

Table 6: Simulated bias and root mean-square error (rMSE) for the estimators of π_k where the BJSM assumptions are satisfied. Four modeling approaches: Bayesian joint stage modeling (BJSM), log-Poisson joint stage modeling (LPJSM), Bayesian first stage modeling (BFSM) and first stage maximum likelihood estimation (FSMLE) are compared. The sample size per treatment arm is 15. π_k is the response rate at six months for treatment k , $k = A, B, C$.

Scenario	BJSM		LPJSM		BFSM		FSMLE		
	Bias	rMSE	Bias	rMSE	Bias	rMSE	Bias	rMSE	
1	π_A	0.004	0.084	0.001	0.099	-0.014	0.106	-0.003	0.119
	π_B	0.007	0.084	0.002	0.099	-0.011	0.104	0.001	0.118
	π_C	0.006	0.082	0.001	0.097	-0.013	0.104	-0.002	0.117
2	π_A	-0.002	0.076	-0.001	0.084	-0.002	0.092	-0.002	0.104
	π_B	-0.003	0.085	0.000	0.101	-0.011	0.104	0.001	0.118
	π_C	-0.007	0.088	0.005	0.111	-0.025	0.113	-0.002	0.125
3	π_A	0.005	0.076	-0.002	0.083	-0.002	0.092	-0.002	0.104
	π_B	0.006	0.084	0.000	0.098	-0.011	0.104	0.001	0.118
	π_C	0.006	0.085	0.005	0.110	-0.025	0.113	-0.002	0.125

Table 7: Simulated width and coverage of 95% CI for the estimators of π_k where the BJSM assumptions are satisfied. Four modeling approaches: Bayesian joint stage modeling (BJSM), log-Poisson joint stage modeling (LPJSM), Bayesian first stage modeling (BFSM) and first stage maximum likelihood estimation (FSMLE) are compared. The sample size per treatment arm is 15. π_k is the true response rate at six months for the treatment k , $k = A, B, C$. CR=Coverage Rate.

Scenario	BJSM		LPJSM		BFSM		FSMLE		
	Width	CR	Width	CR	Width	CR	Width	CR	
1	π_A	0.319	0.936	0.372	0.913	0.386	0.930	0.441	0.947
	π_B	0.320	0.928	0.374	0.917	0.389	0.934	0.444	0.947
	π_C	0.320	0.937	0.373	0.920	0.388	0.934	0.443	0.948
2	π_A	0.278	0.920	0.317	0.898	0.327	0.943	0.376	0.801
	π_B	0.323	0.922	0.376	0.912	0.389	0.934	0.444	0.947
	π_C	0.346	0.938	0.428	0.928	0.423	0.899	0.478	0.943
3	π_A	0.279	0.926	0.308	0.892	0.327	0.943	0.376	0.801
	π_B	0.320	0.926	0.368	0.918	0.389	0.934	0.444	0.947
	π_C	0.341	0.947	0.422	0.926	0.423	0.899	0.478	0.943

Table 8: Simulated bias and root mean-square error (rMSE) for the estimators of π_k where the BJSM assumptions are satisfied. Four modeling approaches: Bayesian joint stage modeling (BJSM), log-Poisson joint stage modeling (LPJSM), Bayesian first stage modeling (BFSM) and first stage maximum likelihood estimation (FSMLE) are compared. The sample size per treatment arm is 60. π_k is the response rate at six months for treatment k , $k = A, B, C$.

Scenario	BJSM		LPJSM		BFSM		FSMLE		
	Bias	rMSE	Bias	rMSE	Bias	rMSE	Bias	rMSE	
1	π_A	0.006	0.046	0.000	0.048	-0.004	0.058	-0.001	0.060
	π_B	0.007	0.045	-0.001	0.048	-0.003	0.057	0.000	0.059
	π_C	0.007	0.044	-0.002	0.048	-0.004	0.057	-0.001	0.059
2	π_A	0.000	0.041	-0.003	0.043	-0.001	0.050	-0.001	0.052
	π_B	0.002	0.047	0.000	0.050	-0.003	0.057	0.000	0.059
	π_C	0.002	0.050	-0.001	0.055	-0.008	0.061	-0.001	0.063
3	π_A	0.004	0.040	-0.002	0.042	-0.001	0.050	-0.001	0.052
	π_B	0.007	0.045	0.000	0.048	-0.003	0.057	0.000	0.059
	π_C	0.010	0.048	-0.002	0.055	-0.008	0.061	-0.001	0.063

