

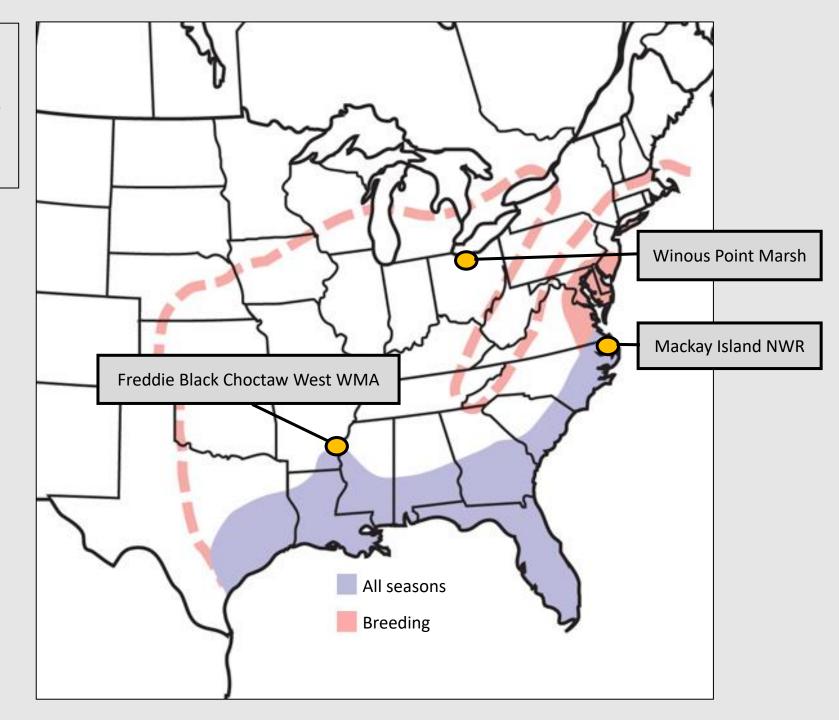
Carol Gause and Megan Linke

**Population Genomics** 

Final Project

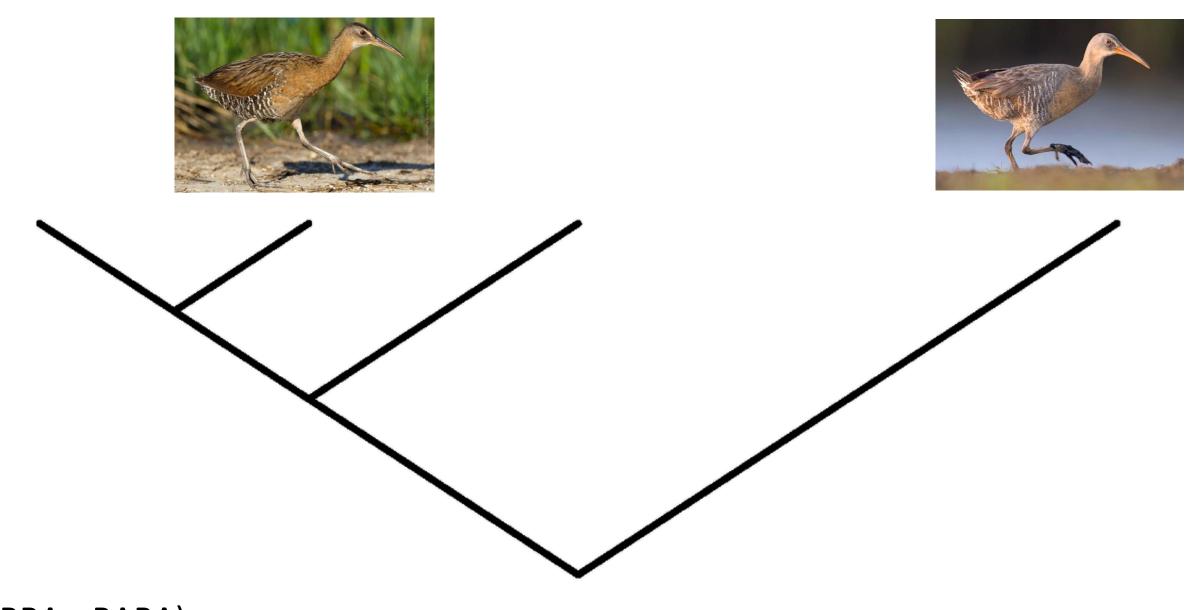
# Comparing three geographically separate populations

- Separated by location and migratory status
- Migration = gene flow?
  - Not all rails migrate



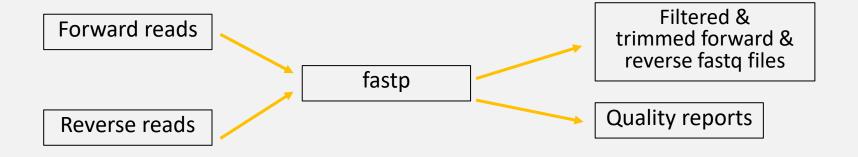
## Migration Routes





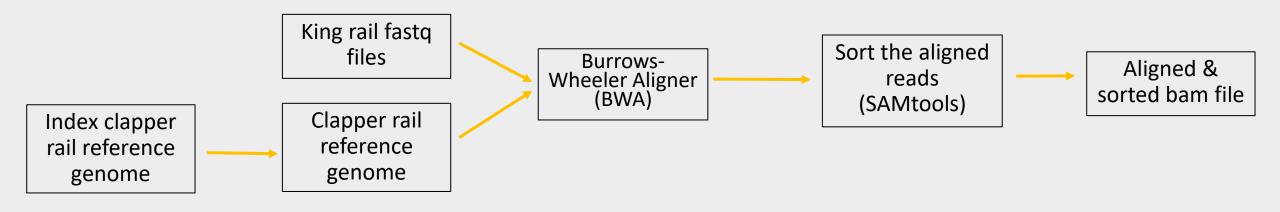
(nABBA-nBABA)
(nABBA+nBABA) = Patterson's D (ABBA-BABA statistic)

