

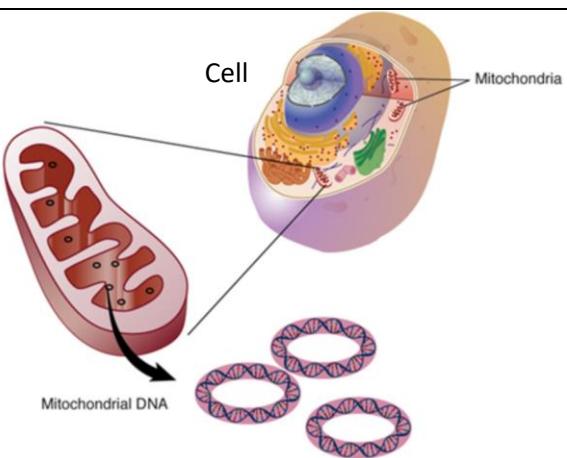
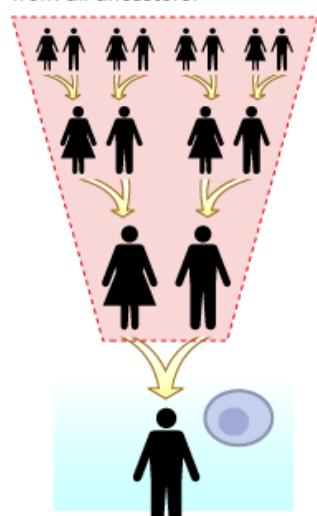
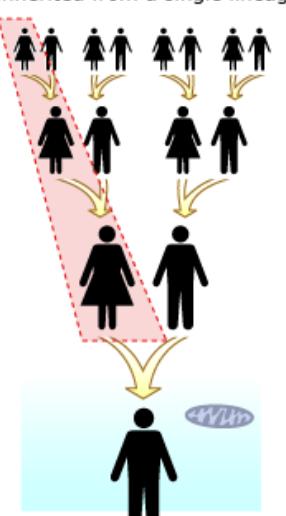
YEAR 10 MATHS. ANALYSIS TASK

Date:

Name:

Marks:

MITOCHONDRIAL DNA (mtDNA)

 <p>Source: http://epi.grants.cancer.gov/mitochondrial/</p> <p>The mitochondria are organelles found in cells that are the sites of energy production. Mitochondrial DNA is the small circular chromosome found inside mitochondria.</p>	<p>A. Nuclear DNA is inherited from all ancestors.</p>  <p>Source: http://evolution.berkeley.edu/evolibrary/news/071101_genealogy</p>	<p>B. Mitochondrial DNA is inherited from a single lineage.</p>  <p>Source: http://evolution.berkeley.edu/evolibrary/news/071101_genealogy</p>
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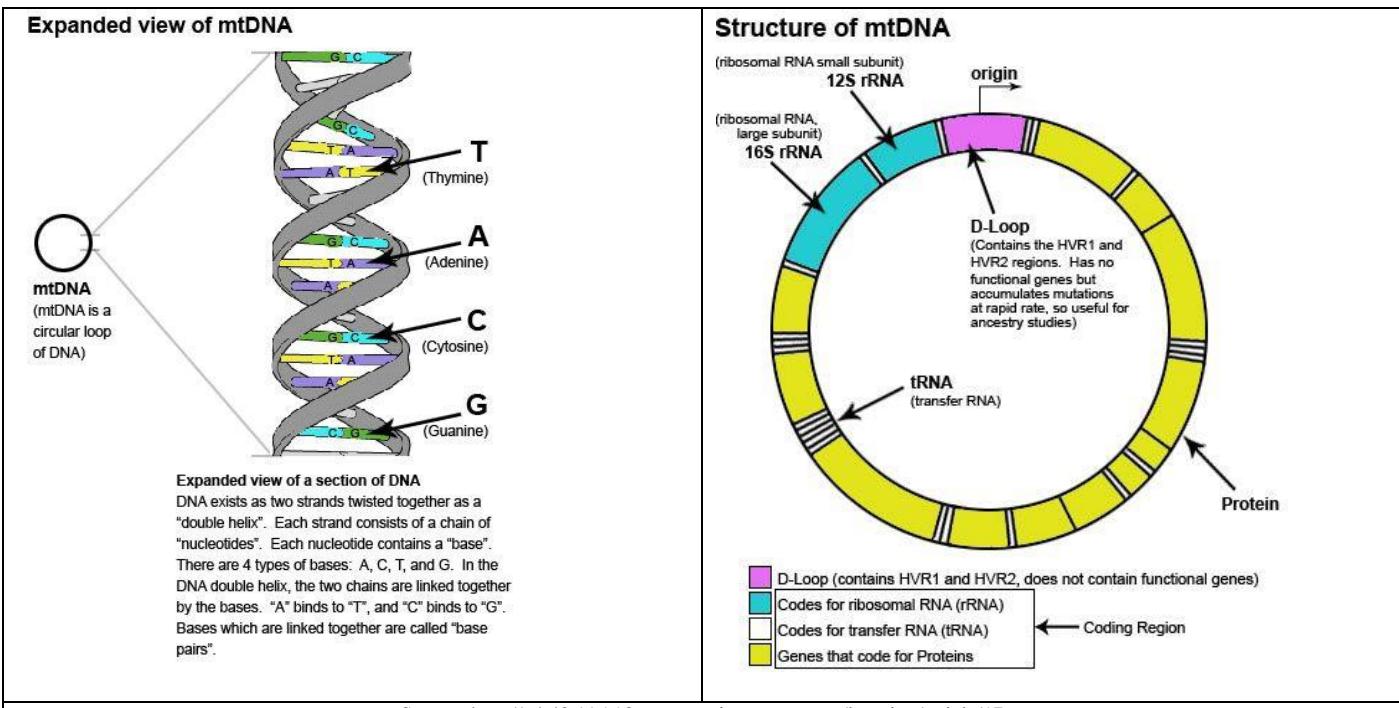
Genetic “Clocks”

