Summary

Practical 10 Genomics\_sequence\_analysis

**Result:**

The result of running output is concluded in the following table.

|  |  |  |  |
| --- | --- | --- | --- |
|  | Human\_mouse | Human\_random | Mouse\_random |
| Hamming distance | 23 | 210 | 219 |
| Percentage identity | 89.6% | 5.4% | 5.9% |
| Biosum62 score | 1091 | -250 | -250 |

(although the scores will be slightly different using different matrix, but the tendency is similar and these scores could indicate the ‘simple’ distance between the sequences.)

**Interpretation:**

There will be more mismatched amino acids, base pairs and gap in more distant sequence and these contributes to the simple ‘sequence distance’.

From lecture there are different types of mutations in the DNA sequence and consequently may result different amino acid which could change the functions, physicochemical properties of protein. However, huge changes in the sequence are less likely to maintain during evolution not only because of the correct system in the organisms but also because large changes may lead to dysfunctional proteins endanger the organisms. Identical or similar sequences or amino acids pairs indicate probably signature of evolutionary constraint and same ancestor in the evolution tree.

Human beings and mice are mammal so their sequences show the similarity.