

code.r

samit

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```
#load library
library(metafor)
library(rmarkdown)

#load data
allom=read.csv("data/allometric_effectsize14.csv")
tls=read.csv("data/tls_effectsize14.csv")

# Calculate effect sizes: log response ratio for TLS vs DEST
es_tls <- escalc(measure = "ROM",
                 m1i = TLS_mean, sd1i = TLS_SD, n1i = n,
                 m2i = DEST_mean, sd2i = DEST_SD, n2i = n,
                 data = tls)

# Calculate effect sizes: log response ratio for ALLOM vs DEST
es_allom <- escalc(measure = "ROM",
                  m1i = ALLOM_mean, sd1i = ALLOM_SD, n1i = n,
                  m2i = DEST_mean, sd2i = DEST_SD, n2i = n,
                  data = allom)

# Meta-analysis TLS vs DEST
res_tls <- rma(yi, vi, data = es_tls, method = "REML")
summary(res_tls)

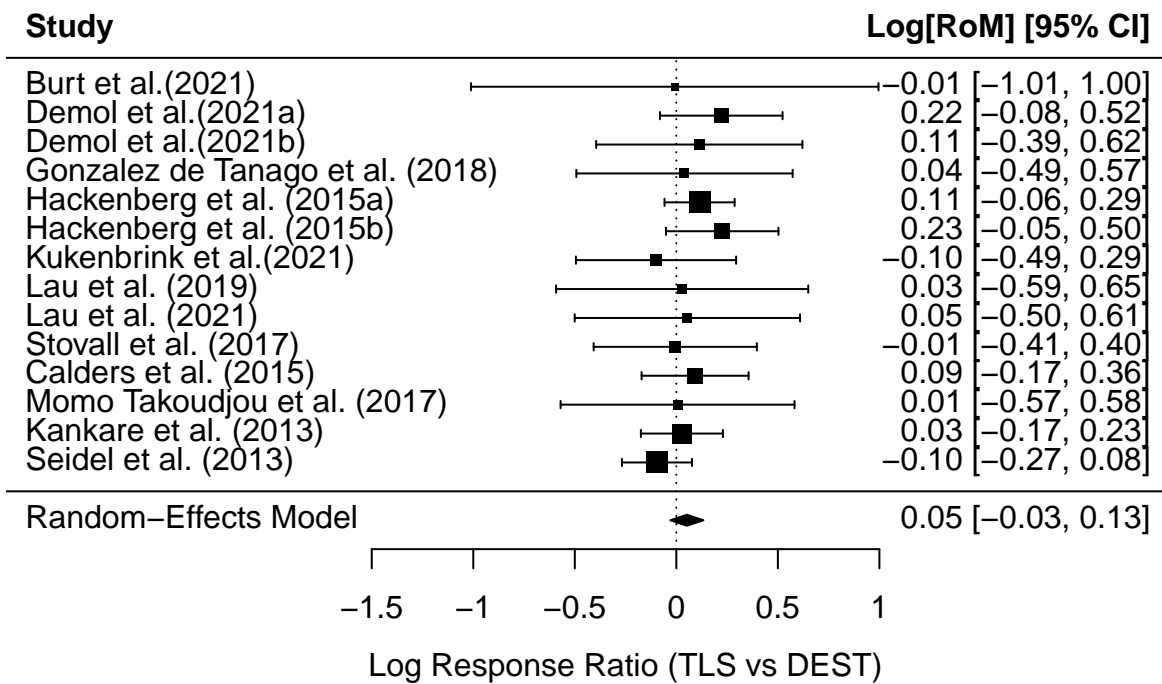
##
## Random-Effects Model (k = 14; tau^2 estimator: REML)
##
##   logLik  deviance      AIC      BIC      AICc
##   5.8214  -11.6428   -7.6428   -6.5129   -6.4428
##
## tau^2 (estimated amount of total heterogeneity): 0.0007 (SE = 0.0075)
## tau (square root of estimated tau^2 value):      0.0264
## I^2 (total heterogeneity / total variability):    2.76%
## H^2 (total variability / sampling variability):   1.03
##
## Test for Heterogeneity:
## Q(df = 13) = 6.9277, p-val = 0.9058
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.0520   0.0415   1.2548   0.2095   -0.0292   0.1333
##
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

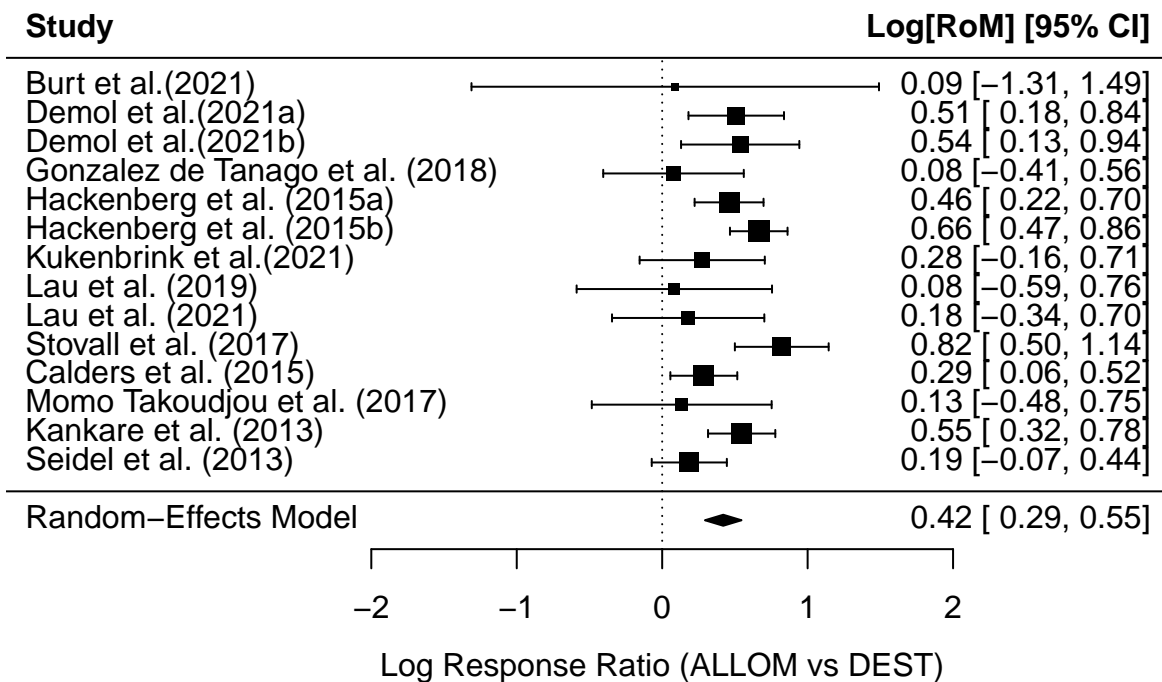
# Meta-analysis ALLOM vs DEST
res_allom <- rma(yi, vi, data = es_allom, method = "REML")
summary(res_allom)