Ticking within every species is a “clock” that measures the length of time a species has existed on the earth. Since DNA is passed on imperfectly from parent to offspring, each generation grows more genetically distant from prior generations. Consequently, with each successive generation, reproductively isolated groups within species grow more and more genetically distant from each other.

This is true for DNA found not only in the nucleus of the cell but also in the cellular energy factories termed *mitochondria*. Mitochondrial DNA is present in both males and females, but unlike nuclear DNA, it is inherited only from mothers.¹

Question 1

- Is there any way to determine how long humans have been in existence for? If yes, what are some of the ways we could determine this?
- What would be some assumptions that you have made?



Source: <http://64.40.115.136.van.ca.siteprotect.com/learning/article/17>

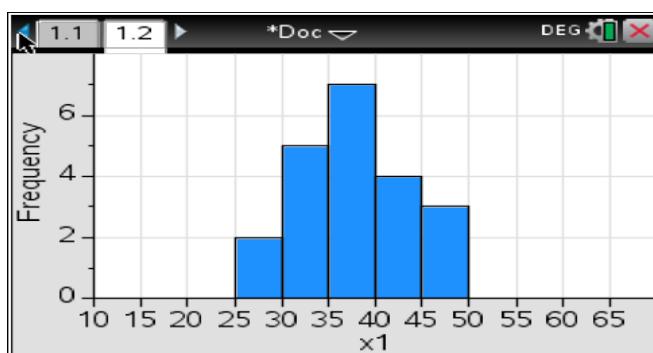
The D-Loop is considered a non-vital part of the mtDNA because it does not have a useful biological function. Thus, whenever a mutation occurs in this region the individual does not die and survives to pass the mutation along to future generations. However, the coding region of the mtDNA is considered essential for the survival of the individual, so usually, whenever a mutation occurs in this region, it is often lethal and the organism dies. Thus, mutations which occur in the coding region are usually not passed down to future generations. For this reason, over a period of thousands of years, many mutations accumulate in the D-Loop, but very little are found in the coding region. Mutations are found at a much lower frequency in the coding region because only the mutations which do not end up being lethal are passed down. When tracing ancestry, scientists usually begin by testing the D-Loop because of its abundance of mutations or “ancestral markers”.

Question 2 Constructing and drawing column graphs with standard deviations.

- (a) (i) For the following data find the mean, median, and standard deviation of the following data.
27, 29, 34, 33, 34, 32, 31, 35, 38, 35, 37, 39, 37, 36, 41, 43, 44, 40, 46, 47, 45

$$\text{Mean} = 37.29 \quad \text{median} = 37 \quad \text{standard deviation} = 5.60$$

- (ii) Draw a histogram for this data using intervals of 5.



- (iii) What is the best measure of spread and centre to use for the data in part (a) and explain why?

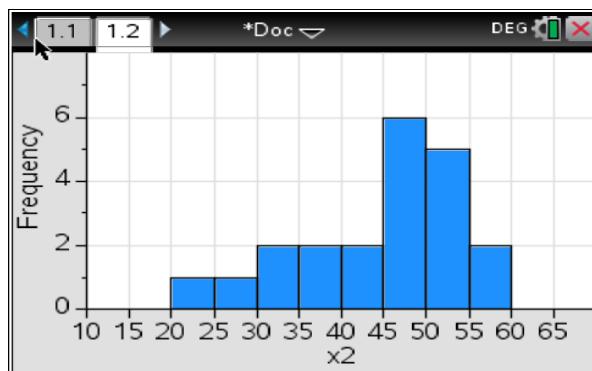
Mean or median for centre and IQR or standard deviation for spread as the data is symmetrical

(b) (i) For the following data find the mean, median, and standard deviation of the following data.

23, 27, 31, 33, 35, 38, 41, 43, 48, 45, 47, 49, 47, 46, 51, 53, 54, 50, 54, 57, 55

Mean = 44.14 median = 47 standard deviation = 9.66

(ii) Draw a histogram for this data using intervals of 5.



(iii) What is the shape of this data/distribution? Negatively skewed (as the tail is toward the negative).

(iv) What is the best measure of spread and centre to use for the data in part (b) and explain why?

