

Gorilla Report

August, Johannes, Jonas, Martin, Michelle, Thomas, Danny
Group K

September 23, 2020

Results

Our implementation produces the expected results on all pairs of species, but as the given output file compares in an almost random order, it has only been manually compared.

We compared the species in HbB_FASTAs-in.txt with the common rat, given by

```
MVHLTDAEKA AVNALWGKVN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS
SASAIMGNPK VKAHGKKVIN AFNDGLKHLD NLKGTFAHLS ELHCDKLHVD
PENFRLLGNM IVIVLGHHLG KEFTPCAQAA FQKVVAGVAS ALAHKYH
```

The closest species to *Rattus rattus* is human, with score 653 and with the following optimal alignment:

```
MVHLTDAEKA AVNALWGKVN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS
SASAIMGNPK VKAHGKKVIN AFNDGLKHLD NLKGTFAHLS ELHCDKLHVD
PENFRLLGNM IVIVLGHHLG KEFTPCAQAA FQKVVAGVAS ALAHKYH
```

```
MVHLTPEEKS AVTALWGKVN VDEVGGEALG RLLVVYPWTQ RFFESFGDLS
TPDAVMGNPK VKAHGKKVLG AFSDGLAHLN NLKGTFAHLS ELHCDKLHVD
PENFRLLGNV LVCVLAHHFG KEFTPPVQAA YQKVVAGVAN ALAHKYH
```

Implementation details

We chose a naive iterative implementation with backward trace back.

For two sequences of length n and m , respectively, our implementation uses $O(nm)$ time and $O(nm)$ space.