Fall 2002 (Przybycien) **42-101 Intro to BME** **NAME: ____________________**

EXAM #1 SOLUTIONS AND GRADING SCHEME

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. *No more than two or three sentences in answer to each question please.*

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

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

where W is mass in kg and H is height in cm. What must the units of the constants 0.0277 and 0.75 be?

Dimensions of 0.75 must match ρ: $0.75 \;[=]\; g/cm^3$ (+3 pts)
Dimensions of $0.0277W^{-0.3}H^{0.725}$ must match ρ:
$0.0277 \;[=]\; (g{*}kg^{0.3})/(cm^3{*}cm^{0.725})$
$[=]\; ((g{*}kg^{0.3})/(cm^{3.725}))\langle 1000\ g/1\ kg\rangle^{0.3}$
$[=]\; g^{1.3}/cm^{3.725}$ (+3 pts)
note that the constant includes the conversion factor of ~7.943 from $\langle 1000\ g/1\ kg\rangle^{0.3}$

2. (6 pts) What is meant by the "oil drop model" of globular proteins?

The hydrophobic amino acids within a protein tend to be in the interior of the protein away from water while the hydrophilic amino acids tend to be on the outside of the protein in contact with water. (+6 pts)

3. (6 pts) Why are phospholipids well-suited for forming cell membranes?

Phosopholipids are amphipathic (+3 pts): they have a hydrophilic head group comprising an alcohol and a phosphate and a hydrophobic tail consisting of two fatty acids. These molecules can form ordered bilayers (+3 pts) with the head groups on the outside and the fatty acid tails in the middle. This bilayer forms an essentially impermeable layer that polar molecules cannot cross without special transport mechanisms; these bilayers can be used by cell to chemically distinguish inside from outside of cell.

4. (6 pts) What is "The Central Dogma"?

The Central Dogma describes the flow of information (+3 pts) within cells. DNA carries the information (+1 pt), in the form of genes coding for proteins, needed to construct cells from generation to generation; mRNA carries working copies (+1 pt) of the genes to ribosomes where the proteins are actually synthesized (+1 pt).

OR:

 DNA → RNA → proteins (+ 6 pts)

5. (6 pts) Suppose you ate a synthetic gelatin made up of poly(D-glycine), i.e. a polymer made up of monomers of D-glycine connected by peptide bonds. What would happen and why?

   This question was supposed to be clever: the body uses only L-amino acids; we don't have enzymes that can recognize and process the D-stereo isomers of amino acids; a peptide comprising D-amino acids would likely pass unprocessed through the gut. However, I must have had my hat on too tightly as I picked glycine, the only non-chiral amino acid (the R-group is "H") of the 20 commonly occuring amino acids, to make up the peptide. Many recognized this error – well done. A gimmie. (+6 pts)

6. (6 pts) I.V. Leeg, a non-CMU biomedical engineer, performs a growth rate study with a bacterial species and a series of increasing substrate concentrations and obtains the following data:

S (g/L)	μ (hr^{-1})
57	1.37
103	1.38
199	1.35
411	1.38

   Iggy is confused by his data. Can you explain this behavior? If the Monod growth model were to be used to describe the growth of this bacterium, could you say anything about the magnitude of the Monod constant K_s?

   The cells are growing as fast as they can (+3 pts); adding more substrate will not make them grow any faster. The variation seen in specific growth rates is probably the result of normal experimental variation and error. When $S >> K_S$ in the Monod model, the cells grow at the maximum specific growth rate; so, $K_S \leq 57$ g/L (+3 pts).

7. (6 pts) A microorganism growing aerobically on glucose exhibits the growth stoichiometry below:

$$C_6H_{12}O_6 + 1.473O_2 + 0.782NH_3 \rightarrow 0.909C_{4.4}H_{7.3}N_{0.86}O_{1.2} + 3.854H_2O + 2CO_2$$

   What is the respiratory ~~coefficient~~ quotient for this organism growing under these conditions?

