Identification of Conserved Regions in CRISPR protein family

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Abstract

The abstract goes here.

I. Introduction

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mds
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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.

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