



Dose-finding in malaria

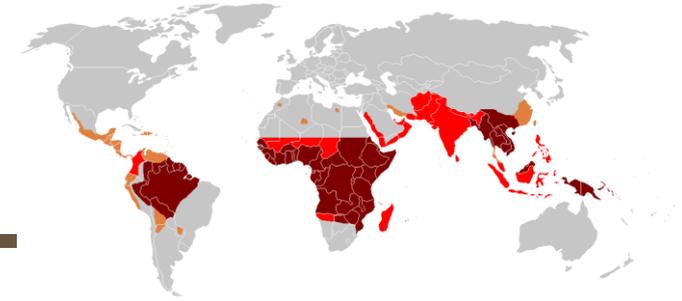
A combination dose-escalation study using Bayesian logistic regression modeling (BLRM)

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19 May 2016

Outline

- Malaria – disease overview
- Program overview and context for dose finding
- Candidate phase 2b study design
- Dose escalation – methodology reminder
 - Safety metrics
 - Bayesian logistic regression model for combination modeling
 - Prior specification and derivation
- Implementing the design
 - Planning
 - Communication
 - Simulations
- Summary



Malaria

Disease overview

- Mosquito-borne infectious disease
 - Human cases date back to 2700 BC
 - Historically associated with “bad air” (*mala aria*) around marshes
- Once common in the US and southern Europe
- Now endemic in a “broad band” around the equator
- 2015 facts & figures (WHO)
 - 214 million cases worldwide
 - 438,000 documented deaths
 - 70% of deaths occur in children under 5 years old
- Treatment:
 - In late 19th century: mustard bath, kerosene massage, lots of whiskey
 - Current: artemisinin-based combination regimens (~95% cure rate)

Program overview

Key question for phase 2b

- Setting:
 - Investigational compound (drug A) under development for treatment of malaria
 - Preferred combination partner (drug B) has been identified
- Phase 2a completed – monotherapy only
 - Multiple-dose and single-dose regimens have been investigated
 - Potential for *single dose cure*
- Key question for phase 2b – is single dose cure feasible?
 - Components to answer question: need a combination dose with
 - satisfactory safety profile
 - efficacy comparable with existing multi-day regimens (~95% cure rate)
- In the context of malaria treatment, higher doses are preferable
- Primary purpose of dose-finding: establish the maximum tolerated dose (MTD)

Program overview

Candidate design for phase 2b

- Candidate phase 2b design:
 - Consider dose escalation methodology often used in phase 1 oncology studies
 - Escalate separately for monotherapy and combination therapy
 - Note: partner drug dose kept constant

- Primary endpoint
 - Rate of occurrence of specific dose-limiting toxicities (DLTs)
 - DLTs are pre-defined according to known program and indication risks

- Components of dose escalation
 - Incorporate contextual information from previous studies
 - Quantify dose-toxicity relationship with BLRM
 - Provide model-based recommendation of the next dose level

Interim analysis algorithm

Inference → *dose recommendations*

- BLRM input – cumulative DLTs and sample size at each studied dose
- Inference:
 - Estimate dose-toxicity relationship
 - Derive safety metrics:
 - Under-dosing DLT probability < 0.05
 - Target dosing DLT probability between 0.05 and 0.20
 - Overdosing DLT probability > 0.20
 - Report interval probability for each candidate dose
- Model-based dose recommendation:
 - Dose with high probability of being in target interval for DLT
 - AND maximal overdose probability of 0.25 (EWOC)
 - Possible recommendations:
escalate, repeat, de-escalate
or stop and declare MTD

Combination BLRM

Modeling the dose-toxicity relationship

$$\begin{aligned}\log(\text{odds}(\pi_{1,d_1})) &= \log(\alpha_1) + \beta_1 \log(d_1) \\ \log(\text{odds}(\pi_{2,d_2})) &= \log(\alpha_2) + \beta_2 \log(d_2) \\ \pi_{12,d_1,d_2}^0 &= \pi_{1,d_1} + \pi_{1,d_2} - \pi_{1,d_1} \pi_{2,d_2} \\ \text{odds}(\pi_{12,d_1,d_2}) &= \text{odds}(\pi_{12,d_1,d_2}^0) \exp(\eta d_1 d_2) \\ (\alpha_1, \beta_1, \alpha_2, \beta_2 > 0)\end{aligned}$$

Dose-toxicity relationship for each individual drug

DLT probability under no interaction

Dose-dependent interaction term on odds scale

- (note: reference/scaling doses dropped in formulas)
- if no dose-dependent interaction desired: simply use $\exp(\eta)$
- no interaction $\Leftrightarrow \eta = 0$
- typically $\eta > 0$, but not necessarily

Combination BLRM

Specifying the priors

MAP* prior for α^* , β^* obtained from hierarchical model

$$r_{d,h} \sim \text{Bin}(\pi_{d,h}, n_{d,h})$$

$$\log(\pi_{d,h} / (1 - \pi_{d,h})) = \log(\alpha_h) + \beta_h \log(d / d^*)$$

$$(\log(\alpha_h), \log(\beta_h)) \sim \text{BVN}((\mu_1, \mu_2), \psi)$$

$$(\log(\alpha^*), \log(\beta^*)) \sim \text{BVN}((\mu_1, \mu_2), \psi)$$

Priors

$$\psi = \begin{pmatrix} \tau_1^2 & \tau_1 \tau_2 \rho \\ \tau_1 \tau_2 \rho & \tau_2^2 \end{pmatrix}$$

$$\mu_1 \sim \text{N}(m_{\mu_1}, s_{\mu_1}^2), \mu_2 \sim \text{N}(m_{\mu_2}, s_{\mu_2}^2)$$

$$\tau_1 \sim \text{LN}(m_{\tau_1}, s_{\tau_1}^2), \tau_2 \sim \text{LN}(m_{\tau_2}, s_{\tau_2}^2), \rho \sim \text{Unif}(-1, 1)$$

Interaction prior – normal prior on η

$$\text{odds}(\pi_{12,d_1,d_2}) = \text{odds}(\pi_{12,d_1,d_2}^0) \exp(\eta d_1 d_2)$$

