Two-Stage DesignsBackground and Examples

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Background

In the EMA's Guideline Two-Stage Designs (TSD) are stated as acceptable when attempting to demonstrate bioequivalence (1): "If this approach is adopted appropriate steps must be taken to preserve the overall type I error of the experiment and the stopping criteria should be clearly defined prior to the study. The analysis of the first stage data should be treated as an interim analysis..." Based on group-sequential designs (GSD) with interim analyses (2-6) a few methods have been published in the context of bioequivalence (7, 8) - which did not achieve regulatory acceptance. Recently numerous frameworks were developed in order to control the type I error (TIE) without requiring the sponsor to perform own simulations (9 – 20). In a review TSDs were classified into two 'Types' (21):

- 1. The *same* adjusted α is applied in both stages (regardless whether a study stops in the first stage or proceeds to the second stage).
- An unadjusted α may be used in the first stage, dependent on interim power.

Both types use an *interim* power estimation as a means to guide the decision tree. Clearly, the former (Fig. 1) was inspired by Pocock's GSD (3, 5) with one interim analysis, whereas the latter (Fig. 2) by conventional BE testing. The rationale of conditionally adjusting α in the first stage is the following: If the sample size of the first stage was planned for a given target power π (based on an assumed T/Rratio *GMR* and *CV*), it is reasonable to evaluate power first (for A – not the *observed T/R* ratio). Interim power $\geq \pi$ implies that assumptions hold and the framework proceeds with *unadjusted* α like a conventional fixed-sample pivotal BE study (left branch of Fig. 2). Since only the CV is used in interim power, no α has to be 'spent'. On the other hand, interim power < π indicates a higher than expected CV, and the framework proceeds to the sequential part, where adjustment is mandatory (right branch of Fig. 2).

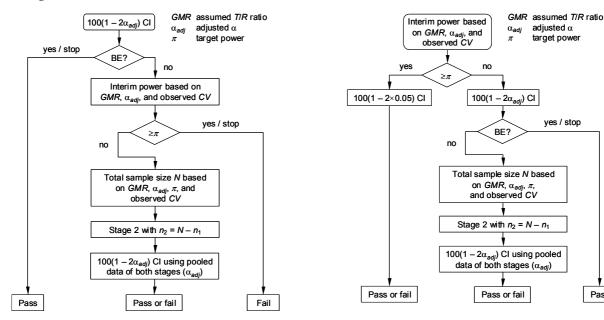


Fig. 1 'Type 1' TSD with adjusted α in both stages.

Fig. 2 'Type 2' TSD with conditionally adjusted α in the first stage.

Pass

In both types futility rules can be introduced to allow early stopping. It should be noted that introducing a futility criterion which is not described in one of the frameworks will not negatively impact the type I error since the chance to proceed to the second stage will be lower than in the original method. However, especially introducing a maximum total sample size (12 – 14), i.e., stopping in stage 1 if the re-estimated $N > N_{max}$) can render such studies unethical (15, 21). Futility criteria based on the observed T/R-ratio or its confidence interval are a better alternative (6, 19). Full adaptive designs (12 - 14),

i.e., re-estimating the sample size based on *both* the observed CV and T/R-ratio) may lead to extreme sample sizes, which – together with a futility criterion on N_{max} – result in low power since the precision of the estimated T/R-ratio in the first stage is poor (22).

In the recent past the EMA's Biostatics Working Party (BSWP) questioned the validity of TSDs based on simulations in terms of control of the type I error. The package AdaptiveBE (23) for R (24) supports both applicants and regulatory assessors in *post hoc* exploring the empiric TIE by means of package Power2Stage (25).

The workflow is outlined in the following:

- 1. The study data have to be specified (stage 1 *GMR*, *CV*, sample size and if applicable the same for the second stage). The applied type of the TSD (adjusted α , eventual futility rules) have to be given. If not specified in the protocol and/or report, by default power and sample size reestimation is done by the noncentral *t*-approximation.
- 2. The empiric TIE is obtained by simulating one million TSD studies according to the conditions given above (significance limit 0.05036, standard error of the estimate 0.00016) under the true Null $\theta_0 = \theta_2$.
 - a. If the empiric TIE is \leq 0.05, the results of the study can be accepted as reported (see Example 1, p 5).
 - b. If the empiric TIE is >0.05, the equation

```
power(\alpha_{adj}, \Theta) - \alpha_{nominal} = 0
```

is numerically solved (26) under the true Null for the study conditions Θ in the interval {tol, $\alpha_{nominal}$ }, where the defaults are $tol = 10^{-8}$ and $\alpha_{nominal} = 0.05$.

