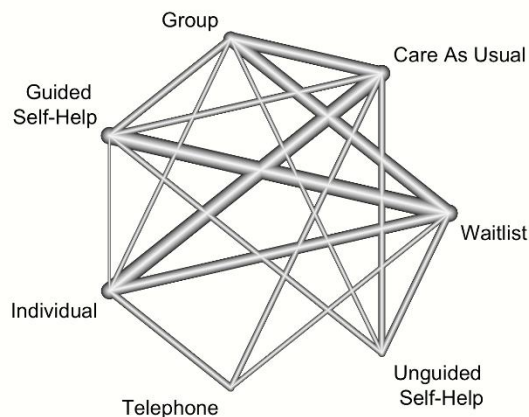


متاآنالیز شبکه ای : تحلیل با R



دکتر محمد حیدری

استادیار اپیدمیولوژی

گروه اپیدمیولوژی و آمار زیستی ، دانشکده پزشکی

دانشگاه علوم پزشکی ارومیه

۲۹ فروردین ۱۴۰۳

ایمیل : Heidari.m@umsu.ac.ir

! "Multilevel" Meta-Analysis

! Structural Equation
Modeling Meta-Analysis

! **Network Meta-Analysis**

! Bayesian Meta-Analysis

Helpful Tools

! Power Analysis

! Risk of Bias Plots

! Reporting &
Reproducibility

! Effect Size Calculation &
Conversion

Appendix

Questions & Answers

Effect Size Formulas

List of Symbols

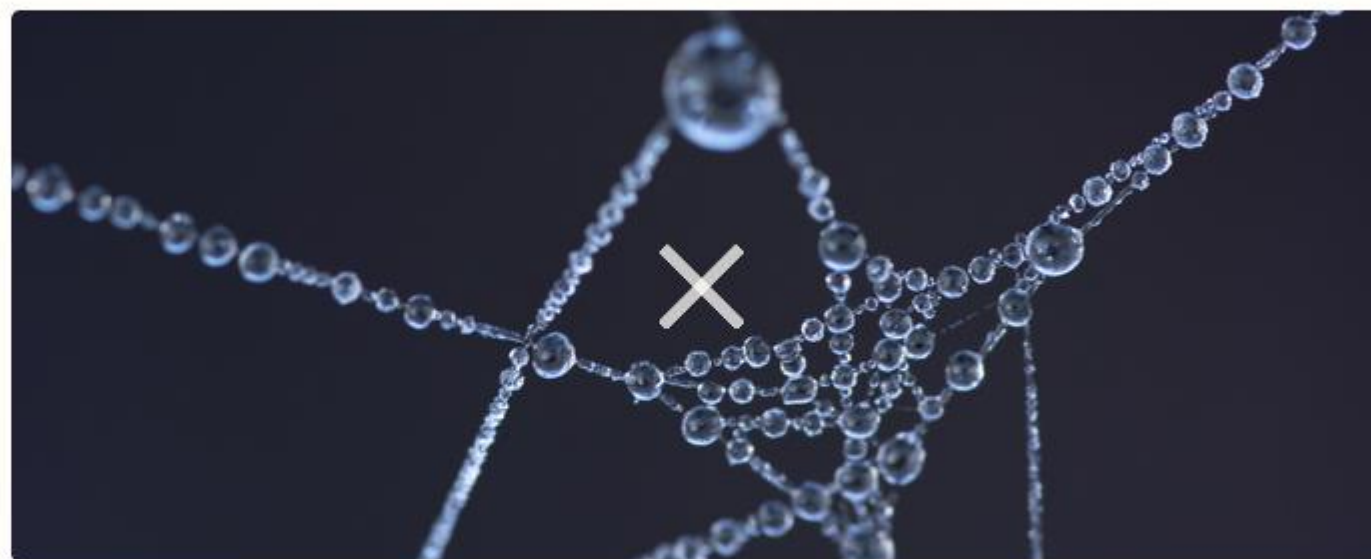
R & Package Information

Corrections & Remarks

Linking this Guide

References

12 Network Meta-Analysis



When we perform meta-analyses of clinical trials or other types of intervention studies, we usually estimate the true effect size of **one** specific treatment. We include studies in which the same type of intervention was compared to similar control groups, for example a placebo. All else being equal, this allows to assess if a

Monhammad Heidari, Ph.D in

Epidemiology

فصل مربوط به متاآنالز شبکه ای از کتاب Rucker و Schwarzer

Use R!

