Broadscale Test of Host-Symbiont Cophylogeny Reveals Key Drivers of Phylogenetic Congruence

Supplementary Material

Alexander Hayward, Robert Poulin & Shinichi Nakagawa

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Contents

Setups

Loading packages and custom functions

```
# loading packages
# devtools::install_github("thomasp85/patchwork")
pacman::p_load(tidyverse, # tidy family and related pacakges below
               kableExtra,
               gridExtra, # may not use this
               purrr,
               magrittr, # extending piping
               pander,   # nice tables
               metafor,  # package for meta-analysis
               MCMCglmm,  # Bayeisan mixed model package
               ggbeeswarm, # making bee-swarm plots possible
               plotly,     # interactive plots using ggplot2
               MuMIn,  # multi-model inference
               lme4,   # lmm & glmm (models)
               broom.mixed, # getting estimates from lmer + glmer objects
               performance, # getting R2 from lmer + glmer objects
               png,         # reading png files
               grid,        # graphic layout manipulation
               patchwork,   # putting ggplots together - you need to install via devtool
               here         # making reading files easy
```

```
                #lmerTest,   # more functions for lme4
                #mi,       # missing data analysis
                #betareg   # dependence of the above
)
```

Custom functions We have 5 custom functions named : `p_to_Zr()`,`I2()`, `R2()`, `get_est()`, `get_pred()`, and `cont_gen()`, all of which are used later (see below for their functionality) and the code are included here.

```
# coustm functions

#' Title: getting Zr and its sampling variance from p value
#'
#' @param data: data frame
#' @param pval: p value
#' @param N: sample size (N: the number of species ) and the degrees of freedom df = N - 2
#'
#' @return
#' @export
#'
#' @examples
p_to_Zr <- function(data, pval, N) {

    # turning them into strings
    pval <- data[[deparse(substitute(pval))]]
    N <- data[[deparse(substitute(N))]]

    # getting t values
    tval <- -qt(pval, N - 2)
    rval <- tval/sqrt((tval^2) + (N - 2))

    # define Zr function Zr <- 0.5*(log(1 + rval) - log(1 - rval)); the same as below
    # r <-tanh(Zr) # turning Zr to r
    Zr <- atanh(rval)

    # getting Var(Zr)
    VZr <- 1/(N - 3)

    # putting all together
    Zrs <- tibble(rval, Zr, VZr)
    data <- bind_cols(data, Zrs)
}

# coverting back Zr to r Just use 'psych' pacakge - fisherz2r(z) -
# <http://personality-project.org/r/psych/help/fisherz.html> or this will do : r
# to Zr is tanh(r)!!

# Functions for processing


# General modeling functions Functions for I2

#' Title Function to obtain total and separate I2 from multilevel-meta-analytic model
#'
```

```r
#' @param model
#' @param method
#'
#' @return
#' @export
#'
#' @examples
I2 <- function(model, method = c("Wolfgang", "Shinichi")) {

    ## evaluate choices
    method <- match.arg(method)

    # Wolfgang's method
    if (method == "Wolfgang") {
        W <- solve(model$V)
        X <- model.matrix(model)
        P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
        I2_total <- sum(model$sigma2)/(sum(model$sigma2) + (model$k - model$p)/sum(diag(P)))
        I2_each <- model$sigma2/(sum(model$sigma2) + (model$k - model$p)/sum(diag(P)))
        names(I2_each) = paste0("I2_", model$s.names)

        # putting all together
        I2s <- c(I2_total = I2_total, I2_each)

        # or my way
    } else {
        # sigma2_v = typical sampling error variance
        sigma2_v <- sum(1/model$vi) * (model$k - 1)/(sum(1/model$vi)^2 - sum((1/model$vi)^2))
        I2_total <- sum(model$sigma2)/(sum(model$sigma2) + sigma2_v)  #s^2_t = total variance
        I2_each <- model$sigma2/(sum(model$sigma2) + sigma2_v)
        names(I2_each) = paste0("I2_", model$s.names)

        # putting all together
        I2s <- c(I2_total = I2_total, I2_each)
    }
    return(I2s)
}

# test <- dataset$fit4.1[[3]] I2(test, method = 'Wolfgang') I2(test, method =
# 'Shinichi')


#' Title: R2 based on Nakagawa & Schielzeth 2013
#'
#' @param model
#'
#' @return
#' @export
#'
#' @examples
R2 <- function(model) {
    warning("Conditional R2 is not meaningful and the same as marginal R2\n")
```

```
    # fixed effect variance
    fix <- var(as.numeric(as.vector(model$b) %*% t(as.matrix(model$X))))

    # marginal
    R2m <- fix/(fix + sum(model$sigma2))
    R2
    # Rm <- round(100*R2m, 3)

    # conditional
    R2c <- (fix + sum(model$sigma2) - model$sigma2[length(model$sigma2)])/(fix +
        sum(model$sigma2))

    R2s <- c(R2_marginal = R2m, R2_coditional = R2c)
    return(R2s)
}


#' Title: the function to get estimates from rma objects (metafor)
#'
#' @param model: rma.mv object
#' @param mod: the name of a moderator
get_est <- function(model, mod = " ") {

    name <- as.factor(str_replace(row.names(model$beta), mod, ""))
    estimate <- as.numeric(model$beta)
    lowerCL <- model$ci.lb
    upperCL <- model$ci.ub

    table <- tibble(name = name, estimate = estimate, lowerCL = lowerCL, upperCL = upperCL)
}


#' Title: the function to get prediction intervals (crediblity intervals) from rma objects (metafor)
#'
#' @param model: rma.mv object
#' @param mod: the name of a moderator
get_pred <- function(model, mod = " ") {
    name <- as.factor(str_replace(row.names(model$beta), mod, ""))
    len <- length(name)

    if (len != 1) {
        newdata <- matrix(NA, ncol = len, nrow = len)
        for (i in 1:len) {
            # getting the position of unique case from X (design matrix)
            pos <- which(model$X[, i] == 1)[[1]]
            newdata[, i] <- model$X[pos, ]
        }
        pred <- predict.rma(model, newmods = newdata)
    } else {
        pred <- predict.rma(model)
    }
    lowerPR <- pred$cr.lb
    upperPR <- pred$cr.ub
```

```
    table <- tibble(name = name, lowerPR = lowerPR, upperPR = upperPR)
}

# Here are links for how to do confidence regions for rma.mv regression lines
# https://www.rdocumentation.org/packages/metafor/versions/1.9-9/topics/predict.rma
# https://stackoverflow.com/questions/50804464/out-of-sample-prediction-for-rma-object-in-metafor


#' Title: Contrast name geneator
#'
#' @param name: a vector of character strings
cont_gen <- function(name) {
    combination <- combn(name, 2)
    name_dat <- t(combination)
    names <- paste(name_dat[, 1], name_dat[, 2], sep = "-")
    return(names)
}
```

Supplementary Methods

Supplementary information for the literature search

Extended Data Table 1: Citations for papers describing the main methods of cophylogeny analysis, based on a *Google Scholar* search conducted on 4th July 2019. Although the paper describing Brooks parsimony analysis has more citations than that describing the Parafit method, relatively few citations correspond to actual cophylogenetic analyses employing the approach, *verses* methodological discussion.

```
# getting the data and formating some variables (turning chraracter vectors to
# factors)
read_csv(here("data/lit_search.csv"), na = "NA") %>% mutate_if(is.character, as.factor) %>%
    kable("html") %>% kable_styling("striped", position = "left")
```

Method

Paper

No. citations

TreeMap

Page RDM. 1994. Parallel phylogenies: reconstructing the history of host–parasite assemblages. Cladistics 10: 155–173.

385

Brooks Parsimony Analysis (BPA)

Brooks DR. 1981. Hennig's parasitological method: a proposed solution. Systematic Zoology 30: 229–249.

362

ParaFit

Legendre P, Desdevises Y, Bazin E. 2002. A statistical test for host–parasite coevolution. Systematic Biology 51: 217–234.

344

JANE

Conow C, Fielder D, Ovadia Y, Libeskind-Hadas R. 2010. Jane: a new tool for the cophylogeny reconstruction problem. Algorithms for Molecular Biology 5: 16.

249

TREEFITTER

Ronquist F. 1995. Reconstructing the history of host–parasite associations using generalised parsimony. Cladistics 11: 73–89.

124

PACO

Balbuena JA, Míguez-Lozano R, Blasco-Costa I. 2013. PACo: a novel procrustes application to cophylogenetic analysis. PloS one. 8(4):e61048.

103

TARZAN

Merkle D, Middendorf M. 2005. Reconstruction of the cophylogenetic history of related phylogenetic trees with divergence timing information. Theory in Biosciences 123: 277–299.

72

COALA

Baudet C, Donati B, Sinaimeri B, Crescenzi P, Gautier C, Matias C, Sagot MF 2014. Cophylogeny reconstruction via an approximate Bayesian computation. Systematic biology, 64(3), 416-431.

23

COMPONENT

Page RDM. 1993. User's manual for component, version 2.0. London, UK: The Natural History Museum.

13

The Cophylogeny Dataset

Table of the dataset

Below is the dataset used for our meta-analysis, followed by explanations of 24 variables extracted from the papers included (not all variables were used for our analyses; variables which were neither 'directly' nor 'indirectly' used in our analyses are indicated by *).

Extended Data Table 2: The meta-analytic dataset of this study.

```
# getting the data and formating some variables (turning chraracter vectors to
# factors)
full_data <- read_csv(here("data/2020-08-12-source-data-dat.csv"), na = "NA") %>%
    mutate_if(is.character, as.factor)

# dataset to compare the same cophylogenies between the two methods

full_pair <- read_csv(here("data/2020-08-12-paried.csv"), na = "NA") %>% mutate_if(is.character,
    as.factor)

# making a scrollable table
kable(full_data, "html") %>% kable_styling("striped", position = "left") %>% scroll_box(width = "100%",
    height = "500px")
```

authors

year

host_tax_broad

host_tax_fine

symbiont_tax_broad

symbiont_tax_fine

symbiont_euk

symbiosis

endo_or_ecto

mode_of_transmission_broad

mode_of_transmission_fine

Visiting_symbiont?

host_tips_linked

host_tips_linked_corrected

host_genera

total_host_symbioint_links

host_range_link_ratio

host_range_taxonomic_breadth

symbiont_tips_linked

symbiont_genera

no_randomizations

p_value

method

Althoff_et_al_2012

2012

Plant

Plant

Invert

Invert

y

Mutualist

Ecto

horizontal

autonomous

visitor

24

24

1

40

2.00

1.35

20

1

1000

0.00100

Parafit

Althoff_et_al_2012

2012

Plant

Plant

Invert

Invert

y

Mutualist

Ecto

horizontal

autonomous

visitor

24

24

1

38

2.24

1.53

17

1

1000

0.00100

Parafit

Arab_et_al_2019

2019

Invert

Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
55
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52
55
1.00
1.00
55
1
999
0.00100
Parafit
Ballinger_et_al_2018
2018
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
11
11
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12

1.00

1.00

12

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999

0.07000

Parafit

Banks_et_al_2006

2006

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

18

18

6

30

2.00

1.60

15

2

10000

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Parafit

Bayerlova_2009

2009

Vert

Tetrapod

Microbe

Virus

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Parasite
Endo
horizontal
contact
resident
21
21
14
31
1.55
1.45
20
1
9999
0.00040
Parafit
Bellec_et_al_2014
2014
Plant
Plant
Microbe
Virus
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Parasite
Endo
horizontal
contact
resident
22
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133
2.61
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51

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Parafit

Bruyndonckxx_et_al_2009

2009

Vert

Tetrapod

Invert

Invert

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Parasite

Ecto

both

contact

resident

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Parafit

Caraguel_et_al___2007

2007

Microbe

Amoeba

Microbe

Protist

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Mutualist

Endo

vertical

vertical

resident

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1

9999

0.00100

Parafit

Carneiro_et_al_2018

2018

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

body fluid

resident

26

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26

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1.00

26

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0.01000

Parafit

Catanach_et_al_2018

2018

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

54

28

5

44

1.07

0.93

41

30

999

0.00100

Parafit

Chen_et_al_2017

2017

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

50
50
11
50
1.00
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50
1
999
0.00100
Parafit
Choi_&_Thines_2015
2015
Plant
Plant
Microbe
Fungus
y
Parasite
Endo
horizontal
autonomous
resident
63
63
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1.00
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Parafit
Conord_et_al_2008
2008

Invert
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Microbe
Bacterium
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Mutualist
Endo
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Parafit
Cornuault_et_al_2012
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Parafit
Cruaud_et_al_2012
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Parafit
Cui_et_al_2014
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Tetrapod
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Virus
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Parasite
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body fluid
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Parafit
Deng_et_al_2013
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Parafit

Desdevises_et_al_2002

2002

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Fish

Invert

Invert

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Parasite

Ecto

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Parafit

Dhami_et_al_2013

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Parafit
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Parafit
Dona_2018
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Parafit
Dowie_et_al_2016
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Endara_et_al_2017
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Endara_et_al_2018
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Parafit
FerrerParis_et_al_2013
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Parafit
FraijaFernandez_et_al_2016
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Garamszegi_2009
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Parafit
Garcia_&_Hayman_2016
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Gavotte_et_al_2007
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Bacterium
Microbe
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Parasite
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Goker_et_al_2011
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Hoglund_et_al_2003

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Invert

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Parafit

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Parasite

Endo

horizontal

environmental

resident

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1.00
1.00
39
21
1000
0.00100
Parafit
Holzer_et_al_2018
2018
Vert
Fish
Invert
Invert
y
Parasite
Endo
horizontal
environmental
resident
69
69
62
101
1.00
1.00
101
15
1000
0.00100
Parafit
Holzer_et_al_2018
2018

Vert
Fish
Invert
Invert
y
Parasite
Endo
horizontal
environmental
resident
69
69
58
75
1.00
1.00
75
21
1000
0.00100
Parafit
Hughes_et_al_2007
2007
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
18
18
6

18
1.06
1.00
17
1
999
0.00010
Parafit
Huyse_&_Volckaert_2005
2005
Vert
Fish
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
resident
8
8
3
22
1.29
1.29
17
1
999
0.09500
Parafit
Irwin_et_al_2012
2012
Vert
Tetrapod
Microbe

Virus
n
Parasite
Endo
horizontal
contact
resident
21
21
14
31
1.55
1.85
20
NA
9999
0.00040
Parafit
Jenkins_et_al_2012
2012
Vert
Tetrapod
Microbe
Protist
y
Parasite
Endo
horizontal
autonomous
resident
52
52
40
138
1.45
NA

95
1
999
0.00100
Parafit
Jesovnik_et_al_2017
2017
Invert
Invert
Microbe
Fungus
y
Mutualist
Ecto
both
environmental
resident
32
6
1
6
1.00
1.00
6
1
999
0.02900
Parafit
Jousselin_et_al_2008
2008
Plant
Plant
Invert
Invert
y
Mutualist

Endo
horizontal
autonomous
resident
15
15
1
15
1.07
1.07
14
6
9999
0.00300
Parafit
Jousselin_et_al_2008
2008
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
13
13
1
13
1.00
1.00
13
1
9999

0.02000
Parafit
Jousselin_et_al_2008
2008
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
16
16
1
18
1.06
1.06
17
2
9999
0.00100
Parafit
Jousselin_et_al_2008
2008
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous

resident

13

13

1

14

1.00

1.00

14

1

9999

0.00300

Parafit

Jousselin_et_al_2009

2009

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

55

22

1

22

1.00

1.00

22

1

9999

0.00100

Parafit

Kaltenpoth_et_al_2014

2014
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
39
39
2
41
1.00
1.00
41
1
1000
0.00100
Parafit
Kawakita_&_Kato_2009
2009
Plant
Plant
Invert
Invert
y
Mutualist
Ecto
horizontal
autonomous
visitor
10
10

7
10
1.00
1.00
10
1
100
0.39000
Parafit
Kawakita_et_al_2004
2004
Plant
Plant
Invert
Invert
y
Mutualist
Ecto
horizontal
autonomous
visitor
18
18
1
18
1.00
1.00
18
1
999
0.00500
Parafit
Kawazoe_et_al_2008
2008
Invert
Invert

Invert
Invert
y
Mutualist
Ecto
vertical
vertical
resident
4
4
1
5
1.25
1.25
4
1
9999
0.00010
Parafit
Kolsch_&___Pedersen_2010
2010
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
41
41
7
41
1.00

1.00

41

1

9999

0.00100

Parafit

Krasnov_&_Shenbrot_2013

2013

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

horizontal

contact

resident

21

21

8

62

3.26

4.37

19

7

999

0.16000

Parafit

Krumbholz_et_al_2009

2009

Vert

Vert

Microbe

Virus

n

Parasite
Endo
horizontal
NA
resident
13
13
13
18
1.00
1.00
18
1
999999
0.49460
Parafit
Ku_&_Hu_2014
2014
Plant
Plant
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
11
11
1
11
1.00
1.00
11
1

9999
0.02000
Parafit
Lanterbecq_et_al_2010
2010
Invert
Invert
Invert
Invert
y
Parasite
Endo/Ecto
horizontal
contact
resident
16
16
12
16
1.00
1.00
16
5
1000
0.01300
Parafit
Latinne_et_al_2018
2018
Vert
Tetrapod
Microbe
Fungus
y
Parasite
Endo
horizontal

enviromental
resident
15
15
6
19
3.17
2.00
6
1
999
0.00900
Parafit
Lauber_et_al_2017
2017
Vert
Vert
Microbe
Virus
n
Parasite
Endo
horizontal
autonomous
resident
30
30
28
30
0.88
1.00
34
8
10000
0.00010
Parafit

Lauron_et_al_2015
2015
Vert
Tetrapod
Microbe
Protist
y
Parasite
Endo
horizontal
vector
resident
18
18
8
83
1.80
NA
46
1
1000
0.66000
Parafit
Lei_&_Olival_2014
2014
Vert
Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
environmental
resident
14

14
11
38
1.00
1.00
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1
999
0.00100
Parafit
Lei_&_Olival_2014
2014
Vert
Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
environmental
resident
4
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4
20
1.00
1.00
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999
0.00100
Parafit
Lei_&_Olival_2014
2014
Vert

Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
environmental
resident
14
14
12
19
1.00
1.00
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999
0.85800
Parafit
Lei_&_Olival_2014
2014
Vert
Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
environmental
resident
9
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8
13

1.00
1.00
13
1
999
0.02900
Parafit
Lei_&_Olival_2014
2014
Vert
Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
environmental
resident
35
35
22
119
1.09
1.17
109
1
999
0.00010
Parafit
Lei_&_Olival_2014
2014
Vert
Tetrapod
Microbe
Bacterium

n
Parasite
Endo
horizontal
environmental
resident
6
6
5
7
1.00
1.00
7
1
999
0.75870
Parafit
LewisRogers_&_Crandall_2009
2009
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
contact
resident
6
6
NA
27
1.00
1.00
27

11
999
0.47000
Parafit
Li_et_al_2017
2017
Plant
Plant
Microbe
Fungus
y
Parasite
Endo
horizontal
vector
Resident
12
12
9
12
1.71
2.00
7
1
999
0.50505
Parafit
Li_et_al_2017
2017
Plant
Plant
Microbe
Fungus
y
Parasite
Endo

horizontal
autonomous
resident
12
12
9
12
1.71
1.57
7
1
999
0.50505
Parafit
Li_et_al_2018
2018
Vert
Vert
Invert
Invert
y
Parasite
Endo
horizontal
trophic
resident
68
68
34
129
1.45
NA
89
89
100000
0.00100

Parafit
Light_&_Hafner_2008
2008
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
44
21
4
21
1.00
1.00
21
1
999
0.00100
Parafit
Liu_et_al_2016
2016
Plant
Plant
Microbe
Fungus
y
Parasite
Endo
NA
environmental
resident

13

13

10

44

1.57

2.71

28

28

9999

0.02510

Parafit

Liu_et_al_2016

2016

Plant

Plant

Microbe

Fungus

y

Parasite

Endo

NA

environmental

resident

19

19

16

76

3.30

3.22

23

23

9999

0.02030

Parafit

Maneesakorn_et_al_2011

2011

Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
12
12
1
12
1.00
1.00
12
1
999
0.00100
Parafit
Martinez_et_al_2011
2011
Invert
Invert
Microbe
Protist
y
Parasite
Endo
horizontal
vector
resident
16
16
1

22

2.44

1.56

9

1

999

0.07500

Parafit

Martinez_San_udo_&_Girolami_2009

2009

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

19

19

10

19

1.12

1.18

17

5

999

0.00300

Parafit

Matthews_et_al_2018

2018

Vert

Tetrapod

Invert

Invert
y
Parasite
Ecto
both
contact
resident
12
12
6
33
1.00
0.58
33
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99900
0.00400
Parafit
Mattiucci_&_nascetti_2008
2008
Vert
Tetrapod
Invert
Invert
y
Parasite
Endo
horizontal
trophic
resident
7
7
15
12
1.33
1.78

9
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100
0.05000
Parafit
Mazzon_et_al_2010
2010
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
17
17
10
17
1.06
1.13
16
3
999
0.00700
Parafit
McFrederick_&_Taylor_2013
2013
Invert
Invert
Invert
Invert
y
NA

Ecto
vertical
vertical
resident
7
7
3
7
1.00
1.00
7
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10000
0.00600
Parafit
McKee_et_al_2016
2016
Vert
Tetrapod
Microbe
Bacterium
n
Parasite
Endo
horizontal
vector
resident
66
66
42
184
1.06
1.09
173
1
10000

0.00010
Parafit
McLeish_&_Van_Noort_2012
2012
Plant
Plant
Invert
Invert
y
Mutualist
Endo
horizontal
autonomous
resident
26
26
1
65
1.00
1.00
65
6
9999
0.18000
Parafit
Megia-palma_et_al_2018
2018
Vert
Reptile
Microbe
Protist
y
Parasite
Endo
horizontal
vector

resident
16
16
8
23
1.53
1.27
15
8
999
0.00400
Parafit
Mehdiabadi_et_al_2012
2012
Invert
Invert
Microbe
Fungus
y
Mutualist
Ecto
both
environmental
resident
99
11
1
11
1.00
1.00
11
1
999
0.00100
Parafit
Mendlova_et_al_2012

2012
Vert
Fish
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
resident
6
6
5
34
1.17
1.21
29
2
999
0.02400
Parafit
Merville_et_al._2013
2013
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
9
9

1
9
1.00
1.00
9
1
999
0.00350
Parafit
Millanes_et_al_2014
2014
Microbe
Fungus
Microbe
Fungus
y
Parasite
Endo
both
environmental
resident
16
16
2
16
1.00
1.00
16
1
999
0.23600
Parafit
Miyaki_et_al_2016
2016
Vert
Fish

Microbe
Bacterium
n
Mutualist
Endo
horizontal
environmental
resident
8
8
4
54
3.18
2.24
17
1
999
0.00100
Parafit
Mondo_et_al_2012
2012
Microbe
Fungus
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
55
5
2
5
1.00

1.00

5

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10000

0.00010

Parafit

Nouioui_et_al_2014

2014

Plant

Plant

Microbe

Bacterium

n

Mutualist

Endo

horizontal

vector

resident

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1.00

1.00

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9999

0.33000

Parafit

Patra_et_al_2018

2018

Vert

Fish

Invert

Invert

y

Parasite
Endo
horizontal
environmental
resident
24
24
24
31
1.00
1.00
31
1
999
0.00100
Parafit
Pellissier_et_al_2013
2013
Plant
Plant
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
visitor
104
104
NA
NA
NA
NA
97
NA

10000
0.00010
Parafit
Perkins_2010
2010
Vert
Fish
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
61
61
50
75
1.00
1.00
75
NA
9999
0.92600
Parafit
Peterson_et_al_2010
2010
Plant
Plant
Microbe
Fungus
y
Parasite
Endo
horizontal

environmental
resident
11
11
1
25
2.08
1.58
12
1
9999
0.00010
Parafit
Polme_et_al_2014.pdf
2014
Plant
Plant
Microbe
Bacterium
n
Mutualist
Endo
horizontal
vector
resident
22
22
1
NA
NA
NA
43
1
999
0.00100
Parafit

Quek_et_al_2004

2004

Plant

Plant

Invert

Invert

y

Mutualist

Ecto

horizontal

autonomous

resident

9

9

1

19

1.90

1.50

10

1

999

0.77900

Parafit

Ramasindrazana_et_al_2017

2017

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

15

15
6
26
2.89
1.78
9
5
999
0.00100
Parafit
Ricklefs_et_al_2004
2004
Vert
Tetrapod
Microbe
Protist
y
Parasite
Endo
horizontal
vector
resident
44
44
1
121
1.86
NA
65
2
100
0.63000
Parafit
Riess_et_al_2018
2018
Plant

Plant
Microbe
Fungus
Y
Parasite
Endo
horizontal
autonomous
resident
11
11
5
11
1.00
1.00
11
2
9999
0.26400
Parafit
Savio_2011
2011
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
horizontal
NA
resident
17
17
10
17

1.00

1.00

17

3

999

0.00700

Parafit

Schardl_et_al_2008

2008

Plant

Plant

Microbe

Fungus

y

Mutualist

Endo

both

NA

resident

25

25

16

25

0.96

1.00

26

2

1000

0.00100

Parafit

Sibbald_et_al_2017

2017

Microbe

Amoeba

Microbe

Protist

y
Mutualist
Endo
horizontal
environmental
resident
7
7
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1.00
1.00
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9999
0.00010
Parafit
Simkova_et_al_2013
2013
Vert
Fish
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
resident
5
5
1
21
1.00
1.00
21

1
999
0.01300
Parafit
Singh_et_al_2016
2016
Microbe
Fungus
Plant
Plant
y
Mutualist
Endo
horizontal
environmental
resident
23
23
1
28
1.40
1.20
20
1
9999
0.00020
Parafit
Singh_et_al_2017
2017
Microbe
Fungus
Plant
Plant
y
Mutualist
Endo

vertical

vertical

resident

23

17

1

25

1.25

1.15

20

1

9999

0.00020

Parafit

Sontowski_et_al_2015

2015

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

14

14

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14

1.00

1.00

14

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100000

0.00300

Parafit
Sorenson_et_al_2004
2004
Vert
Tetrapod
Vert
Tetrapod
y
Parasite
Ecto
horizontal
autonomous
resident
33
33
10
34
1.62
1.43
21
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1000
0.00100
Parafit
Souza_et_al_2018
2018
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
both
body fluid
resident

8

8

8

19

1.06

1.00

18

1

999

0.00500

Parafit

Stireman_et_al_2010

2010

Plant

Plant

Invert

Invert

y

Parasite

Endo

horizontal

autonomous

resident

15

15

10

39

1.39

1.25

28

1

9999

0.00080

Parafit

Sudakaran_et_al_2015

2015

Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
NA
NA
resident
16
16
7
22
1.00
1.00
22
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1000
0.97800
Parafit
Sudakaran_et_al_2015
2015
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
NA
NA
resident
14
14
6

26

1.00

1.00

26

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1000

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Parafit

Summers_&_Rouse_2014

2014

Invert

Invert

Invert

Invert

y

Parasite

Endo/Ecto

horizontal

autonomous

resident

53

53

36

78

1.13

1.23

69

10

9999

0.00050

Parafit

Susoy_&_Herrmann_2014

2014

Invert

Invert

Invert

Invert
y
Mutualist
Ecto
vertical
vertical
resident
35
35
7
37
1.42
1.31
26
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9999
0.00010
Parafit
Swafford_&_Bond_2010
2010
Invert
Invert
Invert
Invert
y
Parasite
Ecto
horizontal
contact
resident
7
7
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1.00
1.00

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9999
0.31900
Parafit
Sweet_&_Johnson_2018
2018
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
13
13
4
14
2.80
1.80
5
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100000
0.00500
Parafit
Sweet_et_al_2016
2016
Vert
Tetrapod
Invert
Invert
y
Parasite

Ecto
both
contact
resident
52
52
25
57
1.33
1.21
43
1
100000
0.00001
Parafit
Sweet_et_al_2016
2016
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
52
52
25
58
1.18
1.14
49
4
100000

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Parafit
Sweet_et_al_2017
2017
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
12
12
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15
1.15
1.23
13
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999
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Parafit
Sweet_et_al_2018a
2018
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact

resident

259

259

163

283

1.63

1.61

174

11

9999

0.00010

Parafit

Sweet_et_al_2018b

2018

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

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11

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13

1.86

1.43

7

1

100000

0.00500

Parafit

Tao_et_al_2013

2013
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
NA
resident
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7
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1.00
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99999
0.17592
Parafit
Toju_et_al_2013
2013
Invert
Invert
Microbe
Bacterium
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Mutualist
Endo
vertical
vertical
resident
27
27

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1.00
1.00
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99999
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Parafit
Urban_&_Cryan_2012
2012
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
30
30
29
30
1.00
1.00
30
1
1000
0.00100
Parafit
Urban_&_Cryan_2012
2012
Invert
Invert

Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
40
40
38
40
1.00
1.00
40
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1000
0.00300
Parafit
Viale_et_al_2015
2015
Invert
Invert
Microbe
Bacterium
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Mutualist
Endo
vertical
vertical
resident
23
23
1
23
1.00

1.00
23
1
9999
0.00100
Parafit
Won_et_al_2008
2008
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
horizontal
contact
resident
15
15
5
15
1.00
1.00
15
1
100
0.37000
Parafit
Xu_et_el_2017
2017
Invert
Invert
Microbe
Bacterium
n

Mutualist
Endo
vertical
vertical
resident
20
20
8
20
1.00
1.00
20
1
999
0.00100
Parafit
Zhang_et_al_2017
2017
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
44
44
24
44
1.00
1.00
44
1

100000

0.00001

Parafit

Badets_et_al_2011

2011

Vert

Tetrapod

Invert

Invert

y

Parasite

Endo

horizontal

autonomous

resident

17

17

13

17

1.00

1.00

17

4

1000

0.01000

TreeMap

Banks_et_al_2006

2006

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

18

18

6

30

2.00

1.60

15

2

1000

0.01000

TreeMap

Bochkov_et_al_2011

2011

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

6

6

NA

9

1.00

1.00

9

6

100

0.01000

TreeMap

Charleston_&_Perkins_2003
2003
Vert
Tetrapod
Microbe
Protist
y
Parasite
Endo
horizontal
vector
resident
9
9
1
9
1.00
1.00
9
1
100
0.03000
TreeMap
Charleston_&_Robertson_2002
2002
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
body fluid
resident
12

