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# Matrix Algorithms for Genome Evolution (MAGE)

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## Abstract

The recent sequencing of more than 1000 human genomes has revealed that two individuals from the same population have millions of genomic variations between them. Closely located mutations are linked together forming haplotypes that change constantly due to recombination events during gametogenesis. Evolution occurs on whole ensembles of these numerous haplotypes, where mutations influence each other and should be considered as a whole entity – a gigantic matrix, unique for every individual genome. Several mathematical theories have attempted to describe the intricate dynamics of genomic variations in populations. However, these theories are conflicting each other, and there is no universally acknowledged understanding of genome evolution. We attempted to model mammalian population genetics using a pure computational approach, taking advantage of the enormous power of modern supercomputers. A software package named Matrix Algorithms for Genome Evolution (MAGE), has been created and tested for modeling evolution of entire chromosomes. We have validated that MAGE can precisely mimic real biological processes that have influence on genome evolution such as: 1) authentic arrangements of genes and functional genomic elements; 2) frequencies of various types of mutations in different nucleotide contexts; 3) non-random distribution of meiotic recombination events along chromosomes. Computer modeling with MAGE made a breakthrough in the appreciation of mutation dynamics. In particular, we demonstrated that a numeric parameter, a number of DNA recombination events per gamete, is crucial factor that influence the population fitness under the observed intense flow of novel mutations (~50 mutations per individual). MAGE can computethe probability of fixation for a mutation with a selection coefficient ***s*** as a function of multiple parameters: 1) mutation influxand the distribution of novel mutations by their selection coefficients; 2) selection pressure (including number of offspring per individual, mating schemes, population size); 3) genomic parameters (such as number of meiotic recombinations, arrangements of genes and their degrees of dominance).

## Biography

Alexei Fedorov has completed his Ph.D in 1993 from the Institute of Molecular Genetics, Russian Academy of Sciences in Moscow. His postdoctoral studies include Walter Gilbert Laboratory at Harvard University. He is an Associate Professor and the Director of Bioinformatics and Genomics/Proteomics Program at the University of Toledo, OH USA. He has published more than 60 papers in reputed journals and serves as an editorial board member for three journals.