Meta-Analysis for Longevity 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 longevity.

2. Setup

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

```r
### Read in effect size data
effectdata <- read.csv("Survival project all pairwise.es.csv")
longdata_warm <- subset(effectdata, Trait.category == "Longevity" &
    warm.cool == "Warm")
longdata_cool <- subset(effectdata, Trait.category == "Longevity" &
    warm.cool == "Cool")

alllong <- rbind(longdata_warm, longdata_cool)

### select data for analysis
rdata <- alllong

rdata <- subset(rdata, Paper.code != "HUM251")

rdata <- rdata %>%
    mutate(c_treattemp = treattemp - 25)
```

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.

```r
### 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.

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

```
## [1] 290
```

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

```
## [1] 316
```

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_longevity_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), R = list(Species.phylo = phylo_matrix),
    test = "t", dfs = "contain", data = rdata, method = "REML")
```

```
summary(meta2)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3569.8004   7139.6008   7149.6008   7175.7500   7149.6444
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed          factor    R
## sigma^2.1   0.0000  0.0001    290     no   Species.phylo  yes
## sigma^2.2   0.0000  0.0003    290     no         species   no
## sigma^2.3   0.9558  0.9776    316     no      study_code   no
## sigma^2.4   7.6624  2.7681   1381     no             obs   no
##
## Test for Heterogeneity:
## Q(df = 1380) = 51322.8613, p-val < .0001
##
## Model Results:
##
## estimate       se      zval     pval     ci.lb    ci.ub
##  -0.1783   0.0979   -1.8205   0.0687   -0.3702   0.0137   .
##
## ---
## 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
##    9.908166e+01     4.027427e-08     9.504325e-07    1.098812e+01    8.809354e+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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3558.8224   7117.6449   7127.6449   7153.7941   7127.6886
##
## Variance Components:
##
##               estim     sqrt   nlvls   fixed         factor     R
## sigma^2.1    0.0000   0.0000     290      no   Species.phylo   yes
## sigma^2.2    0.0000   0.0003     290      no         species    no
## sigma^2.3    0.6821   0.8259     316      no      study_code    no
## sigma^2.4    7.9265   2.8154    1381      no             obs    no
##
## Test for Heterogeneity:
## Q(df = 1380) = 69550.4868, p-val < .0001
##
## Model Results:
##
## estimate       se      zval     pval     ci.lb     ci.ub
##  -0.1901   0.0946   -2.0088   0.0446   -0.3756   -0.0046   *
##
## ---
## 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
##    9.908064e+01     1.014580e-10    7.633043e-07    7.850134e+00   9.123051e+01
```

Model without phylogeny

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

```
## without phylogeny
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 = 1381; method: REML)
## 
##      logLik    Deviance         AIC         BIC        AICc
## -3558.8224   7117.6449   7125.6449   7146.5643   7125.6740
## 
## Variance Components:
## 
##             estim    sqrt  nlvls  fixed       factor
## sigma^2.1  0.0000  0.0003    290     no      species
## sigma^2.2  0.6821  0.8259    316     no   study_code
## sigma^2.3  7.9265  2.8154   1381     no          obs
## 
## Test for Heterogeneity:
## Q(df = 1380) = 69550.4868, p-val < .0001
## 
## Model Results:
## 
## estimate      se     tval   df    pval    ci.lb    ci.ub
##  -0.1901  0.0946  -2.0088  289  0.0455  -0.3764  -0.0038  *
## 
## ---
## 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
## 9.908064e+01  9.571908e-07  7.850129e+00  9.123051e+01
```

Model without phylogeny or species

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

```
summary(meta4)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##      logLik    Deviance        AIC         BIC        AICc
## -3558.8224   7117.6449   7123.6449   7139.3344   7123.6623
##
## Variance Components:
##
##            estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6821  0.8259    316     no  study_code
## sigma^2.2  7.9265  2.8154   1381     no         obs
##
## Test for Heterogeneity:
## Q(df = 1380) = 69550.4868, p-val < .0001
##
## Model Results:
##
## estimate      se     zval     pval     ci.lb     ci.ub
##  -0.1901  0.0946  -2.0088   0.0446   -0.3756   -0.0046  *
##
## ---
## 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
##    99.080643      7.850129   91.230514
```

Model without phylogeny, species or study_code

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

```
summary(meta7)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3577.8245   7155.6489   7159.6489   7170.1086   7159.6576
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed  factor
## sigma^2      8.6967  2.9490   1381     no     obs
##
## Test for Heterogeneity:
## Q(df = 1380) = 69550.4868, p-val < .0001
##
## Model Results:
##
## estimate       se     zval     pval    ci.lb     ci.ub
##  -0.2047   0.0817  -2.5071   0.0122  -0.3648   -0.0447  *
##
## ---
## 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
## 99.08988 99.08988
```

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 meta3 . We continue our analysis using meta4 as our base model.

4. Meta-regressions

Starting with the best fitting random-effect model from Section 3, "meta4" 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, which we expect to havea non-linear relationship to longevity.

