Grant Messner
Section 2

Bi 1 HW 3

1a)

N_k: $\boldsymbol{\frac{dN_k}{dt} = -\lambda N_k}$

N_{Ar}: $\frac{dN_k(0)}{dt} = \frac{dN_k}{dt} + \frac{dN_{Ar}}{dt} = 0$

$$\frac{dN_{Ar}}{dt} = -\frac{dN_k}{dt} = \lambda N_k$$

$$\boldsymbol{\frac{dN_{Ar}}{dt} = \lambda N_k}$$

These expressions are related by the fact that $\frac{dN_k}{dt} + \frac{dN_{Ar}}{dt} = -\lambda N_k + \lambda(N_k(0) - N_{Ar}) = \lambda(N_k(0) - N_{Ar} - N_k) = \lambda(0) = 0$, which makes sense because the any decrease in N_k is matched by an increase in N_{Ar}, so there is no net change.

1b) $N_k(t) = N_k(0)e^{-\lambda t}$

1c) $N_k(0) = N_k(t) + N_{Ar}(t)$

$$\frac{N_k(0)}{N_k(t)} = 1 + \frac{N_{Ar}(t)}{N_k(t)}$$

$$\frac{N_{Ar}(t)}{N_k(t)} = \frac{N_k(0)}{N_k(t)} - 1 = \frac{N_k(0)}{N_k(0)e^{-\lambda t}} - 1$$

$$\frac{N_{Ar}(t)}{N_k(t)} = e^{\lambda t} - 1 \rightarrow \boldsymbol{t} = \boldsymbol{\frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)} + 1\right)}{\lambda}}$$

1d) $t = \frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)}+1\right)}{\lambda}$

For all samples, we first find the number of moles of ^{40}K in the sample, using the mass percentages given, the molar mass of K_2O, and the $\frac{^{40}K}{K_{total}}$ ratio given. Next, we found the number of ^{40}Ar moles which is simply the numbers in the table given if we have a 1 g sample. Lastly, we rearranged equation 1c to give us the age directly, $t = \frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)}+1\right)}{\lambda}$, and plugged directly into here to get the age.

<u>Sample 1:</u> $1g\ sample * \frac{.00657\ g\ K_2O}{1g\ sample} * \frac{1\ mol\ K_2O}{96\ g\ K_2O} * \frac{2\ mol\ K}{1\ mol\ K_2O} * \frac{1.2*10^{-4}\ mol\ ^{40}K}{1\ mol\ K_{total}}$

$= 1.64 * 10^{-8}\ mol\ ^{40}K$

$$1g\ sample * \frac{2.91 * 10^{-12}\ mol\ ^{40}Ar}{1\ g\ sample} = 2.91 * 10^{-12}\ mol\ ^{40}Ar$$

$\lambda = 5.8 * 10^{-11}\ yr^{-1}$

So $t = \frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)}+1\right)}{\lambda} = \frac{\ln\left(\frac{2.91*10^{-12}\ mol\ ^{40}Ar}{1.64*10^{-8}\ mol\ ^{40}K}+1\right)}{5.8*10^{-11}\ yr^{-1}} = \mathbf{3.06 * 10^6\ yr}$

<u>Sample 2:</u> $1g\ sample * \frac{.00755\ g\ K_2O}{1g\ sample} * \frac{1\ mol\ K_2O}{96\ g\ K_2O} * \frac{2\ mol\ K}{1\ mol\ K_2O} * \frac{1.2*10^{-4}\ mol\ ^{40}K}{1\ mol\ K_{total}}$

$= 1.88 * 10^{-8}\ mol\ ^{40}K$

$$1g\ sample * \frac{3.18 * 10^{-12}\ mol\ ^{40}Ar}{1\ g\ sample} = 3.18 * 10^{-12}\ mol\ ^{40}Ar$$

$\lambda = 5.8 * 10^{-11}\ yr^{-1}$

So $t = \frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)}+1\right)}{\lambda} = \frac{\ln\left(\frac{3.18*10^{-12}\ mol\ ^{40}Ar}{1.88*10^{-8}\ mol\ ^{40}K}+1\right)}{5.8*10^{-11}\ yr^{-1}} = \mathbf{2.91 * 10^6}\ \boldsymbol{yr}$

<u>Sample 3:</u> $1g\ sample * \frac{.00680\ g\ K_2O}{1g\ sample} * \frac{1\ mol\ K_2O}{96\ g\ K_2O} * \frac{2\ mol\ K}{1\ mol\ K_2O} * \frac{1.2*10^{-4}\ mol\ ^{40}K}{1\ mol\ K_{total}}$

$= 1.69 * 10^{-8}\ mol\ ^{40}K$

$$1g\ sample * \frac{3.08 * 10^{-12}\ mol\ ^{40}Ar}{1\ g\ sample} = 3.08 * 10^{-12}\ mol\ ^{40}Ar$$

$\lambda = 5.8 * 10^{-11}\ yr^{-1}$

So $t = \frac{\ln\left(\frac{N_{Ar}(t)}{N_k(t)}+1\right)}{\lambda} = \frac{\ln\left(\frac{3.08*10^{-12}\ mol\ ^{40}Ar}{1.69*10^{-8}\ mol\ ^{40}K}+1\right)}{5.8*10^{-11}\ yr^{-1}} = \mathbf{3.14 * 10^6}\ \boldsymbol{yr}$

Mean age: $\frac{3.06*10^6+2.91*10^6+3.14*10^6}{3} = \mathbf{3.04 * 10^6}\ \boldsymbol{yr}$

2a) Assume that:

- A human genome is $3 * 10^9$ base pairs long
- During replication, an error is made once every 10^{10} base pairs

This gives us $3 * \frac{10^9}{10^{10}} \approx \mathbf{3 * 10^{-1}}$ **mutations** per genome duplication.