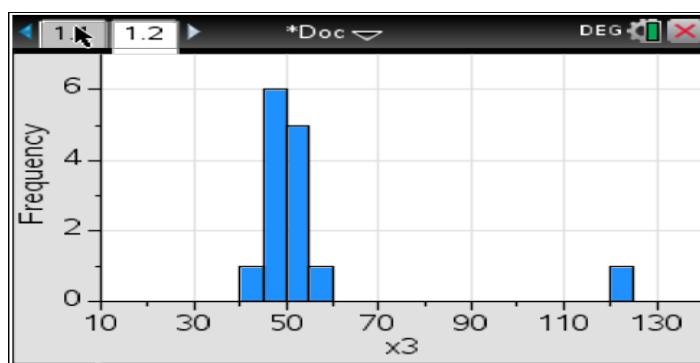
As the data is skewed, we would use median for centre and IQR for spread.

(c) (i) For the following data find the mean, median, and standard deviation of the following data.

43, 48, 45, 47, 49, 47, 46, 51, 53, 54, 50, 54, 57, 124

Mean = 54.86 median = 49.5 standard deviation = 20.29

(ii) Draw a histogram for this data using intervals of 5.



(iii) Is there an outlier in part (c)? Justify your answer with appropriate working out.

Yes.

$$Q3 + 1.5 \times IQR = 54 + 1.5 \times (54 - 47) = 64.5$$

(iv) What is the best measure of spread and centre to use for the data in part (c) and explain why?

We would use the median and IQR because there is an outlier.

[4+5+6 = 15 marks]

Question 3

Average mutation rate for the human D-loop region. (Summary from various studies*)

Research Paper	Number of mutation	Generations (G)	Years (26 years x G)	Mutations/year (5d.p.)
Study 1	0	292	7592 (=292x26)	0 or 0.00000
Study 2	8	508	13208	0.00061
Study 3	0	228	5928	0
Study 4	4	220	5720	0.00070
Study 5	14	327	8502	0.00165
Study 6	6	705	18330	0.00033
Study 7	0	108	2808	0

*Data Modified for the ease of calculation for this assignment

Show your teacher the table before proceeding

(a) Complete the above table. Hence, calculate the average mutations per year. **0.00047**

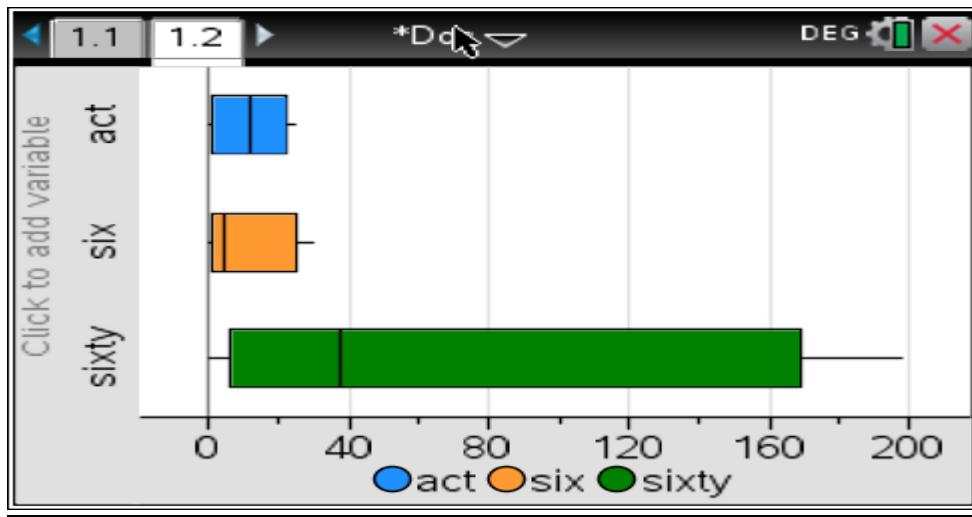
[3+1=4 marks]

(b) Write down the 5-number summary (Min, Q1, Med, Q3 and Max) of the mutation rate.

Min 0, Q1 0, Med 0.00033, Q3 0.00070, Max 0.00165 [1 mark]

(c) In the table below is a 5 figure summary of the human mtDNA rates, on your CAS use the information to draw up parallel box plots (show your teacher once this is done).

5 Figure number summary	actual	6,000 year model	60,000 year model
Minimum	0	0	0
Q1	2	1	12
Median	12	4	38
Q3	20	20	139
Maximum	25	30	198



[2 marks]

Question 4

- (a) Letting r be the average mutation rate calculated in question 3(a), and t = the number of years, show that the mtDNA differences (D) between two identical twins after 10000 years will be 9.4 mutations. Use $D = 2rt$ (Note: constant mutation rate through time is assumed)

$$D = 2xrxt = 2 \times 0.00047 \times 10000 = 9.4 \text{ mutations (Q.E.D. Shown)}$$

[1 mark]

- (b) Calculate the mtDNA differences (use $D=2rt$) between two humans if

humans have been existed for 6000 years

$$2 \times 0.00047 \times 6000 = 5.76$$

humans have been existed for 60,000 years

$$2 \times 0.00047 \times 60000 = 56.4$$

[2 marks]

Question 5 Predictions and modelling.