*Meta-analytic predictive

Combination BLRM

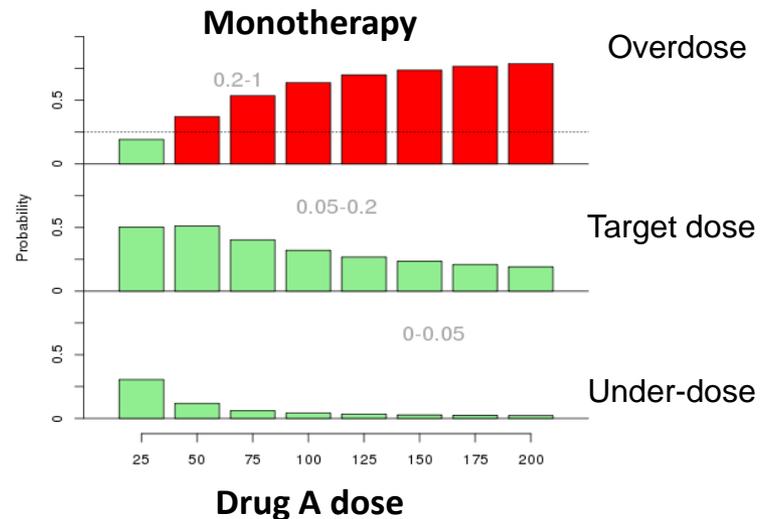
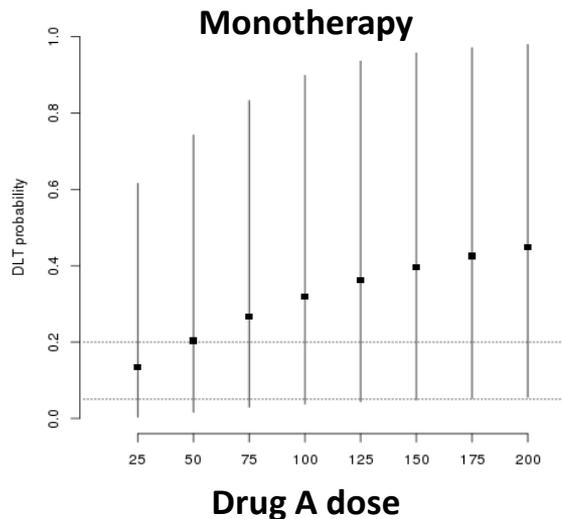
Deriving the MAP prior

- Contextual information from patient studies of drug A:
 - Two single-dose studies – several dose levels
 - One multiple-dose study – one dose level
 - Summed and treated as single dose in meta-analysis
- Differential discounting of historical information:
 - Assumption of **multi-dose = single-dose x days** is crude, needs attention!
 - Approach: Split prior data into strata (single vs. multiple-dose)
 - ...and assume larger prior variability in multiple-dose stratum
- Deriving the MAP prior:
 - The described model can be easily fit with BUGS/JAGS/Stan...
 - Approximate MAP prior with bivariate normal mixture
 - Mixture components can be written directly in the protocol

Summary of contextual information

Prior distributions for dose-toxicity

- MAP prior fitted to the available dose-DLT data and robustified
- A priori: 25mg is MTD, 50m too toxic, but *substantial uncertainty*



- Main source of information for drug B: [drug label](#)
 - Single dose of drug B at recommended dose expected to be relatively safe
- No dose-response data, so two assumptions for dose of interest:
 - $\Pr(\text{DLT} < 0.2) = 0.95$ and $\Pr(\text{DLT} < 0.05) = 0.5$
 - Converted into a bivariate normal prior to fit with the combination BLRM setup

Implementing the design

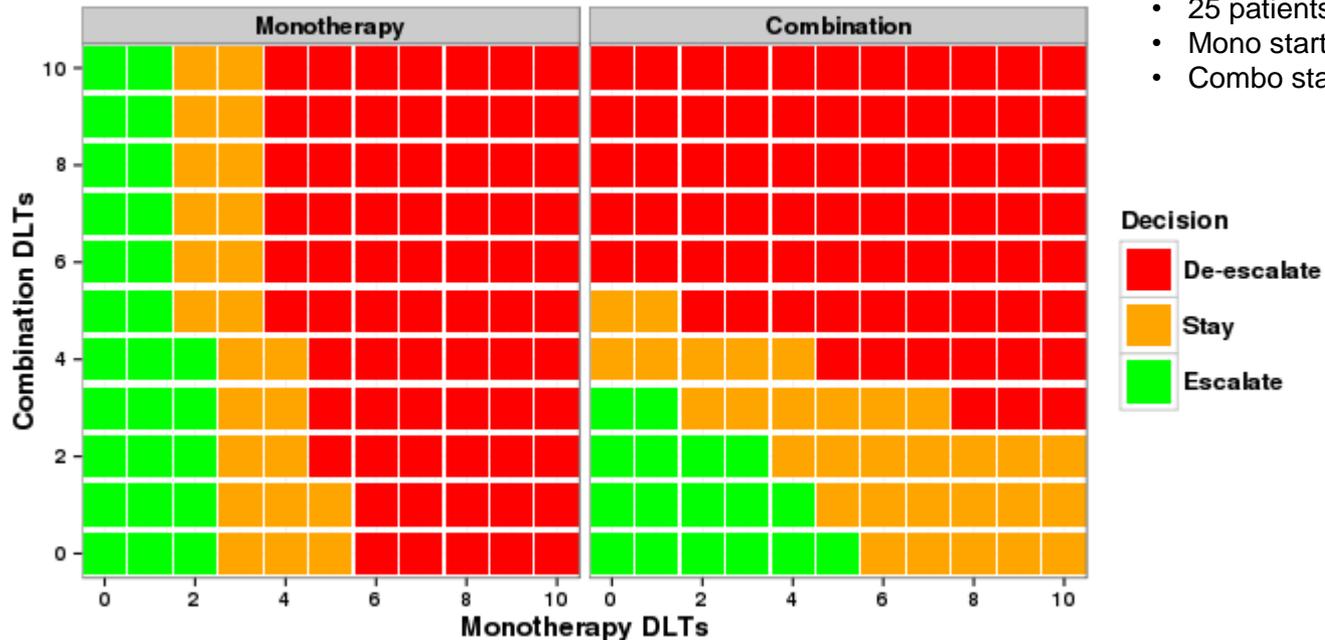
Planning, simulating, communicating!

- Many (though not all) members of clinical team were unfamiliar with this type of design
- Clear visual communication essential to ensure clarity regarding
 - Methodology – quantification of uncertainty in DLT rates
 - Credibility – sanity checks that reasonable recommendations will be made
 - End-to-end understanding – illustration of a hypothetical trial
- Robustness assessment – does the design perform as desired?
- Simulation plan written to
 - Define dose-toxicity scenarios for evaluation
 - Define metrics for comparison of competing design options
 - Agree on key design parameters such as sample size
 - In a cohort/overall

First interim analysis

Dose recommendation

- Question:
 - “Given all the assumptions for the prior...”
 - “...and given the agreed-upon limits for dose toxicity categories...”
 - “...does the design make reasonable recommendations in light of actual data?”
- Address by showing grid of outcomes for first IA



