Reference-scaling and Control of the Type I Error

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Study Designs

The more ‘sophisticated’ a design is, the more information can be extracted.

- **Hierarchy of designs:**
  - Full replicate (RTRT | TRTR or RTR | TRT)
    - Partial replicate (RRT | RTR | TRR)
      - 2×2×2 crossover (RT | TR)
        - Parallel (R | T)

- **Variances which can be estimated:**

Parallel:	total variance (between + within subjects)
2×2×2 crossover:	+ between, within subjects
Partial replicate:	+ within subjects (of R)
Full replicate:	+ within subjects (of R and T)

High variability

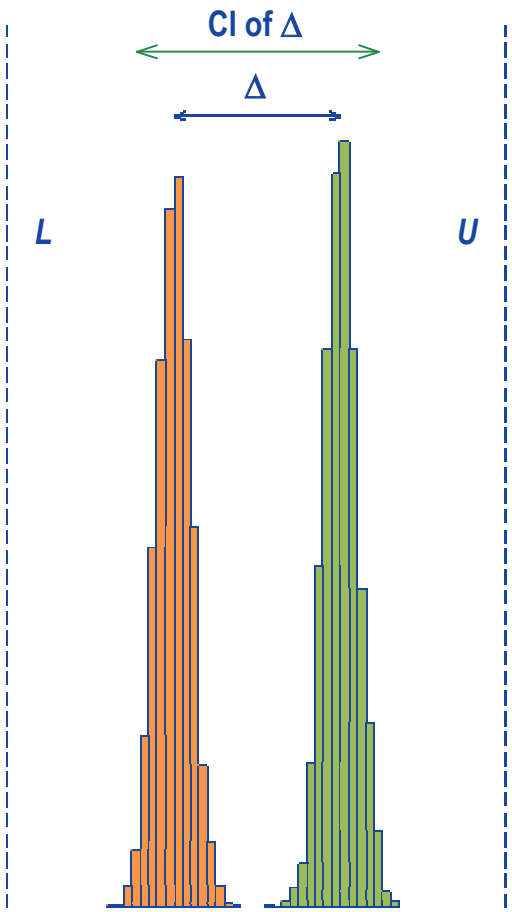
High (within-subject) variability can be

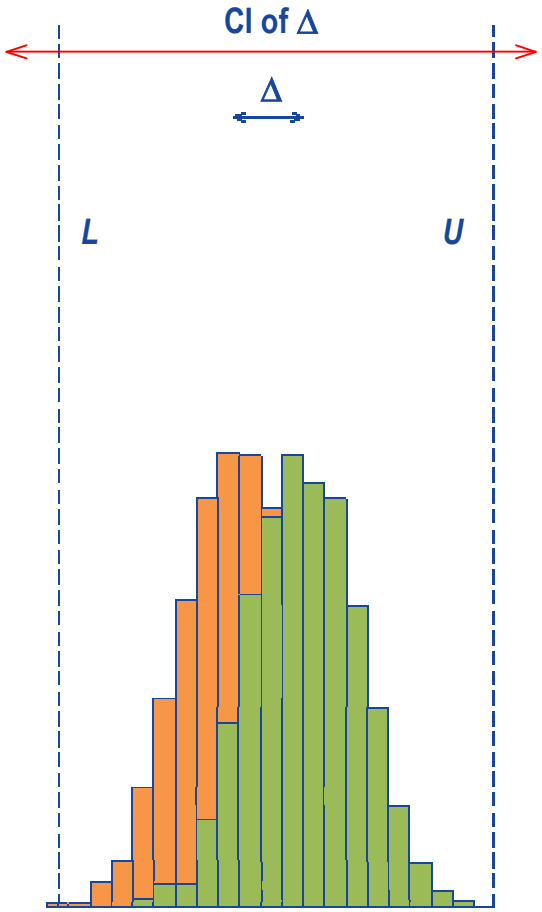
- an intrinsic property of the drug itself (low absorption and/or inter-occasion clearance) and/or
- attributed to the product's performance
  - Physiology (enteric coated formulations and gastric emptying)
  - Absorption: rate of drug release and absorption window
  - Influence of excipients and/or food
    - on gastric motility and/or
    - on transporters

