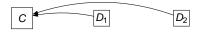
Part 2

Graphical Approaches to Multiple Testing

Structured families of hypotheses

Example

- A parallel group study with
 - Two treatments and a control



- One primary and one secondary endpoint
 - For example, FEV1 and time to exacerbation in a COPD trial (see Part 1)
- Structure:
 - Four hypotheses of interest
 - Two are primary (FEV1 for low and high dose)
 - Two secondary (time to exacerbation for low and high dose)

Key question in case of several study objectives/hypotheses:

What is their precise role?

Primary?		Required for study success?
Secondary?	\Leftrightarrow	For additional label claims?
Tertiary?		Just exploratory?

- Type I error rate control may be only required for some (maybe just one primary) hypothesis
- Classification is specific to the study, needs discussion within clinical teams and with regulatory agencies

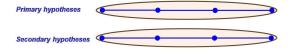
The primary hypothesis may be

- Clinically more important than the secondary hypothesis
 - Example: Glucose level in blood (e.g. HbA1c) and weight loss in diabetes
- Key to approval, although not clinically more important
 - Example: FEV1 and time to exacerbation in COPD
- Prerequisite for possible significance in the secondary hypothesis
 - Example: non-inferiority needs to be established before testing superiority

Structured hypotheses

Traditional multiple testing methods assume

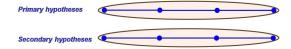
- No order (all hypotheses equally important)
- Strict hierarchy (e.g. H_2 only tested if H_1 is rejected before)
- Strict hierarchy in blocks:



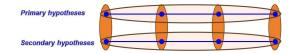
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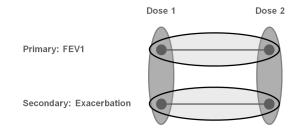
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- Strict hierarchy (e.g. H₂ only tested if H₁ is rejected before)
- Strict hierarchy in blocks:



Concrete applications often impose more structure through successiveness property between primary and corresponding secondary hypotheses:



- The two doses are equally relevant
- FEV1 increase and reduction in time to exacerbation within a dose group are successive
 - That is, for the same dose, time to exacerbation is only of interest if FEV1 increase has been shown before



How to construct decision strategies that reflect such complex requirements?

Need for suitable multiple test procedures

Standard multiple comparison procedures ...

- include Bonferroni, Holm, Hochberg, Dunnett, etc.
- control the FWER at level α
- are not suitable, because they treat all hypotheses equally and do not address the underlying structure of the test problem

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An intuitive procedure that does not control the FWER

- Test H₁, H₂ with Holm at level α; if at least one is rejected, test the "descendant" secondary hypothesis at level α/2.
- This procedure (or many variants thereof) does not control the FWER at level α; actual error rate can be up to 3α/2.

• Often applied to clinical trials with structured families of hypotheses and several levels of multiplicity

- Multiple endpoints (e.g. HbA1c and body weight)
- Multiple treatments of the same drug (e.g. dose or regimen)
- Multiple populations (e.g. full and sub-population)
- Combined non-inferiority and superiority testing
- Reflect the difference in importance as well as the relationship between the various study objectives
- Can be represented as weighted closed test procedures

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Hypotheses:

- $H_1, \ldots, H_m : m$ elementary null hypotheses
- $2^m 1$ intersection hypotheses

 $H_J = H_{j_1} \cap H_{j_2} \cap \ldots \cap H_{j_k}, J = \{j_1, \ldots, j_k\} \subseteq \{1, \ldots, m\}$

Closed test procedure (CTP):

- Test each H_J with a suitable α -level test
- Reject an elementary hypothesis *H_j*, if all intersection hypotheses containing the index *j* can be rejected
- This controls the FWER strongly at level α

- Test H₁,..., H_m at level α with weights w₁,..., w_m ≥ 0 such that w₁ + ... + w_m ≤ 1, i.e. w₁α + ... + w_mα ≤ α
- Assume *m* unadjusted p-values *p*₁,...,*p_m*
- Weighted Bonferroni test (for the global null hypothesis): Reject H = H₁ ∩ ... ∩ H_m if p_j ≤ w_jα for at least one j
- Alternatively, define weighted p-values p̃_j = p_j/w_j and reject H if min_j p̃_j ≤ α
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Consonance

- CTP is consonant, if the following condition is satisfied: If $H = H_1 \cap \ldots \cap H_m$ is rejected, then reject at least one H_i
- Desirable property of CTP, as it ensures rejection of an individual null after rejecting the global null
- Consonance enables construction of sequentially rejective procedures, reducing the number of tests from 2^m – 1 to m
- Not all CTP are consonant
 - Assume m = 2 and test H_1 , H_2 using a CTP
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- Reject H_J , if $p_j \leq w_j(J)\alpha$ for at least one $j \in J$
- If for every pair $I, J \subseteq \{1, ..., m\}$ with $J \subseteq I$ the monotonicity $w_j(I) \le w_j(J)$ for all $j \in J$

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 Resulting CTP can be performed as sequentially rejective procedure based on weighted p-values p̃_j(J) = p_j/w_j(J), starting with J = {1,...,m}:

