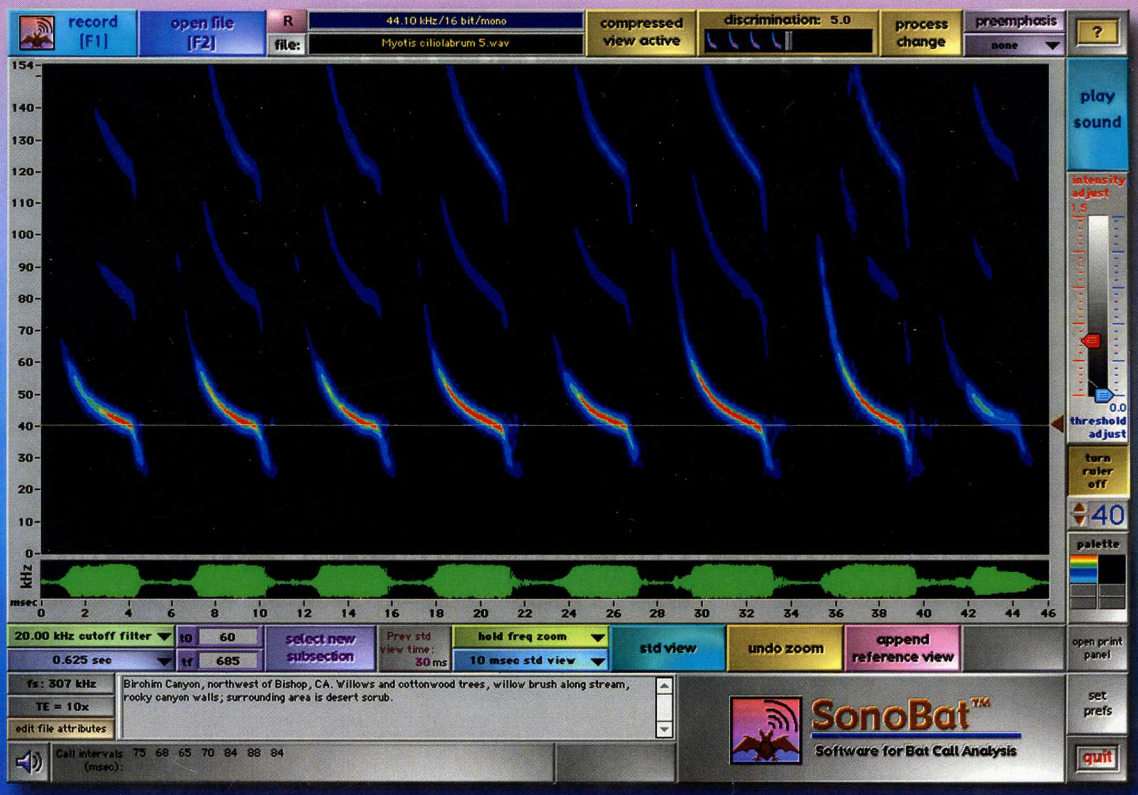
SonoBat 2

software for bat call analysis



User's Guide

SonoBat 2.2

May 2004

SonoBat

Joe Szewczak is the designer and programmer of SonoBat.

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Introduction

SonoBat is a powerful tool for viewing and analyzing full-spectrum sound data. It is especially designed to work with ultrasound and pulsatile sounds like that emitted by bats. SonoBat accepts sound from any sound source, but in particular, it is well suited for working with bat sounds recorded using time expansion bat detectors or high speed data acquisition of ultrasound. SonoBat allows you to

- view call sequences in an easy to interpret sonogram
- play call sounds
- display calls in a variety of modes
- filter out unwanted low frequency noise
- enhance harmonic elements of a call sequence
- manipulate screen-positioned cursors to quantify low/high frequency, bandwidth, duration, heel, slopes, characteristic frequencies, harmonics
- write call data to an external file
- compare unknown bat calls to those from known bats

Chapter 1 takes you through the steps of viewing sample call sequences to help familiarize you with the most common features of SonoBat. Chapter 2 covers zooming and making side-by-side comparisons of unknown calls with reference calls from positively identified bats. Chapter 3 covers the quantitative functions available with SonoBat and Chapter 4 provides instructions and tips for recording bat calls with SonoBat. Most topics are covered with a general overview, a detailed example and any additional information and tips that will help you to get the most out of your bat calls. The examples make extensive use of sample files provided on the SonoBat CD.

1 Processing & Displaying Calls

This section explains the features, settings, controls and functions needed to open, process, adjust and view bat call recordings in SonoBat.

Starting Terminology

- A *sonogram* is a visual picture of the frequency, time and amplitude components of a sound. Also called a *spectrogram*.
- A *call* is a single, discrete sound emitted by a bat.
- A *call sequence* is a series of calls emitted by a bat.
- *File* and *recording* refer to a bat call or call sequence that has been collected by an ultrasonic detector and saved as a .wav file.

Opening SonoBat the First Time

Windows: Start SonoBat from the Start/Programs/SonoBat menu.

Macintosh: Locate the SonoBat program file you copied to your hard drive and double-click on it.

The main SonoBat window appears. Take a moment to familiarize yourself with the general arrangement of the screen:

- The large, black, main window will display the sonogram.
- Buttons across the top of the sonogram are used for switching to the recorder panel, opening files, processing files and changing processing settings.
- Buttons on the right side of the window are used for post-processing functions such as playing sounds, printing and adjusting the intensity of the sonogram.
- The bottom portion of the window is predominantly used for advanced features such as comparing one call to another,

displaying detailed parameters about a call, and other advanced settings.

- Many of the buttons on the right and bottom portion of the screen appear grayed-out until a file has been opened. Other buttons will appear when you are in different modes.

We will cover the use of all buttons, controls and settings in this Guide.

Setting preferences for sample file directories

Examples throughout the Guide use sample files provided on the SonoBat CD in a directory named SonoBat files. If you have not already copied this directory to your hard drive, please do so now before proceeding. Follow the steps below to set up the path to the two sample directories. Details about example files versus reference views will be covered in later sections.

1. Click on the **set prefs** button in the lower right portion of the SonoBat window.
2. Locate the **default analysis call path** label and click on the related **Click to browse to directory** button.
3. Using standard directory navigation techniques, locate the **SonoBat files** directory copied to your hard drive during installation.
4. *Windows:* Double-click on the **example files** directory.

   Macintosh: Click once on the **example files** directory to highlight it.
5. *Windows:* Click **Select Cur Dir** on the lower right corner of the dialogue box.

   Macintosh: Click on the **choose** button on the lower right of the file dialogue.
6. Locate the **default reference call path** label and click on the related **Click to browse to directory** button.
7. Using standard directory navigation techniques, locate the **SonoBat files** directory copied to your hard drive during installation.

8 *Windows:* Double-click on the **`ref views`** directory.

Macintosh: Click once on the **`ref views`** directory to highlight it.

9 *Windows:* Click **`Select Cur Dir`** on the lower right corner of the dialogue box.

Macintosh: Click on the **`choose`** button on the lower right of the file dialogue.

10 Click **`Save`**. The preferences panel will close.

Processing and Viewing Call Sequences

SonoBat offers two modes of displaying a call sequence: *compressed view* and *real time view.*

- Real time view displays the calls over time as they were emitted by the bat and saved to the file. The entire unabridged file is shown in low resolution and the time scale accurately reflects call *duration* and the *intervals* between calls.
- Compressed view mode reduces the silent intervals between calls, leaving more room on the screen to better display the details of the calls within the sequence. The time scale accurately reflects call *duration*, but not the *intervals* between calls. Interval times shown start with the interval between the first and second call shown. If the number of intervals displayed is not equal to one minus the number of calls displayed, then there are some overlapping calls, or non-bat noise discriminated.

The following examples look at the same file in each mode.

Real time view example

1 Click once on the **`compressed view active`** button to change it to **`real time view active`**.

2 Click on the **`open file`** button in the top left portion of the SonoBat window

3 Navigate to the **Example files** directory.

4 Select the file **Pipistrellus hesperus 3**.

5 SonoBat displays a **processing...** status bar in the middle of the sonogram window while the file processing is in progress.

6 Seven calls appear in the sonogram and oscillogram (below the sonogram) when processing is complete.

7 The name of the file is shown above the sonogram, just below the file format data. Note the time interval shown below the oscillogram runs from 0 to 594 msec, the complete time for this file.

8 Click once on the **play sound** button in the upper right corner of the screen. Note how a thin orange indicator line moves along the oscillogram to assist you in matching the sounds and pictures.

Tip: When using the SonoBat file selection dialogues, you can change the sorting order of the list between filename and date by clicking on the column labels at the top of the list window.

Tip: You can quickly move about the SonoBat file selection dialogues by clicking in their slider bar furrow. The slider will jump to that position.

Compressed view example

1 Click once on the **real time view active** button to change it to **compressed view active.**

2 SonoBat displays a **processing...** status bar in the middle of the sonogram window while the file processing is in progress.

3 Five calls appear in the sonogram and oscillogram when processing is complete.

4 Click once on the **play sound** button in the upper right corner of the screen. Note how the orange line moves along the oscillogram, jumping from one call to the next instead of moving smoothly as it did in real time mode. Remember that the time between calls has been removed. The time scale still accurately reflects call *duration*, but not the *intervals* between calls. The time interval of the

oscillogram now runs from 0 to just 38 msec. Of the 594 msec in this file, 556 msec have been removed as noncall intervals.

5 Look in the lower left corner next to the sound output icon and notice that the true time elapsed between calls is displayed for you. No information has been lost; removing the silent intercall intervals allows you to view calls in higher resolution.

6 Notice the start time (`t0`) and end time (`tf`) of the displayed sequence are shown below the oscillogram toward the left side of the panel. The values for this sequence are 0 to 594 msec whether in real time or compressed view mode.

7 Go back to real time mode (click the `compressed view active` button and then `reprocess`). The time displayed on the oscillogram plot goes from 0 to 594 msec and no call intervals are displayed.

Resolution in real time view

Calls can be viewed in low or high resolution in real time view. Use the switch next to the real time/compressed view button to change resolution.

You can also zoom in on one or more calls. See "Zooming in real time mode" in the Call Analysis chapter.

More on real time view vs. compressed view

Why does the real time view display seven calls and the compressed view only five calls? Real time view displays the entire contents of the file. Sometimes real time mode will show faint calls that are not recognized by the discrimination algorithm used for compressed view mode. In compressed view mode SonoBat is more selective about displaying sounds and attempts to eliminate sounds that are atypical of discrete and complete bat calls. SonoBat depends on a clear distinction of amplitude level between calls and background sound to make best guesses on which sounds are bat calls and which are not.

Most of the time you will want to be working in compressed view mode for fast maximum call resolution. However real time mode is handy when there is too much noise for effective call discrimination, or when you

want to display the real time relationship between calls and intercall intervals, as for a feeding buzz. Real time mode is also helpful for displaying calls missed by compression discrimination when call amplitude may vary significantly.

The automatic call interval calculation depends upon a clear distinction of amplitude level between calls and background sound. Thus, calls in recordings with considerable background noise will not discriminate well, and may yield spurious interval times, or some calls of low amplitude may be missed. If the interval times do not appear consistent, view the call in real time mode to manually check the call interval sequence.

Experiment with viewing a feeding buzz in real time and compressed view modes with the sample file `Myotis volans 1`. Click on the `real time view active` / `compressed view active` button to toggle between view modes.

Adjusting the Intensity and Threshold

Unlike the frequency and time parameters that can be represented with absolute numbers, the intensity of a call varies with the distance and orientation of the bat from the microphone. Intensity should be thought of in relative terms and is predominantly used to determine the portion of the call in which the bat uses maximum power. SonoBat allows you to adjust the intensity (amplitude) representation of the sonogram and the minimum intensity displayed of the sonogram.

Adjusting threshold and intensity example

Let's explore the intensity controls in SonoBat:

1. Open the file `Myotis ciliolabrum 2` in compressed view mode.
2. The intensity control panel is under the `play sound` button. Two settings can be adjusted. The blue control slides up and down to adjust the relative minimum intensity displayed.
3. Slide the `threshold adjust` control up and down and observe how the call structure is revealed as extraneous noise in the file is

muted when the threshold is raised. Raising the threshold further results in loss of the weaker, lower amplitude components of the call. Maximizing the threshold adjustment simulates how a call would look if recorded at lower amplitude, as when the bat is farther from the detector microphone.

4 Slide the red **`intensity adjust`** control up and down to increase and decrease the contrast of the amplitude. Moving the control toward the top of the scale will reveal intensity contours in gray scale mode (selectable from the **`palette`** control).

Processing Long Call Sequences

All the files we have opened so far have fit neatly into a single sonogram. Sometimes a file will be too large to process in a single pass due to memory limitations, but also to enable a practical view of a sequence. For files larger than your **`max file segment to process`** setting, SonoBat displays the entire oscillogram and prompts you to choose a portion for processing and display in a sonogram. The size of the file segment that SonoBat can process in a single pass is set with the **`max file segment to process`** pulldown on the lower left of the SonoBat panel, beside the end time indicator, **`tf`**.

Long call sequence example

We can see how this works with the sample file **`Eumops perotis.`**

Note: If after opening the file, your **`max file segment to process`** setting does not show 1.5 sec, see "More on long files" below.

1 Open the file **`Eumops perotis`** in **`compressed view active`** mode with the default **`5 kHz cut off filter.`**

2 A noisy oscillogram with four vague calls appears below a blank sonogram. A flashing button on the lower right alerts you to the fact that SonoBat needs instructions from you before it can process the sonogram.

3 A default section of the oscillogram from 100–1600 msec has been pre-selected by SonoBat. The default section is demarcated at the

beginning by a thin yellow line and at the end by a thin red line. The start and end time indicators, `t0` and `tf` also indicate these values. This section includes two calls.

4 Click on the flashing button or hit your `Enter` key to accept the default subsection.

5 Two calls are shown. If you play the sound, expect long pauses before and between the calls.

6 Click `select new subsection`.

7 The original oscillogram is presented again.

8 Position your cursor over the yellow line at 100 msec, hold down the mouse button and slide it smoothly to the right until it reaches 1700 msec. Notice that the red end-of-file line moves to the right as you move the yellow line. If you inadvertently add too much vertical motion to the mouse as you drag right, the oscillogram will flash unhappily. Simply keep the cursor in the oscillogram window when you drag left and right.

9 Click on the flashing button or hit your `Enter` key to process your new selection.

10 Two different calls are shown; the call on the left reveals multiple harmonics.

More on long files

At its default **max file segment to process** setting, SonoBat can process a file subsection of 750 msec for a sequence sampled at 44.1 kHz and a time expansion factor of 10x. (1.50 sec for a sequence sampled at 22.05 kHz). SonoBat offers eleven other choices. Why wouldn't you want to select the largest possible file segment (16 sec for a 44.1 kHz file, 32 sec for a 22.05 kHz file)? The maximum file segment that you can process depends on the available RAM and system resources of your computer. Trying to process segments too large for your computer will result in SonoBat crashing with "out of memory" messages. In addition, even if your system could process very large subsections, they may render too many calls in each sonogram to easily view the calls.

You can change the **max file segment to process** setting while the **select subsection** button is flashing. Note the red end-of-file line move accordingly as you choose more or fewer points to process.

If the entire file size is less than 3x the **max file segment to process** setting, a change in the filter setting (see next section) will be processed and rendered in the oscillogram view. This may help to reveal calls present in noisy sequences. To see how this works, open the file **Myotis yumanensis 3** with the **5 kHz cutoff filter** active. You should see the **select subsection** bar. Change the filter setting to **20 kHz cutoff** and you will see the bat calls show more clearly in the oscillogram trace to guide your selection.

A change in the default **max file segment to process** setting will remain in effect for the duration of your SonoBat session. However, you may save a new setting as your default by clicking on the **set prefs** button in the lower right corner of the window. The preferences panel will open. Toward the bottom of the prefs panel you will see the **max file segment to process** pulldown control. Select the desired value and hit the **Save** button. This setting will then be active when you begin your next and subsequent SonoBat sessions.

