Meta-analysis on the effects of temperature on sexual selection

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# 1.0 - Setting up and Data Exploration

### 1.1 - Load Packages

pacman::p\_load(metafor, MCMCglmm, tidyverse, rotl, magrittr, kableExtra, rmarkdown, gridExtra, psych, metaAidR, bindrcpp, pander)

### 1.2 - Load Data

First, lets load the data into R:

data <- read.csv("../data\_Temp\_SS.csv", stringsAsFactors = FALSE)

Now that it is in we can view the data structure. Note that all factors should be characters. Also, we need to do some cleaning of the data before continuing as well as a little data exploration to check the data for consistencies, such as spelling mistakes etc.

str(data)

## 'data.frame': 49 obs. of 29 variables:  
## $ study : int 1 1 1 1 13 13 13 13 13 24 ...  
## $ author : chr "Berger" "Berger" "Berger" "Berger" ...  
## $ year : int 2014 2014 2014 2014 2006 2006 2006 2006 2006 2014 ...  
## $ journal : chr "Evolution" "Evolution" "Evolution" "Evolution" ...  
## $ vol : int 68 68 68 68 20 20 20 20 20 28 ...  
## $ sex : chr "males" "females" "males" "females" ...  
## $ genus : chr "Callosobruchus" "Callosobruchus" "Callosobruchus" "Callosobruchus" ...  
## $ species : chr "maculatus" "maculatus" "maculatus" "maculatus" ...  
## $ group : chr "insect" "insect" "insect" "insect" ...  
## $ source : chr "fig. 1" "fig. 1" "fig. 1" "fig. 1" ...  
## $ variable : chr "Total number of offspring (LRS)" "Total number of offspring (LRS)" "Total number of offspring (LRS)" "Total number of offspring (LRS)" ...  
## $ depend : int 0 0 0 0 0 0 0 0 0 1 ...  
## $ Tadapt : chr "27-29" "27-29" "27-29" "27-29" ...  
## $ T1 : int 29 29 29 29 25 25 25 25 25 15 ...  
## $ T2 : int 36 36 36 36 30 30 30 30 30 25 ...  
## $ X\_T1 : num 53.646 54.692 48.751 48.983 0.331 ...  
## $ Err\_T1 : num 3.8019 2.2098 3.2825 2.116 0.0134 ...  
## $ N\_T1 : num 41 41 32 32 31 31 31 31 31 20 ...  
## $ X\_T2 : num 29.312 33.488 19.071 22.047 0.324 ...  
## $ Err\_T2 : num 3.379 2.24 2.116 2.21 0.013 ...  
## $ N\_T2 : num 41 41 32 32 27 27 27 26 26 20 ...  
## $ Err\_T1\_Type : chr "SE" "SE" "SE" "SE" ...  
## $ Err\_T2\_Type : chr "SE" "SE" "SE" "SE" ...  
## $ temp.range : chr "stress" "stress" "stress" "stress" ...  
## $ temp.treatment.stage: chr "lifetime" "lifetime" "lifetime" "lifetime" ...  
## $ endo.ecto : chr "ecto" "ecto" "ecto" "ecto" ...  
## $ fitness : chr "direct" "direct" "direct" "direct" ...  
## $ prop : int 0 0 0 0 0 0 0 0 0 1 ...  
## $ notes : chr "lome" "lome" "ofuya" "ofuya" ...

There are clearly a few things that need to be sorted. First, we need to convert all SE estimates to their corresponding SD. We can apply a couple simple functions to do this. We can then subset the data out for males and females, we’ll run a subset analysis for each dataset as we expect very strong differences between these effect sizes, and potentially differences in how moderators affect the effects.

# Convert everything to SD from SE  
se\_to\_sd <- function(se, n){  
 sd = se\*sqrt(n)  
 return(sd)  
}  
  
convert\_to\_SD <- function(data){  
 data$Err\_T1 <- ifelse(data$Err\_T1\_Type == "SE", se\_to\_sd(data$Err\_T1, data$N\_T1), data$Err\_T1)  
 data$Err\_T2 <- ifelse(data$Err\_T2\_Type == "SE", se\_to\_sd(data$Err\_T2, data$N\_T2), data$Err\_T2)  
 return(data)  
}  
  
data <- convert\_to\_SD(data)  
  
# Add in a species identifier  
data$spp <- gsub(" ", "", paste0(data$genus, "\_", data$species))  
  
# Add a new variable describing the temperature difference between treatments. We will scale this so that when we fit models the intercept is automatically at the "average" temperature across studies  
data$deltaT <- as.numeric(scale(data$T2 - data$T1))  
  
# Extract male data, and because errors are converted to SD now, we can exclude the Err\_type columns. We also want to add an observation-level random effect  
males <- filter(data, sex == "males")[, -match(c("Err\_T1\_Type","Err\_T2\_Type"), colnames(data))]  
males$obs <- 1:nrow(males)  
  
females <- filter(data, sex == "females")[, -match(c("Err\_T1\_Type","Err\_T2\_Type"), colnames(data))]  
females$obs <- 1:nrow(females)

We’ll now use the males and females datasets throughout for data exploration and summary statistics before we do some meta-analysis with subsets of them. We can generate the effect sizes and corresponding sampling variance for each dataset. We can use Wolfgang’s very excellent, and comprehensive, escalc function to generate (bias corrected) versions of lnVR and lnCVR and also lnRR, which we can then add to the dataset. We’ll create separate datasets so it’s clear which effect size we are using, but these could easily be all merged into one. We just find it easier to have them separated so that we can change the dataset. What we want to do is “subtract” log(T1) from log(T2), summary statistics. In other words, when the effect size is negative, it means that the higher temperature (T2) has a smaller mean or variance compared with the lower temperature (T1). When the effect size is positive, it means that T1 has a smaller mean or variance than T2. We can see how this works quite easily by checking results form a few simple ratios. For example, log(2/1) = 0.69 is positive and we can see that the numerator is larger than the denominator. In contrast, log(1/2) = -0.69 is the same estimate, but negative and we can see that the numerator is smaller than the denominator. All we are essentially doing then is calculating the following ratio: log(T2/T1). We can even convert this to a more interpretable value, which will will do a little later, by exponentiating the resulting value. So, for example, exp(log(1/2)) = 0.5, which means that the numerator (i.e., T2) is 50% smaller than the denominator. To give you another example, if exp(log(1.5/2)) = 0.75, which means that the numerator (i.e., T2) is 25% smaller than the denominator. If, for example, the ratios were reversed such that, we have exp(log(2/1.5)) = 1.33 then this would mean that the numerator is 33.33% larger than the denominator. This same interpretation applies to lnVR and lnCVR when we talk about variances.

lnRR\_males <- metafor::escalc(measure= "ROM", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = males)  
 lnVR\_males <- metafor::escalc(measure= "VR", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = males)  
 lnCVR\_males <- metafor::escalc(measure= "CVR", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = males)

We can then do the same for the females:

lnRR\_females <- metafor::escalc(measure= "ROM", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = females)  
lnVR\_females <- metafor::escalc(measure= "VR", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = females)  
lnCVR\_females <- metafor::escalc(measure= "CVR", m1i= X\_T2, m2i = X\_T1, sd1i= Err\_T2, sd2i= Err\_T1, n1i =N\_T2, n2i=N\_T1, append = TRUE, data = females)

Now we have size datasets with the effect size, yi, being the relevant ratio of means, standard deviations and coefficient of variations, for males and females and vi being the corresponding sampling variance. These datasets can then be substituted into the models to estimate overall effects, how moderators impact variance and the variation in effects overall.

### 1.3 - Data Exploration

Now that we have the males and females data created we can start some data exploration. We can first view these datasets, the raw data, if we want first. Since we have three different effect sizes, we’ll just view the lnRR datasets for both sexes, but the raw data for each are provided should the reader be interested in looking at them all.

We’ll look at the female data first. It’s smaller:

# Word / pdf table  
 pander(lnRR\_females)

Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| study | author | year | journal | vol |
| 1 | Berger | 2014 | Evolution | 68 |
| 1 | Berger | 2014 | Evolution | 68 |
| 9 | Dubey | 2016 | Journal of Thermal Biology | 58 |
| 9 | Dubey | 2016 | Journal of Thermal Biology | 58 |
| 14 | Grazer | 2012 | Evolutionary Ecology | 26 |
| 23 | Martinossi-Allibert | 2017 | Journal of Evolutionary Biology | 30 |
| 30 | Sambucetti | 2014 | Entomologia Experimentalis et Applicata | 154 |
| 30 | Sambucetti | 2014 | Entomologia Experimentalis et Applicata | 154 |
| 4 | Tregenza | 2003 | Evolution | 57 |
| 8 | Plesnar-Bielak | 2012 | Proceedings of the Royal Society B-Biological Sciences | 279 |
| 8 | Plesnar-Bielak | 2012 | Proceedings of the Royal Society B-Biological Sciences | 279 |
| 8 | Plesnar-Bielak | 2012 | Proceedings of the Royal Society B-Biological Sciences | 279 |
| 11 | McCabe | 1997 | Evolution | 51 |
| 11 | McCabe | 1997 | Evolution | 51 |
| 11 | McCabe | 1997 | Evolution | 51 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |

Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| sex | genus | species | group | source |
| females | Callosobruchus | maculatus | insect | fig. 1 |
| females | Callosobruchus | maculatus | insect | fig. 1 |
| females | Menochilus | sexmaculatus | insect | table A3 |
| females | Menochilus | sexmaculatus | insect | table A3 |
| females | Tribolium | castneum | insect | fig. 2 |
| females | Callosobruchus | maculatus | insect | fig. 2 |
| females | Drosophila | buzzatii | insect | fig. 2 |
| females | Drosophila | buzzatii | insect | fig. 2 |
| females | Scathophaga | stercoraria | insect | fig. 2 |
| females | Rhizoglyphus | robini | arachnid | text |
| females | Rhizoglyphus | robini | arachnid | raw |
| females | Rhizoglyphus | robini | arachnid | raw |
| females | Drosophila | melanogaster | insect | fig. 8 |
| females | Drosophila | melanogaster | insect | fig. 8 |
| females | Drosophila | melanogaster | insect | fig. 8 |
| females | Aquarius | remigis | insect | fig. 5 |
| females | Aquarius | remigis | insect | fig. 5 |
| females | Aquarius | remigis | insect | fig. 5 |

Table continues below

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| variable | depend | Tadapt | T1 | T2 | X\_T1 |
| Total number of offspring (LRS) | 0 | 27-29 | 29 | 36 | 54.69 |
| Total number of offspring (LRS) | 0 | 27-29 | 29 | 36 | 48.98 |
| Number of eggs (Fecundity/Reproductive success) | 0 | NA | 15 | 35 | 77.4 |
| Number of eggs (Fecundity/Reproductive success) | 0 | NA | 15 | 35 | 79.65 |
| Reproductive success | 0 | 30 | 30 | 34 | 179.2 |
| Total fitness (survival & LRS) | 0 | 27-29 | 29 | 37 | 0.9919 |
| Proportion of mated flies | 0 | NA | 25 | 33 | 0.4159 |
| Proportion of mated flies | 0 | NA | 25 | 33 | 0.5858 |
| Mean proportion of eggs hatched | 0 | NA | 11 | 19 | 0.556 |
| Mean number of eggs per female | 0 | 24 (18 gen at 28) | 24 | 28 | 163.9 |
| Mean number of eggs per female | 0 | 24 (18 gen at 28) | 24 | 28 | 143.1 |
| Mean number of eggs per female | 0 | 24 (18 gen at 28) | 24 | 28 | 118.3 |
| Lifetime number of progeny | 0 | 25 | 18 | 25 | 553.4 |
| Lifetime number of progeny | 0 | 25 | 18 | 25 | 493.6 |
| Lifetime number of progeny | 0 | 25 | 18 | 25 | 730.6 |
| log(abdomin length) | 0 | NA | 20 | 25 | 0.775 |
| log(abdomin length) | 0 | NA | 20 | 25 | 0.7906 |
| log(abdomin length) | 0 | NA | 20 | 25 | 0.8133 |

