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Comment: Analyzing Propensity Score Matched Count Data

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Abstract

We offer an explanation to the simulation result of Austin (2009) regarding rate ratios, and argue that unmatched analysis of propensity score matched count data results in conservative statistical inferences on the rate ratios.

KEYWORDS: propensity score, statistical inference, Poisson, rate ratio

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In a recent simulation study, Austin (2009) reported empirical results on Type I error rates, coverage of confidence intervals and variance estimation in propensity-score matched analyses, which included four types of models: linear model of Gaussian data for mean differences, logistic model of binary data for odds ratios, Cox model of lifetime data for hazard ratios, and Poisson model of count data for rate ratios. The results showed that for mean difference, odds ratio and hazard ratio, the unmatched analyses led to slightly more conservative statistical inference than the matched analyses, as evidenced by small decrease in Type I error rates and small increases in confidence interval coverage and variance estimators (Tables 1-3 of Austin (2009)). However, for rate ratios, the simulation suggested the opposite conclusion that the unmatched analysis was much more liberal than the matched analysis, as shown by a substantial increase in Type I error, and close to or more than 50% reduction in confidence interval coverage and estimated variance. We offer an explanation for this phenomenon, and show that it may have been the result of overdispersion created by the propensity score matching process. We show that after proper adjustment for overdispersion, a similar conclusion can be drawn for the rate ratio, that the unmatched analysis of count data also leads to slightly conservative statistical inference on the rate ratio.

According to Equations (1) and (6) of Austin (2009), the probability of being in the treatment group, as opposed to the control, is modeled by $\text{logit}(\Pr(T = 1)) = \beta^T \mathbf{X}$ in the simulation; the outcome variable Y was generated via a Poisson regression model, which satisfies $E(Y|T, \mathbf{X}) = \text{Var}(Y|T, \mathbf{X}) = \exp(\theta T + \alpha^T \mathbf{X})$, where θ is the log rate ratio of the treatment. We can show that

$$\begin{aligned} \text{Var}(Y|T) &= \text{Var}\{E(Y|\mathbf{X}, T)|T\} + E\{\text{Var}(Y|\mathbf{X}, T)|T\} \\ &> E\{\text{Var}(Y|\mathbf{X}, T)|T\} = E\{E(Y|\mathbf{X}, T)|T\} \\ &= E(Y|T) \end{aligned}$$

Since $E(Y|T) = E\{E(Y|\mathbf{X}, T)|T\} = \exp(\theta T) \mathbf{E}\{\exp(\alpha^T \mathbf{X})|T\}$ and the distribution of $\mathbf{X}$, following the propensity score matching, is independent of T , we have that $\mathbf{E}\{\exp(\alpha^T \mathbf{X})|T\}$ is independent of T and serves as the intercept in the Poisson regression of Y on T with the matched data. Note that in this Poisson regression, the conditional variance $\text{Var}(Y|T)$ exceeds the conditional mean $E(Y|T)$ and hence there is overdispersion.

The following table shows a simulation under the same design as in Austin (2009). The sample size was 1000 and the result was based on 5000 repetitions.

There were roughly equal numbers of treated and control subjects in the data, and about 50% of them could be matched. It can be seen that with adjustment for overdispersion (method “*Poisson 2*”), the unmatched analysis is a little more conservative than the matched GEE analysis (method “*GEE*”). But if we ignore overdispersion (method “*Poisson*”), the simulation would suggest the opposite conclusion. The underlying reason for this is that Poisson regression without overdispersion adjustment gave much smaller variance estimators in this case. The correlation between the matched pairs, as estimated by the GEE working correlation, was roughly at 0.1. Note that the matched analysis via GEE model did not suffer from overdispersion problem because with the GEE, as long as the mean structure is correctly specified and robust sandwich type variance estimator is used, mis-specifying the variance structure does not affect the statistical inference.

Table 1. Simulation results on the rate ratio

θ	method	Mean Est	Emp Std	Ave Std	% Rejection	% Coverage
0	<i>Poisson</i>	0.002107	0.1561	0.06093	43.48	56.52
	<i>GEE</i>	0.002113	0.1563	0.1586	4.29	95.71
	<i>Poisson 2</i>	0.002107	0.1561	0.1703	2.52	97.48
log(1.5)	<i>Poisson</i>	0.4124	0.1589	0.05559	97.60 †	51.48
	<i>GEE</i>	0.4125	0.1588	0.15720	75.86 †	95.48
	<i>Poisson 2</i>	0.4124	0.1589	0.17250	71.04 †	97.92

Mean Est: average of point estimators $\hat{\theta}$; *Emp Std*: standard deviation of $\hat{\theta}$; *Ave Std*: average of estimated standard error of $\hat{\theta}$; *% Rejection*: percentage that the null hypothesis $\theta = 0$ is rejected at 0.05 level; *% Coverage*: coverage probability of 95% confidence interval. *Poisson*: unmatched Poisson regression; *Poisson 2*: unmatched Poisson regression with overdispersion adjustment; *GEE*: generalized estimating equation with exchangeable working correlation. †Under the non-null hypothesis, *% Rejection* is the empirical statistical power of the test.

References

Austin PC (2009). Type I Error Rates, Coverage of Confidence Intervals, and Variance Estimation in Propensity-Score Matched Analyses. *The International Journal of Biostatistics*, Vol. 5, Iss. 1, Article 13.