

A Multiple Comparison Procedure for Hypotheses with Gatekeeping Structures

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Outline

- A clinical trial example
- Problem Set-up

- Proposed procedure
- Comparison with alternative procedures
- Application to the clinical trial
- Conclusions

A Clinical Trial*

- **Population: Patients with psoriasis**
- **Treatments: 1:1:1:1 randomization**
 - Placebo (P)
 - Low dose regimen (L)
 - Medium dose regimen (M)
 - High dose regimen (H)
- Endpoints

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- 1. PASI change from baseline at week 24
- 2. sPGA change from baseline at week 24
- Objectives with strong control of FWER
 - 1. Claim significant improvement in PASI change for one or more dose groups
 - 2. Claim significant improvement in sPGA change for significant dose group(s)
- Sample size: 280 = 4 x 70

* Some design features and data are modified for illustrative purpose.

Statistical Problem

Endpoint	Mean Difference					
	L-P	M-P	H-P			
PASI	π ₁₁	π ₁₂	π ₁₃			
sPGA	π ₂₁	π ₂₂	Π ₂₃			

Data

- $H_{vi}: \pi_{vi} = 0$
- Individual Z-scores

$$Y_{\nu}^{l} = \sum_{j=1}^{n_{l}} Y_{\nu,j}^{l}, l = 0, 1, ..., K; \nu = 1, 2, ..., p$$
$$Z_{\nu}^{l} = \sqrt{\frac{K+1}{N}} (Y_{\nu}^{l} - Y_{\nu}^{0}), l = 1, ..., K; \nu = 1, 2, ..., p$$

- Which of {H_{vl}: γ =1,2; I=1,2,3} can be rejected with a strong $Z_{\nu}^{l} \prec n(\sqrt{\frac{N}{K+1}}\pi_{\nu l}, \hat{\sigma}_{\nu l}^{2} + \hat{\sigma}_{\nu 0}^{2})$ significant level?
- No normality assumption for $p_{\nu l} = P(\sqrt{\frac{1}{\hat{\sigma}_{\nu l}^2 + \hat{\sigma}_{\nu 0}^2}}Z_{\nu}^l > z_{\nu l})$ PASI and sPGA changes

Some Available MCPs

- For the combined family of F₁ and F₂, use weighted bonferroni procedures (or graphical representation)
 - Bretz, Maurer, and Hommel 2011 SIM

- Use Bonferroni for F₁ and F₂ individually, and then mix them for the combined family with a bonferroni mixing function
 - Dmitrienko and Tamhane (2011) SIM
- Use truncated Hommel test for F₁ and F₂ individually, and then mix them for the combined family with a bonferroni mixing function
 - Brechenmacher, Xu, Dmitrienko, Tamhane, A.C. (2011) JPS

Points for Consideration

- Many MCPs are implemented based on marginal p-values {p_{vl}:γ=1,2,l=1,2,3}
 - Can they be improved by considering the correlation among individual test statistics?
- Some assume individual test statistics are positively correlated
 - May not be easily verified in some cases
- How do we choose initial local alpha?
- Power assessment of a MCP

Joint asymptotic distribution

Endpoint	Mean Difference						
	L-P	M-P	H-P				
PASI	π ₁₁ =π ₁	π ₁₂ =π ₃	π ₁₃ =π ₅				
sPGA	π ₂₁ =π ₂	π ₂₂ =π ₄	π ₂₃ =π ₆				
. (1 1)	1 0 1	1 0 0					

$$(\gamma, l) \equiv \gamma + p(l-1), \gamma = 1, 2, l = 1, 2, 3$$

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$$Z_{v}^{l} \prec n\left(\sqrt{\frac{1}{K+1}}\pi_{vl}, \hat{\sigma}_{vl}^{2} + \hat{\sigma}_{v0}^{2}\right)$$

$$(Z_{1},..., Z_{pK}) \prec n\left(\sqrt{\frac{N}{K+1}}(\pi_{1},..., \pi_{pK})', \hat{V}\right)$$

$$\hat{V} = \begin{pmatrix} C^{0} + C^{1} & C^{0} & C^{0} \\ C^{0} & C^{0} + C^{2} & C^{0} \\ C^{0} & C^{0} & C^{0} + C^{3} \end{pmatrix}$$

 C^{l} = sample covariance matrix of random vector $(Y_{1}^{l},...,Y_{p}^{l})$

Proposed Procedure: Overview

- For any intersection of H₁,...,H₆, H(e) with e=(e₁,...,e₆), define an α level test
 - Truncated Dunnett type for F₁ family

