

# Adaptive Trial Designs for Public and Global Health

Vaccine and Cluster Randomized Trials go Bayesian

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# Background

# **Global and Public Health Trial Characteristics**

#### > Typically large

- > Are run for a long time
- > Multi-center, logistically challenging
- > Are funded by the taxpayer or nonprofits
- > Potentially high impact
- > Could benefit greatly from saving time and resources



#### **Bayesian Adaptive Trial Designs**

> Are simulation-guided, and are therefore flexible – but also computer-intensive.

Consists of multiple arms and multiple stages with early arm-stopping options.

> The decision boundaries are set for the *posterior probability of efficacy* 

 $p_i^{ ext{effic}} = \mathbb{P}\left( ext{Treatment} \ i \ ext{is efficacious} | ext{data}
ight)$ 

for trials testing treatments against a common control, or the posterior probability of superiority

 $p_i^{ ext{sup}} = \mathbb{P}\left( ext{Treatment} \ i ext{ is the most efficacious} | ext{data} 
ight)$ 

for trials comparing all therapies against each other. These get updated at every interim readout.

Potential gains include earlier EUA application, fewer patients receiving futile treatments, fewer overall patients treated and shorter run times.



# Multi-arm, Multi-stage Vaccine Trials

# **Modelling Assumptions**

> All arms' case counts follow Poisson processes.

> Vaccine effects (VEs) are measured in terms of the rate reduction relative to control.

Once a certain total number of cases has been recorded, data are unblinded and case distribution across groups is analyzed.

Some transformation of the VEs can be shown to follow a multinomial distribution.

> Using a conjugate Dirichlet prior distribution, the posterior distribution is also Dirichlet.



#### The Main Idea

▶ If we define

$$heta_i = rac{q_i(1-\mathrm{VE}_i)}{q_{\mathrm{ctrl}}+\sum_{j=1}^K q_j(1-\mathrm{VE}_j)},$$

where  $q_i$  is the allocation probability of the  $i^{
m th}$  vaccine, and assign m heta a Dirichlet prior, then

$$oldsymbol{ heta}ig|n_1(t),\ldots n_K(t),n_{ ext{ctrl}}(t)$$

will also follow a Dirichlet distribution, where  $n_i(t)$  denotes the number of infections recorded in the  $i^{th}$  vaccine group.

> Inference on the VEs is achievable via the back-tranform

$$ext{VE}_i = 1 - rac{ heta_i}{ heta_ ext{ctrl}} rac{q_ ext{ctrl}}{q_i}$$



#### What We Did

- Seneralized the model used by Pfizer/BioNTech to any number of arms with any allocation ratio.
- Calculated the joint VE distribution and showed that inference can be restricted to paired vaccineplacebo comparisons.
- > Proposed a principled way for choosing a prior distribution.
- $\blacktriangleright$  Derived closed form expressions for all inferential quantities, including  $p^{
  m effic}$  .
- We can now run 100,000 simulations in ~1 minute on a standard PC.



# **Trial Design Example**

> Three vaccine groups and a common control (placebo).

 $\blacktriangleright$  A  $\sqrt{3}$  : 1 : 1 : 1 Dunnett allocation ratio to minimize the average VE uncertainty.

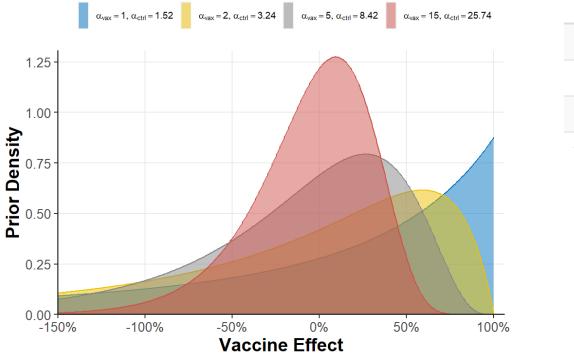
- > We assume VEs of 50%, 37.5% and 25%.
- > Interim analysis take place when an average of 10.5 events are observed across the remaining arms.
- $\blacktriangleright$  Early stopping due to efficacy occurs if  $p^{
  m effic} > 99.025\%$  at any analysis.
- Early stopping due to futility occurs if  $p^{\rm effic} < 25\%$ , 50% or 75% in the first, second or third analysis, respectively.



