

# Novel approaches in adaptive designs and $\alpha$ adjustment, e.g., with futility criteria and for parallel design studies

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## Simulation-based (2×2×2 crossover)

#### No futility criteria, unlimited stage 2 sample size

Reference	Туре	Method	GMR	Power (%)	CV (%)	$lpha_{adj}$	TIE <sub>max</sub>
Potvin et al. [3]	1	В	0.95	80	10 – 100	0.0294	0.0489
	2	С					0.0512*
Montague et al. [4]	2	D	0.90			0.0280	0.0517*
	1	В	0.05	90	10 - 80	0.0284	0.0497
Fuglsang [5]	2	C/D	0.95			0.0274	0.0501
	2	C/D	0.90			0.0269	0.0503

## Futility criteria on CI, $N_{\text{max}}$ 42 (low CV), 180 (high CV)

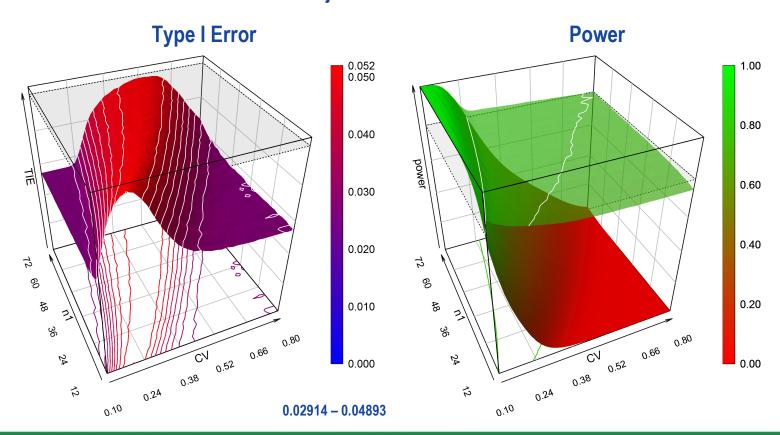
Reference	Type	Method	GMR	Power (%)	CV (%)	Futility region	$\alpha_{adj1}$	α <sub>adj2</sub>	<b>TIE</b> <sub>max</sub>
Xu et al. [11]	1	Е	- - 0.95 -	80	10 – 30 –	0.9374 - 1.0667	0.0249	0.0363	0.0490
	2	F				0.9374 - 1.0667 0.9492 - 1.0535	0.0248	0.0364	0.0496
	1	Ε			30 – 55 –	0.9305 - 1.0747	0.0254	0.0357	0.0453
	2	F				0.9350 - 1.0695	0.0259	0.0349	0.0455





## **Operating Characteristics (Type 1 TSD** [3])

GMR 0.95, power 80%,  $\alpha_{adi}$  0.0294 (Potvin et al. 'Method B')







## Repeated Confidence Intervals / Inverse Normal Method [15–18] adapted for BE [19-21]; aka »Maurer's method« [21]

- **Controls the Type I Error in the strict sense** 
  - Analytically proven
  - Confirmed in simulations
- Two approaches
  - Standard Combination Method
  - Maximum Combination Test (recommended [20,21])
- Weights of the stages have to be pre-specified
  - The adjusted  $\alpha$  depends on the weights
    - The more weights differ, the more adjustment
    - Robust against misspecification
    - The same adjusted  $\alpha$  is used in both stages
  - Simulations can be performed to find suitable weights





#### »Maurer's method« [21]

- My recommendations
  - Stage 1 sample size
    - 80% of fixed sample design for assumed GMR and CV
      - » Reasonably high probability to stop already in stage 1 for BE
      - » Overall power higher than fixed sample design
  - If CV expected to be not more than 75% larger than assumed
    - Standard Combination Method more powerful, requires less adjustment [22]
- Sample size re-estimation
  - A fixed GMR is used by default
  - Can be fully adaptive, i.e., based on the GMR of stage 1
- Minimum and maximum stage 2 sample sizes can be pre-specified
  - At least four subjects in two sequences are required in stage 2
  - Too small stage 2 negatively affects power





#### »Maurer's method« [21]

- Optional futility criteria for stopping in the interim
  - GMR outside specified limits (default 0.80 – 1.25)
  - 90% confidence interval of the GMR entirely outside specified limits (default  $0.95 0.95^{-1}$ )
  - Maximum total sample size (default  $4 \times n_1$ )
- Futility criteria
  - Combinations are possible
  - Reduce the Type I Error
  - Negatively affect power
    - Fairly robust on GMR or CI
    - Very sensitive on  $N_{\text{max}}$
  - Simulations highly recommended