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- Holds for weighted Holm procedure, fixed sequence test, Bonferroni-based fallback and gatekeeping procedures, etc

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 J → *J*/{*i*}
 Go to step 1.
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Consonance for Closed Weighted Bonferroni Tests

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Graphical Approach

Notation

- Null hypotheses H_1, \ldots, H_m
- Initial allocation of the significance level $\alpha = \alpha_1 + \ldots + \alpha_m$
- Unadjusted p-values p_1, \ldots, p_m

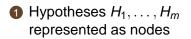
Notation

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- Initial allocation of the significance level α = α₁ + ... + α_m
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" α propagation"

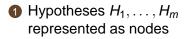
If a hypothesis H_i can be rejected at level α_i (i.e. $p_i \leq \alpha_i$), reallocate its level α_i to the remaining, not yet rejected hypotheses (according to a prefixed rule) and continue testing with the updated α levels.

Conventions





 (H_2)



2 Split of significance level α as weights α₁,..., α_m

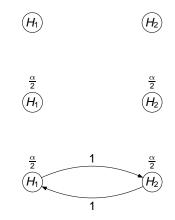


 H_1

 $\alpha_2 = \frac{\alpha}{2}$ (H_2)

 H_2

- **1** Hypotheses H_1, \ldots, H_m represented as nodes
- 2 Split of significance level α as weights α₁,..., α_m
- "α propagation" through weighted, directed edges



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Bonferroni (H_1) (H_2) Holm (H_1) (H_2)

H₂

H₁

Bonferroni Test (m = 2)



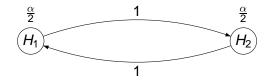


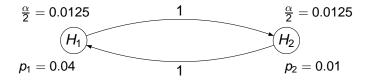


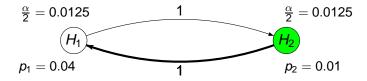
Remarks

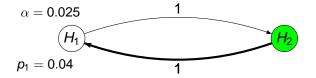
- Single-step procedures (e.g. Bonferroni) have no α propagation (i.e. no edges between nodes)
- Stepwise procedures (e.g. Holm) include α propagation and are thus more powerful

Bonferroni-Holm test (m = 2)









$$\alpha = 0.025$$

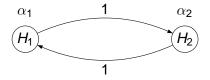
$$(H_1)$$

$$p_1 = 0.04$$



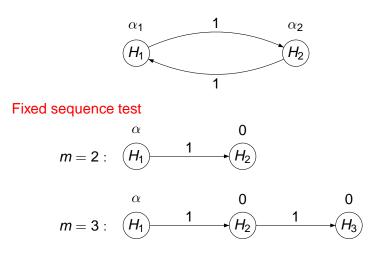
Weighted Bonferroni-Holm test

Use α_1, α_2 with $\alpha_1 + \alpha_2 = \alpha$ instead of $\alpha_1 = \alpha_2 = \alpha/2$



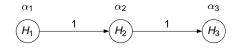
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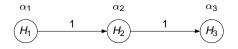
Fallback procedures (m = 3)

Original fallback

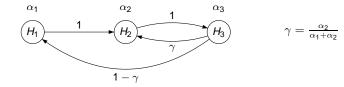


Fallback procedures (m = 3)

Original fallback

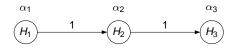


Improved fallback I

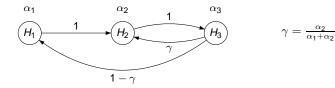


Fallback procedures (m = 3)

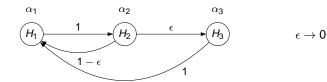
Original fallback



Improved fallback I



Improved fallback II



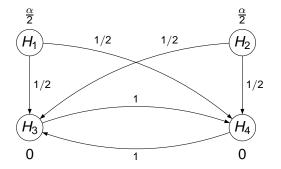
Parallel Gatekeeping

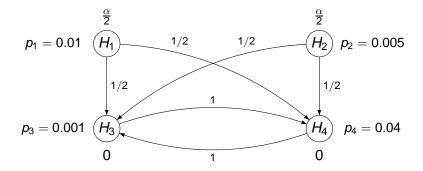
Intersection hypothesis	Weights			
	H_1	H_2	H_3	H_4
$\overline{H_1\cap H_2\cap H_3\cap H_4}$	0.5	0.5	0.0	0.0
$H_1 \cap H_2 \cap H_3$	0.5	0.5	0.0	0.0
$H_1 \cap H_2 \cap H_4$	0.5	0.5	0.0	0.0
$H_1 \cap H_2$	0.5	0.5	0.0	0.0
$H_1 \cap H_3 \cap H_4$	0.5	0.0	0.25	0.25
$H_1 \cap H_3$	0.5	0.0	0.5	0.0
$H_1 \cap H_4$	0.5	0.0	0.0	0.5
H_1	0.5	0.0	0.0	0.0
$H_2 \cap H_3 \cap H_4$	0.0	0.5	0.25	0.25
$H_2 \cap H_3$	0.0	0.5	0.5	0.0
$H_2 \cap H_4$	0.0	0.5	0.0	0.5
H_2	0.0	0.5	0.0	0.0
$H_3 \cap H_4$	0.0	0.0	0.5	0.5
H_3	0.0	0.0	1.0	0.0
H_4	0.0	0.0	0.0	1.0

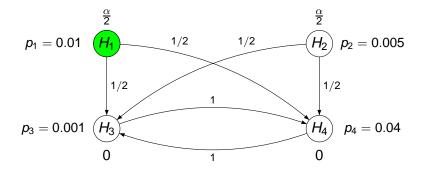
Table I. Weights assigned to the intersection hypothesis tests.

