Partition Testing in Dose-Response Studies with Multiple Endpoints

Yi Liu¹, Jason Hsu¹, and Stephen Ruberg²

¹Statistics, The Ohio State University, Columbus, OH, USA ²Eli Lilly and Company, Indianapolis, Indiana, USA

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Abstract

Dose-response studies with multiple endpoints can be formulated as closed testing or partition testing problems. When the endpoints are primary and secondary, whether the order in which the doses are to be tested is pre-determined or sample-determined lead to different partitioning of the parameter space corresponding to the null hypotheses to be tested. We use the case of two doses and two endpoints to illustrate how to apply the partitioning principle to construct multiple tests that control the appropriate error rate. Graphical representation can be useful in visualizing the decision process.

1 Historical aspect of dose-response trials in pharmaceutics

Pharmaceutical drug development has long been divided into four Phases with Phase II being the part of the development cycle where dose response studies are conducted. The goal is usually to identify the best dose to use in confirmatory Phase III trials. While this has been the framework for several decades, there are still many drugs that fail to confirm efficacy and safety in Phase III (estimates range from 30-50%) with a substantial number of failures attributed to improper dose selection. Thus, the importance of the design and analysis of dose response studies is as relevant today as it has ever been.

In the past, efficacy of a new drug was typically demonstrated by showing its superiority to a placebo (called a *negative* control). However, in recent years, when treatments known to be effective exist, and the disease does not cause mortality or irreversible morbidity, efficacy of a new drug might be defined as superiority or non-inferiority to a known effective treatment (called an *active* control). In the case of non-inferiority trials, the determination of non-inferiority might be based on what is a clinically meaningful difference. See [1]. Even in the case of superiority trials against a negative control, the definition of superiority might consider risk versus benefit, if there is toxicity concerns for the drug. (see [2].) Some early discussion of these concepts can be seen in [3, 4, 5, 6].

Dose-response studies may have multiple endpoints. A *primary endpoint* is one such that efficacy of a new drug relative to the control in this single endpoint constitutes evidence of efficacy. *Secondary endpoints* are ones that efficacy of a new treatment in any secondary endpoints supports evidence of efficacy, but by themselves (i.e. in the absence of efficacy in a primary endpoint) do not constitute evidence of efficacy.

When there are primary and secondary endpoints, inference on the secondary endpoint is given only if the compound is efficacious for the primary endpoint at that dose. This ordering guides the selection of test statistics for each intersection hypothesis in closed testing (as in [7]). We give a different perspective in this article, which is the ordering guides the partitioning of the parameter space in using the partitioning principle to construct multiple tests that control the appropriate FWER.

In some (but not all) dose-response studies, it may be appropriate to pre-determine the order in which inferences on the doses are given. For example, one might start with the high dose and proceed to inference on the low dose only if the high dose shows efficacy. We show how this second "ordering" further guides the partitioning of the parameter space. The resulting partitioning test is in the form of a decision tree which can be represented graphically.

Interestingly, the joint distribution of t test statistics for multiple endpoints is *not* what is usually called the multivariate t distribution. This article discusses the computation of this distribution in the bivariate case which, to avoid confusion, we call the *dual* t distribution. We show, for example, that using algorithms for multivariate t distributions results in slightly liberal critical values, while computing as if the t statistics were independent results in somewhat conservative critical values.

Section 2 gives a motivating example of a dose-response study with multiple endpoints. Section 3 shows how the partitioning principle forms null hypotheses when inferences are ordered by dose, and the corresponding multiple test is a step-down test. Section 4 extends the partitioning principle of forming null hypotheses to when inferences are ordered by dose and by endpoint. The corresponding multiple test has a graphical representation. That section also contains a study of issues in the computation of critical values. Section 5 provides a numerical illustration of methods developed in this article, using the real data example in section 2.

2 A motivating example for dose-response studies

Consider, for example, [8], a 26-center double-blind trial comparing the effect of five doses of the anti-psychotic drug "Seroquel" (Quetiapine) and the placebo with parallel design on a total of 361 patients. For illustration purpose, we will focus on two of the doses (75 mg/day and 600 mg/day) with the primary endpoint being Clinical Global Impression (CGI) Global Improvement score and the secondary endpoint being CGI Severity of Illness score. Summary statistics for these two doses and endpoints are presented in Table 1.

		Dose		
Endpoint		0 mg/day (Placebo)	75 mg/day	600 mg/day
	Sample size	51	52	51
CGI Global Improvement score	Mean	4.78	4.22	3.58
(Primary)	SE ^a	0.23	0.22	0.23
CGI Severity of Illness score	Mean	5.2	4.8	4.4
(Secondary)	SE	1.2	1.3	1.5

Table 1: Summary statistics of two doses and two endpoints in [8]

^aStandard error

Throughout the paper, the placebo (0 mg/day), low dose (75 mg/day) and high dose (600 mg/day) groups will be indexed as i = 0, 1, 2. Primary and secondary endpoints will be indexed by superscripts L = P, S. For discussion involving only the primary endpoint, the superscript P will be dropped for convenience.