##
## Random-Effects Model (k = 14; tau^2 estimator: REML)
##
##   logLik  deviance      AIC      BIC     AICc
## -0.5407   1.0813   5.0813   6.2112   6.2813
##
## tau^2 (estimated amount of total heterogeneity): 0.0232 (SE = 0.0207)
## tau (square root of estimated tau^2 value):      0.1522
## I^2 (total heterogeneity / total variability):   45.87%
## H^2 (total variability / sampling variability):   1.85
##
## Test for Heterogeneity:
## Q(df = 13) = 22.8723, p-val = 0.0432
##
## Model Results:
##
## estimate      se      zval      pval    ci.lb    ci.ub
##  0.4197  0.0641  6.5478  <.0001  0.2941  0.5454  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Forest plots
forest(res_tls, slab = tls$Author, xlab = "Log Response Ratio (TLS vs DEST)", main = "")
```



```
forest(res_allom, slab = allom$Author, xlab = "Log Response Ratio (ALLOM vs DEST)", main = "")
```



```
# Egger's test for asymmetry
```

```
reg_tls=regtest(res_tls, model = "lm")
```

```
reg_allom=regtest(res_allom, model = "lm")
```

```
reg_tls
```

```
##
```

```
## Regression Test for Funnel Plot Asymmetry
```

```
##
```

```
## Model:      weighted regression with multiplicative dispersion
```

```
## Predictor: standard error
```

```
##
```

```
## Test for Funnel Plot Asymmetry: t = 0.2500, df = 12, p = 0.8068
```

```
## Limit Estimate (as sei -> 0):   b = 0.0360 (CI: -0.1122, 0.1841)
```

```
reg_allom
```

```
##
```

```
## Regression Test for Funnel Plot Asymmetry
```

```
##
```

```
## Model:      weighted regression with multiplicative dispersion
```

```
## Predictor: standard error
```

```
##
```

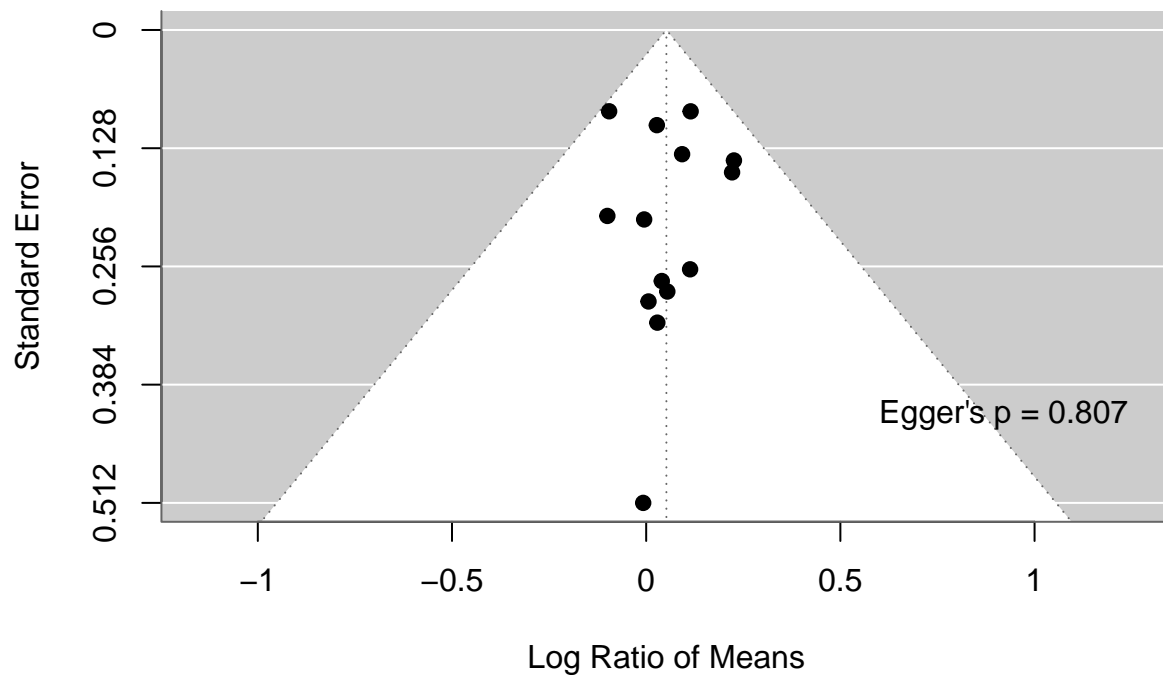
```
## Test for Funnel Plot Asymmetry: t = -1.6537, df = 12, p = 0.1241
```

```
## Limit Estimate (as sei -> 0):   b = 0.6530 (CI: 0.3585, 0.9476)
```

```
# Funnel plots for publication bias
funnel(res_tls, main = "a. Funnel Plot: TLS vs DEST")