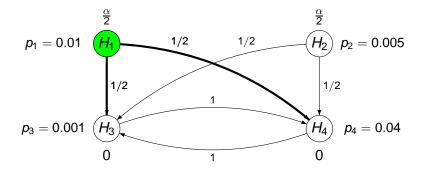
(Dmitrienko, Offen & Westfall, 2003)

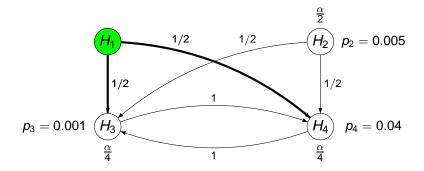
Parallel Gatekeeping

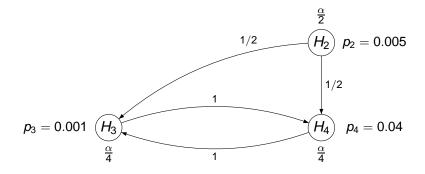






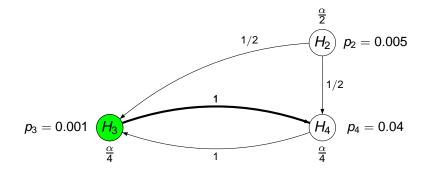


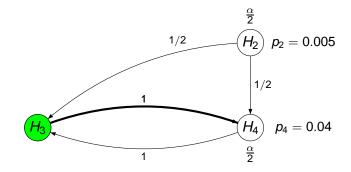


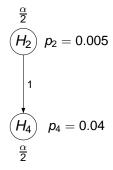


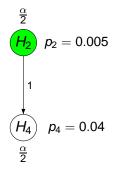
Procedure not successive:

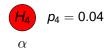
 H_4 could be rejected without having H_2 rejected











General Definition

- $\alpha = (\alpha_1, \dots, \alpha_m), \sum_{i=1}^m \alpha_i = \alpha$, initial levels
- **G** = (g_{ij}) : $m \times m$ transition matrix g_{ij} with $0 \le g_{ij} \le 1$, $g_{ii} = 0$ and $\sum_{j=1}^{m} g_{ij} \le 1$ for all $i = 1, \dots, m$.
- g_{ij} : fraction of the level of H_i that is propagated to H_j
- **G** and α determine the graph and the multiple test

Update algorithm

Set $J = \{1, ..., m\}$. **1** Select a *j* such that $p_j \leq \alpha_j$. If no such *i* exists, stop, otherwise reject H_i . Set $J = \{1, ..., m\}$.

- **1** Select a *j* such that $p_j \le \alpha_j$. If no such *j* exists, stop, otherwise reject H_j .
- Output the graph:

 $J \to J/\{j\}$ $\alpha_{\ell} \to \begin{cases} \alpha_{\ell} + \alpha_{j}g_{j\ell}, & \ell \in J \\ 0, & \text{otherwise} \end{cases}$ $g_{\ell m} \to \begin{cases} \frac{g_{\ell m} + g_{\ell j}g_{jm}}{1 - g_{\ell j}g_{j\ell}}, & \ell, m \in J, \ell \neq m, g_{\ell j}g_{j\ell} < 1 \\ 0, & \text{otherwise} \end{cases}$

B Go to step 1.

Set $J = \{1, ..., m\}$.

- **1** Select a *j* such that $p_j \le \alpha_j$. If no such *j* exists, stop, otherwise reject H_j .
- Output the graph:

$$J \to J/\{j\}$$

$$\alpha_{\ell} \to \begin{cases} \alpha_{\ell} + \alpha_{j}g_{j\ell}, & \ell \in J \\ 0, & \text{otherwise} \end{cases}$$

$$g_{\ell m} \to \begin{cases} \frac{g_{\ell m} + g_{\ell j}g_{jm}}{1 - g_{\ell j}g_{j\ell}}, & \ell, m \in J, \ell \neq m, g_{\ell j}g_{j\ell} < 1 \\ 0, & \text{otherwise} \end{cases}$$

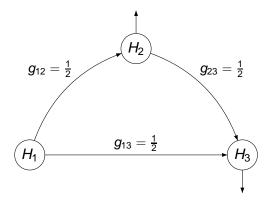
3 Go to step 1.

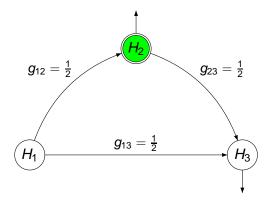
Theorem

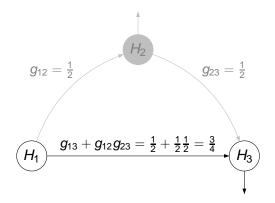
The initial levels α , the transition matrix **G** and the algorithm define a unique sequentially rejective test procedure that controls the FWER strongly at level α .

