

## Exercise sheet 10: Introduction to Mapping

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### Exercise 1

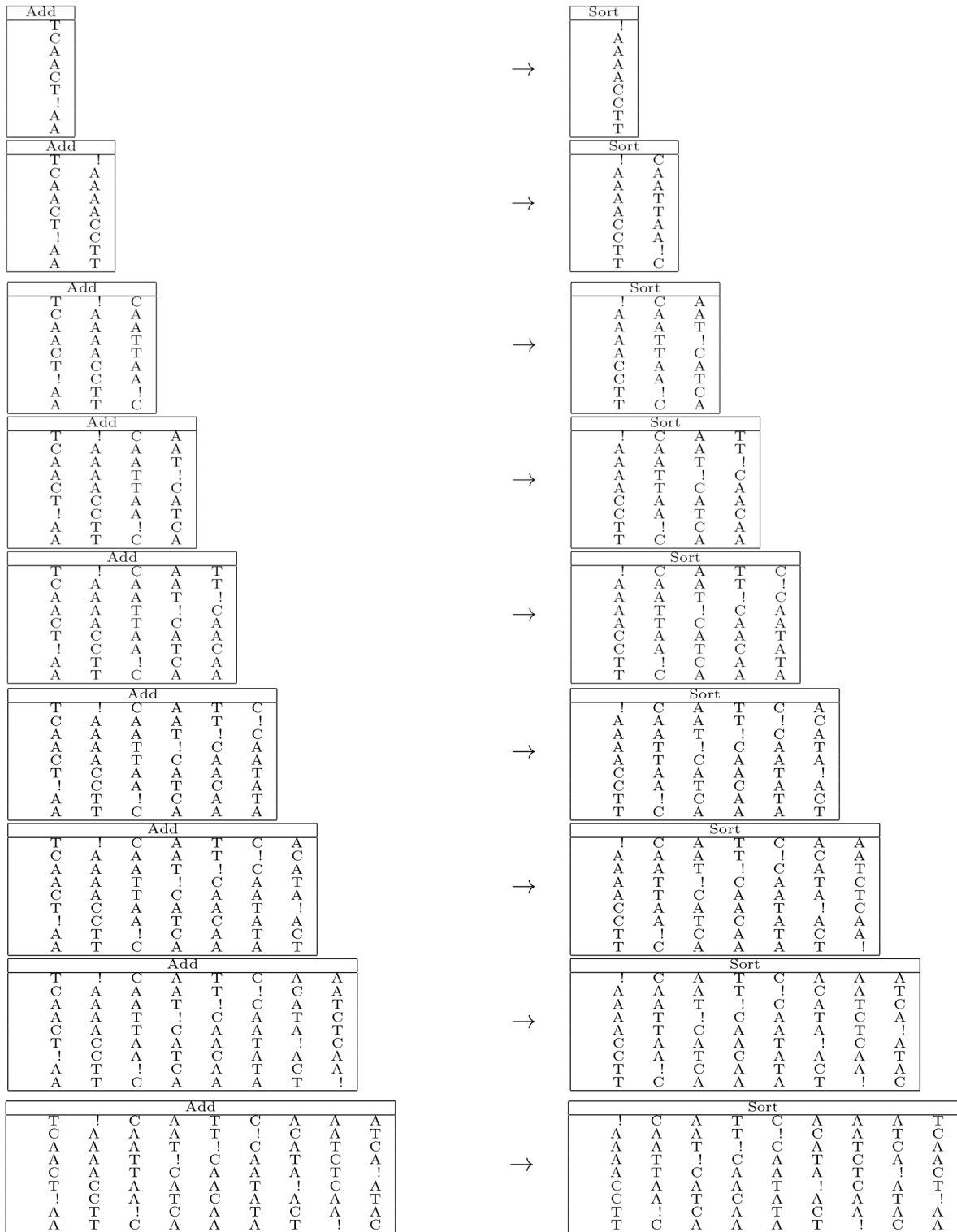
**Question 1A** Extract the Burrows-Wheeler Transform  $B(S)$  of  $S = TGGTGGTTGA\$$ .

