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Part I: Short Answer Questions (48 pts)

Short written answer/short calculation questions – I'll be looking for key words, diagrams and/or calculations that backup your answers in this section. *Responses to each question in this section should typically be less than one bluebook page*.

1. (6 pts) A correlation for male body density, ρ , in g/cm³ is given by the equation:

$$\rho = 0.0277 W^{-0.3} H^{0.725} + 0.75$$

where W is mass in kg and H is height in cm. Modify this equation, maintaining the general form

 $\rho = (\text{constant 1})W^{-0.3}H^{0.725} + (\text{constant 2})$

so that W may be plugged-in with units of lbm and H may be plugged-in with units of inches to yield ρ in g/cm³. [Note: 1 kg = 2.2 lbm and 1 inch = 2.54 cm]

$$\rho = 0.0227 \left((Win \ lbm) \left\langle \frac{1 \text{kg}}{2.2 \text{lbm}} \right\rangle \right)^{-0.3} \left((Hin \ inches) \left\langle \frac{2.54 \text{cm}}{1 \text{inch}} \right\rangle \right)^{0.725} + 0.75$$
$$\rho = 0.05653 (Win \ lbm)^{-0.3} (Hin \ inches)^{0.725} + 0.75$$

(4 pts: plugging in conversion factors; 1 pt: constant 1; 1 pt: constant 2 unchanged)

2. (6 pts) For the chemical structures given below, identify each as belonging to one of the following chemical species categories: {lipids/fatty acids} or {proteins/amino acids} or {carbohydrates/sugars} or {nucleic acids/nucleotides}. Give one sentence for each compound that describes the logic supporting your choice of category.



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Compound A: PROTEIN/AMINO ACID (AKA Asp-Phe dipeptide; AKA aspartame). Recognize N terminus and C terminus (although methylated), internal peptide bond, CHON content or amino group – central carbon with sidechain – carboxyl group structure.

Compound B: NUCLEIC ACID/NUCLEOTIDE (AKA cyclic AMP).

Recognize generic phosphate – 5-carbon sugar – nitrogenous base structure. Compound C: CARBOHYDRATE/SUGAR(AKA starch).

Recognize $C_nH_{2n}O_n$ stoichiometry or ether-linked cyclic monosaccharides.

Compound D: LIPIDS/FATTY ACID(AKA oxostearate).

Recognize long nydrophobic hydrocarbon chain terminated with a carboxylic acid group.

Compound E: NUCLEIC ACID/NUCLEOTIDE (AKA poly(U) RNA). Recognize polymer of generic phosphate – 5-carbon sugar – nitrogenous base

structure.

Compound F where "R" = compound D LIPIDS/FATTY ACID (AKA palmitoylphosphatidylcholine).

Recognize two fatty acids and a phosphaste derivative of an alcohol attached to a central glycerol molecule.

(0.5 pts for each ID and 0.5 pts for each supporting logic statement)

3. (6 pts) The vast majority of the commonly occurring amino acids are said to be chiral. What does it mean to be chiral and what is it about amino acids that make them chiral?

A chiral molecule has a non-superimposable mirror image (3 pts). This occurs for compounds containing carbon atoms that have four different species bonded to them (sp^3 hybdridization) such as amino acids where the central carbon has an H atom, an amino group, a carboxyl group and a sidechain bonded to it (3 pts).

4. (6 pts) The influenza virus (family Orthomyxoviridae), depending on species, has a genome (the genetic information or hereditary material possessed by an organism) containing about 13,500 single-stranded ribonucleotide bases. This single-stranded RNA is distributed among 8 separate coding strands allowing the virus, upon infecting a cell, to produce 8 different proteins. Use this information to estimate the average molecular weight of the flu virus proteins. You may assume that 95% of the ribonucleotide bases actually code for protein and the average molecular weight of an amino acid is 110 g/mol.

$$(13500nt) \left(\frac{95codingnt}{100nt}\right) \left(\frac{1codon}{3codingnt}\right) = 4275codons$$

$$\left(\frac{4275codons - 8stopcodons}{8gene}\right) = 533.37 \approx 533codons / gene$$

$$\left(\frac{533codons}{gene}\right) \left(\frac{1gene}{1protein}\right) \left(\frac{1aa}{1codon}\right) \left(\frac{110g / mol}{1aa}\right) = 58630g / mol / protein \approx 59000g / mol / protein$$

<mark>(1.5 pt: 3 nt per codon; 1.5 pt: 1 gene per protein; 1.5 pt 1 aa per codon; 1 pt: 59 kDa</mark> answer; 0.5 pt: 2 sig figs)

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5. (6 pts) A growth rate study with a bacterial species at a series of increasing substrate concentrations, S, is performed; the data are reproduced in the table at the right in terms of specific growth rates, μ . Assuming the Monod growth model is a reasonable model for this data, estimate the constant K_s from this data. Report your estimate with its associated units and give the reasoning behind your estimate.