- Union test to maintain gatekeeping structure
- Joint distribution to compute local type I error
- Use Maucus' closed test principle to derive a strongly controlled MCP

$$(Z_{1},..., Z_{pK}) \prec n(\sqrt{\frac{N}{K+1}}(\pi_{1},..., \pi_{pK})', \hat{V})$$

$$(W_{1},..., W_{pK}) \prec n((0,..., 0)', \hat{V})$$

$$U_{e,\hat{V}(e)}(u) = P(\max\{W_{j}: e_{j} = 1\} \leq u)$$

$$p(e) = 1 - U_{e,\hat{V}(e)}(\max\{Z_{j}: e_{j} = 1\})$$

$$\alpha$$
 level test for H(e) :
max{ $Z_j : e_j = 1$ } $\geq U_{e,\hat{V}(e)}(1 - \alpha)$

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$$c(1, \alpha) = U_{e^{M}, \hat{V}(e^{M})}(1 - \alpha), e^{M} = (1, 0, 1, 0, 1, 0)$$

$$f(v_{1}, e, \alpha) = v_{1}U_{e,\hat{V}(e)}(1 - \alpha) + (1 - v_{1})c(1, \alpha)$$

$$\geq U_{e,\hat{V}(e)}(1 - \alpha)$$

Dunnett-type test for F₁ and for F₂

For any e within F_1 , construct a truncated α level test for H(e): max {Z : e = 1} > $f(v = \alpha)$

 $\max\{Z_j: e_j=1\} \ge f(v_1, e, \alpha)$

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For any e within F_2 , construct an un - truncated α level test for H(e): $\max\{Z_j : e_j = 1\} \ge U_{e,\hat{Y}(e)}(1 - \alpha)$

Union Test for Mixed Intersections

$$e = e^{1} + e^{2}, e^{1} \in F_{1}, e^{2} \in F_{2}$$

$$H(e) = H(e^{1}) \cap H(e^{2})$$

$$C(e) = \{\max\{Z_{j} : e_{j}^{1} = 1\} \ge f(v_{1}, e^{1}, \alpha)\} \cup \{\max\{Z_{j} : e_{j}^{2} = 1\} \ge g(v_{1}, e, \alpha)\}$$

$$P(C(e) \mid H(e)) = \alpha \text{ for finding } g(v_{1}, e, \alpha)$$

Special case for $e^1 = e^M$: $C(e) = \{\max\{Z_j : e_j^1 = 1\} \ge f(v_1, e^1, \alpha)\}$

Modification with Logical Constraint

e = (0,1,1,0,1,1) with common treatment H(3)

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 $e^1 = (0,0,1,0,1,0)$ for endpoint 1 and treatment M and H $e^2 = (0,1,0,0,0,1)$, for endpoint 2 and treatment L and H $H(e) = H(e^1) \cap H(e^2)$

$$C(e) = \{ \max\{Z_j : e_j^1 = 1\} \ge f(v_1, e^1, \alpha) \}$$

e = (0,1,1,0,1,0) without common treatment $e^{1} = (0,0,1,0,1,0)$ for endpoint 1 and treatment M and H $e^2 = (0,1,0,0,0,0)$, for endpoint 2 and treatment L $H(e) = H(e^1) \cap H(e^2)$ $C(e) = \{\max\{Z_i : e_i^1 = 1\} \ge f(v_1, e^1, \alpha)\} \bigcup \{\max\{Z_i : e_i^2 = 1\} \ge g(v_1, e, \alpha)\}$ 12

gene Simulation Model								
	Endpoint	Mean Difference						
		L-P	M-P					
	1	π ₁₁ =π ₁	π ₁₂ =π ₃					
	2	π ₂₁ =π ₂	π ₂₂ =π ₄					

Random sample from $(Y_1^l, Y_2^l) \prec n((m_1^l, m_2^l)', \Sigma^l), l = 0, 1, 2$

$$\begin{split} V = & \begin{pmatrix} 2.0 & -0.7 & 1.0 & 0 \\ -0.7 & 2.0 & 0 & 1.0 \\ 1.0 & 0 & 2.0 & -0.8 \\ 0 & 1.0 & -0.8 & 2.0 \end{pmatrix} \\ Y_{\nu}^{l} = \sum_{j=1}^{n_{l}} Y_{\nu,j}^{l}, l = 0, 1, 2; \nu = 1, 2, p_{\nu l} = P(\sqrt{\frac{1}{\hat{\sigma}_{\nu l}^{2} + \hat{\sigma}_{\nu 0}^{2}}} Z_{\nu}^{l} > z_{\nu l}) \\ H_{i} : \pi_{i} = 0, i = 1, 2, 3; F_{1} = \{H_{1}, H_{3}\}, F_{2} = \{H_{2}\} \\ \text{simulation runs : 10,000} \end{split}$$

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Bonferroni Mixing

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Reject H(I) if $\begin{cases} p_i(I_i) \leq \alpha & \text{if } I = I_i \ (i = 1, 2), \\ \phi_I(p_1(I_1), p_2(I_2)) \leq \alpha & \text{if } I = I_1 \cup I_2, I_1 \text{ and } I_2 \text{ are nonempty.} \end{cases}$

$$\phi_I(p_1(I_1), p_2(I_2)) = \min\left(p_1(I_1), \frac{p_2(I_2)}{1 - e_1(I_1|\alpha)/\alpha}\right)$$

