

Table 1: Treatment effect bias for Generative Models G, A, B and C over 10,000 replications

GM	T	N	β_0			SR
			Bias	SD	MC-SE	
G	10	30	-0.052	0.247	0.002	0.999
		100	-0.056	0.135	0.001	1.000
		200	-0.054	0.094	0.001	1.000
	30	30	-0.023	0.205	0.002	0.998
		100	-0.025	0.112	0.001	0.998
		200	-0.024	0.078	0.001	0.997
A	10	30	0.000	0.238	0.002	0.999
		100	-0.002	0.130	0.001	0.999
		200	0.000	0.092	0.001	0.998
	30	30	0.000	0.202	0.002	0.998
		100	-0.002	0.110	0.001	0.997
		200	0.000	0.077	0.001	0.996
B	10	30	0.005	0.132	0.001	1.000
		100	0.004	0.071	0.001	1.000
		200	0.004	0.049	0.000	1.000
	30	30	0.001	0.073	0.001	1.000
		100	0.000	0.039	0.000	1.000
		200	0.000	0.028	0.000	1.000
C	10	30	0.002	0.220	0.002	0.999
		100	0.000	0.121	0.001	0.999
		200	0.003	0.086	0.001	1.000
	30	30	-0.001	0.194	0.002	0.998
		100	-0.002	0.107	0.001	0.998
		200	0.000	0.075	0.001	0.999

Note. GM: generative model. T: number of timepoints. N: sample size. Bias: $\frac{1}{n_{\text{sim}}} \sum_{i=1}^{n_{\text{sim}}} \hat{\beta}_{0i} - \beta_0$, which represents the difference between the mean of the estimated parameter values $\hat{\beta}_0$ and the prespecified treatment effect $\beta_0 = 1$. SD: $\sqrt{\frac{1}{(n_{\text{sim}}-1)} \sum_{i=1}^{n_{\text{sim}}} (\hat{\beta}_{0i} - \bar{\beta}_0)^2}$, which is the standard deviation of estimates across replications. MC-SE: $\frac{\text{SD}}{\sqrt{n_{\text{sim}}}}$, which represents the Monte Carlo SE of bias. SR: model fitting success rate.