Computing Oak Divergence Using MUMMER Alignments

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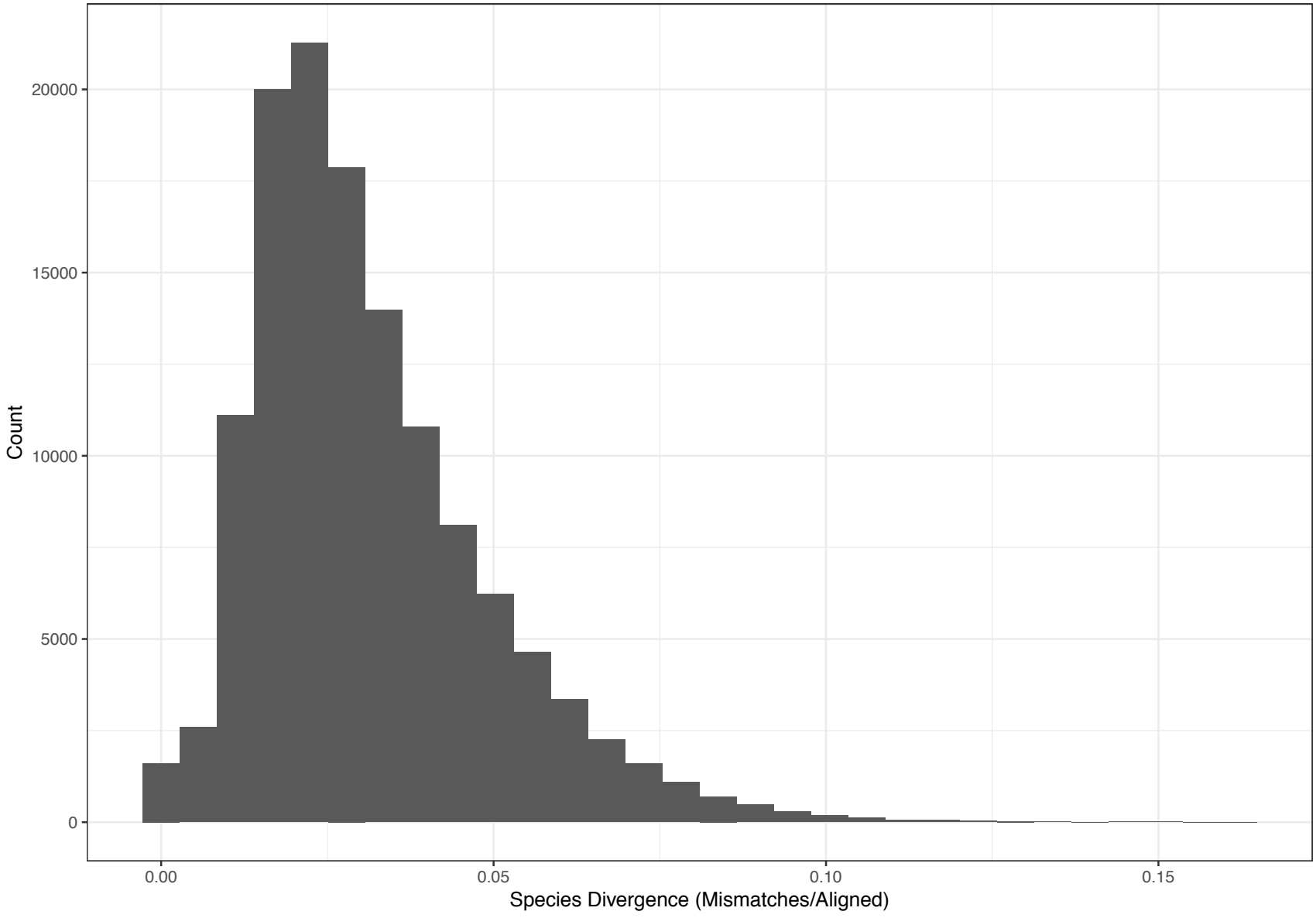
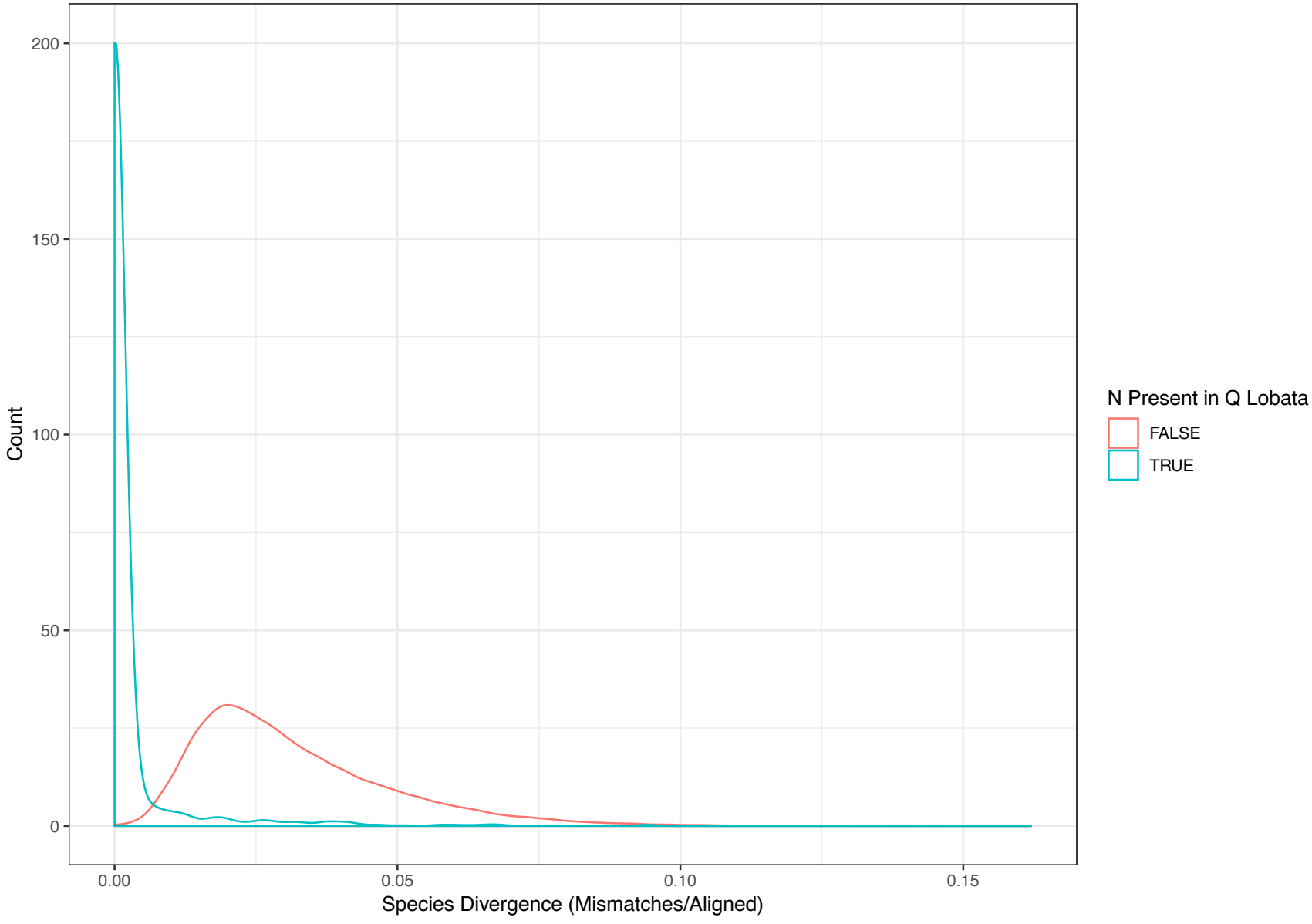
Processing of Data

