Efficient construction of a compressed de Bruijn graph for pan-genome analysis

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What the heck is pan-genome analysis?

Next generation sequencers produce vast amounts of DNA sequence information:

- multiple genomes of the same or closely related species are available
- 1000 Genomes Project: goal was to sequence the genomes of at least 1000 humans from all over the world and to produce a catalog of all variations (SNPs, indels, etc.) in the human population
- the genomic sequences together with this catalog is called the "pan-genome" of the population

Related work

There are several approaches that try to capture variations between many individuals/strains in a population graph:

- Schneeberger et al. (Genome Biology 2009), Huang et al. (Bioinformatics 2013), Rahn et al. (Bioinformatics 2014) require a multi-alignment as input
- Marcus et al. (Bioinformatics 2014) use a compressed de Bruijn graph of maximal exact matches (MEMs) as a graphical representation of the relationship between genomes
- the contracted de Bruijn graph introduced by Cazaux et al. (CPM 2014) cannot be used

Definition

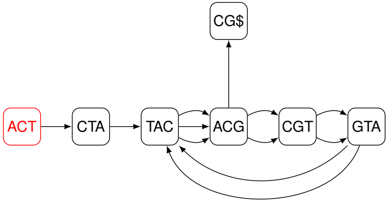
Uncompressed de Bruijn graph

Given $k > 0$ and string S, the de Bruijn graph of S

- contains a node for each distinct length k substring of S, called a k-mer
- two nodes u and v are connected by a directed edge (u, v) if $u = S[i..i + k - 1]$ and $v = S[i + 1..i + k]$

Example

The uncompressed and compressed de Bruijn graphs for $k = 3$ and the string $S =$ ACTACGTACGTACG\$



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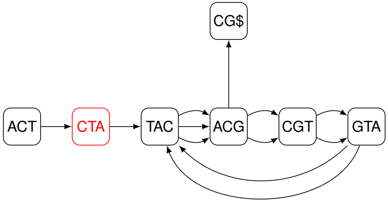

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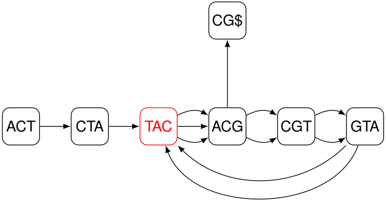

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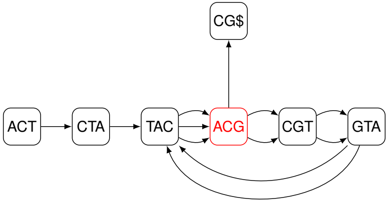

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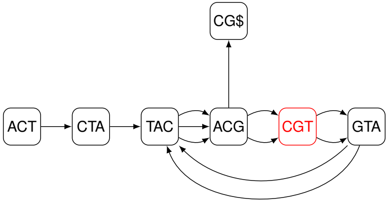

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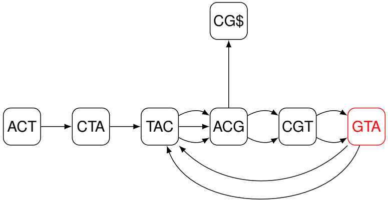

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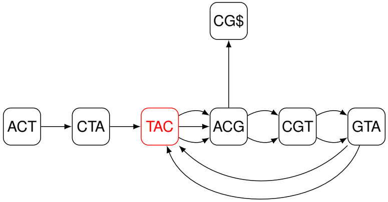

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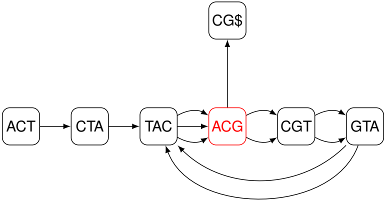

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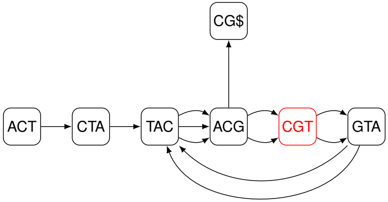

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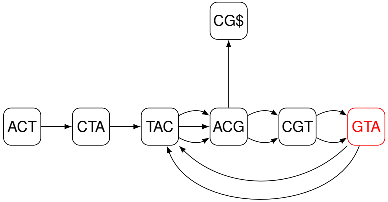

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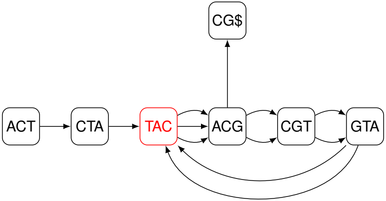