- c. The study is recalculated with the adjusted α (interim, and if applicable the sample size re-estimation, and the final analysis).
 - i. If results of both evaluations agree, the study can be accepted as reported. Although there might be an inflation of the TIE with the pre-specified α , none of the confidence limits is close to the acceptance range and thus, no relevant impact on the consumer risk is expected (see Example 2, p 6).
 - ii. If results do not agree (*i.e.*, the study passes with the pre-specified α and fails with the adjusted α), the potential relative increase of the consumer risk is given (see Example 3, p 7).

Based on the study conditions the code 'guesses' which of the published frameworks might have been used. The frameworks were validated for a range of stage 1 sample sizes and CVs in the interim (Working range of the frameworks, p 8). Hence, if at least one of the two were outside the validated matrix of n_1/CV -combinations it shows a lack of understanding of the applicant. However, as long as the TIE is controlled, the study should still be acceptable.

It should be noted that in simulations of the references always *exactly* the re-estimated stage 2 sample size n_2 was used. Naturally, if in a study more subjects are dosed in the second stage (based on an assumed dropout-rate) and at the end of the study more than n_2 subjects are eligible, the chance to demonstrate BE increases and thus, potentially the TIE. Therefore, especially in such cases assessing the TIE is recommended.

Can we expect that the Type I Error after optimization will *always* be \leq 0.05 in simulations? Only if we use a *fixed* seed of the (pseudo) random generator – which is generally recommended in simulations for reproducibility. Let us explore the location of the maximum TIE for 'Method C' (9; at CV 22%, n_1 12) with power and sample size re-estimation by the noncentral t-approximation (Fig. 3).

With the specified α 0.0294 we obtain an empiric TIE of 0.05143 (red circle). If we repeat the estimation with *random* seeds we get the magenta rhombi. If we assess lower alphas (*i.e.*, would adjust more), naturally the TIE decreases (yellow circles). With a fixed seed (blue circle) we get an optimized α of 0.02832 (TIE 0.05000) which is far below the significance limit for one million simulations (0.05036, binomial test) and – hopefully – acceptable for the EMA's BSWP.

Now we repeat the optimization with random seeds and get the cluster of lightblue circles. The blue lines give the 50, 75, and 95 percentile ellipses (based on the bivariate normal distribution). Of course, one could use their mean (the square) as a

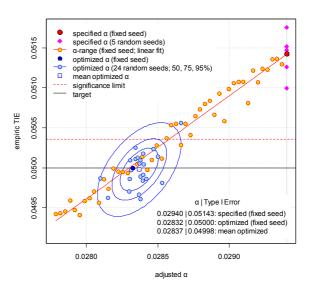


Fig. 3 'Type 2' TSD with conditionally adjusted α in the first stage.

'best' estimate (here 0.02832), but would that really help? First, it is not reproducible any more (for every run of the code one will get another value) and second there is no guarantee that the TIE will be always ≤ 0.05 . More about it in the next example. The run-time is demanding (almost three hours on my machine) and I do not think that one gets a substantial gain.

The following examples explore the maximum TIE for 'Method D' (10; at CV 20%, n_1 12) with the noncentral t-approximation.

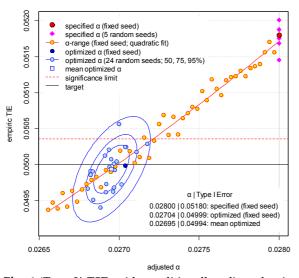


Fig. 4 'Type 2' TSD with conditionally adjusted α in the first stage; first run.

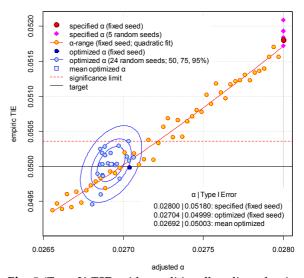


Fig. 5 'Type 2' TSD with conditionally adjusted α in the first stage; second run.

With the specified α 0.0280 we obtain an empiric TIE of 0.05180 (Fig. 4). Note that this 'exact' match with the reported 0.0518 is due to chance. Here we are using the noncentral *t*-approximation, whereas (10) used the shifted central *t*-approximation. Using the same we would get a TIE of 0.05153 (see Example 3, p 7). Since the seed is not given in the reference, differences are to be expected. As in the previous example magenta rhombi show results with random seeds. The mean of optimized alphas is slightly lower (0.02695, TIE 0.04994) than the first estimate (0.02704, TIE 0.04999), but the mean TIE can be >0.05 as shown in yet another run (Fig. 5).