Table 9: Simulated width and coverage of 95% CI for the estimators of π_k where the BJSM assumptions are satisfied. Four modeling approaches: Bayesian joint stage modeling (BJSM), log-Poisson joint stage modeling (LPJSM), Bayesian first stage modeling (BFSM) and first stage maximum likelihood estimation (FSMLE) are compared. The sample size per treatment arm is 60. π_k is the true response rate at six months for the treatment k , $k = A, B, C$. CR=Coverage Rate.

Scenario	BJSM		LPJSM		BFSM		FSMLE		
	Width	CR	Width	CR	Width	CR	Width	CR	
1	π_A	0.176	0.942	0.188	0.946	0.221	0.931	0.229	0.947
	π_B	0.176	0.951	0.188	0.942	0.222	0.933	0.230	0.948
	π_C	0.176	0.952	0.187	0.938	0.221	0.935	0.229	0.948
2	π_A	0.157	0.932	0.162	0.931	0.191	0.935	0.199	0.922
	π_B	0.181	0.947	0.190	0.945	0.222	0.932	0.230	0.948
	π_C	0.200	0.955	0.215	0.936	0.238	0.938	0.246	0.931
3	π_A	0.154	0.940	0.158	0.935	0.191	0.935	0.199	0.922
	π_B	0.176	0.949	0.186	0.940	0.222	0.932	0.230	0.948
	π_C	0.192	0.960	0.212	0.938	0.238	0.938	0.246	0.931

Table 10: Simulated bias and root mean-square error (rMSE) for the estimators of π_k when assumptions are violated. Three modeling approaches: Bayesian joint stage modeling (BJSM), Bayesian joint stage modeling with multiple linkage parameters (BJSMM), and log-Poisson joint stage modeling (LPJSM) are compared. The sample size per treatment arm is 15. π_k is the response rate at six months for treatment k , $k = A, B, C$.

Scenario		BJSM		BJSMM		LPJSM	
		Bias	rMSE	Bias	rMSE	Bias	rMSE
4	π_A	-0.023	0.078	-0.020	0.077	-0.027	0.085
	π_B	-0.006	0.085	-0.004	0.084	-0.007	0.099
	π_C	0.020	0.086	0.024	0.087	0.038	0.116
5	π_A	-0.010	0.073	-0.006	0.074	-0.010	0.080
	π_B	-0.005	0.085	-0.001	0.085	-0.006	0.099
	π_C	0.016	0.093	0.015	0.091	0.020	0.115
6	π_A	-0.031	0.077	-0.026	0.076	-0.036	0.084
	π_B	-0.009	0.085	-0.003	0.084	-0.012	0.097
	π_C	0.043	0.096	0.044	0.097	0.052	0.123
7	π_A	0.012	0.073	0.014	0.075	0.016	0.085
	π_B	-0.002	0.084	0.002	0.085	0.001	0.099
	π_C	-0.011	0.098	-0.015	0.094	-0.015	0.114
8	π_A	0.024	0.079	0.030	0.081	-0.003	0.079
	π_B	0.034	0.088	0.040	0.091	0.001	0.093
	π_C	0.041	0.091	0.047	0.094	0.004	0.106
9	π_A	-0.016	0.071	-0.016	0.070	0.001	0.088
	π_B	-0.034	0.083	-0.034	0.082	0.002	0.105
	π_C	-0.056	0.095	-0.055	0.094	0.005	0.114
10	π_A	-0.034	0.077	-0.028	0.076	-0.043	0.086
	π_B	-0.013	0.085	-0.007	0.084	-0.025	0.098
	π_C	0.069	0.107	0.072	0.110	0.072	0.132
11	π_A	0.012	0.071	0.015	0.071	-0.001	0.082
	π_B	0.007	0.075	0.010	0.074	0.002	0.096
	π_C	-0.001	0.073	0.002	0.072	0.005	0.106
12	π_A	-0.043	0.077	-0.037	0.075	-0.051	0.086
	π_B	-0.013	0.085	-0.007	0.084	-0.022	0.098
	π_C	0.070	0.108	0.072	0.110	0.078	0.137