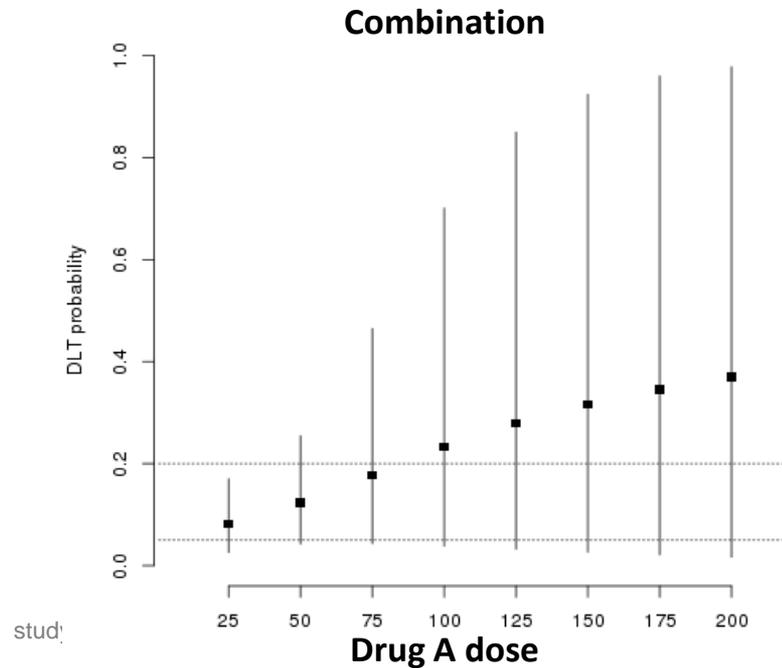
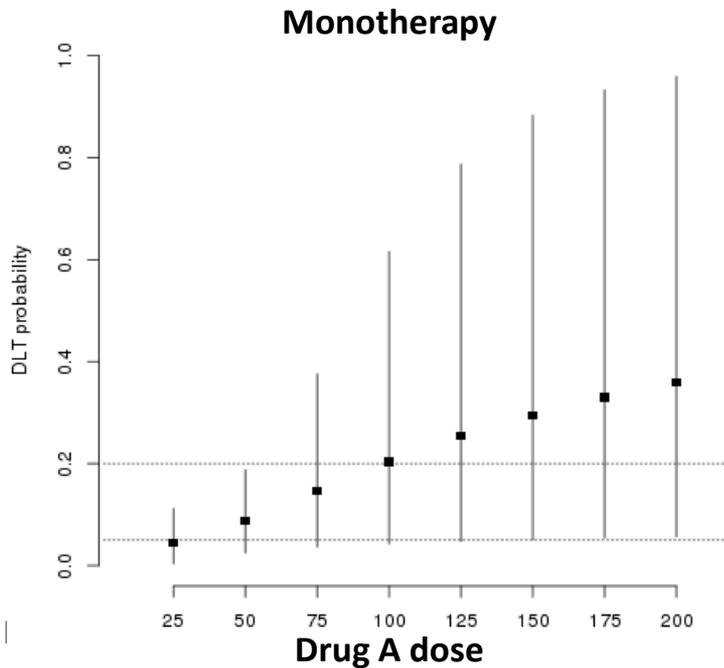
Example – Complete study

Using maximal escalation rule

Cohort 1

Monotherapy 2/25; Combination 1/25

	Dose	25	50	75	100	125
Mono	# Patients	0	25	0	0	0
	# DLT		2			
Comb	# Patients	25	0	0	0	0
	# DLT	1				

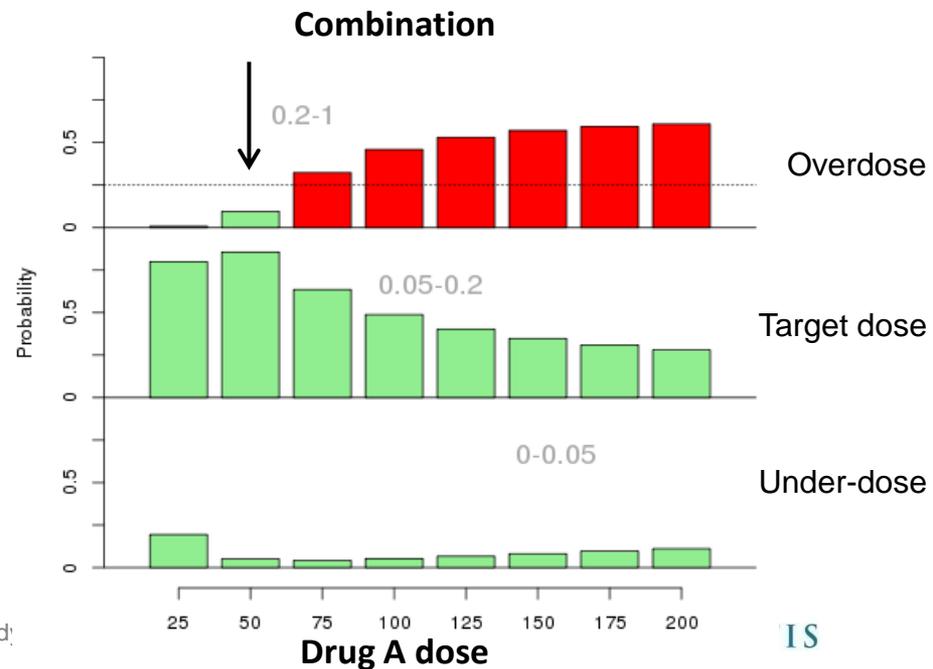
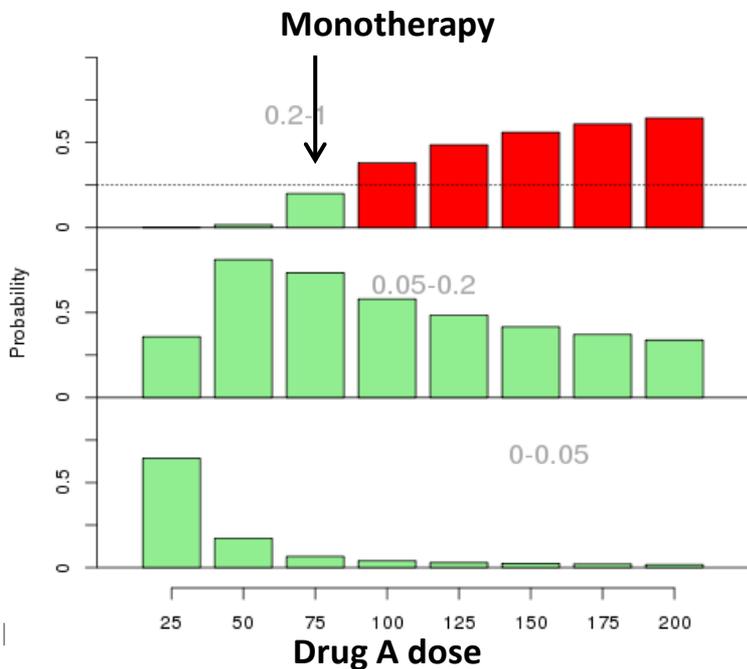


