Introduction to Quantitative Biology
Homework 6

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The submission includes two files - Homework6.m and Caller.m
Homework6.m contains the function for simulating the molecule's movement which returns the mean displacement array along the x and y direction.
Caller.m calls the function for three values of number of simulations - 100, 1000 and 10000 (Challenge Problem). For executing our program, Caller.m file is run.

The following were calculated:-

- Mean displacement in x direction (meanx)
- Mean displacement in y direction (meany)
- Absolute value of Mean displacement (meandisp)
- Mean square displacement (meanrsq)

For **1000 simulations** we got the following values :-

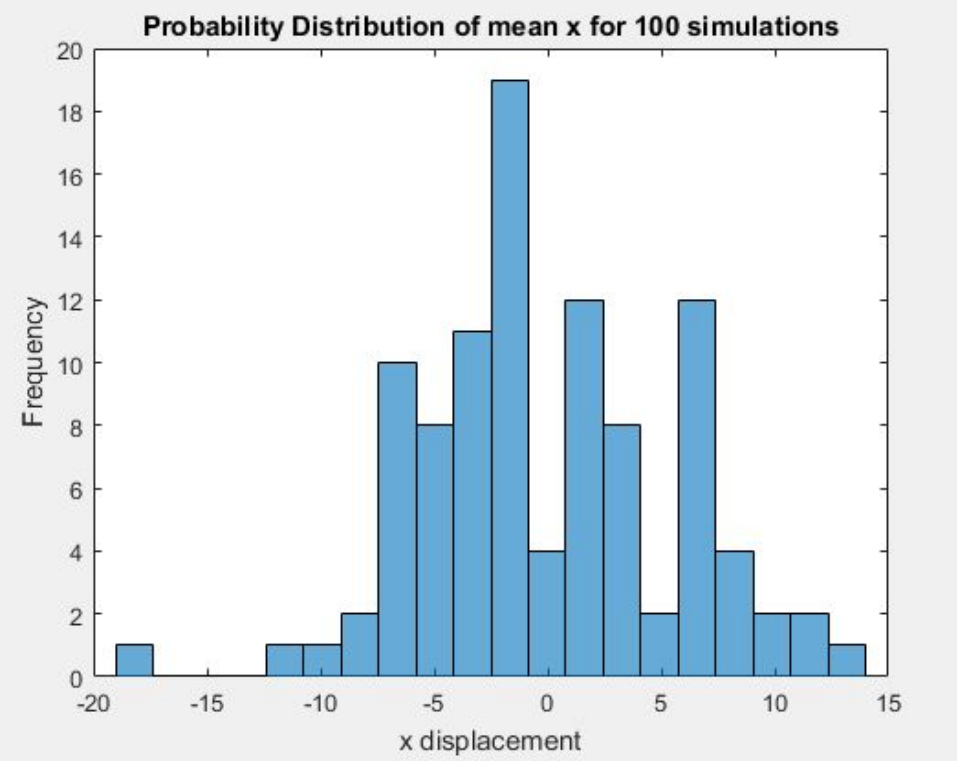
- **meanx** = Approximately 0 (within -2.00 to 1.00)
- **meany** = Approximately 0 (within -2.00 to 1.00)
- **meandisp** = Approximately 0 (sqrt(meanx^2 + meany^2))
- **meanrsq** = Approximately 500 (which is 1000/2 since for 1D movement it is 1000 and for 2D is 500)

