



A Scalable Pipeline for Single-Pulse Analysis of Animal Vocalizations



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Abstract

The study of animal vocalizations is of central importance to the fields of ecology and population biology. In recent years, a myriad of new methods have been developed for working on animal vocalizations. Many, if not most of these center on the use of spectrograms or summary numerical representations of the elements of the vocalization signals themselves as the basis for analysis. In previous posters, the author has introduced a new method for animal vocalizations which is termed single-pulse analysis. This methods presents a robust and intuitive approach to analyzing vocalizations whose structure consists of self-similar pulses. In this poster, we present a scalable and parallelizable pipeline for performing single pulse analysis.

This study is indebted to the Macaulay Library of the Cornell Lab of Ornithology for generously allowing us to download and use their frog calls for our research.

Introduction

- Vocalizations play a central role in the study of animal ecology [1,4].
- There have been many methods developed for analyzing these vocalizations [1,4,7].
- Early methods focused on simple statistics and vocalization parametrizations [2].
- Modern methods tend to focus on Spectrographic analysis [1].
- There have even been some attempts to integrate machine learning into vocalization Analysis. These have resulted in methods like the WASIS approach [7].
- This study builds on previous work in prior years.
- The basis of this study is Single-Pulse Analysis. This was presented in earlier posters as a new method for approaching repetitive, pulse-like vocalizations by considering individual pulses in their time-domain wave forms as shapes which can be analyzed through a Geometric Morphometric framework [8].
- This method builds on that work.
- Here we develop a full pipeline for Single Pulse Analysis of multiple vocalizations which can be scaled up and is easily parallelizable.

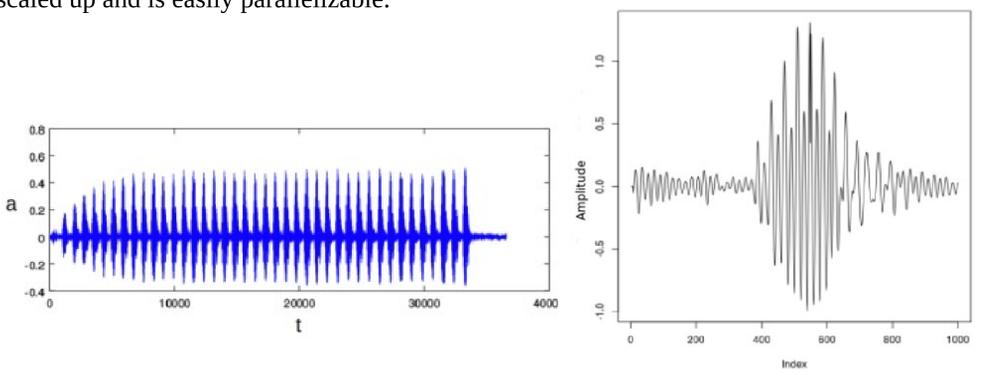


Figure 1: Figure 1 shows a plot of a mating call of *Hyla chrysoscelis* side-by-side with a plot of one of the pulses from a *Hyla chrysoscelis* call.

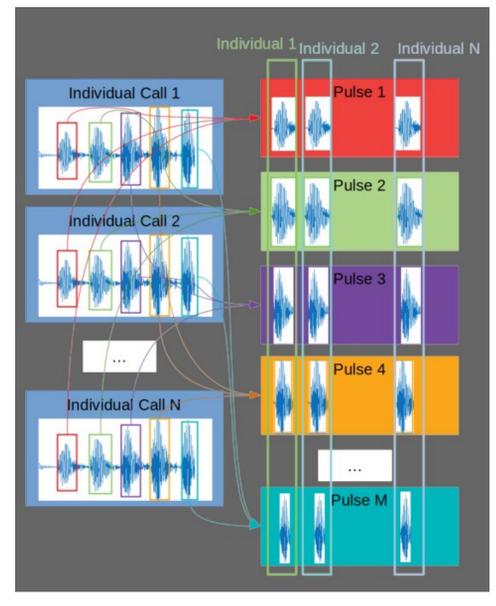


Figure 3: Figure 3 shows the process of re-arranging the extracted pulses from each call into Pulse-Matrices.