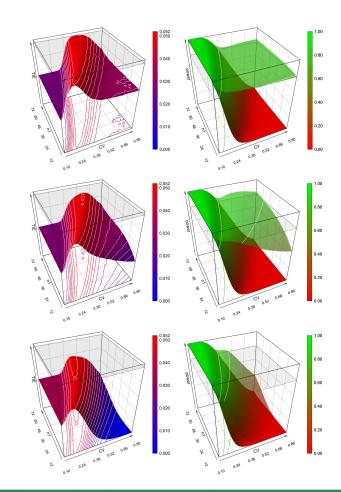


## **Operating Characteristics (Exact [21])**

Fixed GMR 0.95 (CV 0.1–0.8,  $n_1$  12–72) No futility Type I Error 0.02598 – 0.04995

Adaptive GMR (CV 0.1–0.8,  $n_1$  12–72) Futility on CI (outside  $0.95 - 0.95^{-1}$ ) Type I Error 0.01678 – 0.04523

Adaptive GMR (CV 0.1–0.8,  $n_1$  12–72) Futility on CI (outside  $0.95 - 0.95^{-1}$ ) Futility on  $N_{\text{max}}$  (> 4× $n_1$ ) Type I Error 0.00006 - 0.03838





### »Maurer's method« [21]

- Contrary to simulation-based methods, data are not pooled
  - Stages are evaluated separately and assessed by (repeated) confidence intervals
    - ANOVA (EMA and most other juridictions)
    - Mixed-effects model (FDA, Health Canada, China's CDE)
    - Additional factors, e.g., for multi-group or multi-site studies can be incorporated in the model
  - Required in the interim analysis by Power2Stage [35]
    - GMR<sub>1</sub>,  $CV_1$ ,  $n_1$ , assumed GMR for sample size re-estimation, target power
    - If additional factors in the model:  $df_1$ , SEM<sub>1</sub>
  - Required in the final analysis by Power2Stage [35]
    - GMR<sub>1</sub>,  $CV_1$ ,  $n_1$
    - GMR<sub>2</sub>,  $CV_2$ ,  $n_2$
    - If additional factors in the model: df<sub>1</sub>, SEM<sub>1</sub>, df<sub>2</sub>, SEM<sub>2</sub>



## Simulation-based (parallel design [14])

#### Two methods implemented in <a href="Power2Stage">Power2Stage</a> [35]

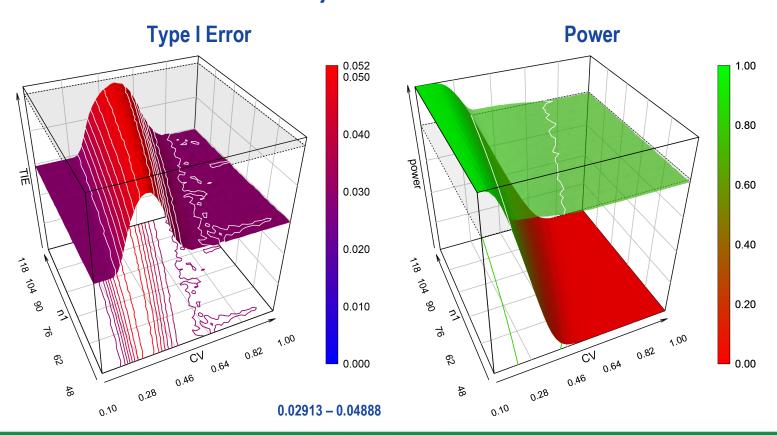
- **ANOVA** 
  - Incorporates a term for stage in the final analysis
    - In line with the EMA's Q&A-document [28]
  - Assumes equal variances
    - Liberal and hence, not recommended
- Welch-Satterthwaite test
  - Approximates degrees of freedom for unequal group sizes and variances
    - No stage term possible; contradicts the EMA's Q&A-document [28]
    - In line with the FDA's guidance [33]
    - Highly recommended
- **Modifications (simulations recommended)** 
  - Fully adaptive, i.e., based on the GMR observed in stage 1
  - Futility criterion on  $N_{\rm max}$





## Operating Characteristics (Type 1 TSD [14])

## GMR 0.95, power 80%, $\alpha_{adi}$ 0.0294, Welch-Satterthwaite test







## **State of Affairs**

#### Simulation-based methods for 2×2×2 crossovers [3–13]

- Ambiguous description in the EMA's guideline, regrettably incurred in other jurisdictions
  - Resulted in unsubstantiated deficiency letters
  - Wariness in the industry about application of adaptive designs
     There are actually more articles describing the theoretical and statistical base for the application of the two-stage design than there are reported studies. [26]
  - Type 2 TSD recommended by the FDA and Health Canada [23,32]