Let μ_i^L denote the mean response of dose group *i* for endpoint *L*, *i* = 0, 1, 2, *L* = *P*, *S*. Define

 $\theta_i^L = \mu_i^L - \mu_0^L$ as the true mean difference between dose group *i* and the placebo for endpoint *L*, i = 0, 1, 2, L = P, S. Let δ^L denote the clinically meaningful difference for endpoint *L*, L = P, S. The family of null hypotheses of interest consists of four null hypotheses with the first two in (1) concerning primary endpoint and the second two in (2) concerning secondary endpoint.

$$H_{01}^{P}: \theta_{1}^{P} \leq \delta^{P} \quad \text{vs.} \quad H_{a1}^{P}: \theta_{1}^{P} > \delta^{P}$$

$$H_{02}^{P}: \theta_{2}^{P} \leq \delta^{P} \quad \text{vs.} \quad H_{a2}^{P}: \theta_{2}^{P} > \delta^{P}$$

$$H_{01}^{S}: \theta_{1}^{S} \leq \delta^{S} \quad \text{vs.} \quad H_{a1}^{S}: \theta_{1}^{S} > \delta^{S}$$

$$H_{02}^{S}: \theta_{2}^{S} \leq \delta^{S} \quad \text{vs.} \quad H_{a2}^{S}: \theta_{2}^{S} > \delta^{S}$$

$$(2)$$

Assume the samples from dose group *i* for endpoint $L, Y_{i1}^L, ..., Y_{in_i}^L, i = 0, 1, 2, L = P, S$, come from a model:

$$Y_{ir}^{L} = \mu_{i}^{L} + \epsilon_{ir}^{L}, \ i = 0, 1, 2, r = 1, ..., n_{i}, L = P, S,$$
(3)

where
$$\begin{pmatrix} \epsilon_{ir}^P \\ \epsilon_{ir}^S \end{pmatrix}$$
 i.i.d. $\sim \mathbf{N} \left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} (\sigma^P)^2 & \rho \sigma^P \sigma^S \\ \rho \sigma^P \sigma^S & (\sigma^S)^2 \end{pmatrix} \right)$ $i = 0, 1, 2, r = 1, ..., n_i$

Define T_i^L , i = 1, 2, L = P, S, in (4) to be the t-statistic for testing the null hypothesis H_{0i}^L , i = 1, 2, L = P, S,

$$T_i^L = \frac{\bar{Y}_{i\cdot}^L - \bar{Y}_{0\cdot}^L - \delta^L}{\hat{\sigma}^L \sqrt{1/n_i + 1/n_0}} \quad i = 1, 2, \ L = P, S,$$
(4)

where $\bar{Y}_{i\cdot}^L = \frac{1}{n_i} \sum_{r=1}^{n_i} Y_{ir}^L$, $\hat{\sigma}^L = \sqrt{\frac{\sum_{i=0}^2 \sum_{r=1}^{n_i} (Y_{ir}^L - \bar{Y}_{i\cdot}^L)^2}{\sum_{i=0}^2 (n_i - 1)}}$, i = 0, 1, 2, L = P, S.

The purpose of dose-response studies is to find which doses are effective. Control of multiple testing error rate should control the probability of incorrectly inferring a dose is efficacious for

some endpoint when in fact it is not. In this situation, controlling the False Discovery Rate (FDR) will not control this probability (see [9]), while controlling the Familywise Error Rate (FWER) strongly for appropriately formulated null hypotheses will. We thus consider methods that strongly control FWER in this article.

With four null hypotheses in (1) and (2), a straight-forward application of the closed testing principle would test $2^4 - 1 = 15$ intersection null hypotheses to control FWER. However, we will show that if inferences are ordered by both endpoints and doses, then testing only four (disjoint) null hypotheses according to the partitioning principle controls FWER. These hypotheses are tested in three steps, with multiplicity adjustment involved in only one of the steps. When there are k > 2doses and m > 2 endpoints, a similar step-down procedure could in theory be developed following the same principle.

3 Multiple tests construction using the partitioning principle

The purpose of this article is to demonstrate how to use the partitioning principle, a fundamental multiple tests constructing technique, to construct multiple tests when there are multiple doses and multiple endpoints. We illustrate the idea with the two hypotheses in (1), concerning the primary endpoint first.

3.1 Closed testing to step-down doses according to sample responses

The closed testing technique of [10] tests all possible non-empty intersections of the hypotheses in (1), leading to the three hypotheses in (5), each at level- α :

 $H_0^{\cap}: \ \ \theta_1 \leq \delta \ \text{and} \ \ \theta_2 \leq \delta \ \ \ \text{(Neither dose is efficacious)}$

$H_{01}:$	$\theta_1 \leq \delta$	(Low dose is not efficacious)	(5)
$H_{02}:$	$\theta_2 \leq \delta$	(High dose is not efficacious)	

The logical implications of testing are:

- If H_0^{\cap} is not rejected, no inference is given even if H_{01} or H_{02} or both are rejected, because H_0^{\cap} implies H_{01} and H_{02} .
- If only H_0^{\cap} and H_{01} (H_{02}) are rejected but not H_{02} (H_{01}), then infer low (high) dose is efficacious.
- If all three hypotheses are rejected, then infer both doses are efficacious.

