Probe Selection Algorithms with Applications in the Analysis of Microbial Communities

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Abstract

We propose two efficient heuristics for minimizing the number of oligonucleotide probes needed for analyzing populations of ribosomal RNA gene (rDNA) clones by hybridization experiments on DNA microarrays. Such analyses have applications in the study of microbial communities. Unlike in the classical SBH (sequencing by hybridization) procedure, where multiple probes are on a DNA chip, in our applications we perform a series of experiments, each one consisting of applying a single probe to a DNA microarray containing a large sample of rDNA sequences from the studied population. The overall cost of the analysis is thus roughly proportional to the number of experiments, underscoring the need for minimizing the number of probes. Our algorithms are based on two well-known optimization techniques, namely, simulated annealing and Lagrangian relaxation, and our preliminary tests demonstrate that both algorithms are able to find satisfactory probe sets for real rDNA data.

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