

Assignment 1

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1 Problem 1

In what follows, r is the radius of the hemispherical caps, l the length and m of the cell. It is given that,

$$r = 0.5\mu\text{m}$$

$$l = 2\mu\text{m}$$

(a) Volume is given by

$$V = \pi r^2 l + \frac{4}{3} \pi r^3 = 2.094\mu\text{m}^3$$

Typical cell volume is $0.6 - 0.7\mu\text{m}^3$

https://en.wikipedia.org/wiki/Escherichia_coli

(b) m is the sum of the mass of water contained and that of the other substances. Since, density of water is

$$10^3 \frac{\text{kg}}{\text{m}^3} = 10^{-6} \frac{\text{pg}}{\mu\text{m}^3}$$

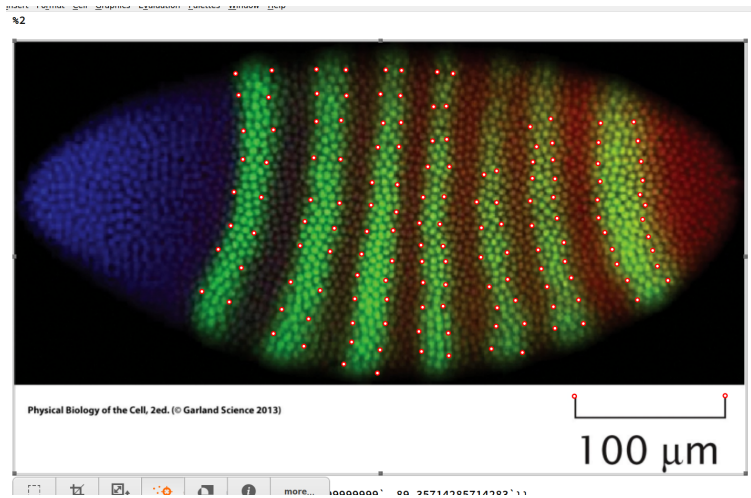
We have

$$m = 10^{-6} \cdot \left(\frac{2}{3} + 1.3 \cdot \frac{1}{3} \right) \cdot V_{\text{pg}} = 2.304 \cdot 10^{-3} \text{pg}$$

Typical cell weight is $1 \cdot 10^{-3} \text{pg}$

https://ecmdb.ca/e_coli_stats

It is evident from the above calculations, that the it is the assumed shape of *E. coli* which deviates greatly from what is true.



2 Problem 2

Let at the end of 9th cycle there be N nuclei at the surface. At the end of 13th cycle, therefore there are $16N$ nuclei, which is given as ≈ 6000 . Hence,

$$N \approx 375$$

Since, every embryo must start from a single fertilized nucleus, at the end of 9th cycle, there must be $2^9 = 512$ nuclei in total. Therefore, the fraction of nuclei which migrated to the surface is

$$\frac{375}{512} \approx 0.7324$$

Following the notation of Problem 1, surface area of the spherocylinder is

$$A = 4\pi r^2 + 2\pi r l = 4.3982 \cdot 10^{-7} \text{m}^2$$

Therefore, the areal density is

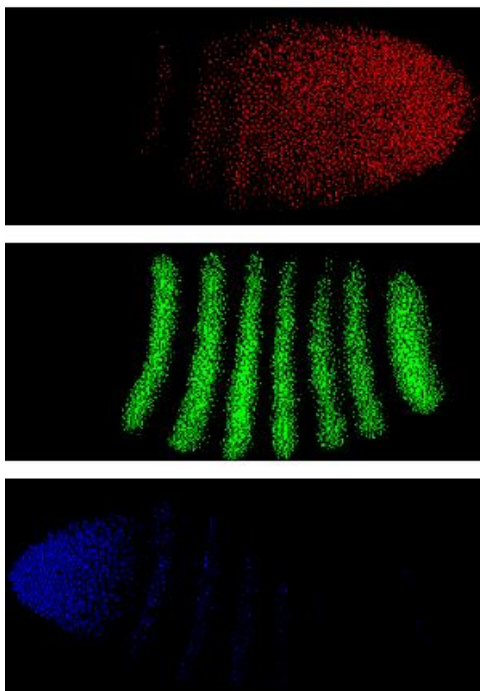
$$1.3642 \cdot 10^{10} \frac{\text{nuclei}}{\text{m}^2}$$

(For the next part, I have used Mathematica.) To calculate the length of the green strips, I marked the ends of widths along the lengths of each strip, and then used the given scale.

