**Search for frame shift signals in bacterial genomes**

1. Petrov1, A. Milenkin2, I. Antonov3

*1Saint Petersburg State University, Universitetskaya emb 7-9, 199034, Saint*

*Petersburg, Russia*

*2Moscow Institute of Physics and Technology, Institutskiy per. 9, Dolgoprudny, 141701, MoscowRegion, Russia*

*3Institute of Bioengineering, Federal Research Centre Fundamentals of Biotechnology, Leninsky prosp. 33- 2, 119071*, *Moscow, Russia*

One of the substances necessary for the biosynthesis of chlorophyll and vitamin B12 are the enzymes Magnesium chelatase and Cobalt chelatase, consisting of three subunits and having similar functions. There are studies showing that in some organisms that synthesize vitamin B12, the cobalt chelatase contains a large cobalt chelatase subunit and two magnesium chelatase subunits. However, the genome of these organisms lacks a gene encoding the small subunits of Magnesium chelatase.

In this project, a database containing more than 1000 genomes of various bacteria containing genes of Magnesium chelatase was analyzed. Among these organisms, more than 100 signal sequences have been identified, with the help of which the reading frame is shifted and the subsequent synthesis of both the medium and the small subunit of Magnesium chelatase from only one gene of the medium subunit. This is possible due to the similar structure of the part of the middle subunit and the small subunit of Magnesium chelatase.

As part of the project, frame shift signals were retrieved from the database, multiple alignments were constructed for them in order to find common subsequences and specific codons responsible for the frame shift. The research revealed the most active appearance of programmed shifts in proteobacteria of the genus *Pseudomonas*.

The corresponding secondary structure was predicted for each bacterial genus separately.

Also, for the convenience of searching for genomes containing chelatase genes and analyzing the corresponding frame shift signals, attempts were made to create a convenient web interface of the existing database.