Table 11: Simulated width and coverage of 95% CI for the estimators of π_k when assumptions are violated. Three modeling approaches: Bayesian joint stage modeling (BJSM), Bayesian joint stage modeling with multiple linkage parameters (BJSMM), and log-Poisson joint stage modeling (LPJSM) are compared. The sample size per treatment arm is 15. π_k is the true response rate at six months for the treatment k , $k = A, B, C$. CR=Coverage Rate.

Scenario		BJSM		BJSMM		LPJSM	
		Width	CR	Width	CR	Width	CR
4	π_A	0.262	0.876	0.268	0.898	0.306	0.844
	π_B	0.319	0.919	0.325	0.926	0.372	0.909
	π_C	0.345	0.952	0.348	0.950	0.426	0.924
5	π_A	0.272	0.921	0.278	0.926	0.300	0.889
	π_B	0.321	0.924	0.327	0.929	0.366	0.908
	π_C	0.352	0.941	0.358	0.947	0.438	0.929
6	π_A	0.256	0.872	0.264	0.894	0.289	0.822
	π_B	0.317	0.920	0.325	0.928	0.363	0.903
	π_C	0.349	0.933	0.354	0.932	0.435	0.921
7	π_A	0.288	0.945	0.291	0.942	0.311	0.926
	π_B	0.325	0.932	0.329	0.930	0.371	0.913
	π_C	0.353	0.912	0.361	0.926	0.439	0.922
8	π_A	0.283	0.928	0.293	0.937	0.292	0.884
	π_B	0.319	0.930	0.329	0.932	0.353	0.912
	π_C	0.332	0.936	0.341	0.928	0.409	0.926
9	π_A	0.270	0.920	0.271	0.925	0.332	0.902
	π_B	0.310	0.912	0.311	0.918	0.394	0.914
	π_C	0.331	0.914	0.332	0.918	0.443	0.928
10	π_A	0.250	0.856	0.261	0.890	0.282	0.794
	π_B	0.311	0.912	0.322	0.927	0.356	0.890
	π_C	0.343	0.892	0.348	0.883	0.433	0.908
11	π_A	0.278	0.938	0.284	0.948	0.303	0.889
	π_B	0.311	0.954	0.318	0.962	0.366	0.913
	π_C	0.324	0.966	0.330	0.970	0.419	0.927
12	π_A	0.244	0.845	0.254	0.879	0.268	0.767
	π_B	0.312	0.912	0.322	0.924	0.360	0.891
	π_C	0.344	0.888	0.348	0.887	0.439	0.903

Table 12: Simulated bias and root mean-square error (rMSE) for the estimators of π_k when assumptions are violated. Three modeling approaches: Bayesian joint stage modeling (BJSM), Bayesian joint stage modeling with multiple linkage parameters (BJSMM), and log-Poisson joint stage modeling (LPJSM) are compared. The sample size per treatment arm is 60. π_k is the response rate at six months for treatment k , $k = A, B, C$.