#### Exact method for 2×2×2 crossovers [21] preferable

- Strict Type I Error control
- Flexible (fully adaptive, futility criteria)

### Simulation-based method for parallel designs [14]

At the time being the only available





### Outlook

#### **Expand the exact method for 2×2×2 crossovers**

- If a PK metric in the first stage is highly variable, perform the second stage in a replicate design intended for reference-scaling
  - Scaling based on  $CV_{WR}$  in the second stage

#### Development of an exact method for parallel designs

Not trivial because unequal sample sizes and variances have to be taken into account

#### Simulation-based methods for RSABE/ABEL

- **Practically impossible** 
  - Stable sample size estimation requires 10<sup>5</sup> simulations taking conditions of the regulatory frameworks into account
  - 10<sup>6</sup> simulations to demonstrate control of the Type I Error
  - With a reasonable narrow grid of  $n_1$  / CV-combinations estimated runtime ≈50 years 24/7 on a current workstation



## Novel approaches in adaptive designs and $\alpha$ adjustment, e.g., with futility criteria and for parallel design studies



#### Thank You!



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#### Simulation-based sequential Two-Stage Designs

- 2×2×2 crossover design
- 1. Gould AL. Group Sequential Extension of a Standard Bioequivalence Testing Procedure. J Pharmacokinet Biopharm. 1995; 23(1): 57-86. https://doi.org/10.1007/BF02353786.
- 2. Hauck WW, Preston PE, Bois FY. A Group Sequential Approach to Crossover Trials for Average Bioequivalence. J Biopharm Stat. 1997; 7(1): 87–96. https://doi.org/10.1080/10543409708835171.
- Potvin D, DiLiberti CE, Hauck WW, Parr AF, Schuirmann DJ, Smith RA. Sequential design approaches for bioequivalence studies with crossover designs. Pharm Stat. 2008; 7(4): 245–262. https://doi.org/10.1002/pst.294.
- Montague TH, Potvin D, DiLiberti CE, Hauck WW, Parr AF, Schuirmann DJ. Additional results for 'Sequential design approaches for bioequivalence studies with crossover designs'. Pharm Stat. 2011; 11(1): 8–13. https://doi.org/10.1002/pst.483.
- 5. Fuglsang A. Seguential Bioequivalence Trial Designs with Increased Power and Controlled Type I Error Rates. AAPS J. 2013; 15(3): 659-61. https://doi.org/10.1208/s12248-013-9475-5.
- Karalis V, Macheras P. An Insight into the Properties of a Two-Stage Design in Bioequivalence Studies. Pharm Res. 2013; 30(7): 1824–1835. https://doi.org/10.1007/s11095-013-1026-3.
- Karalis V. The role of the upper sample size limit in two-stage bioequivalence designs. Int J Pharm. 2013; 456(1): 87–84. https://doi.org/10.1016/j.jpharm.2013.08.013.
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- 10. Zheng Ch, Zhao L, Wang J. Modifications of sequential designs in bioequivalence trials. Pharm Stat. 2015; 14(3): 180-8. https://doi.org/10.1002/pst.1672.





- 11. Xu J, Audet C, DiLiberti CE, Hauck WW, Montague TH, Parr AF, Potvin D, Schuirmann DJ. Optimal adaptive sequential designs for crossover bioequivalence studies. Pharm Stat. 2016; 15(1): 15–27. https://doi.org/10.1002/pst.1721.
- 12. Molins E. Cobo E. Ocaña J. Two-stage designs versus European scaled average designs in bioequivalence studies for highly variable drugs: Which to choose? Stat Med. 2017; 36(30): 4777–88. https://doi.org/10.1002/sim.7452.
- 13. Molins E, Labes D, Schütz H, Cobo E, Ocaña J. An iterative method to protect the type I error rate in bioequivalence studies under two-stage adaptive 2×2 crossover designs. Biom J. 2021; 63(1): 122–33. https://doi.org/10.1002/bimi.201900388.
- Parallel design
- 14. Fuglsang A. Seguential Bioequivalence Approaches for Parallel Designs. AAPS J. 2014; 16(3): 373–8. https://doi.org/10.1208/s12248-014-9571-1.

#### **Adaptive designs**

- Conditional power, repeated confidence intervals
- 15. Bauer P, Köhne K. Evaluation of Experiments with Adaptive Interim Analyses. Biometrics. 1994; 50(4): 1029– 41. https://doi.org/10.2307/2533441.
- 16. Lehmacher W, Wassmer G. Adaptive Sample Size Calculations in Group Sequential Trials. Biometrics. 1999; 55(4): 1286–90. https://doi.org/10.1111/j.0006-341X.1999.01286.x.
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- 18. Wassmer G, Brannath W. Group Sequential and Confirmatory Adaptive Designs in Clinical Trials. Switzerland: Springer; 2016. ISBN 978-3-319-32560-6. https://doi.org/10.1007/978-3-319-32562-0.