- **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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3555.9039   7111.8079   7119.8079   7140.7243   7119.8370
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6742  0.8211    316     no  study_code
## sigma^2.2  7.9293  2.8159   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 69486.0682, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.5364, p-val = 0.2152
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt   -1.3024  0.9023  -1.4434  0.1489  -3.0708  0.4661
## reftemp    0.0447  0.0361   1.2395  0.2152  -0.0260  0.1155
##
## ---
## 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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3356.9436   6713.8872   6721.8872   6742.8036   6721.9163
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  1.1335  1.0647    316     no  study_code
## sigma^2.2  5.3123  2.3048   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 48854.1415, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 489.6259, p-val < .0001
##
## Model Results:
##
##              estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt       -0.3127  0.0926  -3.3784  0.0007  -0.4941  -0.1313  ***
## c_treattemp   -0.1907  0.0086 -22.1275  <.0001  -0.2076  -0.1738  ***
##
## ---
## 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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3326.1091   6652.2183   6660.2183   6681.1347   6660.2474
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6254  0.7908    316     no  study_code
## sigma^2.2  5.2758  2.2969   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 46542.1152, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 557.0028, p-val < .0001
##
## Model Results:
##
##                estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt          1.3461  0.1047  12.8548  <.0001   1.1409   1.5514   ***
## warm.coolWarm   -3.0965  0.1312 -23.6009  <.0001  -3.3537  -2.8394   ***
##
## ---
## 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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3326.1091   6652.2183   6660.2183   6681.1347   6660.2474
##
## Variance Components:
##
##              estim    sqrt   nlvls   fixed      factor
## sigma^2.1   0.6254  0.7908     316      no  study_code
## sigma^2.2   5.2758  2.2969    1381      no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 46542.1152, p-val < .0001
##
## Test of Moderators (coefficients 1:2):
## QM(df = 2) = 562.6656, p-val < .0001
##
## Model Results:
##
##                estimate      se      zval     pval    ci.lb    ci.ub
## warm.coolCool    1.3461  0.1047   12.8548   <.0001   1.1409   1.5514   ***
## warm.coolWarm   -1.7504  0.1051  -16.6536   <.0001  -1.9564  -1.5444   ***
##
## ---
## 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), data = rdata, test = "t", dfs = "contain",
    method = "REML")
```

```
summary(meta_trait_diff)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -3343.4388   6686.8776   6694.8776   6715.7940   6694.9067
##
## Variance Components:
##
##            estim    sqrt   nlvls   fixed      factor
## sigma^2.1  0.9889  0.9944     316      no  study_code
## sigma^2.2  5.2509  2.2915    1381      no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 46581.0991, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 520.9053, p-val < .0001
##
## Model Results:
##
##           estimate       se      zval     pval    ci.lb    ci.ub
## intrcpt    -0.2817   0.0894   -3.1495   0.0016  -0.4570  -0.1064    **
## diff       -0.1969   0.0086  -22.8234   <.0001  -0.2138  -0.1800   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Treatment temperature as a cubic effect