### Step 1: Preprocessing using fastp



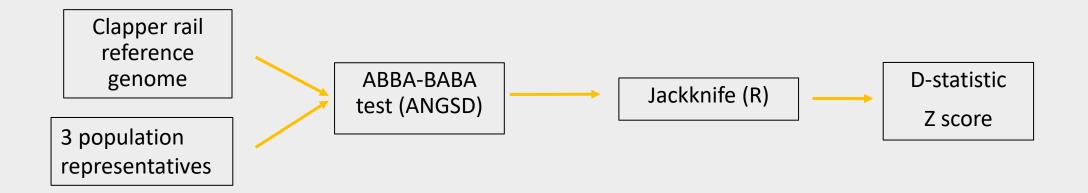
Filtering result	
reads passed filters:	103.512868 M (97.867706%)
reads with low quality:	2.206578 M (2.086240%)
reads with too many N:	4.294000 K (0.004060%)
reads too short:	44.416000 K (0.041994%)

#### Step 2: Mapping



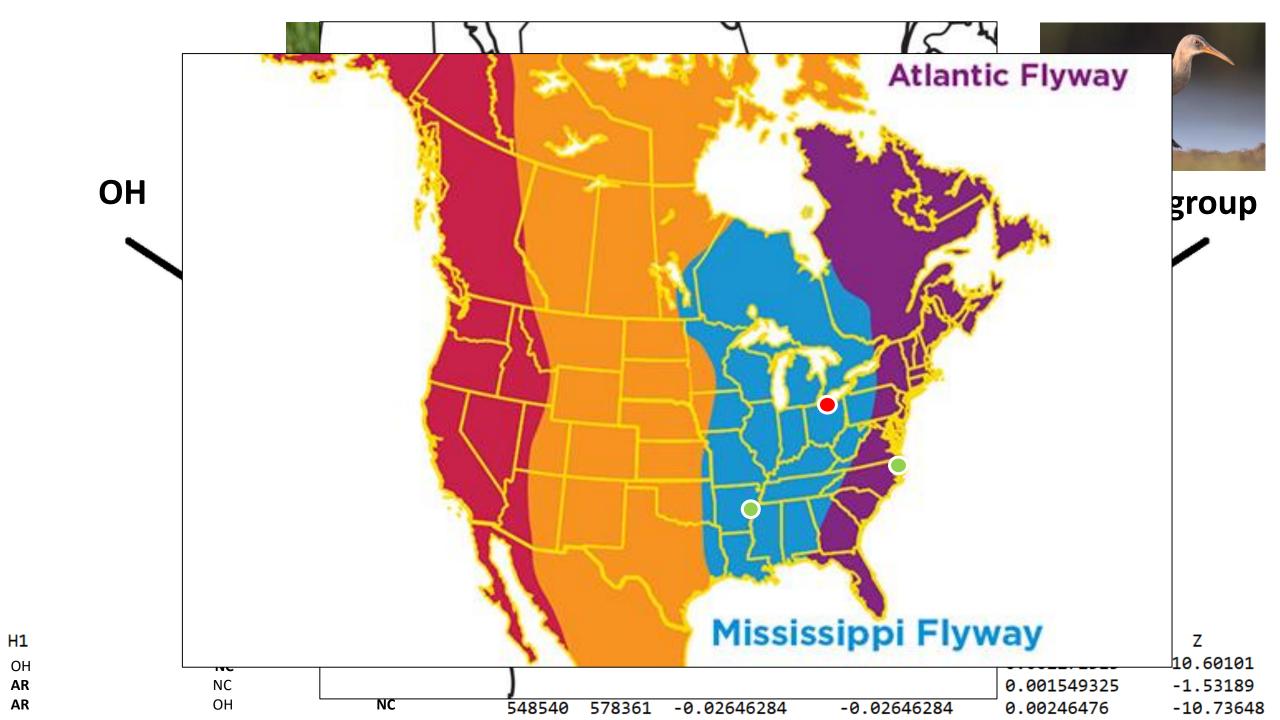
```
-rw-rw-r-- 1 gausec21 gausec21 10G Apr 26 19:02 11105.bam — AR -rw-rw-r-- 1 gausec21 gausec21 13G Apr 26 19:03 6026.bam — OH -rw-rw-r-- 1 gausec21 gausec21 6.7G Apr 26 19:04 RK02.bam — NC
```

#### Step 3: ABBA-BABA test



Individual population representatives were chosen carefully:

- All females
- ~1 year sample window
- Sampled during the breeding season
- Resident population individuals are confirmed residents



Questions?

