Exercise sheet 10: Introduction to Mapping

Exercise 1

1a)

Extract the Burrows-Wheeler Transform B(S) of S = TGGTGGTTGA\$.

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Solution B(S) = AGTTTGGT\$GG

i	SA[i]	SA[i]-th suffix	Rotation	Last column
1	11	\$	\$TGGTGGTTGA	A
2	10	A\$	A\$TGGTGGTTG	G
3	9	GA\$	GA\$TGGTGGTT	T
4	2	GGTGGTTGA\$	GGTGGTTGA\$T	Τ
5	5	GGTTGA\$	GGTTGA\$TGGT	T
6	3	GTGGTTGA\$	GTGGTTGA\$TG	G
7	6	GTTGA\$	GTTGA\$TGGTG	G
8	8	TGA\$	TGA\$TGGTGGT	Τ
9	1	TGGTGGTTGA\$	TGGTGGTTGA\$	\$
10	4	TGGTTGA\$	TGGTTGA\$TGG	G
_11	7	TTGA\$	TTGA\$TGGTGG	G

1b)

Invert the Burrows-Wheeler-Transform B(S) = TCAACT\$AA to obtain S.

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Hint 1 You can get the first column F(S) of the Burrows Wheeler Matrix via counting and sorting the letters since it has a very predictably structure.

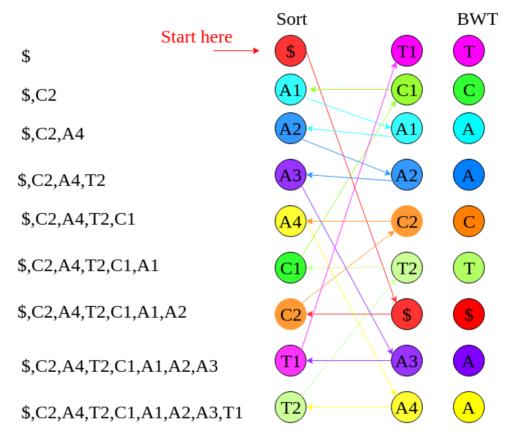
$$F(S) = \$AAAACCTT$$

Hint 2 Use the last-first mapping to assign indices to the corresponding letters in the first F(S) and the last column B(S)

$$F(S) = \$_1 A_1 A_2 A_3 A_4 C_1 C_2 T_3 T_4$$

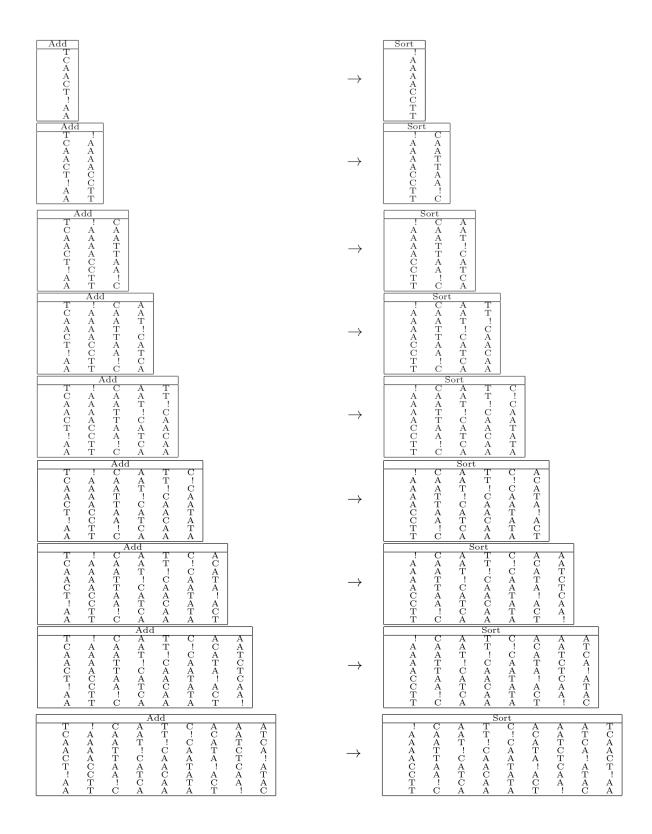
$$B(S) = T_1 C_1 A_1 A_2 C_2 T_2 \$_1 A_3 A_4$$

Solution 1



Inverse BWT: \$CATCAAAT

Solution 2 Step-by-step method:

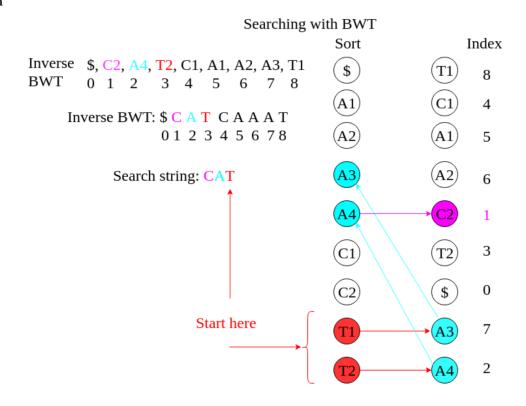


1c)

Search for CAT in B(S) = TCAACT\$AA.

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Solution



Exercise 2

Read the publication on the bwa-mem aligner at https://arxiv.org/abs/1303.3997 and pay particular attention to the re-seeding and chaining features of the algorithm. Now consider a read R = CCCCGTTTT and a reference genome T = ...CCCCATTTT...CCCCGA...AGTTTT... and explain step-by-step how re-seeding and chaining let bwa-mem let recover the correct best alignment of R to T.

2a)

What are the original SMEMs that get generated?

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Solution The original MEMs are CCCCG and GTTTT.

2b)
Would these SMEMs lead to discovery of the best possible alignment?
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Solution No, because it would not lead to a best possible match in the reference genome. The current seeds are too specific and we may miss the seeds that lead to the best mapping (CCC- CATTTT), therefore we need to reseed.
2c)
Which shortened new SMEMs are discovered with re-seeding (assume re-seeding gets perfor- med despite the below-threshold length of the SMEMs)?
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Solution Re-seeding around the central base of each MEM leads to discovery of CCCC and TTTT (both occur once more often than the originals).
2 d)
What is the effect of chaining of colinear seeds?
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Solution The two new seeds are colinear on R and T , and can be merged into a chain, so only one local alignment has to be performed.
Exercise 3 - Programming assignment
Under Construction