**The use of Bayesian hierarchical models for adaptive randomization in biomarker-driven phase II studies**

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The use of biomarker-driven designs has increased in cancer clinical trials, in attempts to efficiently answer questions of both treatment effects and biomarker performance as a companion diagnostic. This has been extended from single marker-enrichment and marker-stratified designs, to “basket”, “umbrella” and “platform” trials which investigate multiple treatments in a heterogeneous population. Bayesian methods and hierarchical models have been proposed for conducting statistical inferences and for applying outcome adaptive randomization in this setting. Recent work has used in silico simulations to quantify potential gains in efficiency under idealized scenarios. Two recent high-profile platform trials, NCI-MATCH (non-adaptive) and I-SPY 2 (adaptive), serve as important case studies for revealing fundamental challenges of platform trials and limitations of both adaptive and non-adaptive designs in adhering to basic principles of clinical trials.