12

12

12

1.00

1.00

12

1

1000

0.01500

TreeMap

Chauvatcharin_et_al_2006

2006

Microbe

Bacterium

Microbe

Virus

n

Parasite

Endo

both

NA

resident

14

14

7

15

1.07

1.00

14

1

1000

0.33100

TreeMap

Clark_et_al_2000

2000

Invert

Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
17
17
4
17
1.00
1.00
17
1
1000
0.00100
TreeMap
Clayton_&_Johnson_2003
2003
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
13
13
6
14

1.08

1.15

13

1

10000

0.00060

TreeMap

Clayton_&_Johnson_2003

2003

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

13

13

6

16

1.60

1.50

10

1

10000

0.15300

TreeMap

Cui_et_al_2012

2012

Vert

Tetrapod

Microbe

Virus

n
Parasite
Endo
horizontal
body fluid
resident
7
7
3
7
1.00
1.00
7
7
10000
0.36600
TreeMap
Dabert_2001___
2001
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
21
21
12
22
1.00
1.00
22

9
10000
0.00100
TreeMap
Deng_et_al_2013
2013
Invert
Invert
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
7
7
4
10
1.00
1.00
10
2
999
0.53000
TreeMap
Desai_et_al_2010
2010
Microbe
Protist
Microbe
Bacterium
n
Mutualist
Ecto

both

contact

resident

9

9

2

8

0.89

1.00

9

1

1000

0.00100

TreeMap

Desdevises_et_al_2002

2002

Vert

Fish

Invert

Invert

y

Parasite

Ecto

horizontal

autonomous

resident

14

14

11

39

1.95

1.65

20

2

999

0.31700

TreeMap
Downie_&_Gullan_2005
2005
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
21
21
16
21
1.00
1.00
21
1
1000
0.00100
TreeMap
Erpenbeck_et_al_2002
2002
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident

6

6

5

6

1.00

1.00

6

1

10000

0.02000

TreeMap

Etherington_et_al_2006

2006

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

contact

resident

7

7

7

8

1.00

1.00

8

1

1000

0.01000

TreeMap

Farrell_1998

1998

Plant
Plant
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
resident
21
21
2
21
1.00
1.00
21
6
1000
0.07000
TreeMap
Gottschling_et_al_2011
2011
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
contact
resident
43
43
40

78
1.00
1.00
78
30
1000
0.00100
TreeMap
Hendricks_et_al_2013
2013
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
19
19
17
20
1.25
1.25
16
1
1000
0.02100
TreeMap
Hosokawa_et_al_2006
2006
Invert
Invert
Microbe

Bacterium
n
Mutualist
Endo
vertical
vertical
resident
7
7
3
7
1.00
1.00
7
1
1000
0.00100
TreeMap
Hugot_1999
1999
Vert
Tetrapod
Invert
Invert
y
Parasite
Endo
horizontal
trophic
resident
10
10
9
11
1.00
1.00

11
6
1000
0.00100
TreeMap
Hugot_et_al_2003
2003
Vert
Tetrapod
Microbe
Fungus
y
Parasite
Endo
horizontal
contact
resident
19
19
12
19
1.00
1.00
19
1
1000
0.00100
TreeMap
Huyse_&_Volckaert_2005
2005
Vert
Fish
Invert
Invert
y
Parasite

Ecto
horizontal
autonomous
resident
8
8
3
22
1.29
1.29
17
1
100
0.02000
TreeMap
IkedaOhtsubo_&_Brune_2009
2009
Microbe
Protist
Microbe
Bacterium
n
Mutualist
Ecto
vertical
vertical
resident
11
11
1
11
1.00
1.00
11
1
1000

0.00100
TreeMap
Jackson_&_Charleston_1994
1994
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
contact
resident
10
10
8
10
1.00
1.00
10
1
100
0.19000
TreeMap
Jackson_&_Charleston_1994
1994
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
bodily fluid

resident
10
10
7
10
1.00
1.00
10
1
100
0.01000
TreeMap
Jackson_&_Charleston_1994
1994
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
contact
resident
11
11
7
12
1.00
1.00
12
1
100
0.05000
TreeMap
Jackson_&_Charleston_1994

1994
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
bodily fluid
resident
13
13
9
15
1.00
1.00
15
1
100
0.18000
TreeMap
Jackson_&_Charleston_1994
1994
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
contact
resident
14
14

7
17
1.00
1.00
17
1
100
0.01000
TreeMap
Jeong_et_al_1999
1999
Plant
Plant
Microbe
Bacterium
n
Mutualist
Endo
horizontal
vector
resident
12
12
12
19
1.06
1.00
18
1
1000
0.23000
TreeMap
Johnson_et_al_2002
2002
Vert
Tetrapod

Invert
Invert
y
Parasite
Ecto
both
contact
resident
25
25
23
25
1.32
1.42
19
19
1000
0.23000
TreeMap
Johnson_et_al_2003
2003
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
28
28
15
31
1.48

1.33
21
1
100
0.03000
TreeMap
Johnson_et_al_2006
2006
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
10
10
NA
11
1.00
1.00
11
11
1000
0.40200
TreeMap
Jousselin_et_al_2008
2009
Plant
Plant
Invert
Invert
y

Mutualist
Endo
horizontal
autonomous
resident
15
15
1
15
1.07
1.07
14
6
10000
0.01000
TreeMap
Jousselin_et_al_2008
2009
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
13
13
1
14
1.00
1.00
14
1

10000

0.01000

TreeMap

Jousselin_et_al_2008

2009

Plant

Plant

Invert

Invert

y

Parasite

Endo

horizontal

autonomous

resident

13

13

1

13

1.00

1.00

13

1

10000

0.01000

TreeMap

Jousselin_et_al_2008

2009

Plant

Plant

Invert

Invert

y

Parasite

Endo

horizontal

autonomous

resident

16

16

1

18

1.06

1.06

17

2

10000

0.01000

TreeMap

Jousselin_et_al_2009

2009

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

55

22

1

22

1.00

1.00

22

1

10000

0.00100

TreeMap

Kawaida_et_al_2013

2013

Invert

Invert

Plant

Plant

y

Mutualist

Endo

vertical

vertical

resident

6

6

1

6

1.00

1.00

6

1

10000

0.00350

TreeMap

Kawakita_et_al_2004

2004

Plant

Plant

Invert

Invert

y

Mutualist

Ecto

horizontal

autonomous

visitor

18

18
1
18
1.00
1.00
18
1
999
0.01900
TreeMap
Kelley_&_Farrell_1998
1998
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
41
41
1
89
6.85
1.92
13
1
100
0.28000
TreeMap
Kikuchi_et_al_2009
2009
Invert

Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
14
14
5
14
1.00
1.00
14
1
1000
0.00100
TreeMap
Lanterbecq_et_al_2010
2010
Invert
Invert
Invert
Invert
y
Parasite
Endo/Ecto
horizontal
contact
resident
16
16
12
16

1.00

1.00

16

5

5000

0.04000

TreeMap

Light_&_Hafner_2008

2008

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

44

21

4

21

1.00

1.00

21

1

1000

0.00100

TreeMap

LimFong_et_al_2008

2008

Invert

Invert

Microbe

Bacterium

n
Mutualist
Endo
vertical
vertical
resident
5
5
1
5
1.00
1.00
5
2
1000
0.11000
TreeMap
Liu_et_al_2013
2013
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
37
37
1
37
1.00
1.00
37

1

1000

0.00100

TreeMap

Liu_et_al_2014

2014

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical

vertical

resident

27

27

3

29

1.00

1.00

29

1

1000

0.01000

TreeMap

LopezVaamonde_et_al_2001

2001

Invert

Invert

Invert

Invert

y

Parasite

Endo

horizontal
autonomous
resident
15
15
1
15
1.00
1.00
15
1
1000
0.00100
TreeMap
LopezVaamonde_et_al_2003
2003
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
33
33
33
77
1.00
1.00
77
1
1000
0.21300

TreeMap
LopezVaamonde_et_al_2005
2005
Invert
Invert
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
28
28
1
35
2.33
1.33
15
1
1000
0.24800
TreeMap
Martin_et_al_1999
1999
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
body fluid
resident

38

38

38

48

1.00

1.00

48

1

1000

0.00100

TreeMap

Martin_et_al_2003

2003

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

body fluid

resident

14

14

14

16

1.00

1.00

16

1

100

0.01000

TreeMap

Martin_et_al_2003

2003

Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
body fluid
resident
9
9
9
9
1.00
1.00
9
1
100
0.05000
TreeMap
Martin_et_al_2003
2003
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
body fluid
resident
17
17
17

23
1.00
1.00
23
1
100
0.21000
TreeMap
Mazzon_et_al_2010
2010
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
17
17
10
17
1.06
1.13
16
3
1000
0.00100
TreeMap
Morelli_&_Spicer_2007
2007
Vert
Tetrapod
Invert

Invert

y

Parasite

Ecto

both

contact

resident

6

6

6

6

1.00

1.00

6

1

10000

0.00950

TreeMap

Muniz_et_al_2013

2013

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

body fluid

resident

17

17

11

17

1.00

1.00

17

1

10000

0.00001

TreeMap

Musser_et_al_2010

2010

Vert

Mammal

Invert

Invert

y

Parasite

Ecto

both

contact

resident

6

6

1

6

1.00

1.00

6

6

100

0.30000

TreeMap

Pagan_et_al_2010

2010

Plant

Plant

Microbe

Virus

n

Parasite

Endo
horizontal
contact
resident
10
10
10
13
1.00
1.00
13
1
1000
0.24000
TreeMap
Page_1996
1996
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
15
15
6
17
1.00
1.00
17
2
1000

0.00100
TreeMap
Page_et_al_1998
1998
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
7
7
1
8
1.00
1.00
8
1
100
0.01000
TreeMap
Page_et_al_2004
2004
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact

resident
12
12
4
12
1.00
1.00
12
1
1000
0.00100
TreeMap
Page_et_al_2004
2004
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
11
11
5
13
1.00
1.00
13
4
100
0.25000
TreeMap
Page_et_al_2004

2004
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
13
13
5
14
1.00
1.00
14
1
100
0.46000
TreeMap
Page_et_al_2004
2004
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident
9
9

3

9

1.00

1.00

9

1

100

0.36000

TreeMap

Paterson_&_Poulin_1999

1999

Vert

Fish

Invert

Invert

y

Parasite

Ecto

horizontal

autonomous

resident

8

8

8

12

1.20

2.20

10

1

100

0.01000

TreeMap

Paterson_et_al_2000

2000

Vert

Tetrapod

Invert
Invert
y
Parasite
Ecto
both
contact
resident
11
11
5
14
1.00
1.00
14
5
100
0.01000
TreeMap
Percy_et_al_2004
2004
Plant
Plant
Invert
Invert
y
Parasite
Ecto
both
autonomous
resident
35
35
8
56
1.22

1.09
46
4
1000
0.00500
TreeMap
PerezLosada_et_al_2006
2006
Vert
Tetrapod
Microbe
Virus
n
Parasite
Endo
horizontal
NA
resident
9
9
9
11
1.00
1.00
11
1
100
0.01000
TreeMap
Perlman_et_al_2003
2003
Invert
Invert
Invert
Invert
y

Parasite
Endo
horizontal
autonomous
resident
16
16
1
17
1.89
1.33
9
1
1000
0.14000
TreeMap
Quek_et_al_2004
2004
Plant
Plant
Invert
Invert
y
Mutualist
Ecto
horizontal
autonomous
resident
9
9
1
9
1.00
1.00
6
1

1000

1.00000

TreeMap

Ramsden_et_al_2008

2008

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

contact

resident

33

33

20

38

1.00

1.00

38

1

1000

1.00000

TreeMap

Reed_et_al_2007

2007

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

horizontal

contact
resident
4
4
4
6
1.20
1.00
5
4
1000
0.05000
TreeMap
Refregier_et_al_2008
2008
Plant
Plant
Microbe
Fungus
y
Parasite
Endo
horizontal
vector
resident
18
18
7
20
1.25
1.25
16
1
3000
0.50000
TreeMap

Riess_et_al_2018
2018
Plant
Plant
Microbe
Fungus
Y
Parasite
Endo
horizontal
autonomous
resident
11
11
5
11
1.00
1.00
11
2
1000
0.33500
TreeMap
Shoemaker_et_al_2002
2002
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
both
NA
resident
20

20
7
23
1.00
1.00
23
1
100
0.47000
TreeMap
Simkova_et_al_2013
2013
Vert
Fish
Invert
Invert
y
Parasite
Ecto
horizontal
autonomous
resident
5
5
1
21
1.00
1.00
21
1
999
0.04500
TreeMap
Six_&_Paine_1999
1999
Microbe

Fungus
Invert
Invert
y
Mutualist
Ecto
horizontal
vector
resident
6
6
1
6
1.00
1.00
6
3
1000
0.03100
TreeMap
Skerikova_et_al_2001
2001
Vert
Fish
Invert
Invert
y
Parasite
Endo
horizontal
trophic
resident
7
7
7
7

1.00

1.00

7

1

10000

0.40000

TreeMap

Smith_et_al_2008b

2008

Vert

Tetrapod

Invert

Invert

y

Parasite

Ecto

both

contact

resident

20

20

3

20

1.00

1.00

20

14

100

0.05000

TreeMap

Sorenson_et_al_2004

2004

Vert

Tetrapod

Vert

Tetrapod

y
Parasite
Ecto
horizontal
autonomous
resident
33
33
10
34
1.62
1.43
21
1
100
0.15000
TreeMap
Subbotin_et_al_2004
2004
Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
16
16
16
21
1.00
1.00
21

4

1000

0.00100

TreeMap

Switzer_et_al_2005

2005

Vert

Tetrapod

Microbe

Virus

n

Parasite

Endo

horizontal

body fluid

resident

46

46

17

51

1.00

1.00

51

1

10000

0.00700

TreeMap

Urban_&_Cryan_2012

2012

Invert

Invert

Microbe

Bacterium

n

Mutualist

Endo

vertical
autonomous
resident
40
40
38
40
1.00
1.00
40
1
1000
0.00100
TreeMap
Urban_&_Cryan_2012
2012
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
autonomous
resident
30
30
29
30
1.00
1.00
30
1
1000
0.00100

TreeMap
Vanhove_et_al_2015
2015
Vert
Fish
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
19
19
10
28
1.00
1.00
28
1
10000
0.04210
TreeMap
Weckstein_2004
2004
Vert
Tetrapod
Invert
Invert
y
Parasite
Ecto
both
contact
resident

11
11
1
11
2.20
1.80
5
1
10000
0.89000
TreeMap
Weiblen_&_Bush_2002
2002
Plant
Plant
Invert
Invert
y
Mutualist
Endo
horizontal
autonomous
resident
19
19
1
19
1.00
1.00
19
1
10000
0.01950
TreeMap
Weiblen_&_Bush_2002
2002

Plant
Plant
Invert
Invert
y
Parasite
Endo
horizontal
autonomous
resident
12
12
1
18
1.00
1.00
18
1
10000
0.12150
TreeMap
Wu_et_al_2008
2008
Plant
Plant
Microbe
Virus
n
Parasite
Endo
horizontal
vector
resident
8
8
8

10
1.00
1.00
10
1
100
0.01000
TreeMap
Xu_et_al_2017
2017
Invert
Invert
Microbe
Bacterium
n
Mutualist
Endo
vertical
vertical
resident
20
20
8
20
1.00
1.00
20
1
1000
0.00100
TreeMap
Yan_et_al_2011
2011
Vert
Fish
Microbe

Virus

n

Parasite

Endo

horizontal

contact

resident

8

8

8

15

1.00

1.00

15

1

999

0.98900

TreeMap

A. **authors**: The authors of the study and the date (citation form).

B. **year**: The year of publication of the study.

C. **host_tax_broad**: Separation of the host group according to broader taxonomic units (e.g. vertebrate, invertebrate, microbe, plant).

D. **host_tax_fine***: Separation of the host group according to narrower taxonomic units (e.g. fish, tetrapod, bird, invertebrate, protist, bacterium, plant, fungus).

E. **symbiont_tax_broad**: Separation of the symbiont group according to broader taxonomic units (e.g. vertebrate, invertebrate, microbe, plant).

F. **symbiont_tax_fine***: Separation of the symbiont group according to narrower taxonomic units (e.g. invertebrate, protist, virus, bacterium, fungus, plant, bird).

G. **symbiont_euk***: Whether the symbiont is eukaryotic (state ='yes'), or prokaryotic (state='no').

H. **symbiosis**: The type of symbiont (e.g. parasite or mutualist). For this we followed the definition used by the authors of the study.

I. **endo_or_ecto**: Whether the symbiont lives outside the host (i.e. is an ectosymbiont), or inside the host (i.e. is an endosymbiont).

J. **mode_of_transmission_broad**: Whether the symbiont is transmitted vertically, horizontally, or both. For this, we followed the route of transmission specified by the authors of the study.

K. **mode_of_transmission_fine***: A finer-scale description of the mode of transmission of the symbiont (e.g. contact, vector, bodily fluid, vertical, trophic).

L. **Visiting_symbiont?*** Whether the symbiont is resident on the host (resident), or makes visits to the host or hosts (visitor).

M. **host_tips_linked**: The number of individual host taxa included in the cophylogenetic analysis.

N. **host_tips_linked_corrected** The same measure as for column N, 'host_tips_linked', but reduced to only include one member of each host species. This is included because some authors include multiple individuals of the same host species. Without correction, this artificially increases the apparent number of host species included in the study.

O. **host_genera**: A count of the number of host genera included in the cophylogenetic analysis.

P. **total_host_symbioint_links** The total number of links between host and symbiont taxa recorded in a study. If all symbionts were strict specialists, this would equal the number of symbionts included in the study. However, because symbionts are often associated with more than one host, this value is often higher than the total number of symbionts included in the study.

Q. **host_range_link_ratio**: An estimation of symbiont host specificity, calculated by dividing the total number of links between hosts and symbionts (i.e. 'total_host_symbiont_links', column Q), by the total number of symbionts included in the study (i.e. 'symbiont_tips_linked', column T).

R. **host_range_taxonomic_breadth**: An alternative estimation of symbiont host specificity, calculated by first summing the number of host taxonomic ranks linked to each symbiont (i.e. single host species = 1, multiple host species in the same genera = 2, multiple host genera = 3, multiple host families = 4, multiple host orders = 5), and dividing by the total number of symbionts included in the study (i.e. 'symbiont_tips_linked', column T).

S. **symbiont_tips_linked** The number of individual symbiont taxa included in the cophylogenetic analysis.

T. **symbiont_genera**: A count of the number of symbiont genera included in the cophylogenetic analysis.

U. **no_randomizations**: The number of phylogenetic randomizations performed during the cophylogenetic analysis.

V. **p_value**: The p-value reported for the cophylogenetic analysis, representing the likelihood that host and symbiont phylogenies display cospeciation.

W. **method**: Whether TreeMap or ParaFit was used to obtain the reported p value.

Table of sample sizes

Below we present our sample sizes for the two separate methods: TreeMap (Page 1994) and ParaFit (Legendre *et al.* 2002) (and combined), in terms of effect sizes, papers, and different levels of categorical variables (factors).

```
# selecting out variables, which we used for our analysis
dat <- full_data %>% select(-symbiont_euk, -mode_of_transmission_fine, -`Visiting_symbiont?`)
pair <- full_pair %>% select(-symbiont_euk, -mode_of_transmission_fine, -`Visiting_symbiont?`)

# making a table of sample sizes for different variables
dat %>% group_by(method) %>%
  summarise(
    `Effect sizes (analyses)` = n(),
    Studies = n(),
    Papers = n_distinct(authors),
    `Vertebrate hosts` = sum(host_tax_broad == "Vert", na.rm = T), # na.rm is important when NA exists
    `Invertebrate hosts` = sum(host_tax_broad == "Invert", na.rm = T),
    `Plant hosts`  = sum(host_tax_broad == "Plant", na.rm = T),
    `Microbe hosts` = sum(host_tax_broad == "Microbe", na.rm = T),
    `Vertebrate symbionts` = sum(symbiont_tax_broad  == "Vert", na.rm = T),
    `Invertebrate symbionts` = sum(symbiont_tax_broad  == "Invert", na.rm = T),
    `Plant symbionts`  = sum(symbiont_tax_broad  == "Plant", na.rm = T),
```

```
    `Microbe symbionts` = sum(symbiont_tax_broad  == "Microbe", na.rm = T),
    `Parastic relationships` = sum(symbiosis == "Parasite", na.rm = T),
    `Mutualistic relatioships` = sum(symbiosis == "Mutualist", na.rm = T),
    `Ecto-symbionts` = sum(endo_or_ecto  == "Ecto", na.rm = T),
    `Endo-symbionts` = sum(endo_or_ecto == "Endo", na.rm = T),
    `Ecto/endo-symbionts` = sum(endo_or_ecto == "Endo/Ecto", na.rm = T),
    `Horizontal transmission` = sum(mode_of_transmission_broad  == "horizontal", na.rm = T),
    `Vertical transmission` = sum(mode_of_transmission_broad == "vertical", na.rm = T),
    `Horizontal/vertical-transmission` = sum(mode_of_transmission_broad == "both", na.rm = T)
  ) -> n_table1

# transposing the table and creating that table and adding a correct number of the papers for `Combined
n_authors <- n_distinct(dat$authors) # the total number of papers
dat$studies <- paste0(dat$authors, dat$host_tax_fine, dat$symbiont_tax_fine, dat$total_host_symbioint_li
n_studies <- n_distinct(dat$studies)
n_table2 <-t(n_table1[,-1])
colnames(n_table2) <- n_table1$method
n_table2 %>% as_tibble(rownames = "Number") %>%
  mutate(Combined = Parafit + TreeMap, Combined = replace(Combined, c(2,3), c(n_studies, n_authors))) %
  rename("Number of" = "Number", "ParaFit (n)" = "Parafit", "TreeMap (n)" = "TreeMap",  "Combined (n)" =
  kable() %>% kable_styling("striped", position = "left") %>%
  scroll_box(width = "100%", height = "250px")
```

Number of	ParaFit (n)	TreeMap (n)	Combined (n)
Effect sizes (analyses)	140	93	233
Studies	140	93	211
Papers	118	78	180
Vertebrate hosts	60	51	111
Invertebrate hosts	39	20	59
Plant hosts	31	18	49
Microbe hosts	10	4	14
Vertebrate symbionts	1	1	2
Invertebrate symbionts	62	49	111
Plant symbionts	3	1	4
Microbe symbionts	74	42	116
Parastic relationships	91	70	161
Mutualistic relatioships	48	23	71
Ecto-symbionts	41	34	75
Endo-symbionts	97	58	155
Ecto/endo-symbionts	2	1	3
Horizontal transmission	84	53	137
Vertical transmission	28	15	43
Horizontal/vertical-transmission	23	25	48

```
  #pander(split.cell = 40, split.table = Inf) # not as nice as kable
```

Note that for the numbers of studies and papers does not add up (TreeMap + ParaFit ≠ Combined), because 22 analyses and 16 papers used both the TreeMap and ParaFit methods (the term "papers" here is our variable `authors`)

Missing data patterns

Below, we present the number of instances of missing data (cells) for all variables used in our meta-analysis.

```
# summaring missingness in our dataset
# funs(sum(is.na(.))) needs to be in funs as is.na has "." = each column
dat %>% summarise_all(~sum(is.na(.))) %>% # map(~sum(is.na(.)) # this is an alterantive way
  t() %>% as_tibble(rownames = "Variable") %>%
  rename("Number of missing data (n)" = "V1") %>%
  #pander(split.cell = 40, split.table = Inf)
  kable() %>% kable_styling("striped", position = "left") %>%
  scroll_box(width = "60%", height = "250px")
```

Variable	Number of missing data (n)
authors	0
year	0
host_tax_broad	0
host_tax_fine	0
symbiont_tax_broad	0
symbiont_tax_fine	0
symbiosis	1
endo_or_ecto	0
mode_of_transmission_broad	5
host_tips_linked	0
host_tips_linked_corrected	0
host_genera	6
total_host_symbioint_links	3
host_range_link_ratio	3
host_range_taxonomic_breadth	7
symbiont_tips_linked	0
symbiont_genera	9
no_randomizations	0
p_value	0
method	0
studies	0

```
# an alternative method using the mi package
#missing_data_tbl <- missing_data.frame(as.data.frame(data))
#show(missing_data_tbl)
```

Meta-analysis

Calculating effect sizes

We created our effect size (correlation coefficient r and its Fisher's z transformation Zr) from p values and associated sample sizes (Rosenthal & Rubin 2003). We used the smaller sample size of either `host_tips_linked_corrected` or `symbiont_tips_linked` as our sample size (i.e., the number of both host and symbiont species) for each effect size (an indicator of congruence). Also, we created a column with a unique ID for each observation (i.e. an observation level random effect), termed `observation`, which is required for the `rma.mv` function in `metafor` (Viechtbauer 2010).

```
dat %<>% # getting sample size & observation level random effect
mutate(., sample_size = if_else(host_tips_linked_corrected >= symbiont_tips_linked,
    symbiont_tips_linked, host_tips_linked_corrected), observation = factor(1:nrow(.)))

# making p = 1 to p = (no_randomization - 1)/no_randomization as p = 1 produces t
# value = Inf
```

```
dat$p_value <- ifelse(dat$p_value != 1, dat$p_value, (dat$no_randomizations - 1)/dat$no_randomizations)

# calculating effect size
dat %<>% p_to_Zr(p_value, sample_size)

# getting sample size for spp sum(dat$sample_size[match(unique(dat$studies),
# dat$studies)])

# getting effect sizes for pair data
pair %<>% # getting sample size & observation level random effect
mutate(., sample_size = if_else(host_tips_linked_corrected >= symbiont_tips_linked,
    symbiont_tips_linked, host_tips_linked_corrected), observation = factor(1:nrow(.)))

# making p = 1 to p = (no_randomization - 1)/no_randomization as p = 1 produces t
# value = Inf
pair$p_value_tree <- ifelse(pair$p_value_tree == 1, 0.999, pair$p_value_tree)
# calculating effect size
pair %<>% p_to_Zr(p_value_para, sample_size) %>% rename(rval_para = rval, Zr_para = Zr,
    VZr_para = VZr) %>% p_to_Zr(p_value_tree, sample_size) %>% rename(rval_tree = rval,
    Zr_tree = Zr, VZr_tree = VZr)
```

Correlating two methods of the same cophylogenetic data

In 16 studies, authors used both `ParaFit` and `TreeMap` on the same cophylogeny dataset, but some of these studies, they used different numbers of randomization between the two methods. Among these 16, 11 studies used `ParaFit` and `TreeMap` with the same or similar number of randomization (e.g., 999 and 1,000). We here correlated effect sizes (Zr) between these two methods. In the following analyses, we assume the p-value based effect size, Zr~equivalent (or just Zr) is equivalent for both methods. In such a case, we would require a tight correlation between the method.

```
# plotting correlations but not displayed A)
cor_1 <- round(with(pair, cor(Zr_para, Zr_tree)), 3)
cor_t1 <- with(pair, cor.test(Zr_para, Zr_tree))

all_plot <- ggplot(pair, aes(Zr_para, Zr_tree)) + geom_point() + geom_smooth(method = "lm") +
    labs(x = "Zr (ParaFit)", y = "Zr (TreeMap)") + annotate("text", x = 1, y = -1,
    label = paste("r = ", cor_1))

# B)
cor_2 <- round(with(pair[pair$match == "y", ], cor(Zr_para, Zr_tree)), 3)
cor_t2 <- with(pair[pair$match == "y", ], cor.test(Zr_para, Zr_tree))

part_plot <- ggplot(pair[pair$match == "y", ], aes(Zr_para, Zr_tree)) + geom_point() +
    geom_smooth(method = "lm") + labs(x = "Zr (ParaFit)", y = "Zr (TreeMap)") + annotate("text",
    x = 1, y = -1, label = paste("r = ", cor_2))

comb_plot <- all_plot + part_plot + plot_annotation(tag_levels = "A", tag_suffix = ")")
# comb_plot
```

There are strong and significant correlations in effect sizes (Zr) between `ParaFit` and `TreeMap` (for all the 16 studies, r = 0.705, t = 3.716, df = 14, p = 0.0023, and for the 11 perfectly matching studies, r = 0.746, t = 3.357, df = 9, p = 0.0084). Therefore, we have made an assumption that effect sizes based on p values from these two methods can be equated in our analyses below.

Meta-analytic model: testing Fahrenholz's rule

First, we checked what random effects should be put into the main model. To do this we fitted two random effects, `authors` (i.e. study IDs) and `observation`; the former term was added to account for non-independence of effect sizes originating from the same papers (i.e., `authors`).

```
# 2 random effects & model AIC note that probably only base stuff works outside
# of main chunck so need to create AIC here
ma_test1 <- rma.mv(yi = Zr, V = VZr, random = list(~1 | authors, ~1 | observation),
    data = dat)
aic1 <- AIC(ma_test1)

# 1 random effect & model AIC
ma_test2 <- rma.mv(yi = Zr, V = VZr, random = ~1 | authors, data = dat)
aic2 <- AIC(ma_test2)
```

The model (`ma_test1`), which included both random factors, had a larger AIC value (316.6) than the model with only one random effect (314.6) . This is because `observation` hardly accounted any variance (< 0.0001) compared to `authors` (0.0876). Therefore, we only included `authors` as our random factor in subsequent analyses.