Using $D = 2 r t$

where D = mtDNA differences between two species

r = mutation rate

t = time of origin (years)

Complete the following tables (use $D = 2rt$)

Species	Average Mutations per year	Average differences observed	mtDNA differences	
			After 6000 years	After 60 000 years
Human	0.00048	10	5.76	56.4

Species	Average Mutations per year	Average differences observed	mtDNA differences	
			After 6000 years	After 20 000 000 years
Fruit fly	0.060	1168	720	2400000

Species	Average Mutations per year	Average differences observed	mtDNA differences	
			After 6000 years	After 18 000 000 years

Round worm	0.136	1655	1632	4896000
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[1+1+1=3 marks]

(b) Draw conclusions from the 3 tables above (Note: 3 marks, 3 different points).

Main points are 1/ the data that is closest to the actual experimental results are the 6000 year old model

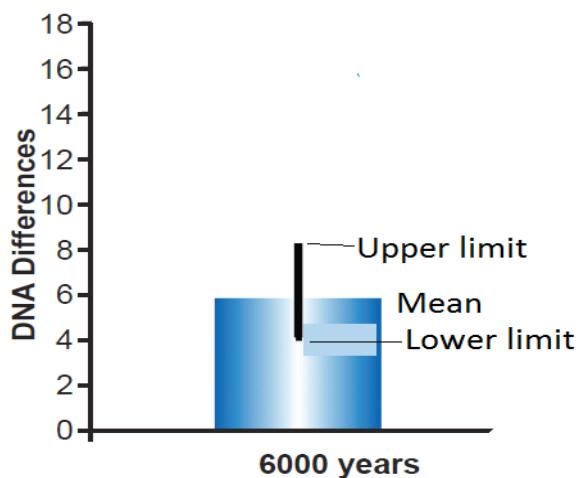
2/ The longer the time period, the further out seems to be the data.

3/ Other points like faster mutation rate in the round worms are easy enough and easy marks, but are not a higher level order conclusion.

[3 marks]

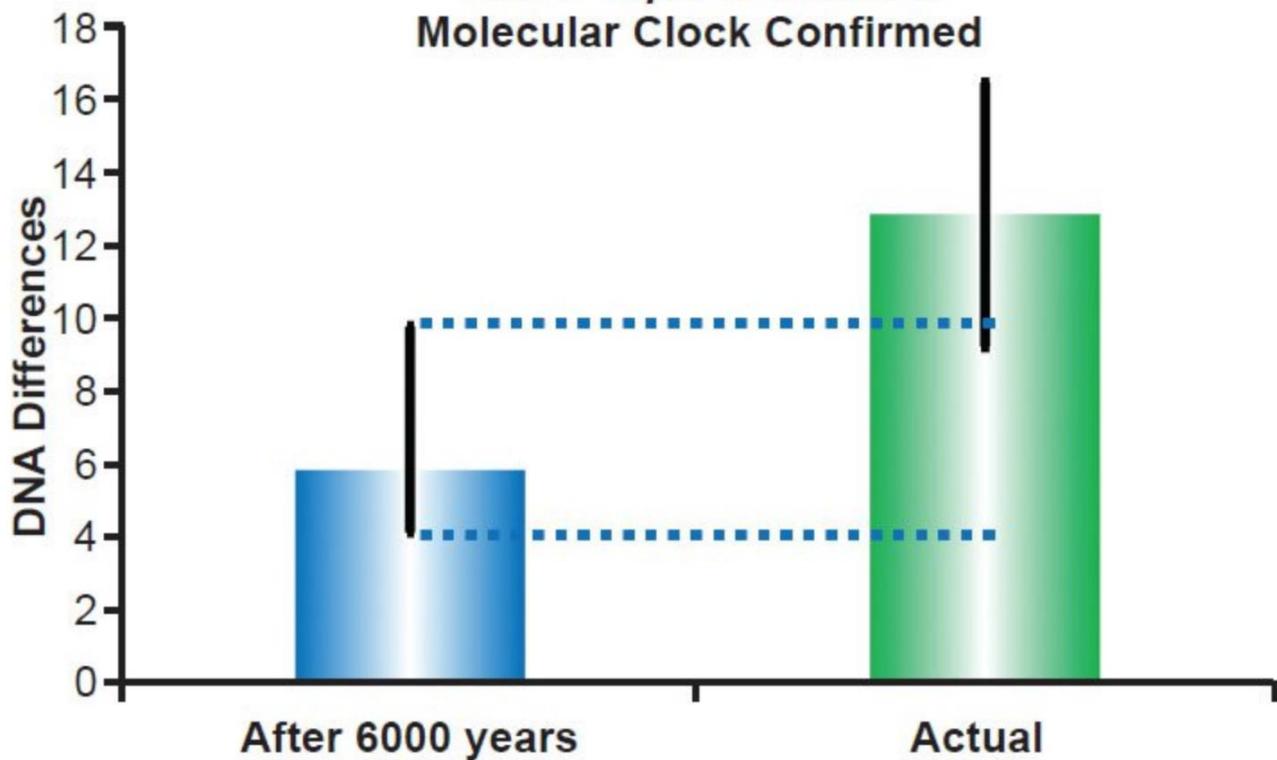
Question 6 Constructing column graphs with error bars.

The following is a single column graph with a mean of 5.8 and an error bar of plus or minus 2 standard deviations ($S_x = 0.9$), where the upper limit is 7.6 and the lower limit is 4.0.