1. Used .coords file and Sorel's "chromosome name to scaffold and orientation table" to convert 2017 Q Lobata alignment coordinates to 2018 Q Lobata alignment coordinates
2. Removed all alignments that weren't on chromosomes
3. Used remaining alignment coordinates to extract nucleotide sequences from Q Robur and Q Lobata
4. Nucleotide sequences were differing lengths because of indels, so globally aligned sequence pairs using NW algorithm. Insertions were indicated with "_". Now Sequences are the same length and have 1-1 alignment.
5. Currently 128,513 Alignment pairs out of 129,162 finished computing (99.5%). 30 Pairs were too large for NW align.

There's some variability of divergence across alignment coordinates



I think runs of N's contribute to this



Aligned N's Count as matches. Only last 6 bases are nucleotides.

```
## [1] "NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
## [1] "NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
## [1] 724
## NNNCAAATCT
```

Divergence Estimates by N

Total Divergence for everything: 0.0275034

Table 1: Table continues below

NPresent	Divergence	Alignments	TotalLength	NumberOfMatches
FALSE	0.02758	126917	498540988	484790888
TRUE	0.002726	1596	1554477	1550239

NumberOfMismatches
13750100
4238

Next Steps

1. Remove Repeats, SNPs near Runs of Ns, and CDS.
2. Sorel also has GATK called variants where Q Robur and Q Lobata were aligned to a reference genome. I think Computing divergence for this should be easier because scripts exist.