Meta-Analysis Reproduction Summary Excluding HUM251

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1. Summary

This document reports the process taken in the model fitting stage of the meta-analysis in thermal reproduction.

2. Setup

We first read in our data and select all of the effect sizes related to reproduction. We do this using the following code.

```
### Read in effect size data
effectdata <- read.csv("Data/Survival project all pairwise.es.csv")
repdata_warm <- subset(effectdata, Trait.category == "Reproduction" &
    warm.cool == "Warm")
repdata_cool <- subset(effectdata, Trait.category == "Reproduction" &
    warm.cool == "Cool")

allrep <- rbind(repdata_warm, repdata_cool)

### select data for analysis
rdata <- allrep
```

Next we create new columns in our dataframe which will serve as random factors in our multi-level meta analysis models. The following initialises four new columns, namely "obs", "study_code", "Species.phylo" and "species". Lastly, we create a column name "precision" which is equal to the inverse standard error.

```
### Create random factors into data frame
rdata$obs <- factor(c(1:nrow(rdata)))  # Unique observation code
rdata$study_code <- factor(rdata$Paper.code)  # Model requires column names study_code
rdata$Species.phylo <- factor(rdata$Species.latin)  # Species names for phylo matrix
rdata$species <- factor(rdata$Species.latin)  # Another species column for random factor

precision <- sqrt(1/rdata$v)  # inverse standard error
rdata[, "precision"] <- precision
```

The number of species and total number of studies present in the data are as follows.

```
nlevels(rdata$species)  # Check number of species
```

```
## [1] 307
```

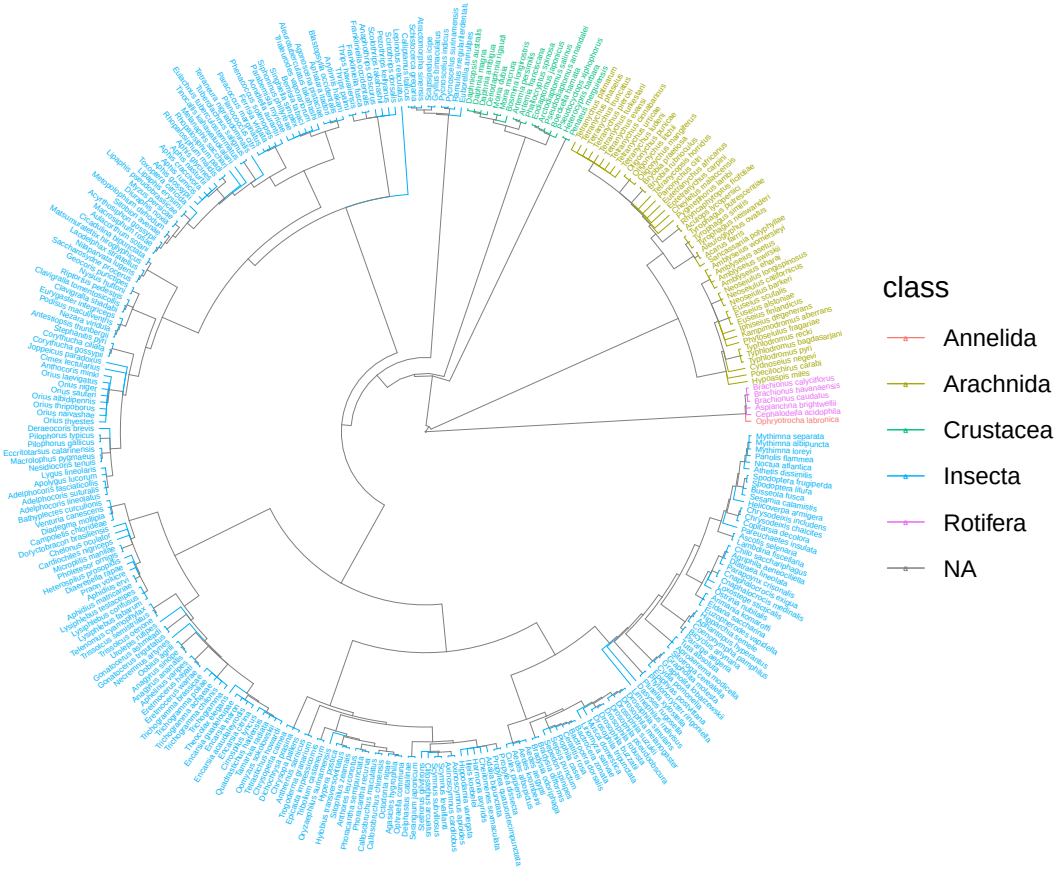
```
nlevels(rdata$study_code)  # Check number of studies
```

```
## [1] 340
```

The final stage in the setup is to import a phylogentic tree of the data. Below is the code used to produce the tree and a plot of the tree itself.

```
## import tree from map
tree1 <- read.nexus("all_reproduction_excHUM251_tree.nex")
tree_grafen = compute.brlen(tree1, method = "Grafen", power = 1)
phylo_matrix <- vcv(tree_grafen, cor = TRUE, model = "Brownian")  # Make phylogenetic matrix
```

```
## character(0)
```