# Add Egger's test p-value to the plot
pval <- formatC(reg_tls$pval, format = "f", digits = 3) # Format p-value to 3 decimal places
text(x = 0.6, y = 0.4, labels = paste0("Egger's p = ", pval), adj = c(0,1), cex = 1)
```

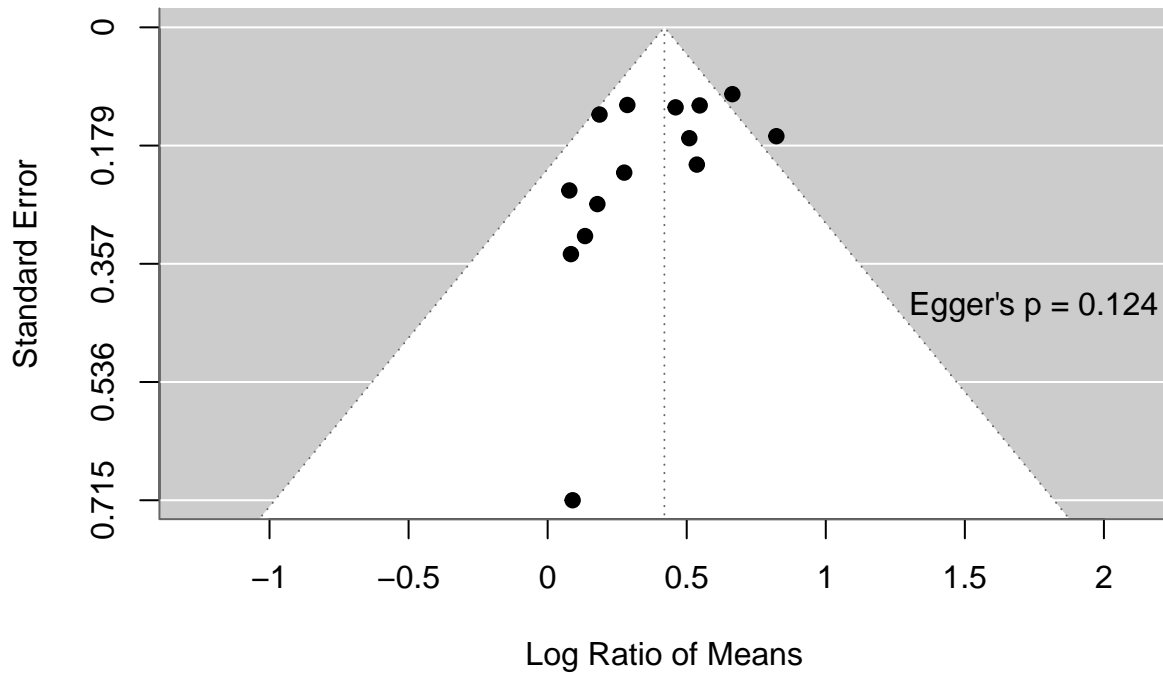
a. Funnel Plot: TLS vs DEST



```
funnel(res_allom, main = "b. Funnel Plot: ALLOM vs DEST")

# Add Egger's test p-value to the plot
pval <- formatC(reg_allom$pval, format = "f", digits = 3) # Format p-value to 3 decimal places
text(x = 1.3, y = 0.4, labels = paste0("Egger's p = ", pval), adj = c(0,1), cex = 1)
```

b. Funnel Plot: ALLOM vs DEST



```
#####
# Moderator analysis (species type)
res_mod_allom <- rma(yi, vi, mods = ~ type+equation_type, data = es_allom, method = "REML")
summary(res_mod_allom)

##
## Mixed-Effects Model (k = 14; tau^2 estimator: REML)
##
##   logLik  deviance      AIC      BIC     AICc
##   3.4604   -6.9209   1.0791   2.6707   7.7458
##
## tau^2 (estimated amount of residual heterogeneity):    0 (SE = 0.0099)
## tau (square root of estimated tau^2 value):           0
## I^2 (residual heterogeneity / unaccounted variability): 0.00%
## H^2 (unaccounted variability / sampling variability):  1.00
## R^2 (amount of heterogeneity accounted for):           100.00%
##
## Test for Residual Heterogeneity:
## QE(df = 11) = 7.5254, p-val = 0.7551
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 15.3469, p-val = 0.0005
##
## Model Results:
##
```

```
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.6400  0.0659   9.7071 <.0001   0.5108  0.7692 ***
## typeneedleleaf  -0.2605  0.1393  -1.8698  0.0615  -0.5335  0.0126 .
## equation_typespecies-specific -0.0970  0.1387  -0.6991  0.4845  -0.3688  0.1749
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Moderator ( equation type)
```

```
res_mod_allom2 <- rma(yi, vi, mods = ~ equation_type-1, data = es_allom, method = "REML")
res_mod_allom2
```

```
##
## Mixed-Effects Model (k = 14; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0 (SE = 0.0095)
## tau (square root of estimated tau^2 value):            0
## I^2 (residual heterogeneity / unaccounted variability): 0.00%
## H^2 (unaccounted variability / sampling variability):   1.00
##
## Test for Residual Heterogeneity:
## QE(df = 12) = 11.0216, p-val = 0.5271
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 119.4176, p-val < .0001
##
## Model Results:
##
##               estimate      se      zval      pval      ci.lb      ci.ub
## equation_typepantropical    0.5816  0.0581  10.0148 <.0001   0.4678  0.6955 ***
## equation_typespecies-specific 0.2825  0.0646   4.3729 <.0001   0.1559  0.4092 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Moderator ( tree type)
```

```
res_mod_allom3 <- rma(yi, vi, mods = ~ type-1, data = es_allom, method = "REML")
res_mod_allom3
```

```
##
## Mixed-Effects Model (k = 14; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0 (SE = 0.0096)
## tau (square root of estimated tau^2 value):            0
## I^2 (residual heterogeneity / unaccounted variability): 0.00%
## H^2 (unaccounted variability / sampling variability):   1.00
##
## Test for Residual Heterogeneity:
## QE(df = 12) = 8.0142, p-val = 0.7840
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 122.4251, p-val < .0001
##
```

```
## Model Results:
##
##           estimate      se   zval   pval   ci.lb   ci.ub
## typebroadleaf    0.6400 0.0659 9.7071 <.0001 0.5108 0.7692 ***
## typeneedleleaf   0.3036 0.0572 5.3101 <.0001 0.1915 0.4157 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# load orchard package
```