Results

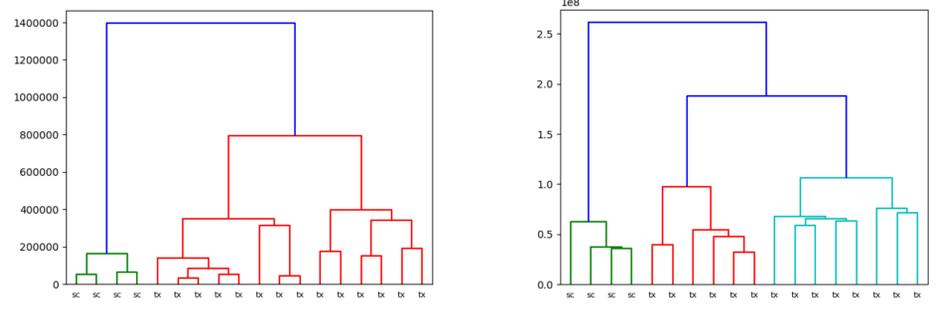


Figure 4: Figure 4 shows a plot of the results of a test of this pipeline. This test was intended to reproduce the results from Gerhardt's classic papers. It shows 2 very clear populations. The figure on the left shows the results using only one pulse from each call while the figure on the right shows the results using all available calls assimilated into a single overall result.

Methods

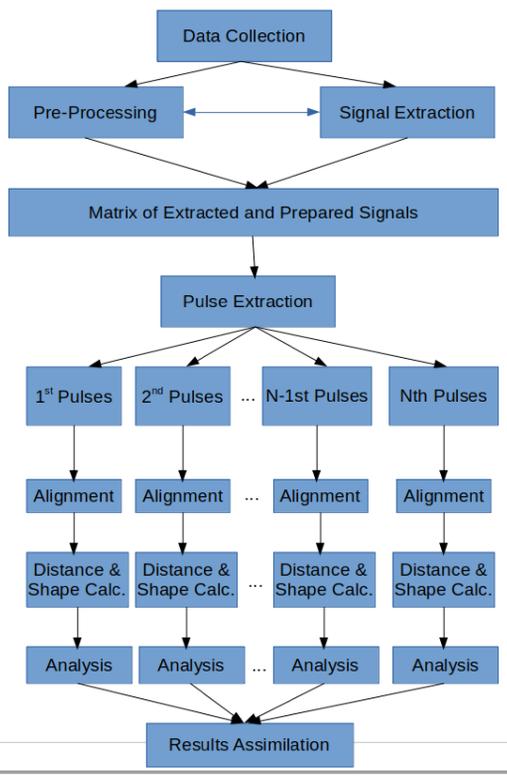


Figure 2: Figure 2 shows a graphical outline of the pipeline being presented in this poster.

- Data was obtained from the MacAulay Library, a subsidiary of the Cornell Lab of Ornithology [2].
- The calls were separated out manually.
- The pulses of each call were extracted using an automated heuristic approach presented in previous posters where a pulse was defined as 1000 timesteps around a peak which itself is defined as the maximum of a neighborhood of points that exceed 4σ of the mean.
- These pulses were then numbered according to their position in the call.
- The pulses were rearranged as in Figure 3 to form Pulse-Matrices.
- These pulses were then aligned using an iterative approach based on Generalized Procrustes Analysis [6].
- From the aligned pulses, a distance matrix was formed for each pulse matrix.
- Clusterings were formed from each distance matrix using Ward's Method.
- These distance matrices were then combined into a weighted average where the weight was based on a method that penalized missing data so that the more data was missing from the matrix, the less influence it would have on the final result.
- The final weighted mean distance matrix was clustered with Ward's Method

Conclusion

- The results demonstrate that this approach works quite well for highly repetitive pulse-like vocalizations.
- The results demonstrated in Dr. Gerhardt's work were faithfully reproduced [4].

Acknowledgements

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