

NSAA Specimen Section 2

Model Solutions





Physics.

1. a. How far away means the displacement.

$$40 \text{ minutes} = 40 \times 60 = 2400 \text{ seconds.}$$

=> By Symmetry the displacement will be zero as the area under the curve is the same above and below the time axis.

$$b. \text{ acceleration} = \frac{\Delta v}{\Delta t} = \frac{-40}{200} = -\frac{1}{5} \text{ ms}^{-2}.$$

$$\Rightarrow v = u + at$$

$$v = 40 + -\frac{1}{5}T \quad T = \text{time after } t = 900s.$$

$$= 40 - \frac{1}{5}(t - 900)$$

$$= 220 - \frac{t}{5}.$$

$$c. \int_{1300}^{1500} v(t) dt = \int_{1300}^{1500} \left(220 - \frac{t}{5}\right) dt$$

$$= \left[220t - \frac{t^2}{10}\right]_{1300}^{1500}$$

$$= (105000) - (117000)$$

$$= -12000m.$$

ii. Area under the line joining B and C (when extended) and the time axis between $t = 1300s$ and $t = 1500s$.





d. when $t = 1000s$, acceleration $= -\frac{1}{5} ms^{-2}$.

$F = ma$ by Newtons second law.

$$= 10000 \times -\frac{1}{5}$$

$= -2000N$. due to the braking forces.

e. when $t = 90s$, acceleration $= \frac{90}{180} = \frac{2}{9} ms^{-2}$.

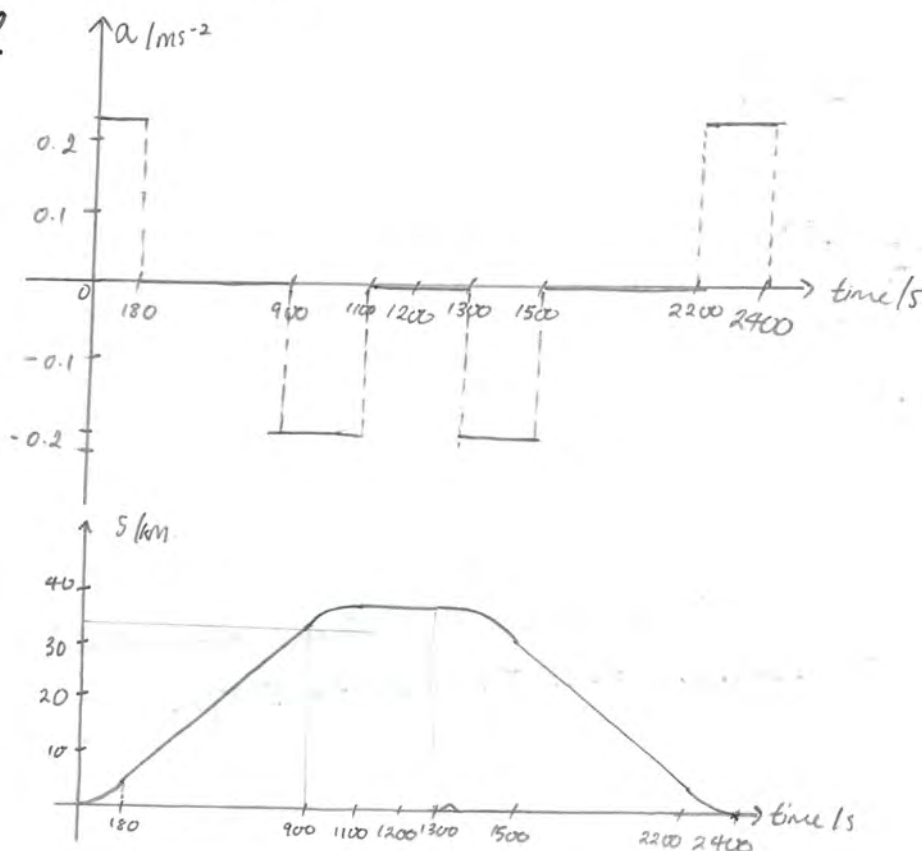
$$F = ma = 10000 \times \frac{2}{9} = \frac{20000}{9} N.$$

$$P = Fv = \frac{20000}{9} \times 920$$

$$= \frac{4000000}{9}$$

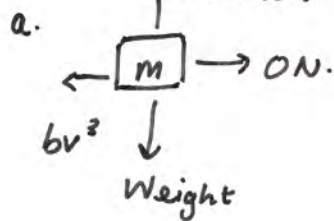
$$= 44.4 kW$$

f.