```
pacman::p_load(devtools, tidyverse, metafor, patchwork, R.rsp, orchaRd, emmeans, ape, phytools, flextable)
```

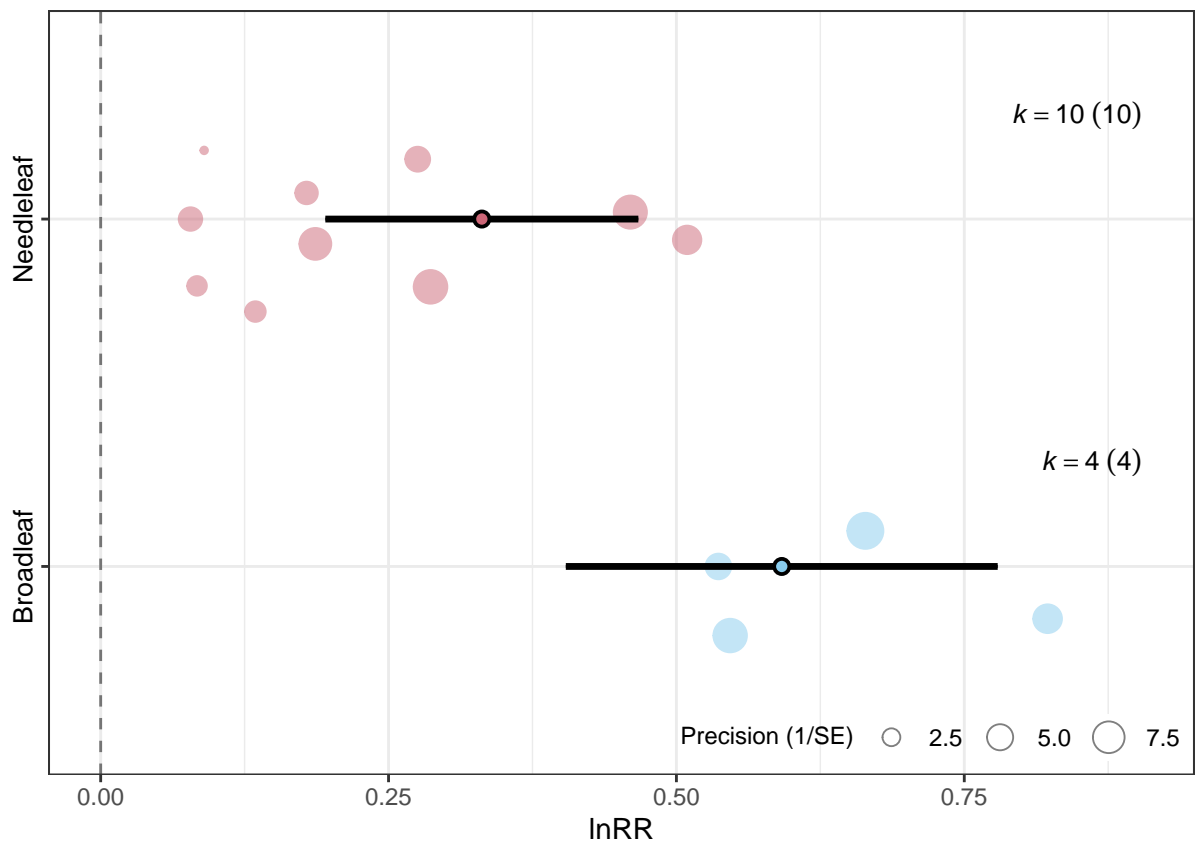
```
# we can create a table of results for moderator
```

```
res2 <- orchaRd::mod_results(res_mod_allom, mod = "type", group = "ID")
res2
```

```
##           name estimate lowerCL upperCL lowerPR upperPR
## 1 Broadleaf 0.5914946 0.4039632 0.7790261 0.4039632 0.7790261
## 2 Needleleaf 0.3310278 0.1951203 0.4669354 0.1951203 0.4669354
```

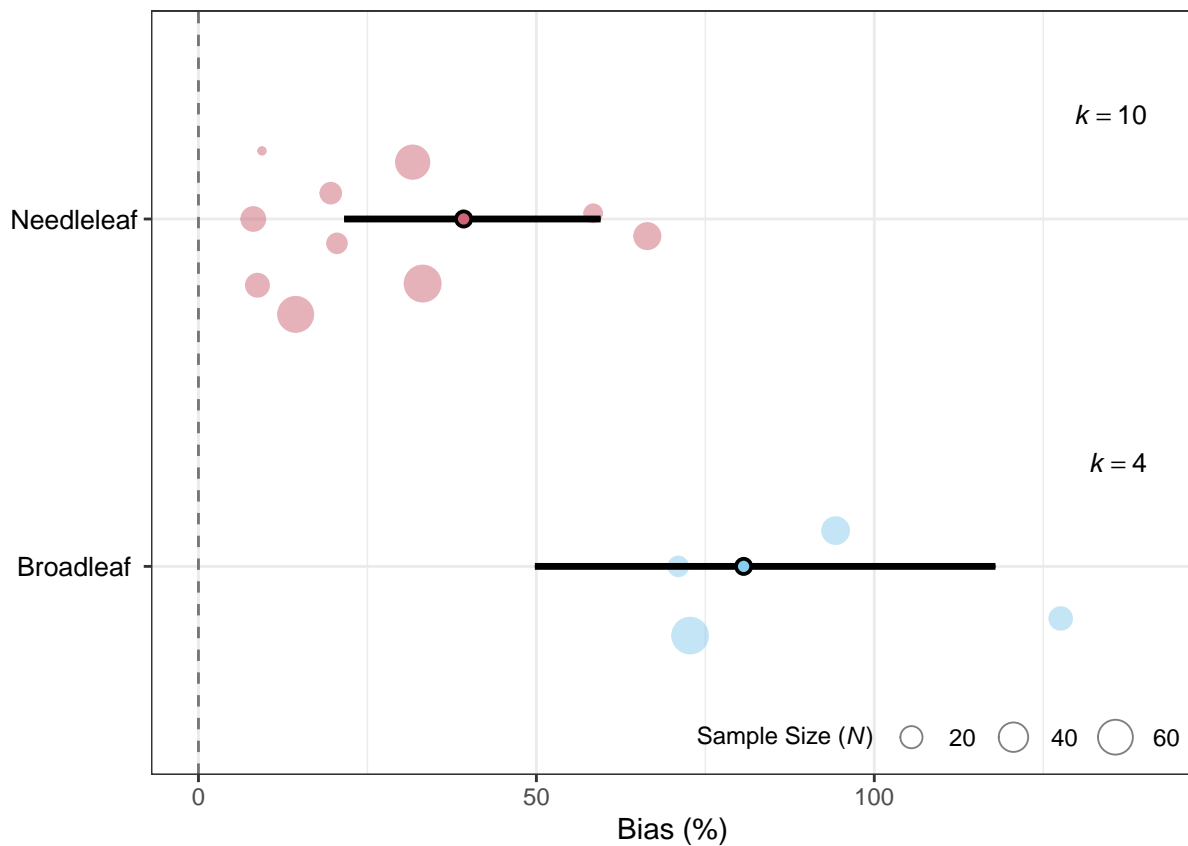
```
p2 <- orchaRd::orchard_plot(res2,
                             mod = "type",
                             group = "Author",
                             xlab = "lnRR")##tree type as moderator
```