<u>S (g/L)</u>	<u>μ (hr⁻¹)</u>
11	0.53
14	0.69
20	1.01
57	1.37
103	1.38
199	1.35

From the data, it looks like the specific growth rate maxes out at about 1.37 hr-1. (2 pts) We know from the form of the Monod model, $\mu = \mu_{max}S/(K_s + S)$, that $S = K_s$ when $\mu = \mu_{max}/2$. (2 pts) This looks like it occurs at $S \sim 14$ g/L. So, a rough estimate is $K_s \sim 14$ g/L. (2 pts)

6. (6 pts) If a bacterial culture is undergoing exponential (Malthusian) growth with a specific growth rate $\mu = 0.97$ hr⁻¹, how long, in hours, will it take for the number of cells present to double in number?

 $N/N_o = exp{\mu t} = 2N_o/N_o = exp{0.97t} \Rightarrow \ln 2/0.97 = t = 0.7145 \approx 0.71 hr$

(3 pts: exponential growth eqn; 2 pts: 0.71 hr; 1 pt: 2 sig figs)

7. (6 pts) A person with type 2 diabetes measures their blood glucose concentration using a new glucose meter five times in a row for practice ahead of a meal, resulting in measurements of 95, 100, 155, 95, and 105 mg glucose/dL whole blood. This person needs to determine their blood glucose concentration so that they can fine-tune their mealtime insulin dose. What glucose concentration should they use in figuring their insulin dose? Justify your answer statistically.

The 155 mg/dL measurement seems suspect as it's much different than the other four measurements (2 pts). Apply the Q test to see if 155 mg/dL could be rejected as an outlier.

$$Q = \left(\frac{suspect \ pt - closest \ pt}{full \ spread \ of \ data}\right) = \left(\frac{155 - 105}{155 - 95}\right) = 0.833 > Q_{crit 99\%} = 0.82$$

So by the Q test, the 155 mg/dL can be rejected as an outlier with greater than 99% confidence. (2 pts) So, punt that data point and average the remainders to calculate the glucose concentration:

 $(95 + 100 + 95 + 105 \text{ mg/dL})/4 = 98.75 \sim 99 \text{ mg glucose/dL whole blood.}$ (1 pt: value; 1 pt: 2 sig figs)

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8. (6 pts) A flow diagram for a undergoing patient extracorporeal dialysis is given at the right. The components of interest for this system are red blood cells, albumin (a protein), glucose, urea (a waste product), sodium ions, potassium ions and water. What is the number of independent mass balances that may be written for this system? Justify your answer.



There are 7 different species present (N = 7, $\frac{2 \text{ pts}}{2 \text{ pts}}$) and two different process units (M = 2, $\frac{2 \text{ pts}}{2 \text{ pts}}$). The number of independent mass balances we can write is M×N = $2 \times 7 = 14$ (2 pts).

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Part II: Detailed Questions (52 points)

- 1. (26 pts) The typical elemental composition of *E. coli*, on a dry basis, is 50±4 wt% C, 20±2 wt% O, 14±1 wt% N, 8.0±1.0 wt% H and 3.0±0.7 wt% P. [The atomic masses of C, O, N, H and P are 12, 16, 14, 1 and 31 g/mol, respectively]
 - a. Determine a stoichiometric formula, $C_aO_bN_cH_dP_e$, representing *E. coli* on a dry basis. Scale the formula such that there is one mole of C per mole of cells, i.e. such that a=1.

Let's work on the basis of 100 g dry *E. coli.* (9 pts) (50 gC)(molC/12 gC) = 4.1667 molC \Rightarrow a = 4.1447/4.1667 = 1.000|0 (20 gO)(molO/16 gO) = 1.2500 molO \Rightarrow b = 1.2500/4.1667 = 0.300|0 (14 gN)(molN/14 gN) = 1.0000 molN \Rightarrow c = 1.0000/4.1667 = 0.240|0 (8.0 gH)(molH/1 gH) = 8.0000 molH \Rightarrow d = 8.0000/4.1667 = 1.919|98 (3.0 gP)(molP/31 gP) = 0.0967 molP \Rightarrow e = 0.0967/4.1667 = 0.023|21

Looking at smallest component, P, <mark>(1 pt)</mark> and figuring on 2 sig figs <mark>(1 pt)</mark>, report result as

CO_{0.300}N_{0.240}H_{1.920}P_{0.023} (2 pts)

b. Compute the molecular weight of E. coli on a dry basis using the scaled stoichiometric formula from part a. Report result as the average \pm one standard deviation using propagation of error techniques.

$$\begin{split} \mathsf{MW} &= \Sigma[\text{atomic stoichiometry atom i}](\text{atomic wt atom i}) \quad \begin{array}{l} \textbf{(4 pts)} \\ \text{sum over all atom types} \\ \mathsf{MW} &= \Sigma[(\text{mass atom i of 100 g total})/(\text{atomic wt atom i})/4.1667](\text{atomic wt atom i}) \\ \mathsf{MW} &= \Sigma[(\text{mass atom i of 100 g total})/4.1667] \\ \mathsf{MW} &= (50+20+14+8.0+3.0)/4.1667 = 100|.0/4.1667 = 23.9|9981 \\ \mathsf{MW} \sim 24.0 \text{ g } \textit{E. coli/mol} \end{split}$$