2. a.



By Newton's Second law \rightarrow :

$$0 - bv^3 = ma$$

$$\Rightarrow ma = -bv^3.$$

b.

$$\text{i. } \int_{v_0}^v \frac{1}{v^3} dv = \left[-\frac{1}{2} v^{-2} \right]_{v_0}^v = -\frac{1}{2v^2} + \frac{1}{2v_0^2} = \frac{1}{2v_0^2} - \frac{1}{2v^2}$$

$$\int_0^t \frac{-b}{m} dt = -\frac{bt}{m}$$

$$\text{ii. } \frac{1}{2v_0^2} - \frac{1}{2v^2} = -\frac{bt}{m}$$

$$\frac{1}{2v_0^2} + \frac{bt}{m} = \frac{1}{2v^2}$$

$$\frac{v^2}{2v_0^2} + \frac{bvt}{m} = \frac{1}{2}$$

$$v^2 \left(\frac{1}{v_0^2} + \frac{2bt}{m} \right) = 1$$

$$v^2 \left(\frac{m + 2btv_0^2}{mv_0^2} \right) = 1$$

$$\Rightarrow v^2 = \frac{v_0^2 m}{m + 2bv_0^2 t}$$





c. $v = \frac{v_0}{2}$

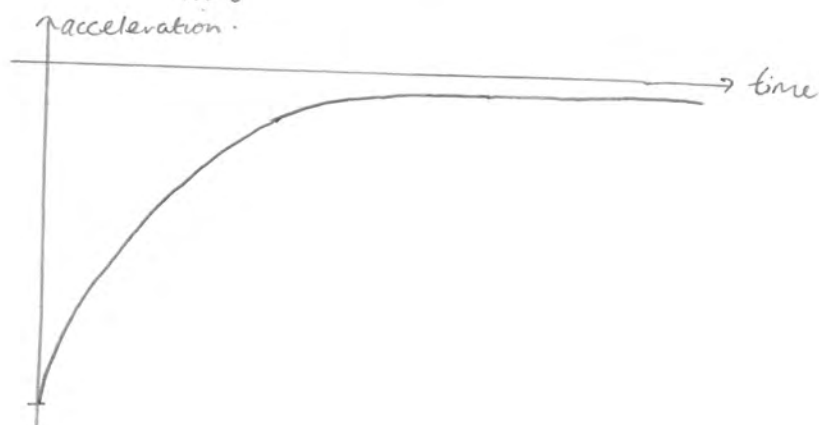
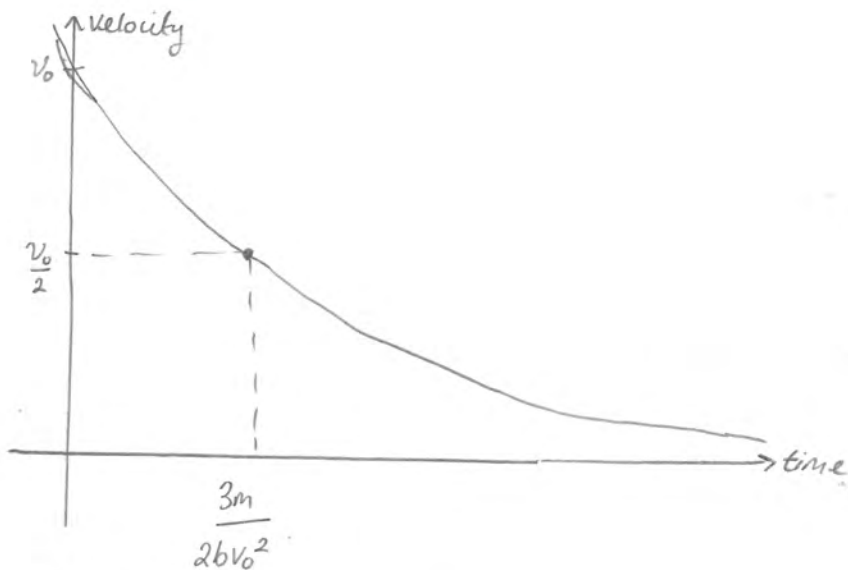
$$\frac{v_0^2}{4} = \frac{v_0^2 m}{m + 2bv_0^2 t}$$