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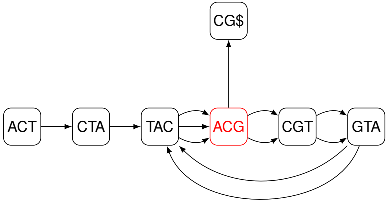

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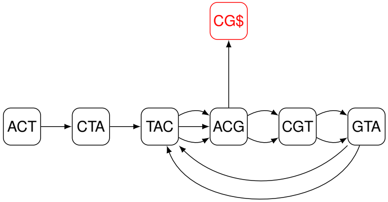

Definition

Compressed de Bruijn graph

A de Bruijn graph can be compressed as follows:

- if node u is the only predecessor of node v and v is the only successor of u (but there may be multiple edges (u, v)), then u and v can be merged into a single node that has the predecessors of u and the successors of v.

Example

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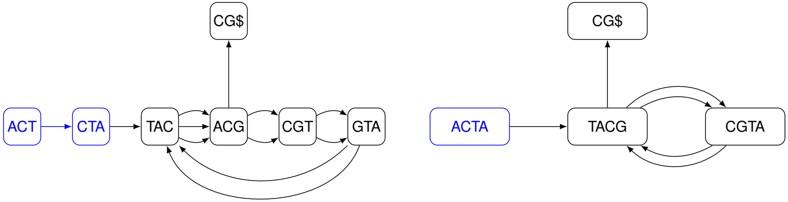

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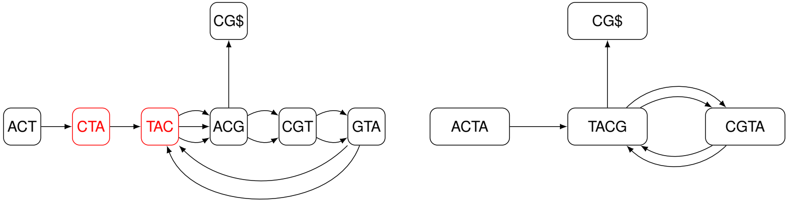

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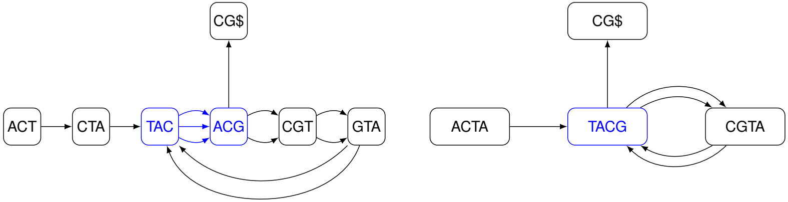

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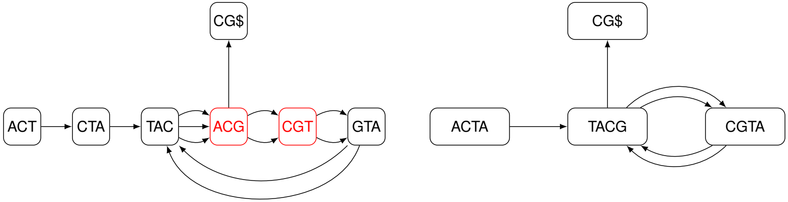

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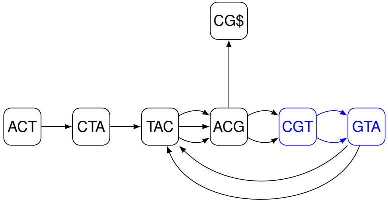

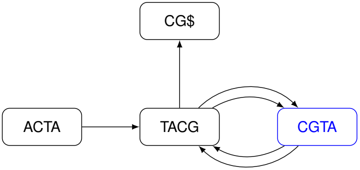

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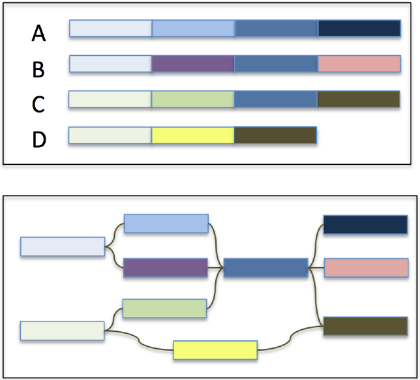

Fig. 1. Overview of a graphical representation of a pan-genome. The four input genomes (A-D) are decomposed into segments shared or specific to the individuals in the population with edges maintaining the adjacencies of the segments.

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Lemma

Of course, the compressed de Bruijn graph can be built from its uncompressed counterpart (a much larger graph), but this is disadvantageous because of the huge space consumption.

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Characterization of nodes in the de Bruijn graph

Let ω be a node in the de Bruijn graph.

