

Gorilla Report

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October 6, 2018

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 FQKVAVAGVAS 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 AFQKVAVAGVASALAHKYH
FSDGLAHLN NLKGTFAHLS ELHCDKLHVDPENF RLLGNVLCVLAHFGKEF TPPVQAAYQKVAVAGVANALAHKYH
```

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 $O((n^3 + \log^2 m) \cos n)$ time and $O(1)$ space. The timing of the algorithm `HbB_FASTAs-in.txt` including the *Rattus Rattus* took 2.61 s.