

Admission Test
Applied Physics - Biomolecular Physics
First Semester 2018

Candidate's Code:

Reminder to the Candidates: The test consists of 10 questions with a value of 1.0 points each, making a maximum value of 5.0 points in the area of physics and 5.0 points in the areas of biological sciences and biochemistry. Candidates who achieved zero in either part of the exam (physics or biological sciences and biochemistry) will be eliminated.

ATTENTION: The candidate must write the test code in the upper right corner of ALL Test sheets.

QUESTIONS OF PHYSICS AREA

Question 1:

Earth spins about its axis resulting in a centripetal acceleration that varies with latitude θ . This acceleration changes local effective gravitational acceleration for different latitudes, leading to an apparent weight for an object. The average radius of Earth is $6,4 \times 10^6 m$ and the gravity of Earth is $g = 9,83 m/s^2$.

- a) Find the expression for centripetal acceleration on Earth in terms of θ .
- b) If centripetal acceleration changes only the magnitude of effective gravitational acceleration (i.e., it does not change its direction in relation to the center of Earth), find the effective gravitational acceleration at the Equator $\theta = 0^\circ$, at $\theta = 45^\circ$ latitude and at the pole $\theta = 90^\circ$.

Question 2:

Karate practitioners know that an expert blow can shatter a concrete block. Consider your hand to have a mass $m = 500g$ to be moving with a speed of $5m/s$ as it strikes the block. In this situation, your hand stops $6mm$ beyond the point of contact.

- a) What impulse does the block exert on your hand?
- b) If collision time is approximately $1,25ms$, what is the average force the block exerts on your hand?

Question 3:

A pendulum consists of a bob of mass m attached to a string of negligible mass and length L . The bob is pulled aside so that the string makes an angle θ_0 with the vertical, and is released from rest. Effects due to air resistance are negligible.

- c) Determine the speed of the bob as it passes through the lowest point of the arc.
- d) Determine the tension in the string as it passes through the lowest point of the arc.
- e) Find the expression for the period of oscillation if the angle θ_0 is small.

Question 4:

Consider the following wave function for a certain standing wave on a string that is fixed at both ends: $y(x, t) = 4,2\text{sen}(0,2x)\text{cos}(300t)$, where y and x are in centimeters and t is in seconds.

- a) What are the wavelength and frequency of this wave?
- b) What is the speed of the transversal waves on this string?
- c) If the string is vibrating in its fourth harmonic, how long is it?

Question 5:

A student wants to make a calorimetry experiment and assembles his own calorimeter with Styrofoam and aluminum. He places 85g of water into the calorimeter. The equilibrium temperature of the system is 17°C . A coin of mass $m = 20\text{g}$ fall inside the calorimeter without being noticed by the student. The student adds extra 85g of water at the temperature of 55°C and the thermal equilibrium is reached at the temperature of 34°C . The specific heat of water is $1\text{ cal/g}^\circ\text{C}$.

- a) Without noticing the coin, what is the heat capacity of the calorimeter determined by the student?
- b) If actual heat capacity is $18\text{ cal/}^\circ\text{C}$, find the initial temperature of the coin. The specific heat of the coin is $0,2\text{ cal/g}^\circ\text{C}$.

