1023-05-1849 **Olgica Milenkovic*** (`milenkov@schof.colorado.edu`), Dept. of Electrical and Computer Enngineering, 425 UCB, Boulder, CO 80305. *On the generalized reversal distance.*

The reversal distance is the smallest number of reversals that one has to perform on a signed permutation in order to convert it to the identity element of the underlying group. This distance measure is frequently used to estimate the number of genome reshuffling events that occured during evolutionary history. We propose to generalize the concept of reversal distance for the case of non-uniform, context-dependent reversal costs. For the purpose of analyzing the combinatorial properties of the generalized reversal distance, we use a set of techniques from classical algebraic coding theory. (Received September 27, 2006)