SEA 2018 report

Contents

1	Experimental setup	1
	1.1 Time measurements	 1
2	WL tests	1
	2.1 Input data	 1
	2.2 Double rank versus single rank	 2
	2.3 Lazy versus nonlazy	 3
	2.4 Double rank and fail versus double rank	
	2.5 Double rank, Lazy, and Rank and fail versus Single rank, nonlazy, and nonfail	 5
	2.6 Maxrep	 6
3	Optimizations on parent operations	7
	3.1 Input data	 7
	3.2 LĈA versus parent sequence	 8
4	Genome tests	10
	4.1 Figure 4	 10
	4.2 Figure 5	

1 Experimental setup

1.1 Time measurements

We run a program k times with and without the optimization and recorded the sum construction time of the MS and RUNS vectors. The plots report (median, with quartile ranges) of the speedup of each optimized time t_i^{opt} relative to the average non-optimized time in the construction time of the MS vector. In other words

$$d^{(i)} = \frac{\bar{t}_{\mathtt{non_opt}}}{t_{\mathtt{opt}}^{(i)}}$$

with $\bar{t}_{\mathtt{non_opt}} = 1/n \sum t_{\mathtt{non_opt}}^{(i)},$ and $i = 1, \dots, k.$

The boxplots report the raw times.

2 WL tests

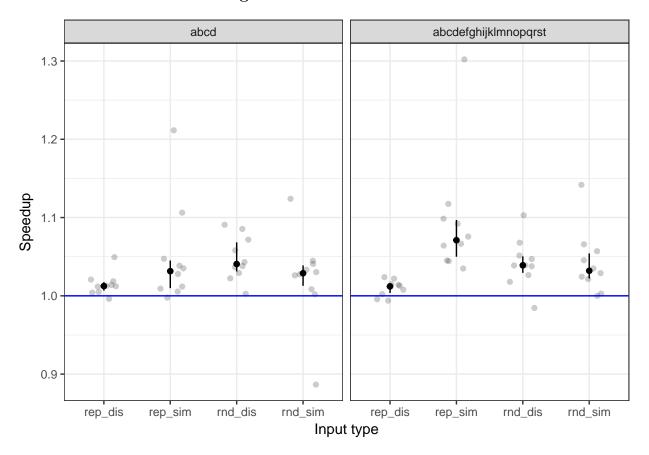
2.1 Input data

We perform tests on the Weiner Link optimizations on 4 types of input.

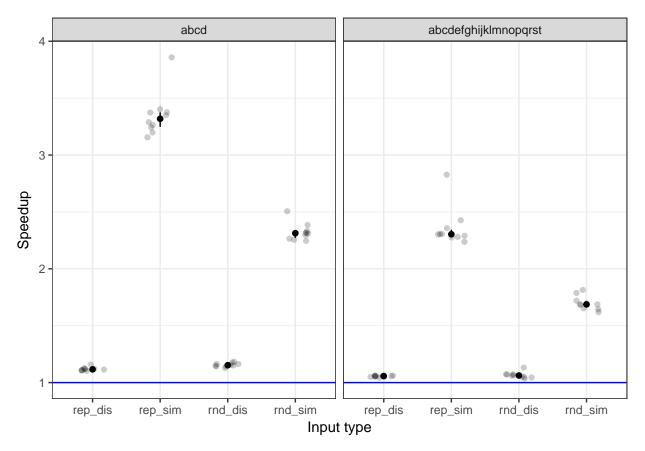
- Index string with repeats, query string random (code: rep_dis)
- Index string with repeats, query string similar to index (code: rep_sim)
- Index string random, query string random (code: rnd_dis)
- Index string random, query string similar to index (code: rnd_sim)

Further, we generate all of the above input data for two alphabet sizes: $\Sigma_1 = 4$ and $\Sigma_2 = 20$. For all input types, the index string is of length 100MB and the query 500KB.