Length of the green strip is: $18.37 \pm 4.99 \mu\text{m}$ To evaluate the number of nuclei in each strip, I isolated the colors, and counted the number of pixels.

Therefore, the number of nuclei corresponding to each dye(I'm considering only a single surface – In the diagram, the surface of the cylinder has been mapped to a rectangle)

- Red: 466
- Green: 660
- Blue: 182



3 Problem 3

3.1 *E. coli*

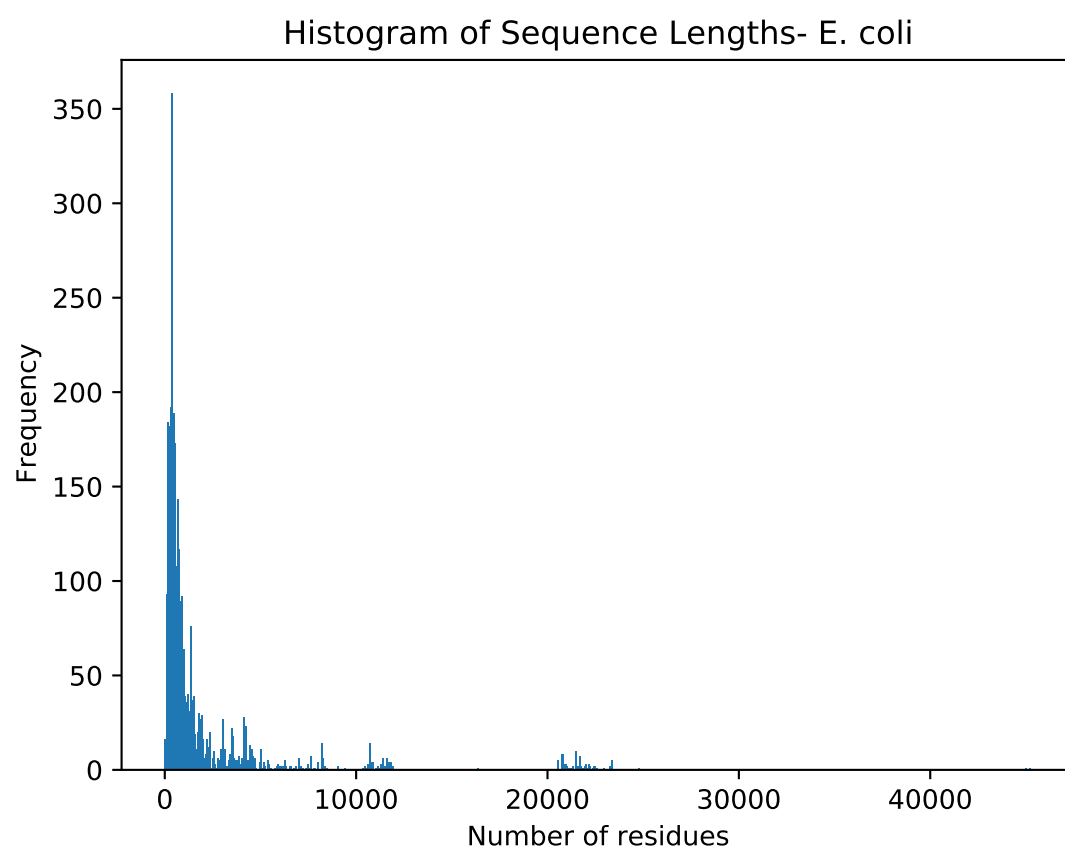
Mean of sequence length: 1892.00
Standard deviation of sequence length: 3872.73
Mean of molecular mass: 289.03
Standard deviation of molecular mass: 775.76