Table continues below

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Err\_T1 | N\_T1 | X\_T2 | Err\_T2 | N\_T2 | temp.range | temp.treatment.stage |
| 14.15 | 41 | 33.49 | 14.34 | 41 | stress | lifetime |
| 11.97 | 32 | 22.05 | 12.5 | 32 | stress | lifetime |
| 4.736 | 20 | 104.3 | 4.53 | 20 | natural | lifetime |
| 3.229 | 20 | 108.5 | 3.774 | 20 | natural | lifetime |
| 180.5 | 60 | 223.2 | 151.6 | 60 | natural | lifetime |
| 0.1553 | 14 | 0.3375 | 0.1278 | 14 | stress | juvenile |
| 0.2171 | 6 | 0.5411 | 0.3256 | 6 | natural | adults |
| 0.211 | 6 | 0.5012 | 0.2164 | 6 | stress | adults |
| 0.4313 | 36 | 0.9113 | 0.4557 | 36 | natural | lifetime |
| 88.25 | 31 | 47.53 | 32.79 | 31 | stress | lifetime |
| 49.84 | 46.8 | 76.15 | 40.45 | 33.4 | stress | lifetime |
| 47.01 | 43.1 | 92.86 | 43.42 | 40.6 | stress | lifetime |
| 382.9 | 88 | 374.1 | 335.7 | 88 | stress | lifetime |
| 348.1 | 88 | 343.7 | 319.8 | 88 | stress | lifetime |
| 364.8 | 88 | 413.1 | 253.6 | 88 | stress | lifetime |
| 0.02237 | 11 | 0.7578 | 0.05618 | 11 | natural | lifetime |
| 0.01512 | 11 | 0.7799 | 0.01542 | 11 | natural | lifetime |
| 0.01723 | 11 | 0.8093 | 0.01378 | 11 | natural | lifetime |

Table continues below

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| endo.ecto | fitness | prop | notes | | |
| ecto | direct | 0 | lome | | |
| ecto | direct | 0 | ofuya | | |
| ecto | direct | 0 | TxT | | |
| ecto | direct | 0 | MxM | | |
| ecto | direct | 0 |  | | |
| ecto | direct | 0 |  | | |
| ecto | direct | 1 | Chumbicha - low | | |
| ecto | direct | 1 | Quilmes - high | | |
| ecto | direct | 1 |  | | |
| ecto | direct | 0 | In text pilot data, wild type | | |
| ecto | direct | 0 | 24\_Polygamy\_SL | | |
| ecto | direct | 0 | 28\_Polygamy\_SL | | |
| ecto | direct | 0 | control lines | | |
| ecto | direct | 0 | small wing selection | | |
| ecto | direct | 0 | large wing selection | | |
| ecto | indirect | 0 | SW population | | |
| ecto | indirect | 0 | DLM population | | |
| ecto | indirect | 0 | SCI population | | |
| spp | | deltaT | obs | yi | vi | |
| Callosobruchus\_maculatus | | -0.1491 | 1 | -0.4905 | 0.006106 | |
| Callosobruchus\_maculatus | | -0.1491 | 2 | -0.7983 | 0.01191 | |
| Menochilus\_sexmaculatus | | 3.649 | 3 | 0.2983 | 0.0002815 | |
| Menochilus\_sexmaculatus | | 3.649 | 4 | 0.3086 | 0.0001427 | |
| Tribolium\_castneum | | -1.026 | 5 | 0.2195 | 0.02461 | |
| Callosobruchus\_maculatus | | 0.1431 | 6 | -1.078 | 0.01199 | |
| Drosophila\_buzzatii | | 0.1431 | 7 | 0.2631 | 0.1057 | |
| Drosophila\_buzzatii | | 0.1431 | 8 | -0.1561 | 0.05271 | |
| Scathophaga\_stercoraria | | 0.1431 | 9 | 0.4941 | 0.02366 | |
| Rhizoglyphus\_robini | | -1.026 | 10 | -1.238 | 0.02471 | |
| Rhizoglyphus\_robini | | -1.026 | 11 | -0.6311 | 0.01104 | |
| Rhizoglyphus\_robini | | -1.026 | 12 | -0.2421 | 0.00905 | |
| Drosophila\_melanogaster | | -0.1491 | 13 | -0.3916 | 0.01459 | |
| Drosophila\_melanogaster | | -0.1491 | 14 | -0.3618 | 0.01549 | |
| Drosophila\_melanogaster | | -0.1491 | 15 | -0.5702 | 0.007115 | |
| Aquarius\_remigis | | -0.7334 | 16 | -0.02248 | 0.0005754 | |
| Aquarius\_remigis | | -0.7334 | 17 | -0.0136 | 6.878e-05 | |
| Aquarius\_remigis | | -0.7334 | 18 | -0.005019 | 6.717e-05 | |

#kable(lnRR\_females) %>%  
 #kable\_styling(font = 11) %>%  
 #scroll\_box(width = "100%", height = "200px")

Then we can look at the male data, it’s a bit more as many studies quantify and seem to be interested mostly in male fitness (or fitness proxies) for sexual selection. At least in the context of temperature manipulations:

# Word / pdf table  
 pander(lnRR\_males)

Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| study | author | year | journal | vol |
| 1 | Berger | 2014 | Evolution | 68 |
| 1 | Berger | 2014 | Evolution | 68 |
| 13 | Fox | 2006 | Functional Ecology | 20 |
| 13 | Fox | 2006 | Functional Ecology | 20 |
| 13 | Fox | 2006 | Functional Ecology | 20 |
| 13 | Fox | 2006 | Functional Ecology | 20 |
| 13 | Fox | 2006 | Functional Ecology | 20 |
| 24 | Mehlis | 2014 | Evolutionary Ecology | 28 |
| 24 | Mehlis | 2014 | Evolutionary Ecology | 28 |
| 24 | Mehlis | 2014 | Evolutionary Ecology | 28 |
| 24 | Mehlis | 2014 | Evolutionary Ecology | 28 |
| 25 | Nguyen | 2013 | Journal of Insect Physiology | 59 |
| 40 | Wilson | 2005 | Animal Behaviour | 70 |
| 32 | Saxon | 2018 | Journal of Evolutionary Bilogy | 31 |
| 23 | Martinossi-Allibert | 2017 | Journal of Evolutionary Biology | 30 |
| 28 | Plesnar-Bielak | 2018 | BMC Evolutionary Biology | 18 |
| 30 | Sambucetti | 2014 | Entomologia Experimentalis et Applicata | 154 |
| 30 | Sambucetti | 2014 | Entomologia Experimentalis et Applicata | 154 |
| 37 | Vasudeva | 2014 | Journal of Evolutionary Biology | 27 |
| 37 | Vasudeva | 2014 | Journal of Evolutionary Biology | 27 |
| 37 | Vasudeva | 2014 | Journal of Evolutionary Biology | 27 |
| 37 | Vasudeva | 2014 | Journal of Evolutionary Biology | 27 |
| 41 | Yenisetti | 2006 | Korean Journal of Genetics | 28 |
| 41 | Yenisetti | 2006 | Korean Journal of Genetics | 28 |
| 6 | Reeve | 2000 | Journal of Evolutionary Biology | 13 |
| 6 | Reeve | 2000 | Journal of Evolutionary Biology | 13 |
| 6 | Reeve | 2000 | Journal of Evolutionary Biology | 13 |
| 7 | Polak | 2012 | Journal of Evolutionary Biology | 25 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |
| 17 | Fairbairn | 2005 | The American Naturalist | 166 |

Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| sex | genus | species | group | source |
| males | Callosobruchus | maculatus | insect | fig. 1 |
| males | Callosobruchus | maculatus | insect | fig. 1 |
| males | Callosobruchus | maculatus | insect | fig. 1A |
| males | Callosobruchus | maculatus | insect | fig. 1A |
| males | Callosobruchus | maculatus | insect | fig. 1A |
| males | Callosobruchus | maculatus | insect | fig. 1A |
| males | Callosobruchus | maculatus | insect | fig. 1A |
| males | Gasterosteus | aculeatus | fish | fig. 1 |
| males | Gasterosteus | aculeatus | fish | fig. 1 |
| males | Gasterosteus | aculeatus | fish | fig. 2B |
| males | Gasterosteus | aculeatus | fish | fig. 2C |
| males | Anisopteromalus | calandrae | insect | fig. 2 |
| males | Gambusia | holbrooki | fish | fig. 4 |
| males | Drosophila | birchii | insect | fig. 1I |
| males | Callosobruchus | maculatus | insect | fig. 2 |
| males | Rhizoglyphus | robini | insect | fig. 4 |
| males | Drosophila | buzzatii | insect | fig. 2 |
| males | Drosophila | buzzatii | insect | fig. 2 |
| males | Callosobruchus | maculatus | insect | fig. 2 |
| males | Callosobruchus | maculatus | insect | fig. 2 |
| males | Callosobruchus | maculatus | insect | fig. 2 |
| males | Callosobruchus | maculatus | insect | fig. 2 |
| males | Phorticella | striata | insect | table 1 |
| males | Phorticella | striata | insect | table 1 |
| males | Drosophila | melanogaster | insect | fig. 2 |
| males | Drosophila | melanogaster | insect | fig. 2 |
| males | Drosophila | melanogaster | insect | fig. 2 |
| males | Drosophila | bipectinata | insect | table 3 |
| males | Aquarius | remigis | insect | fig. 5 |
| males | Aquarius | remigis | insect | fig. 5 |
| males | Aquarius | remigis | insect | fig. 5 |

Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| variable | depend | Tadapt | T1 | T2 |
| Total number of offspring (LRS) | 0 | 27-29 | 29 | 36 |
| Total number of offspring (LRS) | 0 | 27-29 | 29 | 36 |
| mg Mass loss (Male Investment) | 0 | NA | 25 | 30 |
| mg Mass loss (Male Investment) | 0 | NA | 25 | 30 |
| mg Mass loss (Male Investment) | 0 | NA | 25 | 30 |
| mg Mass loss (Male Investment) | 0 | NA | 25 | 30 |
| mg Mass loss (Male Investment) | 0 | NA | 25 | 30 |
| Mean Fertilization Success at 100,000 sperm (%) | 1 | NA | 15 | 25 |
| Mean Fertilization Success at 1,000,000 sperm (%) | 1 | NA | 15 | 25 |
| Sperm Linearity (PCA) | 2 | NA | 15 | 25 |
| Mean Motile Sperm (%) | 2 | NA | 15 | 25 |
| Number of Sperm in Vesicles | 0 | 30 | 30 | 36 |
| Number of Copulations Per Minute | 0 | NA | 18 | 26 |
| Total number of offspring | 0 | NA | 17 | 24 |
| Total fitness (survival & LRS) | 0 | 27-29 | 29 | 37 |
| Percentage of egg sired by fighers (reproductive success) | 0 | 24 (EE at 18 for 14 gen)) | 18 | 24 |
| Proportion of mated flies | 0 | NA | 25 | 33 |
| Proportion of mated flies | 0 | NA | 25 | 33 |
| Sperm number (1000x) | 1 | 27 | 25 | 33 |
| Sperm Length (mm) | 1 | 27 | 25 | 33 |
| Sperm number (1000x) | 2 | 27 | 25 | 33 |
| Sperm Length (mm) | 2 | 27 | 25 | 33 |
| Copulation duration | 0 | NA | 15 | 29 |
| Copulation duration | 0 | NA | 15 | 29 |
| Proportion of wild-type progeny sired (fertility) | 0 | 25 | 18 | 25 |
| Proportion of wild-type progeny sired (fertility) | 0 | 25 | 18 | 25 |
| Proportion of wild-type progeny sired (fertility) | 0 | 25 | 18 | 25 |
| CT1 Comb Number | 0 | NA | 25 | 29 |
| log(genital length) | 0 | NA | 20 | 25 |
| log(genital length) | 0 | NA | 20 | 25 |
| log(genital length) | 0 | NA | 20 | 25 |

Table continues below

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| X\_T1 | Err\_T1 | N\_T1 | X\_T2 | Err\_T2 | N\_T2 | temp.range |
| 53.65 | 24.34 | 41 | 29.31 | 21.64 | 41 | stress |
| 48.75 | 18.57 | 32 | 19.07 | 11.97 | 32 | stress |
| 0.3309 | 0.07481 | 31 | 0.3238 | 0.06756 | 27 | natural |
| 0.3436 | 0.08064 | 31 | 0.2984 | 0.08625 | 27 | natural |
| 0.327 | 0.07153 | 31 | 0.2882 | 0.0603 | 27 | natural |
| 0.3065 | 0.06058 | 31 | 0.2603 | 0.05971 | 26 | natural |
| 0.2614 | 0.07679 | 31 | 0.2105 | 0.05695 | 26 | natural |
| 37.9 | 28.98 | 20 | 60.69 | 36.05 | 20 | natural |
| 89 | 14.28 | 20 | 77.36 | 29.39 | 20 | natural |
| 0.4829 | 1.36 | 12 | 0.6836 | 1.852 | 12 | natural |
| 30.99 | 12.71 | 12 | 24.05 | 10.82 | 12 | natural |
| 3203 | 1211 | 56 | 1425 | 1296 | 30 | stress |
| 0.322 | 0.255 | 14 | 0.2302 | 0.1505 | 14 | natural |
| 100.4 | 74.35 | 20 | 172.6 | 87.26 | 20 | natural |
| 1.006 | 0.3741 | 14 | 0.07857 | 0.07287 | 14 | stress |
| 49 | 29.89 | 37 | 41.1 | 33.38 | 16 | stress |
| 0.5925 | 0.1737 | 6 | 0.3602 | 0.1647 | 6 | natural |
| 0.4065 | 0.1745 | 6 | 0.6426 | 0.1485 | 6 | stress |
| 69.23 | 26.18 | 18 | 37.8 | 24.84 | 18 | stress |
| 0.166 | 0.008973 | 18 | 0.1668 | 0.01188 | 18 | stress |
| 58.33 | 48.78 | 18 | 45.58 | 52.7 | 18 | stress |
| 0.1702 | 0.005066 | 18 | 0.1665 | 0.009039 | 18 | stress |
| 186.4 | 19.1 | 25 | 202.1 | 38.25 | 25 | natural |
| 192.2 | 25.7 | 25 | 229.5 | 56.65 | 25 | natural |
| 0.204 | 0.08148 | 13 | 0.1681 | 0.04403 | 13 | stress |
| 0.195 | 0.1377 | 13 | 0.1454 | 0.04848 | 13 | stress |
| 0.1591 | 0.08497 | 13 | 0.14 | 0.04043 | 13 | stress |
| 5.835 | 0.6737 | 134 | 5.74 | 0.9376 | 134 | natural |
| 0.3961 | 0.04639 | 11 | 0.3933 | 0.03454 | 11 | stress |
| 0.4048 | 0.01413 | 11 | 0.3991 | 0.01346 | 11 | natural |
| 0.4754 | 0.01626 | 11 | 0.4625 | 0.0465 | 11 | natural |

