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A Guide to Processing Bat Acoustic Data for the North American Bat Monitoring Program (NABat) version 1.2

By Dane Smith, Brian E. Reichert, Cori Lausen, Susan Loeb, Ted Weller, Ryan Allen, Eric Britzke, Tara Hohoff, Jeremy Siemers, Braden Burkholder, and Michelle Verant

Open-File Report 2020–XXXX

U.S. Department of the Interior
U.S. Geological Survey

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U.S. customary units to International System of Units

Multiply	By	To obtain
Length		
mile (mi)	1.609	kilometer (km)
mile, nautical (nmi)	1.852	kilometer (km)
yard (yd)	0.9144	meter (m)

International System of Units to U.S. customary units

Multiply	By	To obtain
Length		
kilometer (km)	0.6214	mile (mi)

Abbreviations

Auto ID	Automated Species Identification
BCID	Bat Call Identification (software)
FFT	Fast Fourier transform
FS	Full spectrum recording format
GPS	Global Positioning System
GRTS	Generalized Random-Tessellation Stratified design
GUANO	Grand Unified Acoustic Notation Ontology, a universal, extensible, open metadata format for acoustic files
KSPro	Kaleidoscope Pro (software)
ms	millisecond (1 ms = 0.001 seconds)
NABat	North American Bat Monitoring Program
USGS	U.S. Geological Survey
WAV	Waveform audio-file format, standard for storing audio bit-stream on personal computers
ZC	Zero-cross audio file format and recording format

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[5]Illinois Natural History Survey
[6]Colorado Natural Heritage Program
[7]Montana Natural Heritage Program
[8]New York State Department of Environmental Conservation
[9]National Park Service

Introduction

The North American Bat Monitoring Program (NABat) is a multi-national, multiagency coordinated monitoring program designed to assess the status and trends of North American bats at local, state, and range-wide scales. NABat monitoring efforts focus on the 47 species of bats shared by Canada, the United States, and Mexico. NABat is composed of a network of partners including local, State, Federal, and provincial Agencies, Tribes, non-governmental organizations, and volunteers collecting bat survey data and invested in bat conservation. Information from NABat can be used to inform land management and conservation decision making.

The success of NABat is predicated on making reliable inferences about bat distributions and their relative abundance from data collected and processed using standardized techniques and protocols in a consistent manner over space and time. In 2015, "A Plan for the North American Bat Monitoring Program (NABat)" (Loeb and others, 2015) was developed, providing the foundation and overall direction needed for the initial implementation of NABat. Loeb and others (2015) represented the first step towards the establishment of standardized protocols, with the understanding that guidance would be refined and more specific protocols would be made available over time.

NABat relies in part on acoustic monitoring using stationary and mobile transect survey methodologies. Currently, however, acoustic data are managed and processed using a variety of methods. These inconsistencies may introduce sources of undocumented, systematic bias that could limit the utility of these combined data for evaluating bat distributions and trends at broader scales. We believe there is a need for more specific guidance on detector settings, protocols for deploying acoustic detectors, and a standardized workflow for analyzing acoustic data. Standardized protocols and workflow can help to establish a common currency from which to improve the interpretation of acoustic data by reducing variation and uncertainty in how bat echolocation calls are collected, processed, and identified to species.

In 2017, the U.S. Geological Survey (USGS) Fort Collins Science Center hosted a workshop of bat acoustic experts with the goal of developing a suggested workflow to help standardize the analysis of acoustic data for NABat (NABat Acoustic Data Analysis Workflow

Workshop, 2017). The guide that follows is a product of that workshop. While accurate and efficient analysis of bat acoustic data requires a minimum level of expertise and training, the suggested workflow is intended to help make this process more repeatable and feasible for a wider pool of potential NABat partners, including those with limited resources and experience. To this end, the workflow was developed with the intention of minimizing the amount of time and effort required for processing bat acoustic data for NABat while following a "conservative" approach that reduces subjectivity and minimizes the potential for species misidentification.

The following provides general recommendations and specific workflows for the process of identifying bat species from acoustic files recorded using both stationary point and mobile transect acoustic monitoring protocols for NABat (Loeb and others, 2015). It focuses exclusively on post-processing of acoustic data. For recommendations on detector settings and detector deployment, download the "NABat Guide to Site Selection for Stationary Point Monitoring" and the "NABat Guide to Acoustic Detector Settings" available on the "Resources" page of the NABat website (https://nabatmonitoring.org/resources).

The described workflow includes data attribution (step 1), noise scrubbing (step 2), automated species identification (auto ID) (step 3), manual vetting (step 4), and submitting data to NABat (step 5). Some auto ID software automates the process and allows you to complete steps 1–3 at once. The workflow varies at step 2 and step 4 for stationary versus mobile transect monitoring because of the inherent differences between objectives (that is, species occupancy versus species relative abundance, respectively). For detailed workflows and tips for using specific software programs see chapters 1–5 and appendixes A and B of this report.
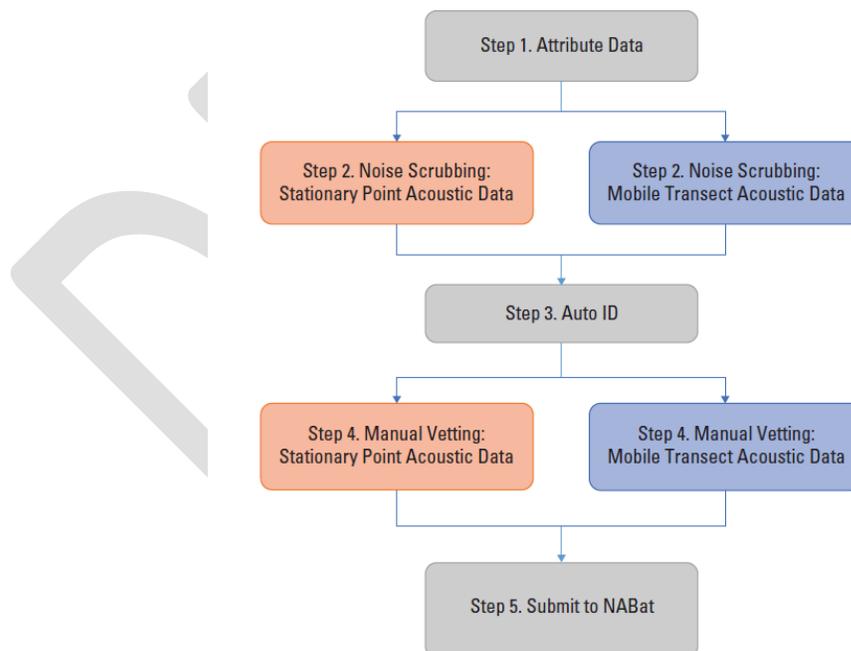
Figure 1. A general workflow for processing recorded acoustic files for the North American Bat Monitoring Program (NABat). Note: Workflow guidance varies between stationary point and mobile transect survey data at steps 2 and 4, because objectives differ between survey methodologies (site occupancy from stationary point acoustic data versus relative abundance of species from mobile transect data).

This document is NOT meant to serve in place of the user manual or official documentation provided by the software developers. It should only serve to help users follow NABat protocols while using the available software. It is strongly recommended that users are familiar with the software user's manual before using this document.

Step 1. Attribute Acoustic Files

Download cards or recorded acoustic files to a hard drive. Be sure to retain all status and log files associated with recordings (these are indispensable for troubleshooting missing data and low data rates).

Naming Acoustic Files

Files are no longer required to conform to NABat naming conventions if a timestamp is provided with the metadata for each recording. Many detectors embed a timestamp into each recording, and the NABat metadata forms for Kaleidoscope and SonoBat (see Chapters 1 and 2) will automatically extract these data and autofill the corresponding columns in the metadata output. However, users should ensure that their data contain timestamps before skipping the renaming process. Furthermore, NABat encourages users to follow the naming conventions below, regardless of whether a timestamp is included in file metadata.

Use **Grid Cell GRTS ID, Site Name, and timestamp** (using 24-hour clock notation) as a prefix for recording filenames (see table 1 for definitions). Each element *must* be separated by an underscore. When put together, **Grid Cell GRTS ID** and **Site Name** provide a unique identifier for each detector deployment.

Examples

- 5867_NW_20160712_210932: This file was recorded in a NABat grid cell with GRTS ID 5867, at the NW site (or quadrant), on July 12, 2016 at 21 hours (or 9 pm) 9 minutes and 32 seconds.
- 5867_DT_20160712_214930: This file was recorded in a NABat grid cell with GRTS ID 5867, on a mobile driving transect (DT), on July 12, 2016 at 21 hours (or 9 pm) 49 minutes and 30 seconds.

To more easily compare surveys across grid cells and sites over time, maintain a consistent naming convention. For your reference, it can be helpful to develop an "authority file" of your naming conventions so (1) each code is unique and (2) additional description can be entered for each code to properly identify the site.

Depending on detector and software system used, this naming prefix can typically be pre-programmed prior to field recording, and (or) can be edited for entire batches of files during post-processing. Additionally, NABat offers a free tool for batch renaming files, available for download at https://github.com/talbertc-usgs/GuanoMDEditor/releases/tag/0.0.1. To rename acoustic files using the NABat tool:

1. Download the renaming tool from the above link, install the program, and open.

2. Click "Browse" to the right of the "Source Directory" box and navigate to the folder containing files you wish to rename. The folder should not contain files for more than one

deployment (the new filenames must include site name). All files within the selected folder will appear in the white boxes beneath the renaming tools.

3. Click the "NABat Auto Correct" box to remove superfluous characters from the filename.

4. Click the "GRTS ID is" box and enter the GRTS ID for your survey.

5. Click the "Site Name is" box and enter the ≤ 6-character site name.

6. Use the "String Replace" fields to remove additional superfluous characters and/or replace dashes and other symbols with underscores where necessary.

7. As you specify edits within the NABat File Renamer, a red preview of the new filenames will appear in the bottom right box. Review the new filenames to ensure you have correctly edited the original names.

8. Once you have properly formatted the filenames, click "Rename Files" in the lower right corner to save the changes. This will overwrite the original filenames, and the newly renamed files will be available in the original folder. If you wish to retain the original filenames and create new files with edited names, choose a destination for the newly named files using the "browse" button to the right of the Output Directory field at the top of the window. If an output directory is specified, the renaming tool will create new files with edited names in the selected folder and retain the original filenames in their previous location.

Assigning Metadata to Acoustic Files

It is important that each recorded acoustic file also be attributed with metadata (that is, information about the recorded file). To meet the data management requirements for NABat, **Grid Cell GRTS ID or Latitude/Longitude, Site Name, Survey Start Time, Survey End Time, Auto ID or Manual ID, Software Type, and Species List** must also be included as metadata for each file (see tables 1 and 2 for definitions). It is also strongly recommended that the information in tables 1 or 2, depending on the survey type, be added as metadata to individual files to help contextualize recordings. This information summarizes the recording situation and should also be included in the metadata CSV upload.

These metadata fields may be represented using the extensible Grand Unified Acoustic Notation Ontology (GUANO) metadata format as presented in table 1. Additional resources for attributing files with metadata are available at https://nabatmonitoring.org/#/resources. See chapters 1–5 of this report for more details on how to assign metadata using specific software.

Table 1. Required and recommended metadata fields for the North American Bat Monitoring Program (NABat) stationary acoustic files. Metadata should be embedded in individual files. [km, kilometer; WGS, World Geodetic System 1984]

GUANO Field	Required / Recommended	Description/Instruction
NABat|Grid Cell GRTS ID*	Required*	GRTS ID number of the NABat grid cell where the survey was conducted. This is also the NABat sampling priority of the grid cell based on the GRTS master sample, for example, lower GRTS ID = higher NABat sampling priority.
NABat|Site Name	Required	A user-defined name (6-character limit) of the specific location (or point) where a detector was deployed within a single grid cell. Being consistent with site names from year to year allows for easier sorting and interpretation of the data.

