

Read each question carefully.

Make sure you answer everything each question asks. Each part of each question is worth an *equal* fraction of the question's point value.

Read the question carefully! Don't answer something different from what I ask for!

Always be as specific as possible! Use information from other questions (especially the figure questions in the back!) to help you. There's nothing untoward about using the material on the exam itself to help you answer a particular question.

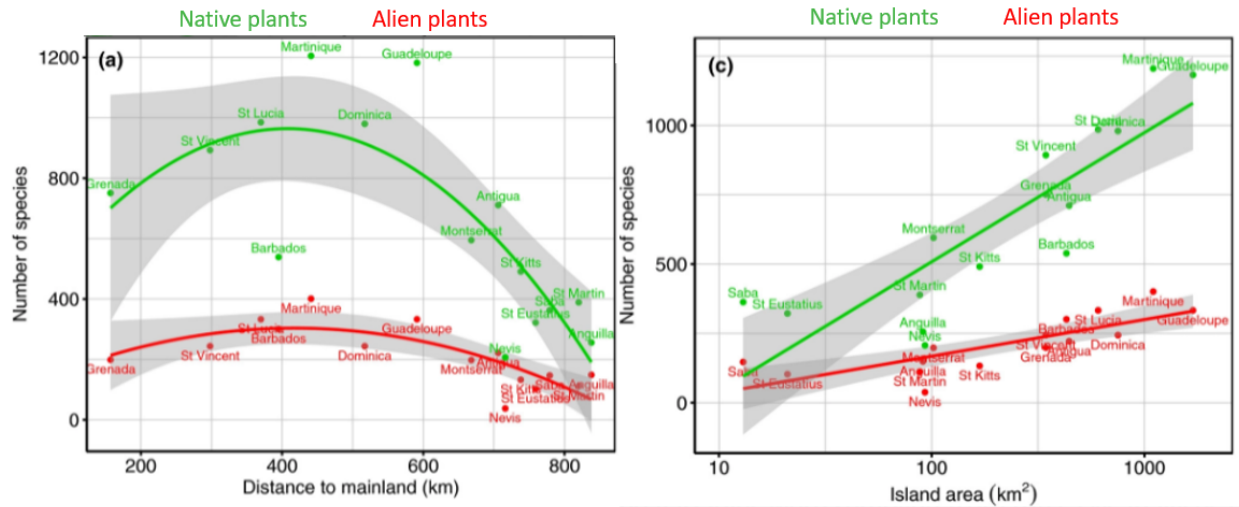
Work within the limits of the data. Your ability to assess what is supported by data is explicitly what I'm testing here (and in your project, and just generally in this class).

Assume anything stated in the question is true.

1. (1 point) *Your coolest friend comes up to you in the hallway and says, “Hey, I just read that paper about Solenodon venom for fun. It got me thinking. They were talking about the KLK1 gene, and how humans also have it, and snakes have it, and these weird venomous Caribbean euliptophylans also have many copies of it, and how those venomous shrews also have many copies. I was wondering, since the same name is used, that would mean that the KLK1 gene itself is homologous between humans, snakes, shrews, and Solenodon. But if genes can be homologous, what about duplicated copies of a gene? Are the extra copies of KLK1 in the shrews homologous to the extra copies in Solenodon?*

How do you answer them?

Function does NOT matter for homology. It explicitly and definitionally does NOT matter. As stated in the question (never argue with the question text) the normal KLK1 gene is homologous between all of these groups. We’ll discuss why later when we do genes more, but for now it was just stated in the question text. For the duplicates, the trick here is that while all the duplicates within Solenodon are homologous (paralogous) to the “normal” copy in shrews (and all the duplicates in shrews are homologous [paralogous] to the “normal” copy in Solenodons) the duplications themselves were independent. That was one of the main points of the paper. The two species separately and independently duplicated the same gene to make venom. So the duplicates aren’t homologous to one another. So a good answer here would need to emphasize that the two groups duplicated these genes independently, and as long as no *strong* statements about them being homologous were made in the answer, I’d count it at least mostly correct.

