R에서의 meta 분석 예 rmeta package 소개

김호
서울대학교 보건대학원

R site : http://cran.r-project.org/
Author of the package
: Thomas Lumley
<tlumley@u.washington.edu>

Catheter Data

Data on the effetiveness of silver sulfadiazine coating on venous catheters for preventing bacterial colonisation of the catheter and bloodstream infection

Name	: Name of principal author
n.trt	: number of coated catheters
n.ctrl	: number of standard catheters
col.trt	: number of coated catheters colonised by bacteria
col.ctrl	: number of standard catheters colonised by bacteria
inf.trt	: number of coated catheters resulting in bloodstream infection
inf.ctrl	: number of standard catheters resulting in bloodstream infection

```
> library(rmeta)
> data(catheter)
> catheter
          Name n.trt n.ctrl col.trt col.ctrl inf.trt inf.ctrl
1       Ciresi   124    127      15       21      13       14
2       George    44     35      10       25       1        3
3       Hannan    68     60      22       22       5        7
4        Heard   151    157      60       82       5        6
5   vanHeerden    28     26       4       10      NA       NA
6         Maki   208    195      28       47       2        9
7      Bach(a)    14     12       0        4      NA       NA
8       Ramsay   199    189      45       63       1        4
9       Appavu    12      7       1        1      NA       NA
10    Trazzera   123     99      16       24       4        5
11     Collins    98    139       2       25       1        4
12     Bach(b)   116    117       2       16       0        3
13 Tennenberg   137    145       8       32       5        9
14  Pemberton    32     40      NA       NA       2        3
15      Logghe   338    342      NA       NA      17       15
```

Cochrane Data

- Data from randomised trials before 1980 of corticosteroid therapy in premature labour and its effect on neonatal death.

name	Identifier for the study
ev.trt	Number of deaths in the treated group
n.trt	Number in the treated group
ev.ctrl	Number of deaths in the control group
n.ctrl	Number in the control group

```
> data(cochrane)
> cochrane
          name ev.trt n.trt ev.ctrl n.ctrl
1     Auckland     36   532       60    538
2        Block      1    69        5     61
3        Doran      4    81       11     63
4        Gamsu     14   131       20    137
5     Morrison      3    67        7     59
6 Papageorgiou      1    71        7     75
7      Tauesch      8    56       10     71
>
```

Fixed effects (Mantel-Haenszel) meta analysis

```
> data(catheter)
> a <- meta.MH(n.trt, n.ctrl, col.trt, col.ctrl,
   data=catheter,
+ names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
> a
Fixed effects ( Mantel-Haenszel ) Meta-Analysis
Call: meta.MH(ntrt = n.trt, nctrl = n.ctrl, ptrt =
   col.trt, pctrl = col.ctrl,
     names = Name, data = catheter, subset = c(13, 6,
   5, 3, 7,
         12, 4, 11, 1, 8, 10, 2))
Mantel-Haenszel OR =0.44    95% CI ( 0.36, 0.54 )
Test for heterogeneity: X^2( 10 ) = 25.36 ( p-value
   0.0047 )
```

```
> summary(a)
Fixed effects ( Mantel-Haenszel ) meta-analysis
Call: meta.MH(ntrt = n.trt, nctrl = n.ctrl, ptrt = col.trt,
   pctrl = col.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 5, 3, 7,
        12, 4, 11, 1, 8, 10, 2))
-------------------------------------
             OR (lower  95% upper)
Tennenberg 0.22    0.10       0.49
Maki       0.49    0.29       0.82
vanHeerden 0.27    0.07       1.00
Hannan     0.83    0.40       1.72
Bach(a)    0.00    0.00        NaN
Bach(b)    0.11    0.02       0.49
Heard      0.60    0.38       0.95
Collins    0.10    0.02       0.41
Ciresi     0.69    0.34       1.42
Ramsay     0.58    0.37       0.92
Trazzera   0.47    0.23       0.94
George     0.12    0.04       0.33
-------------------------------------
Mantel-Haenszel OR =0.44 95% CI ( 0.36,0.54 )
Test for heterogeneity: X^2( 10 ) = 25.36 ( p-value 0.0047 )
> plot(a)
```

8	32	
129	113	
137	145	

$$OR = \frac{8 \times 113}{32 \times 129}$$

$$Var \ln OR = \left\{ \frac{1}{8} + \frac{1}{113} + \frac{1}{32} + \frac{1}{145} \right\}$$

For i-th study

	case	control	
Res	a_i	b_i	
No	c_i	d_i	
			n_i

$OR_i = a_i d_i / b_i c_i$

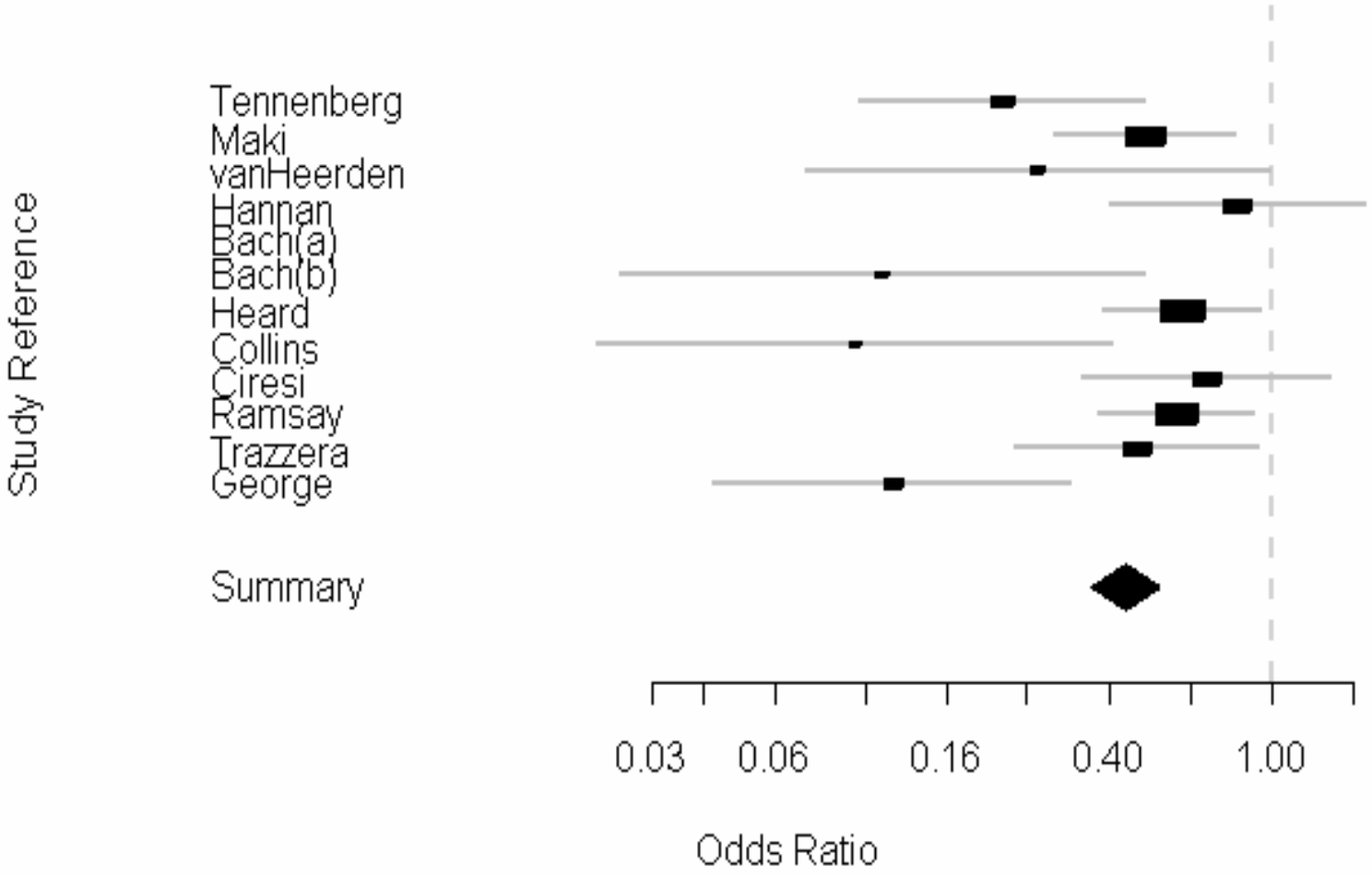
$Var(\ln OR) = 1/a_i + 1/b_i + 1/c_i + 1/d_i$

