

Gorilla Report

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Results

Our implementation produces the expected results on all pairs of species.

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

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

The closest species to *Rattus rattus* is [*HomoSapiens*], with the following optimal alignment:

```
MVHLTDAEKA AVNALWGKVN PDDVGGEALGRLL VVYPWTQRYFDSFGDLSSAS AIMGNPKVKAHGKKVINA
MVHLTPEEKSAVTAL WGKVNVDDEVGGEALGRLL VVYPWTQRFESFGDLSTPD AVMGNPVKAHGKKVLGA

FNDGLKHLN NLKGTFAHLS ELHCDKLHVDPENF RLLGNMIVIVLGHHLGKEF TPCAQA AFQKVVAGVASALAHKYH
FSDGLAHLN NLKGTFAHLS ELHCDKLHVDPENF RLLGNVLCVLAHHFGKEF TPPVQAAYQKVVAGVANALAHKYH
```

Implementation details

After implementing both we chose the iterative implementation because of a better resolution time. For two sequences of length n and m , respectively, our implementation uses $O(nm)$ time and $O(2nm)$ space. The timing of the algorithm `HbB_FASTAs-in.txt` including the *Rattus Rattus* took 2.61 s.