#### 2×2×2 crossover design

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- 20. Patterson SD, Jones B. Bioequivalence and Statistics in Clinical Pharmacology. Boca Raton: Chapman & Hall / CRC Press; Second edition 2017. p. 141–87.
- 21. Maurer W, Jones B, Chen Y. Controlling the type 1 error rate in two-stage sequential designs when testing for average bioequivalence. Stat Med. 2018; 37(10): 1-21. https://doi.org/10.1002/sim.7614. Supplementary Information for "Controlling the Type I error rate in two-stage sequential adaptive designs when testing for Average Bioequivalence". https://onlinelibrary.wiley.com/action/downloadSupplement?doi=10.1002/sim.7614&file=sim7614-sup-0001supplementary.pdf.
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#### **Reviews**

- 23. García-Arieta A, Gordon J. Bioequivalence Requirements in the European Union: Critical Discussion. AAPS J. 2012; 14(4): 738-48. https://doi.org/10.1208/s12248-012-9382-1.
- 24. Davit B, Braddy AC, Conner DP, Yu LX. International Guidelines for Bioequivalence of Systemically Available Orally Administered Generic Drug Products: A Survey of Similarities and Differences. AAPS J. 2013; 15(4): 974-90. https://doi.org/10.1208/s12248-013-9499-x.
- 25. Schütz H. Two-stage designs in bioequivalence trials. Eur J Clin Pharmacol. 2015; 71(3): 271–81. https://doi.org/10.1007/s00228-015-1806-2.
- 26. Kaza M, Sokolvskyi A, Rudzki PJ. 10th Anniversary of a Two-Stage Design in Bioequivalence. Why Has it Still Not Been Implemented? Pharm Res. 2020; 37(7): Article number 140. https://doi.org/10.1007/s11095-020-02871-3.



Lee J, Feng K, Xu M, Gong X, Sun W, Kim J, Zhang Z, Wang M, Fang L, Zhao L. Applications of Adaptive Designs in Generic Drug Development. Clin Pharm Ther. 2020; 110(1): 32-5. https://doi.org/10.1002/cpt.2050.

#### **Guidelines**

- EMA, CHMP. Guideline on the Investigation of Bioequivalence. CPMP/EWP/QWP/1401/98 Rev. 1/ Corr. https://www.ema.europa.eu/en/documents/scientific-quideline/quideline-investigation-bioequivalencerev1 en.pdf. London. 20 January 2010.
- EMA, CHMP. Questions & Answers: positions on specific questions addressed to the Pharmacokinetics Working Party (PKWP). EMA/618604/2008 Rev. 13. https://www.ema.europa.eu/en/documents/scientificguideline/guestions-answers-positions-specific-questions-addressed-pharmacokinetics-workingparty en.pdf. London. 19 November 2015.
- 30. EMA, CHMP. Guideline on multiplicity issues in clinical trials. Draft. EMA/CHMP/44762/2017. https://www.ema.europa.eu/en/documents/scientific-guideline/draft-guideline-multiplicity-issues-clinicaltrials en.pdf. London, 15 December 2016.
- 31. WHO Expert Committee on Specifications for Pharmaceutical Preparations. Multisource (generic) pharmaceutical products: Guidelines on registration requirements to establish interchangeability. WHO Technical Report Series No. 992, Annex 6. https://www.who.int/docs/default-source/medicines/norms-andstandards/guidelines/regulatory-standards/trs1003-annex6-who-multisource-pharmaceutical-productsinterchangeability.pdf. Geneva. 2017.

#### Guidance

32. Health Canada. Conduct and Analysis of Comparative Bioavailability Studies. Cat: H13-9/6-2018E-PDF. https://www.canada.ca/content/dam/hc-sc/documents/services/drugs-health-products/drugproducts/applications-submissions/guidance-documents/bioavailability-bioequivalence/conduct-analysiscomparative.pdf. Ottawa. Adopted 2012/02/08, revised 2018/06/08.





- 33. FDA, CDER. Statistical Approaches to Establishing Bioequivalence. https://www.fda.gov/media/70958/download. Rockville, MD. January 2001.
- 34. FDA, CDER/CBER. Adaptive Designs for Clinical Trials of Drugs and Biologics. https://www.fda.gov/media/78495/download. Silver Spring, MD. November 2019.