Cohort 1

Monotherapy 2/25; Combination 1/25

Both mono and comb may escalate, 75mg and 50mg respectively

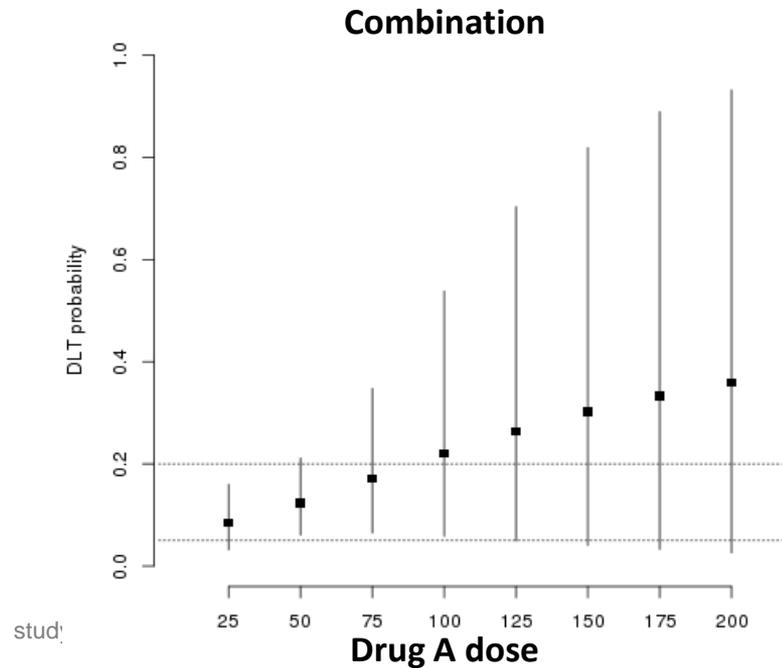
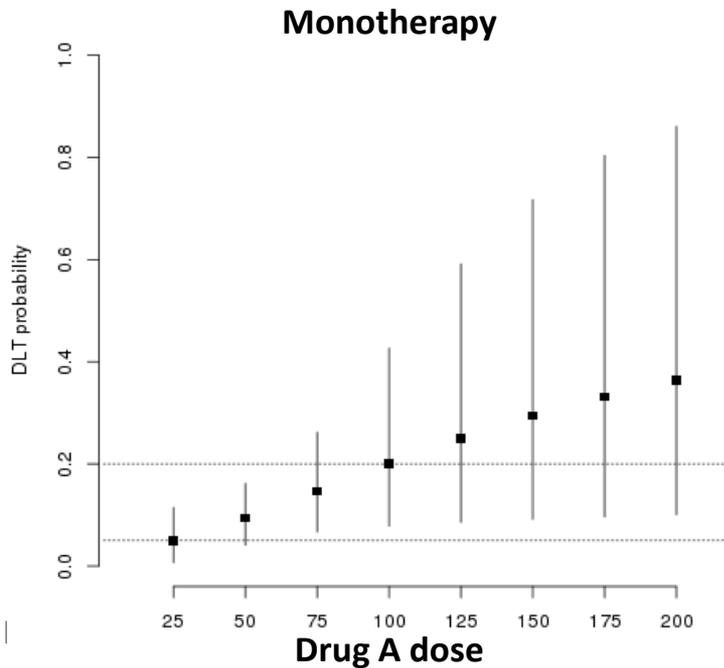
	Dose	25	50	75	100	125
Mono	# Patients	0	25	0	0	0
	# DLT		2			
Comb	# Patients	25	0	0	0	0
	# DLT	1				



Cohort 2

Monotherapy 4/25; Combination 3/25

	Dose	25	50	75	100	125
Mono	# Patients	0	25	25	0	0
	# DLT		2	4		
Comb	# Patients	25	25	0	0	0
	# DLT	1	3			

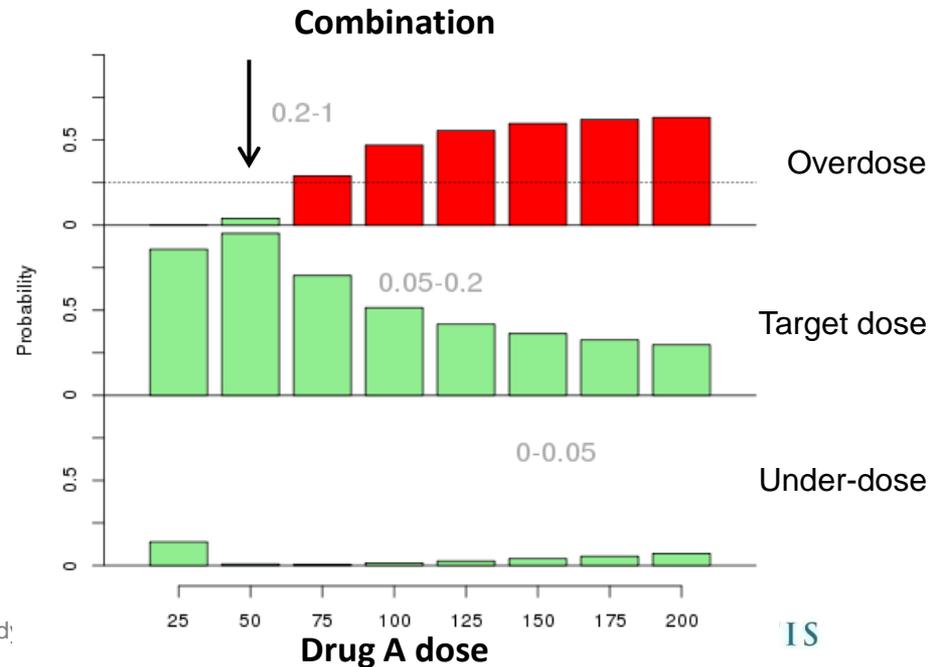
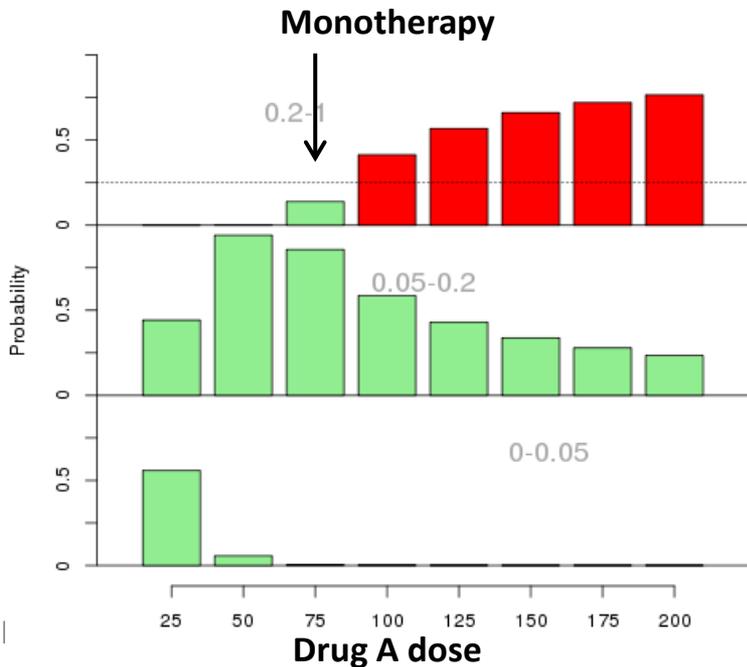


Cohort 2

Monotherapy 4/25; Combination 3/25

Mono and comb should repeat 75mg and 50mg respectively, escalation not possible due to EWOC