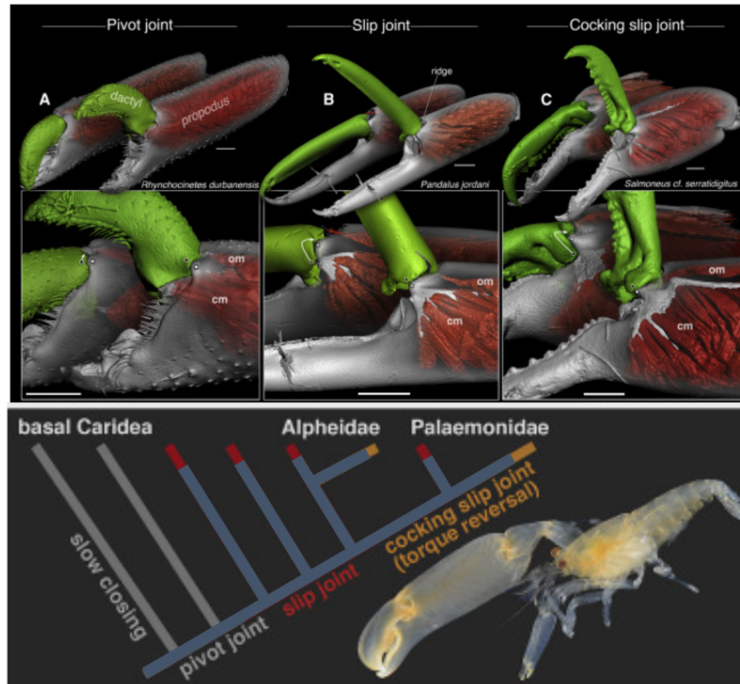


3. (1 point) Above are data showing the number of plant species on the islands of the Lesser Antilles. In green are shown data for native plants (plants that existed on these islands before the arrival of Europeans), while data for alien (invasive) plants are shown in red. A second-order polynomial (quadratic) curve was fit to the distance data, and a first-order polynomial (straight line) was fit to the island area data.

(a) Which of the two rates that control species diversity on islands differs most between native & alien plants?

(b) Propose an alternative measurement that could be taken to better explain what predicts the rate you specified in part (a) for alien species.

(a) Immigration rate. Normally, farther islands = lower immigration, but the points are essentially flat for alien species. You can calculate it roughly by looking at the difference in the levels of the best-fit lines. Alien plants are arriving via human activity, not via natural dispersal, and so distance isn't functioning the same between the two sorts of plants. (b) Almost any human activity measure makes sense here. Island GDP, number of ports, human population, number of farms, w/e. The trick is to name an actual measurement. "The environment" could mean anything. Things like "survival rate" could be useful, but



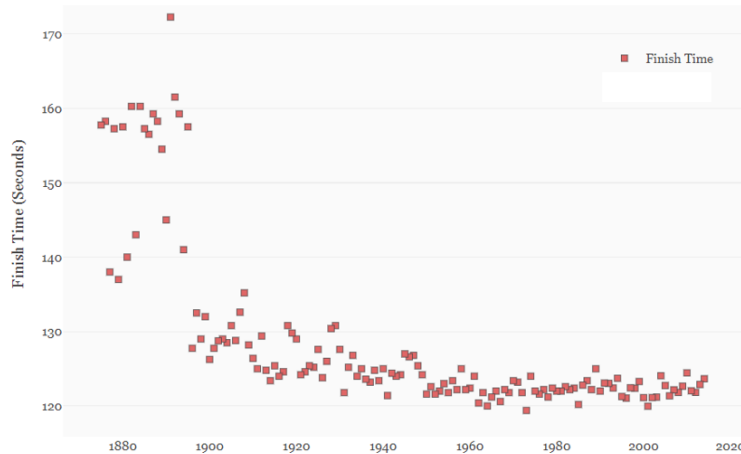
4. (1 point) *Pistol shrimp* are amazing. They have specialized giant claws, with an elaborate joint that allows them to be cocked like a pistol. These small shrimp do not use their claws to grab things as other crustaceans do, though. Instead, the upper portion of the claw (the dactyl) is held upon under tension and can be “fired” also like a pistol. The dactyl snaps shut so fast, a jet of water is fired out. The snapping of this shrimp is one of the loudest sounds produced in nature, and the water forced forward from it’s claw can kill a small fish several centimeters away (quite far for such a tiny shrimp!). Two clades (Alpheidae and Palaemonidae) have shrimp with these specialized snapping claws, and none of the other 50,000+ species of Crustacea have anything like this, nor does any other of the more than a million other species of arthropod. The above diagram show shrimp claw anatomy, and both Palaemonidae and Alpheidae with the cocking slip joint have the same arrangement of opening muscles (om) and closing muscles (cm). The shape of the joint mechanism that allows the shrimp to “fire” is also identical between the two groups. The same genes are used to create the special joint by affecting the same population of cells during development in the two groups. Above is also shown an evolutionary tree of shrimp, with different types of claws color-coding the ends of the branches. These entirely distinct, anatomically, genetically, and developmentally-identical claws found only in these two small groups of shrimp and in no other arthropods are not completely homologous.

