

Chapter 02 Bibliography

Matthew D. Buehler

SNPs vs Microsatellites

Shawna J Zimmerman et al. “An empirical comparison of population genetic analyses using microsatellite and SNP data for a species of conservation concern”. In: *BMC genomics* 21 (2020), pp. 1–16, SNP/Micro Comparison Grouse

Demographic Parameters

Population Connectivity

Desislava Petkova et al. “Visualizing spatial population structure with estimated effective migration surfaces”. In: *Nature genetics* 48.1 (2016), pp. 94–100, EEMS Description Steven M Musmann et al. “BA3-SNPs: Contemporary migration reconfigured in BayesAss for next-generation sequence data”. In: *Methods in Ecology and Evolution* 10.10 (2019), pp. 1808–1813, BAYESASS3

Conservation Genomics

Soraia Barbosa et al. “Integrative approaches to guide conservation decisions: using genomics to define conservation units and functional corridors”. In: *Molecular Ecology* 27.17 (2018), pp. 3452–3465, Delimiting Conservation Units

Population Genetics Bibliography

Barbosa et al.: Integrative approaches to guide conservation decisions: using genomics to define conservation units and functional corridors

barbosa2018IntegrativeConservationGenomics

Soraia Barbosa, Frederico Mestre, Thomas A White, Joana Paupério, Paulo C Alves, and Jeremy B Searle. “Integrative approaches to guide conservation decisions: using genomics to define conservation units and functional corridors”. In: *Molecular Ecology* 27.17 (2018), pp. 3452–3465.

Annotations: **USE THIS PAPER TO SET UP THE CONSERVATION UNITS FOR EIS.** This paper delineates and proposes a unit schema for defining populations for conservation. First is the Conservation Unit (CU) or the Evolutionary Significant Unit. This designation lumps populations based on their genetic composition and should be separated, ideally, by phylogeographic history (e.g., the GA and FL EIS populations). These conservation units would be delimited using all loci in a genomic dataset. ESUs can be subdivided further into management units and adaptive units. Management units are the short term currency of conservation, clustering populations based on their neutral genetic diversity. This delimits populations that are genetically unique from one another. Adaptive units are identified using potential adaptive loci. I could use outlier methods to identify putatively adaptive loci in the RAD data. Reseq data would be a better method for delimiting the AUs. In small populations, genetic drift may inflate the number of detected MUs, however, in large populations MUs may be falsely suppressed due to lingering ancestral alleles. This paper outlines a way to identify functional corridors for species accounting for gene flow between populations, as well as, habitat. Essentially, combine environmental and genetic connectivities to find overlaps in where gene flow is occurring and how it correlates with suitable habitats.

Mussmann et al.: BA3-SNPs: Contemporary migration reconfigured in BayesAss for next-generation sequence data

mussmann2019ba3snps

Steven M Mussmann, Marlis R Douglas, Tyler K Chafin, and Michael E Douglas. “BA3-SNPs: Contemporary migration reconfigured in BayesAss for next-generation sequence data”. In: *Methods in Ecology and Evolution* 10.10 (2019), pp. 1808–1813.

Petkova et al.: Visualizing spatial population structure with estimated effective migration surfaces

petkova2016EEMSDescription

Desislava Petkova, John Novembre, and Matthew Stephens. “Visualizing spatial popula-

tion structure with estimated effective migration surfaces”. In: *Nature genetics* 48.1 (2016), pp. 94–100.

Annotations: This paper describes the program EEMS. EEMS is based on a stepping stone model and estimates the rate in which genetic similarity decays between samples. This scheme has benefits over using PCAs or clustering methods because EEMS accounts for the geographic proximity of samples when comparing to genetic similarities. Although PCAs have been used to investigate the effects of IBD, these analyses have to be done *posthoc*. Clustering methods are susceptible to k estimation deviation caused by sampling bias. EEMS is unable to detect gene flow directionality because the base model assumes symmetric equal gene flow between populations. In the same vein that effective population size represents the idealized population size needed to maintain the levels of genetic diversity observed in a population, EEMS calculates effective migration rates that idealize the migration rate parameters under a stepping stone model that would produce the genetic decay or similarity between the given samples. EEMS also calculates effective diversity parameters within each deme that reflects the expected genetic dissimilarity between two individuals within a deme. This is somewhat analogous to expected heterozygosity within the deme. Demes with higher effective diversity are going to have higher levels of heterozygosity. For the resistance grids, their size is arbitrary so multiple scales should be tried based on the sampling density.

Zimmerman et al.: An empirical comparison of population genetic analyses using microsatellite and SNP data for a species of conservation concern

zimmerman2020empirical

Shawna J Zimmerman, Cameron L Aldridge, and Sara J Oyler-McCance. “An empirical comparison of population genetic analyses using microsatellite and SNP data for a species of conservation concern”. In: *BMC genomics* 21 (2020), pp. 1–16.

Annotations: This paper identified the differences between SNP and microsatellite markers for estimating demographic parameters (H_o , H_e , F_{is} , A_R) and population differentiation (f_{st} , g_{st} , $jostD$). Generally they found that the demographic parameters were correlated with each other except for H_o . Again found a high level of correlation between the population differentiation statistics, note that F_{st} and G_{st} are considered fixation indices and $JostD$ is considered an allelic differentiation metric. G_{st} estimates were higher in the microsatellites, however, the theoretical max heterozygosity for microsats is double that of SNPs, and given G_{st} is based on heterozygosity, it makes sense that this metric is higher. Finally, the authors found that there was similar ability of SNPs from a smaller sub-set of individuals to cluster genetically similar samples, compared to a full microsatellite dataset. There should be some caution used when placing too much emphasis on the ESUs or conservation units. Adaptive variation may be adaptive for a specific contemporary environment, but focusing on purifying the genetics of ESUs may lead to loss of future adaptive potential. There is the potential to consider the clustering of populations based on the presence of putatively adaptive alleles.