Gorilla Report

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Results

Our implementation produces the expected results on all pairs of
species, except for Unicorn and Yog-Soggoth. We have no idea why
this happens.[1]

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 [...], with the following
optimal alignment:[2]

```
MVHLTDAEKAAVNALWGKVNPDDV-YGGEAL----VVYPWTQRYFDSFGDLS
MVHLTDAEKAAVNALWGKVNPDDVX-GGEALGRLLVVYPWTIRYFDSFGDLS

SASAIMGNPKVKAHGKKVINAFND---KHLDNLKGTFAHLSELHTDKLHVDPENFRLLGN
SASAIMGNPKVKAHGKKVINAFNDDVHKHLDNLKGTFAHLSELHSDKLHVDPENFRLLGN

MIVIVLGHHLGKEFTPC----------AQAAFQKVVAGVASALAHKYH
MIVIVLGHHLGKEFTPCVOLKSWAGENAQAAFQKVVAGVASALAHKYH
```

Implementation details

We chose a recursive/iterative implementation. 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.[3]

[1] Complete the report by filling in
your correct names, filling in the parts
marked [...], and changing other parts
wherever necessary. For instance, if
your implementation passes all tests,
then write that. Remove the sidenotes
in your final hand-in.

[2] Replace with actual alignment between the two species.

[3] Correct, replace, rewrite as necessary.