

SHRiMP

Summary

SHRiMP is a an aligner from the University of Toronto which uses a vectored Smith-Waterman for alignment. Although it is slow, it detects alignments with high sensitivity and accuracy. It supports color space data.

Available on

[Fourierseq](#) - current version: 2.2.1 (updated 11/14/11).

[Phylocluster](#) - version: 2.0

User documentation

- To get started using SHRiMP, read through the [the SHRiMP documentation](#).

How to run SHRiMP

SHRiMP (rmapper) results can vary greatly based upon the input parameters. So please select parameters accordingly.

The base commands on Fourierseq are:
for color space:

```
gmapper-cs
```

and for base space:

```
gmapper-ls
```

The input parameters that we typically use with color space data are the following:

```
gmapper-cs -p opp-in -N 4 -1 F3/V3BC17_RNA.csfasta -2 F5/V3BC17_RNA.csfasta /home/scott/Downloads/mouse.rna.fna  
> bc17.sam 2> bc17.log &
```

Tip: To view the actual alignments in base space as part of the output file, add -p option (prettyprint).