In all references the power approximation by the shifted central *t*-distribution was used for speed reasons (tenths of millions of studies had to be simulated). In actual studies likely the approximation

by the noncentral *t*-distribution or even the exact method (Owen's Q) will be used. Both algorithms are available in commercial (SAS, NQuery) and open-source (R package PowerTOST (27)) software. The former is also implemented in PASS. In the following a comparison of results:

	TI	E by meth	od	adjusted α by				agreement†		
	a	b	С	a	b	С	a	b	С	
Example 1, p 5	0.04307	0.04269	0.04287		not n	ecessary				
Example 2, p 6	0.05062	0.05083	0.05087	0.02858	0.02856	0.02856	yes	yes	yes	
Example 3, p 7	0.05153	0.05180	0.05180	0.02709	0.02704	0.02704	no	no	no	

[†] agreement in conclusions: Analyses by optimized α (if necessary) vs. the pre-specified α .

Note: If an inflated TIE is detected with the exact method, adjusting α can take some [sic] hours.

Example 1 'Method B' (9): *GMR* 0.95, π 0.80, α_1 0.0294, α_2 0.0294. Stage 1 *MSE* 0.032634, ln(T)–ln(R) 0.08396, n_1 12; final *MSE* 0.045896, ln(T)–ln(R) 0.014439, N 20.

```
1
2
            Study conditions and assessment of empiric Type I Error
                                       2×2×2 crossover
            Design
 4
            TSD Type
                                       1 (Potvin et al. 2008, Method B)
                                       0.80
 5
6
7
            Target power
                                       0.95 (fixed)
            GMR used
            Interim power check:
                                       yes
 8
            Futility criterion:
                                       none
                                    : not specified
: not specified
: 0.0294, 0.0294
: 94.12%, 94.12%
 9
            Minimum n2
10
            Maximum N
            Specified \alpha 1, 2
11
12
            Specified CIs
13
14
            Data for the interim analysis
15
                                        18.21% (0.032634)
            CV (MSE)
PE (]n(T)-ln(R))
16
                                       108.76% (0.08396)
17
18
            Sample size
19
20
21
            Data for the final (pooled) analysis
                                         21.67% (0.045896)
22
            CV (MSE)
23
            PE (\ln(T)-\ln(R))
                                       101.45% (0.014439)
24
25
26
            Total sample size
                                        20
            TIE for specified \alpha: 0.04307 (\leq0.05)
27
                                       Applied adjustment is justified.
28
29
30
            Interim analysis (specified \alpha 1 0.0294)
            94.12% CI: 92.93-127.28% (failed to demonstrate BE)
31
            Power : 0.5049 (approx. via shifted central t)
Second stage with 8 subjects (N=20) is justified.
32
33
34
35
            Power based on interim data (specified \alpha)
36
                                       approx. via shifted central t
37
            Method
38
                                       0.5248
            Stage 1
39
40
            Both stages : 0.8560
Studies in stage 2 : 44.2%
Expected total sample size
41
42
               Average
43
               Median
44
45
               5, 95 percentiles: 12, 34
            Final analysis of pooled data (specified \alpha 2 0.0294)
46
47
            94.12% CI: 88.45-116.38% (BE concluded)
48
            Post hoc power (irrelevant;
Based on GMR : 0.6627
49
                                                for validation purposes)
50
            Based on PE
                                     : 0.7685
```

a shifted central *t*-approximation: check.TSD(..., pmethod="shifted")

b noncentral *t*-approximation: check.TSD(..., pmethod="nct")

c exact method: check.TSD(..., pmethod="exact")

```
Since no inflation of the Type I Error is expected, can accept the reported analysis.
```

In 'Type 1' TSDs BE is assessed with the adjusted α in the interim first and then power. Since the study failed to demonstrate BE (line 31) and power is lower than π 0.8 (line 32), the second stage can be initiated (line 33). Otherwise, the study should have stopped already in the interim. The code estimates the sample size of the second stage (based on the *GMR*, π , and α ₂). Lines 35–44 give the result of simulating power (argument pa=TRUE). The average total sample size (called ASN by some authors) is 17.5. With the default setting (pa=FALSE) this part is not shown.