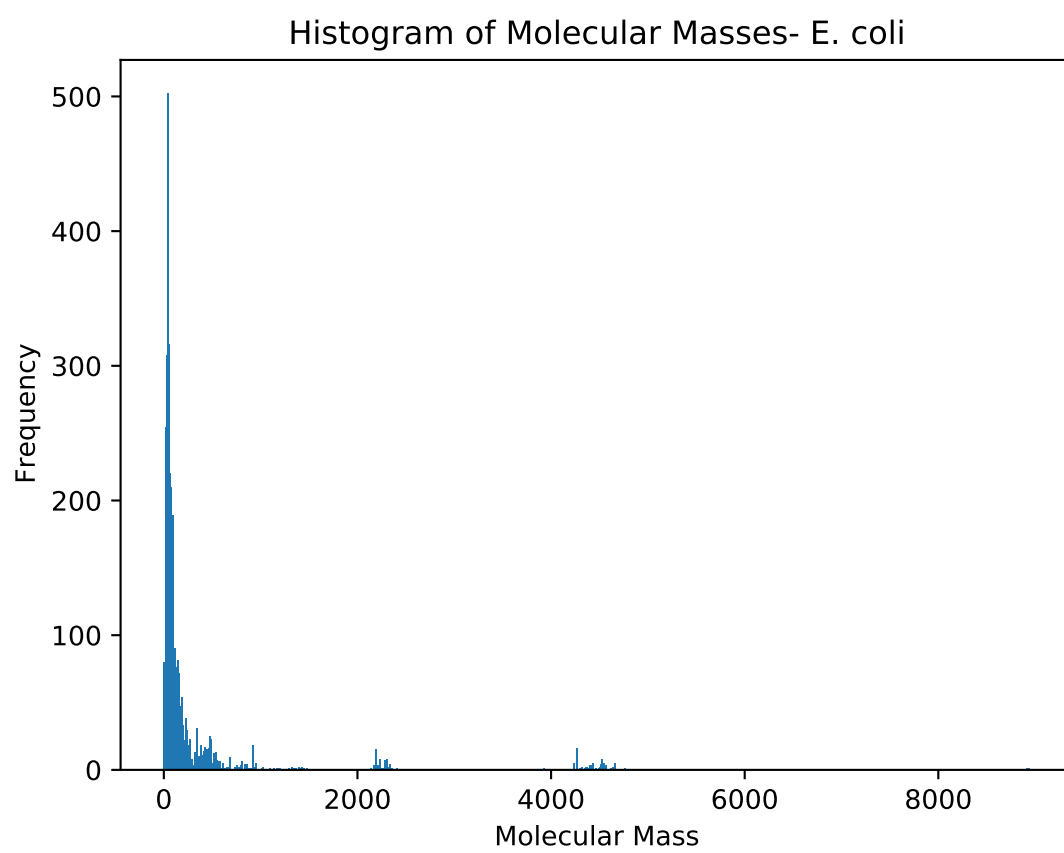
3.2 *S. cerevisiae*

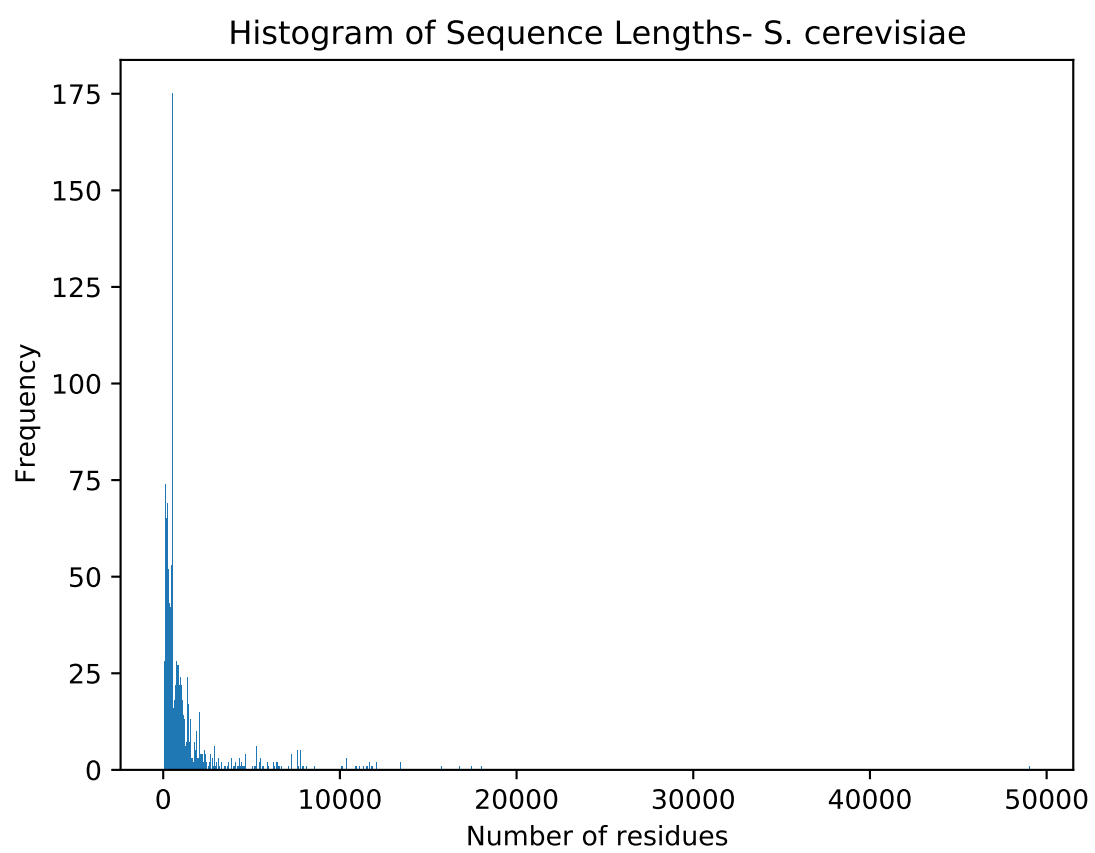
Mean of sequence length: 1287.90
Standard deviation of sequence length: 2444.49
Mean of molecular mass: 154.78
Standard deviation of molecular mass: 313.31

