

# 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.

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## 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

[1]

### 3 Hypothesis: SRA82660 sequence is not part of the *Neurospora crassa* genome

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

```

TEST IF SRA82660 SEQUENCE IS PART OF THE Neurospora crassa GENOME(Golden/ReferenceModel)
// Golden/Reference Model
1  if [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.
5
6  return

```

## 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](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.