We ran intercept models (meta-analyses) with 3 different datasets (`ParaFit`, `TreeMap` and both combined; see the explanation of `method` above). Also, we note that we used adjustments for test statistics and confidence intervals (`test = "t"`), which is similar to (but not the same as) those proposed by Kanpp and Hartung (Knapp & Hartung 2003); probably this approach is a more conservative.

```
# think about making this into a tibble meta-analysis with Parafit
ma_parafit <- rma.mv(yi = Zr, V = VZr, random = ~1 | authors, test = "t", subset = which(method ==
    "TreeMap"), data = dat)

# meta-analysis with TreeMap
ma_treemap <- rma.mv(yi = Zr, V = VZr, random = ~1 | authors, test = "t", subset = which(method ==
    "Parafit"), data = dat)

# meta-analysis with all the data combined
ma_all <- rma.mv(yi = Zr, V = VZr, test = "t", random = ~1 | authors, data = dat)
```

Running Multilevel Meta-analytic models with 3 datasets **Supplementary Table 1:** Overall effects (meta-analytic means), 95% confidence intervals (CIs), variance components (V) and heterogeneity, I^2 (I2) (Higgins *et al.* 2003) from the `metafor` model using the 3 datasets (`ParaFit`, `TreeMap` and both combined, or `All`). Note that in these models, $I^2_{[\text{total}]} = I^2_{[\text{authors}]}$ (see (Nakagawa & Santos 2012; Senior *et al.* 2016)), as we only have one random factor.

```
# getting I2 for the models could use map()
i2_treemap <- I2(ma_treemap)
i2_parafit <- I2(ma_parafit)
i2_all <- I2(ma_all)
# creating a table
tibble(Dataset = c("Parafit", "TreeMap", "All"), `Overall mean (Zr)` = c(ma_parafit$b,
    ma_treemap$b, ma_all$b), `Lower CI [0.025]` = c(ma_parafit$ci.lb, ma_treemap$ci.lb,
    ma_all$ci.lb), `Upper C  [0.975]` = c(ma_parafit$ci.ub, ma_treemap$ci.ub, ma_all$ci.ub),
    `V[authors]` = c(ma_parafit$sigma2, ma_treemap$sigma2, ma_all$sigma2), `I2[total]` = c(i2_parafit[1]
        i2_treemap[1], i2_all[1])) %>% kable("html", digits = 3) %>% kable_styling("striped",
    position = "left")
```

Dataset

Overall mean (Zr)

Lower CI [0.025]

Upper C [0.975]

V[authors]

I2[total]

Parafit

0.545

0.452

0.638

0.077

0.482

TreeMap

0.586

0.514

0.658

0.082

0.627

All

0.573

0.513

0.633

0.088

0.600

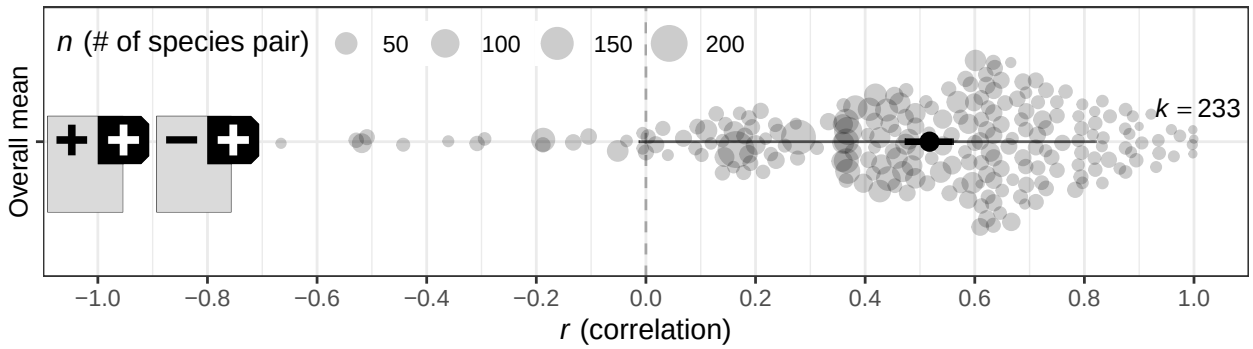
These models all gave consistent results including heterogeneity. Given these results, we proceeded with only analyzing the whole dataset (`All`) from here on.

```
# https://stackoverflow.com/questions/41919023/ggplot-adding-image-on-top-right-in-two-plots-with-diffe
# how to add png files to the figure (above) reading image
image_mutualism <- readPNG(here("images/mutualism_transparentbg.png"))
image_parasitism <- readPNG(here("images/parasitism_transparentbg.png"))

# creating a table of results
pred_ma <- get_pred(ma_all)
effect_ma <- get_est(ma_all) %>% left_join(pred_ma)

# creating a forest plot
fig_ma <- ggplot(data = effect_ma, aes(x = tanh(estimate), y = "Overall mean")) +
    scale_x_continuous(limits = c(-1, 1), breaks = seq(-1, 1, by = 0.2)) + geom_quasirandom(data = dat,
    aes(x = tanh(Zr), y = "Overall mean", size = (1/VZr) + 3), groupOnX = FALSE,
    alpha = 0.2) + # precition interval (PI)
geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)), height = 0, show.legend = F,
```

```
    size = 0.5, alpha = 0.6) + # CI
geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)), height = 0, show.legend = F,
    size = 1.2) +
geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) + # creating dots and different
geom_point(size = 3, shape = 21, fill = "black") + annotate("text", x = 0.93, y = 1.15,
    label = paste("italic(k)==", length(dat$Zr)), parse = TRUE, hjust = "left", size = 3.5) +
    labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n),
        " (# of species pair)"))) + theme_bw() + theme(legend.position = c(0, 1),
    legend.justification = c(0, 1)) + theme(legend.direction = "horizontal") + # theme(legend.backgroun
theme(legend.background = element_blank()) + theme(axis.text.y = element_text(size = 10,
    colour = "black", hjust = 0.5, angle = 90)) + annotation_custom(rasterGrob(image_mutualism),
    xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) + annotation_custom(rasterGrob(image_parasitism),
    xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2)
# ggsave(plot = fig_ma, filename = 'fig_2a.pdf', height = 2, width = 8) ggploty 0
# does not work (Error in unique.default(x) : unimplemented type 'expression' in
# 'HashTableSetup')
fig_ma
```




```
# for Fig 3

a <- ggplot(data = effect_ma, aes(x = tanh(estimate), y = "Overall mean")) + scale_x_continuous(limits =
    1), breaks = seq(-1, 1, by = 0.2)) + geom_quasirandom(data = dat, aes(x = tanh(Zr),
    y = "Overall mean", size = (1/VZr) + 3), groupOnX = FALSE, alpha = 0.2) + # precition interval (PI)
geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)), height = 0, show.legend = F,
    size = 0.5, alpha = 0.6) + # CI
geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)), height = 0, show.legend = F,
    size = 1.2) +
geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) + # creating dots and different
geom_point(size = 3, shape = 21, fill = "black") + annotate("text", x = 0.93, y = 1.15,
    label = paste("italic(k)==", length(dat$Zr)), parse = TRUE, hjust = "left", size = 3.5) +
    labs(x = "", y = "", size = expression(paste(italic(n), " (# of species pairs)")),
        tag = "a") + theme_bw() + theme(legend.position = c(0, 1), legend.justification = c(0,
    1)) + theme(legend.direction = "horizontal") + # theme(legend.background = element_rect(fill = 'whi
theme(legend.background = element_blank()) + theme(axis.text.y = element_text(size = 10,
    colour = "black", hjust = 0.5, angle = 90)) + annotation_custom(rasterGrob(image_mutualism),
    xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) + annotation_custom(rasterGrob(image_parasitism),
    xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2)
```

Figure 3a: A forest plot showing the meta-analytic mean (mean effect size) with its 95% confidence interval (thick line) and 95% prediction interval (thin line), with observed effect sizes based on various sample sizes.

Meta-regression

We ran a univariate meta-regression model for each of the following moderators: 1) `symbiosis`, 2) `host_tax_broad`, 3) `symbiont_tax_broad`, 4) `host_range_link_ratio`, 5) `host_range_taxonomic_breadth`, 6) `mode_of_transmission_broad`, and 7) `endo_or_ecto`. The results from these models are presented in the main text.

In addition to these, we ran three more univariate models: 1) `host_tax_symbiosis` (equivalent to the interaction term between `symbiosis` and `host_tax_symbiosis`; `symbiosis*host_tax_symbiosis`), 2) `symbiont_tax_symbiosis` (`symbiosis*symbiont_tax_broad`), 3) `host_symbiont_tax` (`host_tax_symbiosis*symbiont_ta` and 4) `symbiosis_transmission` (`symbiosis*mode_of_transmission_broad`). These moderators are created below:

```
dat %<>%
    # host_tax_broad*symbiosis (host_tax_symbiosis)
  mutate(host_tax_symbiosis = str_c(host_tax_broad, symbiosis),
         host_tax_symbiosis = ifelse(host_tax_symbiosis == "InvertNA", NA, host_tax_symbiosis),
         host_tax_symbiosis = factor(host_tax_symbiosis),
         # symbiont_tax_broad*symbiosis (symbiont_tax_symbiosis)
         symbiont_tax_symbiosis = factor(str_c(symbiont_tax_broad, symbiosis)),
         # host_tax_broad*symbiont_tax_broad (host_symbiont_tax)
         host_symbiont_tax  = factor(str_c(host_tax_broad, symbiont_tax_broad)),
         # symbiosis*mode_of_transmission_broad (symbiosis_transmission)
         symbiosis_transmission  = factor(str_c(symbiosis, mode_of_transmission_broad)),
         # whether p values were the smallest value given the number of randamization - limit_researche
         limit_reached = if_else(abs((1/p_value) - no_randomizations) <= 1, 1, 0))
```

Univariate (uni-predictor) analyses

We first conducted a series of meta-regression models with one predictor.

```
# meta-regression: mutiple intercepts
mr_symbiosis1 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiosis - 1, test = "t", random = ~1 |
    authors, data = dat)
# meta-regression: contrast
mr_symbiosis2 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiosis, test = "t", random = ~1 |
    authors, data = dat)
```

The type of symbiosis: parasitism vs. mutualism **Supplementary Table 2:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (Nakagawa & Schielzeth 2013) (R2) from the meta-regression with `symbiosis`.

```
# getting marginal R2
r2_symbiosis1 <- R2(mr_symbiosis1)

# getting estimates
res_symbiosis1 <- get_est(mr_symbiosis1, mod = "symbiosis")
res_symbiosis2 <- get_est(mr_symbiosis2, mod = "symbiosis")

# creating a table
tibble(`Fixed effect` = c(as.character(res_symbiosis1$name), cont_gen(res_symbiosis1$name)),
    Estimate = c(res_symbiosis1$estimate, res_symbiosis2$estimate[2]), `Lower CI [0.025]` = c(res_symbi
        res_symbiosis2$lowerCL[2]), `Upper CI  [0.975]` = c(res_symbiosis1$upperCL,
```

```
        res_symbiosis2$upperCL[2]), `V[authors]` = c(mr_symbiosis1$sigma2, rep(NA,
        2)), R2 = c(r2_symbiosis1[1], rep(NA, 2))) %>% kable("html", digits = 3) %>%
    kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Mutualist

0.652

0.551

0.752

0.085

0.037

Parasite

0.529

0.457

0.601

NA

NA

Mutualist-Parasite

-0.123

-0.244

-0.002

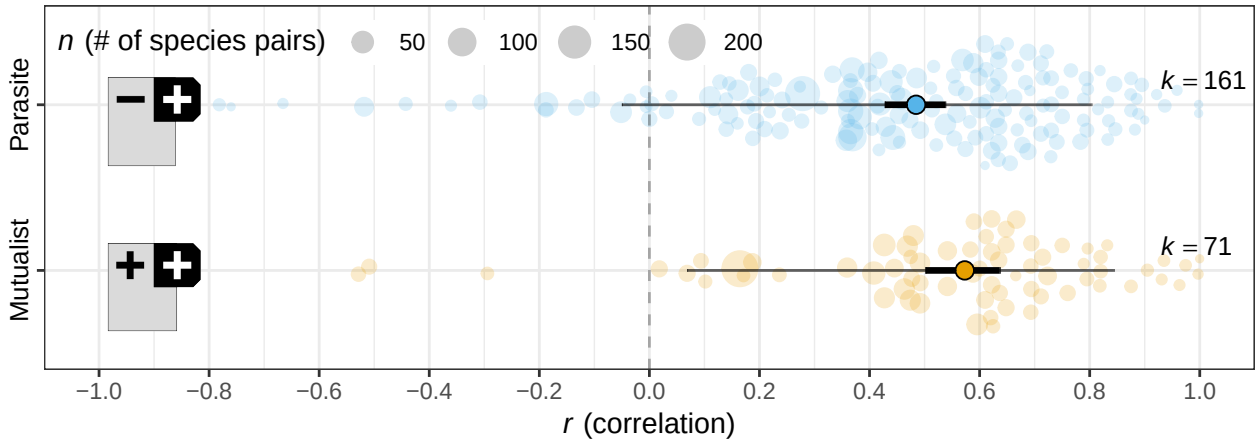
NA

NA

```
# adding sample size (k) for each category
k_symbiosis <- dat %>% group_by(symbiosis) %>% count()
# getting estimates and predicitons
pred_symbiosis <- get_pred(mr_symbiosis1, mod = "symbiosis")
res_symbiosis1 <- left_join(res_symbiosis1, k_symbiosis, by =  c("name" = "symbiosis"))  %>% left_join(
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_symbiosis <- ggplot(data = res_symbiosis1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiosis)),
                   aes(x= tanh(Zr), y = symbiosis, size = ((1/VZr) + 3), colour = symbiosis), groupOnX =
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size =
  # 95 %CI
```

```
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Mutualist" = "#E69F00", "Parasite" = "#56B4E9")) +
  scale_fill_manual(values = c("Mutualist" = "#E69F00", "Parasite" = "#56B4E9")) +
  annotate('text', x = 0.93, y = c(1.15, 2.15), label= paste("italic(k)==", res_symbiosis1$n), parse = 
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_mutualism), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2)

fig_symbiosis
```




```
# fig 3

b <- ggplot(data = res_symbiosis1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiosis)),
                   aes(x= tanh(Zr), y = symbiosis, size = ((1/VZr) + 3), colour = symbiosis), groupOnX =
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Mutualist" = "#E69F00", "Parasite" = "#56B4E9")) +
  scale_fill_manual(values = c("Mutualist" = "#E69F00", "Parasite" = "#56B4E9")) +
  annotate('text', x = 0.93, y = c(1.15, 2.15), label= paste("italic(k)==", res_symbiosis1$n), parse = 
```

```
  labs(x = "", y = "", tag = "b") +
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_mutualism), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2)
```

Figure 3b: A forest plot showing the group-wise means (the categorical variable `symbiosis`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```
# reordering
dat$host_tax_broad <- factor(dat$host_tax_broad, levels = c("Microbe", "Plant", "Invert",
    "Vert"))

# meta-regression: mutiple intercepts
mr_host_tax_broad1 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad - 1, test = "t",
    random = ~1 | authors, data = dat)

# meta-regression: contrast 1
mr_host_tax_broad2 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad, test = "t",
    random = ~1 | authors, data = dat)

# meta-regression: contrast 2
mr_host_tax_broad3 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(host_tax_broad, ref = "Plant"),
    test = "t", random = ~1 | authors, data = dat)

# meta-regression: contrast 3
mr_host_tax_broad4 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(host_tax_broad, ref = "Invert"),
    test = "t", random = ~1 | authors, data = dat)
```

The effect of host taxa **Supplementary Table 3:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `host_tax_broad`.

```
# getting marginal R2
r2_host_tax_broad1 <- R2(mr_host_tax_broad1)

# getting estimates
res_host_tax_broad1 <- get_est(mr_host_tax_broad1, mod = "host_tax_broad")
res_host_tax_broad2 <- get_est(mr_host_tax_broad2, mod = "host_tax_broad")
# the name bit does not work if relevel....
res_host_tax_broad3 <- get_est(mr_host_tax_broad3, mod = "host_tax_broad")
res_host_tax_broad4 <- get_est(mr_host_tax_broad4, mod = "host_tax_broad")

# creating a table
tibble(`Fixed effect` = c(as.character(res_host_tax_broad1$name), cont_gen(res_host_tax_broad1$name)),
    Estimate = c(res_host_tax_broad1$estimate, res_host_tax_broad2$estimate[-1],
        res_host_tax_broad3$estimate[-(1:2)], res_host_tax_broad4$estimate[-(1:3)]),
    `Lower CI [0.025]` = c(res_host_tax_broad1$lowerCL, res_host_tax_broad2$lowerCL[-1],
        res_host_tax_broad3$lowerCL[-(1:2)], res_host_tax_broad4$lowerCL[-(1:3)]),
```

```
    `Upper CI  [0.975]` = c(res_host_tax_broad1$upperCL, res_host_tax_broad2$upperCL[-1],
        res_host_tax_broad3$upperCL[-(1:2)], res_host_tax_broad4$upperCL[-(1:3)]),
    `V[authors]` = c(mr_host_tax_broad1$sigma2, rep(NA, 9)), R2 = c(r2_host_tax_broad1[1],
        rep(NA, 9))) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
    scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Microbe

0.910

0.659

1.160

0.084

0.143

Plant

0.408

0.280

0.536

NA

NA

Invert

0.649

0.538

0.761

NA

NA

Vert

0.561

0.475

0.647

NA

NA

Microbe-Plant

-0.502

-0.783

-0.220

NA

NA

Microbe-Invert

-0.261

-0.535

0.014

NA

NA

Microbe-Vert

-0.349

-0.613

-0.084

NA

NA

Plant-Invert

0.241

0.071

0.411

NA

NA

Plant-Vert

0.153

-0.001

0.308

NA

NA

Invert-Vert

-0.088

-0.226

0.050

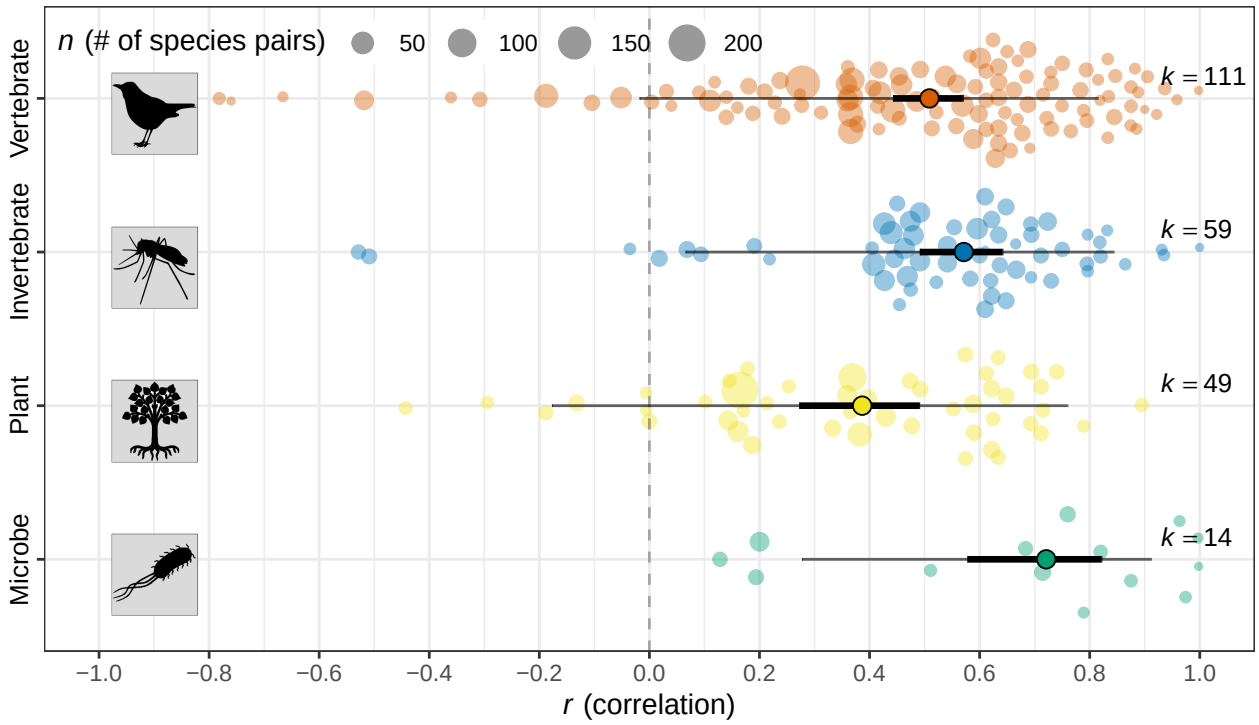
NA

NA

```r
# getting images
image_invertebrate_host <- readPNG(here("images/invertebrate_host_transparentbg.png"))
image_microbe_host <- readPNG(here("images/microbe_host_transparentbg.png"))
image_vertebrate_host <- readPNG(here("images/vertebrate_host_transparentbg.png"))
image_plant_host <- readPNG(here("images/plant_host_transparentbg.png"))

# adding sample size (k) for each category
k_host_tax_broad <- dat %>% group_by(host_tax_broad) %>% count()
# getting estimates and predicitons
pred_host_tax_broad <- get_pred(mr_host_tax_broad1, mod = "host_tax_broad")
res_host_tax_broad1 <- left_join(res_host_tax_broad1, k_host_tax_broad, by =  c("name" = "host_tax_broa
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_host_tax_broad <- ggplot(data = res_host_tax_broad1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(host_tax_broad)),
                   aes(x= tanh(Zr), y = host_tax_broad, size = ((1/VZr) + 3), colour = host_tax_broad),
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ve
  scale_fill_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_y_discrete(labels = c("Microbe" = "Microbe",  "Plant" = "Plant",  "Invert"= "Invertebrate",  "V
  annotate('text', x = 0.93, y = 1:4 + 0.15, label= paste("italic(k)==", res_host_tax_broad1$n), parse=
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_plant_host), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1, xmax = -0.8, ymin = 2.6, ymax = 3.2
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1, xmax = -0.8, ymin = 3.6, ymax = 4.2)

fig_host_tax_broad
```




```
# fig 3c
c <- ggplot(data = res_host_tax_broad1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(host_tax_broad)),
                   aes(x= tanh(Zr), y = host_tax_broad, size = ((1/VZr) + 3), colour = host_tax_broad),
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = (
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_fill_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_y_discrete(labels = c("Microbe" = "Microbe",  "Plant" = "Plant",  "Invert"= "Invertebrate",  "V
  annotate('text', x = 0.93, y = 1:4 + 0.15, label= paste("italic(k)==", res_host_tax_broad1$n), parse="
  labs(x = "", y = "", size = expression(paste(italic(n), " (# of species pairs)")) , tag = "c") +
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_plant_host), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1, xmax = -0.8, ymin = 2.6, ymax = 3.2)
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1, xmax = -0.8, ymin = 3.6, ymax = 4.2)
```

Figure 3c: A forest plot showing the group-wise means (the categorical variable `host_tax_broad`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```r
# reordering
dat$symbiont_tax_broad <- factor(dat$symbiont_tax_broad, levels = c("Microbe", "Plant",
    "Invert", "Vert"))

# sizes <- factor(sizes, levels = c('small', 'medium', 'large')) sizes > [1]
# small large large small medium > Levels: small medium large meta-regression:
# mutiple intercepts
mr_symbiont_tax_broad1 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiont_tax_broad - 1,
    test = "t", random = ~1 | authors, data = dat)

# meta-regression: contrast 1
mr_symbiont_tax_broad2 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiont_tax_broad, test = "t",
    random = ~1 | authors, data = dat)

# meta-regression: contrast 2
mr_symbiont_tax_broad3 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(symbiont_tax_broad,
    ref = "Plant"), test = "t", random = ~1 | authors, data = dat)

# meta-regression: contrast 3
mr_symbiont_tax_broad4 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(symbiont_tax_broad,
    ref = "Invert"), test = "t", random = ~1 | authors, data = dat)
```

The effect of symbiont taxa **Supplementary Table 4:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `symbiont_tax_broad`.

```r
# getting marginal R2
r2_symbiont_tax_broad1 <- R2(mr_symbiont_tax_broad1)

# getting estimates
res_symbiont_tax_broad1 <- get_est(mr_symbiont_tax_broad1, mod = "symbiont_tax_broad")
res_symbiont_tax_broad2 <- get_est(mr_symbiont_tax_broad2, mod = "symbiont_tax_broad")
res_symbiont_tax_broad3 <- get_est(mr_symbiont_tax_broad3, mod = "symbiont_tax_broad")
res_symbiont_tax_broad4 <- get_est(mr_symbiont_tax_broad4, mod = "symbiont_tax_broad")

# creating a table
tibble(`Fixed effect` = c(as.character(res_symbiont_tax_broad1$name), cont_gen(res_symbiont_tax_broad1$
    Estimate = c(res_symbiont_tax_broad1$estimate, res_symbiont_tax_broad2$estimate[-1],
        res_symbiont_tax_broad3$estimate[-(1:2)], res_symbiont_tax_broad4$estimate[-(1:3)]),
    `Lower CI [0.025]` = c(res_symbiont_tax_broad1$lowerCL, res_symbiont_tax_broad2$lowerCL[-1],
        res_symbiont_tax_broad3$lowerCL[-(1:2)], res_symbiont_tax_broad4$lowerCL[-(1:3)]),
    `Upper CI  [0.975]` = c(res_symbiont_tax_broad1$upperCL, res_symbiont_tax_broad2$upperCL[-1],
        res_symbiont_tax_broad3$upperCL[-(1:2)], res_symbiont_tax_broad4$upperCL[-(1:3)]),
    `V[authors]` = c(mr_symbiont_tax_broad1$sigma2, rep(NA, 9)), R2 = c(r2_symbiont_tax_broad1[1],
        rep(NA, 9))) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
    scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Microbe

0.576

0.494

0.658

0.087

0.073

Plant

1.188

0.703

1.674

NA

NA

Invert

0.549

0.460

0.639

NA

NA

Vert

0.496

-0.172

1.163

NA

NA

Microbe-Plant

0.613

0.120

1.105

NA

NA

Microbe-Invert

-0.027

-0.148

0.095

NA

NA

Microbe-Vert

-0.080

-0.753

0.592

NA

NA

Plant-Invert

-0.639

-1.133

-0.146

NA

NA

Plant-Vert

-0.693

-1.518

0.132

NA

NA

Invert-Vert

-0.054

-0.727

0.620

NA

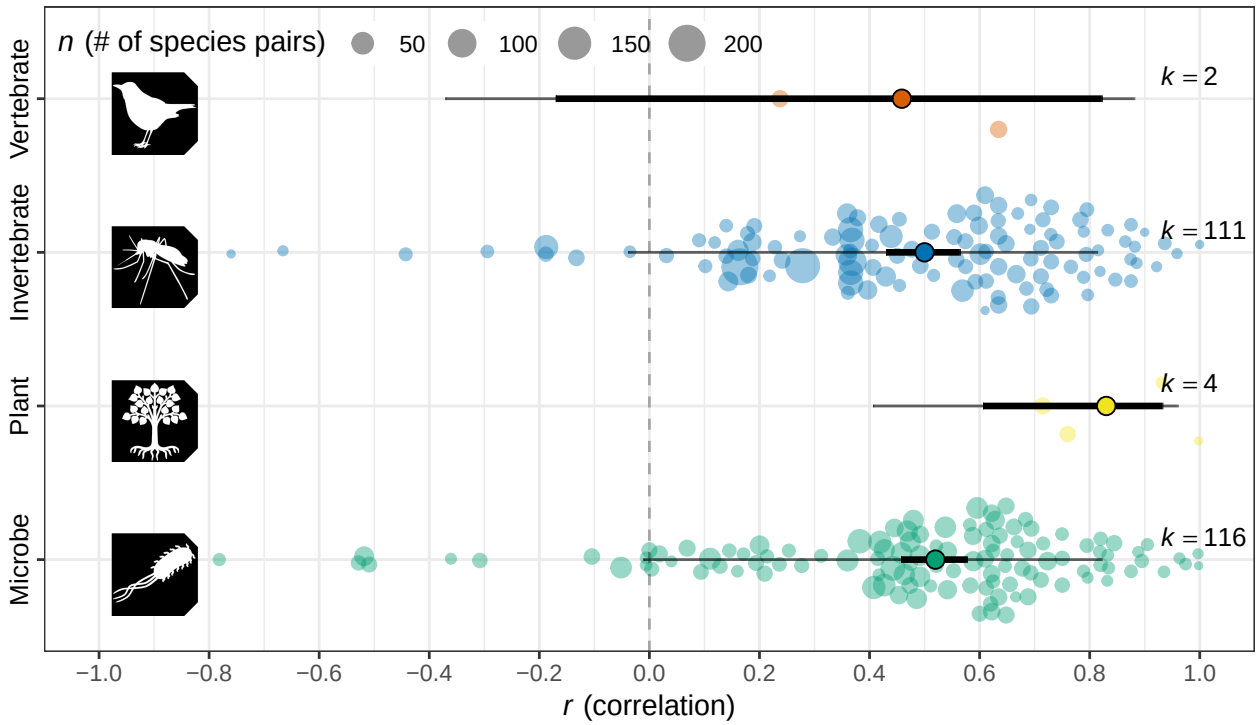
NA

```
# getting images
image_invertebrate_parasite <- readPNG(here("images/invertebrate_parasite_transparentbg.png"))
image_microbe_parasite <- readPNG(here("images/microbe_parasite_transparentbg.png"))
image_vertebrate_parasite <- readPNG(here("images/vertebrate_parasite_transparentbg.png"))
image_plant_parasite <- readPNG(here("images/plant_parasite_transparentbg.png"))

# adding sample size (k) for each category
k_symbiont_tax_broad <- dat %>% group_by(symbiont_tax_broad) %>% count()
# getting estimates and predicitons
pred_symbiont_tax_broad <- get_pred(mr_symbiont_tax_broad1, mod = "symbiont_tax_broad")
res_symbiont_tax_broad1 <- left_join(res_symbiont_tax_broad1, k_symbiont_tax_broad, by =  c("name" = "sy
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_symbiont_tax_broad <- ggplot(data = res_symbiont_tax_broad1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiont_tax_broad)),
```

