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## Search for Regions with Periodicity Using the Random Position Weight Matrices in Different Genomes

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The present study developed a mathematical method for determining tandem repeats in a DNA sequence. A multiple alignment of periods was calculated by direct optimization of the position-weight matrix (PWM) without using the pair wise alignments or searching for similarity between periods. A new mathematical algorithm for periodicity search was developed using the random PWMs. The developed algorithm was applied in analyzing the DNA sequences of the different genome. A total of more than  $60 \times 10^3$  regions were found to possess a periodicity with the length of 2 to 50 bases. On the average, a periodicity of  $\sim 5000$  nucleotides was found to be associated with each region. A significant portion of the revealed regions possess periods consisting of 10 and 11 nucleotides, multiple of 10 nucleotides and periods in the vicinity of 35 nucleotides. Only  $\sim 30\%$  of the periods found were discovered previously. This study discussed the origin of periodicity with insertions and deletions.

### Biography:

Eugene V. Korotkov is a professor at the Department of Applied Mathematics in Moscow Engineering Physics Institute and Principal Investigator in Bioinformatics Department of Bioengineering Centre, Russian Academy of Sciences. He graduated from the National Nuclear Research University (MEPhI), Department of Experimental and Theoretical Physics in 1974. He completed PhD thesis in radiobiology. Then, from 1980 to 1995 he worked at the Institute of Chemical Physics, NN Semenov and since 1995, he is working with the Center 'Bioengineering', Russian Academy of Sciences. His research interests are in developing new methods for the analysis of symbolical sequences and time series.