NABat|Latitude *	Recommended*	Latitude (WGS) of the stationary point where detector was deployed
NABat|Longitude*	Recommended*	Longitude (WGS) of the stationary point where detector was deployed
NABat|Activation start time	Required	Time when detector was activated to start recording. Note that this may be different than deployment start time.
NABat|Activation end time	Required	Time when detector was deactivated. Note that this may be different than deployment end time.
NABat|Detector type	Recommended**	Brand and model (restricted entry)
NABat|Detector Serial Number	Recommended	Serial number of detector/recording device
NABat|Microphone type	Recommended**	Brand and model (restricted entry)
NABat|Microphone Serial Number	Recommended	Serial number of microphone device
NABat|Microphone orientation	Recommended**	Direction the microphone was pointed (restricted entry)
NABat|Microphone height	Recommended	Height (meters) of microphone above ground
NABat|Distance to clutter	Recommended	Distance (meters) between microphone and nearest clutter; for example: vegetation, buildings, or other structure
NABat|Type of clutter	Recommended**	Nearest clutter type; for example: vegetation, buildings, or other structure (restricted entry)
NABat|Percent clutter	Recommended	Percent of clutter surrounding microphone
NABat|Distance to water	Recommended	Distance (meters) between microphone and nearest water
NABat|Water type	Recommended	Broad type of nearest water
NABat|Habitat type	Recommended**	Broad habitat type surrounding microphone (restricted entry)
NABat|Land unit code	Recommended	A user-defined 4-letter abbreviation describing your study area, region, park, state, or land unit. For example: if the survey is conducted in a park or refuge, use park or refuge codes (YELL for Yellowstone National Park, etc.). If the survey is not carried out in a park or refuge, the user creates a 4-letter abbreviation for land unit code based on the region or larger surrounding area (for example: SOCA for South Carolina, 3LMA for Three Lakes Wildlife Management Area). Note that multiple sites (Site Names) can exist within the same land unit code.
NABat|Contact information	Recommended	Contact information for person/entity that recorded the file
NABat|Weatherproofing	Recommended	Indicate whether weather proofing was used on microphone (TRUE|FALSE)
NABat|Unusual occurrences	Recommended	Indicate whether unusual occurrences took place during the recording session that may impact the interpretation of results (for example: power to detector may have been low, time not adjusted for daylight savings time, recording was interrupted due to dead batteries, filled data card, microphone or cable damage, schedule programming error, late deployment, etc.).
NABat|Nightly Low Temperature	Recommended	The nightly low temperature (C)
NABat|Nightly High Temperature	Recommended	The nightly high temperature (C)
NABat|Nightly Low Relative Humidity	Recommended	The nightly low Relative Humidity (%)
NABat|Nightly High Relative Humidity	Recommended	The nightly low Relative Humidity (%)
NABat|Nightly Low Weather Event	Recommended	Notes on a light significant weather event (e.g. Light Snow)
NABat|Nightly High Weather Event	Recommended	Notes on a heavy significant weather event (e.g. Heavy Rain)
NABat|Nightly Low Wind Speed	Recommended	The nightly low Wind Speed (km/h)
NABat|Nightly High Wind Speed	Recommended	The nightly high Wind Speed (km/h)
NABat|Nightly Low Cloud Cover	Recommended	The nightly low Cloud Cover (%)
NABat|Nightly High Cloud Cover	Recommended	The nightly high Cloud Cover (%)
NABat|Software type	Required**	The type of software used for file processing, auto ID, and vetting (restricted entry)
NABat|Species List	Required	Name of the species list created or selected in your NABat project homepage. The species list should include all species considered in the auto and manual ID process. Users with specific knowledge of local species assemblages and projects that cover large areas may use multiple species lists based on the location of the deployment.

* Either GRID Cell GRTS ID <u>OR</u> Latitude/Longitude are required. If Lat/Long are provided and GRTS Cell is unspecified, NABat will auto-assign the appropriate cell.

** Restricted categorical field. For a full list of accepted entries, see
https://www.sciencebase.gov/catalog/file/get/5e3de185e4b0edb47be3d6e6?name=NABat_Metadata_Fields.

Table 2. Required and recommended metadata fields for the North American Bat Monitoring Program (NABat) mobile acoustic transect files. Metadata should be embedded in individual files. [C, Celsius; km, kilometer; WGS, World Geodetic System 1984]

GUANO Field	Required / Recommended	Description/Instruction
NABat|Grid Cell GRTS ID*	Required*	GRTS ID number of the NABat grid cell where the survey was conducted. This is also the NABat sampling priority of the grid cell based on the GRTS master sample; for example, lower GRTS ID = higher NABat sampling priority.
NABat|Site Name	Required	A user-defined name (6-character limit) of the specific mobile transect route within a single grid cell. Being consistent with route names from year to year allows for easier sorting and interpretation of the data. If stationary point surveys were conducted within the same grid, the corresponding stationary point name, with an additional identifier like "DT" (mobile driving transect), would be appropriate (e.g. SWDT, NEDT, etc.)
NABat|Latitude *	Recommended*	Latitude (WGS) of the specific point where each file was recorded
NABat|Longitude*	Recommended*	Longitude (WGS) of the specific point where each file was recorded
NABat|Activation start time	Required	Time when detector was activated to start recording
NABat|Activation end time	Required	Time when detector was deactivated
NABat|Detector type	Recommended**	Brand and model (restricted entry)
NABat|Detector Serial Number	Recommended	Serial number of detector/recording device
NABat|Microphone type	Recommended**	Brand and model (restricted entry)
NABat|Microphone Serial Number	Recommended	Serial number of microphone device
NABat|Microphone placement	Recommended	Where the microphone was mounted during the mobile transect
NABat|Habitat type	Recommended	Broad habitat type surrounding microphone
NABat|Contact information	Recommended	Contact information for person/entity that recorded the file
NABat|Comments	Recommended	Indicate whether unusual occurrences took place during the recording session that may impact the interpretation of results; for example, power to detector was low, time not adjusted for daylight savings time, recording was interrupted due to dead batteries, filled data card, microphone or cable damage, schedule programming error, late deployment, etc.
NABat|Nightly Low Temperature	Recommended	The nightly low temperature (C)
NABat|Nightly High Temperature	Recommended	The nightly high temperature (C)
NABat|Nightly Low Relative Humidity	Recommended	The nightly low Relative Humidity (%)
NABat|Nightly High Relative Humidity	Recommended	The nightly low Relative Humidity (%)
NABat|Nightly Low Weather Event	Recommended	Notes on a light significant weather event (e.g. Light Snow)
NABat|Nightly High Weather Event	Recommended	Notes on a heavy significant weather event (e.g. Heavy Rain)
NABat|Nightly Low Wind Speed	Recommended	The nightly low Wind Speed (km/h)
NABat|Nightly High Wind Speed	Recommended	The nightly high Wind Speed (km/h)
NABat|Nightly Low Cloud Cover	Recommended	The nightly low Cloud Cover (%)
NABat|Nightly High Cloud Cover	Recommended	The nightly high Cloud Cover (%)
NABat|Software type	Required**	The type of software used for file processing, auto ID, and vetting (restricted entry)
NABat|Species List	Required	Name of the species list created or selected in your NABat project homepage. The species list should include all species considered in the auto and manual ID process. Users with specific knowledge of local species assemblages and projects that cover large areas may use multiple species lists based on the location of the deployment.

* Either GRID Cell GRTS ID <u>OR</u> Latitude/Longitude are required unless a spatial file of the survey route is provided. If Lat/Long are provided and GRTS Cell is unspecified, NABat will auto-assign the appropriate cell. If neither GRTS ID or Lat/Long are provided, the NABat database will estimate locations based on start/end times of the survey and route length.

** Restricted categorical field. For a full list of accepted entries, see
https://www.sciencebase.gov/catalog/file/get/5e3de185e4b0edb47be3d6e6?name=NABat_Metadata_Fields.

Step 2. Noise Scrubbing

Acoustic sampling for bats results in the recording of both bat echolocation calls and extraneous noise (that is, non-bat files). In some circumstances, files with extraneous noise can represent a large proportion of the recorded files. The goal of noise scrubbing is to identify and separate files with only extraneous noise from files with bat echolocation calls. Noise scrubbing reduces storage requirements and increases efficiency of the call identification process.

Multiple automated methods can be used to remove extraneous noise. At its core, the noise scrubbing process represents an inherent balancing act between removing non-bat sounds and low quality bat echolocation calls. An optimized noise scrubbing process will result in retention of recordings of bats potentially identifiable to species while retaining a trivial number of non-bat recordings. Achieving this balance will depend on the software employed, the parameters specified, and the recording situation. For example, in areas with high levels of background noise, it may be necessary to remove a larger proportion of low-quality echolocation recordings in order to minimize the number of files that do not contain bat echolocation recordings.

Scrubbing Stationary versus Mobile Datasets

For NABat stationary acoustic monitoring, where the goal is to document species presence based on identification of high-quality echolocation recordings, noise scrubbing specifications should be more stringent to retain mostly high quality calls. Whereas for NABat mobile acoustic transects, where the goal is to document the relative abundance of each bat species, noise scrubbing should be more lenient, where parameters are set to retain all potential bat recordings.

In general, the software packages described here provide robust methods for separating bat echolocation calls from non-bat, extraneous noise and are easily customizable to be more stringent or lenient in the files that pass. However, the various methods for automated noise filtering differ. Some programs have a separate file scrubber used as a standalone step (e.g., SonoBat [chapter 2] and SCAN'R [not presented here]) while other software programs integrate file scrubbing into the process of auto ID (e.g. BCID [chapter 3] and EchoClass [chapter 4]). Still others have it optionally as an integrated or standalone step (e.g., Kaleidoscope [chapter 1]). For zero-cross (ZC) files, scrubbing can also be done in AnaLookW v4.2g (Titley Scientific, 2016 [chapter 5]) using a filter prior to being analyzed in one of the auto ID programs. When starting with a new program, it may be helpful to review samples of stationary and mobile acoustic datasets post scrubbing to determine appropriate settings.

Step 3. Auto ID

The objective of using auto ID, or automated species identification, is to rapidly determine a species classification for large amounts of data in order to determine probable

presence for the species of interest. Auto ID includes additional filtering to select pulses that are suitable for identification and then classify pulses and files. Classification methods vary among software programs but all rely on statistical comparisons of unknown pulses to classifiers or algorithms developed from a known call library of selected species. A critical part of this process is that the user must select the correct set of species to be used in this classification process. This is an important step as the user needs to make sure that all of the possible species in the state or region are included in the species set (including accounting for potential range expansions) while excluding species that are unlikely to occur. Note that some software classifiers may have limited species support. Many software suites include pre-loaded regional or state species lists, but users are advised to review these template lists to ensure all species that are potentially present in the survey area are included. Additionally, NABat requires users to create a species list on their project homepage indicating which species were considered when identifying calls. Users may create multiple species lists within a single project when necessary. The name of the species list used to identify calls must be included in the metadata upload (see step 5). To create a species list:

1. Login to NABat and navigate to your project homepage (https://sciencebase.usgs.gov/nabat/#/home).

2. Click the "Species Lists" tab beneath your project name at the top of the page.

3. Click the green edit button in the top right of the page.

4. Click the "Add +" button in the top right of the page.

5. Create a name for the new species list (user defined) and add a brief description.

6. Using the drop-down menu under "Definition," click the box beside all species which were/will be considered during auto and manual species identification.

7. Click the green "Save" button in the in the top right of the page.

8. Include the species list name in your metadata upload exactly as it appears on your project homepage.

Software programs for auto ID have varying levels of customization for species classification, including the degree of similarity required between known (underlying reference library) and unknown recordings for a species-level identification to be made by the program. In general, a more conservative (which hopefully leads to an increase in accuracy) level of classification is desired. These specifics are included in chapters 1–5. Some programs embed species classification labels as metadata into the files of bat recordings (e.g., SonoBat, Kaleidoscope Pro, BCID, and AnaLookW). Metadata formats are evolving; currently not all metadata written to a file by one program will be read by another program. Some software allows you to access and view files with auto ID metadata from within the software (SonoBat and Kaleidoscope Pro) while others require an additional software viewer be used if recordings are to be visualized (for example, AnaLookW can be used to view files that have been processed with BCID, EchoClass, or Kaleidoscope Pro).

Step 4. Manual Vetting

Auto ID software programs are limited by various issues in the analysis process that can lead to inaccurate species classifications. Generally, programs are unable to account for deviations from expected call structure due to atypical bat behavior, approach calls, cluttered environments, presence of social calls, recorded call quality issues, multiple individual bats and/or species in a recording, trends across a sequence of call pulses, and inherent overlap that exists in call metrics, pulse shape, and (or) sequence pattern between some species. Both automated classification programs and manual vetting can also be limited by their underlying libraries of known calls. When there are biases in the reference library (for example, proportion of certain pulse shapes, under-representation of a particular species, and misidentification of recorded species), identification of unknown calls can also be inaccurate.

The goal of manual vetting acoustic files for NABat is to eliminate species misclassifications resulting from the automated identification process, because species misclassifications can lead to false-positive errors (that is, documenting that a species was present in a grid cell when it was not). To meet this goal, manual vetting should focus on ensuring that auto ID classifiers have not misclassified files based on poor recording quality, non-search phase components of calls, recordings with multiple bats that may cause one or more bats to vary their echolocation outside the known norms for the species, or echolocation calls from species other than the species suggested from the auto ID. Manual vetting is a qualitative process that requires users with extensive experience.

General Recommendations:

1. Accept the fact that not all call sequences can be, or should be, definitively identified to a species using diagnostic characteristics measurable in sound viewing/analysis software.

2. View the recording in "real-time" (most viewers will default to showing recordings in "compressed view") to help visualize inter-pulse intervals (the relatively long periods of silence in between call pulses). Ensure that there is a consistent inter-pulse interval indicating that the bat was performing a typical "search-phase" call type and not performing a behavior such as an inspection or acquisition ("approach-phase" call type). Approach-phase behaviors result in call pulses with parameters that differ from search phase calls such as higher frequencies, broader bandwidth, and steeper slopes. Approach-phase pulses often show a high degree of overlap among species. To examine pulse shape parameters, view in "compressed time."

