**DNA to Free Energy**

*Goal*: Use the method describe in the referenced papers [1, 2] to compute the average free energy for each position in the E. coli genome. Write results to a separate file. (See Figure 1 below for a listing of free energy values.)

Practice:

1. Suppose this is your dataset of energy values by position (e.g. Energy1 is the free energy at position 1.)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Sequence* | *Energy1* | *Energy2* | *Energy3* | *Energy4* | *Energy5* |
| Seq1 | -2.30 | -5.61 | -1.00 | -2.82 | -4.32 |
| Seq2 | -1.43 | -7.56 | -0.53 | -1.44 | -3.89 |
| Seq3 | -0.56 | -4.83 | -0.98 | -2.09 | -5.01 |

Calculate the following values by hand.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Avg(energy1) | Avg(energy2) | Avg(energy3) | Avg(energy4) | Avg(energy5) |
|  |  |  |  |  |

Input: datafile

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Sequence* | *Energy1* | *Energy2* | *Energy3* | *Energy4* | *Energy5* |
| Seq1 | -2.30 | -5.61 | -1.00 | -2.82 | -4.32 |
| Seq2 | -1.43 | -7.56 | -0.53 | -1.44 | -3.89 |
| Seq3 | -0.56 | -4.83 | -0.98 | -2.09 | -5.01 |

Output: Array of free energy values for each position

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Avg(energy1) | Avg(energy2) | Avg(energy3) | Avg(energy4) | Avg(energy5) |