95% C.I. = exp(lnOR ± sqrt(Var(lnOR))

Pooled estimator (Mental-Haenszel) $\sum_{i=1}^{k} \frac{a_i d_i}{b_i c_i}$

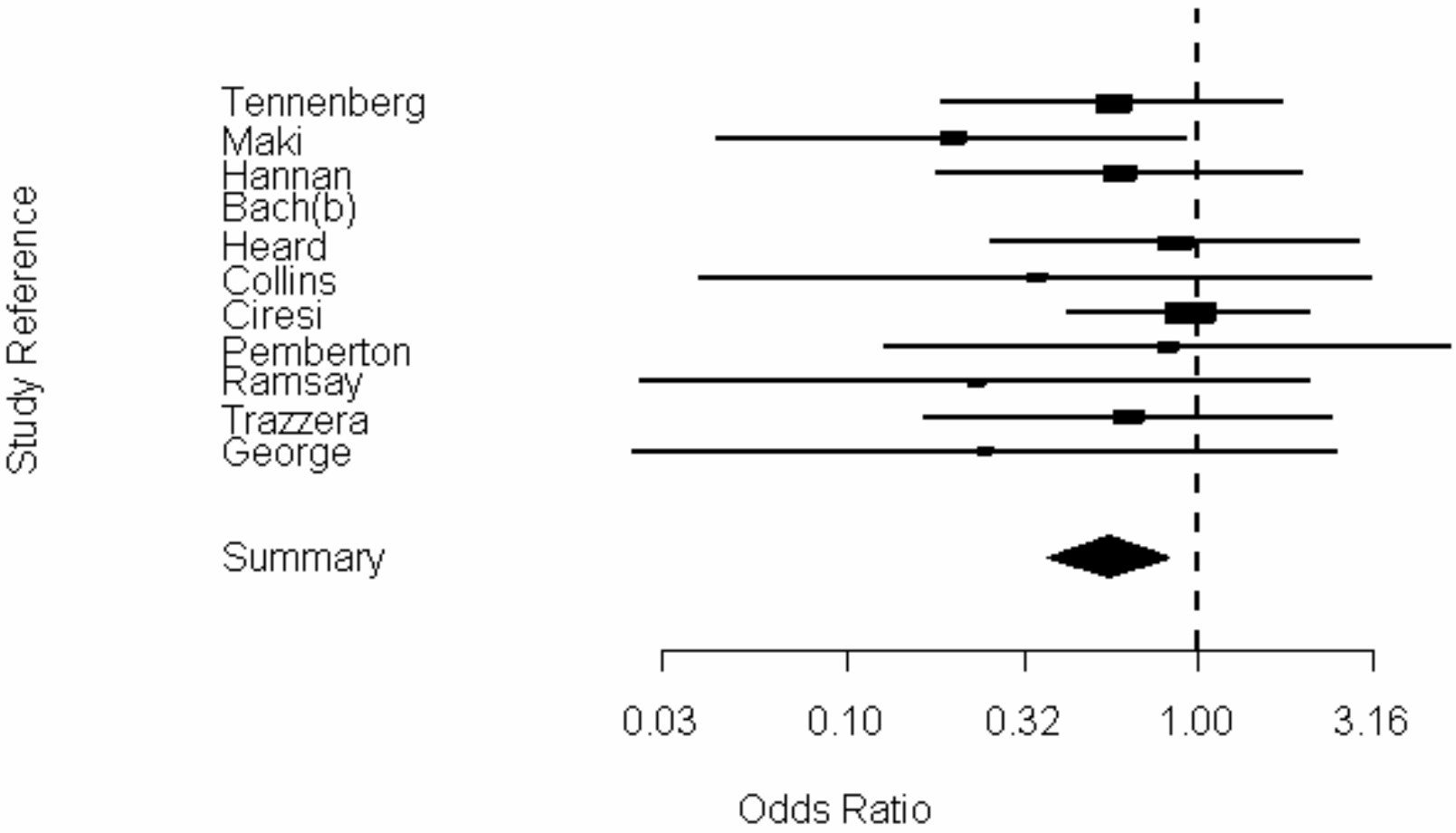
Hetero test

$$Q = \sum_{i=1}^{k} w_i (\ln OR_i - \ln MHOR)^2, w_i = Var(\ln OR_i)$$


Study Reference
Tennenberg
Maki
vanHeerden
Hannan
Bach(a)
Bach(b)
Heard
Collins
Ciresi
Ramsay
Trazzera
George
Summary
0.03
0.06
0.16
0.40
1.00
Odds Ratio

```
> d <- meta.MH(n.trt, n.ctrl, inf.trt, inf.ctrl,
    data=catheter,
+ names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
> d
Fixed effects ( Mantel-Haenszel ) Meta-Analysis
Call: meta.MH(ntrt = n.trt, nctrl = n.ctrl, ptrt = inf.trt,
    pctrl = inf.ctrl,
     names = Name, data = catheter, subset = c(13, 6, 3,
    12, 4,
         11, 1, 14, 8, 10, 2))
Mantel-Haenszel OR =0.56    95% CI ( 0.37, 0.84 )
Test for heterogeneity: X^2( 9 ) = 5.32 ( p-value
    0.8056 )
```