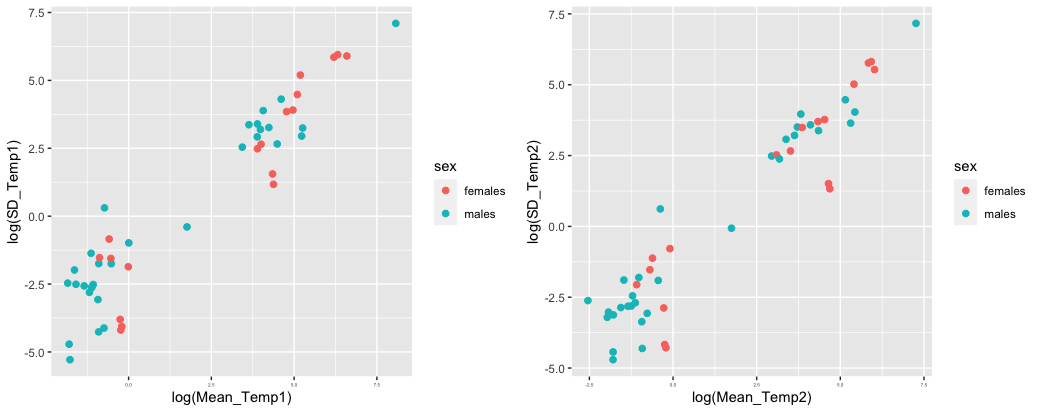
Table continues below

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| temp.treatment.stage | endo.ecto | fitness | prop | notes |
| lifetime | ecto | direct | 0 | lome |
| lifetime | ecto | direct | 0 | ofuya |
| lifetime | ecto | indirect | 0 | Burkina Faso\_Azuki |
| lifetime | ecto | indirect | 0 | Burkina Faso\_Cowpea |
| lifetime | ecto | indirect | 0 | Burkina Faso\_Mung |
| lifetime | ecto | indirect | 0 | South India\_Azuki |
| lifetime | ecto | indirect | 0 | South India\_Cowpea |
| adults | ecto | indirect | 1 |  |
| adults | ecto | indirect | 1 |  |
| adults | ecto | indirect | 0 |  |
| adults | ecto | indirect | 1 |  |
| early | ecto | indirect | 0 |  |
| adults | ecto | direct | 0 |  |
| lifetime | ecto | direct | 0 |  |
| juvenile | ecto | direct | 0 |  |
| lifetime | ecto | direct | 1 |  |
| adults | ecto | direct | 1 | Chumbicha - low |
| adults | ecto | direct | 1 | Quilmes - high |
| lifetime | ecto | indirect | 0 | replicate 1 |
| lifetime | ecto | indirect | 0 | replicate 1 |
| lifetime | ecto | indirect | 0 | replicate 2 |
| lifetime | ecto | indirect | 0 | replicate 2 |
| adults | ecto | indirect | 0 | Mysore |
| adults | ecto | indirect | 0 | Ahmedabad |
| lifetime | ecto | direct | 1 | control line 1 |
| lifetime | ecto | direct | 1 | control line 2 |
| lifetime | ecto | direct | 1 | control line 3 |
| lifetime | ecto | indirect | 0 |  |
| lifetime | ecto | indirect | 0 | SW population |
| lifetime | ecto | indirect | 0 | DLM population |
| lifetime | ecto | indirect | 0 | SCI population |
| spp | deltaT | obs | yi | vi |
| Callosobruchus\_maculatus | -0.1491 | 1 | -0.6044 | 0.01831 |
| Callosobruchus\_maculatus | -0.1491 | 2 | -0.9386 | 0.01684 |
| Callosobruchus\_maculatus | -0.7334 | 3 | -0.02174 | 0.003262 |
| Callosobruchus\_maculatus | -0.7334 | 4 | -0.1408 | 0.00487 |
| Callosobruchus\_maculatus | -0.7334 | 5 | -0.1262 | 0.003164 |
| Callosobruchus\_maculatus | -0.7334 | 6 | -0.1636 | 0.003285 |
| Callosobruchus\_maculatus | -0.7334 | 7 | -0.2166 | 0.005601 |
| Gasterosteus\_aculeatus | 0.7275 | 8 | 0.4709 | 0.04689 |
| Gasterosteus\_aculeatus | 0.7275 | 9 | -0.1402 | 0.008506 |
| Gasterosteus\_aculeatus | 0.7275 | 10 | 0.3477 | 1.273 |
| Gasterosteus\_aculeatus | 0.7275 | 11 | -0.2534 | 0.03088 |
| Anisopteromalus\_calandrae | -0.4413 | 12 | -0.81 | 0.03012 |
| Gambusia\_holbrooki | 0.1431 | 13 | -0.3355 | 0.07531 |
| Drosophila\_birchii | -0.1491 | 14 | 0.5414 | 0.04018 |
| Callosobruchus\_maculatus | 0.1431 | 15 | -2.55 | 0.07131 |
| Rhizoglyphus\_robini | -0.4413 | 16 | -0.1757 | 0.05128 |
| Drosophila\_buzzatii | 0.1431 | 17 | -0.4975 | 0.04918 |
| Drosophila\_buzzatii | 0.1431 | 18 | 0.458 | 0.03961 |
| Callosobruchus\_maculatus | 0.1431 | 19 | -0.605 | 0.03194 |
| Callosobruchus\_maculatus | 0.1431 | 20 | 0.004561 | 0.0004442 |
| Callosobruchus\_maculatus | 0.1431 | 21 | -0.2466 | 0.1131 |
| Callosobruchus\_maculatus | 0.1431 | 22 | -0.02195 | 0.0002128 |
| Phorticella\_striata | 1.896 | 23 | 0.08051 | 0.001853 |
| Phorticella\_striata | 1.896 | 24 | 0.177 | 0.003153 |
| Drosophila\_melanogaster | -0.1491 | 25 | -0.1933 | 0.01755 |
| Drosophila\_melanogaster | -0.1491 | 26 | -0.2935 | 0.04692 |
| Drosophila\_melanogaster | -0.1491 | 27 | -0.1277 | 0.02835 |
| Drosophila\_bipectinata | -1.026 | 28 | -0.01642 | 0.0002986 |
| Aquarius\_remigis | -0.7334 | 29 | -0.007057 | 0.001948 |
| Aquarius\_remigis | -0.7334 | 30 | -0.01432 | 0.0002141 |
| Aquarius\_remigis | -0.7334 | 31 | -0.02745 | 0.001025 |

#kable(lnRR\_males) %>%  
 #kable\_styling(font = 11) %>%  
 #scroll\_box(width = "100%", height = "200px")

We can also have a look at the mean-variance relationship in these data:

p1 = ggplot(data, aes(x=log(X\_T1), y=log(Err\_T1), col = sex)) +   
 geom\_point(size=2) +   
 #theme\_bw() +   
 theme(axis.text.x=element\_text(size=rel(0.4))) +   
 labs(x = "log(Mean\_Temp1)", y = "log(SD\_Temp1)")  
  
 p2 = ggplot(data, aes(x=log(X\_T2), y=log(Err\_T2), col = sex)) +   
 geom\_point(size=2) +   
 #theme\_bw() +   
 theme(axis.text.x=element\_text(size=rel(0.4))) +   
 labs(x = "log(Mean\_Temp2)", y = "log(SD\_Temp2)")  
  
 grid.arrange(p1,p2, nrow =1)



# 2.0 - Multi-level Meta-analytic Models (MLMA)

Now that the datasets are cleaned, effect sizes generated and explored a bit we are now ready to start meta-analysing. We first start with multi-level meta-analytic models (MLMA). These are essentially intercept-only random effects models that account for the known sampling variance of effects along with additional sources of non-independence, such as study and species in a single model. These models are useful for exploring heterogeneity in effects, estimating overall meta-analytic means to understand how temperature affects sexual selection across the entire population of studies and species included in our sample. Effect sizes here are not totally comparable because, as we are well aware, across studies they use different temperatures. However, we are aware of this and what this will essentially do is increase the heterogeneity in effects. Alternatively, this will somewhat get captured by the study-level / species-level random effect because temperature is likely a major driver of between study differences. So, for now, we will assume that effect sizes are comparable and then we can control for temperature differences in meta-regression models below.

## 2.1 - Males

We’ll first have a look at the male data and each of the effect sizes of interest.

#### LnRR

MLMA\_male\_lnRR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnRR\_males)  
 summary(MLMA\_male\_lnRR)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.2572 30.5144 38.5144 44.1192 40.1144   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.4318 0.6571 14 no study   
## sigma^2.2 0.0033 0.0570 11 no spp   
## sigma^2.3 0.0000 0.0000 31 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 30) = 261.2501, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.2932 0.1811 -1.6191 0.1054 -0.6480 0.0617   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a high between-study variance in effects, which isn’t totally surprising given what we discussed above. We also see that the overall meta-analytic mean is -0.29 with a 95% CI = -0.65 to 0.06, which tells us that the mean in the T2 treatment tends to be smaller than the mean in the T1 treatment. More specifically, the higher temperature is about 25.41% smaller than the mean at the lower temperature. The overall estimate isn’t significant (approaching it though), but the sample size is small, so we should stay focused on the estimate and its uncertainty.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

tab <- metaAidR::I2(MLMA\_male\_lnRR, MLMA\_male\_lnRR$vi)  
 # kable(tab)%>%  
 # kable\_styling(font = 14)  
 #  
 pander(tab)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0.9865 | 0.9703 | 0.9948 |
| **spp** | 0.0085 | 0.0022 | 0.0214 |
| **total** | 0.995 | 0.9899 | 0.9977 |

#### lnVR

MLMA\_male\_lnVR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMA\_male\_lnVR)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -19.1939 38.3878 46.3878 51.9926 47.9878   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2583 0.5082 14 no study   
## sigma^2.2 0.0004 0.0191 11 no spp   
## sigma^2.3 0.0212 0.1457 31 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 30) = 144.0839, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.0624 0.1480 -0.4213 0.6736 -0.3524 0.2277   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a moderate between-study variance in effects. We also see that the overall meta-analytic mean is -0.06 with a 95% CI = -0.35 to 0.23, which tells us that the variance in the T2 treatment tends to be smaller than the variance in the T1 treatment, although this is a very small effect size overall. More specifically, the higher temperature is about 6.04% smaller than the lower temperature.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

tabF <- metaAidR::I2(MLMA\_male\_lnVR, MLMA\_male\_lnVR$vi)   
 pander(tabF)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0.7743 | 0.5958 | 0.8805 |
| **spp** | 0.0012 | 3e-04 | 0.0029 |
| **total** | 0.8463 | 0.7281 | 0.9167 |

#### lnCVR

MLMA\_male\_lnCVR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMA\_male\_lnCVR)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -18.3442 36.6884 44.6884 50.2932 46.2884   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0691 0.2630 14 no study   
## sigma^2.2 0.0448 0.2116 11 no spp   
## sigma^2.3 0.0237 0.1539 31 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 30) = 77.8102, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## 0.2195 0.1212 1.8111 0.0701 -0.0180 0.4571 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a small between-study variance in effects. We also see that the overall meta-analytic mean is 0.22 with a 95% CI = -0.02 to 0.46, which tells us that the variance (controlling for the mean) in the T2 treatment tends to be higher than the variance (controlling for the mean) in the T1 treatment. This effect is approaching significance at p = 0.05. More specifically, the variance (controlling for the mean change) in higher temperature is about 24.55% larger compared to the lower temperature.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

tab2 <- metaAidR::I2(MLMA\_male\_lnCVR, MLMA\_male\_lnCVR$vi)   
 pander(tab2)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0.3434 | 0.1662 | 0.5277 |
| **spp** | 0.2225 | 0.0906 | 0.3905 |
| **total** | 0.6885 | 0.5821 | 0.7771 |

The one challenge with these effects is that they contain directionality, however, as is indicated in our review, directionality may not be so easily predicted and there are good theoretical reasons to believe that such clear directional predictions do not likely exist. Hence, we can test this by analysing the magnitude of the response. Here we need to do a couple tricks to account for uncertainty and avoid bias.

