

Comprehensive evaluation of CRM, mTPI, and 3+3 relative to a benchmark

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Outline of Talk

- ▶ Methods compared
- ▶ Summary estimates used to compare methods
- ▶ Simulation study

Methods compared

- ▶ Continual reassessment method (CRM)
- ▶ Modified toxicity probability interval (mTPI)
- ▶ 3+3
- ▶ Benchmark

CRM

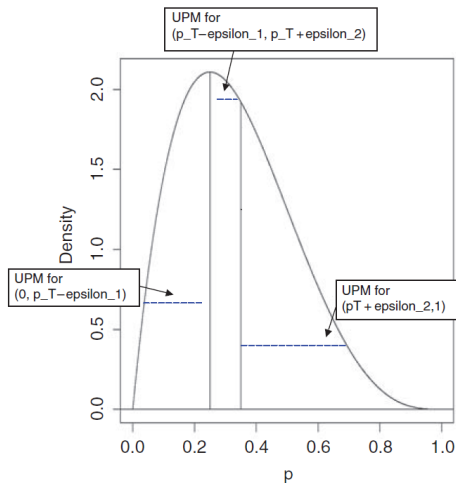
- ▶ 2-stage design
- ▶ Stage 1
 - ▶ Cohort size of 1
 - ▶ Increase until heterogeneity is observed responses
- ▶ Stage 2
 - ▶ `dfcrm` package used to make dose recommendations specifying a power model to model DLT probabilities
 - ▶ Skeleton generated with the `getprior` function from `dfcrm`
 - ▶ `getprior(0.06,0.2,2,# of dose levels)`
 - ▶ Trial terminated if at dose 1 and the lower bound of 90% confidence interval of the probability of toxicity is greater than the target toxicity

mTPI

- ▶ Decisions are based on an equivalence interval
 - ▶ $[p_T - \epsilon_1, p_T + \epsilon_2]$
- ▶ Safety stopping measures
 - ▶ Terminate early if probability of toxicity, given data, too high
 - ▶ Exclude doses in future if probability of toxicity too high
- ▶ <http://compgenome.org/NGDF/>
 - ▶ Specifying a cohort size of 3 and $\epsilon_1 = \epsilon_2 = 0.05$
- ▶ Next dose chosen by maximum unit probability mass (UPM)

mTPI

Posterior probability distribution



Benchmark

- ▶ Suppose we know each patient's toxicity tolerance
 - ▶ tolerance generated from uniform $(0,1)$ distribution
- ▶ For a specified toxicity curve, know when each patient would have a DLT
- ▶ Example:
 - ▶ 4 dose levels
 - ▶ Toxicity curve: $(0.1, 0.19, 0.30, 0.39)$

Benchmark

True toxicity curve: (0.1, 0.19, 0.30, 0.39)

Patient	Tolerance	Toxicity at dose level i			
		1	2	3	4
1	0.349	0	0	0	1
2	0.462	0	0	0	0
3	0.222	0	0	1	1
4	0.517	0	0	0	0
\vdots	\vdots	\vdots	\vdots	\vdots	\vdots
23	0.074	1	1	1	1
24	0.382	0	0	0	1
Est. Tox. Rate		0.06	0.22	0.27	0.40

Benchmark

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Summary estimates used to compare methods

- ▶ Percent correct selection (PCS)
- ▶ Accuracy index
- ▶ Other basic statistics:
 - ▶ Proportion of toxicities observed
 - ▶ Average number of subjects allocated to a dose

Percent correct selection (PCS)

- ▶ The probability of selecting the true MTD
- ▶ Percent of dose selection within 5% and 10% of the target toxicity rate

Accuracy Index

- ▶ For dose selection:

- ▶ $A_N = 1 - K \times \frac{\sum_{k=1}^K \rho_k \times \text{Probability of selecting dose } k}{\sum_{k=1}^K \rho_k}$

- ▶ K is the number of doses

- ▶ $\rho_k = |p_k - \theta|$, where p_k is the true toxicity probability at dose k and θ is the target toxicity

- ▶ Also used for subject allocation

Cheung (2011)

