

Meta-Analysis Reproduction Summary Excluding HUM251

Fay Frost

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 phylogenetic 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
```

```
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")
```

```
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
```

```
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 = ~c_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      -1.3476  0.1399  -9.6331  <.0001   -1.6218   -1.0734  ***  
## c_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

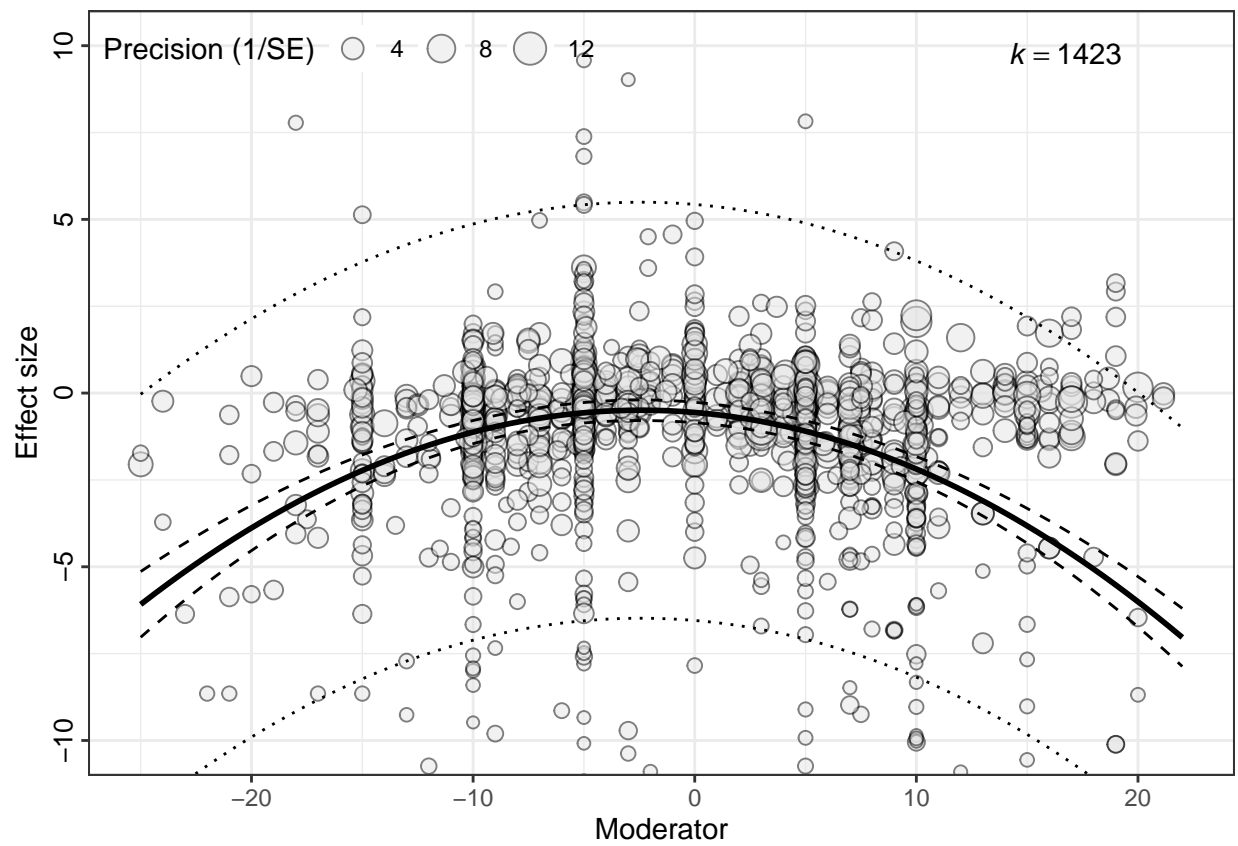
We expect that treatment temperature will have a quadratic effect on reproduction. In other words, we expect that reproduction will decrease either side of an optimum temperature for each species. We also assume that this optimum temperature will be close to the control temperature. That said, we investigate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

```
meta_trait_treat2 <- rma.mv(es, VCV_shared, mod = ~poly(c_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
## intrcpt          -0.5574  0.1565   -3.5615  0.0004   -0.8642
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0531  0.0080   -6.6545 <.0001   -0.0688
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0110  0.0008  -12.9197 <.0001   -0.0126
##      ci.ub
## intrcpt          -0.2507 ***
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0375 ***
## poly(c_treattemp, degree = 2, raw = TRUE)2  -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
```

