

# *Gorilla Report*

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## *Results*

Our implementation produces the expected results on all pairs of species. Even though the alignments are not precisely the same as the out-files, they are optimal solutions (I.E. of optimal cost/value). The output after solving the smallest input file (the Toy-file) is:

```
File: Toy_FASTAs-in.txt
Sphinx--Bandersnatch: 5
KQRK
KA-K
Sphinx--Snark: -8
KQR-K-----
KQRIKAAKABK
Bandersnatch--Snark: -18
K---A-K---
KQRIKAAKABK
```

## *Implementation details*

We have chosen the bottom-up approach, creating an  $m \times n$  matrix. This matrix is filled with values for the possible alignments, taking  $O(m * n)$  time and space to create.