

# Group sequential designs for clinical trials

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# Intro: clinical trials

- Clinical trials
  - studies examining the effects of medical treatments on living beings (usually humans)
  - participants are usually accrued over time
  - ethical considerations



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# Intro: clinical trial jargon

- Endpoint
  - the outcome variable
- Arm
  - treatment group
- Randomization
  - random allocation of participants to arms
- RCT
  - randomized controlled trial

# Intro: fixed-sample designs (FSD)

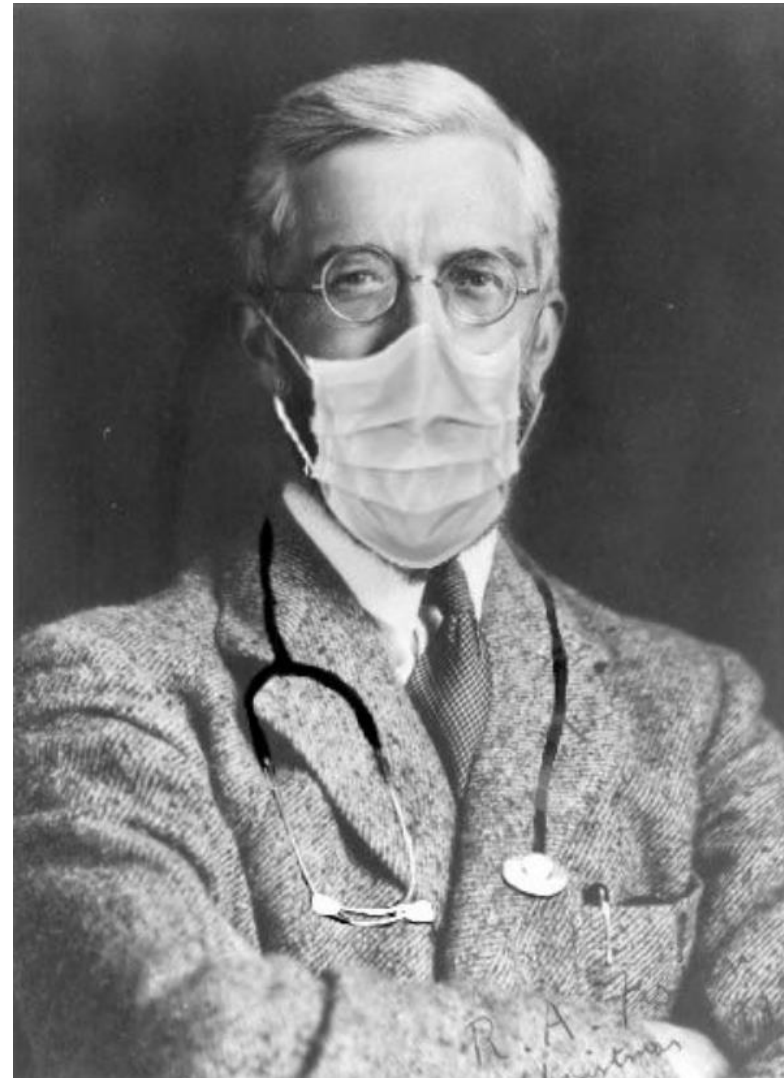
- Predetermined sample size
- No analysis until all data collected