3. Limit the potential species list for a particular acoustic survey site by the potential geographic ranges of species; if a species is less likely to be present and does not have large overlap in call characteristics with more common species in the area, include it in the analysis. Otherwise, if a species is unlikely and has overlapping call characteristics with other species in the area, it is likely best to not include this species in the potential species list, until there is more evidence to justify looking for it acoustically.

4. Review a single species at a time in order to be consistent and efficient in your manual review. This can be achieved in some programs (e.g., Kaleidoscope Pro, SonoBat, BCID, and AnaLookW) by sorting species-labelled files (metadata embedded in files following automated ID) and then viewing files in order by species. If sorting of files is not available within the automated ID software, then an associated viewer software can be

used (for example, BCID engages AnaLookW as a viewer following auto ID), or a results output file can simply be viewed in a tabular program or database (e.g., Microsoft Excel file) where files can be sorted by species, and then viewed in a separate viewer (for example, ZC recordings analyzed in EchoClass can be manually viewed in AnaLookW).

5. Review the entire sequence. Look for long call sequences, for example, those with multiple consecutive pulses in a sequence, especially pulses that have consistent inter-pulse intervals and consistent shapes, slopes, and bandwidths. The more calls with definitive features, the more confident the identification.

6. You may want to examine recordings immediately before or after a file to determine if they provide any context in which to understand a particular pulse pattern (for example, if a bat has circled within range of the microphone, generating multiple files, a sequence of varying pulse shapes may better elucidate the species identification).

7. Assess recordings that have a good "signal to noise" ratio (identified by crisp, clean, non-saturated oscillograms in full-spectrum recordings) and without non-bat noise, echoes, or distortions in the call-pulses that can skew the qualitative or quantitative measures of the individual call pulses.

8. If available, use established regional keys or rulesets for acoustic species identification (for example, see appendix A. *Case Study: Using Rule Sets to Process Acoustic Data for USDA Forest Service Lands in Northern California*).

9. Files that are manually-vetted should be assigned one of the following: a standard 4 or 6-letter species label (table 3), species couplet (e.g., MYCAMYYU, LANOTABR), frequency class (HighF, LowF), NoID, or NOTBAT (see table 4 for species couplet, group, and frequency class labels). Whether you choose 4- or 6-letter species labels, be consistent and avoid mixing labels for a single species. Most software programs will tag automated identifications with "Species Auto ID" and manually vetted identifications with "Species Manual ID" (e.g. Species Auto ID:MYSO, Species Manual ID:LABO). However, if the software does not automatically include the appropriate tag, users should manually include this prefix so that species IDs can be read by the NABat database and extracted for metadata uploads.

Table 3. Species labels to be used when labeling acoustic files and submitting data to the North American Bat Monitoring Program (NABat) modified from Loeb and others (2015). Regardless of whether you choose 4- or 6-letter labels, be consistent and avoid mixing labels for a single species.

Common name	Scientific name	4-letter label	6-letter label
Pallid bat	*Antrozous pallidus*	ANPA	ANTPAL
Jamaican fruit-eating bat	*Artibeus jamaicensis*	ARJA	ARTJAM
Antillean fruit-eating bat	*Brachyphylla cavernarum*	BRCA	BRACAV
Mexican long-tongued bat	*Choeronycteris mexicana*	CHME	CHOMEX
Rafinesque's big-eared bat	*Corynorhinus rafinesquii*	CORA	CORRAF
Townsend's big-eared bat	*Corynorhinus townsendii*	COTO	CORTO
Virginia big-eared bat	*Corynorhinus townsendii virginianus*		COTOVI
Hairy-legged vampire bat	*Diphylla ecaudata*	DIEC	DIPECA

Big brown bat	*Eptesicus fuscus*	EPFU	EPTFUS
Spotted bat	*Euderma maculatum*	EUMA	EUDMAC
Florida bonneted bat	*Eumops floridanus*	EUFL	EUMFLO
Greater bonneted bat	*Eumops perotis*	EUPE	EUMPER
Underwood's bonneted bat	*Eumops underwoodi*	EUUN	EUMUND
Allen's big-eared bat	*Idionycteris phyllotis*	IDPH	IDIPHY
Silver-haired bat	*Lasionycteris noctivagans*	LANO	LASNOC
Western red bat	*Lasiurus blossevillii*	LABL	LASBLO
Eastern red bat	*Lasiurus borealis*	LABO	LASBOR
Hoary bat	*Lasiurus cinereus*	LACI	LASCIN
Southern yellow bat	*Lasiurus ega*	LAEG	LASEGA
Northern yellow bat	*Lasiurus intermedius*	LAIN	LASINT
Minor red bat	*Lasiurus minor*	LAMI	LASMIN
Seminole bat	*Lasiurus seminolus*	LASE	LASSEM
Western yellow bat	*Lasiurus xanthinus*	LAXA	LASXAN
Mexican long-nosed bat	*Leptonycteris nivalis*	LENI	LEPNIV
Lesser long-nosed bat	*Leptonycteris yerbabuenae*	LEYE	LEPYER
California leaf-nosed bat	*Macrotus californicus*	MACA	MACCAL
Pallas' mastiff bat	*Molossus*	MOMO	MOLMOL
Peter's ghost-faced bat	*Mormoops megalophylla*	MOME	MORMEG
Southwestern myotis	*Myotis auriculus*	MYAR	MYOAUR
Southeastern myotis	*Myotis austroriparius*	MYAU	MYOAUS
California myotis	*Myotis californicus*	MYCA	MYOCAL
Western small-footed myotis	*Myotis ciliolabrum*	MYCI	MYOCIL
Long-eared myotis	*Myotis evotis*	MYEV	MYOEVO
Gray bat	*Myotis grisescens*	MYGR	MYOGRI
Keen's myotis	*Myotis keenii*	MYKE	MYOKEE
Eastern small-footed myotis	*Myotis leibii*	MYLE	MYOLEI
Little brown bat	*Myotis lucifugus*	MYLU	MYOLUC
Arizona myotis	*Myotis occultus*	MYOC	MYOOCC
Northern long-eared bat	*Myotis septentrionalis*	MYSE	MYOSEP
Indiana bat	*Myotis sodalis*	MYSO	MYOSOD
Fringed myotis	*Myotis thysanodes*	MYTH	MYOTHY
Cave bat	*Myotis velifer*	MYVE	MYOVEL
Long-legged myotis	*Myotis volans*	MYVO	MYOVOL
Yuma myotis	*Myotis yumanensis*	MYYU	MYOYUM
Greater bulldog bat	*Noctilio leporinus*	NOLE	NOCLEP
Evening bat	*Nycticeius humeralis*	NYHU	NYCHUM
Pocketed free-tailed bat	*Nyctinomops femorosaccus*	NYFE	NYCFEM
Big free-tailed bat	*Nyctinomops macrotis*	NYMA	NYCMAC
Canyon bat	*Parastrellus hesperus*	PAHE	PARHES
Tri-colored bat	*Perimyotis subflavus*	PESU	PERSUB
Red fruit bat	*Stenoderma rufum*	STRU	STERUF

Brazilian free-tailed bat	*Tadarida brasiliensis*	TABR	TADBRA

Table 4. Species couplet, group, and frequency class labels recommended for labelling files with recordings of species that are acoustically similar and can occur sympatrically (adapted from Loeb and others, 2015). Also included are labels for files without bat recordings (NOTBAT) and for files that contain a bat pulse, but no grouping or user-defined category applies. For consistency, always place the species names making up a couplet label in alphabetical order.

Common name	Scientific name	Label
Pallid bat, Big brown bat	*Antrozous pallidus, Eptesicus fuscus*	ANPAEPFU
Big brown bat, Eastern red bat	*Eptesicus fuscus, Lasiurus borealis*	EPFULABO
Big brown bat, Silver-haired bat	*Eptesicus fuscus, Lasionycteris noctivagans*	EPFULANO
Big brown bat, Little brown bat	*Eptesicus fuscus, Myotis lucifugus*	EPFUMYLU
Western red bat, Canyon bat	*Lasiurus blossevillii, Parastrellus hesperus*	LABLPAHE
Eastern red bat, Seminole bat	*Lasiurus borealis, Lasiurus seminolus*	LABOLASE
Eastern red bat, Little brown bat	*Lasiurus borealis, Myotis lucifugus*	LABOMYLU
Eastern red bat, Evening bat	*Lasiurus borealis, Nycticeus humeralis*	LABONYHU
Eastern red bat, Tri-colored bat	*Lasiurus borealis, Perimyotis subflavus*	LABOPESU
Hoary bat, Silver-haired bat	*Lasiurus cinereus, Lasionycteris noctivagans*	LACILANO
Hoary bat, Mexican free-tailed bat	*Lasiurus cinereus, Tadarida brasiliensis*	LACITABR
Silver-haired bat, Mexican free-tailed bat	*Lasiurus noctivagans, Tadarida brasiliensis*	LANOTABR
Long-eared or Keen's myotis, and Northern bat	*Myotis evotis, Myotis keenii, Myotis septentrionalis*	LEMY
Unknown species in the *Leptonycteris* genus	*Leptonycteris sp.*	LESP
Little brown bat, Indiana bat	*Myotis lucifugus/Myotis sodalis*	LUSO
California myotis, Western small-footed myotis	*Myotis californicus, Myotis ciliolabrum*	MYCAMYCI
California myotis, Yuma myotis	*Myotis californicus, Myotis yumanensis*	MYCAMYYU
Western small-footed myotis, Long-legged myotis	*Myotis ciliolabrum, Myotis volans*	MYCIMYVO
Western long-eared myotis, Fringed myotis	*Myotis evotis, Myotis thysanodes*	MYEVMYTH
Little brown bat, Western small-footed myotis	*Myotis lucifugus, Myotis ciliolabrum*	MYLUMYCI
Little brown bat, Northern long-eared bat	*Myotis lucifugus, Myotis septentrionalis*	MYLUMYSE
Little brown bat, Long-legged myotis	*Myotis lucifugus, Myotis volans*	MYLUMYVO
Bat, but no grouping or user-defined category applies		NoID
Not a bat		NOTBAT
Noise		NOISE
Unknown species in the *Nyctinomops* genus	*Nyctinomops sp.*	NYSP

User-defined categories		
User-defined frequency class	*Various species with pulses that have a minimum frequency of approximately 15-25 kHz*	25k
User-defined frequency class	*Various species with pulses that have a minimum frequency of approximately 35-45 kHz*	40k
User-defined frequency class	*Various species of Myotis with pulses that have a minimum frequency of approximately 15-25 kHz*	40kMyo

User-defined frequency class	*Various species with pulses having a minimum frequency lower than ~30 kHz*	LowF/LoF
User-defined frequency class	*Various species with pulses having a minimum frequency higher than ~30 kHz*	HighF/HiF
User-defined frequency class	*Call file with both a low frequency and high frequency bat species*	HiLo

For Stationary Point Acoustic Data

1. Because the goal is to determine site occupancy for each species, examine and manually ID at least one high quality, confidently identified recording per species per detector per night (that is, a voucher file) that was identified using an acoustic ID program. Where possible, select noise-free, long duration call sequences that can be confidently distinguished from conspecifics.

2. High quality recordings generally result from a loud signal as a bat approaches closer to a microphone. Some potential indicators of higher quality recordings for some species (e.g., *Myotis* spp.) include high bandwidth calls. High bandwidth indicates that the bat has approached the microphone close enough for high frequencies to be recorded. Close approach of bats can also be assumed in the presence of harmonics (in full-spectrum recordings), but note that some calls may be oversaturated if the bat approached the microphone too closely (as seen in clipped, or "squared off," oscillograms and the presence of aliasing, instead of true harmonics); sequences with oversaturated pulses should not be considered in the analysis process.

3. When corroborating automated species identification, focus your review on low clutter, search phase calls, and take precautions to avoid using approach phase calls, feeding buzzes, and social calls for most species.

   A. High quality recordings for auto ID have consistent inter-pulse intervals indicative of typical search-phase behavior. Be careful not to include approach phase calls when a bat is responding to an object in its flight path, as these calls take on a different shape that is generally less desirable for differentiating species, and can confound auto ID.

   B. Recordings should have been made in relatively uncluttered environments; however, low clutter calls can be difficult to obtain. For example, even when detectors are placed far from buildings, dense vegetation, or other hard surfaces bats often produce high clutter sequences when approaching the ground or in close proximity to other bats or while checking out the microphone if it is a novel item of interest on the landscape.

   C. Look at the entire sequence in both "compressed" and "real time" views. This will help you see the whole picture (e.g., multiple bats and or species in the recording or non-search phase calls, indicating the types of convergent approach-phase and acquisition-phase call types that all bats are capable of producing).

   D. Adjust filters, thresholds, and other viewer settings as needed.

   E. If possible, play the recording in real-time or time-expansion to listen for a consistent cadence between call pulses.

F. Examining files within a short period of time (for example less than 2 seconds) immediately prior and following the file of interest may add context to better identify the species.