3. Random effects models

In this section we determine which random effects to include in our model. For each model I have provided the code used to specify the structure of the model and a summary of the results. We begin with a model that includes all of the random factors we created earlier.

```
# Adding four random factors
meta2 <- rma.mv(es, v, random = list(~1 | Species.phylo, ~1 |
    species, ~1 | study_code, ~1 | obs), test = "t", dfs = "contain",
    R = list(Species.phylo = phylo_matrix), data = rdata, method = "REML")
```

```
summary(meta2)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -4119.6114   8239.2228   8249.2228   8275.5219   8249.2651
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed         factor    R
## sigma^2.1   0.0000  0.0000    307     no  Species.phylo  yes
## sigma^2.2   0.0000  0.0004    307     no        species   no
## sigma^2.3  10.2889  3.2076    340     no     study_code   no
## sigma^2.4   5.0483  2.2468   1423     no            obs   no
##
## Test for Heterogeneity:
## Q(df = 1422) = 37705.7968, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb    ci.ub
##  -1.5435  0.1886  -8.1844  <.0001  -1.9131  -1.1739  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
i2_ml(meta2, method = c("ratio"))  # Heterogeneity at each random factor level
```

```
##         I2_Total I2_Species.phylo       I2_species    I2_study_code           I2_obs
##     9.945130e+01     3.084327e-10     1.214829e-06     6.671656e+01     3.273474e+01
```

Accounting for non-independence of data points from the same experiment

The data has a nested structure. Each study (study_code) may have a number of experiments (effect.size.code) which share a common control temperature. Each effect size has its own unique code, obs. Effect sizes from the same experiment which share a control temperature are thought to be non-independent. The following code create a covariance matrix "VCV_shared" which assumes a correlation of 0.5 between effect sizes from the same experiment. We include this structure in our proceeding models.

```
rdata$shared_control <- factor(rdata$Effect.size.code)
VCV_shared <- impute_covariance_matrix(vi = rdata$v, cluster = rdata$shared_control,
    r = 0.5)
```

```
# Add new variance matrix into the mixed-effects
# meta-analysis model
```

```r
meta3 <- rma.mv(es, VCV_shared, random = list(~1 | Species.phylo,
    ~1 | species, ~1 | study_code, ~1 | obs), test = "t", dfs = "contain",
    R = list(Species.phylo = phylo_matrix), data = rdata, method = "REML")
```

```r
summary(meta3)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3838.5316   7677.0632   7687.0632   7713.3623   7687.1055
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed         factor    R
## sigma^2.1  0.0000  0.0000    307     no  Species.phylo  yes
## sigma^2.2  0.0000  0.0002    307     no        species   no
## sigma^2.3  5.0925  2.2567    340     no     study_code   no
## sigma^2.4  4.3215  2.0788   1423     no            obs   no
##
## Test for Heterogeneity:
## Q(df = 1422) = 39436.4596, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb    ci.ub
##  -1.3309  0.1399  -9.5102  <.0001  -1.6052  -1.0566  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
i2_ml(meta3, method = c("ratio"))  # Heterogeneity at each random factor level
```

```
##         I2_Total I2_Species.phylo       I2_species    I2_study_code           I2_obs
##     9.910914e+01     3.211305e-09     6.034366e-07     5.361290e+01     4.549624e+01
```

Model without phylogeny

We also originally included a variance-covariance matrix for phylogenetic relatedness of the included species as a random effect in the model (Chamberlain et al., 2012), but this has now been removed as its inclusion did not improve model fit and the phylogenetic signal was very weak.

```
## without phylogeny but with shared control
meta5 <- rma.mv(es, VCV_shared, random = list(~1 | species, ~1 |
    study_code, ~1 | obs), test = "t", dfs = "contain", data = rdata,
    method = "REML")
```

```
summary(meta5)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3838.5316   7677.0632   7685.0632   7706.1024   7685.0914
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0003    307     no     species
## sigma^2.2  5.0925  2.2567    340     no  study_code
## sigma^2.3  4.3215  2.0788   1423     no         obs
##
## Test for Heterogeneity:
## Q(df = 1422) = 39436.4596, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb    ci.ub
##  -1.3309  0.1399  -9.5102  <.0001  -1.6052  -1.0566  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
i2_ml(meta5, method = c("ratio"))  # Heterogeneity at each random factor level
```

```
##      I2_Total    I2_species I2_study_code        I2_obs
##  9.910913e+01  6.890664e-07  5.361289e+01  4.549624e+01
```

Model without phylogeny or species

```
## without phylogeny or species
meta4 <- rma.mv(es, VCV_shared, random = list(~1 | study_code,
    ~1 | obs), test = "t", dfs = "contain", data = rdata, method = "REML")
```

```
summary(meta4)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3838.5316   7677.0632   7683.0632   7698.8426   7683.0801
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.0925  2.2567    340     no  study_code
## sigma^2.2  4.3215  2.0788   1423     no         obs
##
## Test for Heterogeneity:
## Q(df = 1422) = 39436.4596, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb    ci.ub
##  -1.3309  0.1399  -9.5102  <.0001  -1.6052  -1.0566  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
i2_ml(meta4, method = c("ratio"))  # Heterogeneity at each random factor level
```

```
##      I2_Total I2_study_code        I2_obs
##      99.10914      53.61290      45.49624
```

Model without phylogeny, species or study_code

```
## without phylogeny, species or study_code
meta7 <- rma.mv(es, VCV_shared, random = list(~1 | obs), test = "t",
    dfs = "contain", data = rdata, method = "REML")
```

```
summary(meta7)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3998.6362   7997.2725   8001.2725   8011.7921   8001.2810
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed  factor
## sigma^2    6.8055  2.6087   1423     no     obs
##
## Test for Heterogeneity:
## Q(df = 1422) = 39436.4596, p-val < .0001
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
##  -1.2600  0.0721  -17.4635  <.0001  -1.4014  -1.1185  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
i2_ml(meta7, method = c("ratio"))  # Heterogeneity at each random factor level
```

```
## I2_Total   I2_obs
## 98.77186 98.77186
```

We can see from the above that the best fitting model according to AIC is “meta4” which includes only the study code and the unique effect size code, obs. There is a AIC difference of 4 between the model meta4 and the next best model meta5 . We continue our analysis using meta4 as our base model.

