1. (1 point) *A common question from folks who do not understand evolution goes roughly along the lines of “if humans evolved from monkeys, why are there still monkeys?” Above is a phylogeny of primates.* In fewer than 100 words, give a clear, precise, and accurate answer to this question.

Monkeys and humans share a common ancestor as shown above. The speciation rate of humans does not mean that the monkeys will go extinction rate will increase because humans were not derived from monkeys. Humans are actually more closely related to the chimps as shown above. The reason why monkeys still exist is because monkeys just share a common ancestor with humans so neither species has to go extinct. Monkeys and humans evolved alongside each other, not from one another.

1. (1 point) Please read this essay by Holly Dunsworth ([https://jonsmitchell.com/biol461/ final/final\_estrogen.pdf)](https://jonsmitchell.com/biol461/final/final_estrogen.pdf) and describe in detail what data you could collect to test whether the childbirth/competition hypothesis or the estrogen/allometry hypothesis for sex-based skeletal differences is better supported. [*Nota bene:* approach your answer as if you were going to add a graph or figure to this paper, and describe how you would generate it]

Two different graphs would need to be created. The first graph would be Pelvic size versus Estrogen production. To determine the correlation between the two, pelvic size and estrogen production levels is the data that would need to be collected. The second graph would be Pelvic size versus Pelvic organ volume. To produce this graph, pelvic size and pelvic organ volume would be the data needed.

1. (3 points) There’s a classic paper in evolutionary biology by Stephen J Gould and Dick Lewontin which you can access at [https://jonsmitchell.com/biol461/final/01\_GouldLewontin. pdf.](https://jonsmitchell.com/biol461/final/01_GouldLewontin.pdf) Note, this paper is old (written and conceived by men who were old in the 1970’s) and uses some outmoded language with respect to some human cultures. Based on your reading of this paper: (a) In your own words, explain why the authors contend that the concepts of *spandrel* and *exaptation* are useful. (b) In less than 100 words, choose what you think the **strongest** argument made in the paper is and *explain why* **you think it is the strongest**. (c) In less than 100 words, choose what you think the **weakest** argument made in the paper is and *explain why* **you think it is the weakest**.

A) The altering of perspective is the reasoning behind why the authors claim that the concepts Known as spandrel and exaptation are considered useful. When studying the different aspects of evolution, the spandrel and exaptation can alter the perspective of the matter. One example that was in the article keened in on the vaulted fan-ceilings, there are open spaces that where intentionally designed to give the fans room to work (structural component) but has taken more of a decoration route within the article. Another example of exaptation would be the lungs of basal fish. The reason why this is an example is because these lungs were the buoyancy organ and gas filled within basal fish, air breathing tetrapod’s lungs were believed to arose from the basal fish lungs. The authors used the spandrels to show their example of exaptation.

B) In my opinion, the strongest argument made throughout this paper was the multiple factors that resulted in hoe evolution takes place. The argument was that although selection is a very important part of evolution, it’s not the only factor to be considered. Drift and Migration are also two factors that contribute to the resulting evolution. When studying evolution in this class, we have learned that all factors need to be taken into consideration, even if some outweigh others.

C) In my opinion, the weakest argument was the fact of Adaptive program objection. The reasoning for this claim is that the authors seemed to be going off of opinionated facts that supported their claim and only their claim. The authors opinion when giving evidence that supported the claim was all we really knew about the article give. The authors “good” article and my “good” article could be completely two different things. Not enough evidence-based support for this claim.

1. (2 points) *Above are data from a paper by Rob Arthur. Using data from fruit flies, he & some colleagues found rates of H3K27me3 occurrence along the genome at sites where a gene had been duplicated. H3K27me3 is a repressive structure, that prevents nearby genes from being expressed. We discussed in class that a duplicated gene can either remain a gene (gaining a new function, a specialized function, a subfunction, etc) or it can be “broken” in which case it becomes a pseudogene (e.g., if the start codon is mutated, no protein is made, and so it’s no longer a gene). The y-axis here is the amount of H3K27me3 in the (reconstructed) ancestor at the location where the duplicated gene ended up. The x-axis shows what happened to that gene in the living fruit fly (lost function so a pseudogene, or still functioned so a new gene). Since gene duplications typically result from errors in meiosis, it’s safe to assume that the location the duplicate ends up is random with respect to it’s fitness effects.* (a) Do these data support selection as the primary force for reducing the effect of duplicated genes? (b) Concisely explain your answer to part a. The paper is accessible here: <https://jonsmitchell.com/biol461/final/final_geneDuplication.pdf>

A) No, the data will not support the selection as the reason for reducing the effects that the duplicated genes will have.

B) Since location is random, the location of the duplicated gene will ultimately have no effect on fitness. If there is a high H3K27me3 expression, then there will be a pseudogene effect on the gene that ended up there due to the randomness of location. Selection would only be selecting for the genes that don’t end up at the locations with the high H3K27me3 expression. Genetic drift and mutation would more than likely influence the duplicated gene reduction than anything else.

1. (2 points) *Fins in fish and limbs in tetrapods are quite different in form and function, although limbs evolved from fins and still retain much of the original genetic network that creates them– albeit with a few modifications. One of the changes to the genetic network involves the timing and location of* Hox *expression. Above is a phylogeny showing the relationship between three species: gar fish, zebrafish, and mouse. These mouse embryoes are transgenic, which means that a researcher added a specific regulatory element called island I from a gar (left), zebrafish (middle), and mouse (right) to the mouse embryo’s DNA. They then used a special stain to see where that added regulatory element was controlling gene expression. The top row of images shows the whole embryo, and features a lot of noise. The lower images show a close-up of the front limb and is more reliable in this particular case.* (a) Which two species are most closely related? (b) Which two species have the most similar pattern of expression? (c & d) If we could sequence the DNA of the common ancestor of these three species and implant it in the mouse, what is the *most likely* pattern of expression we’ll observe in the limb? The paper is accessible here:

<https://jonsmitchell.com/biol461/final/final_limbRegulation.pdf>

A) Gar and the Zebra fish are the two that are most closely related according to the phylogeny tree.