# Set the prior  
prior <- list(R=list(V = 1, nu =0.002), G = list(G1 = list(V=1, nu = 0.002), G2 = list(V=1, nu = 0.002)))  
  
# Run the Bayesian MLMA model  
model\_magnitude\_bayes\_males <- MCMCglmm(yi ~ deltaT, mev = lnCVR\_males$vi, random = ~study + spp, data = lnCVR\_males, prior = prior, burnin = 10000, nitt = 1000000, thin = 100, verbose = FALSE)  
summary(model\_magnitude\_bayes\_males)

##   
## Iterations = 10001:999901  
## Thinning interval = 100  
## Sample size = 9900   
##   
## DIC: -42   
##   
## G-structure: ~study  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## study 0.0637 0.000191 0.218 10919  
##   
## ~spp  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## spp 0.105 0.000212 0.367 9934  
##   
## R-structure: ~units  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## units 0.0313 0.000217 0.109 9610  
##   
## Location effects: yi ~ deltaT   
##   
## post.mean l-95% CI u-95% CI eff.samp pMCMC  
## (Intercept) 0.2179 -0.0908 0.4894 9900 0.13  
## deltaT 0.1844 -0.1432 0.5576 9900 0.26

model\_magnitude\_bayes\_malesVR <- MCMCglmm(yi ~ deltaT, mev = lnVR\_males$vi, random = ~study + spp, data = lnVR\_males, prior = prior, burnin = 10000, nitt = 1000000, thin = 100, verbose = FALSE)  
summary(model\_magnitude\_bayes\_malesVR)

##   
## Iterations = 10001:999901  
## Thinning interval = 100  
## Sample size = 9900   
##   
## DIC: -44   
##   
## G-structure: ~study  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## study 0.292 0.000628 0.664 9900  
##   
## ~spp  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## spp 0.0571 0.000138 0.226 9900  
##   
## R-structure: ~units  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## units 0.0313 0.000211 0.113 9234  
##   
## Location effects: yi ~ deltaT   
##   
## post.mean l-95% CI u-95% CI eff.samp pMCMC  
## (Intercept) -0.0341 -0.3981 0.3126 9900 0.84  
## deltaT 0.1321 -0.3342 0.5955 9900 0.54

# Extract posteriors  
sol <- model\_magnitude\_bayes\_males$Sol  
VCV <- model\_magnitude\_bayes\_males$VCV[,-match("sqrt(mev):sqrt(mev).meta", colnames(model\_magnitude\_bayes\_males$VCV))]  
  
sol\_VR <- model\_magnitude\_bayes\_malesVR$Sol  
VCV\_VR <- model\_magnitude\_bayes\_malesVR$VCV[,-match("sqrt(mev):sqrt(mev).meta", colnames(model\_magnitude\_bayes\_malesVR$VCV))]  
  
# Can get the same I2.  
I2(model\_magnitude\_bayes\_males, v = lnCVR\_males$vi)

## I2\_Est. 2.5% CI 97.5% CI  
## study 0.0068 5e-04 0.70  
## spp 0.0084 8e-04 0.80  
## total 0.7465 5e-01 0.93

Now that the Bayesian model is run, we have the overall meta-analytic mean and its posterior distribution, we can apply the posterior to the folded normal:

# Get the folded normal function. This takes the mean and the SD for the "normal" and returns the "mean" on the folded. We can use the entire posterior distribution which then gives us the CI for the mean.  
mu.fnorm <- function(mu, sigma){  
 dnorm(mu, 0, sigma)\*2\*sigma^2 + mu\*(2\*pnorm(mu, 0, sigma) -1)  
}  
  
magnitude\_mean\_males <- mu.fnorm(sol[,1], sqrt(rowSums(VCV)))  
magnitude\_males\_mean <- data.frame(mean\_mag = mean(magnitude\_mean\_males), L\_CI = HPDinterval(magnitude\_mean\_males)[1], U\_CI = HPDinterval(magnitude\_mean\_males)[2])   
  
magnitude\_mean\_males\_VR <- mu.fnorm(sol\_VR[,1], sqrt(rowSums(VCV\_VR)))  
magnitude\_males\_mean\_VR <- data.frame(mean\_mag = mean(magnitude\_mean\_males\_VR), L\_CI = HPDinterval(magnitude\_mean\_males\_VR)[1], U\_CI = HPDinterval(magnitude\_mean\_males\_VR)[2])

##### lnVR - Magnitude

magnitude\_males\_mean\_VR

## mean\_mag L\_CI U\_CI  
## 1 0.5 0.27 0.76

##### lnCVR - Magnitude

magnitude\_males\_mean

## mean\_mag L\_CI U\_CI  
## 1 0.4 0.22 0.62

OK, so, now we can see that the magnitude change in the log ratio of CV between treatments, is on average quite large, and does not overlap zero.

## 2.2 - Females

Now we’ll look at the female data and each of the effect sizes of interest.

#### LnRR

MLMA\_female\_lnRR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnRR\_females)  
 summary(MLMA\_female\_lnRR)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -8.1837 16.3674 24.3674 27.7003 27.7008   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0211 0.1452 9 no study   
## sigma^2.2 0.1760 0.4195 8 no spp   
## sigma^2.3 0.0464 0.2154 18 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 17) = 1220.5820, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.1440 0.1698 -0.8482 0.3964 -0.4769 0.1888   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a high between-species variance in effects. We also see that the overall meta-analytic mean is -0.14 with a 95% CI = -0.48 to 0.19, which tells us that the mean in the T2 treatment tends to be smaller than the mean in the T1 treatment, consistent (but lower) than the male effect. More specifically, the higher temperature is about 13.41% smaller than the lower temperature. The overall estimate isn’t significant, but again (even more so here) the sample size is small, so we should stay focused on the estimate and its uncertainty.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

tab3 <- metaAidR::I2(MLMA\_female\_lnRR, MLMA\_female\_lnRR$vi)  
 pander(tab3)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0.0948 | 0.0188 | 0.2351 |
| **spp** | 0.6905 | 0.3812 | 0.8799 |
| **total** | 0.9974 | 0.9949 | 0.9989 |

#### lnVR

MLMA\_female\_lnVR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_females)  
 summary(MLMA\_female\_lnVR)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.2177 12.4354 20.4354 23.7682 23.7687   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0122 0.1105 9 no study   
## sigma^2.2 0.0000 0.0000 8 no spp   
## sigma^2.3 0.0505 0.2248 18 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 17) = 45.0805, p-val = 0.0002  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.0868 0.0829 -1.0465 0.2953 -0.2493 0.0757   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a moderate between-study variance in effects. We also see that the overall meta-analytic mean is -0.09 with a 95% CI = -0.25 to 0.08, which tells us that the variance in the T2 treatment tends to be smaller than the variance in the T1 treatment, although this is a very small effect size overall amounting to the higher temperature being about 8.31% smaller.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

tab4 <- metaAidR::I2(MLMA\_female\_lnVR, MLMA\_female\_lnVR$vi)   
 pander(tab4)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0.1298 | 0.0352 | 0.2691 |
| **spp** | 0 | 0 | 0 |
| **total** | 0.6619 | 0.5109 | 0.774 |

#### lnCVR

MLMA\_female\_lnCVR <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_females)  
 summary(MLMA\_female\_lnCVR)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.4026 12.8052 20.8052 24.1380 24.1385   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0000 0.0000 9 no study   
## sigma^2.2 0.1279 0.3577 8 no spp   
## sigma^2.3 0.0000 0.0000 18 no obs   
##   
## Test for Heterogeneity:  
## Q(df = 17) = 51.1258, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## 0.0882 0.1424 0.6193 0.5357 -0.1909 0.3673   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Here we can see from the model output that there a small between-study variance in effects. We also see that the overall meta-analytic mean is 0.09 with a 95% CI = -0.19 to 0.37, which tells us that the variance (controlling for the mean) in the T2 treatment tends to be higher than the variance (controlling for the mean) in the T1 treatment. Nonetheless, is a small effect amounting to the variance (controlling for the mean change) in higher temperature being about 9.22% larger compared to the lower temperature.

We can also get estimates of the between study, phylogenetic (if we have one), species and total heterogenity.

table5 <- metaAidR::I2(MLMA\_female\_lnCVR, MLMA\_female\_lnCVR$vi)  
 pander(table5)

|  |  |  |  |
| --- | --- | --- | --- |
|  | I2\_Est. | 2.5% CI | 97.5% CI |
| **study** | 0 | 0 | 0 |
| **spp** | 0.6917 | 0.4048 | 0.8624 |
| **total** | 0.6917 | 0.4048 | 0.8624 |

Again, we can have a look at the magnitudes

# Set the prior  
prior <- list(R=list(V = 1, nu =0.002), G = list(G1 = list(V=1, nu = 0.002)))  
  
# Run the Bayesian MLMA model  
model\_magnitude\_bayes\_feamles <- MCMCglmm(yi ~ deltaT, mev = lnCVR\_females$vi, random = ~study, data = lnCVR\_females, prior = prior, burnin = 10000, nitt = 1000000, thin = 100, verbose = FALSE)  
summary(model\_magnitude\_bayes\_feamles)

##   
## Iterations = 10001:999901  
## Thinning interval = 100  
## Sample size = 9900   
##   
## DIC: -32   
##   
## G-structure: ~study  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## study 0.163 0.000269 0.48 10680  
##   
## R-structure: ~units  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## units 0.0351 0.000236 0.145 9343  
##   
## Location effects: yi ~ deltaT   
##   
## post.mean l-95% CI u-95% CI eff.samp pMCMC  
## (Intercept) 0.1721 -0.1464 0.4699 9900 0.22  
## deltaT -0.0824 -0.3017 0.1602 9900 0.41

model\_magnitude\_bayes\_feamles\_VR <- MCMCglmm(yi ~ deltaT, mev = lnVR\_females$vi, random = ~study, data = lnVR\_females, prior = prior, burnin = 10000, nitt = 1000000, thin = 100, verbose = FALSE)  
summary(model\_magnitude\_bayes\_feamles\_VR)

##   
## Iterations = 10001:999901  
## Thinning interval = 100  
## Sample size = 9900   
##   
## DIC: -2.7   
##   
## G-structure: ~study  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## study 0.0255 0.000169 0.0956 9900  
##   
## R-structure: ~units  
##   
## post.mean l-95% CI u-95% CI eff.samp  
## units 0.0561 0.00034 0.146 9900  
##   
## Location effects: yi ~ deltaT   
##   
## post.mean l-95% CI u-95% CI eff.samp pMCMC  
## (Intercept) -0.0859 -0.2701 0.1024 9900 0.33  
## deltaT 0.0548 -0.0887 0.1865 9900 0.40

# Extract posteriors  
sol\_f <- model\_magnitude\_bayes\_feamles$Sol  
VCV\_f <- model\_magnitude\_bayes\_feamles$VCV[,-match("sqrt(mev):sqrt(mev).meta", colnames(model\_magnitude\_bayes\_feamles$VCV))]  
  
sol\_f\_VR <- model\_magnitude\_bayes\_feamles\_VR$Sol  
VCV\_f\_VR <- model\_magnitude\_bayes\_feamles\_VR$VCV[,-match("sqrt(mev):sqrt(mev).meta", colnames(model\_magnitude\_bayes\_feamles\_VR$VCV))]  
  
# Can get the same I2.  
I2(model\_magnitude\_bayes\_feamles, v = lnCVR\_females$vi)

## I2\_Est. 2.5% CI 97.5% CI  
## study 0.0091 0.0027 0.89  
## total 0.8152 0.4856 0.96

Now that the Bayesian model is run, we have the overall meta-analytic mean and its posterior distribution, we can apply the posterior to the folded normal:

# Get the folded normal function. This takes the mean and the SD for the "normal" and returns the "mean" on the folded. We can use the entire posterior distribution which then gives us the CI for the mean.  
  
magnitude\_mean\_females <- mu.fnorm(sol\_f[,1], sqrt(rowSums(VCV\_f)))  
magnitude\_females\_mean <- data.frame(mean\_mag = mean(magnitude\_mean\_females), L\_CI = HPDinterval(magnitude\_mean\_females)[1], U\_CI = HPDinterval(magnitude\_mean\_females)[2])   
  
magnitude\_mean\_females\_VR <- mu.fnorm(sol\_f\_VR[,1], sqrt(rowSums(VCV\_f\_VR)))  
magnitude\_females\_mean\_VR <- data.frame(mean\_mag = mean(magnitude\_mean\_females\_VR), L\_CI = HPDinterval(magnitude\_mean\_females\_VR)[1], U\_CI = HPDinterval(magnitude\_mean\_females\_VR)[2])

##### lnVR - Magnitude

magnitude\_females\_mean\_VR

## mean\_mag L\_CI U\_CI  
## 1 0.24 0.1 0.39

##### lnCVR - Magnitude

magnitude\_females\_mean

## mean\_mag L\_CI U\_CI  
## 1 0.38 0.18 0.66

OK, so, now we can see that the magnitude change in the log ratio of CV between treatments, is on average quite large, and does not overlap zero.

