This page presents the code needed to solve the Problem Set #2 in "Introduction to Biophysics" course. All the files connected to the PS2 are modifications of the initial code from PNelson code .

"PS2_task3_a.ipynb"

This file outputs the number of mistakes and total time of translation for several mRNAs for 3 different models: the Hopfield-Ninio model where selectivity is through unbinding (HN), a model that discriminates mainly by forward rates (FRD), and a model that uses *in vitro* measured rates (Realistic).

For this part I rewrote the definition of the **ribosim** function by adding the parameters for the FRD model. Also I noticed some mistakes in the parameters of HN model ($k_{add,c}$ was 0.01 instead of 0.001 and ϕ_{-1} was 5 instead of 94). I put $\phi_{-1} = 94$ as it should be and $k_{add,c} = 0.005$ because with the right value the calculations were too long..

*here I needed to use the numpy version 1.16.1 to exlude an error with np.load comand

"PS2_task3_b.ipynb"

This code outputs the number of mistakes and average translation rate (for one certain chain and with the respect to the number of experiments) for 3 mentioned models.

For this part I put $k_{add,c} = 10^3$ for all 3 models. I calculated the average rate for each mRNA chain by considering

$$\text{rate}_i = \frac{\text{length of the chain}_i}{\text{total translation time for the chain}_i}$$

I wrote this value to the array **rate**. Also I calculated and output the average rate with the respect to the number of experiments (number of chains), so

$$\text{ave\_rate} = \frac{\sum_i \text{rate}_i}{\text{number of chains}}$$

"PS2_task3_c.ipynb"

This code outputs plot which depicts the function of wrong AAs VS a function of the average rate on a semi-log scale. I increased the number of chains to highlight that values are distributed in a distinguishable separate areas.