**Abstract**

* 100-200 word summary of the paper.
* [Here](https://www.nature.com/documents/nature-summary-paragraph.pdf) is a good format to follow.

This paper presents the first complete mitochondrial DNA genome of the jack silverside, an omnivorous fish species found along the Pacific coast. For this study, the specimen was collected from California. The DNA from the tissue archived at the Natural History Museum of Los Angeles County was extracted, sequenced, and analyzed. This process produced around 125 million 150 bp paired-end reads. FastQC and SMART2 were utilized to conduct quality assessment and assembly into a complete mitogenome. A partial sequence of the cytochrome b gene was used as a reference. This study was conducted to enhance the understanding of *A. californiensis’s* evolutionary position in the Atherinpsidae family and to provide insights into its conservation needs and ecological adaptations.

**Introduction**

* Introduce the biological problem and the existing software tools that are available to solve the problem, a subset of the problem, or a closely related problem.
* End the introduction with a brief summary/preview of what you developed.

We have developed a software tool that makes the process of assembling and analyzing marine genomic data more streamlined. The tool simplifies the workflow, making it more accessible to researchers with limited bioinformatics background. The complete source code and documentation is available in the GitHub repository.

* Be sure to include a link to your Project Code GitHub repository.

<https://github.com/rozgaw/MitogenomeAssemblyPipeline.git>

* 1-2 paragraphs

**Implementation**

* Include details about the development of the application/pipeline in ENGLISH (not a list of classes/functions).
* What is your input/output? What programming language(s)/packages/modules did you use? What functionality did you develop? - GetOrganelle (has dependencies - list bowtie and spades and etc), MitoFish

We utilized existing tools such as GetOrganelle, which requires dependencies such as Bowtie for indexing and aligning sequences, and SPAdes for genome assembly. Additionally, we used MitoFish, a mitochondrial genome database for fish, to aid in the annotation and comparison of our assembled genomes.

* How did you evaluate accuracy and/or complexity?

**Results and Discussion**

* Show results run on test data.
* Include 1-2 figures and/or tables as appropriate.
* How does your project improve what was known/done previously?
* Describe the limitations of your application. How could the tool you developed be improved in the future?

Full paper is 2 pages maximum (1000-1300 words), not including the References.

**References**

* References cited in the text must be listed at the end. References should be formatted using the NLM/ICMJE Style, which is used by [PLOS journals](http://journals.plos.org/plosone/s/submission-guidelines#loc-references). Use a free reference manager like Zotero or Mendeley to help.