We expect that treatment temperature will have a non-linear effect on longevity. We expect that the relationship will be cubic. More specifically, we expect that longevity will increase at cooler temperature and decrease at more extreme higher temperature. We also assume that this optimum temperature will be close to the control temperature. That said, we investigate **treattemp** as a cubic fixed effect.

```
meta_trait_treat3 <- rma.mv(es, VCV_shared, mod = ~poly(c_treattemp,
    degree = 3, raw = TRUE), random = list(~1 | study_code, ~1 |
    obs), test = "t", dfs = "contain", data = rdata, method = "REML")
```

```
summary(meta_trait_treat3)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3289.3464   6578.6928   6590.6928   6622.0588   6590.7541
##
## Variance Components:
##
##             estim     sqrt   nlvls   fixed      factor
## sigma^2.1   0.6631   0.8143     316      no   study_code
## sigma^2.2   4.9962   2.2352    1381      no          obs
##
## Test for Residual Heterogeneity:
## QE(df = 1377) = 45364.6017, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 650.3631, p-val < .0001
##
## Model Results:
##
##                                              estimate       se      zval      pval      ci.lb
## intrcpt                                       -0.0693   0.0986   -0.7027    0.4822    -0.2626
## poly(c_treattemp, degree = 3, raw = TRUE)1    -0.2894   0.0125  -23.2134    <.0001    -0.3139
## poly(c_treattemp, degree = 3, raw = TRUE)2    -0.0031   0.0008   -3.6610    0.0003    -0.0047
## poly(c_treattemp, degree = 3, raw = TRUE)3     0.0006   0.0001   10.6070    <.0001     0.0005
##                                                 ci.ub
## intrcpt                                        0.1240
## poly(c_treattemp, degree = 3, raw = TRUE)1    -0.2650   ***
## poly(c_treattemp, degree = 3, raw = TRUE)2    -0.0014   ***
## poly(c_treattemp, degree = 3, raw = TRUE)3     0.0008   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

For completeness we also investigate treatment temperature as a quadratic 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 = 1381; method: REML)
```

```
##
##      logLik    Deviance       AIC         BIC        AICc
## -3342.2747   6684.5495   6694.5495   6720.6914   6694.5932
##
## Variance Components:
##
##             estim    sqrt   nlvls  fixed      factor
## sigma^2.1  1.1454  1.0702     316     no  study_code
## sigma^2.2  5.1999  2.2803    1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1378) = 48666.3566, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 525.2602, p-val < .0001
##
## Model Results:
##
##                                        estimate      se      zval     pval     ci.lb
## intrcpt                                 -0.0166  0.1093   -0.1517   0.8794   -0.2309
## poly(c_treattemp, degree = 2, raw = TRUE)1   -0.1974  0.0086  -22.8527   <.0001   -0.2143
## poly(c_treattemp, degree = 2, raw = TRUE)2   -0.0045  0.0009   -5.0642   <.0001   -0.0063
##                                          ci.ub
## intrcpt                                 0.1977
## poly(c_treattemp, degree = 2, raw = TRUE)1   -0.1805   ***
## poly(c_treattemp, degree = 2, raw = TRUE)2   -0.0028   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Below is a bubble plot of the fitted cubic model.
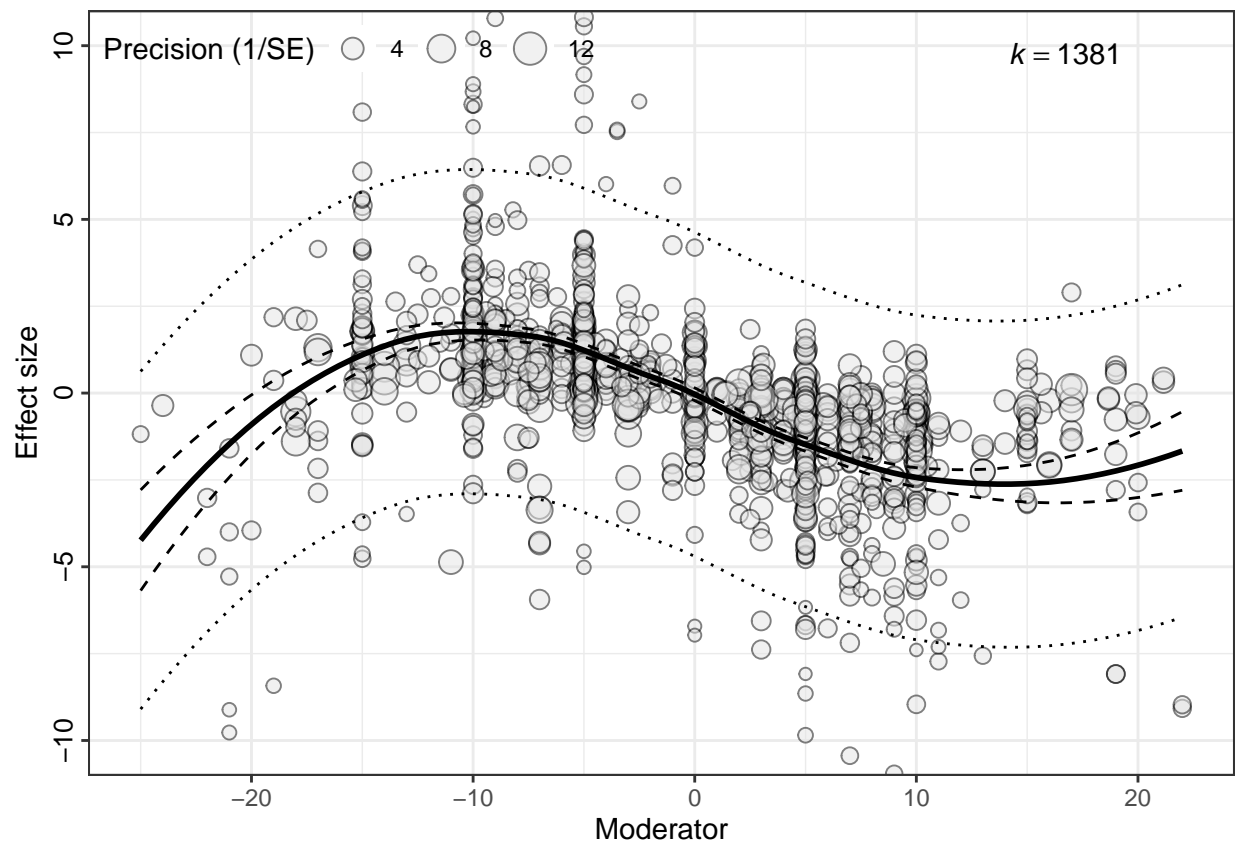
Modelling response with binned treatment temperatures

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

```
table(rdata$bin.temp)

