orchaRd: An R package for drawing orchard plots from meta-analyses and meta-regressions with categorical moderators

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Introduction

`orchaRd` allows users to create pretty orchard plots that contain both confidence intervals (CIs) and prediction intervals (PIs) around point estimates for different categorical moderators, plots the effect size distribution over top such estimates and weights effect sizes by their precision (1/standard error, SE) or sample size. `orchaRd` takes a `metafor` object of class `rma.mv` or `rma` (Viechtbauer, 2010) and plots the results for the meta-analytic or meta-regression model. Currently, only meta-regression models with a single moderator variable are allowed or intercept only meta-analytic models. `orchaRd` uses `ggplot2` (Wickham, 2009) for plotting, and as such, layers can be added directly to make plots customizable to the users needs.

Citing orchaRd

To cite `orchaRd` in publications one can use the following reference:

Nakagawa, S. et al. 2020. The Orchard Plot: Cultivating Forest Plots for Use in Ecology, Evolution and Beyond. *Research Synthesis Methods*, in review

Installation

To install `orchaRd` use the following code in R:

```
install.packages("devtools")
install.packages("tidyverse")
install.packages("metafor")
install.packages("patchwork")
devtools::install_github("itchyshin/orchard_plot", subdir = "orchaRd", force = TRUE,
    build_vignettes = TRUE)

library(orchaRd)
library(patchwork)
library(tidyverse)
library(metafor)
```

Installation will make the primary functions accessible to users along with their help files. You will also need the `tidyverse` and `metafor` packages.

Examples of how it works

In this vignette we'll walk the reader through a number of case studies and show you how you can create beautiful looking orchard plots. We overview three different case studies that make use of different effect sizes and moderators. The datasets associated with each case study come as part of the `orchaRd` package.

Example 1: Dietary Restriction and Lifespan

English and Uller (2016) performed a systematic review and meta-analysis on the effects of early life dietary restriction (a reduction in a major component of the diet without malnutrition; e.g. caloric restriction) on average age at death, using the standardised mean difference (often called d). They found that, across the whole dataset, there was little evidence for an effect of dietary restriction on mean age at death. Here we'll use the dataset to first calculate the effect size measures and then fit an intercept only, meta-analytic model.

```
data(english)

# We need to calculate the effect sizes, in this case d
english <- escalc(measure = "SMD", n1i = NStartControl, sd1i = SD_C, m1i = MeanC,
    n2i = NStartExpt, sd2i = SD_E, m2i = MeanE, var.names = c("SMD", "vSMD"), data = english)

english_MA_int <- rma.mv(yi = SMD, V = vSMD, random = list(~1 | StudyNo, ~1 | EffectID),
    data = english)
summary(english_MA_int)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -44.5943   89.1887   95.1887  102.1809   95.5220
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0614  0.2478     21     no   StudyNo
#> sigma^2.2  0.0760  0.2756     77     no  EffectID
#>
#> Test for Heterogeneity:
#> Q(df = 76) = 297.4722, p-val < .0001
#>
#> Model Results:
#>
#> estimate      se    zval    pval    ci.lb   ci.ub
#>   0.0572  0.0729  0.7845  0.4327  -0.0856  0.2000
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We have fit a meta-analytic model and thus the only estimate we see is the overall effect size on the effects of caloric restriction on mean death across all studies examined. Now that we have fit our meta-analytic model we can get the confidence intervals and prediction intervals with a few functions in the `orchaRd` package. If one is interested in getting the table of results we can use the `mod_results` function. This will allow users to make nice tables of the results if needed. We can do that as follows:

```
res1 <- mod_results(english_MA_int, mod = "Int")
print(res1)
#>      name   estimate     lowerCL  upperCL   lowerPR   upperPR
#> 1 Intrcpt 0.05715615 -0.08563968 0.199952 -0.683237 0.7975493
```

If we instead want to create an orchard plot and visualise the results we can do so quite simply as:

```
orchard_plot(english_MA_int, mod = "Int", xlab = "Standardised mean difference",
    transfm = "none")
```

In 1, we simply add in the metafor model and it will create a default orchard plot. Alternatively, we could also add in the table of results, and try to change the colour of the 'trunk' (estimate) and 'fruit' (effect sizes) from the default (orange) to grey by just adding `ggplot` functions.

```
orchard_plot(res1, xlab = "Standardised mean difference", transfm = "none") + scale_fill_manual(values = "gre
```

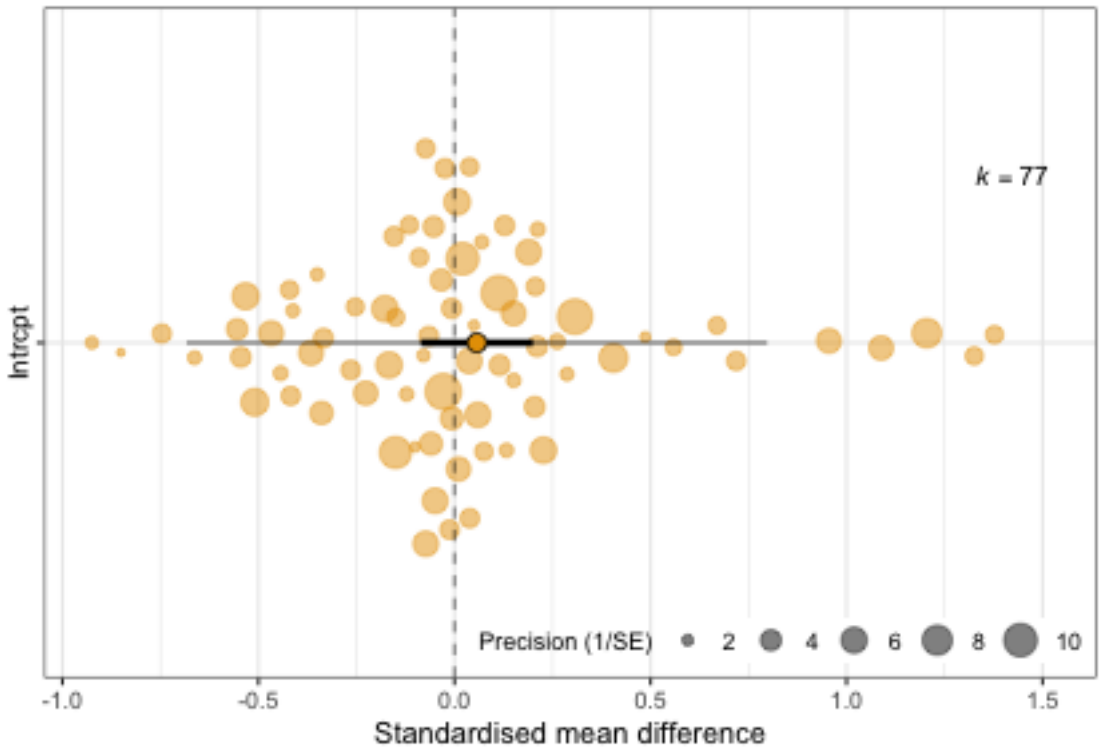

Figure 1: Orchard plot of the impact caloric restriction using standardised mean difference

