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BIO 594 0004

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18 April 2019

Discussion Summary: Climate Change and Conservation Biology

For this week’s discussion of climate change and conservation biology, the class read Bay et al.’s 2018 paper on climate-driven population declines in the yellow warbler and Jordan et al.’s paper on climate-related adaptation in eucalyptus trees. To start our discussion participants were asked to share what they liked and disliked about each paper, what they found interesting, and what questions they had relating to the contents of the two papers. We later asked the group to explain the figures within the Bay et al. paper, identify and explain the study’s main findings and results, leading to a discussion about how the concepts and modeling the research team was trying to do is difficult and new for the field. After extensive conversation on the Bay et al. paper, we brought the conversation over to the Jordan et al. paper and discussed the importance of standing genetic variation for adaptation potential as well as the ethical side of assisted adaptation and migration. Overall the group led a productive discussion shedding light on the potential for using a genomics-approach for conservation and how predictions can be made from high-throughput data such that used in Jordan et al. and Bay et al.

When asked to share what their general thoughts on the Bay et al. and Jordan et al. papers the group generally liked these two studies and appreciated the novelty of their approaches to answering questions relating to genomic and conservation biology. In regards to the Bay et al. paper participants found the machine learning aspect of the paper to be very interesting as well as the authors’ use of the genomic vulnerability metric. Participants also appreciated the clarity of the methods in the eucalyptus paper: dataset development was clear, data filtering standards were stated, and the methods in which they distinguished neutral and outlier SNPs was well-stated.

After gathering the group’s collective thoughts and questions about the two papers we then asked participants to break off into smaller groups to discuss the different figures in the Bay et al. study and report their findings to the class. Group 1 started by explaining Figures 1A and 1B. 1A and 1B compared genetic distance with geographical distance and ‘environmental distance.’ They explained that environmental distance metric was calculated using pairwise comparisons of different environmental parameters between sampling sites and while accounting for magnitude. It was unclear if the researchers accounted for collinearity between environmental parameters when estimating this metric, which could be a potential caveat in the study. Figure 1C showed the top environmental factors affecting genetic distance with the first three being environmental variables relating to precipitation and the fourth relating to temperature. Finally, figure 1D plotted the top four environmental factors on a PCA plot. Each environmental parameter was assigned a color that coordinated with a map of sampling locations. Group 2 then went on the explain figure 2. A few potential weak points of Figure 2 were pointed out, specifically about how Figure 2A and Figure 2B did not visually reflect the same information but were then used to find a correlation between the two. The group talked about how they would expect both the predicted genomic vulnerability and current population trend graphs to either both be patchy or smoother. As well as that their sample sites included Alaska and the upper North America region, but those locations were not included in the population trends and genomic vulnerability modeling maps. For some of the class, this issue caused problems for them in agreeing with the research team’s genomic vulnerability measurement and using that to predict population levels and adaptation potential of populations. One member of the class brought up the potential for migration, which could influence the genomic vulnerability measurement unless the metric only refers to populations in an area and if a population migrated then that population would be gone anyway. The migration aspect is important to think about if the model is to apply to all ecosystems, including benthic marine organisms like coral reefs. It was also mentioned that the research team could have used more ecological data in their model. The class member thought this because the genomic vulnerability predictions (Figure 2A) didn’t seem to match the current trends in population levels (Figure 2B).

Figure 3 depicts a diagram of chromosome 5 and SNP upstream of DEAF1 gene. This was considered the most significant SNP, shown in the first section of Figure 3. The paper stated that the DEAF1 gene was used in migratory and flight functions for birds, indicating these traits could be under selection. The class discussed that it would be difficult to apply this model and cohesive story to non-model organisms that don’t have as much background genomic data to work with like a constructed or annotated genome. A class member suggested using this model in a smaller geographical region to prove the genomic vulnerability metric is accurate. This would allow the research team to use more fine-scale environmental data and could help with the disconnect discussed earlier between Figure 2A and 2B, the genomic vulnerability metric predictions and the current population trends. If the environmental data was widespread for the regions the team did use, the map shown in Figure 2B would be generalizing areas, which could lead to the patchiness shown as well.

Although there were some discrepancies and concerns with the figures and methods, we ended the Bay et al. discussion with talking about how the concepts and modeling the research team was trying to do is difficult and new for the field. The research team was trying to come up with a metric with new, high throughput genomic data as a predictor for adaptation potential and survivability of populations. Because of the recent growth in quality of genomic data we are able to obtain, studies like this can start to be explored. Carlos mentioned that he liked the paper because it pushes boundaries of science and doesn’t use genomic data to use methods we have been using in the past and what would be in our comfort zone. I agreed that to move science forward, newer methods and concepts have to be put out there for review and criticism in order to improve a model like this. Carlos mentioned that he thinks this is a direction that NSF and funding sources are looking to go with the future of climate change research. The authors take home message was that the greater the expected allele shift to keep up with climate change, the greater that population’s susceptibility to climate change stressors would be. This conclusion is similar to the Jordan et al paper that highlighted the importance of standing genetic variation and reiterated that higher survival would be associated with the smaller allele frequency shifts to match future predictions.

The class then moved on to discuss the Jordan et al. paper, which a class member previously commented that they thought the methods were very clear and the SNP filtering and choice of adaptive loci was held to high standards. This made the overall story of the paper and conclusions believable for the class. One member of the class commented that they thought it was important that the research team used multiple outlier tests to detect adaptive loci, and they differentiated between types of putatively adaptive loci. This paper emphasized the importance of standing genetic variation and incorporating that into restoration efforts is critical for the long-term efficacy of those conservation practices. The class discussed their thoughts on conservation practices and restoration and gave their opinions on what conservation practice, if any, is worth the time, money, and efforts spent to enact these plans. One member of the class said they thought species that weren’t humans would be fine because Earth’s biodiversity has persisted through several mass extinctions. I would personally strongly disagree because this mass extinction is anthropogenically driven, could have been avoided, and still has the potential to be at least partially mitigated. Therefore it is unethical for humans to continue to drive the carbon dioxide levels in the atmosphere that eventually harm every type of ecosystem on the planet. Other mass extinctions have been limited to a geographical area, not affected every species on the planet. Another member of the class felt strongly in favor of restoration practices and is including efforts for conservation in her dissertation projects. But they also felt strongly about restoration practices being based on scientific research. I personally agree with and feel that it isn’t worth the time and energy spent if it is not going to be effective long-term.

Overall, the class discussion was productive and shed light on the potential for using genomics in conservation, and specifically how predictions could be made from high-throughput data like the datasets used in Jordan et al. and Bay et al. Both papers propose methods to make predictions for adaptive potential in a rapidly changing environment. Both papers are also recently published and will likely influence the direction of using genomics to evaluate climate change and guide management practices as well as restoration efforts. We found it interesting that even within a small group of similar people, all biological science students in Rhode Island, opinions still largely differ. And when that difference in opinion is scaled up to state or even national level, it becomes clear why issues like climate change are so highly debated and why making any effort at a national level to change the trajectory we’re on is so difficult.

**References:**

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