Simulation results

General model:

$$\mu(t|Z) = f(t, \beta_0^\top Z) g(\gamma_0^\top Z),$$

where for fixed $x \in \mathbb{R}$, $f(\cdot, x)$ is an unspecified density function on $[0, \tau]$, and $g(x)$ is unknown but monotone in x. We assume $\|\beta_0\| = \|\gamma_0\| = 1$.

Simulation settings used in the paper:

- Z is generated from a multivariate truncated normal distribution satisfying $Z \sim N_2(0, I_2)$ and $\|Z\| \leq 1$.
- Censoring time is an exponential distribution with mean $10 \cdot (1 + |z_1|)$.
- Recurrent event times are generated from Poisson process with rate functions:

  M1: $\mu(t|Z) = \mu_0(t) \exp(\gamma_0^\top Z)$
  - $\mu_0(t) = \frac{2}{1+t}$.
  - $\beta_0 = (\beta_1, \beta_2) = (0, 0)$, $\gamma_0 = (\gamma_1, \gamma_2) = (0.28, 0.96)$.

  M2: $\mu(t|Z) = \mu_0(t) + \alpha_0^\top Z$
  - $\mu_0(t) = e^{0.1t}$.
  - $\beta_0 = \gamma_0 = \alpha_0 = (0.6, 0.8)$.

  M3: $\mu(t|Z) = \mu_0\{t \exp(\alpha_0^\top Z)\}$
  - $\mu_0(t) = e^{-t}$.
  - $\beta_0 = \gamma_0 = \alpha_0 = (0.6, 0.8)$.

  M4: $\mu(t|Z) = \mu_0\{t, \exp(\beta_0^\top Z)\} \exp(\gamma_0^\top Z)$
  - $\mu_0(t, x) = \frac{t \cdot (1-t)^{1+x}}{B(2, 1+x)}$
  - $\beta_0 = (0.6, 0.8)$, $\gamma_0 = (0.28, 0.96)$

- Set $\tau = 10$ for **M1, M2, M3** and $\tau = 1$ for **M4**.
- **M1-ind** solves γ_0 under shape-independence.

Table 1: Point estimator (PE), empirical standard error (ESE) and asymptotic standard error (ASE) for **M1**–**M4** with 1000 replications.

	$n = 50$			$n = 100$			$n = 200$			$n = 500$		
	PE	ESE	ASE	PE	ESE	ASE	PE	ESE	ASE	PE	ESE	ASE
	Scenario **M1**; without assuming shape-independent.											
β_1	0.302	0.626	0.488	0.196	0.662	0.502	0.151	0.667	0.515	0.102	0.679	0.520
β_2	0.300	0.654	0.493	0.276	0.670	0.515	0.264	0.681	0.526	0.152	0.712	0.539
γ_1	0.273	0.114	0.133	0.276	0.082	0.087	0.274	0.076	0.060	0.279	0.037	0.036
γ_2	0.955	0.032	0.038	0.957	0.025	0.025	0.958	0.029	0.018	0.960	0.010	0.011
	Scenario **M1**; assuming shape-independent.											
γ_1	0.264	0.118	0.141	0.272	0.077	0.089	0.276	0.054	0.059	0.275	0.033	0.035
γ_2	0.957	0.031	0.038	0.959	0.021	0.023	0.960	0.015	0.016	0.961	0.009	0.010
	Scenario **M2**.											
β_1	-0.194	0.655	0.566	-0.435	0.456	0.522	-0.592	0.197	0.379	-0.597	0.073	0.099
β_2	-0.296	0.669	0.567	-0.606	0.486	0.520	-0.743	0.245	0.396	-0.797	0.054	0.094
γ_1	0.591	0.116	0.132	0.599	0.086	0.092	0.593	0.076	0.067	0.597	0.051	0.047
γ_2	0.792	0.099	0.109	0.793	0.068	0.078	0.800	0.052	0.053	0.797	0.085	0.036
	Scenario **M3**.											
β_1	-0.080	0.670	0.576	-0.376	0.513	0.545	-0.584	0.172	0.407	-0.602	0.057	0.088
β_2	-0.304	0.673	0.570	-0.594	0.492	0.528	-0.775	0.170	0.388	-0.795	0.042	0.083
γ_1	-0.415	0.493	0.531	-0.561	0.220	0.397	-0.594	0.083	0.150	-0.599	0.047	0.050
γ_2	-0.567	0.514	0.522	-0.765	0.225	0.371	-0.798	0.055	0.140	-0.797	0.056	0.039
	Scenario **M4**.											
β_1	-0.070	0.672	0.569	-0.312	0.548	0.547	-0.556	0.269	0.445	-0.597	0.063	0.132
β_2	-0.271	0.686	0.570	-0.534	0.564	0.533	-0.743	0.259	0.419	-0.798	0.047	0.125
γ_1	0.251	0.217	0.231	0.266	0.142	0.153	0.274	0.094	0.102	0.280	0.059	0.062
γ_2	0.941	0.068	0.078	0.953	0.041	0.042	0.957	0.025	0.029	0.958	0.017	0.019

Table 2: Summary of rejection proportions based on the simulation scenarios **M1**–**M4**. The rejection proportions are computed based on $n = 50, 100, 200, 500$ observations with 1000 replications at $\alpha = 0.05$. The resampling size is 200.

	n			
	50	100	200	500
M1	0.031	0.037	0.046	0.052
M2	0.281	0.700	0.960	1.000
M3	0.382	0.831	0.996	1.000
M4	0.287	0.686	0.963	1.000