Sequence similarity does not always accurately represent relatedness. In this hypothetical tree, the evolution of three species is indicated by *thick light blue bars* and the evolution of specific genes is indicated by *thin red and blue lines* within the bars. An early gene duplication gave rise to the $\alpha$ and $\beta$ genes; thus all of the $\alpha$ genes are paralogs of the $\beta$ genes. Over time, the $\alpha$ and $\beta$ genes diverged such that their functions now differ (indicated by red and blue). The multiple forms of the $\alpha$ genes arose through speciation events, and thus all are orthologs of each other (and likewise for all the $\beta$ genes). If species 3 had a slower rate of evolution than the other two, then the $\alpha$ and $\beta$ paralogs within species 3 will be more similar to each other (as measured by summing the branch lengths connecting them) than either is to their orthologs in other species. (Redrawn from Eisen J.A. *Genome Res.* **8**: 163–167, Table 4, © 1998 CSHLP.)

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