We describe a new mathematical method for finding very diverged short tandem repeats containing a single indel. The method involves comparison of two frequency matrices: a first matrix for a subsequence before shift and a second one for a subsequence after it. A measure of comparison is based on matrix similarity. The approach developed was applied to analysis of the genomes of C.elegans, D.melanogaster and S.cerevisiae. They were investigated regarding the presence of tandem repeats having repeat length equal to 2 and 4-11 nucleotides. A number of phase shift regions for these genomes was approximately 2.2x10^4, 1.5x10^4 and 1.7x10^2, respectively. Type I error was less than 5%. The mean length of fuzzy periodicity and phase shift regions was about 220 nucleotides.

The regions of fuzzy periodicity having single insertion or deletion occupy substantial parts of the genomes: 5%, 3% and 0.3%, respectively. Only less than 10% of these regions have been detected previously. That is, the number of such regions in the genomes of C.elegans, D.melanogaster and S.cerevisiae is dramatically higher than it has been revealed by any known methods. We suppose that some found regions of fuzzy periodicity could be the regions for protein binding.