Kaleidoscope Viewer

You must have a Kaleidoscope Viewer or Kaleidoscope Pro license to use the Kaleidoscope Viewer features.

Kaleidoscope Viewer is a spectrogram viewer capable of opening *.wac*, *.wav*, and *.??#* files. It can also be used to view and edit meta data and quickly review automatic identification results.

You can open a file in the Kaleidoscope Viewer from the main Kaleidoscope window by using the "File->Open" menu. The Kaleidoscope Viewer is also launched automatically after batch processing with automatic classification.

The Waveform Plot

The plot on the top is an oscillogram of the audio signal and represents amplitude on the vertical axis and time on the horizontal axis. Note that this plot is only available for full spectrum (e.g. *.wav* and *.wac* files) and would appear blank for zero crossing (e.g. *.??#* files) because zero crossing files do not contain any amplitude information.

Pressing the 🟥 / 🟥 button toggles between linear and log scales. The ■ and ■ buttons located to the right of the plot can be used to zoom in and zoom out of the vertical amplitude axis, and a vertical scroll bar can be used to scroll in the vertical direction.

Moving the mouse over the waveform plot shows a cursor and displays the time position in seconds and the amplitude value in either a linear or log (dB) scale. Moving the cursor while holding the left button down lets you create a selection box. The boundaries and deltas of the selection box are displayed in the status bar at the bottom of the Kaleidoscope Viewer window. The selection box can be cleared with a left click of the mouse.

If you right-click inside the selection box, a pop-up menu will appear offering you additional actions you can take on the selection. At this time, the only action supported is "Zoom to fit" which will expand the selection to fit the available window area.

Up to two horizontal reference lines can be set with a right-click of the mouse. The reference lines can be cleared with a double right-click.

The Spectrogram Plot

The plot below the waveform plot described above is the spectrogram plot and represents frequency on the vertical axis and time on the horizontal axis.

For full spectrum recordings (e.g. *.wav* and *.wac* files), the color intensity corresponds to the power level of the signal at a given frequency and at a given point in time. The brightness slider indicated by ■ / ● can be used to decrease or increase the signal power color on a dB scale from -96dB to +96dB. The contrast slider indicated by ◉ / ▣ can be used to decrease or increase the dynamic range represented by the color gradient on a dB scale from -96dB to 0dB.

For zero crossing recordings (e.g. *.??#* files), dots representing a sequence of zero crossing points are shown.

Kaleidoscope can convert full spectrum data to zero crossing data, and will show zero crossing dots superimposed on top of the color spectrogram plot. The ⁙ / ⧄ button toggles display of zero crossing dots on and off while the ⧅ / ☒ button toggles display of full spectrum data on and off.

To the right of the spectrogram plot, the ■ and ■ buttons can be used to zoom in and out of the vertical frequency axis and a vertical scroll bar can be used to scroll in the vertical direction. The ■ button toggles to a "zoom to fit" mode which will fit the vertical scale to the nyquist frequency.

Moving the mouse over the spectrogram plot shows a cursor and displays the time position in seconds, the frequency in Hz, and (for full spectrum recordings) the amplitude value in dB. Moving the cursor while holding the left button down lets you create a selection box. The boundaries and deltas of the selection box are displayed in the status bar at the bottom of the Kaleidoscope Viewer window. The selection box can be cleared with a left click of the mouse.

If you right-click inside the selection box, a pop-up menu will appear offering you additional actions you can take on the selection. At this time, the only action supported is "Zoom to fit" which will expand the selection to fit the available window area.

Up to two horizontal reference lines can be set with a right-click of the mouse. The reference lines can be cleared with a double right-click.

For Kaleidoscope Pro users, if you have a classifier installed, you can toggle on and off a visualization of our training data reference call clusters for comparing with your recordings with control-left-click. When turned on, blueish shapes of calls are superimposed on top of the spectrogram using the current frequency and time scales. The calls can be scrolled left and right by holding the control button while dragging the mouse left or right across the spectrogram or by using the left and right arrow keys. During training, we cluster together similar calls from the training set. The visualization represents a histogram of calls as if we layered all of the cluster members on top of each other. The yellow areas represent the path where most of the calls line up, and the blue region around them represent the variation of calls represented.

You can also open a blank window to look at just the reference call clusters with "Open Reference" from the menu.

Shared Waveform and Spectrogram Controls

The waveform and spectrogram plots share a number of controls. Just below the spectrogram plot, the ■ and ■ buttons can be used to zoom both plots in and out on the horizontal (time) axis. The ■ button toggles a "zoom to fit" mode which will fit the horizontal scale to the entire recording duration. A scroll bar lets you scroll through time. The ▣ / ◙ button toggles inverse video mode. And the ▥ / ▥ button toggles between compressed time and normal time views. Note that the compressed time view is based on Kaleidoscope's zero crossing conversion. If no zero crossing signals meeting the filter criteria are met, the compressed view will look blank.

You can left click and drag a region on the spectrogram frequency axis ruler to the left of the spectrogram plot to establish a bandpass filter, and the waveform plot is updated with the filter applied. The filter can be cleared with a left-click on the frequency ruler.

Spectral Analysis

The ■ button pops up an analysis window. This shows a spectral plot with frequency on the vertical axis and dB level on the horizontal axis. If a region of the spectrogram is selected with a box, the spectral plot shows data corresponding to the contents of the box. Otherwise, the spectral plot shows data for the time period displayed on the spectrogram (or fragmented periods in compressed mode).

A red line represents the power spectrum of the full spectrum signal. A dotted black and white line represents a weighted zero crossing histogram representing how long the zero crossing signal spends in a given frequency.

