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*Genomic Midpoints: Computation and Evolutionary Implications*

In joint work with graduate student Yannet Interian, I have developed a method for computing genomic midpoints, which minimize the sum of the distances to three given genomes. In contrast to the GRIMM synteny method which uses an ad hoc procedure to find a very good solution, our algorithm use local search methods to perform a more wide-ranging investigation of the set of possibilities. An advantage of our method is that it can easily produce 100 good solutions. As in the reconstruction of phylogenies, comparing these solutions helps us understand the confidence we can have in various features of our predicted midpoint. We illustrate our methods using comparative maps of of human-lemur-tree shrew, human-cow-cat, and human-mouse-rat.