We use t-statistics T_1 and T_2 defined in (4) (with superscript *P* dropped) to test the three intersection hypotheses in (5) with critical values $d_{\alpha,2,\nu}$ (the upper α quantile of Dunnett distribution with 2 and $\nu = \sum_{i=0}^{2} (n_i - 1)$ degrees of freedom) and $t_{\alpha,\nu}$ (the upper α quantile of t distribution with ν degrees of freedom). Let (1), (2) denote the random indices such that $T_{(1)} < T_{(2)}$, then the rejection rules can be shown in Table 2.

Hypothesis	Rejection rule	Test level
$H_0^{\cap}: \theta_1 \leq \delta \text{ and } \theta_2 \leq \delta$	$T_{(2)} > d_{\alpha,2,\nu}$	α
$H_{01}:\theta_1\leq\delta$	$T_1 > t_{\alpha,\nu}$	α
$H_{02}:\theta_2\leq\delta$	$T_2 > t_{\alpha,\nu}$	α

Table 2: Decision rules for closed testing with two doses single primary endpoint

Since the critical values satisfy $d_{\alpha,2,\nu} > t_{\alpha,\nu}$, a step-down procedure with sample-determined steps exists, as follows:

- Step 1: If $T_{(2)} > d_{\alpha,2,\nu}$, infer dose (2) is efficacious and go to step 2; else stop.
- Step 2: If $T_{(1)} > t_{\alpha,\nu}$, infer dose (1) is efficacious and stop; else stop.

3.2 Partition to step-down doses

If higher dosage is expected to be more efficacious, then one may choose to always test the high dose first. If high dose is effective, then proceed to test low dose; otherwise, stop. We can formally state this pre-determined sequence of testing as:

Condition A (order in doses): The low dose can not be claimed efficacious unless the high dose has shown evidence of efficacy.

The partitioning principle of [11] and [12] is a general principle for constructing multiple tests. Under *condition A*, [13] partition the null space, $\{\boldsymbol{\theta} \in \mathbb{R}^2 | \theta_1 \leq \delta \text{ or } \theta_2 \leq \delta\}$ into two disjoint subspaces $\{\boldsymbol{\theta} \in \mathbb{R}^2 | \theta_2 \leq \delta\}$ and $\{\boldsymbol{\theta} \in \mathbb{R}^2 | \theta_1 \leq \delta \text{ and } \theta_2 > \delta\}$ corresponding to the two hypotheses:

$$H_{02}^{\downarrow}: \quad \theta_2 \leq \delta \quad (\text{ High dose is not efficacious})$$

$$H_{01}^{\downarrow}: \quad \theta_1 \leq \delta \text{ and } \theta_2 > \delta \quad (\text{ Low dose is not efficacious but high dose is})$$
(6)

The logical implications of testing are:

- If H[↓]₀₂ is not rejected (regardless of H[↓]₀₁), then no inference is given, since "neither dose is efficacious" (which is contained in H[↓]₀₂) is not rejected.
- If H[↓]₀₂ and H[↓]₀₁ are rejected, then since the union of H[↓]₀₂ and H[↓]₀₁ is "either low dose or high dose is not efficacious", the implication is "both high dose and low dose are efficacious".
- If H_{02}^{\downarrow} is rejected but H_{01}^{\downarrow} is not rejected, then one infers high dose is efficacious.

The interesting thing is, in testing H_{0i}^{\downarrow} , i = 1, 2 simultaneously, no multiplicity adjustment is needed to control FWER, the probability of rejecting any true null hypothesis. This is because the null spaces of H_{0i}^{\downarrow} , i = 1, 2 are disjoint. In other words, at most one null hypothesis can be true: it cannot be the case that high dose is ineffective (H_{02}) and that high dose is effective but low dose is ineffective (H_{01}) , for example. We thus test each H_{0i}^{\downarrow} , i = 1, 2, at level- α .

Level α tests for each H_{0i}^{\downarrow} , i = 1, 2, are of course not unique. Note, however, a level- α test for $H_{01} : \theta_1 \leq \delta$ is also a level- α test for $H_{01}^{\downarrow} : \theta_1 \leq \delta$ and $\theta_2 > \delta$. For example, a test which rejects no more than 5% of the time when low dose is ineffective, regardless of whether high dose is effective, will reject no more than 5% of the time in particular when low dose is ineffective and high dose is effective.

So the simplest level- α test for H_{0i}^{\downarrow} is to use a one-sided two-sample size α t-test based on $T_i, i = 1, 2$ defined in (4) for each H_{0i}^{\downarrow} as shown in Table 3.