   The respiratory quotient, RQ, is defined as the ratio of the moles CO_2 produced to the moles O_2 consumed (+3 pts). So, RQ = 2 mol CO_2/1.473 mol O_2 = 1.358 mol CO_2/mol O_2 (+3 pts).

8. (6 pts) Compare the function of a promoter with that of the Shine-Delgarno box.

   A promoter is a DNA sequence upstream of a gene where RNA polymerase binds to begin transcription (+3 pts), making an mRNA copy of the gene; the Shine-Delgarno box is an RNA sequence upstream of the coding region of an mRNA transcript where a ribosome binds to begin translation (+3 pts), making the protein coded by the gene. Both a promoter and the Shine-Delgarno box give and indication of where processing of a nucleic acid should start.

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Part II: Detailed Questions (52 points)

1. (26 pts) Consider the microorganismic growth stoichiometry below:

$$C_6H_{12}O_6 + 1.473O_2 + 0.782NH_3 \rightarrow 0.909C_{4.4}H_{7.3}N_{0.86}O_{1.2} + 3.854H_2O + 2CO_2$$

Cells and glucose are added to a solution such that biomass is present at 1.48 g dry cells/L and glucose is present at 95 g/L. At this glucose concentration, the cells have a specific growth rate of 1.63 hr^{-1}. How long, in hours, will it take the cells to consume 5.0% of the glucose given the stoichiometry above?

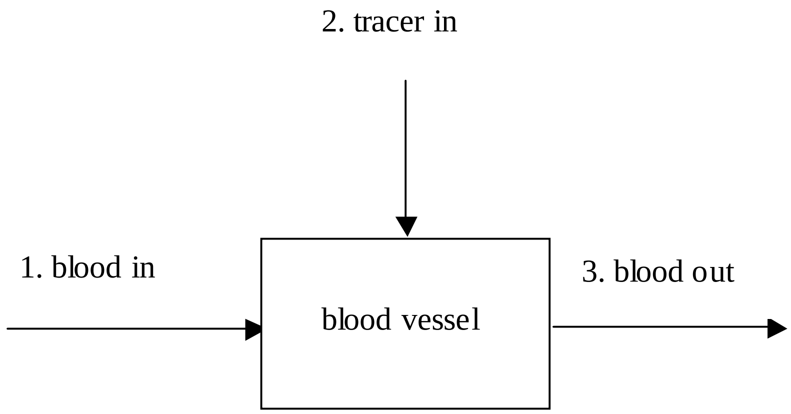
Strategy: 1. find $X(t_{5\%})$ when $S(t_{5\%}) = 0.95S(0)$ via $X(t) – X(0) = -Y_{x/s}(S(0) – S(t))$, will need to find $Y_{x/s}$ from stoichiometry and convert to mass basis using molecular weights of cells and glucose and 2. use Malthusian (exponential) growth kinetics with the specified specific growth rate to determine the time corresponding to $X(t_{5\%})$ via $X(t) = X(0)\exp\{\mu t\}$.

$Y_{x/s}$ = [(0.909 mol X)(4.4*12 + 7.3*1 + 0.86*14 + 1.2*16 g X/mol X)]
÷ [(1 mol S)(180 g S/mol S)] (+8 pts)
= 0.4613 g X/g S

$X(t_{5\%})$ = $X(0) + Y_{x/s}(S(0)–S(t_{5\%})) = X(0) + Y_{x/s}(S(0)-0.95S(0)) = X(0) + 0.05Y_{x/s}S(0)$
(+ 8 pts)
= (1.48 g X/L) + 0.05(0.4613 g X/g S)(95 g S/L)
= 3.6712 g X/L

$t_{5\%}$ = $(1/\mu)\ln\{X(t_{5\%})/X(0)\}$ (+8 pts)
= (1/1.63 hr-1)ln{(3.6712 g X/L)/(1.48 g X/L)}
= 0.5573 hr
≈ 0.56 hr (+1 pt #; +1 pt sig figs)

2. (26 pts) A radioactive tracer experiment is performed in order to measure the flow rate of blood in a blood vessel (stream 3). The concentration of the tracer in the inlet and outlet blood streams is determined via autoradiography. A schematic of the experiment is given below.