Guido Schwarzer
James R. Carpenter
Gerta Rücker

Meta- Analysis with R

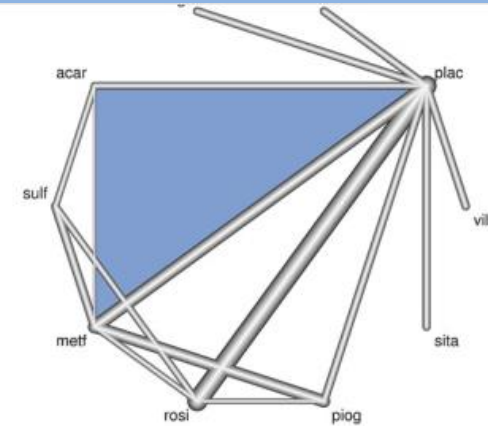


Fig. 8.3 A graph of the network for the diabetes data, generated using the `netgraph` function. The treatments are equally spaced on the perimeter of the circle. Any two treatments are connected by a line when there is at least one study comparing the two treatments. The thickness of the line is proportional to the inverse standard error of the direct treatment comparison. The *shading* indicates the three-arm study

8.3.3 A More Detailed Look at the Output

Next, we view the output stored in the R object `nm1` using the `print` function. We split this into several chunks which we discuss in turn.

```
> print(nm1, digits=2)
Original data (with adjusted standard errors for multi-arm studies):
```

	treat1	treat2	TE	seTE	seTE.adj	narms	multiarm
DeFronzo1995	metf	plac	-1.90	0.14	0.14	2	
Lewin2007	metf	plac	-0.82	0.10	0.10	2	
Willms1999	acar	metf	0.20	0.36	0.39	3	*
Davidson2007	plac	rosi	1.34	0.14	0.14	2	
*** Output truncated ***							
Moulin2006	benf	plac	-1.01	0.14	0.14	2	
Willms1999	metf	plac	-1.20	0.38	0.41	3	*
Willms1999	acar	plac	-1.00	0.47	0.82	3	*

مقاله کره ای خوب و راهنمای عملی تحلیل ها

Open Access

Volume: 41, Article ID: e2019013, 10 pages
<https://doi.org/10.4178/epih.e2019013>

METHODS



Network meta-analysis: application and practice using R software

Sung Ryul Shim^{1,2}, Seong-Jang Kim^{3,4}, Jonghoo Lee⁵, Gerta Rücker⁶

¹Department of Preventive Medicine, Korea University College of Medicine, Seoul, Korea; ²Urological Biomedicine Research Institute, Soonchunhyang University Hospital, Seoul, Korea; ³Department of Nuclear Medicine, Pusan National University Yangsan Hospital, Pusan National University School of Medicine, Yangsan, Korea; ⁴Biomedical Research Institute for Convergence of Biomedical Science and Technology, Pusan National University Yangsan Hospital, Yangsan, Korea; ⁵Department of Internal Medicine, Jeju National University Hospital, Jeju National University School of Medicine, Jeju, Korea; ⁶Institute of Medical Biometry and Statistics, Faculty of Medicine and Medical Center, University of Freiburg, Freiburg, Germany

The objective of this study is to describe the general approaches to network meta-analysis that are available for quantitative data synthesis using R software. We conducted a network meta-analysis using two approaches: Bayesian and frequentist methods. The corresponding R packages were “gemtc” for the Bayesian approach and “netmeta” for the frequentist approach. In estimating a network meta-analysis model using a Bayesian framework, the “rjags” package is a common tool. “rjags” implements Markov chain Monte Carlo simulation with a graphical output. The estimated overall effect sizes, test for heterogeneity, moderator effects, and publication bias were reported using R software. The authors focus on two flexible models, Bayesian and frequentist, to deter-