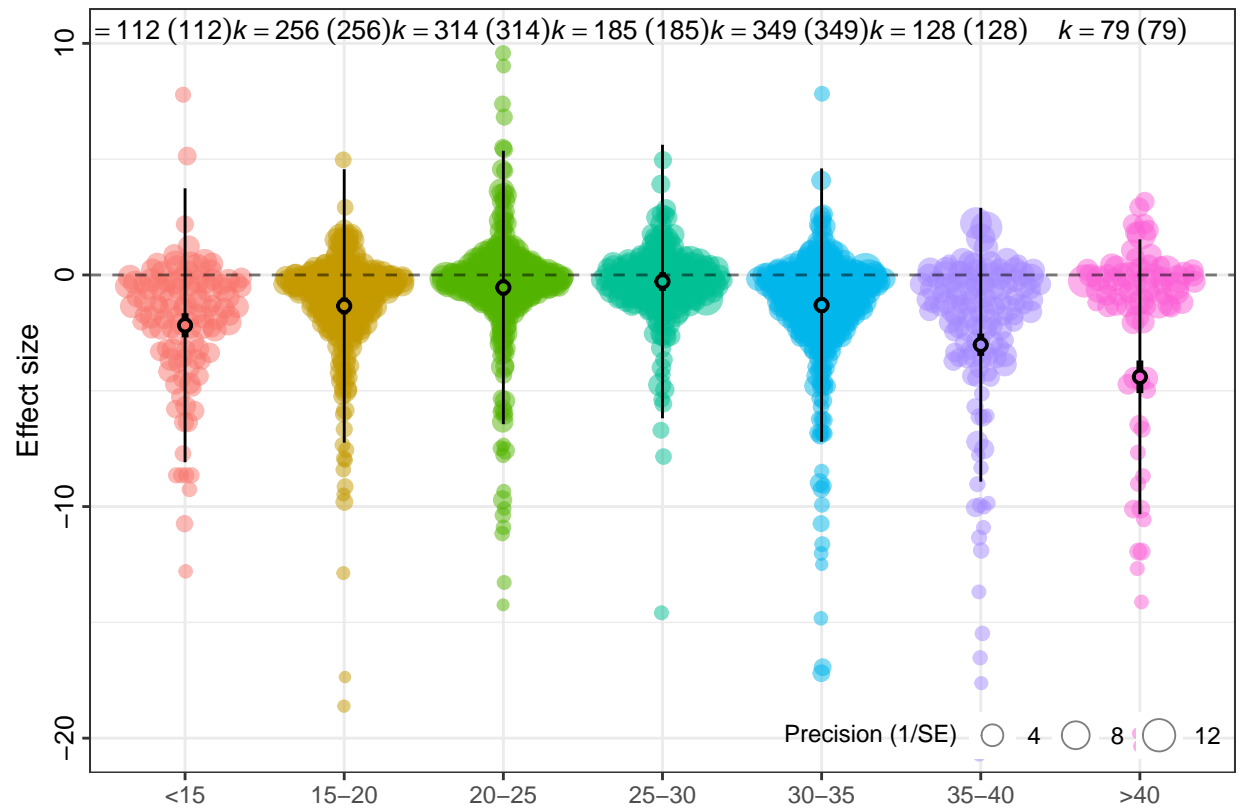
```
## bin.temp30-35 -1.3021 0.1721 -7.5644 <.0001 -1.6395 -0.9647 ***
```

```
## 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
```



Other fixed effects

Here are tabled number of counts for each level of our moderators.

```
table(rdata$Class)
```

```
##
##  Annelida Arachnida Crustacea  Insecta  Rotifera
##      2      215      46      1134      26
```

```
table(rdata$Habitat)
```

```
##
##  Aquatic      Both Terrestrial
##      72      37      1314
```

```
table(rdata$Sex.exposed)
```

```
##
##      Both      Female      Male Parthenogenetic      Unsure
##      891      312      6      211      3
```

```
table(rdata$Fertilisation.mode)
```

```
##
##  External      Internal Parthenogenetic
##      2      1253      4
```

```
table(rdata$Agricultural.importance)
```

```
##
## Control agent      No      Other      Pest
##      414      229      42      738
```

```
table(rdata$Lab.or.field)
```

```
##
##  Field      Lab      Mix Semi-natural
##      8      1380      6      29
```

```
table(rdata$Exposure.duration)
```

```
##
##      < 24 hours      1 to 5 days      Mix More than 5 days Natural variation
##      88      45      22      1260      8
```

```
table(rdata$Life.stage.of.animal)
```

```
##
##  Adult      Egg      Embryo Juvenile      Larvae      Mix      Pupae
##      510      14      3      67      13      788      28
```

Given the imbalance in number of effect sizes in each level, taxonomic class and habitat moderators do not seem like they are going to be useful.

