

ON NEW SCALARIZATION TECHNIQUES IN MULTIOBJECTIVE OPTIMIZATION

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Most of the methods for multiobjective optimization utilize some scalarization technique where several goals of the original multiobjective problem are converted into a single-objective problem. One common scalarization technique is to use the achievement scalarizing functions. In our latest research [1, 2], we introduce a new family of two-slope parameterized achievement scalarizing functions for multiobjective optimization. This family generalizes both parametrized ASF and two-slope ASF. With these two-slope parameterized ASF, we can guarantee (weak) Pareto optimality of the solutions produced, and every (weakly) Pareto optimal solution can be obtained. The parameterization of this kind gives a systematic way to produce different solutions from the same preference information. With two weighting vectors depending on the achievability of the reference point, there is no need for any assumptions about the reference point. In addition to theory, we give graphical illustrations of two-slope parameterized ASF and analyze sparsity of the solutions produced in convex and nonconvex test problems.

References

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RECONSTRUCTION OF DISEASE TRANSMISSIONS FROM VIRAL QUASISPECIES GENOMIC DATA

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Genomic analysis is becoming a major tool for outbreak investigations. Existing computational frameworks for inference of transmission history from viral genomic data often do not consider intra-host diversity of pathogens and rely on additional epidemiological data, such as sampling times and exposure intervals. This impedes analysis of outbreaks of highly mutable viruses associated with chronic infections, such as HIV and HCV, whose transmissions are often carried out through minor intra-host variants, while the epidemiological information is unavailable or has a limited use.

The proposed framework QUENTIN (QUasispecies Evolution, Network-based Transmission INference)[1] addresses the above challenges by evolutionary analysis of intra-host viral populations sampled by deep sequencing and Bayesian inference using general properties of