**Online materials**

metafor/R[[1]](#footnote-1)を使ったメタアナリシス

「診療ガイドラインのためのGRADEシステム（第2版）」（相原、凸版メディア、2015年出版）のオンライン追加資料です。<http://www.grade-jpn.com/online_supplementals/online_supplemental_materials.html>

* 詳細は書籍の**4.4.3章**を参照ください。
* 本資料のファイル名：Metafor\_heparin.docx （相原守夫、2014年9月作成）
* 以下の内容は、更新される可能性がありますので、上記URLに表示する年月日を参考にしてください。

R： version 3.0.3

データ： heparin4metafor.xlsx　(heparin.RData)

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| ##Rを立ち上げ、インストールしたmetaforを読みこむ |
| データを読みこむ。   * ディレクトリの変更（データのある場所を指定） * Rコマンダーを使って、（この例では、データ名を“heparin”に指定し）、エクセルデータを読みこむ（csvか、テキストデータでも可）。 * もしくは、R console に、　**>dat <- get(heparin)** |
| ##データを表示  **>heparin**  **>print(heparin[,-c(8:9)], row.names=FALSE)** |
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| ### meta-analysis of the log relative risks using a random-effects model  **> dat = escalc(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=heparin, append=TRUE)**  **> res <- rma(yi, vi, data = dat)**  **> res** |
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| **> confint(res)** |
| ###log odds-ratio  **>res <- rma(measure="OR", ai=tpos, bi=tneg, ci=cpos, di=cneg, slab=paste(author, year, sep=", "), data=heparin)**  **>res**  （結果略） |
| ###forest plot  **>forest(res)** |
| **>forest(res, slab = paste(heparin$author, heparin$year, sep = ", "), xlim = c(-16, 6), at = log(c(0.05, 0.25, 1, 4)), atransf = exp, ilab = cbind(heparin$tpos, heparin$tneg, heparin$cpos, heparin$cneg), ilab.xpos = c(-9.5, -8, -6, -4.5), cex = 0.9)**  **>op <- par(cex = 0.75, font = 2)**  **> text(c(-9.5, -8, -6, -4.5), 10, c("outcome+", "outcome-", "outcome+", "outcome-"))**  **> text(c(-8.75, -5.25), 11, c("Heparin", "Control"))**  **> text(-16, 10, "Author(s) and Year", pos = 4)**  **> text(6, 10, "Relative Risk [95% CI]", pos = 2)**  **> par(op)** |
| ###forest plot (pooled estimates by control rate)  **>forest(dat$yi, dat$vi, atransf = exp, ylim = c(-3.5, 16),at = log(c(0.05, 0.25, 1, 4, 20)), xlim = c(-9, 7),slab = paste(dat$author, dat$year, sep = ", "))**  **>res <- rma(yi, vi, mods = cbind(controlrate), data = dat)**  **> preds <- predict(res, newmods = c(0.4, 0.6, 0.8))**  **> addpoly(preds$pred, sei = preds$se, atransf = exp,mlab = c("controlrate 0.4", "controlrate 0.6", "controlrate 0.8"))**  **> text(-9, 15, "Author(s) and Year", pos = 4, font = 2)**  **> text(7, 15, "Relative Risk [95% CI]", pos = 2, font = 2)**  **> abline(h = 0)** |
| ##funnel plot (Random-effects model without moderators)  **>** **res <- rma(yi, vi, data = dat)**  **>** **funnel(res, main = "Random-Effects Model")** |
| ##funnel plot (mixed-effects model with moderators: modulator as controlrate)  **>res <- rma(yi, vi, mods = cbind(controlrate), data = dat)**  **>funnel(res, main = "Mixed-Effects Model")** |
| ### contour-enhanced funnel plot centered at 0 (see Peters et al., 2008)  **>funnel(res, level=c(90, 95, 99), shade=c("white", "gray", "darkgray"),refline=0, atransf=exp, at=log(c(.25, .5, 1, 2, 4)))** |
| ### classical Egger test  **> regtest(res, model="lm")** |
| ###Fail-Safe N Analysis (File Drawer Analysis)  **>fsn(yi, vi, data=dat)**  **>fsn(yi, vi, data=dat, type="Orwin")**  **>fsn(yi, vi, data=dat, type="Rosenberg")** |
