Computational tools for biological sequence alignment are indispensable to modern molecular biology. Nowadays, the functional, structural, and evolutionary relationships of a novel protein or nucleic acid sequence are often inferred by finding similar sequences of known function in a database. Here, we investigate sequence alignment statistics. We model the alignment of random sequences heuristically with Markov additive processes. Its optimal alignment score is explained by ascending ladder scores of the Markov random walk process. In sequence alignment, the heuristic suggests a numerical acceleration scheme for simulating an important asymptotic parameter for the sequence alignment statistics. (Received September 17, 2013)