2b) Assume that:

- 23 genome duplications occur in forming an egg
- There are $3 * 10^{-1}$ mutations per genome duplication

Thus, we have $23 * 3 * 10^{-1} = \mathbf{7}$ **mutations** passed along to the child

2c) Assume that:

- A developed sperm cell has undergone the bare minimum number of divisions at age 15
- After puberty, the sperm cell undergoes another division about every 16 days
- Puberty begins at age 15, and the male reproduces at age 30, giving 15 years between the time the cells start dividing and the time the male reproduces
- Each year takes up about 365 days

The bare minimum number of divisions that occur at puberty (age 15) from both mitosis and meiosis is about **34 divisions**. There are a total of 15 years $* \frac{365 \text{ days}}{1 \text{ year}} * \frac{1 \text{ division}}{16 \text{ days}} = 342$ divisions that occur between ages 15 and 30, so there are $342 + 34 =$ **380 divisions** that occur overall for the 30 year old male.

2d) Assume that:

- As before, there are $3 * 10^{-1}$ mutations per genome duplication
- The 15 year old male has undergone 34 divisions, and the 30 year old has undergone 380 divisions

Thus, there are a total of $380 * 3 * 10^{-1} \approx$ **100 mutations** by age 30, when the man reproduces.

2e) Assume that:

- The total number of mutations in an offspring's DNA is the sum of the mutations from the mother and the father

The total number of mutations is thus $7 + 100 \approx$ **100 mutations** in the offspring.

The mother contributes $\frac{7}{100} = \mathbf{7\%}$ as many mutations as the father does.

2f) See .ipynb file

3a) Assume that:

- There are a total of 4 generations between the great-great-grandmother and her great-great-grandchild
- There are roughly 100 mutations per generation (from 2e)

Thus, there are roughly $4 * 100 =$ **400 mutations** from great-great-grandmother to great-great-grandchild.

3b) Assume that:

- The mutation rate per generation is the same from dinosaur to human (100 mutations per generation)
- There are about $3 * 10^6$ years since Lucy lived
- A new generation occurs roughly every 30 years

This means that there have been about $\frac{3*10^6}{30} = 10^5$ generations since Lucy lived, and with 100 mutations per generation, we have $100 * 10^5 = \mathbf{10^7}$ **mutations** that differ from Lucy's genome.

3c) Assume that:

- There are 10^7 mutations that have occurred since Lucy, and 400 that have occurred since the great-great-grandmother
- These occur in a genome $3 * 10^9$ base pairs in length
- This 5000 base pair segment is average in terms of mutation number relative to the rest of the genome

The ratio of mutations per base pair is $\frac{10^7}{3*10^9} \approx 3 * 10^{-3}$, so we will expect to see $5000 * 3 * 10^{-3} \approx$ **10 mutations** in this 5000 base pair segment different from Lucy. The ratio of mutations per base pair since the great-great-grandmother is $\frac{4*10^2}{3*10^9} \approx 10^{-7}$, and we would expect $5000 * 10^{-7} = \mathbf{5 * 10^{-4}}$ **mutations** in the 5000 base pair segment different from the great-great-grandmother. This method might not work well if not enough time has passed, as we are very likely to not see any mutations at all in a 5000 base pair segment (like the $5 * 10^{-4}$ mutations for the great-great-grandmother).

4a) Assume that:

- The error rate is mitochondrial DNA is $3 * 10^{-5} \frac{\text{mutations}}{\text{bp}*\text{generation}}$
- The entire mitochondrial genome is 17000 bp

Thus, the expected number of mutations is $1.7 * 10^4 \text{bp} * \frac{3*10^{-5}\text{mutations}}{\text{bp}*\text{generation}}$

$\mathbf{= 6 * 10^{-1} \frac{mutations}{generation}}$.

4b) Assume that:

- The expected number of mutations per generation is $6 * 10^{-1} \frac{\text{mutations}}{\text{generation}}$ (from 4a)
- There are a total of 4 generations between the great-great-grandmother and her great-great-grandchild

Therefore, we would expect the mitochondrial DNA's of the great-great-grandmother and her great-great-grandchild to differ by $4 * \frac{6*10^{-1}\text{mutations}}{\text{generation}} \approx$ **2 mutations.**

4c) Assume that:

- The mutation rate per generation is the same from dinosaur to human ($6 * 10^{-1} \frac{\text{mutations}}{\text{generation}}$)
- There are about $3 * 10^6$ years since Lucy lived
- A new generation occurs roughly every 30 years

The number of generations that have passed is thus $\frac{3*10^6}{30} = 10^5$ generations. We would therefore expect 10^5 generations $* \frac{6*10^{-1}\text{ mutations}}{\text{generation}} = \mathbf{6 * 10^4}$ **mutations** to have occurred since then. This method will not work well if too much time has passed since it will eventually predict more mutations than there base pairs, as it does here (there are only about $2 * 10^4$ base pairs)!