#### **Prior Selection**

 $\blacktriangleright$  Prior candidates are required to have a prior probability of efficacy of 50%.

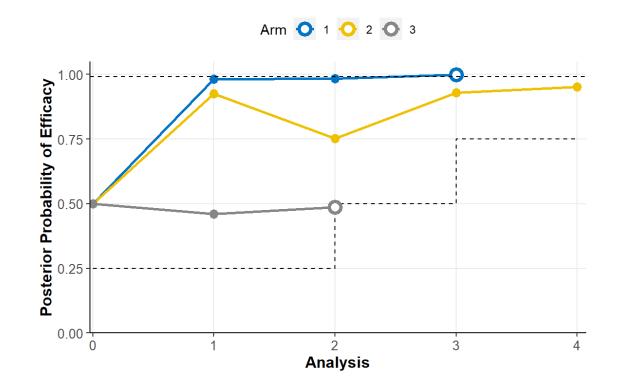
> We compare multiple candidates and use summaries and density plots.



$lpha_{ m vax}$	$lpha_{ m ctrl}$	Mean	Median	95% Crl	
1.00	1.52	-2.33	0.00	[-16.85; 0.97]	
2.00	3.24	-0.55	0.00	[-5.27; 0.88]	
5.00	8.42	-0.17	0.00	[-2.01; 0.70]	
15.00	25.74	-0.05	0.00	[-0.87; 0.49]	



## A Sample Trial



> In this randomly simulated trial, the third vaccine arm was stopped for futility after two analyses

> The first vaccine was found to be efficacious after three analyses.

> The second vaccine arm completed four analyses without meeting the efficacy threshold.

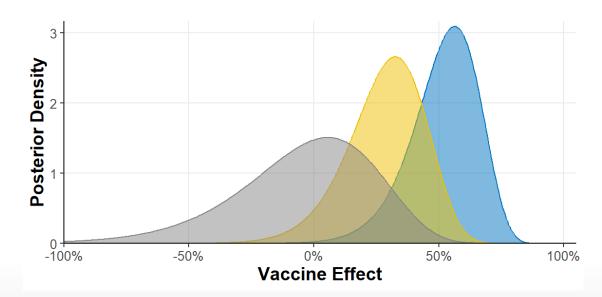


#### **Posterior Inference**

> Point and interval estimation is based on the posterior VE distribution –

Arm	Stopping reason	Analysis 1 cases	Analysis 2 cases	Analysis 3 cases	Analysis 4 cases	Efficacy	Pr(Efficacy Data)	VE [95% Crl]
Control		20	36	57	72			
1	Early efficacy	4	10	15		Yes	99.8%	53.4% [20.7%; 74.2%]
2	End of trial	6	17	23	29	No	95.2%	29.8% [-6.3%; 54.8%]
3	Early futility	12	21			No	48.6%	-0.9% [-69.7%; 41.4%]

Arm 1 Arm 2 Arm 3





#### **Operating Characteristics (100k simulations)**

Arm	VE	Power	$\mathbb{P}(\mathrm{Stop}=1)$	$\mathbb{P}(\mathrm{Stop} \leq 2)$	$\mathbb{P}(\mathrm{Stop} \leq 3)$	
All	0%	2.5%	23.9%	53.2%	79.0%	
1	50%	81.3%	17.8%	43.1%	70.9%	
2	37.5%	50.1%	10.8%	25.9%	50.4%	
3	25%	22.8%	10.3%	24.1%	48.2%	

 $\blacktriangleright$  Trial inputs were calibrated for a 2.5% type I error rate and  $\ge 80\%$  power for a vaccine with 50% VE.

> A high probability of early stopping – but not necessarily fewer doses administered.



#### Adaptive Cluster Randomized Trials

# Some CRT Background

- > Trials in which the cluster (e.g., a village) is the randomization unit.
- > As an example: laying attractive toxic sugar baits outside the village to reduce malaria infections.
- > Induces two variance components: subject-to-subject and cluster-to-cluster.
- > The variance inflation is governed by the cluster size and the *intrucluster correlation coefficient* (ICC).
- > A large ICC or cluster size can significantly inflate the sample size.