4. To expedite review, focus manual vetting efforts on call sequences that were assigned an automated species identification. These files are more likely to contain high quality call sequences, unlike the files that did not receive an automated species identification. Spreadsheet outputs can be sorted in order of auto ID confidence by looking at the number of call pulses that contributed to the identification. In this way the longest call sequences and decisions most likely to be correct are presented first.

5. Review auto ID files that have been assigned to a given species category. Confirm species identification for a minimum of one file per species per night (voucher file).

6. For example, if an auto ID assigns a file a label of Species *X* because all 40 pulses in the sequence are assigned to that species, then this would be your voucher file for that species that night. If it is assigned to Species *X* but only 20 of 40 pulses matched to this species label, and the other 20 assigned to Species *Y* for which you think the sequence could equally be either species due to a lack of any diagnostic features, then you might consider a species label *XY*. Then continue to review other files that were strongly assigned the Species *X* label until one is found that represents a good voucher file. If a species' identification cannot be manually confirmed by examining the files with the highest auto ID confidence scores, you may also want to examine high quality recordings that were not assigned a species-specific auto ID label (e.g., "NoID"). This is because sometimes the presence of more than one bat in a recording can confound auto-identification, despite a high quality recording.

For Mobile Transect Acoustic Data

1. The goal for collecting mobile transect acoustic data for NABat is to evaluate relative species abundance. Therefore, manually vet *all* files, focusing first on the files that were assigned an automated species identification, as these are likely to be of higher quality. Sort the files by species and use the same criteria as described above for stationary point acoustic datasets.

2. For files that did not receive an auto ID (that is, file-level classification results were left blank, or labeled HighF, LowF or NoID), if possible, apply filters or a sort function to enable like recordings to be viewed in series. For example, some auto ID software provides a suggestion of species pulse shapes that may be present in a file even if an auto ID could not be achieved. Alternatively, use the general call shape and characteristic frequency to sort "NoID" files by phonic group so that you have fewer species to consider at one time in the manual vetting process. For example, all low frequency bats may be viewed in series before all high frequency bats.

3. When appropriate, assign a label to "NoID" files, preferentially using couplets, or categories that contain only two species (e.g., LABOMYLU for pulses that have minimum frequencies ~40 kilohertz (kHz) but undulate to some extent); recordings that could be of more than two possible species will receive a generic group category such as "Low Frequency bat" (e.g., LowF or 25k Hz).

4. Because the goal of transects is to determine relative species abundance, it is also important to identify recordings that contain more than one individual bat and/or species. Be sure to assign multiple labels as appropriate.

The Manual Vetting Process

1. Assess call sequence quality.

   There are cases when auto ID is questionable due to reduced call quality. The presence of the following quality issues likely impact the effectiveness of auto ID software. Downgrade the species identification to a species group if one or more of the following issues exist.

   A. Excessive noise.

   B. Classifier chose inappropriate calls (pulses) for classification (for example social calls, quiet/out of range calls), included noise as part, or in place of a call, or used non-search phase or high clutter calls.

   C. Identification is confounded by multiple species or individuals present in the call sequence.

   D. Insufficient number of pulses present for confident identification.

   E. Destructive interference caused by echoes.

2. Examine call sequence and call characteristics.

   If the auto ID is correct, the basic measures of the calls and sequence (e.g. characteristic frequency, duration, slopes, call intervals, and so forth) should be within the typical ranges observed for that species. Sometimes these call characteristics are measured incorrectly by the auto ID software, leading to assignment of a pulse sequence of an unlikely species. When the call characteristics are not within the range typically observed for the species identified, downgrade the species identification to a species group.

3. Look for evidence of alternative species identification.

   Many call sequences have characteristics that fall within the ranges of multiple species. Depending on the potential species present, look for any evidence that the recording is actually of another species. Appendix C provides a "Bat Auto ID Species Confusion Matrix" as a quick look-up guide indicating which species are commonly confused by auto ID software. If there is strong evidence of another species, or a high degree of ambiguity (e.g., 50 percent of the pulses match Species *X*, and 50 percent match a highly similar Species *Y*), downgrade the species identification from the auto ID to a species group "*XY*" (e.g., EPFULANO). If there is no evidence of another species, and the recording is of a high-quality bat pass, accept the auto ID as correct for that file. However, auto ID software is currently evolving, and there are known cases of areas where one species might repeatedly be called another species. There are many reasons why this might be the case, such as regional differences in some species echolocation repertoires that may not be reflected in underlying libraries or unreliable known calls in a program's library. If the expert analyst can provide suitable justification for changing a

species identification from auto ID to another species label, then such justification can be provided in an appended note, such as in the file metadata.

4. Look for evidence of multiple individuals in the file.

Depending on how the detector was deployed in relation to surrounding habitat features, flight paths, and so forth, passive recordings (from stationary point surveys) can include multiple individuals in a file. This is especially true if the microphone is located near a potential roost. Sometimes you can identify new roosts, or night roosts, acoustically by such recordings, so these instances are important to document. For example, in a passive dataset, a note in the metadata might be used to indicate there are many bats, or a suspected/known roost, and so forth. This should also be included in the submission of covariate information to NABat.

If multiple bats occur in a single recording from a mobile driving transect, users should include a separate row for each bat in the metadata CSV upload. Aside from the species ID, all other metadata should remain the same, and the NABat database will recognize the two rows as a single recording with two bat species (further guidance on uploading metadata is presented in the following section).

Step 5. Submit to NABat

The following steps are required for submitting acoustic monitoring data to NABat:

1. **Request an Account** on the NABat website by visiting https://sciencebase.usgs.gov/nabat/#/home and clicking on "Request an Account." When your account is approved, you will receive a confirmation email with a link to create a username and password. Detailed guidance on creating a new user account is available at https://www.sciencebase.gov/catalog/file/get/5e3de185e4b0edb47be3d6e6?name=Create _NABat_User_Account.pdf

2. **Create a New NABat Project** by visiting https://sciencebase.usgs.gov/nabat/#/home, logging in, and clicking the "Projects" tab at the top of the page.

   A. A list of current projects will appear (for new users this list will be blank unless another Project Leader has added you to an existing NABat Project). Click "Add New Project."

   B. Enter required project information including Project Name, Owning Organization, and Project Description. Identify your role in the project. If you would like to allow other existing NABat users (that is, those with registered accounts) to access your project, click "Add User," identify their role in the project, and assign appropriate permissions.

   C. Use the drop-down menu under the GRTS Selection section to indicate whether your sample design follows NABat guidelines.

   D. Use the drop-down menu under the GRTS Selection section to select the appropriate Grid Sample Frame.

E. Indicate your data sharing preferences using the drop-down menus in the NABat Data Use and Sharing Agreement. Data sharing preferences can be changed at any time by clicking the Data Use & Sharing tab from within your project homepage.

F. When all required fields have been completed, click "Proceed to Cell Selection" in the bottom right of the page.

G. When the cell selection tool loads, users can either claim GRTS cells for survey or proceed to your new project and make GRTS cell selections at a later time.

   i. If you wish to claim GRTS cells:

Use the available filters at the top of the map and/or the available map layers to navigate to the area of interest. Add individual cells to the evaluation table by double clicking or bulk select cells using the "Draw Polygon" feature or uploading a .geojson or .kml file of your study area. Filtered cells will be outlined in blue and can be added to the evaluation table by clicking the "Add Filtered Cells to List" button in the top right of the map filters. Once all the cells of interest are added to the table on the right half of the page, use the legend (located above the evaluation table) to indicate what type of survey(s) you will conduct by clicking the corresponding button(s). Next, sort the cells into ascending order by clicking the arrows beside the GRTS Cell ID column header, then use the drop-down menus to the right of the GRTS Cell ID to indicate which cells you will survey (begin with the highest priority – lowest GRTS number) and provide justification for the cells you do not plan to survey.

   ii. If you wish to proceed to your newly-created project and select GRTS cells at a later time:

Claiming cells is not required to create a new project. Cells can be claimed at any time, and survey data can be uploaded for cells that have not yet been claimed. Users who wish to skip the cell selection step can proceed to step H.

H. Click "Save Project."

3. **Prepare metadata CSV**: Site and call metadata must be saved in a comma delimited (CSV) file and uploaded to your NABat project page. This can be accomplished either by entering the metadata manually or embedding and extracting metadata using one of the various automated identification software programs. Guidance specific to each program is presented in the following chapters. **Users with audio files that already contain required metadata who wish only to extract those data into the NABat bulk upload template should refer to the footnotes at the end of the Stationary Point Data and Mobile Transect Data sections of chapter 1.** To enter metadata manually:

A. Login to the NABat Partner Portal (**https://sciencebase.usgs.gov/nabat/#/home**) and navigate to your project homepage.

B. Click the "Upload Survey Data" button in the top right corner of the page and select the type of survey (Stationary Acoustic Point or Mobile Acoustic Transect).

C. Select "Full Metadata" from the pop-up window.

D. In the bulk upload preview window, click the green "Download Template" button and save the file to your machine.

E. Using the guidance provided in the template (formatting tips and accepted categorical entries are provided in the second row), complete all required fields and any others for which you have data. In many cases, "Audio Recording Name," "Auto ID," and "Manual ID" columns can be filled by copying and pasting values from software outputs. Required fields are indicated in the preview window.

F. When all required fields have been filled (and any others for which you have data), save the file with a unique name. The NABat system will automatically overwrite duplicate filenames with the most recent version, so it is critical that the filename is not duplicated in future uploads.

4. **Submit metadata to NABat:** Once you have registered your project, chosen GRTS cells for survey, collected data, and prepared a bulk metadata CSV:

A. Click on the "Upload Survey Data" button in the top right corner of your project homepage and select the type of survey.

B. Select "Full Metadata" in the pop-up window**.**

C. Click the blue "Select File" button and navigate to your metadata CSV.

D. A preview window will appear with errors highlighted in red. Use the drop-down menus beneath the column headers to determine accepted formatting and inputs and correct any errors identified in the preview. Save the updated file, click the refresh button in the top left of the preview window, and navigate to the corrected file.

E. Ensure that all errors identified in the preview have been corrected and submit the metadata file to your project page.

F. When the metadata CSV has successfully uploaded, it will appear under the "Bulk Upload Status" tab of your project homepage. The number of rows processed and number rows with errors will be listed. **The upload preview only scans a portion of the upload, and some errors cannot be identified until the document is processed. Review the "Bulk Upload Status" tab to ensure the upload processed without errors.**

G. If errors are present in the uploaded document, click the blue hyperlink in the "Errors Found" column to download a CSV identifying which rows have errors and what error occurred (final two columns of the document). Errors can either be corrected in the original document, which can then be re-uploaded, or corrected directly in the error report, which can then be uploaded as a supplement to the original file. Rows with errors are dropped/ignored by the NABat system, so it is crucial that errors are corrected. Otherwise, metadata for those rows will not be saved in the NABat database.

5. **Users with mobile transect data should also provide spatial data outlining the transect route.** These data can be provided either by uploading a .geojson or .kml file of the route or by drawing the transect route in the project map. **To upload a .geojson or .kml file:**

A. From your project homepage, scroll down to the project map, located below the project details.

B. Click the "KML | GeoJson" button in the top right of the map. Navigate to your .geojson/.kml file and click "Open."

C. Navigate to the .geojson/.kml file and click "Open."

D. A dialogue box will appear with the option to edit route details. Name the transect, provide a description (if you wish), select "Transect Route" from the Survey Type drop-down menu, and save.

E. The route can now be linked to your transect metadata by listing the transect name you just saved as the "Location Name" in the transect metadata CSV. The names *must match exactly*. This will link the route you just saved to the route metadata. Route objects should be uploaded before route metadata. If metadata for the route has already been uploaded, navigate back to the project homepage, click the "Bulk Upload Status" tab, and click the "Reprocess" button beside the route metadata upload. Future surveys of this location can also be linked to the same spatial object as long as the "Location Name" provided matches the name of the spatial object exactly.

To draw a mobile transect route using the cell selection tool:

A. From your project homepage, scroll down to the project map, located below the project details.

B. Navigate to the GRTS cell where you wish to draw a mobile transect route (the search bar above the map includes a variety of filters including GRTS Cells, land jurisdiction, state, county, etc.).

C. Click the "Mark a transect route" button in the top left of the map to begin drawing the transect.

D. Click along your desired route. The mapping tool will drop points with each click and connect the points with a line. The mapping tool will also display the total length of the route.

E. When finished, either click "Finish" beside the "Make a transect route" button or click the last point on the route.

F. A dialogue box will appear with the option to edit route details. Name the transect, provide a description (if you wish), select "Transect Route" from the Survey Type drop-down menu, and save.

G. The route can now be linked to your transect metadata by listing the transect name you just saved as the "Location Name" in the transect metadata CSV. The names *must match exactly*. This will link the route you just saved to the route metadata. Route objects must be uploaded before route metadata. If metadata for the route has already been uploaded, navigate back to the project homepage, click the "Bulk Upload Status" tab, and click the "Reprocess" button beside the route metadata upload. Future surveys of this location can also be linked to the same spatial object as long as the "Location Name" provided matches the name of the spatial object exactly.

