PBL MODULE 2 - Population Structure, Genetic Variation, and Conservation

General Info about this PBL assignment

There will be 3.5 classes available to do the assignment. In two classes you will be actively analyzing data (note the 2nd class is a work from home day – use this time valuably). The third class should be used to finish writing the document (thus strategize to have readings done and data fully analyzed by the start of the last class.

Background:

Within a remote artic region of Nunavut Canada, lies a landlocked freshwater lake called Lake Illiyardjuk (meaning orphan in Inuit). Within Lake Illiyardjuk resides an endemic, landlocked population of Illiyardjuk Walrus (*Odobenus rosmarus fictiousi*). This walrus subspecies derives from walruses that became trapped in Lake Illiyardjuk after the last glacial period (approximately 10,000 years ago). The Illiyardjuk Walrus population experienced a serious anthropogenic bottleneck during the 20th century and, despite a conservation recovery attempt in 1979 where 20 marine walruses were added to the lake, the lake population only numbers around 300 walruses. Previous studies based on both nuclear and mitochondrial DNA have shown that the Illiyardjuk Walrus has low genetic variability, especially compared to marine walrus populations (microsatellite-based estimates of expected heterozygosities of marine walruses range from $H_E = 0.80$ to $H_E = 0.89$. As the lake population has remained completely isolated for hundreds of generations, the fate of its gene pool is determined largely by population size and internal population structure.

Lake Illiyardjuk covers over 4,400 km^2, but the lake is very fragmented, with narrow straits separating its main basins. Telemetry studies have shown that adult Illiyardjuk walruses are relatively sedentary, but have also indicated that population connectivity could be maintained by dispersal of immature individuals nearing adulthood that may leave their birth areas to eventually find mates. However, little is known about how often this occurs or whether it is largely males or females that are dispersing within the lake population. Studies on marine walruses indicate that both sexes disperse from the natal region.

A scenario of substantial gene flow was supported by a previous study, showing weak differentiation at microsatellite loci between the northern and southern parts of the lake, albeit genetic sampling was low. However, another study recently reported strong mtDNA differentiation among the five main basins of Lake Illiyardjuk: Northern region, Kinapak region, Hawani region, Perpaluktok region, and Southern region (Figure 1). These contradictory results could be explained by the low amount of data in the earlier microsatellite assessment, but also by sex-biased gene flow.
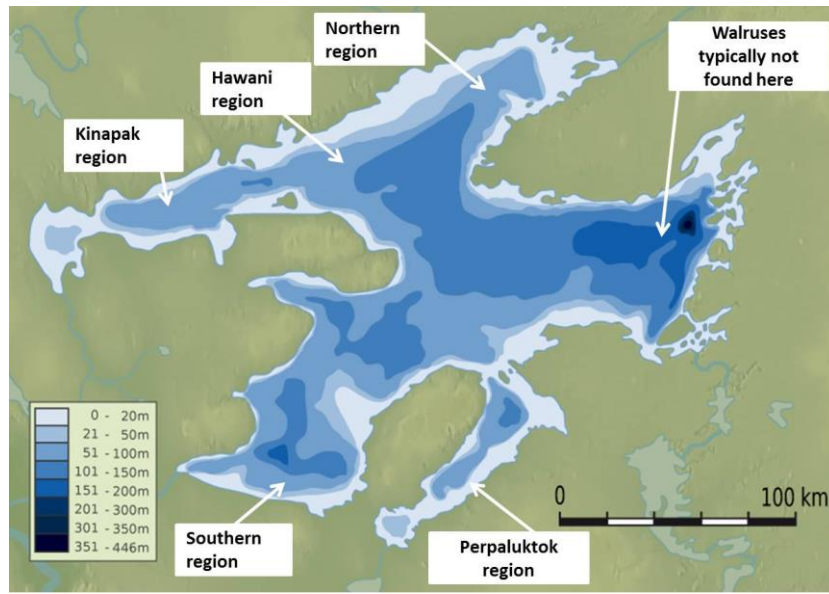
Figure 1. Lake Illiyardjuk and its 5 divided breeding regions.

Based on pleas from the Inuit near Lake Illiyardjuk, who revere the walrus, a local graduate student interested in evolution and conservation began to work on the walrus populations. She wanted to determine what processes were at play for the Illiyardjuk Walrus for the purposes of conservation of this critically endangered species and thus, genotyped individuals based on microsatellite loci. Unfortunately, the student disappeared during a collecting trip and was believed to be eaten by polar bears (a common occurrence in this region). She managed to genotype 172 individuals prior to her presumed death.

Your company has been hired by the local Inuit population to analyze the data. Your job is to examine the genetic diversity, population structure, and dispersal patterns in the Illiyardjuk Walrus based on the student's data and notebook. You will answer the following questions (see below).