- If ω is not the start node, then it has at least two different predecessors if and only if the length k prefix of ω is a left-maximal repeat.
- It has at least two different successors if and only if the length k suffix of ω is a right-maximal repeat.

Example: left- and right-maximal repeat

$S =$ ACTACGTACGTACG$ contains the repeat ACG

Example: left- and right-maximal repeat

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$\Rightarrow$ ACG is not left-maximal

Example: left- and right-maximal repeat

$S =$ `ACTACGTACGTACG$` contains the repeat `ACG`

Left-context: `ACTACGTACGTACG$`

Left-context(`ACG`) = {`T`} is a singleton set

⇒ `ACG` is not left-maximal

⇒ node `ACG` has just one predecessor

Example: left- and right-maximal repeat

$S =$ ACTACGTACGTACG\$ contains the repeat ACG

Left-context: ACTACGTACGTACG\$

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Right-context: ACTACGTACGTACG\$

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Right-context(ACG) = {T, $} is not a singleton set

⇒ ACG is right-maximal

⇒ node ACG has (at least) two different successors

Idea of the algorithm

Compute all right-maximal k-mers, using an index of the text.

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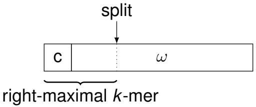
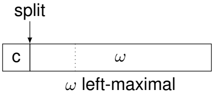
The left-extension of a string ω must stop if

- the length k prefix of $c\omega$ is a right-maximal repeat for some $c \in \Sigma$.
- (the length k prefix of) ω is a left-maximal repeat





Algorithm

Add the intervals of all right-maximal k-mers to a queue Q.
Add the interval [1..1] to Q (the stop node ends with \$).

while the queue Q is not empty **do**

- remove an interval from Q
- extend the corresponding string ω to the left: this yields $c\omega$
- **if** the length k prefix of $c\omega$ is a right-maximal repeat **then** add an edge to the graph
- **else if** ω is a left-maximal repeat **then** add an edge to the graph and add the interval of the length k prefix of $c\omega$ to Q
- **else** proceed with the $c\omega$-interval

Preproccessing

i	LCP	B	BWT	$S[SA[i] \ldots |S|]$
1	−1	0	C	$
2	0	0	$	ACTAGTTTTCTAGTCC$
3	1	0	T	AGTCC$
4	3	0	T	AGTTTTCTAGTCC$
5	0	0	C	C$
6	1	0	T	CC$
7	1	0	T	CTAGTCC$
8	5	0	A	CTAGTTTTCTAGTCC$
9	0	0	A	GTCC$
10	2	0	A	GTTTTCTAGTCC$
11	0	0	C	TAGTCC$
12	4	0	C	TAGTTTTCTAGTCC$
13	1	0	G	TCC$
14	2	0	T	TCTAGTCC$
15	1	0	T	TTCTAGTCC$
16	2	0	T	TTTCTAGTCC$
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4	3	0	T	AGTTTTTCTAGTCC$
5	0	0	C	C$
6	1	0	T	CC$
7	1	0	T	CTAGTCC$
8	5	0	A	CTAGTTTTTCTAGTCC$
9	0	0	A	GTCC$
10	2	0	A	GTTTTTCTAGTCC$
11	0	0	C	TAGTCC$
12	4	0	C	TAGTTTTTCTAGTCC$
13	1	0	G	TCC$
14	2	0	T	TCTAGTCC$
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Compressing

i	B	BWT	$S[SA[i] \dots |S|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
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4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
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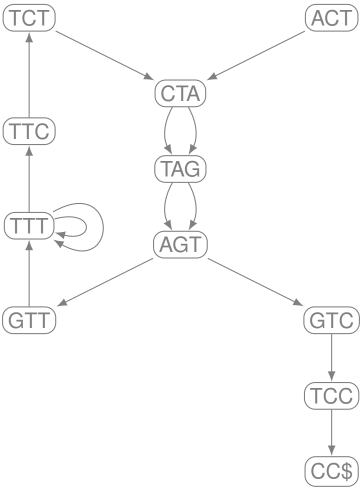

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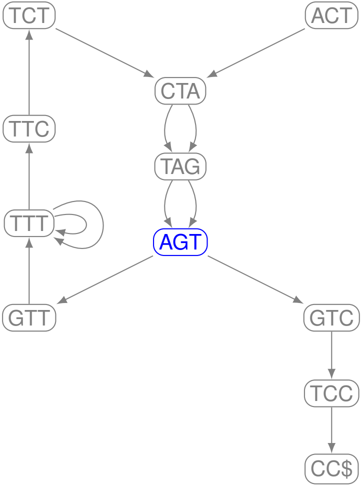