```
                    aes(x= tanh(Zr), y = symbiont_tax_broad, size = ((1/VZr) + 3), colour = symbiont_tax_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_fill_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_y_discrete(labels = c("Microbe" = "Microbe",  "Plant" = "Plant",  "Invert"= "Invertebrate",  "V
  annotate('text', x = 0.93, y = 1:4 + 0.15, label= paste("italic(k)==", res_symbiont_tax_broad1$n), pa
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2)
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -1, xmax = -0.8, ymin = 2.6, ymax = 
  annotation_custom(rasterGrob(image_vertebrate_parasite), xmin = -1, xmax = -0.8, ymin = 3.6, ymax = 4

fig_symbiont_tax_broad
```



```r
# fig 3d
d <- ggplot(data = res_symbiont_tax_broad1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiont_tax_broad)),
                   aes(x= tanh(Zr), y = symbiont_tax_broad, size = ((1/VZr) + 3), colour = symbiont_tax_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = (
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_fill_manual(values = c("Microbe" = "#009E73",  "Plant" = "#F0E422",  "Invert"= "#0072B2",  "Ver
  scale_y_discrete(labels = c("Microbe" = "Microbe",  "Plant" = "Plant",  "Invert"= "Invertebrate",  "V
  annotate('text', x = 0.93, y = 1:4 + 0.15, label= paste("italic(k)==", res_symbiont_tax_broad1$n), pa
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -1, xmax = -0.8, ymin = 0.6, ymax = 1.2)
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -1, xmax = -0.8, ymin = 2.6, ymax =
  annotation_custom(rasterGrob(image_vertebrate_parasite), xmin = -1, xmax = -0.8, ymin = 3.6, ymax = 4
```

Figure 2d: A forest plot showing the group-wise means (the categorical variable `symbiont_tax_broad`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```r
# meta-regression
mr_host_range_link_ratio <- rma.mv(yi = Zr, V = VZr, mods = ~log(host_range_link_ratio),
    random = ~1 | authors, data = dat)
```

Testing specialization 1: host range **Supplementary Table 5:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `log(host_range_link_ratio)`.

```r
# getting marginal R2
r2_host_range_link_ratio <- R2(mr_host_range_link_ratio)

# getting estimates: name does not work for slopes
res_host_range_link_ratio <- get_est(mr_host_range_link_ratio, mod = "log(host_range_link_ratio)")

# creating a table
tibble(`Fixed effect` = c("Intercept", "log(host_range_link_ratio)"), Estimate = c(res_host_range_link_
    `Lower CI [0.025]` = c(res_host_range_link_ratio$lowerCL), `Upper CI  [0.975]` = c(res_host_range_li
    `V[authors]` = c(mr_host_range_link_ratio$sigma2, NA), R2 = c(r2_host_range_link_ratio[1],
        NA)) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept

0.577

0.509

0.645

0.09

0

log(host_range_link_ratio)

0.009

-0.156

0.173

NA

NA

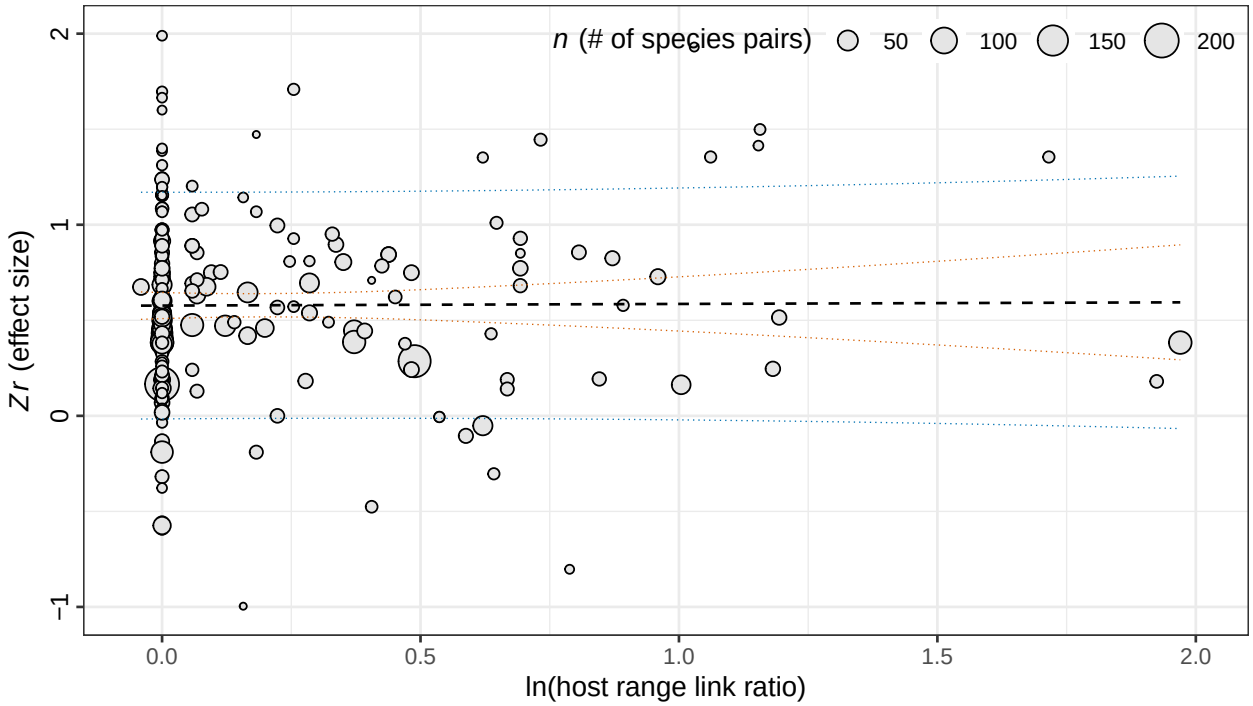
```
# newmods <- seq(-0.3, 2.2, by = 0.1)
# pred_host_range_link_ratio <-predict.rma(mr_host_range_link_ratio, newmods = newmods)
# ribbon_dat <- tibble(newmods = newmods, ymin = pred_host_range_link_ratio$ci.lb, ymax = pred_host_ran
pred_host_range_link_ratio <-predict.rma(mr_host_range_link_ratio)

# plotting

fig_host_range_link_ratio <-  dat %>%
  filter(!is.na(host_range_link_ratio))  %>% # getting ride of NA values
  mutate(ymin = pred_host_range_link_ratio$ci.lb,
         ymax = pred_host_range_link_ratio$ci.ub,
         ymin2 = pred_host_range_link_ratio$cr.lb,
         ymax2 = pred_host_range_link_ratio$cr.ub,
         pred = pred_host_range_link_ratio$pred) %>%
  ggplot(aes(x = log(host_range_link_ratio), y = Zr, size = (1/VZr) + 3, )) +
  geom_point(shape = 21, fill = "grey90") +
  #geom_ribbon(aes(ymin = ymin, ymax = ymax), fill = "#0072B2")  + # not quite sure why this does not w
  geom_smooth(aes(y = ymin2), method =  "loess", se = FALSE, lty =  "dotted", lwd = 0.25, colour = "#00
  geom_smooth(aes(y = ymax2), method =  "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#007
  geom_smooth(aes(y = ymin), method =  "loess", se = FALSE,lty = "dotted", lwd = 0.25, colour ="#D55E00
  geom_smooth(aes(y = ymax), method =  "loess", se = FALSE, lty ="dotted", lwd = 0.25, colour ="#D55E00
  geom_smooth(aes(y = pred), method =  "loess", se = FALSE, lty ="dashed", lwd = 0.5, colour ="black") +
  ylim(-1, 2) + xlim(-0.05, 2) +
  #geom_abline(intercept = mr_host_range_link_ratio$beta[[1]], slope = mr_host_range_link_ratio$beta[[2
  labs(x = "ln(host range link ratio)", y = expression(paste(italic(Zr), " (effect size)")), size = exp
  guides(fill = "none", colour = "none") +
  # themses
  theme_bw() +
```

```
  theme(legend.position= c(1, 1), legend.justification = c(1, 1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90))

fig_host_range_link_ratio
```



Supplementary Figure 1: A bubble plot showing a predicted regression line for the contentious variable `log(host_range_link_ratio)`, indicating 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines) with observed effect sizes based on various sample sizes.

```
# meta-regression
mr_host_range_taxonomic_breadth <- rma.mv(yi = Zr, V = VZr, mods = ~log(host_range_taxonomic_breadth),
    random = ~1 | authors, data = dat)
```

Testing specialization 2: taxonomic breadth **Supplementary Table 6:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `log(host_range_taxonomic_breadth)`.

```
# getting marginal R2
r2_host_range_taxonomic_breadth <- R2(mr_host_range_taxonomic_breadth)

# getting estimates: name does not work for slopes
res_host_range_taxonomic_breadth <- get_est(mr_host_range_taxonomic_breadth, mod = "log(host_range_taxo

# creating a table
tibble(`Fixed effect` = c("Intercept", "log(host_range_taxonomic_breadth)"), Estimate = c(res_host_rang
    `Lower CI [0.025]` = c(res_host_range_taxonomic_breadth$lowerCL), `Upper CI  [0.975]` = c(res_host_
    `V[authors]` = c(mr_host_range_taxonomic_breadth$sigma2, NA), R2 = c(r2_host_range_taxonomic_breadth
```

```
        NA)) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept

0.590

0.522

0.658

0.088

0

log(host_range_taxonomic_breadth)

0.005

-0.188

0.198

NA

NA

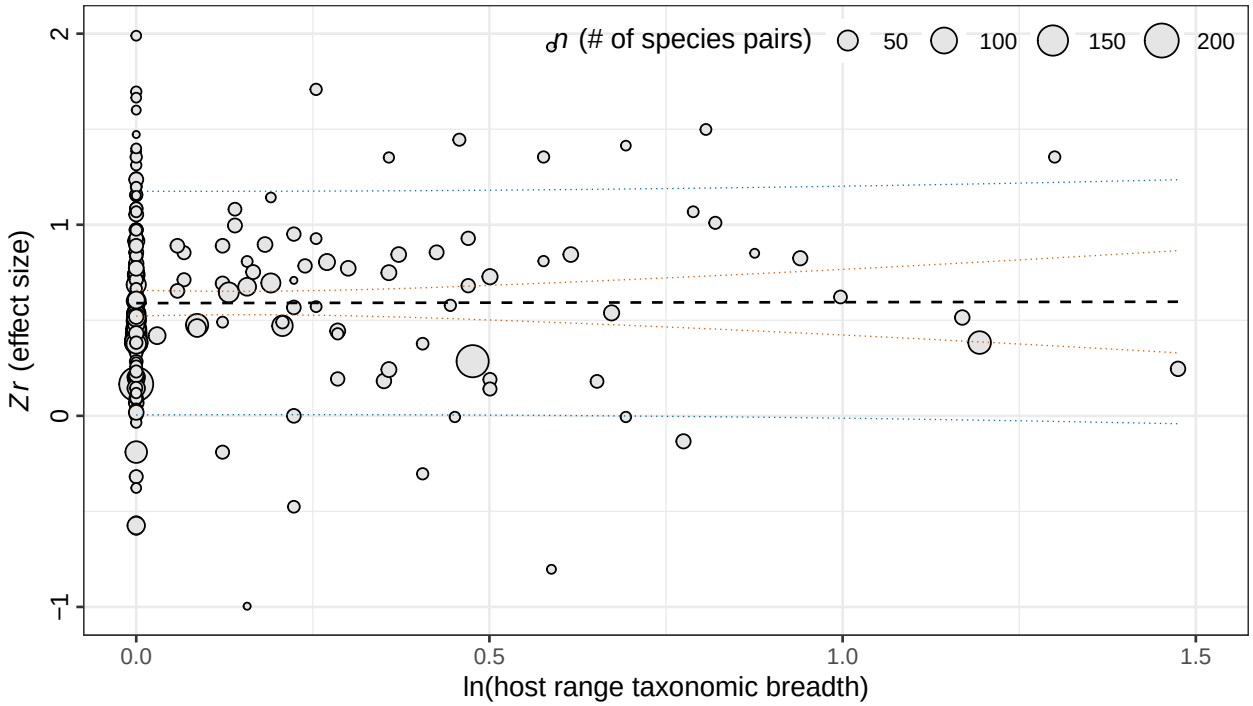
```
pred_host_range_taxonomic_breadth <-predict.rma(mr_host_range_taxonomic_breadth)

# plotting

fig_host_range_taxonomic_breadth <-  dat %>%
  filter(!is.na(host_range_taxonomic_breadth))  %>% # getting ride of NA values
  mutate(ymin = pred_host_range_taxonomic_breadth$ci.lb,
         ymax = pred_host_range_taxonomic_breadth$ci.ub,
         ymin2 = pred_host_range_taxonomic_breadth$cr.lb,
         ymax2 = pred_host_range_taxonomic_breadth$cr.ub,
         pred = pred_host_range_taxonomic_breadth$pred) %>%
  ggplot(aes(x = log(host_range_taxonomic_breadth), y = Zr, size = (1/VZr) + 3, )) +
  geom_point(shape = 21, fill = "grey90") +
  #geom_ribbon(aes(ymin = ymin, ymax = ymax), fill = "#0072B2")  + # not quite sure why this does not w
  geom_smooth(aes(y = ymin2), method =  "loess", se = FALSE, lty =  "dotted", lwd = 0.25, colour = "#007
  geom_smooth(aes(y = ymax2), method =  "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#0071
  geom_smooth(aes(y = ymin), method =  "loess", se = FALSE,lty = "dotted", lwd = 0.25, colour ="#D55E00
  geom_smooth(aes(y = ymax), method =  "loess", se = FALSE, lty ="dotted", lwd = 0.25, colour ="#D55E00
  geom_smooth(aes(y = pred), method =  "loess", se = FALSE, lty ="dashed", lwd = 0.5, colour ="black") +
  ylim(-1, 2) + xlim(0, 1.5) +
  #geom_abline(intercept = mr_host_range_link_ratio$beta[[1]], slope = mr_host_range_link_ratio$beta[[2
  labs(x = "ln(host range taxonomic breadth)", y = expression(paste(italic(Zr), " (effect size)")), size
  guides(fill = "none", colour = "none") +
  # themses
  theme_bw() +
```

```
  theme(legend.position= c(1, 1), legend.justification = c(1, 1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90))

fig_host_range_taxonomic_breadth
```



Supplementary Figure 2: A bubble plot showing a predicted regression line for the contentious variable `log(log(host_range_taxonomic_breadth)`, indicating 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines) with observed effect sizes based on various sample sizes.

```
# reordering
dat$endo_or_ecto <- factor(dat$endo_or_ecto, levels = c("Endo/Ecto", "Endo", "Ecto"))

# meta-regression: mutiple intercepts
mr_endo_or_ecto1 <- rma.mv(yi = Zr, V = VZr, mods = ~endo_or_ecto - 1, test = "t",
    random = ~1 | authors, data = dat)

# meta-regression: contrast 1
mr_endo_or_ecto2 <- rma.mv(yi = Zr, V = VZr, mods = ~endo_or_ecto, test = "t", random = ~1 |
    authors, data = dat)

# meta-regression: contrast 2
mr_endo_or_ecto3 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(endo_or_ecto, ref = "Endo"),
    test = "t", random = ~1 | authors, data = dat)
```

The place of symbiosis: ednosymbiosis vs. ectosymbiosis **Supplementary Table 7:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `endo_or_ecto`.

```r
# getting marginal R2
r2_endo_or_ecto1 <- R2(mr_endo_or_ecto1)

# getting estimates
res_endo_or_ecto1 <- get_est(mr_endo_or_ecto1, mod = "endo_or_ecto")
res_endo_or_ecto2 <- get_est(mr_endo_or_ecto2, mod = "endo_or_ecto")
res_endo_or_ecto3 <- get_est(mr_endo_or_ecto3, mod = "endo_or_ecto")

# creating a table
tibble(`Fixed effect` = c(as.character(res_endo_or_ecto1$name), cont_gen(res_endo_or_ecto1$name)),
    Estimate = c(res_endo_or_ecto1$estimate, res_endo_or_ecto2$estimate[-1], res_endo_or_ecto3$estimate
    `Lower CI [0.025]` = c(res_endo_or_ecto1$lowerCL, res_endo_or_ecto2$lowerCL[-1],
        res_endo_or_ecto3$lowerCL[-(1:2)]), `Upper CI  [0.975]` = c(res_endo_or_ecto1$upperCL,
        res_endo_or_ecto2$upperCL[-1], res_endo_or_ecto3$upperCL[-(1:2)]), `V[authors]` = c(mr_endo_or_
        rep(NA, 5)), R2 = c(r2_endo_or_ecto1[1], rep(NA, 5))) %>% kable("html", digits = 3) %>%
    kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Endo/Ecto

0.510

0.029

0.990

0.09

0.004

Endo

0.564

0.491

0.637

NA

NA

Ecto

0.600

0.489

0.710

NA

NA

Endo/Ecto-Endo

0.054

-0.431

0.540

NA

NA

Endo/Ecto-Ecto

0.090

-0.403

0.583

NA

NA

Endo-Ecto

0.036

-0.097

0.168

NA

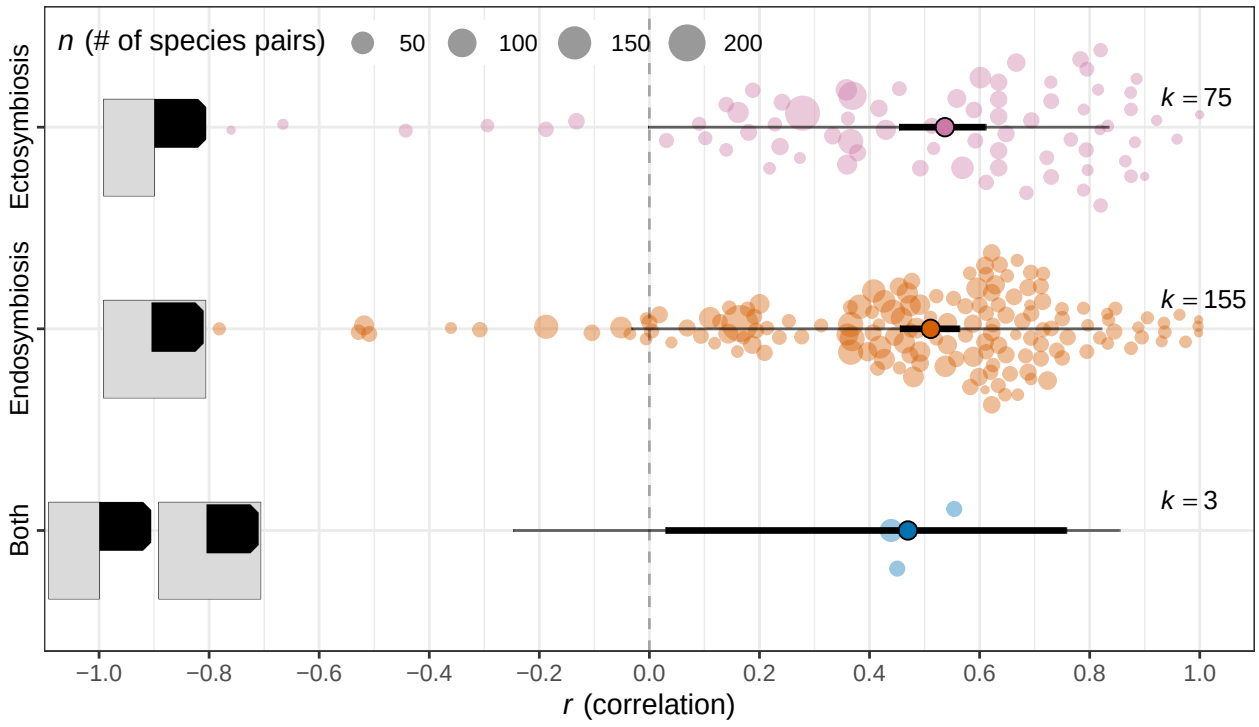
NA

```
# getting images
image_endoparasite <- readPNG(here("images/endoparasite_transparentbg.png"))
image_ectoparasite <- readPNG(here("images/ectoparasite_transparentbg.png"))

# adding sample size (k) for each category
k_endo_or_ecto <- dat %>% group_by(endo_or_ecto) %>% count()
# getting estimates and predicitons
pred_endo_or_ecto <- get_pred(mr_endo_or_ecto1, mod = "endo_or_ecto")
res_endo_or_ecto1 <- left_join(res_endo_or_ecto1, k_endo_or_ecto, by =  c("name" = "endo_or_ecto"))  %>%
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_endo_or_ecto <- ggplot(data = res_endo_or_ecto1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(endo_or_ecto)),
                   aes(x= tanh(Zr), y = endo_or_ecto, size = ((1/VZr) + 3), colour = endo_or_ecto), grou
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size =
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size =
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Endo/Ecto" = "#0072B2",  "Endo" = "#D55E00",  "Ecto"= "#CC79A7")) +
  scale_fill_manual(values = c("Endo/Ecto" = "#0072B2",  "Endo" = "#D55E00",  "Ecto"= "#CC79A7")) +
  scale_y_discrete(labels = c("Endo/Ecto" = "Both",  "Endo" = "Endosymbiosis",  "Ecto"= "Ectosymbiosis"
  annotate('text', x = 0.93, y = 1:3 + 0.15, label= paste("italic(k)==", res_endo_or_ecto1$n), parse=TRU
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
```

```
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction = "horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # adding images
  annotation_custom(rasterGrob(image_endoparasite), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_ectoparasite), xmin = -1, xmax = -0.8, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_ectoparasite), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_endoparasite), xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2)

fig_endo_or_ecto
```




```
# fig 3e

e <- ggplot(data = res_endo_or_ecto1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(endo_or_ecto)),
                   aes(x= tanh(Zr), y = endo_or_ecto, size = ((1/VZr) + 3), colour = endo_or_ecto), grou
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = (
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("Endo/Ecto" = "#0072B2",  "Endo" = "#D55E00",  "Ecto"= "#CC79A7")) +
```

```
  scale_fill_manual(values = c("Endo/Ecto" = "#0072B2",  "Endo" = "#D55E00",  "Ecto"= "#CC79A7")) +
  scale_y_discrete(labels = c("Endo/Ecto" = "Both",  "Endo" = "Endosymbiosis",  "Ecto"= "Ectosymbiosis")
  annotate('text', x = 0.93, y = 1:3 + 0.15, label= paste("italic(k)==", res_endo_or_ecto1$n), parse=TRU
  labs(x = "", y = "", size = expression(paste(italic(n), " (# of species pairs)")), tag = "e" ) +
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # adding images
  annotation_custom(rasterGrob(image_endoparasite), xmin = -1, xmax = -0.8, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_ectoparasite), xmin = -1, xmax = -0.8, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_ectoparasite), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_endoparasite), xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2)
```

Figure 3e: A forest plot showing the group-wise means (the categorical variable `endo_or_ecto`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```
# meta-regression: mutiple intercepts
mr_mode_of_transmission_broad1 <- rma.mv(yi = Zr, V = VZr, mods = ~mode_of_transmission_broad -
    1, test = "t", random = ~1 | authors, data = dat)

# meta-regression: contrast 1
mr_mode_of_transmission_broad2 <- rma.mv(yi = Zr, V = VZr, mods = ~mode_of_transmission_broad,
    test = "t", random = ~1 | authors, data = dat)

# meta-regression: contrast 2
mr_mode_of_transmission_broad3 <- rma.mv(yi = Zr, V = VZr, mods = ~relevel(mode_of_transmission_broad,
    ref = "vertical"), test = "t", random = ~1 | authors, data = dat)
```

The effect of the mode of transmission **Supplementary Table 8:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `mode_of_transmission_broad`.

```
# getting marginal R2
r2_mode_of_transmission_broad1 <- R2(mr_mode_of_transmission_broad1)

# getting estimates
res_mode_of_transmission_broad1 <- get_est(mr_mode_of_transmission_broad1, mod = "mode_of_transmission_
res_mode_of_transmission_broad2 <- get_est(mr_mode_of_transmission_broad2, mod = "mode_of_transmission_
res_mode_of_transmission_broad3 <- get_est(mr_mode_of_transmission_broad3, mod = "mode_of_transmission_

# creating a table
tibble(`Fixed effect` = c(as.character(res_mode_of_transmission_broad1$name), cont_gen(res_mode_of_trans
    Estimate = c(res_mode_of_transmission_broad1$estimate, res_mode_of_transmission_broad2$estimate[-1]
        res_mode_of_transmission_broad3$estimate[-(1:2)]), `Lower CI [0.025]` = c(res_mode_of_transmissi
        res_mode_of_transmission_broad2$lowerCL[-1], res_mode_of_transmission_broad3$lowerCL[-(1:2)]),
    `Upper CI  [0.975]` = c(res_mode_of_transmission_broad1$upperCL, res_mode_of_transmission_broad2$upp
        res_mode_of_transmission_broad3$upperCL[-(1:2)]), `V[authors]` = c(mr_mode_of_transmission_broad
        rep(NA, 5)), R2 = c(r2_mode_of_transmission_broad1[1], rep(NA, 5))) %>% kable("html",
    digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

both

0.620

0.497

0.742

0.068

0.148

horizontal

0.486

0.412

0.559

NA

NA

vertical

0.763

0.642

0.884

NA

NA

both-horizontal

-0.134

-0.277

0.009

NA

NA

both-vertical

0.143

-0.029

0.316

NA

NA

horizontal-vertical

-0.277

-0.419

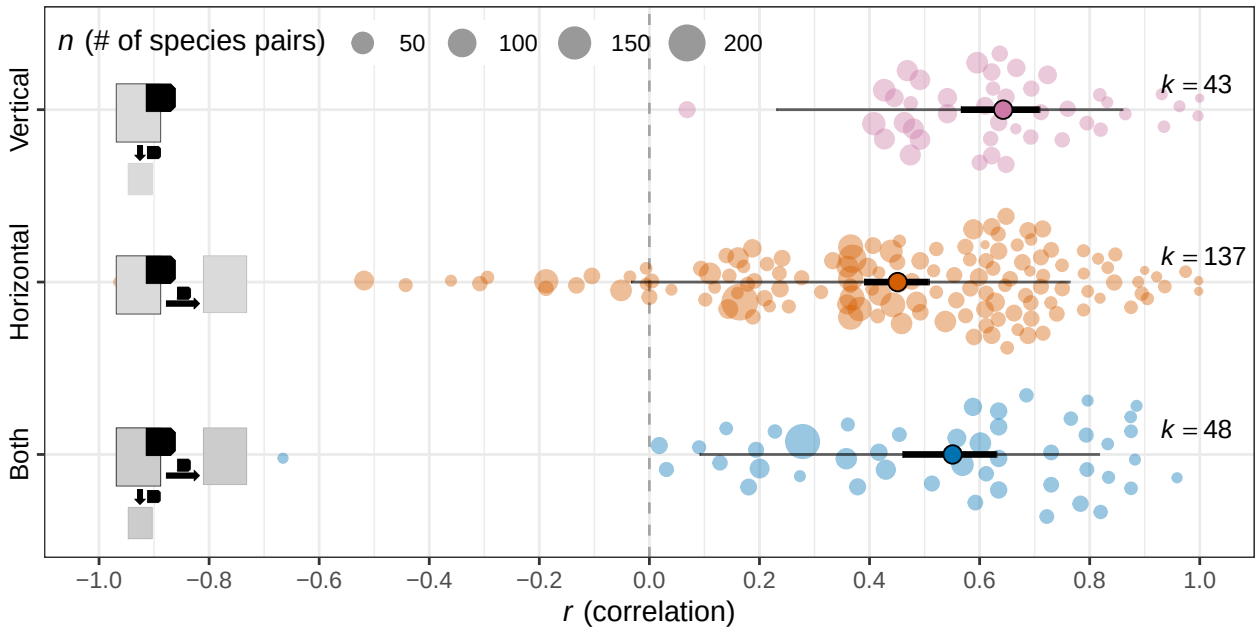
-0.135

NA

NA

```
# getting images
image_horizontal <- readPNG(here("images/horizontal_transparentbg.png"))
image_vertical <- readPNG(here("images/vertical_transparentbg.png"))
image_both <- readPNG(here("images/horizontal_vertical_transparentbg.png"))
# adding sample size (k) for each category
k_mode_of_transmission_broad <- dat %>% group_by(mode_of_transmission_broad) %>% count()
# getting estimates and predicitons
pred_mode_of_transmission_broad <- get_pred(mr_mode_of_transmission_broad1, mod = "mode_of_transmission_
res_mode_of_transmission_broad1 <- left_join(res_mode_of_transmission_broad1, k_mode_of_transmission_br
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_mode_of_transmission_broad <- ggplot(data = res_mode_of_transmission_broad1, aes(x = tanh(estimate)
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(mode_of_transmission_broad)),
                   aes(x= tanh(Zr), y = mode_of_transmission_broad, size = ((1/VZr) + 3), colour = mode_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("both" = "#0072B2",  "horizontal" = "#D55E00",  "vertical"= "#CC79A7")) 
  scale_fill_manual(values = c("both" = "#0072B2",  "horizontal" = "#D55E00",  "vertical"= "#CC79A7")) +
  scale_y_discrete(labels = c("both" = "Both",  "horizontal" = "Horizontal",  "vertical"= "Vertical")) +
  annotate('text', x = 0.93, y = (1:3 + 0.15), label= paste("italic(k)==", res_mode_of_transmission_broa
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction = "horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # adding images
  annotation_custom(rasterGrob(image_horizontal), xmin = -1, xmax = -0.7, ymin = 1.4, ymax = 2.2) +
  annotation_custom(rasterGrob(image_vertical), xmin = -1, xmax = -0.7, ymin = 2.4, ymax = 3.2) +
  annotation_custom(rasterGrob(image_both), xmin = -1, xmax = -0.7, ymin = 0.4, ymax = 1.2)

fig_mode_of_transmission_broad
```




```
# fig 3f

f <- ggplot(data = res_mode_of_transmission_broad1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(mode_of_transmission_broad)),
                   aes(x= tanh(Zr), y = mode_of_transmission_broad, size = ((1/VZr) + 3), colour = mode_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = (
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values = c("both" = "#0072B2",  "horizontal" = "#D55E00",  "vertical"= "#CC79A7"))
  scale_fill_manual(values = c("both" = "#0072B2",  "horizontal" = "#D55E00",  "vertical"= "#CC79A7")) +
  scale_y_discrete(labels = c("both" = "Both",  "horizontal" = "Horizontal",  "vertical"= "Vertical")) +
  annotate('text', x = 0.93, y = (1:3 + 0.15), label= paste("italic(k)==", res_mode_of_transmission_broa
  labs(x = "", y = "", size = expression(paste(italic(n), " (# of species pairs)")), tag = "f" ) +
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # adding images
  annotation_custom(rasterGrob(image_horizontal), xmin = -1, xmax = -0.7, ymin = 1.4, ymax = 2.2) +
  annotation_custom(rasterGrob(image_vertical), xmin = -1, xmax = -0.7, ymin = 2.4, ymax = 3.2) +
  annotation_custom(rasterGrob(image_both), xmin = -1, xmax = -0.7, ymin = 0.4, ymax = 1.2)
```

Figure 2f: A forest plot showing the group-wise means (the categorical variable `mode_of_transmission_broad`), indicating 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```r
# reordering
dat$symbiosis_transmission <- factor(dat$symbiosis_transmission, levels = c("Mutualistboth",
    "Mutualisthorizontal", "Mutualistvertical", "Parasiteboth", "Parasitehorizontal"),
    labels = c("MutualistBoth", "MutualistHorizontal", "MutualistVertical", "ParasiteBoth",
        "ParasiteHorizontal"))

# meta-regression: mutiple intercepts
mr_symbiosis_transmission1 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiosis_transmission -
    1, test = "t", random = ~1 | authors, data = dat)

# # meta-regression: contrasts x 10 getting the level names out
level_names <- levels(dat$symbiosis_transmission)

# helper function to run metafor meta-regression
run_rma <- function(name) {
    rma.mv(yi = Zr, V = VZr, mods = ~relevel(symbiosis_transmission, ref = name),
        test = "t", random = ~1 | authors, data = dat)
}

# results of meta-regression including all contrast results; taking the last
# level out ([-length(level_names)])
mr_symbiosis_transmission <- map(level_names[-length(level_names)], run_rma)
```

