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# Modeling of prokaryotic genome evolution using coding signal as selection pressure

Protein coding genes in prokaryotic chromosomes are subjected to two different asymmetric mutational pressures associated with various replication mechanisms of DNA strands (leading and lagging). To simulate evolution of prokaryotic protein coding sequences under this asymmetric mutational pressure, we elaborated a simulation model based on the Borrelia burgdorferi genome. As the mutational pressure we applied nucleotide substitution matrices empirically found for the leading and lagging DNA strands of the genome. The selection pressure was based on the modified algorithm for protein coding gene finding, trained on annotated B. burgdorferi protein coding genes. We simulated the evolution of genes from differently replicating strand under the constant, opposite and changing mutational conditions, mimicking sequence inversions.