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Optimization in Pharmacogenomics

High-throughput sequencing provides the means to determine the allelic decomposition— the exact sequence content of all gene copies present in the sample— for any gene of interest. When applied to pharmaceutical genes, such decomposition can be used to inform the drug treatment and dosage decisions. However, many clinically and functionally important genes are highly polymorphic and have undergone structural alterations, and as such present a significant challenge for the existing genotyping methods. Here we present a combinatorial optimization framework based on integer linear programming that is able to efficiently solve this problem for various pharmacogenes, including those with structural alterations. We also show how to adapt these linear programs for the emerging long-range barcoded sequencing datasets.