```
    scale_colour_manual(values = "grey")
#> Scale for 'fill' is already present. Adding another scale for 'fill', which will replace the
#> existing scale.
#> Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the
#> existing scale.
```

Figures 1 & 2 above show that overall estimate from a random-effects meta-analysis of 77 effect sizes is centered on zero, with a 95% CI that spans the line of no-effect. The prediction intervals clearly demonstrate the high level of heterogeneity, with effect sizes less than -0.5 and greater than 0.5 predicted to be observed.

In a subsequent publication, Senior et al. (2017) analysed this dataset for the effects of dietary-restriction on among-individual variation in the age at death using the log coefficient of variation ratio. A major prediction in both English & Uller (2016) and Senior et al. (2017) was that the type of manipulation, whether the study manipulated quality of food versus the quantity of food would be important. As such, we can fit a meta-regression model to test whether the moderator "Manipulation Type" impacts our results on the mean and variance. Note that we need a meta-regression model with a categorical variable for `orchard_plot` (i.e. the intercept less model).

```
# First we need to calculate the lnCVR
english <- escalc(measure = "CVR", n1i = NStartControl, sd1i = SD_C, m1i = MeanC,
    n2i = NStartExpt, sd2i = SD_E, m2i = MeanE, var.names = c("lnCVR", "vlnCVR"),
    data = english)

# Now we can fit the meta-regression model (contrast)
english_MR0 <- rma.mv(yi = SMD, V = vSMD, mods = ~ManipType, random = list(~1 | StudyNo,
    ~1 | EffectID), data = english)
summary(english_MR0)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -44.2108   88.4216   96.4216  105.6916   96.9931
#>
#> Variance Components:
```

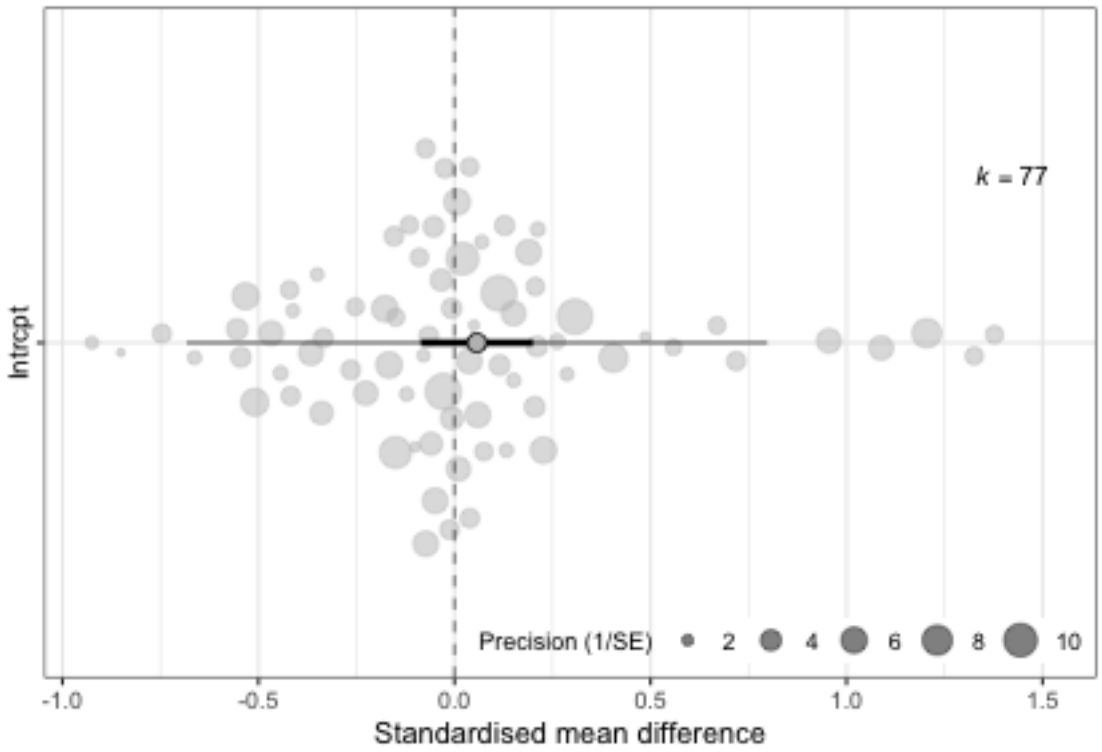

Figure 2: Orchard plot of the impact caloric restriction using standardised mean difference but instead of using the metafor model, using the model results table

```
#>
#>              estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0655  0.2560     21     no   StudyNo
#> sigma^2.2  0.0761  0.2758     77     no  EffectID
#>
#> Test for Residual Heterogeneity:
#> QE(df = 75) = 295.5324, p-val < .0001
#>
#> Test of Moderators (coefficient 2):
#> QM(df = 1) = 0.0414, p-val = 0.8388
#>
#> Model Results:
#>
#>                    estimate      se    zval    pval    ci.lb   ci.ub
#> intrcpt              0.0469  0.0924  0.5079  0.6115  -0.1342  0.2281
#> ManipTypeQuantity    0.0283  0.1390  0.2035  0.8388  -0.2442  0.3008
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Now we can fit the meta-regression model without the intercept we need this
# intercept-less model for the orchard plot
english_MR <- rma.mv(yi = SMD, V = vSMD, mods = ~ManipType - 1, random = list(~1 |
    StudyNo, ~1 | EffectID), data = english)
summary(english_MR)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -44.2108   88.4216   96.4216  105.6916   96.9931
```

```
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0655  0.2560     21     no   StudyNo
#> sigma^2.2  0.0761  0.2758     77     no  EffectID
#>
#> Test for Residual Heterogeneity:
#> QE(df = 75) = 295.5324, p-val < .0001
#>
#> Test of Moderators (coefficients 1:2):
#> QM(df = 2) = 0.6532, p-val = 0.7214
#>
#> Model Results:
#>
#>                    estimate      se    zval    pval    ci.lb   ci.ub
#> ManipTypeQuality     0.0469  0.0924  0.5079  0.6115  -0.1342  0.2281
#> ManipTypeQuantity    0.0752  0.1122  0.6704  0.5026  -0.1447  0.2951
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Again, we can create a table of results
res2 <- mod_results(english_MR, mod = "ManipType")
print(res2)
#>       name   estimate    lowerCL   upperCL    lowerPR   upperPR
#> 1  Quality 0.04693124 -0.1341875 0.2280500 -0.7125254 0.8063879
#> 2 Quantity 0.07521998 -0.1446838 0.2951238 -0.6944086 0.8448485

