

# Adaptive Designs in Clinical Trials

Thevaa Chandereng

Biostatistics & Medical Informatics  
University of Wisconsin–Madison

`thevaachandereng.github.io`  
`github.com/thevaachandereng`

# Overview

Adaptive Process

Introduction to RAR

BATTLE-1 Trial

Other Issues with RAR

Blocked RAR

Incorporation of Historical Data

bayesCT

Future Work

# Adaptive Designs in Clinical Trials

FDA

Adaptive Design Clinical Trials for Drugs and Biologics  
Guidance for Industry, November 2019

# Adaptive Designs in Clinical Trials

## FDA

Adaptive Design Clinical Trials for Drugs and Biologics  
Guidance for Industry, November 2019

“An adaptive design is defined as a clinical trial design that allows for **prospectively planned modifications** to one or more aspects of the design based on accumulating data from subjects in the trial. ”

# Adaption on-the-fly

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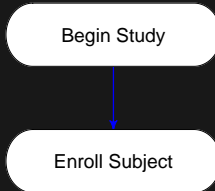
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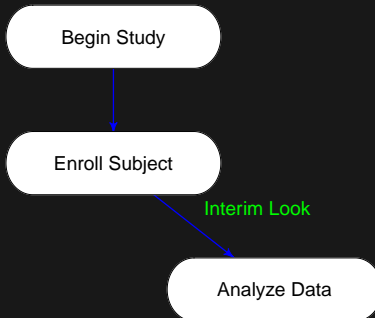
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- ▶ Dynamically incorporate historical data.

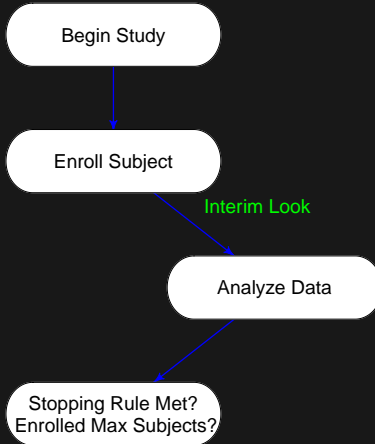
# Adaptive Process



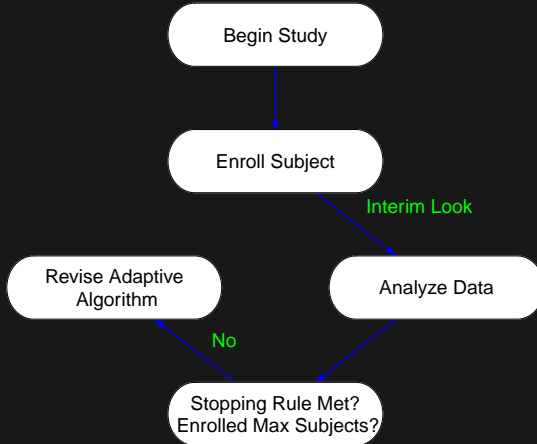
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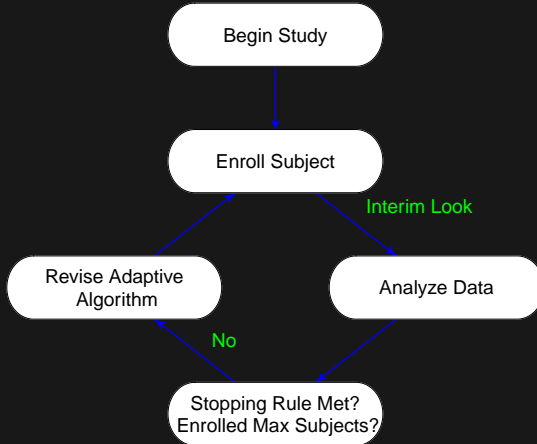
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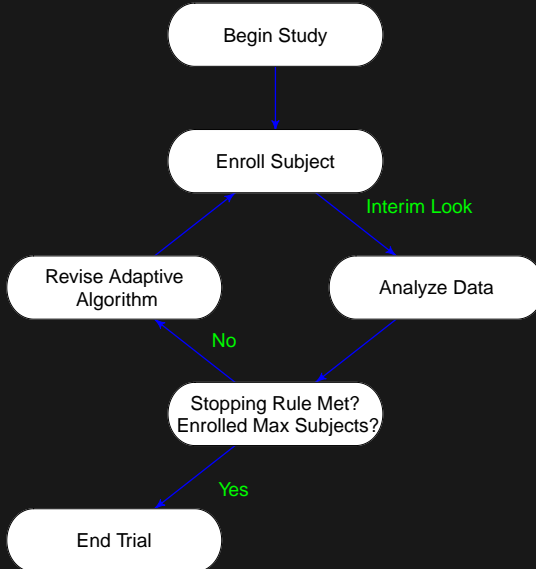
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# What is a Response Adaptive Randomization (RAR) Design?

- ▶ RAR designs utilize accumulating information on outcomes as the trial progresses in order to alter the treatment assignment probabilities and assign more patients to the better-performing treatment arm.
- ▶ Previous outcomes are used to tilt the randomization probabilities in favor of the treatment currently observed to have superior results.

