

# ruby-libssw

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## Summary

Ruby-libssw is the Ruby binding of libssw, a library that uses the Smith-Waterman algorithm to find the best pairwise alignment of two sequences. ruby-libssw was created using fiddle, the Ruby standard library. Ruby-libssw can be used to create local alignments of nucleotide and amino acid sequences in the Ruby language.

Code : <https://github.com/kojix2/ruby-libssw>

## Statement of need

(“SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications | PLOS ONE”  
n.d.)

## Benchmark

## Examples

```
require 'libssw'

ref_str = "AAAAAAAAACGTTAAAAAAAAA"
ref_int = SSW::DNA.to_int_array(ref_str)
# [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 2, 3, 3, 0, 0, 0, 0, 0, 0, 0, 0]

read_str1 = "ACGTT"
read_str2 = SSW::DNA.revcomp(read_str1)
# "AACGT"

read_int1 = SSW::DNA.to_int_array(read_str1)
# [0, 1, 2, 3, 3]
read_int2 = SSW::DNA.to_int_array(read_str2)
# [0, 0, 1, 2, 3]

mat = SSW.create_scoring_matrix(SSW::DNA::Elements, 2, -2)
# mat = [2, -2, -2, -2, 0,
#        -2, 2, -2, -2, 0,
#        -2, -2, 2, -2, 0,
#        -2, -2, -2, 2, 0,
#        0, 0, 0, 0, 0]

profile1 = SSW.init(read_int1, mat)
align1 = SSW.align(profile1, ref_int, 3, 1, 1, 0, 0)
pp align1.to_h
# {
```

```

# :score1      => 10,
# :score2      => 0,
# :ref_begin1  => 8,
# :ref_end1    => 12,
# :read_begin1 => 0,
# :read_end1   => 4,
# :ref_end2    => 0,
# :cigar       => [80],
# :cigar_len   => 1,
# :cigar_string => "5M"
# }

profile2 = SSW.init(read_int2, mat)
align2   = SSW.align(profile2, ref_int, 3, 1, 1, 0, 0)
pp align2.to_h
# {
# :score1      => 10,
# :score2      => 0,
# :ref_begin1  => 7,
# :ref_end1    => 11,
# :read_begin1 => 0,
# :read_end1   => 4,
# :ref_end2    => 0,
# :cigar       => [80],
# :cigar_len   => 1,
# :cigar_string => "5M"
# }

puts SSW.build_path(read_str1, ref_str, align1)
# 5M
# ACGTT
# ||||
# ACGTT

```

## Reference

“SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications | PLOS ONE.”  
n.d. Accessed May 24, 2022. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0082138>.