HVD

HVDP

Highly Variable Drugs / Drug Products





Counterintuitive concept of BE:

Two formulations with a large difference in means are declared bioequivalent if variances are low, but not BE – even if the difference is quite small – due to high variability

Modified from Tothfálusi *et al.* (2009), Fig. 1

Highly Variable Drugs / Drug Products

It may be almost impossible to demonstrate BE of HVD(P)s with a reasonable sample size

- **Example: *CV* 70%, *GMR* 0.90, target power 80%, 2×2×2 design**

```
library(PowerTOST)
sampleN.TOST(CV=0.7, theta0=0.9, targetpower=0.9, design="2x2x2")
++++++++++++ Equivalence test - TOST ++++++++++++
            Sample size estimation
-----------------------------------------------
Study design:  2x2 crossover
log-transformed data (multiplicative model)
alpha = 0.05, target power = 0.8
BE margins = 0.8 ... 1.25
True ratio = 0.9,  CV = 0.7
Sample size (total)
 n     power
358   0.801175
```

- **Since HVD(P)s are considered to be safe and efficacious some jurisdictions accept a larger 'not clinically relevant' difference**
  - **The BE limits can be *scaled* based on the variability of the reference**

HVD(P)s – Reference-scaling

It may be almost impossible to demonstrate BE with a reasonable sample size

- Reference-scaling (*i.e.*, widening the acceptance range based of the variability of the reference) introduced 2010 by the FDA and EMA and by Health Canada in 2016
  - Requires a replicate design, where at least the reference product is administered twice (though not necessarily to all subjects)
  - Smaller sample sizes compared to the standard 2×2×2 design but outweighed by increased number of periods
  - Similar total number of individual treatments
  - Any replicate design can be evaluated for 'classical' (unscaled) Average Bioequivalence (ABE) as well. Switching CV_{wR} 30%:
    - FDA: *AUC* and C_{max}
    - EMA: C_{max}; MR products additionally: $C_{ss,min}$, $C_{ss,τ}$, partial *AUC*s
    - Health Canada: *AUC*

HVD(P)s – Reference-scaling

Models (in log-scale)

- **ABE Model**
  - A difference Δ of $\leq$20% is considered to be clinically not relevant
  - The limits [*L*, *U*] of the acceptance range are fixed to
    $\log(1-\Delta) = \log((1-\Delta)^{-1})$ or $L \sim -0.2231$ and $U \sim +0.2231$
  - The consumer risk is fixed with 0.05. BE is concluded if the $100(1-2\alpha)$ confidence interval lies entirely within the acceptance range

$$-\theta_A \leq \mu_T - \mu_R \leq +\theta_A$$

- **SABEL Model**
  - Switching condition θ_S is derived from the regulatory standardized variation σ_0 (proportionality between acceptance limits in log-scale and σ_{wR} in the highly variable region)

$$-\theta_S \leq \frac{\mu_T - \mu_R}{\sigma_{wR}} \leq +\theta_S$$

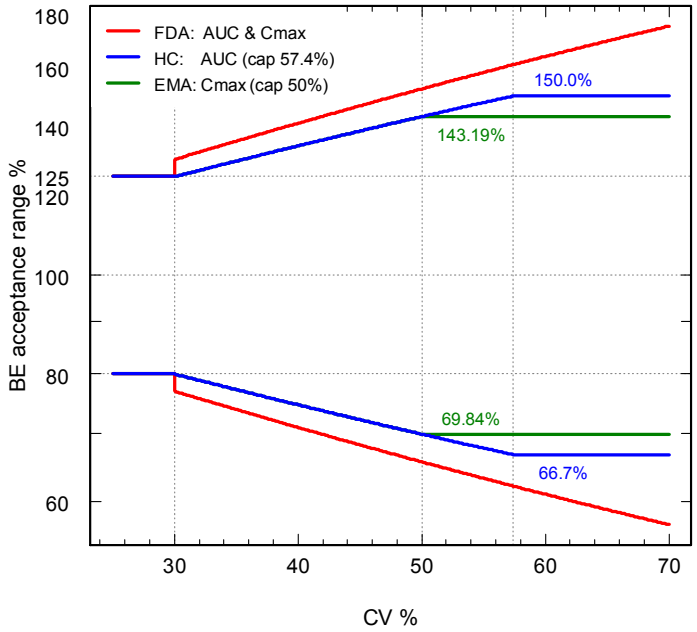
HVD(P)s – Reference-scaling

Regulatory Approaches

- Bioequivalence limits derived from σ_0 and σ_{wR}

$$\theta_s = \frac{\log(1.25)}{\sigma_0}, \quad [L,U] = e^{\pm\theta_S \cdot \sigma_{wR}}$$