# What is a Response Adaptive Randomization (RAR) Design?

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- ▶ Previous outcomes are used to tilt the randomization probabilities in favor of the treatment currently observed to have superior results.
- ▶ The trial needs to be short to be able to obtain the outcome of the trial for future randomization

# Objective of Trials

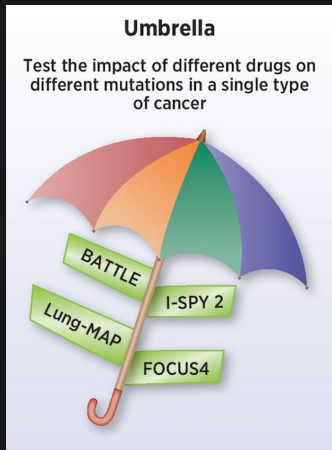
- ▶ maximize power to detect clinically relevant difference;
- ▶ minimize total cost of the trial;
- ▶ minimize the number of failures;
- ▶ control type I error under nominal level;
- ▶ maximize the individual's experience in the trial

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- ▶ maximize the individual's experience in the trial
- ▶ maximize the probability to provide the best treatment

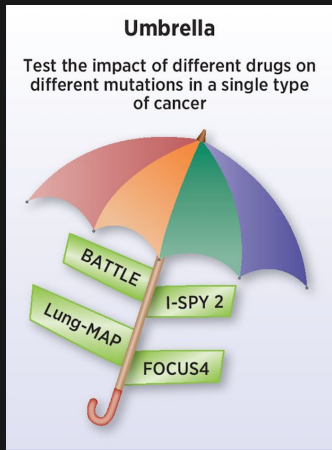
# BATTLE-1 Trial

## Biomarker-integrated Approaches of Targeted Therapy for Lung Cancer Elimination (BATTLE - 1)



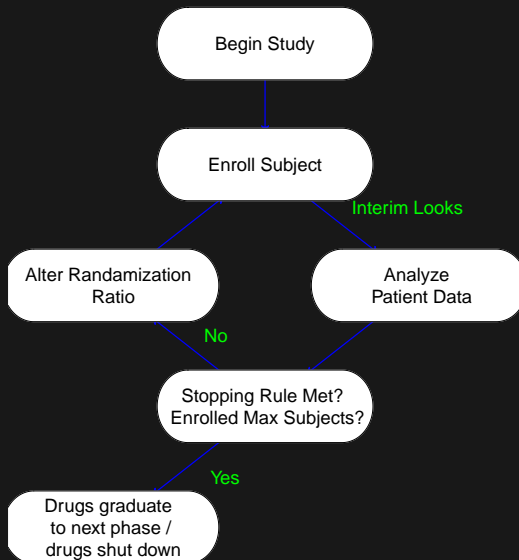
# BATTLE-1 Trial

## Biomarker-integrated Approaches of Targeted Therapy for Lung Cancer Elimination (BATTLE - 1)



- ▶ 4 treatments, 5 biomarker;
- ▶ primary end point, 8-week disease control rate;
- ▶ treat more patients in promising groups based on biomarker profile;
- ▶ suspend ineffective groups early

# Design of BATTLE-1 Trial



- ▶ 1st interim look: at least one patient in each treatment and biomarker groups
- ▶ All subsequent interim looks: patient by patient

# BATTLE-1 Trial



# BATTLE-1 Trial

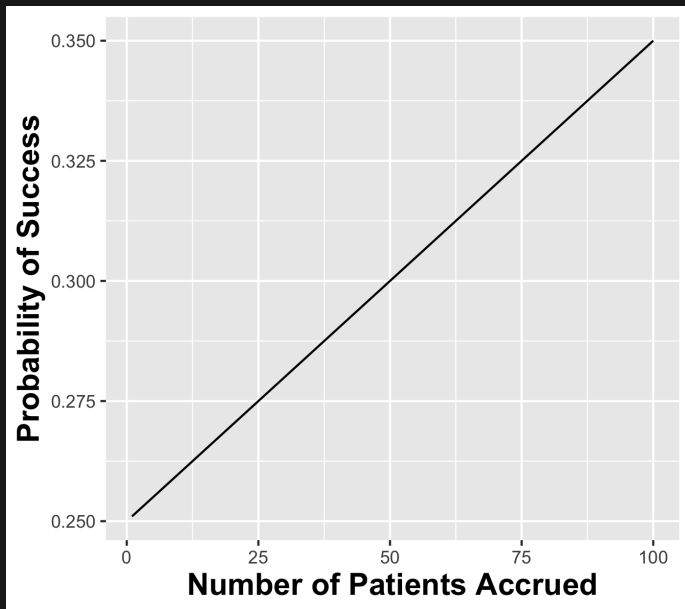
“More smokers enrolled in the latter part of the study compared to the beginning of the study”.

# BATTLE-1 Trial

“More smokers enrolled in the latter part of the study compared to the beginning of the study”.

