Basel Biometric Society Meeting on Covariate Adjustment in Clinical Trials Discussion

Tim P. Morris 25 March 2025



Senn

Two clarifications, which may be useful

- 1. In the first of the three consequences, the 'mean square error effect', the comparator is an **analysis** that **ignores covariates** completely.
- 2. In the second consequence, the 'Variance inflation factor', the comparator changes to a **design** that **perfectly balances covariates**.

My proposition is then that VIF is not really to do with covariate adjustment, since the consequences of imbalance vs. perfect balance affect the estimator whether or not you adjust; adjustment is the way we acknowledge this in inference.

Senn: Two annotations (I think) to the table

			Effect	
		Estimated	Imbalance	Second
		mean square	effect	-order
		error effect	or VIF	precision
Influence	Design	No*	Yes	No
	Model	Yes	Yes	Yes
	Outcome	Yes	No	No

'Model' = model used by the analyst

'Outcome' = model/mechanism that produced the data

I think it also provides a useful perspective on

- How this works out for 'ANCOVA2' (Tsiatis et al., 2008), subsequently further justified by Lin (2013). I will return to this for Jack Kuipers' talk.
- Estimators based on weighting, for example inverse-probability-of-treatment weighting (Williamson et al., 2014), and overlap weighting (Zeng et al., 2020). Note: these papers do not 'cheat', but they do not use propensity scores in the way Stephen prescribes!

Kuipers

I was very interested by this talk and the accompanying paper but it is less familiar to me and so I feel less qualified to comment and throw in further interpretations.

My own reason not to adjust would be the possibility of small-sample bias (I have bonus slides if time). To be clear, I don't see this as a real problem (Tackney et al., 2023).

An apparent contradiction. Tsiatis et al. (2008) showed that for E(Y|do(X = 1)) - E(Y|do(X = 0)) adjustment cannot harm (large-sample) relative precision with linear outcome models, two treatment arms and 1:1 randomization.

More generally, from Lin (2013):

'OLS adjustment cannot hurt asymptotic precision when a full set

of treatment × covariate interactions is included'

(Note: covariates must be centered.)

So my question is simply: what is different here? The estimator itself or finite sample size?

Magirr

I was initially a 'conditionalist', after reading Hauck et al. (1998). The claim is that a clinical trial should aim to 'predict the direction and size of a treatment benefit for a patient with specific covariate values' (personalized treatment effects), not average effects for groups of patients.

- · Laudable (aim)
- · Laughable (estimation)

My guess is that Dominic is too diplomatic to come out swinging for marginal measures.

An epidemiology 101 'trick' makes life simple: estimate the treatment effect after **restricting** the analysis, for example to males aged YY with stage X disease and...

'What's that? Your trial only had two such participants? Too bad. That's the information you have.' [Note: Stephen earlier described this as 'a fool's errand']

Touted solution is then to buy information with assumptions, e.g. logit $P(Y = 1) = \alpha_0 + \alpha_1 \mathbb{I}(\text{trt} = 1) + \alpha_2 X$.

This only targets the average conditional effects (for each combination of covariates) if the model is right. It's probably not right, however hard we wish.

Do you ever believe any risk prediction model is 'correct'?

If a prediction model is not correct, adjustment for a prognostic score using a model for a conditional estimand will targets a sort of amorphous hybrid of conditional and marginal measures.

This is a strong nudge towards marginal measures when using supercovariates.

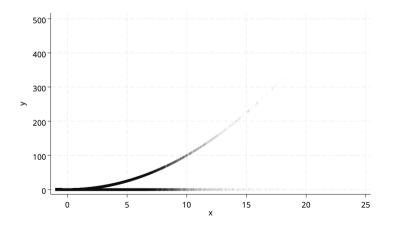
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Bias bonus

I want to start with a point that none of the speakers have mentioned: covariate adjustment can lead to small-sample bias.

This is mentioned in the supplementary materials of Tackney et al. (2023) but I think not widely known.

1 million data points; true average effect \approx 2



Bias of ANCOVA assuming E[Y] a linear function of X

