Identification of Conserved Regions in CRISPR protein family

Christine Baek
Computational Biology
Carnegie Mellon University
baek@cmu.edu

Qi Chu
Computational Biology
Carnegie Mellon University
qchu@andrew.cmu.edu

Yanyu Liang
Computational Biology
Carnegie Mellon University
yanyul@andrew.cmu.edu

***Abstract*—The abstract goes here.**

I. Introduction

This demo file is intended to serve as a "starter file" for IEEE conference papers produced under LaTeX using IEEEtran.cls version 1.8b and later. I wish you the best of success.

mds

August 26, 2015

A. Subsection Heading Here

Subsection text here.

1) Subsubsection Heading Here: Subsubsection text here.

II. Methods

We used 3 differenr approaches .. blahblahblah. All used the same .fa sequence, etc. etc. talk about the data itself here, and why we used 3 different methods.

A. Sequence Alignment using Dynamic Programming

1) Model & Algorithm Overview: talk about overview of what the method does (method itself, not in detail of how you used it)

2) Pros and Cons: of using the method - what is it capable of, what are the limitations ?

3) Protocol: implementation details - justifications for decisions you made when you ran the experiment, parameters, etc.

4) Analysis: Discuss METHOD for analysis, not the actual result/analysis itself.

B. Gibbs Sampling

1) Model & Algorithm Overview: talk about overview of what the method does (method itself, not in detail of how you used it)

2) Pros and Cons: of using the method - what is it capable of, what are the limitations ?

3) Protocol: implementation details - justifications for decisions you made when you ran the experiment, parameters, etc.

4) Analysis: Discuss METHOD for analysis, not the actual result/analysis itself.

C. HMM

1) Model & Algorithm Overview: talk about overview of what the method does (method itself, not in detail of how you used it)

2) Pros and Cons: of using the method - what is it capable of, what are the limitations ?

3) Protocol: implementation details - justifications for decisions you made when you ran the experiment, parameters, etc.

4) Analysis: Discuss METHOD for analysis, not the actual result/analysis itself.

III. Results

IV. Conclusion

The conclusion goes here.

Acknowledgment

The authors would like to thank...

References

[1] H. Kopka and P. W. Daly, *A Guide to LaTeX*, 3rd ed. Harlow, England: Addison-Wesley, 1999.

[2] K. S. Makarova, Y.I. Wolf, O.S. Alkhnbashi, E.V. Koonin et al., *An updated evolutionary classification of CRISPR-Cas systems* http://dx.doi.org/10.1038/nrmicro3569