

## CSC 314, Exam I Review

Note: the format of Exam I will be similar to the format of previous Labs, but will also include multiple choice, short-answer, or matching questions. The material will cover biological terms and concepts including inheritance, cells and DNA, nucleotide sequences, protein sequences, gene expression, and python programming.

You will be allowed to bring *one* page of notes (front and back, handwritten or typed) to the exam. A copy of the genetic code (page 13 of the Gene Expression notes) will also be provided. The use of computers will not be allowed.

### Biological concepts

- *Inheritance*
  - Law of Segregation
  - Law of Independent Assortment
  - Alleles
  - Punnet Squares
  - Homozygous vs. Heterozygous
  - Dominant vs. recessive traits
  - Phenotype vs. Genotype
  - Complexities
    - Incomplete Dominance
    - Codominance
    - Multiple Alleles
    - Pleiotropy
    - Epistasis
    - Polygenic Inheritance
  - Chromosomal basis of inheritance:
    - Homologous Chromosomes
    - Linked Genes
    - Sex Determination and Sex-Linked Genes
    - Recombination and crossing over
- *Cells and Cell Structure*
  - Differences between eukaryotic and prokaryotic cells
  - Function of: plasma membrane, nucleus, mitochondria, ribosomes, Golgi apparatus, endoplasmic reticulum
- *Overview of Biological molecules*
  - Polymer vs. Monomer, in DNA and protein
  - Dehydration synthesis vs. hydrolysis
- *Nucleic Acids*
  - DNA vs. RNA, 5' vs. 3'
  - Nucleotide components
  - Complementary base pairing

- *Proteins and protein structure* - primary, secondary, tertiary, and quaternary structure
- *Gene expression*
  - Transcription
    - primary transcript and pre-mRNA
    - sense strand vs. anti-sense/template strand
    - promoter, TATA box, RNA polymerase, direction of transcription
    - RNA processing, introns/exons, 5' cap, poly-A tail
    - Alternative splicing
  - The Genetic Code (including using the table on page 13)
  - Translation
    - tRNA and anti-codons
    - ribosomes: P, A, and E site
    - termination and release factor
    - polyribosome
    - signal sequence
  - Mutations
    - Substitutions: silent, missense, and nonsense mutations
    - Insertions and deletions, frameshift mutations

## **Python programming concepts**

- Printing text or variable values
- User input (*raw\_input* function)
- Arithmetic
- Strings
  - slicing
  - methods/operations – *upper, count, find, in, replace, len*
- *if, elif, else* statements
- defining and using functions
- for loops and *range* function
- reading text from files (*open* function, for loops, reading methods)
- dictionaries
- lists and string immutability

***Note: The questions below are not a comprehensive review, but contain exercises based on concepts that may appear on the first exam. In addition to doing these exercises, you should look over previous labs and your notes.***

1. Assume that for a particular type of dog, brown fur is dominant to white fur. A male who is homozygous dominant mates with a female who is heterozygous.
  - a. What is the probability that a male puppy produced from this union has brown fur?
  - b. What is the probability that a female puppy produced from this union has brown fur?
2. Repeat the previous problem, but assume that fur color is a sex-linked trait (on the X chromosome). The male parent has brown fur and the female is a carrier. Note that dogs have 39 pairs of chromosomes, but the same sex chromosomes (X and Y) as humans.
3. If a male with type AB blood mates with a female having type O blood, what are the possible blood types of the offspring, and what are the expected genetic ratios?
4. Find the complement of the following DNA sequences (make sure to label the 5' and 3' ends)

a. 5'-GCGGTAAGCA-3'

b. 3'-GCGATGAGCA-5'

5. Specify the mRNA sequence that would be transcribed from the following DNA *template* strand:

5'-TCAATGAACGATCAT-3'

6. Assume that the nucleotide in bold was mutated from A->G on the *template* strand.

5'-TCAATGA**A**CGATCAT-3'

Would the resulting mutation be a missense mutation, a silent mutation, or a nonsense mutation? You must justify your answer to receive credit.

7. Write a python script that reads in nucleotide sequences from two files, *sample1.txt* and *sample2.txt*. The script outputs the length of each sequence and then outputs which sequence is longer. Note #1: You may assume that each file contains the sequence and nothing else (i.e., there is no header). However, the sequence may span multiple lines.
8. Write a function in Python that takes a nucleotide sequence as input, and returns a list containing the number of A's, C's, G's, and T's. Note that the sequence may be in either lower- or uppercase. Use this function to output the number of A's, C's, G's, and T's in the sequence AGTGAGAGTAG.
9. Suppose that a python dictionary exists and is of the form

```
translate = {"ATG": "Met", "CUU": "Leu",  
            "UCU": "Ser", "UGU": "Cys",  
            "UGA": "Stop", ...}
```

That is, a key exists for each codon and its corresponding value is the appropriate amino acid determined by the genetic code.

Using the dictionary above, write statements in Python in order to translate an RNA sequence stored in a string named *RNA*.