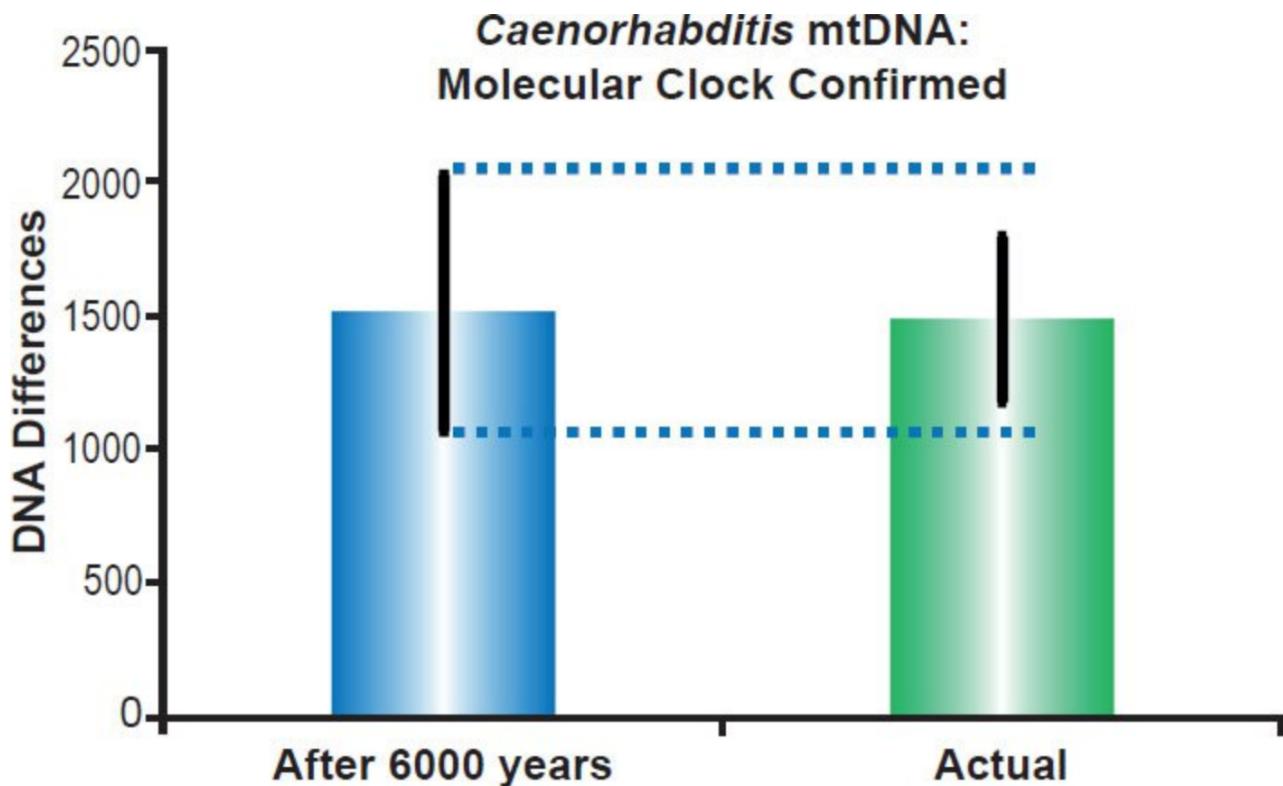


- (a) On the same graph (below) draw a column graph that includes the following data: 1/ Humans after 6000 years where the mean is 5.8 DNA differences and standard deviation is 0.9 (show the error bar plus and minus 2 standard deviations), compared to 2/ the actual data for humans where the mean is 10.0 DNA differences and standard deviation is 1.5 (i.e. draw 2 columns on the 1 graph).

***Homo sapiens* mtDNA:
Molecular Clock Confirmed**



- (b) On the same graph (draw below) draw a column graph that includes the following data: 1/ Roundworms after 6000 years where the mean is 1632 DNA differences and the standard deviation is 250 (show the error bar plus and minus 2 standard deviations), compared to 2/ the actual data for roundworms where the mean is 1655 DNA differences and standard deviation is 125.



- (c) Would it be practical to plot (i) the mutations data for the humans for 60,000 years with the 6000 years and the actual data for humans and (ii) the mutations data for the roundworms after 18,000,000 years with the 6000 years and actual data for roundworms on the same column graphs? Discuss why or why not.

One might be able to put up to 60 on the vertical scale (but a bit of a stretch), but no way can we put a normal (linear scale) on the roundworm as it would have to go into the millions (could do it with a logarithmic scale).

[3+3+3 =9marks]

Question 7 What have I learnt?

Write down 3 things you have learnt

Scale is linear, i.e. longer the dates, the further out it will be from the new data. Various other things are good too.