```
p2
```




```
p6_per <- orchaRd::orchard_plot(res_mod_allom,
                                mod = "type", group = "Author",
                                xlab = "Bias (%)",
                                angle = 0, N = "n",
                                g = FALSE,
                                transfm = "percentr") #plot with log ratio transformed to percentage
```

p6_per



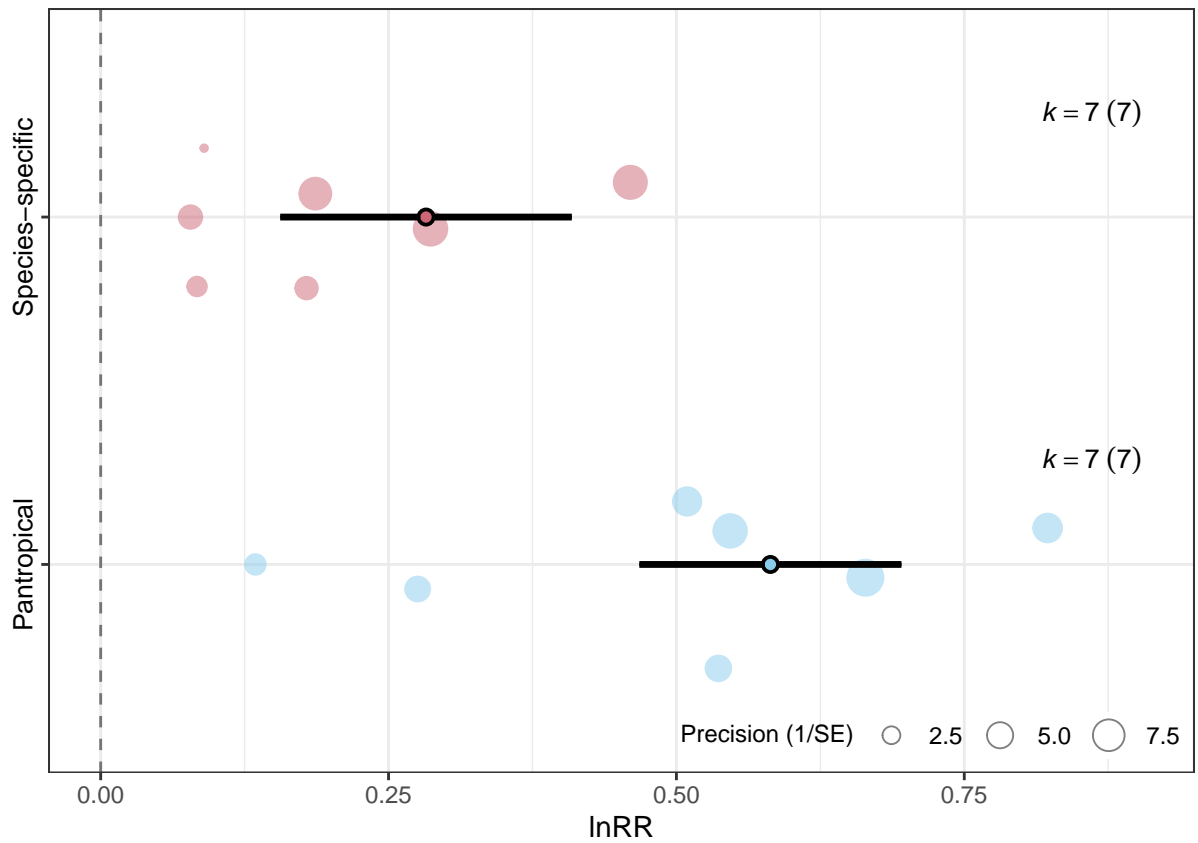
```
res3 <- orchaRd::mod_results(res_mod_allom2,
                              mod = "equation_type",
                              group = "Author") #equation type as moderator
```

res3

```
##           name estimate lowerCL upperCL lowerPR upperPR
## 1   Pantropical 0.5816295 0.4678003 0.6954587 0.4678003 0.6954587
## 2 Species-specific 0.2825495 0.1559073 0.4091917 0.1559073 0.4091917
```

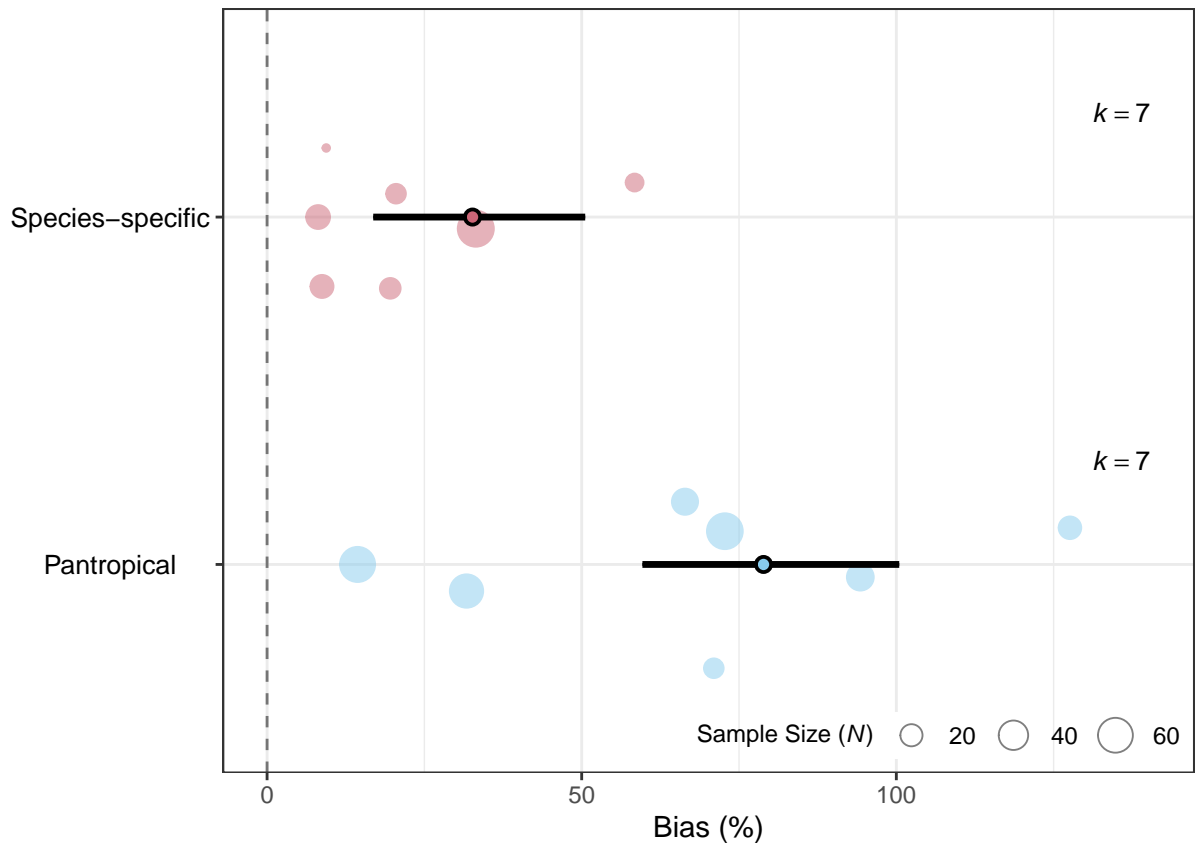
```
p3 <- orchaRd::orchard_plot(res3,
                             mod = "equation_type",
                             group = "Author",
                             xlab = "lnRR") ## equation type as moderator
```

p3



