Assignment #2: Genetic Dirft

[A2-1] Yes-No Answers

[A2-2] Correlation

[A2-3] Textbook Case of Speciation

[A2-1] Yes-No Answers

Random genetic drift …

[yes/no] is a random factor and therefore the outcome cannot be predicted.

[yes/no] depends on population size.

[yes/no] is more likely to remove rare alleles.

[yes/no] decreases genetic diversity over time.

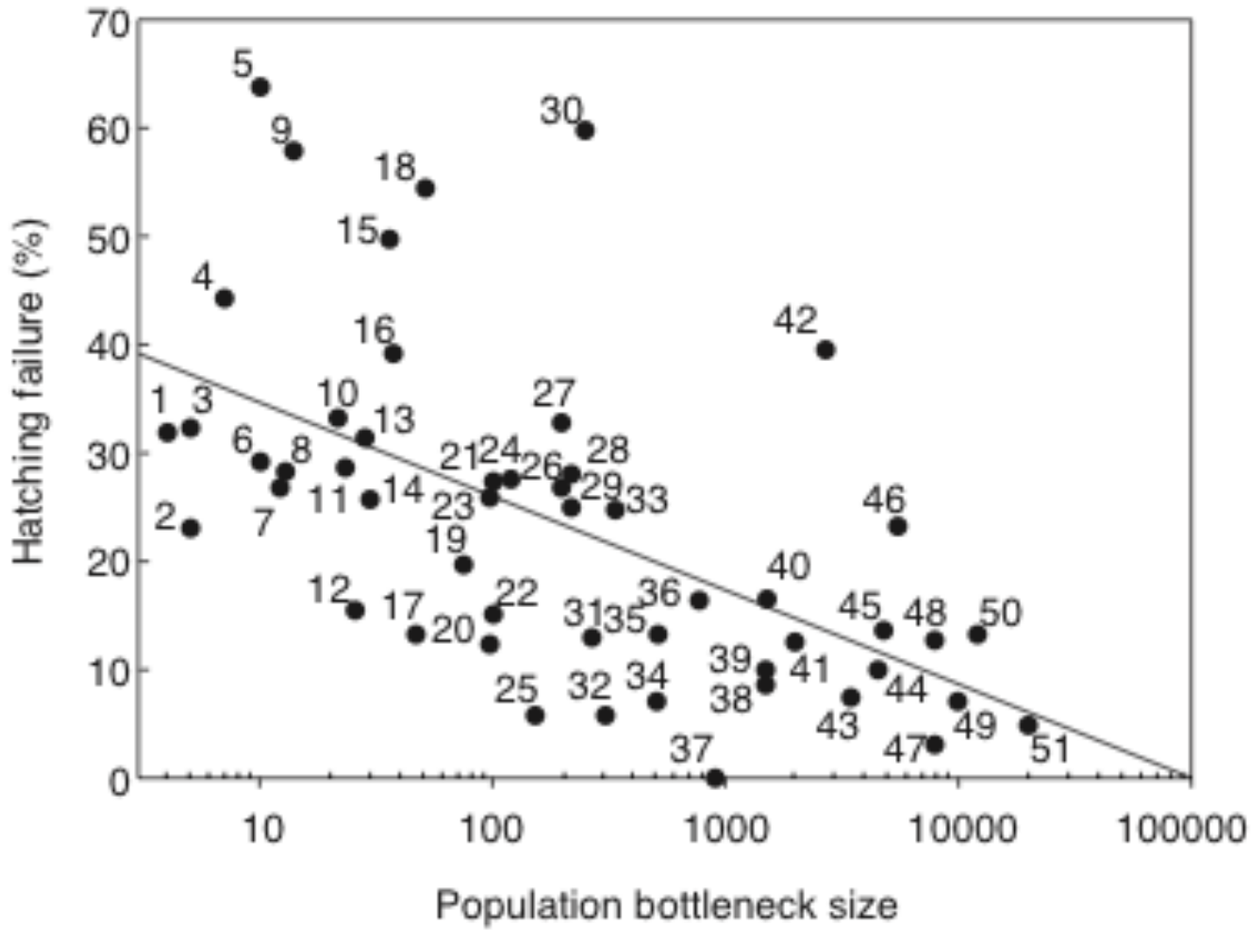
[yes/no] is driving a population away from H-W equilibrium.

[yes/no] is bringing subpopulation closer to each other

[yes/no] is reducing the number of alles in a population over time.