The following statistics are also calculated and displayed:

Power Min
Estimate of minimum signal frequency. This is determined by following the peak frequency down to the noise floor.
Power Max
Estimate of the maximum signal frequency. This is determined by following the peak frequency up to the noise floor.
Power Mean
This is the power-weighted mean frequency of the spectrum
Power Peak
This is the peak frequency of the spectrum
ZC Min
This is the minimum frequency represented by a zero crossing dot
ZC Max
This is the maximum frequency represented by a zero crossing dot
ZC Mean
This is the average frequency of all zero crossing dots
ZC Peak
This is the peak frequency of the time-weighted zero crossing histogram

Playback

The ▶/■ (Play/Stop) buttons are used to play full spectrum data on your computer speakers. The playback can be at "Normal" speed or fast or slow by factors of 8, 10, 16, or 20 times. If a region is selected, the region is played. Otherwise the area shown on the screen is played. No sound is presently produced for zero crossing recordings but we may change this at a later date.

Time Expansion

The time expansion factor can be used to specify if the file open in the viewer is time expanded. The "TE Auto" choice will automatically determine the time expansion factor from meta data first, or the sample rate second.

Automatic Identification

If classification is enabled (from the main Kaleidoscope window), the pulse-by-pulse classification result will be shown at the top of the spectrogram plot indicating the species and cluster number associated with the classification. When all of the pulses in the file have been classified, the pass-level analysis is performed. If a final identification is determined, the matching pulse-by-pulse values will be shown as bright while other values will remain grayed out. The final identification is also loaded into the identification button label in the meta data panel (see below). You can toggle between enabling and disabling automatic classification with the ■ / ⧄ button to improve the performance..

File and Folder Navigation

The title bar the top of the Kaleidoscope Viewer window displays the folder name containing the current file and the current file name. For *.wac* files, it also displays the current trigger number out of how many triggers e.g. "(1 of 3)" indicates the first trigger out of three triggers in the file. The ■ and ■ buttons will change the view to the previous or next file in the folder respectively. The ■ and ■ buttons will change the view to the last file of the previous folder or the first file of the next folder respectively. For *.wac* files, the ■ and ■ buttons will change the view to the previous trigger or the next trigger in the file.

When the Kaleidoscope Viewer is linked to a results table (see below), the previous/next file buttons are replaced with ‹ and › and are used to go to the previous and next file in the results table instead.

Meta Data

The ■ button toggles between showing and hiding the meta data panel below at the bottom of the Kaleidoscope Viewer window. This panel displays meta data contained in the file such as timestamps and GPS coordinates. An editable field contains field notes. Another editable field contains the manual identification. Below this field is a button that is populated with the results of automatic identification.

At the bottom of the Meta Data panel are 24 user-defined buttons used to assign manual identifications to the meta data. The button labels can be pre-loaded from the classifiers from the "File->Load labels" Kaleidoscope Viewer menu. The buttons can be customized by right-clicking inside the button and typing in a new label. Left clicking a button loads the customized label value into the manual identification field.

There are thus three ways to assign a manual identification to the meta data. First, you can simply type an identification into the identification field and press return. Second, you can press the automatic identification button located below this field which is prepopulated with an automatic identification if determined. Third, you can press one of the user-defined buttons. If the "Auto next file" checkbox is checked, the ■ or › next file button is automatically activated after the manual identification has been set. In this way, you can quickly review and assign identifications to files.

Results Table

A results table can be loaded from either the "id.csv" file created after a batch run with automatic classification enabled or from a "metaid.csv" file created after a batch run on input files containing metadata without automatic classification. See Automatic Identification for more information.

The results table is automatically loaded after a batch run with automatic classification enabled. The table can be manually loaded from the "File->Load Results..." menu on the main Kaleidoscope window. This causes a Kaleidoscope Results window and a Kaleidoscope Viewer window to appear and these two windows are linked together. The results window is a spreadsheet view into the underlying *.csv* file and shows a subset of available columns with a row for each output. Rows can be sorted by clicking on column headers. Clicking on a column header again will reverse the sort order. Clicking on a row causes the linked viewer window to open and display the corresponding file.

The ‹ and › buttons in the viewer will advance the linked results window to the previous or next row and open the corresponding file. If a manual identification is updated in the viewer, the corresponding entry in the results table is also updated. In this way the files can be quickly reviewed with manual classifications added and the spreadsheet is updated at the same time. When finished, you can save the spreadsheet with the "File->Save" or "File->Save as..." menu on the results window. The resulting *.csv* file can then be opened in spreadsheet software and pivot tables can be easily created to summarize results.

Settings

The Kaleidoscope Viewer inherits many of its settings from the main Kaleidoscope window at the time the Viewer window is opened. This includes the output time expansion factor (used to determine the correct sample rate with the assumption that you are opening output files and not input files), as well as filtering and classification parameters. From the Kaleidoscope Viewer window, you can reopen the main

Kaleidoscope window by using the "File->Settings" menu. To reload these settings into the viewer, use the "File->Reload" menu. This will apply the new settings to the viewer window and reopen the currently displayed file.

As a convenience, the time expansion factor is also controlled by a choice box so you can coneniently set the correct time expansion factor. This is critical for auto id. Make sure the vertical frequency axis represents the true frequencies of the bats, and not divided down (or up) by time expansion.

Advanced Settings

The "File->Advanced Settings..." menu can be used to change internal parameters. The FFT Size is the order of the Fast Fourier Transform (default 256). The Window Size is the number of windowed samples included in each FFT with any remaining samples between the Window Size and FFT Size zero-stuffed. These windows are then 50% overlapped to form vertical slices in the spectrogram plot representing half the number of windowed samples. The Max Cache Size is how much computer memory will be used to load samples and FFT data. The maximum number of samples is shown. Large files that can't fit within the available memory will be broken into pieces, and you can navigate forward and backward through these pieces using the ■ and ■ buttons.