6. **Submit acoustic files (all audio recordings not scrubbed as NOISE) to NABat.**

A. Click the "Upload Audio Recordings" button on your project homepage, navigate to the folder containing files you wish to upload, and click "Select Files."

B. Audio files can be uploaded individually, but uploading a compressed .tar.gz file is highly recommended. Compressed .tar.gz files can be created using the NABat renaming tool (guidance in step 1). The NABat system will instantly begin to extract audio files from .tar.gz uploads, but the process could take some time.

C. When files have been successfully uploaded and extracted, the NABat database will attempt to match the filename to filenames listed in the metadata CSV uploads. The number of successfully matched files will appear under the "Acoustic Data" tab of your project homepage. The number of "Missing Acoustic Files" will also be listed. If you believe all audio files for a deployment have been uploaded but the "Acoustic Data" tab shows missing files, follow the guidance below to identify the missing files:

   i. Click the blue hyperlink corresponding to the deployment with missing files in the "Survey Event" column of the "Acoustic Data" tab. This will expand the deployment information in the user interface.

   ii. Scroll down through the deployment details to the "Echolocation Measurements" section.

   iii. Click the box beside "Unmatched Only" in the "Audio Recording" column. This will display information for all recordings which have metadata but no associated audio recording.

   iv. Compare the unmatched filenames listed in the "Echolocation Measurements" interface to the names of your audio recordings. If the names do not match exactly, use the NABat file renaming tool to make the appropriate changes to your audio filenames. When you are certain the filenames match exactly, try uploading the files again, following the above guidance. If the problem persists, contact NABat support.

Chapter 1. Processing Acoustic Data Using Kaleidoscope Pro Version 5.3.8

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Stationary Point Data

1. Open Kaleidoscope and click "Browse" to select the input directory of the folder containing your .wav/.zc files. It's best to select a folder containing all data for a single detector deployment (all nights at a single site). This is the broadest selection for which all files will share the same metadata (Site Name, Latitude, Longitude, etc.).

2. Download the required NABat metadata forms from https://www.sciencebase.gov/catalog/item/5dcdd2b5e4b069579760b15a (NABat_Metadata_Form_Kaleidoscope_Stationary.xml for use with steps 1-9 and NABat_Stationary_Meta_Output_Only_KPRO.xml for use with steps 12-18). Next, click the drop-down menu above the "Default Project Form" and select "Add or Replace a Project Form." Navigate to NABat_Metadata_Form_Kaleidoscope_Stationary.xml and select the file. The NABat metadata form will now load in the bottom of the INPUTS section (the left half of the Kaleidoscope window).

3. Complete all metadata fields for which you have data. **GRTS Cell ID or Latitude/Longitude**, **Location Name**, **Survey Start Time**, **Survey End Time**, **Software Type**, and **Species List** are required. Some fields require specific formatting. Hover the pointer over a field for formatting tips and/or a list of accepted entries.

4. Once all required metadata fields (and any additional fields for which you have data) have been completed, select the desired output directory to save processed files by clicking "Browse" in the top right of the window.

5. Once the output directory has been selected, choose "Nightly" from the "Create subdirectories" drop-down menu to keep new files organized by detector night (recommended, not required). Next, select the type of output files you wish to create (WAV or ZC). **In order to successfully export metadata, you *must* select WAV or ZC files in the OUTPUTS window and create copies of the original files during this step.** These copies will contain embedded metadata that will be the source of the "meta" output spreadsheet you will upload to NABat. If your files end in the # extension (certain Anabat models), select the "8.3 filenames" and "Use .zc instead of .??#" options. The NABat database will not accept files that end in the .# extension and Kaleidoscope will drop all values after the "." in filenames if the "8.3 filenames" option is not selected. This may lead to duplicate filenames and upload errors.

6. Click the "Auto ID for Bats" tab at the top of the window. Select "Bats of North America" from the "Classifiers" drop-down menu. Select "+ 1 More Accurate (Conservative)" from the drop-down menu at the top right. Next, select your state/region from the drop-down menu below the list of species. Species can be manually added or removed based on specific knowledge of species assemblages in your area, but this must be reflected in your NABat species list.

7. Click the "Signal Parameters" tab.

    A. Minimum and maximum frequency range should be appropriate for the expected bat community.

    B. Minimum and maximum length of detected pulses should be one to 50 milliseconds (ms) for mobile transects and 2–50 ms for stationary points. This will potentially exclude a few bat recordings in stationary datasets but will ensure more high-quality recordings for species identification.

    C. Minimum number of pulses should be three.

    D. Leave the maximum inter-syllable gap at its default value of 500 ms. This applies only to the cluster analysis process, which is not part of this workflow.

8. Click "Process Files" in the bottom right corner of the window.

9. When Kaleidoscope has finished processing, review the automated identifications and confirm or change the Kaleidoscope ID (manual ID). For stationary surveys, NABat guidance calls for one manual verification per species per night in order to establish presence/absence.

10. If the detector model you're using automatically embeds a timestamp into recordings, these data should auto-populate and appear in the "Audio Recording Time" column of the Kaleidoscope "meta" output. If so, you may skip the renaming process. However, before uploading metadata to NABat, you should ensure that the "Audio Recording Time" column contains data. Otherwise, filenames must adhere to the NABat file naming format, and users should rename files before proceeding.

11. Repeat steps 1-9 for all deployments you wish to process. Once all deployments have been processed, steps 12-18 will allow users to simultaneously export metadata for all processed deployments into a single bulk upload CSV.

12. Return to the batch processing window, click "Browse" in the "Input directory" window, and select the parent folder containing all your processed deployments (the new files you created with metadata and IDs in steps 1-9). Select a new output directory. If the box beside "WAV files" or "ZC files" is still checked, unselect the box (you won't create new files during this process, only a "meta" file containing NABat metadata).

13. Click the "Auto ID for Bats" tab and select "DISABLED" in the "CLASSIFIERS" drop-down menu.

14. Replace the NABat_Metadata_Form_Kaleidoscope_Stationary.xml file from step 2 with NABat_Stationary_Meta_Output_Only_KPRO.xml. The data entry window will no longer display NABat metadata fields. The form will still export the embedded metadata from steps 1-9.

15. Click "Process Files" in the bottom right corner of the window.

16. Navigate to the current output directory folder and open the "meta" file. Check to ensure all fields for which you entered data are filled and ensure one or both of the Auto ID/Manual ID columns are filled.

17. Rename the file with a descriptive and unique name and save. The NABat system will automatically overwrite duplicate filenames with the most recent version, so it is critical that your filename is unique.

18. Follow the guidance presented in step 5 of the introduction to this document to upload the metadata CSV to your NABat project page.

* The free version of Kaleidoscope 5.3.8 can be used with files that already contain required metadata (regardless of the software used to embed the metadata) to export those data into the NABat bulk upload template.

Mobile Transect Data

1. Open Kaleidoscope and click "Browse" to select the input directory of the folder containing your .wav/.zc files.

2. Download the required NABat metadata forms from https://www.sciencebase.gov/catalog/item/5dcdd2b5e4b069579760b15a (NABat_Metadata_Form_Kaleidoscope_Mobile.xml for use with steps 1-9 and NABat_Mobile_Meta_Output_Only_KPRO.xml for use with steps 12-18). Next, click the drop-down menu above the "Default Project Form" and select "Add or Replace a Project Form." Navigate to NABat_Metadata_Form_Kaleidoscope_Mobile.xml and select the file. The NABat metadata form will now load in the bottom of the INPUTS section (the left half of the Kaleidoscope window).

3. Complete all metadata fields for which you have data. **GRTS Cell ID or Latitude/Longitude**, **Location Name**, **Survey Start Time**, **Survey End Time**, **Software Type**, and **Species List** are required. Hover the pointer over a field for formatting tips and/or a list of accepted entries. If you saved the transect route as a spatial object using the NABat cell selection tool, ensure that the "Location Name" matches the name of the corresponding route that was previously saved. If your mobile transect passes through > 1 cell and you have a record of the X,Y location where each file was recorded (using an external GPS or a GPS enabled detector) leave the GRTS Cell ID field blank. The NABat system will use the X,Y locations to auto-assign the correct GRTS cell to each recording. Otherwise, files recorded outside the primary cell will produce a Latitude/Longitude-GRTS ID mismatch error. If Latitude/Longitude are embedded in your files, the Kaleidoscope metadata form will extract those values and auto-populate the metadata output. If Latitude/Longitude values were downloaded from a GPS unit, see step 17.

4. Once all required metadata fields (and any additional fields for which you have data) have been completed, select the desired output directory by clicking "Browse" in the top right of the window.

5. Choose "Nightly" from the "Create subdirectories" drop-down menu to keep new files organized by detector night (recommended, not required). Next, select the type of output files you wish to create (WAV or ZC). In order to successfully export metadata, you *must* select WAV or ZC files in the OUTPUTS window and create copies of the original files during this step. These copies will contain embedded metadata that will be the source of the "meta" output spreadsheet you will upload to NABat. If your files end in the # extension (certain Anabat models), select the "8.3 filenames" and "Use .zc instead of .??#" options. The NABat database will not accept files that end in the .# extension and Kaleidoscope will drop all values after the "." in filenames if the "8.3 filenames" option is not selected. This may lead to duplicate filenames and upload errors.

6. Click the "Auto ID for Bats" tab at the top of the window. Select "Bats of North America" from the "Classifiers" drop-down menu. Select "+ 1 More Accurate (Conservative)" from the drop-down menu at the top right. Next, select your state/region from the drop-down menu below the list of species. Species can be manually added or removed based on specific knowledge of species assemblages in your area, but this must be reflected in your NABat species list.

7. Click the "Signal Parameters" tab.

    A. Minimum and maximum frequency range should be appropriate for the expected bat community.

    B. Minimum and maximum length of detected pulses should be one to 50 milliseconds (ms) for mobile transects and 2–50 ms for stationary points. This will ensure that all potential bat recordings are included in the mobile transect dataset (some noise files that do not contain bats will also be included). This is to ensure no bat files are missed in the measuring of relative abundance in the mobile transect dataset, even though it is anticipated that more of the auto-identified files will remain as NoID or changed in manual vetting, such as downgrading to a species group or frequency class.

    C. Minimum number of pulses should be three.

    D. Leave the maximum inter-syllable gap at its default value of 500 ms. This applies only to the cluster analysis process, which is not part of this workflow.

8. Click "Process Files" in the bottom right corner of the window.

9. When Kaleidoscope has finished processing, review the automated identifications and confirm or change the Kaleidoscope ID (manual ID). For mobile transects, NABat guidance calls for manual verification of all recordings in order to estimate abundance.

10. If the detector model you're using automatically embeds a timestamp into each file, these data should auto-populate and appear in the "Audio Recording Time" column of the Kaleidoscope "meta" output. If so, you may skip the renaming process. However, before uploading metadata to NABat, you should ensure that the "Audio Recording Time" column contains data. Otherwise, filenames must adhere to the NABat file naming format, and users should rename files before proceeding.

11. Repeat steps 1-9 for all deployments you wish to process. Once all deployments have been processed, steps 12-18 will allow users to simultaneously export metadata for all processed deployments into a single bulk upload CSV.

12. Return to the batch processing window, click "Browse" in the "Input directory" window, and select the parent folder containing all your processed deployments (the new files you created with metadata and IDs in steps 1-9). Select a new output directory. If the box beside "WAV files" or "ZC files" is still checked, unselect the box (you won't create new files during this process, only a "meta" file containing NABat metadata).

13. Click the "Auto ID for Bats" tab and select "DISABLED" in the "CLASSIFIERS" drop-down menu.

14. Replace the NABat_Metadata_Form_Kaleidoscope_Mobile.xml file from step 2 with NABat_Mobile_Meta_Output_Only_KPRO.xml. The data entry window will no longer

display NABat metadata fields. The form will still export the embedded metadata from steps 1-9.

15. Click "Process Files" in the bottom right corner of the window.

16. Navigate to the current output directory folder and open the "meta" file. Check to ensure all fields for which you entered data are filled and ensure the Auto Id/Manual Id columns are filled.

17. Users who recorded latitude and longitude of recordings with an external GPS unit must manually add X,Y locations to the bulk metadata spreadsheet. Users with GPS enabled detectors that embed X,Y locations into each file (the latitude/longitude columns of your CSV will already contain data) can skip to step 18. Users with no X,Y locations must provide a spatial object of the route (see step 5 on page 18). NABat will use the survey start/end times, timestamps of the files, and the user-provided spatial object to estimate locations. In this case, users must leave the GRTS ID column blank.

    A. Download the X,Y locations from your GPS unit or detector. This is typically in the form of a text file with a column for filename, latitude, and longitude.

    B. Import the text file into Excel:

        i. Open a new spreadsheet, click the "Data" tab, select "From File," and "From Text/CSV."

        ii. Navigate to the GPS text file and click "Open."

        iii. A dialogue box will appear with a preview of the data to be imported. The GPS text files are typically tab delimited. If your data is properly sorted into columns, click "Load." If not, use the "Delimiter" drop-down menu to select the appropriate delimiter and click "Load."