```
p7_per <- orchaRd::orchard_plot(res_mod_allom2,
                                mod = "equation_type",
                                group = "Author",
                                xlab = "Bias (%)",
                                angle = 0,
                                N = "n", g = FALSE,
                                transfm = "percentr") ## transformed to percentage
```

p7_per



```
##### Continuous Moderator ( dbh)
res_mod_allom4 <- rma(yi, vi,
  mods = ~ mean_dbh,
  data = es_allom,
  method = "REML")##for allometric estimates
res_mod_allom4
```

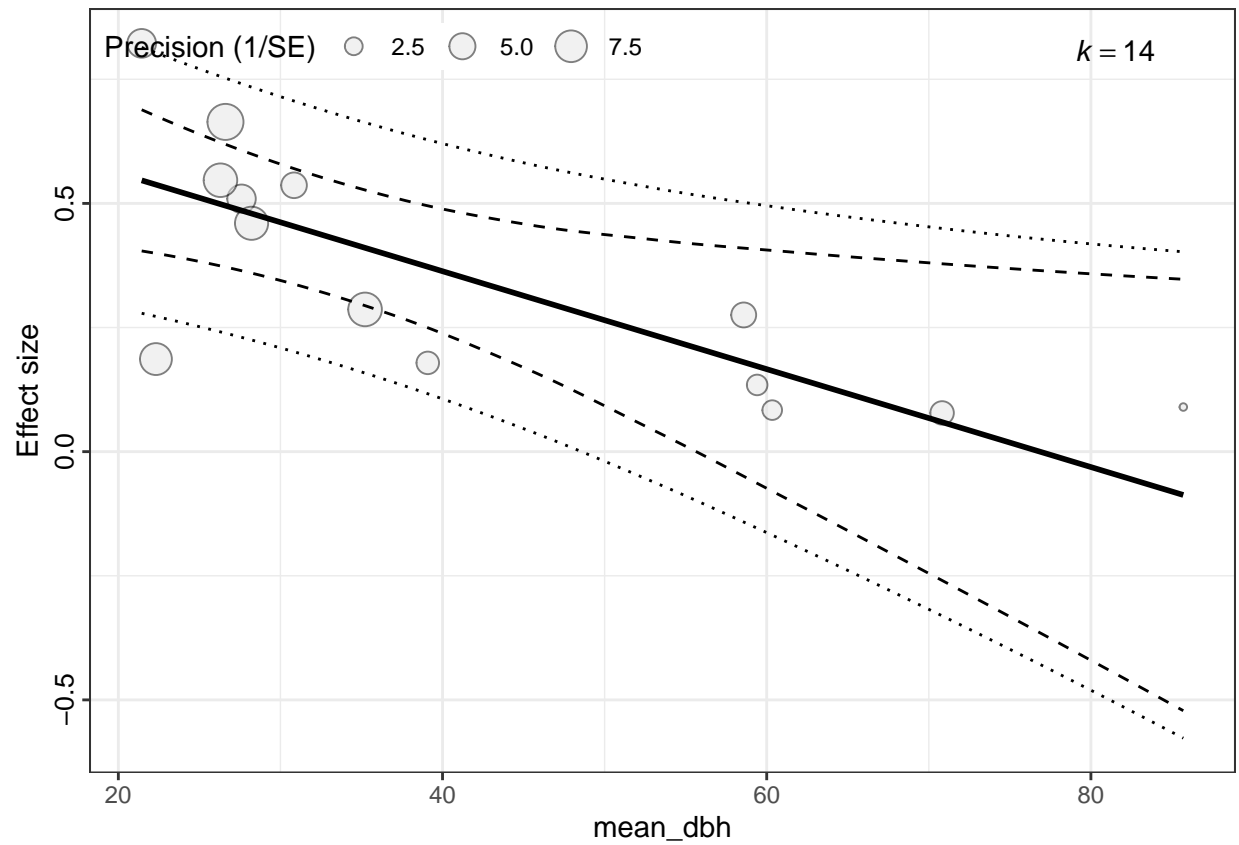
```
##
## Mixed-Effects Model (k = 14; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0.0132 (SE = 0.0161)
## tau (square root of estimated tau^2 value):            0.1149
## I^2 (residual heterogeneity / unaccounted variability): 33.18%
## H^2 (unaccounted variability / sampling variability):    1.50
## R^2 (amount of heterogeneity accounted for):            43.04%
##
## Test for Residual Heterogeneity:
## QE(df = 12) = 15.0391, p-val = 0.2393
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 5.8184, p-val = 0.0159
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
```

```
## intrcpt      0.7578  0.1478   5.1259  <.0001   0.4681   1.0476  ***
## mean_dbh     -0.0099  0.0041  -2.4121  0.0159  -0.0179  -0.0018   *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