The moderators with the good spreads are (providing we do some recategorisation) are: 1. Sex exposed.

2. Life stage.

Sex exposed

We could lump categories so that we have cases where males are included (Both, Male), versus cases with just females (Female, Parthenogenetic), with Unsure removed. I would predict that the 'Both' category would show the biggest drop for reproduction, but there will be no difference for lifespan

```
table(new_data$Sex.exposed)
```

```
##
## Both Female
## 897 523
```

```
meta_treat_sex <- rma.mv(es, VCV_shared_sex, mod = ~poly(c_treattemp,
  degree = 2, raw = TRUE) * Sex.exposed, random = list(~1 |
  study_code, ~1 | obs), data = new_data, method = "REML")
```

```
summary(meta_treat_sex)
```

```
##
## Multivariate Meta-Analysis Model (k = 1420; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -3721.9875    7443.9749    7459.9749    7502.0083    7460.0774
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  5.8194  2.4123   339     no  study_code
## sigma^2.2  3.4443  1.8559  1420     no      obs
##
## Test for Residual Heterogeneity:
## QE(df = 1414) = 36971.0150, p-val < .0001
##
## Test of Moderators (coefficients 2:6):
## QM(df = 5) = 222.5186, p-val < .0001
##
## Model Results:
##
##                                     estimate      se      zval
## intrcpt                           -0.6791  0.1935  -3.5089
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0233  0.0098  -2.3823
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0098  0.0010  -9.6886
## Sex.exposedFemale                    0.3007  0.3120   0.9635
## poly(c_treattemp, degree = 2, raw = TRUE)1:Sex.exposedFemale -0.0818  0.0154  -5.2981
## poly(c_treattemp, degree = 2, raw = TRUE)2:Sex.exposedFemale -0.0036  0.0016  -2.2121
##                                     pval      ci.lb      ci.ub
## intrcpt                           0.0005  -1.0584  -0.2998 ***
## poly(c_treattemp, degree = 2, raw = TRUE)1  0.0172  -0.0425  -0.0041  *
## poly(c_treattemp, degree = 2, raw = TRUE)2  <.0001  -0.0118  -0.0078 ***
## Sex.exposedFemale                    0.3353  -0.3109   0.9123
## poly(c_treattemp, degree = 2, raw = TRUE)1:Sex.exposedFemale <.0001  -0.1121  -0.0515 ***
## poly(c_treattemp, degree = 2, raw = TRUE)2:Sex.exposedFemale 0.0270  -0.0067  -0.0004  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Life-stage

We could lump categories so that we have cases where only adults were exposed (Adult), versus cases where immature stages were exposed (Juvenile, Larvae, Pupae, Mix)- perhaps after excluding 'Egg' and 'Embryo' because these categories are a bit weird. I would predict that exposure of juveniles is worse than just exposure of adults

```
table(ls_data$Life.stage.of.animal)
```

```
##
##      Adult Immature
##      510      896
```

```
meta_treat_ls <- rma.mv(es, VCV_shared_life, mod = ~poly(c_treattemp,
  degree = 3, raw = TRUE) * Life.stage.of.animal, random = list(~1 |
  study_code, ~1 | obs), data = ls_data, method = "REML")
```