4. Meta-regressions

Starting with the best fitting random-effect model from Section 3, "meta8" we now include single factors as a fixed effect. We initially explore the fixed factors

- **reftemp**: The experiment's control (reference) temperature.
- **treattemp**: The treatment temperature
- **warm.cool** : A categorical variable indicating whether treatment is warmer or cooler than the reference temperature
- **diff**: The difference between the reference and treatment temperature.

Reference temperature

```
meta_trait_ref <- rma.mv(es, VCV_shared, mod = ~reftemp, random = list(~1 |
    study_code, ~1 | obs), test = "t", dfs = "contain", data = rdata,
    method = "REML")
```

```
summary(meta_trait_ref)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3835.2711   7670.5423   7678.5423   7699.5787   7678.5705
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.0483  2.2468    340     no  study_code
## sigma^2.2  4.3315  2.0812   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39262.5694, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.6304, p-val = 0.2016
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    0.1221  1.1464   0.1065  0.9152  -2.1248  2.3689
## reftemp   -0.0588  0.0461  -1.2769  0.2016  -0.1492  0.0315
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Treatment temperature

```
meta_trait_treattemp <- rma.mv(es, VCV_shared, mod = ~treattemp,
    random = list(~1 | study_code, ~1 | obs), test = "t", dfs = "contain",
    data = rdata, method = "REML")
```

```
summary(meta_trait_treattemp)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3828.1823   7656.3646   7664.3646   7685.4011   7664.3929
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.1036  2.2591    340     no  study_code
## sigma^2.2  4.2445  2.0602   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39389.3398, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 16.9542, p-val < .0001
##
## Model Results:
##
##            estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt     -0.4771  0.2496  -1.9113  0.0560  -0.9663   0.0122    .
## treattemp   -0.0348  0.0085  -4.1175  <.0001  -0.0514  -0.0182  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Warm vs Cool

```
meta_trait_warm <- rma.mv(es, VCV_shared, mod = ~warm.cool, random = list(~1 |
    study_code, ~1 | obs), test = "t", dfs = "contain", data = rdata,
    method = "REML")
```

```
summary(meta_trait_warm)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3828.9782   7657.9564   7665.9564   7686.9928   7665.9846
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.0837  2.2547    340     no  study_code
## sigma^2.2  4.2511  2.0618   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39145.1933, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 15.6100, p-val < .0001
##
## Model Results:
##
##                estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt         -1.0722  0.1540  -6.9633  <.0001  -1.3739  -0.7704  ***
## warm.coolWarm   -0.5057  0.1280  -3.9509  <.0001  -0.7565  -0.2548  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We model warm versus cool without and intercept so we can visualise the estimates easier.

```
meta_trait_warm_nointer <- rma.mv(es, VCV_shared, mod = ~warm.cool -
    1, random = list(~1 | study_code, ~1 | obs), data = rdata,
    test = "t", dfs = "contain", method = "REML")
```