# 3.0 - Multi-level Meta-regression Models (MLMR)

Given our very limited sample size, we can only hope to run some simple meta-regression models exploring how a few hypothesized variables impact variation in effects.

## 3.1 - Males

### 3.1.1 - When we control for temperature differences between treatments within a study what is the average effect size at an “average” temperature?

Here we want to simply control for the fact that effect sizes across studies are done with experimental temperature treatments that vary in temperature. What we want to now estimate is: 1) whether the magnitude of the effect get larger with greater temperature difference between the treatments and 2) what the average effect is when we control for temperature (i.e., scaled temperature)

#### lnRR

MLMR\_male\_lnRR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnRR\_males)  
 summary(MLMR\_male\_lnRR\_T)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -14.3093 28.6186 38.6186 45.4551 41.2273   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.4791 0.6922 14 no study   
## sigma^2.2 0.0008 0.0290 11 no spp   
## sigma^2.3 0.0000 0.0001 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 29) = 253.2062, p-val < .0001  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 0.0146, p-val = 0.9039  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.2957 0.1897 -1.5588 0.1190 -0.6676 0.0761   
## deltaT 0.0323 0.2675 0.1208 0.9039 -0.4919 0.5565   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_male\_lnVR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -18.2272 36.4544 46.4544 53.2909 49.0631   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2708 0.5204 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0216 0.1471 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 29) = 137.4662, p-val < .0001  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 0.4828, p-val = 0.4871  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.0566 0.1512 -0.3743 0.7082 -0.3530 0.2398   
## deltaT 0.1469 0.2114 0.6949 0.4871 -0.2675 0.5613   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_male\_lnCVR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -17.3978 34.7956 44.7956 51.6320 47.4043   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0258 0.1607 14 no study   
## sigma^2.2 0.1101 0.3318 11 no spp   
## sigma^2.3 0.0244 0.1561 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 29) = 73.0960, p-val < .0001  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 1.6889, p-val = 0.1937  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt 0.2031 0.1336 1.5205 0.1284 -0.0587 0.4649   
## deltaT 0.1917 0.1475 1.2996 0.1937 -0.0974 0.4808   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: When we standardise the temperature comparisons across the studies, for an average temperature difference of 7.51 degrees Celsius there is no strong evidence for the mean of direct and indirect fitness estimates being impacted in males

### 3.1.2 - Are there differences between direct and indirect estimates of fitness, after accounting for temperature?

Here we want to explore if the results are moderated by whether or not our effect size was generated with some measure of direct fitness estimate (what we really want) versus if it comes from an indirect estimate, or trait that is linked with fitness. What we will do to test this, is fit a model

#### lnRR

MLMR\_male\_lnRR\_T\_Fitness <- metafor::rma.mv(yi ~ -1 + deltaT + fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnRR\_males)  
 summary(MLMR\_male\_lnRR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -12.9404 25.8809 37.8809 45.8741 41.8809   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.4579 0.6767 14 no study   
## sigma^2.2 0.0327 0.1808 11 no spp   
## sigma^2.3 0.0000 0.0000 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 201.3877, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 2.8837, p-val = 0.4099  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0133 0.2700 0.0493 0.9607 -0.5158 0.5425   
## fitnessdirect -0.4619 0.2773 -1.6659 0.0957 -1.0054 0.0815 .   
## fitnessindirect -0.0938 0.2682 -0.3498 0.7265 -0.6196 0.4319   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_male\_lnVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1 + deltaT+ fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -14.3719 28.7439 40.7439 48.7371 44.7439   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.1111 0.3334 14 no study   
## sigma^2.2 0.0164 0.1279 11 no spp   
## sigma^2.3 0.0270 0.1643 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 85.9664, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 10.1907, p-val = 0.0170  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1319 0.1541 0.8560 0.3920 -0.1701 0.4339   
## fitnessdirect -0.3949 0.1705 -2.3156 0.0206 -0.7292 -0.0607 \*   
## fitnessindirect 0.2800 0.1523 1.8384 0.0660 -0.0185 0.5785 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_male\_lnCVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1+deltaT+ fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -16.1884 32.3768 44.3768 52.3700 48.3768   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0930 0.3049 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0220 0.1484 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 67.3331, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 8.8985, p-val = 0.0307  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1044 0.1375 0.7592 0.4477 -0.1651 0.3739   
## fitnessdirect 0.0523 0.1658 0.3157 0.7522 -0.2726 0.3773   
## fitnessindirect 0.3900 0.1348 2.8926 0.0038 0.1258 0.6543 \*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: We see a slight effect of temperature between a 7.51 degrees Celsius difference on the mean, when looking at direct fitness estimates the actual variance for fitness decreases significantly, where as for indirect estimates of traits the variance at higher temperatures actually increases (marginally significant). However, this effect is explained by changes in the mean as lnCVR, we see now change on direct estimates of fitness but a even stronger increase in variance for indirect traits linked with fitness.

### 3.1.3 - Do stressful temperature comparisons lead to stronger effect sizes, when accounting for temperature differences across studies?

Some studies clearly manipulate temperatures outside or on the extreme of the normal range of temperatures. We hypothesized that stressful temperatures will likely result in a greater increase in variance.

#### lnRR

MLMR\_male\_lnRR\_T\_stress <- metafor::rma.mv(yi ~ -1 +deltaT +temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnRR\_males)  
 summary(MLMR\_male\_lnRR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.3547 30.7093 40.7093 47.3703 43.4366   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.4900 0.7000 14 no study   
## sigma^2.2 0.0000 0.0004 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 245.2598, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 2.6866, p-val = 0.4425  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0343 0.2703 0.1269 0.8991 -0.4954 0.5640   
## temp.rangenatural -0.3071 0.1926 -1.5940 0.1109 -0.6846 0.0705   
## temp.rangestress -0.2850 0.1930 -1.4769 0.1397 -0.6633 0.0932   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_male\_lnVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.0145 30.0290 42.0290 50.0223 46.0290   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2255 0.4748 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0125 0.1118 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 108.1396, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 6.5856, p-val = 0.0863  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0898 0.1945 0.4614 0.6445 -0.2915 0.4710   
## temp.rangenatural 0.2091 0.1760 1.1880 0.2348 -0.1359 0.5540   
## temp.rangestress -0.3378 0.1822 -1.8541 0.0637 -0.6949 0.0193 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_male\_lnCVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -17.0755 34.1509 46.1509 54.1442 50.1509   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0874 0.2956 14 no study   
## sigma^2.2 0.0644 0.2537 11 no spp   
## sigma^2.3 0.0189 0.1375 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 73.0902, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 3.6760, p-val = 0.2986  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1355 0.1625 0.8338 0.4044 -0.1830 0.4540   
## temp.rangenatural 0.2721 0.1603 1.6968 0.0897 -0.0422 0.5863 .   
## temp.rangestress 0.1486 0.1788 0.8313 0.4058 -0.2018 0.4990   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: We see a strong effect of temperature on mean (decreased at higher temps) over a 7.51 degrees Celsius difference when the temperatures being manipulated fall within the stressed range. When controlling for the effect of temperature on the mean, we see a strong increase in total variance in direct and indirect fitness estimates over a 7.51 degrees Celsius difference.

## 3.2 - Females

### 3.2.1 - When we control for temperature differences between treatments within a study what is the average effect size at an “average” temperature?

Here we want to simply control for the fact that effect sizes across studies are done with experimental temperature treatments that vary in temperature. What we want to now estimate is: 1) whether the magnitude of the effect get larger with greater temperature difference between the treatments and 2) what the average effect is when we control for temperature (i.e., scaled temperature)

#### lnRR

MLMR\_female\_lnRR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|obs), data = lnRR\_females)  
 summary(MLMR\_female\_lnRR\_T)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -7.8779 15.7559 23.7559 26.8462 27.3922   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2198 0.4688 9 no study   
## sigma^2.2 0.0457 0.2139 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 16) = 385.8987, p-val < .0001  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 0.9715, p-val = 0.3243  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.2277 0.1701 -1.3387 0.1807 -0.5611 0.1057   
## deltaT 0.1222 0.1240 0.9856 0.3243 -0.1208 0.3653   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_female\_lnVR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|obs), data = lnVR\_females)  
 summary(MLMR\_female\_lnVR\_T)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -5.9243 11.8486 19.8486 22.9390 23.4850   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0097 0.0986 9 no study   
## sigma^2.2 0.0516 0.2271 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 16) = 41.6782, p-val = 0.0004  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 0.8655, p-val = 0.3522  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.0896 0.0812 -1.1025 0.2703 -0.2488 0.0697   
## deltaT 0.0568 0.0610 0.9303 0.3522 -0.0628 0.1764   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_female\_lnCVR\_T <- metafor::rma.mv(yi ~ deltaT, V = vi, random = list( ~1|study, ~1|obs), data = lnCVR\_females)  
 summary(MLMR\_female\_lnCVR\_T)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -7.0090 14.0181 22.0181 25.1085 25.6545   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.1572 0.3964 9 no study   
## sigma^2.2 0.0000 0.0000 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 16) = 45.5188, p-val = 0.0001  
##   
## Test of Moderators (coefficient 2):  
## QM(df = 1) = 0.5210, p-val = 0.4704  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt 0.1576 0.1486 1.0610 0.2887 -0.1336 0.4488   
## deltaT -0.0775 0.1073 -0.7218 0.4704 -0.2878 0.1329   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: Result holds really when we account for temperature. Females don’t seem to be affected much, with the caveat of it being lower powered.

### 3.2.2 - Are there differences between direct and indirect estimates of fitness, when controlling for temperature?

Here we want to explore if the results are moderated by whether or not our effect size was generated with some measure of direct fitness estimate (what we really want) versus if it comes from an indirect estimate, or trait that is linked with fitness.

#### lnRR

MLMR\_female\_lnRR\_T\_fitness <- metafor::rma.mv(yi ~ -1 + deltaT + fitness, V = vi, random = list( ~1|study, ~1|obs), data = lnRR\_females)  
 summary(MLMR\_female\_lnRR\_T\_fitness)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.9180 13.8360 23.8360 27.3763 30.5027   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2453 0.4953 9 no study   
## sigma^2.2 0.0455 0.2132 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 152.0483, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 2.7106, p-val = 0.4384  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1420 0.1340 1.0598 0.2892 -0.1206 0.4047   
## fitnessdirect -0.2731 0.1922 -1.4210 0.1553 -0.6497 0.1036   
## fitnessindirect 0.0905 0.5198 0.1741 0.8618 -0.9284 1.1094   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_female\_lnVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1+ deltaT+ fitness, V = vi, random = list( ~1|study, ~1|obs), data = lnVR\_females)  
 summary(MLMR\_female\_lnVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -4.3822 8.7644 18.7644 22.3047 25.4311   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0000 0.0000 9 no study   
## sigma^2.2 0.0460 0.2145 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 35.9947, p-val = 0.0018  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 7.0893, p-val = 0.0691  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0801 0.0549 1.4588 0.1446 -0.0275 0.1878   
## fitnessdirect -0.1466 0.0735 -1.9948 0.0461 -0.2905 -0.0026 \*   
## fitnessindirect 0.2979 0.2243 1.3282 0.1841 -0.1417 0.7374   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_female\_lnCVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1 + deltaT+ fitness, V = vi, random = list( ~1|study, ~1|obs), data = lnCVR\_females)  
 summary(MLMR\_female\_lnCVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.3614 12.7228 22.7228 26.2630 29.3894   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.1949 0.4415 9 no study   
## sigma^2.2 0.0000 0.0000 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 45.5067, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 1.2831, p-val = 0.7332  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT -0.0745 0.1208 -0.6166 0.5375 -0.3113 0.1623   
## fitnessdirect 0.1523 0.1742 0.8747 0.3817 -0.1890 0.4937   
## fitnessindirect 0.1970 0.4860 0.4053 0.6853 -0.7556 1.1496   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: Over a 7.51 degrees Celsius temperature difference we don’t see much evidence that there are differences between direct and indirect estimates.

### 3.2.3 - Do stressful temperature comparisons lead to stronger effect sizes, when accounting for temperature differences across studies?

