QUANTUM ALGORITHMS AND SEQUENCE ALIGNMENT

M.V.Altaisky[1], P.Filatov [2], Yu.Ovodkov, [3]

[1]*Joint Institute for Nuclear Research, Dubna, 141980, Russia;*
e-mail: altaisky@mx.iki.rssi.ru, ph. 65598, fax 65145
[2] *National Hematology Research Center of RAMS,*
4a Novo-Zykovsky pr., Moscow, 125167, Russia,
e-mail: ffelix@blood.ru
[3]*International University «Dubna»,*
Universitetskaya 19, Dubna, 141980, Russia
e-mail: ovodkovv@mail.ru

In present paper we analyze the similarity between the modern paradigm of quantum information processing and the (64/20 redundant) triplet genetic code. It is shown that the DNA sequence alignment problem, which is one of the most resource consuming problems in bioinformatics, can be considered as a problem for quantum computations performed by pentabits $|\phi\rangle = \alpha_0|0\rangle + \alpha_1|A\rangle + \alpha_2|C\rangle + \alpha_3|T\rangle + \alpha_4|G\rangle$ instead of traditional qubits. The formal analogy between pentabit computing and traditional quantum computing, taken together with functional properties of the four nucleotides, implies a metric on the space of DNA sequences. This metric can be used for both classical and quantum algorithms of sequence alignment. As a practical example the phylogeny based on the S segment nucleocapsid protein gene for hantaviruses is calculated.