##
##    <15    >40  15-20  20-25  25-30  30-35  35-40
##    110     55    249    316    189    354    108

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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3299.9928   6599.9856   6617.9856   6665.0150   6618.1176
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed      factor
## sigma^2.1   0.7395  0.8599    316     no  study_code
## sigma^2.2   5.0928  2.2567   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1374) = 46257.8558, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 611.7116, p-val < .0001
##
## Model Results:
##
##                estimate      se      zval    pval    ci.lb    ci.ub
## bin.temp<15      0.9640  0.2503    3.8505  0.0001   0.4733   1.4546  ***
## bin.temp>40     -2.1798  0.3798   -5.7387  <.0001  -2.9243  -1.4353  ***
## bin.temp15-20    1.8019  0.1599   11.2684  <.0001   1.4885   2.1153  ***
## bin.temp20-25    1.1145  0.1435    7.7674  <.0001   0.8333   1.3957  ***
## bin.temp25-30   -0.8034  0.1823   -4.4072  <.0001  -1.1607  -0.4461  ***
## bin.temp30-35   -1.7814  0.1366  -13.0396  <.0001  -2.0492  -1.5137  ***
## bin.temp35-40   -2.7791  0.2403  -11.5643  <.0001  -3.2502  -2.3081  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
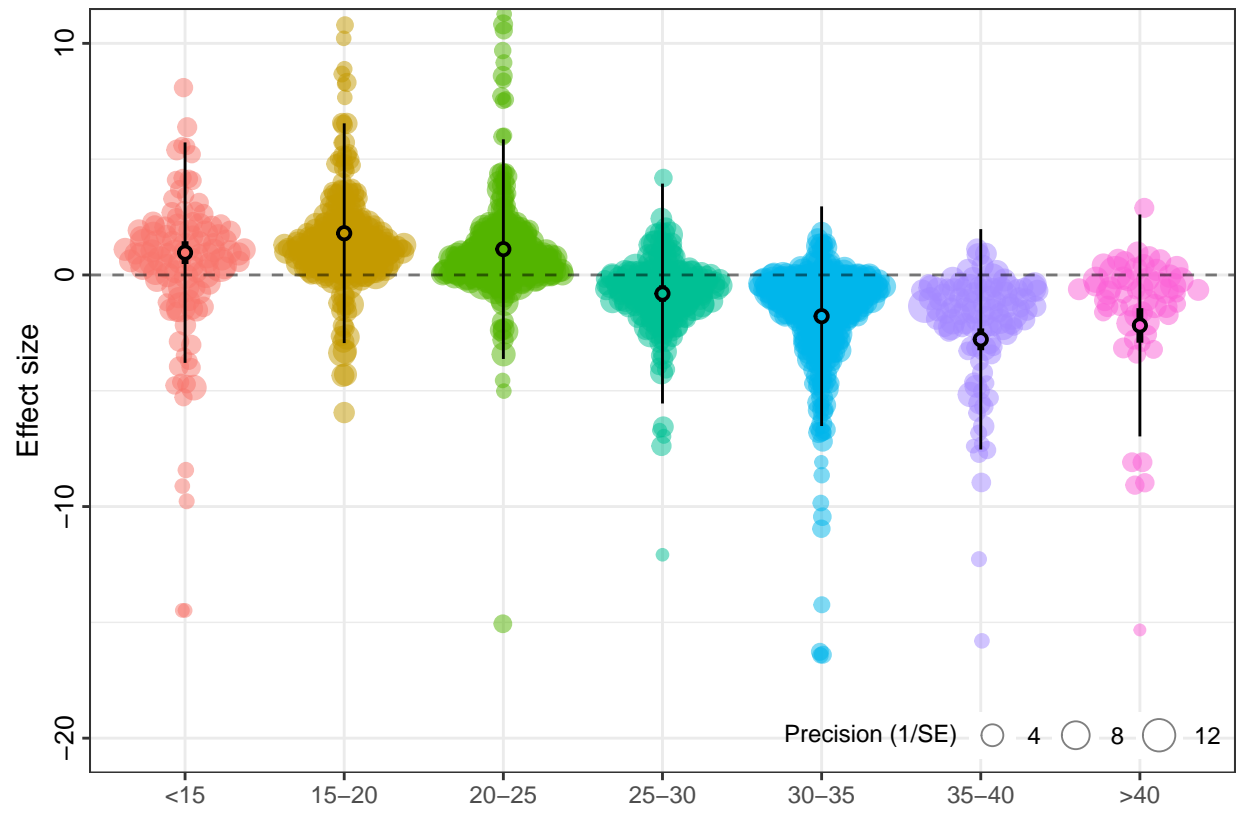
Other fixed effects

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

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

```
##
##  Annelida Arachnida Crustacea   Insecta  Rotifera
##         2       219        28      1106        26
```

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

```
##
##     Aquatic        Both Terrestrial
##          56          55        1270
```

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

```
##
##           Both          Female            Male Parthenogenetic          Unsure
##            573             599               4             202               3
```

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

```
##
##     External     Internal Parthenogenic
##            2         1221             4
```

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

```
##
## Control agent            No         Other          Pest
##           426           203            60           692
```

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

```
##
##         Field           Lab           Mix Semi-natural
##             8          1350             6            17
```

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

```
##
##        < 24 hours        1 to 5 days        2 to 5 days               Mix  More than 5 days
##                72                 19                  2                17              1265
## Natural variation
##                 6
```

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

```
##
##    Adult       Egg   Embryo  Juvenile    Larvae       Mix     Pupae
##      485        14        3        49        13       794        23
```

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
##    577    801
```

```
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 = 1378; method: REML)
##
##      logLik   Deviance        AIC        BIC       AICc
## -3276.2624   6552.5247   6572.5247   6624.7504   6572.6866
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6732  0.8205    315     no  study_code
## sigma^2.2  5.0249  2.2416   1378     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1370) = 45026.3714, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 646.1653, p-val < .0001
##
## Model Results:
##
##                                                    estimate       se      zval
## intrcpt                                             -0.0811   0.1539   -0.5269
## poly(c_treattemp, degree = 3, raw = TRUE)1          -0.2885   0.0190  -15.2255
## poly(c_treattemp, degree = 3, raw = TRUE)2          -0.0028   0.0012   -2.2842
## poly(c_treattemp, degree = 3, raw = TRUE)3           0.0006   0.0001    7.7222
## Sex.exposedFemale                                    0.0236   0.2012    0.1172
## poly(c_treattemp, degree = 3, raw = TRUE)1:Sex.exposedFemale  -0.0020   0.0254   -0.0802
## poly(c_treattemp, degree = 3, raw = TRUE)2:Sex.exposedFemale  -0.0006   0.0017   -0.3499
## poly(c_treattemp, degree = 3, raw = TRUE)3:Sex.exposedFemale   0.0000   0.0001    0.0102
##                                                      pval    ci.lb     ci.ub
## intrcpt                                            0.5983  -0.3828    0.2206
## poly(c_treattemp, degree = 3, raw = TRUE)1         <.0001  -0.3257   -0.2514  ***
## poly(c_treattemp, degree = 3, raw = TRUE)2         0.0224  -0.0052   -0.0004    *
## poly(c_treattemp, degree = 3, raw = TRUE)3         <.0001   0.0005    0.0008  ***
## Sex.exposedFemale                                  0.9067  -0.3708    0.4180
## poly(c_treattemp, degree = 3, raw = TRUE)1:Sex.exposedFemale  0.9361  -0.0519    0.0478
## poly(c_treattemp, degree = 3, raw = TRUE)2:Sex.exposedFemale  0.7264  -0.0040    0.0028
## poly(c_treattemp, degree = 3, raw = TRUE)3:Sex.exposedFemale  0.9919  -0.0002    0.0002
```