The combined effect of symbiosis and mode of transmission **Supplementary Table 9:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `symbiosis_transmission`.

```r
# getting marginal R2
r2_symbiosis_transmission1 <- R2(mr_symbiosis_transmission1)

# getting estimates
res_symbiosis_transmission1 <- get_est(mr_symbiosis_transmission1, mod = "symbiosis_transmission")
res_symbiosis_transmission <- map(mr_symbiosis_transmission, ~get_est(.x, mod = "symbiosis_transmission

# a list of the numbers to take out unnecessary contrasts
contra_list <- Map(seq, from = 1, to = 1:4)

# you need to flatten twice: first to make it a list and make it a vector
estimates <- map2(res_symbiosis_transmission, contra_list, ~.x[-(.y), "estimate"]) %>%
    flatten() %>% flatten_dbl()
lowerCLs <- map2(res_symbiosis_transmission, contra_list, ~.x[-(.y), "lowerCL"]) %>%
    flatten() %>% flatten_dbl()
upperCLs <- map2(res_symbiosis_transmission, contra_list, ~.x[-(.y), "upperCL"]) %>%
    flatten() %>% flatten_dbl()

# creating a table
tibble(`Fixed effect` = c(as.character(res_symbiosis_transmission1$name), cont_gen(res_symbiosis_transmi
    Estimate = c(res_symbiosis_transmission1$estimate, estimates), `Lower CI [0.025]` = c(res_symbiosis_
        lowerCLs), `Upper CI  [0.975]` = c(res_symbiosis_transmission1$upperCL, upperCLs),
    `V[authors]` = c(mr_symbiosis_transmission1$sigma2, rep(NA, (5 + choose(5, 2)) -
        1)), R2 = c(r2_symbiosis_transmission1[1], rep(NA, (5 + choose(5, 2)) - 1))) %>%
    kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
    scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

MutualistBoth

0.719

0.349

1.089

0.069

0.142

MutualistHorizontal

0.490

0.322

0.659

NA

NA

MutualistVertical

0.757

0.635

0.880

NA

NA

ParasiteBoth

0.608

0.477

0.739

NA

NA

ParasiteHorizontal

0.486

0.405

0.566

NA

NA

MutualistBoth-MutualistHorizontal

-0.229

-0.635

0.178

NA

NA

MutualistBoth-MutualistVertical

0.038

-0.352

0.428

NA

NA

MutualistBoth-ParasiteBoth

-0.111

-0.504

0.281

NA

NA

MutualistBoth-ParasiteHorizontal

-0.234

-0.612

0.145

NA

NA

MutualistHorizontal-MutualistVertical

0.267

0.059

0.475

NA

NA

MutualistHorizontal-ParasiteBoth

0.118

-0.095

0.331

NA

NA

MutualistHorizontal-ParasiteHorizontal

-0.005

-0.187

0.177

NA

NA

MutualistVertical-ParasiteBoth

-0.149

-0.329

0.030

NA

NA

MutualistVertical-ParasiteHorizontal

-0.272

-0.419

-0.125

NA

NA

ParasiteBoth-ParasiteHorizontal

-0.122

-0.276

0.031

NA

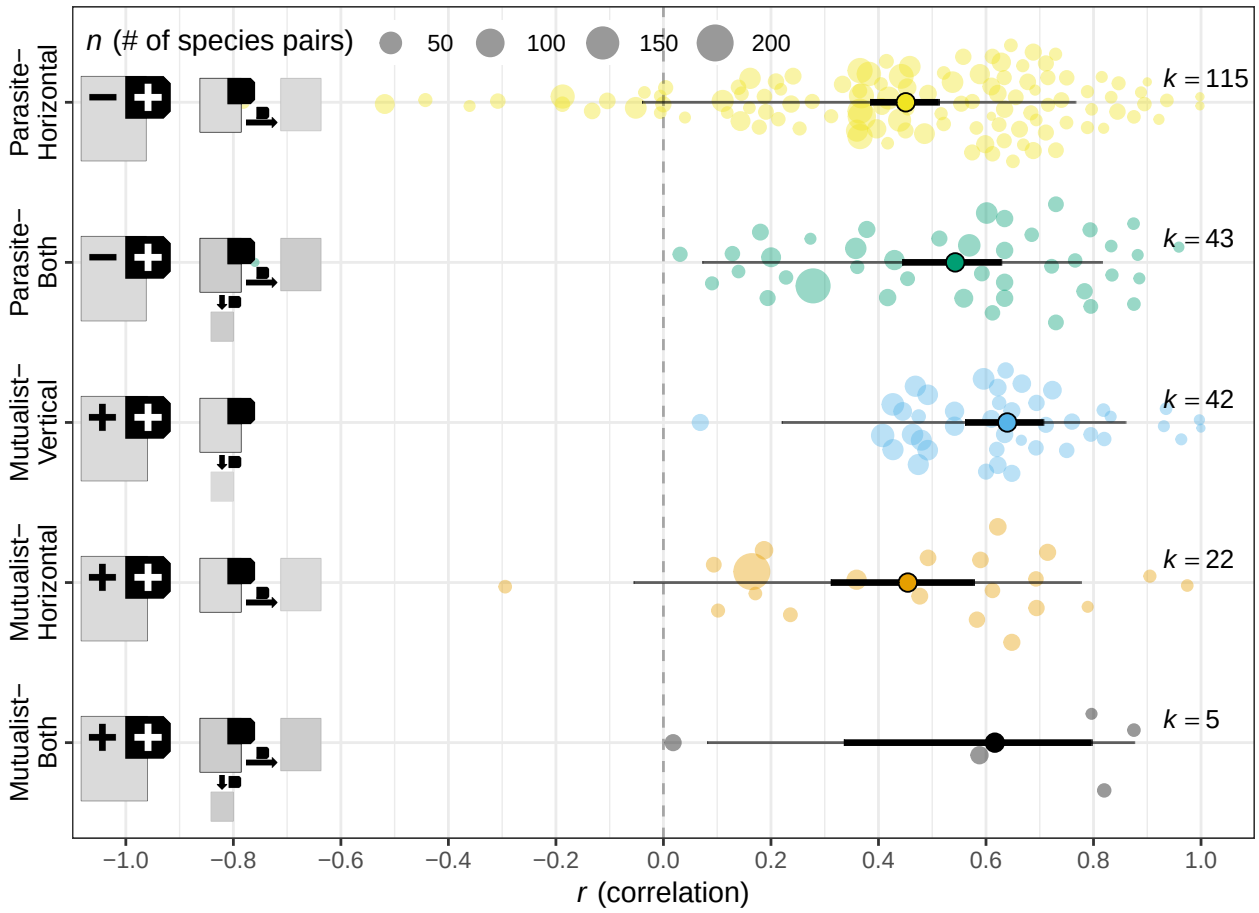
NA

```
# colour list
colour_ls <- c("#000000", "#E69F00", "#56B4E9", "#009E73",  "#F0E422",  "#0072B2",  "#D55E00", "#CC79A7

# adding sample size (k) for each category
k_symbiosis_transmission <- dat %>% group_by(symbiosis_transmission) %>% count()
# getting estimates and predicitons
pred_symbiosis_transmission <- get_pred(mr_symbiosis_transmission1, mod = "symbiosis_transmission")
res_symbiosis_transmission1 <- left_join(res_symbiosis_transmission1, k_symbiosis_transmission, by =  c
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_symbiosis_transmission <- ggplot(data = res_symbiosis_transmission1, aes(x = tanh(estimate), y = nar
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiosis_transmission)),
                   aes(x= tanh(Zr), y = symbiosis_transmission, size = ((1/VZr) + 3), colour = symbiosis
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 0
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
```

```
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values =   c("MutualistBoth"= colour_ls[1], "MutualistHorizontal"= colour_ls[2], "
  scale_fill_manual(values = c("MutualistBoth"= colour_ls[1], "MutualistHorizontal"= colour_ls[2], "Mut
  scale_y_discrete(labels = c("MutualistBoth" = "Mutualist-\nBoth", "MutualistHorizontal" = "Mutualist-
  annotate('text', x = 0.93, y = 1:5 + 0.15, label= paste("italic(k)==", res_symbiosis_transmission1$n)
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_both), xmin = -0.9, xmax = -0.6, ymin = 0.4, ymax = 1.2) +
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_horizontal),xmin = -0.9, xmax = -0.6, ymin = 1.4, ymax = 2.2) +
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_vertical), xmin = -0.9, xmax = -0.6, ymin = 2.4, ymax = 3.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1.1, xmax = -0.9, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_both), xmin = -0.9, xmax = -0.6, ymin = 3.4, ymax = 4.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1.1, xmax = -0.9, ymin = 4.6, ymax = 5.2) +
  annotation_custom(rasterGrob(image_horizontal), xmin = -0.9, xmax = -0.6, ymin = 4.4, ymax = 5.2)

fig_symbiosis_transmission
```



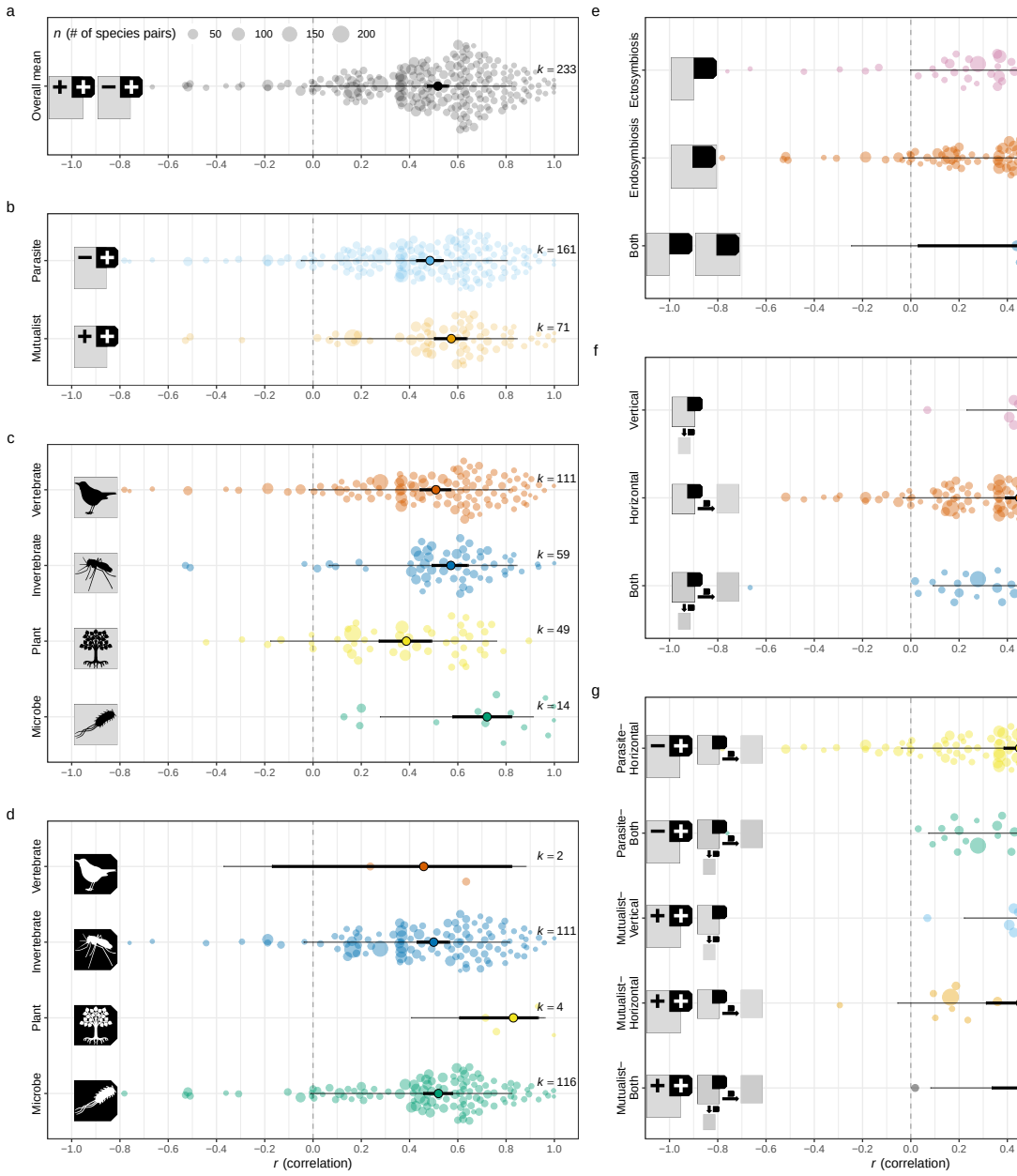

```
## fig 3
g <- ggplot(data = res_symbiosis_transmission1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiosis_transmission)),
                   aes(x= tanh(Zr), y = symbiosis_transmission, size = ((1/VZr) + 3), colour = symbiosis
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values =   c("MutualistBoth"= colour_ls[1], "MutualistHorizontal"= colour_ls[2], "
  scale_fill_manual(values = c("MutualistBoth"= colour_ls[1], "MutualistHorizontal"= colour_ls[2], "Mut
  scale_y_discrete(labels = c("MutualistBoth" = "Mutualist-\nBoth", "MutualistHorizontal" = "Mutualist-
  annotate('text', x = 0.93, y = 1:5 + 0.15, label= paste("italic(k)==", res_symbiosis_transmission1$n)
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position="none") +
  theme(axis.text.y = element_text(size = 10, colour ="black",hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_both), xmin = -0.9, xmax = -0.6, ymin = 0.4, ymax = 1.2) +
```

```
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_horizontal),xmin = -0.9, xmax = -0.6, ymin = 1.4, ymax = 2.2) +
  annotation_custom(rasterGrob(image_mutualism), xmin = -1.1, xmax = -0.9, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_vertical), xmin = -0.9, xmax = -0.6, ymin = 2.4, ymax = 3.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1.1, xmax = -0.9, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_both), xmin = -0.9, xmax = -0.6, ymin = 3.4, ymax = 4.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -1.1, xmax = -0.9, ymin = 4.6, ymax = 5.2) +
  annotation_custom(rasterGrob(image_horizontal), xmin = -0.9, xmax = -0.6, ymin = 4.4, ymax = 5.2)
```

Figure 3g: A forest plot showing the group-wise means (the categorical variable `symbiosis_transmission`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

```
# building fig 3 using patchwork
fig3 <- (a/b/c/d + plot_layout(heights = c(1.6, 2, 3.7, 3.7))) | (e/f/g + plot_layout(heights = c(2.8,
    2.8, 4.4)))  #+ plot_annotation(tag_levels = 'a', tag_suffix = ')')

fig3
```



Putting together Figure 3

```
# ggsave('../figs/fig3.png', width = 14, height = 14) ggsave('../figs/fig3.pdf',
# width = 14, height = 14)
```

Figure 3: putting all 7 panels together: Figure 3a - Figure 3g (see the main text)

Additional analyses (uni-predictor)

These are extra analyses not discussed in the main text.

```
# reordering
dat$host_tax_symbiosis <- factor(dat$host_tax_symbiosis, levels = c("MicrobeMutualist",
    "MicrobeParasite", "PlantMutualist", "PlantParasite", "InvertMutualist", "InvertParasite",
```

```
    "VertMutualist", "VertParasite"))

# meta-regression: mutiple intercepts
mr_host_tax_symbiosis1 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_symbiosis - 1,
    test = "t", random = ~1 | authors, data = dat)

# # meta-regression: contrasts x 10 getting the level names out
level_names <- levels(dat$host_tax_symbiosis)

# helper function to run metafor meta-regression
run_rma <- function(name) {
    rma.mv(yi = Zr, V = VZr, mods = ~relevel(host_tax_symbiosis, ref = name), test = "t",
        random = ~1 | authors, data = dat)
}

# results of meta-regression including all contrast results; taking the last
# level out ([-length(level_names)])
mr_host_tax_symbiosis <- map(level_names[-length(level_names)], run_rma)
```

The combined effect of host taxa and symbiosis (parasitism vs. mutualism) **Supplementary Table 10:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `host_tax_symbiosis`.

```
# getting marginal R2
r2_host_tax_symbiosis1 <- R2(mr_host_tax_symbiosis1)

# getting estimates
res_host_tax_symbiosis1 <- get_est(mr_host_tax_symbiosis1, mod = "host_tax_symbiosis")
res_host_tax_symbiosis <- map(mr_host_tax_symbiosis, ~get_est(.x, mod = "host_tax_symbiosis"))

# a list of the numbers to take out unnecessary contrasts
contra_list <- Map(seq, from = 1, to = 1:7)

# you need to flatten twice: first to make it a list and make it a vector
estimates <- map2(res_host_tax_symbiosis, contra_list, ~.x[-(.y), "estimate"]) %>%
    flatten() %>% flatten_dbl()
lowerCLs <- map2(res_host_tax_symbiosis, contra_list, ~.x[-(.y), "lowerCL"]) %>%
    flatten() %>% flatten_dbl()
upperCLs <- map2(res_host_tax_symbiosis, contra_list, ~.x[-(.y), "upperCL"]) %>%
    flatten() %>% flatten_dbl()

# creating a table
tibble(`Fixed effect` = c(as.character(res_host_tax_symbiosis1$name), cont_gen(res_host_tax_symbiosis1$n
    Estimate = c(res_host_tax_symbiosis1$estimate, estimates), `Lower CI [0.025]` = c(res_host_tax_symbi
        lowerCLs), `Upper CI  [0.975]` = c(res_host_tax_symbiosis1$upperCL, upperCLs),
    `V[authors]` = c(mr_host_tax_symbiosis1$sigma2, rep(NA, (8 + choose(8, 2)) -
        1)), R2 = c(r2_host_tax_symbiosis1[1], rep(NA, (8 + choose(8, 2)) - 1))) %>%
    kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
    scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

MicrobeMutualist

1.348

1.006

1.689

0.074

0.302

MicrobeParasite

0.435

0.088

0.782

NA

NA

PlantMutualist

0.401

0.217

0.585

NA

NA

PlantParasite

0.412

0.262

0.562

NA

NA

InvertMutualist

0.647

0.525

0.768

NA

NA

InvertParasite

0.604

0.371

0.837

NA

NA

VertMutualist

1.499

0.467

2.531

NA

NA

VertParasite

0.550

0.467

0.633

NA

NA

MicrobeMutualist-MicrobeParasite

-0.913

-1.400

-0.426

NA

NA

MicrobeMutualist-PlantMutualist

-0.947

-1.335

-0.559

NA

NA

MicrobeMutualist-PlantParasite

-0.936

-1.309

-0.563

NA

NA

MicrobeMutualist-InvertMutualist

-0.701

-1.063

-0.338

NA

NA

MicrobeMutualist-InvertParasite

-0.743

-1.157

-0.330

NA

NA

MicrobeMutualist-VertMutualist

0.151

-0.936

1.238

NA

NA

MicrobeMutualist-VertParasite

-0.798

-1.149

-0.446

NA

NA

MicrobeParasite-PlantMutualist

-0.034

-0.426

0.359

NA

NA

MicrobeParasite-PlantParasite

-0.023

-0.401

0.355

NA

NA

MicrobeParasite-InvertMutualist

0.212

-0.155

0.580

NA

NA

MicrobeParasite-InvertParasite

0.170

-0.248

0.587

NA

NA

MicrobeParasite-VertMutualist

1.064

-0.025

2.153

NA

NA

MicrobeParasite-VertParasite

0.115

-0.241

0.472

NA

NA

PlantMutualist-PlantParasite

0.011

-0.211

0.233

NA

NA

PlantMutualist-InvertMutualist

0.246

0.026

0.466

NA

NA

PlantMutualist-InvertParasite

0.203

-0.094

0.500

NA

NA

PlantMutualist-VertMutualist

1.098

0.049

2.146

NA

NA

PlantMutualist-VertParasite

0.149

-0.053

0.351

NA

NA

PlantParasite-InvertMutualist

0.235

0.042

0.428

NA

NA

PlantParasite-InvertParasite

0.192

-0.085

0.469

NA

NA

PlantParasite-VertMutualist

1.087

0.044

2.129

NA

NA

PlantParasite-VertParasite

0.138

-0.033

0.309

NA

NA

InvertMutualist-InvertParasite

-0.043

-0.306

0.220

NA

NA

InvertMutualist-VertMutualist

0.852

-0.187

1.891

NA

NA

InvertMutualist-VertParasite

-0.097

-0.244

0.050

NA

NA

InvertParasite-VertMutualist

0.894

-0.164

1.952

NA

NA

InvertParasite-VertParasite

-0.054

-0.295

0.187

NA

NA

VertMutualist-VertParasite

-0.949

-1.984

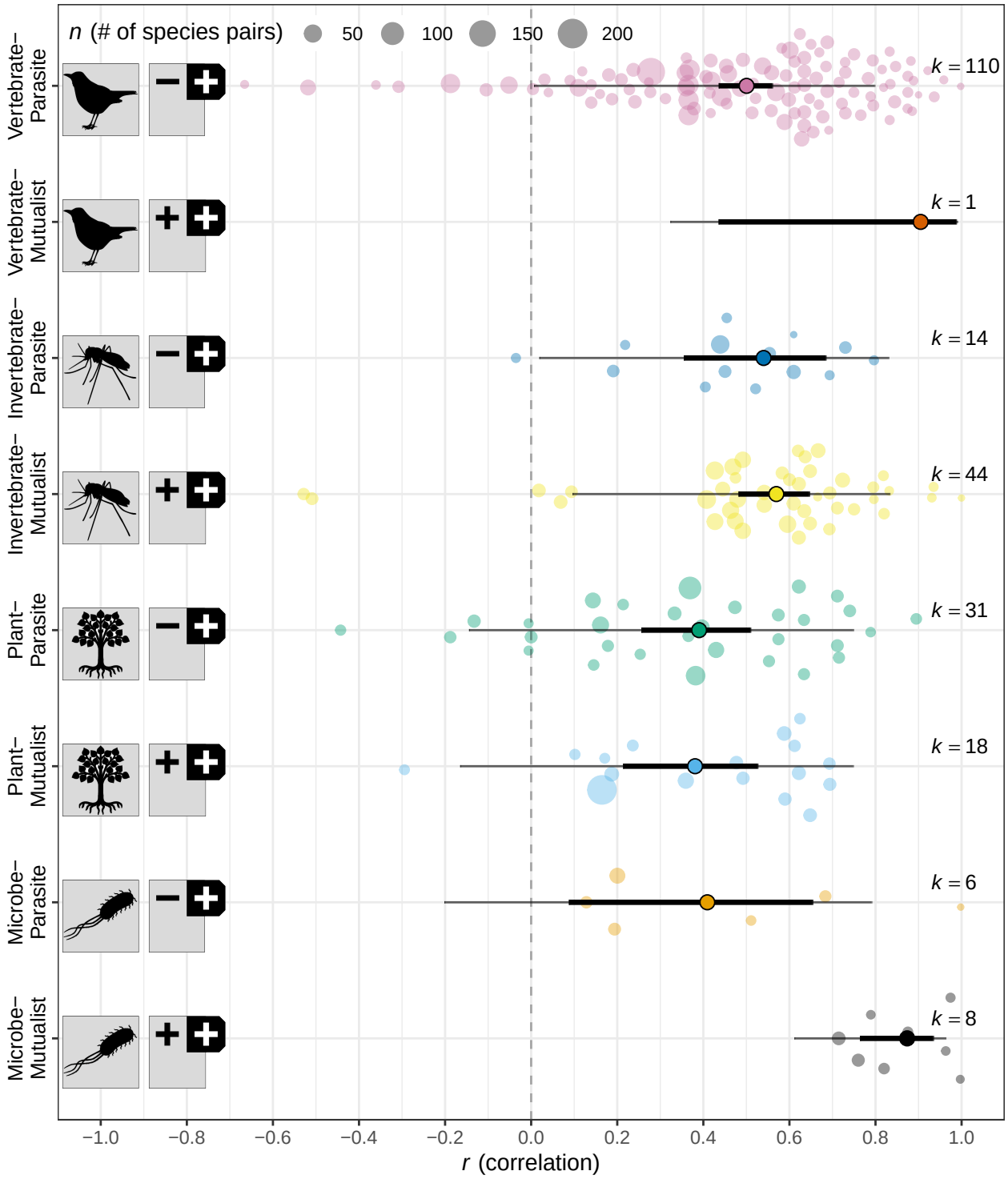
0.087

NA

NA

```
# adding sample size (k) for each category
k_host_tax_symbiosis <- dat %>% group_by(host_tax_symbiosis) %>% count()
# getting estimates and predicitons
pred_host_tax_symbiosis <- get_pred(mr_host_tax_symbiosis1, mod = "host_tax_symbiosis")
res_host_tax_symbiosis1 <- left_join(res_host_tax_symbiosis1, k_host_tax_symbiosis, by =  c("name" = "ho
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_host_tax_symbiosis <- ggplot(data = res_host_tax_symbiosis1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(host_tax_symbiosis)),
                   aes(x= tanh(Zr), y = host_tax_symbiosis, size = ((1/VZr) + 3), colour = host_tax_symb
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 0
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values =   c("MicrobeMutualist"= colour_ls[1], "MicrobeParasite"= colour_ls[2],  "M
  scale_fill_manual(values = c("MicrobeMutualist"= colour_ls[1], "MicrobeParasite"= colour_ls[2],  "Plan
  scale_y_discrete(labels = c("MicrobeMutualist"= "Microbe-\nMutualist", "MicrobeParasite"= "Microbe-\nP
  annotate('text', x = 0.93, y = 1:8 + 0.15, label= paste("italic(k)==", res_host_tax_symbiosis1$n), par
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
  # putting pictures in
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1.1, xmax = -0.9, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_parasitism),xmin = -0.9, xmax = -0.7, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_plant_host), xmin = -1.1, xmax = -0.9, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_plant_host), xmin = -1.1, xmax = -0.9, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 4.6, ymax = 5
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 4.6, ymax = 5.2) +
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 5.6, ymax = 6
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 5.6, ymax = 6.2) +
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 6.6, ymax = 7.2)
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 6.6, ymax = 7.2) +
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 7.6, ymax = 8.2)
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 7.6, ymax = 8.2)
```

```
fig_host_tax_symbiosis
```



Supplementary Figure 3: A forest plot showing group-wise means (the categorical variable `host_tax_symbiosis`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

Splitting host taxonomy by mode of symbiosis revealed that the observed higher phylogenetic congruence of host-symbiont cophylogenies involving a microbial host is driven primarily by greater congruence between

microbial hosts and mutualist symbionts. Congruence is also relatively high for invertebrate hosts that harbour a mutualistic symbiont, while congruence appears to be lowest for plant hosts that harbour a parasitic symbiont.

```
# reordering
dat$symbiont_tax_symbiosis <- factor(dat$symbiont_tax_symbiosis, levels = c("MicrobeMutualist",
    "MicrobeParasite", "PlantMutualist", "PlantParasite", "InvertMutualist", "InvertParasite",
    "VertParasite"))

# meta-regression: multiple intercepts
mr_symbiont_tax_symbiosis1 <- rma.mv(yi = Zr, V = VZr, mods = ~symbiont_tax_symbiosis -
    1, test = "t", random = ~1 | authors, data = dat)

# # meta-regression: contrasts x 10 getting the level names out
level_names <- levels(dat$symbiont_tax_symbiosis)

# helper function to run metafor meta-regression
run_rma <- function(name) {
    rma.mv(yi = Zr, V = VZr, mods = ~relevel(symbiont_tax_symbiosis, ref = name),
        test = "t", random = ~1 | authors, data = dat)
}

# results of meta-regression including all contrast results; taking the last
# level out ([-length(level_names)])
mr_symbiont_tax_symbiosis <- map(level_names[-length(level_names)], run_rma)
```