Filters

In the perfect field recording situation there would be no chirping insects, no babbling brooks and no rustling leaves to interfere with loud and clear

bat calls. As this perfect situation is rare, you may often have non-bat call "noise" in your recordings that you want to minimize or hide. In addition, you might occasionally see glimmers of quiet harmonics in a call and wish that you could turn up the intensity for a closer look. SonoBat offers four filter settings to help you get the most out of your call sequences:

- *unfiltered*—all sounds are displayed, regardless of frequency; this setting may be useful for calls that extend into the audible range
- *5 kHz cut off*—preferentially eliminates sounds below 5 kHz; sounds below this frequency often carry interfering environmental noise and rarely carry true bat call components
- *20 kHz cut off*—preferentially eliminates sounds below 20 kHz; this filter may be useful for reducing noise in higher frequency calls (around 40 kHz and above)
- *harmonic emphasis*—this setting progressively emphasizes higher frequencies and can reveal subtle harmonic components of calls

The `5 kHz cut off filter` is the default filter setting in SonoBat. The filter setting button is just below the oscillogram on the left of the panel. Changing the filter setting initiates an immediate reprocessing of the sonogram.

Note: The 5 kHz and 20 kHz values above apply to typical files with a 10x time expansion factor. The filter values will adjust proportionally for other time expansion factors.

Filter examples

The following files will help you understand the range of filter settings:

- `Two bats`—open in `compressed view active` mode with the default `5 kHz cut off filter`. Reprocess with the `unfiltered` and `20 kHz cut off` filter and observe how

the non-bat noise is eliminated or reduced to cleanly separate the calls.

- **Antrozous pallidus 3**—open in **compressed view active** mode with the default 5 kHz cut off filter and **preemphasis** set to **none** (pulldown menu at upper right). Notice the small spot at 80 kHz in the first call. With the default threshold setting at 0.0, we can't turn up the intensity to see more of what's happening at 80 kHz. Switch to the **harmonic emphasis** filter and **reprocess**. Note the subtle harmonic now revealed at 80 kHz.
- **Filter demo**—open in **real time active** mode with the **unfiltered** setting and **preemphasis** set to **none** (pulldown menu at upper right). This file is a synthesized sound of 10 msec long pure tones of consistent amplitude, increasing in frequency 5 kHz each step. Watch the beginning of the oscillogram and sonogram and reprocess with the **5 kHz cut off filter**. Notice that the sound around 5 kHz is significantly reduced but is not entirely eliminated. Repeat with the other three filter settings to view the filter effects.

Preemphasis

Preemphasis processing accentuates differences in the audio signal, particularly low amplitude components, and helps to render these components visible in the sonogram display. However, preemphasis may also magnify noise and undesirable portions of a signal. For strong signals of high quality, preemphasis will probably contribute little additional information. In contrast to the **harmonic emphasis** filter, preemphasis treats all frequencies more *equally*. Thus if you wish to reveal and compare the relative strengths of harmonic components, use the preemphasis function.

The harmonic emphasis filter and preemphasis may be used together to coax out high frequency structures.

Preemphasis vs. harmonic emphasis example

To view the action of **preemphasis** processing:

1. Open the file **Myotis californicus 3** in compressed view active mode with the default **5 kHz cut off** filter and **preemphasis** set to **none**.
2. Depending upon your **max file segment to process** setting, a flashing button on the lower right prompts you to select a subsection of the file. Drag the vertical yellow cursor to the left so that the selected subsection includes the first call. (If you don't see the yellow cursor, it may be hidden behind the second call at 100 msec.) Then click on the flashing button or hit your **Enter** key to accept the subsection.
3. The processed sonogram reveals strong fundamental tones, and harmonics going off the top of the screen (if the sampling frequency is set to the default of 300 kHz).
4. Change the filter to **harmonic emphasis**. Click on the flashing button or hit your **Enter** key to accept the same subsection if needed.
5. Bits of an intermediate harmonic are now visible in the sequence.
6. But are the top harmonics (the third harmonics) actually stronger than the intermediate harmonics (the second harmonics), or is this an artifact of the harmonic emphasis filter which preferentially emphasizes higher frequencies?
7. Reset the filter setting to the default **5 kHz cut off** and set **preemphasis** to **medium** using the pull-down on the upper right side of the sonogram window.
8. Click on the flashing button or hit your **Enter** key to accept the same subsection if needed.
9. We can now confirm that the third harmonics are stronger than the second harmonics.
10. Return the **preemphasis** control to none for subsequent examples.

More on preemphasis

Too much preemphasis can fill a sonogram with unwanted features.

1. Open the file **`Euderma maculatum 1`**.
2. Reset the **`preemphasis`** control to **`full`**. The sequence will reprocess using the new **`preemphasis`** setting.
3. Ugly vertical features appear o the middle call, and all the calls take on a more ragged appearance. This is an example of too much preemphasis processing in which signal noise becomes over-emphasized.

Adjusting the Discrimination Level

In compressed view mode, SonoBat reads the file and determines where each call begins and ends, attempting to distinguish bat calls from noise with a discrimination algorithm. For maximum flexibility, you can adjust using the discrimination setting using the control at the top of the sonogram window.

- Increase the discrimination setting to prevent calls with abrupt starts and stops from being inadvertently truncated.
- Decrease the discrimination setting to prevent noise from being misinterpreted as bat call. When noise is misidentified as bat call, call duration and intercall intervals are inaccurate.

SonoBat calculates the call intervals from the centers of the file segments that it discriminates as call portions. Changing the discrimination setting may increase or decrease the amount of sound that is interpreted as call, which in turn may slightly shift the value of the reported call intervals. For best results, the minimum discrimination setting that reveals all calls (even if displayed as truncated) is ideal for calculating call intervals. Take care to check on the real time view that calls are not missed.

To execute a change in the discrimination setting, you must push the **`process change`** button.

The default discrimination setting is 6.4.

- Windows *users:* right-click on the discrimination control to reset to the default setting.
- *Macintosh users:* command-click to reset the discrimination control to reset to the default setting.

Discrimination control with truncated bat call example

Let's see how increasing the discrimination control can prevent calls with abrupt starts and stops from being truncated:

1. Slide the discrimination control from the default setting of 6.4 to a setting of 3.0 and open the sample file **`Euderma maculatum 1`** in compressed view mode, leaving all other settings in their default mode.
2. Note how calls abut each other in the oscillogram and show funny little vertical artifacts at the end of each call. Also note that there are two interval times reported, as you would expect for three calls.
3. Slide the discrimination control to a setting of 9.0. The control shows you that more space will be retained between each call.
4. Click **`process change`**.
5. Note the increased spacing between calls in the oscillogram and the absence of truncation in the sonogram window. There are now three call interval times reported. The first call interval time is a spurious result because some non-call sound component was recognized as a call at this improper discrimination setting.
6. Return the discrimination setting to the default setting of 6.4.

Discrimination control with noisy bat call example

Let's see how decreasing the discrimination control can improve discrimination of noise to call:

1. Open the sample file **`Myotis ciliolabrum 3`** in compressed view mode with **`preemphasis`** set to **`none`** and leaving all other settings in their default mode.
2. Six calls are shown with six call intervals of 177, 61, 26, 69, 82 and163. Recall that the number of call intervals should be equal to the number of calls minus one. The first interval is for the time between the first and second call, and so on.
3. Reprocess the call in **`real time active mode`**. The long intervals shown between calls 1 and 2, and 5 and 6 correlate well with the calculations from SonoBat. Some noise between calls 2 and 5 is being interpreted as a bat call and generating a spurious call interval.
4. Reprocess the call in **`compressed view active`**.
5. Slide the discrimination control to a setting of 3.0. The control shows you that less space will be retained between each call.
6. Click **`process change`**.
7. Six calls are shown again, but this time with five call intervals of 177, 88, 79, 81 and 162. Decreasing the discrimination setting provided more accurate call intervals.

Discrimination control with pure tones example

Another convenient way to see how the discrimination control works is to examine a synthesized sound of four pure tones separated by 10 msec intervals:

1. Open the sample file **`Discrimination demo`** in **`real time view`** mode with **`preemphasis`** set to **`none`** and leaving all other settings in their default mode.
2. Note how each call and interval between calls is 10 msec.

3 Change the view to **`compressed view active`**. Note that the discrimination control appears as soon as you click on compressed view active.

4 Set the discrimination control to 10.0, the maximum setting.

5 Click **`process change`**.

6 Note the spacing between the four sounds in the sonogram and oscillogram. The intercall intervals are reported as 20 msec, this is measured from the center to center of the calls.

7 Set the discrimination control to 1.0 and **`process change`**.

8 Note the spacing between the four sounds in the sonogram and oscillogram decreased, but the intercall intervals are still reported as 20 msec.

9 Try different settings between 1.0 and 10.0 to see how the discrimination setting changes the interval spacing between the sounds.

Sampling Frequency

Two sampling frequencies are important in determining the maximum frequency that can be displayed in SonoBat:

- the sampling frequency of your *ultrasound detector*
- the sampling frequency of your *recording device*

Common detector and recording sampling frequency combinations are shown below.

detector sampling frequency (kHz)	recording sampling frequency (kHz)	maximum frequency (kHz)
300	22.05	110.25
300	44.10	150
307	22.05	110.25
307	44.10	154
350	22.05	110.25
350	44.10	175

Higher sampling rates yield greater frequency resolution. SonoBat automatically detects the recording sampling rate of a file and displays it above the sonogram, and above the filename.

Sampling frequency example

Let's examine the same sequence saved in 22.5 kHz format and 44.10 kHz format:

1. Open the sample file **`Lasionycteris noctivagans 2`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4.)

Tip: You can right-click (Windows) or command-click (Macintosh) to get a pop-up menu that let's you reinitialize any control to its default setting.

2. The recording format, **`22.05 kHz/8 bit/mono`**, is automatically determined and shown at the top of the screen.
3. The maximum frequency shown on the *y*-axis is 110.
4. Six calls are visible, some with multiple harmonics. The funny components of opposite slope to the main call component are aliases of higher frequency components (more on those later).
5. Open the sample file **`Lasionycteris noctivagans 3`**. Select the default subsection. This is the same call, saved in 44.10 kHz format. The additional information makes the file just large enough to require you to select a subsection for processing.
6. Hit the **`Enter`** key to accept the default segment, which will include all six calls.
7. The sampling format is now shown at **`44.10 kHz/16 bit/mono`**.
8. The maximum frequency shown on the *y*-axis is now 150.
9. An additional harmonic is revealed for each of the calls as a result of the higher resolution.

How SonoBat determines the sampling frequency of a file

The sampling frequency (`fs`) used to process the call is displayed in the lower left corner of the window and determined in one of two ways:

1. If the call being processed was recorded using SonoBat, the sampling frequency of the file was set at the time of recording and saved as an attribute of the file. SonoBat reads the sampling frequency stored with the file and processes the sonogram appropriately. See the chapter on the recording for more information.
2. If the file being processed was not recorded with SonoBat, defaults set with the `set prefs` button are used to determine the sampling frequency. See the "Setting Preferences" section of the Call Analysis chapter for more information.

If a file does not have a sampling frequency assigned, or you believe that the one assigned is incorrect, use the `edit file attributes` button in the lower left corner of the window to change the sampling frequency. That way the files will always be opened and appropriately processed without relying on default settings that may be incorrect for a file. You must *reopen* the file in order for your changes to take effect. Clicking `process change` or other controls that reprocess the file already open will not show your changes.

The Ruler

Later in this Guide we'll cover instructions on using SonoBat to generate extensive call parameter data such as maximum frequency, minimum frequency, duration and slope for a single call. For a quicker look at frequency over a range of calls, SonoBat has a handy ruler that toggles on and off with a button found on the right side of the sonogram.

Frequency of the ruler is shown below the button. Move the ruler by sliding the brown triangle at the right side of the ruler or clicking the up & down arrows next to the ruler frequency display.

"Turn down" frequency with ruler example

In the next example we'll see how the ruler can help reveal an important piece of information for a *Myotis californicus* call sequence.

1. Open the sample file `Myotis californicus 3` with the filter set to 20 kHz and the discrimination set to 4.0.
2. *Myotis* calls typically have a trailing hook, or tail, that is of lower amplitude than other portions of the call, and is only completely resolved on calls recorded from bats passing close to the detector.
3. Turn the ruler on by clicking on the `turn ruler on` button on the right side of the screen.
4. Click on the brown triangle along the right edge of the sonogram and slide the marker up or down until the ruler is positioned where you want it. Read the frequency along the kilohertz axis or in the box below the ruler button. Position the ruler at the lowest frequency of the calls, about 37 kHz.
5. Move the `threshold adjust` control up to simulate different recording ranges. Notice how the minimum frequency of the calls increases as we simulate greater distance from the microphone.
6. Now that we have determined that minimum frequency for this bat can be deceptive, observe that the frequency at which the calls turn down is more diagnostic and reliable. Position the ruler at 48 kHz and again adjust the threshold up and down. Note that the "turn down" frequency remains constant.
7. Click on `turn ruler off`.

More on the ruler

When the analysis mode is enabled, the action of the ruler can become sluggish because of increased processor activity.

Sonogram Appearance

SonoBat gives you two options for the background color of the sonogram (black or white) and oscillogram and two options for the colors of the sonogram (color or gray scale). Using the same file still open from the previous section (**Myotis californicus 3**), toggle the palette controls found just below the ruler button to see the four possible color combinations. Adjust the intensity control to optimize appearance in the different palettes.

In gray scale mode, SonoBat represents the relative amplitude intensity by cycling the gray tone through light and dark to create a contour effect. Move the intensity control up and down to see how this changes the appearance of the sonogram view.

Adding Notes

It's easy to add notes to a file. Notes can be added at the time of recording or viewing. See the chapter on recording for instructions on how to add a note during recording. To add a note while viewing a file:

1. Click on the **edit file attributes** button in the lower left corner of the window.
2. Type your text in box below the **edit file note** label.
3. Click **Save.**
4. A dialogue box will ask whether or not you want to replace the existing file of the same name. Click **Replace.**
5. Your new text will not appear in the note window until you reopen the file.

If you are using a Windows computer and you get an error message when you try to save a note, the Read Only file attribute from the CD were probably copied over from the CD to your hard drive. To change the file permissions:

1. Locate the examples directory with Windows Explorer.
2. Right-click on the directory.
3. Choose **Properties.**
4. Uncheck **Read Only.**

5 Select **Apply changes to this folder, subfolders and files.**

6 Click **OK.**

7 Click **OK** again.

Setting Sonogram Preferences

A variety of default file paths, processing parameters and recording settings can be saved using the preferences panel invoked from the **set prefs** button in the lower right portion of the SonoBat screen. See the chapter on recording for a list of recording preferences.

The following items can be set as preferences with changes taking place after the preferences are saved:

- maximum file segment to process
- R or L channel to process for stereo files
- default detector sampling frequency (**fs**) used for interpreting files with no SonoBat-encoded sampling frequency attribute
- sound on/off
- default time expansion factor for processing files with no encoded time expansion (standard is 10×, but other time expansion factors are available)
- the default directory used to store calls for analysis
- the default directory used to store reference views (See the next chapter for details on creating and using reference views.)

Printing

To print a copy of the currently displayed sonogram, click on the **open print panel** button on the lower right side of the screen, just below the palette controls.

- The print panel will open with the default settings of a white background and gray scale sonogram. The palette controls are available in the print panel if you want to change the default selections.
- Threshold and intensity adjustments are also available in the print panel if you want to change the settings.
- The file name will print at the top of the page for reference.
- The time parameters of the file will print below the sonogram
- Type your comments in either or both of the comment boxes.
- Click **page setup** from the file menu and then **printer setup** to change from portrait to landscape mode.
- Choose **print** or **cancel** to return to the main sonogram window.

Help

The **?** button on the upper right corner of the screen provides instructions on how to view on-screen help messages about SonoBat features and functions. There are two ways to access on-line help text:

Method 1:

- *Windows Users:* right-click on any screen element (panel, button, control, etc.) and select **`description`** from the pop-up menu.
- *Macintosh Users:* command-click on any screen element (panel, button, control, etc.) and select **`description`** from the pop-up menu.

Method 2:

- *Windows Users:* Use **`control-h`** to open the help window and then move the cursor over the screen element for which you want to view the help text.
- *Macintosh Users:* Use **`command-h`** to open the help window and then move the cursor over the element for which you want to view the help text.

If the text of a long help message runs off the help message window, move the help window to the upper left of your screen and enlarge it by dragging the lower right corner. The help message may change as you resize the help window, but when you move the cursor back over the original element for which you wish to view the help message, it will open larger to reveal the hidden text.

Quitting

Click on the **`quit`** button in the lower right portion of the window. You can also quit using the key sequence shift-F4. On the Macintosh, SonoBat will also quit using command-Q.