```
summary(meta_trait_warm_nointer)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3828.9782   7657.9564   7665.9564   7686.9928   7665.9846
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.0837  2.2547    340     no  study_code
## sigma^2.2  4.2511  2.0618   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39145.1933, p-val < .0001
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 106.1596, p-val < .0001
##
## Model Results:
##
##                estimate      se      zval    pval    ci.lb    ci.ub
## warm.coolCool   -1.0722  0.1540   -6.9633  <.0001  -1.3739  -0.7704  ***
## warm.coolWarm   -1.5778  0.1532  -10.2985  <.0001  -1.8781  -1.2776  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Difference

```
meta_trait_diff <- rma.mv(es, VCV_shared, mod = ~diff, random = list(~1 |
    study_code, ~1 | obs), test = "t", dfs = "contain", data = rdata,
    method = "REML")
```

```
summary(meta_trait_diff)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3828.8765   7657.7529   7665.7529   7686.7894   7665.7812
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.1566  2.2708    340     no  study_code
## sigma^2.2  4.2399  2.0591   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39327.3415, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 15.6189, p-val < .0001
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt   -1.3368  0.1404  -9.5227  <.0001  -1.6120  -1.0617  ***
## diff      -0.0339  0.0086  -3.9521  <.0001  -0.0508  -0.0171  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Treatment temperature as a quadratic effect

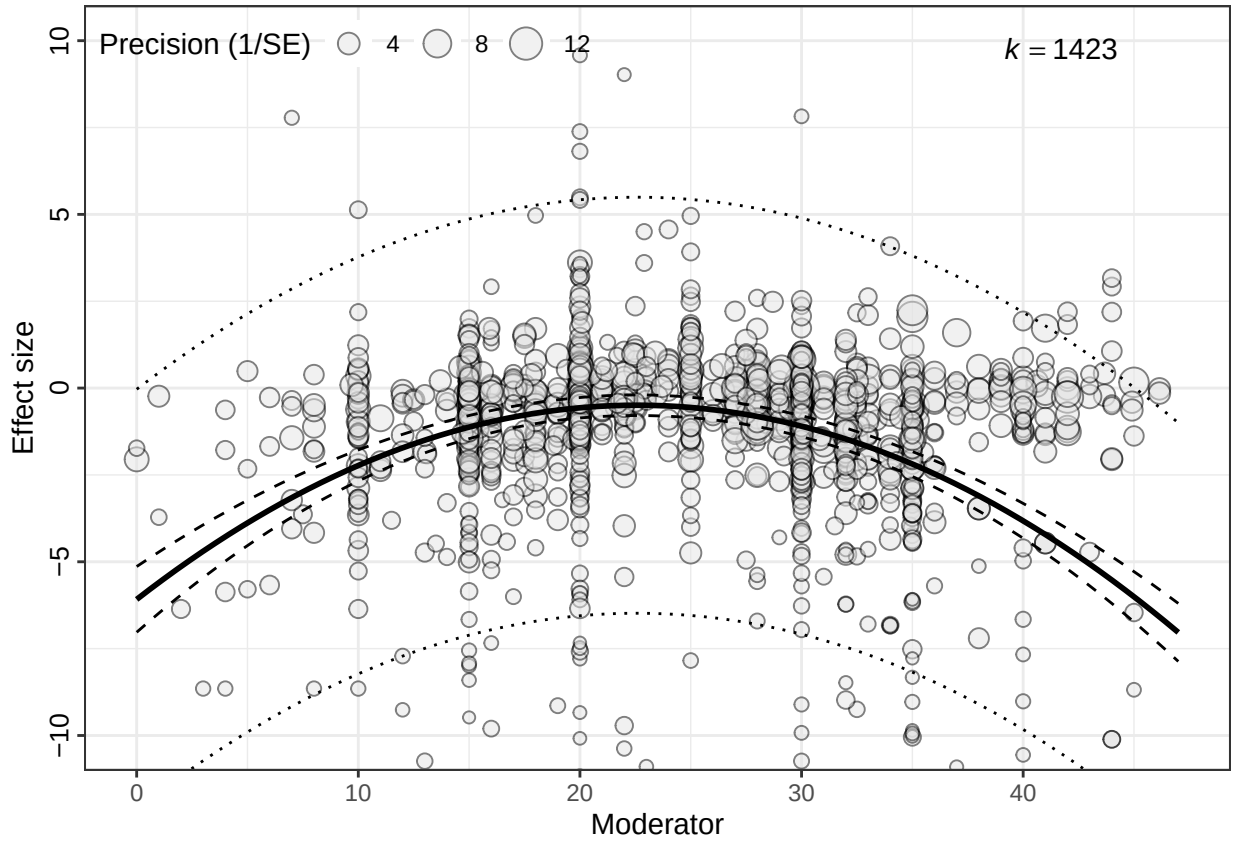
We expect that treatment temperature will have a quadratic effect on reproduction. In other words, we expect that reproduction will decrease either side of an optimum temperature for each species. We also assume that this optimum temperature will be close to the control temperature. That said, we investigate **treattemp** as a quadratic fixed effect.

```
meta_trait_treat2 <- rma.mv(es, VCV_shared, mod = ~poly(treattemp,
    degree = 2, raw = TRUE), random = list(~1 | study_code, ~1 |
    obs), test = "t", dfs = "contain", data = rdata, method = "REML")
```

```
summary(meta_trait_treat2)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3750.0876   7500.1753   7510.1753   7536.4673   7510.2177
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.7801  2.4042    340     no  study_code
## sigma^2.2  3.5306  1.8790   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1420) = 37352.2717, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 186.7480, p-val < .0001
##
## Model Results:
##
##                                          estimate      se      zval    pval    ci.lb    ci.ub
## intrcpt                                   -6.0828  0.4976  -12.2239  <.0001  -7.0581  -5.1075  ***
## poly(treattemp, degree = 2, raw = TRUE)1   0.4951  0.0418   11.8515  <.0001   0.4133   0.5770  ***
## poly(treattemp, degree = 2, raw = TRUE)2  -0.0110  0.0008  -12.9197  <.0001  -0.0126  -0.0093  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Below is a bubble plot of the fitted quadratic model.



Modelling response with binned treatment temperatures

The last model we will try is one with categorised or 'binned' treatment temperatures. We categories our effect sizes into one seven bins depending on the treatment temperature. The bins and the number of effect sizes in each bin are given below

```
## [1] "<15"   ">40"   "15-20" "20-25" "25-30" "30-35" "35-40"
```