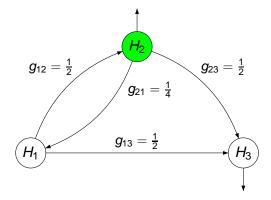
Proof idea:

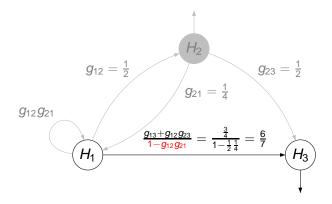
- The graph and algorithm define weighted Bonferroni tests for each intersection hypothesis
- The algorithm defines a shortcut for the resulting consonant closed test, which does not depend on the rejection sequence











Generic Example

Example

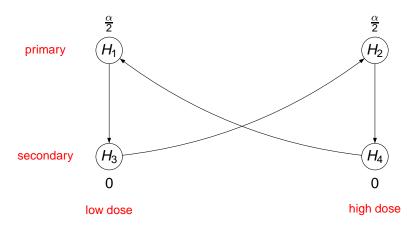
- Two primary hypotheses *H*₁, *H*₂ For example,
 - low/high dose for primary endpoint or non-inferiority claim
- Two secondary hypotheses *H*₃, *H*₄ For example,
 - low/high dose for secondary endpoint or superiority claim

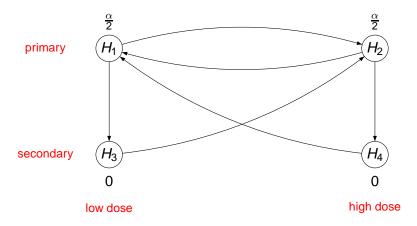
Example

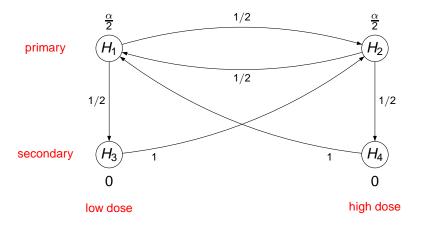
- Two primary hypotheses *H*₁, *H*₂ For example,
 - low/high dose for primary endpoint or non-inferiority claim
- Two secondary hypotheses *H*₃, *H*₄ For example,
 - low/high dose for secondary endpoint or superiority claim

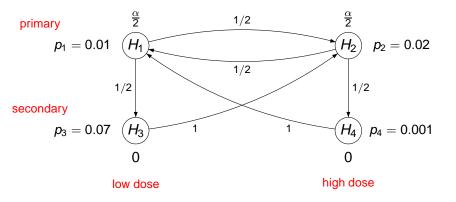
Proposed graphs

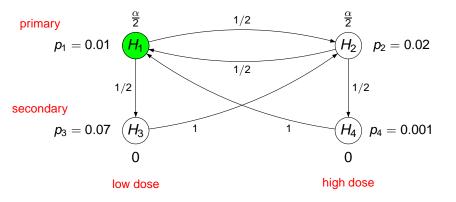
- ... are successive, control FWER, and display possible decision paths
- ... can be finetuned to reflect clinical considerations or treatment effect assumptions

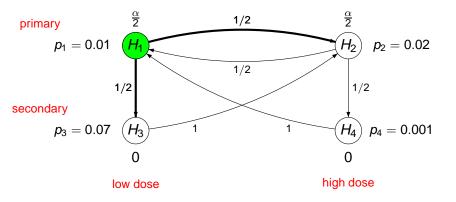


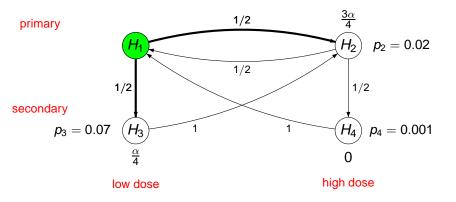


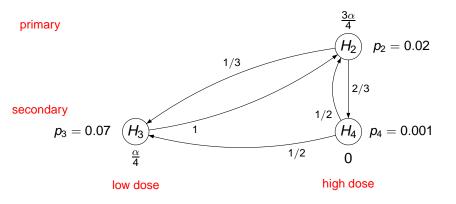


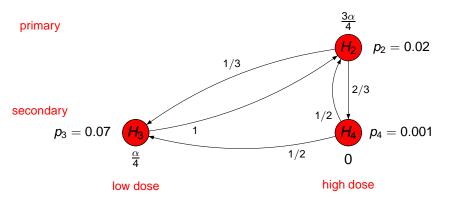


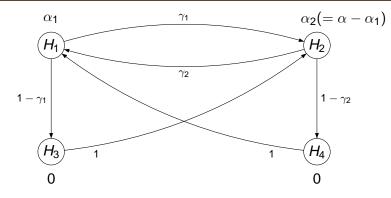












Resulting graph ...

needs to be finetuned with respect to α_1 , γ_1 , and γ_2 , based on:

- further clinical considerations, or
- assumptions about effect sizes, correlations, etc.

