

VoICE USV Walkthrough Introduction:

The walkthrough for VoICE USV are in the following pages. I strongly recommend your doing the tutorial before proceeding with your own data.

In this tutorial, I will score similarity between the vocalizations of one mouse and then assign them to canonical call types. VoICE USV offers the option to blind the user to the animal's genotype, which I will not do here. The sample data are included in the VoICE USV download .zip file, in a folder entitled "sample_data_usv."

The screenshots here are from the Mac OS X version of VoICE USV, but the Windows version should be nearly identical.

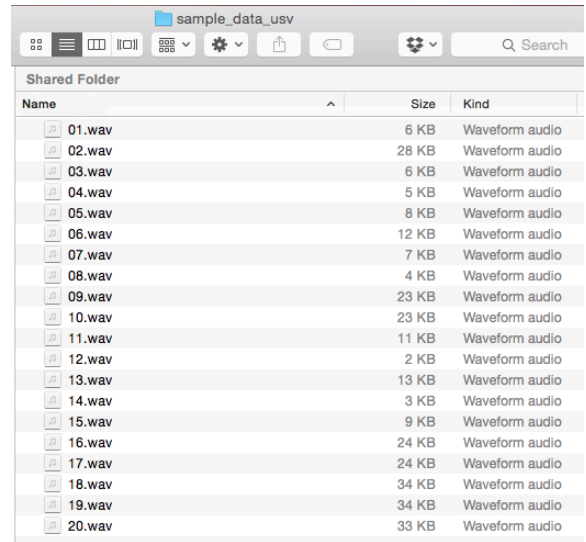
Please be sure that you have VoICE USV and its dependencies properly installed before beginning these tutorials.

[See the README for instructions on how to install VoICE's dependencies.](#)

VoICE USV Walkthrough

The data you start with is a folder containing USVs in individual .WAV files. This folder is entitled "sample_data_usv". It contains 20 USVs, each in their own .WAV files.

(Note: When collecting your USVs, please ensure that filenames are sequential. We do not have a recommendation as how to generate your individual .WAV files. We have used custom-written MATLAB code to generate these .wav files that we do not provide in the software package.)



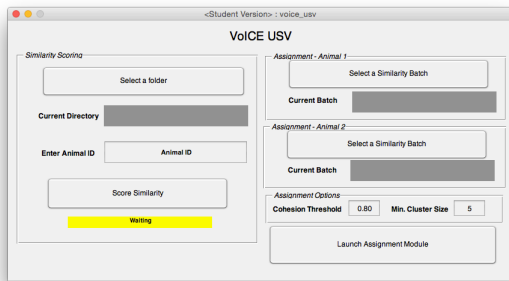
Name	Size	Kind
01.wav	6 KB	Waveform audio
02.wav	28 KB	Waveform audio
03.wav	6 KB	Waveform audio
04.wav	5 KB	Waveform audio
05.wav	8 KB	Waveform audio
06.wav	12 KB	Waveform audio
07.wav	7 KB	Waveform audio
08.wav	4 KB	Waveform audio
09.wav	23 KB	Waveform audio
10.wav	23 KB	Waveform audio
11.wav	11 KB	Waveform audio
12.wav	2 KB	Waveform audio
13.wav	13 KB	Waveform audio
14.wav	3 KB	Waveform audio
15.wav	9 KB	Waveform audio
16.wav	24 KB	Waveform audio
17.wav	24 KB	Waveform audio
18.wav	34 KB	Waveform audio
19.wav	34 KB	Waveform audio
20.wav	33 KB	Waveform audio

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Step 1: Score Similarity Between USVs

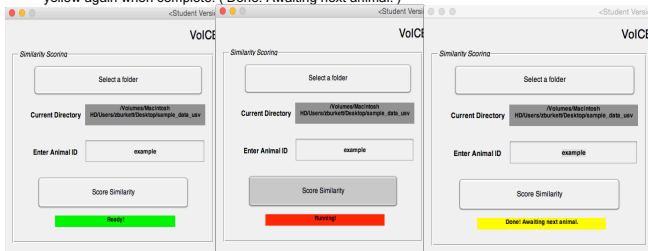
VoICE USV is contained within two modules. To launch, type "voice_usv" at the MATLAB command prompt. The interface will then open.



Press 'Select a folder' and then navigate to "sample_data_usv" and hit 'Open'.

Enter an animal ID for the similarity batch, here I will use "example". Once a valid ID has been entered, the yellow status bar will change to green and say 'Ready!'.

Press 'Score Similarity'. The yellow status bar will turn red while similarity is scored ('Running!'), then yellow again when complete. ('Done! Awaiting next animal.')

