4. CBBAAC$ has a suffix array [6,3,4,2,1,5,0].

CBBAAC$

$ - 6
AAC$ - 3
AC$ - 4
BAAC$ - 2
BBAAC$ - 1
C$ - 5
CBBAAC$ - 0

5. $TAGACT
ACT$TAG
AGACT$T
CT$TAGA
GACT$TA
T$TAGAC
TAGACT$

6.

 a. The hamming distance could be less than n because the mutate function doesn't track which positions in the string have already been mutated, so the character at the same position may be changed more than once. This would result in a hamming distance less than n because at the end of the function there would be less than n mutations still present in the string.

 b. The hamming distance could be equal to n if every random index was unique. This would mean that n different characters would be changed in the copy, so the hamming distance would be n.

 c. The hamming distance could not be more than n because at most n unique indexes could be chosen by the code, and the indexes are always substituted, not inserted or deleted. There is not a situation where more than n characters would be changed in the copy and so the hamming distance could not be more than n.

7.   T = AAA$
       BWT(T) = AAA$

       BWM(T) is
       $AAA
       A$AA
       AA$A
       AAA$

8. Since the $ must occur at the end of the string, the only two options for T are ab$ and ba$. The BWT of ab$ is b$a, and the BWT of ba$ is ab$. This means that only b$a and ab$ are valid BWTs.

$ab - not valid
$ba - not valid
a$b - not valid
ab$ - valid
b$a - valid
ba$ - not valid

9.

	Empty	C	A	A	A	T	G
empty	0	1	2	3	4	5	6
C	1	0	1	2	3	4	5
C	2	1	1	2	3	4	5
A	3	2	1	1	2	3	4
A	4	3	2	1	1	2	3
T	5	4	3	2	2	1	2
T	6	5	4	3	3	2	3
G	7	6	5	4	4	3	2

10. This is not possible because the difference between hamming and edit distance is insertion/deletion, but hamming distance requires that the strings are the same length. If the strings are the same length, an insertion would require a deletion at the end to perfectly align, and vice versa. For instance, in the case below, the insertion at index 2 of Y brings the strings into alignment, but it requires a deletion at the end of the string to align the lengths, thus the edit distance would be 2 rather than 1.

X: GCGTAT
Y: GCTATG
Hamming: MMSSSS
Edit: MMIMMMD

11.

X: GCGTAT
Y: GCTATG

Edit:MMIMMMD = 2
X: GCGTAT-
Y: GC-TATG

Hamming: MMSSSS = 4