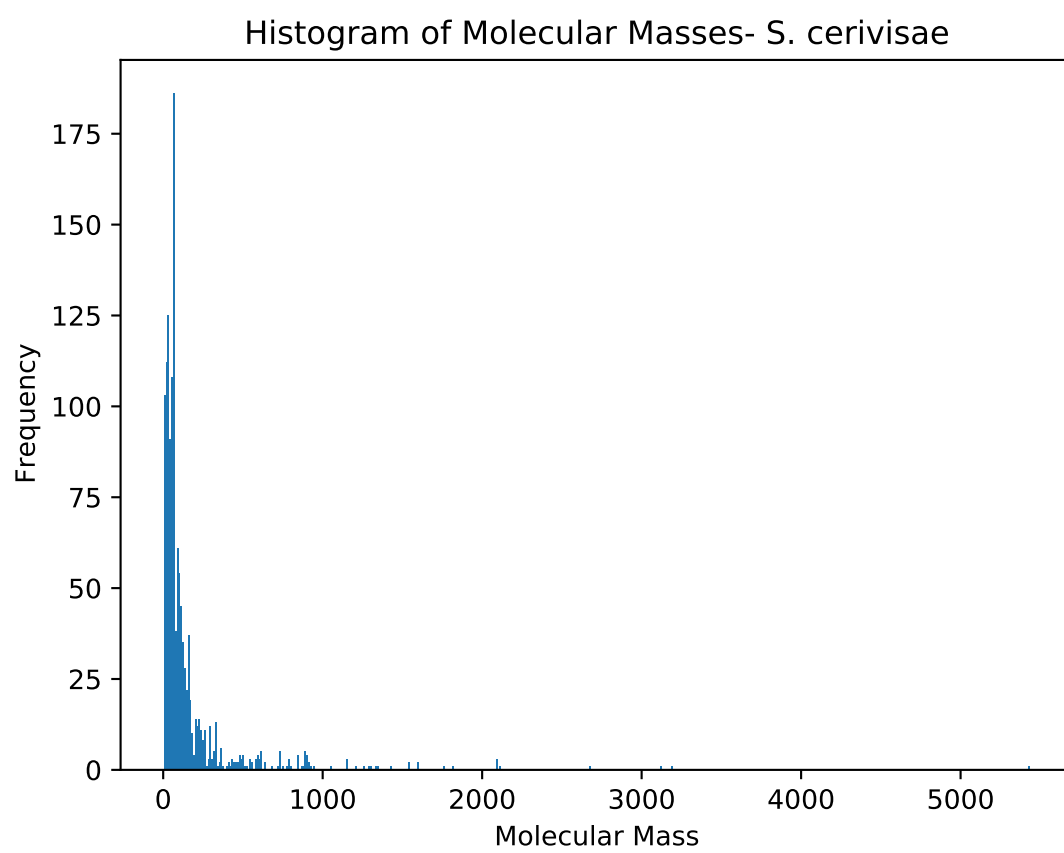
3.3 Humans

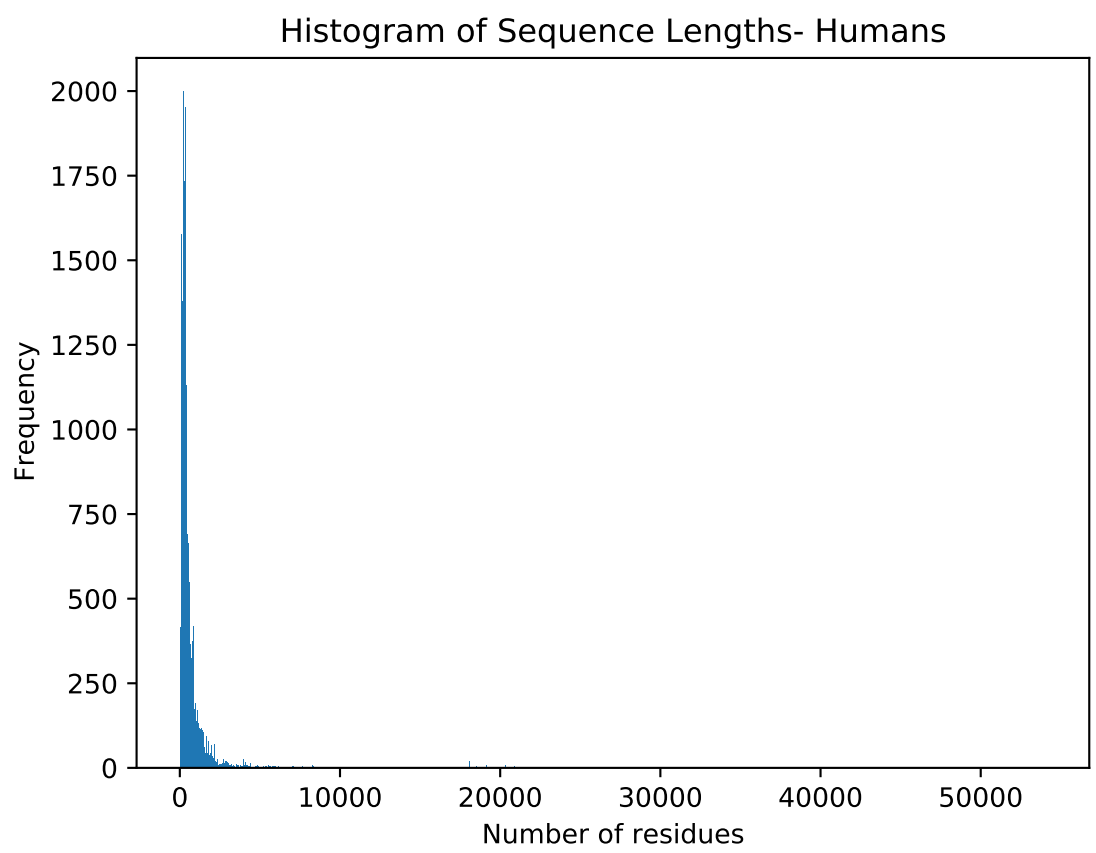
Mean of sequence length: 630.74
Standard deviation of sequence length: 1263.08
Mean of molecular mass: 74.21
Standard deviation of molecular mass: 181.93