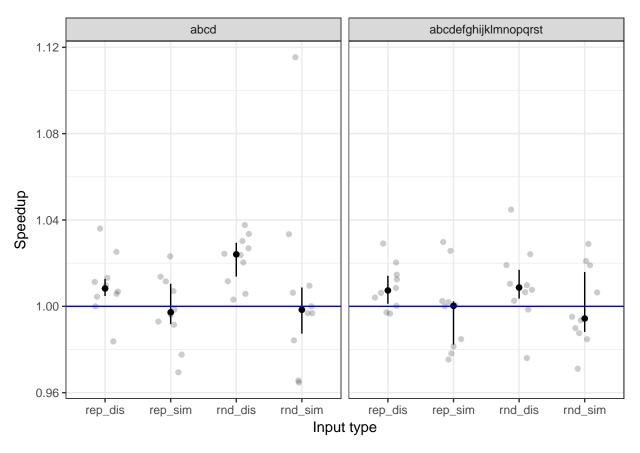
2.2 Double rank versus single rank



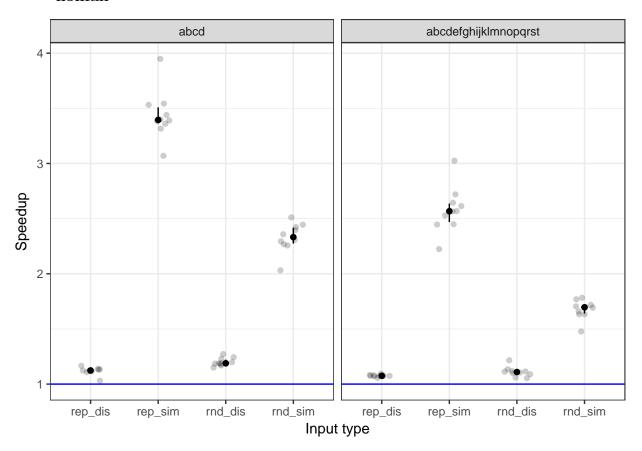
2.3 Lazy versus nonlazy



2.4 Double rank and fail versus double rank

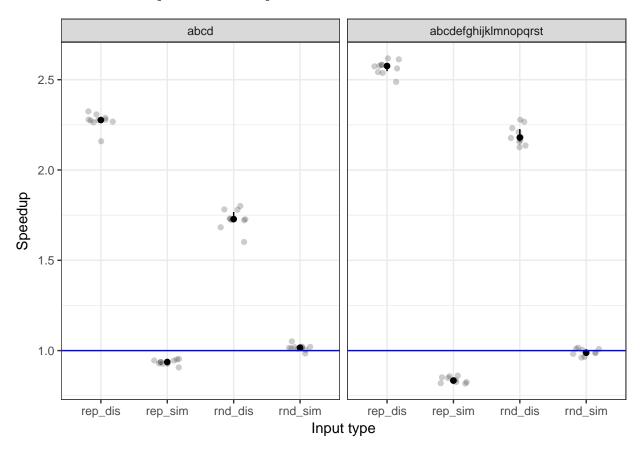


2.5 Double rank, Lazy, and Rank and fail versus Single rank, nonlazy, and nonfail

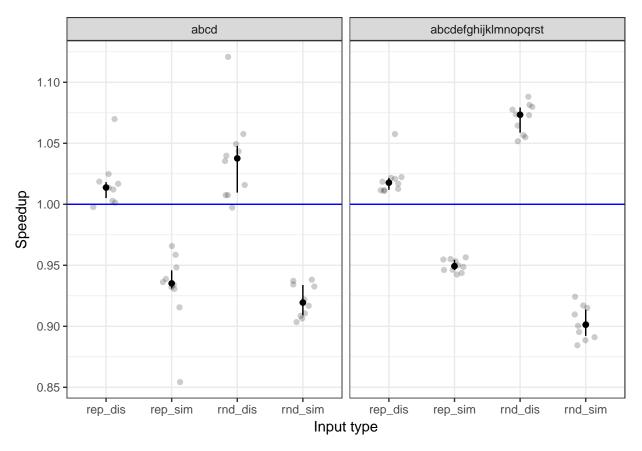


2.6 Maxrep

2.6.1 Vanilla Maxrep vs. non-maxrep



2.6.2 Rank&check Maxrep versus Vanilla Maxrep



3 Optimizations on parent operations

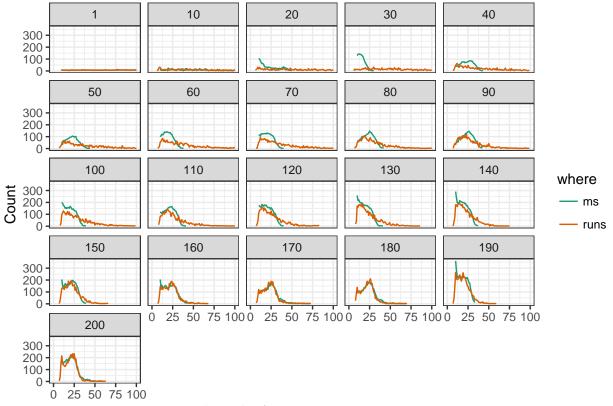
3.1 Input data

We generate the index input string with repetitions as follows. We generate a random seed block b of length 200. Next, we generate blocks of the same length b_k by introducing k mutations on b. The index string of length 10MB is $b \circ b_k^{(1)} \ldots \circ b_k^{(4999)}$.

The query string is obtained as a concatenation of labels from nodes of the suffix tree of s. We select nodes with node depth of at least 10 and string length at most 170 for a total string length of 103KB. We separate the labels with a sentinel character that does not appear in s.

Furthermore, we perform experiments for various choices of $1 \ge k \ge |b|$.

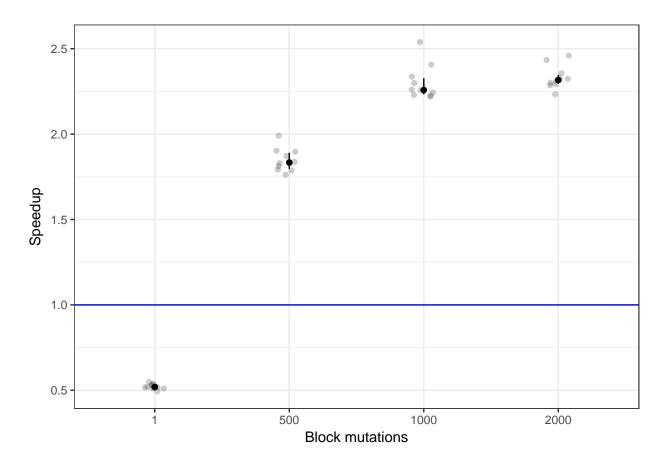
The plot below shows a histogram of the length of consecutive parent operations. This quantity is important since the speedup of this optimization is proportional to the length of sequence of parent operations. Importantly, the optimization might not even be beneficial if the length of the sequence of parent operations is less than 3.