Hypothesis	Rejection rule	Test level
$H_0^{\cap}: \theta_2 \leq \delta$	$T_2 > t_{\alpha,\nu}$	α
$H_{01}: \theta_1 \leq \delta \text{ and } \theta_2 > \delta$	$T_1 > t_{\alpha,\nu}$	α

Table 3: Decision rules for partition testing to step-down doses

In terms of the rejection rules in Table 3, the pre-determined D-steps (D stands for doses) proceeds as follows.

- Step 1: If $T_2 > t_{\alpha,\nu}$, infer high dose is efficacious and go to step 2; else stop.
- Step 2: If $T_1 > t_{\alpha,\nu}$, infer low dose is efficacious and stop; else stop.

Note that, even though the method above controls FWER regardless of whether the shape of the true response function, it is recommended only when the response is expected to be monotonically increasing (for otherwise it might stop too soon and miss an efficacious dose).

4 Partition testing with two doses and two endpoints

Suppose the dose-response study has both a primary endpoint and a secondary endpoint, so that the family of null hypotheses of interest includes both those in (1) and (2). We will show that, in addition to stepping through doses, the partitioning principle can also be used to derived multiple tests that step through endpoints in a pre-determined sequence.

4.1 Partition to step-down endpoints

Multiple testing procedures for dose-response studies with a primary endpoint and hierarchically ordered secondary endpoints were developed in [7]. In the case of two doses and two endpoints (one secondary endpoint), the procedure has to satisfy the condition that for the same dose, the secondary endpoint is tested only if primary endpoint is claimed to be efficacious, which is formally stated as:

Condition B (order in endpoints): For the same dose, a secondary endpoint can not be claimed efficacious unless its primary endpoint has been shown to be efficacious.

Within each endpoint, Dunnett's method was used in [7] to adjust multiplicity for multiple doses. The FWER of the whole procedure was controlled at α using the principle of closed testing. Figure 1 is a graphical representation of their procedure with two doses and two endpoints.

The procedure in [7] can be reproduced by partitioning the parameter space with constraints on



Figure 1: Decision process in [7]

S means "Stop", c is calculated based on sample correlation between endpoints.

ordered endpoints for each dose, similar to partitioning to step-down through the doses technique as illustrated in section 4. For example, for high dose, we would test the following two hypotheses in a step-down fashion (pre-determined E-steps).

 $H_{02}^{P\downarrow}: \qquad \theta_2^P \le \delta^P \qquad (Primary endpoint is not effective)$

4.2 Partitioning to step-down both doses and endpoints

The procedure developed in [7] steps through the endpoints in a pre-determined sequence, satisfying *condition B*, but not necessarily steps through the doses in a pre-determined sequence.

To step through both doses and endpoints, we test the following four partition hypotheses in a step-down fashion (pre-determined DE-steps):

- Step 1: Test $H_{02}^{P\downarrow}: \theta_2^P \leq \delta^P$ (High dose is not effective for primary endpoint).
 - If rejected, infer high dose for the primary endpoint is effective and proceed to step 2;
 else stop.
- Step 2: Test two hypotheses:

 $H_{01}^{P\downarrow}$: $\theta_1^P \leq \delta^P$ and $\theta_2^P > \delta^P$ (Low dose is not effective, but high dose is effective for primary endpoint)

 $H_{02}^{S\downarrow}$: $\theta_2^S \leq \delta^S$ and $\theta_2^P > \delta^P$ (High dose is not effective for secondary endpoint, but is effective for primary endpoint)

- If both hypotheses are rejected, infer both doses are effective for primary endpoint,
 high dose is also effective for secondary endpoint and proceed to the next step.
- Otherwise, if only H^{P↓}₀₁ is rejected, infer both doses are effective for primary endpoint and stop.
- If only $H_{02}^{S\downarrow}$ is rejected, infer high dose is effective for both endpoints and stop.
- Step 3: Test $H_{01}^{S\downarrow}$: $\theta_1^S \leq \delta^S$ and $\theta_2^S > \delta^S$ and $\theta_1^P > \delta^P$ and $\theta_2^P > \delta^P$ (Low dose is not effective for secondary endpoint, but is effective for primary endpoint and high dose is

effective for both endpoints.)

- If rejected, infer both doses are effective for both endpoints and stop. Otherwise stop.

The direction of these steps is presented in Table 4:

Endpoint\Dose	Low	High		
Primary	Step 2 ^b	$\leftarrow Step \ 1$		
	\downarrow	\downarrow		
Secondary	Step 3	$\leftarrow Step \ 2^b$		

Table 4: Direction of the pre-determined DE-steps

^bProceed only if both hypotheses in step 2 are rejected

4.2.1 Decision tree

The rejection rules for these hypotheses in each step are presented in Table 5 in the form of usual t-statistics T_i^L , i = 1, 2, L = P, S, as defined in (4).