In the final analysis BE is demonstrated. *Post hoc* power is only given to compare the result with the reference (with the default setting this part is not shown). The assessment is given in the box.

Example 2 Data from above but 'Method C': α_0 0.05, α_1 = α_2 0.0294.

```
Study conditions and assessment of empiric Type I Error
 1
 3
            Design
                                       2×2×2 crossover
            TSD Type
                                       2 (Potvin et al. 2008, Method C)
 5
            Target power
                                       0.80
                                    : 0.95 (fixed)
 6
            GMR used
 7
            Interim power check: yes
 8
            Futility criterion
                                       none
            Minimum n2
                                       not specified
            Maximum N : not specified Specified \alpha 1, 2 : 0.050 \mid 0.0294, 0.0294 Specified CIs : 90.00\% \mid 94.12\%, 94.12\% TIE for specified \alpha: 0.05062 (>0.05)
10
11
12
13
                                       Applied adjustment is not justified.
14
15
16
            Interim analysis (specified \alpha 1 \ 0.0294)
17
18
            94.12% CI: 92.93-127.28% (failed to demonstrate BE)
                        : 0.6494 (approx. via shifted central t)
19
            Second stage with 8 subjects (N=20) is justified.
20
21
22
            Power based on interim data (specified \alpha)
23
24
            Method
                                      approx. via shifted central t
25
                                       0.5449
            Stage 1
26
            Both stages
                                       0.8635
27
            Studies in stage 2
                                       40.6%
            Expected total sample size (N)
28
29
                                    : 17.4
               Average
30
               Median
31
               5, 95 percentiles: 12, 34
32
33
            Final analysis of pooled data (specified α2 0.0294)
34
35
            94.12% CI: 88.45-116.38% (BE concluded)
36
37
            \alpha-optimization (objective function: TIE - 0.05 \rightarrow 0)
38
39
                                       approx. via shifted central t
            Method
40
            Convergence
                                       18 iterations (run-time 5.15 min)
                                       5.07E-09
41
            Estimated precision:
            Adjusted α 1, 2 : 0.050 | 0.02858, 0.02858
Adjusted CIs : 90.00% | 94.28%, 94.28%
TIE for adjusted α : 0.04992 (n.s. >0.05)
            Adjusted \alpha 1, 2
42
43
44
45
46
            Interim analysis (adjusted α1 0.02858)
47
48
            94.28% CI: 92.82-127.44% (failed to demonstrate BE)
            Power : 0.6494 (approx. via shifted central t)
Second stage with 8 subjects (N=20) is justified.
49
50
51
52
            Final analysis of pooled data (adjusted \alpha2 0.02858)
53
54
55
            94.28% CI: 88.36-116.49% (BE concluded)
56
57
               Since conclusions of both analyses agree,
58
               can accept the original analysis.
59
```

In 'Type 2' TSDs power in the interim is assessed first. If power is at least π (here 0.8), this implies that the assumptions (*CV*, *GMR*) which lead to the sample size of the first stage seemingly are correct. According to the framework in this case no adjustment has to be done (BE can be assessed with α_0 0.05) since the study will stop in the interim (pass or fail). In the example power is less than the target (line 19) and therefore, BE must be assessed with α_1 0.0294. The study failed to demonstrate BE in the interim (line 18), and therefore, the second stage can be initiated (line 20).

Since an inflation of the TIE (0.05062) is expected, α is optimized (lines 40–47). With an α_2 of 0.02858 the TIE is controlled (0.04992). The interim with this α justifies a second stage as well (lines 49–53).

In the final analysis with the specified α 0.0294 (lines 33–35) BE is easily demonstrated (*CI* well within the acceptance range). Repeating the final analysis with the adjusted α 2 0.02858 (lines 52–54) shows BE as well. The assessment is given in the box.