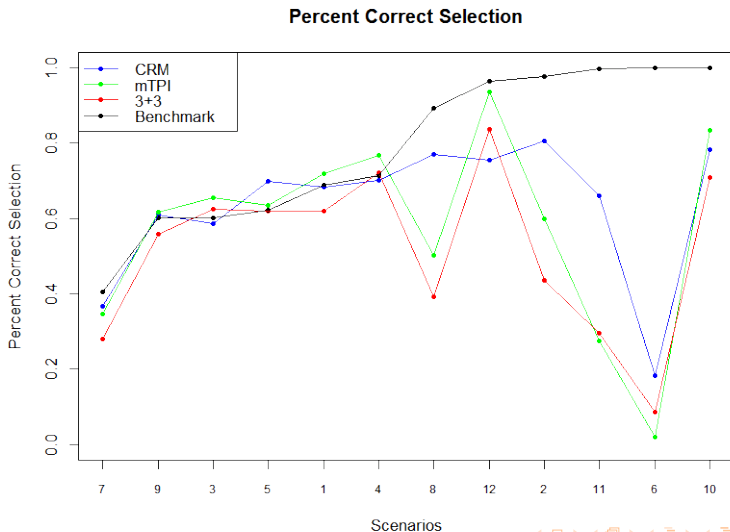
Dose curve selection

- ▶ 10,000 curves were simulated using order statistics from a Beta distribution (8 dose levels)
- ▶ K-means clustering used to partition these curves into 12 groups
- ▶ Curves within groups were averaged to create the 12 curves used in the simulations

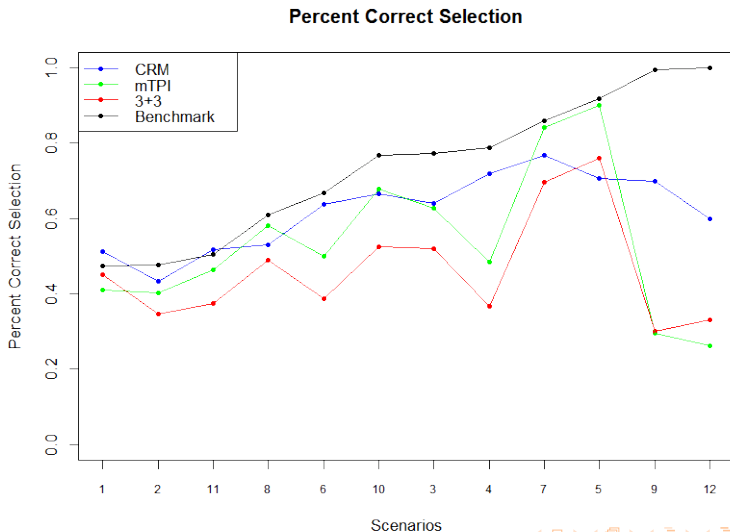
Simulation setup

- ▶ 2,000 simulations
- ▶ Target toxicity rate $\theta = 0.2$
- ▶ Varying number of dose levels
 - ▶ 3 dose levels $\rightarrow n=18$
 - ▶ 4 dose levels $\rightarrow n=24$
 - ▶ 6 dose levels $\rightarrow n=36$
 - ▶ 8 dose levels $\rightarrow n=48$
- ▶ dfcrm package in R used for CRM
- ▶ <http://compgenome.org/NGDF/> used for mTPI

