Protein synthesis and chance

A “stochastic” model of protein synthesis

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In the process of protein synthesis there is a “stochastic” component, i.e., involving random chance, which influences the time the process takes. This aspect has been investigated by two research scientists at the International School for Advanced Studies (SISSA) in Trieste.

Gene expression (the functional activation of genes within a cell) is a crucial process for life. An important step in this process is protein synthesis, whereby the single amino acids, the “building blocks” that make up the strand of protein, are strung together like beads on a necklace. Even though this mechanism had previously been described in detail, some “stochastic” aspects had been neglected: in the chain of events that characterizes protein synthesis there is a certain random component that influences the time it takes for the protein to be assembled. A research
team at SISSA has investigated this aspect and described the process of protein translation by using a mathematical model. The study has just been published in the scientific journal Physical Review E.

In mathematics, a stochastic system refers to a process that is subject to random changes, which fluctuate, however, around an average value. For the sake of simplicity, the system can be described considering only the average value, i.e., in a “deterministic” manner, where, given the conditions, the variable can assume only a single definite value. In actual fact, however - and this is true for many biological processes – the “cloud of values” that a variable can assume when the process is repeated over time can affect the efficiency of the process.

A group of scientists at SISSA has analyzed the stochastic nature of the protein translation process, testing it with computer simulations. “We considered a specific aspect of translation: the distribution of binding times (BT) that is the time needed for tRNA (a molecule capable of transporting amino acids) to carry the proper amino acid to the ‘matrix’ (mRNA) which ‘prints’ the proteins according to a specific code”, explains Pierangelo Lombardo, who carried out the research together with Luca Caniparoli – both from SISSA. “This time interval is not always the same, but it varies in a more or less random manner”.

“Imagine you know there is an average BT value, for example 1, which can be used conventionally when describing the system. In actual fact, however, each time we observe the process the value may be 1.1, 0.9, 0.7, 1.3 and so on. The value assumed each time by the BT changes in a stochastic, though not completely random, manner because it distributes into a cloud with a specific shape around the mean”, continues Lombardo. “The shape of this cloud is not indifferent, as it has an effect on the time needed for process of protein synthesis. What we found in our study is that the BT fluctuates more (i.e., the cloud is more spread out) than previously thought and consequently so does the time needed for protein translation”.

“Observations like this extend our knowledge on protein synthesis processes”, he concludes. “Knowing how translation times decrease and increase may also be useful to understand under which conditions these mechanism can fail“.
More in detail...

Gene expression consists in building proteins (or other macromolecules) starting from the genetic information contained in the DNA. The process occurs inside the cells. The original matrix of proteins are genes, small parts of DNA contained in the cell nucleus. The sequence of elements (nucleotides) making up the DNA contains the information needed for building proteins.

Simplifying the process greatly, we can say that first a sort of carbon copy is made of the sequences encoded in the gene. This first step is called “transcription”: a portion of DNA is copied into a small RNA molecule, termed mRNA or messenger RNA. This portion travels to the parts of the cell where the second step, translation (or protein synthesis), takes place with the help of structures called ribosomes which “read” the mRNA sequence and collect the material needed to build the protein.

Proteins, in fact, are made up of long chains of amino acids, the tiny building blocks normally found dissolved in the cytoplasmic fluid. Some small RNA molecules, called tRNA and different from mRNA, bind specifically to amino acids giving rise to tRNA-amino acid complexes. These complexes then go and interlock, like the teeth of a zipper, with the chain of mRNA, one after the other into the proper sequence of amino acids, which bind to each other to form the strand of protein.

IMAGE:

- Credit: Duncan Hull (http://bit.ly/1drKXXk)

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