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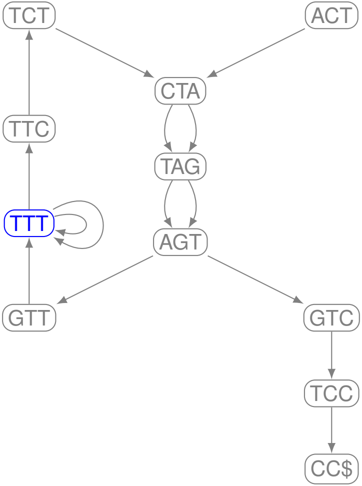

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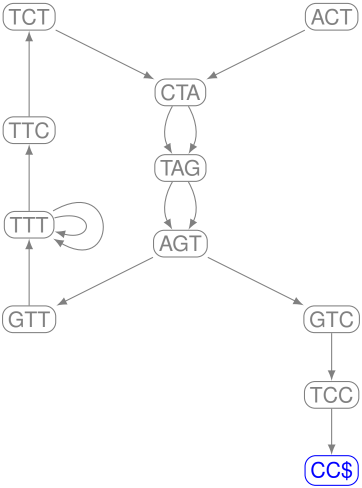

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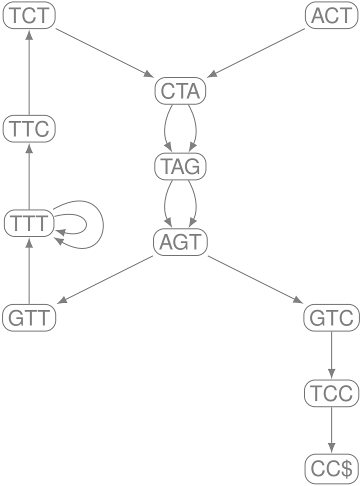

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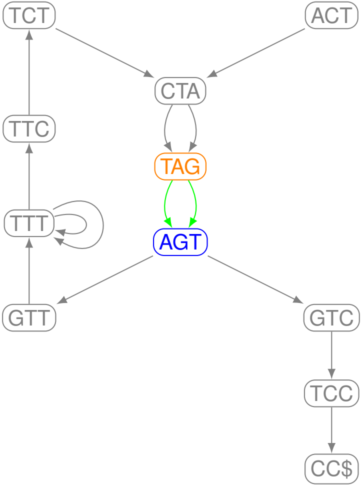
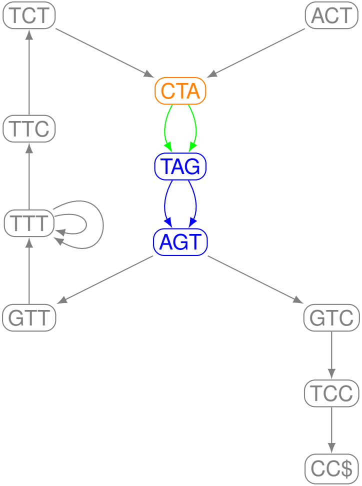
Compressing



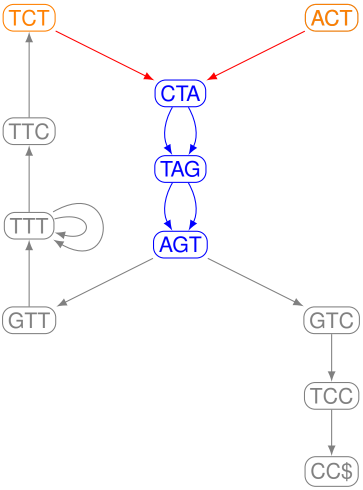
i	B	BWT	$S[SA[i] \ldots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



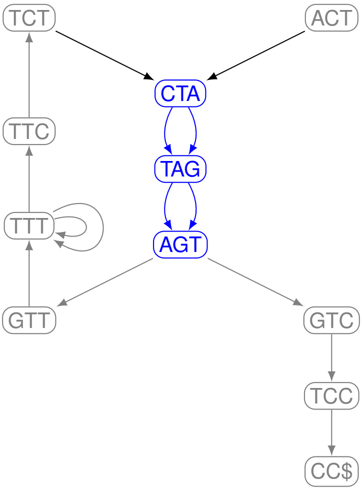
i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