- Error function for Bonferroni test
 - Dmitrienko and Tamhane (2011) SIM
- Error function for truncated Hommel test
 - Brechenmacher, Xu, Dmitrienko, Tamhane, A.C. (2011) JPS

$$e_1(I_1|\alpha) = |I_1|\alpha/n_1 \qquad e(I|\alpha,\gamma) = (\gamma + (1-\gamma)|I|/n)\alpha \text{ if } |I| > 0$$

Colorno				Dee					
Ceigene		MUR	ation	Res	Suits				
	pi	В	BC	н	НС	FB	FBC	D	DC
	0	0%	0%	2%	2%	1%	1%	2%	2%
	0	0%	0%	0%	0%	0%	0%	0%	0%
	0	0%	0%	1%	1%	1%	1%	2%	2%
	0.45	1%	1%	83%	83%	83%	83%	83%	83%
	0	0%	0%	0%	0%	0%	0%	2%	0%
	0	1%	1%	2%	2%	2%	2%	2%	2%
	0	2%	2%	3%	3%	2%	3%	2%	2%
	0	0%	0%	1%	0%	1%	0%	2%	0%
	0.45	2%	2%	<mark>82%</mark>	<mark>82%</mark>	<mark>82%</mark>	<mark>82</mark> %	83%	83%
	0	0%	0%	1%	1%	1%	1%	1%	1%
	0.45	0%	0%	1%	0%	1%	1%	2%	1%
	0	0%	0%	2%	2%	2%	2%	2%	2%
	0.45	1%	1%	<mark>82%</mark>	<mark>82%</mark>	<mark>82%</mark>	<mark>82%</mark>	83%	83%
	0.45	1%	1%	60%	47%	60%	60%	72%	61%
	0	1%	1%	2%	2%	2%	2%	2%	2%
	0.45	72%	72%	86%	86%	85%	86%	85%	85%
	0	1%	1%	2%	2%	2%	2%	2%	1%
	0.45	72%	72%	87%	87%	85%	85%	85%	85%
	0	1%	1%	3%	3%	2%	2%	2%	2%
	0.45	1%	1%	64%	2%	64%	2%	75%	1%
	0.45	1%	1%	83%	83%	83%	83%	84%	84%
	0.45	73%	73%	88%	88%	88%	88%	86%	86%
	0.45	64%	64%	81%	74%	81%	76%	83%	74%
	0.45	73%	73%	88%	88%	87%	87%	86%	86%

Application to the Clinical Trial*

Population: Patients with psoriasis

- Placebo (P): n=79; Low dose regimen (L): n=66; Medium dose regimen (M): n=70; High dose regimen (H): n=72
- Standardized PASI and sPGA changes adjusted by P group
 - Z=(24.32, 2.36, 38.25, 5.67, 52.77, 7.32)
 - V=(78.227.6842.913.9642.913.967.681.623.960.723.960.7242.913.9692.309.2842.913.963.960.7242.913.960.729.281.823.960.7242.913.9642.913.9696.007.663.960.723.960.727.661.64)
- C(1,0.025)=22.43 and compute f(1,0.025,e), all of which are smaller than 23. Thus, L, M, H are better than P in PASI
- Compute g bounds and decision rules
 - Gatekeeping: M and H are better than P (L cannot be concluded)
 - Gatekeeping with constraint: same result in this case
- * Some design features and data are modified for illustrative purpose.

Graphical Approach to the trial data



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updated graph after sequentially rejecting H11, H12, H13, H22 and H23

	Endpoint 1			Endpoint 2		
	H11	H12	H13	H21	H22	H23
raw P-value	0.003	3E-05	<1E-05	0.032	1.4E-05	<1E-05
alpha by step						
0	0.00833	0.00833	0.00833	0	0	0
1	0	0.012495	0.00833	0.004165	0	0
2	0	0	0.013322	0.006661	0.004992	0
3	0	0	0	0.008324	0.008318	0.008324
4	0	0	0	0.012478	0	0.012478
5	0	0	0	0.024907	0	0
NULL Rejected	1	1	1	0	1	1

Conclusions

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Propose a MCP based on jointly asymptotic multivariate distribution

- Utilize internal correlation among marginal tests statistics
- Avoid assumption of normal distribution
- Avoid assumption of positive correlation among individual test statistics
- Show to have improvement over graphical procedure and bonferroni mixing for gatekeeping procedure in numerical examples under study

Apply the procedure to a real clinical trial data

- Easy implementation with computational package of multivariate normal distribution
- Application to group sequential design with multiple endpoints could be extended