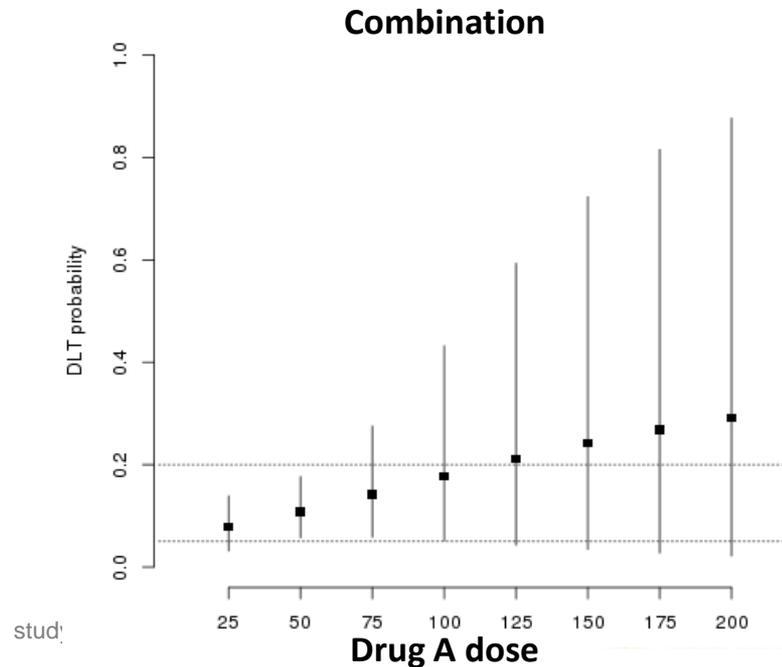
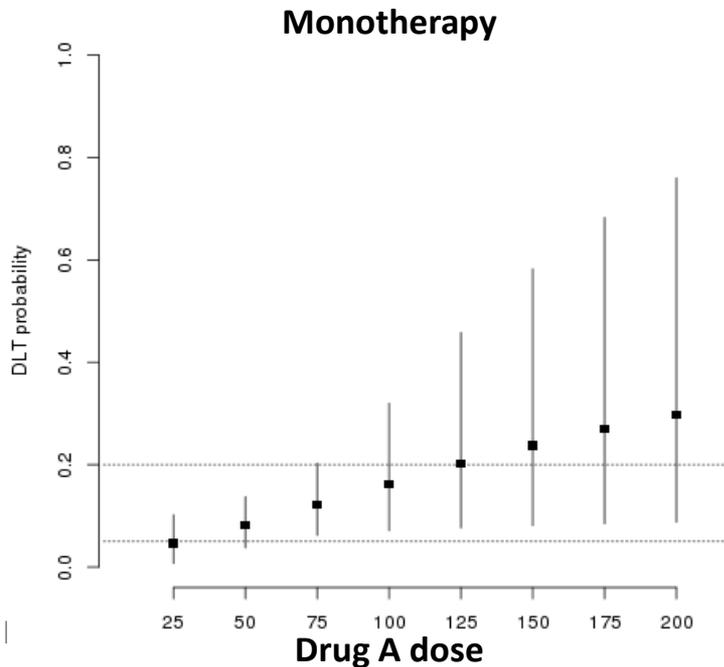
	Dose	25	50	75	100	125
Mono	# Patients	0	25	25	0	0
	# DLT		2	4		
Comb	# Patients	25	25	0	0	0
	# DLT	1	3			



Cohort 3

Monotherapy 2/25; Combination 2/25

	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	0	0
	# DLT		2	6		
Comb	# Patients	25	50	0	0	0
	# DLT	1	5			

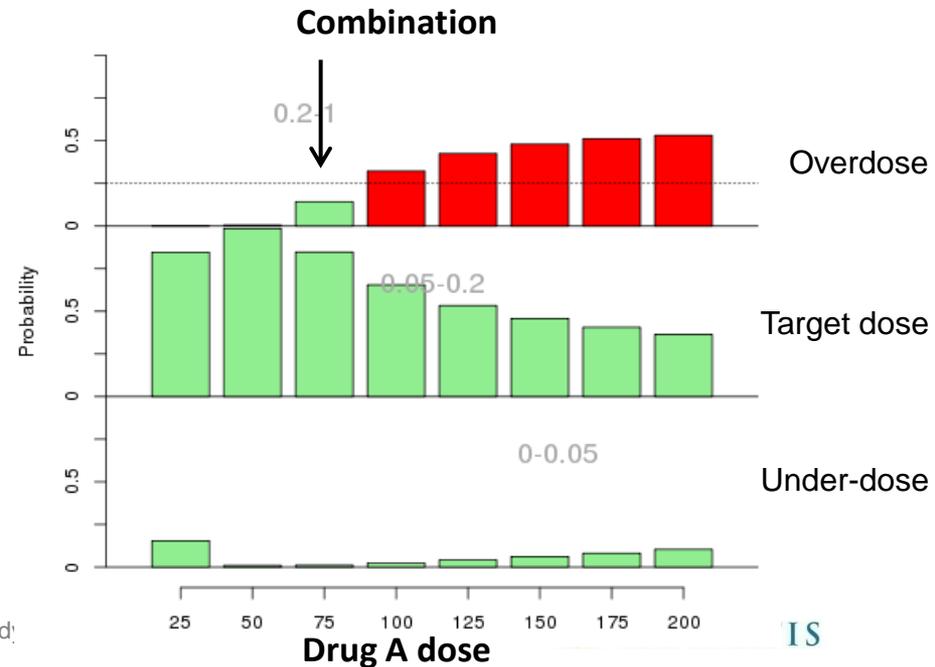
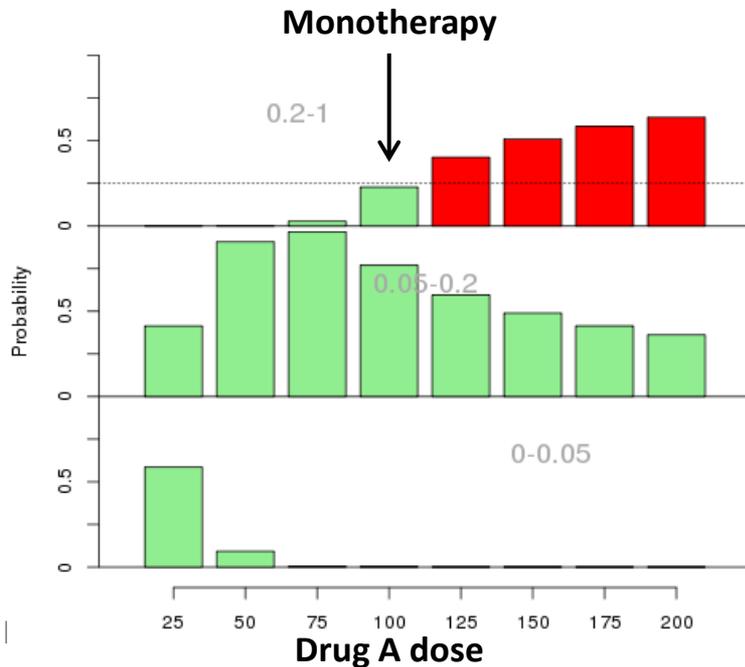