# Intro: group sequential designs (GSD)

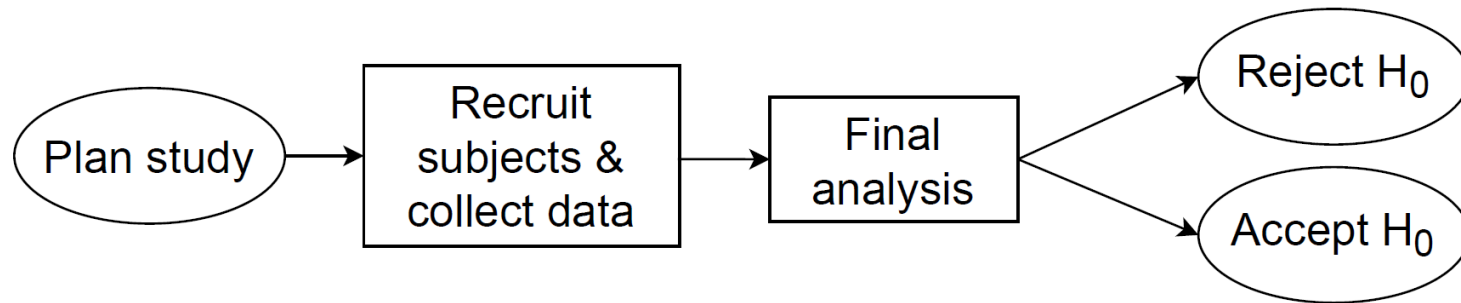
- Analyze data from an ongoing trial
- Early stopping for efficacy or futility
- Sample size depends on the data



# Intro: FSD vs GSD

or: how I learned to stop worrying and accept the null

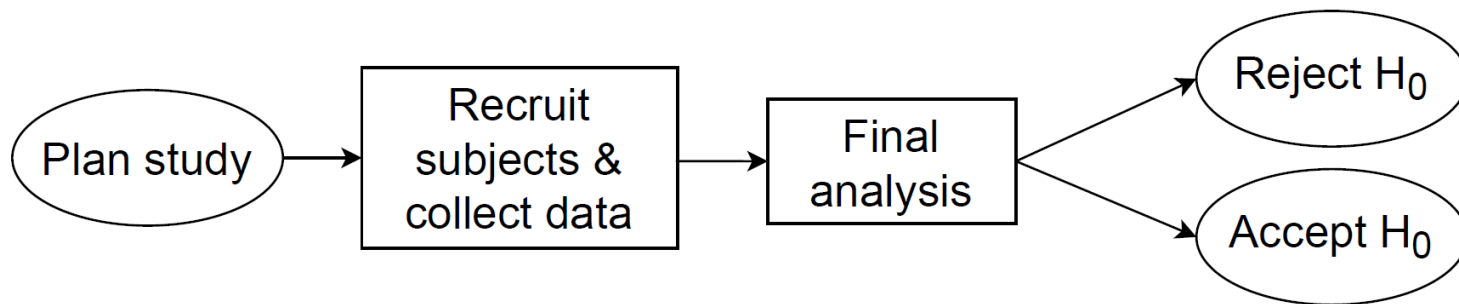
Fixed design



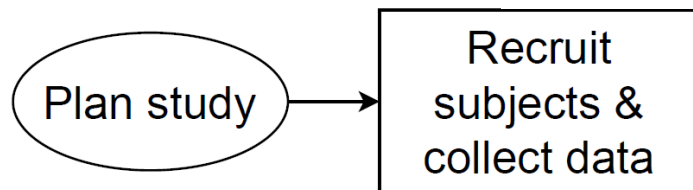
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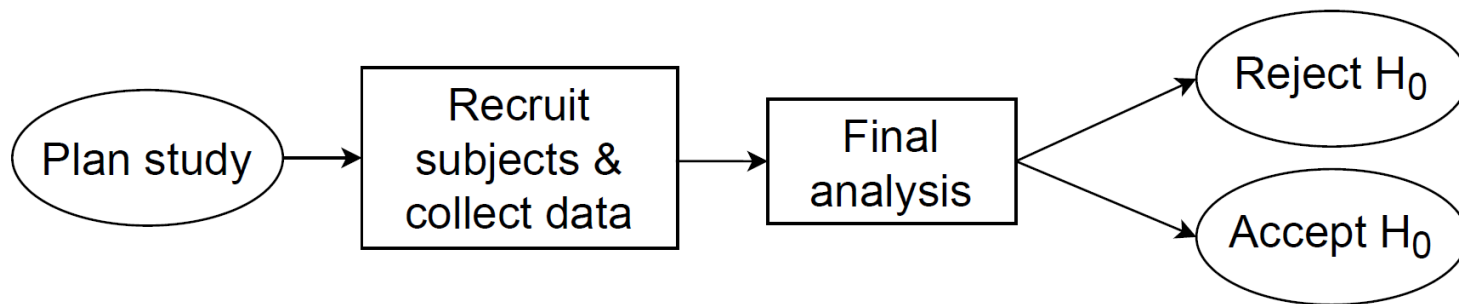
Group sequential design