Time trends are nearly universally ignored among RAR proponents.

# Time-trends in RAR



# Time-trends in Clinical Trials

- ▶ Thall et al. (2015) investigated type-I error under a **linear time-trend induced** in the traditional response-adaptive randomization design and showed that the type-I error is significantly above the nominal level.
- ▶ Chappell (2011) used an artificial example to illustrate changes in proportion of success over time in a binomial trial draws a wrong conclusion.

# Issues with RAR

Common problems with RAR methods that are proposed (besides time-trends):

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- ▶ Thall et al. (2015): “... AR may behave pathologically in that it carries a nontrivial risk of creating a large sample size imbalance in favor of the inferior treatment”.
- ▶ Poor/extreme schemes to alter the allocation ratios.

# Blocked Design for RAR

Karrison et al. (2003) introduced a stratified group-sequential method for RAR.



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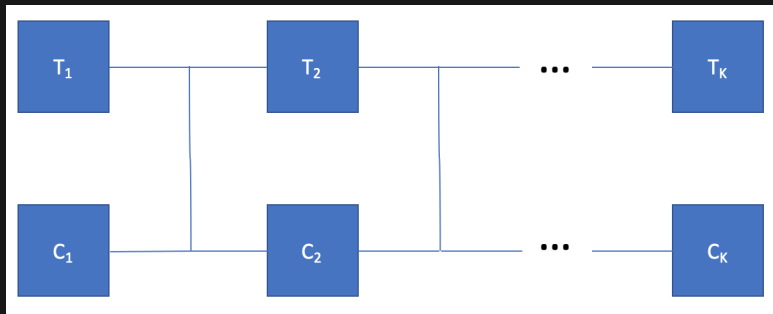
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But never expanded it on the characteristics of blocked RAR!

What is the optimal block size?

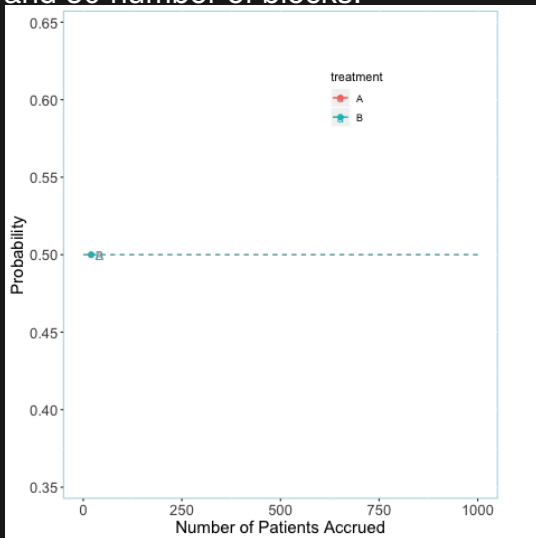
# Blocked Design for RAR

- ▶ Group-sequential procedure.
- ▶ Update allocation ratio for groups rather than patients.



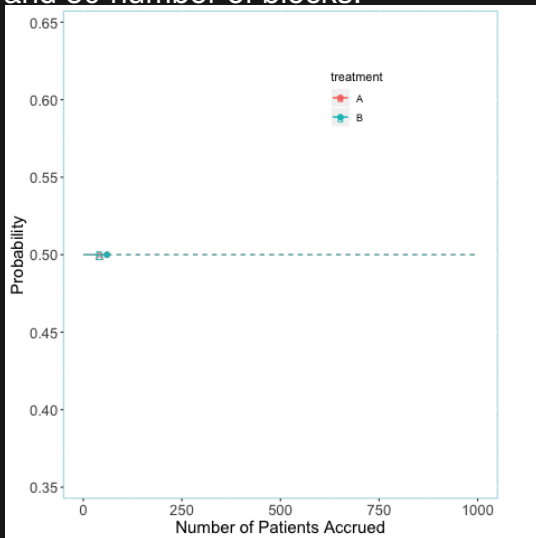
# Example RAR

A single simulation for RAR with  $p_A = 0.07$ ,  $p_B = 0.05$  with N of 1000 and 50 number of blocks.



