# GENERAL STATISTICAL METHODOLOGIES FOR ADAPTIVE DESIGN

## **Background**

The Pharmaceutical Research and Manufacturers of America (PhRMA) working group on adaptive design defined adaptive designs as "a clinical study design that uses accumulating data to decide how to modify aspects of the study as it continues without undermining the validity and integrity of the trial" While both validity and integrity are important, statistical methods are mainly designed to safeguard validity, which means to provide the correct statistical inferences. E.g., the overall pre-specifiedType I error rate must be maintained.

In general, varies statistical methods to control Type I Error in adaptive clinical trials can be classified into the followingcategories:

1) Repeat testing such as group sequential trials, 2)Multiple hypothesis testing or multiple comparison, 3)Combination of pre- and post- adaptation data.

In more complex adaptive trials where statistical methodologies are not available to ensure the Type I Error rate is controlled at its nominal level, the so called strict control, simulations areusually used to demonstrate the operating characteristic.

## **Repeat Testing**

The earliest development of adaptive clinical trials is perhaps the group sequential trials where a trial can be stopped early if there is strong evidence of efficacy during any planned interim analysis.

- ❖ Pocock crossing boundary
- **<sup>❖</sup>** O'Brien and Fleming crossing boundaries
- ❖ The alpha spending function developed by Lan and DeMets<br>(1983) (1983)

Violation of assumption - the information accumulated each time between interim analyses is statistically independent.

Scharfstein et al. (1997) demonstrated that sequential Wald statistics behave like a standardized partial sum of independent normal variables and thus have independent increments.

Chen et al. (2014) extended the alpha spending function methodology to derive stopping boundaries for testing different hypotheses at different interim analyses.

### **Combination Test of Pre- and Post- Adaptation Data**

Let  $p_1$  denote the p-value based only on the first stage data and  $p_2$  denote the p-value based only on the second stage data.

• If  $a < p_1 \le b$ , proceed to the second stage, reject  $H_0$  if the combination function,  $C(p_1, p_2) \le c$ .

where  $I_{[C(x,y)\leq c]}$  is an indicator function. Some combination functions are discussed below.

The combination methods can be applied to different adaptive designs to provide combined critical values or to combine p-values from pre-

 $a + \int_a^b \int_0^1 I_{[{\mathcal C}(x,y) \leq c]} dy dx = \alpha,$ 

function:

inverse of the function.

## **Multiple Hypothesis Testing**

The stepwise multiple comparison procedures based on the closure principle, also known as closed testing methods, can also be applied to adaptive clinical trials. These methods are very often used in combination with the stage-wise combination method to allow for additional flexibility. Under the closed testing principal, reject a hypothesis,  $H_i$ , if all intersection hypotheses,  $H_I = \bigcap_{i \in I} H_i$ , are rejected at level  $\alpha$ . For example, the general Bonferroni method, although somewhat conservative, is valid for all correlation structure. A single stage Dunnett procedure was discussed in Bretz's (2006) seamless Phase II/III design.

## **Bayesian Approach in Adaptive Designs**

The Bayes theorem fits naturally in the adaptive design framework (learning and confirming cycle).

- $\triangleright$  The prior distribution,  $P(\theta)$ , represents the prior linear that the state of the prior knowledge.
- The posterior distribution, *P(*θ*|y)*, represents the knowledge gained after learning from the data, *<sup>y</sup>*. The Type I error or Type II error concept does not exist

 in the Bayes theorem. These probabilities, or so called operating characteristics, are usually obtained viasimulations.

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## Brannath's et al (2002) proposed overall p-value for combination tests that was defined by  $P_C\big(p_1,p_2\big)=\begin{cases} p_1 & \text{if $p_1\leq a$ or $p_1>b$}\\ a+\int_a^b\int_0^1\mathbf{1}_{[C(x,y)\leq C(p_1,p_2)]}dydx & otherwise \end{cases},$

Muller and Schafer (2001) also considered a more complex combination rule based on a conditional error function for adaptive group sequential

where  $C(p_1, p_2)$  can be any combination function.

and can be expressed as  $c = \frac{\sqrt{n_1}z_1 + \sqrt{n_2}z_{A(z_1)}}{\sqrt{n_1+n_2}}$ .

trials.

and post-adaptation.

• If  $p_1 \le a$ , reject  $H_0$ ,

• If  $p_1 > b$ , accept  $H_0$ ,

function.

The value c can be solved by the following:

Proschan and Hunsberger (1995) considered a conditional error

 $A(z_1) = CP_0(n_2, c|z_1) = \begin{cases} 0, & z_1 < z_b \\ 1 - \Phi(\sqrt{z_a^2 - z_1^2}), & z_b \leq z_1 \leq z_a, \\ 1, & z_1 > z_a \end{cases}$ 

where  $z_1$  denotes the observed stage 1 test statistic,  $z_h$  and  $z_a$  are the stage 1 critical value to accept or reject  $H_0$ . They need to be selected

such that  $\int_{-\infty}^{\infty} A(z_1)(z_1) dz_1 = \alpha$ , where  $\phi(z_1)$  denotes the density

of the standard normal distribution. The critical value for stage 2 is a

function of stage 1 and stage 2 sample size  $n_1$  and  $n_2$ ,  $z_1$ , and  $z_{A(z_1)}$ ,

effect size in adaptive group sequential trials. Consider a twostage design with sample size  $n_1$  and  $n_2$ . At the end of stage 1, sample size for stage 2 can be increased to  $m_2(m_2 \ge n_2)$ based on observed effect size. Let  $z_1$  and  $z_2$  be the test statistics (realization of  $Z_1$  and  $Z_2$ ) based on the n<sub>1</sub> and m<sub>2</sub> observation. The test statistics at the end of stage 2 is modified to  $z^*$  by keeping the original weights.

Cui et al (1999) developed a down weighting combination

strategy for sample size adjustment based on the observed

Lehmacher and Wassmer (1999) proposed an inverse normal

 $C(p_1, p_2) = 1 - \Phi[w_1\Phi^{-1}(1-p_1) + w_2\Phi^{-1}(1-p_2)],$ with weights  $0 < w_i < 1$  and  $w_1^2 + w_2^2 = 1$ , where  $\Phi$  and  $\Phi^{-1}$  denote the standard normal distribution function and the

$$
z^* = z_1 \sqrt{\frac{n_1}{n_1 + n_2}} + z_2 \sqrt{\frac{n_2}{n_1 + n_2}}.
$$

Bauer and Kieser (1999) proposed a Fisher's combination function,  $C(p_1, p_2) = p_1 \times p_2$ , for independent samples. When there is no early stopping, simply reject  $H_0$  at the end of the second stage if  $p_1 \times p_2 \leq c_\alpha = \exp[-\frac{1}{2}\chi^2_4(1-\alpha)].$ 

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