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**Title:** Great expectations—gene order rearrangement made (sort of) easy

**Abstract:** Evolutionary relationships can be derived by studying the order in which the genes appear. Common gene order changing operations in nature are the reversal and the block transposition. A relatively simple method to estimate the evolutionary distance between two species is to compute the minimal number of reversals or block transpositions needed to transform the gene order of one of the species into the second species' gene order. This number is called the edit distance and it gives a lower limit for the evolutionary distance that is reliable for closely related species but unreliable for distantly related species. Better estimates can be obtained by means of the expected edit distance between two genomes separated by  $t$  operations, a function of  $t$  that is hard significantly harder to compute than the corresponding edit distances.