

Identification of Conserved Regions in CRISPR protein family

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Abstract

The abstract goes here.

I. INTRODUCTION

TODO: Christine : brief intro

A. CRISPR/Cas

TODO: Christine writes about CRISPR bg Subsection text here.

B. Past Approaches

TODO: Qi : summarize the HMMer approach?

C. Approaches in This Paper

TODO: everyone?

D. Goal of Paper

TODO: Yanyu : short discussion of our goal in this paper

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. **TODO:** Christine : fill in this section, and why protein sequence

A. Data Retrieval

TODO: Qi : talk about source of data

B. 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.

C. 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.

D. 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

Individual results for each

TODO: put in appropriate figures, and any analysis for each

A. *Sequence Alignment using Dynamic Programming*

B. *Gibbs Sampling*

C. *HMM*

IV. CONCLUSION

TODO: we need to do this one together

TODO: please include any other resources or papers you referenced

REFERENCES

- [1] H. Kopka and P. W. Daly, *A Guide to L^AT_EX*, 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>