

**CPS363: Introduction to Bioinformatics**  
**Homework 3: Reversal Distance**  
**(15 pts)**

**Due:** 11:59pm March 2, 2021 (Tuesday)

Late submissions accepted with penalty until 11:59pm March 3 (Wednesday).

**Files to turn in:** source code files, input and output files, and a readme file.

Write a program called “`ibprs.py`” which implements the “Improved Break Point Reversal Sort” algorithm which we discussed in class. The program takes an input of a text file which contains a list of permuted numbers (each number represents a gene number ) and sorts the numbers by reducing the number of breakpoints based on decreasing strips. The program should output each step of sorting, including the number of breakpoints for the permutation of each step. It also needs to output the reversal distance (i.e., the number of reversals) to the identity permutation. For example, your program should be run as the following:

```
$ python ibprs.py inputFile outputFile
```

First test your program with the examples we discussed in class. Then create at least 3 test cases to test your program and include these input and output files in your submission.