Homework 1

Total: 10 points

1. DNA sequencing (DNA-seq)

   a. What is the goal of polymerase chain reaction (PCR)? How does PCR relate to/help with DNA sequencing? (0.5 pt)

   b. What role do dideoxynucleotides play in Sanger sequencing? What are the products of replicating **AGACGTAAGCA** with **ddATP**? (1 pt)

   c. How does sequencing-by-synthesis differ from traditional Sanger sequencing with respect to their sequencing procedures? List at least three different aspects and briefly describe each aspect for both techniques. (1 pt)

   d. What are advantages (and potential limitations) of Illumina sequencing vs. Sanger sequencing? List at least two advantages or limitations. (1 pt)

2. Gene expression and RNA sequencing (RNA-seq)

   a. What are typical elements of a gene? (0.5 pt)

   b. Briefly describe how gene expression can be regulated at the transcriptional level by transcription factors and at the translational level by alternative splicing. (1 pt)

   c. On average, there are around 8 exons per gene. For a gene with 8 exons, assuming that all possible combinations of exons can be read through into proteins, how many types of proteins could potentially be made? (0.5 pt)

   d. For the same gene, if exactly 5 exons are to be retained in the final transcript, how many types of proteins can be made? (0.5 pt)

   e. What does RNA-seq measure? (0.5 pt)

   f. Choose the right sequencing technique (RNA-seq or DNA-seq) to measure each of the following: 1) genes that are differentially expressed between two individuals, 2) genetic variation across two species, 3) alternative splicing sites. (0.5 pt)

   g. Briefly describe the experimental procedure of RNA-seq. (1 pt)

3. Online tutorial 1: Linux environment setup

Please go through Tutorial 1 and make sure you set up Linux environment (for Windows users) and install Miniconda together with several packages. Attach a screenshot(s) for each of the following:

   a. Show the Python path after activating the "rnaseq" environment by using command "which python" (1 pt)
      (Attach here)

   b. Show all the packages you installed for the "rnaseq" environment in Miniconda by using command "conda list" (1 pt)
      (Attach here)