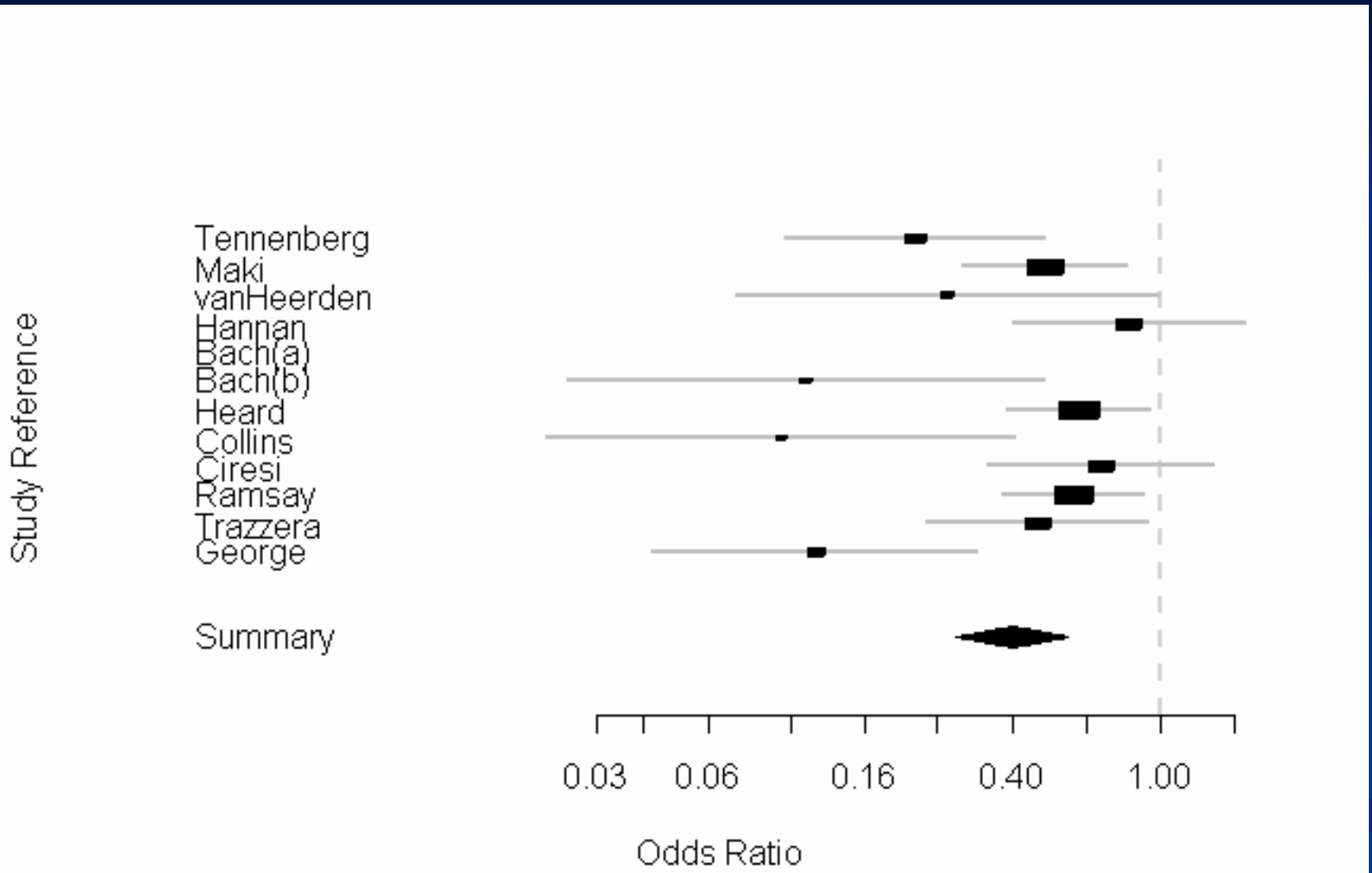
```
> summary(d)
Fixed effects ( Mantel-Haenszel ) meta-analysis
Call: meta.MH(ntrt = n.trt, nctrl = n.ctrl, ptrt = inf.trt, pctrl
   = inf.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 3, 12, 4,
        11, 1, 14, 8, 10, 2))
------------------------------------
             OR (lower  95% upper)
Tennenberg 0.57    0.19       1.75
Maki       0.20    0.04       0.94
Hannan     0.60    0.18       2.00
Bach(b)    0.00    0.00        NaN
Heard      0.86    0.26       2.89
Collins    0.35    0.04       3.16
Ciresi     0.95    0.43       2.10
Pemberton  0.82    0.13       5.24
Ramsay     0.23    0.03       2.11
Trazzera   0.63    0.17       2.42
George     0.25    0.02       2.50
------------------------------------
Mantel-Haenszel OR =0.56 95% CI ( 0.37,0.84 )
Test for heterogeneity: X^2( 9 ) = 5.32 ( p-value 0.8056 )
> ## plot with par("fg")
> plot(d, colors=meta.colors(NULL))
```


Study Reference
Tennenberg
Maki
Hannan
Bach(b)
Heard
Collins
Ciresi
Pemberton
Ramsay
Trazzera
George
Summary
0.03
0.10
0.32
1.00
3.16
Odds Ratio

Random effects (DerSimonian-Laird) meta analysis

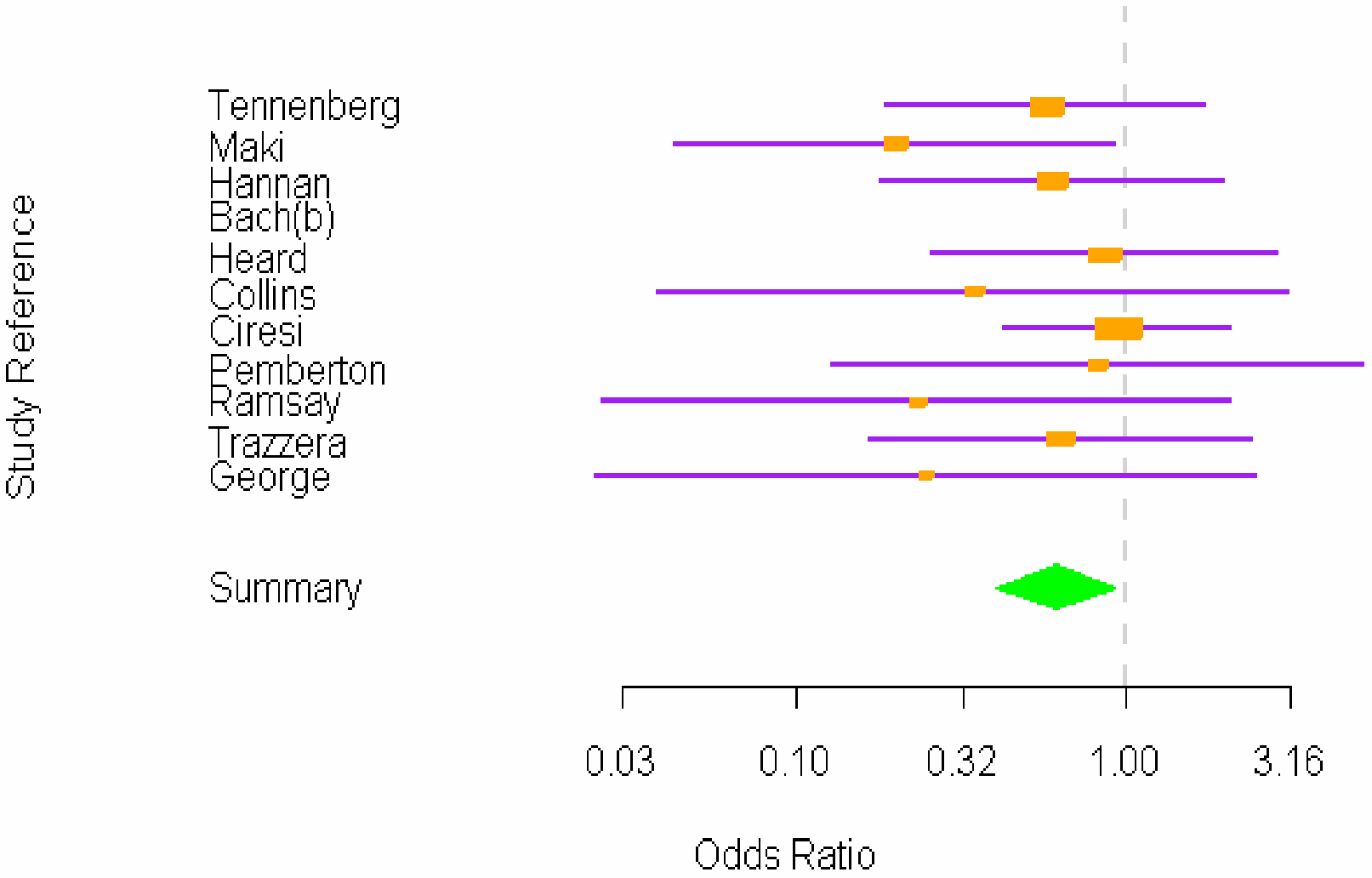
```
> data(catheter)
> b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
+ names=Name, subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
Warning message:
Studies with 0/Inf statistic omitted in: meta.DSL(n.trt, n.ctrl, col.trt,
    col.ctrl, data = catheter, names = Name,
> b
Random effects ( DerSimonian-Laird ) meta-analysis
Call: meta.DSL(ntrt = n.trt, nctrl = n.ctrl, ptrt = col.trt, pctrl =
    col.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 5, 3, 7,
        12, 4, 11, 1, 8, 10, 2))
Summary OR= 0.4    95% CI ( 0.28, 0.57 )
Estimated random effects variance: 0.19
```

```
> summary(b)
Random effects ( DerSimonian-Laird ) meta-analysis
Call: meta.DSL(ntrt = n.trt, nctrl = n.ctrl, ptrt = col.trt,
   pctrl = col.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 5, 3, 7,
        12, 4, 11, 1, 8, 10, 2))
-------------------------------------
             OR (lower  95% upper)
Tennenberg 0.22    0.10       0.49
Maki       0.49    0.29       0.82
vanHeerden 0.27    0.07       1.00
Hannan     0.83    0.40       1.72
Bach(a)    0.00    0.00        NaN
Bach(b)    0.11    0.02       0.49
Heard      0.60    0.38       0.95
Collins    0.10    0.02       0.41
Ciresi     0.69    0.34       1.42
Ramsay     0.58    0.37       0.92
Trazzera   0.47    0.23       0.94
George     0.12    0.04       0.33
-------------------------------------
SummaryOR= 0.4  95% CI ( 0.28,0.57 )
Test for heterogeneity: X^2( 10 ) = 24.9 ( p-value 0.0055 )
Estimated random effects variance: 0.19
(  1 studies with zero or infinite odds ratio omitted )
> plot(b)
```