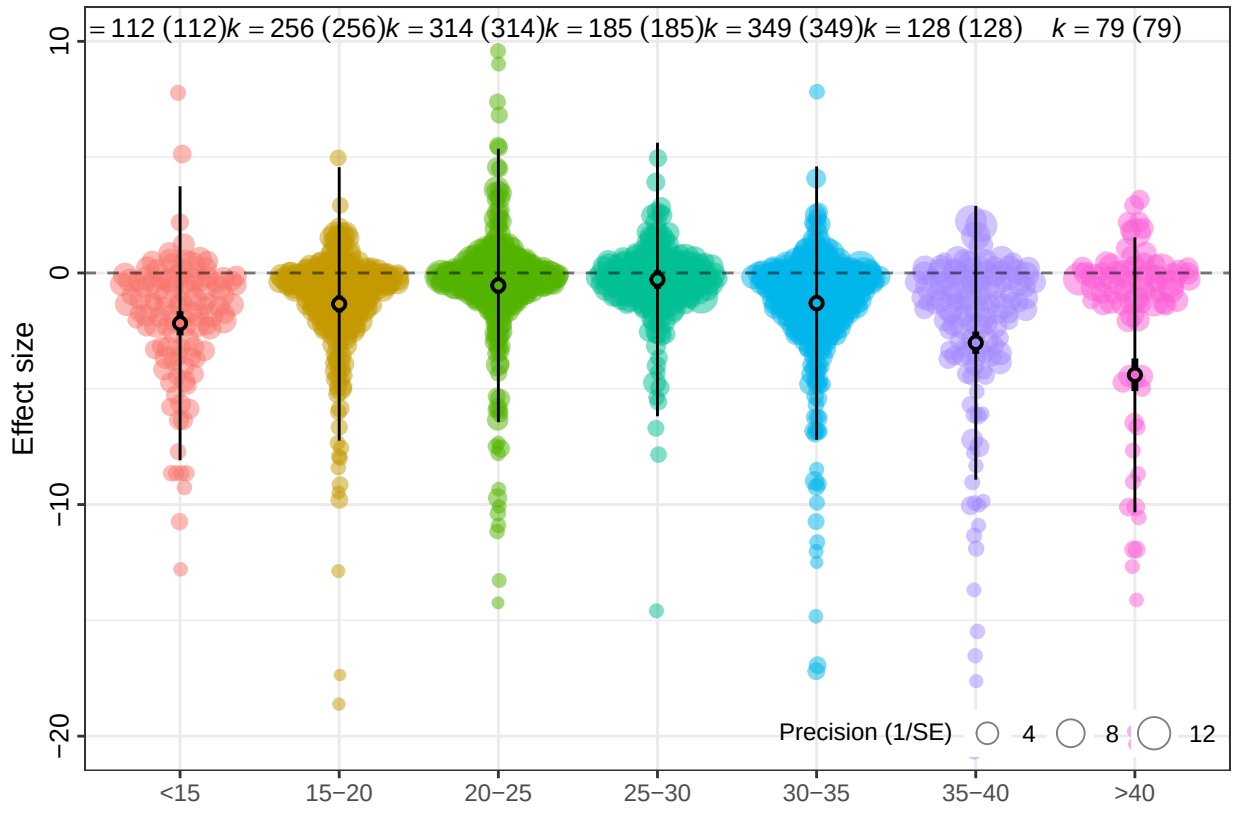
```
table(rdata$bin.temp)
```

```
##
##   <15   >40 15-20 20-25 25-30 30-35 35-40
##   112    79   256   314   185   349   128
```

```
meta_trait_bintemp <- rma.mv(es, VCV_shared, mod = ~bin.temp -
    1, random = list(~1 | study_code, ~1 | obs), data = rdata,
    method = "REML")
```

```
summary(meta_trait_bintemp)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3731.3772   7462.7544   7480.7544   7528.0547   7480.8824
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.5217  2.3498    340     no  study_code
## sigma^2.2  3.5140  1.8746   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1416) = 36953.4464, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 295.5739, p-val < .0001
##
## Model Results:
##
##                estimate      se      zval    pval    ci.lb    ci.ub
## bin.temp<15     -2.1735  0.2644   -8.2216  <.0001  -2.6916  -1.6553  ***
## bin.temp>40     -4.3977  0.3593  -12.2402  <.0001  -5.1018  -3.6935  ***
## bin.temp15-20   -1.3375  0.1864   -7.1768  <.0001  -1.7028  -0.9722  ***
## bin.temp20-25   -0.5414  0.1761   -3.0741  0.0021  -0.8866  -0.1962   **
## bin.temp25-30   -0.2829  0.2065   -1.3701  0.1707  -0.6876   0.1218
## bin.temp30-35   -1.3021  0.1721   -7.5644  <.0001  -1.6395  -0.9647  ***
## bin.temp35-40   -3.0130  0.2457  -12.2614  <.0001  -3.4946  -2.5314  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


= 112 (112)k = 256 (256)k = 314 (314)k = 185 (185)k = 349 (349)k = 128 (128) k = 79 (79)
Effect size
10
0
−10
−20
Precision (1/SE)
4
8
12
<15
15−20
20−25
25−30
30−35
35−40
>40

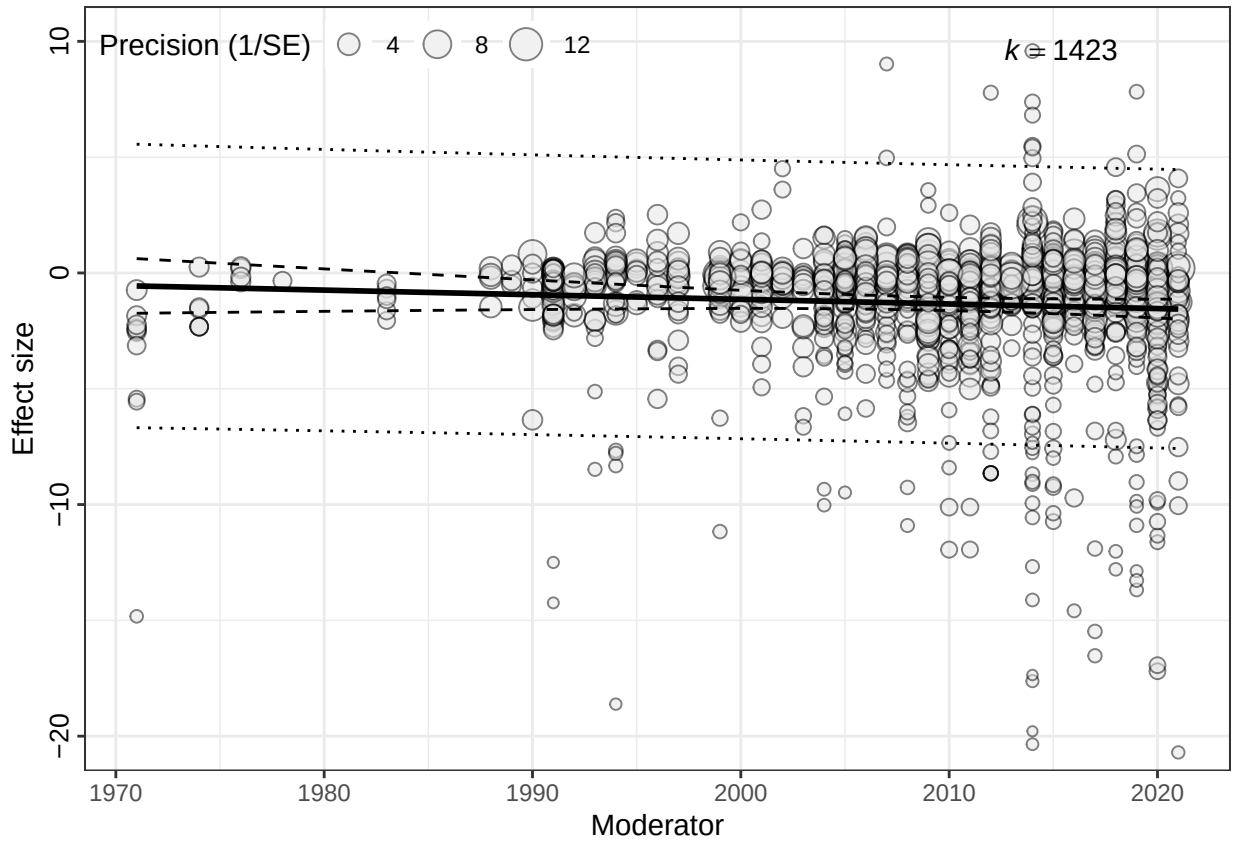
Publication Bias.

We fit meta-regression model with year as a moderator to see whether there is an publication bias. In other words, is effect size strongly correlated with publication year. We found now evidence to suggest that year has an effect on the report effect sizes. A summary of the model is given below.