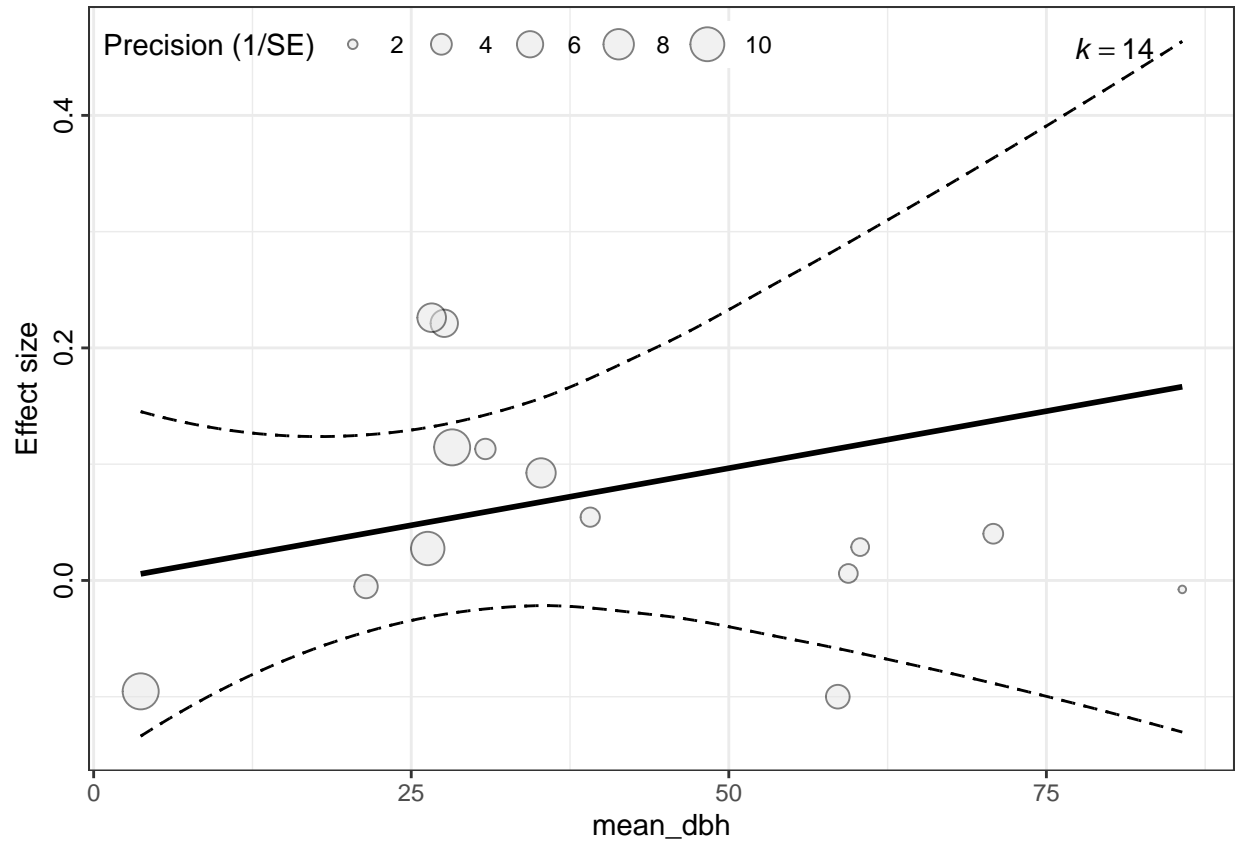
```
res_mod_tls <- rma(yi, vi,
                  mods = ~ mean_dbh,
                  data = es_tls,
                  method = "REML") ## for TLS based estimates
res_mod_tls
```

```
##
## Mixed-Effects Model (k = 14; tau^2 estimator: REML)
##
## tau^2 (estimated amount of residual heterogeneity):      0 (SE = 0.0079)
## tau (square root of estimated tau^2 value):             0
## I^2 (residual heterogeneity / unaccounted variability): 0.00%
## H^2 (unaccounted variability / sampling variability):    1.00
## R^2 (amount of heterogeneity accounted for):             100.00%
##
## Test for Residual Heterogeneity:
## QE(df = 12) = 6.2960, p-val = 0.9004
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.6316, p-val = 0.4268
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.0016  0.0777  -0.0208  0.9834   -0.1539   0.1506
## mean_dbh       0.0020  0.0025   0.7947  0.4268   -0.0029   0.0068
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Bubble plots for continuous moderator
lim_bubble <- orchaRd::mod_results(res_mod_allom4, #allometric model
                                mod = "mean_dbh",
                                group = "ID")
orchaRd::bubble_plot(lim_bubble,
                    group = "Article",
                    mod = "mean_dbh",
                    xlab = "mean_dbh",
                    legend.pos = "top.left")
```



```
lim_bubble <- orchaRd::mod_results(res_mod_tls, ## tls model
                                   mod = "mean_dbh",
                                   group = "ID")
orchaRd::bubble_plot(lim_bubble,
                     group = "Article",
                     mod = "mean_dbh",
                     xlab = "mean_dbh",
                     legend.pos = "top.left")
```



```
##leave one out test Sensitivity analysis
```

```
loo_test_allom <- leave_one_out(res_allom, group = "Author")##for allometric
loo_test_allom
```

	name	estimate	lowerCL	upperCL	lowerPR	upperPR
## 1	Burt et al.(2021)	0.4221940	0.2958521	0.5485358	0.09734864	0.7470393
## 2	Demol et al.(2021a)	0.4085859	0.2716171	0.5455546	0.05595518	0.7612166
## 3	Demol et al.(2021b)	0.4093169	0.2749095	0.5437242	0.06299050	0.7556432
## 4	Gonzalez de Tanago et al. (2018)	0.4386830	0.3130087	0.5643573	0.12827358	0.7490924
## 5	Hackenberg et al. (2015a)	0.4104071	0.2693323	0.5514819	0.04730818	0.7735060
## 6	Hackenberg et al. (2015b)	0.3885874	0.2628390	0.5143359	0.10195734	0.6752175
## 7	Kukenbrink et al.(2021)	0.4274571	0.2958010	0.5591131	0.09221082	0.7627033
## 8	Lau et al. (2019)	0.4300672	0.3030205	0.5571139	0.10786896	0.7522655
## 9	Lau et al. (2021)	0.4306043	0.3019355	0.5592731	0.10492284	0.7562858
## 10	Stovall et al. (2017)	0.3906925	0.2700475	0.5113376	0.11340942	0.6679757
## 11	Calders et al. (2015)	0.4352041	0.3000881	0.5703202	0.10000727	0.7704010
## 12	Momo Takoudjou et al. (2017)	0.4296631	0.3019270	0.5573992	0.10546866	0.7538575
## 13	Kankare et al. (2013)	0.4010300	0.2621729	0.5398871	0.04856437	0.7534956
## 14	Seidel et al. (2013)	0.4518285	0.3278383	0.5758187	0.16532875	0.7383282