```
summary(meta_treat_ls)
```

```
##
## Multivariate Meta-Analysis Model (k = 1406; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -3628.5929    7257.1858    7277.1858    7329.6138    7277.3444
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  5.6736  2.3819   339     no  study_code
## sigma^2.2  3.1344  1.7704  1406     no      obs
##
## Test for Residual Heterogeneity:
## QE(df = 1398) = 35515.0429, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 225.6003, p-val < .0001
##
## Model Results:
##
##                                     estimate      se
## intrcpt                           -0.7501  0.2483
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.0010  0.0178
## poly(c_treattemp, degree = 3, raw = TRUE)2  -0.0070  0.0012
## poly(c_treattemp, degree = 3, raw = TRUE)3  -0.0001  0.0001
## Life.stage.of.animalImmature              0.3158  0.3055
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature -0.0450  0.0224
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature -0.0081  0.0016
## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature -0.0001  0.0001
##                                     zval      pval
## intrcpt                           -3.0205  0.0025
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.0566  0.9548
## poly(c_treattemp, degree = 3, raw = TRUE)2  -5.7093 <.0001
## poly(c_treattemp, degree = 3, raw = TRUE)3  -1.2547  0.2096
## Life.stage.of.animalImmature              1.0336  0.3013
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature -2.0054  0.0449
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature -5.0127 <.0001
```

```

## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature -1.3023 0.1928
##                                     ci.lb    ci.ub
## intrcpt                           -1.2368 -0.2634
## poly(c_treattemp, degree = 3, raw = TRUE)1 -0.0359 0.0339
## poly(c_treattemp, degree = 3, raw = TRUE)2 -0.0094 -0.0046
## poly(c_treattemp, degree = 3, raw = TRUE)3 -0.0003 0.0001
## Life.stage.of.animalImmature             -0.2830 0.9146
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature -0.0890 -0.0010
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature -0.0113 -0.0049
## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature -0.0004 0.0001
##
## intrcpt                                **
## poly(c_treattemp, degree = 3, raw = TRUE)1
## poly(c_treattemp, degree = 3, raw = TRUE)2      ***
## poly(c_treattemp, degree = 3, raw = TRUE)3
## Life.stage.of.animalImmature
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature      *
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature      ***
## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Sub-analysis on pest species

```
pest_data <- subset(rdata, Agricultural.importance == "Pest")

VCV_shared_pest <- impute_covariance_matrix(vi = pest_data$v,
  cluster = pest_data$shared_control, r = 0.5)

meta_pest <- rma.mv(es, VCV_shared_pest, mod = ~poly(c_treattemp,
  degree = 2, raw = TRUE), random = list(~1 | study_code, ~1 |
  obs), data = pest_data, method = "REML")
```

```
summary(meta_pest)
```

```
##
## Multivariate Meta-Analysis Model (k = 738; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -1665.5404    3331.0807    3341.0807    3364.0801    3341.1630
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  1.9983  1.4136   167     no  study_code
## sigma^2.2  3.0740  1.7533   738     no      obs
##
## Test for Residual Heterogeneity:
## QE(df = 735) = 19340.0145, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 49.6619, p-val < .0001
##
## Model Results:
##
##                                     estimate      se      zval      pval      ci.lb
## intrcpt                           -0.5928  0.1512  -3.9214  <.0001  -0.8892
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0241  0.0097  -2.4982  0.0125  -0.0431
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0073  0.0011  -6.9279  <.0001  -0.0093
##                                     ci.ub
## intrcpt                           -0.2965 ***
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0052  *
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0052  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

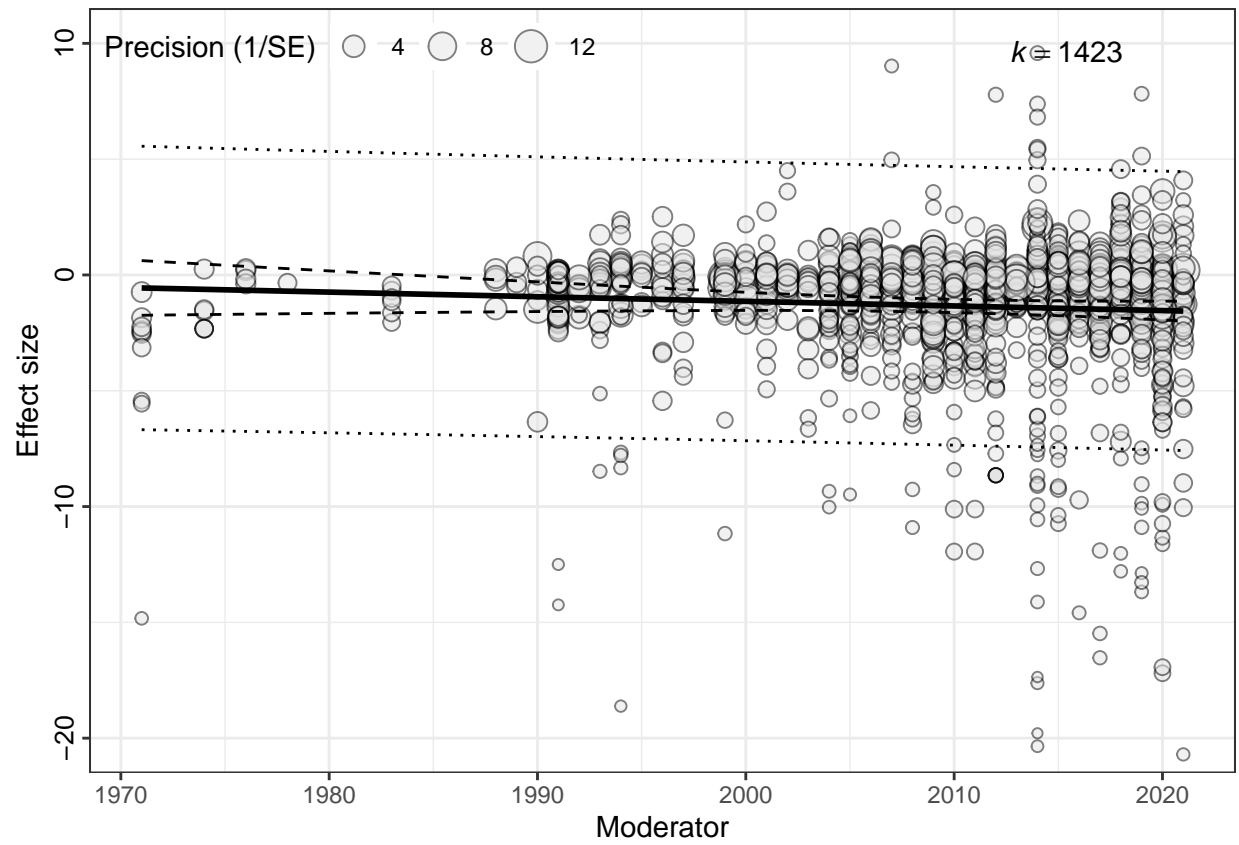
Publication Bias.

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
```