The combined effect of symbiont taxa and symbiosis (parasitism vs. mutualism) **Supplementary Table 11:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `symbiont_tax_symbiosis`.

```
# getting marginal R2
r2_symbiont_tax_symbiosis1 <- R2(mr_symbiont_tax_symbiosis1)

# getting estimates
res_symbiont_tax_symbiosis1 <- get_est(mr_symbiont_tax_symbiosis1, mod = "symbiont_tax_symbiosis")
res_symbiont_tax_symbiosis <- map(mr_symbiont_tax_symbiosis, ~get_est(.x, mod = "symbiont_tax_symbiosis

# a list of the numbers to take out unnecessary contrasts
contra_list <- Map(seq, from = 1, to = 1:6)

# you need to flatten twice: first to make it a list and make it a vector
estimates <- map2(res_symbiont_tax_symbiosis, contra_list, ~.x[-(.y), "estimate"]) %>%
    flatten() %>% flatten_dbl()
lowerCLs <- map2(res_symbiont_tax_symbiosis, contra_list, ~.x[-(.y), "lowerCL"]) %>%
    flatten() %>% flatten_dbl()
upperCLs <- map2(res_symbiont_tax_symbiosis, contra_list, ~.x[-(.y), "upperCL"]) %>%
    flatten() %>% flatten_dbl()

# creating a table
tibble(`Fixed effect` = c(as.character(res_symbiont_tax_symbiosis1$name), cont_gen(res_symbiont_tax_syml
    Estimate = c(res_symbiont_tax_symbiosis1$estimate, estimates), `Lower CI [0.025]` = c(res_symbiont_
        lowerCLs), `Upper CI  [0.975]` = c(res_symbiont_tax_symbiosis1$upperCL, upperCLs),
    `V[authors]` = c(mr_symbiont_tax_symbiosis1$sigma2, rep(NA, (7 + choose(7, 2)) -
```

```
    1)), R2 = c(r2_symbiont_tax_symbiosis1[1], rep(NA, (7 + choose(7, 2)) - 1))) %>%
  kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
  scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

MicrobeMutualist

0.687

0.570

0.804

0.082

0.357

MicrobeParasite

0.472

0.361

0.583

NA

NA

PlantMutualist

1.052

0.560

1.545

NA

NA

PlantParasite

3.453

1.404

5.503

NA

NA

InvertMutualist

0.474

0.269

0.680

NA

NA

InvertParasite

0.555

0.461

0.648

NA

NA

VertParasite

0.496

-0.157

1.149

NA

NA

MicrobeMutualist-MicrobeParasite

-0.215

-0.376

-0.054

NA

NA

MicrobeMutualist-PlantMutualist

0.366

-0.140

0.872

NA

NA

MicrobeMutualist-PlantParasite

2.766

0.713

4.820

NA

NA

MicrobeMutualist-InvertMutualist

-0.212

-0.449

0.024

NA

NA

MicrobeMutualist-InvertParasite

-0.132

-0.282

0.018

NA

NA

MicrobeMutualist-VertParasite

-0.191

-0.855

0.472

NA

NA

MicrobeParasite-PlantMutualist

0.580

0.076

1.085

NA

NA

MicrobeParasite-PlantParasite

2.981

0.928

5.034

NA

NA

MicrobeParasite-InvertMutualist

0.002

-0.231

0.236

NA

NA

MicrobeParasite-InvertParasite

0.082

-0.063

0.228

NA

NA

MicrobeParasite-VertParasite

0.023

-0.639

0.686

NA

NA

PlantMutualist-PlantParasite

2.401

0.293

4.509

NA

NA

PlantMutualist-InvertMutualist

-0.578

-1.111

-0.045

NA

NA

PlantMutualist-InvertParasite

-0.498

-0.999

0.003

NA

NA

PlantMutualist-VertParasite

-0.557

-1.375

0.261

NA

NA

PlantParasite-InvertMutualist

-2.979

-5.039

-0.919

NA

NA

PlantParasite-InvertParasite

-2.899

-4.951

-0.847

NA

NA

PlantParasite-VertParasite

-2.958

-5.109

-0.806

NA

NA

InvertMutualist-InvertParasite

0.080

-0.138

0.298

NA

NA

InvertMutualist-VertParasite

0.021

-0.663

0.706

NA

NA

InvertParasite-VertParasite

-0.059

-0.719

0.601

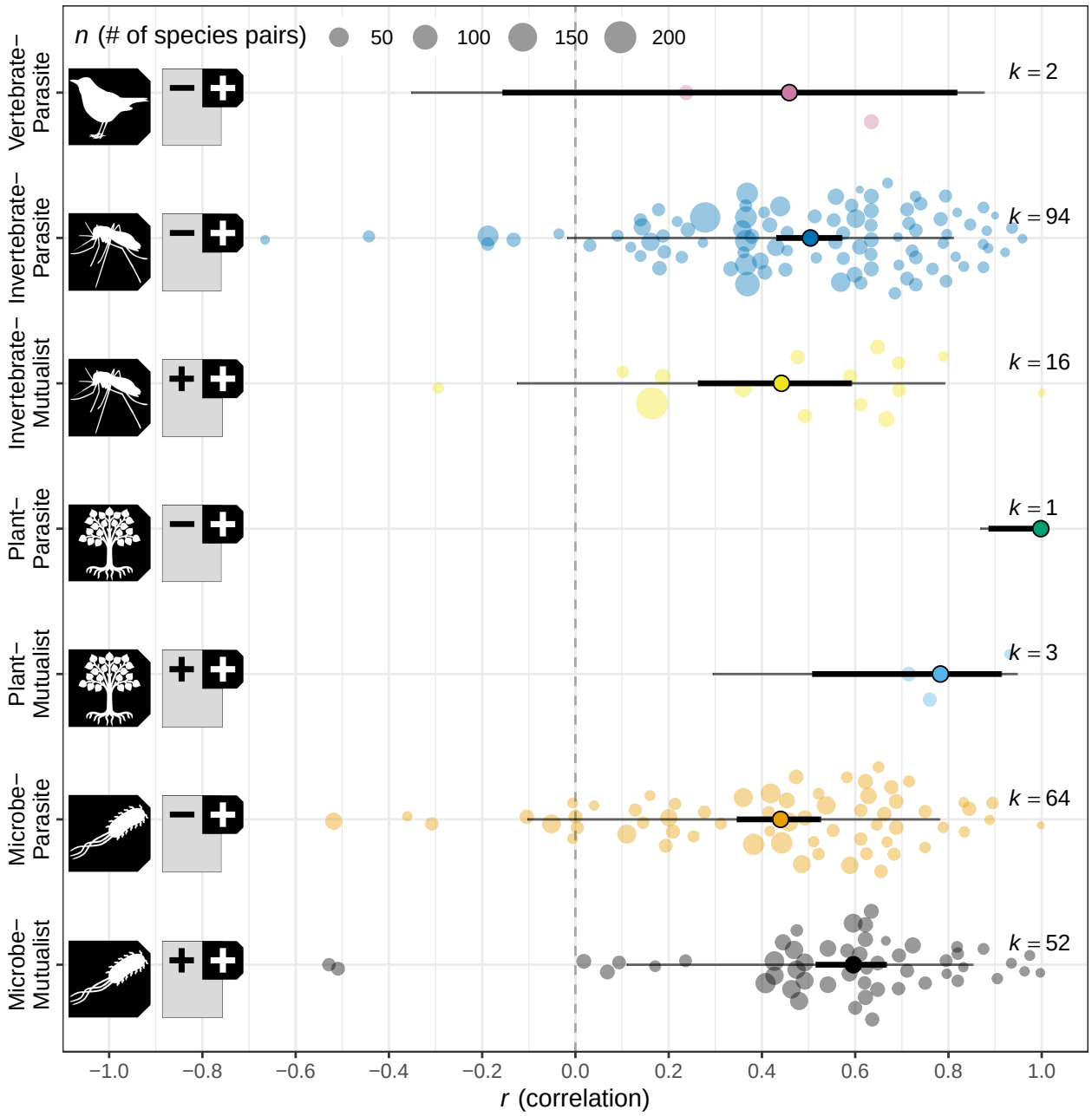
NA

NA

```
# adding sample size (k) for each category
k_symbiont_tax_symbiosis <- dat %>% group_by(symbiont_tax_symbiosis) %>% count()
# getting estimates and predicitons
pred_symbiont_tax_symbiosis <- get_pred(mr_symbiont_tax_symbiosis1, mod = "symbiont_tax_symbiosis")
```

```r
res_symbiont_tax_symbiosis1 <- left_join(res_symbiont_tax_symbiosis1, k_symbiont_tax_symbiosis, by =  c
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_symbiont_tax_symbiosis <- ggplot(data = res_symbiont_tax_symbiosis1, aes(x = tanh(estimate), y = nar
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(symbiont_tax_symbiosis)),
                   aes(x= tanh(Zr), y = symbiont_tax_symbiosis, size = ((1/VZr) + 3), colour = symbiont_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 0
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  # setting colours
  scale_color_manual(values =   c("MicrobeMutualist"= colour_ls[1], "MicrobeParasite"= colour_ls[2],  "M
  scale_fill_manual(values = c("MicrobeMutualist"= colour_ls[1], "MicrobeParasite"= colour_ls[2],  "Plan
  scale_y_discrete(labels = c("MicrobeMutualist"= "Microbe-\nMutualist", "MicrobeParasite"= "Microbe-\nP
  annotate('text', x = 0.93, y = 1:7 + 0.15, label= paste("italic(k)==", res_symbiont_tax_symbiosis1$n)
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0, 1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
    # putting pictures in
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -1.1, xmax = -0.9, ymin = 1.6, ymax = 2.2
  annotation_custom(rasterGrob(image_parasitism),xmin = -0.9, xmax = -0.7, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -1.1, xmax = -0.9, ymin = 2.6, ymax = 3.2)
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -1.1, xmax = -0.9, ymin = 3.6, ymax = 4.2)
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -1.1, xmax = -0.9, ymin = 4.6, ymax
  annotation_custom(rasterGrob(image_mutualism), xmin = -0.9, xmax = -0.7, ymin = 4.6, ymax = 5.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -1.1, xmax = -0.9, ymin = 5.6, ymax
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 5.6, ymax = 6.2) +
  annotation_custom(rasterGrob(image_vertebrate_parasite), xmin = -1.1, xmax = -0.9, ymin = 6.6, ymax =
  annotation_custom(rasterGrob(image_parasitism), xmin = -0.9, xmax = -0.7, ymin = 6.6, ymax = 7.2)

fig_symbiont_tax_symbiosis
```



Supplementary Figure 4: A forest plot showing group-wise means (the categorical variable `symbiont_tax_symbiosis`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

Splitting symbiont taxonomy by mode of symbiosis revealed much less variation, except for higher congruence exhibited by cophylogenies involving a plant symbiont (instances of which are relatively rare), and the finding that cophylogenies involving a microbial mutualist symbiont are slightly more congruent than the remaining categories.

```
# reordering
dat$host_symbiont_tax <- factor(dat$host_symbiont_tax, levels = c("MicrobeInvert",
    "MicrobeMicrobe", "MicrobePlant", "PlantInvert", "PlantMicrobe", "InvertInvert",
```

```
    "InvertMicrobe", "InvertPlant", "VertInvert", "VertMicrobe", "VertVert"))

# meta-regression: multiple intercepts
mr_host_symbiont_tax1 <- rma.mv(yi = Zr, V = VZr, mods = ~host_symbiont_tax - 1,
    test = "t", random = ~1 | authors, data = dat)

# # meta-regression: contrasts x 10 getting the level names out
level_names <- levels(dat$host_symbiont_tax)

# helper function to run metafor meta-regression
run_rma <- function(name) {
    rma.mv(yi = Zr, V = VZr, mods = ~relevel(host_symbiont_tax, ref = name), test = "t",
        random = ~1 | authors, data = dat)
}

# results of meta-regression including all contrast results; taking the last
# level out ([-length(level_names)])
mr_host_symbiont_tax <- map(level_names[-length(level_names)], run_rma)
```

The combined effect of host and symbiont taxa **Supplementary Table 12:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `host_symbiont_tax`.

```
# getting marginal R2
r2_host_symbiont_tax1 <- R2(mr_host_symbiont_tax1)

# getting estimates
res_host_symbiont_tax1 <- get_est(mr_host_symbiont_tax1, mod = "host_symbiont_tax")
res_host_symbiont_tax <- map(mr_host_symbiont_tax, ~get_est(.x, mod = "host_symbiont_tax"))

# a list of the numbers to take out unnecessary contrasts
contra_list <- Map(seq, from = 1, to = 1:10)

# you need to flatten twice: first to make it a list and make it a vector
estimates <- map2(res_host_symbiont_tax, contra_list, ~.x[-(.y), "estimate"]) %>%
    flatten() %>% flatten_dbl()

lowerCLs <- map2(res_host_symbiont_tax, contra_list, ~.x[-(.y), "lowerCL"]) %>% flatten() %>%
    flatten_dbl()

upperCLs <- map2(res_host_symbiont_tax, contra_list, ~.x[-(.y), "upperCL"]) %>% flatten() %>%
    flatten_dbl()

# creating a table
tibble(`Fixed effect` = c(as.character(res_host_symbiont_tax1$name), cont_gen(res_host_symbiont_tax1$nam
    Estimate = c(res_host_symbiont_tax1$estimate, estimates), `Lower CI [0.025]` = c(res_host_symbiont_t
        lowerCLs), `Upper CI  [0.975]` = c(res_host_symbiont_tax1$upperCL, upperCLs),
    `V[authors]` = c(mr_host_tax_symbiosis1$sigma2, rep(NA, (11 + choose(11, 2)) -
        1)), R2 = c(r2_host_symbiont_tax1[1], rep(NA, (11 + choose(11, 2)) - 1))) %>%
    kable("html", digits = 3) %>% kable_styling("striped", position = "left") %>%
    scroll_box(width = "100%", height = "300px")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

MicrobeInvert

1.069

-0.208

2.346

0.074

0.213

MicrobeMicrobe

0.842

0.547

1.137

NA

NA

MicrobePlant

1.108

0.583

1.632

NA

NA

PlantInvert

0.353

0.191

0.515

NA

NA

PlantMicrobe

0.505

0.289

0.721

NA

NA

InvertInvert

0.721

0.493

0.950

NA

NA

InvertMicrobe

0.620

0.491

0.750

NA

NA

InvertPlant

1.665

0.388

2.942

NA

NA

VertInvert

0.613

0.497

0.729

NA

NA

VertMicrobe

0.502

0.369

0.635

NA

NA

VertVert

0.496

-0.171

1.162

NA

NA

MicrobeInvert-MicrobeMicrobe

-0.227

-1.538

1.084

NA

NA

MicrobeInvert-MicrobePlant

0.039

-1.342

1.419

NA

NA

MicrobeInvert-PlantInvert

-0.716

-2.003

0.572

NA

NA

MicrobeInvert-PlantMicrobe

-0.564

-1.860

0.731

NA

NA

MicrobeInvert-InvertInvert

-0.348

-1.645

0.950

NA

NA

MicrobeInvert-InvertMicrobe

-0.449

-1.733

0.835

NA

NA

MicrobeInvert-InvertPlant

0.596

-1.210

2.402

NA

NA

MicrobeInvert-VertInvert

-0.456

-1.739

0.826

NA

NA

MicrobeInvert-VertMicrobe

-0.567

-1.851

0.717

NA

NA

MicrobeInvert-VertVert

-0.574

-2.014

0.867

NA

NA

MicrobeMicrobe-MicrobePlant

0.266

-0.336

0.868

NA

NA

MicrobeMicrobe-PlantInvert

-0.489

-0.825

-0.152

NA

NA

MicrobeMicrobe-PlantMicrobe

-0.337

-0.703

0.028

NA

NA

MicrobeMicrobe-InvertInvert

-0.121

-0.494

0.252

NA

NA

MicrobeMicrobe-InvertMicrobe

-0.222

-0.544

0.100

NA

NA

MicrobeMicrobe-InvertPlant

0.823

-0.488

2.134

NA

NA

MicrobeMicrobe-VertInvert

-0.229

-0.546

0.088

NA

NA

MicrobeMicrobe-VertMicrobe

-0.340

-0.664

-0.017

NA

NA

MicrobeMicrobe-VertVert

-0.346

-1.076

0.383

NA

NA

MicrobePlant-PlantInvert

-0.754

-1.303

-0.206

NA

NA

MicrobePlant-PlantMicrobe

-0.603

-1.170

-0.036

NA

NA

MicrobePlant-InvertInvert

-0.387

-0.959

0.186

NA

NA

MicrobePlant-InvertMicrobe

-0.487

-1.028

0.053

NA

NA

MicrobePlant-InvertPlant

0.557

-0.824

1.938

NA

NA

MicrobePlant-VertInvert

-0.495

-1.032

0.042

NA

NA

MicrobePlant-VertMicrobe

-0.606

-1.147

-0.065

NA

NA

MicrobePlant-VertVert

-0.612

-1.461

0.236

NA

NA

PlantInvert-PlantMicrobe

0.152

-0.118

0.421

NA

NA

PlantInvert-InvertInvert

0.368

0.088

0.648

NA

NA

PlantInvert-InvertMicrobe

0.267

0.060

0.474

NA

NA

PlantInvert-InvertPlant

1.312

0.024

2.599

NA

NA

PlantInvert-VertInvert

0.260

0.061

0.459

NA

NA

PlantInvert-VertMicrobe

0.148

-0.061

0.358

NA

NA

PlantInvert-VertVert

0.142

-0.544

0.828

NA

NA

PlantMicrobe-InvertInvert

0.216

-0.098

0.531

NA

NA

PlantMicrobe-InvertMicrobe

0.115

-0.136

0.367

NA

NA

PlantMicrobe-InvertPlant

1.160

-0.135

2.455

NA

NA

PlantMicrobe-VertInvert

0.108

-0.137

0.353

NA

NA

PlantMicrobe-VertMicrobe

-0.003

-0.256

0.250

NA

NA

PlantMicrobe-VertVert

-0.009

-0.710

0.692

NA

NA

InvertInvert-InvertMicrobe

-0.101

-0.364

0.162

NA

NA

InvertInvert-InvertPlant

0.944

-0.354

2.241

NA

NA

InvertInvert-VertInvert

-0.108

-0.353

0.136

NA

NA

InvertInvert-VertMicrobe

-0.219

-0.484

0.045

NA

NA

InvertInvert-VertVert

-0.226

-0.931

0.479

NA

NA

InvertMicrobe-InvertPlant

1.045

-0.239

2.328

NA

NA

InvertMicrobe-VertInvert

-0.007

-0.181

0.166

NA

NA

InvertMicrobe-VertMicrobe

-0.118

-0.304

0.067

NA

NA

InvertMicrobe-VertVert

-0.125

-0.804

0.555

NA

NA

InvertPlant-VertInvert

-1.052

-2.335

0.230

NA

NA

InvertPlant-VertMicrobe

-1.163

-2.447

0.121

NA

NA

InvertPlant-VertVert

-1.169

-2.610

0.271

NA

NA

VertInvert-VertMicrobe

-0.111

-0.287

0.065

NA

NA

VertInvert-VertVert

-0.117

-0.794

0.559

NA

NA

VertMicrobe-VertVert

-0.006

-0.686

0.674

NA

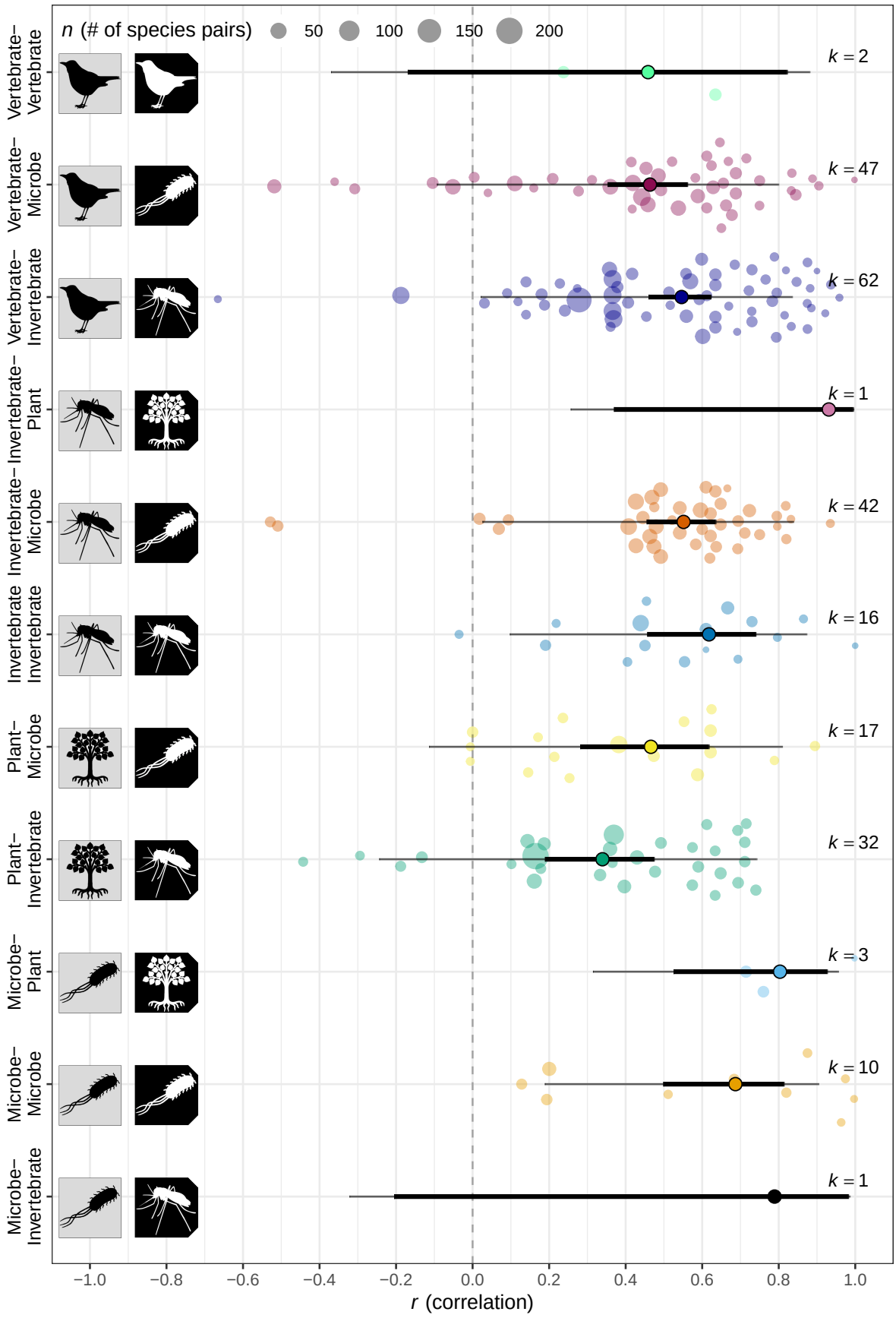
NA

```
# colour list
#colour_ls <- c("#000000", "#E69F00", "#56B4E9", "#009E73",  "#F0E422",  "#0072B2",  "#D55E00", "#CC79A

# adding sample size (k) for each category
k_host_symbiont_tax <- dat %>% group_by(host_symbiont_tax) %>% count()
# getting estimates and predicitons
pred_host_symbiont_tax <- get_pred(mr_host_symbiont_tax1, mod = "host_symbiont_tax")
res_host_symbiont_tax1 <- left_join(res_host_symbiont_tax1, k_host_symbiont_tax, by =  c("name" = "host_
#res_symbiosis1
# drawing a funnel plot - fig 2b
fig_host_symbiont_tax <- ggplot(data = res_host_symbiont_tax1, aes(x = tanh(estimate), y = name)) +
  scale_x_continuous(limits=c(-1, 1), breaks = seq(-1, 1, by = 0.2) ) +
  geom_quasirandom(data = dat %>% filter(!is.na(host_symbiont_tax)),
                   aes(x= tanh(Zr), y = host_symbiont_tax, size = ((1/VZr) + 3), colour = host_symbiont_
  # 95 %precition interval (PI)
  geom_errorbarh(aes(xmin = tanh(lowerPR), xmax = tanh(upperPR)),  height = 0, show.legend = F, size = 0
  # 95 %CI
  geom_errorbarh(aes(xmin = tanh(lowerCL), xmax = tanh(upperCL)),  height = 0, show.legend = F, size = 1
  geom_vline(xintercept = 0, linetype = 2, colour = "black", alpha = 0.3) +
  # creating dots and different size (bee-swarm and bubbles)
  geom_point(aes(fill = name), size = 3, shape = 21) + #
  # setting colours
  scale_color_manual(values =  c("MicrobeInvert" = colour_ls[1],  "MicrobeMicrobe"= colour_ls[2], "Micro
  scale_fill_manual(values = c("MicrobeInvert" = colour_ls[1],  "MicrobeMicrobe"= colour_ls[2], "Microbe
  scale_y_discrete(labels = c("MicrobeInvert" = "Microbe-\nInvertebrate",  "MicrobeMicrobe"= "Microbe-\n
  annotate('text', x = 0.93, y = 1:11 + 0.15, label= paste("italic(k)==", res_host_symbiont_tax1$n), par
  labs(x = expression(paste(italic(r), " (correlation)")), y = "", size = expression(paste(italic(n), "
  guides(fill = "none", colour = "none") +
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0,1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90)) +
    # putting pictures in
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1.1, xmax = -0.9, ymin = 0.6, ymax = 1.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -0.9, xmax = -0.7, ymin = 0.6, ymax
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1.1, xmax = -0.9, ymin = 1.6, ymax = 2.2) +
  annotation_custom(rasterGrob(image_microbe_parasite),xmin = -0.9, xmax = -0.7, ymin = 1.6, ymax = 2.2
  annotation_custom(rasterGrob(image_microbe_host), xmin = -1.1, xmax = -0.9, ymin = 2.6, ymax = 3.2) +
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -0.9, xmax = -0.7, ymin = 2.6, ymax = 3.2)
  #
  annotation_custom(rasterGrob(image_plant_host), xmin = -1.1, xmax = -0.9, ymin = 3.6, ymax = 4.2) +
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -0.9, xmax = -0.7, ymin = 3.6, ymax
  annotation_custom(rasterGrob(image_plant_host), xmin = -1.1, xmax = -0.9, ymin = 4.6, ymax = 5.2) +
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -0.9, xmax = -0.7, ymin = 4.6, ymax = 5.
  #
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 5.6, ymax = 6
```

```
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -0.9, xmax = -0.7, ymin = 5.6, ymax
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 6.6, ymax = 7
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -0.9, xmax = -0.7, ymin = 6.6, ymax = 7.1
  annotation_custom(rasterGrob(image_invertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 7.6, ymax = 8
  annotation_custom(rasterGrob(image_plant_parasite), xmin = -0.9, xmax = -0.7, ymin = 7.6, ymax = 8.2)
  #
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 8.6, ymax = 9.2)
  annotation_custom(rasterGrob(image_invertebrate_parasite), xmin = -0.9, xmax = -0.7, ymin = 8.6, ymax
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 9.6, ymax = 10.1
  annotation_custom(rasterGrob(image_microbe_parasite), xmin = -0.9, xmax = -0.7, ymin = 9.6, ymax = 10
  annotation_custom(rasterGrob(image_vertebrate_host), xmin = -1.1, xmax = -0.9, ymin = 10.6, ymax = 11
  annotation_custom(rasterGrob(image_vertebrate_parasite), xmin = -0.9, xmax = -0.7, ymin = 10.6, ymax =


fig_host_symbiont_tax
```


n (# of species pairs)
50
100
150
200
Vertebrate–Vertebrate
Vertebrate–Microbe
Vertebrate–Invertebrate
Invertebrate–Plant
Invertebrate–Microbe
Invertebrate Invertebrate
Plant–Microbe
Plant–Invertebrate
Microbe–Plant
Microbe–Microbe
Microbe–Invertebrate
k = 2
k = 47
k = 62
k = 1
k = 42
k = 16
k = 17
k = 32
k = 3
k = 10
k = 1
−1.0
−0.8
−0.6
−0.4
−0.2
0.0
0.2
0.4
0.6
0.8
1.0
r (correlation)

Supplementary Figure 4: A forest plot showing the group-wise means (the categorical variable `host_symbiont_tax`) with their 95% confidence intervals (thick lines) and 95% prediction intervals (thin lines), with observed effect sizes based on various sample sizes.

