Cython assignment

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1. The general modifications that you have done in your code

The code of both the original and the improved versions can be founr in sections 4 and 5.

The general modifications imply static type declarations where possible. That means that variables will be defined using C types, such as int, char or list, while functions will be defined using cdef or cpdef (in case it needs to be accessed from actual python interpreters). I also added memory views to numpy matrixes to efficiently access those matrixes.

Some Cython parameters were also tweaked to allow faster runtimes and/or to properly execute the functions as they were coded.

2. The performance of your code as millions of cells processed per second, and factor out this performance indicating the codification efficiency, the processor throughput and the H/W speed.

The overall performance improvements are compared below:

Original version:

Improved version:

Perf stats of the improved version

biom-4-3@aolin-login:~/Escritorio/github/masters/module_v/APM-II/late_ass\$ perf stat python -c 'import my_imp as align; align.align("seq20K.txt", "seq20K.out")'

Performance counter stats for 'python -c import my_imp as align;

```
0,998 CPUs utilized
   22152,61 msec task-clock
         78
                context-switches
                                               0,004 K/sec
                 cpu-migrations
                                          #
                                              0,000 K/sec
    3379879
                 page-faults
                                          # 0,153 M/sec
74645953879
                 cvcles
                                             3,370 GHz
                 stalled-cycles-frontend
                                          # 39,89% frontend cycles idle
29777446271
 8305212734
                 stalled-cycles-backend
                                              11,13% backend cycles idle
                 instructions
                                             2,10 insn per cycle
156420710761
                                               0,19 stalled cycles per insn
                                          # 1022,483 M/sec
22650669559
                 branches
                                               0,04% of all branches
    9990243
                 branch-misses
22,192649466 seconds time elapsed
17,409475000 seconds user
4,742222000 seconds sys
```

align.align("seq20K.txt", "seq20K.out")':

Performance metrics

OpRate

Operations/Instructions:
20000 * 10/156420710761=0.0000012786

Instructions per cycle (IPC)
2,10

Clock frequency
n_cycles/elapsed time (s):
74645953879/22,192649466=3363544041.61 (cells per second)

CPU time
instructions/(IPC * clock frequency)
156420710761/(2,10 * 3363544041.61)=22.1451099857 (H/W speed)

3. The reasons that make your code faster than the original Python version.

- 1. Tweak Cython to assume that some errors are not present in the code. That includes @cython.wraparound(False) and @cython.initializedcheck(False).
- 2. Use memory views were possible. It is the case for the dp_matrix that we use in many of the functions.
- 3. Define variables as C data types, specially focusing on the most computationally expensive function (align_edit_distance). That includes:
- Defining both input and output variables in the function definitions.
- Change strings to chars, python int and lists to C int and lists.
- Encode and decode chars when neded to call functions or python methods.