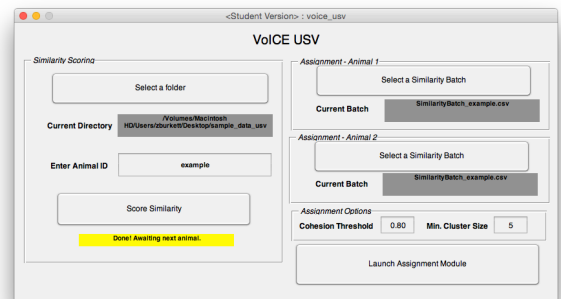


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Step 2: Assign Clustered Syllables to Canonical Call Types

After scoring similarity, the folder in the 'Current Directory' field of the 'Similarity Scoring' panel will contain a .CSV file, which is the result of the similarity batch. Select this file in both the 'Animal 1' and 'Animal 2' panels by pressing the 'Select a Similarity Batch' button in each.

(Important Note: If the user wishes to be blind to the animal's genotype when assigning calls, select similarity batches from animals of different genotypes in 'Animal 1' and 'Animal 2' panels.)



Once similarity batches are loaded, the user can optionally edit the 'Cohesion Threshold' and 'Min. Cluster Size' fields in the Assignment Options panel.

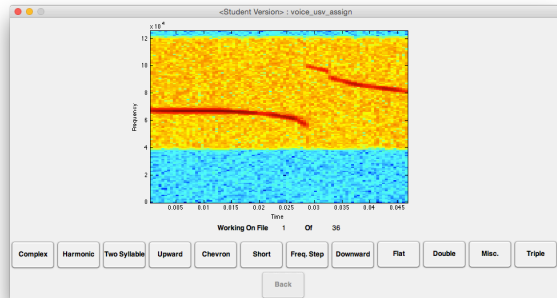
Cohesion Threshold: Clusters must display an average level of correlation with their eigencall at or above this threshold in order to be assigned by inspection of the call most like the eigencall. Otherwise, calls within the cluster are assigned individually.

Min. Cluster Size: Clusters must be at least this large in order to be considered for classification by inspection of the call most like the eigencall. Otherwise, calls within the cluster are assigned individually.

For the purposes of this tutorial, we are analyzing only 20 total calls. Thus, I will decrease the minimum cluster size to 2 and proceed by pressing 'Launch Assignment Module.'

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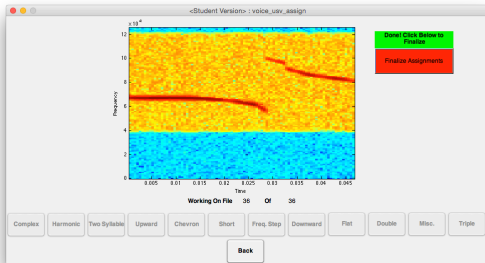
The Assignment Module



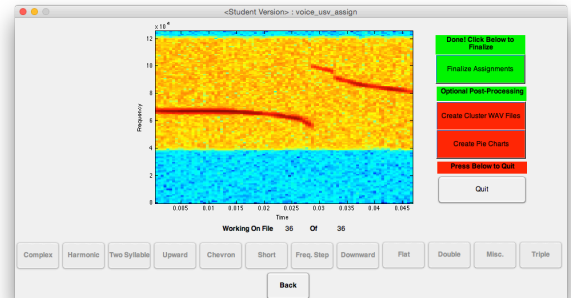
The assignment module is self-explanatory. Based on your selections in the previous window, the total number of calls that the user must assign will be higher or lower.

Proceed with assigning calls to their canonical categories, as defined by Scattoni et al. in 2008. (**Note:** detailed descriptions of the call categories are in this manuscript.)

When all syllables are assigned, the buttons will turn gray and new options will appear.



First, hit the red 'Finalize Assignments' button. New options will then appear.



Create Cluster WAV Files will generate four folders within the directory for each animal in the analysis.

1. **joined_clusters_clusters**: A directory containing a single .WAV file containing all of the calls for each cluster, as determined by the automated tree trimming algorithm.
2. **sorted_syllables_clusters**: A directory containing subdirectories for each cluster, as determined by the automated tree trimming algorithm, with a .WAV file for each call in that cluster.
3. **joined_clusters_pie**: A directory containing a single .WAV file containing all of the calls for each call type, as determined by the user assignments in the assignment module.
4. **sorted_syllables_pie**: A directory containing subdirectories for each call type, as determined by the user assignments in the assignment module, with a .WAV file for each call of that call type.

Create Pie Charts will generate "pieChart.pdf" within the directory for each animal in the analysis. This chart displays the percentage distribution of each call type, as determined by the user assignments in the assignment module.

This concludes the VoICE USV tutorial.