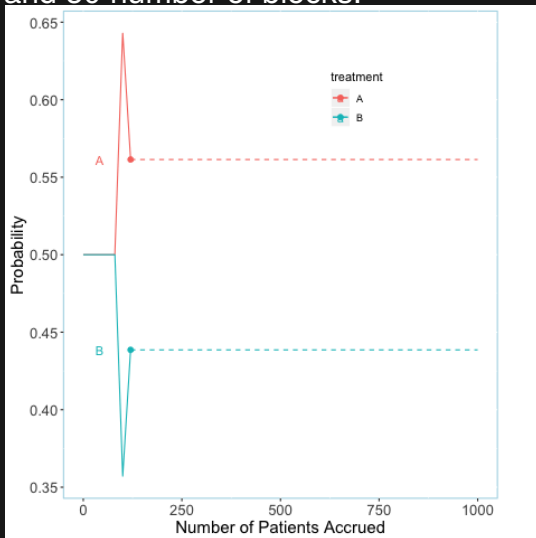
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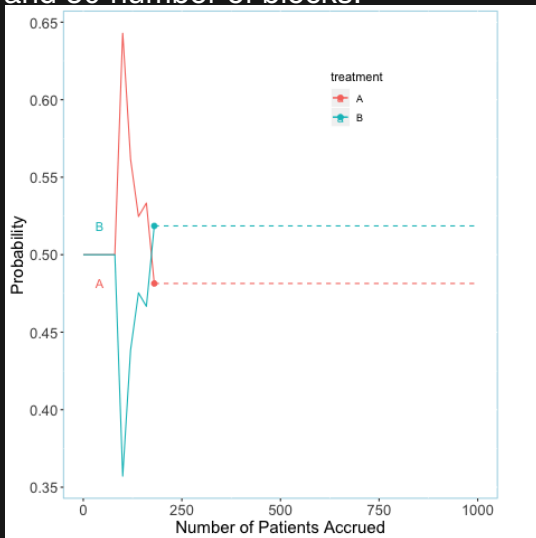
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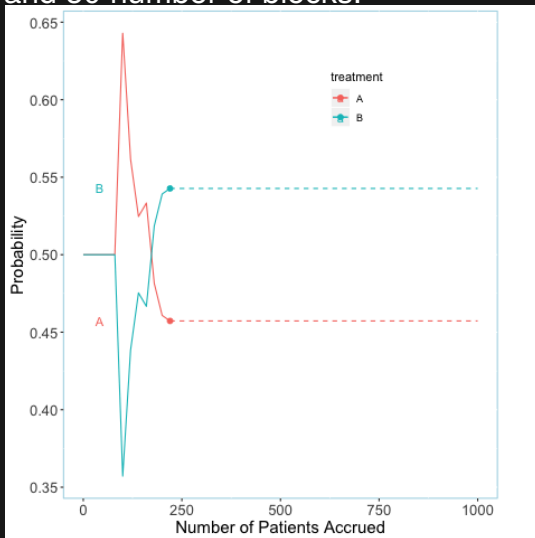
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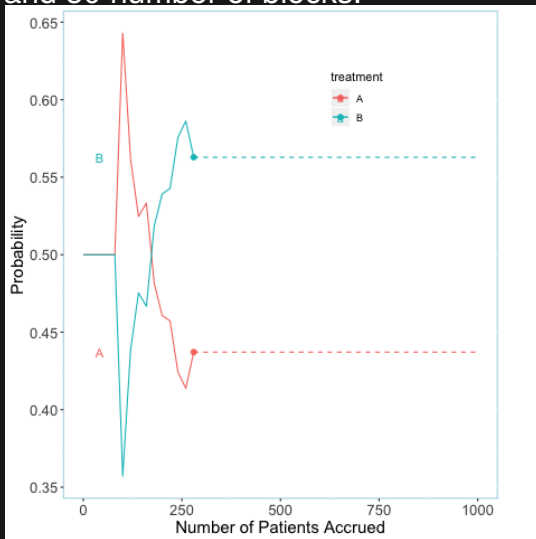
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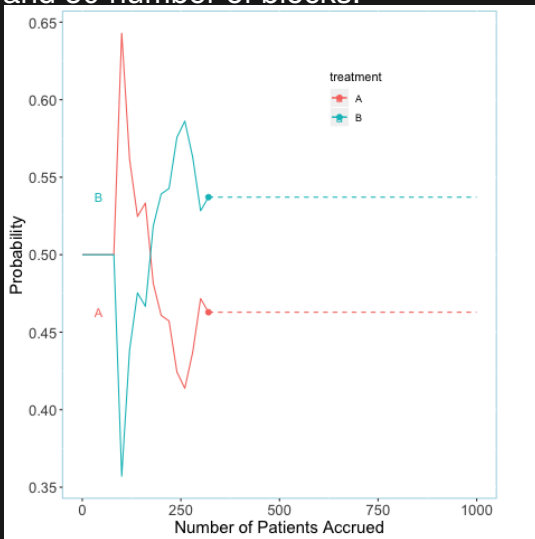
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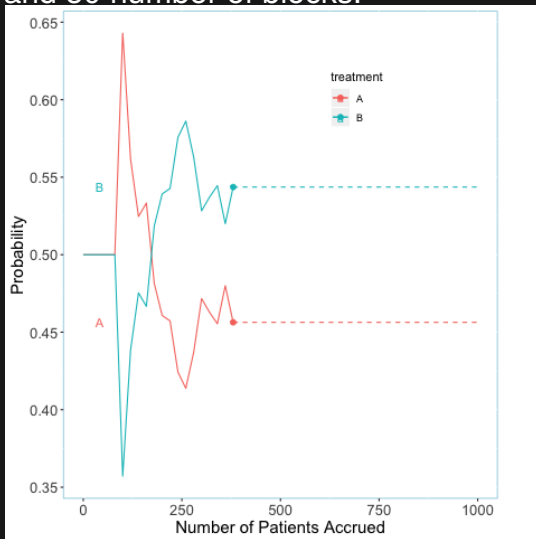
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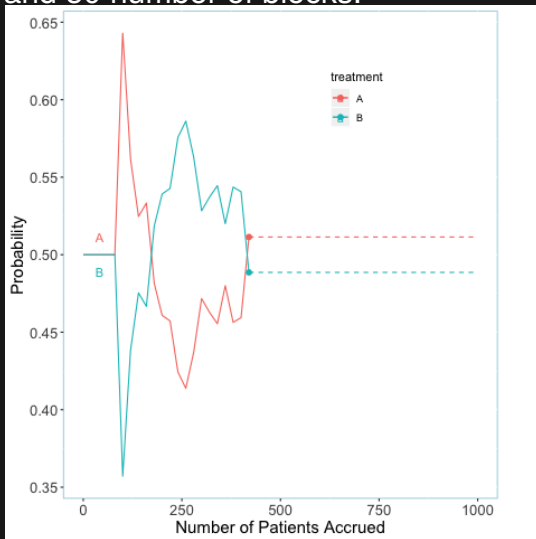