Scenario		BJSM		BJSMM		LPJSM	
		Bias	rMSE	Bias	rMSE	Bias	rMSE
4	π_A	-0.025	0.048	-0.022	0.046	-0.030	0.051
	π_B	-0.005	0.046	-0.001	0.046	-0.007	0.049
	π_C	0.029	0.055	0.034	0.057	0.033	0.064
5	π_A	-0.011	0.040	-0.005	0.041	-0.012	0.042
	π_B	-0.005	0.046	0.003	0.046	-0.005	0.049
	π_C	0.022	0.055	0.012	0.053	0.014	0.058
6	π_A	-0.035	0.051	-0.028	0.048	-0.039	0.055
	π_B	-0.011	0.046	-0.001	0.046	-0.012	0.049
	π_C	0.046	0.066	0.044	0.065	0.046	0.073
7	π_A	0.014	0.041	0.018	0.044	0.016	0.044
	π_B	0.001	0.046	0.009	0.047	0.002	0.049
	π_C	-0.002	0.054	-0.018	0.058	-0.021	0.061
8	π_A	0.022	0.045	0.027	0.049	-0.003	0.039
	π_B	0.035	0.055	0.041	0.060	0.000	0.046
	π_C	0.047	0.063	0.054	0.070	-0.001	0.053
9	π_A	-0.014	0.041	-0.016	0.041	-0.002	0.044
	π_B	-0.025	0.049	-0.028	0.050	0.001	0.052
	π_C	-0.040	0.059	-0.042	0.060	-0.002	0.058
10	π_A	-0.041	0.055	-0.032	0.050	-0.046	0.060
	π_B	-0.019	0.047	-0.007	0.045	-0.025	0.053
	π_C	0.070	0.083	0.075	0.087	0.067	0.087
11	π_A	0.011	0.039	0.013	0.040	-0.002	0.041
	π_B	0.011	0.041	0.014	0.042	0.001	0.048
	π_C	0.010	0.040	0.013	0.041	-0.002	0.055
12	π_A	-0.050	0.060	-0.040	0.054	-0.054	0.065
	π_B	-0.018	0.047	-0.007	0.045	-0.022	0.052
	π_C	0.073	0.085	0.074	0.087	0.072	0.092

Table 13: Simulated width and coverage of 95% CI for the estimators of π_k when assumptions are violated. Three modeling approaches: Bayesian joint stage modeling (BJSM), Bayesian joint stage modeling with multiple linkage parameters (BJSMM), and log-Poisson joint stage modeling (LPJSM) are compared. The sample size per treatment arm is 60. π_k is the response rate at six months for the treatment k , $k = A, B, C$. CR=Coverage Rate.

Scenario		BJSM		BJSMM		LPJSM	
		Width	CR	Width	CR	Width	CR
4	π_A	0.147	0.857	0.153	0.884	0.157	0.838
	π_B	0.177	0.938	0.185	0.950	0.188	0.938
	π_C	0.197	0.938	0.198	0.920	0.214	0.918
5	π_A	0.152	0.928	0.158	0.935	0.153	0.907
	π_B	0.178	0.944	0.187	0.951	0.186	0.937
	π_C	0.202	0.939	0.212	0.955	0.220	0.94
6	π_A	0.142	0.800	0.150	0.858	0.148	0.780
	π_B	0.174	0.934	0.185	0.950	0.184	0.928
	π_C	0.200	0.878	0.205	0.894	0.219	0.884
7	π_A	0.161	0.958	0.165	0.944	0.158	0.934
	π_B	0.182	0.952	0.189	0.952	0.187	0.940
	π_C	0.203	0.932	0.218	0.924	0.221	0.919
8	π_A	0.152	0.917	0.159	0.911	0.149	0.934
	π_B	0.169	0.895	0.178	0.882	0.178	0.938
	π_C	0.179	0.835	0.187	0.810	0.206	0.938
9	π_A	0.153	0.924	0.153	0.923	0.170	0.930
	π_B	0.173	0.903	0.174	0.906	0.200	0.943
	π_C	0.186	0.882	0.186	0.877	0.223	0.938
10	π_A	0.136	0.757	0.147	0.836	0.144	0.713
	π_B	0.168	0.909	0.181	0.943	0.180	0.894
	π_C	0.193	0.723	0.197	0.703	0.218	0.789
11	π_A	0.149	0.948	0.153	0.950	0.154	0.933
	π_B	0.165	0.957	0.170	0.964	0.185	0.940
	π_C	0.171	0.970	0.175	0.968	0.211	0.941
12	π_A	0.133	0.679	0.143	0.786	0.137	0.621
	π_B	0.168	0.912	0.181	0.944	0.183	0.900
	π_C	0.193	0.699	0.197	0.705	0.220	0.766