2 Taking a Closer Look

This section covers zooming in on calls, saving calls with a standard time scale and making side-by-side comparisons of calls from different files.

Zooming

Depending on the number of calls contained in a file and the maximum file segment to process setting, a sonogram might contain anywhere from one call to two dozen or more calls. Interpreting the details of call structure may be difficult when too many calls are present. You might also want to highlight the best calls for closer examination. SonoBat provides multiple levels and two types of zooming:

- *hold freq zoom:* frequency (y) axis is unchanged while time is maximized to spread the call across the entire x axis
- *full zoom:* frequency and time are both maximized to fill the screen

Zooming example

1. Open the sample file **`Myotis yumanensis 2`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. The last four calls appear to be the better part of the recording.
3. Use the cursor to drag a selection box around the last four calls.
4. If you make a mistake, click the **`undo zoom`** button below the oscillogram and try again.
5. Notice how the shape of the call changes. This is the default zoom behavior: the time (*x*) axis is stretched while the frequency (*y*) axis remains unchanged and goes from 0 to 110 kHz. This is the **`hold freq zoom`**, as indicated on the pull-down button below the oscillogram.
6. Click **`undo zoom`**.

7 Use the pull-down menu to change the zoom type from **`hold freq zoom`** to **`full zoom`**.

8 Reselect the last four calls again by dragging a selection box around them.

9 Notice how the four calls fill the window and the frequency axis now goes from about 35 to 100 kHz (the exact frequency will depend on how you drew your selection box).

10 Click **`undo zoom`** so you are ready to proceed with the next section.

More on selecting calls for zooming

When you use **`hold freq zoom`**, SonoBat is not fussy about selecting calls for zooming. You only need to zoom some horizontal band to define a time range for the zoom. However, if you accidentally make a teeny tiny selection (like an inadvertent double-click), SonoBat can display some peculiar looking sonograms. Click on **`undo zoom`** when that happens and try again.

When you use **`full zoom`**, SonoBat will enlarge only the specific portion of the call that you selected. Try using the full zoom to enlarge just the "tails" of these *Myotis* calls.

Zooming in real time mode

Though you may zoom on calls while in real time mode, resolution will be low. As the real time mode displays the entire recording in one pass, resolution is sacrificed and not improved with zooming.

Standard Views

Zooming in on one or more calls is handy for getting a closer look at call structures, but it's difficult to compare one call shape to another when the values on the *x*-axis change with every call. SonoBat uses the concept of a *standard view* to display one call over a specific period of time.

To use the standard view function:

1. Select a call as for zooming. The call is enlarged.
2. Click on the **`std view`** button (below the oscillogram).
3. The call is displayed in high resolution over half of the sonogram window, over the period of time selected in the standard view pull-down below the zoom pull-down.
4. The time of the call within the file is displayed next to the zoom pull-downs.
5. Click **`end std view`** to return to the full call sequence.
6. The time within the current sonogram window for the call that you just viewed is now displayed next to the zoom pull-downs.

Standard view example

We'll continue with the sample file **`Myotis yumanensis 2`** opened in the previous section to explore the standard zoom feature.

1. Return to an unzoomed **`Myotis yumanensis 2`** sonogram (with the default **`hold freq zoom`**).
2. Drag to select any part of the longest call at 60 msec.
3. Some portion of the call is enlarged.
4. Click on the **`std view`** button (below the oscillogram).
5. The call is displayed in high resolution between 0 and 15 msec on an axis that goes to 30 msec. All standard calls will be displayed on this time scale when the standard zoom setting is on **`15 msec std view`**. This is the default setting and is displayed below the oscillogram.

6 The starting time position of the selected call within the time period covered by the opened file is shown to the left of the zoom and frequency pull-down menus. For this example you should see "std view time: 555 msec," indicating that this zoomed call occurred 55 msec into the file.

7 Click `end std view` when you are finished to return to the original sonogram.

8 Click `real time view active` and reprocess to see the location of the call in the file (60 msec).

Standard view in real time mode example

You may also select calls in real time mode for display in standard view, though the selection mechanism works just a bit differently than in compressed view mode. Let's try it out:

1 Open the sample file `Pipistrellus hesperus 1` in `real time view active` mode.

2 Select the default subsection by hitting the `Enter` key.

3 Drag to select the second call, but position the call snugly against the left side of the selection box, dragging the right side of the selection box nearly to the next call.

4 Click `std view`.

5 If you've selected the call badly (as instructed), you will get one big mess of a standard view. In `real time active` mode, the center of your zoom selection determines the center of the standard view. You must position the center of your selected call in the middle of the selection box. It may be helpful to first do a coarse zoom, then the final standard zoom.

6 Click `end std view`.

7 Drag to select the first four calls.

8 The four calls are distributed across the entire sonogram in low resolution.

9 Drag to select one of the calls, taking care to position your choice in the middle of the selection box.

10 Click `std view`.

11 A high-resolution standard view of the call is displayed.
12 Click `end std view` to return to the full sonogram.

Standard view settings

SonoBat provides twelve choices for standard views:

- 5 msec
- 7.5 msec
- 10 msec
- 15 msec (default)
- 20 msec
- 30 msec
- 40 msec
- 50 msec
- 100 msec
- 200 msec
- 500 msec
- 1000 msec

By setting the standard view length to be the minimum required without truncating a call, i.e., 10 msec for calls less than 10 msec long, you will maximize the magnification of the call. This is especially helpful when placing cursors on the call, a topic that is covered in the next chapter.

Long call standard view example

Working with the same length standard view will make it easier for you to place bat call shapes in a consistent frame of reference, however a range of standard views are provided to accommodate calls of different duration. Trying to apply to a short standard view to a long call will result in truncation of the call. To test this:

1. Open the **Eumops perotis** sample file using the default 5 kHz filter setting and with **preemphasis** set to **none** and discrimination control at 6.4.
2. Select the default subsection by hitting the **Enter** key.
3. Drag to select the first of the two calls.
4. Click **std view**, leaving the default setting of **15 msec std view**.
5. Note how the call appears jammed up at 0 msec and stretches all the way to 15 msec.
6. Change the pull-down standard view setting to **40 msec std view**.
7. The call is reprocessed for the new standard view time selection.
9. Note that the call is no longer jammed up to the 0 point on the *x*-axis and fits nicely within the sonogram window.
10. Click **end std view** to return to the original sonogram.

Reference Views

No matter how fine your memory or how fast your computer, it's difficult to compare one call to another by processing two calls in a row, trying to remember the first one while looking at the second. It's possible to take extensive notes on key call parameters (we'll learn an easier way to do that later) but the ideal way to compare calls is to view them side by side. SonoBat gives you two methods for making side-by-side comparisons:

- appending a reference view to a call sequence
- appending a reference view to a single call in standard view

SonoBat displays the reference view on the same time and frequency scale as the current sonogram or standard view.

To append a reference view to a call sequence or a standard view:

1. Click **`append reference view`**.
2. Navigate to the folder **`SonoBat files/ref views`** and select a file.
3. The reference view is appended on the right side of the sonogram, over the same time scale as used in the call on the left side of the sonogram.

Reference view appended to a call sequence example

Let's see how reference views can help us identify a call from an unknown bat. First we'll append a single reference view to a call sequence (multiple calls):

1. Open the file **`Reference view demo 1`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Click on the **`append reference view`** button.
3. Navigate to the folder **`SonoBat files/ref views`** and select the file **`Myci_FreeFliteOwensVly`**.

4 A single call is appended on the right side of the sonogram, separated from the original call sequence by a green line. This call is from a free flying *Myotis ciliolabrum*. Details about the reference view you just appended are shown in the lower right portion of the screen.

5 Turn the ruler on and position it at the approximate ending frequency of the original call sequence (47–50 kHz), excluding the variable trailing hook (tail). With the minimum frequency of the *Myotis ciliolabrum* call at approximately 40 kHz, we don't have a good match.

6 Click **append reference view** to try another reference view.

7 Navigate to the folder **SonoBat files/ref views** and select the file **Myev_LngVly#1**.

8 The first reference view is deleted and the new reference view for *Myotis evotis* is appended to our original sequence.

9 With the minimum frequency of the *Myotis evotis* call at approximately 36 kHz, we still don't have a good match.

10 Click **append reference view** to try another reference view.

11 Navigate to the folder **SonoBat files/ref views** and select the file **Myca_SilvCyn#2**.

12 Though the intensity of the appended reference view from *Myotis californicus* is slightly stronger than our unknown calls, the shape and minimum frequency are sufficiently similar to suggest that our unknown call sequence is likely to be *Myotis californicus*.

13 Click **append reference view** to try another reference view.

14 Navigate to the folder **SonoBat files/ref views** and select the file **Myca_SilvCyn#1**. This one is an even better match. The intensity distribution, shape, and minimum frequency of this appended reference view from *Myotis californicus* is similar to our unknown calls, and suggests that our unknown call sequence is likely to be *Myotis californicus*. The match is particularly good with the third call in the sequence. Place the ruler at 51 kHz and not the consistency of the frequency at which all the calls turn down.

Reference view appended to a single call example

Now let's append a reference view to a single call in standard view. The call sequence was recorded before the sky was dark from a small bat with erratic flight. We postulate the bat is *Pipistrellus hesperus:*

1. Open the file **`Reference view demo 2`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Set the standard view time to 10 msec and drag to select a portion of the second call.
3. Click **`std view`**.
4. Turn on the ruler and move it to help your eye track the minimum frequency (~49 kHz if you center the ruler on the center of the frequency envelope).
5. Click **`append reference view`**.
6. Navigate to the folder **`SonoBat files/ref views`** and select the file **`Pihe_SilvCyn#3`**.
7. Our hunch was good!

Appending a compiled reference view

SonoBat also gives you the capability to compare *compilations* of reference views to the call that is currently being processed. These compiled reference views are created by combining multiple reference views into a single compiled view using the RefCompiler utility. For example, compiled reference views allow you to compare a sequence or individual call against a species repertoire at a glance. See the section "Saving Your Own Reference Views" below and "Making Your Own Compiled Reference View" later in this chapter for details on how to create a compiled reference view.

Compiled reference view example

Appending a compiled reference view is the same as appending a single reference view:

1. Open the sample file **Eptesicus fuscus** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Click on the **append reference view** button.
3. Navigate to the folder **SonoBat files/ref views** and select the file **@Epfu_Compiled.wav**.
4. Five reference calls are appended on the right side of the sonogram, separated from the original call sequence by a green line. The filenames of the individual reference views from which the compiled view was made are shown in the note in the lower right portion of the screen.
5. The calls in this sequence most closely resemble the first call in the compiled sequence, **Epfu_WMRS#1**. Click on **append reference view** and navigate to that reference view for a more detailed comparison.

Saving Your Own Reference Views

Where do these handy reference views come from and how you can get more of them? Reference views are created by picking out any call from a file and saving it to be used as a comparison call. Reference views are typically created from files for which the species of bat is known with a high degree of confidence, and compared against calls from unknown bats. Reference views are saved as .wav files and may include detailed notes about the bat, location and other circumstances under which the call was collected, e.g., cluttered, over a pond, just after hand-release, etc.

To create your own reference view:

1. Drag to select the call you would like to save as a reference view.
2. Click **std view**.
3. Click **save std view**.

4 Enter a call note in the box to the right of the "enter reference call" label.

5 Click **`Note Entered`**.

6 A dialogue box appears prompting you for a name for your reference view. Navigate to the **`SonoBat files/ref views`**. Name the file and click **`Save`**. (Do not append the file extension ".wav." SonoBat will do this for you.)

Along with the text you typed in the note box, four other pieces of information are automatically stored with your reference view:

1 The name of the source file for the reference view.
2 The position of the call in the original file (in msec).
3 The time expansion factor of the source file.
4 The detector sampling frequency of the source file.

The file name of the reference view is displayed dynamically in the reference view note, but not stored.

Creating a reference view example

The sample file **`Antrozous pallidus 2`** was collected from an *A. pallidus* during a hand release. Let's create a reference view from this reference call sequence:

1 Open the sample file **`Antrozous pallidus 2`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2 Drag to select one of the calls.
3 Click **`std view`**.
4 Click the **`save std view`** button at the far right of the view buttons.
5 A text box opens below the button. A prompt to enter a call note is shown to the left of the text box.
6 Type in "**`Antrozous pallidus, hand released.`**"

7 The name of the original reference call sequence, **Antrozous pallidus 2**, will automatically be appended to the note with the label "source file," along with the msec position of the call in the original sequence. Thus you have the complete reference to relocate the original call in the full .wav file.

8 Click **Note Entered** on the lower right corner of the screen when you are finished.

9 A dialogue box appears prompting you for a name for your reference view. Navigate to the **SonoBat files/ref views** folder if necessary. The file name will be appended automatically to the note with the label "reference call file." Type the name **Anpa_hr**.

10 Click **Save**.

Appending a new reference view example

Put your new reference view created in the example above to work:

1 Open the sample file **Reference view demo 3** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).

2 Drag to select the middle call.

3 Click **std view**.

4 Click **append reference view**.

5 Select the reference view **Anpa_hr** you created in the section above.

6 What do you think? Is the reference view a good match? The minimum and maximum frequencies of the two calls show some similarities, though duration and slope differ. In fact, **reference view demo 3** is from *Eptesicus fuscus*.

Tip: If you are creating multiple reference views from the same call sequence, use the standard copy and paste commands to copy note text from one reference view to another.

Reference view format & file attributes

Reference views are stored as .wav files. Reference views created with SonoBat 1.2 or earlier were saved in a different format and must be converted to .wav files. A reference view converter and instructions are supplied on the SonoBat CD.

Reference view files automatically store the time expansion factor of their parent file. Should you ever need to compare reference views of a time expansion different from the file you are analyzing, SonoBat will automatically convert the reference view to match.

Creating Your Own Compiled Reference Views

A RefCompiler utility comes with SonoBat and makes it easy to combine multiple reference views into a single reference view file so that you can see a range of calls for a single species or similar species in the same window.

Sample compiled reference views are found in the SonoBat Files/Ref View directory and are named @xxxx_Compiled.wav.

To create your own compiled reference view:

1. Locate the RefCompiler in the Start/Programs/SonoBat/RefCompiler menu or in the folders copied over during installation. If you used the RefCompiler installer, it will be in the same directory as the SonoBat program and share its preference file. This will make it easier as it will default to the same reference view directory that you have specified for SonoBat.
2. A dialogue box launches for you to locate and choose the first reference view. Click the **`change directory`** button and navigate to your **`ref views`** directory if that directory was not displayed by default.

   Windows: Double-click on the **`ref views`** directory, then click **`Select Cur Dir`** on the lower right corner of the dialogue box.

   Macintosh: Click once on the **`ref views`** directory to highlight it, then click on the **`choose`** button on the lower right of the file dialogue.

4 Click on a reference view.

5 The selected reference view is displayed in the Compiler. Move the yellow and green lines to tighten up the selected call but leave a little space on either side so that the calls won't overlap.

6 Click **`select segment`**.

7 Repeat steps 4–6 for each reference call desired.

8 Click **`select segment and end`** when you are finished adding reference calls.

9 The selected reference views are shown side-by-side in the window on the right. The original filename for each is shown in the note below the compiled view.

10 Reorder if desired using the pull down array below the compilation sonogram, then click **`reordering done, save file`**.

11 Enter any additional notes that you would like displayed with the compiled view.

12 Click **`edit note, save file`**. We suggest using an "@" as the first character in a compilation filename. That will distinguish it from other ref views and move it to the top of the ref view dialogue listing when displayed in alphabetic order.

13 Navigate to the reference views directory and save the file. The ".wav" extension will be added automatically.

Compiling a reference view example

Normally the first step in creating a compiled reference view is to create each of the individual reference views. In this example, we'll compile four Myotis reference views already available in the ref views directory:

- *Myotis californicus:* Myca_OVL#1
- *Myotis ciliolabrum:* Myci_OVL_#1
- *Myotis evotis:* Myev_LngVly#1
- *Myotis yumanensis:* Myyu_Graeagle_Zip2

1 Launch the RefCompiler.

*Win*dows: find the compiler in the Start/Programs/SonoBat/RefCompiler menu.

Macintosh: find the compiler in the SonoBat folders you dragged to your hard drive during installation.

2 A dialogue box launches for you to locate and choose the first reference view. Click the **`change directory`** button.

