Lazy vs. non lazy

O. Denas

12/28/2016

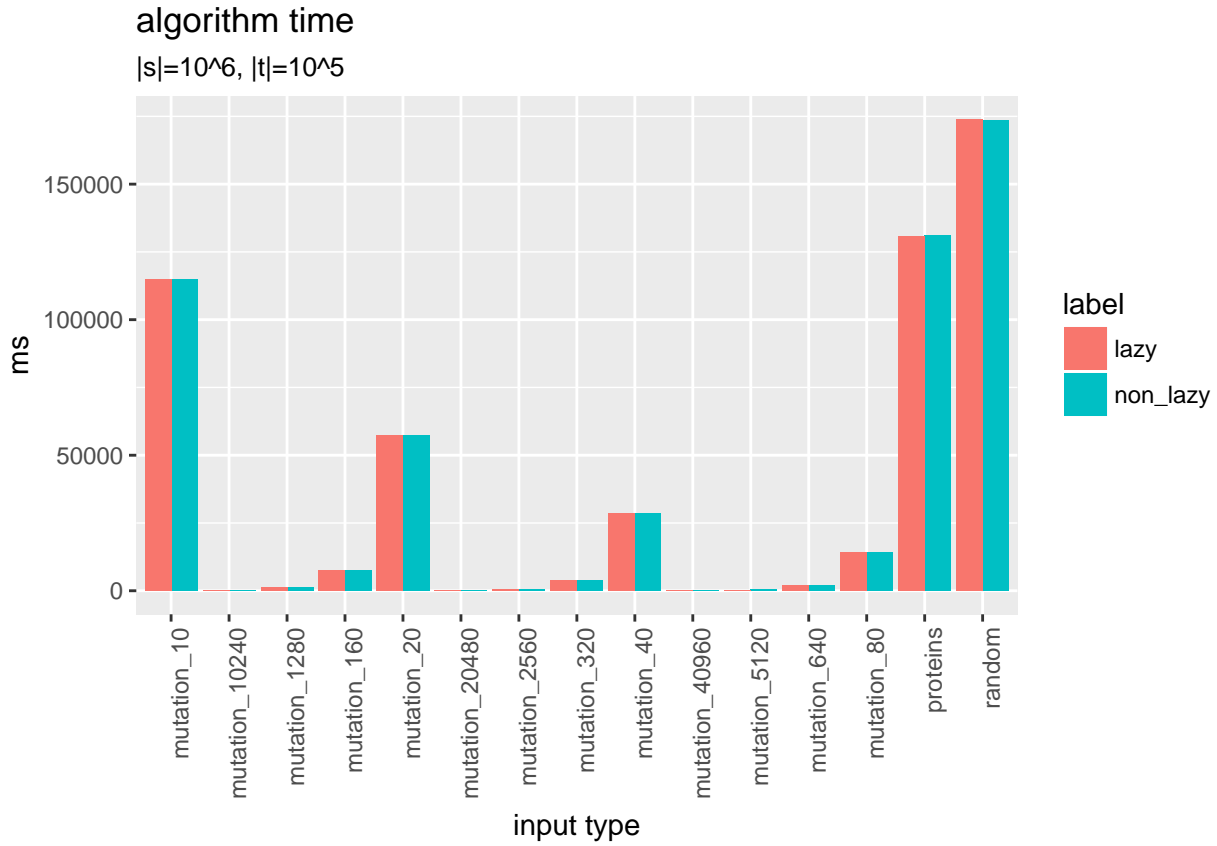## Contents

1 Double vs. single rank

algorithm time on protein data

$|s|=10^6, |t|=10^5$
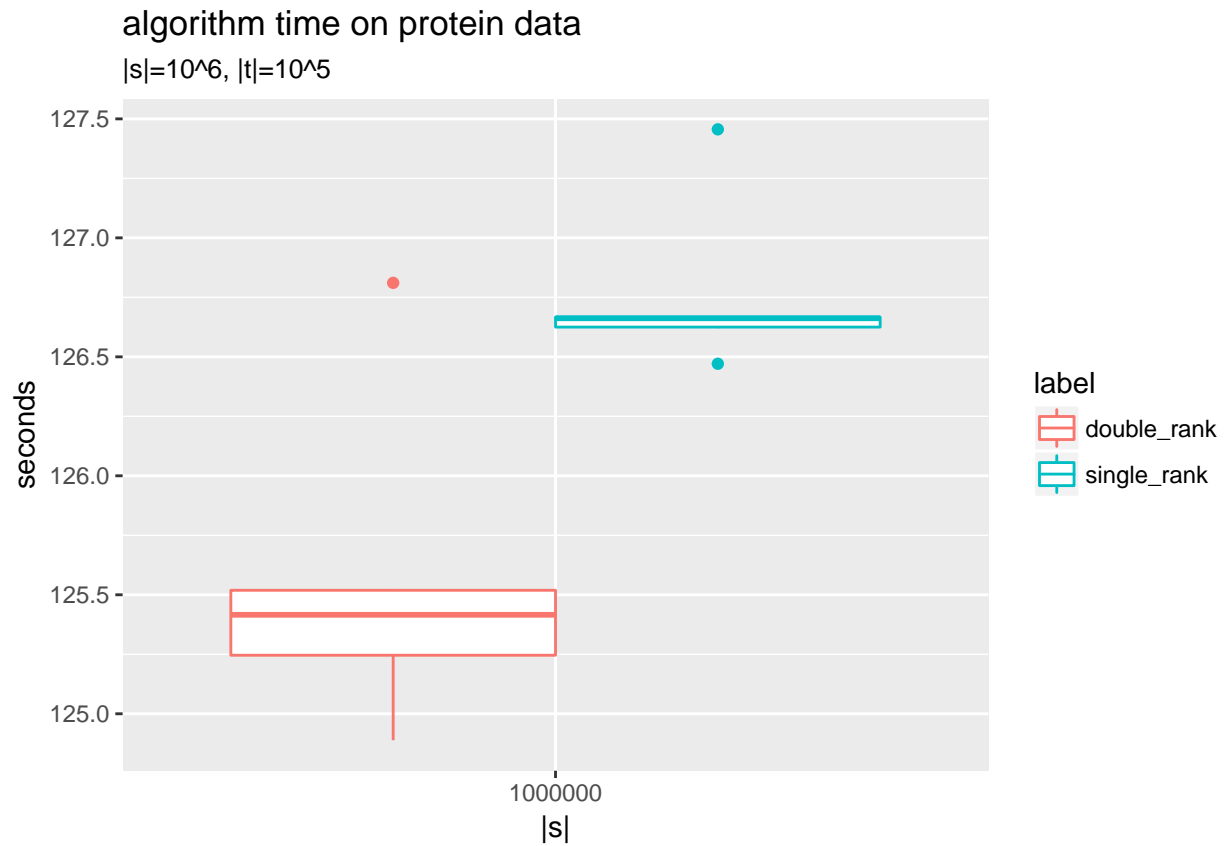
2 Lazy vs non-lazy

2.1 Run time

algorithm time

|s|=10^6, |t|=10^5


```
##               unit value_lazy value_nonlazy
## 1      mutation_10     115088        115048
## 2   mutation_10240        223           262
## 3    mutation_1280       1120          1168
## 4     mutation_160       7456          7497
## 5      mutation_20      