- FDA
  - Scaling σ_{wR} 0.25 (θ_S 0.893) but applicable at CV_{wR} ≥30%
  - Discontinuity at CV_{wR} 30%
- EMA
  - Scaling σ_0 0.2936 (θ_S 0.760)
  - Upper cap at CV_{wR} 50%
- Health Canada
  - Like EMA but upper cap at CV_{wR} 57.4%



HVD(P)s – Reference-scaling

Regulatory Approaches

- Scaled limits based on variability of the reference
  - EMA IR C_{max} only; MR (additionally $C_{max,ss}$, $C_{min,ss}$, $C_{τ,ss}$, partial *AUC*s)
  - FDA C_{max} and *AUC*
  - HC *AUC* only

EMA	
CV_{wR}	BE limits (%)
≤30	80.00 – 125.00
35	77.23 – 129.48
40	74.62 – 134.02
45	72.15 – 138.59
≥50	69.84 – 143.19

FDA	
CV_{wR}	BE limits (%)
≤30	80.00 – 125.00
35	73.83 – 135.45
40	70.90 – 141.04
45	68.16 – 146.71
50	65.60 – 152.45
60	60.96 – 164.04
80	53.38 – 187.35
100	47.56 – 210.25

HC	
CV_{wR}	BE limits (%)
≤30	80.00 – 125.00
35	77.23 – 129.48
40	74.62 – 143.02
45	72.15 – 138.59
50	69.84 – 143.19
≥57.4	66.67 – 150.00

HVD(P)s – Reference-scaling

The EMA's Approach

- Average Bioequivalence with Expanding Limits – ABEL (crippled from Endrényi and Tóthfalusi 2009)
  - Justification that the widened acceptance range is clinically not relevant (important – different to the FDA)
  - Assumes identical variances of T and R [*sic*] like in a 2×2×2
  - All fixed effects model according to the Q&A-document preferred
  - Mixed-effects model (allowing for unequival variances) is 'not compatible with CHMP guideline'…
  - Scaling limited at a maximum of CV_{wR} 50% (*i.e.*, to 69.84 – 143.19%)
  - *GMR* within 80.00 – 125.00%
  - Demonstration that CV_{wR} >30% is not caused by outliers (box plots of studentized intra-subject residuals?)…
  - ≥12 subjects in sequence RTR of the 3-period full replicate design

HVD(P)s – Reference-scaling

The EMA's Approach

- Pitfalls and suggestions
  - The applicant should justify that the calculated intra-subject variability is a reliable estimate and that it is not the result of outliers
    - EMA Q&A-document (Rev. 7, March 2011), Data set I:
      RTRT | TRTR full replicate, 77 subjects, unbalanced, incomplete
    - CV_{wR} 46.96% → apply ABEL (>30%)
    - Scaled acceptance range: 71.23 – 140.40%
    - Method A: 90% CI 107.11 – 124.89% ⊂ AR; PE 115.66% ⊂ 80.00 – 125.00%
    - Method B: 90% CI 107.17 – 124.97% ⊂ AR; PE 115.73% ⊂ 80.00 – 125.00%
    - But there *are* two severe outliers!
      By excluding subjects 45 and 52, the CV_{wR} drops to 32.16%
    - New scaled acceptance range: 78.79 – 126.93%
      Almost no more gain compared to the conventional ABE limits
    - Outliers have to be only excluded for the calculation of CV_{wR} but *kept* for the calculation of the CI