Length of parent sequence

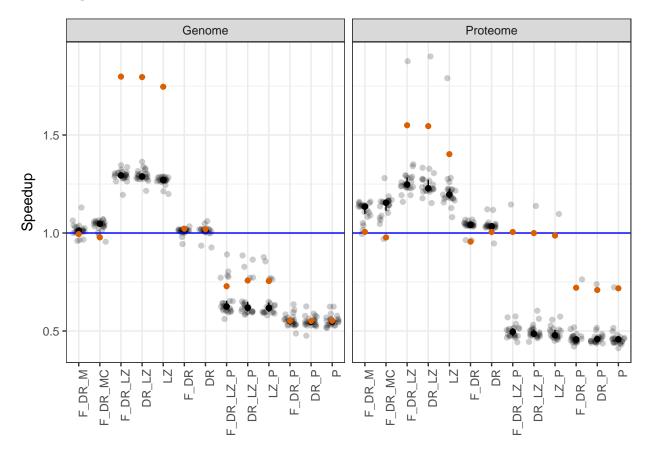
3.2 LCA versus parent sequence

```
## # A tibble: 40 x 5
## # Groups:
               ntrial [10]
##
      ntrial
                  k
                      lca pseq
                                     value
##
       <int> <fctr> <int> <int>
                                     <dbl>
           1
                      887
                             459 0.5174746
##
    1
                  1
##
    2
           1
               1000
                       207
                             476 2.2995169
##
    3
               2000
                             487 2.2863850
           1
                      213
##
    4
           1
                500
                      225
                             408 1.8133333
##
    5
           2
                 1
                      863
                             448 0.5191194
##
    6
           2
               1000
                      209
                             469 2.2440191
           2
   7
##
               2000
                      216
                            502 2.3240741
                500
##
    8
           2
                      234
                             430 1.8376068
    9
           3
                      861
                             459 0.5331010
##
                  1
                             479 2.3365854
           3
## 10
               1000
                      205
## # ... with 30 more rows
```



4 Genome tests

4.1 Figure 4



4.2 Figure 5

