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Genomic sequencing has permitted us the opportunity to use comparative genomics to reconstruct species evolution. However, genomic diversity has made the connection between an ancestral genome and present day species computationally challenging. A genome undergoes rearrangements, translocation and speciation of genes. Just modeling the rearrangements of genes that a genome undertakes is difficult. If we try to model the rearrangements of a single chromosome to another chromosome and attempt to compute the minimum number of rearrangements that a chromosome must undergo to become another chromosome, then we have an NP-hard problem. To address this issue, we will instead construct the geodesic path between two genomes. As an example of this technique, we tackle the geodesic path between the tobacco genome and the *Lobelia fervens* genome using the calculus of variations. (Received September 18, 2009)