

Gorilla Report

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October 5, 2022

Results

Our implementation produces the expected results on all pairs of specie. We tested our output against the out-file and there were no differences, when they were sorted accordingly.

We compared the species in HbB_FASTAs-in.txt with the a Gorilla, given by

```
MVHLTPEEKS AVTALWGKVN VDEVGGEALG RLLVVYPWTQ RFFESFGDLS
TPDAVMGNPK VKAHGKKVLG AFSDGLAHLN NLKGT FATLS ELHCDKLHVD
PENFKLLGNV LVCVLAHHFG KEFTPPVQAA YQKV VAGVAN ALAHKYH
```

The closest species to a Gorilla is a Spider, with the following optimal alignment:

```
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLS
-VHLTGEEKAAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLS

TPDAVMGNPKVKAHGKKVLGAFSDGLAHLNKLKGT FATLSELHCDKLHVD
TPDAVMSNPKVKAHGKKVLGAFSDGLAHLNKLKGTFAQLSELHCDKLHVD

PENFKLLGNVLVCVLAHHFGKEFTPPVQAA YQKV VAGVANALAHKYH
PENFRLLGNVLVCVLAHHFGKEFTPQLQAA YQKV VAGVANALAHKYH
```

Implementation details

We chose a iterative bottom-up implementation. For two sequences of length n and m , respectively, our implementation uses $O(mn)$ time and $O(mn)$ space.