# we fit a meta-regression (contrast) for the log coefficient of variation
senior_MR0 <- rma.mv(yi = lnCVR, V = vlnCVR, mods = ~ManipType, random = list(~1 |
    StudyNo, ~1 | EffectID), data = english)
summary(senior_MR0)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -32.0740   64.1481   72.1481   81.4180   72.7195
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0275  0.1657     21     no   StudyNo
#> sigma^2.2  0.0470  0.2169     77     no  EffectID
#>
#> Test for Residual Heterogeneity:
#> QE(df = 75) = 215.7242, p-val < .0001
#>
#> Test of Moderators (coefficient 2):
#> QM(df = 1) = 1.3308, p-val = 0.2487
#>
#> Model Results:
#>
#>                    estimate      se     zval    pval    ci.lb   ci.ub
#> intrcpt             -0.1310  0.0678  -1.9333  0.0532  -0.2639  0.0018  .
#> ManipTypeQuantity    0.1217  0.1055   1.1536  0.2487  -0.0851  0.3285
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Let's fit a meta-regression without the intercept
senior_MR <- rma.mv(yi = lnCVR, V = vlnCVR, mods = ~ManipType - 1, random = list(~1 |
    StudyNo, ~1 | EffectID), data = english)
summary(senior_MR)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -32.0740   64.1481   72.1481   81.4180   72.7195
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0275  0.1657     21     no   StudyNo
#> sigma^2.2  0.0470  0.2169     77     no  EffectID
#>
#> Test for Residual Heterogeneity:
#> QE(df = 75) = 215.7242, p-val < .0001
#>
#> Test of Moderators (coefficients 1:2):
#> QM(df = 2) = 3.7419, p-val = 0.1540
#>
#> Model Results:
#>
#>                    estimate      se     zval    pval    ci.lb   ci.ub
#> ManipTypeQuality    -0.1310  0.0678  -1.9333  0.0532  -0.2639  0.0018  .
#> ManipTypeQuantity   -0.0093  0.0825  -0.1131  0.9099  -0.1711  0.1524
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# creating a table of results
res3 <- mod_results(senior_MR, "ManipType")
print(res3)
#>       name     estimate    lowerCL     upperCL    lowerPR   upperPR
#> 1  Quality -0.131037178 -0.2638834 0.001809059 -0.6821678 0.4200934
#> 2 Quantity -0.009336131 -0.1710708 0.152398490 -0.5681339 0.5494616


# We can now plot SMD and lnCVR beside each other and compare the results
p1 <- orchard_plot(english_MR, mod = "ManipType", xlab = "Standardised mean difference",
    transfm = "none")

p2 <- orchard_plot(senior_MR, mod = "ManipType", xlab = "log(CV ratio) (lnCVR)",
    transfm = "none")
```

```
p1/p2
```

Our orchard plot for the log coefficient of variation demonstrates that, while restrictions on dietary quality and quantity do not affect the average age at death (top of Figure 3), among-individual variation may be altered by quality restrictions (bottom of Figure 3). The effect is negative suggesting that the coefficient of variation in the control group is lower than that in the treatment group, and the 95% CI does not span zero. Again though, the effect is heterogeneous; a substantial number of positive effects are still predicted.

In many circumstances we want to present both the overall mean meta-analytic estimate (i.e., our intercept-only model) and the mean effect size in different levels of our categorical moderator variable. This provides overall support across all studies included in the meta-analysis while effects across different levels of our categorical variable provide more detailed information about how mean effect size might vary across different groups.

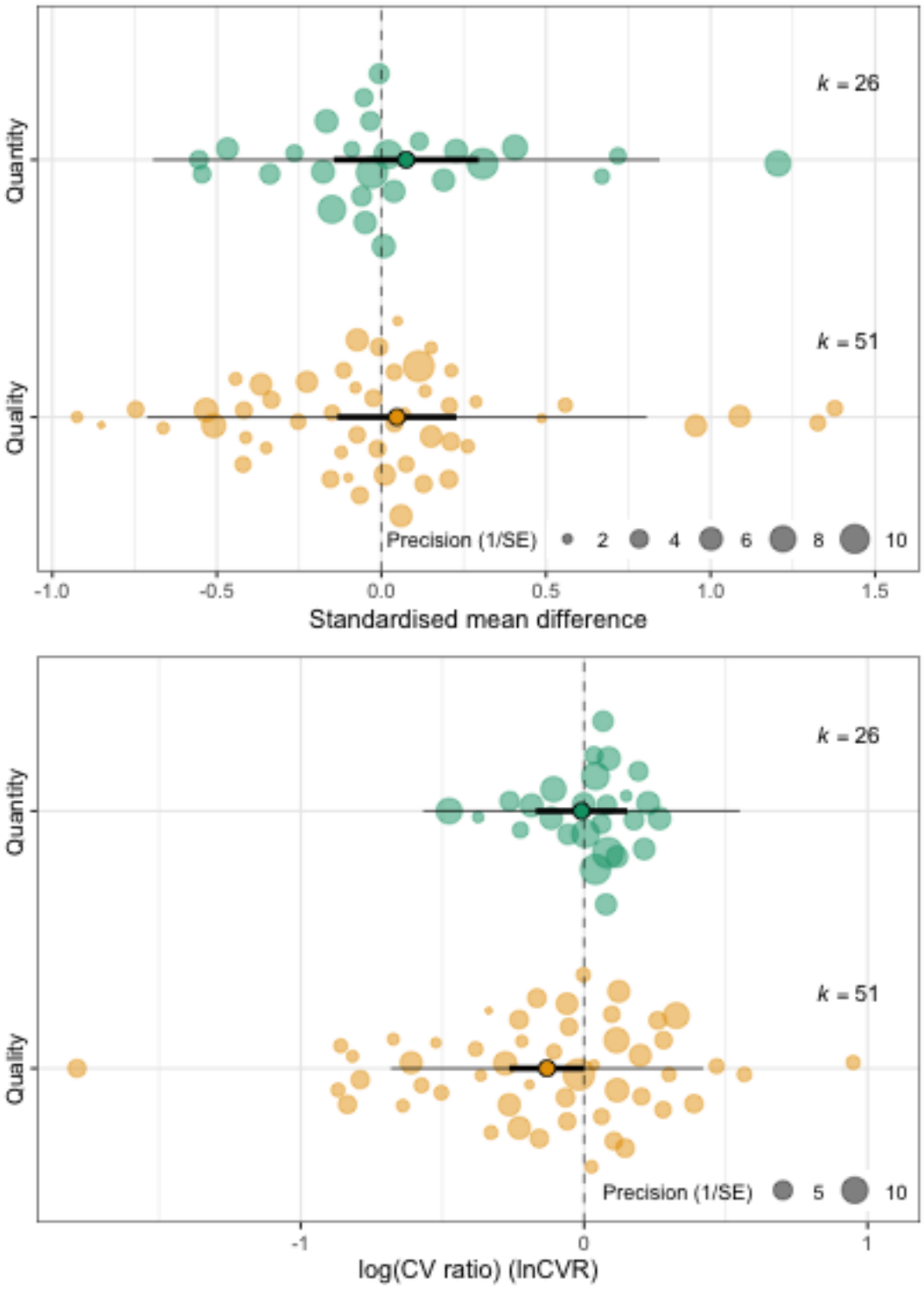

Figure 3: Orchard plot of diet qualities impact on SMD (top) and log coefficient of variation (bottom)

