ERRATUM





Erratum to: A representation of a compressed de Bruijn graph for pan-genome analysis that enables search

Timo Beller and Enno Ohlebusch^{*}

Erratum to: Algorithms Mol Biol (2016) 11:20 DOI 10.1186/s13015-016-0083-7

After publication of the original article [1], the authors noticed errors in Algorithm 2 and the caption of Table 4. In Algorithm 2, the term "rank₁(B_l , i - 1) + 1" should be included on line 28 and not line 29. In addition, in the caption of Table 4, the word "BV_r" should be replaced by "B_r" and the word "BV_l" should be replaced by "B_l". The correct versions of Algorithm 2 and Table 4 are included in this erratum.

Table 4 Breakdown of the space usage of the variantsof Algorithm A4

Algorithm	Part	62 E.coli	7 x Chr1	7 x HG
A4	wt-bwt	0.42 (23.83%)	0.44 (36.23%)	0.43 (22.68%)
A4	Nodes	0.10 (5.94%)	0.03 (2.61%)	0.04 (2.02%)
A4	B _r	0.16 (8.93%)	0.16 (12.86%)	0.16 (8.25%)
A4	BI	0.14 (8.04%)	0.14 (11.57%)	0.14 (7.42%)
A4	wt-doc	0.93 (53.26%)	0.45 (36.73%)	1.13 (59.63%)
A4compr1	wt-bwt	0.42 (28.57%)	0.44 (47.83%)	0.43 (26.85%)
A4compr1	Nodes	0.10 (7.12%)	0.03 (3.44%)	0.04 (2.39%)
A4compr1	Br	0.00 (0.23%)	0.00 (0.12%)	0.00 (0.09%)
A4compr1	BI	0.00 (0.23%)	0.00 (0.12%)	0.00 (0.08%)
A4compr1	wt-doc	0.93 (63.85%)	0.45 (48.49%)	1.13 (70.59%)
A4compr2	wt-bwt	0.16 (13.03%)	0.22 (31.01%)	0.22 (15.62%)
A4compr2	Nodes	0.10 (8.67%)	0.03 (4.55%)	0.04 (2.76%)
A4compr2	Br	0.00 (0.28%)	0.00 (0.16%)	0.00 (0.10%)
A4compr2	BI	0.00 (0.28%)	0.00 (0.16%)	0.00 (0.10%)
A4compr2	wt-doc	0.93 (77.74%)	0.45 (64.11%)	1.13 (81.42%)

The first column shows the algorithm used in the experiment (the *k*-mer size is 50). The second column specifies the different data structures used: wt-bwt stands for the wavelet tree of the BWT (including rank and select support), nodes stands for the array of nodes (the implicit graph representation), B_r and B_l are the bit vectors described in "Computation of right-maximal *k*-mers and node identifiers" section (including rank support), and wt-doc stands for the wavelet tree of the document array. The remaining columns show the memory usage in bytes per base pair and, in parentheses, their percentage

*Correspondence: Enno.Ohlebusch@uni-ulm.de Institute of Theoretical Computer Science, Ulm University, James-Franck-Ring 027/537, 89069 Ulm, Germany



© The Author(s) 2016. This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/ publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.

Al	gorithm 2 Construction of the implicit compressed de Bruijn graph.
1:	function CREATE-COMPRESSED-GRAPH(k, BWT)
2:	create an empty graph G
3:	create an empty queue Q
4:	$(B_r, B_l) \leftarrow \text{create-bit-vectors}(k, BWT, G, Q)$
5:	$rightMax \leftarrow rank_1(B_r, n)/2$
6:	$leftMax \leftarrow rank_1(B_l, n)$
7:	for $s \leftarrow 1$ to d do \triangleright add the stop nodes for the d sequences
8:	$id \leftarrow rightMax + leftMax + s$
9:	$G[id] \leftarrow (1, s, 1, s)$
10:	enqueue(Q, id)
11:	$B_l[s] \leftarrow 0$
12:	while Q is not empty do
13:	$id \leftarrow dequeue(Q)$
14:	repeat
15:	$extendable \leftarrow false$
16:	$lb \leftarrow G[id].lb$
17:	$rb \leftarrow lb + G[id].size - 1$
18:	$list \leftarrow getIntervals([lbrb])$
19:	for each $(c, [i.j])$ in <i>list</i> do
20:	$ones \leftarrow rank_1(B_r, i)$
21:	if ones is even and $B_r[i] = 0$ then
22:	if $c \notin \{\#, \$\}$ then
23:	if $list$ contains just one element then \triangleright Case 1
24:	$extendable \leftarrow true$
25:	$G[id].len \leftarrow G[id].len + 1$
26:	$G[id].lb \leftarrow i$
27:	else > Case 2
28:	$newId \leftarrow rightMax + rank_1(B_l, i-1) + 1$
29:	$G[newId] \leftarrow (k, i, j - i + 1, i)$
30:	enqueue(Q, newId)
31:	until not extendable

ما د زیر 20 f +b الت الم D . . .1 ...

The online version of the original article can be found under doi:10.1186/s13015-016-0083-7.

Received: 9 November 2016 Accepted: 9 November 2016 Published online: 28 November 2016

Reference

1. Beller T, Ohlebusch E. A representation of a compressed de Bruijn graph for pan-genome analysis that enables search. Algorithms Mol Biol. 2016;11:20. doi:10.1186/s13015-016-0083-7.

Submit your next manuscript to BioMed Central and we will help you at every step:

- We accept pre-submission inquiries
- Our selector tool helps you to find the most relevant journal
- We provide round the clock customer support
- Convenient online submission
- Thorough peer review
- Inclusion in PubMed and all major indexing services

Submit your manuscript at www.biomedcentral.com/submit

• Maximum visibility for your research

