

## PS4 DNA Sequence Alignment

In this project, I had to use the Needleman-Wunsch method to find the best alignment for two strings. In this assignment OO designs that were implemented were classes, and data structures used were arrays to create a 2d array in order to implement the Needlema-Wunsch method. In this assignment I learned different ways to use valgrind in order to find memory leaks, and the SFML library in order to determine the run time for different sequences.

One problem that I ran into was that I got stuck on how to delete a 2d array to get rid of memory leaks, but to solve this problem I used google to help me with it.

```
adam@adam-XPS-13-9360: ~/Desktop/COMP4/PS4
File Edit View Search Terminal Help
adam@adam-XPS-13-9360:~/Desktop/COMP4/PS4$ ls
bothgaps20.txt  ED.cpp  ED.o    main.o  readme.txt  test.txt
ED              ED.hpp  main.cpp  Makefile  sequence
adam@adam-XPS-13-9360:~/Desktop/COMP4/PS4$ ./ED < bothgaps20.txt
Edit distance: 12
a a 0
- z 2
- z 2
b b 0
c c 0
d d 0
e e 0
f f 0
g g 0
h h 0
i i 0
z - 2
z - 2
z - 2
z - 2
j j 0
k k 0
l l 0
m m 0
n n 0
o o 0
p p 0

Execution time is 0.000147 seconds
adam@adam-XPS-13-9360:~/Desktop/COMP4/PS4$
```