

Alu-Derived Orthologous Chromosome Classification for the Primate Order

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Orthologous chromosomes between any family of related species have been difficult thus far to obtain, often requiring substantial biochemical testing and computationally-intensive genomic analysis. By employing computational strategies on repeated non-coding DNA, numerous advantages to accurately determining orthologous chromosomes between species can be ascertained. Throughout the primate genome, the Alu repeated element covers 10% of the genome among higher order primates, spanning across each chromosome. These non-protein-coding sequences replicate themselves repeatedly, with each iteration allowed to mutate more than their protein-coding counterparts. Therefore, upon examining the genetic sequences of such “junk” DNA, increasingly specific distinctions can be made between any two compared primate genomes. We propose a novel strategy of matching known Alu repeats by subfamily between two species, thereby ascertaining the not only the frequency of specific Alu elements conserved, but also which where each matched pair is located on the species’ chromosomes. By collecting Alu-identified primate genomes the University of California Santa Cruz Table Browser, this methodology was applied to 12 species-specific genomes. After comparing the Alu elements between each of the primates and subsequent frequency analysis, we were able to accurately highlight what chromosomes were conserved across members of the Order Primate. In addition, we were able to use our alignment with currently accepted literature to produce orthologous chromosomes for numerous species previously not compared against one another. In conclusion, we propose a far less computationally and resource intensive solution to determining conserved chromosomal relationships among primates.