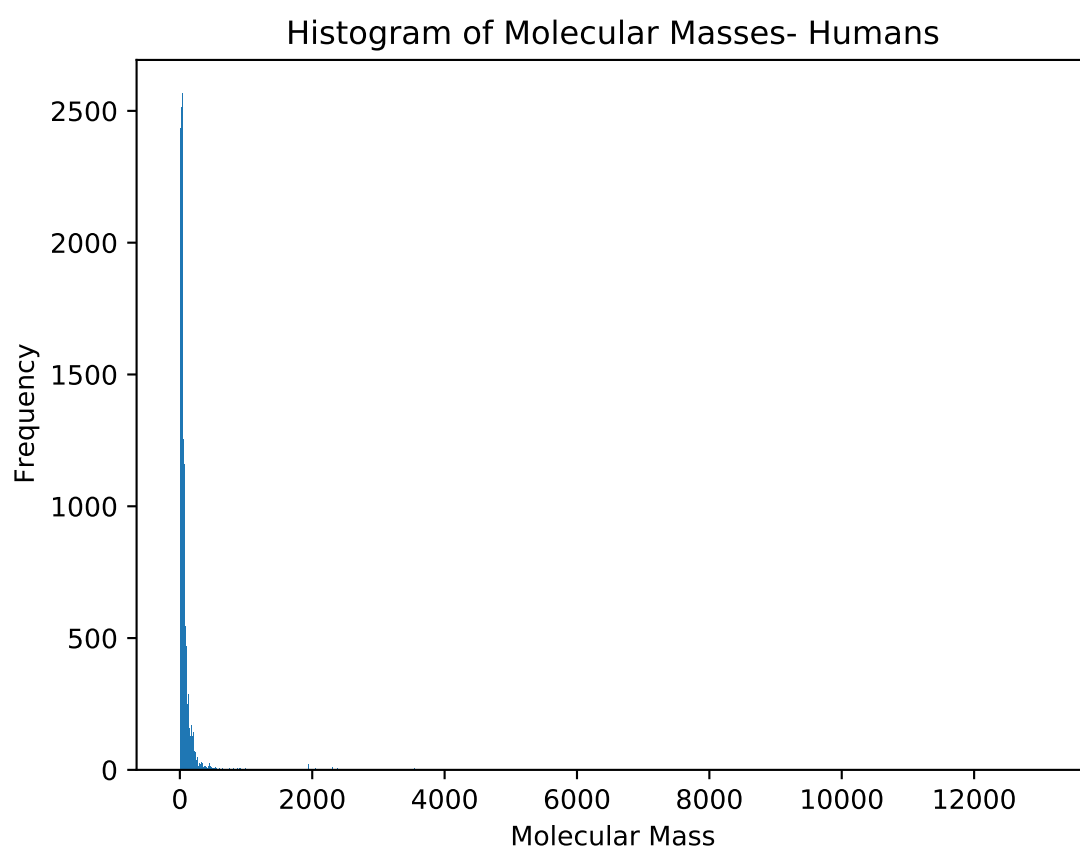












4 Problem 4

The probability of having 0 and 6 is

$$p^3 q^3$$

. The probability of having 1 and 5 is

$$\binom{3}{1} p^4 q^2 + \binom{3}{1} p^2 q^4$$

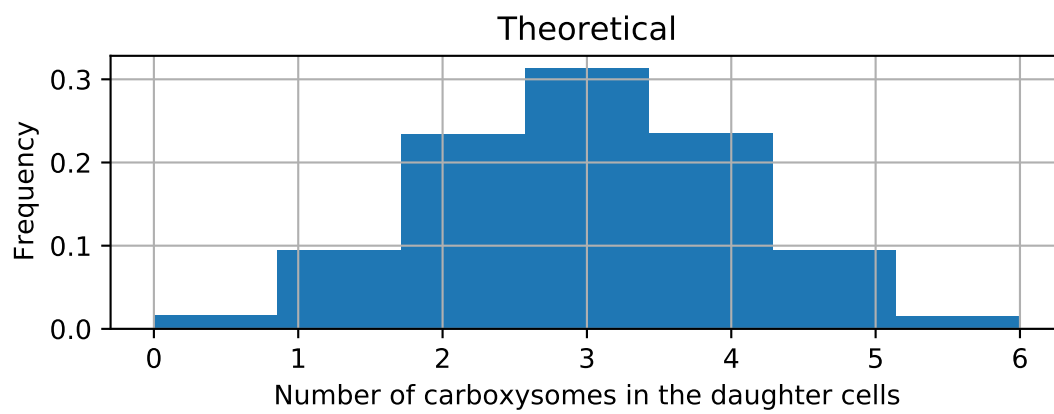
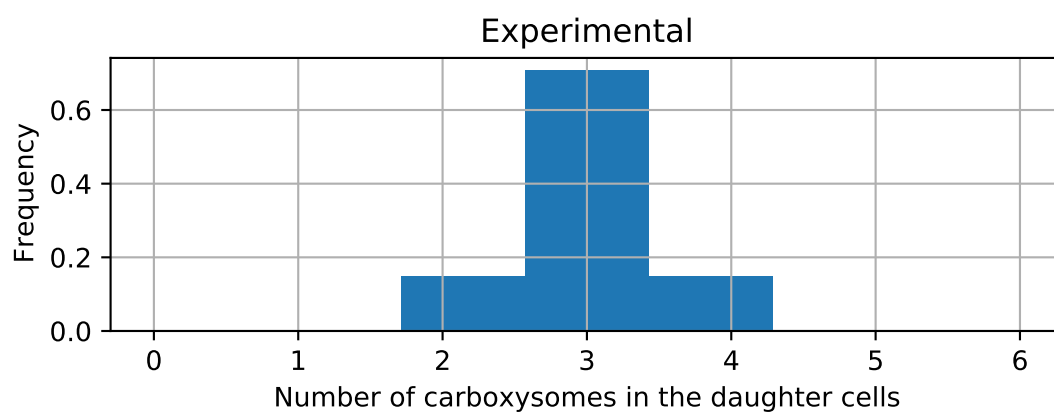
The probability of having 2 and 4 in one cell is

