Workshop Description:

Randomization inference is a widely-used and appealing approach for analyzing treatment effects in randomized experiments, as it is finite-sample valid and does not require any distributional assumptions. However, naive application of randomization inference may suffer from severe size distortion in the presence of sample attrition, where outcome data are missing for some units. In this paper, we propose new, computationally efficient methods for randomization inference that remain valid under a broad class of potentially informative missingness mechanisms, allowing a unit's missingness to depend on its (unobserved) potential outcomes. Specifically, we construct valid p-values for testing both sharp and bounded null hypotheses on treatment effects via a worst-case consideration of the classical Fisher randomization test. Leveraging distribution-free test statistics, these worst-case p-values admit closed-form solutions. Importantly, by incorporating both potential outcomes and potential missingness indicators into the test statistic, our approach connects to a range of partial identification bounds in the literature, which in some sense suggests the sharpness of our tests. Moreover, our methods can exploit structural assumptions such as monotone missingness, which are commonly adopted in applications due to their plausibility and ability to substantially improve inferential power. We illustrate the proposed methods through both simulation studies and an empirical application. An R package implementing the proposed methods is publicly available.

Target Audience:

Statisticians, Biostatisticians, and Practitioners who conduct clinical trials/experiments.

Speaker:

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Reply