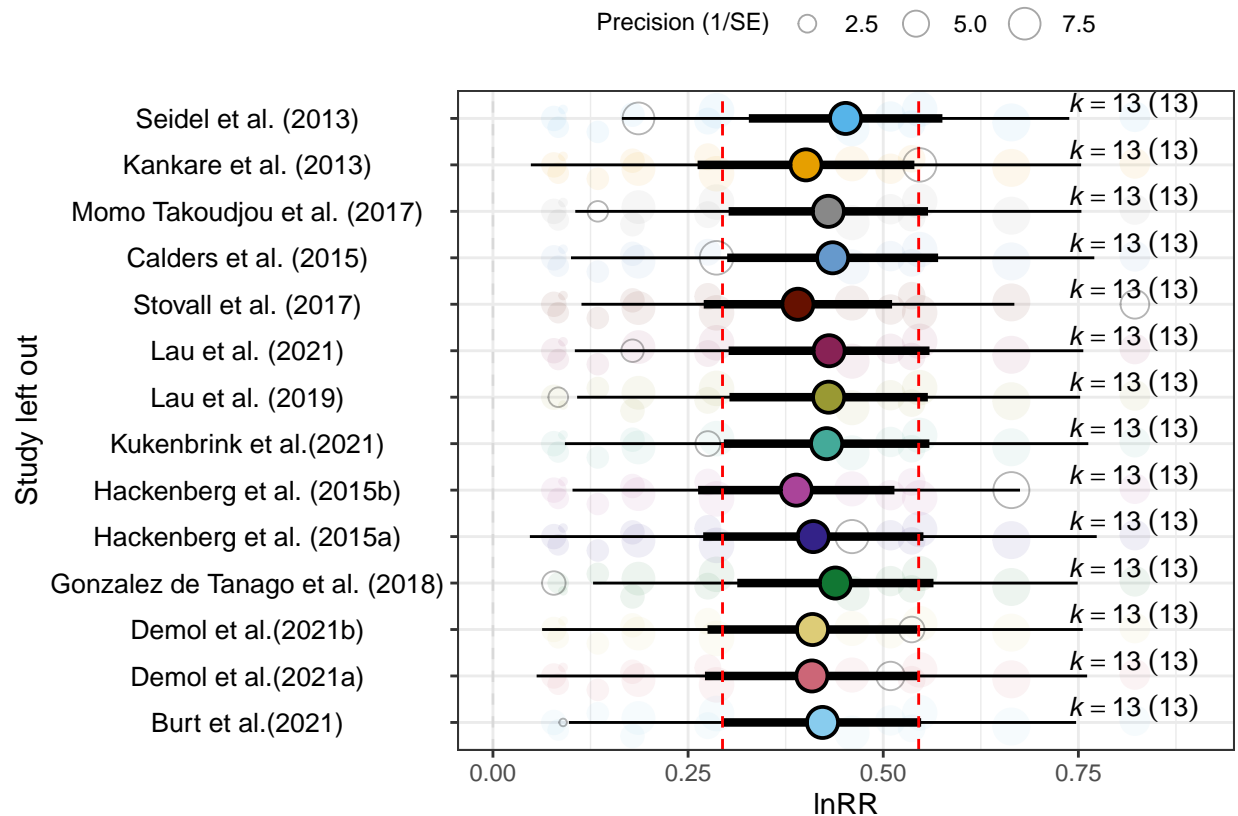
```
loo_test_tls <- leave_one_out(res_tls, group = "Author")##for tls
loo_test_tls
```

	name	estimate	lowerCL	upperCL	lowerPR	upperPR
## 1	Burt et al.(2021)	0.05254492	-0.029285369	0.1343752	-0.045945606	0.1510354

```
## 2          Demol et al.(2021a) 0.03892167 -0.044097873 0.1219412 -0.051114010 0.1289573
## 3          Demol et al.(2021b) 0.05071888 -0.032383406 0.1338212 -0.051703756 0.1531415
## 4 Gonzalez de Tanago et al. (2018) 0.05265376 -0.030450794 0.1357583 -0.050367951 0.1556755
## 5          Hackenberg et al. (2015a) 0.03667480 -0.055178356 0.1285280 -0.073292178 0.1466418
## 6          Hackenberg et al. (2015b) 0.03561735 -0.046872426 0.1181071 -0.046872426 0.1181071
## 7          Kukenbrink et al.(2021) 0.05927891 -0.025026704 0.1435845 -0.046921335 0.1654792
## 8          Lau et al. (2019) 0.05269131 -0.029925828 0.1353085 -0.048573091 0.1539557
## 9          Lau et al. (2021) 0.05228209 -0.030657221 0.1352214 -0.050085649 0.1546498
## 10         Stovall et al. (2017) 0.05509098 -0.029450659 0.1396326 -0.053009397 0.1631913
## 11         Calders et al. (2015) 0.04892040 -0.039148059 0.1369889 -0.068094515 0.1659353
## 12         Momo Takoudjou et al. (2017) 0.05327194 -0.029587565 0.1361314 -0.048942817 0.1554867
## 13         Kankare et al. (2013) 0.05833392 -0.035006370 0.1516742 -0.074612090 0.1912799
## 14         Seidel et al. (2013) 0.09012103 0.001171097 0.1790710 0.001171097 0.1790710
```

```
#plot the sensitivity analysis
```

```
orchard_leave1out(leave1out = loo_test_allom,
  xlab = "lnRR",
  ylab = "Study left out",
  trunk.size = 1.2,
  branch.size = 1.5,
  alpha = 0.08,
  legend.pos = "top.out")
```



```
orchard_leave1out(leave1out = loo_test_tls,
  xlab = "lnRR",
```

```

ylab = "Study left out",
trunk.size = 1.2,
branch.size = 1.5,
alpha = 0.08,
legend.pos = "top.out")

```