4. Original code

ALIGN with EDIT DISTANCE

```
def align_edit_distance ( pattern, text ):
  dp_matrix= [[0 for _ in range(len(text)+1)] for _ in range(len(pattern)+1)]
  for v in range(len(pattern)+1):
   dp_matrix[v][0] = v
  for h in range(len(text)+1):
   dp_matrix[0][h] = h
  # Compute DP Matrix
  for h in range(1,len(text)+1):
   for v in range(1,len(pattern)+1):
      dp_{matrix}[v][h] = min (dp_{matrix}[v-1][h-1] + (0 if pattern[v-1]==text[h-1] else 1),
                             dp_{matrix}[v][h-1] + 1,
                             dp_matrix[v-1] [h] + 1)
  return dp_matrix
## Backtrace to generate OPTIMUM CIGAR
def backtrace_matrix ( pattern, text, dp_matrix ):
 v = len(pattern)
 h = len(text)
  cigar = []
  while v>0 and h>0:
    if dp_matrix[v][h] == dp_matrix[v-1][h] + 1:
      v -= 1
      cigar.insert(0,"D")
   elif dp_matrix[v][h] == dp_matrix[v][h-1] + 1:
      cigar.insert(0,"I")
    else:
      v -= 1
      h -= 1
      if pattern[v] == text[h]:
       cigar.insert(0,"M")
      else:
        cigar.insert(0,"X")
  if v>0:
   for _ in range(v): cigar.insert(0,"D")
   for _ in range(h): cigar.insert(0,"I")
  return cigar
def write_cigar( C, ofile ):
  last="A"
  count=0
  ofile.write("CIGAR=")
  for v in C:
   if v == last:
      count += 1
   else:
      if count != 0:
       ofile.write(str(count)+last)
      last=v
```

```
count=1
  if count != 0:
   ofile.write(str(count)+last)
  ofile.write("\n")
  return
def align(in_filename, out_filename):
  in_filename: input file containing pairs of sequences to align
  out_filename: output file with alignment cigars for input pairs
  ## Opening input & output
  infile = open(in_filename)
  outfile = open(out_filename, 'w')
  pattern= infile.readline()
  text
        = infile.readline()
  N=0
  while (len(pattern) and len(text) > 1):
         = align_edit_distance ( pattern[1:], text[1:] )
   cigar = backtrace_matrix ( pattern[1:], text[1:], dp )
   outfile.write(str(N)+"\t")
   write_cigar ( cigar, outfile )
   pattern= infile.readline()
   text = infile.readline()
   N += 1
  infile.close()
  outfile.close()
if __name__ == "__main__":
  import argparse as arg
  parser = arg.ArgumentParser(prog='ARGUMENTS', usage='%(prog)s [options]')
 parser.add_argument("input", type=str, help="File containing ALL pairs of genome sequences")
  parser.add_argument("output", type=str, help="Output file name.")
  args = parser.parse_args()
  align(str(args.input), str(args.output))
5. Improved code
## ALIGN with EDIT DISTANCE
import numpy as np
import cython
@cython.wraparound(False)
@cython.initializedcheck(False)
cpdef int [:,:] align_edit_distance (char *pattern,char *text ):
  vsz= len(pattern)+1
```

```
hsz= len(text)+1
  cdef int v, h
  cdef int [:, :] dp_matrix
  dp_matrix = np.zeros( (vsz,hsz), dtype= np.int32 )
  for v in range(vsz):
   dp_matrix[v,0] = v
  for h in range(hsz):
   dp_matrix[0,h] = h
 for v in range(1,vsz):
   for h in range(1,hsz):
      dp_{matrix}[v,h] = min (dp_{matrix}[v-1,h-1] + (0 if pattern[v-1] == text[h-1] else 1),
                            dp_{matrix}[v,h-1] + 1,
                            dp_matrix[v-1,h] + 1)
 return dp_matrix
## Backtrace to generate OPTIMUM CIGAR
cdef list backtrace_matrix ( char *pattern, char *text, int [:,:] dp_matrix ):
  cdef int vsz, hsz, v, h
  cdef list cigar
 vsz= len(pattern)+1
 hsz= len(text)+1
 v = vsz-1
 h = hsz-1
  cigar = []
  while v>0 and h>0:
    if dp_matrix[v,h] == dp_matrix[v-1,h] + 1:
      v -= 1
      cigar.insert(0,"D")
   elif dp_matrix[v,h] == dp_matrix[v,h-1] + 1:
      h = 1
      cigar.insert(0,"I")
   else:
      v -= 1
     h -= 1
      if pattern[v] == text[h]:
       cigar.insert(0,"M")
      else:
        cigar.insert(0,"X")
  if v>0:
   for _ in range(v): cigar.insert(0,"D")
  if h>0:
   for _ in range(h): cigar.insert(0,"I")
 return cigar
cdef void write_cigar( list C, object ofile ):
  last="A"
  count=0
 ofile.write("CIGAR=")
 for v in C:
```

```
if v == last:
      count += 1
   else:
      if count != 0:
       ofile.write(str(count)+last)
     last=v
      count=1
  if count != 0:
   ofile.write(str(count)+last)
 ofile.write("\n")
 return
## MAIN FUNCTION
cpdef align( infilename, outfilename ):
 ## Opening input & output
  infile = open(infilename)
 outfile = open(outfilename, 'w')
 pattern= infile.readline()
  text = infile.readline()
 N=0
  while (len(pattern) and len(text) > 1):
          = align_edit_distance ( pattern[1:].encode('utf-8'), text[1:].encode('utf-8') )
   cigar = backtrace_matrix ( pattern[1:].encode('utf-8'), text[1:].encode('utf-8'), dp )
   outfile.write(str(N)+"\t")
   write_cigar ( cigar, outfile )
   pattern= infile.readline()
   text = infile.readline()
   N += 1
  infile.close()
  outfile.close()
```