Sequence Concatenator Report

Generated: 2025-06-25 19:54:47

Input Files:

- input1.fasta
- input2.nex.nex

Summary:
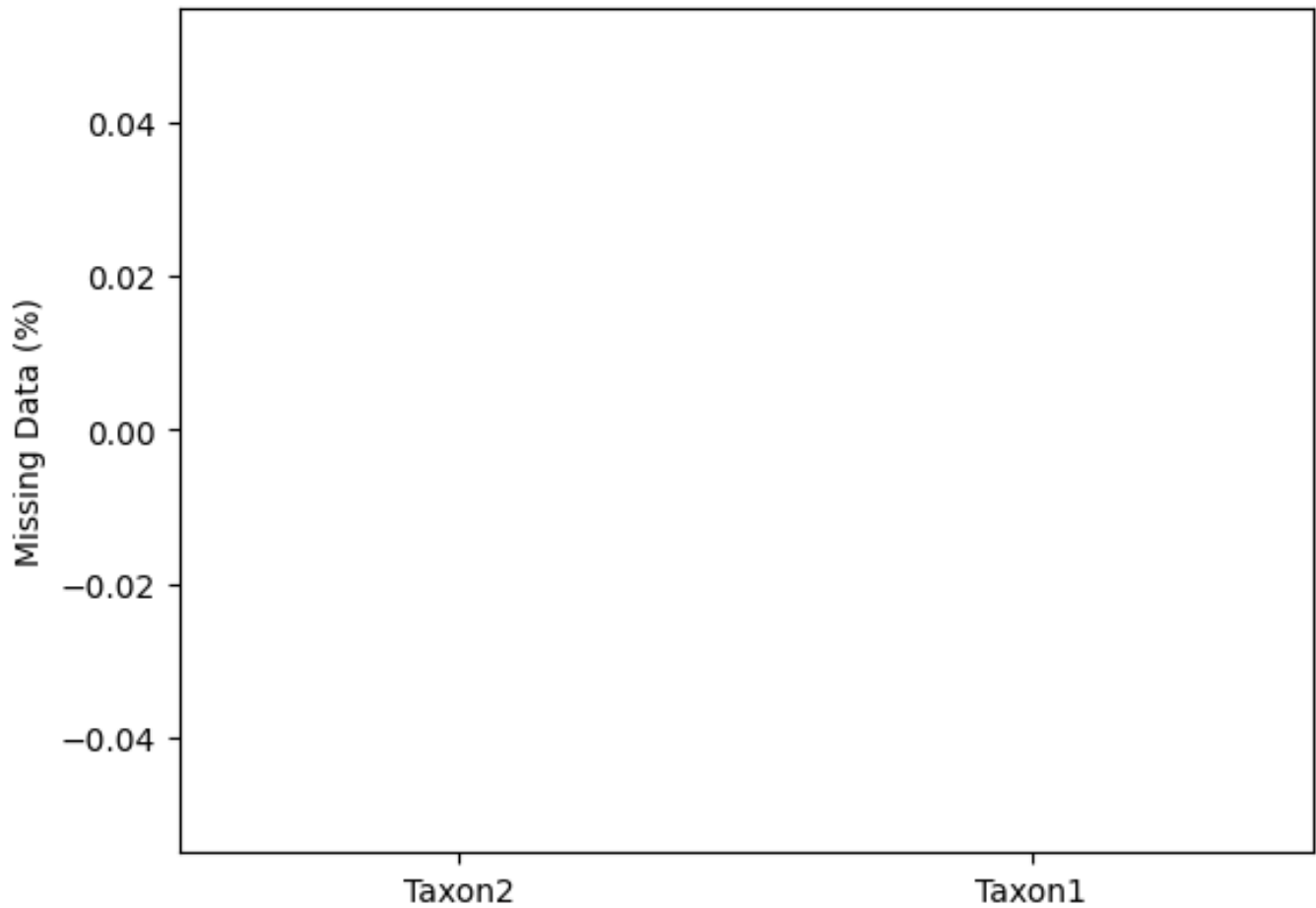
Taxa: 2
Alignment length: 12 bp
Missing data: 0 (0.0%)

Partitions:

- gene1: 1-6
- gene2: 7-12

Partition Lengths