

Standardized maximin D -optimal designs for pharmacological models

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Locally optimal designs are frequently used to estimate parameters in nonlinear models. They are easy to construct but require a single set of nominal values for the unknown parameters. An alternative approach is to use a maximin approach, which allows the user to specify a range of values for each parameter of interest. Maximin optimal designs provide some protection against the worst case scenario and are increasingly proposed for estimating parameters in nonlinear models. However, they are hard to find and study because of two-tier optimization process. We implement an algorithm based on particle swarm optimization (PSO) to find standardized maximin optimal designs for several pharmacological models, including four inhibition models commonly used in enzyme kinetics. We then show how numerical results from our algorithm enable us to identify formulae for the standardized maximin optimal designs which can be verified via the equivalence theorems. Finally we show the comparisons among locally, maximin optimal and standardized maximin optimal designs.