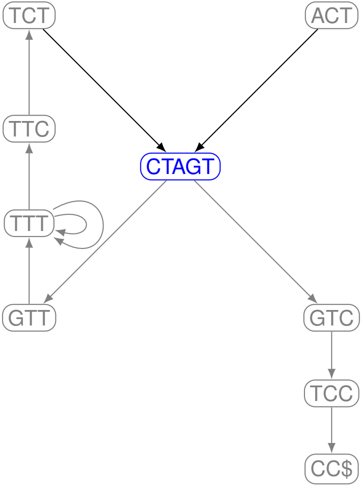
i	B	BWT	$S[SA[i]\ldots\|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[\mathrm{SA}[i]\ldots\|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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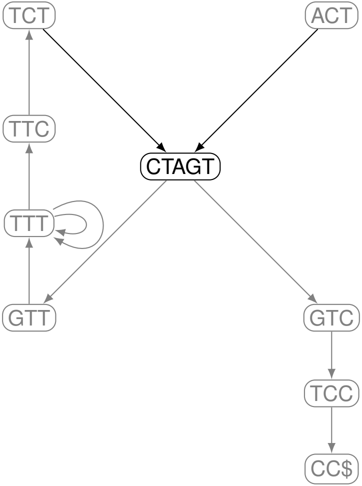
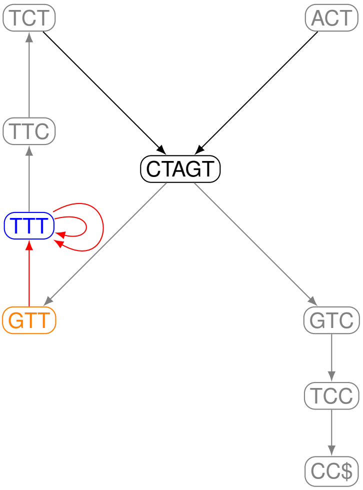
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



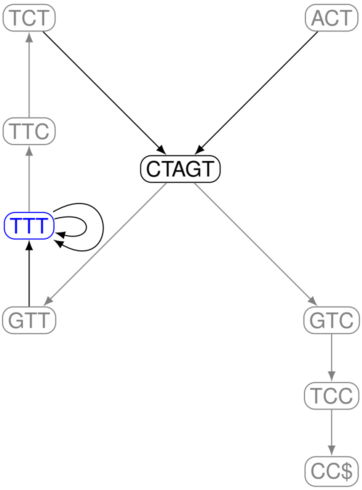
i	*B*	BWT	*S*[SA[*i*] . . . |*S*|]
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



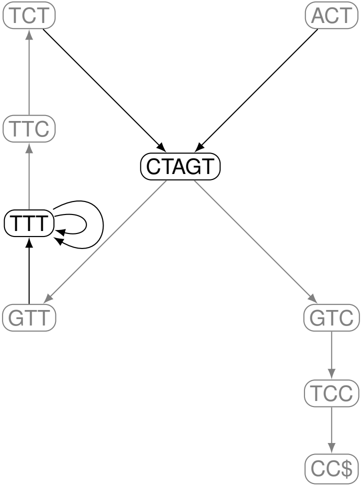
i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



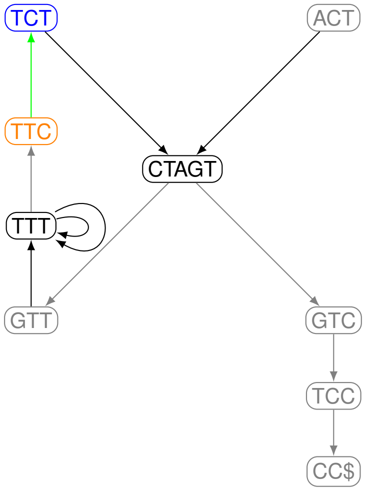
i	B	BWT	$S[SA[i] \ldots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