$$\frac{1}{4} = \frac{m}{m + 2bv_0^2 t}$$

$$\Rightarrow 2bv_0^2 t = 3m$$

$$t = \frac{3m}{2bv_0^2}$$

d.

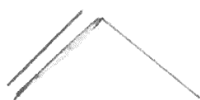
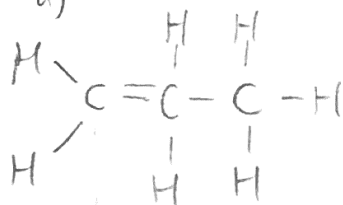




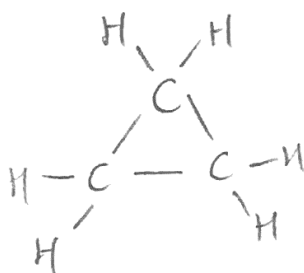
NSAA Specimen Section 2 - Chemistry

Q3

a)

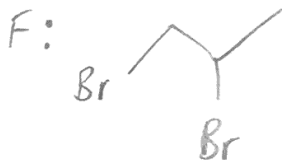


propene
alkene



cyclopropane
cycloalkane

b)



c)



* why - despite there being no UV light, cyclopropane can still undergo addition reactions which result in the ring being broken. This is because the bond angles are 60° rather than 109.5° , so there is more repulsion between bonding pairs, and therefore the system is more stable when the ring is broken

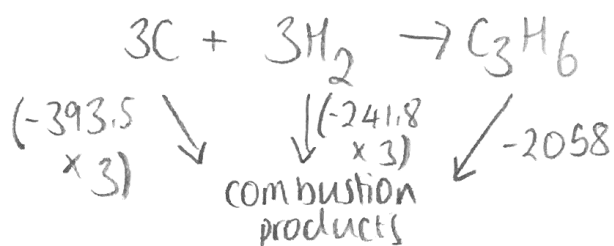


d)

(i)

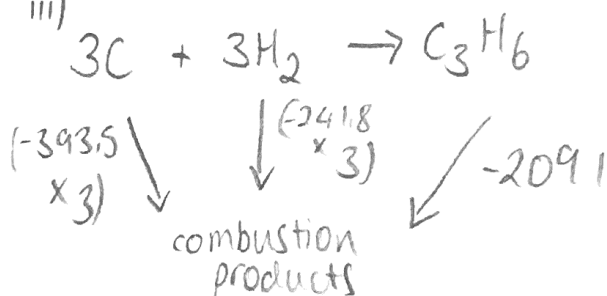


(ii)



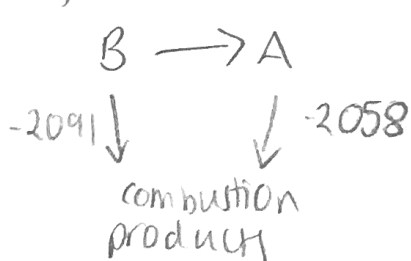
$$-1180.5 - 725.4 + 2058 = \underline{152.1 \text{ kJ mol}^{-1}}$$

iii)



$$-1180.5 - 725.4 + 2091 = \underline{185.1 \text{ kJ mol}^{-1}}$$

iv)



$$-2091 + 2058 = -33 \text{ kJ mol}^{-1}$$

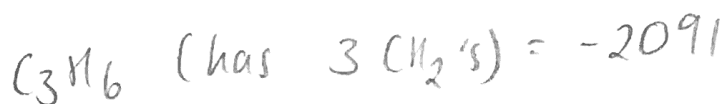
It is negative indicating that energy is released and it is therefore an exothermic reaction. This suggests that A is more stable than B.