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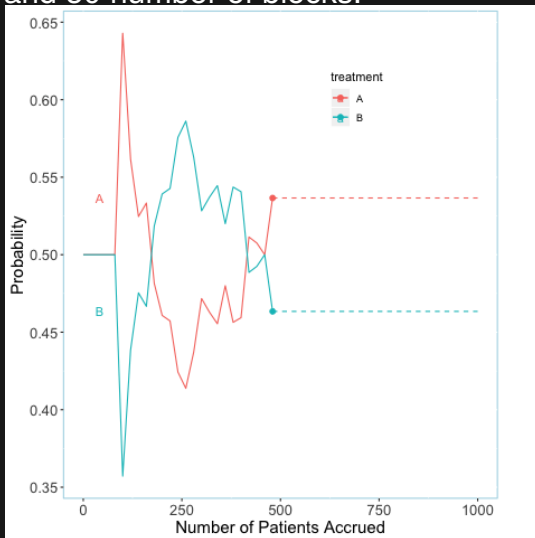
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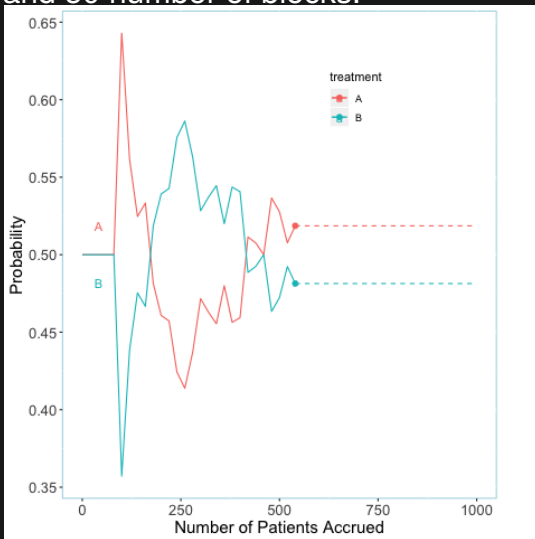
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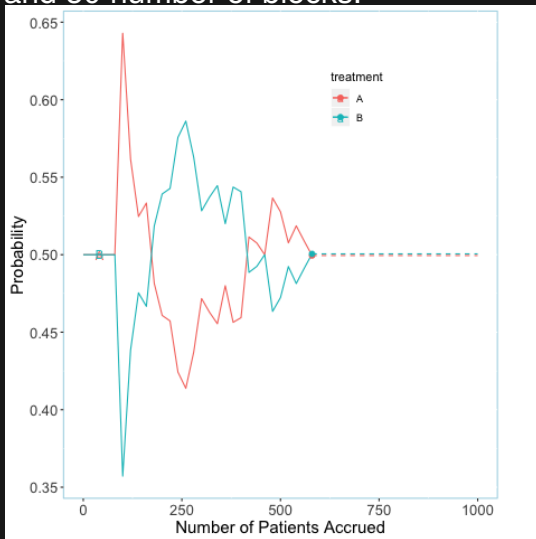
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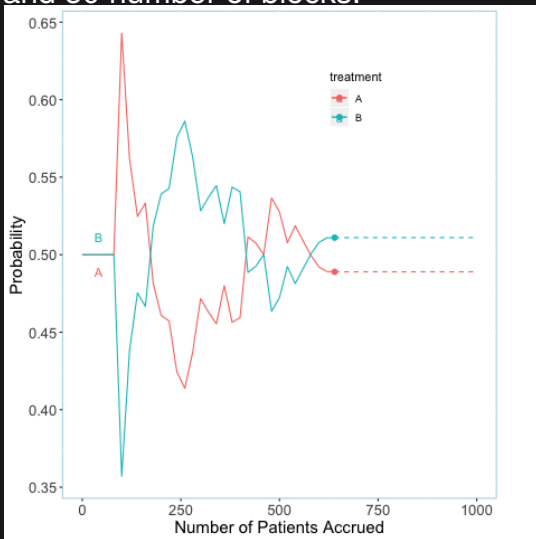
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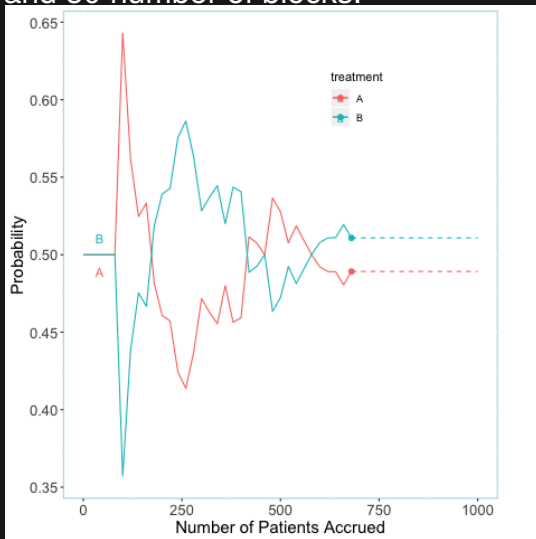
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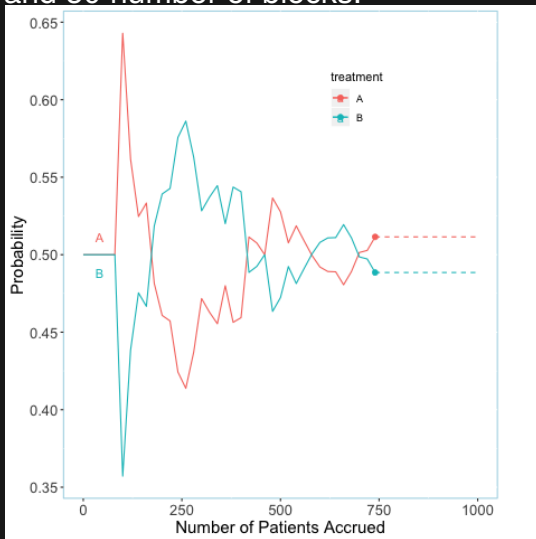