```r
# We will re-fit the meta-analytic and meta-regression models without the
# intercept just to remind the reader what models we would like to compare

english_MA_int <- rma.mv(yi = SMD, V = vSMD, random = list(~1 | StudyNo, ~1 | EffectID),
    data = english)

summary(english_MA_int)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -44.5943   89.1887   95.1887  102.1809   95.5220
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0614  0.2478     21     no   StudyNo
#> sigma^2.2  0.0760  0.2756     77     no  EffectID
#>
#> Test for Heterogeneity:
#> Q(df = 76) = 297.4722, p-val < .0001
#>
#> Model Results:
#>
#> estimate      se    zval    pval    ci.lb   ci.ub
#>   0.0572  0.0729  0.7845  0.4327  -0.0856  0.2000
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

english_MR <- rma.mv(yi = SMD, V = vSMD, mods = ~ManipType - 1, random = list(~1 |
    StudyNo, ~1 | EffectID), data = english)
summary(english_MR)
#>
#> Multivariate Meta-Analysis Model (k = 77; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -44.2108   88.4216   96.4216  105.6916   96.9931
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed    factor
#> sigma^2.1  0.0655  0.2560     21     no   StudyNo
#> sigma^2.2  0.0761  0.2758     77     no  EffectID
#>
#> Test for Residual Heterogeneity:
#> QE(df = 75) = 295.5324, p-val < .0001
#>
#> Test of Moderators (coefficients 1:2):
#> QM(df = 2) = 0.6532, p-val = 0.7214
#>
#> Model Results:
#>
#>                    estimate      se    zval    pval    ci.lb   ci.ub
#> ManipTypeQuality     0.0469  0.0924  0.5079  0.6115  -0.1342  0.2281
#> ManipTypeQuantity    0.0752  0.1122  0.6704  0.5026  -0.1447  0.2951
#>
#> ---
```

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

# Again, we can create a table of results for the various models
res_english_MA_int <- mod_results(english_MA_int, mod = "Int")
res_english_MR <- mod_results(english_MR, mod = "ManipType")

# Now, we can use the submerge function to merge together the mod_results so they
# can be plotted all together in the orchard plot
res_MA_MR_merged <- submerge(res_english_MA_int, res_english_MR)
print(res_MA_MR_merged)
#>       name   estimate     lowerCL   upperCL    lowerPR   upperPR
#> 1  Intrcpt 0.05715615 -0.08563968 0.1999520 -0.6832370 0.7975493
#> 2  Quality 0.04693124 -0.13418752 0.2280500 -0.7125254 0.8063879
#> 3 Quantity 0.07521998 -0.14468379 0.2951238 -0.6944086 0.8448485

# We can now plot the overall SMD and the mean SMD in each level of the diet
# manipulation type. We will also re-label the 'Intrcpt' to make it more clear
# that this refers to the overall meta-analytic mean.
orchard_plot(res_MA_MR_merged, mod = "ManipType", xlab = "Standardised mean difference",
    transfm = "none") + scale_y_discrete(labels = c(Intrcpt = "Overall"))
```

Figure 4 now provides the overall mean estimate and the mean estimate in each level of the diet manipulation categories in one figure. These combined figures are more typical of what readers can expect in meta-analytic papers.

Example 2: Predation and Invertebrate Community

Eklof et al. (2012) evaluated the effects of predation on benthic invertebrate communities. Using the log response ratio they quantified differences in abundance and/or biomass of gastropods and Amphipods in groups with and without predation in an experimental setting.

Here again, we can create orchard plots of the model results, but we'll show how a few simple things can be modified. Again, we can fit the meta-analytic model first:

```
data(eklof)

# Calculate the effect size
eklof <- escalc(measure = "ROM", n1i = N_control, sd1i = SD_control, m1i = mean_control,
    n2i = N_treatment, sd2i = SD_treatment, m2i = mean_treatment, var.names = c("lnRR",
        "vlnRR"), data = eklof)

# Add the observation level factor
eklof$Datapoint <- as.factor(seq(1, dim(eklof)[1], 1))

# Also, we can get the sample size, which we can use for weighting if we would
# like
eklof$N <- rowSums(eklof[, c("N_control", "N_treatment")])

# fit a meta-regression with the intercept (contrast)
eklof_MR0 <- rma.mv(yi = lnRR, V = vlnRR, mods = ~Grazer.type, random = list(~1 |
    ExptID, ~1 | Datapoint), data = eklof)

summary(eklof_MR0)
#>
#> Multivariate Meta-Analysis Model (k = 34; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -51.9349  103.8698  111.8698  117.7328  113.3513
#>
#> Variance Components:
```

