

above

if  $(row-1) \geq 0$   $\xrightarrow{\text{yes}}$  return  $[(row-1), col]$   $\rightarrow$  end  
else  $\xrightarrow{\text{no}}$  return  $-1 * (col+1)$   $\rightarrow$  end

left

if  $(col-1) \geq 0$   $\xrightarrow{\text{yes}}$  return  $[row, (col-1)]$   $\rightarrow$  end  
else  $\xrightarrow{\text{no}}$  return  $-1 * (row+1)$   $\rightarrow$  end

above-left

if  $(row-1) \geq 0$  And  $(col-1) \geq 0$   $\xrightarrow{\text{yes}}$  return  $[(row-1), (col-1)]$   
else  $\xrightarrow{\text{no}}$  if  $col = 0$   $\xrightarrow{\text{yes}}$  return  $-1 * row$   $\rightarrow$  end  
else  $\xrightarrow{\text{no}}$  return  $-1 * col$   $\rightarrow$  end

open\_file

if ifstream can be opened for filename  $\xrightarrow{\text{yes}}$  file = ifstream  
else  $\xrightarrow{\text{no}}$  file = file & return false  $\rightarrow$  end  
return true

get\_id\_and\_sequence

if newid  $\neq$  ""  $\xrightarrow{\text{yes}}$  id = newid, sequence = sequence, return true  
else  $\xrightarrow{\text{no}}$  id & sequence are unchanged, return false  $\rightarrow$  end

Start

↓  
open reference file

↓  
open comparison file

↓  
read id + sequence from reference

↓  
convert sequence to protein sequence

↓  
while program can read comparison id/sequence

↓  
convert comparison sequence to protein sequence

↓  
call needleman-wunsch

↓  
call create-comparison

↓  
call print-comparison

end