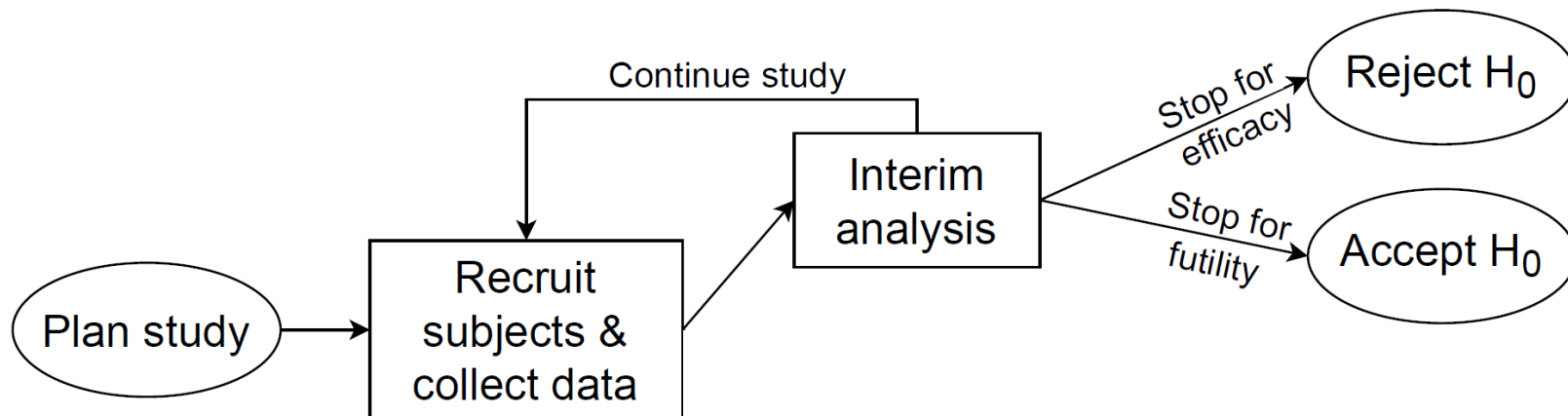
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## Fixed design