    C. When the data has loaded, click the "Sort and Filter" button and select "Custom Sort."

    D. Sort the document by the column containing your filenames.

    E. Open the CSV containing your transect metadata. Follow step C to sort the metadata CSV by the "Audio Recording Name" column.

    F. The "meta" CSV and GPS spreadsheet should now be sorted by filename. Ensure the filename columns match.

    G. If the documents are sorted properly, copy and paste the latitude and longitude columns from the GPS file into the corresponding columns in the metadata CSV.

18. Rename the file with a descriptive and unique name and save. The NABat system will automatically overwrite duplicate filenames with the most recent version, so **it is critical that your filename is unique**.

19. Follow the guidance presented in step 5 of the introduction to this document to upload the metadata CSV to your NABat project page.

* The free version of Kaleidoscope 5.3.7 can be used with files that already contain required metadata (regardless of the software used to embed the metadata) to export those data into the NABat bulk upload template.

Chapter 2. Processing Full Spectrum Acoustic Data Using SonoBat 4.3.0

By Dane Smith[1] and Ted Weller[3]

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Step 1. Assign Metadata

Stationary Point Data

1. Open SonoBat Data Wizard.

2. Click the folder icon in the top right corner of the window and navigate to the folder containing your .wav/.zc files. Select a folder that contains all recordings for a single deployment (all nights at a single site). This is the broadest selection for which all files will share the same metadata (e.g. Latitude, Longitude, Site Name).

3. Select "NABat Attributer" from the drop-down menu in the top left of the window.

4. Specify an output directory to save the final files by clicking the folder in the center of the window (there is also an option to "rename and attribute in place"). Notice that the right panel of the window now displays all the existing file metadata. This will be augmented with NABat metadata fields. Required NABat fields and optional NABat fields are outlined in table 1.

5. Click the "NABat Metadata" button. Enter metadata in the pop-up window that appears. Use arrows at the bottom of the window to proceed through all pages and close the window by clicking "Finish" on the final page.

6. **Software Type** and **Species List** are required fields that must be entered manually. **Microphone Serial Number**, **Microphone Orientation**, and **weather covariates** are not required, but must also be entered manually if you wish to include these data. To manually add a new metadata field, click one of the yellow dropdown triangles in the right half of the widow and select "Add new …"

   a. In the popup menu, enter the desired NABat field name **exactly** as it appears in table 2 (include the NABat| as well).

   b. Click the drop-down menu in the bottom left corner of the window and select "Create advanced metadata field" from the available options.

   c. Input the value for that field and click "Accept."

7. Once all required NABat metadata (and any other metadata you collected) has been added, click the "Attribute Files" button in the bottom center of the window.

Mobile Transect Data

1. Open SonoBat Data Wizard.

2. Click the folder icon in the top right corner of the window and navigate to the folder containing your .wav/.zc files. Select a folder that contains all recordings for a single

deployment (all nights at a single site). This is the broadest selection for which all files will share the same metadata (e.g. Latitude, Longitude, Site Name).

3. Select "NABat Attributer" from the dropdown menu in the top left of the window.

4. Specify an output directory to save the final files by clicking the folder in the center of the window (there is also an option to "rename and attribute in place"). Notice that the right panel of the window now displays all the existing file metadata. This will be augmented with NABat metadata fields. Required NABat fields and optional NABat fields are outlined in table 1.

5. Click the "NABat Metadata" button. Select the box beside "Mobile Transect" so that it reads "True."

6. The SonoBat NABat attributer does not reflect the most recent changes to the NABat database structure, and several fields can be ignored while others must be entered manually. However, this tool is useful for entering required fields. If your mobile transect passes through > 1 cell and you have a record of the X,Y location where each file was recorded (using an external GPS or a GPS enabled detector) leave the Start/End GPS and NABat Grid Cell ID fields blank. The NABat system will use the X,Y locations to auto-assign the correct Grid Cell to each recording. Otherwise, files recorded outside the primary cell will produce a Latitude/Longitude-Grid Cell mismatch error.

7. Complete the fields for **Site Name**, **Monitoring Start Time**, and **Monitoring End Time**, and click the arrow (bottom right) to proceed to the next page. These are required fields and must be completed before uploading data to NABat.

8. Complete the fields for **Surveyor** and **Habitat Type** (not required) and ignore the remaining fields. Click the arrow to proceed to the next page.

9. Complete fields for **Detector Type**, **Detector Serial Number**, and **Microphone Type** (not required) and ignore the remaining fields. Click the arrow to proceed to the next page.

10. Click "Finish" in the bottom right.

11. **Software Type** and **Species List** are required fields that must be entered manually. **Microphone Serial Number**, **Microphone Placement**, and **weather covariates** are not required, but must also be entered manually if you wish to include these data. To manually add a new metadata field, click one of the yellow dropdown triangles in the right half of the widow and select "Add new …"

    a. In the popup menu, enter the desired NABat field name **exactly** as it appears in table 2 (include the NABat| as well).

    b. Click the drop-down menu in the bottom left corner of the window and select "Create advanced metadata field" from the available options.

    c. Input the value for that field and click "Accept."

12. Repeat step 11 for all metadata fields for which you have data.

13. Click "Attribute Files" in the bottom center of the window.

Step 2. Noise Scrubbing using SonoBat Scrubber and Attributer

Follow these steps to remove non-bat files from dataset:

5. Open the SonoBat Data Wizard and select "Batch File Scrubber" from the drop-down menu in the top right corner of the window.

6. Select "Medium Scrub" option from the drop-down menu on the left side of the window.

7. For sites with low frequency bats (less than < 20 kHz), select "Search 5 kHz and above for bats." Low frequency bats include *Euderma maculatum, Eumops spp., Lasiurus cinereus* and *Nyctinomops spp.* It is likely that most locations will have at least one low frequency bat species. However, for sites outside the suspected range of low frequency species, choose "Search 20 kHz and above for bats."

8. Click "Scrub" in the bottom of the window.

Step 3. Auto ID

Follow these steps to SONOBATCH the entire directory containing the recording session of interest:

1. Open SonoBat and click "SonoBatch" in the bottom left corner of the window.

2. Click the folder icon in the top center of the window and navigate to the folder containing files you wish to process.

3. Select the classifier most appropriate for your location and recording conditions using the drop-down menus on the left side of the window.

4. Ensure "Append species codes to filenames?" is **not** selected.

5. Select "autofilter" in areas without low-frequency bat species and "auto-low" in areas with low-frequency bats present.

6. Set "acceptable call quality" to 0.80.

7. Set "sqnc decision threshold" to 0.90.

8. Set "max number of calls to consider" to 16.

9. Click "Process" in the bottom center of the window.

Step 4. Manual Vetting

Manually vet the SONOBATCH output based on objectives (stationary point vs. mobile transect acoustic monitoring).

Stationary Point Data

Follow these steps to confirm species detections per detector per night:

1. Open the project vetting window by clicking "SonoVet" in the bottom left corner of the SonoBat window.

2. Click "Add to Project" and navigate to the folder containing recordings with automated IDs.

3. In the Vetting table, add a Monitoring Night column by right-clicking on the header bar, selecting "Insert before," "SonoBat Data," "MonitoringNight."

4. In the "Settings" tab, click the + button beside "Sort" and add fields as follows: MonitoringNight, 1st, #Maj, #Accp, 2nd, Fc mean, Dur mean. This sorts the results by night and species and files with the highest probability of being confirmed by manual vetting will appear at the top.

Note: "Save Layout" can be used to quickly apply these settings to future SONOVET projects.

5. For each monitoring night, confirm species ID for one file per species per night. Files are displayed in SonoBat by clicking on the file row. Keep reviewing auto ID files where "SppAcc" = *species X* until you confirm the species, or until you have reviewed what you would consider a reasonable number of files (for example, if the species cannot be confirmed after review of the 10 "most likely" files, you might assume non-detection for that species on that night).

6. For each file reviewed, select a standard identification code in the Species Manual ID column by right clicking the Species Manual ID cell. Species codes can be added by selecting "Config Manual ID Defaults." Accepted species codes are provided in tables 3 and 4.

Mobile Transect Data Only

The objective is to confirm species detections for all files. Follow the steps as above, but continue vetting all files, even those that have not been assigned an auto ID.

Step 5. Export Metadata

1. Open SonoBat universal and click the "SonoVet" button in the lower left corner.

2. Click "Add to Project" and navigate to the parent folder containing all the .wav/.zc files that have been processed, renamed, and attributed with metadata. This can include multiple deployments and will allow the user to export metadata for all processed files into a single document. NABat requests that users provide metadata for scrubbed NOISE files. However, SonoBat automatically ignores any folder labeled "Noise Files," "Deleted Files," or "Scrubbed Files." To ensure scrubbed files load in the SonoVet table, rename folders containing scrubbed files as "NOTBAT" before loading folders in SonoVet.

3. Click the "Settings" tab on the top menu bar and click the "Load Layout" button to load the NABat metadata form, available for download at https://www.sciencebase.gov/catalog/file/get/5dcdd2b5e4b069579760b15a?name=NABat_Metadata_Form_SonoBat_4.xml (Stationary Acoustic Surveys)

   https://www.sciencebase.gov/catalog/file/get/5dcdd2b5e4b069579760b15a?name=NABat_Metadata_Form_SonoBat_Mobile.xml (Mobile Acoustic Transects)

4. Click the "Vetting Table" tab from the top menu bar. Ensure all required fields have values and that all fields for which you entered data are filled.

5. If everything is correct, click the "Export" tab from the top menu bar. Select a destination folder to save the metadata file and use the drop-down menu in the bottom center of the window to select Output null as "" or Output null as an empty cell.

6. Click "Save to File."

7. The resulting text file must be converted to a CSV (comma delimited). Open a new Excel workbook, click the Data tab, "Get Data," "From File," "From Text/CSV."

    a. In the pop-up window, navigate to the SonoBat text file and click "Import." Select "Tab" as the delimiter and click "Load" in the bottom right of the window. Your data will now open in an Excel spreadsheet.

8. The specific software version must now be manually added to the document. Highlight the "Software Type" column and, using the find/replace function, replace "SonoBat" with "SonoBat 3.x," "SonoBat 4.2," or "SonoBat 4.x," depending on your specific software version.

9. Scrubbed files must be labeled as NOISE. Highlight the "Auto ID" column and, using the find/replace function, replace empty cells with "NOISE."

10. Users who recorded latitude and longitude of recordings with an external GPS unit must manually add X,Y locations to the bulk metadata spreadsheet. Users with GPS enabled detectors that embed X,Y locations into each file (the latitude/longitude columns of your CSV will already contain data) can skip to step 10. Users with no X,Y locations must provide a spatial object of the route. This can be accomplished either by uploading a .geojson/.kml or drawing the route in the NABat Cell Selection Tool. NABat will use the survey start/end times, timestamps of the files, and the user-provided spatial object to estimate locations. In this case, users must leave the GRTS ID column blank.

    a. Download the X,Y locations from your GPS unit or detector. This is typically in the form of a text file with a column for filename, latitude, and longitude.

    b. Import the text file into Excel:

        i.   Open a new spreadsheet, click the "Data" tab, select "From File," and "From Text/CSV."

        ii. Navigate to the GPS text file and click "Open."

        iii. A dialogue box will appear with a preview of the data to be imported. The GPS text files are typically tab delimited. If your data is properly sorted into columns, click "Load." If not, use the "Delimiter" drop-down menu to select the appropriate delimiter and click "Load."

    c. When the data has loaded, click the "Sort and Filter" button and select "Custom Sort."

    d. Sort the document by the column containing your filenames.

    e. Open the CSV containing your transect metadata. Follow step c to sort the metadata CSV by the "Audio Recording Name" column.

    f. The "meta" CSV and GPS spreadsheet should now be sorted by filename. Ensure the filename columns match.

     g. If the documents are sorted properly, copy and paste the latitude and longitude columns from the GPS file into the corresponding columns in the metadata CSV.

11. Save the file as a CSV (Comma delimited) with a unique and descriptive name. The NABat system will automatically overwrite duplicate filenames with the most recent version, so it is critical that your filename is unique.

12. Follow the guidance presented in step 5 of the introduction to this document to upload the metadata CSV to your project page.

Chapter 3. Processing Acoustic Data Using Bat Call Identification ver. 2.7d (BCID)

By Ryan Allen[10]

[10]Bat Call Identification, Inc.

Step 1. Attribute files

In BCID (Bat Call Identification, v2.7d, 2015), data can be attributed in two ways — both have advantages and disadvantages.

1. Use **Header** tab in BCID — Anything that you type in this area will appear in the header of the ZC file for any file in your tree that passes the filter. The advantages are you can set the filter to look for something very specific and label files as such and can label an entire file tree at once. The disadvantage is that files that do not pass the filter (that is, noise files, poor quality calls) will not be labeled. (However, this can save a lot of processing time).

2. Use **Global Header Change** in AnaLookW—You can change the headers of the file using the global header change options in AnaLookW. Make sure you "MARK" all files first, as changes will not take place on unmarked files (see chapter 5). This method will allow you to change all the files including noise files but may be more time consuming.

