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A Flexible Framework for Determining Weighted Genome Rearrangement Distance

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EVALUATION

Q 1 Please summarize the main findings of the study.



Reviewer 1 | 28 Jun 2020 | 20:47

#1

This manuscript addresses the problem of determining the weighted rearrangement distance between two genomes. The authors describe their approach as a "path deformation" in the genome space, where the minimal-distance path corresponds to the one with minimal weight sum. To find the path with minimal distance between the genomes, they construct an initial path between them. Then, this path is modified using a library of "rewriting rules" that was generated when constructing the initial path. Their approach relies on the fact that the set of inversions can be regarded as a rewriting system, and then by the use of the Knuth–Bendix Algorithm can be transformed into a confluent rewriting system (assuming that the rearrangement operators are invertible!). Thus, the path with minimal weight is guaranteed to exist regardless of the initial path and can be found by the Knuth–Bendix algorithm.

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Q 2 Please highlight the limitations and strengths.



Reviewer 1 | 28 Jun 2020 | 20:47

#1

I think this manuscript presents an interesting framework that can be used to calculate the weighted rearrangement distance. However, it seems their approach so far is only applicable for small examples. They admit that this because of the lack of software that is optimized for the type of tools needed for their approach and also because their approach is only applicable to models involving inversions and translocations but not insertions and deletions. Nonetheless, as a theoretical framework and as a proof of concept, I still think that a revised manuscript is publishable.

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Q 3 Please comment on the methods, results and data interpretation. If there are any objective errors, or if the conclusions are not supported, you should detail your concerns.

Reviewer 1 | 28 Jun 2020 | 20:47

#1

1. What is the complexity of the approach? Can you comment on the complexity of the Knuth–Bendix Algorithm? Also, is the path with minimal weight unique?
2. How large is the genome space? This framework was tested only in very short examples (of seven regions?) Would that be a genome with seven genes?

Add comment

Q 4

Check List

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#1

- Is the English language of sufficient quality?
- Yes
- Is the quality of the figures and tables satisfactory?
- Yes
- Does the reference list cover the relevant literature adequately and in an unbiased manner?
- Yes
- Are the statistical methods valid and correctly applied? (e.g. sample size, choice of test)
- Not Applicable
- Are the methods sufficiently documented to allow replication studies?
- Yes
- Are the data underlying the study available in either the article, supplement, or deposited in a repository? (Sequence/expression data, protein/molecule characterizations, annotations, and taxonomy data are required to be deposited in public repositories prior to publication)
- Not Applicable
- Does the study adhere to ethical standards including ethics committee approval and consent procedure?
- Not Applicable
- Have standard biosecurity and institutional safety procedures been adhered to?
- Not Applicable

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Q 5

Please provide your detailed review report to the editor and authors (including any comments on the Q4 Check List):

Reviewer 1 | 28 Jun 2020 | 20:47

#1

- I suggest that the authors address the following comments before publication.
- Major Revisions:
1. What is the complexity of the approach? Can you comment on the complexity of the Knuth–Bendix Algorithm? Also, is the path with minimal weight unique?
2. I suggest to change or remove the adjective “flexible” from the title. The way it is described in the manuscript, this framework might not be very flexible as it is only applicable to models involving inversions and translocations but not insertions and deletions. Maybe it could be changed to “A group–theoretic framework for ...”.
3. The abstract is not very informative about the approach. It just says that they use the theory of rewriting systems and exploit the Knuth–Bendix algorithm. Adding a brief description of how they use these tools would be helpful.
- Minor Revisions:
1. In line 121, is says “For genomes π_1 and π_2 , if there is ... such that, where ... , and so on”. It seems this statement is incomplete. Were you trying to define something?
2. What is Γ in definition 3.1? It is not described until later in Section 4.
3. How large is the genome space? This framework was tested only in very short examples (of seven regions?) Would that be a genome with seven genes?
4. When constructing a library of rules for alternate paths, can you use dynamic programing to find the least weighted path.

Add comment

QUALITY ASSESSMENT

Q 6

Originality



Q 7

Rigor





Q 8

Significance to the field

Q 9

Interest to a general audience

Q 10

Quality of the writing

Q 11

Overall quality of the study

REVISION LEVEL

Q 12 What is the level of revision required based on your comments:

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#1

Moderate revisions

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