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Corrigendum: A logrank test-based method for sizing clinical trials with two co-primary time-to-event endpoints (10.1093/biostatistics/kxs057)

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In the article by Tomoyuki Sugimoto *et al*. ('A logrank Test-Based Method for Sizing Clinical Trials With Two Co-Primary Time-to-Event Endpoints'), there were errors on pages 409–421 of issue 14(3) of *Biostatistics*.

In Section 4.2 on p. 418, the article described "the total sample size is 928 commonly for the three copulas when $\rho = 0$. When $\rho = 0.3, 0.5$, and 0.8, they are 928, 926, and 924 for the Clayton copula; 926, 922, and 920 for the Gumbel copula; and 926, 924, and 920 for the Frank copula." However, these numbers were calculated with the two hazard ratios $\psi_1 = 1.77$ and $\psi_2 = 1.39$, not $\psi_1^{-1} = 1.77$ and $\psi_2^{-1} = 1.39$. The corrected numbers are as follows:

ρ	Clayton	Gumbel	Frank
0.0	1220	1220	1220
0.3	1218	1210	1212
0.5	1216	1202	1204
0.8	1210	1188	1188

Also Figure 1 on p. 419 is corrected as below. The authors apologize for these errors.

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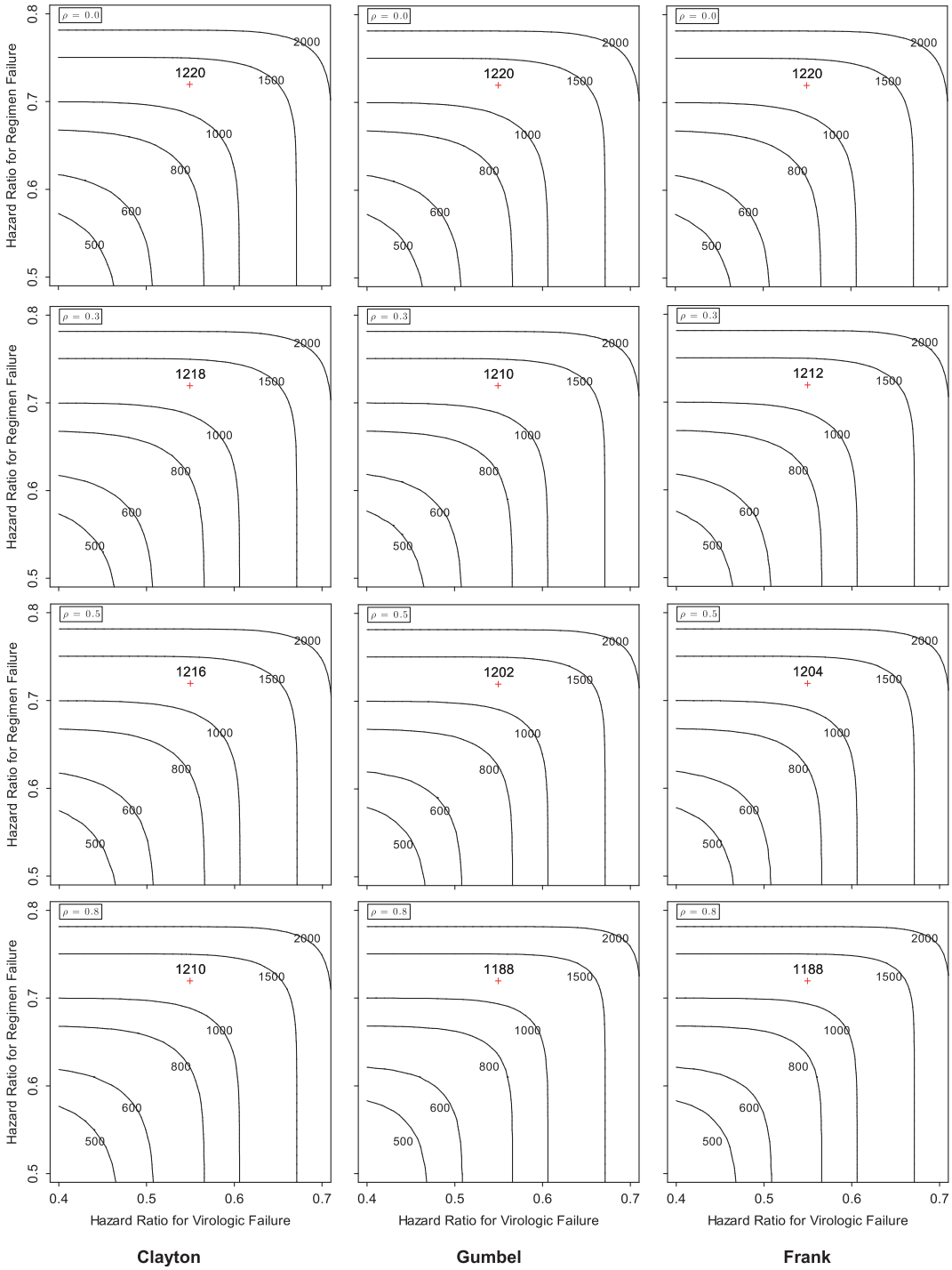

Fig. 1. Contour plots of the required total sample size with the hazard ratios of time-to-events of virologic and regimen failures, and correlation for the three copulas. The sample size was calculated to detect the joint reduction for both time-to-event outcomes with the overall power of 0.90 at the one-sided significance level of 0.0125, where $\rho = \rho^{(1)} = \rho^{(2)} = 0.0,\ 0.3,\ 0.5$ and 0.8; $S_1^{(1)}(96) = 0.75$ and $S_2^{(1)}(96) = 0.55$; $\tau_2 = 0$, and $\tau_f = 96$; $a^{(1)} = 0.5$.