## Group sequential design

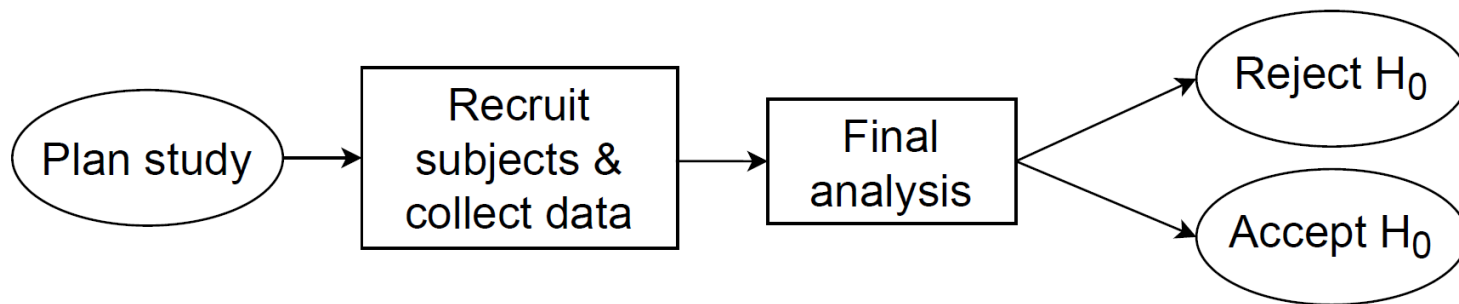




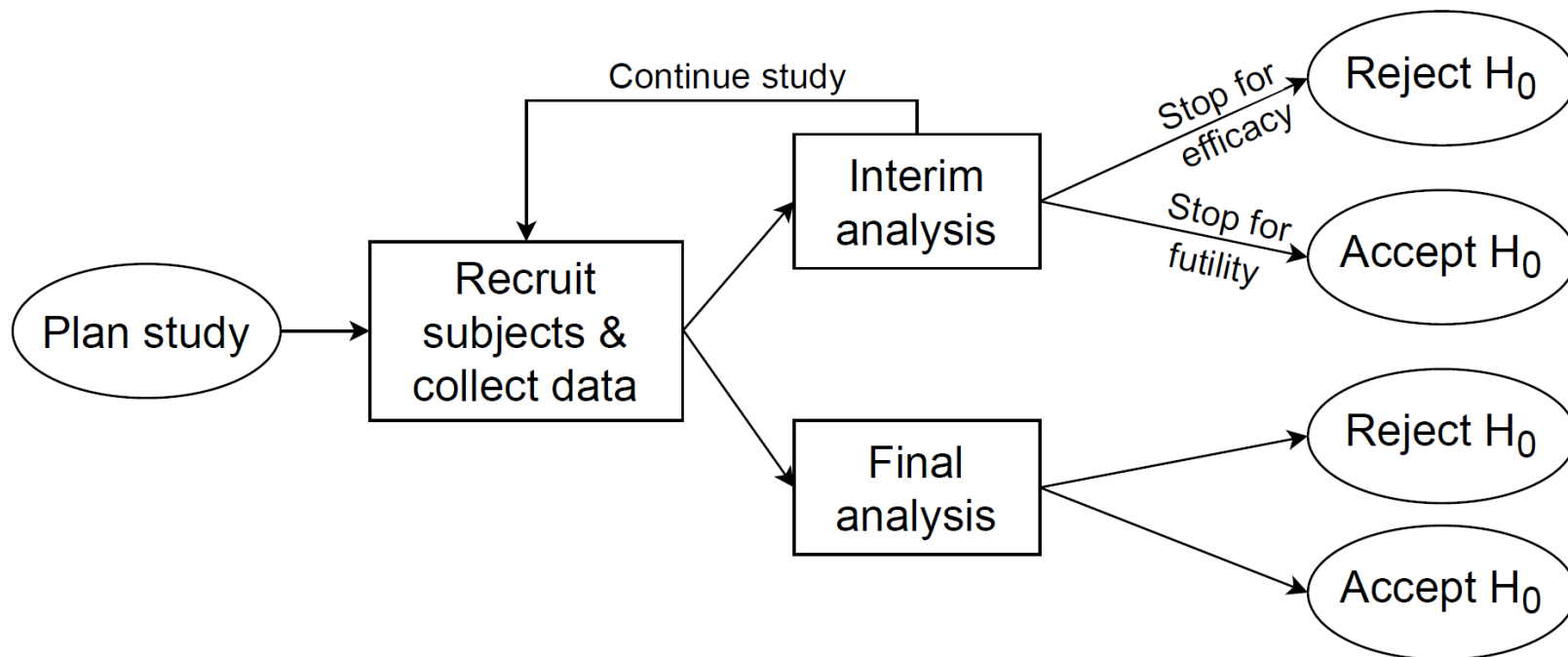
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## Fixed design