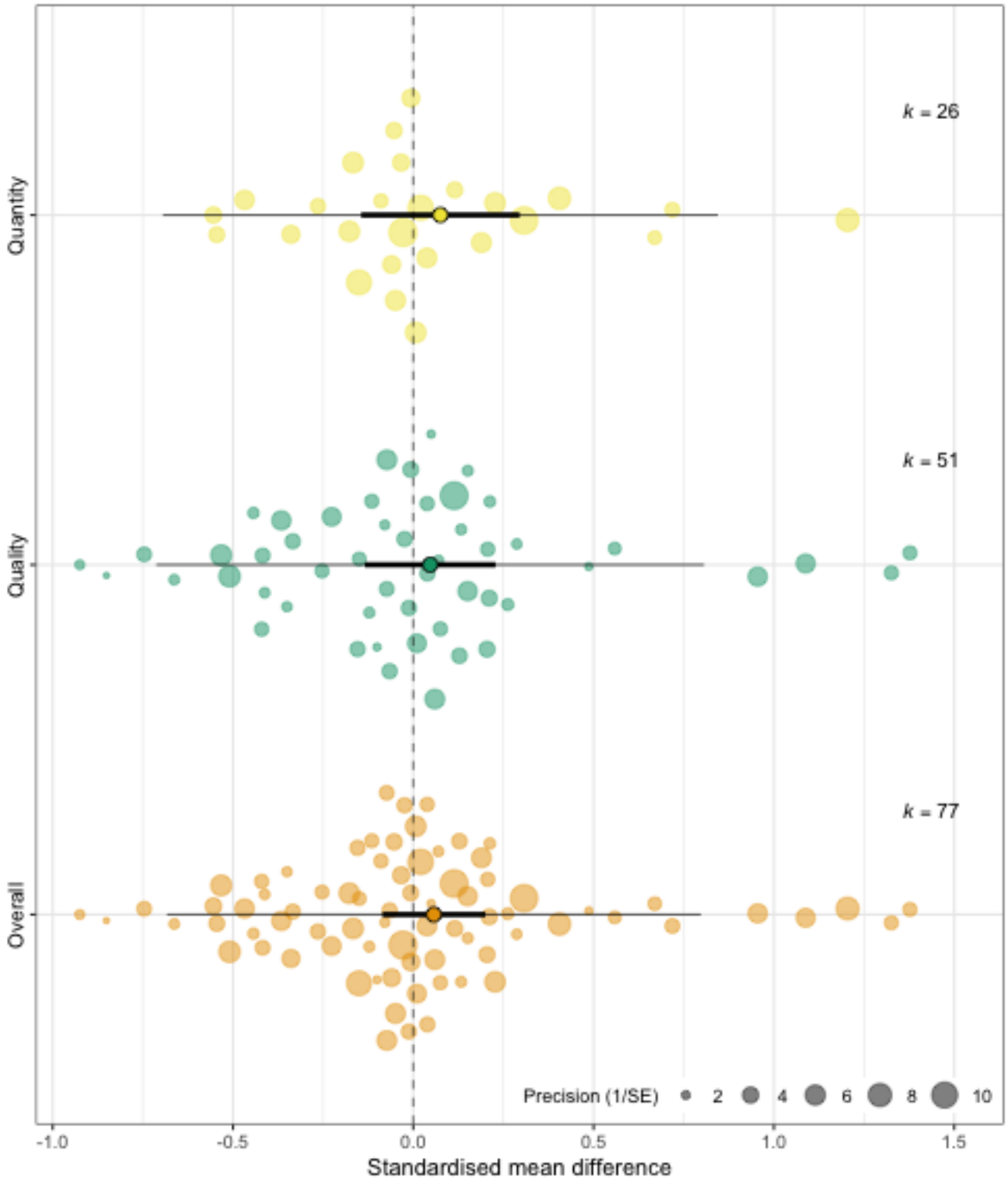

Figure 4: Orchard plot of overall mean SMD for the impact of diet quality on lifespan (bottom) and the effect of different diet manipulations on lifespan (middle and top)

```
#>
#>              estim    sqrt  nlvls  fixed     factor
#> sigma^2.1  0.5075  0.7124     18     no     ExptID
#> sigma^2.2  0.6703  0.8187     34     no  Datapoint
#>
#> Test for Residual Heterogeneity:
#> QE(df = 32) = 195.9943, p-val < .0001
#>
#> Test of Moderators (coefficient 2):
#> QM(df = 1) = 0.8891, p-val = 0.3457
#>
#> Model Results:
#>
#>                       estimate      se     zval    pval    ci.lb    ci.ub
#> intrcpt                -0.8095  0.3099  -2.6119  0.0090  -1.4170  -0.2021  **
#> Grazer.typegastropod    0.3285  0.3484   0.9429  0.3457  -0.3544   1.0114
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# fit a meta-regression without the intercept and we can use this model for the
# orchard plot
eklof_MR <- rma.mv(yi = lnRR, V = vlnRR, mods = ~Grazer.type - 1, random = list(~1 |
    ExptID, ~1 | Datapoint), data = eklof)
```

Above we have fit a meta-regression model using "Grazer Type" as a moderator which is predicted to explain variation in log response ratios. We can demonstrate a few simple changes users can make, but we note here that users can make far more complex changes down the line if needed, but we'll save explaining these more complex changes for the last example. The first is the angle at which the y-axis labels are positioned (bottom of Figure 5):

```
p3 <- orchard_plot(eklof_MR, mod = "Grazer.type", xlab = "log(Response ratio) (lnRR)",
    transfm = "none")

p4 <- orchard_plot(eklof_MR, mod = "Grazer.type", xlab = "log(Response ratio) (lnRR)",
    transfm = "none", angle = 45)

p3/p4
```

The other thing we can change is the type of scaling we wish to use. Let's say we are interested in scaling the effect size by the total sample size of the study we use a vector of N, sample size (bottom of Figure 6):

```
p5 <- orchard_plot(eklof_MR, mod = "Grazer.type", xlab = "log(Response ratio) (lnRR)",
    transfm = "none")

p6 <- orchard_plot(eklof_MR, mod = "Grazer.type", xlab = "log(Response ratio) (lnRR)",
    transfm = "none", angle = 45, N = eklof$N)
#> Warning in if (N != "none") {: the condition has length > 1 and only the first element will be used

p5/p6
```

Overall, our orchard plot shows the results of a re-analysis of their data. The estimated mean effects are negative for both gastropods and amphipods suggesting that mean abundance/biomass in the control group is lower than in the treatment groups, although the effect is largest, and is statistically significant, for amphipods. In both cases the prediction intervals reveal the extent of heterogeneity, with positive effects predicted to be observed.