Some studies clearly manipulate temperatures outside or on the extreme of the normal range of temperatures. We hypothesized that stressful temperatures will likely result in a greater increase in variance. Here, there is strong overlap between the study and species and we have a very small sample size, so we’ll just fit study for now (more levels) and should capture any between species variance.

#### lnRR

MLMR\_female\_lnRR\_T\_stress <- metafor::rma.mv(yi ~ -1 +deltaT + temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnRR\_females)  
 summary(MLMR\_female\_lnRR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -2.4271 4.8541 14.8541 18.3944 21.5208   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0112 0.1061 9 no study   
## sigma^2.2 0.0527 0.2296 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 80.5931, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 43.0588, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0475 0.0526 0.9047 0.3656 -0.0555 0.1506   
## temp.rangenatural 0.1565 0.1116 1.4018 0.1610 -0.0623 0.3753   
## temp.rangestress -0.5906 0.0988 -5.9776 <.0001 -0.7843 -0.3970 \*\*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR

MLMR\_female\_lnVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+ temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnVR\_females)  
 summary(MLMR\_female\_lnVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -4.9064 9.8128 19.8128 23.3530 26.4794   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0000 0.0000 9 no study   
## sigma^2.2 0.0559 0.2364 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 37.9091, p-val = 0.0009  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 5.5369, p-val = 0.1364  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0238 0.0612 0.3893 0.6971 -0.0961 0.1438   
## temp.rangenatural 0.0668 0.1277 0.5232 0.6008 -0.1835 0.3171   
## temp.rangestress -0.1975 0.0961 -2.0549 0.0399 -0.3858 -0.0091 \*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR

MLMR\_female\_lnCVR\_T\_stress <- metafor::rma.mv(yi ~ -1+deltaT+temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnCVR\_females)  
 summary(MLMR\_female\_lnCVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -4.1583 8.3167 18.3167 21.8569 24.9833   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0588 0.2424 9 no study   
## sigma^2.2 0.0000 0.0000 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 28.6289, p-val = 0.0179  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 10.9297, p-val = 0.0121  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT -0.0129 0.0773 -0.1674 0.8671 -0.1645 0.1386   
## temp.rangenatural -0.1619 0.1568 -1.0320 0.3021 -0.4693 0.1455   
## temp.rangestress 0.4247 0.1410 3.0122 0.0026 0.1484 0.7011 \*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: We see a strong effect of temperature on mean (decreased at higher temps) over a 7.51 degrees Celsius difference when the temperatures being manipulated fall within the stressed range. When controlling for the effect of temperature on the mean, we see a significant increase in total variance in direct and indirect fitness estimates over a 7.51 degrees Celsius difference.

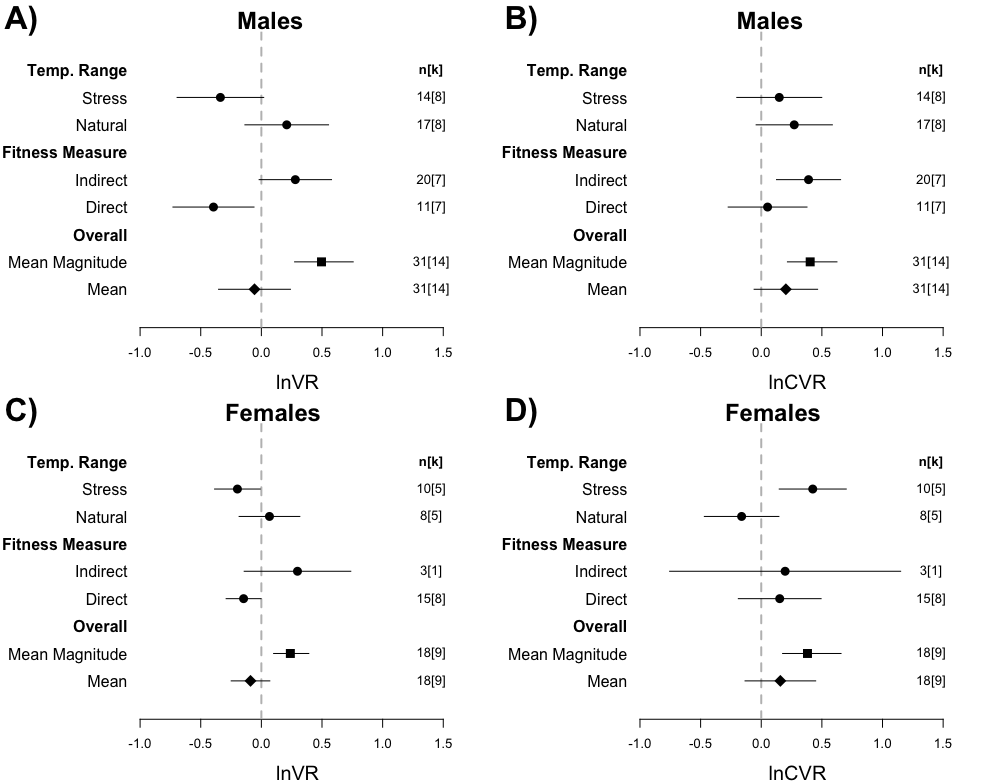
# 4.0 - Summary of Meta-analytic Results

We can summarise the overall results with some forest plots for males and females. We’ll use corrected. We will just use the lnVR and lnCVR results here. First we need to extract the relevant data.

# Get the sample sizes and sizes  
 # Overall  
 n\_all <- data.frame(data %>% group\_by(sex) %>% summarise(n = n(), k = length(unique(study))))  
  
 # Direct vs indirect  
 n\_direct <- data.frame(data %>% group\_by(sex, fitness) %>% summarise(n = n(), k = length(unique(study))))  
  
 # Stress vs not  
 n\_stress <- data.frame(data %>% group\_by(sex, temp.range) %>% summarise(n = n(), k = length(unique(study))))  
  
 N <- rbind(n\_all, n\_all, n\_direct[,c("sex", "n", "k")], n\_stress[,c("sex", "n", "k")])  
 male\_N <- subset(N, sex == "males")  
 female\_N <- subset(N, sex == "females")  
  
 location\_y <- c(1,2, 4,5, 7, 8)  
  
 # Get the model estimates and CIs  
 # Males  
 all\_T\_m\_lnVR <- cbind(MLMR\_male\_lnVR\_T$b[1,], MLMR\_male\_lnVR\_T$ci.lb[1], MLMR\_male\_lnVR\_T$ci.ub[1])  
 all\_T\_m\_lnCVR <- cbind(MLMR\_male\_lnCVR\_T$b[1,], MLMR\_male\_lnCVR\_T$ci.lb[1], MLMR\_male\_lnCVR\_T$ci.ub[1])  
  
 mag\_T\_m\_lnVR <- as.matrix(magnitude\_males\_mean\_VR)  
 mag\_T\_m\_lnCVR <- as.matrix(magnitude\_males\_mean)  
  
 fitness\_T\_m\_VR <- cbind(MLMR\_male\_lnVR\_T\_Fitness$b[c(2:3),], MLMR\_male\_lnVR\_T\_Fitness$ci.lb[c(2:3)], MLMR\_male\_lnVR\_T\_Fitness$ci.ub[c(2:3)])  
 fitness\_T\_m\_CVR <- cbind(MLMR\_male\_lnCVR\_T\_Fitness$b[c(2:3),], MLMR\_male\_lnCVR\_T\_Fitness$ci.lb[c(2:3)], MLMR\_male\_lnCVR\_T\_Fitness$ci.ub[c(2:3)])  
  
 stress\_T\_m\_VR <- cbind(MLMR\_male\_lnVR\_T\_stress$b[c(2:3),], MLMR\_male\_lnVR\_T\_stress$ci.lb[c(2:3)], MLMR\_male\_lnVR\_T\_stress$ci.ub[c(2:3)])  
 stress\_T\_m\_CVR <- cbind(MLMR\_male\_lnCVR\_T\_stress$b[c(2:3),], MLMR\_male\_lnCVR\_T\_stress$ci.lb[c(2:3)], MLMR\_male\_lnCVR\_T\_stress$ci.ub[c(2:3)])  
  
 # Make a big tables for males  
 lnVR\_males\_ests <- cbind(rbind(all\_T\_m\_lnVR, mag\_T\_m\_lnVR, fitness\_T\_m\_VR, stress\_T\_m\_VR), male\_N, location\_y)  
 lnCVR\_males\_ests <- cbind(rbind(all\_T\_m\_lnCVR, mag\_T\_m\_lnCVR, fitness\_T\_m\_CVR, stress\_T\_m\_CVR), male\_N, location\_y)  
  
 # Females  
 all\_T\_f\_lnVR <- cbind(MLMR\_female\_lnVR\_T$b[1,], MLMR\_female\_lnVR\_T$ci.lb[1], MLMR\_female\_lnVR\_T$ci.ub[1])  
 all\_T\_f\_lnCVR <- cbind(MLMR\_female\_lnCVR\_T$b[1,], MLMR\_female\_lnCVR\_T$ci.lb[1], MLMR\_female\_lnCVR\_T$ci.ub[1])  
  
 mag\_T\_f\_lnVR <- as.matrix(magnitude\_females\_mean\_VR)  
 mag\_T\_f\_lnCVR <- as.matrix(magnitude\_females\_mean)  
  
 fitness\_T\_f\_VR <- cbind(MLMR\_female\_lnVR\_T\_Fitness$b[c(2:3),], MLMR\_female\_lnVR\_T\_Fitness$ci.lb[c(2:3)], MLMR\_female\_lnVR\_T\_Fitness$ci.ub[c(2:3)])  
 fitness\_T\_f\_CVR <- cbind(MLMR\_female\_lnCVR\_T\_Fitness$b[c(2:3),], MLMR\_female\_lnCVR\_T\_Fitness$ci.lb[c(2:3)], MLMR\_female\_lnCVR\_T\_Fitness$ci.ub[c(2:3)])  
  
 stress\_T\_f\_VR <- cbind(MLMR\_female\_lnVR\_T\_stress$b[c(2:3),], MLMR\_female\_lnVR\_T\_stress$ci.lb[c(2:3)], MLMR\_female\_lnVR\_T\_stress$ci.ub[c(2:3)])  
 stress\_T\_f\_CVR <- cbind(MLMR\_female\_lnCVR\_T\_stress$b[c(2:3),], MLMR\_female\_lnCVR\_T\_stress$ci.lb[c(2:3)], MLMR\_female\_lnCVR\_T\_stress$ci.ub[c(2:3)])  
  
 # Make a big tables for males  
 lnVR\_females\_ests <- cbind(rbind(all\_T\_f\_lnVR, mag\_T\_f\_lnVR, fitness\_T\_f\_VR, stress\_T\_f\_VR), female\_N, location\_y)  
 lnCVR\_females\_ests <- cbind(rbind(all\_T\_f\_lnCVR, mag\_T\_f\_lnCVR, fitness\_T\_f\_CVR, stress\_T\_f\_CVR), female\_N, location\_y)

Now that we have everything we need we can plot the subset analyses together with overall effects for each of the effect sizes and males and females. We will focus on lnVR and lnCVR as these are the measures we are most interested in.