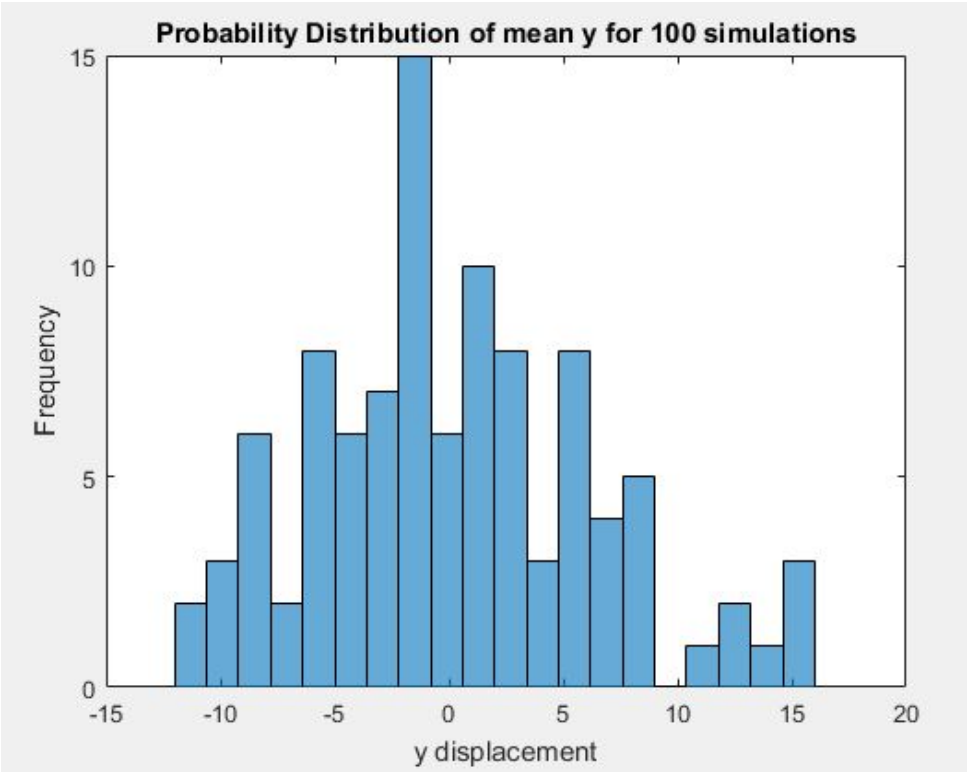
CHALLENGE PROBLEM

Graphs were plotted for mean displacements verses their frequencies for three different number of simulations namely 100, 1000, 10000. The nature of the graphs come out to be a **gaussian** distribution with **mean at 0** and as we increase the number of simulations the distribution is **more spread out** over x and y axes.

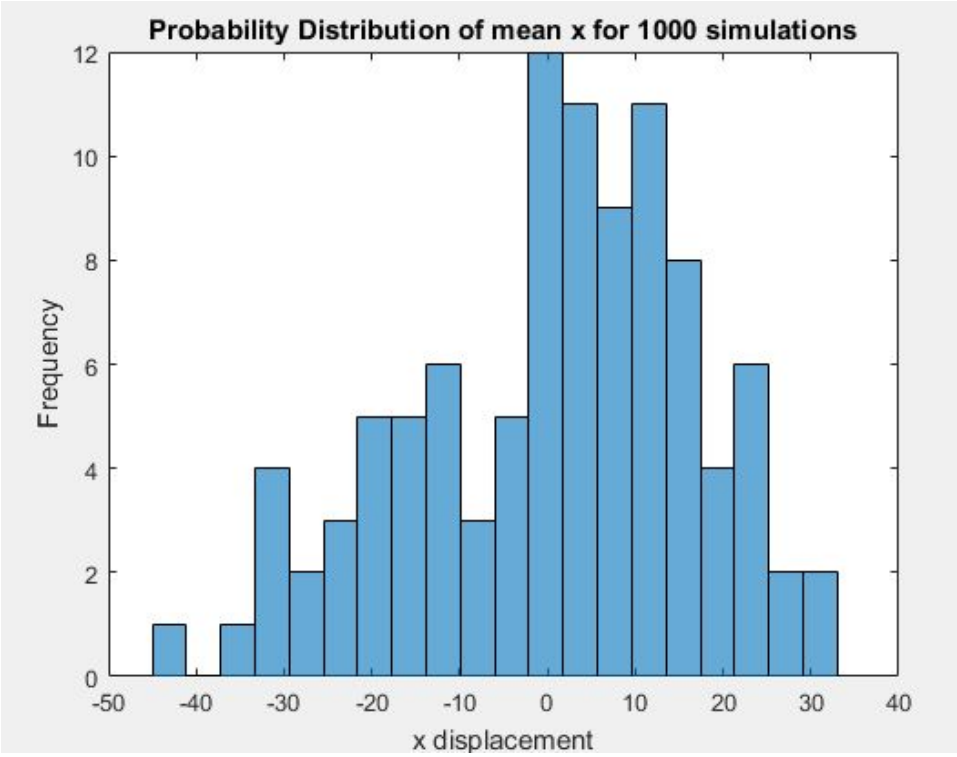
The following graphs were obtained:

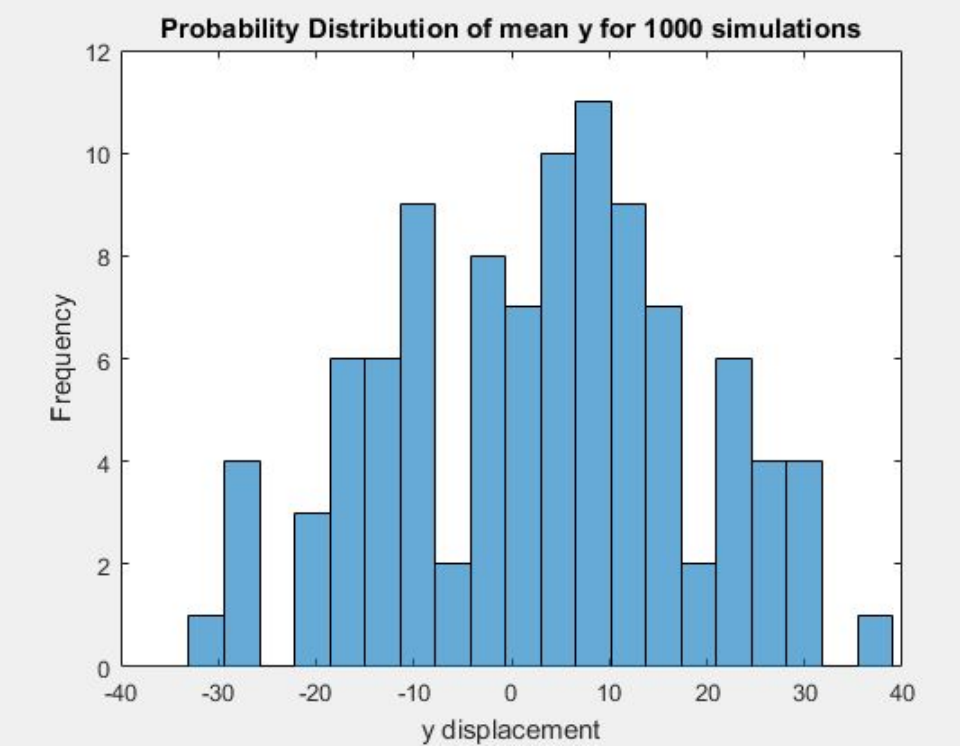
No. of Simulations = 100



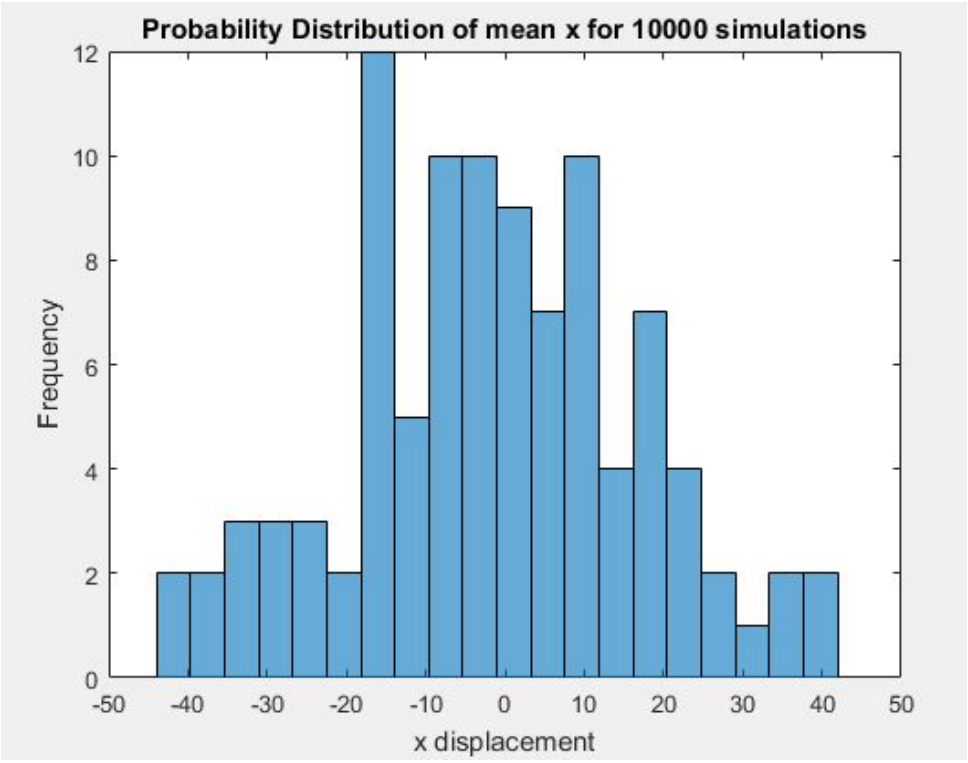


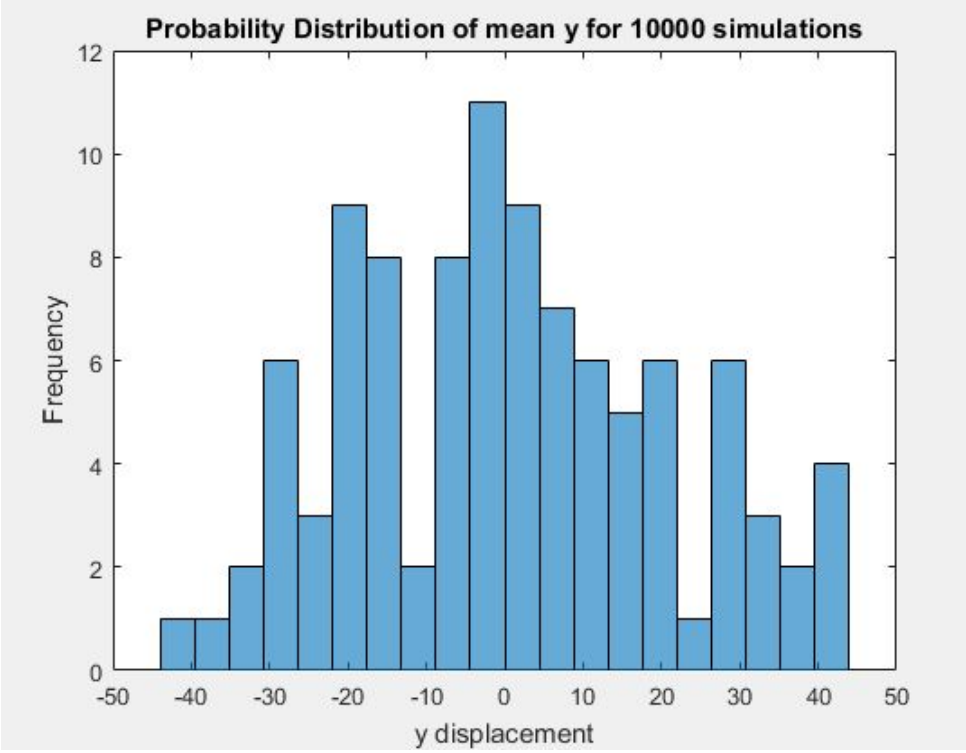
No. of Simulations = 1000





No. of Simulations = 10000




Probability Distribution of mean y for 10000 simulations
Frequency
y displacement
0
2
4
6
8
10
12
-50
-40
-30
-20
-10
0
10
20
30
40
50