Study Reference
Tennenberg
Maki
vanHeerden
Hannan
Bach(a)
Bach(b)
Heard
Collins
Ciresi
Ramsay
Trazzera
George
Summary
0.03
0.06
0.16
0.40
1.00
Odds Ratio

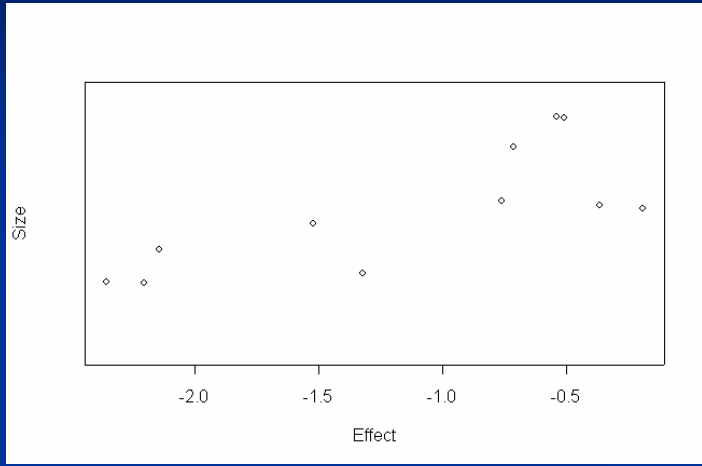
```
> e <- meta.DSL(n.trt, n.ctrl, inf.trt, inf.ctrl, data=catheter,
+ names=Name, subset=c(13,6,3,12,4,11,1,14,8,10,2))
Warning message:
Studies with 0/Inf statistic omitted in: meta.DSL(n.trt, n.ctrl, inf.trt,
    inf.ctrl, data = catheter, names = Name,
> e
Random effects ( DerSimonian-Laird ) meta-analysis
Call: meta.DSL(ntrt = n.trt, nctrl = n.ctrl, ptrt = inf.trt, pctrl = inf.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 3, 12, 4,
        11, 1, 14, 8, 10, 2))
Summary OR= 0.61    95% CI ( 0.4, 0.93 )
Estimated random effects variance: 0
```

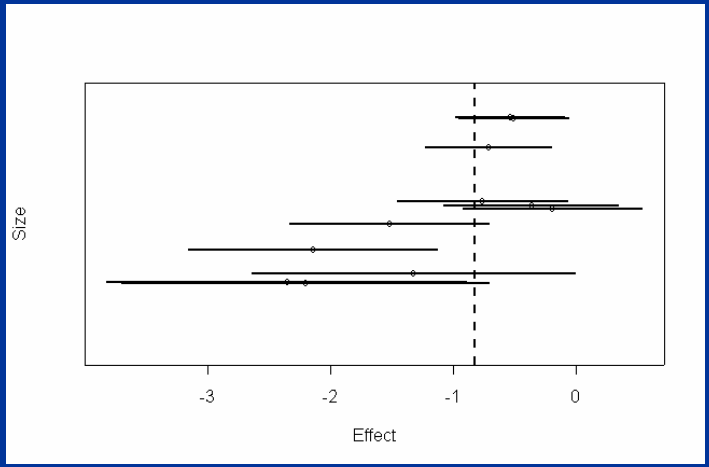
```
> summary(e)
Random effects ( DerSimonian-Laird ) meta-analysis
Call: meta.DSL(ntrt = n.trt, nctrl = n.ctrl, ptrt = inf.trt, pctrl =
   inf.ctrl,
    names = Name, data = catheter, subset = c(13, 6, 3, 12, 4,
        11, 1, 14, 8, 10, 2))
-------------------------------------
             OR (lower  95% upper)
Tennenberg 0.57    0.19       1.75
Maki       0.20    0.04       0.94
Hannan     0.60    0.18       2.00
Bach(b)    0.00    0.00        NaN
Heard      0.86    0.26       2.89
Collins    0.35    0.04       3.16
Ciresi     0.95    0.43       2.10
Pemberton  0.82    0.13       5.24
Ramsay     0.23    0.03       2.11
Trazzera   0.63    0.17       2.42
George     0.25    0.02       2.50
-------------------------------------
SummaryOR= 0.61  95% CI ( 0.4,0.93 )
Test for heterogeneity: X^2( 9 ) = 5.14 ( p-value 0.8222 )
Estimated random effects variance: 0
(  1 studies with zero or infinite odds ratio omitted )
> ##tasteless
> plot(e, colors=meta.colors(summary="green",lines="purple",box="orange"))
```

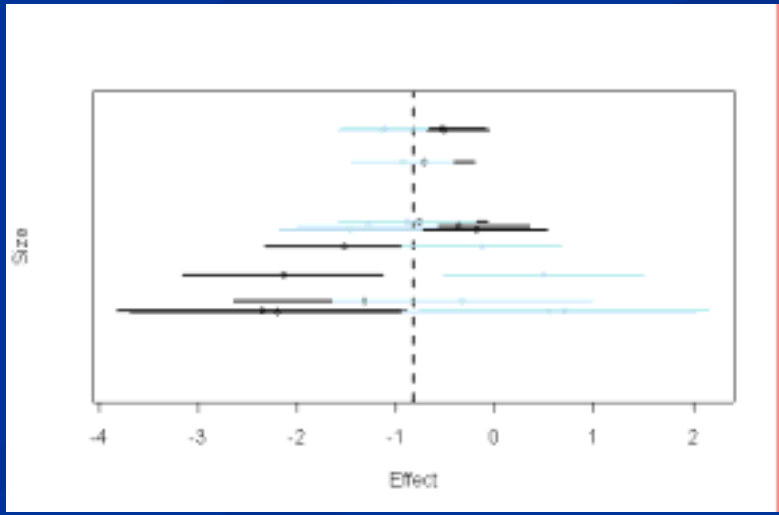

Study Reference
Tennenberg
Maki
Hannan
Bach(b)
Heard
Collins
Ciresi
Pemberton
Ramsay
Trazzera
George
Summary
0.03
0.10
0.32
1.00
3.16
Odds Ratio

Funnel plot

```
>data(catheter)
>a <- meta.MH(n.trt, n.ctrl, col.trt,
    col.ctrl, data=catheter,
+names=Name,
    subset=c(13,6,5,3,7,12,4,11,1,8,10,2))
>funnelplot(a$logOR, a$selogOR)
>funnelplot(a$logOR, a$selogOR,
+plot.conf=TRUE, summ=a$logMH,
    mirror=TRUE)
>funnelplot(a, plot.conf=TRUE)
```