HVD(P)s – Reference-scaling

The EMA's Approach

- Pitfalls and suggestions
  - Incomplete data (missing periods)
    - Even if one has no data of T (*e.g.*, a subject dropped out after the second period in sequence RRT) *do not* exclude the subject from the calculation of CV_{wR}. The estimate will be more accurate.
    - Must be unambigously stated in the protocol
      Example for the partial replicate design (TRR|RTR|RRT)
      - » Data set for the estimation of CV_{wR}
        All subjects with two administrations of R regardless of any other missing periods
      - » Data set for the calculation of the 90% confidence interval
        All subjects with at least one administration of T and at least one administration of R

HVD(P)s – Reference-scaling

The EMA's Approach

- Pitfalls and suggestions
  - If ever possible avoid the partial replicate design (TRR|RTR|RRT)
    - Since the test product is not repeated, it is not possible to estimate CV_{wT}
      - » Even if you plan the pivotal study in a partial replicate (why?), a full replicate pilot study will give you an incentive in the sample size if $CV_{wT} < CV_{wR}$
        Example: CV_{wT} 35%, CV_{wR} 50%, *GMR* 0.90, power 80%, sample sizes:

TRRT|RTTR	22
RT|RTR	34
TRR|RTR|RRT	33

        If your pilot was a partial replicate, you have to *assume* that $CV_{wT} = CV_{wR}$

TRRT|RTTR	28
TRT|RTR	42
TRR|RTR|RRT	39
    - If there are problems in the evaluation or questions from an authority it is rather difficult to assess its properties in simulations

HVD(P)s – Reference-scaling

The EMA's Approach

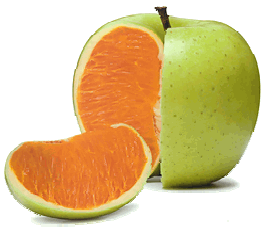
- Pitfalls and suggestions
  - ≥12 subjects in sequence RTR of the 3-period full replicate design (Q&A-document, Rev. 12 June 2015)
    - With sample sizes for the commonly applied T/R-ratio of 0.90 for HVD(P)s and ≥80% power this issue is practically not relevant.
    - Would affect only studies with extreme dropout-rates (>42%)!

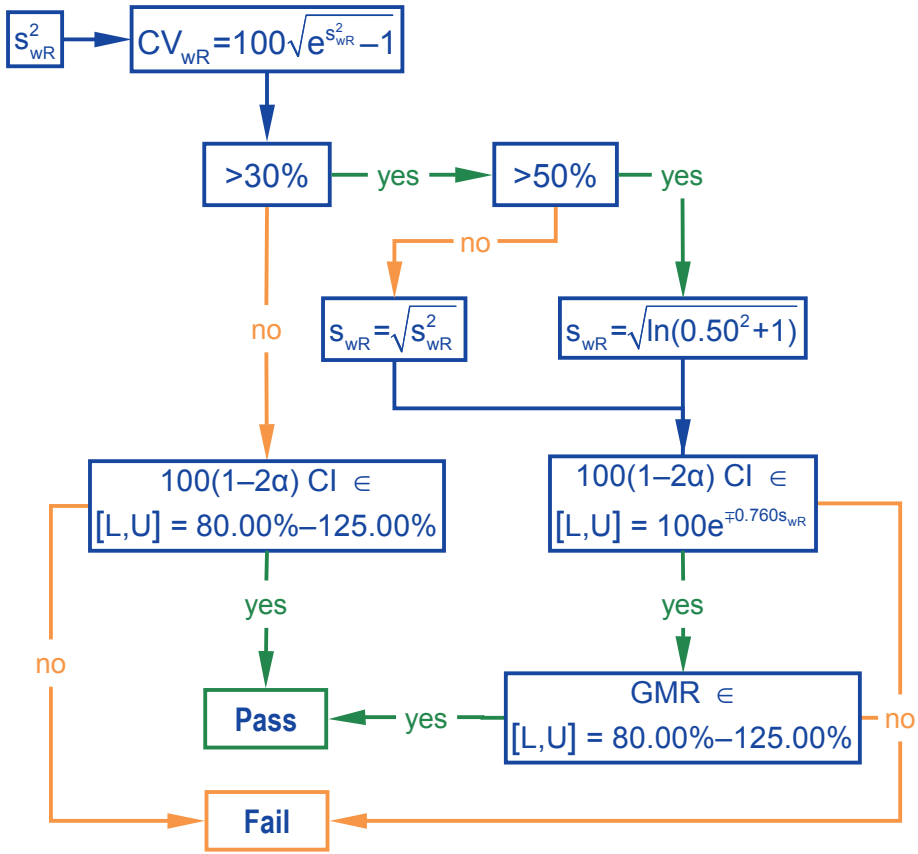
CV_{wR} (%)	N	n_{RTR}	max. dropout-rate (%)
25	42	21	42.9
30	50	25	52.0
40	40	20	47.8
50	42	21	42.9
60	48	24	50.0
70	60	30	60.0
80	74	37	67.6