e)



$$\frac{-3920}{6} = -653.33 \text{ kJ mol}^{-1}$$

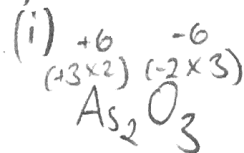


$$\frac{-2091}{3} = -697 \text{ kJ mol}^{-1}$$

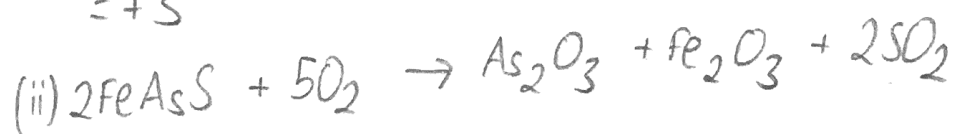
Actual $\Delta_c H^\circ$ can vary depending on the chemical environment of the bonds.

- Q4

a)



$$= +3$$

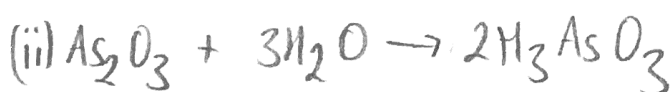


b)

(i)



pyramidal (107°)





iii)

20.6g of As_2O_3 per dm^3

Moles of As_2O_3 (197.84) in $1 \text{ dm}^3 =$

$$\frac{\text{mass}}{\text{mr}} = \text{moles} \quad \frac{20.6}{197.84} = 0.104$$

2 moles of H_3AsO_3 formed from 1 mole of As_2O_3 so

$0.104 \times 2 = 0.208$ moles of H_3AsO_3 in 1 dm^3

$$\frac{\text{mol}}{\text{vol}} = \text{conc} \quad \frac{0.208}{1} = \underline{0.208 \text{ mol dm}^{-3}}$$

c)

(i)

mass of As_2O_3 in 1 dm^3 saturated sol = 20.6g

mass of As_2O_3 in 1 dm^3 dilute sol = $\frac{20.6}{10^{30}}$

$$= 2.06 \times 10^{-29} \text{ g}$$

$$1000 \text{ cm}^3 = 2.06 \times 10^{-29} \text{ g}$$

$$100 \text{ cm}^3 = \underline{2.06 \times 10^{-30} \text{ g}}$$

(ii)

volume needed for fatal dose:

$2.06 \times 10^{-29} \text{ g}$ in 1 dm^3 ($\div 2.06 \times 10^{-28}$)

$$= 0.1 \text{ g} \quad \text{in} \quad \frac{4.854 \times 10^{27} \text{ dm}^3}{4.854 \times 10^{24} \text{ m}^3}$$

=





(ii) continued:

$$\text{km}^3 \xrightarrow{\times 10^9} \text{m}^3$$

$$\begin{aligned}\text{volume of earth} &= 1.08 \times 10^{12} \text{ km}^3 \\ &= 1.08 \times 10^{21} \text{ m}^3\end{aligned}$$

$$\begin{aligned}\text{fraction of volume of Earth needed} &= \frac{4.854 \times 10^{24}}{1.08 \times 10^{21}} \\ &= \frac{4500}{1}\end{aligned}$$