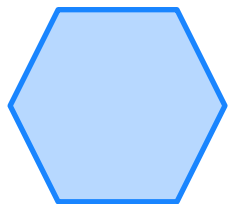
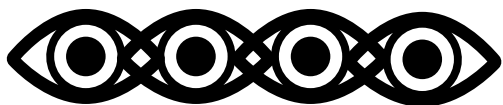
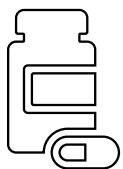
## Group sequential design



# Intro: GSD jargon

- Look
  - analysis of the data to-date
- Expected sample size (ESS)
  - average sample size if the trial were to be repeated
- Maximum information
  - Fisher information of the parameter estimated for the test, calculated at the maximum sample size
- Information fraction
  - fraction of the maximum information that has been collected when a look is performed; proportional to sample size
- Information ratio
  - ratio of the maximum information (sample size) of a GSD to the information (sample size) of an equivalent FSD

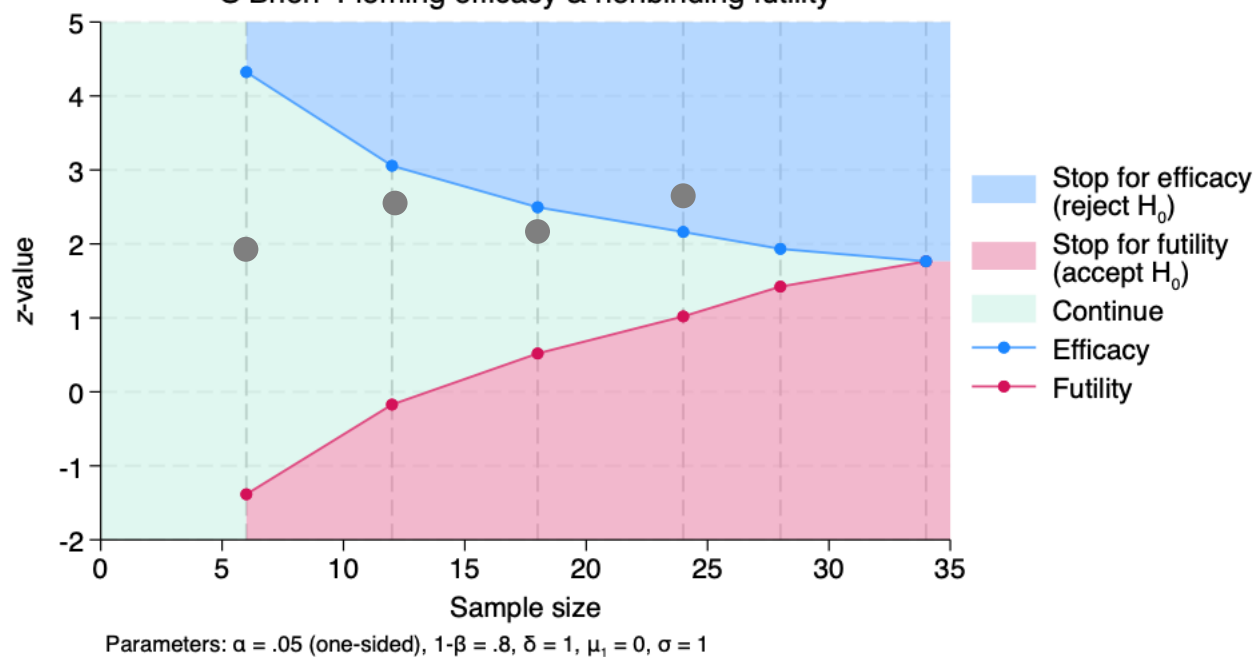
# Intro: GSD in action



Treatment is effective

Group sequential design for a two-sample means test

O'Brien–Fleming efficacy & nonbinding futility



# Intro: GSD theory

Test statistic  $Z_k$  is calculated using all observations through look  $k$

$(Z_1, Z_2, \dots, Z_K)$  is multivariate normal with

$$\text{Cov}(Z_j, Z_k) = \sqrt{\frac{I_j}{I_k}}$$

where information fraction  $I_k = n_k/n_K$

# gs commands

- **gsbounds**

- calculate stopping boundaries & information ratio

- **gsdesign**

- calculate stopping boundaries & sample sizes
- calls **power** and **gsbounds** under the hood



