## Web-based Supplementary Materials for

A comparative study of adaptive dose-finding designs for phase I oncology trials of combination therapies

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## Tables of main results

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Table			27	39	34	35	33		Ave	9	11	10	6	11			0.72	0.82	0.71	0.76	0.69										
			22	31	30	28	22			က	10	6	7	က			0.4	0.56	0.37	0.46	0.31										
			YYC	CDP	BW	WCO	MHH			YYC	CDP	BW	WCO	HHM			YYC	CDP	BW	WCO	HHM										

## Additional scenarios with 'imperfect' MTDC

We also compared the operating characteristics among the 5 methods under 6 scenarios with  $3 \times 3$ ,  $4 \times 4$ , and  $3 \times 4$  dose combination matrices with "imperfect" MTDC's, as shown in Table 3. By 'imperfect' we mean that there is no combination with DLT rate exactly equal to the target rate  $\phi$ . In these cases, selecting combinations, as the MTDC, with DLT rates that are within a certain range would be considered acceptable. Table 3 highlights any combination with a DLT rate within 0.05 of the target and we deem them "acceptable" if chosen as the MTDC. Under each scenario, 1000 trials were simulated. The target toxicity probability is set to  $\phi = 0.30$  in Scenarios 1 and 2,  $\phi = 0.33$  in Scenarios 3–6. The sample size is n = 22 in Scenarios 1 and 2, n = 32 in Scenarios 3 and 4, and n = 36 in Scenarios 5 and 6.

For the YYC method, we assumed gamma(2, 2) as the prior distribution for  $\alpha$  and  $\beta$ , and gamma(0.1, 0.1) as the prior distribution for  $\gamma$ . The values of the marginal a priori DLT rates,  $p_j$ , are set to (0.10, 0.20, 0.30) for J = 3, and (0.10, 0.20, 0.30, 0.40) for J = 4, respectively. The same settings are made for  $q_k$ . The fixed probability cut-offs for dose escalation and deescalation are  $c_e = 0.80$  and  $c_d = 0.45$ , respectively, which are also default values used by the software. For the BW method, the variance parameter  $\sigma^2$  is set to 3 in order to stabilize the implementation of the R package **rjags**. The prior probability of each dose combination is shown in Table 4. For the WCO method, we chose a subset of possible dose-toxicity orders based on ordering the combinations by rows, columns, and diagonals of the drug combination matrix, as suggested by Wages and Conaway [1]. We utilized eight possible orderings in all scenarios. A uniform prior,  $\tau(m)$ , was placed on the orderings. The skeleton values,  $p_{ik}(m)$ , were generated according to the algorithm of Lee and Cheung [2] using the **getprior** function in R package dfcrm [3]. Specifically, for  $3 \times 3$  combinations, we used getprior(0.05,0.30,4,9); for  $4 \times$ 4 combinations, we used getprior(0.05,0.30,7,16); and for  $3 \times 4$  combinations, we used getprior(0.05,0.30,6,12). The location of these skeleton values was adjusted to correspond to each of the six orderings using the **getwm** function in R package **pocrm**. All simulation results were carried out using the functions of **pocrm** with a cohort size of 1 in both stages. For each simulated trial, no stopping rule was specified so as to exhaust the pre-specified maximum sample sizes above. We performed the HHM method using the SAS/IML in SAS 9.3 (SAS Institute Inc., NC). The fixed intercept  $\beta_0$  is set to be -3 throughout.  $c_1$  and  $c_2$  are commonly set to 0.05. We set  $x_1 = 1, 2, 3$  and  $x_2 = 1, 2, 3$  for  $3 \times 3$  dose combinations,  $x_1 = 1, 2, 3, 4$ and  $x_2 = 1, 2, 3, 4$  for  $4 \times 4$  dose combinations, and  $x_1 = 1, 2, 3$  and  $x_2 = 1, 2, 3, 4$  for  $3 \times 4$ dose combinations, respectively.

Overall, the results in Table 5 seem to be consistent with the results in the main paper. The WCO (37.1%) and CDP (38.3%) methods again yielded the highest average recommendation rates for MTDC's around the target rate by at least 6% over the nearest competitior (YYC; 31.5%). These gains appear to be more substantial than in the cases in which there is a "perfect" MTDC, however this is based on a small set of six scenarios.

Table 3: Six scenarios for two-agent combination trials with an "imperfect" MTDC. Combinations with true DLT probabilities within 5% of the target rate ( $\phi$ ) are considered acceptable and are indicated in bold type.

						А				Target	Sample
		1	2	3	4	1	2	3	4	Rate $(\phi)$	Size
		Scenario 1					Scen	ario 2		0.30	22
	3	0.20	0.50	0.66		0.18	0.50	0.60			
	2	0.06	0.33	0.50		0.12	0.18	0.50			
	1	0.02	0.20	0.33		0.06	0.12	0.33			
			Scena	ario 3			Scen	ario 4			
	4	0.35	0.40	0.42	0.45	0.43	0.65	0.79	0.95	0.33	32
В	3	0.28	0.31	0.35	0.36	0.35	0.51	0.75	0.91		
	2	0.15	0.19	0.23	0.30	0.20	0.39	0.63	0.88		
	1	0.05	0.09	0.20	0.25	0.05	0.25	0.50	0.80		
			Scena	ario 5		Scenario 6					
	3	0.30	0.40	0.50	0.60	0.40	0.68	0.80	0.99	0.33	36
	2	0.05	0.15	0.25	0.35	0.20	0.35	0.50	0.70		
	1	0.01	0.10	0.15	0.20	0.01	0.10	0.20	0.30		

						А				
		1	2	3	4		1	2	3	4
			$3 \times 3$					$4 \times 4$		
	4					0.33	0.42	0.50	0.60	
	3	0.30	0.40	0.50		0.22	0.33	0.42	0.50	
	2	0.20	0.30	0.40		0.11	0.22	0.33	0.42	
	1	0.10	0.20	0.30		0.02	0.11	0.22	0.33	
В										
			$3 \times 4$							
	3	0.33	0.40	0.47	0.54					
	2	0.22	0.29	0.36	0.43					
	1	0.10	0.17	0.25	0.33					

Table 4: Prior toxicity probabilities we used in the simulation studies in the BW method in additional simulations with an 'imperfect' MTDC.

Table 5: Summary of the operating characteristics of the 5 methods in 6 scenarios containing an "imperfect" MTDC. The table reports the percentage of simulated trials that each emthod selected, as the MTDC, an acceptable combination, defined as one with true DLT rate within 0.05 of the target rate  $\phi$ .

Scenarios													
Method	1	2	3	4	5	6	Avg.						
	Recommendation rates (%) for												
combos within 5% of $\phi$													
YYC	37.2	23.0	43.0	18.1	29.6	41.1	31.5						
CDP	47.7	29.9	49.5	24.7	29.4	47.6	38.3						
BW	22.5	10.5	17.1	2.9	12.6	11.5	13.8						
WCO	46.4	23.4	48.3	22.3	36.5	50.2	37.1						
HHM	30.5	7.3	26.9	11.4	27.9	37.5	22.4						

## References

- [1] Wages NA, Conaway MR. Specifications of a continual reassessment method design for phase I trials of combined drugs. *Pharmaceutical Statistics* 2013; **12**:217–224.
- [2] Lee SM, Cheung YK. Model calibration in the continual reassessment method. *Clinical Trials* 2009; 6:227–238.
- [3] Wages NA, Varhegyi N. pocrm: an R-package for phase I trials of combinations of agents. Computer Methods and Programs in Biomedicine 2013; **112**: 211–218.