

Apparently simple fragments

Computers are devices that help us in everyday life. Many people cannot imagine functioning without them. They lead us to our destination, help us to cook dinner, provide entertainment, and even help save lives. In all of these areas, computers use algorithms - simple recipes for how to step-by-step perform a given operation. A distinctive group of algorithms are those that we consider as intelligent. It is amazing that people are trying to create something that will imitate human reasoning. Many people imagine artificial intelligence as it is shown in science fiction movies. Indeed, there are many technological achievements that first appeared in the mind of a science fiction writer.

Some of these algorithms help us to understand life at the molecular level - but wait, what exactly does it mean to try to understand something at the molecular level? If we look at a living organism under a microscope, e.g. a human, we will see that it is made up of cells. A cell is considered to be the smallest living thing - yes, we are made up of very small pieces that lead their own lives. The combination of tens of trillions of such small living pieces builds complex beings like humans.

The cell can be compared to a factory that processes raw materials while taking care of its condition. It can also be compared to a ship that transports passengers and leads its own life. If we take a closer look at it, we will see that it is made of proteins. They perform various functions. Some of them are its basic building blocks, others join chemicals, and yet others play a key role in the cell, e.g. they help conduct electrical impulses in our brain - thanks to them we are able to think.

Proteins are composed of amino acids and they look like beads twisted into a string. There are 20 different types of such beads that build proteins. Commonly, these strings have a large variety of beads, but there are also fragments whose diversity of beads is very low. They are composed of only one, two or three types of beads. Scientists for a very long time liked to look at only these beautiful parts with a large diversity of beads, and that is what they studied. Not so long ago, studies of these with little diversity have also begun.

To understand what sizes we are talking about, imagine that we are enlarging the amino acid into a grain of sand. After such an operation, the cell will be the size of a supermarket, and the human body will be the size of the sun. It seems quite simple to see phenomena in the world around us, such as a falling apple, the attraction of metals by a magnet or the conductivity of electricity. Spotting similar phenomena at the molecular level takes months or even years of work in the laboratory. Therefore, it is a time-consuming and costly process. However, It is possible to significantly speed up this process and estimate the biological functions of proteins by finding fragments that we have already discovered and studied.

Scientists' interested in fragments that have high diversity of amino acids. This has led to the development of algorithms that can assist in their analysis. The consequence of the lack of interest in fragments of little diversity has resulted in the lack of methods for automatic computer analysis of these fragments. The aim of the project is to create algorithms that will help us study the phenomena occurring in fragments with a low diversity of amino acids in proteins.

Discovering functions of protein fragments entails a number of applications, both for scientists in other fields, as well as for everyday life. Thanks to this information, we are able to understand genetic diseases, design new medicines, enrich plants with vitamins that are scarce in a given region, and many more.