Example 3 'Method D' (10): *GMR* 0.90, π 0.80, α_0 0.05, $\alpha_1 = \alpha_2$ 0.0280. Stage 1 *CV* 20%, *PE* 0.92, n_1 12; final *CV* 23.315%, *PE* 0.88, *N* 45 (estimated 46; but one dropout in the second stage). Only part of the output is shown below.

```
2
            Study conditions and assessment of empiric Type I Error
            Design
TSD Type
 3
                                      2×2×2 crossover
 4
                                       2 (Montague et al. 2011, Method D)
 5
                                      0.80
            Target power
 6
7
            GMR used
                                      0.90 (fixed)
            Interim power check: yes
 8
            Futility criterion
                                      none
 9
            Minimum n2
                                      not specified
10
            Maximum N
                                      not specified
                                      0.050 | 0.0280, 0.0280
90.00% | 94.40%, 94.40%
            Specified \alpha 1, 2
11
12
            Specified CIs
            TIE for specified \alpha: 0.05153 (>0.05)
13
14
                                      Applied adjustment is not justified.
15
            Interim analysis (specified \alpha 1 \ 0.028)
16
17
            94.40% CI: 77.25-109.57% (failed to demonstrate BE)
            Power : 0.3407 (approx. via shifted central t)
Second stage with 34 subjects (N=46) is justified.
19
20
21
            Final analysis of pooled data (specified \alpha 2 0.028)
22
23
24
25
26
            94.40% CI: 80.00-96.80% (BE concluded)
            \alpha-optimization (objective function: TIE - 0.05 \rightarrow 0)
27
28
            Method
                                      approx. via shifted central t
29
            Convergence
                                      19 iterations (run-time 5.56 min)
30
            Estimated precision: 5.18E-09
            Adjusted α 1, 2 : 0.050 | 0.02709, 0.02709
Adjusted CIs : 90.00% | 94.58%, 94.58%
TIE for adjusted α : 0.04998 (n.s. >0.05)
31
32
33
34
35
            Interim analysis (adjusted α1 0.02709)
36
37
            94.58% CI: 77.13-109.74% (failed to demonstrate BE)
            Power : 0.3407 (approx. via shifted central t)
Second stage with 34 subjects (N=46) is justified.
38
39
40
41
            Final analysis of pooled data (adjusted α2 0.02709)
42
43
            94.58% CI: 79.94-96.88% (failed to demonstrate BE)
44
            Post hoc power (irrelevant; for validation purposes)
45
46
47
               Accepting the reported analysis could in-
48
               crease the relative consumer risk by ~3.1%.
```

This example represents one of the borderline cases; the reported lower confidence limit in the final analysis (lines 20–22) is at the acceptance range. CV 20% and n_1 12 is the location of the maximum in-

flation of the TIE of this method (both according to the authors' results and obtained by the R-package Power2Stage).

Conclusions in the final analyses do *not* agree (the study *passes* with the 94.40% CI but *fails* with the 94.58% *CI*). See lines 24, 43, and the assessment given in the box.

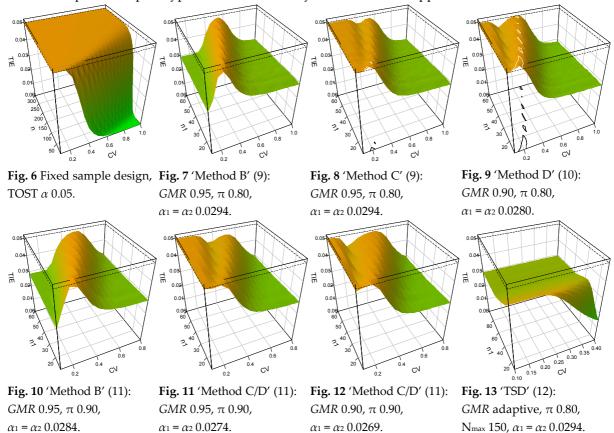
Note that this represents also a case where already the mandatory rounding of the *CI* according to the guideline (1) slightly inflates the TIE (even in fixed sample designs). The 94.40% *CI* is actually 79.99842–96.80191%. The study passes only due to rounding the lower confidence limit up to 80.00%.

