

Supplementary Material 1. Sample data

Table S1. The sample data for continuous outcomes

study	n1	m1	s1	n2	m2	s2	md	sd	se	cohen_d	cohen_se	g
Mitsui2003	7	23.2	4.2	5	39.0	7.4	-15.8	5.7	3.337	-2.772	0.814	1
Mitsui2005a	12	28.2	0.9	11	35.9	1.4	-7.7	1.2	0.486	-6.608	1.060	1
Mitsui2005b	8	27.9	2.0	10	33.4	1.2	-5.5	1.6	0.759	-3.438	0.744	1
Mitsui2011	10	27.9	2.0	9	36.1	2.7	-8.2	2.4	1.082	-3.481	0.728	1
Telmeltas2009_1	10	43.4	5.7	5	61.8	9.4	-18.4	7.1	3.866	-2.607	0.726	0
Telmeltas2009_2	9	53.1	7.9	5	61.8	9.4	-8.7	8.4	4.697	-1.033	0.591	0
WBPark2010_1	9	9.7	4.1	11	9.6	4.2	0.1	4.2	1.870	0.024	0.449	1
WBPark2010_2	6	10.3	4.5	9	8.1	7.4	2.2	6.4	3.391	0.345	0.531	1
YHu2012	8	33.8	3.8	8	40.7	4.0	-6.9	3.9	1.941	-1.783	0.591	0
YingJin2011_1	9	36.2	1.7	10	42.3	4.1	-6.1	3.2	1.465	-1.917	0.555	1
YingJin2011_2	6	37.2	2.0	10	42.3	4.1	-5.1	3.5	1.799	-1.467	0.578	1

n1, treatment group sample size; m1, treatment group mean; s1, treatment group standard deviation; n2, control group sample size; m2, control group mean; s2, control group standard deviation; md, mean difference; sd, pooled sd; se, pooled standard error; cohen_d, SMD; cohen_se, standard error of SMD; g, group. Shim SR et al.[2].

Table S2. The sample data for binary outcomes

study	tp	fp	fn	tn	or	lnor	orse	g
study1	16	49	12	53	1.442	0.366	0.430	1
study2	10	30	8	32	1.333	0.288	0.538	1
study3	19	61	14	66	1.468	0.384	0.394	1
study4	80	320	25	375	3.750	1.322	0.241	0
study5	11	29	8	32	1.517	0.417	0.531	0
study6	18	47	16	49	1.173	0.159	0.400	0

or, odds ratio; lnor, log odds ratio; orse, standard error of odds ratio; g, group. Hwang SD & Shim SR[1].

Supplementary Material 2. R 중재 메타분석 코드

#예제자료는 shim_con(Appendix 1), hwang_bin.csv(Appendix 2) 임.

```
#"meta" 패키지 불러오기
library(meta)
```

▶ 연속형(continuous data) 예제자료

```
#데이터 코딩 및 불러오기
data_con <- read.csv("shim_con.csv", header=TRUE)

##중합효과크기 계산##

#원자료로 계산
#SMD를 쓰려면 method.smd="Hedges"(default,보정된 Hedges가 권고됨) or "Cohen",
MD를 쓰려면 smd="MD" 로 표시.
ma_con <- metacont(n1, m1, s1, n2, m2, s2, sm="SMD", method.smd="Hedges",
study,byvar=g ,data=data_con)
print(ma_con, digits=3)

#forest plot
forest(ma_con, comb.fixed=TRUE, comb.random=TRUE,digits=3,rightcols=c("effect", "ci"))
#meta-regression
metareg(ma_con,g,method.tau="REML", digits=3)
bubble(metareg(ma_con,g,method.tau="REML"))

##publication bias##

#funnel plot
funnel(ma_con, comb.fixed=TRUE, comb.random=FALSE)

#출판편향 통계적 검정
#metabias method.bias="linreg"(egger test) / method.bias="rank"(begg test)
ma_con
metacont(n1,m1,s1,n2,m2,s2,sm="SMD",method.smd="Hedges",study,data=data_con)
metabias(ma_con, method.bias="linreg")
metabias(ma_con, method.bias="rank") <-
```

▶ 이분형(binary data) 예제자료

```
#데이터 코딩 및 불러오기
data_bin <- read.csv("hwang_bin.csv", header=TRUE)

##중합효과크기 계산##

#원자료로 계산
```

```

ma_bin <- metabin(tp,tp+fp,fn,fn+tn, sm="OR", method ="Inverse", study,byvar=g,
data=data_bin)
print(ma_bin, digits=3)

#forest plot
forest(ma_bin, comb.fixed=TRUE, comb.random=TRUE,digits=3,rightcols=c("effect", "ci"))

#meta-regression
metareg(ma_bin,g,method.tau="REML", digits=3)
bubble(metareg(ma_bin,g,method.tau="REML"))

##publication bias##

#funnel plot
funnel(ma_bin, comb.fixed=TRUE, comb.random=FALSE)
#출판편향 통계적 검정
#metabias method.bias="linreg"(egger test) / method.bias="rank"(begg test)
ma_bin <- metabin(tp,tp+fp,fn,fn+tn, sm="OR", method ="Inverse", study, data=data_bin)
metabias(ma_bin, method.bias="linreg", k.min=5)
metabias(ma_bin, method.bias="rank", k.min=6)

```

▶ 자료유형 상관없이 메타분석

```

##연속형자료의 효과크기와 표준오차로 계산##
ma_con_es <- metagen(cohen_d, cohen_se, sm="Cohen(SMD)",study,byvar=g,
data=data_con)
print(ma_con_es, digits=3)
forest(ma_con_es, comb.fixed=TRUE, comb.random=TRUE,digits=3,rightcols=c("effect",
"ci"))

##이분형자료의 효과크기와 표준오차로 계산##
ma_bin_es <- metagen(lnor, orse, sm="OR", study,byvar=g, data=data_bin)
print(ma_bin_es, digits=3)
forest(ma_bin_es, comb.fixed=TRUE, comb.random=TRUE,digits=3,rightcols=c("effect",
"ci"))

##유병률자료의 효과크기와 표준오차로 계산##
prop_es <- metagen(p, se, sm="Proportion", backtransf=FALSE,studlab=study,byvar=g,
data=data_prop) #untransformed
print(prop_es, digits=3)
forest(prop_es, comb.fixed=TRUE, comb.random=TRUE,digits=3, rightcols=c("effect", "ci"))
prop_es_ln <- metagen(lnp, se, sm="Proportion", backtransf=TRUE, studlab=study,
byvar=g, data=data_prop) #ln transformed
print(prop_es_ln, digits=3)
prop_es_logit <- metagen(logitp, se, sm="Proportion", backtransf=TRUE, studlab=study,
byvar=g, data=data_prop) #logit transformed
print(prop_es_logit, digits=3)

```