3 Navigate to and open the **`ref views`** directory supplied with SonoBat (copied from the CD to your computer). Do not select a reference view. Click **`Select Cur Dir`**.

4 Click on Name to sort the ref views by name. Scroll down and select Myca_OVL#1.

5 The selected reference view is displayed in the RefCompiler. Move the yellow and green lines to tighten up the selected call.

6 Click **`select segment`**.

7 The reference view directory is displayed for you to choose the second reference view. Select Myci_OVL_#1.

8 The selected reference view is displayed in the RefCompiler. Move the yellow and green lines to tighten up the selected call.

9 Click **`select segment`**.

10 The reference view directory is displayed for you to choose the second reference view. Select Myev_LngVly#1.

11 Click **`select segment`**.

12 The reference view directory is displayed for you to choose the second reference view. Select Myyu_Graeagle_Zip2.

13 The selected reference view is displayed in the RefCompiler. Move the yellow and green lines to tighten up the selected call.

14 Click **`select segment and end`**.

15 The selected reference view is displayed in the RefCompiler. Move the yellow and green lines to tighten up the selected call.

16 Click **`select segment and end`**.

17 The four reference views are now shown side-by-side in the window on the right. The original filename for each is shown in the note below the compiled view.

18 Click **`reordering done, save file`**.

19 Click **`edit note, save file`**.

20 Navigate to the reference views directory and name the file `@Myotids_Compiled`. The .wav extension will be added automatically.

Second compiled reference view example

Let's see how the compiled reference view we created above can be used to help us figure out a call.

1 Open the file `Reference view demo 4`.

2 Select the sixth call and click `standard view`.

3 Click `append reference view`. Select the newly created `@Myotids_Compiled.wav` file.

Note: If you do not see the file, see the note that follows this list.

4 The four calls are appended and the name of each reference view are shown in the note. Turn the ruler on to help compare the calls. The second call, a *Myotis ciliolabrum* looks like a potential match.

Newly compiled reference view does not appear in list

If you left SonoBat running in the background while creating a compiled reference view, it will not appear in the Ref Views directory unless you trick SonoBat into reloading the directory contents. Click `change directory`, navigate again to the `ref views` and select it as previously described. SonoBat reloads the reference view directory and the newly created file appears.

3 Call Analysis

In addition to creating and appending reference views as a quick visual means to identify calls from unknown bats, SonoBat allows you to collect data on all common call components such as minimum frequency, maximum frequency, duration, slope and harmonics. We will use several examples to explore all of the analysis functions and write call data out to a file.

Quantitative analysis functions

SonoBat automatically determines quantitative measurements for multiple features of a single call.

- On screen cursors can be moved to relocate the beginning and end of a call, etc., with the quantitative data changing accordingly.
- The analysis functions are invoked by clicking `enable analysis` while in standard view mode.
- Data are displayed in the lower left portion of the window and can be written to a file by clicking on the `write data to file` button. See the section below on "Writing call data to a file" for more information.

Enabling analysis example

1. Open the sample file `Lasionycteris noctivagans 1` with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Select the default subsection (beginning at 100 msec).
3. Click and drag to select the second call.
4. Click on the `std view` button. Select a `standard view length` of 10 msec if that is not already the selection.
5. Click on the `enable analysis` button just left of the `end std view` button.

6 Two cursors, **Hi f** and **Lo f**, appear on the call. A bevy of labels and numbers appear in the lower left portion of the screen. The following information is shown for the call we selected:

- **Hi f** (high frequency) = 58.2 kHz
- **Lo f** (low frequency) = 18.1 kHz
- **bandwth** (bandwidth) = 40.1 kHz; (37.0 minus 21.3)
- **duration** = 6.2 ms (microseconds, from **Hi f** to **Lo f**)
- **fmax** (frequency at maximum amplitude) = 27.2 kHz
- **slope** (from **Hi f** to **Lo f**) = 6.47 kHz/msec

Initial values for these six parameters are determined by SonoBat based on SonoBat's interpretation of where the call begins and ends. How well SonoBat succeeds in recognizing the beginning and ending of the call depends on several factors including how much noise is in the recording and whether or not there are call echoes. Change the initial values by moving the **Hi f** and **Lo f** cursors displayed on the call. See the "Placing cursors properly" section below for more details.

6 Position your cursor directly over the open circle below the **Hi f** label. The cursor changes when you are in position to grab it. Click to select the circle and drag to move it to a new location on the call. The values for **Hi f, bandwth, duration** and **slope** change as you move the cursor.

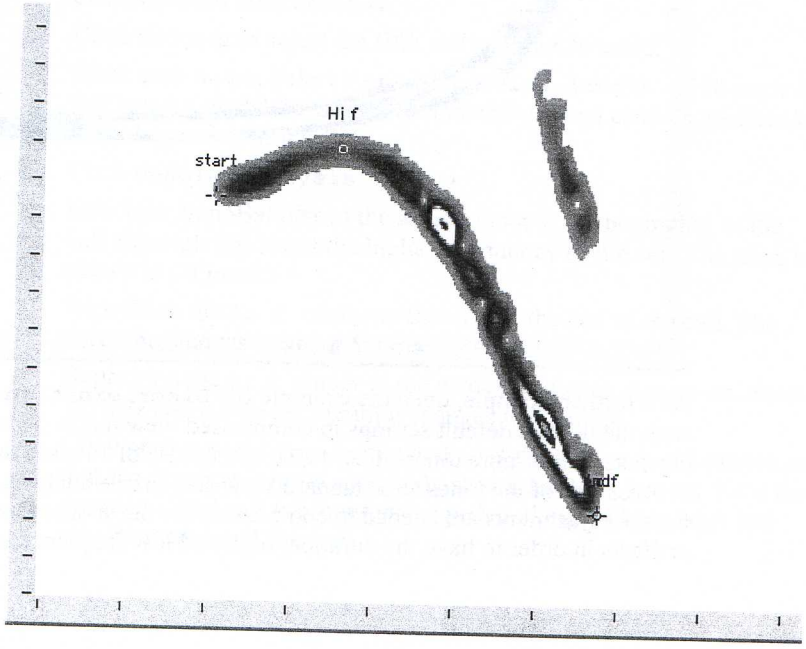
7 Repeat step 6 for the **Lo f** cursor. The values for **Lo f, bandwth, duration** and **slope** change as you move the cursor.

8 Click the **end analysis** button.

Placing cursors properly

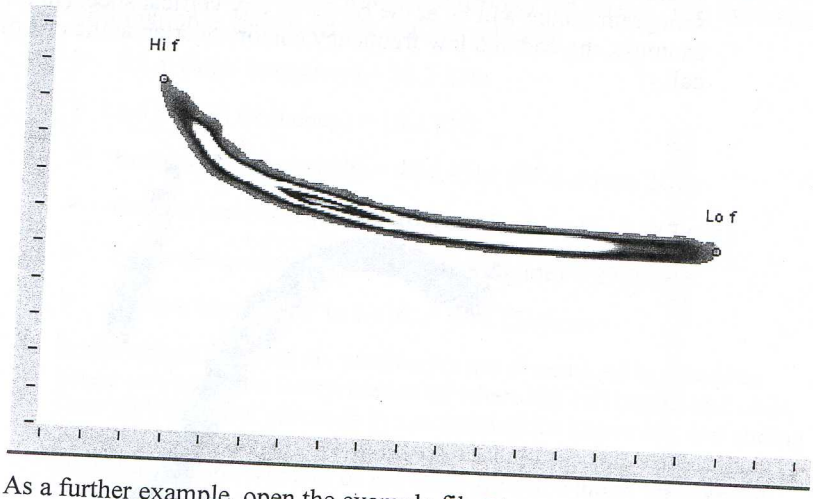
Even with pure, single frequency tones the sonogram image of a tone will extend over a range of frequencies. To properly interpret frequency information, it is important to understand that the operating frequency represented by the sonogram image is at the *center* of the frequency envelope, as shown by the correct positioning of the cursors below. Imagine a line running through the middle of the frequency envelope.

You can also think of the frequency envelope as being constructed from a series of vertical slices. The precise frequency represented by the sonogram image will be at the *center* of any vertical slice. (In this example, the end and low frequency cursors overlap at the end of the call.)*



* For further examples and methods of cursor placement and parameter interpretation, see the special section at the end of this chapter.

The image below shows properly placed analysis cursors at the beginning and end of the call:



As a further example, open the example file **`Discrimination demo`** with the normal default settings in compressed view mode. This file consists of four pure tones of 20, 40, 60 and 80 kHz of 10 msec duration. Process one of the tones as a standard view and enable analysis. Some cursor adjustments are needed to compensate for the sudden-onset artifacts in order to have the duration, high and low frequencies exact.

Cursor placement and duration

SonoBat initially calculates call duration based on the positions of the **`Hi f`** and **`Lo f`** cursors. For some bat calls, the highest and lowest frequencies may not correspond to the start and end of the call. You can invoke separate start and end cursors for calculating duration by clicking on the **`duration`** button in the analysis panel. Start and end cursors appear on the sonogram and can be moved independently of the **`Hi f`** and **`Lo f`** cursors. Toggling the **`duration`** button off will return the duration calculation to the **`Hi f`** and **`Lo f`** cursors.

Cursor placement and duration example

1. Open the sample file **`Myotis volans 1`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Click and drag to select the fifth call at about 30 msec.
3. Click **`std view`**. Select a **`standard view length`** of 10 msec if that is not already the selection. Note the unusual cane-shaped hook at the beginning of the call.
4. Click **`enable analysis`**.
5. Note how SonoBat placed the **`Hi f`** cursor at the beginning of the call although this is not the highest frequency of the call. Duration is shown at 5.4 msec.
7. Reposition the **`Lo f`** cursor so that it is at the end of the call. The duration changes to about 5.0 msec.
8. Reposition the **`Hi f`** cursor to the actual frequency maximum, about 102 kHz and notice the duration changes to 3.1 msec.
9. Click on the **`duration`** button and reset the start and end cursors so that the duration is more accurately shown as about 5 msec. Now the duration of the call is properly designated along with the high and low frequencies of this call.

High and low characteristic frequency

While the high and low frequency cursors are typically used to define the *absolute* highest and lowest frequencies of a call, the high and low *characteristic* frequencies are used to describe the *predominant* trend of the call shape.

Click the **lo f_c** button to invoke a low characteristic frequency cursor, **lo fc**, and the **hi f_c** button to invoke the high characteristic frequency cursor, **hi fc**. Select and drag the cursors on the sonogram.

The high and low characteristic frequencies can also be used to enable slope calculation to reflect the general trend of the call slope by eliminating short, highly curved segments at the beginning or end of a call. See the section below on "Slope and heel" for more information.

Characteristic frequency example

1. Open the sample file **Myotis ciliolabrum 5** with
   - compressed view mode active
   - 20 kHz cutoff filter
   - discrimination control at 5
   - standard view time at 10 msec
2. Click and drag to select the seventh call around 42 msec. Select a **standard view length** of 10 msec if that is not already the selection.
3. Click **std view**.
4. Click **enable analysis**.
5. Note how SonoBat had difficulty determining the end of the call and placed the **Lo f** cursor on some noise.
6. Reposition the **Lo f** cursor to about 26 kHz, in the middle of the envelope at the end of the main call.
7. Reposition the **Hi f** cursor to about 96 kHz, in the middle of the envelope at the top of the main call.

8 The slope has been calculated at about 16.5 but these end points don't accurately reflect the main shape of the call.

9 Recall our earlier discussion about how Myotid calls often display inconsistent trailing "hooks," while maintaining a more consistent frequency at which the calls turn down to begin the trailing hook (the lower characteristic frequency). Click the **lof_c**, button to invoke a **lof_c** cursor, **lo fc**.

10 Move the **lo fc** cursor to a point in the call at the beginning of the steeply descending hook, about 39 kHz. The slope is recalculated using the **lo fc** cursor rather than the **lof_c** cursor and now indicates a slope of about 14.8 kHz/msec with the **lo fc** cursor at 39.2 kHz. (Your placements may vary a bit.)

11 The **hif_c** button can be used in a similar fashion for calls that have beginning features inconsistent with the trend of the main call.

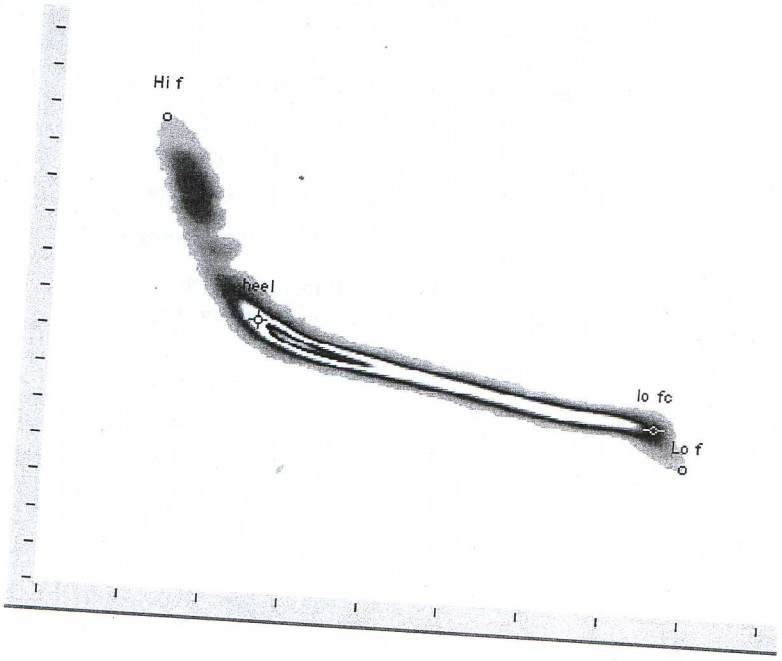
12 Click **end analysis**.

Slope and heel

Not all calls have a smooth curve throughout their sweep. A distinctive change in curvature or point of. inflection is displayed in many calls. This is sometimes referred to as the *heel* of a call. Manually placing a cursor on the heel causes SonoBat to calculate separate values for the upper and lower call slopes, which SonoBat reports in units of kHz/msec. Invoke the heel cursor by clicking on the button within the analysis panel, then drag to an appropriate position on the sonogram.

This cursor is labeled "`up/lo`" rather than "heel" because there are instances in which it may be invoked to designate upper and lower slopes of the call even when there is no definite heel. An additional button that toggles between "`heel no`" and "`heel yes`" enables a judgement of heel presence to be passed along to the spreadsheet when the "`write data to file`" button is pushed.

The figure below shows the placement of the up/lo (heel) cursor for a call with two different slopes.



Slope and heel example

In the next example, we'll place a cursor on the heel to calculate separate values for the upper and lower call slopes.

1. Open the sample file **`Myotis yumanensis 4`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. You will see some low frequency noise in the file. Change the filter setting to **`20 kHz cut off`**. SonoBat will automatically reprocess and clean up the sequence.
3. Click and drag to select the sixth call displayed at about 38 msec.
4. Click **`std view`**. Select a **`standard view length`** of 10 msec if that is not already the selection.
5. Click **`enable analysis`**.
6. Accepting the default **`Hi f`** and **`Lo f`** cursors, note that the slope is calculated at about 11 kHz/msec. However, as you can see the cursors are not placed exactly at the beginning and end of the call. SonoBat's guess moves them close, but depends upon you to get them just right.
7. We can see that this call does not have a smooth curve throughout its sweep. There is a distinctive change in curvature at about 65 kHz when the call goes from steep to flat.
8. Click on the **`up/lo`** button, next to slope.
9. An **`up/lo`** cursor appears on the sonogram. Drag the cursor to the "heel" of the call. Note that two new values appear next to the **`up/lo`** button.
   - **`upper`** refers to the slope of the first and steepest portion of the call; about 19 kHz/msec in our example
   - **`lower`** refers to the slope of the second and shallower portion of the call; about 4 kHz/msec in our example
10. Click **`end analysis`**.

More on upper and lower slopes

Remember that when the characteristic frequency cursors are invoked (`lof`$_c$ and `hif`$_c$), the slope calculations change to become based on these cursors. For example, to most accurately describe the lower slope of the call in the previous example, you would want to invoke the `lof`$_c$ cursor and place it at the end of the trend of the lower slope, just before it turns down to the terminal tail. Try that and see how the lower slope changes. Once you have positioned the cursor, you can turn it on an off and view the difference in the lower slope calculation with and without it.