All global positioning system (GPS) data should be entered into files using AnaHead located within AnaLookW at this time. BCID will work to include this in the near future, making it easier on the user.

Data files can be arranged in any manner the user sees fit, provided that all of the files to be analyzed are nested in the file directory selected to analyze the current "chosen" folder. We recommend a format of Grid Cell/Detector/Date for NABat.

Step 2. Noise Scrubbing

While the noise filtering process in BCID is relatively integrated, there are some options that the user should be aware of. First, the user can change any of the parameters in the noise filter that they wish, but this should be done in a deliberate manner. In addition, BCID recommends reporting significant changes in a header data type format. The filter that was used can be read on the last tab of the BCID output file.

The most important items that users can adjust within the filter are Minimum Number of Calls to be considered in order to make an identification and the Min DP (Minimum Discriminant Probability). Increasing both or either of these numbers will have an effect on both false and true positives. Use a minimum of three calls for NABat.

Given the guidance in this document, BCID recommends experimenting with these numbers, especially the Min DP, as increasing it from the default of 0.00 can help reduce false positives because the number is based on several values that deal with call quality.

If you wish to view the files as the software does in order to test your filter, create the filter under the filter tab within the BCID software and then load the filter into AnaLookW and view your files. This can also be useful for moving "noise" files into separate folders.

Step 3. Auto ID

If you are using full spectrum files, you must first run them through the wav to zero-cross converter within the BCID software or other similar software packages.

The most important thing you can do is choose the correct species for your area. Under the species tab in BCID, you can choose a state or territory and then all of the species known to occur within that region will appear. Those that are widespread will be checked; those that are geographically isolated will be left unchecked. Those that are greyed out are not available for identification in the software.

We recommend setting the Create ANL file under the Advanced tab. This will allow the user to view the files in the next stage (manual vetting) by species label in AnaLookW. In addition, there is the option of adding the predicted species label into the header of the file by checking the corresponding box.

The final step is to use the Add Folders to Project button under the Project tab. Select the folder at the highest level you would like your files analyzed. All files within and below the chosen folder will be included in the analysis and any labeling, etc. that you have chosen for the software to perform. Once all files are chosen, return to Project tab and click Analyze files. This will produce a .txt document will all the files, IDs, etc. and a Microsoft Excel file with three tabs: (1) all of the files broken down by folders, (2) summaries of all folders, and (3) settings used, including the filter parameters and species selected.

Step 4. Manual Vetting

The easiest method of manual vetting files in BCID is to use the ANL file that can be created by BCID under the "Advanced" tab and opened in AnaLookW. This will allow users to open a virtual folder of all files that BCID has classified to species and quickly review them to determine if any of the files are consistent with calls produced by that particular species. Adjust header labels following guidance for manual vetting described above.

After manually vetting a dataset, one could re-run the auto ID, testing various values of the Min DP setting to determine the Min DP value that produces the results most similar to your manual vetting for a particular site, geographic region, etc. This could be informative for future analyses of datasets from this site. It is important to understand that both the software and manual vetting can be incorrect on occasion. The goal is to find the number where one can achieve the largest volume of data while ensuring the accuracy of the results. Once this number is determined, the software can be run using this number and the robustness of the results should be much more reliable.

Step 5. Submit to NABat

Follow the guidance presented in steps 3-5 of the introduction to this document to create a metadata CSV and upload it to your NABat project page.

Chapter 4. Processing Zero-Cross Acoustic Data Using EchoClass v 3.1

By Eric Britzke[4]

[4]U.S. Army Corps of Engineers

The following describes a recommended workflow using EchoClass for processing acoustic data for the North American Bat Monitoring Program (NABat) where data were collected as or converted to zero-cross files (*.00# file format).

Step 1. Attribute files

The first step in this process is attaching metadata to the files. The current version of EchoClass relies on the directory structure to provide information on the files instead of adding this metadata to the individual files (Britzke, 2012). Thus, in order to attach metadata to the individual files, follow the guidance included in chapter 5 (Recommended Workflow for Processing Zero-Cross Acoustic Data using AnaLookW).

Tips for organizing your data

The following information is taken from Britzke (2012). The data file structure must have at least two levels (no maximum) of folders for the program to run. *Additionally, the structure must be consistent throughout for each run of the software*. Keep the folder names short and do not include the "&" symbol in any folders or filenames. All of the recorded call files must be in a folder named with 8 numeric characters (e.g., 20120805). This can either be the date that the files were recorded or a single download date, as EchoClass uses this information to look for files but reads date data from the individual file. As the output of the analysis software includes information from the directory structure, (following the example below) the directory structure will populate the output with project and site information that is then ready for inclusion in a report.

Example file structure

```
Bats2012
      Project1
              Grid Cell1
                      Site1
                              20120601
                              20120602
                      Site2
                              20120701
```

- If you select the folder 20120601 the output file will be empty.

- If you select the folder Site1 you would get results from all folders named with 8 numeric characters under the Site1 folder (e.g., 20120601 and 20120602).

- If you select the folder Project1 you will get results from all the folders named with 8 numeric characters in all of the sites under the Project1 folder (e.g., 20120601, 20120602, and 20120701).

- If you select the folder Bats2012 you will get results from all the folders named with 8 numeric characters in all of the sites of all of the projects under the Bats2012 folder.

Global Positioning System (GPS) Information

Mobile Transect Acoustic Monitoring

- Make sure the gps.txt file downloaded with CFC read is located within each date folder.

- GPS_and_Sunset_Master.xls Excel spreadsheet must be placed in the data directory but can remain empty. For GPS data, the sheet must be entitled Mobile GPS Locations.

- Geographic coordinates for each bat file will be added to the latitude/longitude columns of the UserID output.

Stationary Point Acoustic Monitoring

- The latitude and longitude of each site must be entered

- Any higher data structure must also be entered

Sunset/Sunrise Times

- For sunset/sunrise the sheet must be named Sunset and Sunrise Times.

- For each Site/Date, enter the appropriate Sunset and Sunrise Times in 24-hr clock notation format

Steps 2 and 3. Noise Scrubbing and Auto ID

Analyzing data with EchoClass is straightforward, as there are few options that can be selected by the user. This was done to improve accuracy, repeatability, and consistency in the results among datasets. When the EchoClass software is launched, the user interface appears.

1. Select the **Browse button** and navigate to the appropriate directory (see examples above).

Chose the appropriate species set. If a species is not listed in a set it will not be an option for identification in this analysis. Thus, if that species is present it will be misclassified as a species that is listed. Because of this, the user should include all possible species which *might* be present in the area.

2. Click **GPS information** if the GPS data are provided in a specific format. This will result in location information being included in the output file.

3. Click **Sunset/Sunrise Times** if you want the activity metrics to be calculated. The user must provide the sunset and sunrise times for each night for the given location. This information will also be reported in the results output.

4. Click the **Process Data** button.

As the program runs, a series of popups will appear and disappear. Once completed, a Microsoft Excel file titled "User ID Report" will be created in your selected working directory (the folder selected in with the browse button).

Supplemental Data Options

For the following options to function correctly, the GPS_and_Sunset_Master.xls Excel spreadsheet must be placed in the data directory selected to run the program on (that is, if project1 is selected, the excel sheet must be located there as well).

Step 5. Submit to NABat

Follow the guidance presented in steps 3-5 of the introduction to this document to create a metadata CSV and upload it to your NABat project page.

Chapter 5. Processing Zero-Cross Acoustic Data Using AnaLookW 4.2n (March 16, 2017)

By Cori Lausen[2]

[2]Wildlife Conservation Society Canada

The following chapter describes a recommended workflow using AnaLookW for processing acoustic data for the North American Bat Monitoring Program (NABat) where data were collected as or converted to zero-cross files (.zc file format).

Step 1. Attribute Files

1. Ensure that minimum attribute data are included for each file (see step 1 in the Introduction of this report for more detail on attribution data. If waypoints are not already included in your files, add GPS coordinates to stationary point acoustic data using Anahead or to transect datasets using GPS Integration Wizard prior to analysis.

    A. Using Anahead (click on "Tools"; "Anahead"), select your folder and highlight all the files; positions; enter manually; enter the latitude and longitude in World Geodetic System 1984 (WGS84) datum.

2. (OPTIONAL, but recommended) Sort your data into nightly subfolders. This is generally advantageous because the stationary point acoustic data for NABat are analyzed by species presence per detector per night. For example, one potential hierarchical folder organization scheme includes assigning a single folder per **GRTS ID** with subfolders for each detector and mobile transect. Within each detector subfolder there should be nightly subfolders.

    A. If you used a Titley Scientific detector, this is most easily achieved at the time of download (for example CFCRead for Anabat has a check box for "split nights").

    B. If you are using auto ID software prior to using AnaLookW, many programs provide the option to sort files by "bat-night."

    C. Any dataset can be split by night using "Tools"; "Folder"; "Split Folder" in AnaLookW.

3. Add location data to file headers if this information is not already in the file metadata. It is highly recommended that this step is completed even if the information is present in the filenames.

    A. In AnaLookW, perform the following for *each folder*: "File"; "Mark All Files"; "Edit"; "Global Header Change." Add the **Grid Cell GRTS ID** and **Site Name** into the **LOC** field. For transect folders, add **Grid Cell GRTS ID** transect.

    B. If you know how to run a scan, you can send each detector's files (all nightly subfolders) through a single filter scan using a "blank" filter so that all files are displayed in a list file (virtual subfolder, much like a playlist in iTunes). You can then open the resulting .anl file in AnaLookW and perform a global header

change on all files here, thus putting info into the header of all files in all nightly subfolders, instead of having to do each folder separately.

Step 2. Noise Scrubbing

To remove non-bat files from your dataset:

Option 1: Kaleidoscope or Kaleidoscope Pro

Run the files through Kaleidoscope or Kaleidoscope Pro (KSPro). You do not need to do any file conversion or auto ID; simply use the drop-down menu in the "Outputs" section to select "Move noise files to NOISE subfolder." Be sure to select the appropriate criteria for the noise scrubber (see KSPro workflow).

Option 2: AnaLookW

In AnaLookW, apply an "AllBats" or customized AntiNoise filter (see Appendix B: Using Filters in AnaLookW). Run a scan ("Filter"; "Scan") using the selected filter across a copy of the dataset (folder tree), setting the output to generate a list file (only check the ANL list box). Opening the resulting .anl file in AnaLookW File Selector enables users to mark all the files that passed the filter, reverse the marks, and delete (or move) all the files now marked (the files which didn't pass the filter).

Step 3. Auto ID

Use one of the following options to obtain ZC files with species labels:

Option 1: Species Labels are Embedded in Files as Metadata During the Auto ID Process

SonoBat

SonoBat is used for files that start as full spectrum. SonoBat will place a species label in the file metadata that should appear in AnaLookW once the full spectrum file is converted to ZC format (see next step). The auto ID label will be in the "Species" field of the **Header** data (ensure that "Append species codes to filenames" is **not** selected). Subsequent manual vetting in AnaLookW will place metadata into the species field that will override the auto ID in the final results file.

After running the auto ID process in SonoBatch, you must convert full spectrum files to ZC files in order for them to be read in to AnaLookW. Full spectrum files can be converted to ZC using KSPro, BCID, or newer versions of AnaLookW ("Tools"; "Converter"; "WAV to AnaBat").

Kaleidoscope Pro

- Kaleidoscope Pro (KSPro) can be used for any recording file type. Before processing files with the auto ID option, check the appropriate boxes to indicate your file type under the "Inputs" section of the "Batch" tab (for example, WAV as input, ZC as output). The auto ID process will place a species label in the ZC file metadata which will be seen in the "Species" field of the **Header** data once in AnaLookW. There will also be

information in parentheses about the auto ID (e.g., matching pulses, alternate IDs — this will depend on the version of KSPro).

Bat Call Identification (BCID)

- BCID can be used for any recording file type. If you use full spectrum files, they must first be converted to ZC within the program. The auto ID process of BCID will place a species label in the ZC file metadata (in the "Species" field of the **Header** data, appended with -bcid). See Chapter 3: Processing Acoustic Data Using Bat Call Identification (BCID ver.2.7d).

Option 2: Species Labels Are Embedded in Files as Metadata Following Application of Filters

- Follow instructions in Appendix B: Additional Guidance for AnaLookW.

Option 3: Species Labels Are Provided in an Excel Spreadsheet

- The Excel spreadsheet provided as output from auto ID software (e.g., spreadsheet produced by EchoClass — see the EchoClass workflow in Chapter 4) can be referred to during manual vetting of the files using AnaLookW as a viewer. Manual vetting will require making changes in the Excel spreadsheet after viewing each file.

Step 4. Manual Vetting

To carry out manual vetting, follow the ruleset laid out in step 4 (after the Introduction) of this report. If you obtained files using option 3 above, view each file in AnaLookW and adjust species labels as appropriate in the Excel spreadsheet. If you obtained files using options 1 or 2, proceed with the following steps for manual vetting.

1. Ensure the Species List is visible. Check the option in "View"; "Species List." This will allow you to add a species label to the metadata of each file by clicking a single button. Load or create a species list using one of the following options.