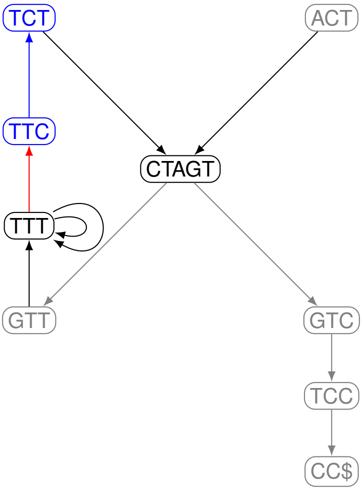
i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i]\ldots|S|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \vert S\vert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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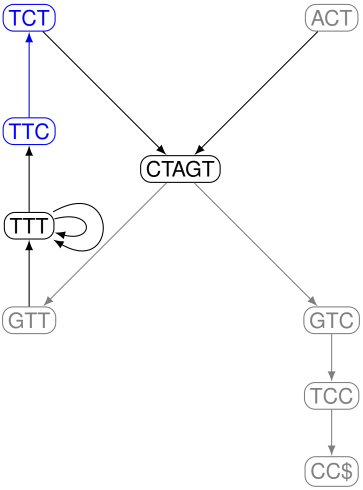
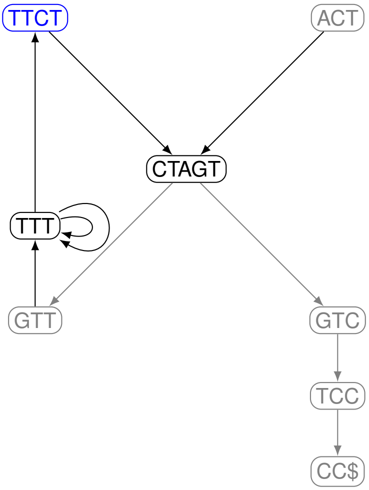
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \dots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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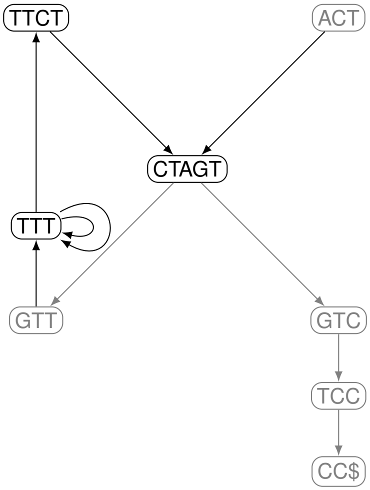
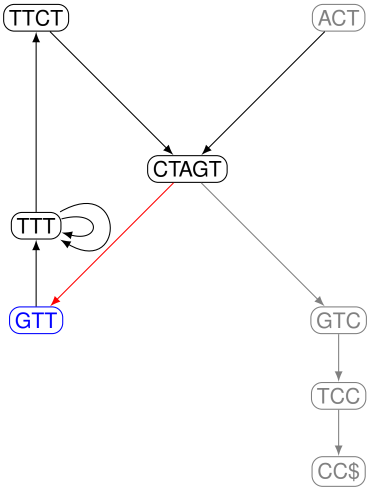
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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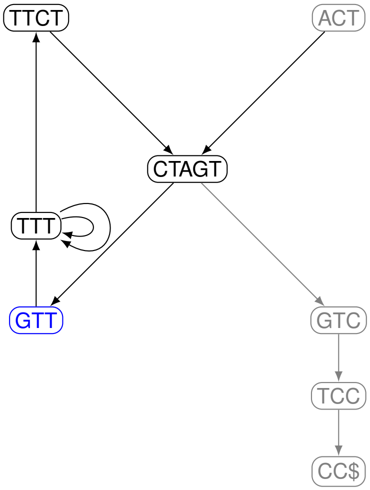
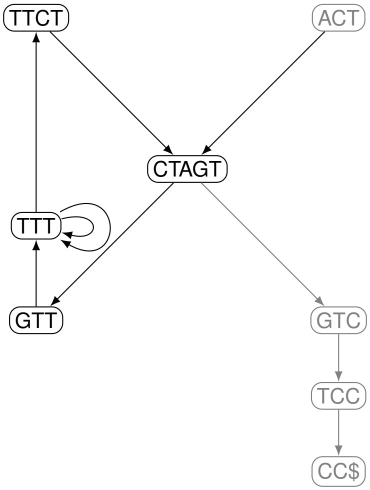
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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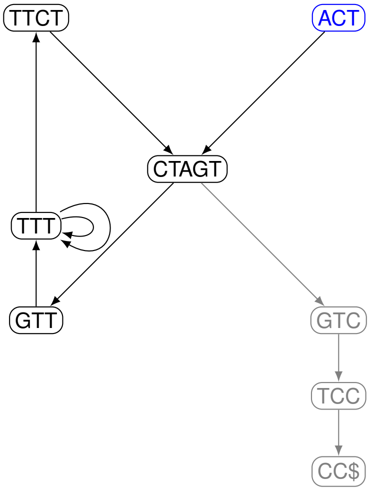
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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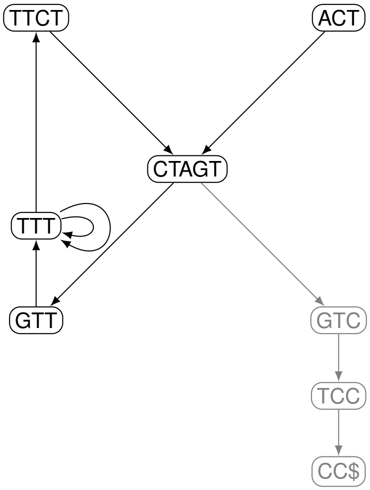
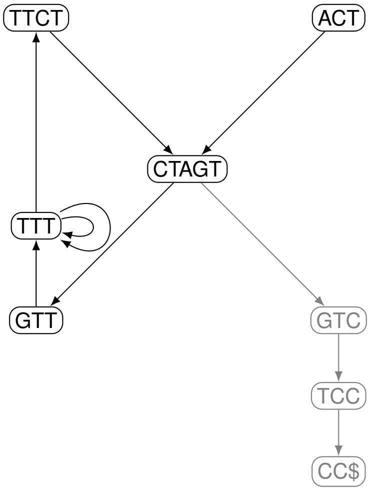
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \dots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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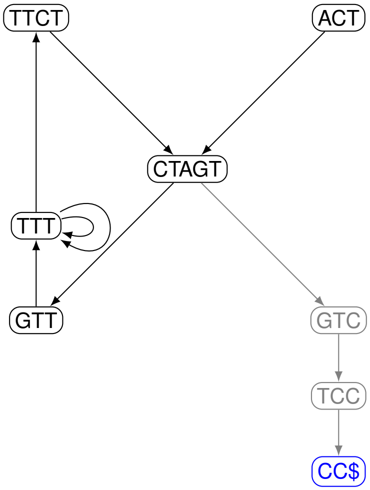
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
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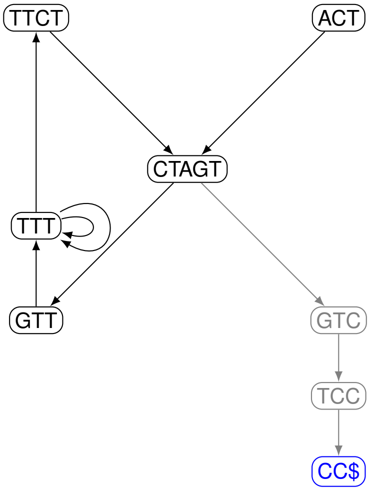
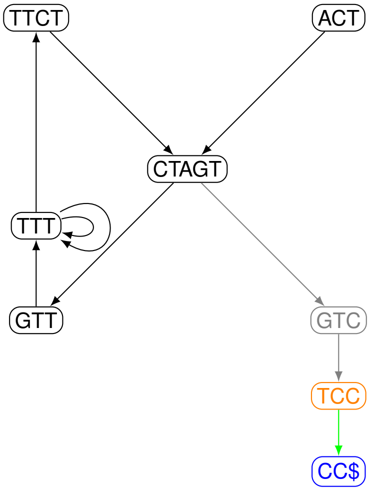
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