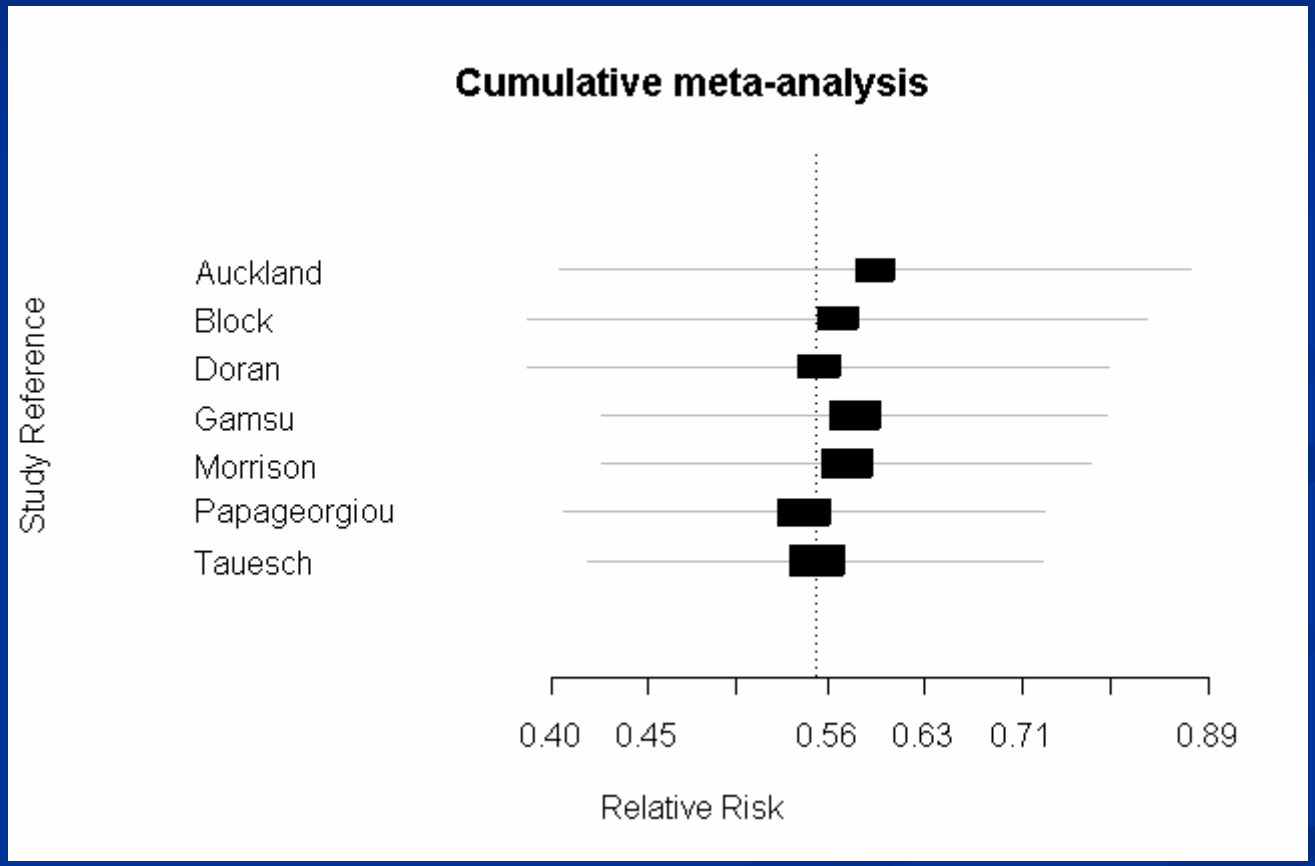




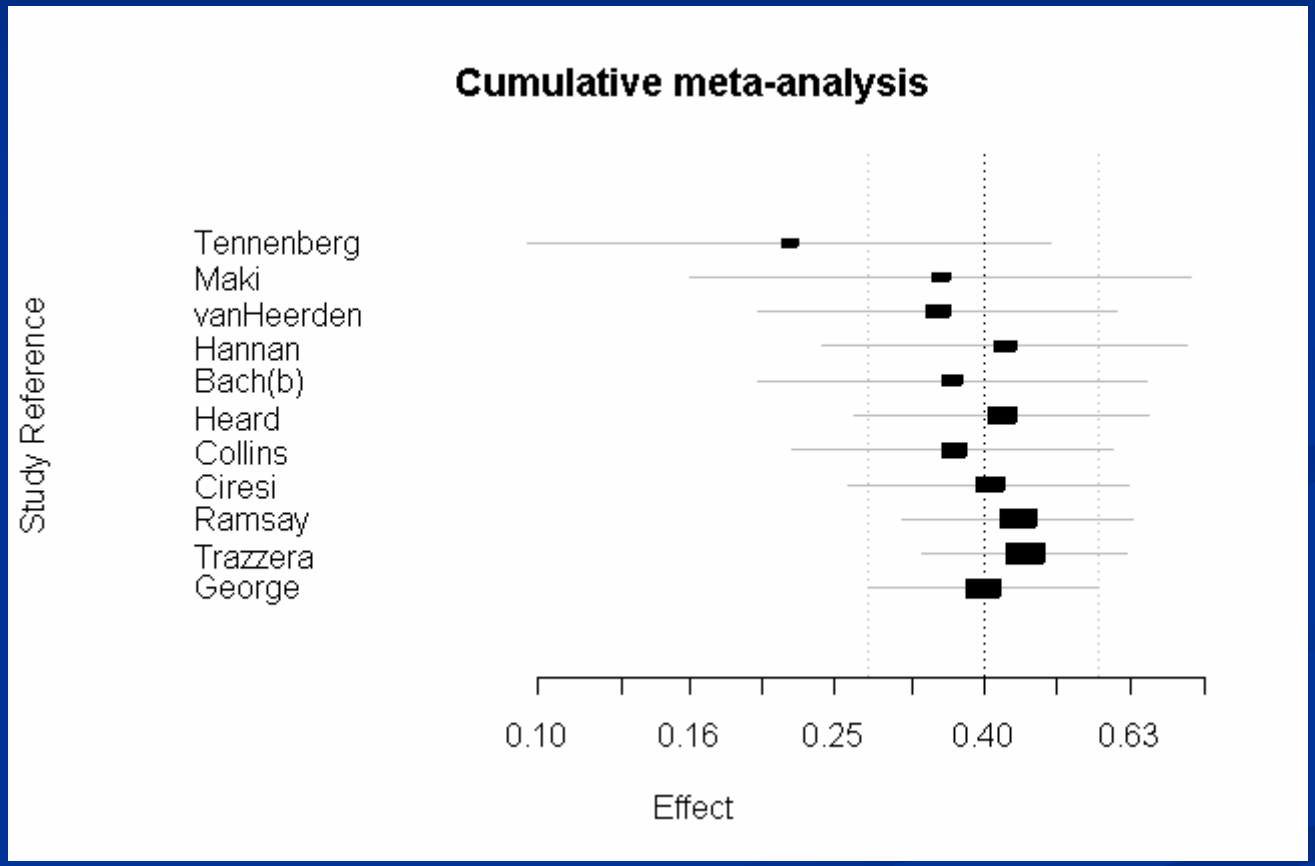


Cummeta: cumulative meta-analysis

```
> data(cochrane)
> steroid<-
    cummeta(n.trt,n.ctrl,ev.trt,ev.ctrl,names=name,data=cochrane,statistic="
    RR",method="meta.MH")
Warning message:
NaNs produced in: pchisq(q, df, lower.tail, log.p)
> plot(steroid)
> summary(steroid)
Cumulative meta-analysis
Call: cummeta(ntrt = n.trt, nctrl = n.ctrl, ptrt = ev.trt, pctrl = ev.ctrl,
    names = name, data = cochrane, method = "meta.MH", statistic = "RR")
-----------------------------------
               RR (lower  95% upper)
Auckland     0.59    0.40       0.87
Block        0.57    0.39       0.83
Doran        0.55    0.39       0.79
Gamsu        0.58    0.43       0.79
Morrison     0.57    0.42       0.77
Papageorgiou 0.54    0.41       0.73
Tauesch      0.55    0.42       0.73
-----------------------------------
```


