1. I would like to tell you about the research in which I am currently participating. This is a study in the field of bacterial immunity in terms of bioinformatics.  
   Bioinformatics has become a buzzword in today’s world of Science. About one or two decades ago, people saw biology and computer science as two entirely different fields. One would learn about living beings and their functions whereas the other would learn about computers and underlying theories. However, at present, there seems to be a mere separation between the two fields and this new field, bioinformatics, has emerged as a combination of both Computer Science and Biology.
2. For further understanding, I should explain the basic concepts. So, first, what is dna in general? Deoxyribonucleic acid, or DNA, is a molecule that contains the instructions an organism needs to develop, live and reproduce. These instructions are found inside every cell, and are passed down from parents to their children. As you can see in the animation, the main components of DNA are the double spiral and the bonds between them. For us, only the connections themselves are interesting. There are only four types, which are located opposite each other on each side of the spiral, and we can encode them in four letters: A, T, C, G. Moreover, A is always opposite T, C is always opposite G. If we untwist the DNA, we find that it is only a sequence of letters or just sequence for short. We can say that all of our past and partly future is just a long sequence of four letters. For human genome if stretched out, it would form very thin thread, about two meters long. Finally, if we know that the genes that encode all the life processes of an organism are only a subsequence of DNA, we can proceed to the core material.
3. All living things have enemies, and bacteria are no exception. They are called bacteriophages. The main idea is to analyze the evolutionary processes of the eternal struggle of bacteria and bacteriophages. In simple terms, genes that promote survival are present in organisms much more often than those that impede survival.
4. The next idea is that functionally linked genes in bacterial genomes are often organized into operons. However, the composition and architecture of operons are highly variable and frequently differ even among closely related genomes. Therefore, to efficiently extract reliable functional predictions for uncharacterized genes from comparative analyses of the rapidly growing genomic databases, dedicated computational approaches are required.  
     
   Last year group of scientists developed a protocol ICITY which use to systematically and automatically identify genes that are likely to be functionally associated with a ‘bait’ gene or locus by using relevance metrics. Given a set of bait loci and a genomic database defined by us, this protocol compares the genomic neighborhoods of the baits to identify genes that are likely to be functionally linked to the baits by calculating the abundance of a given gene within and outside the bait neighborhoods and the distance to the bait.   
     
   We used the ICITY protocol to determine the existence of a functional relationship between the recently discovered DGR operons and the bacterial immune system.
5. Currently, about 700 bacteria are found in which DGR is present. It should be noted that in each genome could be any number of DGRs. We formed a dataset containing the genomes of these bacteria and applied the ICITY protocol to this dataset. As a result of the protocol, about 100 quite convincing outcomes were obtained. The two pictures provide examples of the organization of such immune systems that include DGR (RT) and the well-known elements of the immune system (cas). Then a phylogenetic tree was built. It reflects the genes most related from an evolutionary point of view. By the methods of cluster analysis, five clusters were formed, which divide the initial data into 5 subsets.

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