Probability to reject at least one hypothesis, i.e. to identify at least one true effect

- depends only on the initial levels $\alpha_1, \ldots, \alpha_k$, and
- on the (unknown) true effect sizes and the correlations between the test statistics.
- For successive procedures only levels, effect sizes and correlations of primary hypotheses are relevant.

Probability to identify several true effects

• depends in addition on the edge weights of the graph.

Case Studies

Late phase development of a new compound as an adjunctive therapy

Structured family of hypotheses

- 1. Four-armed trial comparing
 - Three dose levels of a new therapy adjunctive to standard-of-care
 - Placebo + standard-of-care as control
- 2. Two hierarchically ordered endpoints
 - Relapse rate and total medication score after 24 weeks
- \Rightarrow Six hypotheses H_{ij}

Dose i = 1 (low), 2 (medium), 3 (high dose) Endpoint j = 1 (relapse rate), 2 (total medication score)

- Primary hypotheses H_{11}, H_{21}, H_{31} ,
- Secondary hypotheses *H*₁₂, *H*₂₂, *H*₃₂.
- (2) Primary hypotheses considered as equally important, but significance of adjacent doses (i.e. reject H_{11} , H_{21} or H_{21} , H_{31}) preferred over significance of non-adjacent significant doses (i.e. reject H_{11} and H_{31})
- (3) Successiveness: A secondary hypothesis cannot be rejected without having rejected the associated parent primary hypothesis.

- Primary hypotheses H₁₁, H₂₁, H₃₁,
 Secondary hypotheses H₁₂, H₂₂, H₃₂.
- (2) Primary hypotheses considered as equally important, but significance of adjacent doses (i.e. reject H_{11} , H_{21} or H_{21} , H_{31}) preferred over significance of non-adjacent significant doses (i.e. reject H_{11} and H_{31})
- (3) Successiveness: A secondary hypothesis cannot be rejected without having rejected the associated parent primary hypothesis.

- Primary hypotheses H_{11}, H_{21}, H_{31} ,
- Secondary hypotheses H_{12} , H_{22} , H_{32} .

(2) Primary hypotheses considered as equally important, but significance of adjacent doses (i.e. reject H₁₁, H₂₁ or H₂₁, H₃₁) preferred over significance of non-adjacent significant doses (i.e. reject H₁₁ and H₃₁)

(3) Successiveness: A secondary hypothesis cannot be rejected without having rejected the associated parent primary hypothesis.

- Primary hypotheses H_{11}, H_{21}, H_{31} ,
- Secondary hypotheses *H*₁₂, *H*₂₂, *H*₃₂.
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- Secondary hypotheses *H*₁₂, *H*₂₂, *H*₃₂.
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- (3) Successiveness: A secondary hypothesis cannot be rejected without having rejected the associated parent primary hypothesis.

(1)

