

(a)

```
$ ./HW3a.py < test1.txt | sort | uniq -c
472 [0, 3, 4, 5, 7, 8]
528 [1, 4, 5, 7, 8, 9]
$ ./HW3a.py < test1.txt | sort | uniq -c
508 [0, 3, 4, 5, 7, 8]
492 [1, 4, 5, 7, 8, 9]
$ ./HW3a.py < test1.txt | sort | uniq -c
501 [0, 3, 4, 5, 7, 8]
499 [1, 4, 5, 7, 8, 9]
$ ./HW3a.py < test2.txt | sort | uniq -c
1000 [4, 5, 6, 8]
```

According to the test, test1.txt will generate 2 correct MWIS with 50% for each, test2.txt will generate 1 correct MWIS with 100% probability.

(b)

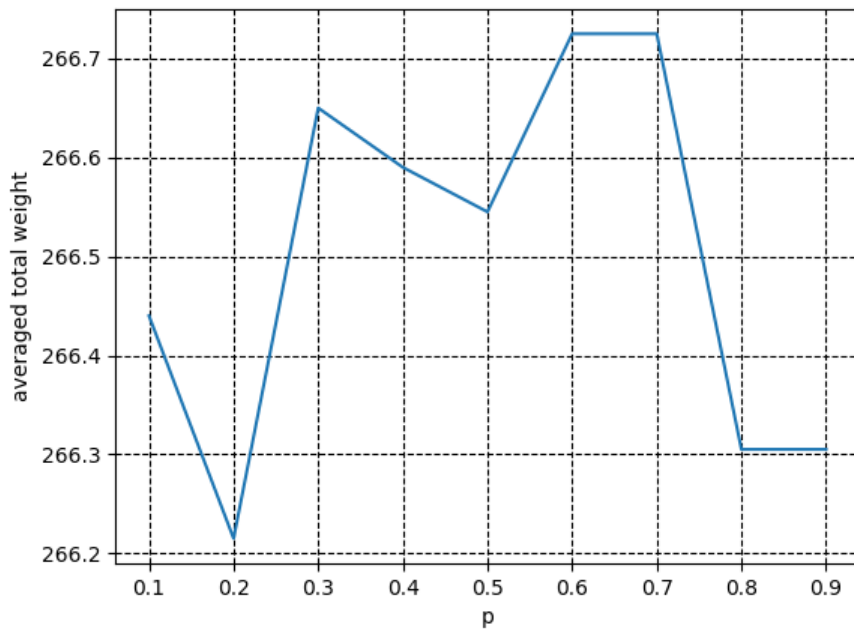
```
$ ./HW3b.py < test1.txt | sort | uniq -c
494 [0, 3, 4, 5, 7, 8]
506 [1, 4, 5, 7, 8, 9]
$ ./HW3b.py < test1.txt | sort | uniq -c
509 [0, 3, 4, 5, 7, 8]
491 [1, 4, 5, 7, 8, 9]
$ ./HW3b.py < test1.txt | sort | uniq -c
519 [0, 3, 4, 5, 7, 8]
481 [1, 4, 5, 7, 8, 9]
$ ./HW3b.py < test2.txt | sort | uniq -c
1000 [4, 5, 6, 8]
```

According to the test, test1.txt will generate 2 correct MWIS with 50% for each, test2.txt will generate 1 correct MWIS with 100% probability, the result isn't affected by probability p.

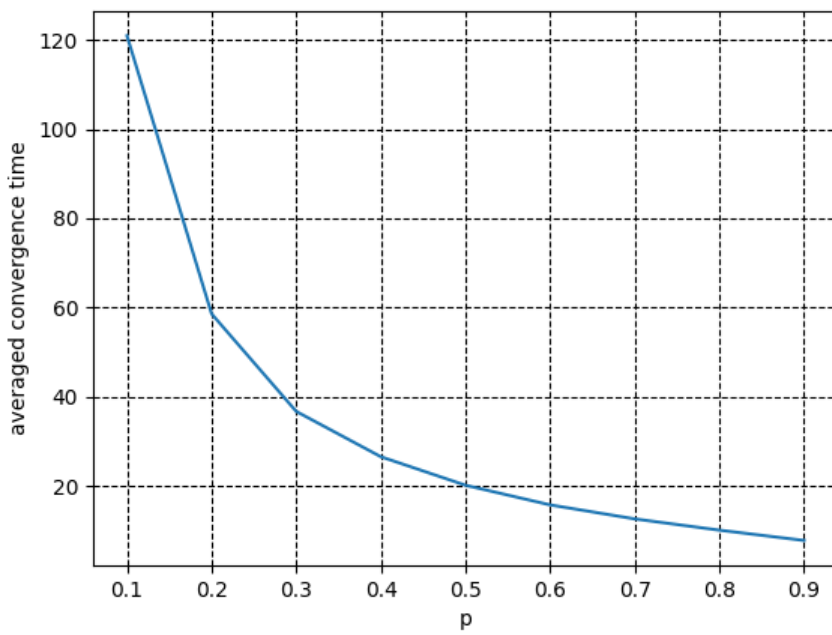
(c)

Test1.txt

Averaged total weight

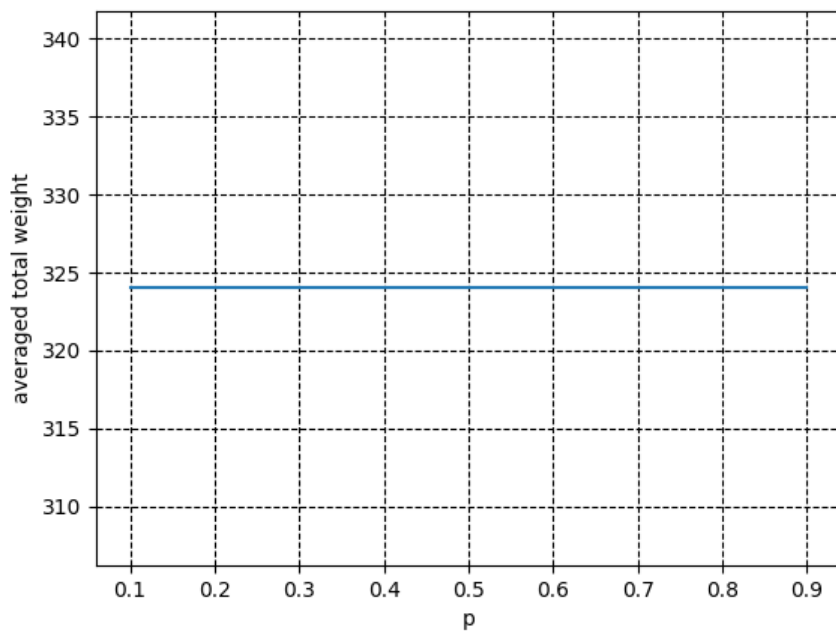


Averaged convergence time



Test2.txt

Averaged total weight



Averaged convergence time

