than one percent of all recordings included social calls. Thus, social calls usually play no role in species determination when using automated recording systems due to their low occurence rate. They do not interfere significantly with the species determination of present species.

3.3.5. Manual species determination via call shape and other measurable parameters

In a sonogram manually or semi-automatically extracted measurements can be used for species determination on the basis of published measurements and own experience. The call shape, which is manually compassed and described in a rather subjective way constitutes also an important criterion for the decision.

The calls of almost all species are variable and are adjusted to the momentary surroundings, function, and flight situation. Therefore, single parameters (e.g., ending frequency) are not sufficient for a reliable determination but several parameters and their interrelation have to be considered. The human perception is quickly overextended with such complex patterns and a statistical, automated species determination mostly beats any manual assessment if enough well measured calls are available. A manual revision is advisable for the verification of single recordings of easily determinable species, for the examination of sequences that were inadequately measured, or if sequences are “polluted” by social calls. It is important to keep in mind that the quality of any manual species determination depends on the user’s ability and experience. Therefore, any user should not overrate him- or herself and should determine doubtful recordings “only” in a conservative manner.

The following table provides a challenge assessment of the manual species determination of European bat species:

* Amateur I: without difficulty and unmistakable even for amateurs.

** Amateur II: without difficulty and unmistakable for amateurs with some practice.

*** Expert I: mostly without difficulty and unmistakable; there are some overlapping instances.

**** Expert II: mainly difficult calling types that can be determined securely.

***** Expert III: very sophisticated - highly risky.

Species/Group	Challenge
Rhinolophus hipposideros	*
Rhinolophus ferrumequinum	*
Genus Plecotus	***
Barbastella barbastellus	**
Vespertilio murinus	*****
Nyctalus noctula	***
Nyctalus leisleri	****
Eptesicus serotinus	****
Eptesicus nilssonii	***
Hypsugo savii	**
Pipistrellus kuhlii	***** (**)
Pipistrellus nathusii	***** (**)
Pipistrellus pipistrellus	**
Pipistrellus pygmaeus	**
Myotis myotis	***
Myotis dasycneme	***
Myotis alcathoe	***
Myotis bechsteinii	****
Myotis nattereri	***
Myotis brandtii/mystacinus	****
Myotis daubentonii	***
Myotis emarginatus	****

This text is not intended to provide an overview of call parameters and call characteristics of central-European species. For such information please refer to the literature: for example the leaflet “Kriterien für die Wertung von Artnachweisen basierend auf Lautaufnahmen” which was developed in cooperation with the Koordinationsstellen für Fledermausschutz in Bayern (http://www.ecoobs.de/downloads/Kriterien_Lautzuordnung_10-2009.pdf). Another good source is http://batecho.eu by Arjan Boonman.

4. Summary of revision advises

- generally check species determinations that are based on only one or a few sequences
- always check rare or not expected species
- identify improperly measured calls, social calls or interfering signals with the call view of bcAdmin
- if this does not clarify the case, examine the sequences by their sonogram in other programs
- doubtful sequences can be determined individually by batIdent
- in case of doubt ignore species assignments of sequences within a block of recordings of similar calling species
- high error probability with low amount of calls
- higher error probability with decreasing sound volume
- higher error probability with increasing number of determined species per sequence
- do not overrate your own abilities when determining species manually

4.1. Known sources of error

- very short calls of *Pipistrellus pipistrellus* and *P. pygmaeus*, and *Myotis*-calls that have not been measured to their end are frequently determined as *Myotis alcathoe* (often as a second species!).
- ending fragments of quiet *Myotis*-calls and short fragments of several other species are sometimes determined as Barbastelle Bat.
- *Myotis bechsteinii* is recognized insufficiently and often only assigned to the species group "Mkm" (*Myotis* small/medium).
- calls of Daubenton's Bats above water are often measured incompletely due to overlapping echoes. Resulting fragments may lead to incorrect species determinations.
- Short calls of Nyctaloid species are uspecific and are identified on genus/group level or incorrectly classified.
- Fragments of echos of nyctaloid calls may be identified as social calls of Pipistrelloid species or Barbastelle calls (rarely).
- *Vespertilio murinus* is hard to identify and oftgen only determined on the level Nycmi. Incorrect classifications as other nyctaloid species occur.
- Calls of *Pipistrellus pipistrellus*, *P. pygmaeus* and *Miniopterus schreibersii* overlap and are often classified as "Phoch" (high calling Pipistrelloids). Incorrect classifications nevertheless occur (approx. 2% of all calls).
- *Pipstrellus nathusii* and *P. kuhlii* use very similar calls and thus often are misclassified (20% error probability).

Analyse

Furthermore software specific errors can occur, as described in the following:

Typical errors of bcDiscriminator

- Social calls of the genus *Pipistrellus* are not recognized and classified as Spec. or a Nyctaloid call.

Typical errors of batIdent

- Daubentons/Pond bat calls are sometimes classified as *Hypsugo savii*.
- *Nyctalus leisleri* calls sometimes get classified as *Eptesicus nilssonii*.
- calls of Tadarida teniotis sometimes get classified as pipistrelloid social calls.

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