HVD(P)s – Reference-scaling

The EMA's Approach

- **Decision Scheme**
  - The Null Hypothesis is *specified* in the face of the data
  - Acceptance limits themselves become random variables
  - Type I Error (consumer risk) might be inflated





HVD(P)s – Reference-scaling

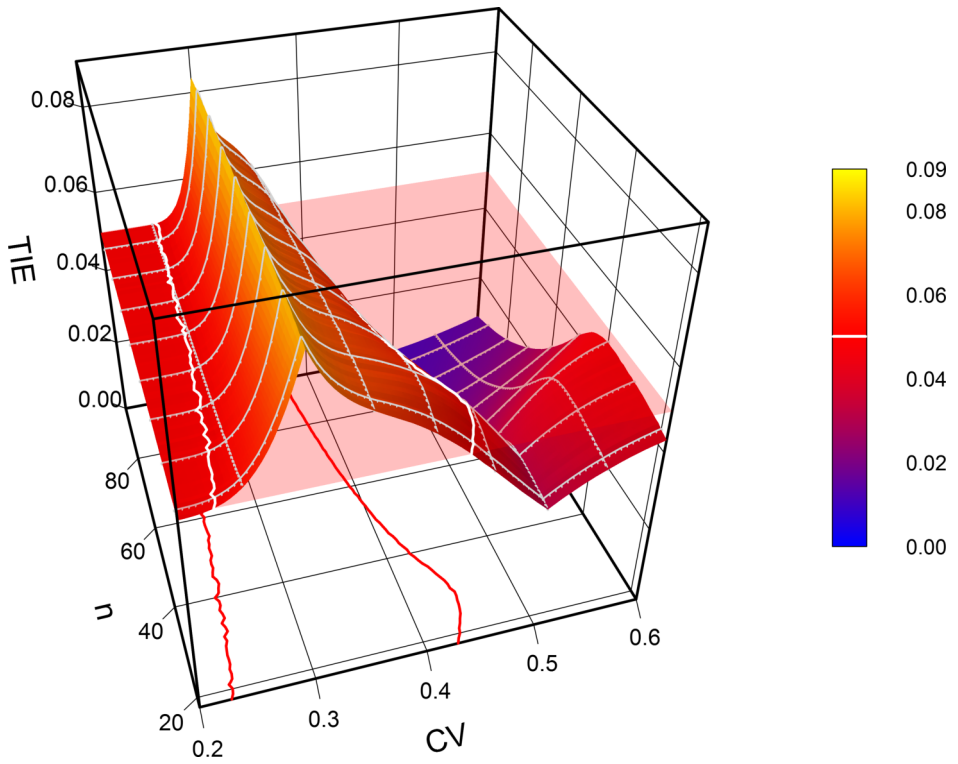
Assessing the Type I Error (TIE)

- TIE = falsely concluding BE at the limits of the acceptance range
  In ABE the TIE is ≤0.05 at 0.80 and ≤0.05 at 1.25
- Due to the decision scheme no direct calculation of the TIE at the scaled limits is possible;
  → extensive simulations required (10^6 BE studies mandatory)
- Inflation of the TIE suspected
  Chow *et al*. 2002, Willavazie & Morgenthien 2006, Chow & Liu 2009, Patterson & Jones 2012
- Confirmed
  - EMA's ABEL: Tóthfalusi & Endrényi 2009, 2017, BEBA-Forum 2013, Wonnemann *et al*. 2015, Muñoz *et al*. 2016, Labes & Schütz 2016, Molins *et al*. 2017
  - FDA's RSABE: Tóthfalusi & Endrényi 2009, BEBA-Forum 2013, Muñoz *et al*. 2016

HVD(P)s – Reference-scaling

Example for ABEL

- RTRT | TRTR
  sample size 18 – 96
  CV_{wR} 20% – 60%
  - TIE_{max} 0.0837
  - Relative increase of the consumer risk 67%!