```
##
## ---
## 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
##       485      879
```

```
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 = 1364; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3247.9257   6495.8514   6515.8514   6567.9744   6516.0150
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6345  0.7966    315     no  study_code
## sigma^2.2  5.0811  2.2541   1364     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1356) = 44716.4367, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 645.5222, p-val < .0001
##
## Model Results:
##
##                                                                estimate      se
## intrcpt                                                         -0.2784  0.1669
## poly(c_treattemp, degree = 3, raw = TRUE)1                      -0.3038  0.0205
## poly(c_treattemp, degree = 3, raw = TRUE)2                      -0.0027  0.0012
## poly(c_treattemp, degree = 3, raw = TRUE)3                       0.0007  0.0001
## Life.stage.of.animalImmature                                    0.3262  0.2076
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature   0.0254  0.0262
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature  -0.0008  0.0017
## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature  -0.0002  0.0001
##                                                                   zval    pval
## intrcpt                                                        -1.6683  0.0953
## poly(c_treattemp, degree = 3, raw = TRUE)1                    -14.8285  <.0001
## poly(c_treattemp, degree = 3, raw = TRUE)2                     -2.2256  0.0260
```

```
## poly(c_treattemp, degree = 3, raw = TRUE)3                                     8.4716  <.0001
## Life.stage.of.animalImmature                                                   1.5716  0.1160
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature        0.9717  0.3312
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature       -0.4373  0.6619
## poly(c_treattemp, degree = 3, raw = TRUE)3:Life.stage.of.animalImmature       -1.4742  0.1404
##                                                                                 ci.lb     ci.ub
## intrcpt                                                                       -0.6054    0.0487
## poly(c_treattemp, degree = 3, raw = TRUE)1                                    -0.3440   -0.2637
## poly(c_treattemp, degree = 3, raw = TRUE)2                                    -0.0051   -0.0003
## poly(c_treattemp, degree = 3, raw = TRUE)3                                     0.0006    0.0009
## Life.stage.of.animalImmature                                                 -0.0806    0.7330
## poly(c_treattemp, degree = 3, raw = TRUE)1:Life.stage.of.animalImmature       -0.0259    0.0768
## poly(c_treattemp, degree = 3, raw = TRUE)2:Life.stage.of.animalImmature       -0.0041    0.0026
## 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 = 692; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -1717.8748   3435.7496   3445.7496   3468.4258   3445.8374
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed       factor
## sigma^2.1  0.2625  0.5124    156     no   study_code
## sigma^2.2  6.8468  2.6166    692     no          obs
##
## Test for Residual Heterogeneity:
## QE(df = 689) = 27343.3537, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 275.5304, p-val < .0001
##
## Model Results:
##
##                                       estimate      se      zval     pval      ci.lb
## intrcpt                                -0.0968  0.1439   -0.6731   0.5009    -0.3788
## poly(c_treattemp, degree = 2, raw = TRUE)1   -0.2131  0.0130  -16.4344   <.0001    -0.2385
## poly(c_treattemp, degree = 2, raw = TRUE)2    0.0001  0.0014    0.0754   0.9399    -0.0026
##                                         ci.ub
## intrcpt                                0.1851
## poly(c_treattemp, degree = 2, raw = TRUE)1   -0.1877  ***
## poly(c_treattemp, degree = 2, raw = TRUE)2    0.0028
##
## ---
## 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 = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3556.2736   7112.5473   7120.5473   7141.4637   7120.5764
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.6932  0.8326    316     no  study_code
## sigma^2.2  7.9235  2.8149   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1379) = 69459.6629, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.7279, p-val = 0.3936
##
## Model Results:
##
##                   estimate       se     zval    pval     ci.lb     ci.ub
## intrcpt            16.8856  20.0142   0.8437  0.3988  -22.3414   56.1127
## Publication.year   -0.0085   0.0100  -0.8532  0.3936   -0.0280    0.0110
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
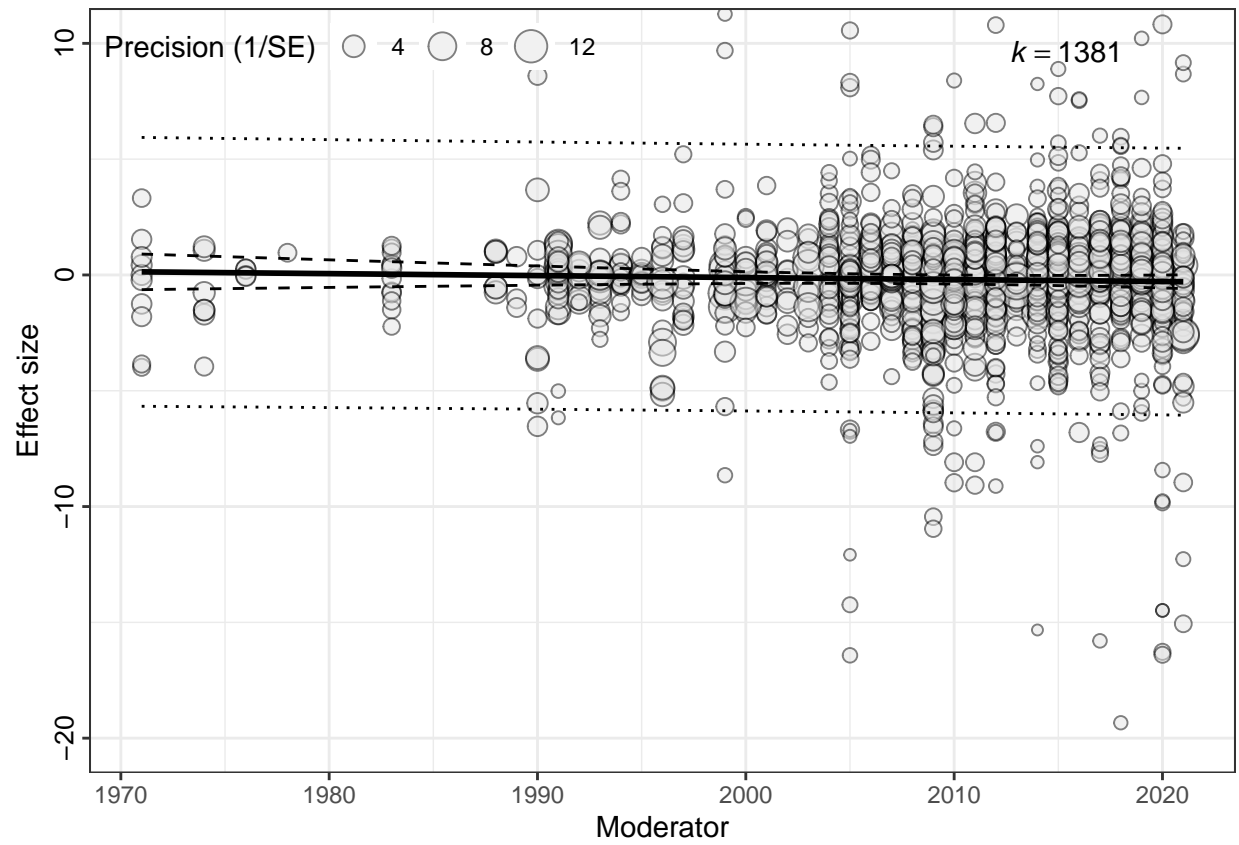
Sensitivty Analysis