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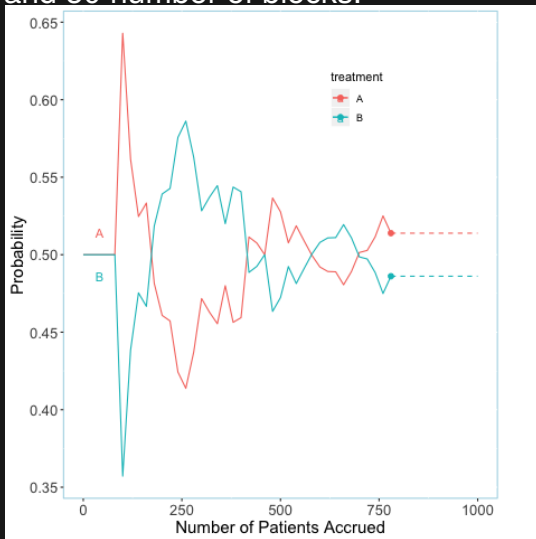
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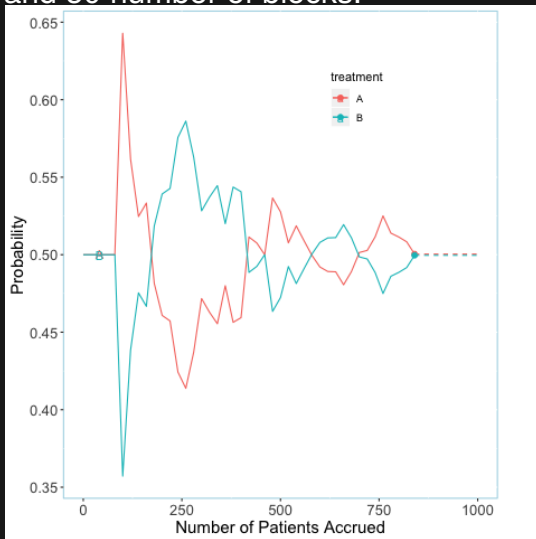
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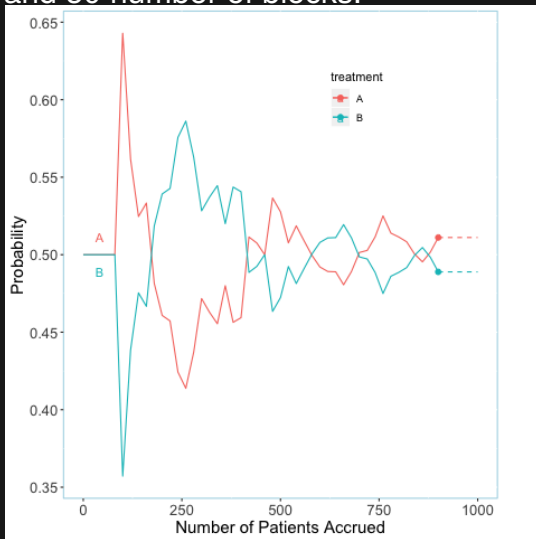
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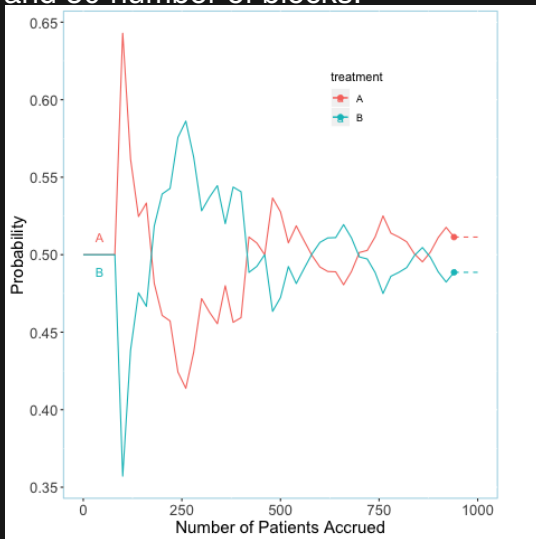
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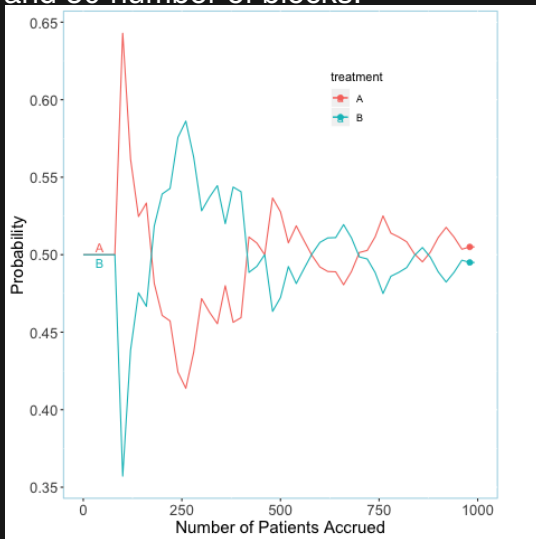
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# Discussion