3 Dose levels

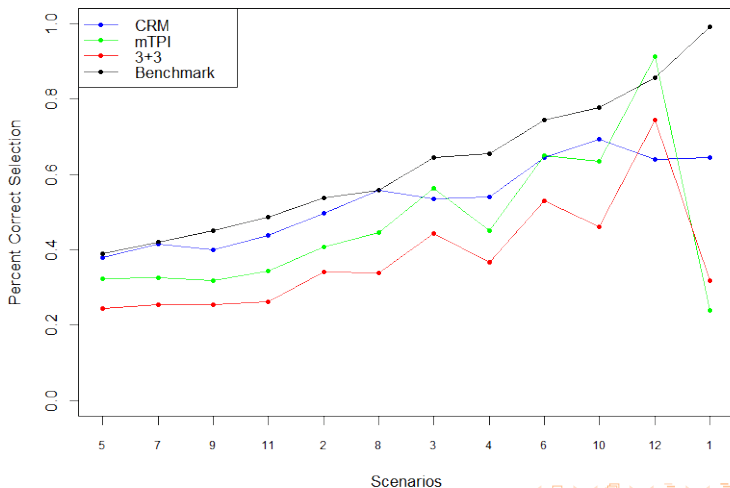


4 Dose levels



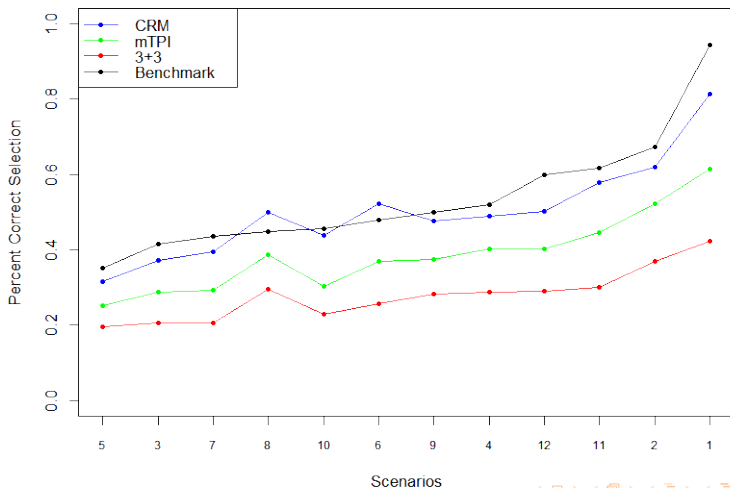
6 Dose levels

Percent Correct Selection



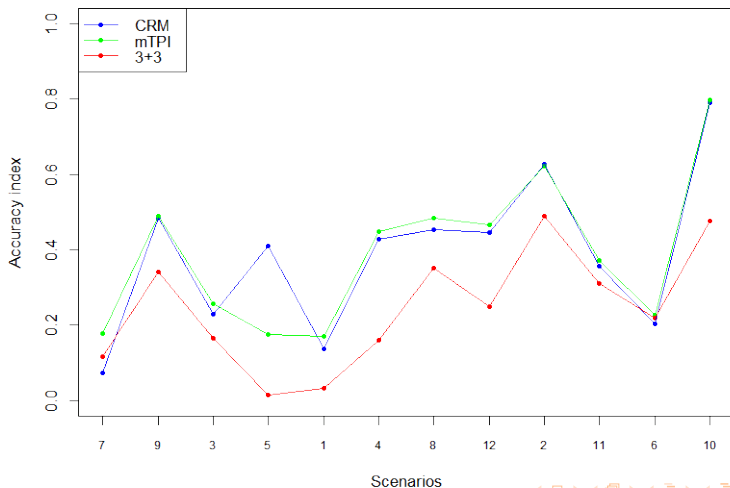
8 Dose levels

Percent Correct Selection



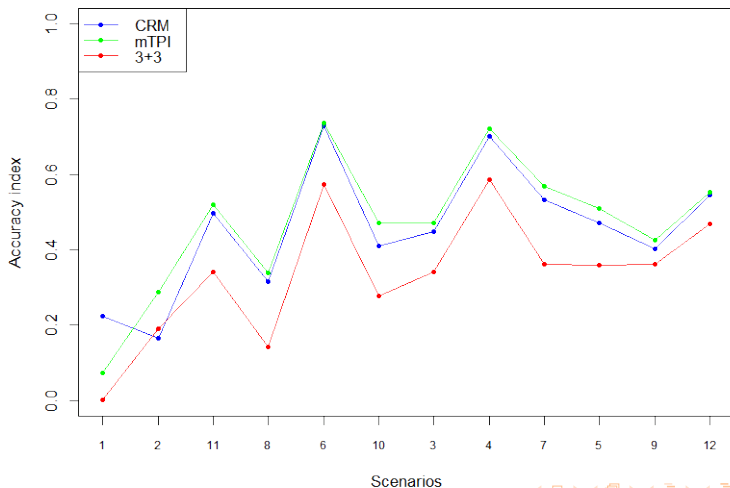
3 Dose levels

Accuracy index for subject allocation



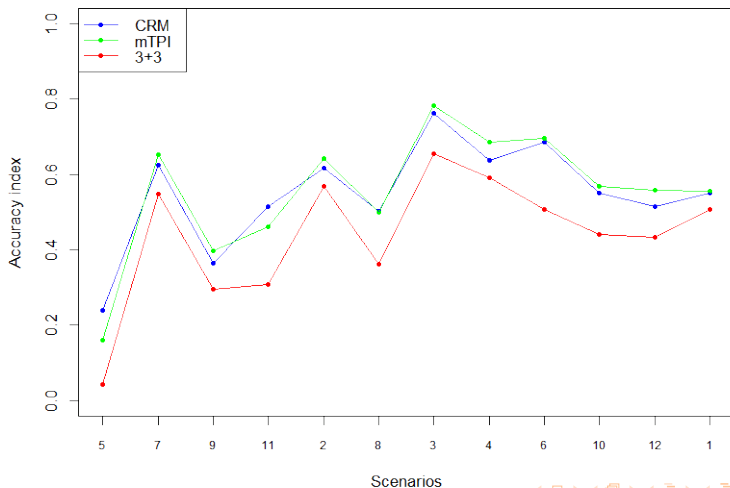
4 Dose levels

Accuracy index for subject allocation



6 Dose levels

Accuracy index for subject allocation



8 Dose levels

Accuracy index for subject allocation