Cumulative meta-analysis
Study Reference
Auckland
Block
Doran
Gamsu
Morrison
Papageorgiou
Tauesch
0.40
0.45
0.56
0.63
0.71
0.89
Relative Risk

```
> data(catheter)
> b <- meta.DSL(n.trt, n.ctrl, col.trt, col.ctrl, data=catheter,
+ names=Name, subset=c(13,6,5,3,12,4,11,1,8,10,2))
> d <- cummeta.summaries(b$logs, b$selogs, names=b$names,
+ method="random", logscale=TRUE)
Warning message:
NaNs produced in: pchisq(q, df, lower.tail, log.p)
> plot(d,summary.conf=TRUE)
> summary(d)
Cumulative meta-analysis
Call: cummeta.summaries(effects = b$logs, stderrs = b$selogs,
   names = b$names,
    method = "random", logscale = TRUE)
-------------------------------------
           Effect (lower  95% upper)
Tennenberg   0.22    0.10       0.49
Maki         0.35    0.16       0.76
vanHeerden   0.35    0.20       0.61
Hannan       0.43    0.24       0.75
Bach(b)      0.36    0.20       0.66
Heard        0.42    0.27       0.67
Collins      0.36    0.22       0.60
Ciresi       0.41    0.26       0.63
Ramsay       0.44    0.31       0.64
Trazzera     0.45    0.33       0.62
George       0.40    0.28       0.57
```


Cumulative meta-analysis
Study Reference
Tennenberg
Maki
vanHeerden
Hannan
Bach(b)
Heard
Collins
Ciresi
Ramsay
Trazzera
George
0.10
0.16
0.25
0.40
0.63
Effect

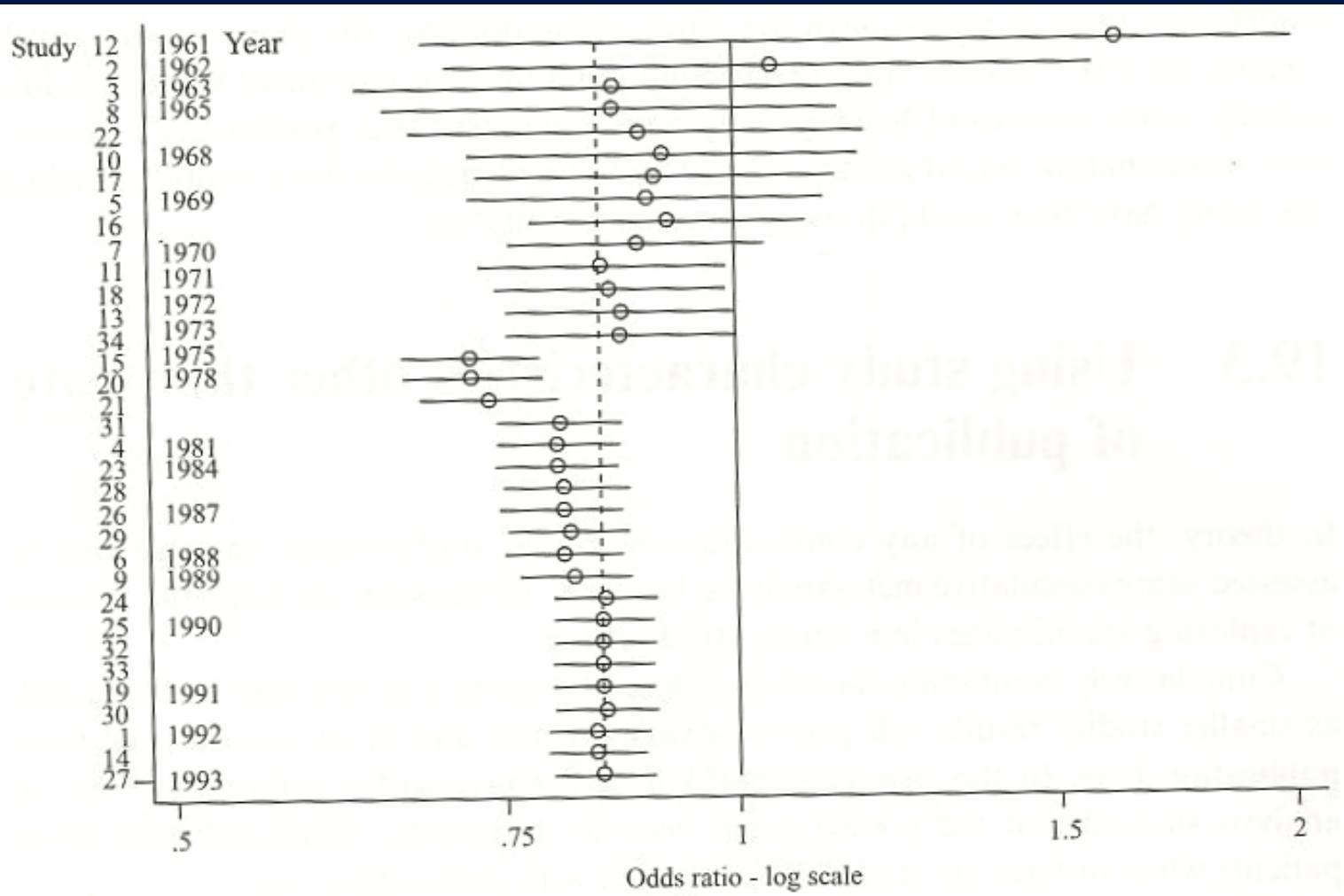


Figure 19.1 Cumulative meta-analysis for total mortality in the cholesterol lowering trials – ordering by year of publication.