Step	Hypothesis	Rejection rule	Test level
1	$H_{02}^{P\downarrow}:\theta_2^P\leq \delta^P$	$T_2^P > c_1$	α
2	$H_{01}^{P\downarrow}: \theta_1^P \leq \delta^P \text{ and } \theta_2^P > \delta^P$	$T_1^P > c_2$	MA ^c
	$H_{02}^{S\downarrow}: \theta_2^S \leq \delta^S \text{ and } \theta_2^P > \delta^P$	$T_2^S > c_2$	MA
3	$H_{01}^{S\downarrow}: \theta_1^S \leq \delta^S \text{ and } \theta_2^S > \delta^S \text{ and } \theta_1^P > \delta^P \text{ and } \theta_2^P > \delta^P$	$T_1^S > c_1$	α

Table 5: Critical values for the pre-determined DE-steps

^cMultiplicity adjustment needed

For step 1 and 3, the simplest choice of critical value c_1 is $t_{\alpha,\nu}$. For step 2, since the null spaces of $H_{01}^{P\downarrow}$ and $H_{02}^{S\downarrow}$ are not disjoint, we need to adjust for multiplicity to make the FWER for the whole procedure controlled at level α .

The decision tree of this step-down procedure with pre-determined DE-steps is presented in Figure 2.



Figure 2: Decision tree for pre-determined DE-steps

4.2.2 Computing the critical value c_2

According to Table 5, we need to find the critical value c_2 accounted for multiplicity for the two hypotheses in step 2. That is, one needs to focus on the joint distribution of (T_1^P, T_2^S) . Notice

that between doses, the observations are independent, but within a dose, observations between endpoints are dependent, the numerators as well as the denominators of T_1^P and T_2^S are correlated through endpoints for the same dose. For one-sided tests, with the rejection rule of the form in (7), the supremum of the probability is obtained at the boundary values (involving θ_1^P and θ_2^S only, since neither T_1^P nor T_2^S involves θ_2^P). The critical value c_2 needs to satisfy:

$$1 - \alpha \leq 1 - \sup_{\theta_{1}^{P} \leq \delta^{P} \text{ and } \theta_{2}^{S} \leq \delta^{S}} \Pr_{\rho} \left\{ T_{1}^{P} > c_{2} \text{ or } T_{2}^{S} > c_{2} \right\}$$

$$= \Pr_{\rho} \left\{ \frac{\bar{Y}_{1.}^{P} - \bar{Y}_{0.}^{P} - \theta_{1}^{P}}{\hat{\sigma}^{P} \sqrt{1/n_{1} + 1/n_{0}}} \leq c_{2} \text{ and } \frac{\bar{Y}_{2.}^{S} - \bar{Y}_{0.}^{S} - \theta_{2}^{S}}{\hat{\sigma}^{S} \sqrt{1/n_{2} + 1/n_{0}}} \leq c_{2} \right\}$$

$$= \Pr_{\rho} \left\{ \frac{Z_{1}}{\hat{\sigma}^{P} / \sigma^{P}} \leq c_{2} \text{ and } \frac{Z_{2}}{\hat{\sigma}^{S} / \sigma^{S}} \leq c_{2} \right\}$$

$$= \int_{0}^{\infty} \int_{0}^{\infty} \Pr_{\rho} \left\{ Z_{1} \leq c_{2} s_{1} \text{ and } Z_{2} \leq c_{2} s_{2} \right\} \gamma_{\rho,\nu}(s_{1}, s_{2}) ds_{1} ds_{2}$$
(8)

where $(Z_1, Z_2) = \left(\frac{\bar{Y}_{1:}^P - \bar{Y}_{0:}^P - \theta_1^P}{\sigma^P \sqrt{1/n_1 + 1/n_0}}, \frac{\bar{Y}_{2:}^S - \bar{Y}_{0:}^S - \theta_2^S}{\sigma^S \sqrt{1/n_2 + 1/n_0}}\right)$ with mean $\mathbf{0} = (0, 0)$, variance 1 and covariance $\rho/(\sqrt{(n_0/n_1 + 1)(n_0/n_2 + 1)}) (= \rho/2$ in the balanced case), $\gamma_{\rho,\nu}(s_1, s_2)$ is the joint density of $\left(\frac{\hat{\sigma}^P}{\sigma^P}, \frac{\hat{\sigma}^S}{\sigma^S}\right)$.

Note that the definition of a bivariate t distribution, as originally introduced by [14] and computed by the ProbMC function in SAS and the qmvnorm function in the R package mvtnorm, requires the denominators in (7) to be the same random variable $\hat{\sigma}^P \equiv \hat{\sigma}^S$, which is not the case here. In fact, computing (7) as if the distribution were bivariate t overestimates the probability, resulting in somewhat liberal critical values, as we will demonstrate. To avoid confusion, we call the distribution of (T_1^P, T_2^S) the *dual t* distribution. (This distribution was studied by [15].)

The probability (8) involves the unknown parameter ρ . Below we describe five ways of approximating (8). The first four methods (normal, bivariate t, dual t and independent standard errors) require ρ be known or approximated. The last method computes by pretending T_1^P and T_2^S are independent, which we prove results in a conservative critical value.