Sensitivity 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 subsetting data i.e. only with data that is between the 2.5th and 97.5th percentile.

Treatment temperature as a quadratic effect (sensitivity analysis)

We re-create the variance-covariance matrix with our new subsetting 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(c_treattemp,  
  degree = 2, raw = TRUE), random = list(~1 | study_code, ~1 |  
  obs), test = "t", dfs = "contain", data = sdata, method = "REML")
```

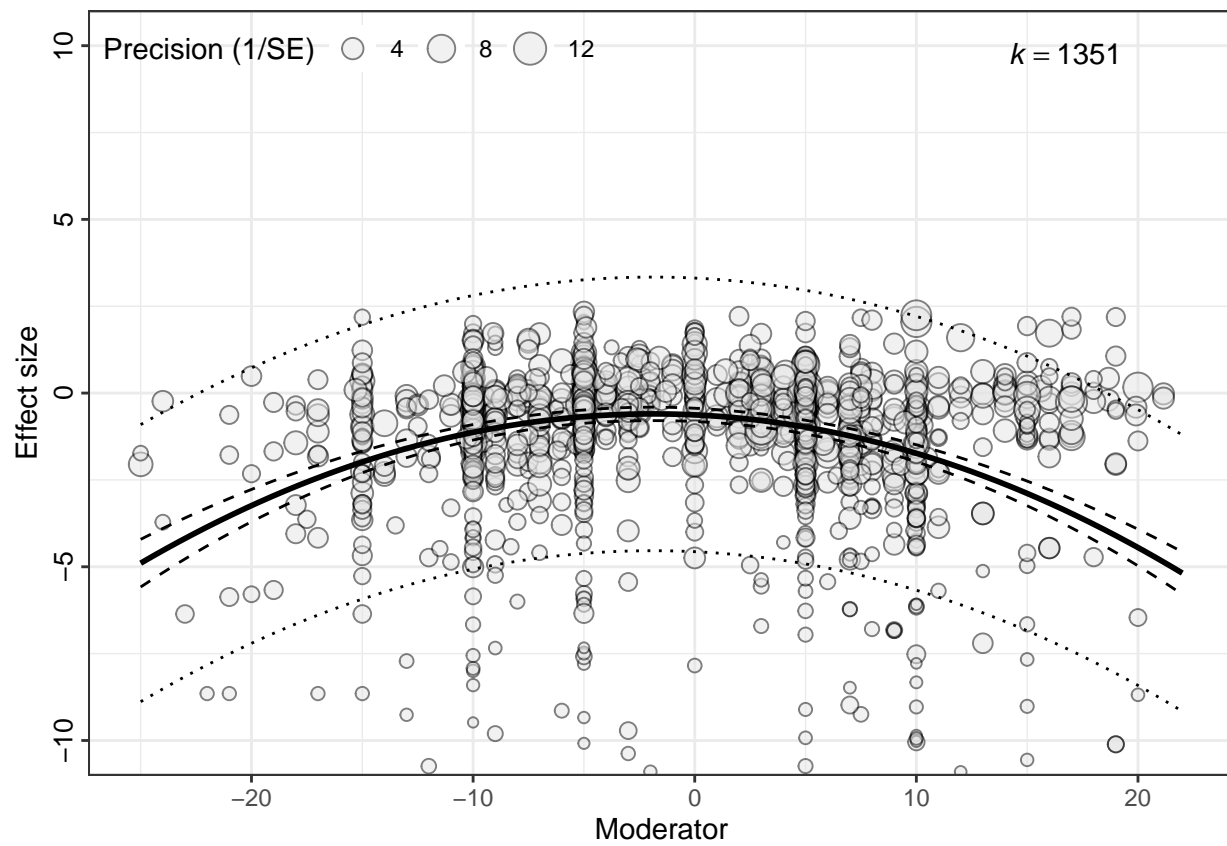
```
summary(meta_sa_treat2)
```

