Consistent treatment selection based on Manski midpoints







Abstract

The fundamental difficulty in comparing efficacies of two treatments based on observational data is that those who actually selected or received a particular treatment may give different responses to it than those who did not select or receive it. Thus, based on those who received one treatment, one cannot estimate the effect in case the treatment is applied to the entire population. Manski (1990) showed, that also in this situation, one may derive bounds for the effect size on the entire population. When only observational data are available, Rudas (2015) suggested, in order to find the better effect, comparing the differences in the numbers the positive versus negative outcomes, in contrast to the usual method, when their ratios are used. He showed that this procedure is consistent in the sense that it never leads to Simpson's paradox. In this research, we develop Manski bounds for these differences, and show that the observed differences are the midpoints of the ranges obtained. We apply the approach to analyze the effects of (1) presidential campaign visits in congressional elections (Keele and Quinn 2017), and (2) defeat in war on revolution (Skocpol 1979).

Treatment selection and effect measures

The task of selecting the best treatment from set \mathcal{D} of available treatments consists of finding

$$d^* = \arg\max_{d \in \mathcal{D}} u(d),$$

where u(d) is the net benefit of treatment d when selected for the whole population. For two treatments ($\mathcal{D} = \{0, 1\}$), this maps to decision function

$$sgn[\delta(u(0), u(1))] := \begin{cases} -1 & \text{if } u(0) > u(1) \\ 0 & \text{if } u(0) = u(1) \\ +1 & \text{if } u(0) < u(1) \end{cases}$$

where $\delta(u(0), u(1))$ is an effect measure.

Often, u(d) is specified as E[Y(d)], where Y(d) is the population distribution of outcome Y under treatment d. For two treatments, this yields effect measure

$$ATE(1) = E[Y(1)] - E[Y(0)].$$

In a setup with two treatments and two outcome values, the population is held by the 2×2 table

$$T = \begin{bmatrix} Y_i = 0 & Y_i = 1 \\ D_i = 0 & p_{10} & p_{11} \\ D_i = 1 & p_{00} & p_{01} \end{bmatrix},$$

in which the cell value p_{dy} is the fraction of units with treatment value d and outcome value y, such that $\sum_{d} \sum_{v} p_{dv} = 1$. Then, and effect measure $\delta(u(0), u(1))$ can be represented as $\delta(T)$, and

$$ATE(1) = \frac{p_{11}}{p_{10} + p_{11}} - \frac{p_{01}}{p_{00} + p_{01}}.$$

Other widely used effect measures include

$$LOR(1) = In \frac{p_{00} + p_{11}}{p_{01} + p_{10}},$$

and
$$LRR(1) = \ln \frac{p_{11}/(p_{10}+p_{11})}{p_{01}/(p_{00}+p_{01})}$$
.

Consistent treatment selection with observational data

For any unit i, at most one of $\{Y_i(0), Y_i(1)\}$ is observable. Thus, only estimates $\{\hat{Y}(0), \hat{Y}(1)\}$ are available, even in population data. In experiments, randomized treatment assignment makes the assumption of $(Y(1), Y(0)) \perp D$ viable. In observational data, confounders X may affect both treatment assignment and outcomes. Thus, only conditional independence $(Y(1), Y(0)) \perp D|X$ holds, and if X is not observed, one cannot estimate $\{Y(0), Y(1)\}$.

Suppose two strata $S \in \{0, 1\}$ held by tables

$$T_{s=0} = \frac{p_{10}^{s=0} p_{11}^{s=0}}{p_{00}^{s=0} p_{01}^{s=0}}$$

$$T_{s=1} = \frac{\begin{vmatrix} p_{10}^{s=1} & p_{11}^{s=1} \\ p_{00}^{s=1} & p_{01}^{s=1} \end{vmatrix}}{\begin{vmatrix} p_{10}^{s=1} & p_{11}^{s=1} \\ p_{00}^{s=1} & p_{01}^{s=1} \end{vmatrix}}$$

where the frequencies sum up to 1 within each table. Under conventional effect measures, the stratified tables may lead to one decision and the combined table to another,

$$sgn[\delta(T_{s=0})] = sgn[\delta(T_{s=1})] \neq sgn[\delta(T)],$$

a consequence of association reversal known as Simpson's paradox. This poses a problem for treatment selection if S is not observed or scientific information lacks whether to condition on it.

Manski midpoints

Manski (1990) showed, that also in settings with observational data and unobserved confounding, one may derive bounds for the effect size on the entire population. For ATE(1) under two treatments and two outcomes, such bounds are

$$[-(p_{01}+p_{10}), p_{00}+p_{11}],$$

with width always equal to 1 as $\sum_{d} \sum_{y} p_{dy} = 1$. Their midpoint equals

$$DI = \frac{1}{2} ((p_{00} + p_{11}) - (p_{01} + p_{10})) = \frac{1}{2} - (p_{01} + p_{10}),$$

which is a special case of DI_k as defined by Rudas (2015a).

Statistical properties

Rudas (2015a) shows that under multinomial sampling with $p_{00} + p_{11} = p$,

$$P(DI > 0) = \sum_{k=\lfloor N/2 \rfloor+1}^{N} {N \choose k} p^k (1-p)^{N-k}, \quad \text{approximated for large N by } \phi \left(\sqrt{N} \frac{p-0.5}{\sqrt{p(1-p)}} \right),$$

where ϕ is the standard normal CDF, and the probability of the correct decision depends only on N and the population value of DI.

Relationship to sensitivity analysis

Discussion

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