(iii)

mass of As_2O_3 in 1dm^3 of dilute solution:

$$\frac{20.6}{1030} = 2.06 \times 10^{-2} \text{ g}$$

moles of As_2O_3 in 1dm^3 :

$$\frac{2.06 \times 10^{-2} \text{ g}}{197.84} = 1.04 \times 10^{-3} \text{ mol}$$

moles of As in 1dm^3 :

$$1.04 \times 10^{-3} \times 2 = 2.08 \times 10^{-3} \text{ mol}$$

number of atoms of As in 1dm^3 :

$$(2.08 \times 10^{-3}) \times (6.02 \times 10^{23}) = 1.254 \times 10^{21}$$

volume required:

$$\begin{aligned}\frac{1}{1.254 \times 10^{-21}} &= 7.97 \times 10^{20} \text{ dm}^3 \\ &= 7.97 \times 10^9 \text{ cm}^3\end{aligned}$$

bottles needed:

$$\frac{7.97 \times 10^9}{28} = 285000000$$



d)

(i)

$$\text{pH} = 7$$

$$\text{H}^+ = 10^{-7}$$

(ii)

$$1 \rightarrow 1 \div 10^2 = 1 \times 10^{-2} \text{ mol dm}^{-3}$$

$$-\log[1 \times 10^{-2}] = 2$$

$$2 \rightarrow 1 \div 10^6 = 1 \times 10^{-6} \text{ mol dm}^{-3}$$

$$-\log[1 \times 10^{-6}] = 6$$

$$3 \rightarrow 1 \div 10^{10} = 1 \times 10^{-10} \text{ mol dm}^{-3}$$

$$-\log[1 \times 10^{-10}] = 10$$

BUT the pH is 7 as the solution (acidic) cannot become alkaline upon dilution with water





NSAA Specimen section 2- Biology

Q5

- a) Each horizontal line represents the DNA sequence belonging to each organism.
- b) In the place of G there would be C and vice versa. In the place of A there would be U and in the place of T there would be A. This results from complementary base pairing when the mRNA nucleotide form temporary hydrogen bonds with the DNA molecules in transcription.
- c) The sequence of organism 3 is least likely to lead to a functional protein because of the deletion of the G base at position 326, resulting in a frame shift mutation. All the codons after this point would code for a different amino acid, resulting in a different primary structure. As the R groups would be in different places, different bonds (hydrogen, ionic, disulfide) and interactions (hydrophobic, hydrophilic) would occur leading to a different tertiary structure. As the function of a protein depends on the specificity of its structure, it is unlikely that the part of the protein that is determined by this sequence will function.
- d)
- (i) Organisms 4 and 5 or 4 and 6 are most closely related to each other as there is only one difference between the sequences in each of the pairs (C instead of T in organism 5 and T instead of A in organism 6). The lack of mutations leading to differences in their sequences in comparison to those of other organisms indicates that the least amount of time has passed since these organisms had a common ancestor.
- (ii) Organisms 3 and 1 or 3 and 5 are least related to each other as they have the greatest number of differences between their sequences (24). This indicates that a long period of time has passed since they had a common ancestor, as many mutations have accumulated in their sequences.





e) The three domains of life are eukaryotes, bacteria and archaea. There are many places where organisms 1 to 6 have the same base but it is different in the sequence of organism 7, suggesting that organism 7 may belong to bacteria or archaea.

f) The differences in these sequences may have arisen from germ line or somatic cell mutation. A mutation is a change in the order of bases on a DNA strand, which can be a point or a frameshift mutation. In the sequences that are very similar, a point mutation will have occurred as only one codon is different. This mutation may be silent (same amino acid coded for), missense (different amino acid coded for) or nonsense (codon becomes a termination triplet). However, it is evident that a frame shift mutation has occurred in the sequence of organism 3 as the deletion of base G has resulted in the codons following the mutation being affected. Mutations create variation between organisms as if they are not silent a different amino acid will be coded for in translation, therefore leading to a protein with a different tertiary structure, which consequently affects its function.

If the mutation has occurred in the germline cells and can, as a result, be passed on to offspring, evolutionary consequences arise depending on whether the mutation was beneficial. Natural selection will occur if the mutation resulted in a characteristic that combats a selection pressure, increasing the chance of survival for an organism. This will mean it is more likely to reach breeding age, where it will pass on the beneficial characteristics to its offspring. This will continue over many generations and the frequency of the allele will increase within the population. If the norm or average phenotype is advantageous, stabilising selection takes place. In comparison, when the extremes are positively selected for it is disruptive selection. If a mutation becomes beneficial as a result of a change in the environment and the most common phenotype is no longer advantageous, directional selection takes place. Sexual selection may occur if the mutation results in an allele coding for a characteristic that improves mating success.