Harmonics

SonoBat provides cursors to enable you to identify up to six harmonics for each call. The lowest call component, called the first harmonic or the fundamental is typically, but not always, the primary call component. Additional harmonics may be visible at various frequencies above the fundamental (h1). Along a vertical cross section, the difference between the fundamental frequency and any harmonic frequency will always be equal to some whole number multiplied by the frequency of the fundamental, i.e.,

fundamental = h1 = 1 × h1
second harmonic = (h1 + h1) = 2 × h1
third harmonic = (h1 + h1 + h1) = 3 × h1
fourth harmonic = (h1 + h1 + h1 + h1) = 4 × h0
and so on.

This scheme describes the physical definition of harmonic components. Thus, although the first *visible* harmonic above the fundamental may actually be a third harmonic at 3 × h1, it is correct to call it a third harmonic based on its frequency. We will show in the examples below how to make such a distinction.

To use the harmonics cursors a call must be in standard view:

1. Click enable analysis.
2. Click on the `h1` button in the analysis panel.
3. The `h1` cursor appears on the sonogram.

4 To explore other harmonic attributes, click on the buttons to select other harmonic indicators.

- The **h1** cursor defaults to the point of *maximum amplitude*, which often provides the optimum x-position to indicate additional harmonics. This will typically be on the fundamental component, but not always. This is also a way to visually indicate where on the call lies the point of maximum frequency.
- The position of the additional harmonic indicators will depend upon the position of the first harmonic cursor (**h1**) according to the relationship described above. All other indicators move as a slave to the **h1** cursor.
- Repositioning the **h1** cursor to another position along the fundamental will move all harmonic indicators along with it.

5 Harmonic values are shown in the analysis panel.

6 The frequency positions of the **h1** cursor and additional indicators are shown below their buttons, which clear when invoked.

Harmonics example one

In the next example, we'll look at a call with four clear harmonics, label each harmonic and determine if they are the true first, second and third harmonic.

1 Open the sample file **Tadarida brasiliensis 3** with the with preemphasis set to none and the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).

2 Adjust the standard view setting to **15 msec std view** and zoom select the middle call.

3 Click **std view**.

4 Click **enable analysis**.

6 Click on the **h1** button in the analysis panel.

4 The **h1** cursor appears on the sonogram. The default position for the **h1** cursor is the point of maximum amplitude, which often provides the optimum x-position to indicate additional harmonics. Note that

the current frequency listing for the `h1` cursor position is the same as the value indicated by the f_{max} indicator.

5 Click on the `h2`, `h3`, and `h4` buttons. Three more harmonic indicators appear above the `h1` cursor. Note that the `h4` indicator does not fall on any visible call component. Its position lies where a fourth harmonic component would be though, if there were one there. However, that component down and to the left of the `h4` indicator may be a fourth harmonic component.

6 Grab hold of the `h1` cursor and move it to the right along the centerline of the call. Note how the additional cursor indicators move in relation to the `h1` cursor. When you get the `h1` to a position at about 8 or 9 msec, it becomes clear that the call component that we suspected as a fourth harmonic is indeed just that because the `h4` indicator falls upon it.

10 Notice the nice progression of harmonic components from the first to the fourth. The fact that they all line up in this regular progression with no skipped components indicates that the `h1` cursor is, in fact, located on a true fundamental component.

Harmonics example two

In the next example, we'll look at a call with multiple harmonics, but not in the typical expected progression from a fundamental component. We will use the harmonic indicators to understand the call structure.

1 Open the sample file `Costa Rica 10` with the preemphasis set to `none`, compressed view mode active, 5 kHz cutoff filter, and discrimination control at 6.4.

2 Accept the default subsection.

3 Adjust the standard view setting to `10 msec std view` and zoom select the fourth call at about 73 msec.

4 Click `std view`.

5 Click `enable analysis`.

6 Click on the `h1`, `h2`, and `h3` buttons in the analysis panel.

7 The `h1` cursor and the two indicators for the second and third harmonic appear on the sonogram. They all land on harmonic

components, but what's going on here? There are components between the ones indicated.

Recall that the **h1** cursor defaults to the point of maximum amplitude for the displayed call. But if the maximum amplitude does not occur on the first harmonic, then the default position of the **h1** cursor will land elsewhere. That is exactly what happened with this example.

8 Grab hold of the **h1** cursor and move it down until it lands on the lower component and the **h2** indicator lands on the component with the maximum amplitude. Notice that the **h3** indicator is now on the previously skipped component above the one with the maximum amplitude.

9 Now click on the **h4**, **h5**, and **h6** buttons in the analysis panel. Notice how they fill out the complete harmonic series, and exactly in the relationship described for a harmonic series.

With the harmonics all properly designated, we can no see that for this bat, the component with the maximum amplitude is actually the second harmonic and not the fundamental. You may find some bats that can actually shift the maximum power among their harmonics.

More on harmonic analysis

Have a look at the sample file `Macrotus californicus` with preemphasis set to none, compressed view mode active, 5 kHz cutoff filter, and discrimination control at 6.4. This is a noisy file, and you will want to switch to `real time view active`. Select calls at 391 and 637 msec and process into standard views. The call at 391 msec switches maximum amplitude from the second to third harmonic, while call at 637 msec retains the maximum amplitude in the second harmonic. Append the reference view `Maca_Sanchez_AZ1` for an example of a *Macrotus californicus* call with the maximum amplitude in it's first harmonic. Recognizing bats with such amplitude switching would be difficult if you could not simultaneously view all harmonic components.

A further use of harmonics

For calls in which all of maximum amplitude remains in the fundamental, the presence or absence of harmonics may serve no other useful function than to indicate that bat made a good close pass by the detector. In many recordings, echo noise can overlap upon the end of a call and obscure particular details that can be important. The presence of harmonics in such cases can help to reveal ending details of calls because the harmonic components are typically less prone to noise obscuration. For example, open the file `Lasiurus blossevillii 3`. Accept the default subsection and apply the 20 kHz cutoff filter. Zoom select the third call and make it into a standard view. From where this call was recorded, a call ending around 40 kHz might be one of several *Myotis* species, or a red bat, *Lasiurus blossevillii*. Myotis calls typically end with a downward trending tail, while having an upward trend to the end of the call may differentiate red bats. That is not very obvious on the fundamental, but is more clearly evident on the harmonic. You can also investigate this with the sample file `Lasiurus blossevillii 2`, which has more noise. Using harmonics in this way can also prove a valuable aid to simply determining where a call ends, particularly for calls of nearly constant frequency.

Writing call data to a file

Call data generated with the analysis functions in SonoBat can easily be written to a file for storage and use in another program.

- Export call data by clicking on **`write data to file`** at the bottom of the window.
- The order the values in the file are listed in the section "Call data output order" below and are available in a text and spreadsheet template on the SonoBat CD.
- SonoBat writes the data file to the same directory that holds your specified analysis file directory.

Writing call data to a file example

1. Reopen the sample file **`Tadarida brasiliensis 1`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. Adjust the standard view setting to **`15 msec std view`** and zoom select the second call.
3. Click **`std view`**, then **`enable analysis`**.
4. Adjust the **`Hi f`** and **`Lo f`** cursors to best designate the beginning and end of the call.
5. Click on the **`write data to file`** button to the right of the call interval panel at the bottom of the screen.
6. Call values are written to the default file **`calldata.txt`** in tab-delimited format.
7. Click **`end std view`** so that we can return to the full call sequence and select another call for analysis.
8. Click and drag to select the third call in the sequence.
9. Follow the steps above to adjust **`Hi f`** and **`Lo f`** cursors, add harmonic cursors, etc. (Did you notice that the other visible harmonic is the third harmonic?)

10 Click **write data to file**. Data for the second call are appended to the same file, **calldata.txt**.

11 Locate the **calldata.txt** file in your SonoBat files folder and double-click to open it with Notepad or SimpleText.

12 The first value in both rows should be the same—the filename we used for our example.

13 The second value in the rows indicates the true position of the call in the call sequence. To verify this, return to SonoBat and reprocess the same call in real time view mode. The time positions for the first and third calls should be about 144 msec and 247 msec.

Call data output order

The data file is written as a text file in tab-delimited format, which may be read by nearly any spreadsheet, word processing or database application. The order of the data is shown in the file **SonoBatTemplate.txt** or **SonoBatTemplate.xls**, both of which are included on the SonoBat CD. These files contain a data header that can be inserted above any saved data file to identify the data columns. Values are saved in this order:

1 filename of call sequence
2 time position of call within the file (msec)
3 duration of call (msec)
4 preceding call interval (msec, see note below for more details)
5 high frequency (kHz)
6 low frequency (kHz)
7 bandwidth (kHz)
8 frequency at maximum amplitude (kHz)
9 maximum amplitude (percent duration)
10 characteristic high frequency
11 characteristic low frequency
12 slope (kHz/msec)
13 hi/lo (heel) position within call (percent of duration)
14 upper slope (kHz/msec)
15 lower slope (kHz/msec)

16 heel obvious? 1 = yes
17 frequency of fundamental, h1 (kHz)
18 frequency of h2 (kHz)
19 frequency of h3 (kHz)
20 frequency of h4 (kHz)
21 frequency of h5 (kHz)
22 frequency of h6 (kHz)

Preceding call interval

To avoid introducing duplicate call interval data in the exported call data file, each call has only one call interval saved with it. The analysis operation saves only the *preceding* call interval into the output file. Preceding call interval was selected because what the bat hears during that interval will best correlate with characteristics of the next call emitted. For example, if the bat detected a target from the echo of its preceding call, it may enter into a pursuit call sequence (feeding buzz) that affects call morphology.

Call data filename

The default filename for writing data to a file is `calldata.txt`. You can change this name by highlighting it in the data filename box (below the filename) and typing over `calldata.txt` with your own filename.

If the new file you specify is open and in use by another application, SonoBat will not be able to write to it, and will return an error message instead.

SonoBat may return an error if the file specified has been altered by another application. Thus, save the original output file as a different file before making changes to it if you wish to continue appending call output to the original file.

Advanced Call Analysis

In this section we'll see how SonoBat extends basic quantitative analysis with the ability to infer high frequency harmonics from aliased call components. This information is advanced and will not be needed for interpreting most bat calls. However, we recommend glancing through it to at least get an impression of what alias sound components are and how to recognize them.

After the section on aliases we'll go over a case study that combines elements from the preceding sections to come up with a solid bat identification.

Alias harmonics

All sounds, whether audible or ultrasonic result from continually changing pressure density fluctuations, or waves, in air (or other media, but here we are concerned with the ones in air). How many of these fluctuations strike our ear or bat detector per time determine the *frequency* of the sound. When we record sound with our computers we convert the original *continuous* fluctuation of air density to a string of numbers that describe *discrete* positions of that motion. This digital representation can be thought of as a connect-the-dots model of the continuous signal. To understand why aliasing occurs, it is important to realize that the dots are acquired as very quick "snap shots" of the signal, separated by the digital sampling interval.

Aliasing occurs when a signal fluctuates in between the snap shots; in other words, the frequency of the signal is greater than the frequency of the sampling snap shots. This leaves the computer ignorant that any additional fluctuation has occurred, and it thus interprets the signal it recorded at a lower frequency, or *alias* of the real signal waveform.

In most digital audio work, aliasing is considered troublesome and unwanted. However, because bat calls are by nature discrete sound structures, it is possible to gain information from the aliased components. To use aliased call components, they must be recognized as such. This is straightforward for frequency modulated call structures because aliased components will have an opposite slope from non-aliased components. However, recognizing alias components of constant frequency call

components is more difficult, although the SonoBat harmonic indicators can help you in this effort. We can interpret aliased information because aliases are generated in a predictable way based on the sampling **fs** frequency of the sound file.

Harmonic and call components with frequencies less than the maximum frequency scale shown on the sonogram will display as structures parallel to and above the fundamental (provided the call file has the appropriate sampling frequency **fs** attributed to it). *Alias* components, on the other hand, will display as structures of *opposite slope* as the fundamental.

- *Non-aliased* components start at the bottom of the sonogram and frequency increases upward following the displayed frequency scale.
- *Aliased* components start in frequency magnitude at the top of the sonogram and increase downward (with equal units). For example, on a sonogram panel with a 110 kHz frequency maximum, an alias component positioned at 85 kHz would actually be a component at 110 + (110 – 85) = 135 kHz.

For a longer primer and some excellent figures to help you visualize aliased components, see the **resources** section of the SonoBat website (www.sonobat.com), these pages are also included on the SonoBat CD and should open up on your web browser.

Alias harmonics example

Now let's put the alias harmonic cursors to work on a call with more than a half dozen harmonics, some of which occur at frequencies well beyond the maximum frequency of our *y*-axis.[1]

1. Open the sample file **Lasionycteris noctivagans 3** in compressed view and preemphasis set to **none**.
2. Click **enter** to accept the default subsection.

[1] In digital sampling theory, the Nyquist criterion sets the maximum frequency for real, non-aliased sounds that can be resolved by a digital representation of a signal. This limit is one half of the sampling frequency. Thus a detector with a sampling frequency of 300 kHz can resolve real sounds up to 150 kHz.

3 Change the filter to **harmonic emphasis**.

4 Check to make sure that the detector sampling frequency attributed to this file (**fs**) is set to 300 kHz. (Lower left of panel.)

5 Zoom select the fourth call.

6 Click **std view**. A standard view length of 10 msec should work.

7 Click **enable analysis**.

8 Just to get our bearings, we're going to start by determining values for the non-aliased harmonics first. Toggle on the first harmonic cursor, **h1**, and the harmonic indicators **h2**, **h3**, **h4**, and **h5**.

9 SonoBat automatically positions the fundamental harmonic cursor, **h1**, at the point of maximum amplitude on the fundamental call component. The other harmonic indicators are all positioned above **h1** in positions where each of their respective harmonics should be, provided that **h1** is on the fundamental. In this case, they show that harmonics two through five are all present.

10 Now toggle on the harmonic indicator **h6**.

11 Notice that while the other cursor indicators proceeded up the screen, **h6** proceeded back down the screen. That is because they indicate aliased harmonics. Look at the indicated frequencies for **h5** and **h6**, 175 and 205 kHz, respectively, despite that the upper limit on the sonogram scale is just 150 kHz. These values represent the real values of the components that they are aliasing.

12 Grab hold of the **h1** cursor and move it to the right, following the centerline of the call. At a position about over the 4 msec mark all the indicators can be made to fall upon harmonic components, real and aliased with clear separation.

13 Next, untoggle harmonic indicators **h6**, **h5**, and **h4** leaving just **h1**, **h2**, and **h3** active. Grab hold of the **h1** cursor and move it to the right off of the call and onto the blank portion of the sonogram panel. Move **h1** upward, watching the movement of **h3** as it nears the top of the panel. Keep going and **h3** seems to bounce off the "ceiling" of the sonogram and continue back downward. Move **h1** back down, and move it back up again, this time watching the indicated frequency for **h3**, particularly as it nears and passes 150 kHz. When it surpasses 150 kHz it is only properly indicating aliased features.

14 Change the data filename to "alias.txt"

15 Click on write data to file.

16 Locate the alias.txt file and open it with a word processing application (SimpleText, NotePad, Word) or spreadsheet. Note the harmonic values at the end of the file.

More on aliased harmonics

Alias components "fold down" around one half of the limiting sampling frequency. For a clear example of this open the sample file **`Lasionycteris noctivagans 2`** in compressed view and preemphasis set to **`none`**. Zoom select the last call in the sequence and create a 15 msec standard view. Enable analysis and push the buttons for cursors one through four. The harmonic indicator **`h4`** initially falls upon the real portion of the fourth harmonic, which displays both an aliased and real portion. Grab hold of the **`h1`** cursor and move it to the left following the centerline of the call. Note how the h4 indicator first moves up as it follows the real portion of the fourth harmonic, then downward as it follows the aliased portion. You can explore more harmonics with both real and alisased components in the file **`Antrozous pallidus 1`**.

Remember that to accurately interpret alias information, the proper sampling frequency **`fs`** must be attributed to the file. Also, either the detector or the recording process can determine the limiting sampling frequency. In the first example above, although the audio file was recorded at 44.10 kHz (which at a time expansion factor of 10x could theoretically resolve up to 220.05 kHz), the sampling frequency of the detector was 300 kHz, which can only resolve up to 150 kHz. The second example in the above paragraph was also recorded with a 300 kHz-sampling detector, but the audio file was saved at 22.05 kHz, which at a time expansion factor of 10x can only resolve up to 110.025 kHz. Although this can be confusing, SonoBat figures it out for you and sets the scales appropriately.

