**Supplementary Materials**

S1

For simplicity, we assume no competing censorings and that the entry time is 0 for all individuals. Assume random effect variable . From the simulation method described in section 3, we know that when . Treat the number of events as a random variable, and it can be shown that , where is the total follow-up time. It follows that

By plugging in numbers, and can be calculated and are shown in Table S1.

Table S1. Expectation and variance of number of events

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |
| U(0.5, 1.5) |  | 2.2 | 2.7 |
|  | 2.8 | 3.7 |
|  | 3.6 | 5.0 |
| U(0.1, 1.9) |  | 5.9 | 9.1 |
|  | 7.5 | 12.9 |
|  | 9.7 | 18.4 |
| U(0.01, 1.99) |  | 10.6 | 296.4 |
|  | 13.6 | 484.8 |
|  | 17.5 | 794.3 |

S2

We simulated data 5,000 times for each Z distribution and parameter setup using the method described in section 3. For each simulated dataset, we record the largest number of events () and calculated the average of this number over 5,000 simulations.

Table S2. Average largest number of events

|  |  |  |
| --- | --- | --- |
| Z distribution | Parameters: treatment vs placebo | Average |
| U(0.5, 1.5) |  | 7.3 |
|  | 7.0 |
| U(0.1, 1.9) |  | 15.9 |
|  | 15.2 |
| U(0.01, 1.99) |  | 59.4 |
|  | 54.8 |

S3

To show differences in the residual distribution using Jung and Jeong’s method and using our new method, we simulated one dataset for each Z distribution using the method described in Part 3 and show the corresponding residuals using two different methods in Figure S1. Baseline survival distributions for treatment and control groups are and respectively. It can be seen that tail part of individual-level residual distribution based on Jung and Jeong’s method is heavier than that based on our new method.

|  |  |
| --- | --- |
| Z distribution | Boxplots of individual-level residuals |
| U(0.5, 1.5) | low_0.5_1.5 |
| U(0.1, 1.9) | medium_0.1_1.9 |
| U(0.01, 1.99) | high_0.01_1.99 |

Figure S1 Boxplots of individual-level residuals based on two different methods, given different Z distributions

S4

To further confirm that residuals calculated using Jung and Jeong’s method have a heavy-tailed distribution, we calculated average kurtosis values from 5,000 simulated datasets.

Table S3. Average kurtosis of residual distribution

|  |  |  |  |
| --- | --- | --- | --- |
|  |  | Jung and Jeong’s method | New method |
| Z distribution | Parameters: treatment vs placebo | Average kurtosis distribution | Average kurtosis of distribution |
| U(0.5, 1.5) |  | 7.7 | 2.7 |
|  | 8.5 | 2.7 |
| U(0.1, 1.9) |  | 22.5 | 2.5 |
|  | 22.9 | 2.5 |
| U(0.01, 1.99) |  | 71.0 | 2.4 |
|  | 69.3 | 2.4 |