- ▶ Blocks with a large number of patients also help reduce the large probability of imbalance in the wrong direction, where more patients are assigned to the inferior treatment compared to traditional RAR.
- ▶ Blocks with fewer patients can reduce the power of the trial because if patients are not randomized to both treatments in a block, the block becomes uninformative.
- ▶ Small number of blocks ( $K = 2, 4$  and  $5$ ) has a good tradeoff between efficiency and ethically treating patients to the best known superior treatment.



# Discussion

- ▶ Large number of blocks should be clearly avoided for both ethical reason and poor design.
- ▶ Statisticians need to be careful with issues of time-trend and methods to alter the randomization ratio.
- ▶ Time-trend can significantly impact the type-I error rate.
- ▶ R package **blockRAR**

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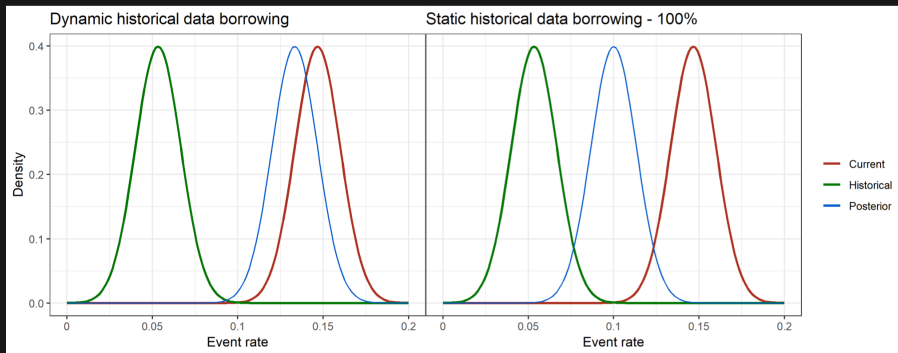
Bound the probability of allocation.

# Historical Data

Historical data from previous studies can be used to lesson sample size, reducing time and expense, as well as decreasing or eliminating patient exposure to sub-par treatments.

- ▶ Previous clinical trials, especially historical control data. Need to ensure same “standard treatment” and inclusion criteria. Published data/reports.
- ▶ Note: historical data already used to determine clinically relevant effect size, guide sample size determination, recruitment rates, etc.
- ▶ Electronic health records