Four different experiments were performed:

expt	tracer in flow rate (mL/min)	tracer in tracer conc (ppm)	blood in tracer conc (ppm)	blood out tracer conc (ppm)
1	1.73	4007	345	732
2	1.67	3999	472	847
3	1.69	4013	507	875
4	1.60	4002	523	900

For this set of experiments, determine the average blood flow rate, in mL/min, with 95% confidence limits for stream 3.

Note: there are two components – tracer, and everything else. The tracer inlet stream is not pure (1,000,000 ppm) tracer. With two components, can write three mass balance expressions, any two of which will be independent.

Strategy: 1. Combine mass balances on tracer and total mass to relate blood outlet flow rate to the blood inlet and outlet tracer concentrations and tracer infusion rate. 2. Since we have sets of data that go together, compute an outlet flow rate for each experiment. 3. Average the outlet flow rates and compute a standard deviation. 4. Use Student's t-table to set 95% confidence limits on outlet flow rate.

Balance on tracer

$\Sigma mdot_{in,tracer} = \Sigma mdot_{out,tracer}$

since mass flow rate tracer = total volume flow rate * tracer concentration, balance becomes

$\Sigma Vdot_{in}\ C_{in,tracer} = \Sigma Vdot_{out}\ C_{out,tracer}$

$Vdot_1 C_1 + Vdot_2 C_2 = Vdot_3 C_3$ (+8 pts)

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Balance on total flow

$\Sigma mdot_{in} = \Sigma mdot_{out}$

since total mass flow rate = total volume flow rate * blood density, balance becomes

$\Sigma Vdot_{in}\ \rho_{blood} = \Sigma Vdot_{out}\ \rho_{blood}$

Dividing out ρ_{blood}:

$Vdot_1 + Vdot_2 = Vdot_3$ (+8 pts)

Since we know $Vdot_2$, $C_{1,tracer}$, $C_{2,tracer}$ and $C_{3,tracer}$, combine tracer and total mass balances to obtain:

$Vdot_3 = Vdot_2(C_{2,tracer} – C_{1,tracer})/(C_{3,tracer} – C_{1,tracer})$

Compute $Vdot_3$ for each experiment, then average (+2 pts); measurements in each experiment go together.

#1: $Vdot_3$ = (1.73 mL/min)(4007 ppm – 345 ppm)/(732 ppm – 345 ppm)
= 16.3702 mL/min

#2: $Vdot_3$ = (1.67 mL/min)(3999 ppm – 472 ppm)/(847 ppm – 472 ppm)
= 15.7069 mL/min

#3: $Vdot_3$ = (1.69 mL/min)(4013 ppm – 507 ppm)/(875 ppm – 507 ppm)
= 16.1009 mL/min

#4: $Vdot_3$ = (1.60 mL/min)(4002 ppm – 523 ppm)/(900 ppm – 523 ppm)
= 14.7650 mL/min

Compute mean and estimated standard deviation (+2 pts)

$<Vdot_3>$ = 15.7358 ml/min

$s(Vdot_3)$ = 0.6081 mL/min

Find confidence limits for (N-1) = (4-1) = 3 degrees of freedom at 95% confidence level

C.L. = $s(Vdot_3)t_{3DOF,95\%}$ /sqrt{N} = (0.6081 mL/min)(3.182*)/sqrt{4} (+4 pts)
= 1.3083 mL/min

** note that Student's t-table I gave you from our web links is in error – the 90% confidence column is actually for 95%, the 95% is for 97.5% and the 99% column is for 99.5%. I will remove this link from our site. Value for 3 DOF and 95% confidence should be 2.353.*

Therefore,

$Vdot_3$ = 15.7358 ± 1.3083 mL/min
≈ 15.7 ± 1.3 mL/min (+1 pt #; +1 pt sig figs)