Model selection (multi-predictor model)

Here we build the best model via an AICc based model selection method implemented in the R package `MuMin`(Barton 2009). For the full model, we had 6 variables: `symbiosis`, `host_tax_broad`, `symbiont_tax_broad`, `mode_of_transmission_broad`, `endo_or_ecto`, & `log(host_range_link_ratio)`. We did not use `log(host_range_taxonomic_breadth)` as it is co-linear with `log(host_range_link_ratio)` and also many of the interaction terms.

```
# creates a new function to run in MuMIn
updated.rma.mv <- updateable(rma.mv)
# updated.rma.mv

# testing the new function use method = 'ML' so that we can compare AIC
mr_full <- updated.rma.mv(yi = Zr, V = VZr, mods = ~symbiosis + host_tax_broad +
    symbiont_tax_broad + mode_of_transmission_broad + endo_or_ecto + log(host_range_link_ratio),
    test = "t", random = ~1 | authors, method = "ML", data = dat)

# ============================== additional methods for 'rma.mv' class (made by
# Kamil Barton) we need this to run model selection with rma.mv in MuMIn
# ==============================
formula.rma.mv <- function(x, ...) return(eval(getCall(x)$mods))

makeArgs.rma.mv <- function(obj, termNames, comb, opt, ...) {
    ret <- MuMIn:::makeArgs.default(obj, termNames, comb, opt)
    names(ret)[1L] <- "mods"
    ret
}

nobs.rma.mv <- function(object, ...) attr(logLik(object), "nall")

coefTable.rma.mv <- function(model, ...) MuMIn:::.makeCoefTable(model$b, model$se,
    coefNames = rownames(model$b))
# ==============================

# testing dredge dredge(full.model, evaluate=F) # show all candidate models n =
# 32 model exisit
candidates <- dredge(mr_full)

# displays delta AICc <2
candidates_aic2 <- subset(candidates, delta < 2)

# model averaging it seems like models are using z values rather than t values
# (which will be OK)
mr_averaged_aic2 <- summary(model.avg(candidates, delta < 2))

# relative importance of each predictor
importance <- importance(candidates)

# use REML if not for model comparision
model1 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad + log(host_range_link_ratio) +
```

```
    mode_of_transmission_broad + symbiosis, test = "t", random = ~1 | authors, method = "REML",
    data = dat)
model2 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad + log(host_range_link_ratio) +
    mode_of_transmission_broad, test = "t", random = ~1 | authors, method = "REML",
    data = dat)
model3 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad + mode_of_transmission_broad +
    symbiosis, test = "t", random = ~1 | authors, method = "REML", data = dat)
model4 <- rma.mv(yi = Zr, V = VZr, mods = ~host_tax_broad + mode_of_transmission_broad,
    test = "t", random = ~1 | authors, method = "REML", data = dat)
```

Supplementary Table 13: The top 2 models (out of 32 possible models) within the ΔAIC difference of 2, and which 6 variables: `symbiosis`, `host_tax_broad`, `symbiont_tax_broad`, `mode_of_transmission_broad`, `endo_or_ecto`, & `log(host_range_link_ratio)` were included (indicated by +); model weights (for the 2 models) and the sum of weights for each of the variables (from the 32 models) are included.

```
# creating a table
tibble(`Model (variable weight)` = c("Model1", "Model2", "Model3", "Model4", "(Sum of weights)"),
    transmission = c(if_else(candidates_aic2$mode_of_transmission_broad == "+", "$+$",
        "NA"), round(importance[1], 3)), host_tax = c(if_else(candidates_aic2$host_tax_broad ==
        "+", "$+$", "NA"), round(importance[2], 3)), symbiosis = c(if_else(candidates_aic2$symbiosis ==
        "+", "$+$", "NA"), round(importance[3], 3)), host_range = c(if_else(candidates_aic2$`log(host_ra
        0, "$+$", "NA"), round(importance[4], 3)), symbiont_tax = c(if_else(candidates_aic2$symbiont_ta
        "+", "$+$", "NA"), round(importance[5], 3)), endo_or_ecto = c(if_else(candidates_aic2$endo_or_e
        "+", "$+$", "NA"), round(importance[6], 3)), delta_AICc = c(candidates_aic2$delta,
        NA), Weight = c(candidates_aic2$weight, NA)) %>% kable("html", digits = 3) %>%
    kable_styling("striped", position = "left")
```

Model (variable weight)

transmission

host_tax

symbiosis

host_range

symbiont_tax

endo_or_ecto

delta_AICc

Weight

Model1

+

+

+

+

NA

NA

0.000

0.266

Model2

+

+

NA

+

NA

NA

0.088

0.255

Model3

+

+

+

NA

NA

NA

0.114

0.252

Model4

+

+

NA

NA

NA

NA

0.321

0.227

(Sum of weights)

0.999

0.794

0.497

0.486

0.163

0.129

NA

NA

Model averaging **Supplementary Table 14:** The average estimates for regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the 2 best meta-regression models.

```
# getting averaged R2 and variance components not provided by the MuMIn package
average_sigma2 <- weighted.mean(x = c(model1$sigma2, model2$sigma2, model3$sigma2,
    model4$sigma2), w = candidates_aic2$weight)
average_R2 <- weighted.mean(x = c(R2(model1)[1], R2(model2)[1], R2(model3)[1], R2(model4)[1]),
    w = candidates_aic2$weight)

# creating a table
tibble(`Fixed effect` = c("Intercept (both-Microbe-Mutulist)", "Microbe-Plant", "Microbe-Invert",
    "Microbe-Vert", "host_range", "both-horizontal", "both-vertical", "Mutulist-Parasite"),
    Estimate = mr_averaged_aic2$coefmat.full[, 1], `Lower CI [0.025]` = mr_averaged_aic2$coefmat.full[,
        1] - mr_averaged_aic2$coefmat.full[, 2] * qnorm(0.975), `Upper CI  [0.975]` = mr_averaged_aic2$
        1] + mr_averaged_aic2$coefmat.full[, 2] * qnorm(0.975), `V[authors]` = c(average_sigma2,
        rep(NA, 7)), R2 = c(average_R2, rep(NA, 7))) %>% kable("html", digits = 3) %>%
    kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept (both-Microbe-Mutulist)

0.902

0.628

1.177

0.071

0.23

Microbe-Plant

-0.428

-0.711

-0.146

NA

NA

Microbe-Invert

-0.320

-0.601

-0.039

NA

NA

Microbe-Vert

-0.273

-0.538

-0.009

NA

NA

host_range

0.045

-0.098

0.188

NA

NA

both-horizontal

-0.076

-0.223

0.071

NA

NA

both-vertical

0.155

-0.100

0.409

NA

NA

Mutulist-Parasite

-0.037

-0.186

0.112

NA

NA

Publication Bias Analysis

Here, we conducted 3 kinds of publication bias analyses: 1) contour-enhanced funnel plots (Peters *et al.* 2008) of residuals (Egger *et al.* 1997; Nakagawa & Santos 2012), 2) a type of Egger regression (Egger *et al.* 1997; Moreno *et al.* 2009), and 3) a regression-based time-lag bias test (Nakagawa & Santos 2012).

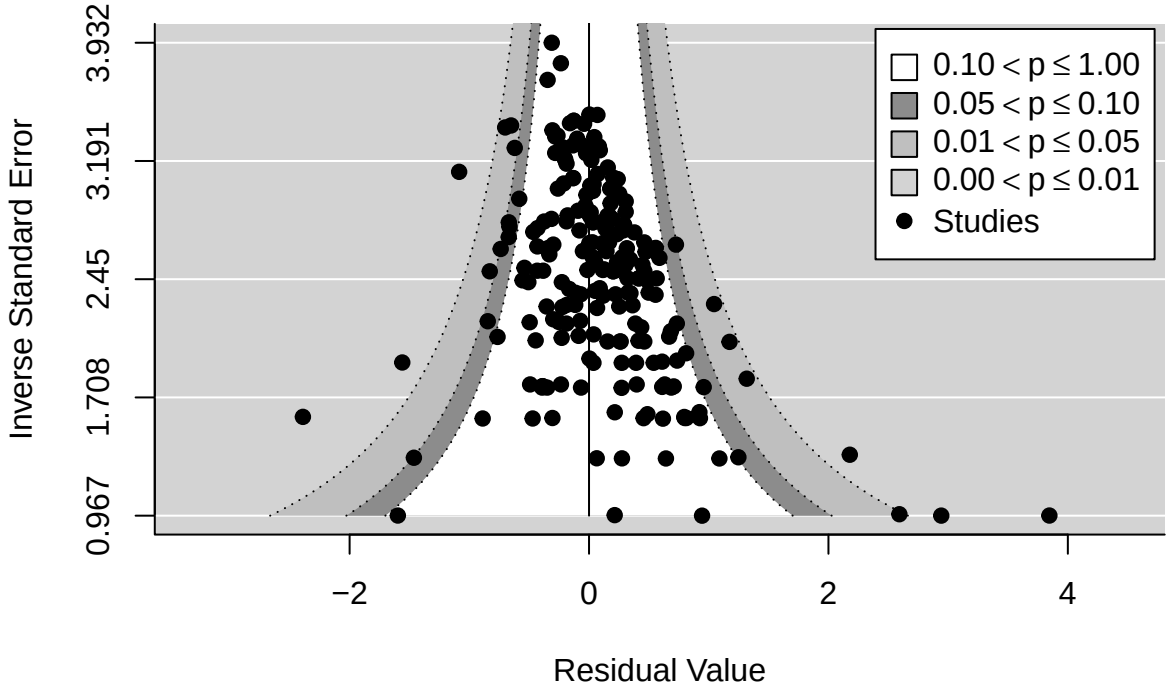
Funnel plot

A normal funnel plot assumes homogeneity (i.e., $I^2 = 0$). Therefore, we controlled for important moderators (i.e., `mode_of_transmission_broad`, `host_tax_broad`, `log(host_range_link_ratio)`, & `symbiosis`).

Residual funnel plot 1 We do not observe normal skewness in our enhanced-counter funnel plot (**Supplementary Figure 5**). This funnel asymmetry seems different from one cased by publication bias(Peters *et al.* 2008); we do not expect a "hollow" in the region with high precision or i.e. inverse standard error (2.4-4) and relative high effect sizes (Zr = 0.5-1.0). The funnel asymmetry is mainly caused by the boundary created by the number of randomizations (see the "Sensitivity Analysis" section where we deal with this skewness).

```
#
res_funnel_plot <- rma.mv(yi = Zr, V = VZr, mods = ~mode_of_transmission_broad +
    host_tax_broad + log(host_range_link_ratio) + symbiosis, random = ~1 | authors,
    data = dat)

funnel(res_funnel_plot, yaxis = "seinv", level = c(90, 95, 99), shade = c("white",
    "gray55", "gray75"), refline = 0, legend = TRUE)
```

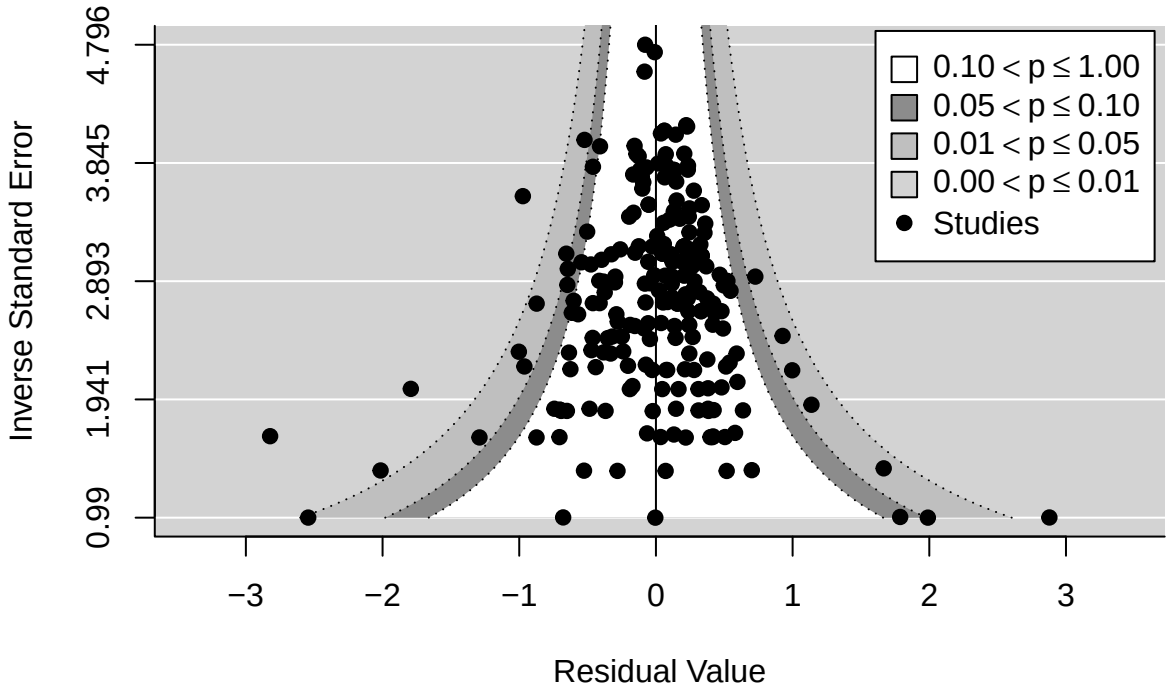


Supplementary Figure 5: A residual funnel plot from the meta-regression model with `mode_of_transmission_broad`, `host_tax_broad`, & `symbiosis`; 'residual value' is on Zr and 'inverse standard error' is precision `1/sqrt(VZr)`.

Residual funnel plot 2 Further, Egger regression analyses (see below) showed that `sqrt(VZr)` (sampling errors [SE] for effect sizes) accounts much heterogeneity, so we added that to our model. The funnel asymmetry we see in **Supplementary Figure 6** (if any) is much less severe than that in **Supplementary Figure 5**.

```
#
res_funnel_plot2 <- rma.mv(yi = Zr, V = VZr, mods = ~sqrt(VZr) + mode_of_transmission_broad +
    host_tax_broad + log(host_range_link_ratio) + symbiosis, random = ~1 | authors,
    data = dat)
```

```
funnel(res_funnel_plot2, yaxis = "seinv", level = c(90, 95, 99), shade = c("white",
    "gray55", "gray75"), refline = 0, legend = TRUE)
```



Supplementary Figure 6: A residual funnel plot from the meta-regression model with `sqrt(VZr)`, `mode_of_transmission_broad`, `host_tax_broad`, `log(host_range_link_ratio)`, & `symbiosis`; 'residual value' is on *Zr* and 'inverse standard error' is precision `1/sqrt(VZr)`.

Egger regression

We applied Egger regression to test whether the funnel asymmetries we observe in our funnel plots are statistical significant or not.

Univariate Egger regression The test (or `sqrt(VZr)`) is significant. However, as mentioned above, this is due to the boundary created by the number of randomizations; this boundary can be seen in **Supplementary Figure 7**

```
#
egger_regression_uni <- rma.mv(yi = Zr, V = VZr, mods = ~sqrt(VZr), random = ~1 |
    authors, data = dat)
```

Supplementary Table 15: Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `sqrt(VZr)`.

```
# getting marginal R2
r2_egger_regression_uni <- R2(egger_regression_uni)

# getting estimates: name does not work for slopes
res_egger_regression_uni <- get_est(egger_regression_uni, mod = "sqrt(VZr)")

# creating a table
tibble(`Fixed effect` = c("Intercept", "sqrt(VZr)"), Estimate = c(res_egger_regression_uni$estimate),
    `Lower CI [0.025]` = c(res_egger_regression_uni$lowerCL), `Upper CI  [0.975]` = c(res_egger_regressi
```

```
    `V[authors]` = c(egger_regression_uni$sigma2, NA), R2 = c(r2_egger_regression_uni[1],
        NA)) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept

0.217

0.093

0.342

0.065

0.437

sqrt(VZr)

1.294

0.874

1.715

NA

NA

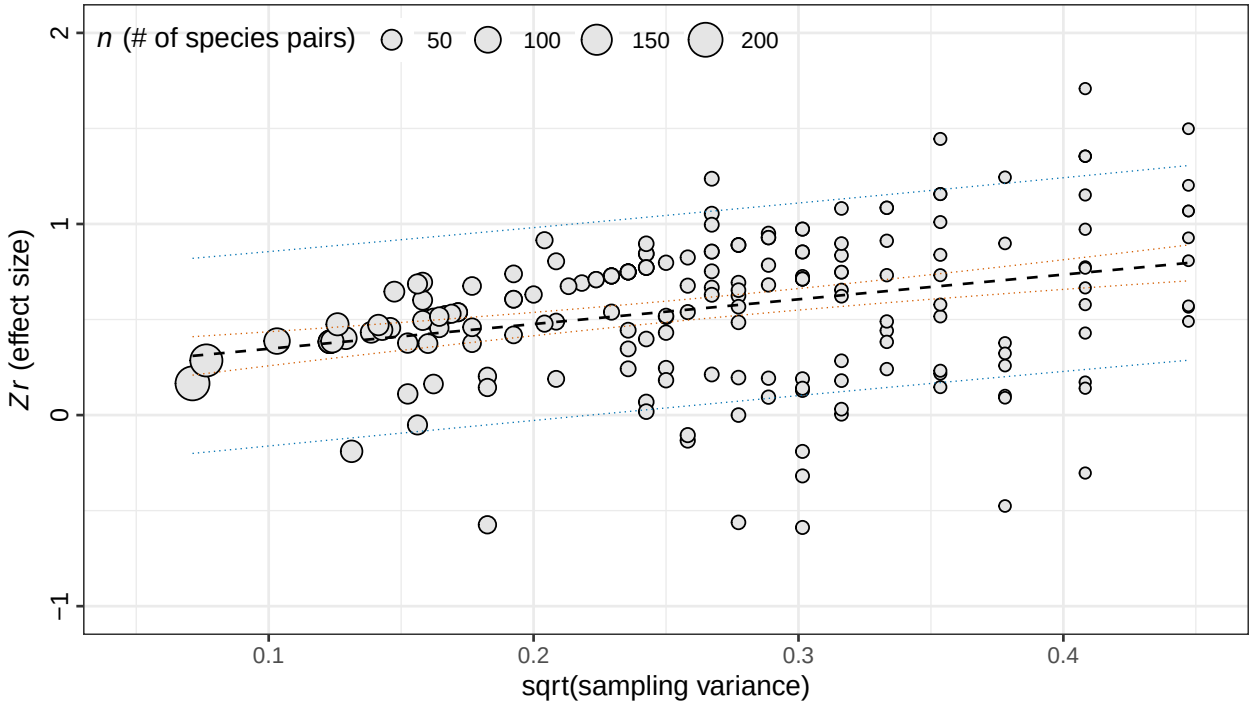
```
pred_egger_regression_uni <- predict.rma(egger_regression_uni)

# plotting

fit_egger_regression_uni <- dat %>% mutate(ymin = pred_egger_regression_uni$ci.lb,
    ymax = pred_egger_regression_uni$ci.ub, ymin2 = pred_egger_regression_uni$cr.lb,
    ymax2 = pred_egger_regression_uni$cr.ub, pred = pred_egger_regression_uni$pred) %>%
    ggplot(aes(x = sqrt(VZr), y = Zr, size = (1/VZr) + 3)) + geom_point(shape = 21,
    fill = "grey90") + # geom_ribbon(aes(ymin = ymin, ymax = ymax), fill = '#0072B2') + # not quite sur
# why this does not work
geom_smooth(aes(y = ymin2), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
    colour = "#0072B2") + geom_smooth(aes(y = ymax2), method = "loess", se = FALSE,
    lty = "dotted", lwd = 0.25, colour = "#0072B2") + geom_smooth(aes(y = ymin),
    method = "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#D55E00") +
    geom_smooth(aes(y = ymax), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
        colour = "#D55E00") + geom_smooth(aes(y = pred), method = "loess", se = FALSE,
    lty = "dashed", lwd = 0.5, colour = "black") + ylim(-1, 2) + xlim(0.05, 0.45) +
    # geom_abline(intercept = mr_host_range_link_ratio$beta[[1]], slope =
# mr_host_range_link_ratio$beta[[2]], alpha = 0.7, linetype = 'dashed', size =
# 0.5) +
labs(x = "sqrt(sampling variance)", y = expression(paste(italic(Zr), " (effect size)")),
    size = expression(paste(italic(n), " (# of species pairs)"))) + guides(fill = "none",
    colour = "none") + # themes
theme_bw() + theme(legend.position = c(0, 1), legend.justification = c(0, 1)) + theme(legend.direction =
```

```
    # theme(legend.background = element_rect(fill = 'white', colour = 'black')) +
theme(legend.background = element_blank()) + theme(axis.text.y = element_text(size = 10,
    colour = "black", hjust = 0.5, angle = 90))

fit_egger_regression_uni
```



Supplementary Figure 7: A bubble plot showing a predicted regression line for the contentious variable `sqrt(VZr)`, indicating 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines), with observed effect sizes based on various sample sizes.

Multivariate Egger regression We also conducted a Egger regression controlling other important moderators (i.e., `mode_of_transmission_broad`, `host_tax_broad`, `log(host_range_link_ratio)`, & `symbiosis`). After controlling for these variables, `sqrt(VZr)` stays significant.

```
#
egger_regression_mul <- rma.mv(yi = Zr, V = VZr, mods = ~sqrt(VZr) + mode_of_transmission_broad +
    host_tax_broad + log(host_range_link_ratio) + symbiosis, random = ~1 | authors,
    data = dat)
```

Supplementary Table 16: Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `sqrt(VZr)`.

```
# getting marginal R2
r2_egger_regression_mul <- R2(egger_regression_mul)

# creating a table
tibble(`Fixed effect` = c("Intercept (both-Microbe-Mutulist)", "sqrt(VZr)", "both-horizontal",
    "both-vertical", "Microbe-Plant", "Microbe-Invert", "Microbe-Vert", "host_range",
    "Mutulist-Parasite"), Estimate = c(egger_regression_mul$b), `Lower CI [0.025]` = c(egger_regression_
    `Upper CI  [0.975]` = c(egger_regression_mul$ci.ub), `V[authors]` = c(egger_regression_mul$sigma2,
        rep(NA, 8)), R2 = c(r2_egger_regression_mul[1], rep(NA, 8))) %>% kable("html",
    digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept (both-Microbe-Mutulist)

0.455

0.153

0.757

0.047

0.607

sqrt(VZr)

1.302

0.888

1.716

NA

NA

both-horizontal

-0.073

-0.209

0.064

NA

NA

both-vertical

0.203

-0.046

0.453

NA

NA

Microbe-Plant

-0.301

-0.568

-0.033

NA

NA

Microbe-Invert

-0.250

-0.516

0.016

NA

NA

Microbe-Vert

-0.145

-0.399

0.109

NA

NA

host_range

0.071

-0.077

0.219

NA

NA

Mutulist-Parasite

-0.076

-0.251

0.100

NA

NA

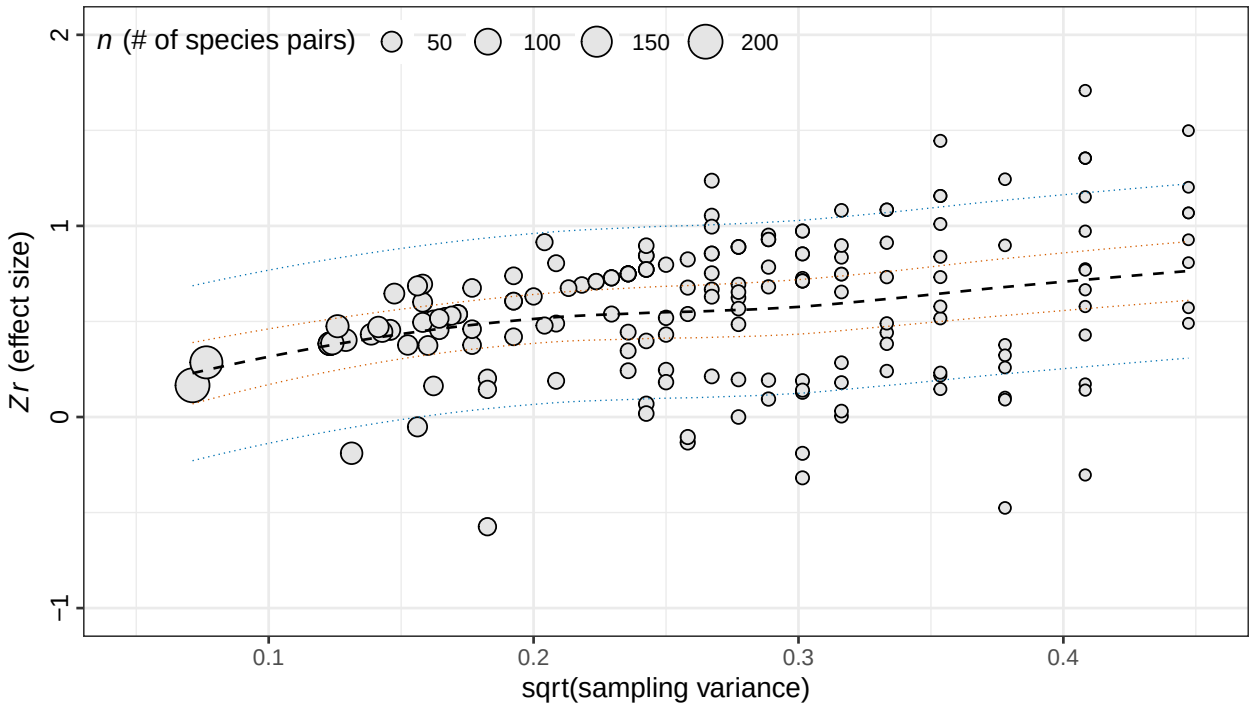
```
pred_egger_regression_mul <-predict.rma(egger_regression_mul)

# plotting

fit_egger_regression_mul <-  dat %>%
  filter(!is.na(mode_of_transmission_broad) & !is.na(host_tax_broad) & !is.na(symbiosis) & !is.na(host_
  mutate(ymin = pred_egger_regression_mul$ci.lb,
         ymax = pred_egger_regression_mul$ci.ub,
         ymin2 = pred_egger_regression_mul$cr.lb,
         ymax2 = pred_egger_regression_mul$cr.ub,
         pred = pred_egger_regression_mul$pred) %>%
  ggplot(aes(x = sqrt(VZr), y = Zr, size = (1/VZr) + 3)) +
  geom_point(shape = 21, fill = "grey90") +
  #geom_ribbon(aes(ymin = ymin, ymax = ymax), fill = "#0072B2")  + # not quite sure why this does not w
  geom_smooth(aes(y = ymin2), method =  "loess", se = FALSE, lty =  "dotted", lwd = 0.25, colour = "#007
  geom_smooth(aes(y = ymax2), method =  "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#007
  geom_smooth(aes(y = ymin), method =  "loess", se = FALSE,lty = "dotted", lwd = 0.25, colour ="#D55E00
  geom_smooth(aes(y = ymax), method =  "loess", se = FALSE, lty ="dotted", lwd = 0.25, colour ="#D55E00
```

```
  geom_smooth(aes(y = pred), method =  "loess", se = FALSE, lty ="dashed", lwd = 0.5, colour ="black") +
  ylim(-1, 2) + xlim(0.05, 0.45) +
  #geom_abline(intercept = mr_host_range_link_ratio$beta[[1]], slope = mr_host_range_link_ratio$beta[[2
  labs(x = "sqrt(sampling variance)", y = expression(paste(italic(Zr), " (effect size)")), size = expres
  guides(fill = "none", colour = "none") +
  # themes
  theme_bw() +
  theme(legend.position= c(0, 1), legend.justification = c(0, 1)) +
  theme(legend.direction="horizontal") +
  #theme(legend.background = element_rect(fill = "white", colour = "black")) +
  theme(legend.background = element_blank()) +
  theme(axis.text.y = element_text(size = 10, colour ="black", hjust = 0.5, angle = 90))

fit_egger_regression_mul
```



Supplementary Figure 8: A bubble plot showing a predicted loess line for the contentious variable `sqrt(VZr)` (given the values of the other 3 variables in the model), with their 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines) with observed effect sizes based on various sample sizes. Note that the lines are not linear as these are based on multivariate predictions of the data points.

Time-lag bias

We do not find any evidence of a time-lag effect (a decline in the magnitude of the effect over time) in either the univariate or multivariate models (**Supplementary Figure 9** and **Supplementary Figure 10**).

```
#
time_lag_effect_uni <- rma.mv(yi = Zr, V = VZr, mods = ~year, random = ~1 | authors,
    data = dat)
```

Univariate time-lag bias **Supplementary Table 17:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[marginal]}$ (R2) from the meta-regression with `year`.