Normal approximation

If the sample sizes n_1, n_2 are large, by Slutsky's Theorem, $\hat{\sigma}^P / \sigma^P$ and $\hat{\sigma}^S / \sigma^S$ converge in probability to one, then the joint distribution of (T_1^P, T_2^S) (under the true mean difference) is asymptotically bivariate normal as (Z_1, Z_2) .

Bivariate t distribution

Assume $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are perfectly correlated, or they are the same, the situation coincides with the bivariate t case. Specifically, the probability in (7) reduces to

$$\int_0^\infty \Pr_{\rho} \left\{ Z_1 \le c_2 s \text{ and } Z_2 \le c_2 s \right\} \gamma_{\nu}(s) ds$$

where $\gamma_{\nu}(s)$ is the density of $\sqrt{\chi_{\nu}^2/\nu}$, and $\nu = \sum_{i=0}^2 (n_i - 1)$ is the degrees of freedom.

Dual t distribution

It can be shown that $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are diagonal elements of a Wishart random matrix (see Appendix). We use simulations from a Wishart distribution (which depends on ρ , the correlation between endpoints from a single individual) and Monte Carlo methods to approximate the probability based on exact dual t distribution of the test statistics (T_1^P, T_2^S) .

Independent Standard Errors $\hat{\sigma}^{P}, \hat{\sigma}^{S}$

The difficulty in computing (7) is caused, in part, by pooling data across doses in estimating the standard errors σ^P , σ^S , resulting in the denominators of test statistics (T_1^P, T_2^S) , $(\frac{\hat{\sigma}^P}{\sigma^P}, \frac{\hat{\sigma}^S}{\sigma^S})$ being

correlated. One can obtain a conservative upper bound of c_2 (see Theorem 1) in solving (9) = $1 - \alpha$ for c_2 by pretending $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are independent, where (9) can be viewed as a simplified version of (8).

$$\int_{0}^{\infty} \int_{0}^{\infty} \Pr_{\rho} \left\{ Z_{1} \le c_{2}s_{1} \text{ and } Z_{2} \le c_{2}s_{2} \right\} \gamma_{\nu}(s_{1})\gamma_{\nu}(s_{2})ds_{1}ds_{2}$$
(9)

Theorem 1 Probability (7) is greater when $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are correlated than when they are independent.

Proof of Theorem 1: We first condition on Z_1 and Z_2 , and note $c_2 > 0$

$$\Pr_{\rho} \left\{ \frac{Z_{1}}{\hat{\sigma}^{P}/\sigma^{P}} \leq c_{2} \text{ and } \frac{Z_{2}}{\hat{\sigma}^{S}/\sigma^{S}} \leq c_{2} \right\}$$

$$= E_{(Z_{1},Z_{2})} \left[\Pr_{\rho} \left\{ \frac{z_{1}}{\hat{\sigma}^{P}/\sigma^{P}} \leq c_{2} \text{ and } \frac{z_{2}}{\hat{\sigma}^{S}/\sigma^{S}} \leq c_{2} \middle| (Z_{1},Z_{2}) = (z_{1},z_{2}) \right\} \right]$$

$$= E_{(Z_{1},Z_{2})} \left[\Pr_{\rho} \left\{ \frac{z_{1}}{\hat{\sigma}^{P}/\sigma^{P}} \leq c_{2} \text{ and } \frac{z_{2}}{\hat{\sigma}^{S}/\sigma^{S}} \leq c_{2} \right\} \right]$$

$$= E_{(Z_{1},Z_{2})} \left[\Pr_{\rho} \left\{ \hat{\sigma}^{P}/\sigma^{P} \geq \frac{z_{1}}{c_{2}} \text{ and } \hat{\sigma}^{S}/\sigma^{S} \geq \frac{z_{2}}{c_{2}} \right\} \right]$$
(10)

Since $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are *associated* (see Theorem 6.1, [16]), for any given Z_1 and Z_2

$$\Pr_{\rho}\left\{\hat{\sigma}^{P}/\sigma^{P} \geq \frac{z_{1}}{c_{2}} \text{ and } \hat{\sigma}^{S}/\sigma^{S} \geq \frac{z_{2}}{c_{2}}\right\} \geq \Pr\left\{\hat{\sigma}^{P}/\sigma^{P} \geq \frac{z_{1}}{c_{2}}\right\} \Pr\left\{\hat{\sigma}^{S}/\sigma^{S} \geq \frac{z_{2}}{c_{2}}\right\}$$
(11)

The result follows. \Box

Independent t statistics T_1^P , T_2^S

To further break down the four dimensional integral in (9), we add the assumption of independent numerators (Z_1, Z_2) of (T_1^P, T_2^S) in addition to independent denominators, which is reasonable since the correlation between Z_1 and Z_2 is only $\rho/2$ in the balanced case. This method is more conservative then the previous method as shown in Theorem 2. **Theorem 2** The probability (9) assuming $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ are independent is greater than the probability assuming test statistics (T_1^P, T_2^S) are independent. (This is equivalent to further assuming the numerators of (T_1^P, T_2^S) , (Z_1, Z_2) are independent.)

