**Abstract**

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

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