# Lets make a plot  
#pdf(file= "fig1.pdf", height = 8.15859, width = 10.41410)  
 par(mar=c(4,8,2,2), mfrow = c(2,2))  
   
 # Males - lnVR  
 plot(location\_y ~ mean\_mag, data = lnVR\_males\_ests, bty="n", xlim = c(-1, 1.6), ylab = "", xlab = "lnVR", yaxt = "n", pch = c(18,15,16, 16, 16, 16), cex = c(2, rep(1.5, 5)), ylim = c(0, 10), cex.lab = 1.5)  
 abline(v = 0, lty = 2, col = "gray", lwd = 2)  
 mtext("Males", font = 2, side=3, adj = 0.4, cex = 1.5)  
 mtext("A)", font = 2, side=3, adj = -0.4, cex = 2)  
 arrows(x0=lnVR\_males\_ests$mean\_mag, y0=lnVR\_males\_ests$location\_y, x1=lnVR\_males\_ests$L\_CI, y1=lnVR\_males\_ests$location\_y, length = 0)  
 arrows(x0=lnVR\_males\_ests$mean\_mag, y0=lnVR\_males\_ests$location\_y, x1=lnVR\_males\_ests$U\_CI, y1=lnVR\_males\_ests$location\_y, length = 0)  
  
 nk <- paste0(lnVR\_males\_ests[,"n"], "[", lnVR\_males\_ests[,"k"], "]")  
 text(nk, y = lnVR\_males\_ests$location\_y, x = 1.4)  
 text("n[k]", y = 9, x = 1.4, font = 2)  
  
 Labels <- c("Mean", "Mean Magnitude", "Direct", "Indirect", "Natural", "Stress")  
 mtext(Labels, at = lnVR\_males\_ests$location\_y, side = 2, las = 1)  
 Headers <- c("Overall", "Fitness Measure", "Temp. Range")  
 mtext(Headers, at = c(3, 6, 9), side = 2, las = 1, font = 2)  
  
 # Males - lnCVR  
 plot(location\_y ~ mean\_mag, data = lnCVR\_males\_ests, bty="n", xlim = c(-1, 1.6), ylab = "", xlab = "lnCVR", yaxt = "n", pch = c(18,15,16, 16, 16, 16), cex = c(2, rep(1.5, 5)), ylim = c(0, 10),cex.lab = 1.5)  
 abline(v = 0, lty = 2, col = "gray", lwd = 2)  
 mtext("Males", font = 2, side=3, adj = 0.4, cex = 1.5)  
 mtext("B)", font = 2, side=3, adj = -0.4, cex = 2)  
 arrows(x0=lnCVR\_males\_ests$mean\_mag, y0=lnCVR\_males\_ests$location\_y, x1=lnCVR\_males\_ests$L\_CI, y1=lnCVR\_males\_ests$location\_y, length = 0)  
 arrows(x0=lnCVR\_males\_ests$mean\_mag, y0=lnCVR\_males\_ests$location\_y, x1=lnCVR\_males\_ests$U\_CI, y1=lnCVR\_males\_ests$location\_y, length = 0)  
  
 nk <- paste0(lnCVR\_males\_ests[,"n"], "[", lnCVR\_males\_ests[,"k"], "]")  
 text(nk, y = lnCVR\_males\_ests$location\_y, x = 1.4)  
 text("n[k]", y = 9, x = 1.4, font = 2)  
  
 Labels <- c("Mean", "Mean Magnitude", "Direct", "Indirect", "Natural", "Stress")  
 mtext(Labels, at = lnCVR\_males\_ests$location\_y, side = 2, las = 1)  
 Headers <- c("Overall", "Fitness Measure", "Temp. Range")  
 mtext(Headers, at = c(3, 6, 9), side = 2, las = 1, font = 2)  
  
 # Females - lnVR  
  
 plot(location\_y ~ mean\_mag, data = lnVR\_females\_ests, bty="n", xlim = c(-1, 1.6), ylab = "", xlab = "lnVR", yaxt = "n", pch = c(18,15,16, 16, 16, 16), cex = c(2, rep(1.5, 5)), ylim = c(0, 10), cex.lab = 1.5)  
 abline(v = 0, lty = 2, col = "gray", lwd = 2)  
 mtext("Females", font = 2, side=3, adj = 0.4, cex = 1.5)  
 mtext("C)", font = 2, side=3, adj = -0.4, cex = 2)  
 arrows(x0=lnVR\_females\_ests$mean\_mag, y0=lnVR\_females\_ests$location\_y, x1=lnVR\_females\_ests$L\_CI, y1=lnVR\_females\_ests$location\_y, length = 0)  
 arrows(x0=lnVR\_females\_ests$mean\_mag, y0=lnVR\_females\_ests$location\_y, x1=lnVR\_females\_ests$U\_CI, y1=lnVR\_females\_ests$location\_y, length = 0)  
  
 nk <- paste0(lnVR\_females\_ests[,"n"], "[", lnVR\_females\_ests[,"k"], "]")  
 text(nk, y = lnVR\_females\_ests$location\_y, x = 1.4)  
 text("n[k]", y = 9, x = 1.4, font = 2)  
  
 Labels <- c("Mean", "Mean Magnitude", "Direct", "Indirect", "Natural", "Stress")  
 mtext(Labels, at = lnVR\_females\_ests$location\_y, side = 2, las = 1)  
 Headers <- c("Overall", "Fitness Measure", "Temp. Range")  
 mtext(Headers, at = c(3, 6, 9), side = 2, las = 1, font = 2)  
  
 # Females - lnCVR  
  
 plot(location\_y ~ mean\_mag, data = lnCVR\_females\_ests, bty="n", xlim = c(-1, 1.6), ylab = "", xlab = "lnCVR", yaxt = "n", pch = c(18,15,16, 16, 16, 16), cex = c(2, rep(1.5, 5)), ylim = c(0, 10), cex.lab = 1.5)  
 abline(v = 0, lty = 2, col = "gray", lwd = 2)  
 mtext("Females", font = 2, side=3, adj = 0.4, cex = 1.5)  
 mtext("D)", font = 2, side=3, adj = -0.4, cex = 2)  
 arrows(x0=lnCVR\_females\_ests$mean\_mag, y0=lnCVR\_females\_ests$location\_y, x1=lnCVR\_females\_ests$L\_CI, y1=lnCVR\_females\_ests$location\_y, length = 0)  
 arrows(x0=lnCVR\_females\_ests$mean\_mag, y0=lnCVR\_females\_ests$location\_y, x1=lnCVR\_females\_ests$U\_CI, y1=lnCVR\_females\_ests$location\_y, length = 0)  
  
 nk <- paste0(lnCVR\_females\_ests[,"n"], "[", lnCVR\_females\_ests[,"k"], "]")  
 text(nk, y = lnCVR\_females\_ests$location\_y, x = 1.4)  
 text("n[k]", y = 9, x = 1.4, font = 2)  
  
 Labels <- c("Mean", "Mean Magnitude", "Direct", "Indirect", "Natural", "Stress")  
 mtext(Labels, at = lnCVR\_females\_ests$location\_y, side = 2, las = 1)  
 Headers <- c("Overall", "Fitness Measure", "Temp. Range")  
 mtext(Headers, at = c(3, 6, 9), side = 2, las = 1, font = 2)

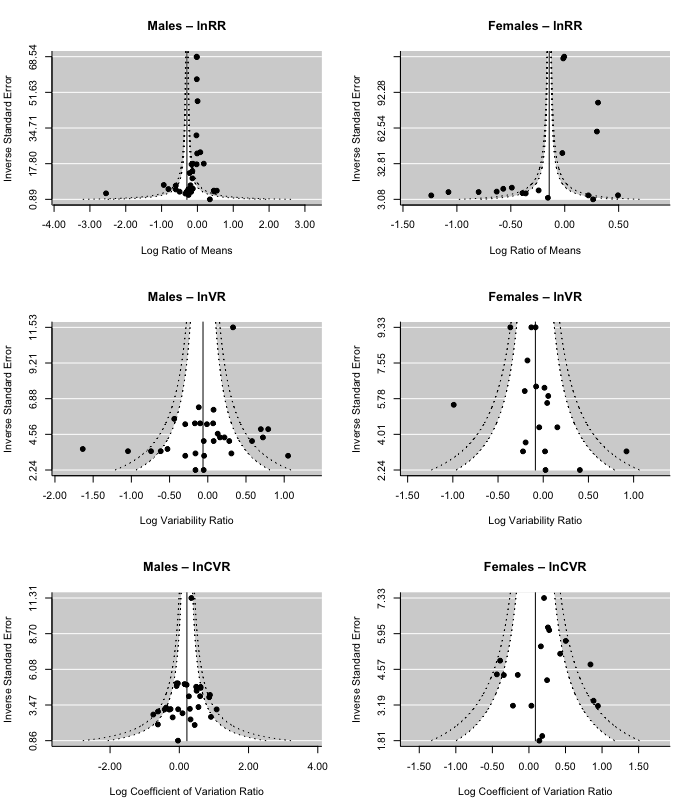


**Figure 1** – Meta-analytic means for a temperature treatment difference of 7.5 degrees Celsius across MLMA and MLMR models for the log variance ratio (lnVR) and the log coefficient of variation ratio (lnCVR) for males and females. n = total number of effect sizes, whereas k = the total number of studies. Mean estimates and 95% credible/confidence intervals are provided. Subset analyses exploring the impact of various moderators on lnVR and lnCVR are provided (‘circles’), along with the overall meta-analytic mean (‘diamond’) and the mean magnitude of variance differences between treatments (‘square’).

# 5.0 - Publication Bias

We should always explore funnel plots. We’ll do that for each effect size estimate for males and females. High levels of heterogeneity can lead to apparent asymmetries in funnel plots, and this is expected to be exacerbated with small sample sizes. We’ll view the raw data first with the random effects models and then explore how funnel asymmetry changes when accounting for moderators

par(mfrow = c(3,2))  
  
# lnRR  
funnel(MLMA\_male\_lnRR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Males – lnRR")  
funnel(MLMA\_female\_lnRR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Females – lnRR")  
  
#lnVR  
funnel(MLMA\_male\_lnVR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Males – lnVR")  
funnel(MLMA\_female\_lnVR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Females – lnVR")  
  
#lnCVR  
funnel(MLMA\_male\_lnCVR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Males – lnCVR")  
funnel(MLMA\_female\_lnCVR, yaxis = "seinv", digits = 2, level = c(0.95, 0.99), main = "Females – lnCVR")



**Figure S1** – Funnel plots of the log response ratio (lnRR), the log variance ratio (lnVR) and log coefficient of variation ratio (lnCVR) as a function of the inverse sampling error for both males and females. Both 95% and 99% pseudo-confidence intervals for sampling variance are provided.

**Conclusions**:There does appear to be some outlying data points and asymmetry in a few plots, but the patterns are not entirely obvious. Publication bias, if it exists, is not entirely clear here, and probably has limited impact on the results. Asymmetry is likely driven more by the limited sample size than actual publication bias.

We can also explore whether there are relationships of the effect sizes with the year of publication to understand whether effects are changing across years. This is unlikely to be the case given that we have so few studies and the empirical work on temperature and sexual selection is rather limited, hence the reason for our synthesis! In any case, we’ll have a look. We will just explore the impact this has in temperature corrected models, so as not to over-parameterize the models too much. Additionally, we will only focus on the mean because there is sound theoretical reasoning to expect a reporting relationship that changes with time on the magnitude of mean changes in temperature. Often, strong mean effect stimulate empirical research into the effects of an experimental manipulation, in the case temperature. At times these are based on strong effects which after corroboration with more empirical research on the topic with larger sample sizes, we begin to see an average decrease in effect sizes as time goes on. So, we expect a negative relationship with year on the mean lnRR:

#### lnRR - Males

MLMR\_male\_lnRR\_T\_year <- metafor::rma.mv(yi ~ deltaT + scale(year), V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnRR\_males)  
 summary(MLMR\_male\_lnRR\_T\_year)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -13.0580 26.1159 38.1159 46.1091 42.1159   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.5038 0.7098 14 no study   
## sigma^2.2 0.0000 0.0001 11 no spp   
## sigma^2.3 0.0000 0.0000 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 250.8972, p-val < .0001  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 0.5952, p-val = 0.7426  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.2673 0.1980 -1.3499 0.1770 -0.6553 0.1208   
## deltaT 0.0209 0.2744 0.0762 0.9392 -0.5169 0.5587   
## scale(year) -0.1484 0.1946 -0.7625 0.4458 -0.5297 0.2330   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnRR - Females

MLMR\_female\_lnRR\_T\_year <- metafor::rma.mv(yi ~ deltaT + scale(year), V = vi, random = list( ~1|study, ~1|obs), data = lnRR\_females)  
 summary(MLMR\_female\_lnRR\_T\_year)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.8048 13.6097 23.6097 27.1499 30.2763   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2324 0.4820 9 no study   
## sigma^2.2 0.0446 0.2113 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 339.7540, p-val < .0001  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 1.7779, p-val = 0.4111  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.2087 0.1751 -1.1919 0.2333 -0.5519 0.1345   
## deltaT 0.1615 0.1340 1.2048 0.2283 -0.1012 0.4242   
## scale(year) -0.1812 0.1957 -0.9261 0.3544 -0.5647 0.2023   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: We do indeed see evidence for a negative relationship on mean lnRR over time for both males and females, but this is not significant. As more studies accumulate we might expect to see this relationship to become stronger.

# 6.0 - Sensitivity Analyses

In this section we’ll explore the impact of some of the assumptions made when extracting and calculating the effect sizes on the inferences drawn from the analyses. Our ability to account for everything is fairly limited given the small sample sizes as so few studies experimentally manipulate temperatures in the context of sexual selection. In any case, we should explore how they impact our inferences as best as we can.