#### Packages for the open-source software R https://www.r-project.org/

- Simulation-based (2×2×2 crossover [3–12] and parallel design [14]), Exact (2×2×2 crossover design [21])
- 35. Labes D, Lang B. Schütz H. Power2Stage: Power and Sample-Size Distribution of 2-Stage Bioequivalence Studies. 2021-11-20; Package version 0.5-4. https://cran.r-project.org/package=Power2Stage.
- Simulation-based (2×2×2 crossover design [13])
- 36. Molins E, Labes D, Schütz H, Ocaña J. betsd: Adjusting significance levels in two-stage adaptive 2×2 crossover designs. 2019; Package version 0.1.5. https://github.com/eduard-molins/betsd.

# Maximum empiric Type I Error (10<sup>6</sup> simulations under the Null)



[Backup]

```
library(Power2Stage)
# Simulation-based (2x2x2 crossover, no futility); References 3, 4, 5
# Exact Power estimation by Owen's Q-function
method <- c("B", "C", "C", "B", "C", "C")
CV.loc \leftarrow c(0.24, 0.22, 0.20, 0.22, 0.10, 0.18)
n1.loc <- c(12, 12, 12, 12, 16, 12)
  <- data.frame(Ref = c(rep("[3]", 2), "[4]", rep("[5]", 3)),</pre>
                     Type = c(1, 2, 2, 1, 2, 2),
                     Method = c("B ", "C ", "D ", "B ", "C/D", "C/D"),
                            = c(0.95, 0.95, 0.90, 0.95, 0.95, 0.90),
                     Power = c(rep(80, 3), rep(90, 3)),
                            = c(rep("10 - 100%", 3), rep("10 - 80%", 3)),
                            = c(rep(0.0294, 2), 0.028, 0.0284, 0.0274, 0.0269))
                     adi
for (i in 1:6) {
  a$TIE.max[i] <- power.tsd(method = method[i], alpha0 = 0.05, alpha = rep(a$adj[i], 2),
                            CV = CV.loc[i], n1 = n1.loc[i], GMR = a\$GMR[i],
                            targetpower = a$Power[i] / 100, pmethod = "exact",
                            theta0 = 1.25)$pBE
}
a$Power <- sprintf("%.0f%%", a$Power)
a$TIE.max <- round(a$TIE.max, 4)
print(a, row.names = FALSE)
```

# Maximum empiric Type I Error (10<sup>6</sup> simulations under the Null)



```
library(Power2Stage)
# Simulation-based (2×2×2 crossover, futility criteria); Reference 11
# Exact Power estimation by Owen's Q-function
method <- rep(c("B", "C"), 2)
CV.loc \leftarrow c(rep(0.3, 2), rep(0.55, 2))
n1.loc \leftarrow c(rep(18, 2), rep(48, 2))
fClower <- c(0.9374, 0.9305, 0.9492, 0.9350) # different futilities on CI
max.n <- c(rep(42, 2), rep(180, 2)) # different futilities on Nmax
b <- data.frame(Ref = rep("[11]", 4), Type = c(1, 2, 1, 2),
                      Method = c("E", "F", "E", "F"), GMR = rep(0.95, 4),
                      Power = rep(80, 4), CV = c(rep("10 - 30%", 2), rep("30 - 55%", 2)),
                      adj1 = c(0.0249, 0.0248, 0.0254, 0.0259), # different alphas
                      adj2 = c(0.0363, 0.0364, 0.0357, 0.0349)) # in the stages
for (i in 1:4) {
  b$TIE.max[i] <- power.tsd.fC(method = method[i], alpha0 = 0.05,
                               alpha = c(b*adj1[i], b*adj2[i]), CV = CV.loc[i], n1 = n1.loc[i],
                               GMR = b$GMR[i], targetpower = b$Power[i] / 100,
                               max.n = max.n[i], fCrit = "CI", fClower = fClower[i],
                               pmethod = "exact", theta0 = 1.25)$pBE
b$Power <- sprintf("%.0f%%", b$Power)
b$TIE.max <- round(b$TIE.max, 4)</pre>
print(b, row.names = FALSE)
```