# gsbounds: syntax

*Calculate efficacy stopping boundaries*

```
gsbounds [ , efficacy(boundary) options ]
```

*Calculate futility stopping boundaries*

```
gsbounds, futility(boundary[ , binding ]) [ options ]
```

*Calculate efficacy and futility stopping boundaries*

```
gsbounds, efficacy(boundary) futility(boundary[ , binding ]) [ options ]
```

<i>boundary</i>	Description
<u>obfleming</u>	classical O'Brien–Fleming bound
<u>pocock</u>	classical Pocock bound
<u>wtsiatis</u> (#)	classical Wang–Tsiatis bound with specified parameter value
<u>errpocock</u>	error-spending Pocock-style bound
<u>errob Fleming</u>	error-spending O'Brien–Fleming-style bound
<u>kdemets</u> (#)	error-spending Kim–DeMets bound with specified parameter value
<u>hsdecani</u> (#)	error-spending Hwang–Shih–de Cani bound with specified parameter value

# gsbounds: syntax

<i>options</i>	Description
Main	
<u>efficacy</u> ( <i>boundary</i> )	boundary for efficacy stopping; if neither <code>efficacy()</code> nor <code>futility()</code> is specified, the default is <code>efficacy(obfleming)</code>
<u>futility</u> ( <i>boundary</i> [ , <u>binding</u> ])	boundary for futility stopping; use <code>binding</code> to request binding futility bounds (default is nonbinding)
<u>nlooks</u> (#)	total number of analyses ( <code>nlooks()</code> – 1 interim analyses and one final analysis)
<u>information</u> ( <i>numlist</i> )	sequence of information levels for analyses; default is evenly spaced
<u>nopvalues</u>	suppress <i>p</i> -values
<u>alpha</u> (#)	overall significance level for all tests; default is <code>alpha(0.05)</code>
<u>power</u> (#)	overall power for all tests; default is <code>power(0.8)</code>
<u>beta</u> (#)	overall probability of type II error for all tests; default is <code>beta(0.2)</code>
<u>upper</u>	upper one-sided test; default is two-sided
<u>lower</u>	lower one-sided test; default is two-sided
<u>onesided</u>	synonym for <code>upper</code>
Graph	
<u>graphbounds</u> [ ( <i>graphopts</i> ) ]	graph boundaries
<u>matlistopts</u> ( <i>general_options</i> )	control the display of boundaries; seldom used
<i>optimopts</i>	optimization options for boundary calculations; seldom used

# gsbounds: output

```
. gsbounds, efficacy(obfleming) nlooks(4)
```

Group sequential boundaries

Efficacy: O'Brien-Fleming

Study parameters:

alpha = **0.0500** (two-sided)