   Option 1: Load a Species List

   - Click the "Load" button to the right of the species label buttons.

   Option 2: Create or edit a Species List

   - Right-click each button and enter a 4-letter species code (table 3) or up to 8 letter frequency group or high/low class label (table 4).

   - Select "Save As" to save your species list.

   Tips for Species Lists

   - Include group labels appropriate for your bat community (tables 3 and 4).

2. Load a file from your dataset. If your files are organized by detector and by nightly subfolders, start with night one of detector one.

3. "File"; "Disperse"

   A. Choose one of the following methods:

- *Method 1*: Select current folder. This will create a sorted .anl file just for the nightly folder you have selected. You will need to repeat this step for each night's folder for each detector.

- *Method 2*: Select a higher order folder. **Include subfolders** (check this box). For example, you might select to "disperse" one detector. This means all nightly subfolders will be included in the "disperse" and you can view all recordings of this detector as though they were in one virtual folder together. This method involves fewer steps overall than *Method 1*, but you will have to pay attention to what nightly subfolder you are in during the vetting process.

  B. Check the option for "List File (.anl)." Check to "Ignore Prefixes," then "Run."

4. "Shift I" (or "File"; "Open Here") and click on "**Sorted.anl**" in whichever folder you directed the disperse to start. Sometimes you need to collapse directory and open it again to see this file. Users can close and reopen the folder in the left viewing pane using the ± button by folder name.

5. Using "Choose Field," review each of the species categories. The goal is to manually verify at least one file per night for each species. Repeat steps 3–5 until all nights of all detectors have been analyzed.

For stationary point acoustic data, you need only confirm one file of each species each night. For mobile transect acoustic data, all bat files should be reviewed.

Required for Mobile Transect data and recommended for stationary point acoustic data:
Review the "No_ID" field. These files did not get an auto ID and if you used filters, also did not get triggered by a filter.

Why are some files No_ID?
Files assigned the label "No_ID" are likely poor quality, high clutter recordings. However, with auto ID, a file is occasionally labelled as "No_ID" even though good quality, identifiable pulses are present. This can occur when the recorded pulses have characteristics of more than one species. However, this can also occur if two equally well-recorded species occur in the same file. Identifying high quality recordings of two species in the same file is especially important if there are species that you think are present in your area but have not been detected in a certain night's dataset. In stationary point acoustic data, this may be the only reason to view "No_ID" bat passes.

Mobile Transect Data Only

The goal for collecting mobile transect acoustic data for NABat is to evaluate relative species abundance. Therefore, ensure that each bat file receives a label. If there are few "No_ID" files, then you may choose to go through all of them. If there are a lot of these files (for example: >100), you may instead opt to run a few filters to group the "No_ID" files into broader categories for easier vetting. For example, you could choose to run a general "40kMyotis" filter if you have one of these available. "Load Filter"; "File"; "Mark if Pass Filter." Remember that once a filter has marked files, you can quickly jump from marked file to next marked file using - / = keys and select on the species button at the top to add the label "40kMyo" (or use "Global Header Change" and label "40kMyo").

Download Results into an Excel Spreadsheet Format.

1. "Tools"; "Anahead"

2. Select the folder in your dataset you want to summarize.

3. "File"; "Download"

4. Repeat 1 and 2 for all subfolders in the dataset.

5. In Windows Explorer, open each Header.txt file that has been created in each folder/sub-folder one at a time and copy/paste the output into an Excel spreadsheet.

Step 5. Submit to NABat

Follow the guidance presented in steps 3-5 of the introduction to this document to create a metadata CSV and upload it to your NABat project page.

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Appendix A. Case Study—Using Rule Sets to Process Acoustic Data for USDA Forest Service Lands in Northern California

By Ted Weller[3]

[3]USDA Forest Service

The standard for which files should be considered for manual vetting will vary by location according to how common a species is expected to be and how likely it is to be confused with other species at the site. Location-based rulesets can be established to direct manual vetting towards files that require the most attention (that is, unusual species, files where SonoBat has lower levels of certainty in its auto ID). Rulesets can be codified to automatically assign species to files for which SonoBat has high levels of confidence and assign files to frequency groups (e.g., HiF, Q40k) where SonoBat has low confidence or gleaned little information from the file. When establishing rulesets, take into consideration the expected probability of a species' detection in deciding how to direct manual vetting efforts. For example, at some sites, a single species can comprise greater than or equal to (≥) 50 percent of the total files recorded. In this case, confirmation of this species can be based on lower levels of certainty by SonoBat (e.g., TABR 2 of 2) than we would normally accept. Rulesets are plastic and evolve over time to improve accuracy of species identification and, importantly, improve efficiency with which assignments to a species or species group are made. Rulesets begin as regional tools and evolve into sub-regional tools as we learn more about the relative probability of species occurring in the parts of the region studied. When appropriate, rulesets can be established for individual sites. In northwest California for example, two sites approximately 100 kilometers (km) apart have different rulesets. At one site, TABR is exceedingly common and LANO is less common, while at the other site, TABR is very uncommon and LANO is common. Hence we review few of the potential TABR files and more LANO files at the first site and all TABR files and very few LANO files at the second site. This saves time at both sites.

In the following, we describe a process for using established rulesets to determine activity levels by species and species groups by night in mountainous areas on USDA Forest Service land in northern California.

1. Vetting table is exported as.txt file, selecting output null as "."

2. Exported .csv file is opened in EXCEL and a Pivot Table is inserted to summarize the data.

The output table includes the number of files confirmed per night populating the species-by-night matrix. Values ≥1 will ultimately be reduced to presence/not-detected values for analysis. Here they represent a crude, proposed method of assigning confidence to species ID per night.

The following rulesets were translated into a PYTHON script (https://github.com/brendan-ward/echoclean) and pointed at text output from a SONOBATCH run.

- For EPFU, LANO, MYCA, MYCI, MYLU, MYVO, MYYU, and PAHE, we will generally only review files if #Maj=#Accp≥3, files with #Maj=4 and #Accp=5, and #Maj=5 and #Accp<=7, and #Maj=6 and #Accp<=8 should also be reviewed.

- When ANPA, COTO, EUMA, EUPE, LABL, LACI, MYEV, MYTH, NYSP, or TABR are listed in the "1st" column, review all files (up to 10 files per night) until at least five files per species per night can be confirmed.

The PYTHON script creates a "Species" column and an "Inspect (Y/N)" column. The species column is populated with a label: species, couplet (EPFULANO), frequency group (50k), or high/low frequency class (HighF) according to SONOBATCH output parameters. Files without adequate information from SONOBATCH are identified simply as "Bat." In some cases, these have been found not to be bats, despite the file having been scrubbed in earlier steps. The relative proportion of files that are not bats appears to depend on site and season (e.g., bird songs and insects can sometimes trick the scrubbers). If it is important to quantify the total number of files produced by bat echolocation ("mobile transect acoustic monitoring" for NABat, Loeb et al. [2015]), low-quality and non-bat files are included in manual vetting efforts.

3. Files highlighted by ruleset (via the Python script) are prioritized for manual vetting.

   A. Output is sorted as follows:

      ▪ Sorting orders the files to be manually vetted by potential species followed by probability that they will ultimately be assigned to that species and groups them according to other potential species in the file and frequency range.

      ▪ Each file with "Inspect=Y" is manually vetted and assigned to species or group. Manual vetting is based on comparison to reference files, regional guidance (with images) written by Ted Weller, and experience of the observer.

4. Following manual vetting, files are re-sorted excluding the "Inspect" column such that potential species ID's are listed in order of SonoBat's guidance.

   A. Patterns in eventual ID's compared to SonoBat ID's are studied to refine the ruleset for each of the species.

5. Night of recording is extracted from the filename and used in a pivot table to create a matrix of number of files assigned to each species or group for each night of recording.

Appendix B. Additional Guidance for AnaLookW

By Cori Lausen[2]

[2]Wildlife Conservation Society Canada

Tips for using AnaLookW

1. "Tools"; "Options"; "Display" will allow you to change colors if needed.

2. "Tools"; "Options"; "change DELAY to 300 ms" (so the user can scroll through files at reasonable speed by holding the closed square bracket or W keys) — *recommended*.

3. Always save files to C drive (not to desktop or My Documents), as AnaLookW does not like files that become too buried in a directory and the desktop is actually an embedded location in your hard drive.

4. Mark all files ("File"; "Marking"; "Mark All"). You then can use the button "Replace" in the top of the AnaLookW screen to replace a field for all marked files (e.g., Highfreq instead of HighF). Recall that there is no "undo" if you make a mistake.

5. To move from file to file that has a label in species field of header (e.g., skipping blank species), hold "Shift" and press the square bracket keys ([or]).

6. To skip between marked files, use the minus (-) and equal (=) keys.

7. Reverse marks as needed, in "File"; "Marking" or right-click on filenames in Anabat File Selector Window (Shift l).

8. "File"; "Mark if Labelled" (only mark those files with a species label).

9. "Edit"; "Delete if Marked." For example, you could "Reverse all Marks" after marking bat files (so marked files are the noise files), then it is possible to move or delete files if you are confident they are all "noise" (non-bat recordings).

10. You can use the "m" key on your keyboard to pull up a measuring screen (or "View"; "Measures"). If you use numeric parameters to help manually vet, you can view measurements of single pulses or averages of pulses on the screen using this "m" key.

11. You do not need to use the "Measures" screen to evaluate "Fmin" if there are many pulses, as this could be misleading. Instead, hold your curser at the bottom of the call of interest and look at the number on bottom right of the screen.

12. Under "View"; "OffDots" you can choose to visualize your "offdots." Filters turn dots "off." By choosing to visualize "offdots" you can see which dots are not passing the filter criteria.

13. You can view your file in a screen next to another screen with a reference file by selecting "View"; "Tile Horizontal" (or "Tile Vertical"). You can then link both screens so they maintain the same settings by selecting the link screen button that looks like two overlapping squares. The screen you are in at the time of clicking the link screen button becomes the "Master" screen while the other screen becomes its "Slave." Alternatively, you can link them both and have both as "Masters."

- If at any point the species field is too full (e.g., when Kaleidoscope Pro fills in a lot of information in parentheses after a space following the species ID label), you can move this information to the "Notes" field using "Copy"; "Paste."

***IMPORTANT** It is critical that the auto ID labels be retained and remain in the "Species Field" so that these data are retained through to the final spreadsheet.*

14. "Buffer" is located to the far right side of the species list. Use this if you want to have a "push button" way of adding a label to the "Species Field" that is more than eight characters long. You can only have two buffer labels (top two) that will add to a "Species Field" when clicked. Enter a label into the "Buffer" by first typing into the "Species Field" exactly what you want to save into the "Buffer." Then click the "Save" button next to the "Buf1+" or "Buf2+" buttons. The "Buf" button is now lit and ready to use as another "Species Label."

Using Filters in AnaLookW

1. Obtain AnaLookW filters. It is recommended that only Strict or "Diagnostic" type species filters be used. (If you are simply scrubbing out noise files from bat files, then an "AllBats" filter can be used.)

   - Filter files (.abf files) can be obtained from trusted sources, or you can create a filter by filling in appropriate parameters.

   - If you are not an advanced user, then these parameters should be obtained from a trusted source. Parameters can be inserted into the filters using "Filter"; "New Filter"; "Save Filter."

2. Apply filter(s).

   Choose one of the following options.

   Option 1: You can apply a filter to any given folder of bat files ("Filter"; "Load Filter," then "File"; "Marking"; "Mark if Pass Filter," then view marked files and (or) perform "Edit"; "Global Header Change").

   Option 2: Use a scan to apply one or more filters at one time. Be sure to only select the output option "ANL." This produces a "scan file" (.anl file format). Recall that using a "Scan" instead of applying a filter on a per folder basis has the advantage of seeing all files of a dataset from all subfolders at once in one "virtual folder" (.anl file). This allows actions to be completed on the dataset all at once, despite the fact they are in separate subfolders (for example, nightly folders). "Scan" files (.abs) are required if you are going to scan with more than one filter at a time.

3. Once a filter/scan has been applied, you should put a species label into the **Species** field of the header so that you know this file has passed a species-level filter. You will use species labels such as LABO. This means you used a filter to identify a file that is likely a LABO bat pass.

   If you applied a single filter to a folder ("Mark if Pass Filter") then simply use "Global Header Change" to apply a label (e.g., LABO for files that passed the LABO filter).

If you applied a scan of a single or multiple filters, use the .anl file to view each field (generally each field is the name of the filter). For each field, "Mark All," then "Global Header Change" to insert a species label into the Header (e.g., LABO). Do so for each field.

Conclusion: All files that passed a strict or diagnostic filter have now had a species label inserted into its metadata. You are ready to manually vet, see chapter 5, step 4, Manual Vetting.

Appendix C. Bat Auto ID Species Confusion Matrix

This appendix provides a "Bat Auto ID Species Confusion Matrix" as a quick look-up guide indicating which species are commonly confused by auto ID software. In the matrix, red cells indicate species not currently included in classifiers used for automated species identification. Grey cells (along diagonal) are not applicable to the matrix.