BIOLOGICAL SCIENCES AND BIOCHEMISTRY QUESTIONS

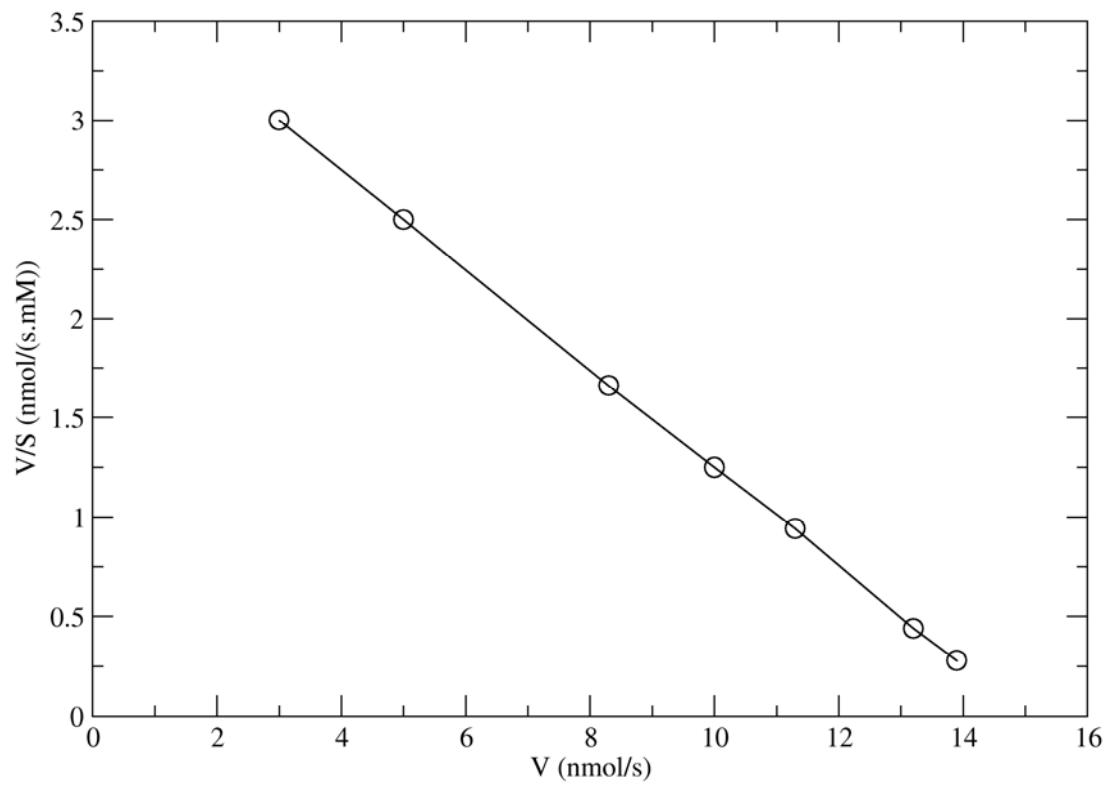
Question 1:

Given the composition of polypeptide chains and the structure of its primary unit, the amino acid, describe the methodology for the separation and characterization of this macromolecule by electrophoresis, as exemplified in the figure below. In your answer, relate the structural features of the macromolecule and its composition to the methodology used for separation and characterization.



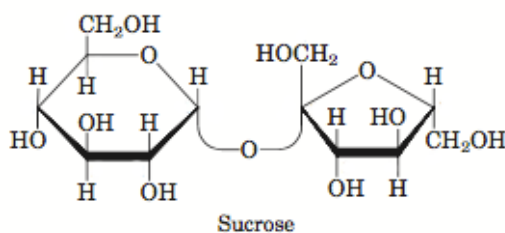
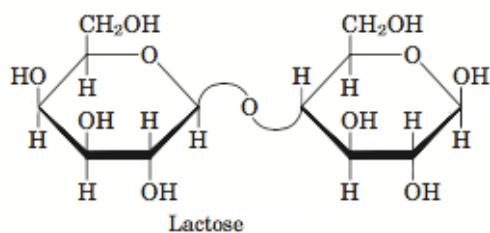
Question 2:

For many enzymes, the kinetics can be described according to the Michaelis-Menten model, which depends of the variables K_M and V_{max} . The data shown in the graph below were obtained for an enzyme following this model. Based on the data in the graph, determine these two kinetic quantities.



Question 3:

The disaccharides lactose and sucrose are formed by units of galactose and glucose and glucose and fructose, respectively. The structures of these disaccharides are shown in the figure below. Describe the glycosidic bonds joining the monosaccharides for these disaccharides and indicate the reducing ends. To indicate the glycosidic bond, use the following abbreviation: Glc((α 1 \rightarrow 1 α)Glc, to indicate, for example, a glycosidic bond between to glucose monosaccharides by carbon atoms at position 1 and with α anomeric conformation.



Question 4:

Regarding the nucleotides and nucleic acids, answer the questions below.

- a) The phosphodiesterases are enzymes that sequentially cleave nucleotides from a nucleotide strand end. Suppose an exonuclease that hydrolyze nucleotides from the 3'-OH end of a oligonucleotide with a free 3'-OH end by cleaving the bond between the 3' hydroxyl group of a ribose or deoxyribose and the phosphate group of the next nucleotide. Suppose that this phosphodiesterase, in particular, is selective and only cleaves a bond just after a purine base. What digestion product(s) would be obtained for a oligonucleotide with sequence (5') GCGCCAUUGC(3')-OH ?

- b) Many eukaryote organisms have specialized systems for the repair of the G-T mismatches in the DNA. These mismatches are corrected to G-C (instead of A-T). Why do the eukaryote cells developed these specific mechanisms for this particular mismatch? Propose a mechanism to explain your answer.

Question 5:

The plasma membrane is basically composed of proteins, phospholipids and sterols. For the bacteria *E. coli*, the protein content can reach as much as 75% of the membrane weight. Many proteins involved in cell signaling are integral proteins. Given that the membrane thickness is around 30 Å and given structural properties of proteins, describe the methodology typically used for the prediction of the topology of integral proteins based on the amino acids sequence, relating the methodology described with the properties of the macromolecules.