Example 3: Maternal-Offspring Morphological Correlations

Finally, we also look at the case discussed by Lim et al. (2014), who meta-analysed the strength of correlation between maternal and offspring size within-species, across a very wide range of taxa. They found that typically there is a moderate

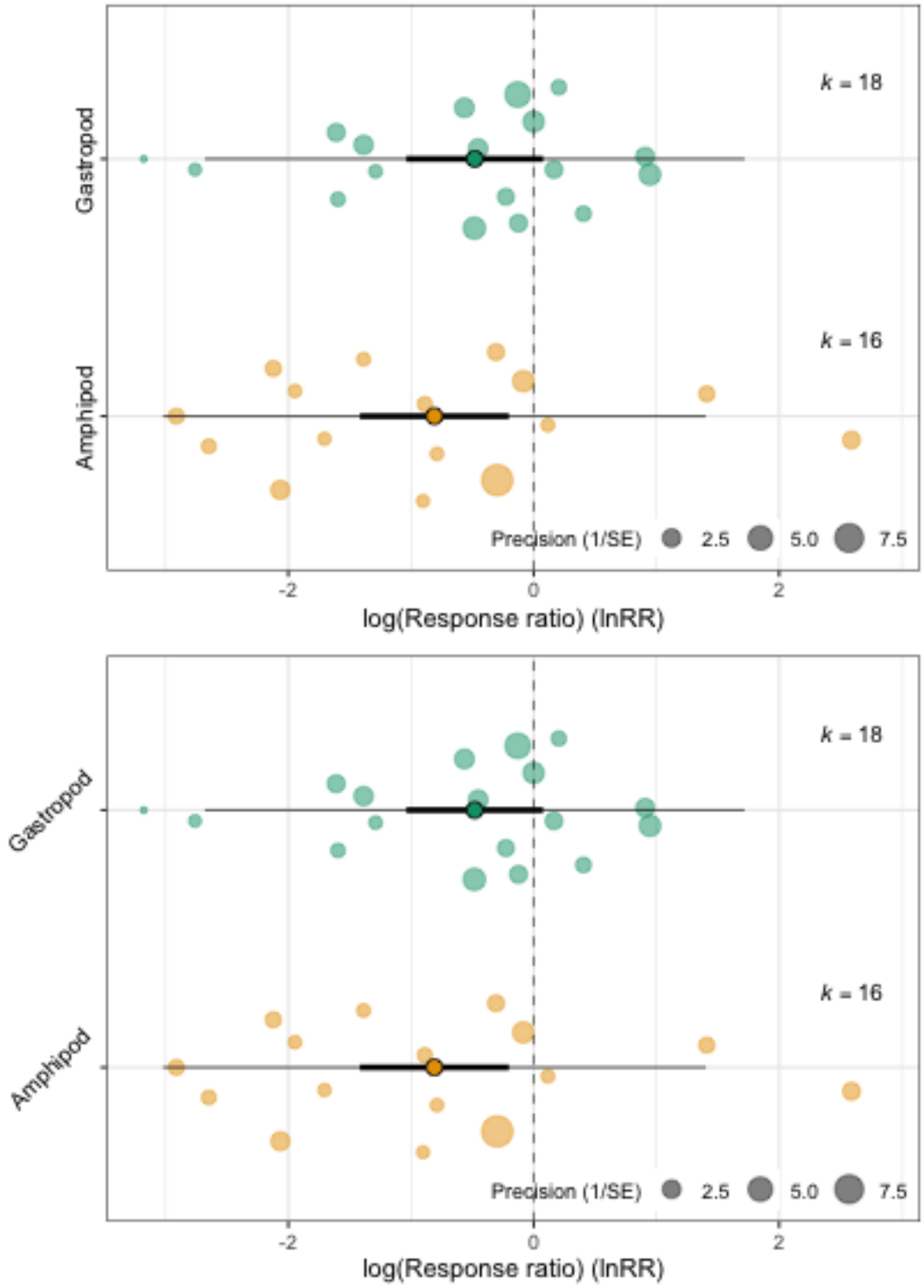

Figure 5: Orchard plots of the effects of predation on benthic invertebrate communities compared using the log response ratio. Top panel is the default plot and bottom panel a plot containing changes in label axes

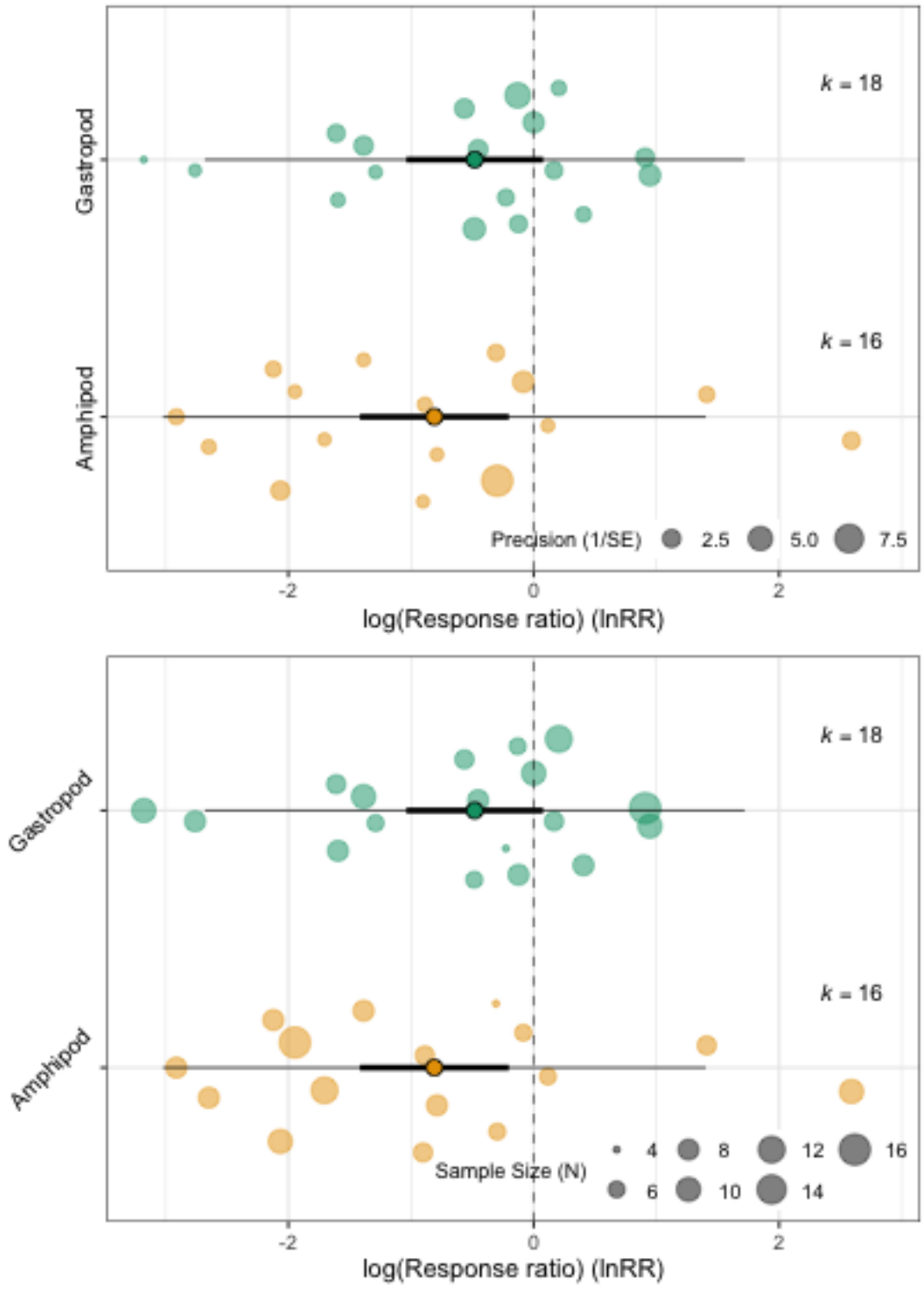

Figure 6: Orchard plots of the effects of predation on benthic invertebrate communities compared using the log response ratio. Top panel is the default plot and bottom panel a plot containing changes in label axes and scaling with sample size instead of precision