```
##  
## 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
## intrcpt          -0.6271  0.1028   -6.1032 <.0001   -0.8285
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0302  0.0059   -5.0861 <.0001   -0.0418
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0080  0.0006  -12.9093 <.0001   -0.0093
##               ci.ub
## intrcpt          -0.4257 ***
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0186 ***
## poly(c_treattemp, degree = 2, raw = TRUE)2  -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 subsetting data.



Modelling response with binned treatment temperatures

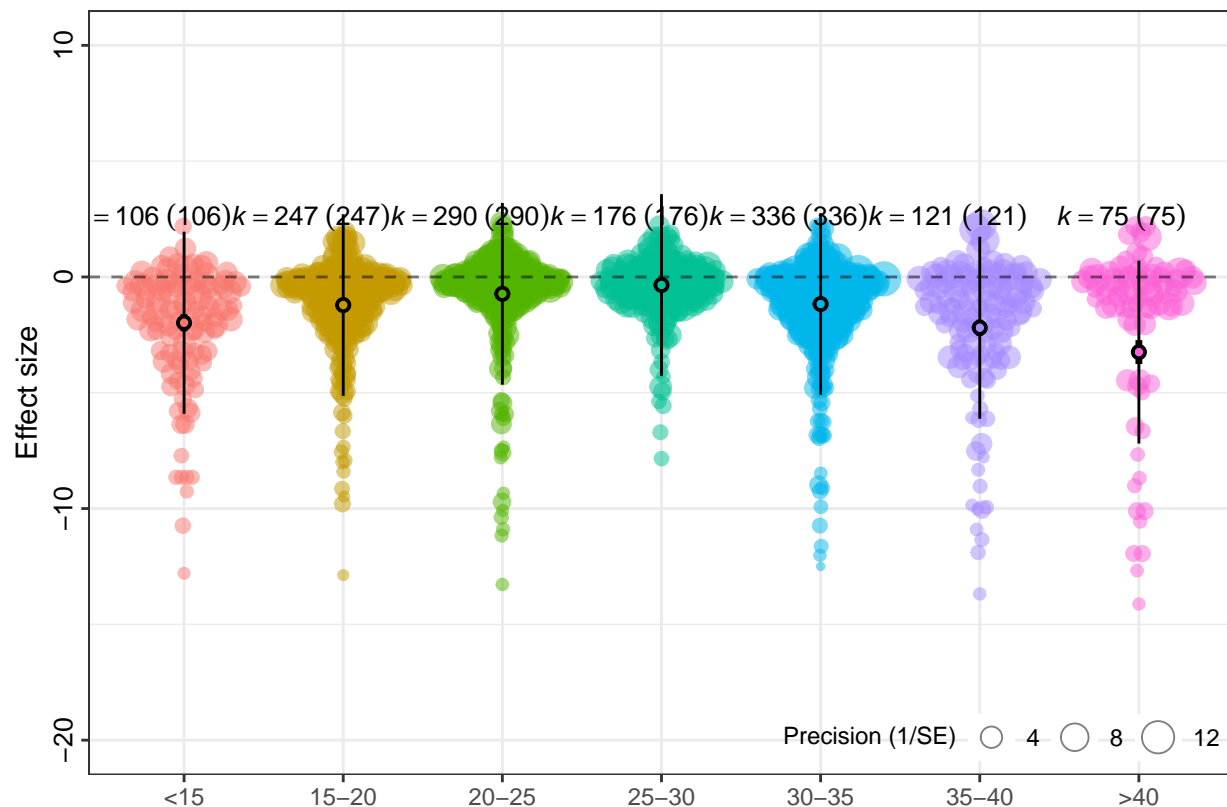
Lastly, we rerun the model where our effect sizes are categorised into one seven bins depending on the treatment temperature. The bins and the number of effect sizes in each bin of the new subsetting data are given below

```
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

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

As a sensitivity analysis we will determine which of our effect sizes do not meet this threshold i.e. are < 3 . We then rerun our best fitting models with these effect sizes removed.