Mitochondrial DNA Differences: Humans

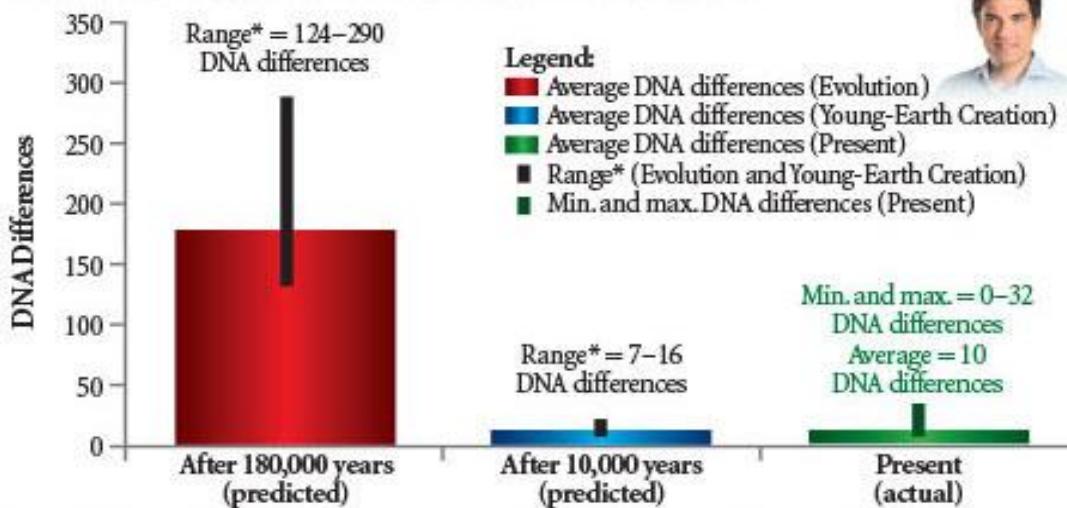
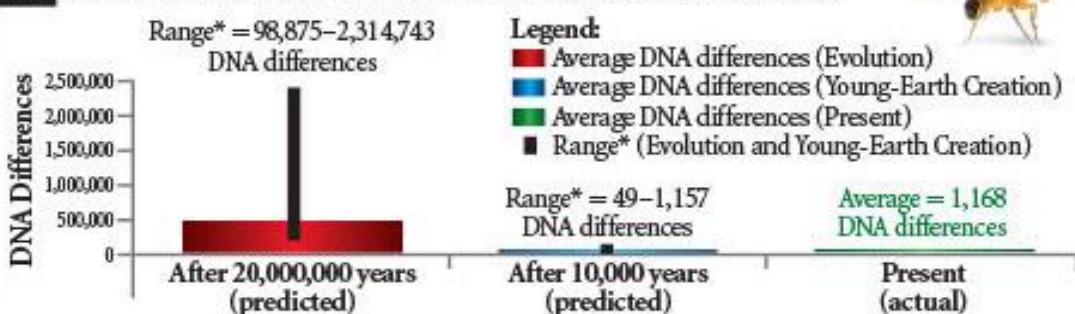


Image credit: Adapted with permission from Answers Research Journal

Figure 1. Present DNA differences among modern humans match the predictions of the young-earth creation model but contradict the predictions of the evolutionary model.

*Range represents the 95% confidence interval.