**Solution**  $B(S) = AGTTTGGT\$GG$

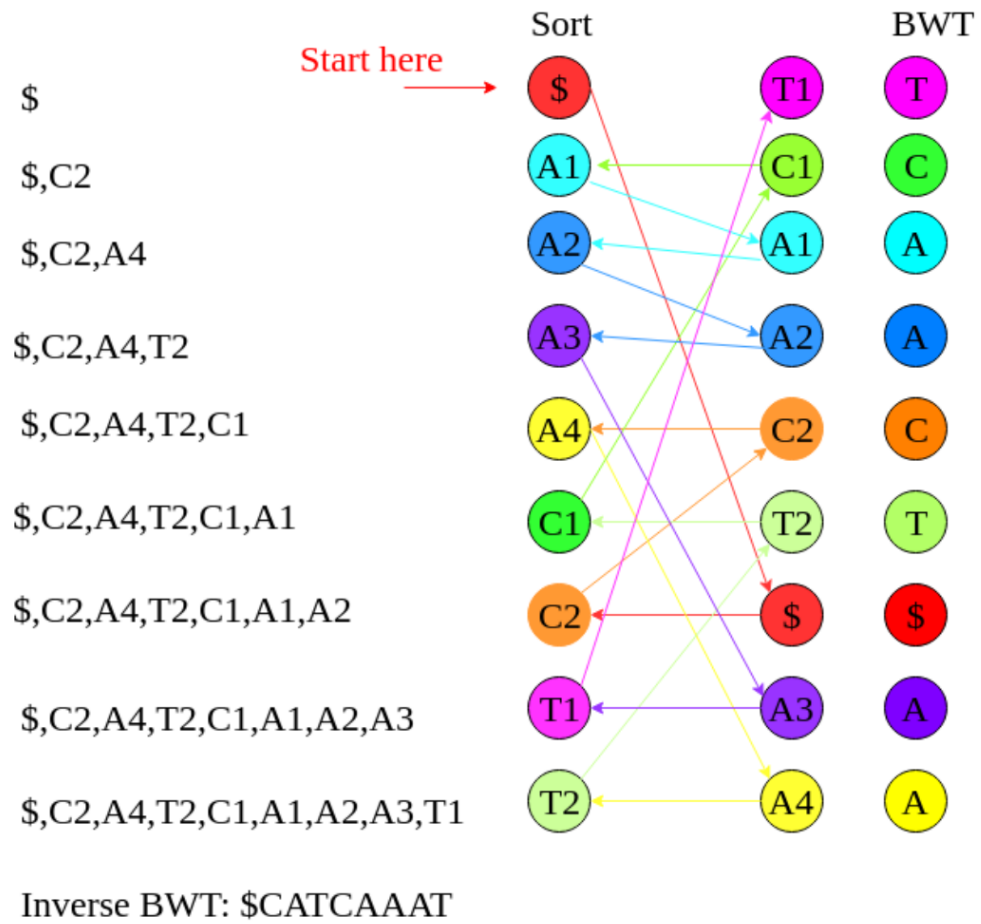
i	SA[i]	SA[i]-th suffix	Rotation	Last column
1	11	\$	\$TGGTGGTTGA	A
2	10	A\$	A\$TGGTGGTTG	G
3	9	GA\$	GA\$TGGTGGTT	T
4	2	GGTGGTTGA\$	GGTGGTTGA\$T	T
5	5	GGTTGA\$	GGTTGA\$TGGT	T
6	3	GTGGTTGA\$	GTGGTTGA\$TG	G
7	6	GTTGA\$	GTTGA\$TGGTG	G
8	8	TGA\$	TGA\$TGGTGGT	T
9	1	TGGTGGTTGA\$	TGGTGGTTGA\$	\$
10	4	TGGTTGA\$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

**Question 1B** Invert the Burrows-Wheeler-Transform  $B(S) = TCAACT\$AA$  to obtain  $S$ .

**Hint** Step-by-step method:

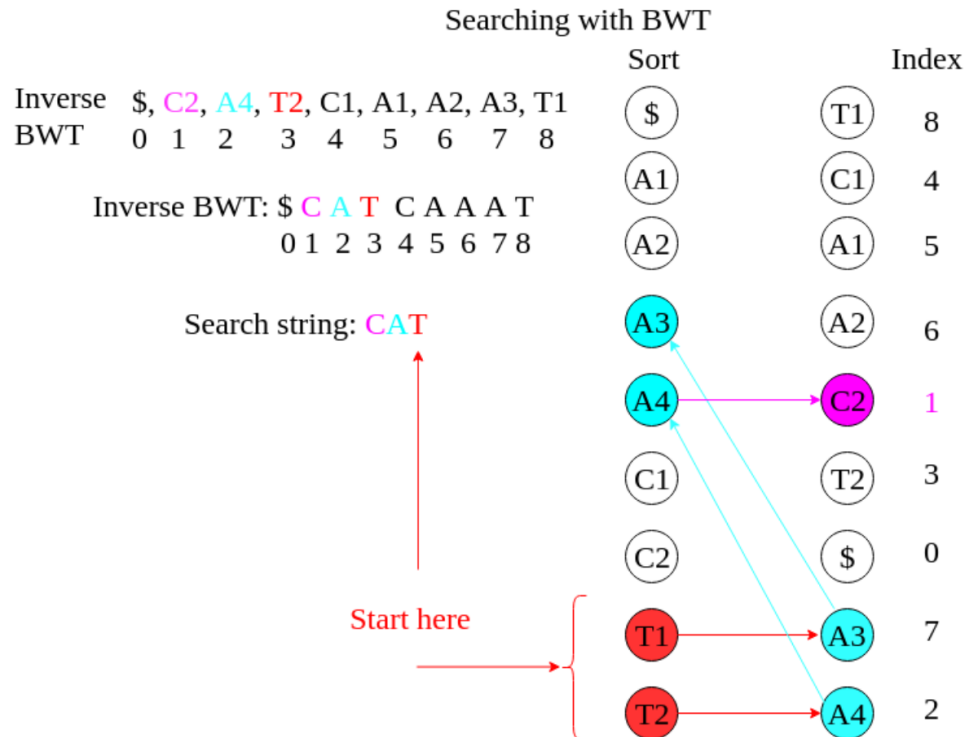


Solution



**Question 1C** Search for  $CAT$  in  $B(S) = TCAACT\$AA$ .

**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  $R = C C C C G T T T T$  and a reference genome  $T = \dots C C C C A T T T T \dots C C C C G A \dots A G T T T T \dots$  and explain step-by-step how re-seeding and chaining let bwa-mem let recover the correct best alignment of  $R$  to  $T$ .

**Question 2A** What are the original MEMs that get generated?

**Solution** The original MEMs are C C C C G and G T T T T.

**Question 2B** Would these MEMs lead to discovery of the best possible alignment?

**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 (C C C - C A T T T T), therefore we need to reseed.

**Question 2C** Which shortened new SMEMs are discovered with re-seeding (assume re-seeding gets performed despite the below-threshold length of the SMEMs)?

**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).

**Question 2D** What is the effect of chaining of colinear seeds?

**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.