Working outline of genomics chapter

Research questions/objectives:

1. Evaluate the genetic structure of the Interior Population
2. Quantify the genetic differentiation of the IP from RMP and PCP lineages
3. Measure gene flow among IP swans to assess contemporary gene flow

Objective paragraph:

* Knowledge of the genetic variability of the IP is necessary for a comprehensive evaluation of the long-term viability of the population and will inform future conservation and management strategies.
* This information will complement ongoing studies of trumpeter swan annual cycle movement patterns to evaluate current migration trends and inform potential resiliency to climate shifts.
* We aim to assess the current genetic structure and connectivity of the IP and evaluate genetic trends since the reintroduction from source populations.

Intro

1. Background on the decline/history of trumpeter swans in North America
2. Overview of IP reintroductions
3. Overview of TRUS population genetic knowledge and info gaps
4. Benefits and potential applications of filling those gaps
5. Study objectives (and predictions?)

Methods

1. Study area description
   1. Overall spatial extent, overall timeframe of captures and deployments, description of habitats and/or ecoregions, dominant spp?
2. Capture/handling and blood extraction details
   1. Took whole blood from…., stored on FTA cards or feather clips, etc
3. DNA Extraction
4. Library prep and sequencing
   1. Mention restriction enzymes, Illumina hardware
5. Bioinformatics from raw sequence files till vcf files post-STACKS
   1. Trimming and filtering
      1. Trimmed adaptor sequences
      2. STACKS::process\_radtags
   2. Alignment
      1. Downloaded reference genome from NCBI (GCA\_019232035.1/GCA\_019232035.1\_ASM1923203v1\_genomic.fna)
      2. Made index with bwa (default parameters)
      3. Ran alignment of samples to ref genome:
         1. Bwa mem (aligned with Burrows-Wheeler Alignment tool)
         2. Samtools view (created sam file)
         3. Samtools sort (saved as bam file)
   3. Ran STACKS::ref\_map.pl (add description)
   4. Ran gstacks modele
6. Popgen analyses