```
# getting marginal R2
r2_time_lag_effect_uni <- R2(time_lag_effect_uni)

# getting estimates: name does not work for slopes
res_time_lag_effect_uni <- get_est(time_lag_effect_uni, mod = "year")

# creating a table
tibble(`Fixed effect` = c("Intercept", "Year"), Estimate = c(res_time_lag_effect_uni$estimate),
    `Lower CI [0.025]` = c(res_time_lag_effect_uni$lowerCL), `Upper CI  [0.975]` = c(res_time_lag_effec
    `V[authors]` = c(time_lag_effect_uni$sigma2, NA), R2 = c(r2_time_lag_effect_uni[1],
        NA)) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept

-4.848

-25.423

15.728

0.089

0.003

Year

0.003

-0.008

0.013

NA

NA

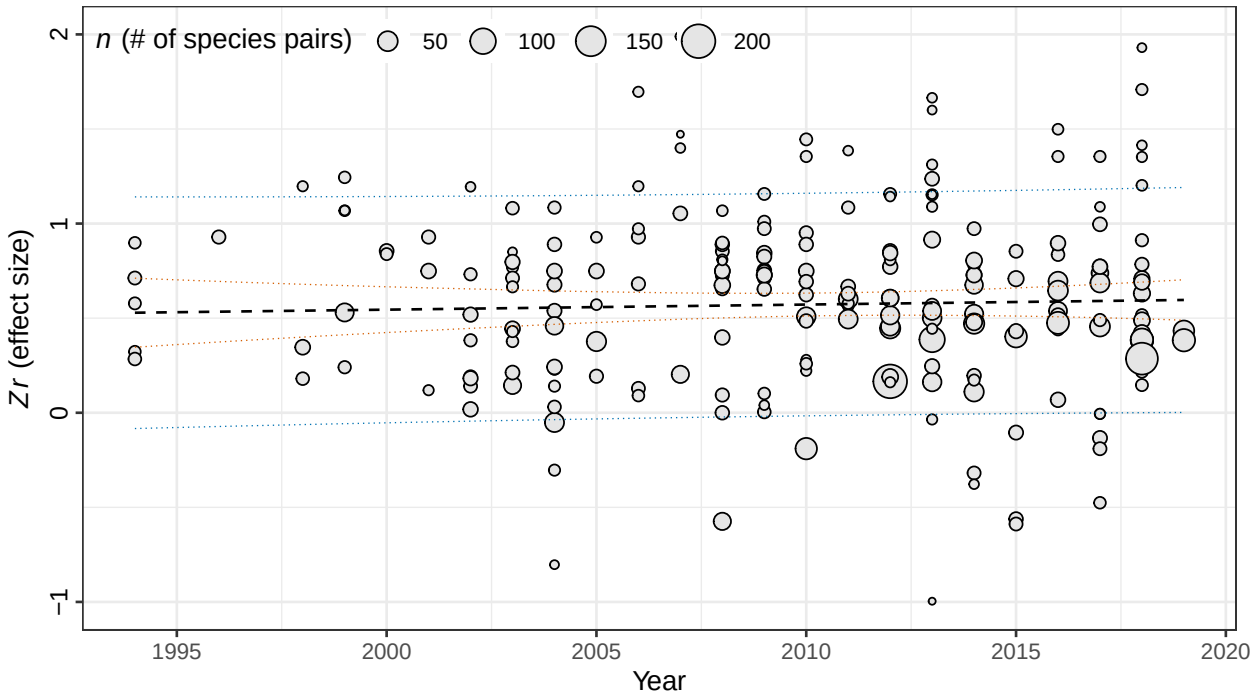
```
pred_time_lag_effect_uni <- predict.rma(time_lag_effect_uni)

# plotting

fit_time_lag_effect <- dat %>% mutate(ymin = pred_time_lag_effect_uni$ci.lb, ymax = pred_time_lag_effec
    ymin2 = pred_time_lag_effect_uni$cr.lb, ymax2 = pred_time_lag_effect_uni$cr.ub,
    pred = pred_time_lag_effect_uni$pred) %>% ggplot(aes(x = year, y = Zr, size = (1/VZr) +
    3)) + geom_point(shape = 21, fill = "grey90") + # geom_ribbon(aes(ymin = ymin, ymax = ymax), fill =
# why this does not work
geom_smooth(aes(y = ymin2), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
    colour = "#0072B2") + geom_smooth(aes(y = ymax2), method = "loess", se = FALSE,
    lty = "dotted", lwd = 0.25, colour = "#0072B2") + geom_smooth(aes(y = ymin),
```

```
    method = "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#D55E00") +
    geom_smooth(aes(y = ymax), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
        colour = "#D55E00") + geom_smooth(aes(y = pred), method = "loess", se = FALSE,
    lty = "dashed", lwd = 0.5, colour = "black") + ylim(-1, 2) + xlim(1994, 2019) +
    scale_x_continuous(breaks = c(1995, 2000, 2005, 2010, 2015, 2020)) + # geom_abline(intercept = mr_h
# mr_host_range_link_ratio$beta[[2]], alpha = 0.7, linetype = 'dashed', size =
# 0.5) +
labs(x = "Year", y = expression(paste(italic(Zr), " (effect size)")), size = expression(paste(italic(n)
    " (# of species pairs)"))) + guides(fill = "none", colour = "none") + # themses
theme_bw() + theme(legend.position = c(0, 1), legend.justification = c(0, 1)) + theme(legend.direction =
    # theme(legend.background = element_rect(fill = 'white', colour = 'black')) +
theme(legend.background = element_blank()) + theme(axis.text.y = element_text(size = 10,
    colour = "black", hjust = 0.5, angle = 90))

fit_time_lag_effect
```



Supplementary Figure 9: A bubble plot showing a predicted regression line for the contentious variable `year`, indicating 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines), with observed effect sizes based on various sample sizes.

```
#
time_lag_effect_mul <- rma.mv(yi = Zr, V = VZr, mods = ~year + mode_of_transmission_broad +
    host_tax_broad + log(host_range_link_ratio) + symbiosis, random = ~1 | authors,
    data = dat)
```

Multivariate time-lag bias **Supplementary Table 18:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the meta-regression with `year`.

```
# getting marginal R2
r2_time_lag_effect_mul <- R2(time_lag_effect_mul)
```

```r
# creating a table
tibble(`Fixed effect` = c("Intercept (both-Microbe-Mutulist)", "Year", "both-horizontal",
    "both-vertical", "Microbe-Plant", "Microbe-Invert", "Microbe-Vert", "host_range",
    "Mutulist-Parasite"), Estimate = c(time_lag_effect_mul$b), `Lower CI [0.025]` = c(time_lag_effect_mu
    `Upper CI  [0.975]` = c(time_lag_effect_mul$ci.ub), `V[authors]` = c(time_lag_effect_mul$sigma2,
        rep(NA, 8)), R2 = c(r2_time_lag_effect_mul[1], rep(NA, 8))) %>% kable("html",
    digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Intercept (both-Microbe-Mutulist)

1.863

-18.349

22.075

0.073

0.234

Year

0.000

-0.011

0.010

NA

NA

both-horizontal

-0.075

-0.228

0.079

NA

NA

both-vertical

0.140

-0.135

0.416

NA

NA

Microbe-Plant

-0.455

-0.748

-0.163

NA

NA

Microbe-Invert

-0.330

-0.619

-0.041

NA

NA

Microbe-Vert

-0.276

-0.552

0.000

NA

NA

host_range

0.095

-0.073

0.262

NA

NA

Mutulist-Parasite

-0.069

-0.260

0.123

NA

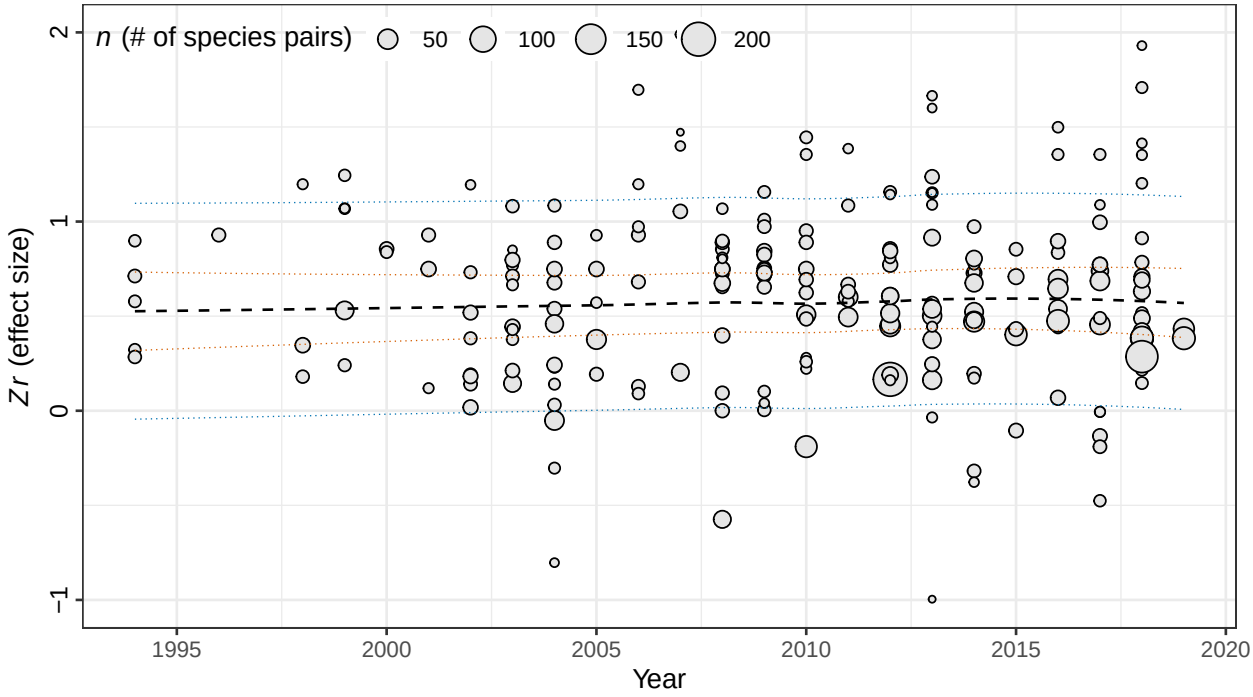
NA

```
pred_time_lag_effect_mul <- predict.rma(time_lag_effect_mul)

# plotting
fit_time_lag_effect_mul <- dat %>% filter(!is.na(mode_of_transmission_broad) & !is.na(host_tax_broad) &
    !is.na(symbiosis) & !is.na(host_range_link_ratio)) %>% mutate(ymin = pred_time_lag_effect_mul$ci.lb
    ymax = pred_time_lag_effect_mul$ci.ub, ymin2 = pred_time_lag_effect_mul$cr.lb,
    ymax2 = pred_time_lag_effect_mul$cr.ub, pred = pred_time_lag_effect_mul$pred) %>%
    ggplot(aes(x = year, y = Zr, size = (1/VZr) + 3)) + geom_point(shape = 21, fill = "grey90") +
    # geom_ribbon(aes(ymin = ymin, ymax = ymax), fill = '#0072B2') + # not quite sure
```

```
# why this does not work
geom_smooth(aes(y = ymin2), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
    colour = "#0072B2") + geom_smooth(aes(y = ymax2), method = "loess", se = FALSE,
    lty = "dotted", lwd = 0.25, colour = "#0072B2") + geom_smooth(aes(y = ymin),
    method = "loess", se = FALSE, lty = "dotted", lwd = 0.25, colour = "#D55E00") +
    geom_smooth(aes(y = ymax), method = "loess", se = FALSE, lty = "dotted", lwd = 0.25,
        colour = "#D55E00") + geom_smooth(aes(y = pred), method = "loess", se = FALSE,
    lty = "dashed", lwd = 0.5, colour = "black") + ylim(-1, 2) + xlim(1994, 2019) +
    scale_x_continuous(breaks = c(1995, 2000, 2005, 2010, 2015, 2020)) + # geom_abline(intercept = mr_h
# mr_host_range_link_ratio$beta[[2]], alpha = 0.7, linetype = 'dashed', size =
# 0.5) +
labs(x = "Year", y = expression(paste(italic(Zr), " (effect size)")), size = expression(paste(italic(n)
    " (# of species pairs)"))) + guides(fill = "none", colour = "none") + # themses
theme_bw() + theme(legend.position = c(0, 1), legend.justification = c(0, 1)) + theme(legend.direction =
    # theme(legend.background = element_rect(fill = 'white', colour = 'black')) +
theme(legend.background = element_blank()) + theme(axis.text.y = element_text(size = 10,
    colour = "black", hjust = 0.5, angle = 90))

fit_time_lag_effect_mul
```



Supplementary Figure 10: A bubble plot showing a predicted loess line for the contentious variable `year` (given the values of the other 3 variables in the model), indicating 95% confidence regions (orange dotted lines) and 95% prediction regions (blue dotted lines) with observed effect sizes based on various sample sizes. Note that the lines are not linear as these are based on multivariate predictions of the data points.

Sensitivity Analysis

The funnel plots above identified the issue of upper bounds for the effect size given a sample size (an upper limit of a p value given the number of randomizations). This boundary would influence our estimates of mean effect sizes and contrasts (i.e., comparing two groups), often making our overall conclusions too conservative. To demonstrate this, we conducted two analyses to show: 1) the number of randomizations

(log(no_randomizations)) do not differ between categories in the 3 important categorical moderators (mode_of_transmission_broad, host_tax_broad, & symbiosis), and, 2) categories with high effect sizes would include "bounded" effect sizes (i.e., from $p = 0.01$, 0.001, or 0.0001; limit_reached) in the 3 moderators.

Sensitivity test 1: the number of randomizations

Below, we showed that none of categorizes have significantly different numbers of randomizations in all mode_of_transmission_broad, host_tax_broad, & symbiosis.

```
# 233 --- Yes = 74 (0.3175966%); No = 159

# symbiosis multiple intercepts
sa_random_symbiosis1 <- lmer(log(no_randomizations) ~ symbiosis - 1 + (1 | authors),
    data = dat)
# contrast
sa_random_symbiosis2 <- lmer(log(no_randomizations) ~ symbiosis + (1 | authors),
    data = dat)
```

The type of symbiosis: parasitism vs. mutualism **Supplementary Table 19:** Regression coefficients (Estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[marginal]}$ (R2), from the regression with symbiosis on log(no_randomizations).

```
# getting marginal R2
r2_sa_random_symbiosis <- r2_nakagawa(sa_random_symbiosis1)

# getting estimates

res_sa_random_symbiosis <- tibble(estiamte = c(fixef(sa_random_symbiosis1), fixef(sa_random_symbiosis2)

ci_sa_random_symbiosis1 <- confint(sa_random_symbiosis1)
ci_sa_random_symbiosis2 <- confint(sa_random_symbiosis2)
res_sa_random_symbiosis %<>% mutate(lowerCL = c(ci_sa_random_symbiosis1[3:4, 1],
    ci_sa_random_symbiosis2[4, 1]))
res_sa_random_symbiosis %<>% mutate(upperCL = c(ci_sa_random_symbiosis1[3:4, 2],
    ci_sa_random_symbiosis2[4, 2]))

# creating a table
tibble(`Fixed effect` = c(as.character(res_symbiosis1$name), cont_gen(res_symbiosis1$name)),
    Estimate = res_sa_random_symbiosis$estiamte, `Lower CI [0.025]` = res_sa_random_symbiosis$lowerCL,
    `Upper CI  [0.975]` = res_sa_random_symbiosis$upperCL, `V[authors]` = c(attr(VarCorr(sa_random_symbi
        "stddev")^2, rep(NA, 2)), `V[residuals]` = c(attr(VarCorr(sa_random_symbiosis1),
        "sc")^2, rep(NA, 2)), R2 = c(r2_sa_random_symbiosis$R2_marginal, rep(NA,
        2))) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

V[residuals]

R2

Mutualist

7.696

7.286

8.106

2.931

0.352

0.004

Parasite

7.619

7.314

7.924

NA

NA

NA

Mutualist-Parasite

-0.077

-0.544

0.389

NA

NA

NA

```
# host_tax_broad mutiple intercepts
sa_random_host_tax_broad1 <- lmer(log(no_randomizations) ~ host_tax_broad - 1 + (1 |
    authors), data = dat)
# contrast 1
sa_random_host_tax_broad2 <- lmer(log(no_randomizations) ~ host_tax_broad + (1 |
    authors), data = dat)
# contrast 2
sa_random_host_tax_broad3 <- lmer(log(no_randomizations) ~ relevel(host_tax_broad,
    ref = "Plant") + (1 | authors), data = dat)

# contrast 3
sa_random_host_tax_broad4 <- lmer(log(no_randomizations) ~ relevel(host_tax_broad,
    ref = "Invert") + (1 | authors), data = dat)
```

The effect of host taxa **Supplementary Table 20:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the regression with `host_tax_broad` on `log(no_randomizations)`.

```r
# getting marginal R2
r2_sa_random_host_tax_broad <- r2_nakagawa(sa_random_host_tax_broad1)

# getting estimates
res_sa_random_host_tax_broad <- tibble(estiamte = c(fixef(sa_random_host_tax_broad1),
                                                    fixef(sa_random_host_tax_broad2)[2:4],
                                                    fixef(sa_random_host_tax_broad3)[3:4],
                                                    fixef(sa_random_host_tax_broad4)[4]))

ci_sa_random_host_tax_broad1<-confint(sa_random_host_tax_broad1)
ci_sa_random_host_tax_broad2<-confint(sa_random_host_tax_broad2)
ci_sa_random_host_tax_broad3<-confint(sa_random_host_tax_broad3)
ci_sa_random_host_tax_broad4<-confint(sa_random_host_tax_broad4)
res_sa_random_host_tax_broad %<>% mutate(lowerCL = c(ci_sa_random_host_tax_broad1[3:6,1],
                                                     ci_sa_random_host_tax_broad2[4:6,1],
                                                     ci_sa_random_host_tax_broad3[5:6,1],
                                                     ci_sa_random_host_tax_broad4[6,1]))
res_sa_random_host_tax_broad %<>% mutate(upperCL = c(ci_sa_random_host_tax_broad1[3:6,2],
                                                     ci_sa_random_host_tax_broad2[4:6,2],
                                                     ci_sa_random_host_tax_broad3[5:6,2],
                                                     ci_sa_random_host_tax_broad4[6,2]))
# creating a table
tibble(
  `Fixed effect` =  c(as.character(res_symbiont_tax_broad1$name), cont_gen(res_symbiont_tax_broad1$name)
  Estimate = res_sa_random_host_tax_broad$estiamte,
  `Lower CI [0.025]` = res_sa_random_host_tax_broad$lowerCL,
  `Upper CI  [0.975]` = res_sa_random_host_tax_broad$upperCL,
  `V[authors]` = c(attr(VarCorr(sa_random_host_tax_broad1)$author,"stddev")^2,  rep(NA, 9)),
  `V[residuals]` =c(attr(VarCorr(sa_random_host_tax_broad1),"sc")^2, rep(NA, 9)),
  `R2` = c(r2_sa_random_host_tax_broad$R2_marginal, rep(NA, 9))) %>% kable("html", digits = 3) %>%
  kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

V[residuals]

R2

Microbe

8.223

7.279

9.168

2.937

0.35

0.071

Plant

7.466

6.856

8.076

NA

NA

NA

Invert

7.650

7.167

8.134

NA

NA

NA

Vert

7.634

7.265

8.003

NA

NA

NA

Microbe-Plant

-0.757

-1.882

0.367

NA

NA

NA

Microbe-Invert

-0.573

-1.634

0.488

NA

NA

NA

Microbe-Vert

-0.589

-1.603

0.425

NA

NA

NA

Plant-Invert

0.184

-0.594

0.962

NA

NA

NA

Plant-Vert

0.168

-0.545

0.881

NA

NA

NA

Invert-Vert

-0.016

-0.599

0.566

NA

NA

NA

```
# mode_of_transmission_broad

sa_random_mode_of_transmission_broad1 <- lmer(log(no_randomizations) ~ mode_of_transmission_broad -
    1 + (1 | authors), data = dat)


# contrast 1
sa_random_mode_of_transmission_broad2 <- lmer(log(no_randomizations) ~ mode_of_transmission_broad +
    (1 | authors), data = dat)

# contrast 2
sa_random_mode_of_transmission_broad3 <- lmer(log(no_randomizations) ~ relevel(mode_of_transmission_broa
    ref = "vertical") + (1 | authors), data = dat)
```

The effect of the model of transmission **Supplementary Table 21:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the regression with `mode_of_transmission_broad` on `log(no_randomizations)`.

```
# getting marginal R2
r2_sa_random_mode_of_transmission_broad <- r2_nakagawa(sa_random_mode_of_transmission_broad1)

# getting estimates
res_sa_random_mode_of_transmission_broad <- tibble(estiamte = c(fixef(sa_random_mode_of_transmission_br
    fixef(sa_random_mode_of_transmission_broad2)[2:3], fixef(sa_random_mode_of_transmission_broad3)[3]))

ci_sa_random_mode_of_transmission_broad1 <- confint(sa_random_mode_of_transmission_broad1)
ci_sa_random_mode_of_transmission_broad2 <- confint(sa_random_mode_of_transmission_broad2)
ci_sa_random_mode_of_transmission_broad3 <- confint(sa_random_mode_of_transmission_broad3)
res_sa_random_mode_of_transmission_broad %<>% mutate(lowerCL = c(ci_sa_random_mode_of_transmission_broa
    1], ci_sa_random_mode_of_transmission_broad2[4:5, 1], ci_sa_random_mode_of_transmission_broad3[5,
    1]))
res_sa_random_mode_of_transmission_broad %<>% mutate(upperCL = c(ci_sa_random_mode_of_transmission_broa
    2], ci_sa_random_mode_of_transmission_broad2[4:5, 2], ci_sa_random_mode_of_transmission_broad3[5,
    2]))
# creating a table
tibble(`Fixed effect` = c(as.character(res_mode_of_transmission_broad1$name), cont_gen(res_mode_of_trans
    Estimate = res_sa_random_mode_of_transmission_broad$estiamte, `Lower CI [0.025]` = res_sa_random_mo
    `Upper CI  [0.975]` = res_sa_random_mode_of_transmission_broad$upperCL, `V[authors]` = c(attr(VarCo
        "stddev")^2, rep(NA, 5)), `V[residuals]` = c(attr(VarCorr(sa_random_mode_of_transmission_broad1
        "sc")^2, rep(NA, 5)), R2 = c(r2_sa_random_mode_of_transmission_broad$R2_marginal,
        rep(NA, 5))) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

V[residuals]

R2

both

7.535

6.978

8.091

2.913

0.363

0.12

horizontal

7.515

7.164

7.866

NA

NA

NA

vertical

8.089

7.509

8.668

NA

NA

NA

both-horizontal

-0.020

-0.678

0.638

NA

NA

NA

both-vertical

0.554

-0.250

1.357

NA

NA

NA

horizontal-vertical

-0.574

-1.251

0.104

NA

NA

NA

Sensitivity test 2: reaching the limits

Below, we show that categories with higher effect sizes were more likely to have "bounded" effect sizes (`limit_reached`) in all `mode_of_transmission_broad`, `host_tax_broad`, & `symbiosis`. This indicates that the higher the estimate of mean effect size is, the more underestimated the mean effect size is. This is true

for differences between two categories; the larger the difference between two, the more underestimated the difference is.

The type of symbiosis: parasitism vs. mutualism **Supplementary Table 22:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[marginal]}$ (R2) from the regression with `symbiosis` on `limit_reached` (compare the effect estimates in **Supplementary Table 2** with the corresponding values in this table).

```
# symbiosis
sa_limit_symbiosis1 <- glmer(limit_reached ~ symbiosis - 1 + (1 | authors), family = "binomial",
    data = dat)

# getting marginal R2
r2_sa_limit_symbiosis <- r2_nakagawa(sa_limit_symbiosis1)

# getting estimates
res_sa_limit_symbiosis <- tibble(estiamte = fixef(sa_limit_symbiosis1))

res_sa_limit_symbiosis %<>% mutate(lowerCL = (tidy(sa_limit_symbiosis1)$estimate[-3] -
    tidy(sa_limit_symbiosis1)$std.error[-3] * qnorm(0.975)))
res_sa_limit_symbiosis %<>% mutate(upperCL = (tidy(sa_limit_symbiosis1)$estimate[-3] +
    tidy(sa_limit_symbiosis1)$std.error[-3] * qnorm(0.975)))
# creating a table
tibble(`Fixed effect` = as.character(res_symbiosis1$name), Estimate = res_sa_limit_symbiosis$estiamte,
    `Lower CI [0.025]` = res_sa_limit_symbiosis$lowerCL, `Upper CI  [0.975]` = res_sa_limit_symbiosis$u
    `V[authors]` = c(attr(VarCorr(sa_limit_symbiosis1)$author, "stddev")^2, rep(NA,
        1)), R2 = c(r2_sa_limit_symbiosis$R2_marginal, rep(NA, 1))) %>% kable("html",
    digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Mutualist

-0.401

-1.074

0.272

1.657

0.051

Parasite

-1.309

-2.015

-0.603

NA

NA

The effect of host taxa **Supplementary Table 23:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the regression with `host_tax_broad` on `limit_reached` (compare the effect estimates in **Supplementary Table 3** with the corresponding values in this table).

```
# host_tax_broad
sa_limit_host_tax_broad1 <- glmer(limit_reached ~ host_tax_broad - 1 + (1 | authors),
    family = "binomial", data = dat)

# getting marginal R2
r2_sa_limit_host_tax_broad <- r2_nakagawa(sa_limit_host_tax_broad1)

# getting estimates
res_sa_limit_host_tax_broad <- tibble(estiamte = fixef(sa_limit_host_tax_broad1))

res_sa_limit_host_tax_broad %<>% mutate(lowerCL = (tidy(sa_limit_host_tax_broad1)$estimate[-5] -
    tidy(sa_limit_host_tax_broad1)$std.error[-5] * qnorm(0.975)))
res_sa_limit_host_tax_broad %<>% mutate(upperCL = (tidy(sa_limit_host_tax_broad1)$estimate[-5] +
    tidy(sa_limit_host_tax_broad1)$std.error[-5] * qnorm(0.975)))
# creating a table
tibble(`Fixed effect` = as.character(res_symbiont_tax_broad1$name), Estimate = res_sa_limit_host_tax_br
    `Lower CI [0.025]` = res_sa_limit_host_tax_broad$lowerCL, `Upper CI  [0.975]` = res_sa_limit_host_ta
    `V[authors]` = c(attr(VarCorr(sa_limit_host_tax_broad1)$author, "stddev")^2,
        rep(NA, 3)), R2 = c(r2_sa_limit_host_tax_broad$R2_marginal, rep(NA, 3))) %>%
    kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

Microbe

-1.211

-2.737

0.316

1.358

0.035

Plant

-1.574

-2.571

-0.578

NA

NA

Invert

-0.579

-1.308

0.150

NA

NA

Vert

-0.937

-1.588

-0.286

NA

NA

The effect of the model of transmission **Supplementary Table 24:** Regression coefficients (estimate), 95% confidence intervals (CIs), variance components (V) and variance explained, $R^2_{[\text{marginal}]}$ (R2) from the regression with `mode_of_transmission_broad` on `limit_reached` (compare the effect estimates in **Supplementary Table 8** with the corresponding values in this table).

```
# mode_of_transmission_broad
sa_limit_mode_of_transmission_broad1 <- glmer(limit_reached ~ mode_of_transmission_broad -
    1 + (1 | authors), family = "binomial", data = dat)

# getting marginal R2
r2_sa_limit_mode_of_transmission_broad <- r2_nakagawa(sa_limit_mode_of_transmission_broad1)

# getting estimates
res_sa_limit_mode_of_transmission_broad <- tibble(estiamte = fixef(sa_limit_mode_of_transmission_broad1)

res_sa_limit_mode_of_transmission_broad %<>% mutate(lowerCL = (tidy(sa_limit_mode_of_transmission_broad
    tidy(sa_limit_mode_of_transmission_broad1)$std.error[-4] * qnorm(0.975)))
res_sa_limit_mode_of_transmission_broad %<>% mutate(upperCL = (tidy(sa_limit_mode_of_transmission_broad
    tidy(sa_limit_mode_of_transmission_broad1)$std.error[-4] * qnorm(0.975)))
# creating a table
tibble(`Fixed effect` = as.character(res_mode_of_transmission_broad1$name), Estimate = res_sa_limit_mode
    `Lower CI [0.025]` = res_sa_limit_mode_of_transmission_broad$lowerCL, `Upper CI  [0.975]` = res_sa_l
    `V[authors]` = c(attr(VarCorr(sa_limit_mode_of_transmission_broad1)$author, "stddev")^2,
        rep(NA, 2)), R2 = c(r2_sa_limit_mode_of_transmission_broad$R2_marginal, rep(NA,
        2))) %>% kable("html", digits = 3) %>% kable_styling("striped", position = "left")
```

Fixed effect

Estimate

Lower CI [0.025]

Upper CI [0.975]

V[authors]

R2

both

-0.928

-1.809

-0.046

1.427

0.078

horizontal

-1.326

-2.031

-0.621

NA

NA

vertical

0.060

-0.750

0.869

NA

NA

Recommendations based on our sensitivity analysis

We have 3 recommendations for future (and past) co-divergence work using TreeMap and ParaFit.

- Researchers need to set the number of randomizations much higher to obtain more accurate p values.
- If possible, the reanalysis of earlier trees would be informative; also, analyses using updated trees is desirable.
- New studies should provide all data available online (including phylogenies in tree format), so that future meta-analyses can incorporate all available data.

Acknowledgements

Many coding materials have been borrowed from these papers (Cally *et al.* 2019; O'Dea *et al.* 2019). We thank Losia Lagisz for preparing small icons and cartoons used in the figures.

R Session Information

```
# pander for making it look nicer
sessionInfo() %>% pander()
```

R version 4.0.3 (2020-10-10)

Platform: x86_64-apple-darwin17.0 (64-bit)

locale: en_AU.UTF-8||en_AU.UTF-8||en_AU.UTF-8||C||en_AU.UTF-8||en_AU.UTF-8

attached base packages: *grid*, *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *here(v.0.1)*, *patchwork(v.1.0.1)*, *png(v.0.1-7)*, *performance(v.0.5.0)*, *broom.mixed(v.0.2.6)*, *lme4(v.1.1-23)*, *MuMIn(v.1.43.17)*, *plotly(v.4.9.2.1)*, *ggbeeswarm(v.0.6.0)*, *MCMCglmm(v.2.29)*, *ape(v.5.4-1)*, *coda(v.0.19-4)*, *metafor(v.2.4-0)*, *Matrix(v.1.2-18)*, *pander(v.0.6.3)*, *magrittr(v.2.0.1)*, *gridExtra(v.2.3)*, *kableExtra(v.1.2.1)*, *forcats(v.0.5.0)*, *stringr(v.1.4.0)*, *dplyr(v.1.0.2)*, *purrr(v.0.3.4)*, *readr(v.1.4.0)*, *tidyr(v.1.1.2)*, *tibble(v.3.0.4)*, *ggplot2(v.3.3.2)* and *tidyverse(v.1.3.0)*

loaded via a namespace (and not attached): *nlme(v.3.1-149)*, *fs(v.1.5.0)*, *lubridate(v.1.7.9.2)*, *insight(v.0.9.6)*, *webshot(v.0.5.2)*, *httr(v.1.4.2)*, *rprojroot(v.2.0.2)*, *tensorA(v.0.36.2)*, *tools(v.4.0.3)*, *TMB(v.1.7.18)*, *backports(v.1.2.0)*, *R6(v.2.5.0)*, *vipor(v.0.4.5)*, *mgcv(v.1.8-33)*, *DBI(v.1.1.0)*, *lazyeval(v.0.2.2)*, *colorspace(v.2.0-0)*, *withr(v.2.3.0)*, *tidyselect(v.1.1.0)*, *compiler(v.4.0.3)*, *cli(v.2.2.0)*, *rvest(v.0.3.6)*, *formatR(v.1.7)*, *pacman(v.0.5.1)*, *xml2(v.1.3.2)*, *labeling(v.0.4.2)*, *bayestestR(v.0.7.2)*, *scales(v.1.1.1)*, *digest(v.0.6.27)*, *minqa(v.1.2.4)*, *rmarkdown(v.2.5)*, *pkgconfig(v.2.0.3)*, *htmltools(v.0.5.0)*, *highr(v.0.8)*, *dbplyr(v.2.0.0)*, *htmlwidgets(v.1.5.1)*, *rlang(v.0.4.9)*, *readxl(v.1.3.1)*, *rstudioapi(v.0.13)*, *farver(v.2.0.3)*, *generics(v.0.1.0)*, *jsonlite(v.1.7.1)*, *Rcpp(v.1.0.5)*, *munsell(v.0.5.0)*, *fansi(v.0.4.1)*, *lifecycle(v.0.2.0)*, *stringi(v.1.5.3)*, *yaml(v.2.2.1)*, *MASS(v.7.3-53)*, *plyr(v.1.8.6)*, *parallel(v.4.0.3)*, *crayon(v.1.3.4)*, *lattice(v.0.20-41)*, *haven(v.2.3.1)*, *splines(v.4.0.3)*, *hms(v.0.5.3)*, *knitr(v.1.30)*, *pillar(v.1.4.7)*, *boot(v.1.3-25)*, *cubature(v.2.0.4.1)*, *corpcor(v.1.6.9)*, *codetools(v.0.2-16)*, *reshape2(v.1.4.4)*, *stats4(v.4.0.3)*, *reprex(v.0.3.0)*, *glue(v.1.4.2)*, *evaluate(v.0.14)*, *data.table(v.1.13.2)*, *modelr(v.0.1.8)*, *vctrs(v.0.3.5)*, *nloptr(v.1.2.2.2)*, *cellranger(v.1.1.0)*, *gtable(v.0.3.0)*, *assertthat(v.0.2.1)*, *xfun(v.0.19)*, *broom(v.0.7.2)*, *viridisLite(v.0.3.0)*, *beeswarm(v.0.2.3)*, *statmod(v.1.4.34)* and *ellipsis(v.0.3.1)*

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