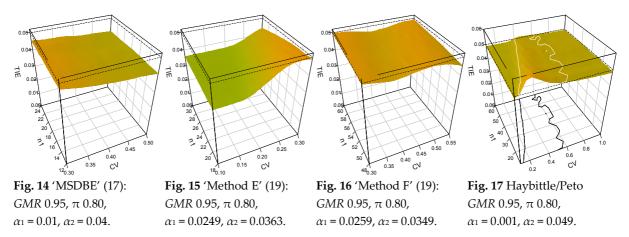
Working range of the frameworks

Ref.	Туре	Method	CV	n_1	GMR	π	α1	Q (2	futility [†]	N _{max} ‡
9	1	В	0.1 - 1.0	12 - 60	0.95	0.80	0.0294	0.0294		
9	2	C	0.1 - 1.0	12 - 60	0.95	0.80	0.0294	0.0294		
10	2	D	0.1 - 1.0	12 - 60	0.90	0.80	0.0280	0.0280		
11	1	В	0.1 - 0.8	12 - 60	0.95	0.90	0.0284	0.0284		
11	2	C/D	0.1 - 0.8	12 - 60	0.95	0.90	0.0274	0.0274		
11	2	C/D	0.1 - 0.8	12 - 60	0.90	0.90	0.0269	0.0269		
12	2	TSD	0.1 - 0.4	12 - 96	0.95	0.80	0.0294	0.0294		UL
13	2	TSD-1	0.2 - 0.4	12 - 60	0.95	0.80	0.0280	0.0280		UL
13	1	TSD-2	0.2 - 0.4	12 - 60	0.95	0.80	0.0294	0.0294		UL
17	1	MSDBE	0.3 - 0.5	12 - 24	0.95	0.80	0.0100	0.0400		
19	1	Е	0.1 - 0.3	18 - 30	0.95	0.80	0.0249	0.0363	0.9374 - 1.0667	42
19	1	Е	0.3 - 0.55	48 - 60	0.95	0.80	0.0254	0.0357	0.9305 - 1.0747	180
19	2	F	0.1 - 0.3	18 - 30	0.95	0.80	0.0248	0.0364	0.9492 - 1.0535	42
19	2	F	0.3 - 0.55	48 - 60	0.95	0.80	0.0259	0.0349	0.9350 - 1.0695	180

- [†] Futility of the $100(1-2\alpha_1)$ confidence interval in the first stage and a fixed upper limit of the total sample size N (19).
- ‡ Futility of 0.80 1.25 on the *GMR* in the first stage and a pre-specified upper limit (UL) of the total sample size N (12, 13).

Some examples of empiric type I errors obtained by the noncentral *t*-approximation:





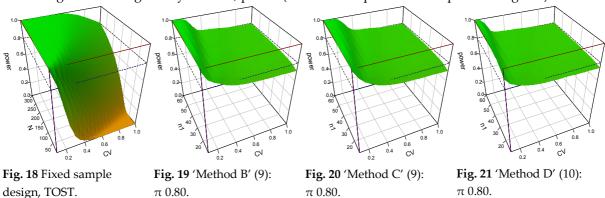
In the fixed sample design with α 0.05 (Fig. 6) we see that TOST is not a uniformly most powerful test; with high *CV*s the test gets conservative (TIE \rightarrow 0).

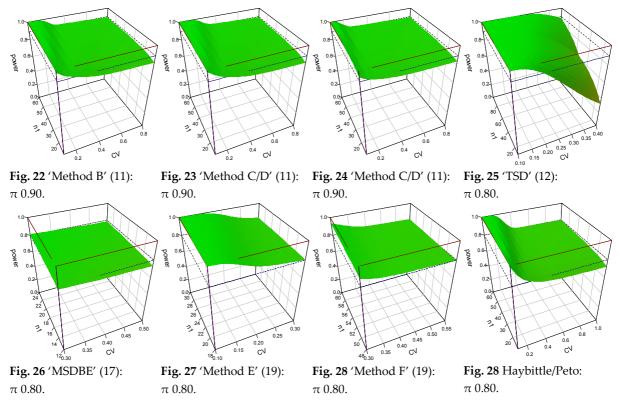
'Type 1' TSDs (Fig. 7, 10) have minima (TIE $\rightarrow \alpha_{adjusted}$). This is observed both with low *CVs* (*i.e.*, in studies mainly stopped in stage 1) and with high *CVs* (studies mainly proceeding to stage 2). Maxima (TIE $\rightarrow \alpha_{nominal}$) are seen with moderate *CVs* and n_1 . 'Type 2' TSD behave like TOST in a fixed sample design with low *CVs* and then like 'Type 1' TSDs (Fig. 8, 9, 11, 12). The adaptive design (Fig. 13) is conservative due to the fact that a certain fraction of studies will not proceed to the second stage because of its two futility rules. Due to the Bonferroni adjustment 'MSDBE' behaves like TOST with $\alpha \sim 0.04$ (Fig. 14). Although not shown, at high *CVs* the method will become conservative as well. The methods of Xu *et al.* (19) show a different pattern due to the two futility rules – regardless whether the are of 'Type 1' (Fig. 15) or 'Type 2' (Fig. 16).

Naïve (mis)use of methods developed for superiority testing in parallel groups (4, 28, 29) may lead to an unacceptably inflated TIE in a wide range of CV/n_1 combinations (Fig. 17: note the different z-axis; at CV 0.25 and n_1 12 the TIE is 0.0584). A valid remedy would be application of an α -spending function (30, 31). Whether such an approach is acceptable according to the guideline – calling for *prespecified* alphas – is unclear.

