

Gorilla Report

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1 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
PENFRLGNM IVIVLGHHLG KEFTPCAQAA FQKVVGAVAS ALAHKYH
```

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

```
Human--Rattus: 653
MVHLTPEEKSAVTALWGKVNVDDEVGGEALGRLLVVYPWTQRFFESFGDL
MVHLTDAEKA AVNALWGKVN PDDVGGEALGRLLVVYPWTQRYFDSFGDL

STPDVAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFAHLSELHCDKLH
SSASAIMGNPKVKAHGKKVINAFNDGLKHLN NLKGTFAHLS ELHCDKLH

VDPENFRLLG NVLVCVLAHFGKEFTPPVQAAYQKVVAGVANALAHKYH
VDPENFRLLG NMIVIVLGHHLGKEFTPCAQA AFQKVVGAVASALAHKYH
```

2 Implementation details

We chose an iterative implementation, where we use an array `T` to keep hold of the trace and values `-1`, `1` and `0` to represent the path taken in the array `M`.

For two sequences of length n and m , respectively, our implementation uses $O(mn)$ time and $O(mn)$ space (for two 2-dimensional arrays of type `int`).