

Sonification of Deep Ocean Microbial Ecology (soniDOME)

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Introduction

The soniDOME Project is a National Academies Keck Futures Initiative (NAKFI) sponsored art-science investigation into novel means to model and experience deep ocean microbial ecosystems, and expand the perceptive foundations of research, all through sound.

We are investigating the sonic display of ecoinformatic data forms to expand current versions of deep ocean information beyond visualizations to explore ecological paradigms and representations of deep ocean microbiology, beginning with sea-ice and deepwater formation in polar regions.

Our work aligns exemplary datasets as sources and structures for sonic transcoding. As an experimental 'reduction to practice' for our methods, a 'master ecological narrative' library of software processes and sound representations is being developed for polar and deep ocean, deep biosphere and mesopelagic microbial ecosystem data sets.

Materials & Methods

This presentation reviews our application of transcoding and sonification processes to the amino acid composition of a long chain fatty acid (LCFA) transport protein (2) of *Colwellia psychrerythraea* 34H (1) as an exemplary dataset for sonic interpretation - one that links sequences and phenotypic data of cold-active bacteria in this genus from sea ice to deep ocean.

Our methods employ custom programming of the visual programming language MAX/MSP (3), for transcoding of amino acids and their physiochemical properties (4) to sonic frequencies. Transcoding of physiochemical properties to frequency include: molecular weight; residue weight ($-H_2O$); acid and base dissociation constants (pKa, pKb, pKx); isoelectric point (pI); and relative hydrophobicity (at pH 2 and 7). The range of frequencies for transcoding of these properties spans 40 Hz to 2000 Hz. In applying transcoding of protein monomers (amino acids) and their properties to sound, we are investigating the use of sonic sensoria for the comparative interpretation of *Colwellia spp.* from cold-active microbial communities in sea ice, the mesopelagic and deep ocean. In prior research (1) *C. psychrerythraea* 34H was selected as a model organism for genomic studies of bacterial cold adaptation.