In general within their validated ranges all frameworks control the type I error. Only in two 'Type 2' TSDs ('Method C' (9) and 'Method D' (10)) for *certain* combinations of CV and n_1 (see the contours in Fig. 8 and 9) a slightly inflated TIE can be expected. Hence, in real studies even for those TSDs the consumer risk will be controlled in the majority of cases.

Although not of a regulatory concern, power (GMRs and alphas as in the previous figures):





TSDs maintain approximately the target (desired) power π . At very low *CV*s power might be higher than the target and drops slightly below the target for lows *CV*s and small n_1 . Power characteristics of the adaptive design (Fig. 25) are not sufficient (15, 21). Only the methods of Xu *et al.* (19) preserve π throughout the entire range (Fig. 26, 27). Their power characteristics are superior to all the other methods.

Validation

		interim							final						
е	Т	r	eported	<pre>check.TSD()</pre>				re	eported		<pre>check.TSD()</pre>				
		CI		π	CI		π	CI		π	CI		π		
1	1	104.27	134.17	75.6	104.27	134.17	75.61	102.83	129.71	NR	102.83	129.70	82.17		
2	2	106.26	131.66	84.1	106.26	131.66	84.12	NP (failed in the interim)							
3	1	92.93	127.28	50.5	92.93	127.28	50.49	88.45	116.38	66.3	88.45	116.38	66.27		
4	2	92.93	127.28	64.9	92.93	127.28	64.94	88.45	116.38	66.3	88.45	116.38	66.27		
5	2		NR		77.25	109.57	34.07		NR		80.00	96.80	67.71		
6	1		NR		67.27	131.41	55.90		NR		80.37	105.31	64.75		
7	1		NR		68.21	132.30	00.00		NR		84.67	106.59	80.06		
8	1	78	114	35.8	78.18	113.74	35.66	91	112	NR	91.04	112.05	88.04		
9	2	78	114	48.7	78.25	113.65	45.57	91	112	NR	90.98	112.12	87.83		
10	1		NR		78.65	109.97	40.92		NR		82.27	102.87	84.51		
11	2		NR		73.75	105.00	34.07		NR		82.42	96.11	85.07		
12	2		NR		83.07	108.65	76.97		NR		84.47	106.84	80.17		
13	2		NR		79.96	112.87	56.50		NR		81.26	104.05	76.97		
14	2	99.07	111.85	99.90	99.07	111.85	99.90		NP (pas	sed in	the in	terim)			

- e Number of internal validation example: check.TSD(valid=TRUE, expl=e)
- T Type of design
- CI $100(1-2\alpha)$ confidence interval
- π Power (in the interim or *post hoc*)
- NR Not reported
- NP Not performed

