

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 AFNDGLKHLN NLKGTFAHLS ELHCDKLHVD
PENFRLLGNM IIVILGHHLG KEFTPCAQAA FQKVVAGVAS ALAHKYH
```

The closest species to *Rattus rattus* is [...], with the following optimal alignment:²

```
MVHLTDAEKA AVNALWGKVN PDDV - YGGEAL - - - VVYPWTQRYFDSFGDLS
MVHLTDAEKA AVNALWGKVN PDDVX - GGEALGRLLVVYPWTIRYFDSFGDLS

SASAIMGNPK VKAHGKKVIN AFND - - - KHLN NLKGTFAHLS ELHTDKLHVD PENFRLLGN
SASAIMGNPK VKAHGKKVIN AFND DVH KHLN NLKGTFAHLS ELHSDKLHVD PENFRLLGN

MIVILGHHLG KEFTPC - - - - - AQA AFQKVVAGVAS ALAHKYH
MIVILGHHLG KEFTPC VOLKSWAGENAQA AFQKVVAGVAS ALAHKYH
```

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.