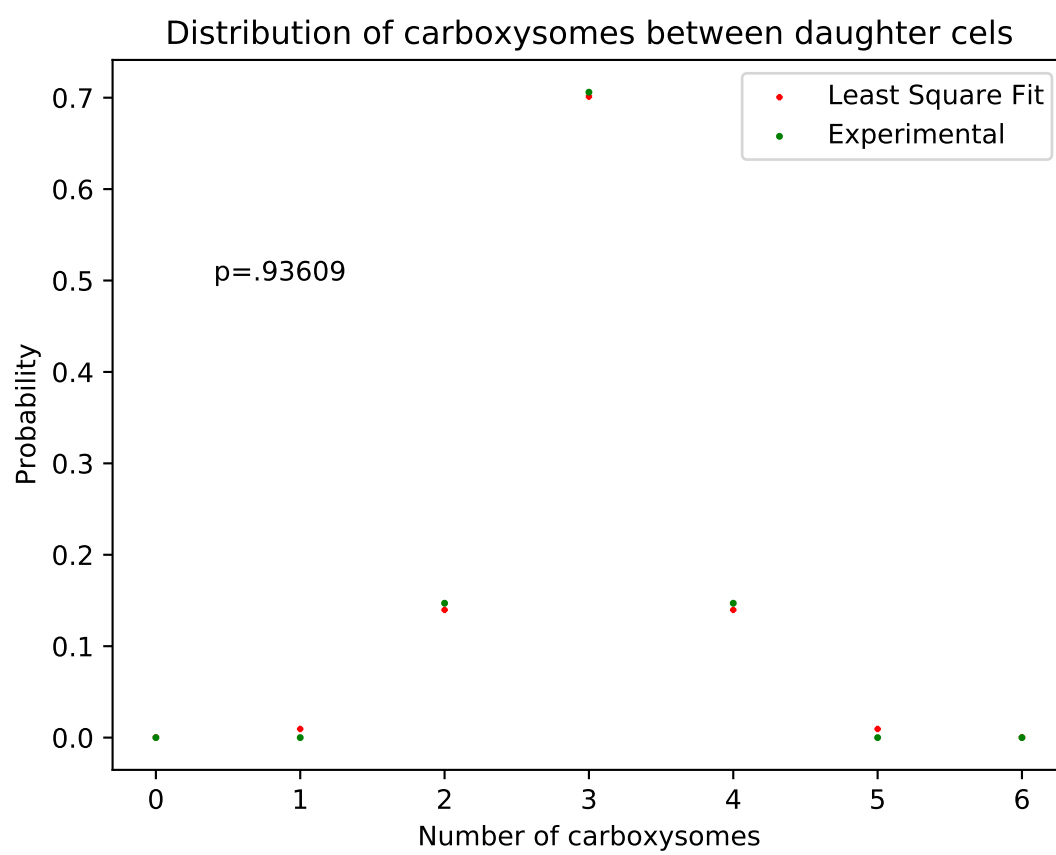
$$\binom{3}{2} p^5 q^1 + \binom{3}{2} p^1 q^5 + \binom{3}{1} \binom{3}{1} p^3 q^3$$

The probability of having 3 in one cell is

$$p^6 + q^6 + \binom{3}{1} \binom{3}{2} p^2 q^4 + \binom{3}{2} \binom{3}{2} p^4 q^2$$

By substituting $p = 0.5 + x$, and minimizing using the least-squares method with respect to the experimental distribution, obtained value for p is 0.936093. Attached, is a scatter plot showing the deviation. Given that, there are only 6 molecules, and the error is about 0.007 ± 0.001 (for the non-zero values), I believe it's a good model.





5 Problem 5

- (a) There are 4^3 possible ways of choosing the bases to form a triplet, each with the same probability. Therefore,

$$p_s = \frac{3}{64}$$

- (b) There are 64 possible codons. Three of these are not allowed (The stop codons), to form an ORF. Therefore, the number of acceptable possibilities is $(64 - 3)^N$.

Required probability is $\left(\frac{61}{64}\right)^N$.

- (c) Codons are of length 3 bases. Since, the DNA is circular, let us pick an arbitrary base and call it the starting point, and label the bases as

$$\dots x_{N-1} x_N x_0 x_1 x_2 \dots$$

Looking at the above sequence, we can see that the codons containing x_0 are

$$x_{N-1} x_N x_0$$

$$x_N x_0 x_1$$

$$x_0 x_1 x_2$$

and their reverse (corresponding to either a clockwise read or an anti-clockwise read – Also respectively, each codon corresponds to reading frames: +2, +1 and +0). Therefore, there are 6 reading frames in total.

- (d) Exact length of the E. coli genome is 4639675 (As per the data in U00096.fna) base pairs, whose remainder with respect to 3 is 1.

Since, when chosen at random, choice of reading frame doesn't matter, let's suppose that I have picked one already. In any reading frame, because of the non-zero remainder, when codons are selected, one base pair will remain ungrouped. I select this as my origin and group bases accordingly. The sequence will look like

$$\dots |XXX|X|XXX|\dots$$

Total number of codons formed is 1546558. Since, this is a very large number, the distribution to a good approximation must be poisson or a sum of poisson distributions. That is, for an ORF of length l , the probability that there will be N such ORFs, when a sequence is chosen at random must be

$$\sum_i e^{-\lambda_i(l)} \lambda_i^N(l) / N!$$

- (e) Take a look at the attached ipython notebook.
 (f) The figures are placed at the end.
 (g) 1
 (h) Plot is placed at the end.