power = **0.8000**

Info. ratio = **1.0238**

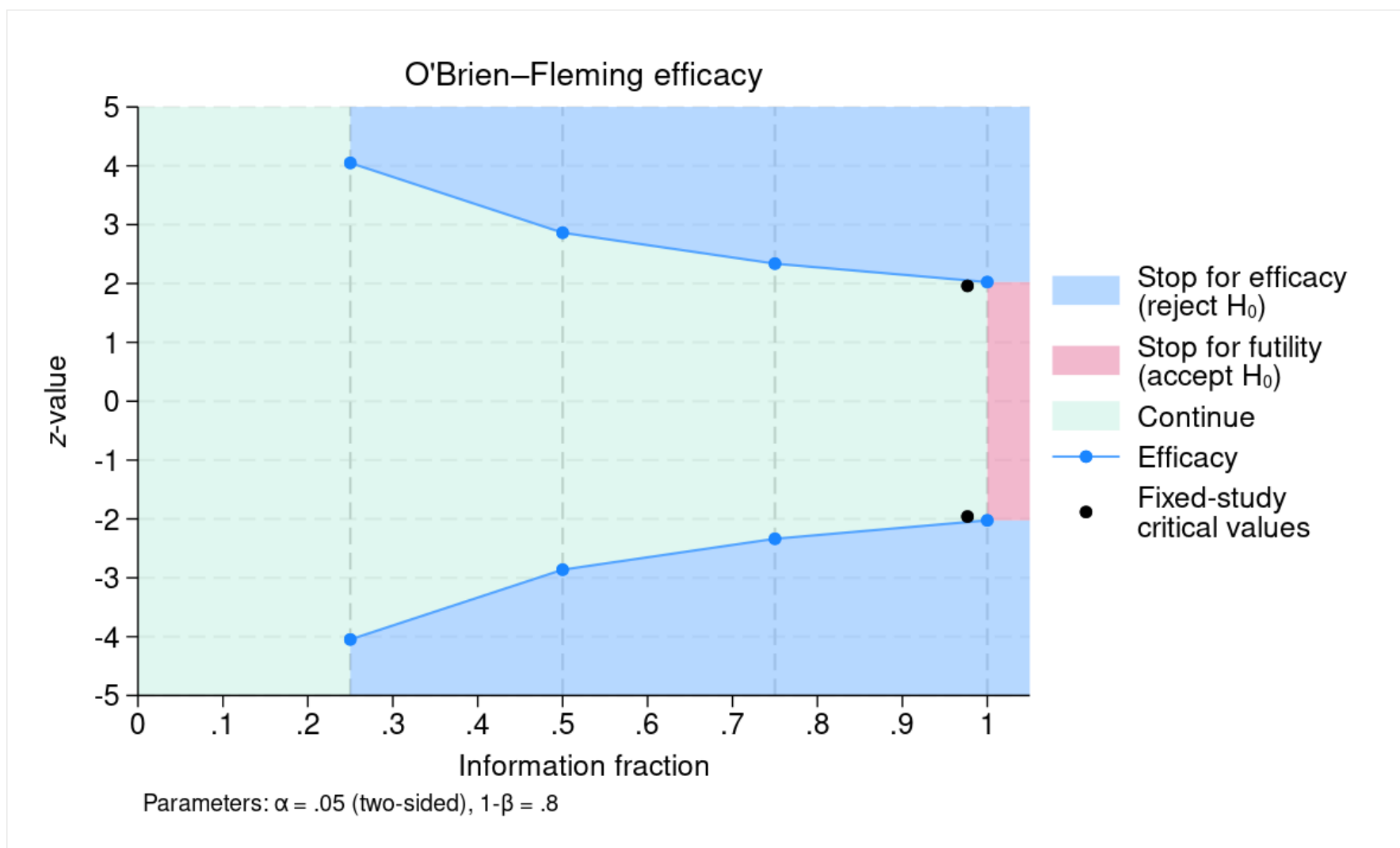
Fixed-study crit. values = **±1.9600**

Critical values and p-values for a group sequential design

Look	Info. frac.	Efficacy		p-value
		Lower	Upper	
1	<b>0.25</b>	<b>-4.0486</b>	<b>4.0486</b>	<b>0.0001</b>
2	<b>0.50</b>	<b>-2.8628</b>	<b>2.8628</b>	<b>0.0042</b>
3	<b>0.75</b>	<b>-2.3375</b>	<b>2.3375</b>	<b>0.0194</b>
4	<b>1.00</b>	<b>-2.0243</b>	<b>2.0243</b>	<b>0.0429</b>

Note: Critical values are for z statistics;  
otherwise, use [p-value boundaries](#).