گام اول : قالب داده ها

A	B	C	D	E	F	G	H	I	
author	TE	seTE	treat1	treat2	treat1.long	treat2.long	versus		
1	Ausbun, 1997	0.092	0.195	ind	grp	Individual	Group	ind vs grp	
2	Crable, 1986	-0.675	0.35	ind	grp	Individual	Group	ind vs grp	
3	Thiede, 2011	-0.107	0.198	ind	grp	Individual	Group	ind vs grp	
4	Bonertz, 2015	-0.09	0.324	ind	grp	Individual	Group	ind vs grp	
5	Joy, 2002	-0.135	0.453	ind	grp	Individual	Group	ind vs grp	
6	Jones, 2013	-0.217	0.289	ind	grp	Individual	Group	ind vs grp	
7	Aaron, 2004	0.103	0.401	ind	grp	Individual	Group	ind vs grp	
8	Breiman, 2001	-0.085	0.516	ind	gsh	Individual	Guided Se	Breiman, 2001	
9	Lucero, 2001	-0.052	0.5	ind	gsh	Individual	Guided Se	ind vs gsh	
10	Amsberry, 2010	-0.109	0.413	ind	gsh	Individual	Guided Se	ind vs gsh	
11	Robinson, 2015	-0.128	0.256	ind	gsh	Individual	Guided Se	ind vs gsh	
12	Burgan, 2012	-0.311	0.139	ind	tel	Individual	Telephone	ind vs tel	
13	Belk, 1986	-0.177	0.083	ind	tel	Individual	Telephone	ind vs tel	
14	Ledbetter, 1984	-0.008	0.231	ind	tel	Individual	Telephone	ind vs tel	
15	Narum, 1986	0.039	0.338	ind	tel	Individual	Telephone	ind vs tel	
16	Breiman, 2001	-0.75	0.513	ind	wlc	Indiv		Breiman, 2001	
17	Wierenga, 2004	-1.438	0.357	ind	wlc	Indiv		ind vs wlc	
18	Eisenberg, 1995	-0.509	0.06	ind	wlc	Indiv		ind vs wlc	
19	Scholer, 2017	-0.965	0.443	ind	wlc	Individual	Waitlist	ind vs wlc	
20	Schlaver, 2004	-1.156	0.344	ind	wlc	Individual	Waitlist	ind vs wlc	

Wide

برای متغیرهای دو حالتی: محاسبه log or

gen logor= $\ln((a/b)/(c/d))$

gen logor= $\log((a/b)/(c/d))$

gen selogor= $\sqrt{(1/a)+(1/b)+(1/c)+(1/d)}$

gen logrr= $\log((a/(a+b))/(c/(c+d)))$

gen selogrr= $\sqrt{(1/a)-(1/(a+b))+(1/c)-(1/(c+d)))}$

	Diseased	Non-diseased	Total
Exposed	A	B	A+B
Non-exposed	C	D	C+D
Total	A+C	B+D	A+B+C+D

نصب پکیج های لازم:

```
library(meta)install.packages(meta)
library(meta)
install.packages(netmeta)
library(netmeta)
install.packages(tidyvers)
library(tidyverse)
#install from githubinstall.packages("remotes")
library(remote)
remotes::install_github("MathiasHarrer/dmetar")
library(dmetar)
```

بخش های اصلی دستور netmeta:

- `m.netmeta <- netmeta(TE = TE, seTE = seTE, treat1 = treat1, treat2 = treat2, studlab = author, data = TherapyFormats, sm = "SMD", fixed = TRUE, random = FALSE, reference.group = "cau", details.chkmultiarm = TRUE, sep.trts = " vs ")`

معرفی ابزارهای آنلاین برای انجام متاآنالیز شبکه ای:

<http://www.nihrcrsu.org/guidance/apps/>

<https://crsu.shinyapps.io/MetaDTA/>

<https://www.nmastudioapp.com/>

<https://addis.drugis.org/manual.html>

قابلیت پکیج shiny در ساختن نرم افزارهای آنلاین:

