

# 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 FQKVVGAVAS ALAHKYH
```

The closest species to *Rattus rattus* is Human, with the following optimal alignment:

```
Human 1.: MVHLTPEEKS AVTALWGKVN VDEVGGEALG RLLVVYPWTQ RFFESFGDLS
Rat    1.: MVHLTDAEKA AVNALWGKVN PDDVGGEALG RLLVVYPWTQ RYFDSFGDLS

Human 2.: TPDVAMGNPK VKAHGKKVLG AFSDGLAHLN NLKGTFAHLS ELHCDKLHVD
Rat    2.: SASAIMGNPK VKAHGKKVIN AFNDGLKHLN NLKGTFAHLS ELHCDKLHVD

Human 3.: PENFRLLGNV LVCVLAHHFG KEFTPPVQAA YQKVVGAVAN ALAHKYH
Rat    3.: PENFRLLGNM IVIVLGHHLG KEFTPCAQAA FQKVVGAVAS ALAHKYH
```

## Implementation details

We chose a recursive implementation. For two sequences of length  $n$  and  $m$ , respectively, our implementation uses  $O(nm)$  time and  $O(nm)$  space.