# Historical Borrowing



# Binomial Outcome Example

## Single-arm binomial count endpoint with incorporation of historical data

Similar event rates between current and historical data

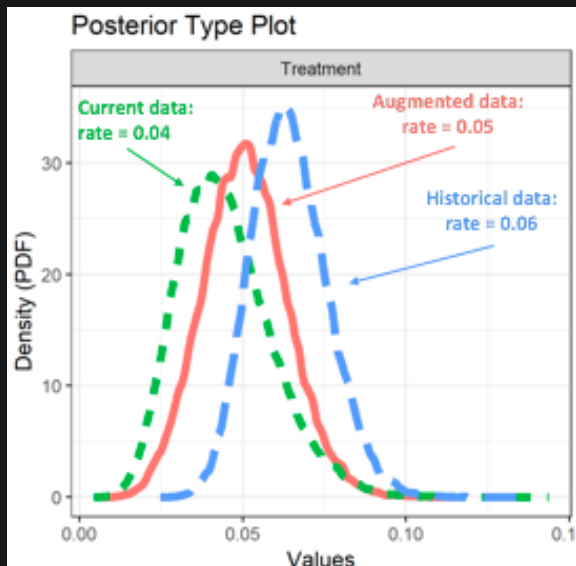
1) Historical data: 28 events in 450 patients

2) Current data: 8 events in 200 patients

- Carry out estimation via bayesDP:

```
library(bayesDP)
# Estimate model via bayesDP using defaults
fit <- bdpbinomial(y_t = 8, N_t = 200,
                  y0_t = 28, N0_t = 450)
```

# Binomial Outcome Example





# bayesCT R Package

**bayesCT R package available:**

**<https://thevaachandereng.github.io/bayesCT/>**

- ▶ CRAN release 0.99.2

## **Analysis types**

- ▶ Single-arm: objective performance criteria trials, treatment data only
- ▶ Two-arm: treatment + control data

## **Function**

- ▶ Incorporation of historical data
- ▶ Allow early stopping for futility and expected success
- ▶ Pipes for modular input & parallelization for fast computing

# Binomial Trial: Single Arm

## Attain Stability Quad Study

$$H_0 : \pi_{treatment} \geq 0.08 \quad H_A : \pi_{treatment} < 0.08$$

- ▶ Lead related complications at 50 days post-implant
- ▶ Enrollment piecewise poisson functions
- ▶ Historical data with 5 failures in 55 samples
- ▶ *Beta*(0.5, 0.5) prior

# Input Parameter

```
value <- binomial_outcome(p_treatment = 0.08) %>%  
  enrollment_rate(lambda = c(0.3, 1),  
                  time   = 25) %>%  
  study_details(total_sample_size   = 900,  
                study_period       = 50,  
                interim_look        = c(600, 700, 800),  
                prop_loss_to_followup = 0.10) %>%  
  hypothesis(delta          = -0.03,  
             futility_prob  = 0.05,  
             prob_accept_ha = 0.95,  
             expected_success_prob = 0.90,  
             alternative     = "less") %>%
```

# Input Parameter: Continued

```
impute(no_of_impute = 1000,  
       number_mcmc = 10000) %>%  
beta_prior(a0 = 0.5,  
          b0 = 0.5) %>%  
historical_binomial(y0_treatment = 5,  
                   N0_treatment = 55,  
                   discount_function = "identity",  
                   y0_control = NULL,  
                   N0_control = NULL,  
                   alpha_max = 1,  
                   fix_alpha = FALSE,  
                   weibull_scale = 0.135,  
                   weibull_shape = 3) %>%  
simulate(no_of_sim = 10000)
```

# Results

Number of Interim Looks	Power = 0.80	Power = 0.90
1	(160, 210)	(280, 300)
2	(160, 190, 220)	(280, 300, 310)
3	(160, 180, 210, 230)	(280, 300, 310, 320)

**Table:** Estimated cumulative sample size vectors that provide 80% and 90% power for binomial trial from the example and prior of Beta(0.5, 0.5)

# bayesCT R Package

## Benefits:

- ▶ ease of developing an entire adaptive trial using this package.
- ▶ functions are simple to understand for regulatory agency (FDA).
- ▶ employable for trials with most common data types.
- ▶ ability for a smaller company with a single statistician to be able to develop an entire adaptive clinical trial code.
- ▶ universal language used for describing Bayesian adaptive trials.
- ▶ working on regulatory agency approval!

# Future Work

Regulatory agencies (FDA) tend to evaluate proposals for adaptive designs with great scrutiny.

- ▶ limited exposure with adaptive designs.
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- ▶ concern on the ability of adaptive designs to control type I error.

However, adaptive trials can speed up the drug discovery process rapidly.



# Future Work in RAR

My future work in RAR will include

- ▶ Study multiple treatments rather than 2 treatments.
- ▶ Continuous outcomes.

# Future Work

My future research work will include

- ▶ developing new adaptive designs that alter the inclusion criteria of patients (adaptive enrichment designs).
- ▶ developing phase II-III seamless designs.
- ▶ creating high-quality open-source computational tools in adaptive designs.

# Acknowledgement

- ▶ Rick Chappell (UW-Madison)
- ▶ David DeMets (UW-Madison)
- ▶ Thomas Cook (UW-Madison)
- ▶ Kyungmann Kim (UW-Madison)
- ▶ Donald Musgrove (Medtronic Inc.)
- ▶ Tarek Haddad (Medtronic Inc.)
- ▶ Peter Thall (MD Anderson)

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**THANK YOU!**