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%
## -6.897064
```

```
print(maxq)
```

```
##     97.5%
## 6.432521
```

The sumamry of the effect sizes is now

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

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -6.8267 -1.2309 -0.0704 -0.1874  0.9824  6.3795
```

We run the cubic 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 cubic effect (sesnsitivity analysis)

We re-create the variance-covariance matrix with our new subsetted 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)
```
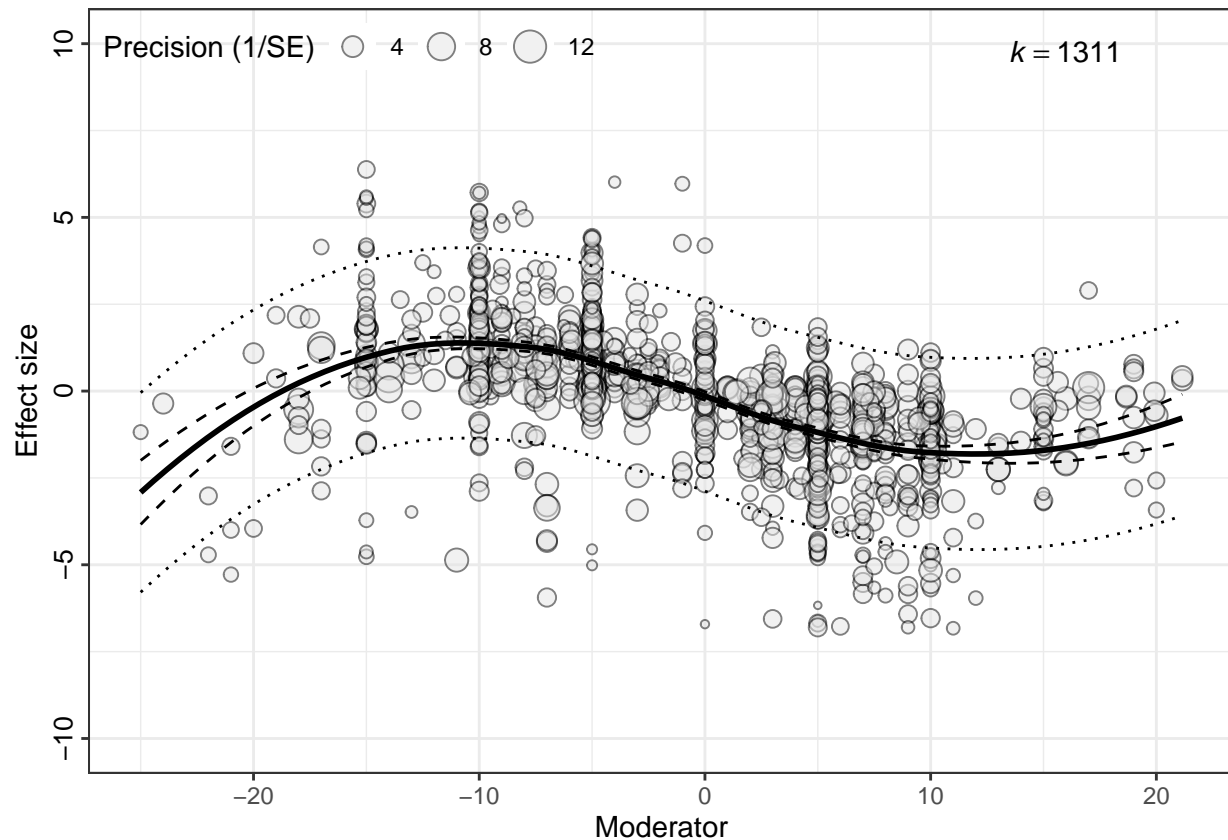
```
meta_sa_treat3 <- rma.mv(es, VCV_shared_sa, mod = ~poly(c_treattemp,
    degree = 3, raw = TRUE), random = list(~1 | study_code, ~1 |
    obs), test = "t", dfs = "contain", data = sdata, method = "REML")
```

