

## Clinical and Research Genomics Assignment #2

From Lecture\_04-05 (April 5<sup>th</sup>):

### RNA-Sequencing, Single-cell Expression, Epitranscriptomes, and Gene Fusions

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**Assignment: Answer questions about RNA-sequencing and their methods**

**Due before 4/15/2022 5PM**

This week has two sections: short-answer questions and a data exercise.

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#### **Tutorial and Problem Sets:**

Complete the tutorial and exercises 'Using Seurat with Multimodal Data'

[https://satijalab.org/seurat/articles/multimodal\\_vignette.html](https://satijalab.org/seurat/articles/multimodal_vignette.html)

#### **Questions:**

State whether the statement is true or false, then explain with one sentence:

- 1) There are 20 types of RNA present in cells.
- 2) Once spliced and 5' capped, an RNA is no longer modified.
- 3) Gene fusions identified by RNA sequencing always correspond to rearrangements in the DNA as well.

#### **Essay Questions:**

- 1) If you were designing an experiment with RNA-Sequencing for each sample:
    - a) How much sequencing is required to assay each sample?
    - b) What are the parameters that affect this depth of sequencing?
    - c) How would you calculate an expression value?
    - d) Which is your favorite RNA consortium, and what project would you like to pursue?
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**Please hand the assignment on the day of the lecture, or email if you cannot attend.**

**For any questions, please contact Chandrima Bhattacharya ([chb4004@med.cornell.edu](mailto:chb4004@med.cornell.edu)), Evan Afshin ([eba2001@med.cornell.edu](mailto:eba2001@med.cornell.edu)), or Professor Mason ([chm2042@med.cornell.edu](mailto:chm2042@med.cornell.edu))**