57327         57366
## 6   mutation_20480        188           228
## 7    mutation_2560        614           664
## 8     mutation_320       3874          3906
## 9      mutation_40      28640         28678
## 10  mutation_40960        138           177
## 11   mutation_5120        352           395
## 12    mutation_640       1858          1893
## 13     mutation_80      14291         14328
## 14        proteins     130850        130961
## 15          random     173818        173748
```
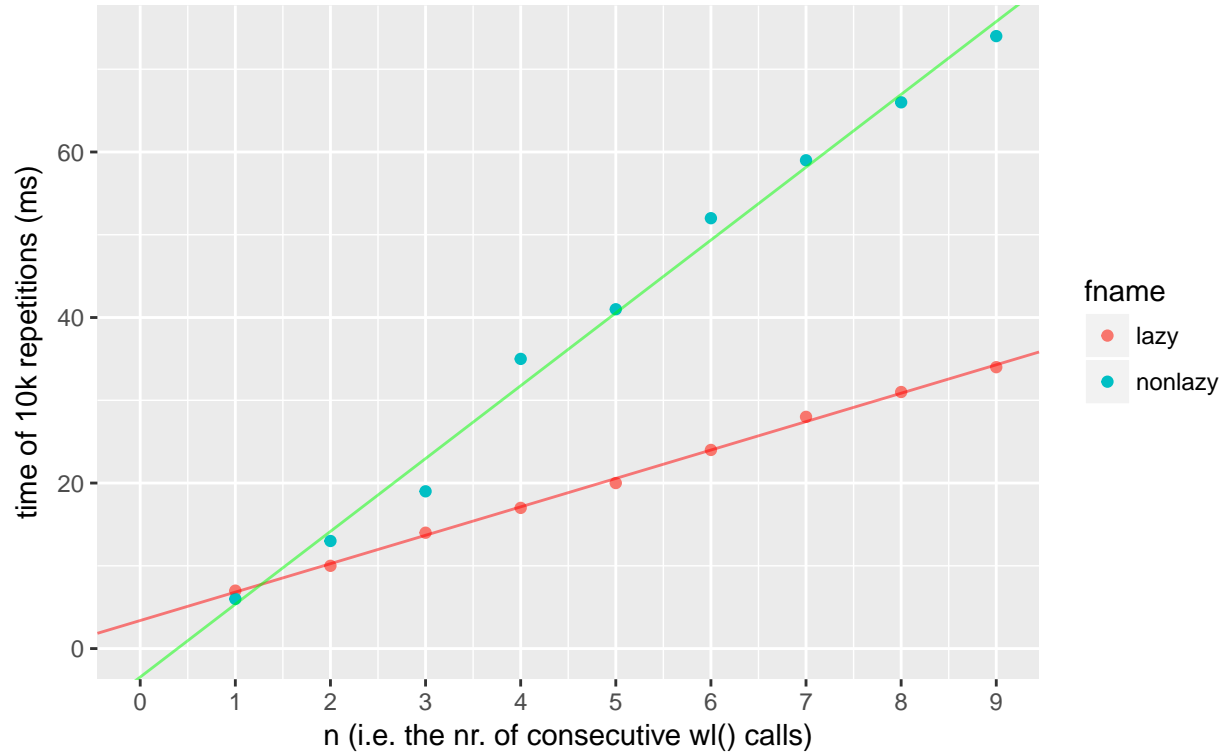
2.2 Sandbox timing

Measure the time of 10k repetitions of

(1) n consecutive `lazy_wl()` calls followed by a `lazy_wl_followup()` and

(2) n consecutive `wl()` calls

rutime of lazy_wl() vs. wl() calls on input size 10^6

lazy: 3.39 + 3.4333*n; nonlazy: −3.44 + 8.8000*n

2.3 Input properties

For various types ("mutation_xxxx" means `s` and `t` are random identical strings with mutations inserted every xxxx characters) of inputs run the MS algorithm and count the number of consecutive `lazy_wl()` calls of length k for $k = 0, 1, 2, 3$.

