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*Topological Metrics on Permutations*

In comparative genomics, biologists measure the similarity between genomes by modelling genome rearrangements. These metrics often correspond to lengths of factorizations of (signed) permutations into products from certain generating sets, for example block interchanges, or signed reversals. We draw an analogy to topological graph theory in which block interchanges naturally correspond to handles and signed reversals correspond to crosscaps, and investigate associated metrics used in comparative genomics.