#### What We Did

- > Proposed the Poisson-Gamma mixture model for CRTs with binary endpoints.
- Showed that some transformation of the mean event rates has conjugate beta prior distributions.
- > Established the mathematical relation between the Gamma random effect parameters and the ICC.
- > Proposed a principled way for choosing prior distributions.
- > Derived the empirical Bayes plug-in estimators for the Gamma shape parameters.
- We can now run 100,000 simulations in ~10 minutes on a standard PC.



# **Modelling Assumptions**

 $\blacktriangleright$  For reasonably large clusters of size  $n_i$ , and a fairly low event rate  $r_i$ , we can model

 $Y_{ij}ig|r_{ij}\sim ext{Poisson}\left(n_ir_{ij}
ight)$ 

the number of cases observed in the  $j^{
m th}$  cluster or the  $i^{
m th}$  arm.

> To capture cluster-to-cluster variability, we model

$$r_{ij}ig|\mu_i,\phi_i\sim \mathrm{Gamma}\left(\phi_i,\mu_i/\phi_i
ight),$$

where  $\mu_i$  is now the mean event rate and  $\phi_i$  a shape parameter.

> The marginal case number distribution can be shown to be negative binomial with

$$p_i = rac{\mu_i n_i}{\phi_i + \mu_i n_i},$$

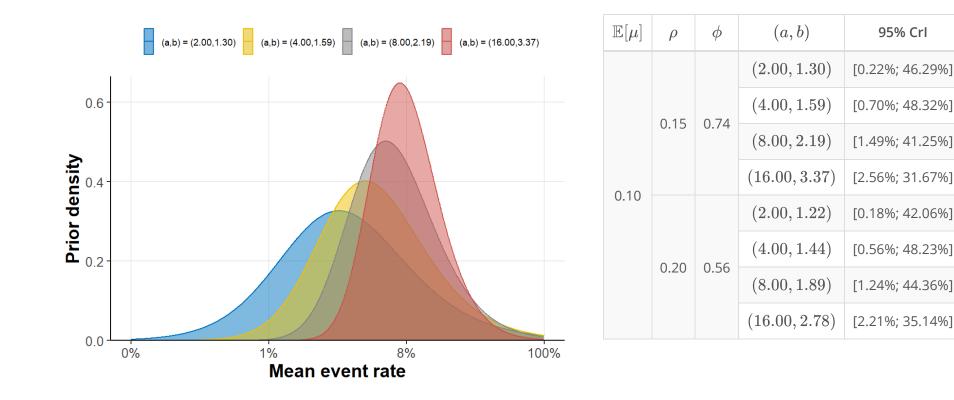
and has a conjugate Beta prior.



#### **Prior Selection**

> All priors are subject to satisfying a pre-specified a priori mean event rate (in this case 10%), assuming an ICC (here 0.15 and 0.2).

 $\blacktriangleright$  We then compare them by their summaries.





# Adaptive Design Example

Suppose that we wish to trial three treatments

 $\blacktriangleright$  Assuming mean event rates of 10%, 7.5% and 5%

 $\blacktriangleright$  A maximum number of 550 clusters divided into three analyses

 $\blacktriangleright$  Average cluster size of 50,

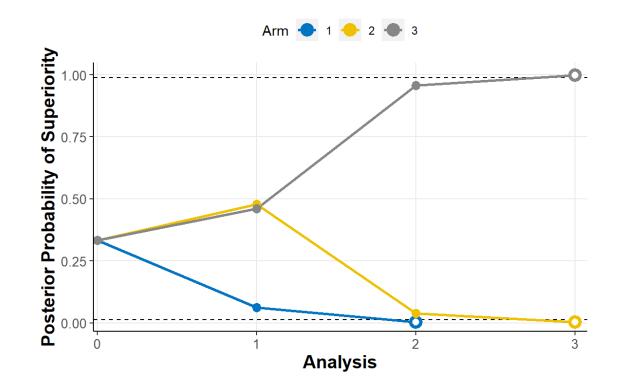
ightarrow An arm gets stopped for futility if  $p^{
m sup} \leq 1.2\%$ 

ightarrow The trial gets stopped if any arm achieves  $p^{
m sup} > 98.8\%$ 

 $\blacktriangleright$  We simulate the data with an ICC of 0.15



## A Sample Trial



> Here first arm was dropped after the second analysis for futility.