nr of consecutive wl() calls
|s|=10^6, |t|=10^5
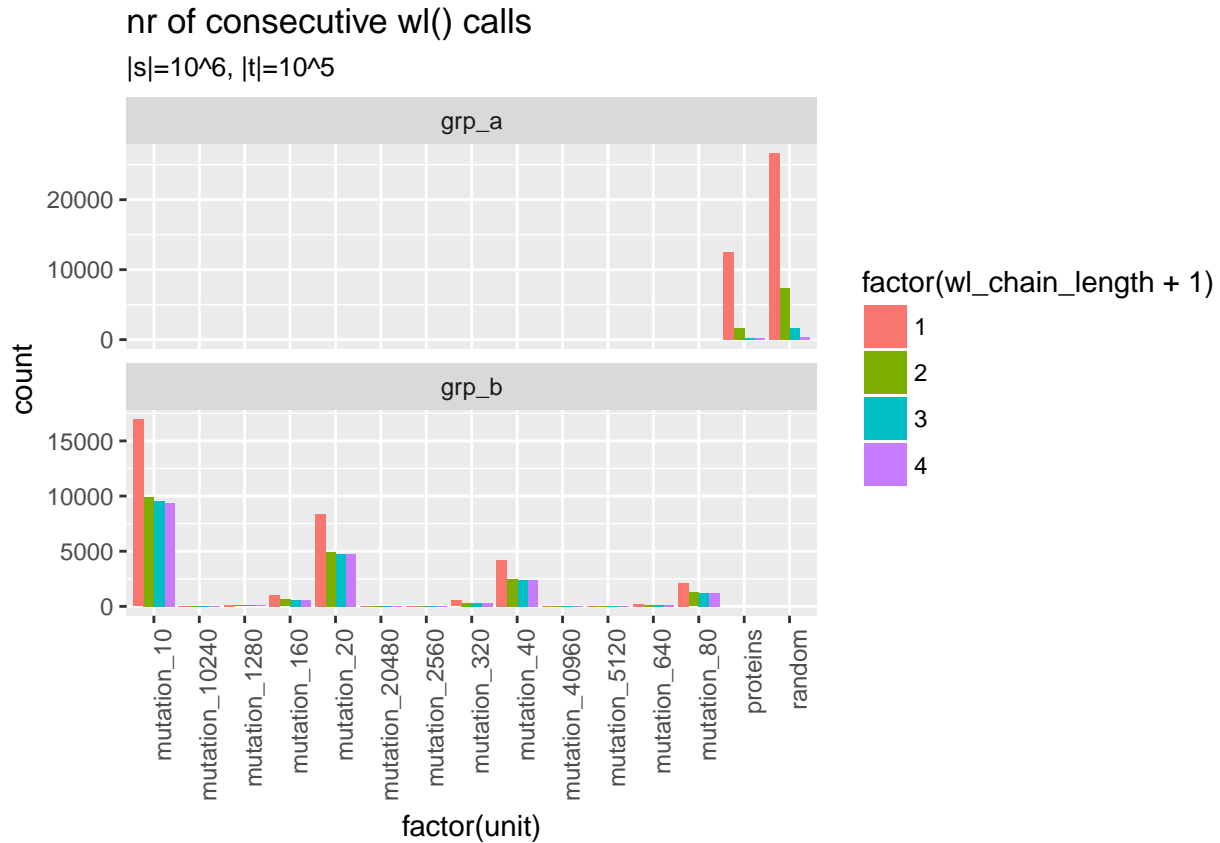
Using the linear fits above, this is the expected toal time the `wl()` or `lazy_wl()` calls should take (in ms).

```
## # A tibble: 15 × 4
##             unit    lazy_t nonlazy_t     diff_ms
##            <chr>     <dbl>     <dbl>       <dbl>
## 1     mutation_10 67.347430 79.858300 -12.510870
## 2  mutation_10240  0.060736  0.072391  -0.011655
## 3   mutation_1280  0.525274  0.626903  -0.101629
## 4    mutation_160  4.240214  5.037445  -0.797231
## 5     mutation_20 33.690606 40.031164  -6.340558
## 6  mutation_20480  0.038526  0.045929  -0.007403
## 7   mutation_2560  0.263940  0.312006  -0.048066
## 8    mutation_320  2.173368  2.582139  -0.408771
## 9     mutation_40 16.906014 20.084384  -3.178370
## 10 mutation_40960  0.027168  0.032862  -0.005694
## 11  mutation_5120  0.142746  0.170649  -0.027903
## 12   mutation_640  1.013312  1.210646  -0.197334
## 13    mutation_80  8.455486 10.045392  -1.589906
## 14       proteins 14.726854 11.100751   3.626103
## 15         random 38.664398 32.073411   6.590987
```