CSCI 490 Term Project B

Planning Report

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-Sample maf data for comparison to true alignment for each species

##maf version=1 scoring=maf\_project.v12

# maf\_project.v12 simali.output.maf HUMAN

a score=0.0

s HUMAN 0 437 + 23304 CTC-----AGATTCCTGTACTTGCATGTGTGGGTA

s CHIMP 0 437 + 23462 CTC-----AGATTCCTGTACTTGCATGTGTGGGTA

s BABOON 0 430 + 24309 CTC-----AGATTTCTGTACTTGCATGTGTGGGTA

s RAT 0 246 + 16222 CTC-----CTATTCCAGCACCTTGATTTGAGGGTG

s MOUSE 0 523 + 15788 CTC-----ACATTTCAGCACCTTGATGTGAGGGTG

s DOG 0 239 + 22528 CGCGTTCTCGATTCCTGGA-TTTCATGTGTGGGTA

s CAT 0 250 + 22812 CTC-----CAATTCCTGGACTTTCATGTGTGGGTA

s PIG 0 215 + 18803 -TC-----TGATTCCTGGACCTACATGTGTGGGTA

s COW 0 222 + 23593 TTC-----TGATTCCTAGGCTTGCATGTGTGGGTA

This program will be written in C++11. It will be based on project 2. Blast will be used to produce computed alignment of each species. The same basic program will be run to compute sensitivity and specificity. New methods will be written to handle inversions. Inversion will be ignored and saved for later computing of overall sensitivity and specificity. Comparisons will be run automatically by running through all selected files in the directory that contains the maf and true alignment files. Once the average sensitivity and specificity has been computed for each alignment standard deviation will be computed and graphed for easy comparison.

Libraries to be used will include:

**#include** <iostream>

**#include** <iomanip>

**#include** <string>

**#include** <fstream>

**#include** <algorithm>

**#include** <map>

**#include** <iterator>

**#include** <cstddef>

**#include** <vector>

**#include** <stdio.h>

**#include** <stdlib.h>

**#include** <ctype.h>

**#include** <cmath>

**#include** <sys/types.h>

**#include** <dirent.h>

**#include** <errno.h>