

System configuration:

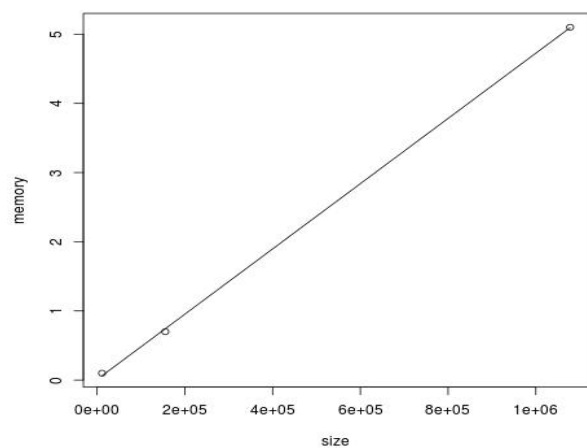
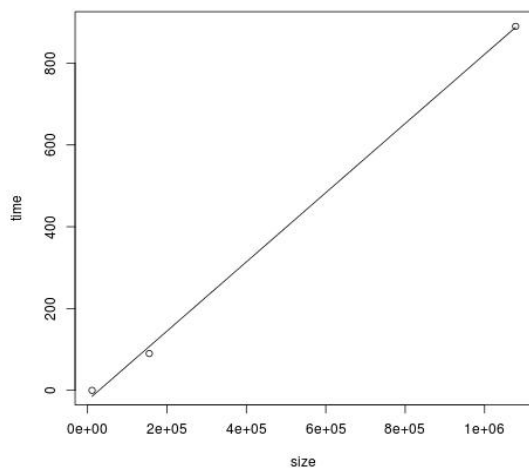
CPU used : Intel® Core™ i5 CPU M 450 @ 2.40GHz × 4
 Clock rate: 1000000 clock per second
 RAM: 3.7 GiB
 Cache size: 3072 KB

Construction time:

Human-BRCA2-cds.out	0 clock	0 ms	11,382 bp	0.1 %MEM
Slyco.out	90000	90 ms	155,461 bp	0.7 %MEM
chr12.out	890000	890 ms	1,078,175 bp	5.1 %MEM

Justification:

The performance observations made above meet my expectations, with linear time and space complexity.



Implementation constant:

~79 byte

Exact matching repeat:

Human-BRCA2-cds.out	length: 14	(7251	9236)	(3389	7078)	(61646404)
Slyco.out	length: 48	(88150	88130)	(153145	153165)	
chr12.out	length: 8375	(451418	460555)			

During Post-order Traversal or DFS, find the internal node with max depth.

Sequence is produced by recursively strcat parent, suffix id is produced recursively on its children.