HVD(P)s – Reference-scaling

What is going on here?

- SABE is stated in model *parameters* …

$$-\theta_S \leq \frac{\mu_T - \mu_R}{\sigma_{wR}} \leq +\theta_S$$

… which are *unknown*

  - Only their *estimates* (*GMR*, s_{wR}) are accessible in the actual study
  - At CV_{wR} 30% the decision to scale will be wrong in ~50% of cases
  - By moving away from 30% the chances of a wrong decision decrease and hence, the Type I Error
  - At high *CV*s (>43%) both the scaling cap and the *GMR*-restriction help to maintain the TIE <0.05)

HVD(P)s – Reference-scaling

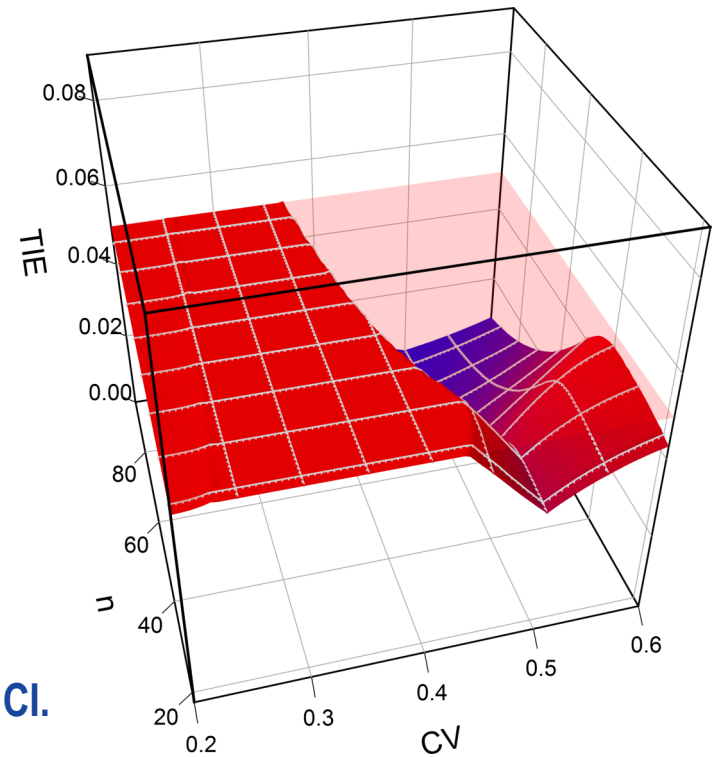
Outlook

- Utopia
  - Agencies collect CV_{wR} from submitted studies. Pool them, adjust for designs / degrees of freedom. The EMA publishes a fixed acceptance range in the product-specific guidance. No need for replicate studies any more. 2×2×2 crossovers evaluated by ABE would be sufficient.
- Halfbaked
  - Hope [*sic*] that *e.g.*, Bonferroni preserves the consumer risk. Still apply ABEL, but with a 95% CI (α 0.025).
  - Drawback: Loss of power, substantial increase in sample sizes.
- Proposal
  - Iteratively adjust α based on the study's CV_{wR} and sample size – in such a way that the consumer risk is preserved (Labes & Schütz 2016, Molins *et al.* 2017)

ABEL (iteratively adjusted α)