Putting it all together

SonoBat provides a wide range of tools to help you analyze and compare bat calls because the challenges of identifying bats acoustically are many and varied. Quality of recording, availability of reference calls, geographic variations, etc. all impose different constraints on our ability

to identify a bat acoustically. Many bat species produce calls that overlap with those from other species. Such calls will not lead to confident species recognition unless other characteristics can be invoked, for example call intervals or visual inspection of foraging flight pattern. Although there may be overlapping call types, within each species' repertoire there may be call types that are distinctive and although less common, those will be the ones that can provide a confident species recognition. Also, knowing which bats to expect at a given location, and which of those may produce similar calls is essential for confident species recognition.

Putting it all together example

Work through the following example to see how you can use a combination of standard views, preemphasis, filters and reference views in order to positively identify an unknown bat call.

1. Open the sample file **`Case study 1`** with the usual default settings (compressed view mode active, 5 kHz cutoff filter, discrimination control at 6.4).
2. The fourth call covers the largest frequency range so let's select that call for a standard view display. It's a short call so set the standard view length to 10 msec.
3. The trailing hook at the end of the call is suggestive of a Myotis call, so let's append some Myotis reference views.
4. Click **`append ref view`** and select **`@Myca_Compiled2.wav`**.
5. Turn on the ruler and compare the characteristic low frequency (the low frequency before the trailing hook). The difference between the lower characteristics of Myotis californicus and our mystery call is too large to be close.
6. Click **`append ref view`** and select **`Myci_Compiled.wav`**.
7. The first reference view is a pretty good match but doesn't show similar harmonic structure. Let's try to coax out some more features.
8. Set the filter to **`harmonic emphasis`** and the preemphasis control to **`full`**.
9. Select the fourth call again and make it a standard view.
10. Click **`append ref view`** and select **`Myci_Compiled.wav`**.

11 The mystery call looks a bit more like the first reference view now. Look in the notes and see that the first call is Myci_OVL_#1. Click **`append ref view`** and select **`Myci_OVL_#1.wav`** to have a more detailed comparison.

12 Part of the first harmonic shows well, like the reference view, but there is no second harmonic. The missing second harmonic probably just indicates that the bat may not have been as close to the detector as the reference view bat was. That would also be the reason why the tail at the end of the call is not as well developed. However, the duration, slope, power distribution and lower characteristic frequency all compare well—a good match!

USDA Redwood Sciences Laboratory Method

Methods for extracting parameters from acoustic files using SonoBat

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Selecting a Call for Analysis

1. Launch SonoBat and engage the **`set prefs`** button in lower right portion of screen (just above the **`quit`** button) to open the preferences panel and set the following preferences:

   Set the **`default analysis call path`** to the directory that you intend to use.

   `Max segment to process` box (towards bottom of window) has a pull down menu that may be set to the program default value of 750msec (best for computers with low ram). Change this to **`2.0 sec`**; a setting that enables most files to open in their entirety. This avoids the extra step of selecting a subsection for processing. (Note: if a 2.0 sec settings demands more memory than your system can manage, you will need to select a lower setting.)

   Save your settings to leave the preferences panel. You must quit and relaunch SonoBat for all preference changes to take effect.

2. SonoBat defaults to **`compressed view`** mode when launched. This simplifies viewing and automatically centers a selected call, but this function requires a clean call signal above background noise to properly center selected calls in the high resolution standard view mode used for extracting call parameters.

However, because many of our calls have background noise, they may be best viewed and processed using **`real time`** mode. To change modes, toggle the

compressed view/real time button (upper right portion of screen) each time you launch the program since this is not an option in **set prefs**. Real time view mode enables manual centering of calls in the high-resolution standard view used for extracting call parameters. Real time view mode allows you to keep the call you have chosen to analyze in the center of the screen and will avoid having the call dissolve away as you zoom in closer using the **msec std view** button. Setting resolution to **high** (an additional option in real time mode) can also help to better resolve noisy recordings to facilitate call selection. However, high resolution rendering will slow processing time. Alternatively, with less noisy calls, you can improve the quality of the positioning of selected calls while still in **real time view** by adjusting the **discrimination** setting to a lower value (press the **reprocess** button to affect this change on a file already open).

3. If the file is larger than your **max segment to process** setting, a control will open requesting you to select a subsection of the full file. The subsection that you select is shown in the oscillogram view of the file and is bounded by yellow and red vertical cursors. Move the yellow cursor to select the strongest section of the call sequence to analyze and press the **enter** key on keyboard to activate the selection.

4. Select the strongest (but not overly saturated* and distorted) call within the displayed file for further analysis. Strong calls will appear with intensities of red and yellow which indicates the strongest signal levels and will often display harmonics. Sometimes call selection will involve a tradeoff between a call with greater intensity and one with more (prominent) harmonics. Thus selection of which particular call to analyze involves some subjectivity. However, the choice between two relatively high quality calls will not typically influence the potential to extract parameters or identify the call.

   If in real time view mode, it may be helpful to first do a coarse zoom to focus on a promising section of the file, and then zoom in further on a particular call to center it on the screen and then click **std view**. (In real time view mode, the std view selection is referenced from the center of the zoomed display, so you can quickly center a call just by a fine zoom onto the center of a call.) Once the call is displayed in std view mode, reduce to the lowest std view time possible without causing truncation of the call, i.e., fill the view with as much of the call as possible without losing any part of it.

* Saturated calls are those in which the signal level exceeded the maximal recording level. If reprocessed with no filter or preemphasis, they will display a flat top in their oscillogram trace. Saturated calls often exhibit

artifactual and aliased harmonics. Aliased harmonics appear at opposite slopes to the fundamental call component. These calls remain usable, but do not be confused by these spurious call components in the sonogram rendering. The loudest recorded calls within a pass may become saturated, but may have strong but unsaturated calls before and after the saturated ones.

5. If the call disappears off the right or left of the std view display, or truncates (appears to lose high or low frequency components or displays vertical artifacts at the start or end of the call), press the **`end std view`** button and repeat step #4 beginning with a longer duration std view (e.g., 30 msec) and reduce incrementally while avoiding truncating the call in the std view display.

6. Many short duration calls may be analyzed at 5 to 7.5 msec to best accentuate call features. In our work at Redwood Sciences Lab, we analyzed some Myotis calls at 10 msec. Rarely did a call have to be measured at >20 msec. Getting a fully shaped call to 5 msec was always the goal, although 7.5 msec seemed to work best overall for us.

7. For calls that appear extra noisy, setting the cutoff filter to 20.00 kHz (lower left portion of screen, SonoBat defaults to 5.00 kHz) can help, although looking at calls in **`real time`** as opposed to **`compressed`** should reduce the need for changing from the default filter setting of 5.00 kHz.

8. In some instances the entire sonogram may appear as a chaotic blue pattern with no discernable calls showing in the oscillogram trace. Such files may result if the bat was too far from the detector to acquire an acceptable signal, or from falsely triggered autorecordings. Nevertheless, such files often contain useful calls when viewed with greater resolution. Engaging the **`play sound`** key and following the moving cursor on the osscillogram trace can sometimes help in locating these weak but useful calls. Zoom in to inspect for calls in any fluctuations in the chaotic blue pattern. Searching for calls in such noise may be enhanced by invoking the 20 kHz filter and changing the **`resolution`** setting to **`high`** if in real time view mode. If none are found, note (in a separate spreadsheet) that no call can be found and move onto the next file.

Extracting Parameters

1. Once a call has been maximized in the std view window, engage the red `enable analysis` key at the bottom center portion of the screen (all analysis tool buttons then appear on the lower left portion of the screen). Two cursors automatically appear on the call: `Hi f` (for high frequency) *near* the high frequency portion of the call, and `Lo f` near the low frequency portion of the call. SonoBat attempts to automatically position these cursors, but this depends upon high quality, clean signals, so generally these will need to be manually adjusted.
2. **The placement of all cursors should be along the centerline of the frequency envelope** (Figure 1). Visualize a line down the center of the call, upon which you should place all cursors (including `Hi f`, `Lo f`, `lo fc` and `up/lo`).
3. Place the `Hi f` cursor at the point of maximum frequency on the call, i.e., along the call centerline and overlapping where the blue* (regardless of shade) of the call changes to the black of silence (Figure 2).
   * If using the color sonogram setting with black background.
4. Move the `Lo f` cursor away from the call and engage the `Lo fc` cursor. This is because the **Lo f** label often obscures the location where you may need to place the `Lo fc` cursor.
5. Place the `Lo fc` cursor at the flattest point on the call (i.e., the point where the slope is changing the least. The intensity of the call should be ignored in selecting this point, and instead focus on the centerline trend of the call (Figures 1 & 2). Changing the palette may help visualize the change of slope without regard to intensity. Note: characteristic frequency (`Lo fc`) may be the same as low frequency (`Lo f`) in some calls.
6. Place the `Lo f` cursor at the point where the call reaches its minimum frequency (i.e., where blue (regardless of shade) turns to black). Note: may be placed at the same spot as `Lo fc`. Be careful to follow the trend in the call and avoid being confused by echo noise which often occurs at the end of the call (Figure 3).
7. Some calls have an obvious change of slope and/or curvature between the initial (upper) sweep beginning at `Hi f` and the lower sweep toward the characteristic frequency (`Lo fc`) (Figure 3). Such an obvious break or inflection point is also called a `heel`. Even without a heel, the initial, or upper slope of a call can be diagnostic and is recorded by invoking the `up/lo` cursor. SonoBat then separately calculates the upper slope between

the **Hi f** cursor and the **up/lo** cursor, and the lower slope between the **up/lo** cursor and the **Lo f** cursor. If the heel is obvious, designate it as so by toggling the **heel no/ heel yes** button to display **heel yes**.

8. To designate the presence of a harmonic, click the **h2** button on the **harmonic explorer**. This should place the **h2** cursor on the harmonic above the fundamental, or first harmonic (typically the primary call component). Clicking the **h2** button forces SonoBat to enter a value on the spreadsheet for the harmonic, which we use as an indication of its presence. If the position of the **h2** cursor does not automatically fall upon a component of the second harmonic, engage **h1** and move it along the fundamental* until **h2** actually appears on the harmonic above the main call component. Then disengage **h1**.
   * The **h2** cursor moves as a slave to **h1**.
9. Once all applicable cursors are in place you are ready to write the data to a **.txt** file. At the bottom center portion of the screen is a black window with a default-named .txt file. Change this to a meaningful name (ex: the RSL bat team uses the site name (e.g., P12a)) and depress the lavender **write data to file** button to execute the write. A line of data will be written to the file *meaningfulname.txt*. in the directory where the calls are stored. If you have your computer's volume set to an audible level you will hear a click. There is no other indication that a save occurred. Pressing the write data to file button multiple times will cause duplicate information from the call to be written to the file.
10. Keep a separate EXCEL sheet (for RSL name sitename_notes.xls) which notes any noteworthy items about calls. Only unusual features not be reflected by parameter extraction should be recorded. These include:

    a. File too noisy for analysis. No call could be identified suitable for measurement --- Delete this file.

    b. More than one call analyzed due to changes in characteristic frequency, presumed presence of multiple bats or multiple species.

Placing cursors properly

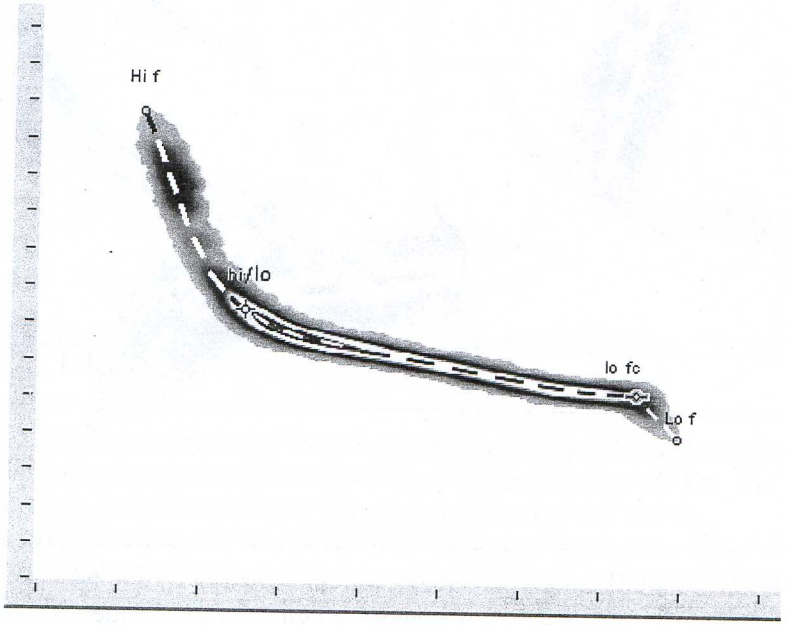


Fig. 1. Even with pure, single frequency tones the sonogram rendering of an acoustic signal will extend over a range of frequencies. In this figure, a dashed line displays the location of the precise frequency information portrayed by this sonogram. To properly interpret frequency data from such a sonogram rendering, visualize a line running through the center of the sonogram rendering, and place all data cursors along that line.

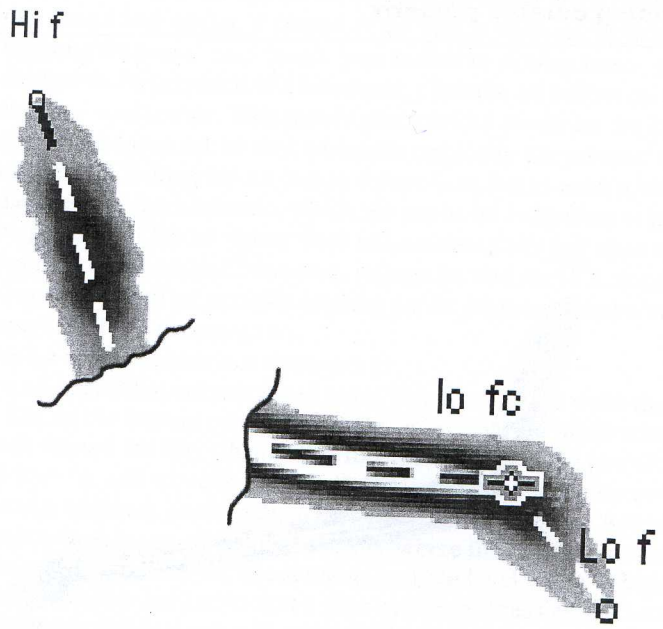


Fig. 2. Detail of cursor placement. All data cursors should be placed along a line running through the center of the frequency envelope. Place the `Hi f` and `Lo f` cursors along this centerline at the points of maximum and minimum frequency, overlapping where the sonogram shading changes to the background shade. The characteristic frequency cursor `Lo fc` should be placed at the point of minimum slope in the call; for Myotis calls, this is the final point in the trend of the call before turning downward into the tail of the call. In the absence of a tail, the `Lo f` and `Lo fc` may occur at the same point (see Fig. 4).

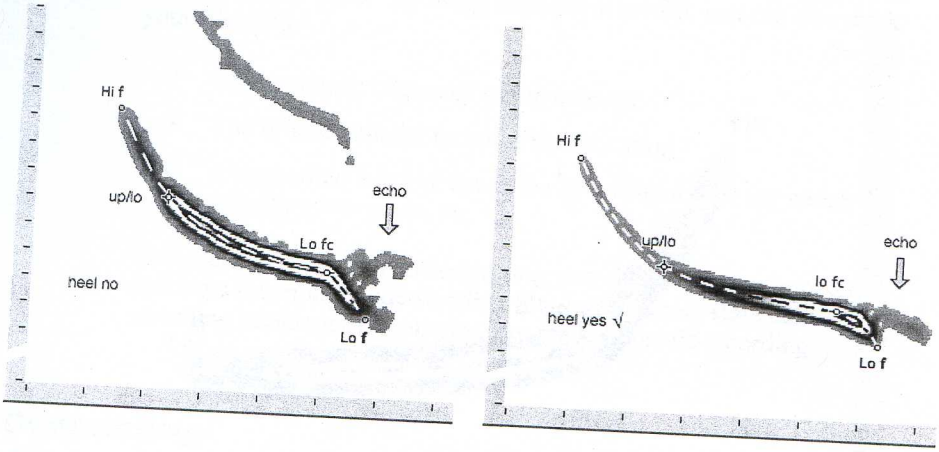


Fig. 3. Further examples of cursor placement. Many calls will exhibit noise from echo returns in addition to the call emitted by the bat. In these cases you must interpret the expected trend of the call to position the cursors. Other calls within the recorded sequence may provide guidance for the call trends, as do harmonic components (left example). Harmonic components follow the fundamental trend of the call, but less often elicit echoes. The left call example has a continuous curvature from its onset to `Lo fc`, and thus exhibits no obvious heel. The `up/lo` cursor is placed on this call to force SonoBat to calculate its approximate upper and lower slopes. The right call example has a discernable* heel and the `up/lo` cursor is placed to indicate that point and to direct SonoBat to calculate its upper and lower slopes. In addition, the `heel no/ heel yes` button was toggled to indicate `heel yes` for this call.