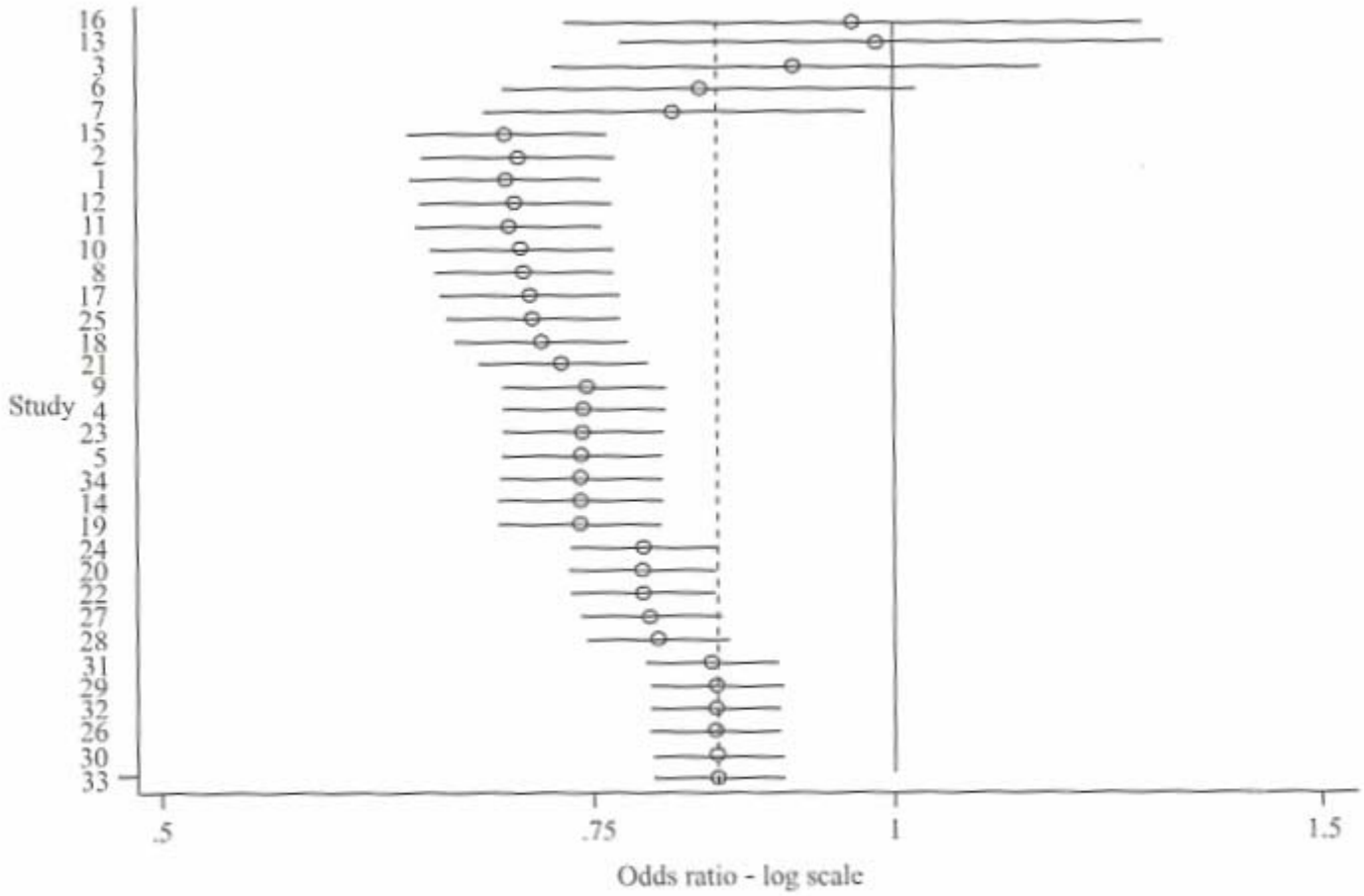
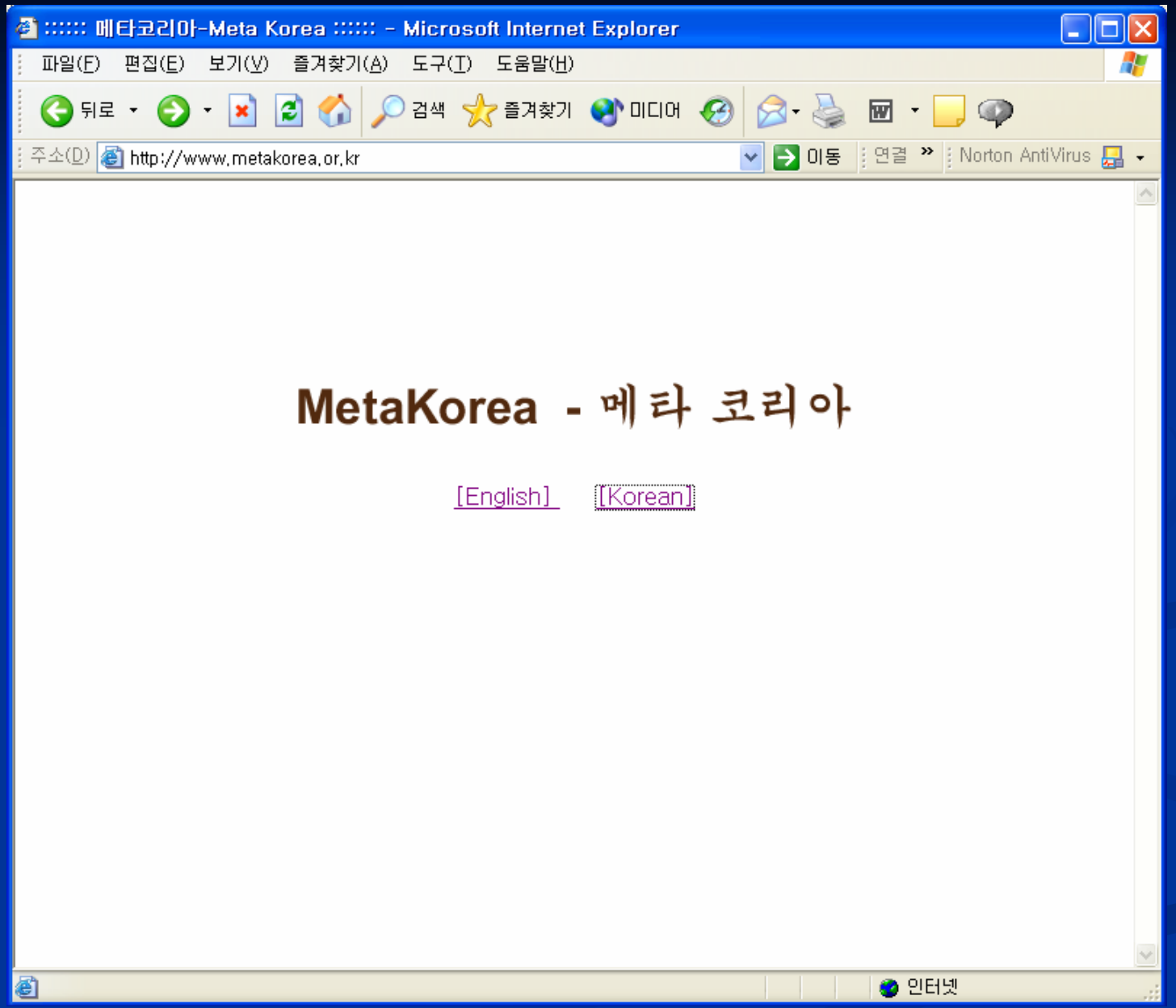
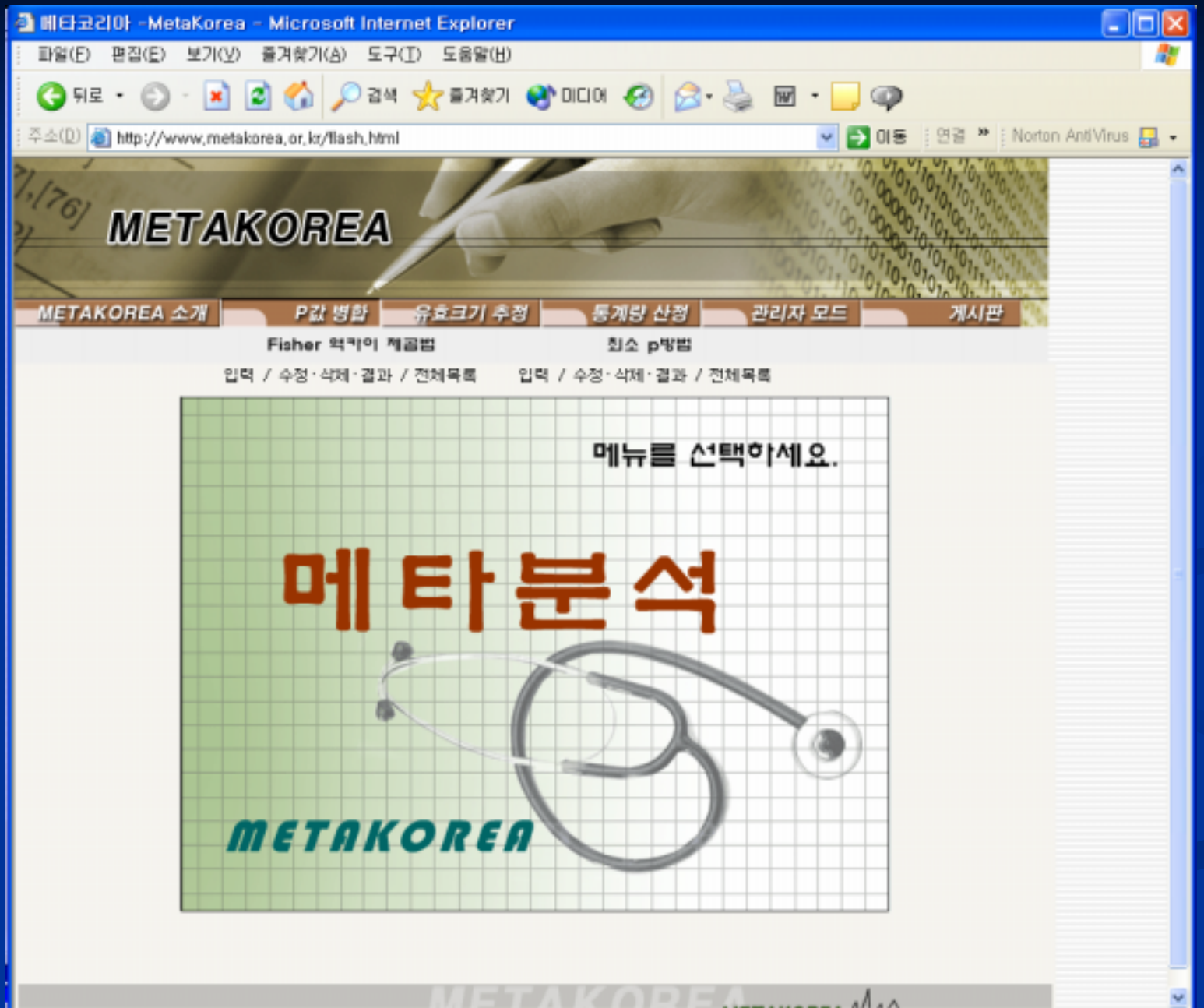
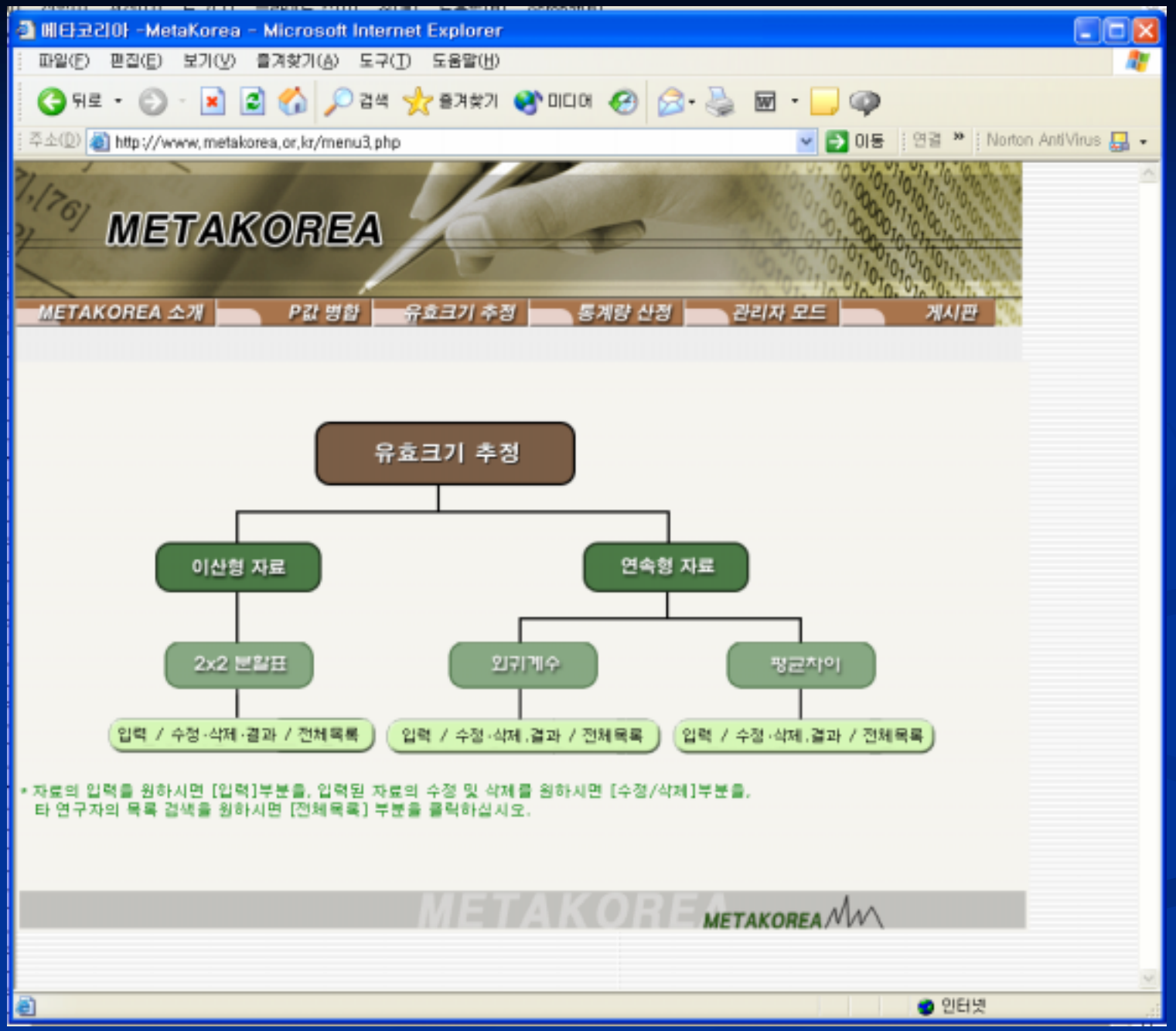