```
meta_year <- rma.mv(es, VCV_shared, mod = ~Publication.year,
    random = list(~1 | study_code, ~1 | obs), data = rdata, test = "t",
    dfs = "contain", method = "REML")
```

```
summary(meta_year)
```

```
##
## Multivariate Meta-Analysis Model (k = 1423; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3835.0508   7670.1016   7678.1016   7699.1381   7678.1299
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  5.0693  2.2515    340     no  study_code
## sigma^2.2  4.3197  2.0784   1423     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1421) = 39431.7962, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.7366, p-val = 0.1876
##
## Model Results:
##
##                   estimate       se     zval    pval     ci.lb    ci.ub
## intrcpt            38.7171  30.3905   1.2740  0.2027  -20.8471  98.2813
## Publication.year   -0.0199   0.0151  -1.3178  0.1876   -0.0496   0.0097
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Precision (1/SE)
4
8
12
k = 1423
10
0
−10
−20
Effect size
1970
1980
1990
2000
2010
2020
Moderator

Sensitivty Analysis

Here, we perform a sensitivity analysis by removing the smallest and largest 2.5% of effect sizes.

The 2.5th and 97.5th percentiles are given below.

```
print(minq)
```

```
##      2.5%
## -14.17649
```

```
print(maxq)
```

```
##    97.5%
## 2.347279
```

The summary of the effective sizes is now

```
summary(sdata$es)
```

```
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -14.1203  -1.8264  -0.6221  -1.3539   0.0000   2.3381
```

We run the quadratic treatment temperature and the binned temperature models again with our new subsetted data i.e. only with data that is between the 2.5Th and 97.5Th percentile.

Treatment temperature as a quadratic effect (sesnsitivity analysis)

We re-create the variance-covariance matrix with our new substted data, which we name sdata. Then we run the meta analysis model again with treatment temperature as quadratic fixed effect,

```
# recreate vcv_shared matrix
VCV_shared_sa <- impute_covariance_matrix(vi = sdata$v, cluster = sdata$shared_control,
    r = 0.5)
```