relapse rate



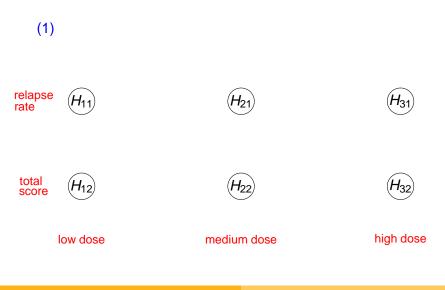


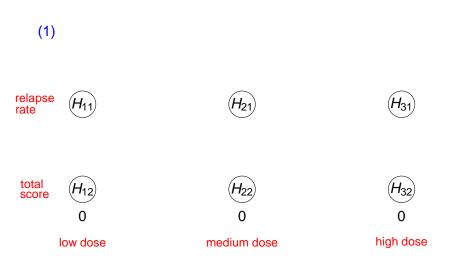
low dose

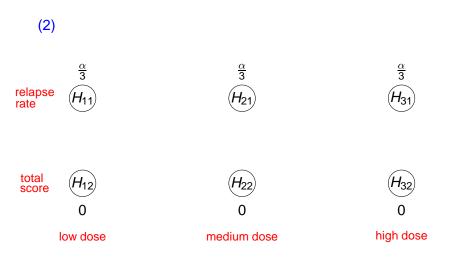
H₁

medium dose

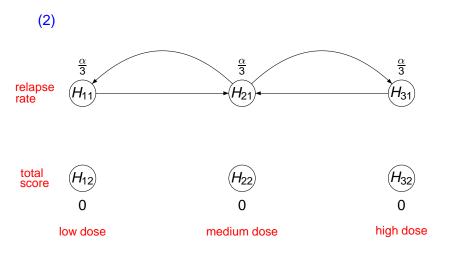
high dose



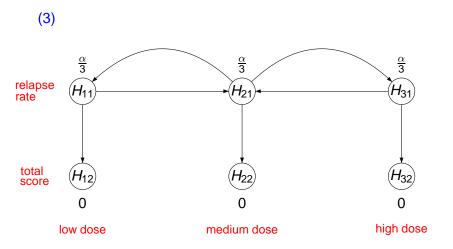




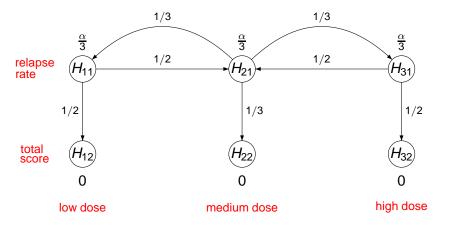
Resulting multiple test procedure



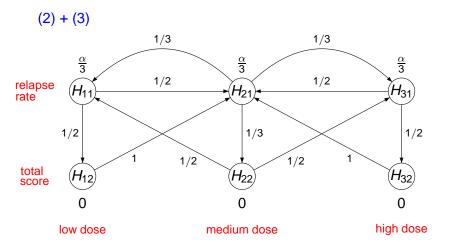
Resulting multiple test procedure



Resulting multiple test procedure



Resulting multiple test procedure



Easily implemented in SAS/IML

```
/* h: indicator whether a hypothesis is rejected (= 1) or not (= 0) (1 x n vector)
   a: initial significance level allocation (1 x n vector)
   w: weights for the edges (n x n matrix)
   p: observed p-values (1 x n vector) */
START mcp(h, a, w, p);
    n = NCOL(h);
   mata = a:
    crit = 0:
    DO UNTIL(crit = 1);
        test = (p < a):
        IF (ANY(test)) THEN DO;
            rej = MIN(LOC(test#(1:n)));
            h[rei] = 1;
            w1 = J(n, n, 0);
            DO i = 1 TO n;
                a[i] = a[i] + a[rej]*w[rej,i];
                IF (w[i,rej]*w[rej,i]<1) THEN DO j = 1 TO n;</pre>
                    w1[i,j] = (w[i,j] + w[i,rej]*w[rej,j])/(1 - w[i,rej]*w[rej,i]);
                END:
                w1[i,i] = 0:
            END:
            w = w1; w[rej,] = 0; w[,rei] = 0;
            a[rej] = 0;
            mata = mata // a;
        END:
        ELSE crit = 1:
    END:
    PRINT h: PRINT (ROUND(mata, 0.0001)): PRINT (ROUND(w.0.01)):
FINISH:
```

```
PROC IML:
START mcp(h, a, w, p);
    . . .
FINISH:
/*** Numerical example ***/
h = \{0 \ 0 \ 0 \ 0 \ 0 \ 0 \};
a = \{0.00833 \ 0.00833 \ 0.00833 \ 0 \ 0 \ 0\};
w = {0 0.5 0
                  0.5 0
                                 0
    0.3333 0 0.3333 0 0.3333 0 .
           0.5 0
    0
                      0 0
                                 0.5.
    0
           1 0
                      0 0
                                 0
    0.5
           0 0.5 0 0
                                 ο.
                      0 0
    0
         1 0
                                 0 };
p = \{0.1 \ 0.008 \ 0.005 \ 0.15 \ 0.04 \ 0.006\};
RUN mcp(h, a, w, p);
QUIT;
```

.

.

gMCP package in R

- Open source package available on CRAN at http://cran.r-project.org/web/packages/gMCP/
- Provides GUI within R through interface to JAVA

🐺 Creating and modifying graphs			
	Hypothesis	Significance Level	P-Value
Variablename to save to: graph	H11	0.016666666666666666	0.0 Reject and pass c
Place new nodes and edges or start the test procedure	H21	0.016666666666666666	0.0 Reject and pass a
	H31	0.016666666666666666	0.0 Reject and pass c
	H12	0.0	0.0 Reject and pass c
0.5 0.5	H22	0.0	0.0 Reject and pass α
H11 0.333 H21 0.333 0.333 H31 0.333 0.333	H32	0.0	0.0 Reject and pass α
	Total c: 0.05		

- Two treatments (A and B) compared with comparator (C)
- Superiority and non-inferiority tests for primary and multiple secondary endpoints.
- Three elementary hypotheses and two families of hypotheses:
 - *H*₁: superiority of A vs. C
 - H₂: non-inferiority of B vs. C
 - *H*₃: superiority of B vs. C
 - \mathcal{H}_4 : multiple secondary variables for A vs. C
 - H₅: multiple secondary variables for B vs. C

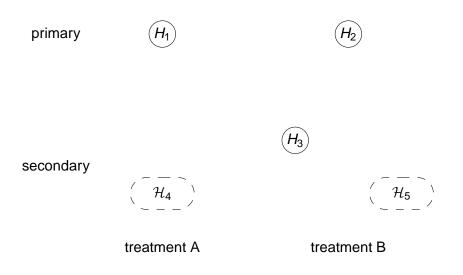
primary

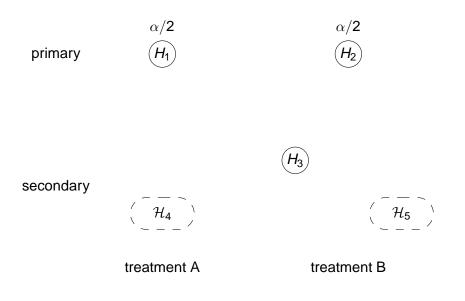


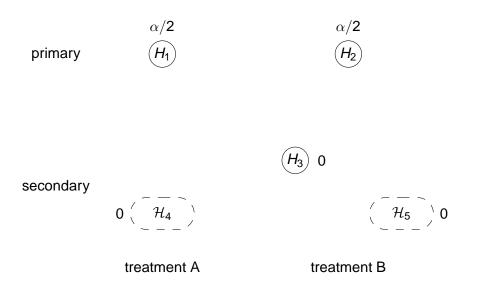


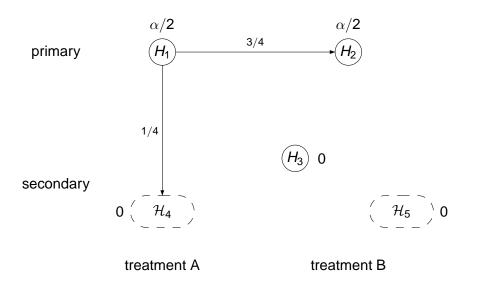
treatment A

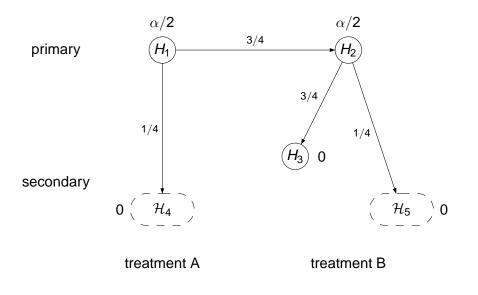
treatment B

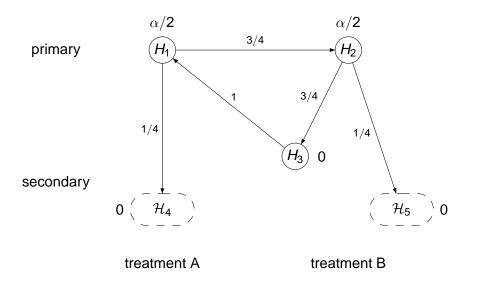


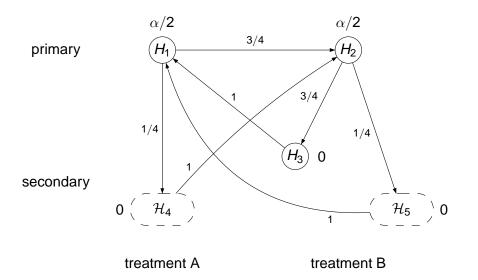




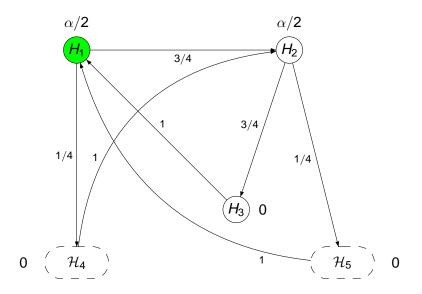




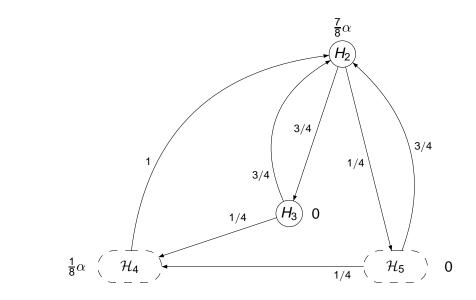




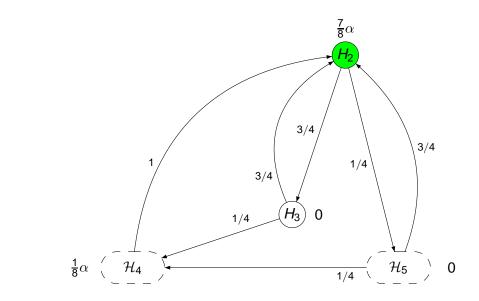
Example

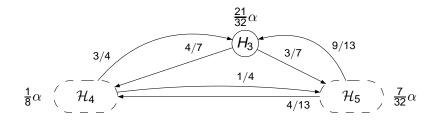


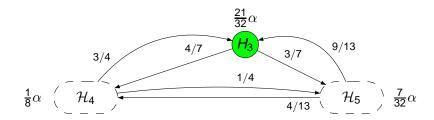
Example



Example







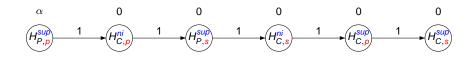


- Gold standard design comparing experimental drug (E) against placebo (P) and active comparator (C)
- Mixture of superiority and non-inferiority tests
- Two primary endpoints: pain, symptoms, resulting in six elementary hypotheses:

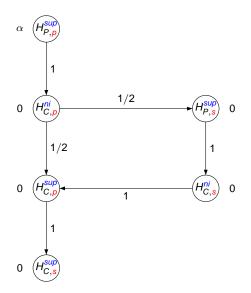
 $H_{P,p}^{sup}$: superiority of E vs. P for pain $H_{P,s}^{sup}$: superiority of E vs. P for symptoms $H_{C,p}^{ni}$: non-inferiority of E vs. C for pain $H_{C,p}^{ni}$: non-inferiority of E vs. C for symptoms $H_{C,p}^{sup}$: superiority of E vs. C for pain

 $H_{C,s}^{sup}$: superiority of E vs. C for symptoms

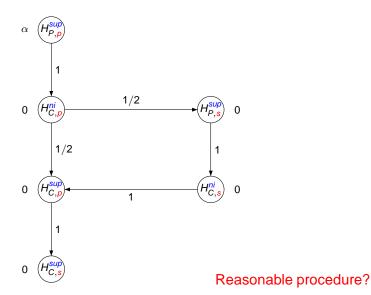
Initial proposal: strict sequence



Next proposal: gatekeeping



Next proposal: gatekeeping



Next proposal: gatekeeping - new display

pain

symptoms

Next proposal: gatekeeping – new display

pain

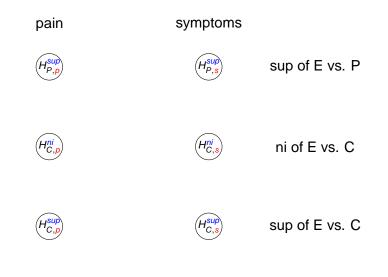
symptoms

sup of E vs. P

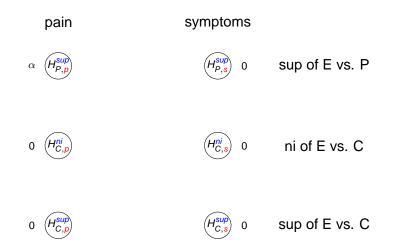
ni of E vs. C

sup of E vs. C

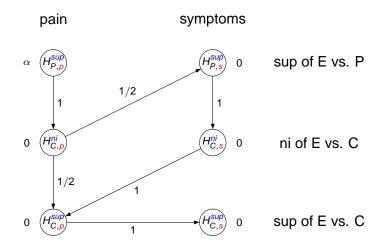
Next proposal: gatekeeping - new display



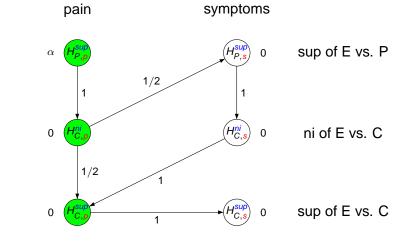
Next proposal: gatekeeping – new display



Next proposal: gatekeeping - new display

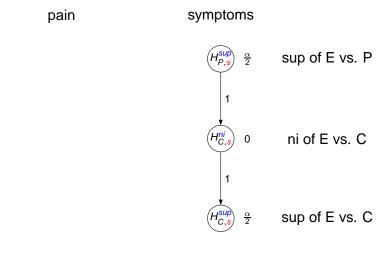


Next proposal: gatekeeping – new display



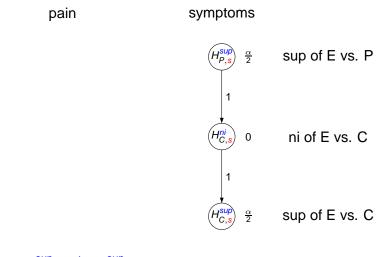
Reject $H_{P,p}^{sup}, H_{C,p}^{ni}, H_{C,p}^{sup}$

Next proposal: gatekeeping - new display

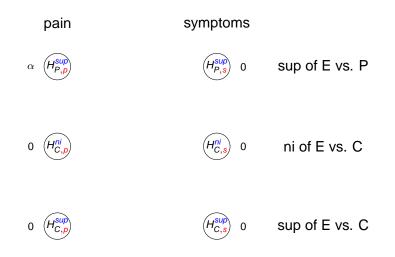


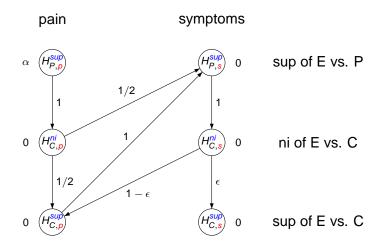
Reject $H_{P,p}^{sup}$, $H_{C,p}^{ni}$, $H_{C,p}^{sup}$

Next proposal: gatekeeping – new display



Reject $H_{P,p}^{sup}$, $H_{C,p}^{ni}$, $H_{C,p}^{sup}$ \Rightarrow Lack of succession property





Case study IV

• Graph describing a test procedure for 4 EEG frequency bands and 5 sub-bands (Ferber et al., 2011)

G. Ferber et al. / Journal of Neuroscience Methods 201 (2011) 204-212

ō 0.2 0.2 α 0.3 03 1/4 1/6 w/2 α, n

• Proposed graphical approach offers the possibility to

- tailor advanced multiple test procedures to structured families of hypotheses,
- visualize complex decision strategies in an efficient and easily communicable way, and
- ensure strong FWER control.
- Approach covers many common gatekeeping procedures as special cases (Holm, fixed sequence, fallback, ...)

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• Approach can be extended to address other problems:

- Adjusted p-values and simultaneous confidence intervals available
- Power and sample size considerations
- Use of weighted and trimmed Simes tests
- Weighted parametric test procedures to exploit correlation
- Multiple testing in group sequential trials and adaptive designs
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 Bretz, Maurer, Maca (2014) Graphical approaches to multiple testing. To appear in: Young and Chen (eds.), *Clinical Trial Biostatistics and Biopharmaceutical Applications*, Taylor & Francis.