| ###Trim-and Fill  **> res <- rma(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, slab=paste(author, year, sep=", "), data=heparin)**  **>res.tf <- trimfill(res)**  **>res.tf**    **>funnel(res.tf)** |
| ###Galbraith plot  **> res <- rma(yi, vi, data = dat, method = "FE")**  **> radial(res, main = "Fixed-Effects Model")**  **> res <- rma(yi, vi, data = dat, method = "REML")**  **> radial(res, main = "Random-Effects Model")** |
| ### L'Abbe plot  **>labbe(res, transf=transf.ilogit, bg="white", xlim=c(0.2,0.6), ylim=c(0.2,0.6), xlab="Control Group Risk", ylab="Intervention Group Risk")** |
| ### Subgroup analysis（がんの種類によるサブ解析）  > dat = escalc(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=heparin, append=TRUE)  > res <- rma(yi, vi, data = dat)  >forest(res, slab = paste(heparin$author, heparin$year, sep = ", "), xlim=c(-16, 6), at=log(c(.05, .25, 1, 4)), atransf=exp, ilab = cbind(heparin$tpos, heparin$tneg, heparin$cpos, heparin$cneg), ilab.xpos=c(-9.5,-8,-6,-4.5), cex=.75, ylim=c(-1, 27), order=order(heparin$cancertype), rows=c(18:13,8:7), mlab="RE Model for All Studies")  > op <- par(cex=.75, font=4)  text(-16, c(19.5,9.5), c("non-SCLC", "SCLC"), pos=4)  par(font=2)  >text(c(-9.5,-8,-6,-4.5), 21, c("Event+", "Event-", "Event+", "Event-"))  text(c(-8.75,-5.25), 22, c("Heparin", "Control"))  text(-16, 21, "Author(s) and Year", pos=4)  text(6, 21, "Relative Risk [95% CI]", pos=2)  par(op)  >res <- rma(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=heparin,  subset=(cancertype==”non-\_sclc”))  addpoly(res, row=11.5, cex=.75, atransf=exp, mlab="RE Model for Subgroup")  >res <- rma(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, data=heparin,  subset=(cancertype==”sclc”))  addpoly(res, row=5.5, cex=.75, atransf=exp, mlab="RE Model for Subgroup") |
| ###メタ回帰（yi, viを利用。共変量としてcontrolrate）  **> metaReg =rma(yi, vi, mods=~controlrate, data=dat)**  **>metaReg** |
| ##メタ回帰（生データを利用。共変量＝controlrateとしてpredict）  >res <- rma(measure="RR", ai=tpos, bi=tneg, ci=cpos, di=cneg, mods = ~ controlrate, data=dat)  > predict(res, transf=exp, addx=TRUE) |
| ### predicted average relative risks for 0.2-1.0 controlrate  （本資料のp3, ###forest plot (pooled estimates by control rate)を参照）  >predict(res, newmods = seq(from = 0.2, to = 1.0, by = 0.2),transf = exp, addx = TRUE) |
| ###回帰曲線  >preds <- predict(res, newmods = (0:1), transf = exp)  >wi <- 1/sqrt(dat$vi)  > size <- 0.5 + 3 \* (wi - min(wi))/(max(wi) - min(wi))  >plot(dat$controlrate, exp(dat$yi), pch = 19, cex = size,xlab = "controlrate", ylab = "Relative Risk",las = 1, bty = "l", log = "y")  #Add a thicker line for the meta-regression and the CIs  >lines(0:1, preds$pred)  >lines(0:1, preds$ci.lb, lty = "dashed")  >lines(0:1, preds$ci.ub, lty = "dashed")  >abline(h = 1, lty = "dotted") |

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| ### influence analysis  > inf <- influence(res)  > inf  > plot(inf, plotdfb = TRUE) |

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| ###Cumulative meta  ### random-effects model  res <- rma(yi, vi, data=dat, slab=paste(author, year, sep=", "))  x <- cumul(res, order=order(dat$year))  forest(x)  forest(x, alim=c(-2,1)) |
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1. metaforは、“META-analysis FOr R”の略である。

   本資料の記載は、Meta-Analysis Package for R (version 1.9-5, 2014/11/24）に準じたものである。<http://www.metafor-project.org/> [↑](#footnote-ref-1)