B) The Mouse and the Gar are the two with the most similar pattern of expression.

C/D) I believe that it will resemble the Gar expression simply based on the fact that the mouse evolved prior to the zebra fish. So, by sequencing the DNA like stated In the question of these three organisms, Gar limb expression will be observed in the limb.

1. (2 points) Please read this paper by Blount et al ([https://elifesciences.org/articles/ 55414)](https://elifesciences.org/articles/55414) and answer the following questions. (a) How does the rate of nonsynonymous mutations vary between Cit+ mutant strains in ctirate-only and glucose+citrate media? (b) What does the difference identified in part (a) suggest about the relative importance of different evolutionary forces?

A) The paper supports the nonsynonymous mutations increase in the citrate media when compared to the glucose + citrate media. This claim is shown in which the citrate only media, on average, had a rate of 3.1 mutations. The paper also shows that the glucose + citrate media, on average, had an average of 1.1 mutations. So, in the citrate only media, the rate of nonsynonymous mutations increased compared to the glucose + citrate media.

B) The difference identified in part A is significant in showing that Cit + outcompeted the others when in the citrate only media. This claim resulted in beneficial nucleotide insertion mutations. The mutation rate increased showing that the mutation was favored throughout the population. There are various evolutionary factors working together with selection favoring this mutation.

1. (2 points) Please read this paper by Zhang et al. ([https://jonsmitchell.com/biol461/ final/05\_Zhangetal.pdf)](https://jonsmitchell.com/biol461/final/05_Zhangetal.pdf) and answer the following questions. (a) Why doesn’t maximal dosing kill the most cancer cells in the long run? (b) What is most troubling about Figure 2d? (c & d) Briefly (*<* 100 words) explain the key result being illustrated by Fig 5.

A) Maximal dosing doesn’t kill most cancer cells when prescribed for long term patients. The reasoning behind maximal dosing not killing all cancer cells is because the cells can adapt and create resistance to the drugs. With the resistance that will form, the cells that attain the resistant traits will grow in overall quantity. Maximal dosage will not kill the cells with resistance but has been known to attack sensitive cells without the resistant traits.

B) The part that is most troubling about figure 2d is the simple fact that the simulation contradicts the hypothesis. The part of the figure that contradicts this is the end of the figure when the T-cells increase drastically. Also, the time in which this simulation occurred was an issue. The drastic increase in T-cells towards the end shows an increase in the resistant cells but also the successfulness of the cycle treatment.

C/D) Figure 5 is a trial instead of a simulation, that being said, the results should show actual data. The on/off medication cycle in Figure 5 shows the least resistant cells in comparison to the maximal dosage. One patient showed the scan progression in Figure A but 14 showed the scan progression in Figure B which deviates from Figure 2d. It is difficult to compare the results of figures that do not have the same parameters. Figure 5 and 2d are the most contradicting, when observing the specifics between figures, they are conducted over two completely different time frame lengths.

1. (2 points) Please read this paper by Smaers et al. ([https://jonsmitchell.com/biol461/ final/final\_brainbody.pdf)](https://jonsmitchell.com/biol461/final/final_brainbody.pdf) and answer the following questions. (a) What is allometry? (b) How does the slope of the regression line between body size and brain size relate to allometry? (c) If a new species of pinniped (seal) evolves and increases its ln body size by 2 units, how do you expect that species’ ln brain size to change? (d) If a new species of eulipotyphlan (shrew) evolves and increases its ln body size by 2 units, how do you expect that species’ ln brain size to change? (e) Briefly (*<* 100 words) explain why relative brain size should not be used as a proxy for intelligence.

A) Allometry is defined as the study of how processes scale such as the rate of growth in shape, function, and size of different structures will change according to the body size and be considered proportional.

B) These two characteristics are increasing in a direct way. The brain will increase in size at its own rate which then will add to total body composition.

C) I would suspect the brain size to be directly proportional. Therefore, I would expect that the brain size will increase, however, I would expect the brain size development to be at a slower rate.

D) It would increase at a slower rate than the body, but it would still increase.

E) Body size to brain size allometry shows a positive correlation. With that being said, relative brain size has no effect on intelligence. With that being said, when the body increases in mass the brain will as well but not at the same growth rate. Populations have different needs, therefore brain region mass may differ, but this still does not prove that brain size has a direct relationship with intelligence level.

1. (2 points) Please read this paper by Shoemaker & Clauset ([https://jonsmitchell.com/ biol461/final/final\_horseEvo.pdf)](https://jonsmitchell.com/biol461/final/final_horseEvo.pdf) and answer the following questions. (a) Does species selection play a major role in the distribution of horse body masses according to these analyses? (b) What is meant by the statement that horse body size is neutral at the macroevolutionary scale? (c & d) Do these results imply that larger individual horses have no fitness advantages over other horses in their own populations?

A) The two major roles in distribution according to these analyses would be gene flow and evolutionary diffusion, not species selection. It does play a role but to say that it is major would not be true.

B) It means that the horse body size doesn’t have an effect throughout the populations. This would be considered the macroevolutionary scale. On a microevolutionary scale, it does an effect because selection is likely to occur within the population.

C/D) I do not believe so. Body size is still considered an important part within the competition aspect of the population. There was an increased number of horses produced as the body size increased. With that being said, there is a higher fitness related to larger body mass size within the population.