Homework for June 26, 2014

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Abstract

This is the homework for June 26, 2014. It contains a description of the comparison of different SAM files. It also contains hypotheses for why the given SRA82660 sequences do not map to chromosome 7 (linkage group VII) of the *Neurospora crassa* species.

1 Acknowledgements*

I acknowledge that I have collaborated with my project teammates Diana Medina and Selene Howe to complete this homework. Specifically, we discussed some hypotheses.

I also acknowledge the help that I have received from the course instructor, Prof. Rodolfo Aramayo, in getting back to my queries about the source of the reference sequence for the *Neurospora crassa* species that was provided to us on Tuesday.

Lastly, I want to thank Ms. Tess L. Pham from the Tutor Zone at Evans Library, which is run by the Academic Success Center at Texas A&M University. Ms. Pham has tutored me about the basics of genetics and gave me feedback about the hypotheses which I proposed. I also want to thank Ms. Priyadharshini Venkat, my classmate for this course, for giving me feedback about my hypotheses and helping me to find alternate golden models for the *Neurospora crassa* species.

2 Comparison of different SAM files

Different types of SAM files have to be compared. Their differences are only based on the different combinations of -v and -m selected, or different combinations of -n and -m selected for -Bowtie [2].

The different combinations of these -v, -n, and -m options of -Bowtie are:

- 1. -v1 -m1
- 2. -v1 -m100
- 3. -v3 -m1
- 4. -v3 -m100
- 5. -n1 -m1
- 6. -n1 -m100

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7. -n3 -m1
8. -n3 -m100
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The -v option is used to determine the number of alignments that have no more than "v" mismatches. This addresses global alignments, where a sequence is matched with another. The -m option reports alignments with a maximum of "m" repeats. The -n option reports alignments with a maximum of "m" repeats. This addresses local alignments, where a region in a sequence is matched with another region in the sequence [1].

3 Hypothesis: SRA82660 sequence is not part of the $Neu-rospora\ crassa\ {f genome}$

A hypothesis is that the SRA82660 sequence is not part of the *Neurospora crassa* genome. That is, it belongs to another species. Proceedure 3

Test if SRA82660 sequence is part of the $Neurospora\ crassa\ {\it Genome}(Golden/ReferenceModel)$

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# Golden/Reference Model
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- $1 \quad \textbf{if} \ [\text{given SRA82660 subsequence does not map to golden model}]$
- 2 Conclusion: The given SRA82660 subsequence is not part of the *Neurospora crassa* species.
- 3 elseif [given SRA82660 subsequence maps to golden model]
- 4 Conclusion: The given SRA82660 subsequence is part of the genome.

6 return

5

References

- [1] Rodolfo Aramayo. Small reads genome mapping 101. Available online from the course Wiki of BIOL 689 Digital Biology at: https://geiger.tamu.edu/gitlab/raramayo/digitalbiology/wikis/05Lecture/SRGenome_Mapping_101.md; June 24, 2014 was the last accessed date, June 24, 2014.
- [2] Ben Langmead and Cole Trapnell. Bowtie: An ultrafast memory-efficient short read aligner. Available online from SourceForge at: http://bowtie-bio.sourceforge.net/index.shtml; April 2, 2014 was the last accessed date, March 14 2014.

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