Proof of Theorem 2:

Assume independence of $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$, we have

$$\Pr_{\rho} \left\{ \frac{Z_1}{\hat{\sigma}^P / \sigma^P} \le c_2 \text{ and } \frac{Z_2}{\hat{\sigma}^S / \sigma^S} \le c_2 \right\}$$
$$= \int_0^\infty \int_0^\infty \Pr_{\rho} \left\{ Z_1 \le c_2 s_1 \text{ and } Z_2 \le c_2 s_2 \right\} \gamma_{\nu}(s_1) \gamma_{\nu}(s_2) ds_1 ds_2$$
since $Cov(Z_1, Z_2) = \rho / \sqrt{(n_0/n_1 + 1)(n_0/n_2 + 1)} > 0$

By Slepian's inequality (Corollary A.3.1 on p. 229 of [17])

$$\geq \int_{0}^{\infty} \int_{0}^{\infty} \Pr\{Z_{1} \leq c_{2}s_{1}\} \Pr\{Z_{2} \leq c_{2}s_{2}\} \gamma_{\nu}(s_{1})\gamma_{\nu}(s_{2})ds_{1}ds_{2} \\ = \int_{0}^{\infty} \Pr\{Z_{1} \leq c_{2}s_{1}\} \gamma_{\nu}(s_{1})ds_{1} \int_{0}^{\infty} \Pr\{Z_{2} \leq c_{2}s_{2}\} \gamma_{\nu}(s_{2})ds_{2} \\ = \Pr\{\frac{Z_{1}}{\hat{\sigma}^{P}/\sigma^{P}} \leq c_{2}\} \Pr\{\frac{Z_{2}}{\hat{\sigma}^{S}/\sigma^{S}} \leq c_{2}\} \\ = \Pr\{T_{1}^{P} \leq c_{2}\} \Pr\{T_{2}^{S} \leq c_{2}\} \square$$

The degrees of conservatism for the methods introduced above are compared in terms of critical value c_2 for different combinations of correlation between endpoints ρ and error degrees of freedom ν in Table 6. Critical values for the dual t and independent standard errors methods are based on 100,000 simulations.

As shown in Table 6, for each combination of ρ and ν , the normal approximation is somewhat liberal and the bivariate t approximation is slightly liberal. Assuming independence of $\frac{\hat{\sigma}^P}{\sigma^P}$ and $\frac{\hat{\sigma}^S}{\sigma^S}$ is slightly conservative, while assuming independence of t statistics is somewhat conservative. It should be noted that, in the setting of simultaneous efficacy and safety studies, [19] considered

				$ ho^{ m d}$		
ν	Method	0	0.2	0.4	0.6	0.8
	Bivariate t ^e	2.0015	1.9972	1.9913	1.9833	1.9730
50	Dual t ^f	2.0026	1.9988	1.9934	1.9851	1.9741
	Ind. SE	2.0028	1.9988	1.9940	1.9866	1.9771
	Ind. T	2.0028	2.0028	2.0028	2.0028	2.0028
	Bivariate t	1.9777	1.9737	1.9682	1.9607	1.9507
100	Dual t	1.9783	1.9744	1.9692	1.9617	1.9513
	Ind. SE	1.9783	1.9745	1.9694	1.9623	1.9527
	Ind. T	1.9783	1.9783	1.9783	1.9783	1.9783
	Bivariate t	1.9660	1.9622	1.9569	1.9495	1.9398
200	Dual t	1.9659	1.9627	1.9572	1.9498	1.9401
	Ind. SE	1.9664	1.9628	1.9573	1.9503	1.9408
	Ind. T	1.9664	1.9664	1.9664	1.9664	1.9664
∞	Normal ^g	1.9545	1.9508	1.9456	1.9385	1.9289

Table 6: Comparing conservatism in terms of critical value c_2

^dNote ρ refers to the correlation between endpoints for a single individual. The correlation between numerators (Z_1, Z_2) of the test statistics, is assumed to be $\rho/2$ in the balanced case.

^eThe critical values of bivariate t are obtained by *qmvt* function in R package *mvtnorm*.

^fWishart is generated first using Bartlett's decomposition and then appropriately transformed (see [18]).

^gThe bivariate normal quantiles are obtained by *qmvnorm* of R package *mvtnorm*.

using the Bonferroni inequality and the bootstrap technique to compute such probabilities.

5 Analysis of the anti-psychotic drug data

We illustrate the step-down procedure with pre-determined DE-steps using the anti-psychotic drug example introduced at the beginning of the paper with $\delta^P = \delta^S = 0$. Using pooled standard error from these three groups, the t-statistics corresponding to each dose and endpoint and the error degrees of freedom are:

$$T_1^P = -1.7499, \quad T_2^P = -3.7318, \quad T_1^S = -0.2116, \quad T_2^S = -0.4212 \text{ and } \nu = 151.$$

If we want to control the FWER at 5% level, then $c_1 = t_{.05,151} = 1.6550$, while $c_2 = 1.9702$, based on the independent t method (which is appropriate because the correlation is unknown). Note in this particular example, a lower score indicates better drug effect. To make it consistent with our hypotheses set up, we take the negatives of the t-statistics and then apply our procedure.