Cohort 3

Monotherapy 2/25; Combination 2/25

Both mono and comb may escalate, 100mg and 75mg respectively

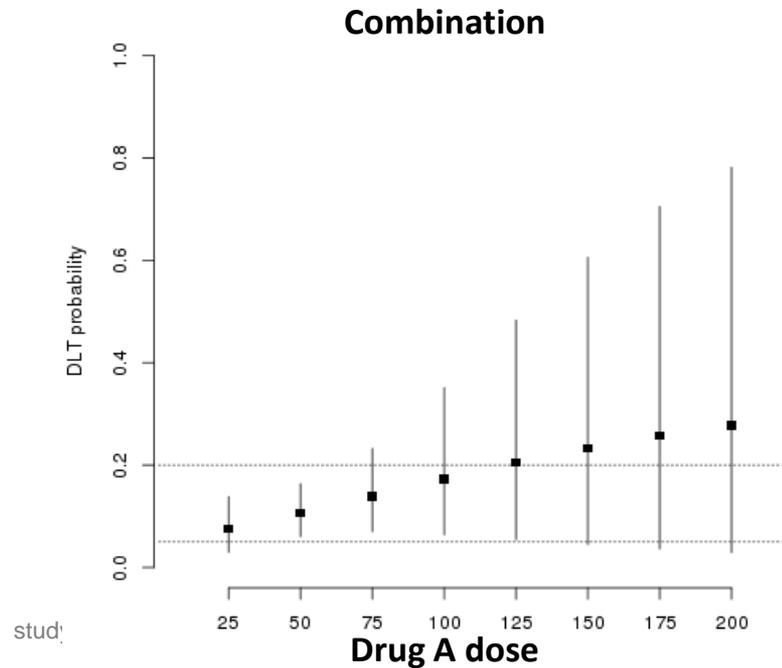
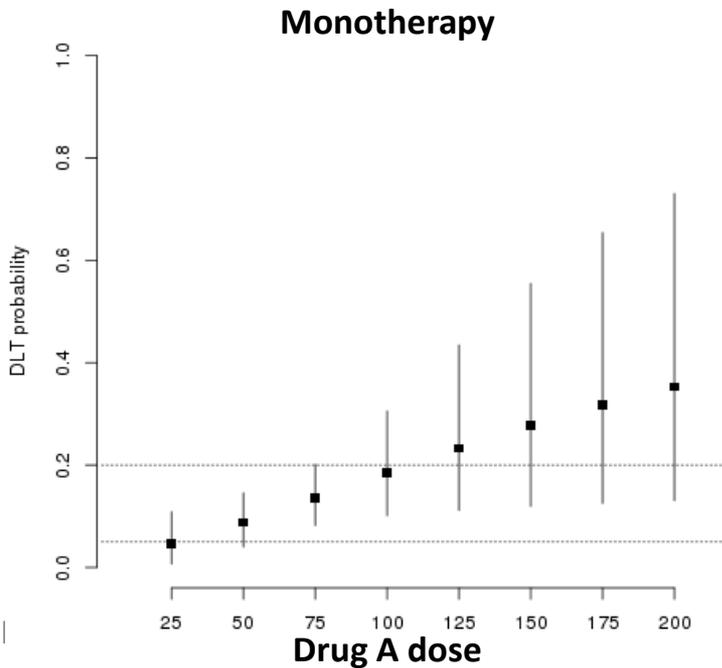
	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	0	0
	# DLT		2	6		
Comb	# Patients	25	50	0	0	0
	# DLT	1	5			



Cohort 4

Monotherapy 6/25; Combination 3/25

	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	25	0
	# DLT		2	6	6	
Comb	# Patients	25	50	25	0	0
	# DLT	1	5	3		

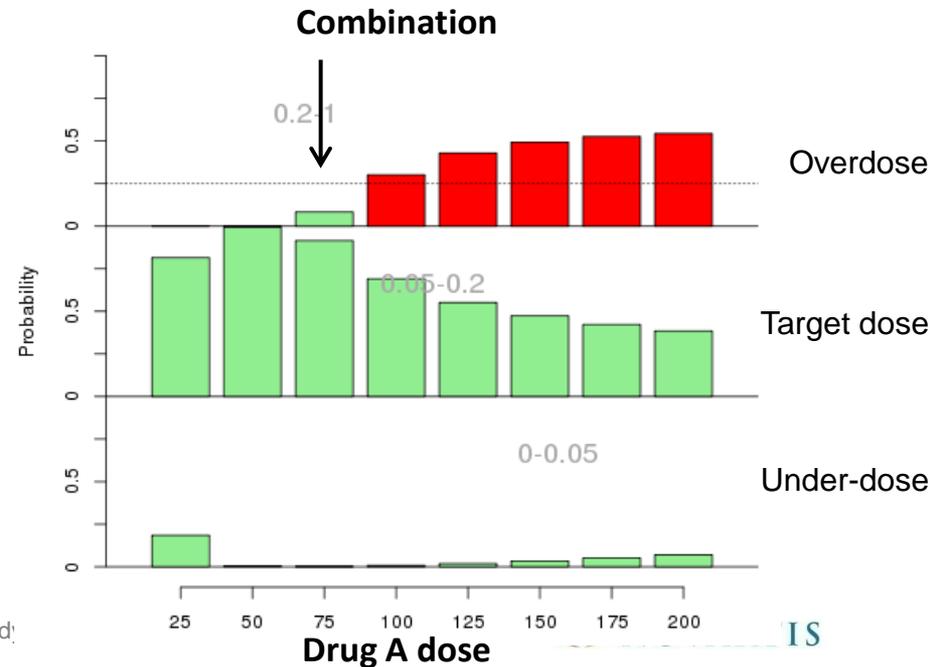
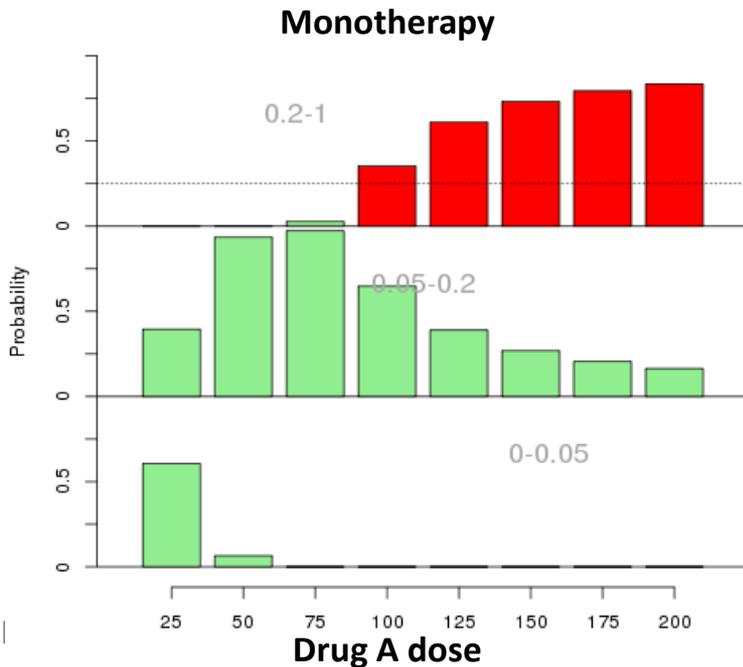


Cohort 4

Monotherapy 6/25; Combination 3/25

Monotherapy MTD established = 75mg;
Continue with combination therapy

	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	25	0
	# DLT			2	6	6
Comb	# Patients	25	50	25	0	0
	# DLT	1	5	3		