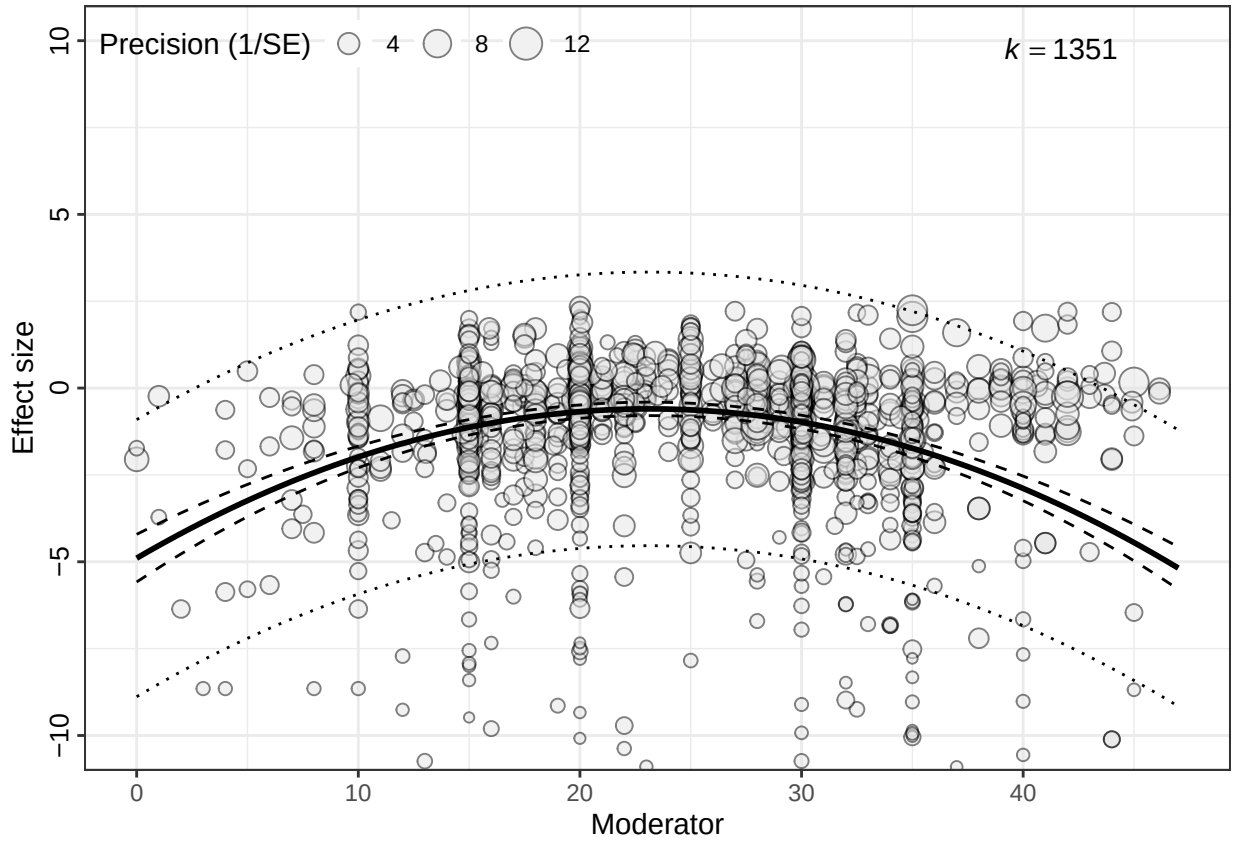
```
meta_sa_treat2 <- rma.mv(es, VCV_shared_sa, mod = ~poly(treattemp,
    degree = 2, raw = TRUE), random = list(~1 | study_code, ~1 |
    obs), test = "t", dfs = "contain", data = sdata, method = "REML")
```

```
summary(meta_sa_treat2)
```

```
##
## Multivariate Meta-Analysis Model (k = 1351; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2741.7575   5483.5151   5493.5151   5519.5470   5493.5598
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  2.1308  1.4597    334     no  study_code
## sigma^2.2  1.8965  1.3771   1351     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1348) = 29193.2105, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 173.9336, p-val < .0001
##
```

```
## Model Results:
##
##                                          estimate      se      zval    pval    ci.lb    ci.ub
## intrcpt                                   -4.8959  0.3601  -13.5956  <.0001  -5.6017  -4.1901  ***
## poly(treattemp, degree = 2, raw = TRUE)1   0.3717  0.0306   12.1579  <.0001   0.3118   0.4316  ***
## poly(treattemp, degree = 2, raw = TRUE)2  -0.0080  0.0006  -12.9093  <.0001  -0.0093  -0.0068  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Below is a bubble plot of the fitted quadratic model to the subsetted data.



Modelling response with binned treatment temperatures

Lastly, we rerun the model where our effect sizes are categorised into one seven bins depending on the treatment temperature. The bins and the number of effect sizes in each bin of the new subsetted data are given below

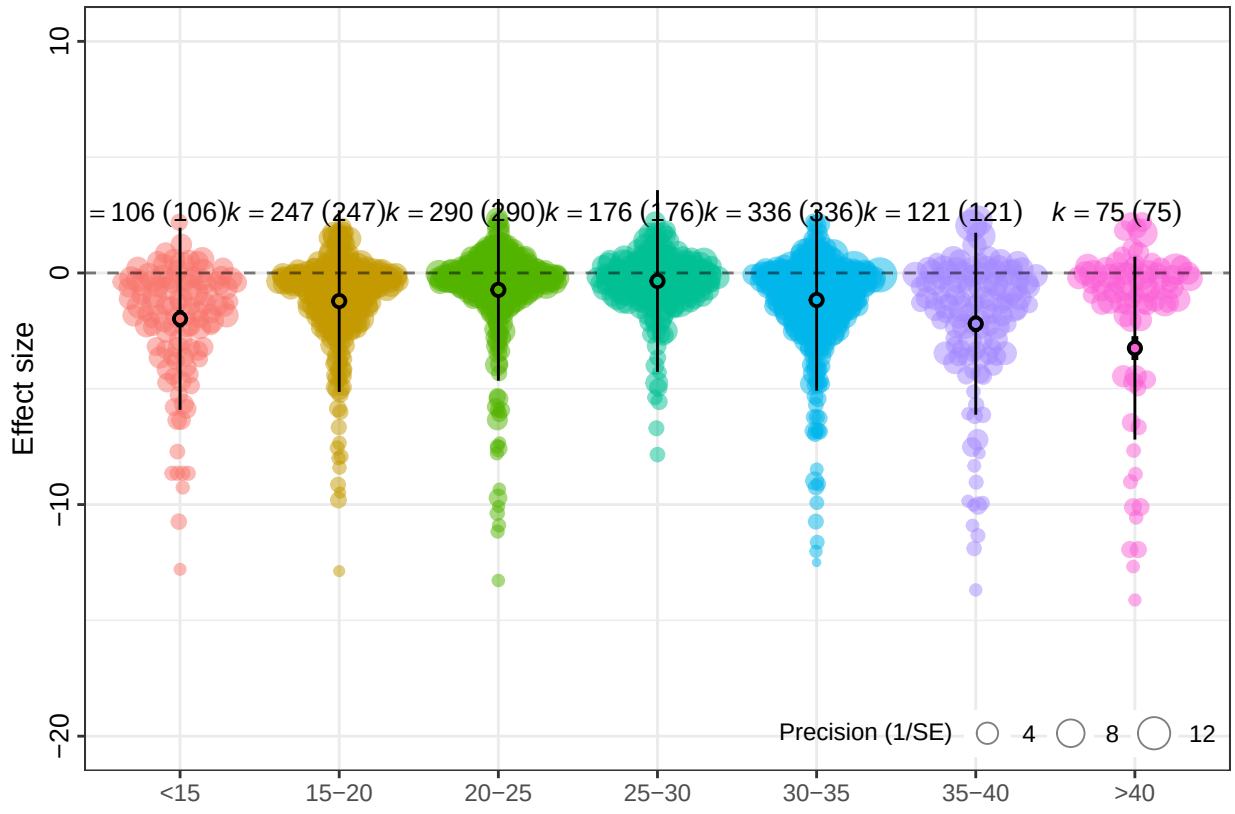
```
table(sdata$bin.temp)
```