* In this call, lines regressed from the trends in the upper and lower portions of the call would intersect at about this point. The call examples in Figs. 1 and 4 have more obvious heels.

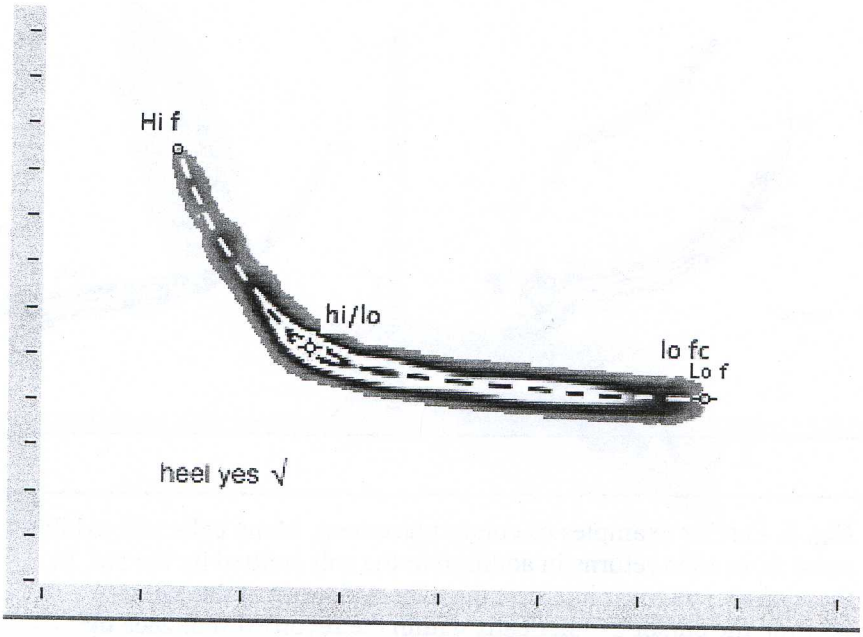


Fig. 4. Example of cursor placement on a call with no final change in slope from the main sweep of the call, e.g., no tail. In such a case, the characteristic frequency cursor `Lo fc` and the low frequency cursor `Lo f` may occupy the same position. By default, the `Lo fc` cursor is not enabled in the SonoBat analysis panel. You may choose to leave it disabled to indicate that the characteristic frequency is not different from the low frequency, (if so, the data spreadsheet will return a zero for lower characteristic frequency), or you may enable the `Lo fc` cursor and place it over the `Lo f` cursor to report its value in the data.

4 Recording

You can use SonoBat to record calls from your detector or tape player, etc. to your computer. By using SonoBat to record, you can also mark your files with:

- The sampling frequency of the detector
- The time expansion factor of the recording
- A note about how the bat or the circumstances under which the recording was made, etc.

This section covers tips on connecting your device to the computer, making a recording, understanding the way detectors store calls, recording preferences, examples, tips, and automatic recording.

Connecting

Sorting out input and output jacks on your sound source and computer is vital for successful call recording. Here are some hints on how to make the process work.

- Connect the output from the detector or tape deck into the computer sound input or microphone jack.
- *Macintosh only:* Set the sound monitoring source to `sound in` using either the Monitors & Sound control panel, or the sound control strip module.
- *Windows only:* The input and output device settings might need to be changed to get the sound to play correctly. Input and output values can be changed using the preferences panel, available from either the main SonoBat window or the recording window.

Stereo output

Whether set to stereo or mono, SonoBat records a single channel. For detectors that have a two-channeled output, i.e. stereo, with the desired time expansion signal on one of the channels, setting the SonoBat recorder to `stereo` instructs the recorder to accept a single channel input and disregard the signal from the other channel.

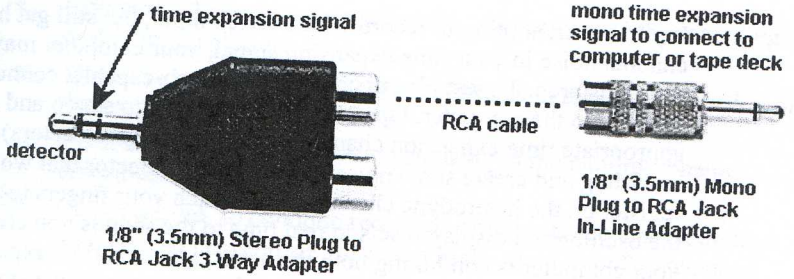
If your computer accepts a stereo input, the SonoBat recording accessory can extract a single time expansion signal from a stereo input without the need for a custom cable. A button on the recorder accessory panel allows you to toggle between stereo and mono input, and a left (`L`) and right (`R`) channel selector button when `stereo` is enabled. This facilitates the use of a standard stereo extension cable, as shown below:



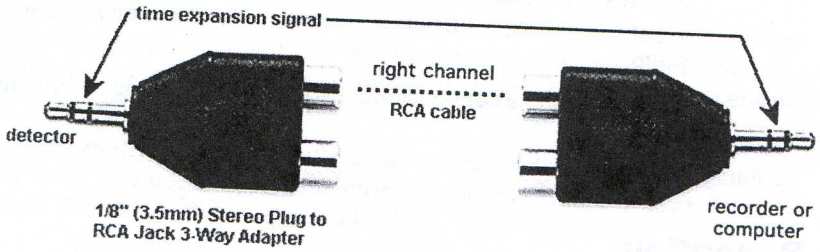
1/8" (3.5 mm) stereo extension cable

Some Pettersson time expansion detectors have a stereo output with a heterodyne signal on the left channel, and the time expansion signal on the right channel. Connecting this signal to the computer using a stereo cable will deliver both signals. Select the `stereo` and the `R` settings to record just the time expansion signal from the right channel.

Extracting a stereo signal using a stereo cable and the SonoBat stereo setting will only work if the computer can accept and process a stereo input. If you get heterodyne noise using a stereo input arrangement, your computer may only accept a single channel input and is mixing the two channels together. In this case use a stereo 3-way adapter as shown below:

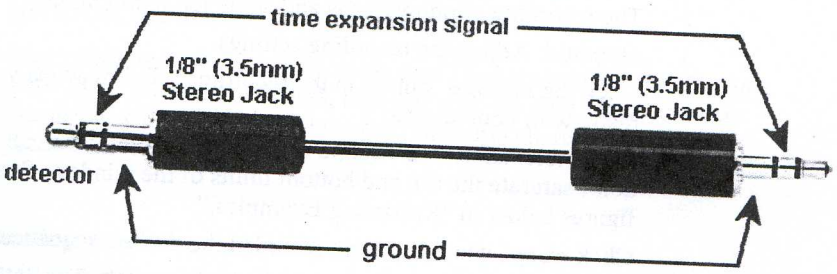


The arrangement above will work for most computers, but not all recorders, some of which need the stereo channels electrically separate. For such equipment, you can patch together a cable in this way:



Connect only the right channel with an RCA patch cable.

Alternatively, a universal custom cable may be fashioned:



Connect middle conductor and base to middle conductor and base, respectively. Do not connect tip conductors.

Example parts list: mouser.com part no.s 171-3311 and 172-2017.

If you are attempting to record with a stereo input, but still get heterodyne channel noise in your time expansion signal, your computer may not support stereo. To test if your computer is stereo-capable, connect your detector to the computer. Open the recorder, set it to stereo and select the appropriate time expansion channel (**R** for Pettersson detectors). Begin recording and create some noise in front of the detector that would register on the heterodyne channel (*e.g.* scratch your fingers together). If the oscillogram display reacts in real time to the sounds you create, then your computer is combining both the heterodyne and time expansion signals. Use one of the adapters shown above to convert the stereo signal from the detector to a mono signal that your computer can accept.

If SonoBat is set to **mono** with a stereo input, both channels will record together. This can result in considerable noise artifact on top of the time expansion signal unless the two channels are separated by the cabling setup.

Changes to the **stereo/mono** setting must be made before initiating a recording.

Recording

1. Click the **record** button on the upper left corner of the main SonoBat window.
2. The recording window opens and waits for sound input.
3. *Optional:* Adjust the recording settings.
4. Click the **record** button in the recording window when you are ready with your source.
5. If possible, adjust the volume on the source so that the call peaks don't saturate the top and bottom limits of the window. See the figures below in "Recording Examples."
6. Click **stop** when you have recorded the desired sequence.
7. *Optional:* Type a note in the box in the lower left. The note will display when the call is analyzed with SonoBat and can be edited again from there. The note will remain in place for the duration of your current SonoBat session unless you change it.
8. *Optional:* Type a file header in the **filename start** text box.

9 *Optional:* Click **edit** to excise non-call portions of the recording, or duplicate calls, etc.

10 Move the left (yellow) and right (red) rules to enclose the portion of the sequence you want to save.

11 Click **save**. The file will be saved using to the naming scheme described below.

12 Click **record** to continue recording additional sequences, or click **end sound recorder** to return to the main SonoBat window.

How SonoBat names files

SonoBat automatically names a file when saved. The file naming scheme appends the date and time to a text header entered in the **filename start** text box. In the absence of any "filename start" text, the filename will be just the date and time.

For example, if collecting calls at Bat Spring on 4 July, 2002, beginning at 7 PM, you might enter "Bat Spring" in the **filename start** text box. The files will then appear like this:

Bat Spring-04Jul02-1900,00.wav

Bat Spring-04Jul02-1901,12.wav

Bat Spring-04Jul02-1901,49.wav

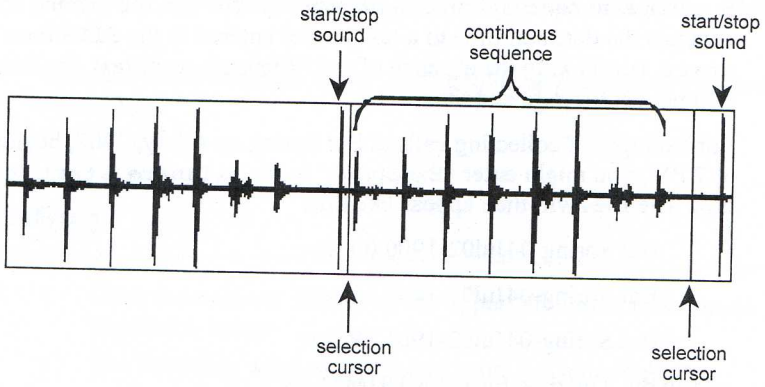
and so on. The time format is HHMM,SS.

Macintosh only: Do not enter more than 12 characters for the filename start. More than 12 characters, together with the date, time, and wav extension, will exceed the Macintosh filename character limit and produce an error.

Looping sequences

The audio output of many time expansion detectors consists of a looping sequence. For proper interpretation of the recorded call sequence, it is essential to avoid saving a selection of the call sequence that includes the transition from end of the recording to the beginning of the recording, which would erroneously juxtapose two calls as if they were emitted by

the bat in that order, though they were not. To do this, you must recognize the beginning and end of the sequence being looped. Many detectors facilitate this with an audible click or other sound at the end of the sequence. Unfortunately, this start/stop sound may not always appear visibly different from the bat calls in the oscillogram display of the recorder, and must be recognized from its pattern in the overall sequence. If your setup allows you to hear the audio input during the recording phase, listen for the start/stop sound, and the second time that you hear it, stop the recording. That way when you switch to edit mode (as shown below), the final signal in the display will be the start/stop sound, and you can use the pattern of the signals to locate the start/stop sound at the beginning of the sequence. Once located, you can move the selection cursors to avoid crossing the start/stop boundary, as shown below.



Alternately, if you cannot hear the audio input during recording, you can record a sequence of sufficient duration to include a continuous segment and then use the recorder's play option to listen to your recording. A moving cursor shows during the playback, which you can use to locate and recognize the appearance of the start/stop sound. Then you can switch to edit mode to select your time-continuous selection for saving.

Tip: Looping sequences may not look precisely alike because the recording oscillogram does not map every point to avoid excessive memory overhead. Use the pattern of the sequence to recognize repeated sequences.

Recording Preferences

To avoid having to set up the recorder each time you use SonoBat, the following recording settings can be saved using the **`set prefs`** button in the bottom portion of the recording window. Changes take place after the preferences are saved:

- sampling format for saving files (22.05 kHz/44.10 kHz and 8 bit/16 bit)
- mono or stereo setting for recording
- right or left channel to used when recording a stereo signal
- default sampling frequency (**`fs`**) to be saved with recording
- sound on/off
- **`input`** & **`output`** settings for Windows recording connections
- default time expansion factor to be saved with recording (standard is 10×, but other time expansion factors are available)
- The **`chart update time`**. This controls the update time for the real time oscillogram when recording. The default value is 0.10 sec and this value works for most systems. However, some systems may transfer data more slowly and this can result in an error message indicating that the program could not retrieve data from the buffer quickly enough. If this happens, increase the chart update time to a greater value.

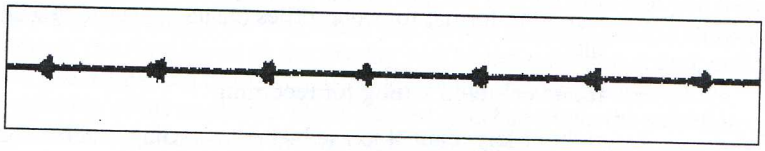
Recording Examples

This oscillogram plot of the recording accessory displays the full scale possible for each selected format. To optimize the signal quality of your recordings, it is important to get a reasonable breadth of signal strength. The signal strength, i.e. amplitude or volume, can be adjusted by either adjusting your computer's recording gain setting to match your detector's tape output (recommended!), or by using your detector's volume control and its headphone output. (See instructions below for adjusting your

computer's recording input gain.) By using your detector's tape output you will not need to make these adjustments each time you use your detector.

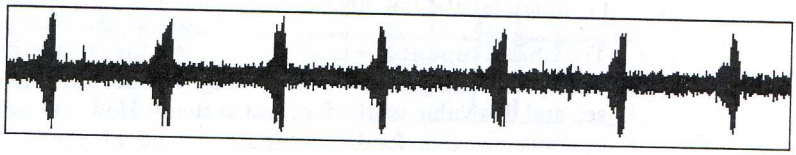
Example 1: volume too low

This recording has the volume set too low for optimum digital representation of the call sequence:



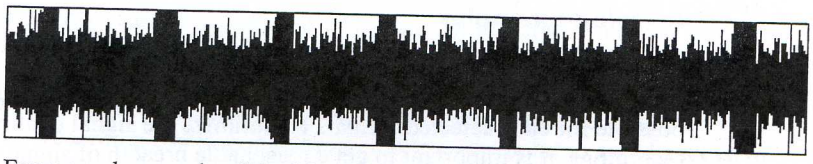
Example 2: volume just right

This recording has the volume set just right. The peaks are resolved and close to filling the recording window, but do not top out at the top of the window:



Example 3: volume too high

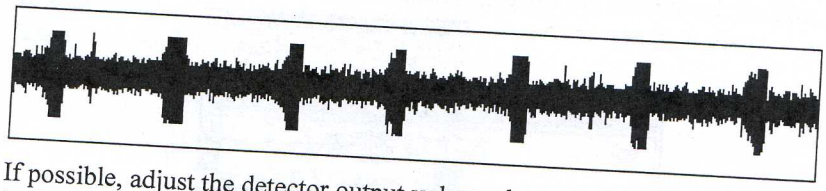
This recording has the volume set too high. The tops of the peaks are saturated and will not be resolved in the digital signal representation of the sequence:



For a good example of the kind of distortion introduced by a recording with the volume set too high, open the example file `volume too high`.