Figure 19.2 Cumulative meta-analysis for total mortality in the cholesterol lowering trials – ordering by baseline risk (descending).


:::::: 메타코리아-Meta Korea :::::: - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
뒤로
검색
즐겨찾기
미디어
주소(D) http://www.metakorea.or.kr
이동
연결
Norton AntiVirus
MetaKorea - 메타 코리아
[English]
[Korean]
인터넷


메타코리아 -MetaKorea - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
뒤로 검색 즐겨찾기 미디어
주소(D) http://www.metakorea.or.kr/flash.html
이동 연결 Norton AntiVirus
METAKOREA
METAKOREA 소개
P값 병합
유효크기 추정
통계량 산정
관리자 모드
게시판
Fisher 역카이 제곱법
최소 p방법
입력 / 수정·삭제·결과 / 전체목록
입력 / 수정·삭제·결과 / 전체목록
메뉴를 선택하세요.
메타분석
METAKOREA


메타코리아 -MetaKorea - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
뒤로 검색 즐겨찾기 미디어
주소(D) http://www.metakorea.or.kr/menu3.php
이동 연결 Norton AntiVirus
METAKOREA
METAKOREA 소개
P값 병합
유효크기 추정
통계량 산정
관리자 모드
게시판
유효크기 추정
이산형 자료
연속형 자료
2x2 분할표
외위계수
평균차이
입력 / 수정·삭제·결과 / 전체목록
입력 / 수정·삭제·결과 / 전체목록
입력 / 수정·삭제·결과 / 전체목록
• 자료의 입력을 원하시면 [입력]부분을, 입력된 자료의 수정 및 삭제를 원하시면 [수정/삭제]부분을,
타 연구자의 목록 검색을 원하시면 [전체목록] 부분을 클릭하십시오.
METAKOREA
인터넷

P-값의 병합

- 연구계획 혹은 치료의 수준이 달라서 효과의 크기를 직접 병합할 수 없는 경우에도 가능
- 단점
  1. 방향이 다르더라도 그대로 병합
  2. 연구의 질이나 표본크기로 가중하지 않음
  3. 각 연구의 효과의 크기를 제시하지 않음

  - 조심해서 사용하여야 함

P-값의 병합; Fisher의 역 카이제곱법

연구	T의 부호	T 값	df	양측 p값	단측 p값	-2log(단측 p값)
1	+	2.907	53	0.0052	0.0026	11.90
2	-	0.199	73	0.8428	0.5786	1.09
3	-	2.233	68	0.0288	0.9856	0.03
4	+	2.108	48	0.0402	0.0201	7.81
5	+	3.694	57	0.0004	0.0002	17.03
합계						38.86~$\chi^2(10)$

출처 : 송혜향 (메타분석법)　　카이제곱의 자유도=2*5　　P=0.00004