# Maximum empiric Type I Error (10<sup>6</sup> simulations under the Null)



[Backup]

```
library(Power2Stage)
# Exact (2×2×2 crossover): Maximum Combination Test, no futility criteria; Reference 21
# Exact Power estimation by Owen's O-function
        <- power.tsd.in(CV = 0.46, n1 = 62, weight = c(0.5, 0.25),
                        max.comb.test = TRUE, ssr.conditional = "error power",
                        fCrit = "No", GMR = 0.95, targetpower = 0.8,
                        pmethod = "exact", theta0 = 1.25)
        <- data.frame(Ref = "[21]", Method = "Maurer's", GMR = 0.95, Power = 80,</pre>
C
                      CV = "10 - 80\%", adj = round(x$alpha[1], 5), TIE.max = x$pBE)
c$Power <- sprintf("%.0f%", c$Power)
print(c, row.names = FALSE)
# Exact (2×2×2 crossover): Standard Combination Method, no futility criteria; Reference 21
# Exact Power estimation by Owen's O-function
        <- power.tsd.in(CV = 0.50, n1 = 70, weight = 0.5,
                        max.comb.test = FALSE, ssr.conditional = "error power",
                        fCrit = "No", GMR = 0.95, targetpower = 0.8,
                        pmethod = "exact", theta0 = 1.25)
        <- data.frame(Ref = "[21]", Method = "Maurer's", GMR = 0.95, Power = 80,</pre>
                      CV = "10 - 80\%", adi = round(x$alpha[1], 5), TIE.max = x$pBE)
d$Power <- sprintf("%.0f%", d$Power)</pre>
print(d, row.names = FALSE)
```



### Evaluation by Power2Stage [35]: Subjects 1–12 [3]

Interim analysis with fixed GMR 0.95

```
interim.tsd.in(GMR1 = 1.0876, CV1 = 0.18213, n1 = 12, GMR = 0.95)
TSD with 2x2 crossover
Inverse Normal approach
- Maximum combination test with weights for stage 1 = 0.5 0.25
- Significance levels (s1/s2) = 0.02635 \ 0.02635
- Critical values (s1/s2) = 1.93741 1.93741
- BE acceptance range = 0.8 ... 1.25
- Observed point estimate from stage 1 is not used for SSR
 - With conditional error rates and conditional estimated target power
Interim analysis after first stage
- Derived key statistics:
   z1 = 3.10000, z2 = 1.70344
   Repeated CI = (0.92491, 1.27891)
  Median unbiased estimate = NA
 - No futility criterion met
- Test for BE not positive (not considering any futility rule)
- Calculated n2 = 6
```

- Decision: Continue to stage 2 with 6 subjects



### Evaluation by Power2Stage [35]: Subjects 1–12 | 13–18 [3]

Final analysis

```
final.tsd.in(GMR1 = 1.0876, CV1 = 0.18213, n1 = 12,
             GMR2 = 1.0893, CV2 = 0.16776, n2 = 6)
TSD with 2x2 crossover
Inverse Normal approach
- Maximum combination test with weights for stage 1 = 0.5 0.25
- Significance levels (s1/s2) = 0.02635 0.02635
- Critical values (s1/s2) = 1.93741 1.93741
- BE acceptance range = 0.8 ... 1.25
Final analysis after second stage
- Derived key statistics:
  z1 = 3.70299, z2 = 2.06106
   Repeated CI = (0.95672, 1.23796)
  Median unbiased estimate = 1.0953
 - Decision: BE achieved
```

 Same conclusion as Potvin et al. 'Method B' [3] but slightly more conservative than its 94.12% CI with 0.9664 – 1.2252

# **Example: Weights and power in stages** (minimum $n_2 = 6$ , futility $N_{\text{max}} = 5 \times n_1$ )



```
library(PowerTOST); library(Power2Stage)
CV <- 0.3
n1 <- 0.8 * sampleN.TOST(CV = CV, print = FALSE)[["Sample size"]] # my recommendation
w1 < -w < -c(seq(0.9, 0.5, -0.1), 0.50)
w2 < -c(seq(0.1, 0.5, 0.1), 0.25)
MCT <- data.frame(Approach = "Maximum Combination Test", w1 = w1, w2 = w2, n1 = n1)
SCM <- data.frame(Approach = "Standard Combination Method", w = w, n1 = n1)
for (i in seq along(w1)) { # nmean is the expected average total sample size E[N]
              <- power.tsd.in(CV = CV, n1 = n1, weight = c(w1[i], w2[i]), GMR = 0.95,
  Х
                              min.n2 = 6, fCrit = "Nmax", fCNmax = 5 * n1)
  MCT$n2[i] <- ceiling(x$nmean) - n1; MCT$adj[i] <- round(x$alpha[1]. 5)</pre>
  MCT$pBE1[i] <- x$pBE s1; MCT$pBE2[i] <- x$pBE</pre>
              <- power.tsd.in(CV = CV, n1 = n1, weight = w[i], max.comb.test = FALSE,</pre>
  Х
                              GMR = 0.95, min.n2 = 6,fCrit = "Nmax", fCNmax = 5 * n1)
  SCM$n2[i] <- ceiling(x$nmean) - n1; SCM$adj[i] <- round(x$alpha[1], 5)</pre>
  SCM$pBE1[i] <- x$pBE s1; SCM$pBE2[i] <- x$pBE</pre>
SCM <- SCM[-nrow(SCM), ]; MCT$Approach[2:nrow(MCT)] <- ""; SCM$Approach[2:nrow(SCM)] <- ""</pre>
print(MCT, row.names = FALSE, right = FALSE)
print(SCM, row.names = FALSE, right = FALSE)
```