```
##
##   <15   >40 15-20 20-25 25-30 30-35 35-40
##   106    75   247   290   176   336   121
```

```
meta_sa_bintemp <- rma.mv(es, VCV_shared_sa, mod = ~bin.temp -
    1, random = list(~1 | study_code, ~1 | obs), data = sdata,
    test = "t", dfs = "contain", method = "REML")
```

```
summary(meta_sa_bintemp)
```

```
##
## Multivariate Meta-Analysis Model (k = 1351; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2735.0546   5470.1092   5488.1092   5534.9399   5488.2442
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  2.0708  1.4390    334     no  study_code
## sigma^2.2  1.9164  1.3843   1351     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1344) = 29044.8493, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 339.9024, p-val < .0001
##
## Model Results:
##
##                estimate      se      zval    pval    ci.lb    ci.ub
## bin.temp<15     -1.9772  0.1899  -10.4114  <.0001  -2.3494  -1.6050  ***
## bin.temp>40     -3.2455  0.2628  -12.3516  <.0001  -3.7605  -2.7305  ***
## bin.temp15-20   -1.2133  0.1286   -9.4342  <.0001  -1.4654  -0.9613  ***
## bin.temp20-25   -0.7288  0.1223   -5.9603  <.0001  -0.9684  -0.4891  ***
## bin.temp25-30   -0.3475  0.1462   -2.3778  0.0174  -0.6340  -0.0611    *
## bin.temp30-35   -1.1681  0.1174   -9.9500  <.0001  -1.3983  -0.9380  ***
## bin.temp35-40   -2.1928  0.1777  -12.3429  <.0001  -2.5410  -1.8446  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Now we completely remove any study that has an effect size in the highest or lowest 2.5%.

```
summary(meta_sub_bintemp)
```

```
##
## Multivariate Meta-Analysis Model (k = 1253; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2377.2698   4754.5396   4772.5396   4818.6888   4772.6852
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  1.4315  1.1965    310     no  study_code
## sigma^2.2  1.5062  1.2273   1253     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1246) = 25250.1123, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 304.1193, p-val < .0001
##
## Model Results:
##
```

```
##                estimate      se      zval    pval    ci.lb    ci.ub
## bin.temp<15     -1.9033  0.1696  -11.2237  <.0001  -2.2356  -1.5709  ***
## bin.temp>40     -2.1787  0.2545   -8.5598  <.0001  -2.6775  -1.6798  ***
## bin.temp15-20   -1.1631  0.1149  -10.1219  <.0001  -1.3884  -0.9379  ***
## bin.temp20-25   -0.6255  0.1090   -5.7381  <.0001  -0.8392  -0.4119  ***
## bin.temp25-30   -0.3477  0.1306   -2.6632  0.0077  -0.6036  -0.0918   **
## bin.temp30-35   -1.1636  0.1050  -11.0774  <.0001  -1.3695  -0.9577  ***
## bin.temp35-40   -1.7249  0.1641  -10.5094  <.0001  -2.0466  -1.4032  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Geary;'s Test

Here we use Geary's test to determine which effect sizes to remove. According to Hedges et al 1999, effect sizes are deemed valid and accurate when the standardized mean of either the control or the treatment group is > 3. In other words, if

$$\frac{\bar{X}}{SD}\sqrt{N} * * \geq 3$$