A Mitochondrial DNA Differences: Fruit Flies



B Mitochondrial DNA Differences: Roundworms

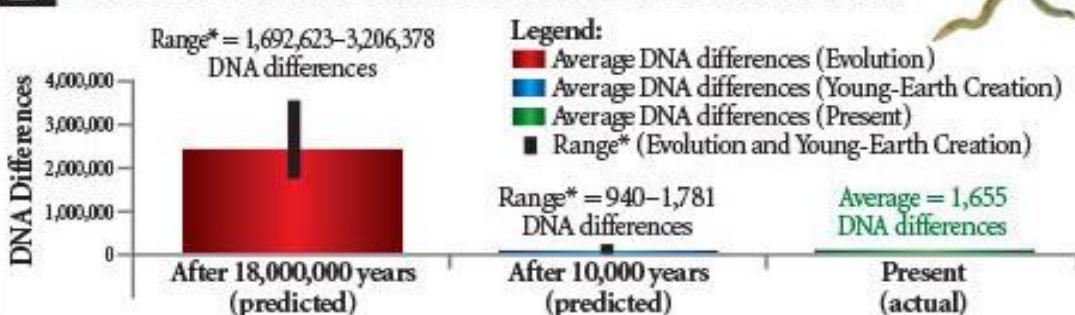


Image credit: Adapted with permission from Answers Research Journal

C Mitochondrial DNA Differences: Water Fleas

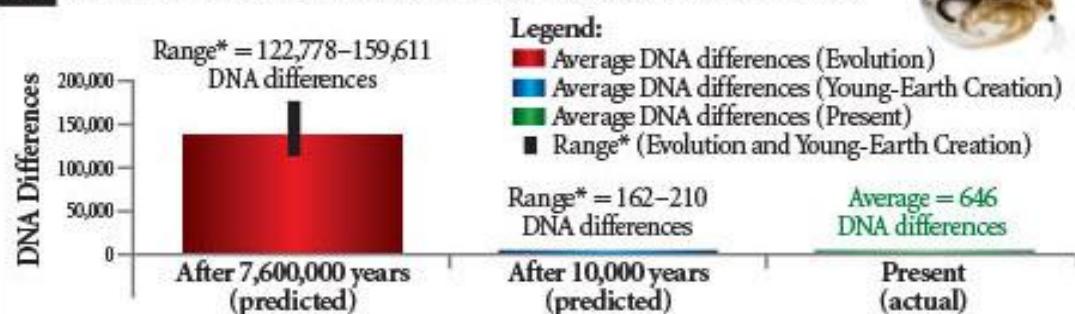
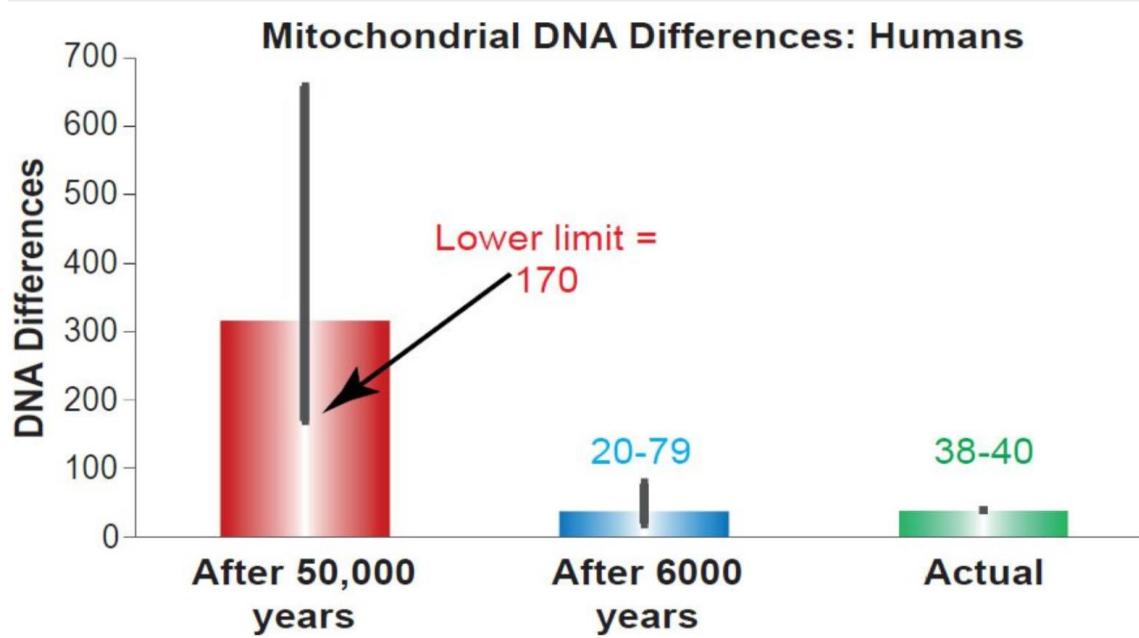
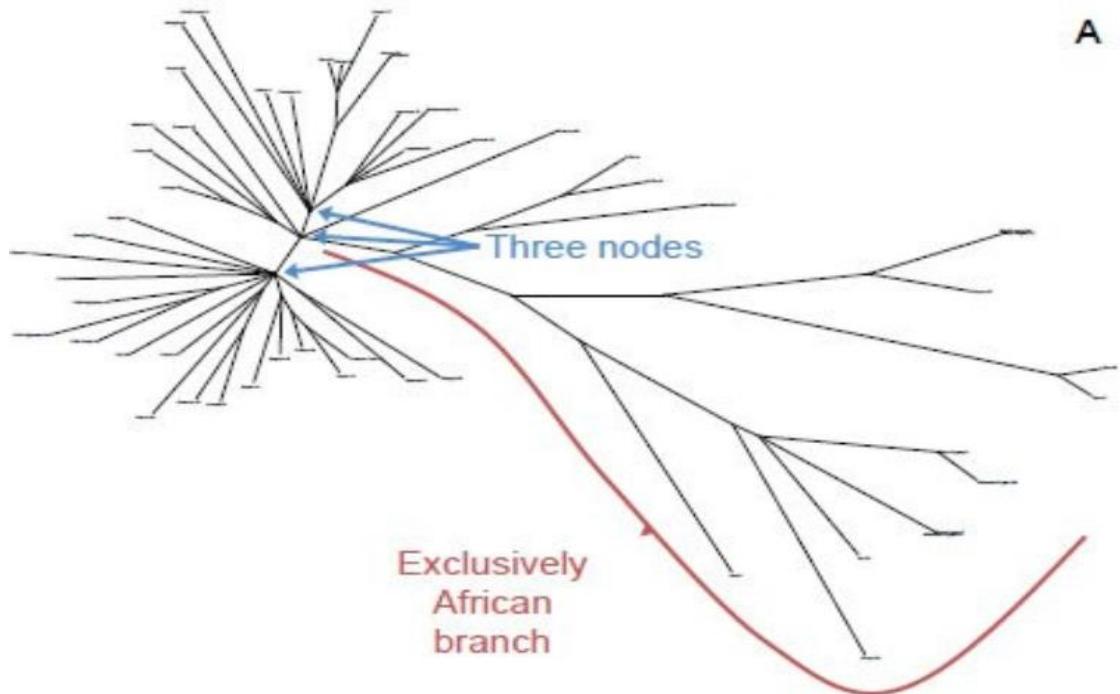
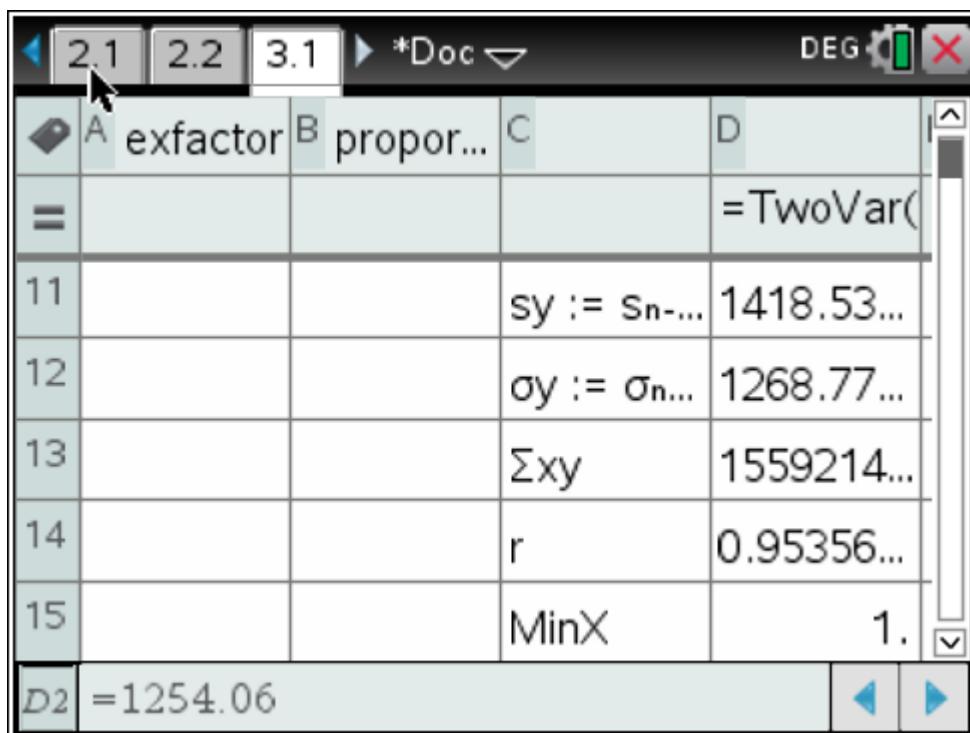
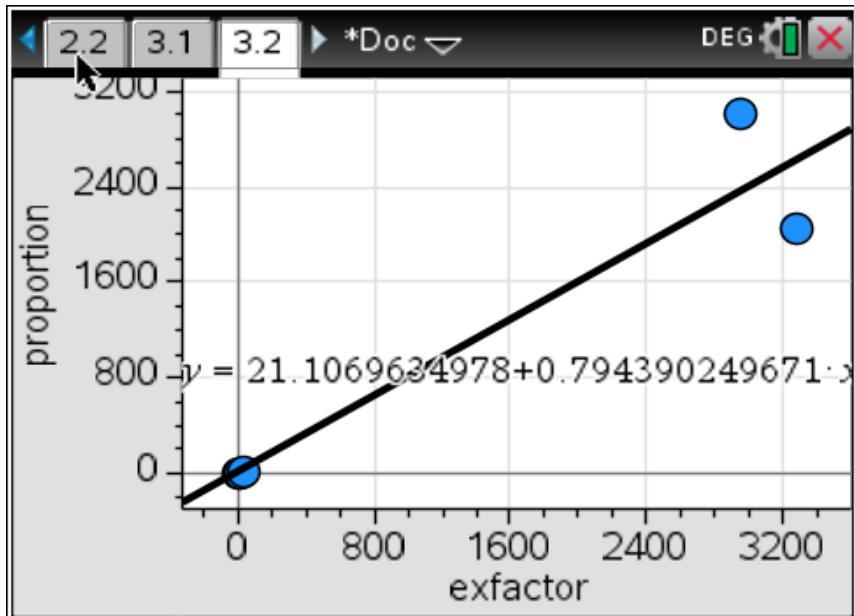