References

- 1 European Medicines Agency, Committee for Medicinal Products for Human Use. *Guideline on the investigation of bioequivalence*. London: 20 January 2011; CPMP/EWP/QWP/1401/98 Rev. 1.
- 2 Armitage P, McPherson CK, Rowe BC. *Repeated significance tests on accumulating data.* J R Stat Soc Ser A. 1969; 132(2): 235–44. doi:10.2307/2343787.
- 3 Pocock SJ. *Group sequential methods in the design and analysis of clinical trials.* Biometrika. 1977; 64(2): 191–9. Open access.
- 4 O'Brien PC, Fleming TR. *A multiple testing procedure for clinical trials*. Biometrics. 1979; 35(3): 549–56. Open access.
- 5 Pocock SJ. *Interim analyses for randomized clinical trials: the group sequential approach.* Biometrics. 1982; 38(1): 153–62.
- 6 Armitage P. *Interim Analysis in Clinical Trials*. Stat Med. 1991; 10(6): 925–37. doi:10.1002/sim.4780100613.
- 7 Gould AL. *Group sequential extension of a standard bioequivalence testing procedure.* J Pharmacokinet Biopharm. 1995; 23(1): 57–86. doi:10.1007/BF02353786.
- 8 Hauck WW, Preston PE, Bois FY. *A group sequential approach to crossover trials for average bioequivalence*. J Biopharm Stat. 1997; 71(1): 87–96. doi:10.1080/10543409708835171.
- 9 Potvin D, DiLiberti CE, HauckWW, Parr AF, Schuirmann DJ, Smith RA. *Sequential design approaches for bioequivalence studies with crossover designs*. Pharm Stat. 2008; 7(4): 245–62. doi:10.1002/pst.294.
- 10 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. doi:10.1002/pst.483.
- 11 Fuglsang A. Sequential bioequivalence trial designs with increased power and controlled type I error rates. AAPS J. 2013; 15(3): 659–61. doi:10.1208/s12248-013-9475-5.
- 12 Karalis V, Macheras P. *An insight into the properties of a two-stage design in bioequivalence studies.* Pharm Res. 2013; 30(7): 1824–35. doi:10.1007/s11095-013-1026-3.
- 13 Karalis V. *The role of the upper sample size limit in two-stage bioequivalence designs*. Int J Pharm. 2013; 456(1): 87–94. doi:10.1016/j.ijpharm.2013.08.013.
- 14 Karalis V, Macheras P. *On the statistical model of the two-stage designs in bioequivalence assessment.* J Pharm Pharmacol. 2014; 66(1): 48–52. doi:10.1111/jphp.12164.
- 15 Fuglsang A. Futility rules in bioequivalence trials with sequential designs. AAPS J. 2014; 16(1): 79–82. doi:10.1208/s12248-013-9540-0.
- 16 Fuglsang A. Sequential bioequivalence approaches for parallel designs. AAPS J. 2014; 16(3): 373–8. doi:10.1208/s12248-014-9571-1.
- 17 Zheng Ch, Zhao L, Wang J. *Modifications of sequential designs in bioequivalence trials*. Pharm Stat. 2015; 14(3):180–8. doi:10.1002/pst.1672.
- 18 Kieser M, Rauch G. *Two-stage designs for cross-over bioequivalence trials*. Stat Med. 2015; 34(16): 2403–16. doi:10.1002/sim.6487.
- 19 Xu J, Audet C, DiLiberti CE, Hauck WW, Montague TH, Parr TH, Potvin D, Schuirmann DJ. *Optimal adaptive sequential designs for crossover bioequivalence studies*. Pharm Stat. 2015; 15(1): 15–27. doi:10.1002/pst.1721.
- 20 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. 29 August 2017; Epub ahead of print. doi:10.1002/sim.7452.

- 21 Schütz H. *Two-stage designs in bioequivalence trials*. Eur J Clin Pharmacol. 2015; 71(3): 271–81. doi:10.1007/s00228-015-1806-2.
- 22 Tsiatis AA, Mehta C. *On the inefficiency of the adaptive design for monitoring clinical trials.* Biometrika. 2003; 90(2): 367–78. doi:10.1093/biomet/90.2.367.
- 23 Schütz H. *AdaptiveBE: Acceptability of Adaptive Bioequivalence Studies*. 2017; R package version 0.8.3.9000. https://github.com/Helmut01/AdaptiveBE
- 24 R Core Team. *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. Vienna, Austria: 2017; https://www.r-project.org/
- 25 Labes D, Lang B, Schütz H. *Power2Stage: Power and Sample-Size Distribution of 2-Stage Bioequivalence Studies*. 2017; R package version 0.4.5.9000. https://CRAN.R-project.org/package=Power2Stage
- 26 Brent RP. Algorithms for minimization without derivatives. Mineola: Dover Publications; 2003.
- 27 Labes D, Schütz H, Lang B. *PowerTOST: Power and Sample Size Based on Two One-Sided t-Tests* (TOST) for (Bio)Equivalence Studies. 2017; R package version 1.4.6.9000. https://cran.r-project.org/package=PowerTOST
- 28 Haybittle JL. *Repeated assessment of results in clinical trials of cancer treatment.* Br J Radiol. 1971; 44: 793–7. doi:10.1259/0007-1285-44-526-793.
- 29 Peto R, Pike MC, Armitage P, Breslow NE, Cox DR, Howard SV, Mantel N, McPherson K, Peto J, Smith PG. *Design and analysis of randomized clinical trials requiring prolonged observation of each patient. II. analysis and examples.* Br J Cancer. 1977; 35: 2–39. doi:10.1038/bjc.1977.1.
- 30 Lan KG, DeMets DL. Discrete sequential boundaries for clinical trials. Biometrika. 1983; 70: 659-63.
- 31 Jennison C, Turnbull BW. *Equivalence tests*. In: Jennison C, Turnbull BW, editors. *Group sequential methods with applications to clinical trials*. Boca Raton: Chapman & Hall/CRC; 1999. p. 142–57.