positive correlation between maternal size and offspring size within species (i.e. larger mothers have larger offspring). However, they also found evidence for relatively strong phylogenetic effects suggesting the strength of the association is dependent on evolutionary lineage.

Here, we have used an orchard plot to represent the results obtained when meta-analysing the data from Lim et al. (2014) by taxonomic phyla.

```
data(lim)

# Add in the sampling variance
lim$vi <- 1/(lim$N - 3)

# Let's fit a meta-regression. The phylogenetic model found phylogenetic effects,
# however, instead we could fit Phylum as a fixed effect and explore them with an
# Orchard Plot
lim_MR <- rma.mv(yi = yi, V = vi, mods = ~Phylum - 1, random = list(~1 | Article,
    ~1 | Datapoint), data = lim)
summary(lim_MR)
#>
#> Multivariate Meta-Analysis Model (k = 357; method: REML)
#>
#>   logLik  Deviance       AIC       BIC      AICc
#> -97.6524  195.3049  213.3049  248.0263  213.8343
#>
#> Variance Components:
#>
#>             estim    sqrt  nlvls  fixed     factor
#> sigma^2.1  0.0411  0.2029    220     no    Article
#> sigma^2.2  0.0309  0.1757    357     no  Datapoint
#>
#> Test for Residual Heterogeneity:
#> QE(df = 350) = 1912.9637, p-val < .0001
#>
#> Test of Moderators (coefficients 1:7):
#> QM(df = 7) = 356.6775, p-val < .0001
#>
#> Model Results:
#>
#>                        estimate      se     zval    pval    ci.lb   ci.ub
#> PhylumArthropoda         0.2690  0.0509   5.2829  <.0001   0.1692  0.3687  ***
#> PhylumChordata           0.3908  0.0224  17.4190  <.0001   0.3468  0.4347  ***
#> PhylumEchinodermata      0.8582  0.3902   2.1992  0.0279   0.0934  1.6230    *
#> PhylumMollusca           0.4867  0.1275   3.8175  0.0001   0.2368  0.7366  ***
#> PhylumNematoda           0.4477  0.3054   1.4658  0.1427  -0.1509  1.0463
#> PhylumPlatyhelminthes    0.4935  0.2745   1.7980  0.0722  -0.0444  1.0314    .
#> PhylumRotifera           0.4722  0.3021   1.5634  0.1180  -0.1198  1.0642
#>
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Now we can plot a default orchard plot, scaling each effect size by N. Also, because we are using Zr, we can use transfm = "tanh" and it will do the conversions for us:

```
orchard_plot(lim_MR, mod = "Phylum", xlab = "Correlation coefficient", alpha = 0.5,
    transfm = "tanh", angle = 45, N = lim$N, cb = FALSE)
#> Warning in if (N != "none") {: the condition has length > 1 and only the first element will be used
```

Now that we have Figure 7 we can do some small changes to make it pretty. Currently, the cb argument is "FALSE", we can change this to "TRUE" to use colour blind friendly colours. Additionally, because we are using `ggplot2` we can add elements to the figure to make it look pretty.

```
orchard_plot(lim_MR, mod = "Phylum", xlab = "Correlation coefficient (r)",
```

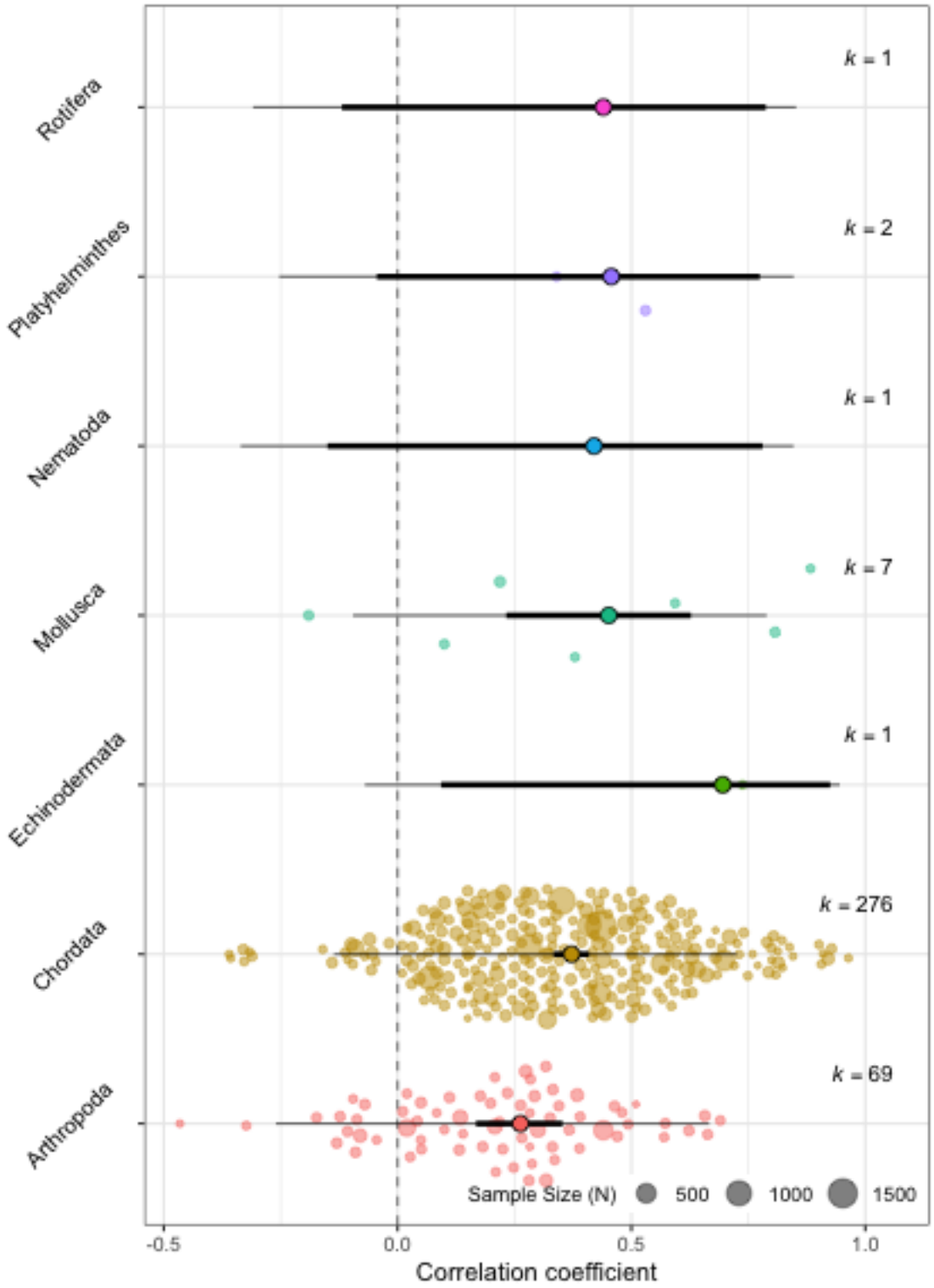

Figure 7: Orchard plot of the the strength of correlation between maternal and offspring size within-species