Figure 2. Present DNA differences among modern fruit flies, roundworms, and water fleas match (or are very close to) the predictions of the young-earth creation model but contradict the predictions of the evolutionary model.

*Range represents the 95% confidence interval.





Reference

1. New Genetic-Clock Research Challenges Millions of Years.
<http://www.icr.org/article/new-genetic-clock-research-challenges>
2. Futuyma, D. J. 2009. *Evolution*. Sunderland, MA: Sinauer Associates.
3. Howell, N. et al. 2003. The pedigree rate of sequence divergence in the human mitochondrial genome: There is a difference between phylogenetic and pedigree rates. *American Journal of Human Genetics*. 72 (3): 659–670.

4. Jeanson, N. T. 2013. Recent, Functionally Diverse Origin for Mitochondrial Genes from ~2700 Metazoan Species. *Answers Research Journal*. 6: 467-501.
5. This is for a subset of the mitochondrial DNA, the “D-loop,” the only region of the human mitochondrial DNA for which a mutation rate has been measured to appropriate statistical confidence.
6. <http://www.icr.org/article/human-mutation-clock-confirms-creation>
7. <http://www.icr.org/article/human-mutation-clock-ticking>
8. <http://www.icr.org/article/icr-gene-project>
9. <http://64.40.115.136.van.ca.siteprotect.com/learning/article/17>