Previous example

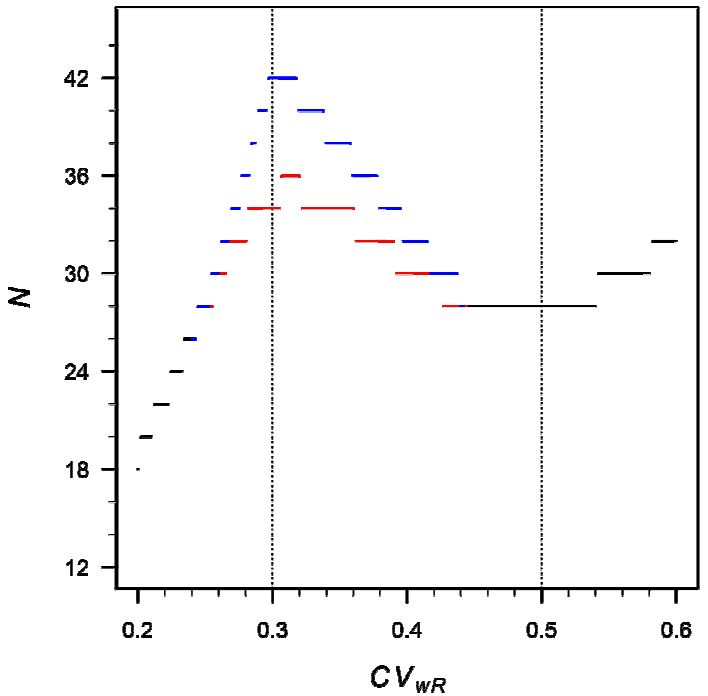
- Algorithm
  - Assess the TIE for the nominal α 0.05.
  - If the TIE $\leq$ 0.05, stop.
  - Otherwise adjust α (downwards) until the TIE = 0.05.
  - At CV_{wR} 30% (dependent on the sample size) α_{adj} is 0.0273 – 0.0300;
    $\rightarrow$ use a 94.00 – 94.54% CI.



ABEL (iteratively adjusted α)

Potential impact on the sample size

- Example: RTRT | TRTR, θ_0 0.90, target power 0.80.
  - Moderate in the critical region (— —).
    - CV_{wR} 30%: 36 → 42 (+17%);
    - CV_{wR} 35%: 34 → 38 (+12%);
    - CV_{wR} 40%: 30 → 32 (+7%).
  - None outside (—).



ABEL (iteratively adjusted α)

Example (RTRT | TRTR, expected CV_{wR} 35%, θ_0 0.90, target power 0.80); R package PowerTOST (≥1.3-3).

- **Estimate the sample size**

```
sampleN.scABEL(CV=0.35, theta0=0.90, targetpower=0.80, design="2x2x4",
               details=FALSE, print=FALSE)[["Sample size"]]
[1] 34
```

- **Estimate the empiric Type I Error for this study**

```
UL <- scABEL(CV=0.35)[["upper"]] # scaled limit (1.2948 for CVwR 0.35)
power.scABEL(CV=0.35, theta0=UL, n=34, design="2x2x4", nsims=1e6)
[1] 0.065566
```

- **Iteratively adjust α**

```
scABEL.ad(CV=0.35, n=34, design="2x2x4")
++++++++++++ scaled (widened) ABEL ++++++++++++
          iteratively adjusted alpha
-----------------------------------------------
CVwR 0.35, n(i) 17|17 (N 34)
Nominal alpha                 : 0.05
True ratio                    : 0.9000
Regulatory settings           : EMA (ABEL)
Empiric TIE for alpha 0.0500  : 0.06557
Power for theta0 0.900        : 0.812
Iteratively adjusted alpha    : 0.03630
Empiric TIE for adjusted alpha: 0.05000
Power for theta0 0.900        : 0.773
```

ABEL (iteratively adjusted α)

- **Optionally compensate for the loss in power (0.812 → 0.773) by increasing the sample size:**

```
sampleN.scABEL.ad(CV=0.35, theta0=0.90, targetpower=0.80, design="2x2x4")
++++++++++++ scaled (widened) ABEL ++++++++++++
            Sample size estimation
        for iteratively adjusted alpha
--------------------------------------------
Study design: 2x2x4 (RTRT|TRTR)
Expected CVwR 0.35
Nominal alpha      : 0.05
True ratio         : 0.9000
Target power       : 0.8
Regulatory settings: EMA (ABEL)
Switching CVwR     : 30%
Regulatory constant: 0.760
Expanded limits    : 0.7723...1.2948
Upper scaling cap  : CVwR 0.5
PE constraints     : 0.8000...1.2500
n  38,   adj. alpha: 0.03610 (power 0.8100), TIE: 0.05000
```

- n 34 → 38 (+12%), power 0.773 → 0.810, α_{adj} 0.0363 → 0.0361

Reference-scaling and Control of the Type I Error

Thank You!
Open Questions?

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