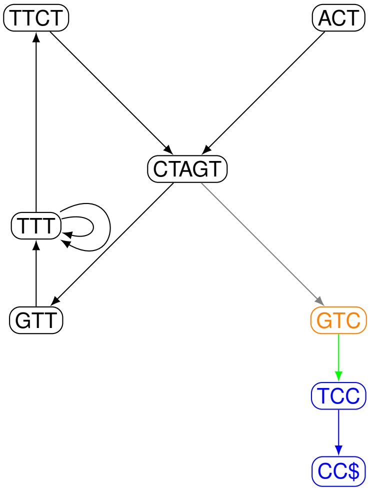
i	B	BWT	$S[SA[i] \ldots \lvert S \rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i] \ldots \|S\|]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
18	1	G	TTTTTCTAGTCC$

Compressing



i	B	BWT	$S[SA[i]\ldots\vert S\vert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
11	0	C	TAGTCC$
12	0	C	TAGTTTTTCT...
13	0	G	TCC$
14	0	T	TCTAGTCC$
15	0	T	TTCTAGTCC$
16	1	T	TTTCTAGTCC$
17	0	T	TTTTCTAGTCC$
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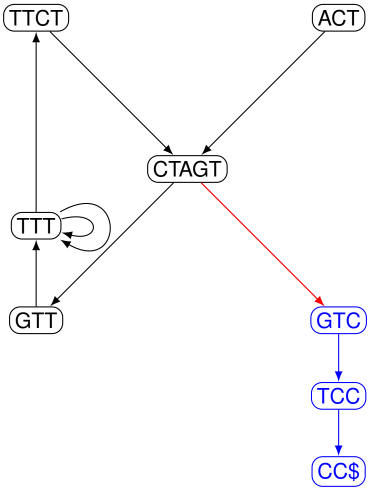