Note least precise masses known to one's place; total mass has 3 sig figs. (1 pt)

For x = f(a,b,c,...), $s^2(x) = (\partial f/\partial a)^2 s^2(a) + (\partial f/\partial b)^2 s^2(b) + (\partial f/\partial c)^2 s^2(c) + ... (2 pts)$ So,

s²(MW) = Σ(∂MW/∂atom i mass of 100g total)²s²(atom i mass) (2 pts) sum over all atom types s²(MW) = Σ(1/4.1667)²s²(atom i mass) = (1/4.1667)²Σs²(atom i mass) s²(MW) = (1/4.1667)² (4² + 2² + 1² + 1.0² + 0.7²) = 1.2954 s(MW) = 1.1|3816 (1 pt)

Match precision of average value (1 pt)

MW = 24.0 ± 1.1 g *E. coli*/mol (2 pts)

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2. (26 pts) In the treatment of acute coronary syndrome ("ACS" - chest pain due to insufficient blood supply to the heart muscle that results from coronary artery disease - also called coronary heart disease), a two-channel infusion pump may be used to deliver heparin (a polysaccharide mixture that reduces blood coagulation) and Integrilin (eptifibatide – a cyclic heptapeptide that inhibits platelet aggregation) to a patient continuously.

Desired doses to treat ACS for an adult male weighing 70 kg are 1000 Units/hr for heparin and 8.25 mg/hr for Integrilin. Integrilin is available as a 100 mL sterile water solution containing 75 mg eptifibatide. Heparin is available as a sterile water solution containing 1000 Units heparin/mL. [There are ~170 Units per every mg of heparin.]

Determine the flow rate of each stream in units of mL/hr and the mass fraction of each component in each stream to treat a 70 kg adult male. [You may assume that all solutions have the density of water.] *Use our seven-step method to solve this problem.*

Label Diagram: (6 pts)



	< U		0 /	0		L I J
h:	0 + (5.8824)	mg h/mL)(md	$ot_{2}/(1000 \text{ mg/m})$	hL) = 5.8824 mg h/	/hr	[eqn 2]
w:	(999.25 mg	w/mL)(mdot ₁)	/(1000 mg/mL)	+ (994.1176 mg w	$m/mL)(mdot_1)/(1000)$	mg/mL)
	= mdot ₃ $- 8$.	25 - 5.8824 n	ng/hr			[ean 3]

T: $mdot_1 mg/hr + mdot_2 mg/hr = mdot_3 mg/hr$ [eqn 4]

DOF Analysis: DOF = 3 unknowns(mdot₁, mdot₂, mdot₃) - 3 equations(3 ind M-bals) = 0 (2 pts)

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Solution Method: (4 pts)

- 1. Solve eqn 1 for $mdot_1$ and $\div \rho_w$ to get volume flow rate in mL/hr
- 2. Solve eqn 2 for $mdot_2$ and $\div \rho_w$ to get volume flow rate in mL/hr
- 3. Solve eqn 4 for mdot₃ and $\div \rho_w$ to get volume flow rate in mL/hr
- 4. Solve for mass fractions by dividing known species mass flow rates by known total stream mass flow rates

Solution: (2 pts)

- 1. mdot1 = 11,000 mg/hr; 11,000 mg/hr/(1000 mg/mL) = 11.000 mL/hr
- 2. mdot2 = 1,000 mg/hr; 1,000 mg/hr/(1000 mg/mL) = 1.000 mL/hr
- 3. mdot3 = 12,000 mg/hr; 12,000 mg/hr/(1000 mg/hL) = 12.000 mL/hr
- 4. stream 1

 $\begin{aligned} x_i &= (0.75 \text{ mg i/mL})(11.000 \text{ mL/hr})/(11,000 \text{ mg/hr}) = 0.00075|0 \\ x_h &= 0 \\ x_w &= 1 - x_i - x_h = 0.99925|0 \end{aligned}$

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stream 2

x_i = 0

x_h = (5.8824 \text{ mg h/mL})(1.000 \text{ mL/hr})/(1,000 \text{ mg/hr}) = 0.00588|24

x_w = 1 - x_i - x_h = 0.99411|76
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stream 3

x_i = 8.25 \text{ mg i/hr/}(12,000 \text{ mg/hr}) = 0.00068|8

x_h = 5.8824 \text{ mg h/hr/}(12,000 \text{ mg/hr}) = 0.00049|0

x_w = 1 - x_i - x_h = 0.99882|2
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smallest concentration (xh in stream 3) sets precision; match in all other streams

Think: <mark>(4 pts)</mark>

- 1. all mdot's and x's > 0, a good thing
- 2. mdot₃ > mdot₁, mdot₂, exiting stream should flow at greater rate than any of the entering streams
- 3. the x_i's and x_h's are small as expected for solutions containing concentrations on the order of milligrams per milliliters; concentrations in stream 3 are diluted with respect to either stream 1 or stream 2 due to the greater flow rate of the exiting stream and presence of only one drug per incoming stream.