# gsbounds: graph



# gsdesign: syntax

```
gsdesign method ... [ , designopts boundopts ]
```

where *method* ... refers to a power *method* that is used for sample-size calculation, *designopts* are options controlling the sample-size calculation, and *boundopts* are options controlling the calculation of the stopping boundaries.

<i>method</i>	Description
<a href="#">onemean</a>	GSD for one-sample mean test
<a href="#">twomeans</a>	GSD for two-sample means test
<a href="#">oneproportion</a>	GSD for one-sample proportion test
<a href="#">twoproportions</a>	GSD for two-sample proportions test
<a href="#">logrank</a>	GSD for a log-rank test
<a href="#">usermethod</a>	user-defined sample-size calculation

gsdesign supports the above methods when they are used to calculate sample size with simple random sampling.  
To use an unsupported method, specify option `methodok`.



# gsdesign: syntax

*designopts*

Description

Main

*methodopts*

method-specific options

alpha(#)

overall significance level for all tests; default is `alpha(0.05)`

power(#)

overall power for all tests; default is `power(0.8)`

beta(#)

overall probability of type II error for all tests;  
default is `beta(0.2)`

onesided

request a one-sided test; default is two-sided

nfractional

report fractional sample size

force

allow calculation with unsupported *methodopts*

methodok

allow calculation with unsupported *method*

poweriteration(*powiteropts*)

iteration options for the calculation of fixed-study sample size;  
not available with *method* `logrank`; seldom used

# gsdesign: output

```
. gsdesign twomeans 50 80, sd1(30) sd2(45) alpha(0.025) power(0.9) onesided efficacy(kdemets(2))
> futility(errobflaming) nlooks(4) graphbounds
```

Group sequential design for a two-sample means test  
Satterthwaite's t test assuming unequal variances  
H0:  $m_2 = m_1$  versus Ha:  $m_2 > m_1$

Efficacy: Error-spending Kim-DeMets,  $\rho = 2.0000$   
Futility: Error-spending O'Brien-Fleming style, nonbinding

Study parameters:  
alpha = **0.0250** (upper one-sided)  
power = **0.9000**  
delta = **30.0000**  
m1 = **50.0000**  
m2 = **80.0000**  
sd1 = **30.0000**  
sd2 = **45.0000**

Expected sample size:  
H0 = **46.96**  
Ha = **53.01**

Info. ratio = **1.1134**  
N fixed = **72**  
N max = **80**  
N1 max = **40**  
N2 max = **40**

Fixed-study crit. value = **1.9600**

Critical values, p-values, and sample sizes for a group sequential design

Look	Info. frac.	Efficacy		Futility		Sample size		
		Upper	p-value	Lower	p-value	N1	N2	N
1	<b>0.25</b>	<b>2.9552</b>	<b>0.0016</b>	<b>-1.3792</b>	<b>0.9161</b>	<b>10</b>	<b>10</b>	<b>20</b>
2	<b>0.50</b>	<b>2.5594</b>	<b>0.0052</b>	<b>0.3580</b>	<b>0.3602</b>	<b>20</b>	<b>20</b>	<b>40</b>
3	<b>0.75</b>	<b>2.3009</b>	<b>0.0107</b>	<b>1.3336</b>	<b>0.0912</b>	<b>30</b>	<b>30</b>	<b>60</b>
4	<b>1.00</b>	<b>2.0920</b>	<b>0.0182</b>	<b>2.0920</b>	<b>0.0182</b>	<b>40</b>	<b>40</b>	<b>80</b>

Note: Critical values are for z statistics; otherwise, use [p-value boundaries](#).



# Resources

- **Overview of features**

- <https://www.stata.com/new-in-stata/group-sequential-designs/>

- **Video overview**

- <https://youtu.be/hO2qW1NLrMk?si=zu1-02rrzzkOw41E>

- **Documentation**

- <https://www.stata.com/manuals/adapt.pdf>

- **Power and sample size calculations**

- <https://www.stata.com/features/power-and-sample-size/>