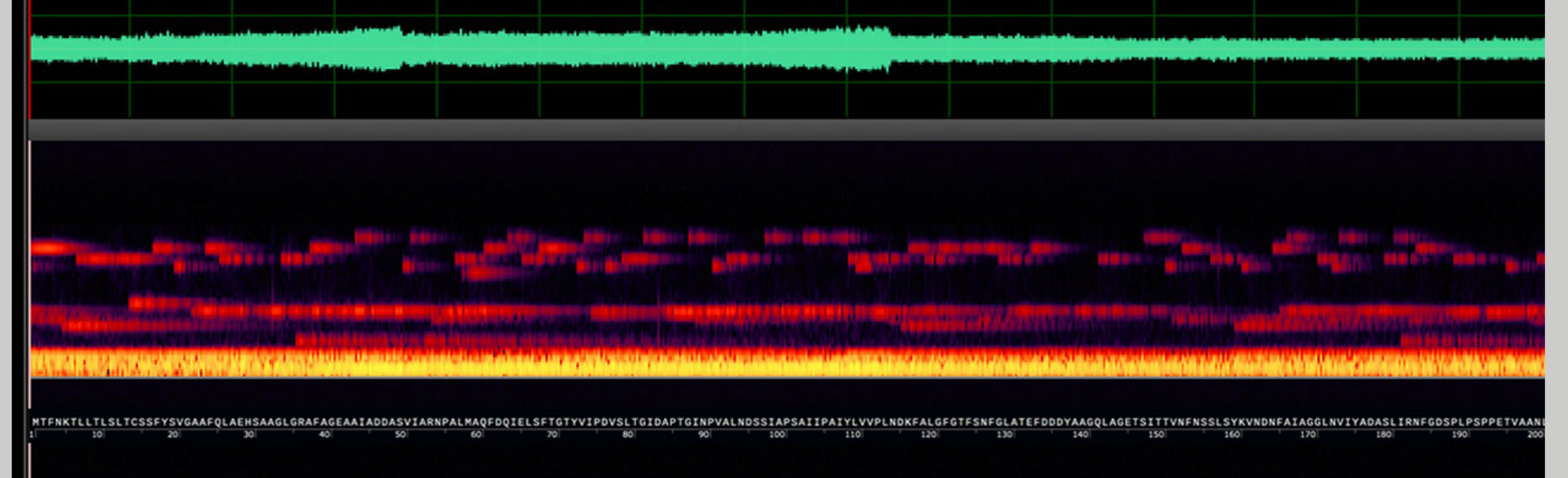
References

- 1) Methe et al (2005), Proc. Nat. Acad. Sci. USA, 102, 10913–10918
- 2) GenBank accession number CP000083.1 (2018). Retrieved from <<https://www.ncbi.nlm.nih.gov/nuccore/CP000083>>
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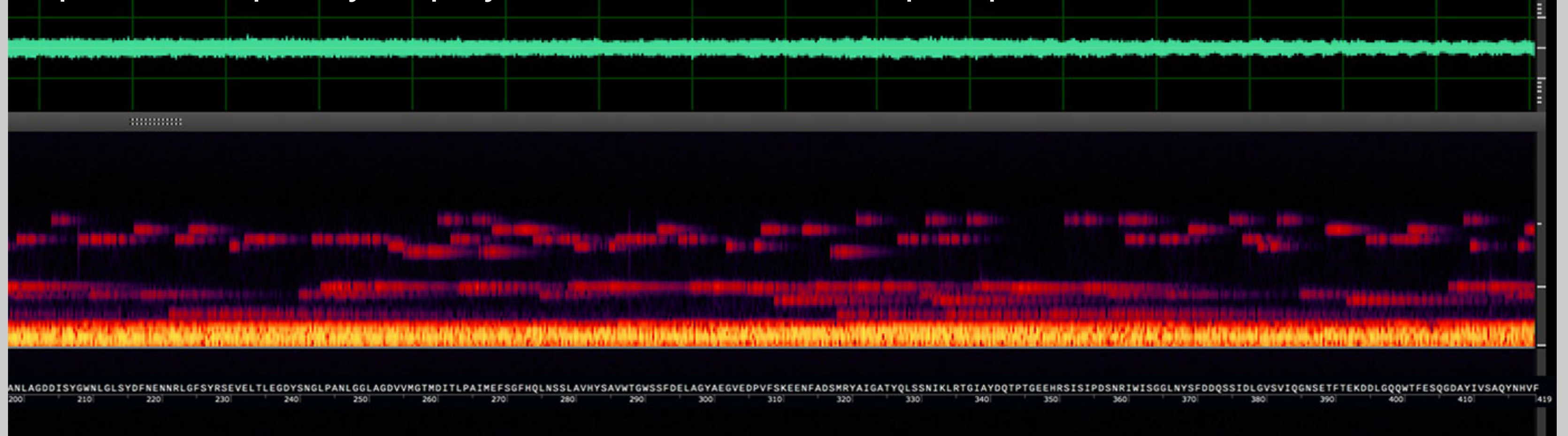
Results

The initial results of this poster publication demonstrate the process of the sonification of a protein of interest through the application of custom-designed and programmed sonification software. Sonic spectrograms, with corresponding reference alignment with the LCFA's transport protein's amino acid sequence, from the software sonification of LCFA transport protein of *C. psychrerythraea* 34H follow.

Spectral frequency display of sonified LCFA transport protein: amino acids 0–200.



Spectral frequency display of sonified LCFA transport protein: amino acids 200–419.



Sound files for online listening are available at: <<https://soundcloud.com/bioticastudio/colwellia-psychrerythraea-34h-lcfa-transport-protein-sonification>>

Conclusions

Transcoding of physiochemical properties to frequency for 22 amino acid monomers of *C. psychrerythraea* 34H LCFA transport protein was accomplished using the visual programming language MAX/MSP. Sonic translations of the equivalent physiochemical properties of sonified amino acid/protein sequences can be run with any of these conditions and remixed into multilayered audio outputs and compositions. By applying this custom software we have the ability to simultaneously listen to multiple equivalents of a wide range of sequence properties with time. Additional variables for sonic conditions include data read speed, frequency range and signal amplitude. Additionally frequency can be audio-filtered and selectively enriched through band pass or notch filtration of the output signals.

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