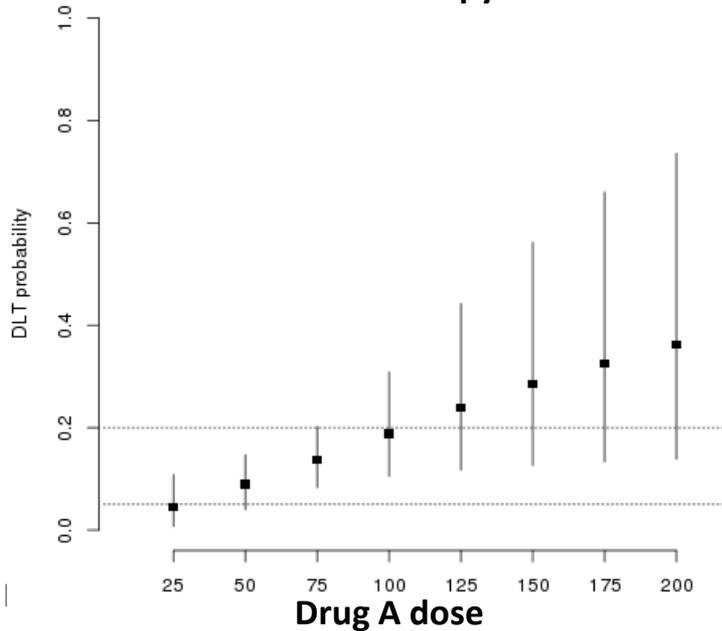


Cohort 5

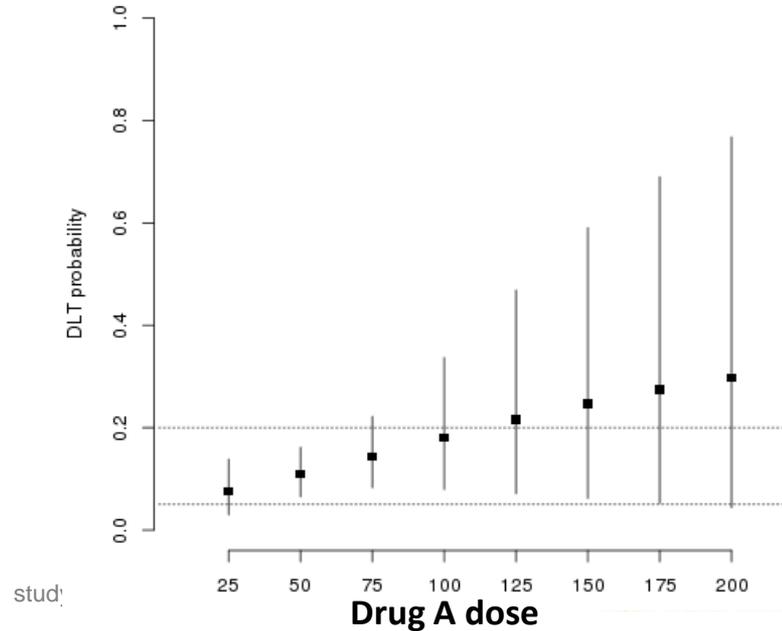
Combination 4/25

	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	25	0
	# DLT		2	6	6	
Comb	# Patients	25	50	50	0	0
	# DLT	1	5	7		

Monotherapy



Combination

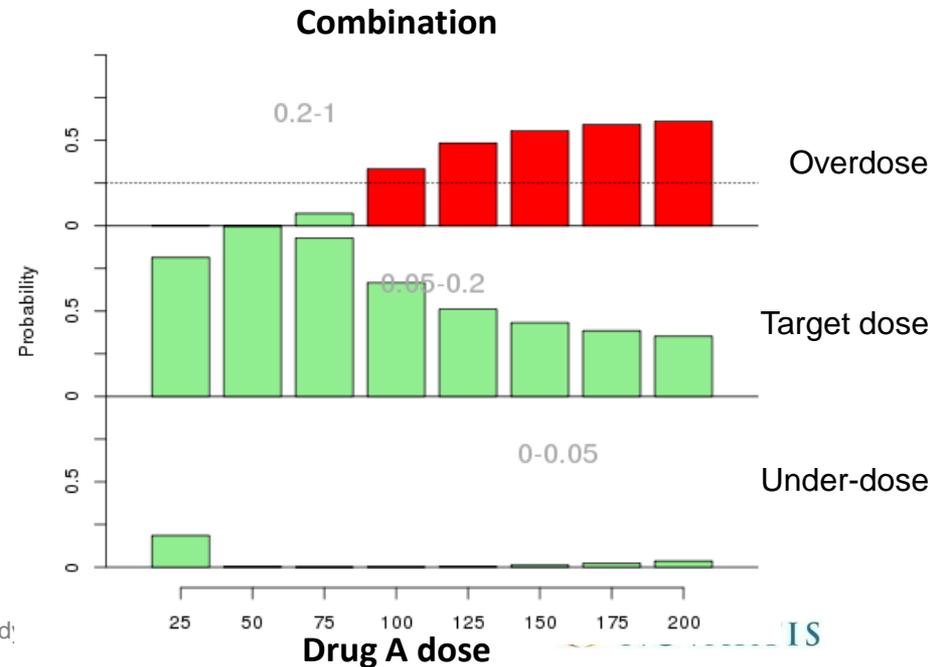
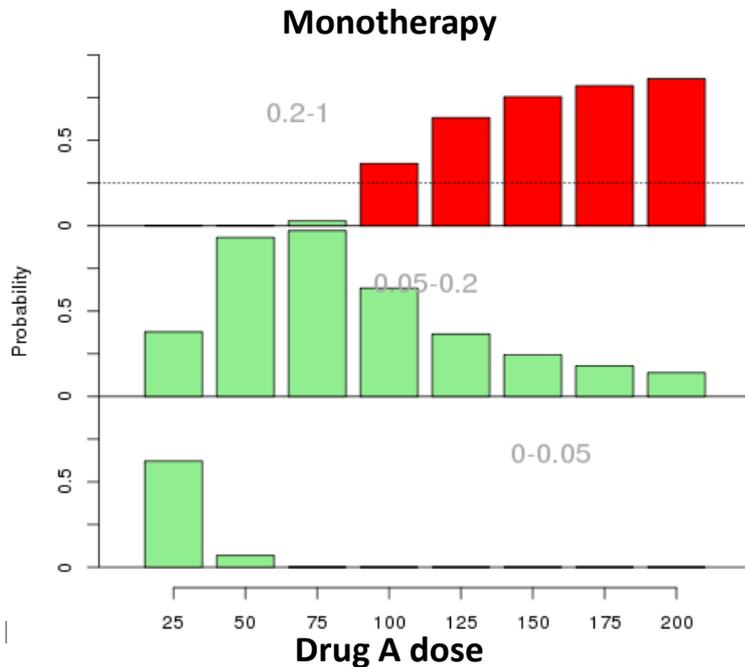


Cohort 5

Combination 4/25

Combination MTD established = 50mg (75mg could also be chosen)

	Dose	25	50	75	100	125
Mono	# Patients	0	25	50	25	0
	# DLT			2	6	6
Comb	# Patients	25	50	50	0	0
	# DLT	1	5	7		



Design evaluation

Simulating study operating characteristics

- A simulation plan was written in collaboration with the clinical team
- Key simulation parameters
 - Cohort size: 10, 20, 25, 30
 - Minimum number of patients enrolled: three cohorts
 - Maximum number of patients enrolled: eight cohorts
 - Minimum enrolled at the MTD combination: two cohorts
- Dose-toxicity scenarios:
 - Mild: 75 borderline under / 100 target / 125 over
 - Moderate 1: 75 target / 50 borderline under / 100 over
 - Moderate 2: 75 borderline over / 50 target
 - Toxic: 50 borderline over / 25 target