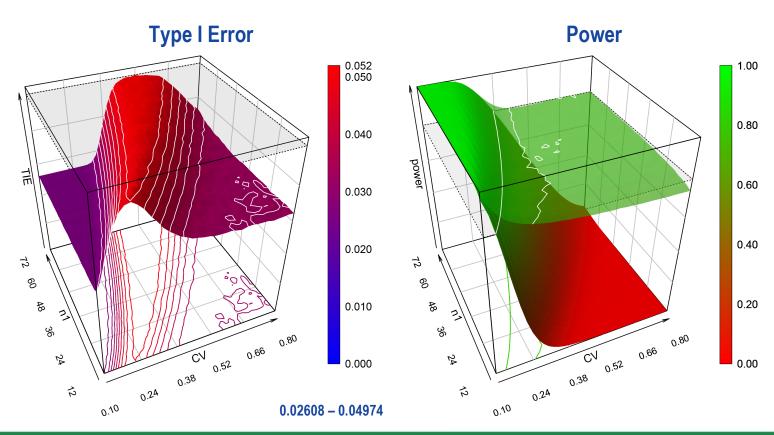
- Similar average total sample sizes like in a fixed sample design
- Always higher power than fixed sample design
- ≈60% chance to stop in the interim for BE





# **Operating Characteristics (Exact [21])**

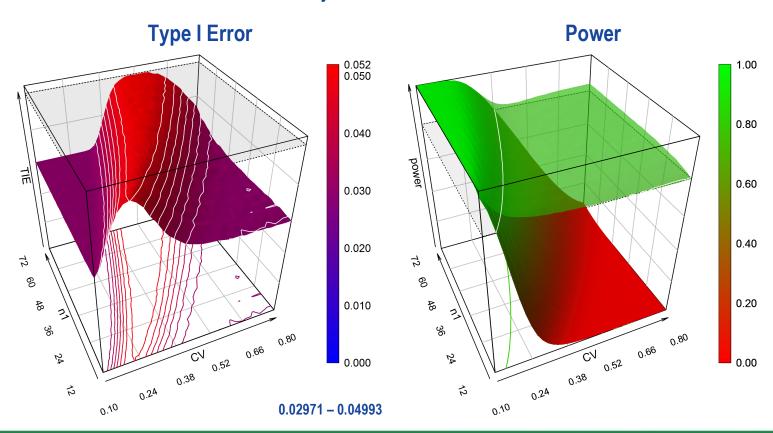
#### **MCT**: weights (0.25, 0.5) instead of the default (0.5, 0.25)





## **Operating Characteristics (Exact [21])**

GMR 0.95, power 80%,  $\alpha_{\text{adj}}$  0.03037 (Standard Combination)





# Standard Combination Method Minimum six subjects in stage 2



#### Interim analysis with fixed GMR 0.95

```
interim.tsd.in(max.comb.test = FALSE, min.n2 = 6,
              GMR1 = 1.0876, CV1 = 0.18213, n1 = 12, GMR = 0.95)
TSD with 2x2 crossover
Inverse Normal approach
 - Standard combination test with weight for stage 1 = 0.5
 - Significance levels (s1/s2) = 0.03037 0.03037
 - Critical values (s1/s2) = 1.87542 1.87542
 - BE acceptance range = 0.8 ... 1.25
 - Observed point estimate from stage 1 is not used for SSR
 - With conditional error rates and conditional estimated target power
Interim analysis after first stage
- Derived key statistics:
  z1 = 3.10000, z2 = 1.70344
  Repeated CI = (0.92491, 1.27891)
  Median unbiased estimate = NA
- No futility criterion met
- Test for BE not positive (not considering any futility rule)
- Calculated n2 = 6
- Decision: Continue to stage 2 with 6 subjects
```