i	B	BWT	$S[SA[i]\ldots\lvert S\rvert]$
1	0	C	$
2	0	$	ACTAGTTTTT...
3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
5	0	C	C$
6	0	T	CC$
7	0	T	CTAGTCC$
8	0	A	CTAGTTTTTC...
9	0	A	GTCC$
10	0	A	GTTTTTCTAG...
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13	0	G	TCC$
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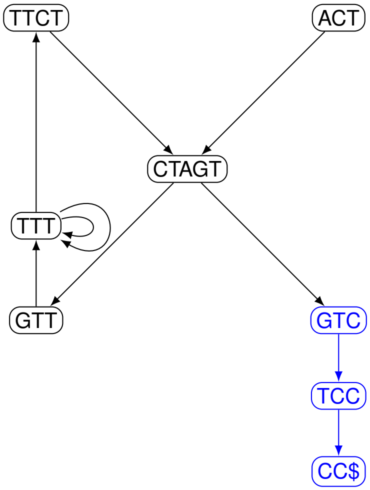

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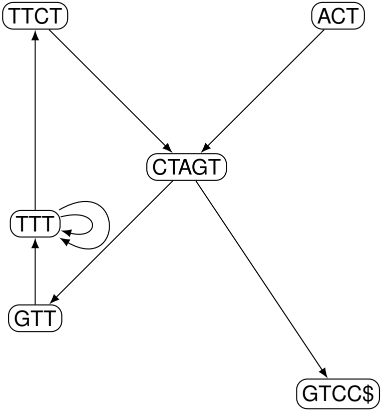

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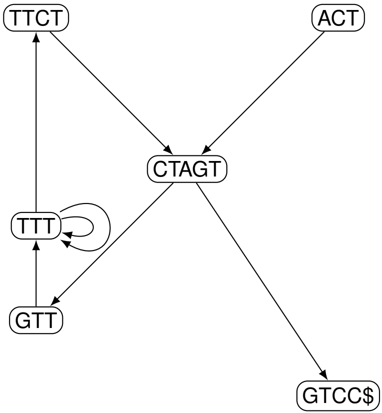

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3	1	T	AGTCC$
4	1	T	AGTTTTTCTA...
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A different representation of the graph

The algorithm computes a compressed de Bruijn graph, in which a node is represented by the quadruple (id, lb, rb, len)

- id is the identifier of the node
- [$lb..rb$] is the suffix array interval
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To model this, a node now contains the sorted list of positions *posList* and the corresponding adjacency list *adjList*.

Implementation

Now the walk through the graph G that gives S is induced by the adjacency lists: if node v is visited for the i-th time, then its successor is the node that can be found at position i in the adjacency list of v.

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The following three algorithms are implemented:

- A1 Uses a comparison based sorting algorithm.
- A2 Uses a non-comparison based sorting algorithm.
- A3 Uses a backward search to track the suffixes of S in G.

Experimental results

Data

- 40-62 different strains of the bacterium *E.coli*
- 7 different human genomes
- *chr1* denotes their first chromosome

The experiments were conducted on a 64 bit Ubuntu 14.04.1 LTS (Kernel 3.13) system equipped with two ten-core Intel Xeon processors E5-2680v2 with 2.8 GHz and 128GB of RAM (but no parallelism was used).

Experimental results

file (Mbp)	k (size)	A1	A2	A3	splitMEM
40 *E.coli*	-	**38** (5.00)	**38** (5.00)	127 (**1.32**)	94 (315)
(199)	25 (1.50)	**55** (6.06)	57 (9.18)	190 (**2.87**)	2,170 (572)
	100 (0.65)	**58** (5.00)	65 (7.89)	207 (**1.63**)	1,684 (572)
	1000 (0.06)	**76** (5.00)	81 (7.08)	190 (**1.49**)	1,671 (572)
62 *E.coli*	-	**64** (5.00)	**64** (5.00)	201 (**1.24**)	134 (316)
(310)	25 (1.57)	**86** (6.06)	93 (9.38)	295 (**2.83**)	-
	100 (0.68)	**92** (5.00)	105 (8.19)	331 (**1.68**)	-
	1000 (0.06)	134 (5.00)	**123** (7.33)	305 (**1.53**)	-
7 *chr1*	-	**399** (5.00)	**399** (5.00)	1,163 (**1.24**)	-
(1,736)	25 (3.10)	**601** (7.70)	646 (11.44)	1,910 (**4.45**)	-
	100 (1.59)	**549** (5.88)	598 (9.70)	1,628 (**2.76**)	-
	1000 (1.50)	**606** (5.86)	621 (9.57)	1,655 (**2.66**)	-
7 *genomes*	-	-	-	**22,038** (**1.24**)	-
(21,201)	25 (3.34)	-	-	**33,247** (**4.84**)	-
	100 (1.16)	-	-	**29,641** (**2.22**)	-
	1000 (1.01)	-	-	**29,962** (**2.04**)	-

Thank you!
Any Questions?