

Synteny in mammalian genome evolution

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The number of chromosome-length genome assemblies has recently exploded, representing many vertebrate clades. These unfragmented assemblies have enabled biologists to study the evolution of gene loci and their positions at unprecedented scales. Synteny blocks, groups of genes with conserved order, have proven to be a key concept in our understanding of genome evolution. To gain further insight into how synteny blocks evolve, we use comparative methods to examine gene order conservation across nearly one hundred mammals. In pairwise comparisons between species, we find a strikingly regular relationship between synteny block sizes and the average amount of protein sequence evolution. We develop a mathematical model that reproduces synteny block size distributions as a function of evolutionary time. Using our model, we seek to identify synteny blocks larger than expected in the absence of selection.