Main Figures

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The Science Table Plot

Many a graduate-level course on causal inference begins with a discussion of the *Science Table*: the complete set of potential outcomes for all individuals in a sample @rubin. The science table – and the potential outcomes within it – become the teaching foundation for a variety of causal inference approaches. Herein, I propose a new teaching visualization, *the science table plot*, which depict individuals according to tehri treated and untreated potential outcomes. While in practice the science table plot, like the science table itself, is fundamentally unobservable, in the classroom the science table plot is a handy companion to the science table, underscoring and clarifying foundational causal inference concepts.

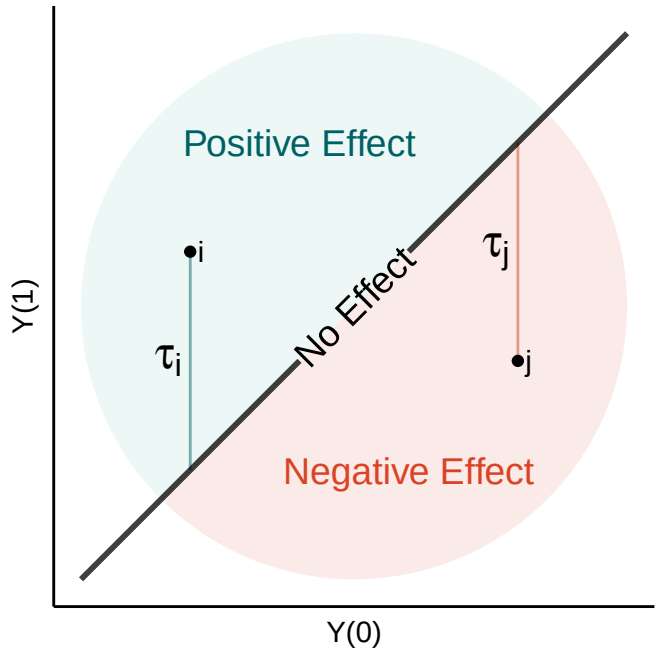

Figure 1: Science table plots. When a subject is graphically plotted according to their potential outcomes, the vertical distance to the diagonal represents their individual treatment effect, and different plot regions correspond to a positive, negative, or neutral response to treatment

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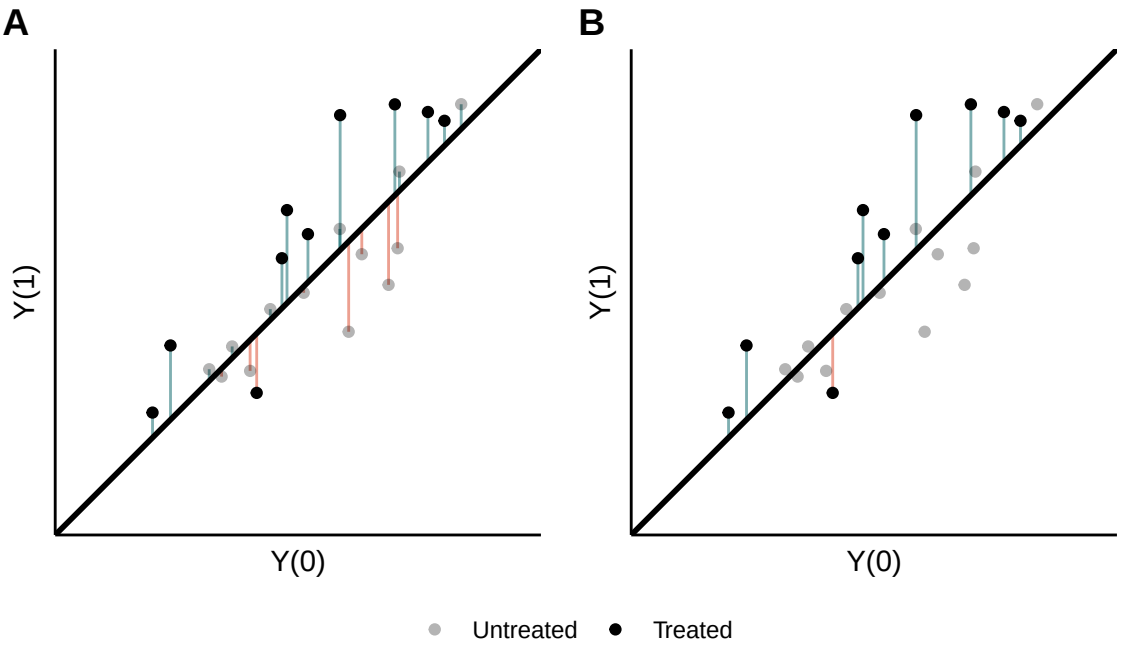
Average Treamtent Effects

When we talk about average treatment effects, it's important to clarify: Average among what group?



SATT and SATE are properties of the sample. When we talk about these estimands, the potential outcomes of the subjects in the sample are all we care about, and the uncertainty in our estimates of sample treatment effects comes from the fact that we cannot observe both potential outcomes in the sample. This is sometimes called the "randomization inference" framework.

Another approach begins with a setting that more closely resembles the set-ups from an undergraduate statistics course. Suppose outcomes and treatments are sampled from some probability distribution $(Y_i(0), Y_i(1), T \sim \Omega)$. Now, instead of being the full scope of our interest, the sample is merely a window into the probability distribution Ω. We might write the effect estimates we care about in terms of expected values over Ω:

$$\tau^{ATE} = E_\Omega[Y(1) - Y(0)], \tau^{ATT} = E_\Omega[Y(1) - Y(0)|T = 1]$$

This is called the "superpopulation" framework. That is, ATE and ATT are properties of the superpopulation from which the sample was drawn. If you could draw two different samples from the same underlying distribution Ω, the SATE for those two samples will almost certainly differ, whereas the ATE will stay the same[1]. Different researchers will favor one framework over the other for a variety of reasons, but students should expect to run into them both. [2]

[1]Sometimes, the ATT and ATE are described as "population" estimands and written PATT and PATE. I'm avoiding that notation here to avoid confusion with the generalizability literature. Often, the supposed superpopulation may not be equivalent to an actual population that exists in practice.

[2]In some settings, it may be difficult to swallow that the observed sample really is all you care about (as in sample estimands). In some settings, it may be difficult to swallow that the superpopulation from which the sample is assumed to be derived is something you care about either.