```
# Read in data with calculated standardised mean
gearydata <- read.csv("Data/Gearys_test_data.csv")

# view the first fews rows of selected columns
gearydata %>%
  dplyr::select(Experiment.code, Trait.category, reftemp, treattemp,
    es, v, gtest) %>%
  head(., 30)

# How many effect sozes have a standardised mean < 3 ?
outliers_lon <- subset(gearydata, Trait.category == "Longevity" &
  gtest < 3) #82
outliers_sur <- subset(gearydata, Trait.category == "Survival" &
  gtest < 3) # 171
outliers_rep <- subset(gearydata, Trait.category == "Reproduction" &
  gtest < 3) # 3
```

There are 256 effect sizes in total that have a $gtest < 3$. 82 of these are longevity effect sizes, 3 are survival and 171 are reproduction.

We remove these effect sizes and rerun the best fitting model from earlier which is the model `meta_trait_treat2`, where temperature is modelled as a quadratic effect on reproduction.

Treatment temperature as a quadratic effect with Geary's outliers removed.

```
# Remove outliers
s.gearydata <- gearydata %>%
  subset(gtest > 3)

# Resubset reproduction dat
gdata_rep_warm <- subset(s.gearydata, Trait.category == "Reproduction" &
```

```

    warm.cool == "Warm")
gdata_rep_cool <- subset(s.gearydata, Trait.category == "Reproduction" &
    warm.cool == "Cool")

all_gdata <- rbind(gdata_rep_warm, gdata_rep_cool)

all_gdata <- all_gdata %>%
    mutate(c_treattemp = treattemp - 25)

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

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

# recalculate v matrix
all_gdata$shared_control <- factor(all_gdata$Effect.size.code)
VCV_shared_ga <- impute_covariance_matrix(vi = all_gdata$v, cluster = all_gdata$shared_control,
    r = 0.5)

summary(meta_ga_treat2)

```

```

##
## Multivariate Meta-Analysis Model (k = 1198; method: REML)
##
##      logLik      Deviance      AIC      BIC      AICc
## -3224.0379    6448.0758    6458.0758    6483.5053    6458.1263
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  6.2549  2.5010   330     no  study_code
## sigma^2.2  4.0534  2.0133   1198     no      obs
##
## Test for Residual Heterogeneity:
## QE(df = 1195) = 33797.9756, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## F(df1 = 2, df2 = 1195) = 71.8333, p-val < .0001
##
## Model Results:
##
##      estimate      se      tval      df      pval      ci.lb
## intrcpt          -0.4916  0.1698   -2.8947   327  0.0041   -0.8257
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0580  0.0097   -5.9797  1195 <.0001   -0.0770
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0114  0.0010  -11.2330  1195 <.0001   -0.0134
##      ci.ub
## intrcpt          -0.1575  **
## poly(c_treattemp, degree = 2, raw = TRUE)1  -0.0390  ***
## poly(c_treattemp, degree = 2, raw = TRUE)2  -0.0094  ***
##

```

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

Below is a bubble plot of the fitted quadratic model.