- Step 1: Is 3.7318 > 1.6550? Yes, go to step 2.
- Step 2: Is 1.7499 > 1.9702 or 0.4212 > 1.9702? No, stop.

So infer high dose (600 mg/day) is efficacious for primary endpoint only, and no evidence of efficacy can be made for low dose (75 mg/day).

6 Conclusion

In this paper, we present a systematic way of constructing null hypotheses by partitioning the parameter space according to conditions that order inferences by dose (high to low), or endpoint (primary to secondary), or both. The hypotheses so constructed automatically form step-down procedures (pre-determined D-steps, E-steps, or DE-steps) and control the proper error rate at a pre-specified level. This way of tests construction can be generalized to situations with k > 2doses and m > 2 endpoints. The technique is as follows. Start by writing down the null hypotheses whose rejections correspond to desired inferences on primary and secondary endpoints. Then, following stated conditions for the decision process, make each null hypothesis in a subsequent step disjoint from null hypotheses in previous steps (by removing from it the union of the null hypotheses whose rejections lead up to it). Adjust for multiplicity within a step (only) if the null hypotheses are not disjoint, but do not adjust for multiplicity between steps.

An important issue in multiple endpoints problems is how to deal with correlations among the test statistics induced by correlations among measurements on the multiple endpoints. We made a systematic study of liberalism and conservatism of five approximation methods.

Graphical representation makes the decision process clear and easy to understand. Multiplicity adjustment may be needed for some steps but not all. There are two general rules. First, if there are two or more statistics involved in one box, then multiplicity adjustment may be needed. Second, if there are two or more branches from a box, and the hypotheses corresponding to these boxes are not disjoint, then further multiplicity adjustment may be needed among those boxes.

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Appendix

Model for dose-response studies with two endpoints

Suppose we have samples $Y_{0r}' = (Y_{0r}^P, Y_{0r}^S), r = 1, ..., n_0$ from a placebo group, and $Y_{1r}' =$ $(Y_{1r}^P, Y_{1r}^S), r = 1, ..., n_1, Y_{2r}' = (Y_{2r}^P, Y_{2r}^S), r = 1, ..., n_2$ from two dose groups, measuring two endpoints. Let $\boldsymbol{\mu}_0 = (\mu_0^P, \mu_0^S)', \boldsymbol{\mu}_1 = (\mu_1^P, \mu_1^S)', \boldsymbol{\mu}_2 = (\mu_2^P, \mu_2^S)'$ be the group means, $\Sigma = \begin{pmatrix} (\sigma^P)^2 & \rho\sigma^P\sigma^S \\ \rho\sigma^P\sigma^S & (\sigma^S)^2 \end{pmatrix}$ be the covariance matrix of ϵ_n , the *n*th row of ϵ , and $\mathbf{1}_n$ be a column vector

of 1s of length n. The model can be written in the following form:

$$\mathbf{Y} = \begin{pmatrix} \mathbf{Y}_{0} \\ \mathbf{Y}_{0} \\$$

$$\mathbf{I} - \mathbf{H} = \begin{pmatrix} I - H_0 & 0 & 0\\ 0 & I - H_1 & 0\\ 0 & 0 & I - H_2 \end{pmatrix} \text{ and } N\hat{\Sigma} = N\mathbf{Y}'(\mathbf{I} - \mathbf{H})\mathbf{Y} = N\sum_{i=0}^{2} \mathbf{Y}'_{i}(I - H_{i})\mathbf{Y}_{i}$$

By Result 7.10. on p. 390 of [20], $N\hat{\Sigma}$ follows the Wishart distribution $W_2(N-3,\Sigma)$, where $N = \sum_{i=0}^{2} n_i$, and N-3 is the degrees of freedom.

Notice, the diagonal elements of $N\hat{\Sigma}$ are $(N-3)(\hat{\sigma}^P)^2$ and $(N-3)(\hat{\sigma}^S)^2$, where $\hat{\sigma}^P = \sqrt{\frac{\sum_{i=0}^2 \sum_{r=1}^{n_i} (Y_{ir}^P - \bar{Y}_i^P)^2}{N-3}}$ and $\hat{\sigma}^S = \sqrt{\frac{\sum_{i=0}^2 \sum_{r=1}^{n_i} (Y_{ir}^S - \bar{Y}_i^S)^2}{N-3}}$. To obtain the joint distribution of $(\frac{\hat{\sigma}^P}{\sigma^P}, \frac{\hat{\sigma}^S}{\sigma^S})$, let $U = diag\{(\sigma^P)^{-1}, (\sigma^S)^{-1}\}$, then $NU'\hat{\Sigma}U \sim W_2\left(N-3, \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}\right)$ with diagonal elements $(N-3)(\frac{\hat{\sigma}^P}{\sigma^P})^2$ and $(N-3)(\frac{\hat{\sigma}^S}{\sigma^S})^2$.