Example 4: detector output saturates below maximum allowed input

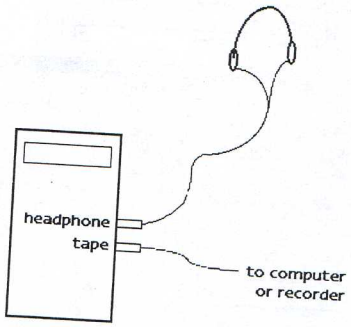
While example 3 shows an input signal whose amplitude exceeds the recorder's maximum allowed input level, it is also possible to saturate the detector's *output* signal at a level below that of the recorder's maximum *input* level. This will appear as a series of flat-topped pulses, all at the same height, but not filling the oscillogram window:



If possible, adjust the detector output volume downward to see a variety in the peak heights, not flat topping at the detector's maximum output level and use 16 bit format for best resolution of the signal.

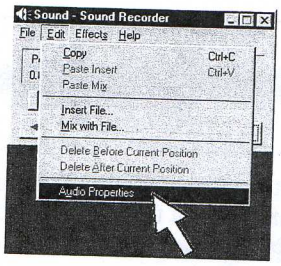
Adjusting your computer's recording gain

To avoid having the need for volume adjustment each time you make a recording, it is best to use the constant volume **tape** output from your detector and match that output with your computer. Your computer should have a sound input adjustment level utility. Once the sound input level of your computer is matched to your detector's **tape** output, that setting will remain saved on your computer for subsequent recording sessions. In addition, you can leave the headphone in it's jack and listen in on the recording as you make it.

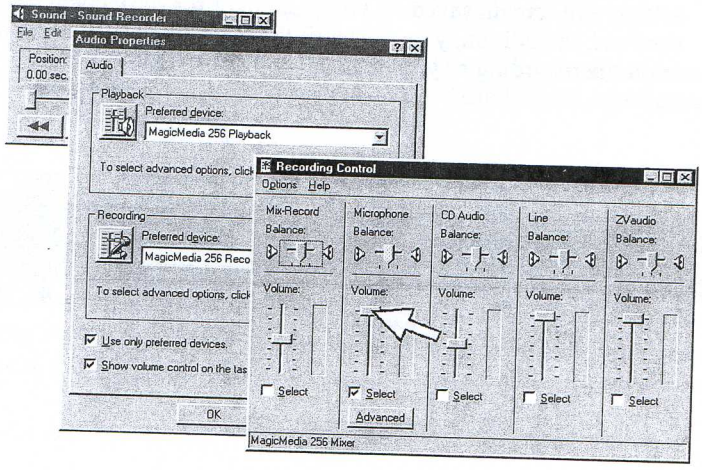


Adjusting sound input level (Windows)

Open the Windows **Sound Recorder**. You will probably find it under the Programs menu–> Accessories–> Entertainment. Select **Audio Properties** from the **Edit** menu:

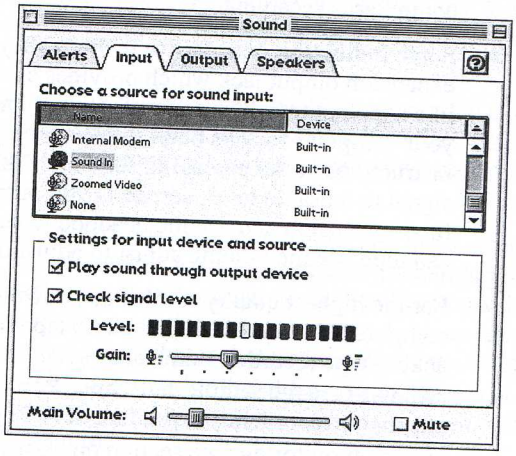


Click on the microphone icon on the **Audio Properties** window and the **Recording Control** panel will open. From there you can adjust the sound input level using the **Microphone Balance** slider control. Check your level using a full volume sound sample from your detector in the SonoBat Recorder. If you can't get the sound level to an acceptable level, you may need to click on the **Advanced** button. That should open another panel with an additional gain setting that you can change.



Adjusting sound input level (Macintosh)

Open the `Sound` Control Panel. Select `Input` and enable `Check signal level`. Adjust the sound input level using the `Gain` slider control. Although a little faux LED meter displays the input level, for best results check your level using a full volume sound sample from your detector in the SonoBat Recorder.



You should select the `source for sound input` to be either `External Mic` or `Sound In`. With `Sound In`, you will here the sound source played through your Mac's speaker as it is recorded.

Recording Tips

- Many users find it helpful to hear the sound input as it is recorded. This is especially helpful for recognizing the start/stop sound in a looping recording. If your computer does not facilitate this (e.g. by using the tape output for the computer), you can still adapt it to do that using an adaptor intended to feed two headphones from a single headphone jack. With such an adaptor you can hear in your headphones the same sound the computer is receiving.
- Some Pettersson detectors (*e.g.* the D 980) have a specific time expansion output jack which provides a constant volume setting like a tape output. To properly set the input signal strength on your computer for this output, follow the gain setting instructions of the preceding section. If that does not bring the signal to a usable level, set the D 980 output for both channels to time-expansion and use the headphone jack for recording. You can then use the volume adjust to adjust the signal.
- For the highest quality recordings, download calls directly to the computer or save to a digital audio tape recorder or high quality analog tape recorder. Some analog tape storage can induce artifacts (see the sample call `Tape Flutter`). However, less expensive recorders can produce satisfactory results for simple species monitoring (see section on "**Unattended recording...**" below.
- For best results with detectors that have a built-in speaker, acquire call data using headphones with the speaker silenced; otherwise the speaker may impart artifact components onto the time expanded audio signal. These will appear as vertical bands through the calls.
- 16-bit quantization allows better resolution of amplitude information. SonoBat analyzes all calls using 16 bit data, so saving in 8-bit format will save disk space, but not improve processing speed.

Using the SonoBat AutoRecorder

This utility allows you to automatically record files and have them saved as SonoBat wav files possessing SonoBat file attributes. The AutoRecorder works like a voice-activated tape in which you adjust the activation threshold. You can use the AutoRecorder in two ways:

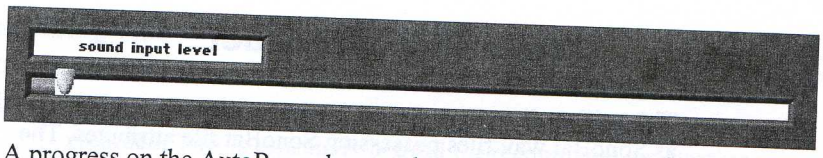
- With a direct connection from your computer to an autotriggering detector (e.g. Pettersson D240x) to automatically collect call sequences. When used in this way, the AutoRecorder appends a date and time stamp to a filename that you can specify.
- To automatically download a tape of auto-recorded call sequences and parse them into SonoBat wav files. This eliminates the onerous task of performing this manually.

When first using the AutoRecorder, you should set the AutoRecorder preferences. (Note: the AutoRecorder maintains a separate preferences file from SonoBat). The AutoRecorder preferences button is located in the lower center of the panel. Select the directory for your autorecorded files and other recording attributes that you desire for your default settings. There is also a setting for the `chart update time`. The default setting is 0.15 seconds; increase the time if you receive an error when running the AutoRecorder.

Tip: It is best to have no other programs running when using the AutoRecorder as it demands much of your computer's attention to stream the audio data to disk. Macintosh users: it will help to turn off filesharing and AppleTalk.

Setting the trigger level

The AutoRecorder works by monitoring the sound input level and begins saving to memory when the input level exceeds the user-specified threshold and then saves that memory to disk when the signal drops below threshold. You must thus set the threshold to a level just above the quiescent level in between call sequences, but below the quietest part of call sequences to get complete sequences recorded to a single file.

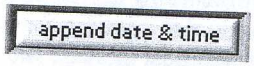


A progress on the AutoRecorder panel displays the signal level in red. The green slider sets the recording trigger threshold. First run the recorder with the lower left button set to **`monitor without saving`**. Push the **`record`** button to begin viewing a detector or tape signal played into the computer. Adjust the green sound input slider control so that it is just above the quiescent signal level during the portions that you do not want to record. A green LED indicator will light when the threshold is exceeded.

When the appropriate threshold is set, change to **`save to disk`** when you are ready to save files.

Selecting the filenaming scheme

The AutoRecorder will name files it saves in one of two user-selectable filenaming schemes. Use the filenaming scheme button to select the scheme of your choice.





When directly attaching an autotriggering detector to the computer, you may prefer the date and time appended to the file name. For example, if for autorecording calls at Bat Spring on 4 July, 2002, you might enter "Bat Spring" in the "filename start" text box. The files will then appear named as

Bat Spring-04Jul02-1900,00.wav
Bat Spring-04Jul02-1901,12.wav
Bat Spring-04Jul02-1901,49.wav

and so on. The time format is HHMM,SS.

For downloading a series of recordings from a tape, you may prefer a file number appended to a filename start with the date of the recording. Otherwise, if you downloaded your calls with **`append date & time`**

active, the dates and times will not reflect the times when you *collected* the call sequences, but rather the times when you *downloaded* them to your computer.

For example, if a tape was collected at Bat Spring on 4 July, 2002, you might enter "Bat Spring-4Jul02" in the "filename start" text box. The files will then appear named as

Bat Spring-04Jul02-T1.wav
Bat Spring-04Jul02-T2.wav
Bat Spring-04Jul02-T3.wav

and so on.

If no filename start was entered, the filename will be an 8-digit number derived from the computer's timing circuitry appended by the file number and the files will be written like

39493557-T1.wav
39493557-T2.wav
39493557-T3.wav

and so on, where the 8-digit prefix will be different for each session.

Unattended recording using tape recorders

Although the highest quality audio work demands a digital audio tape (DAT) recorder, satisfactory results can be obtained using less expensive voice-activated portable cassette recorders such as the Sony TCM465V Pressman (about $50 US). Such a set up performs well for inventory and monitoring studies such as establishing species presence or absence, or for acquiring data for species accumulation curves. Together with an auto-triggering detector like the Pettersson D 240x, such a set up forms a small and easily protected package to implement in a field setting. Many inexpensive tape recorders have significant variability in their tape drive motor speed that results in frequency flutter, but in our experience, these Sony units have good tape speed control and the voice-activation interfaces well with the detector signal. (Note, there is a manual speed adjustment however; just be sure to leave that at unity). Also, these units record only mono sound, so they must be connected to the detector to receive only the time expansion signal as shown in the above comments about cabling arrangements.

These recorders have an automatic gain control which ramps up the volume during the quiet intercall intervals. This fills the sonograms with

annoying noise between the calls, but as you can see from these examples, the calls themselves are nicely rendered and entirely suitable for species recognition. It may be necessary to render the calls with **`real time view active`** for best selection of calls for

Set the detector to auto-trigger and set the recorder to voice-activated record and then return at a later time to recover your data. Then download the recorded call sequences using the AutoRecorder as described in the preceding section.

Appendix A Example Files

The following table lists the files used as exercises in this Guide. You will find additional files included on your SonoBat CD that you can explore.

File name	*(fs) of recording/ (fs) of detector*	*file description*
Antrozous pallidus 1	22.05/300	three calls
Antrozous pallidus 2	22.05/300	five calls
Antrozous pallidus 3	44.10/300	three strong calls, some harmonics
Case study 1	44.10/307	Same as Myotis ciliolabrum 4; seven calls
Costa Rica 10	44.10/350	Ten calls with harmonics
Discrimination demo	22.05	Synthesized sound sequence, four 10 msec pulses at 20, 40, 60 and 80 kHz
Eptesicus fuscus	44.10/300	Five calls with harmonics
Euderma maculatum 1	44.10/307	Three calls
Eumops perotis	22.05/350	Long file with four calls, seven harmonics shown on third call when processed with harmonic emphasis on
Filter demo	22.05	Synthesized tones of increasing frequency. Process in real time.
Lasionycteris noctivagans 1	44.10/307	Nine calls
Lasionycteris noctivagans 2	22.05/300	Six calls with harmonics and alias harmonics, changing through sequence.

Lasionycteris noctivagans 3	44.10/300	Same sequence as above, but saved at 44.10 kHz.
Lasiurus blossevillii 2	44.10/300	Thirteen clear calls among noise.
Lasiurus blossevillii 3	44.10/300	Multiple calls, second bat in background
Macrotus californicus	32.00/307	Macrotus calls showing power switching between harmonics. Noisy file recorded with digital video camera using automatic gain control.
Myotis californicus 3	44.10/350	Seven calls with portion of harmonics going off top of screen at 175 kHz
Myotis ciliolabrum 2	44.10/300	Seven calls with some harmonics and alias harmonics
Myotis ciliolabrum 3	44.10/300	Noisy call with echoes; good example of how reducing the discrimination increases accuracy of call interval calculation
Myotis ciliolabrum 5	44.10/307	Ten calls with excellent harmonics
Myotis volans 1	44.10/300	Feeding buzz with 26 calls. Unrepresentative call type for this species. See other Myotis volans files for typical calls.
Myotis yumanensis 2	22.05/300	Seven calls
Myotis yumanensis 3	44.10/350	Two strong calls amid weaker ones
Myotis yumanensis 4	44.10/307	Seven calls with visible echoes
Pipistrellus hesperus 1	44.10/300	Long file with feeding buzz
Pipistrellus hesperus 3	44.10/300	Five calls

Reference view demo 1	44.10/300	Same as Myotis californicus 2; long file with seven calls.
Reference view demo 2	44.10/300	Same as Pipistrellus hesperus 2; nine calls with characteristic P. hesperus harmonic
Reference view demo 3	44.10/300	Same as Eptesicus fuscus; five calls with a harmonic
Reference view demo 4	22.05/300	Same as Myotis ciliolabrum 1; eight calls
Tadarida brasiliensis 1	44.10/307	Five calls
Tadarida brasiliensis 3	44.10/300	One strong call with harmonics
Tape Flutter	22.05/350	Long file showing wow & flutter artifacts from tape recording
TwoBats	44.10/300	Two different bats
volume too high	44.10	Three calls of increasing over saturation

SonoBat for Windows Quick Installation Guide

Recommended System requirements: Pentium with at least 256 MB of RAM. Similar to other graphic-intensive programs, SonoBat thrives on memory. Increasing RAM will enhance SonoBat performance and allow you to process longer segments of call sequences. Computer display with at least 1024 x 768 pixels (xga).

Double click **Setup.exe** to run the installer utility.

The installation will install all the necessary files and create three entries on your Start Menu, the main SonoBat program, the AutoRecorder utility, the SonoBat RefCompiler utility, and the BatchAttributer utility.

Note: In addition to a "SonoBat 2.9" folder in your "Programs" folder, the installer may also create a folder named "National Instruments." That folder contains essential files for SonoBat to work.

Next, copy the "**SonoBat files**" folder on the CD to your hard drive to get the updated example and reference files. From here you can take off with the **User's Guide**.

Open SonoBat 2.9 from your program menu. Click on the "**set prefs**" button on the lower right of the panel. The preferences panel will open. To begin, you should set the "**default anlaysis call path**" to the "**Examples files**" folder in the SonoBat files folder that you copied to your hard drive*. Set the "**default reference call path**" to the "**ref views**" folder in the SonoBat files folder. Also set the "**max segment to process**" setting to 4.0 seconds. (Go back and set to a shorter time if your computer has memory limitations.) **Save** to exit from the prefs panel.

* To set the folder, click the "Browse" button and navigate through your directories until the files within the desired directly are displayed. Then click the **Select Current Directory** button on the lower right of the window.

Note to Windows Vista users

Upon entering your SonoBat registration code or attempting to set your preferences, SonoBat may report an error condition like:

LabView: could not write to binary file.

This results when SonoBat attempts to update its preference file, which we have always conveniently located in the SonoBat program folder. Under Vista though, User Access Control prevents such changes to program folder contents.

As a workaround, simply move the **SonoBat 2.6 Suite** folder to another location, perhaps where you keep your SonoBat files. Fortunately, Vista will keep track of the program links from your start menu and everything should run fine with SonoBat in a new home beyond the helpful purview of User Access Control.

In a future version of SonoBat, we will find another location for the prefs file to avoid this problem.

The enclosed cable is a custom cable for connecting a Pettersson detector to your computer or recording device, e.g., iRiver IFP series. Notice that the cable is asymmetrical; the 90° stereo end connects to the **detector**. It will separate and deliver only the time expansion signal at the other end. If you use the **mono** setting when recording with the SonoBat recorder utility you will only get the time expansion signal. You can set your default to mono on the Prefs panel. If you use **stereo**, select the **Right** channel.