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Optimizing multi-arm clinical trials for personalized medicine using a genetic algorithm

Personalized medicine aims to improve treatment decisions using patient-specific covariates. In diseases with heterogeneous treatment responses, estimating treatment-covariate interactions is essential for identifying effective therapies across patient subgroups. Multi-arm clinical trials provide an efficient framework for evaluating several treatments simultaneously; however, the design problem becomes increasingly challenging as the numbers of treatments and covariates increase. In this work, we propose a statistical criterion for evaluating multi-arm trial designs based on interaction estimation across all potential subject covariates, including both continuous and categorical variables. To address the resulting combinatorial optimization problem, we develop a genetic algorithm that efficiently searches for statistically efficient treatment assignments. The proposed approach generates efficient designs by minimizing the maximum subject-covariate variance across treatment groups, thereby reducing uncertainty in treatment assignment under the individualized treatment rule considered. Extensive numerical experiments, including a real clinical trial application, demonstrate that the proposed algorithm consistently outperforms existing methods, yielding more efficient multi-arm trial designs. The proposed methodology provides a flexible and scalable framework for designing multi-arm clinical trials in personalized medicine.

Special/ Invited session

Classification

Mainly methodology

Keywords

Personalized medicine, Multi-arm clinical trials, Genetic algorithm, Individualized treatment rule

Primary author: VAZQUEZ, Alan (Tecnologico de Monterrey)

Co-authors: CERVANTES, Karla (Tecnologico de Monterrey); Dr WONG, Weng-Kee (University of California, Los Angeles)

Presenter: CERVANTES, Karla (Tecnologico de Monterrey)

Track Classification: Design of Experiments