

1. Given the structural coordinates (X, Y, Z in Angstroms) from a PDB file of DODECAMERIC B-DNA (*pdb code: 7RQT*) below:

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ATOM    3  C5' DC A  1    19.866  33.675  23.763
ATOM  227  C5' DG A 12    19.940  23.152  -8.211
ATOM   247  C5' DC B 13     9.164  10.482 -9.907
ATOM   471  C5' DG B 24    17.248  17.538  28.728
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calculate the following:

- a) End to End distance between C5' atoms in both the chains A and B
2. Contour length of DNA: Double stranded DNA from bacteriophage λ has a contour length of 17 μm . Each base pair has a bond length b of 3.5 \AA .
 - a. Compute the number of base pairs in the molecule
 - b. Compute Molecular weight of DNA
3. Why is it difficult to BEND free DNA in solution? What is the length of a Kuhn segment in DNA.
4. What is DNA condensation? When was it first observed?
5. Perform a 1D Monte Carlo Simulation of random walk.
 - a. Start at 0 in X-axis (1 dimension only)
 - b. Toss a coin
 - i. Heads: Move right one step (+1)
 - ii. Tails: Move left one step (—1)
 - c. Repeat for 100 tosses
 - d. Calculate mean square displacement $\langle r^2 \rangle$ from position 0.
 - e. Average over 100 trials
6. How can one convert a B-DNA in solution to A-DNA?
7. In a protein-DNA interaction, where DNA has one or more specific sites with unique sequence, how does the protein eventually find its specific site and bind to it?