```
summary(meta_sa_treat3)
```

```
##
## Multivariate Meta-Analysis Model (k = 1311; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -2303.7299   4607.4598   4619.4598   4650.5127   4619.5244
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.5165  0.7187    313     no  study_code
## sigma^2.2  1.4322  1.1967   1311     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1307) = 28230.5429, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 1103.6042, p-val < .0001
##
```

```
## Model Results:
##
##                                            estimate      se      zval    pval    ci.lb
## intrcpt                                     -0.1607  0.0667   -2.4094  0.0160  -0.2914
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.2229  0.0073  -30.3953  <.0001  -0.2373
## poly(c_treattemp, degree = 3, raw = TRUE)2  -0.0009  0.0005   -1.7016  0.0888  -0.0020
## poly(c_treattemp, degree = 3, raw = TRUE)3   0.0005  0.0000   13.3619  <.0001   0.0004
##                                               ci.ub
## intrcpt                                     -0.0300    *
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.2085  ***
## poly(c_treattemp, degree = 3, raw = TRUE)2   0.0001    .
## poly(c_treattemp, degree = 3, raw = TRUE)3   0.0006  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Below is a bubble plot of the fitted cubic 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
##   102    50   233   299   186   342    99
```

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

```
summary(meta_sa_bintemp)
```

```
##
## Multivariate Meta-Analysis Model (k = 1311; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2325.8125   4651.6249   4669.6249   4716.1837   4669.7640
##
## Variance Components:
##
```

```
##                estim    sqrt  nlvls  fixed       factor
## sigma^2.1   0.5448  0.7381    313     no  study_code
## sigma^2.2   1.5006  1.2250   1311     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1304) = 29286.7914, p-val < .0001
##
## Test of Moderators (coefficients 1:7):
## QM(df = 7) = 1016.8182, p-val < .0001
##
## Model Results:
##
##                 estimate      se      zval    pval    ci.lb    ci.ub
## bin.temp<15       0.9793  0.1540    6.3583  <.0001   0.6774   1.2812  ***
## bin.temp>40      -1.5440  0.2451   -6.2987  <.0001  -2.0245  -1.0636  ***
## bin.temp15-20     1.2743  0.0991   12.8569  <.0001   1.0800   1.4685  ***
## bin.temp20-25     0.8315  0.0895    9.2937  <.0001   0.6561   1.0068  ***
## bin.temp25-30    -0.6775  0.1094   -6.1911  <.0001  -0.8920  -0.4630  ***
## bin.temp30-35    -1.4249  0.0851  -16.7388  <.0001  -1.5918  -1.2581  ***
## bin.temp35-40    -1.9753  0.1467  -13.4636  <.0001  -2.2629  -1.6878  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
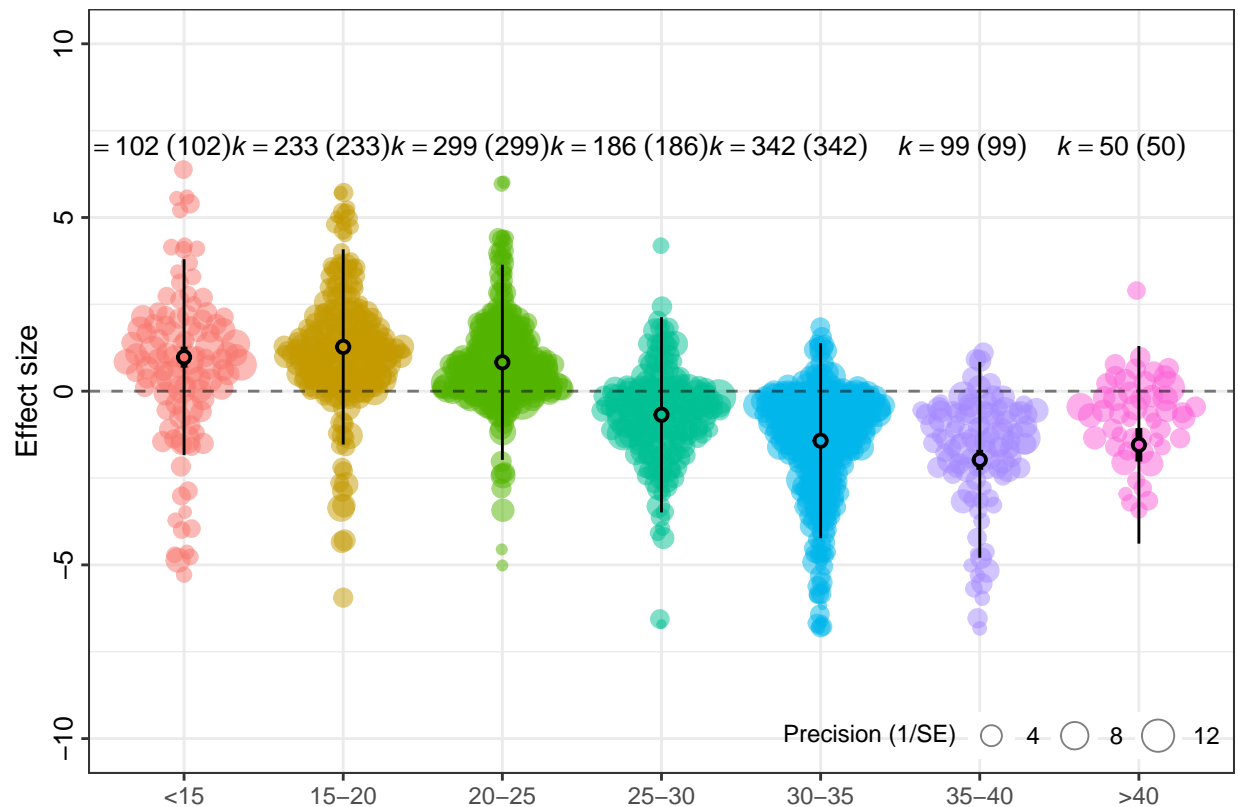
Other fixed effects

