Report on Mapping problem of Restriction Enzymes

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Problem Statement

Write a program to generate a restriction map for a specific RE & compare your result with Mapper. Give RE & Genomic Sequence used.

Report

RE & Genome

Selected RE = NaeI which has recognition site "GCCGGC"

Selected Genomic Sequence = PBR322

Code Explanation

First of all using `regex` python library I match all the substring in Genomic sequence and and extracted it's starting index. Then using those indices I made a list of fragments i.e. parts / substring of the genomic sequence after action of RE. Then printed the total number of fragments and their position and length.

Comparing result with online Mapper

As we can see Total Fragments in Output of the code is 5 and on the online Mapper Frequence column is having value 4 i.e. total number of restriction site for Enzyme "NaeI". It is in accordance with our findings and also the fragments index is according to the data found in online mapper when run for the same Genomic sequence.

Name	Sequence	Frequence	Positions/Cutsite
AaaI	CGGCCG	1	939/940
AagI	ATCGAT	1	23/25
AasI	GACNNNNNNGTC	2	2162/2169, 2575/2582
AatII	GACGTC	1	4284/4289
AccI	GTMKAC	2	651/653, 2244/2246
NaeI	GCCGGC	4	401/404, 769/772, 929/932, 1283/1286
NarI	GGCGCC	4	413/415, 434/436, 548/550, 1205/1207
NbII	CGATCG	1	3733/3737
NciI	CCSGG	10	170/172, 534/536, 1258/1260, 1484/1486, 1812/1814, 2118/2120, 2153/2155, 2852/2854, 3548/3550, 3899/3901
NcuI	GAAGA	11	464/477, 3123/3136, 738, 1009, 1601, 2352, 3214, 3969, 4047, 4156, 4352
NdaI	GGCGCC	4	413/415, 434/436, 548/550, 1205/1207