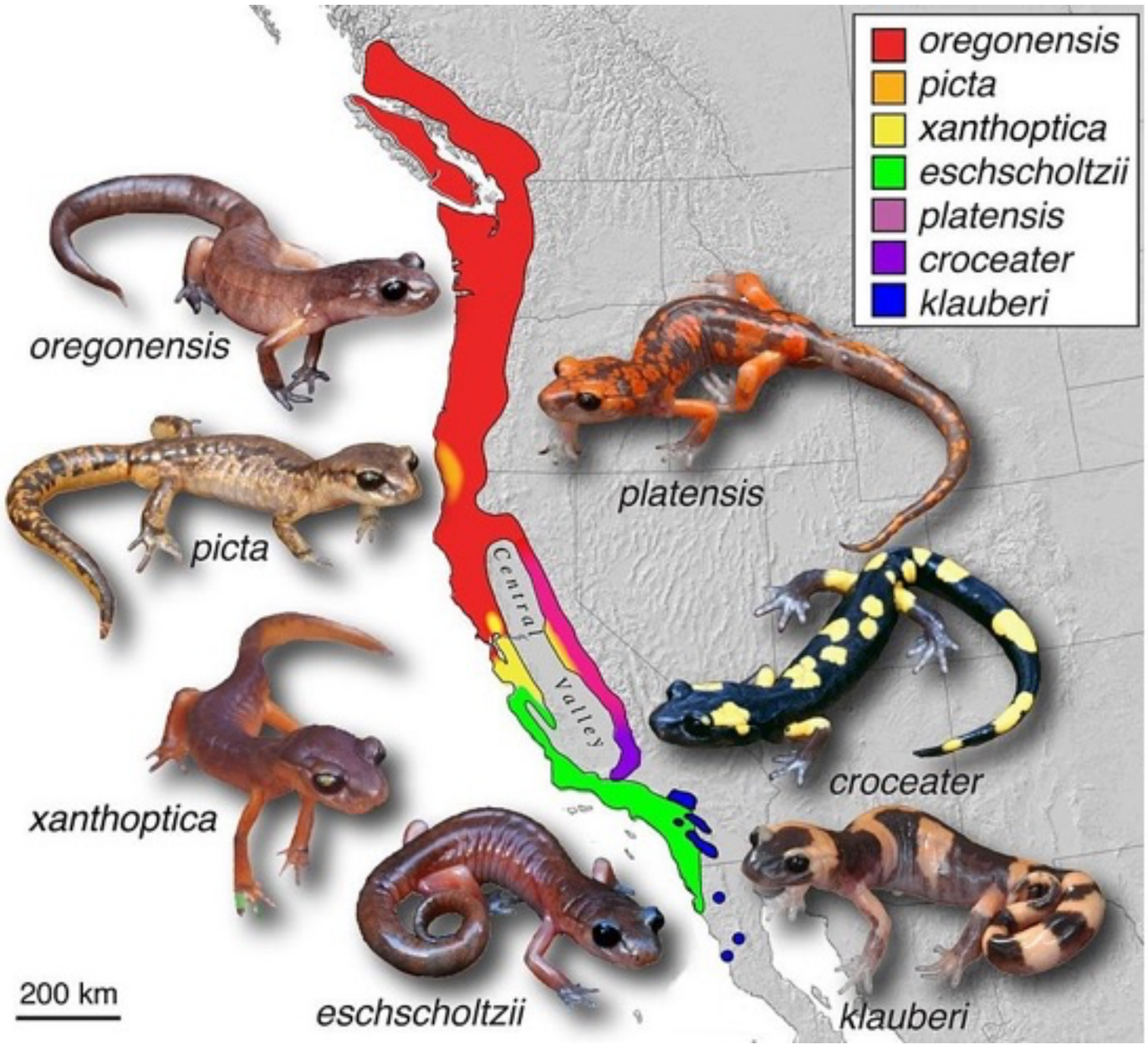
[yes/no] is leading to fixation of alleles.

[**A2-2] Correlation -** In 2010, Heber and Briskie reported a **correlation between** the population **bottleneck size** and **hatching failure** in birds. Can you explain the observation?



Effect of bottleneck size (smallest number of individuals recorded in the population) and percentage hatching failure in 51 bird species. Hatching failure is plotted on a linear scale and bottleneck size is plotted on a logarithmic scale, although both were log transformed in analyses (Heber and Briskie, 2010).

[A2-3] Textbook Case of Speciation



The ensatina is a fairly common salamander. From southern British Columbia in Canada to northern Baja California in Mexico, it can be found lurking under logs in forests along the entire western coast of North America. But it's in California where the little amphibian's story takes an intriguing turn.
Depending on where you are, whether east of California's Central Valley in the mountains of the Sierra Nevada, or west of the valley on the Coast Ranges, the ensatinas you encounter can look strikingly different. While the intermediate populations can interbreed, the forms at the southern ends of the loop are so different that they can no longer mate successfully everywhere they meet.

Explain what happen to the salamnder in evolutionary terms?