Design evaluation

Simulating study operating characteristics

- Metrics for evaluation:
 - Proportion of patients receiving target dose, overdose, and under dose
 - Probability of recommending a target dose, overdose, or an under dose as the MTD
 - Expected total sample size
- Simulations done with an internally developed library (R & JAGS)
- High-performance computing cluster for fast execution
- For simplicity, each arm (mono/comb) was simulated separately
 - Simulated OCs are thus likely “conservative” as the real trial will use information from both arms at each IA
- For each simulation configuration:
 - Summary of metrics – high-level check of OC and suitable for protocol
 - Detailed diagnostic plots – essential for fine-tuning of design parameters

Simulation output

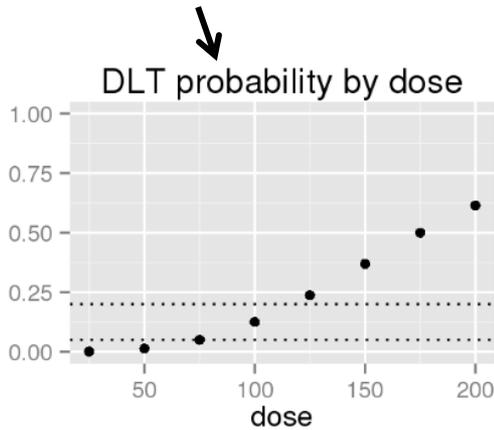
High-level summary table

```
## [1] mild
## Levels: mild
## Metric I : 57.83 - Average proportion of patients in target dose region ( $\geq 5\%$  -  $20\%$ )
## Metric II : 25.14 - Average proportion of patients in over dose region ( $\geq 20\%$ )
## Metric III : 17.03 - Average proportion of patients in under dose region ( $< 5\%$ )
## Metric IV : 81.40 - Proportion of trials with MTD in target dose region ( $\geq 5\%$  -  $20\%$ )
## Metric V : 13.70 - Proportion of trials with MTD in over dose region ( $\geq 20\%$ )
## Metric VI : 0.40 - Proportion of trials with MTD in under dose region ( $< 5\%$ )
## Stopped : 4.50
##
## Average N : 148.45
## Average DLT: 18.20
```

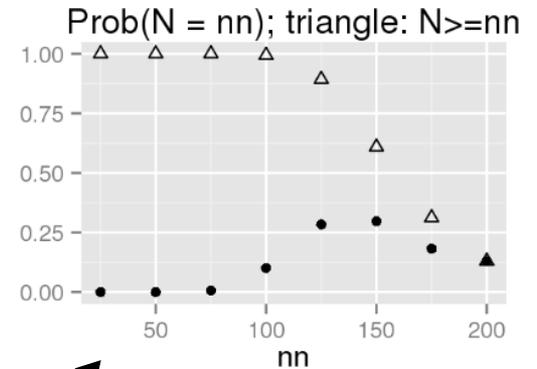
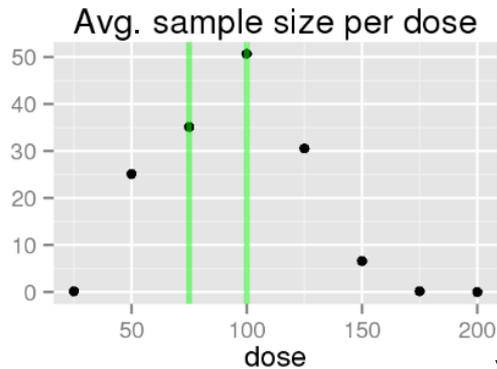
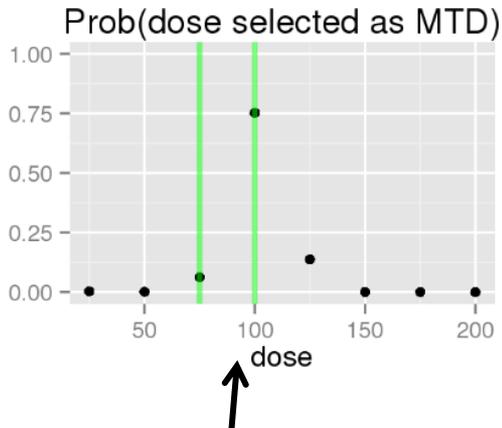
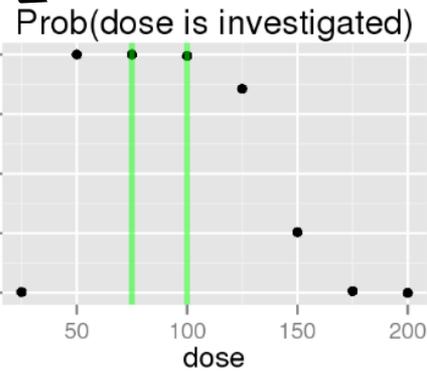
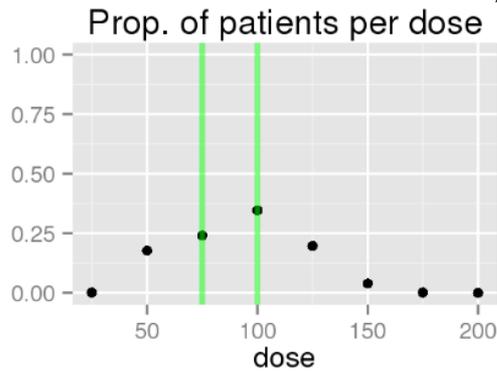
Simulation output

Detailed diagnostic plots

Reasonable doses?



How often is each dose investigated?



Reasonable selections?

How many patients (per dose/overall)?

Discussion

- Historically, dose finding in malaria has been limited
 - Desirable to administer doses as high as possible (efficacy, resistance)
 - Ethically questionable to treat with doses expected to be subtherapeutic
- Dose finding program tailored to estimate the upper limit for dosing
- Methodology for Bayesian phase 1 oncology trials translates naturally to our setting
- Necessary (though perhaps not sufficient) ingredients
 - Open-minded clinical team
 - Frequent discussions with study team – favor visualizations over statistical jargon
 - Hypothetical examples of dose-escalation recommendations
 - Of course...
 - Familiarity with Bayesian statistics
 - Effort/willingness to conduct fairly large-scale simulations to evaluate the design

References & acknowledgements

■ Selected references:

- Neuenschwander B, Matano A, Tang Z, Wandel S, Roychoudhury S, Bailey S. A Bayesian Industry Approach to Phase I Combination Trials in Oncology. In: *Statistical Methods in Drug Combination Studies*, Boca Raton, FL: Chapman & Hall/CRC Press. Edited by Zhao, W. and Yang, H. 2015
- Neuenschwander B, Capkun-Niggli G, Branson M, Spiegelhalter DJ. Summarizing historical information on controls in clinical trials. *Clin Trials* 2010
- Schmidli H, Gsteiger S, Roychoudhury S, O'Hagan A, Spiegelhalter DJ, Neuenschwander B. Robust meta-analytic-predictive priors in clinical trials with historical control information. *Biometrics* 2014

■ Acknowledgments:

- Novartis malaria clinical team
- Simon Wandel and Sebastian Weber (Novartis oncology)

Thank you!

Questions?