(a) What is the best evidence that the special claws in these two shrimp groups are *not* completely homologous?

(b) Given that the common ancestor of the two types of shrimp did not have this special joint, what else do these data tell us about that ancestor?

(a) The distribution across taxa is all screwy. It implies multiple losses if they were homologous, and so it’s strong evidence against it. (b) There’s some homologous pattern in the shrimp that allows them to evolve this trait. You don’t yet need to know what kind of thing it is (in this case, a homologous set of genetic regulatorys that form a network that preadapts/potentiates shrimp in this group to evolve these claws), but the fact that this type of claw has only evolved twice and in

two related groups tells us that the common ancestor of those two groups must have had something special about it to *allow* for the evolution of that claw. These data tell us absolutely nothing about the ancestor's behavior, ecology, diet, habitat, or defenses.



5. (1 point) *The Kentucky Derby is a horse-race held every year in Kentucky. Lots of very wealthy people spend a truly obscene amount of money preparing for it. Horses that win the Kentucky Derby and other high-profile races are then used as studs, and are rented to horse-breeders to father the next generation of horses for, again, absurdly high amounts of money. The Kentucky Derby involves many horses that run the track at different speeds. The fastest horse, the one that runs the track in the least time, is the winner. A winning horse will father many times the number of foals as a losing horse, and even a losing horse will father many more foals than one that did not qualify for the race. A ton of money and effort has gone into breeding the fastest possible horses. Above are data showing winning time around the 1.25 mile long track since the late-1800's. Although training, equipment, and jockey techniques have all changed over the decades, assume these changes have been too slight to have a noticeable impact on horse speed.*

(a) Based on all of the data above, if I gathered wild horses and ran them through the Kentucky Derby, then bred the winners, would their speed be faster, slower, or the same in later generations?

(b) Based on all of the data above, is the speed at which a horse runs the Kentucky Derby currently evolving by selection?

(c & d) Propose a **single** explanation for your answer in (b) consistent with the above data & information.

(a) Faster. It's clearly the case that speed can evolve in horse populations based on the first few decades. (b) No. Evolving = changing over time, and the race times haven't changed in decades. It clearly WAS evolving early on, but seems to have stopped around 1950. (c/d) To evolve by selection something needs (1) variation, (2) differential reproduction based on that variation, and (3) for that variation to be heritable. There is obviously differential reproduction due to the practicing of studding, so an answer involving 2 is not consistent. Horse speed is also obviously variable, as not every horse wins so an answer involving 1 is not consistent. The heritability is the weakest link here—it is clearly the case that race speed *was* heritable, but it seems to no longer be. We don't yet know enough as a class to identify that reason (it's a selection limit resulting from additive genetic variation + a epistatic tradeoff between sprint speed and endurance), but even without knowing why heritability changed, identifying that it did so is all you need for full credit.