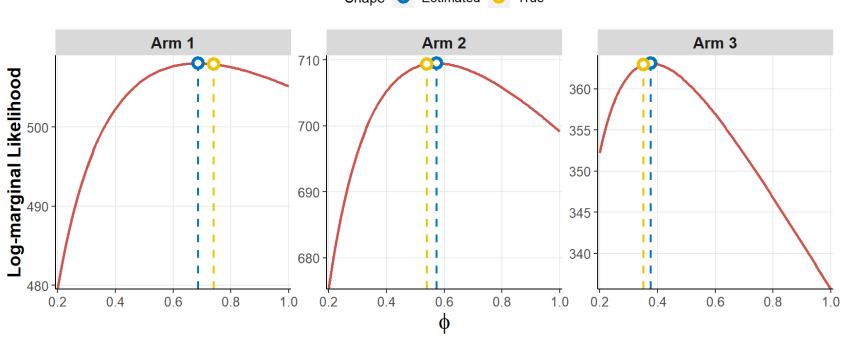
> The third treatment was found to be the superior of the three after the third analysis.

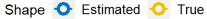


# Shape Parameter Estimation via Empirical Bayes

 $\blacktriangleright$  The negative binomial model is conditional on knowing the values of the shape parameters  $\phi_i$ .

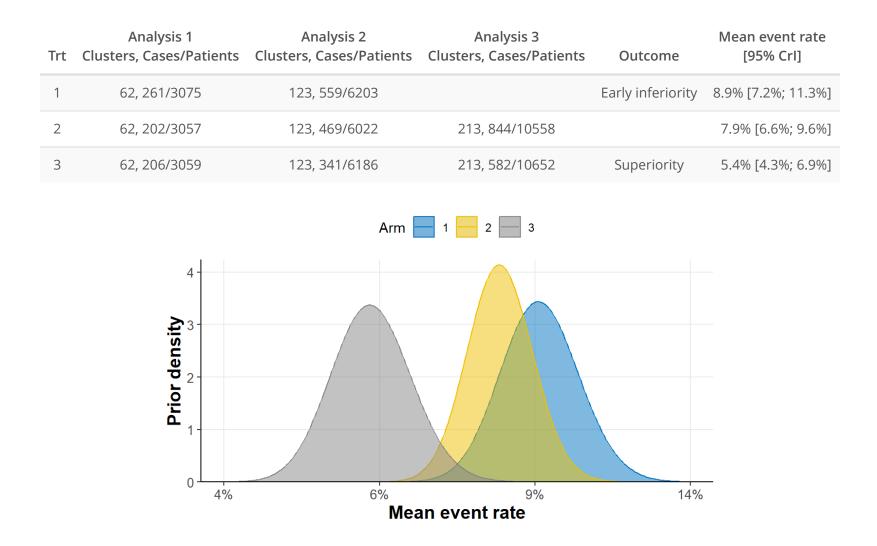
> As plug-in estimates, we propose maximizing the log-marginal likelihood components.







#### **Posterior Estimation and Inference**





### **Operating Characteristics (100K Simulations)**

Mean event rates	Mean no. of clusters	% of patients in Arm 1	% of patients in Arm 2	% of patients in Arm 3	True positive rate	False positive rate
(10.0%, 7.5%, 5.0%)	412.1	20.9%	38.8%	40.3%	80.6%	0.0%
(10.0%, 10.0%, 10.0%)	545.7	33.3%	33.3%	33.3%	-	2.0%
(10.0%, 5.0%, 5.0%)	532.0	13.0%	43.5%	43.5%	_	9.7%

> Note that the "null hypothesis" here includes every scenario where there is no clear-cut winner.

- > "False positives" include detection of one of two equally effective treatments.
- > For a "true positive", we must not only detect difference but also declare the correct winner.
- > In a standard trial, the 1-2 comparison alone at the 5% level (one-sided) would require 528 clusters.
- > Also note the proportion of patients receiving the worst treatment.



# **Concluding Remarks**

#### Famous Last Words

Global health trials could use every bit of efficiency.

> Adaptive trial designs provide just that – but require many simulation runs.

> We propose innovative, MCMC-free, Bayesian vaccine and cluster randomized trial designs.

> Response adaptive randomization (RAR) is unlikely to be applicable here.

> Consider time to outcome and enrollment rate: could your trial benefit from adaptations?

> Possible extensions: time-varying VE; stepped-wedge CRTs.

> Ask us for the preprint!

# Thank you!



# Bibliography

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