Habitat

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

```
summary(meta_bintemp_habitat)
```

```
##
## Multivariate Meta-Analysis Model (k = 1381; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3265.9266   6531.8532   6571.8532   6676.2020   6572.4791
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed       factor
## sigma^2.1  0.5992  0.7741    316     no  study_code
## sigma^2.2  5.0846  2.2549   1381     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1363) = 43855.7469, p-val < .0001
##
## Test of Moderators (coefficients 2:18):
## QM(df = 17) = 638.3230, p-val < .0001
##
## Model Results:
##
##                                   estimate       se       zval     pval     ci.lb     ci.ub
## intrcpt                            -0.3772   1.4059    -0.2683   0.7885   -3.1327    2.3783
## bin.temp>40                        -3.1879   0.4479    -7.1176   <.0001   -4.0657   -2.3100   ***
## bin.temp15-20                       2.2452   1.5226     1.4745   0.1403   -0.7391    5.2295
## bin.temp20-25                       1.9369   1.6151     1.1993   0.2304   -1.2286    5.1025
## bin.temp25-30                      -1.6073   1.5002    -1.0714   0.2840   -4.5478    1.3331
## bin.temp30-35                      -0.3674   1.7231    -0.2132   0.8312   -3.7446    3.0099
## bin.temp35-40                      -3.8301   0.3435   -11.1515   <.0001   -4.5033   -3.1570   ***
## HabitatBoth                        -4.2719   2.2027    -1.9393   0.0525   -8.5891    0.0454    .
## HabitatTerrestrial                  1.4782   1.4285     1.0348   0.3008   -1.3216    4.2780
## bin.temp15-20:HabitatBoth           2.2173   2.3714     0.9350   0.3498   -2.4306    6.8652
## bin.temp20-25:HabitatBoth           2.8733   2.4362     1.1794   0.2382   -1.9015    7.6481
## bin.temp25-30:HabitatBoth           3.7067   2.4508     1.5124   0.1304   -1.0968    8.5101
## bin.temp30-35:HabitatBoth           1.5093   2.4692     0.6112   0.5410   -3.3303    6.3488
## bin.temp35-40:HabitatBoth           3.6738   2.8372     1.2948   0.1954   -1.8871    9.2346
## bin.temp15-20:HabitatTerrestrial   -1.4870   1.5509    -0.9588   0.3377   -4.5267    1.5527
## bin.temp20-25:HabitatTerrestrial   -1.9102   1.6402    -1.1647   0.2442   -5.1249    1.3044
## bin.temp25-30:HabitatTerrestrial   -0.1171   1.5319    -0.0764   0.9391   -3.1195    2.8854
## bin.temp30-35:HabitatTerrestrial   -2.4634   1.7461    -1.4108   0.1583   -5.8858    0.9590
##
## ---
## 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)  # 3
outliers_rep <- subset(gearydata, Trait.category == "Reproduction" &
    gtest < 3)  # 171
```

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_lon_warm <- subset(s.gearydata, Trait.category == "Longevity" &
    warm.cool == "Warm")
gdata_lon_cool <- subset(s.gearydata, Trait.category == "Longevity" &
    warm.cool == "Cool")

all_gdata <- rbind(gdata_lon_warm, gdata_lon_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)
```

```
meta_ga_treat3 <- rma.mv(es, VCV_shared_ga, mod = ~poly(c_treattemp,
    degree = 3, raw = TRUE), random = list(~1 | study_code, ~1 |
    obs), test = "t", dfs = "contain", data = all_gdata, method = "REML")
```

```
summary(meta_ga_treat3)
```

```
##
## Multivariate Meta-Analysis Model (k = 1310; method: REML)
##
##      logLik    Deviance         AIC         BIC        AICc
## -3195.6635   6391.3269   6403.3269   6434.3753   6403.3916
##
## Variance Components:
##
##             estim     sqrt  nlvls  fixed      factor
## sigma^2.1  0.6337   0.7960    311     no  study_code
## sigma^2.2  5.1381   2.2667   1310     no         obs
##
## Test for Residual Heterogeneity:
## QE(df = 1306) = 44067.8973, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## F(df1 = 3, df2 = 1306) = 215.6771, p-val < .0001
##
## Model Results:
##
##                                           estimate       se      tval      df      pval      ci.lb
## intrcpt                                    -0.0537   0.1011   -0.5316     307    0.5954    -0.2526
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.3003   0.0130  -23.1438    1306    <.0001    -0.3258
## poly(c_treattemp, degree = 3, raw = TRUE)2  -0.0030   0.0009   -3.4836    1306    0.0005    -0.0047
## poly(c_treattemp, degree = 3, raw = TRUE)3   0.0007   0.0001   10.5347    1306    <.0001     0.0005
##                                             ci.ub
## intrcpt                                    0.1452
## poly(c_treattemp, degree = 3, raw = TRUE)1  -0.2749  ***
## poly(c_treattemp, degree = 3, raw = TRUE)2  -0.0013  ***
## poly(c_treattemp, degree = 3, raw = TRUE)3   0.0008  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Below is a bubble plot of the fitted quadratic model.