# Standard Combination Method Minimum six subjects in stage 2



#### Final analysis

```
final.tsd.in(max.comb.test = FALSE,
            GMR1 = 1.0876, CV1 = 0.18213, n1 = 12,
            GMR2 = 1.0893, CV2 = 0.16776, n2 = 6)
TSD with 2x2 crossover
Inverse Normal approach
 - Standard combination test with weight for stage 1 = 0.5
 - Significance levels (s1/s2) = 0.03037 \ 0.03037
 - Critical values (s1/s2) = 1.87542 1.87542
 - BE acceptance range = 0.8 ... 1.25
Final analysis after second stage
- Derived key statistics:
  z1 = 3.70299, z2 = 2.06106
  Repeated CI = (0.96127, 1.23210)
  Median unbiased estimate = 1.0884
- Decision: BE achieved
```

 Same conclusion as Maximum Combination Test; slightly less conservative than its Cl 0.9567 – 1.2380 due to  $\alpha_{\text{adi}}$  0.03037 instead of 0.02635





```
library(Power2Stage)
# Simulation-based (parallel design): Welch-Satterthwaite test; Reference 14
# Exact Power estimation by Owen's O-function
TIE.max \leftarrow power.tsd.p(method = "B", alpha = rep(0.0294, 2),
                       CV = 0.52, n1 = 116, GMR = 0.95,
                       targetpower = 0.8, test = "welch",
                       pmethod = "exact", theta0 = 1.25)$pBE
        <- data.frame(Ref = "[14]", Type = 1, Method = "B ", GMR = 0.95, Power = 80,</pre>
                      CV = "10 - 100%", adj = 0.0294, TIE.max = TIE.max)
e$Power <- sprintf("%.0f%%", e$Power)
print(e, row.names = FALSE)
```

# **Example: Power** (parallel design [14])



```
library(PowerTOST); library(Power2Stage)
CV <- 0.45 # total (pooled from within- and between-subject) CV
n1 <- floor(0.8 * sampleN.TOST(CV = CV, design = "parallel",</pre>
                                                                                     print = FALSE)[["Sample size"]]) # my recommendation
power.tsd.p(method = "B", alpha = rep(0.0294, 2), CV = CV, rowthind n1 = rowthin
                                 pmethod = "exact", test = "welch", npct = c(0.05, 0.25, 0.5, 0.75, 0.95))
TSD with 2 parallel groups
Method B: alpha (s1/s2) = 0.0294 0.0294
CIs based on Welch's t-test
Target power in power monitoring and sample size est. = 0.8
Power calculation via exact method
CV1 and GMR = 0.95 in sample size est. used
No futility criterion
BE acceptance range = 0.8 ... 1.25
CV = 0.45; ntot(stage 1) = 128 (nT, nR = 64, 64); GMR = 0.95
1e+05 \text{ sims at theta0} = 0.95 (p(BE) = 'power').

    100,000 simulations by default

p(BE)
                        = 0.82637

    Probability to stop in the interim for success ≈59%

p(BE) s1 = 0.59414

    Probability to procees to second stage ≈41%

Studies in stage 2 = 40.55%
Distribution of n(total)

    Expected average total sample size E[N] 156

- mean (range) = 155.5 (128 ... 316)

    Final power larger than fixed sample design's 80%

- percentiles
                                                                                                                                                    with 160 subjects
  5% 25% 50% 75% 95%
128 128 128 188 224
```

# **Example: Empiric Type I Error** (parallel design [14])

library(PowerTOST); library(Power2Stage)



```
CV <- 0.45 # total (pooled from within- and between-subject) CV
n1 <- floor(0.8 * sampleN.TOST(CV = CV, design = "parallel",</pre>
                                print = FALSE)[["Sample size"]]) # my recommendation
power.tsd.p(method = "B", alpha = rep(0.0294, 2), CV = CV, n1 = n1,
            pmethod = "exact", test = "welch", npct = 0.5, theta0 = 1.25)
TSD with 2 parallel groups
Method B: alpha (s1/s2) = 0.0294 0.0294
CIs based on Welch's t-test
Target power in power monitoring and sample size est. = 0.8
Power calculation via exact method
CV1 and GMR = 0.95 in sample size est. used
No futility criterion
BE acceptance range = 0.8 ... 1.25
CV = 0.45; ntot(stage 1) = 128 (nT, nR = 64, 64); GMR = 0.95
1e+06 sims at theta0 = 1.25 (p(BE) = TIE 'alpha'). • At the limits of the BE range one million simula-
p(BE)
         = 0.044659
                                                        tions by default
p(BE) s1 = 0.029288

    Probability to pass in the interim close to the level

Studies in stage 2 = 96.94%
                                                        of the test
Distribution of n(total)
- mean (range) = 190.5 (128 ... 330)

    Type I Error controlled (<0.05, significance limit of</li>

- percentiles
                                                        the binomial test 0.05036)
50%
```

190