|  |  |
| --- | --- |
| **Description** | **File name** |
| BLAST results | alignmenthittable[1,2,6,7,8,9,10].csv |
| Top BLAST hits | alignfinal.txt |
| Script for getting top blast hit | align.sh |
| Fasta files for 10 blast results for top hits in alignment | sequence[1,2,6,7,8,9,10].fasta |
| Script for muscle build, search, and hits | HMM\_script.sh |
| Muscle alignments | sequence[1,2,6,7,8,9,10].txt |
| HMM builds | sequence[1,2,6,7,8,9,10].hmm |
| HMM searches | sequence[1,2,6,7,8,9,10]\_[Control[1-2]protein.fasta\_cl, Obese[1-2]protein.fasta\_cl].txt |
| Short answer primate sequences | sequence[1,6]\_primate.fasta |
| Short answer nonmammal sequences | sequence[1,6]\_nonmammal.fasta |
| Muscle alignments | sequence[1,6]\_primate.txt |
| Muscle alignments | sequence[1,6]\_nonmammal.txt |
| HMM builds | sequence[1,6]\_primate.hmm |
| HMM builds | sequence[1,6]\_nonmammal.hmm |
| HMM searches | sequence[1,6]\_primate\_[Control[1-2]protein.fasta\_cl, Obese[1-2]protein.fasta\_cl].txt |
| Total hits in searches | HMM\_hits.txt |
| Individual hit tables for graphing | sequence[1,2,6,7,8,9,10]\_hits.txt |
| Script for bar graphs of hits | biogroupproject.py |
| Final bar graphs for each sequence | sequence[1,2,6,7,8,9,10]hits.pdf |

Table 1. Relevant files and descriptions in Bioinformatics\_Group\_Project