```
            transfm = "tanh", angle = 45, N = lim$N, cb = TRUE) +
  theme(
    legend.position = c(0.05, 0.99),

    legend.justification = c(0, 1),

    legend.key.size = unit(1, "mm")) +
  theme(
    legend.direction = "horizontal",

    legend.title = element_text(size = 8),

    legend.text = element_text(size = 10)) +

  scale_x_continuous(expand = c(0.1, 0.1))
#> Warning in if (N != "none") {: the condition has length > 1 and only the first element will be used
```

As in Figure 8, New elements can be added to the `orchard_plot` to modify it as one sees fit. It will overwrite existing elements, often telling you it does so with warning messages (these are nothing to be concerned about in most cases).

From our orchard plots above, it is clear that the analysis is dominated by data from chordates and arthropods, with the other Phyla being much more poorly represented. Second, there is a difference between the strength of a typical correlation within these two well represented groups (the correlation is stronger in chordates), which arguably would explain the phylogenetic signals detected by Lim et al. (2014). Lastly, although there are differences within the typical correlation between Chordates and Arthropods, there remains a large overlap in predicted range of individual effect sizes; individual species within Phyla are still highly variable.

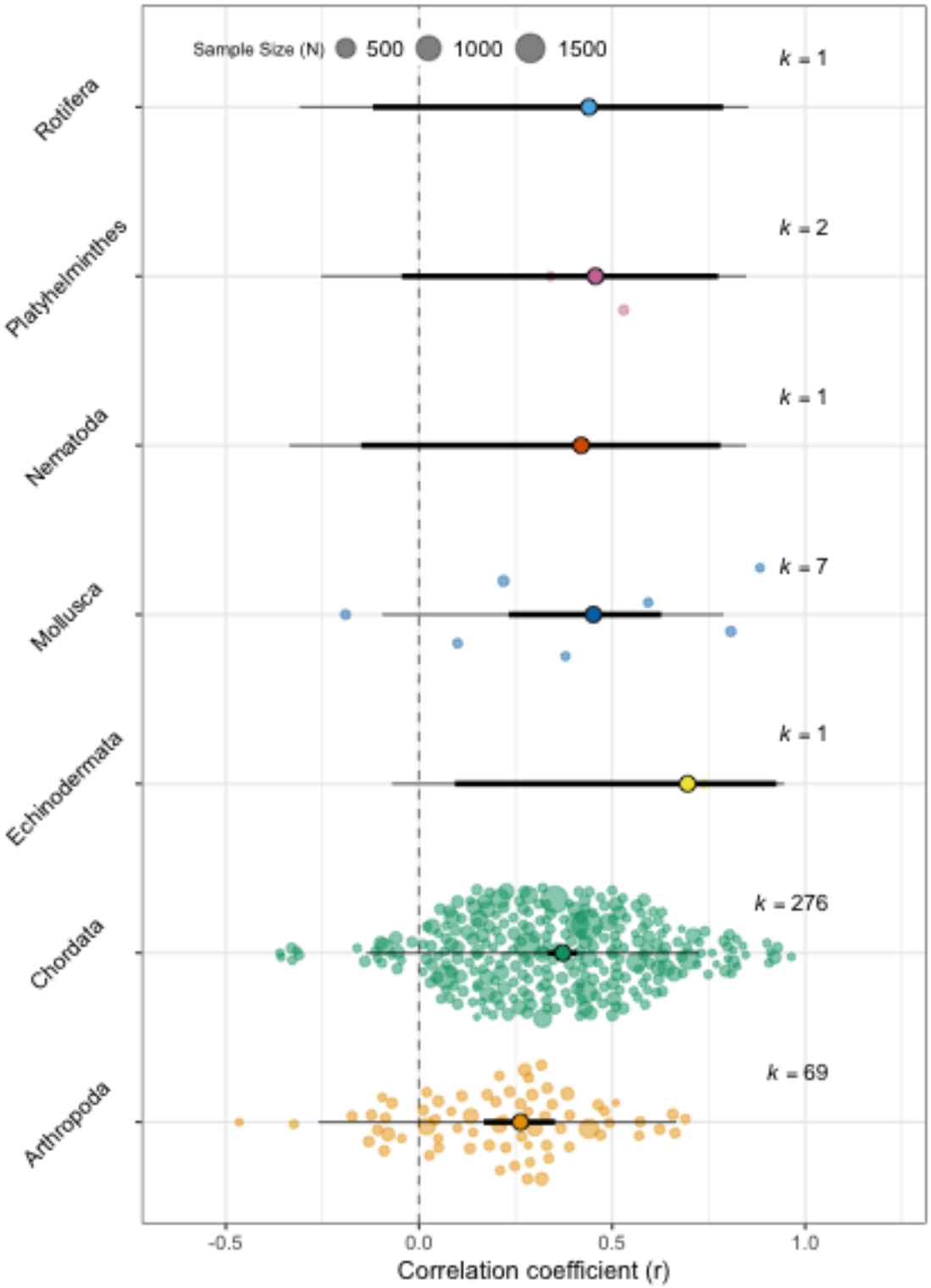

Figure 8: Orchard plot of the the strength of correlation between maternal and offspring size within-species

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