In comparison, genetic drift can occur. This is more common in small populations as the appearance of a new allele has a greater impact.

Mutations cause variation by increasing the number of alleles in the gene pool, allowing species to adapt and change over time. Differences between the sequences in different organisms are present because of the selection pressures they are exposed to, which allows the evolution of different species to converge and diverge over extended periods of time.



Q6

- a) Organisms are classified as being in the same species if they can mate with each other to produce fertile offspring. I would carry out an experiment which would involve mating each of the snails with each other - if fertile offspring were produced (can breed with each other) then they belong to the same species.
- b) Natural selection is the mechanism by which the proportion of beneficial alleles within a population increases because the phenotype they result in provides a survival advantage. Stable polymorphisms are relatively rare because certain selection pressures such as specific predators are constantly present. In most cases one phenotype increases the chance of survival more than another, leading to directional selection. The most advantageous allele becomes the most common, and as a result variation is not maintained.
- c) Variation is maintained as the most common phenotype is not the most advantageous. As birds develop better search images of the most abundant forms, those with the most common phenotype are less likely to survive and reach breeding age. This means those with the rarer phenotypes suffer less predation, are more likely to survive and the alleles are selected for. This results in this phenotype becoming more common, leading to the birds developing better search images of them. This cycle continues resulting in the variation in snail shells being maintained.
- d)
- | | |
|--------------|----------------------------|
| B - unbanded | F1 genotypes: 100% Bb |
| b - banded | F1 phenotypes: 100% banded |
- | | | |
|---|----|----|
| | B | B |
| b | Bb | Bb |
| b | Bb | Bb |



e)

	B	b
B	BB	Bb
b	Bb	bb

F2 genotypes: 25% BB $\frac{1}{4} \times 240 = 60$
 50% Bb $\frac{1}{2} \times 240 = 120$
 25% bb $\frac{1}{4} \times 240 = 60$

F2 phenotypes: 75% unbanded (BB, Bb) = 180
 25% banded (bb) = 60

f)

The null hypothesis for this study would be that there is no statistically significant difference between the proportions of pink, banded snails in habitat A and habitat B. I would carry out the mark and recapture method on the pink, banded snails and the other snails in the two areas.

The dependent variable is the proportion of pink, banded snails and the independent variable is the habitat. Many variables need to be controlled to ensure that the habitat is the only factor affecting the difference in proportions, maintaining the validity of the study. There would include the day and time the experiment was carried out on in the different habitats, the type of non-toxic paint used to label them, the individual classifying the snails as being pink and banded, and the size of the area the snails were collected from, because they would all affect the dependent variable. To carry out the experiment I would spend the same, suitable amount of time in each area (depending on the size) catching pink, banded snails and other snails, recording the numbers in a table. To reduce bias regarding what is a pink, banded snail I would use a key. I would mark them all with non toxic paint (the minimum amount to avoid increasing the chances of being eaten) and release them back into the wild. One day later at the same time I would spend the same length of time catching pink, banded snails and other snails. I have chosen this short time interval to limit the bias created through assuming that this is a closed population - it reduces the chance that individuals will be born, die or emigrate.





Doing separate calculations for the two groups I would use the formula $\frac{1^{\text{st}} \text{ sample} \times 2^{\text{nd}} \text{ sample}}{2^{\text{nd}} \text{ sample previously marked}}$ to estimate the population

size. This would allow me to find the proportion of the pink banded snails in the snail population. I would repeat the test over many weeks to calculate the average population size and therefore proportions over the period of time - these repeats would make the calculations more accurate because it would reduce the effect of outliers.

On a bar graph I would have one bar representing the average population size of pink banded snails and one representing the average population size of the other snails for each environment. Using the standard deviation values calculated from the repeats and plotting them as bars I can see whether the results are statistically different or not.