Questions to answer for final report: (much of the data is likely best summarized in tables or graphs). **They do not need to be answered in any order, just have a logical write up.**

For all questions, you should explain what the results mean in terms of the current status of the lake walrus.

1. How does observed heterozygosity compare with expected across the 5 main breeding areas.
    a. What is the inbreeding coefficient (F – called fixation index in genalex) across the 5 breeding areas?

2. Has heterozygosity increased, stayed consistent, or decreased through time?
    a. Has inbreeding increased, stayed consistent, or decreased through time?

3. What is the mean inbreeding coefficient (Fis) for all populations?

4. What is the mean fixation index (Fst) for all populations?

5. What is the mean number of migrants (N_m) for all populations?

6. Are the five main breeding areas within the lake differentiated?
   a. How does the microsatellite data (Fst values) compare to the mitochondrial data?
   b. What do the Fst values suggest about dispersal across the breeding regions?
   c. What do Nei's genetic distance and genetic identity values suggest about population differentiation?

7. What are migration rates of males and females for the five main breeding areas?
   a. What does the number of migrants for each sex suggest about dispersal across the breeding regions?

Based on the above data and its implications, answer: Will the population be able to maintain variability? What conservation recommendations would you make for this population in terms of long term survival? **Make sure you justify your answer clearly and concisely.**

Methods derived from the missing student's notebook:

DNA was collected from tissue samples from Illiyardjuk walruses found dead. The majority of the sampled individuals were pups (<1 yrs; 76%) (Refer to Table 1). All specimens had been stored at -20°C. Microsatellite loci were amplified using original primers. PCR products were sequenced and allele peaks scored using GeneMapper v. 4.0 (Applied Biosystems). In addition to the microsatellite dataset (See the two excel files), there was mtDNA sequences from 145 individuals from the same population. However, all sequence data was lost and only calculated F_{ST} values across the populations were recorded by the student before her death (See third excel file).

The genotyped individuals originated from different parts of Lake Illiyardjuk and represent a time span of three decades (1980 – 2010). Of the five regions, the following number of samples were collected:

- Northern Illiyardjuk ($N = 15$)
- Kinapak region ($N = 20$)
- Hawani region ($N = 79$)
- Perpaluktok region ($N = 43$)
- Southern Illiyardjuk ($N = 15$)

Of the collected samples from individuals, the following samples were collected for each decade:

- the 1980s ($N = 59$)

- 1990s ($N = 48$)
- 2000s ($N = 65$)

A decade may be an appropriate time span to detect temporal changes, since the estimated generation time of the walrus is approximately 10 years.

Additional Research
You may want to do additional reading to help you form a cogent and intelligent argument and make appropriate recommendations based on the data (and your opinion based on reading). Feel free to share insights with your peers.
Some helpful papers may include: (Frankham, 1995; Lowe & Allendorf, 2010; Prugnolle & De Meeûs, 2002; Slatkin, 1987). Papers are uploaded to webcourses.

Report Format and Guidelines
Your report should be a <u>maximum</u> of 5 pages (not including references, figures and tables). Please only include necessary tables. Longer is not better, be concise! Use pages with 1" margins, a minimum of 11pt Times New Roman font (excluding Figures and Tables, minimum 8 pt. font) and single spacing at minimum. Set up your report as a scientific paper testing specific hypotheses. Include a title and your name. Outline the questions as the hypotheses you are testing. Your report should include a **very brief** introduction (no need to repeat what I know about the walruses), Brief Methods (just the ones **you** actually used), Results & Discussion (combined is fine), and a Conclusion. Your conclusion should summarize your key findings and make justified recommendations for conservation. An abstract is not necessary. Ensure all questions are adequately addressed. Your paper should be well cited where necessary and follow APA style. EndNote is recommended (I use APA 6th style). **Make sure to put in appropriate figure and table titles and legends.**

E.g.

Husband, B. C., & Schemske, D. W. (1996). Evolution of the magnitude and timing of inbreeding depression in plants. *Evolution*, *49*(8), 54-70.

References Cited:

Frankham, R. (1995). Conservation genetics. *Annual Review of Genetics, 29*(1), 305-327.
Lowe, W. H., & Allendorf, F. W. (2010). What can genetics tell us about population connectivity? *Molecular Ecology, 19*(15), 3038-3051.
Prugnolle, F., & De Meeûs, T. (2002). Inferring sex-biased dispersal from population genetic tools: a review. *Heredity, 88*(3), 161-165.
Slatkin, M. (1987). Gene flow and the geographic structure of natural populations. *Science, 236*(4803), 787-792.