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# Solution of TPC2, 23 April 2025 # # Peter Stallinga, Universidade do Algarve # # #

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.macro print (%ttt) li $v0, 4

la $a0, %ttt syscall

.end\_macro

.data

filename: .asciiz "dna.txt"

searchstring: .asciiz "TGGGTGCGTTTGCCACACGCCTTTTATTTGTCTAGCCGTAACCAGAA"

foundstring: .asciiz ">>>> FOUND!" notfoundstring: .asciiz "NOT FOUND!!!!" buffer: .space 256

.text

la $a0, filename li $a1, 0

li $a2, 0

li $v0, 13 syscall

move $t9, $v0

readname:

move $a0, $t9 la $a1, buffer li $a2, 1

li $v0, 14

syscall # read 1 char from file

blez $v0, exiterror # if read error then exit li $v0, 11

lb $a0, buffer

syscall # print char beq $a0, 10, newline

j readname

newline:

move $t0, $zero # $t0: match counter; how many letters are correct

readDNA:

move $a0, $t9 la $a1, buffer li $a2, 1

li $v0, 14

syscall # read 1 char

blez $v0, exiterror # if read error then exit

lb $t2, buffer # in $t2 we have letter of sequence in file beq $t2, 10, readname # if newline, we have a new name

blez $t2, exitprogram # if EoF end program la $a0, searchstring

add $a0, $a0, $t0

lb $t1, ($a0) # in $t1 we now have letter char[$t0] of searchstring beqz $t1, match # if end of searchstring we have found the sequence!

bne $t2, $t1, mismatch # if mismatch then goto mismatch addi $t0, $t0, 1 # so far so good. $t0++

j readDNA

mismatch:

move $t0, $zero # reset $t0 counter

j readDNA # continue

match:

print foundstring # print "FOUND!"

exitprogram: li $v0, 16

move $a0, $t9

syscall # close file terminate:

li $v0, 10 # return(0) syscall

exiterror:

print notfoundstring j exitprogram