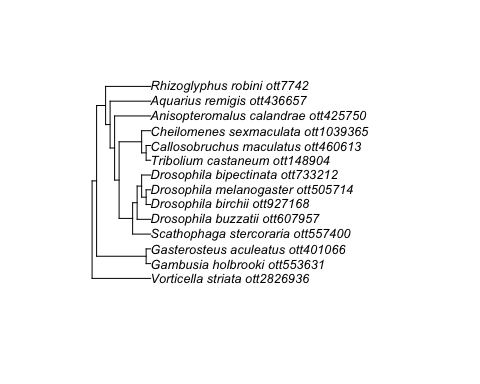
### 6.1 - Phylogeny

We can have a look at finding a somewhat resolved phylogenetic tree of the taxa using the open tree of life. Trying time tree, there are too many unresolved taxa. To start, we need to first get the unique list of taxa in our data. We’ll do this for the entire dataset and then we can prune the tree should we need to do this.

spp\_names <- unique(data$spp)  
  
 # Search rotl  
 tl <- tnrs\_match\_names(spp\_names)  
  
 # Generate the tree with the list of ott\_ids  
 tree\_tmp <- tol\_induced\_subtree(ott\_ids=tl$ott\_id)

##   
Progress [---------------------------------] 0/245 ( 0) ?s  
Progress [==============================] 245/245 (100) 0s

# Have a look  
 plot(tree\_tmp, cex = 0.8)

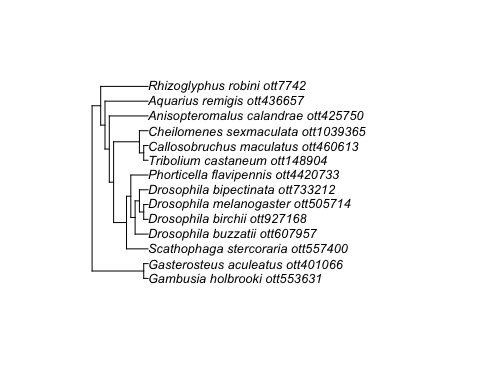


While the tree looks reasonably resolved, as we can see, there are a few problems here, even with rotl. *Drosophila melanogaster* is not found, and is then identified as a bird! *Phorticella striata* is identified as a single-celled organism, yet is supposed to be a fly. We can fix these obvious problems by manually finding the ott\_id online for these taxa and adding them to the ott\_id list:

ott\_id <- tl$ott\_id  
  
 # Add in the correct id for Drosophila and Phorticella  
 ott\_id[c(12, 10)] <- c("505714", "4420733")  
  
 # Generate the tree with the list of ott\_ids  
 tree <- tol\_induced\_subtree(ott\_ids=ott\_id)

##   
Progress [---------------------------------] 0/223 ( 0) ?s  
Progress [==============================] 223/223 (100) 0s

# Have a look  
 plot(tree, cex = 0.8)



OK, now it looks more sensible. The taxa are placed into what looks to be about their correct taxonomic positions. Note that for *Phorticella striata* we used a different, and presumably closely related species *Phorticella flavipennes* given the other species was not identified in an online search. But, this is a Drosophlid like species and so its taxonomic position is correct within the tree. We will use this tree to attempt to understand whether there is evidence for a phylogenetic signal in these data:

phylo\_branch <- compute.brlen(tree, method = "Grafen", power = 0.5)  
 phylo\_branch$tip.label <- gsub("\_ott[0-9]+", "", phylo\_branch$tip.label)  
  
 # Prune male tree  
 lnCVR\_males$spp <- ifelse(lnCVR\_males$spp == "Phorticella\_striata", "Phorticella\_flavipennis", lnCVR\_males$spp)  
 lnVR\_males$spp <- ifelse(lnVR\_males$spp == "Phorticella\_striata", "Phorticella\_flavipennis", lnVR\_males$spp)  
 male\_tree <- drop.tip(phylo\_branch, phylo\_branch$tip.label[-match(unique(lnCVR\_males$spp), phylo\_branch$tip.label)])  
   
 # Prune female tree  
 lnVR\_females$spp <- ifelse(lnVR\_females$spp == "Menochilus\_sexmaculatus", "Cheilomenes\_sexmaculata", lnVR\_females$spp)  
 lnCVR\_females$spp <- ifelse(lnCVR\_females$spp == "Menochilus\_sexmaculatus", "Cheilomenes\_sexmaculata", lnCVR\_females$spp)  
  
 # Fix a spelling mistake  
 lnVR\_females$spp <- ifelse(lnVR\_females$spp == "Tribolium\_castneum", "Tribolium\_castaneum", lnVR\_females$spp)  
 lnCVR\_females$spp <- ifelse(lnCVR\_females$spp == "Tribolium\_castneum", "Tribolium\_castaneum", lnCVR\_females$spp)  
  
 female\_tree <- drop.tip(phylo\_branch, phylo\_branch$tip.label[-match(unique(lnCVR\_females$spp), phylo\_branch$tip.label)])  
   
 # Check trees are ultrametric  
 is.ultrametric(male\_tree)

## [1] TRUE

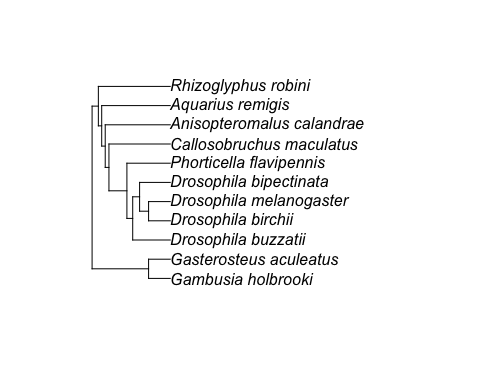
is.ultrametric(female\_tree)

## [1] TRUE

# Phylogenetic correlation matrix.   
 P\_males <- vcv(male\_tree, model="Brownian", corr = TRUE)  
 P\_females <- vcv(female\_tree, model="Brownian", corr = TRUE)

We can plot the subset of taxa for each sex. For the males we have the following tree:

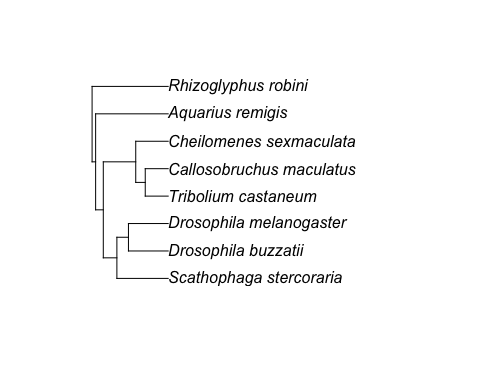
plot(male\_tree)



**Figure S2** – Phylogenetic tree (tree topology) used to control for non-independence among taxa in our male dataset.

and for the females, we have the following tree:

plot(female\_tree)



**Figure S3** – Phylogenetic tree (tree topology) used to control for non-independence among taxa in our female dataset.

Now that we have the phylogenies we can re-run a few models including the correlation structure. We’ll do males, and then females:

# Males  
 MLMA\_male\_lnVR\_phylo <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_males), data = lnVR\_males)  
 summary(MLMA\_male\_lnVR\_phylo)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -19.1939 38.3878 46.3878 51.9926 47.9878   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.2587 0.5086 14 no study no   
## sigma^2.2 0.0000 0.0000 11 no spp yes   
## sigma^2.3 0.0212 0.1457 31 no obs no   
##   
## Test for Heterogeneity:  
## Q(df = 30) = 144.0839, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.0627 0.1479 -0.4240 0.6716 -0.3526 0.2272   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

MLMA\_male\_lnCVR\_phylo <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_males), data = lnCVR\_males)  
 summary(MLMA\_male\_lnCVR\_phylo)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -18.3405 36.6810 44.6810 50.2858 46.2810   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.0815 0.2855 14 no study no   
## sigma^2.2 0.0382 0.1954 11 no spp yes   
## sigma^2.3 0.0233 0.1526 31 no obs no   
##   
## Test for Heterogeneity:  
## Q(df = 30) = 77.8102, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## 0.2534 0.1423 1.7810 0.0749 -0.0255 0.5323 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#Females  
MLMA\_female\_lnVR\_phylo <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_females), data = lnVR\_females)  
 summary(MLMA\_female\_lnVR\_phylo)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.1436 12.2872 20.2872 23.6201 23.6206   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.0000 0.0000 9 no study no   
## sigma^2.2 0.0174 0.1319 8 no spp yes   
## sigma^2.3 0.0482 0.2196 18 no obs no   
##   
## Test for Heterogeneity:  
## Q(df = 17) = 45.0805, p-val = 0.0002  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## -0.0952 0.0977 -0.9745 0.3298 -0.2866 0.0963   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

MLMA\_female\_lnCVR\_phylo <- metafor::rma.mv(yi ~ 1, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_females), data = lnCVR\_females)  
 summary(MLMA\_female\_lnCVR\_phylo)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -7.6917 15.3835 23.3835 26.7163 26.7168   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.1452 0.3810 9 no study no   
## sigma^2.2 0.0000 0.0000 8 no spp yes   
## sigma^2.3 0.0000 0.0000 18 no obs no   
##   
## Test for Heterogeneity:  
## Q(df = 17) = 51.1258, p-val < .0001  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## 0.1494 0.1434 1.0418 0.2975 -0.1317 0.4305   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

We can see from the above, controlling for tree topology doesn’t change the results much at all.

### 6.2 - Effect sizes derived from proportions

Much of the literature currently reports data as proportions, average and some measure of error. We are well aware that proportion data is not normally distributed as its bound between 0 and 1, however, when reported as an average it does have error and so long as its not “extreme” (i.e., close to 0 and 1), should behave as though it is normal. Nonetheless, this may affect conclusions and so we test if there were significant differences between effect sizes generated with proportion data after temperature correction. This is expected to have potentially stronger effects on variance so we will stick to our main analyses:

# Males  
 MLMA\_male\_lnVR\_prop <- metafor::rma.mv(yi ~ 1 + deltaT + prop, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMA\_male\_lnVR\_prop)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -17.7090 35.4179 47.4179 55.4111 51.4179   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2790 0.5282 14 no study   
## sigma^2.2 0.0000 0.0001 11 no spp   
## sigma^2.3 0.0246 0.1569 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 131.2961, p-val < .0001  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 0.5432, p-val = 0.7621  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.0382 0.1687 -0.2266 0.8207 -0.3688 0.2924   
## deltaT 0.1507 0.2153 0.7000 0.4839 -0.2712 0.5726   
## prop -0.0714 0.2617 -0.2730 0.7848 -0.5843 0.4415   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

MLMA\_male\_lnCVR\_prop <- metafor::rma.mv(yi ~ 1 + deltaT + prop, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMA\_male\_lnCVR\_prop)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.9079 31.8158 43.8158 51.8090 47.8158   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0569 0.2386 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0383 0.1957 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 62.2306, p-val = 0.0002  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 4.7095, p-val = 0.0949  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt 0.3596 0.1090 3.2994 0.0010 0.1460 0.5732 \*\*\*   
## deltaT 0.1549 0.1227 1.2621 0.2069 -0.0856 0.3953   
## prop -0.4140 0.2143 -1.9321 0.0534 -0.8339 0.0060 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#Females  
MLMA\_female\_lnVR\_prop <- metafor::rma.mv(yi ~ 1 +deltaT + prop, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_females), data = lnVR\_females)  
 summary(MLMA\_female\_lnVR\_prop)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -5.4666 10.9333 22.9333 27.1816 33.4333   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.0000 0.0000 9 no study no   
## sigma^2.2 0.0140 0.1185 8 no spp yes   
## sigma^2.3 0.0518 0.2277 18 no obs no   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 39.4920, p-val = 0.0005  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 1.6333, p-val = 0.4419  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt -0.1205 0.0992 -1.2150 0.2244 -0.3150 0.0739   
## deltaT 0.0506 0.0613 0.8261 0.4087 -0.0695 0.1708   
## prop 0.2363 0.2522 0.9367 0.3489 -0.2581 0.7307   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

MLMA\_female\_lnCVR\_prop <- metafor::rma.mv(yi ~ 1 + deltaT + prop, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(spp = P\_females), data = lnCVR\_females)  
 summary(MLMA\_female\_lnCVR\_prop)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -6.0200 12.0400 24.0400 28.2883 34.5400   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.1470 0.3834 9 no study no   
## sigma^2.2 0.0000 0.0000 8 no spp yes   
## sigma^2.3 0.0000 0.0000 18 no obs no   
##   
## Test for Residual Heterogeneity:  
## QE(df = 15) = 39.4823, p-val = 0.0005  
##   
## Test of Moderators (coefficients 2:3):  
## QM(df = 2) = 1.7371, p-val = 0.4196  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## intrcpt 0.2302 0.1592 1.4459 0.1482 -0.0819 0.5423   
## deltaT -0.0763 0.1043 -0.7315 0.4645 -0.2807 0.1281   
## prop -0.4105 0.3776 -1.0872 0.2770 -1.1506 0.3296   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusion**: There appears to be a slight difference between effect sizes generated with proportion data for male lnCVR where they had a smaller CV relative to other non-proportion traits. While this is not significant, it’s worth controlling for this in models.

Just to be safe, and although our models are getting heavy on the parameters, we will also explore how accounting for these different types of effect sizes affect the inferences drawn for lnVR and lnCVR, the effects most of interest to us:

#### lnVR - Males - Fitness

MLMR\_male\_lnVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1 + deltaT+ prop +fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -14.0443 28.0885 42.0885 51.1594 47.9833   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.1273 0.3568 14 no study   
## sigma^2.2 0.0140 0.1183 11 no spp   
## sigma^2.3 0.0271 0.1647 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 27) = 85.9034, p-val < .0001  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 9.5252, p-val = 0.0492  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1271 0.1614 0.7875 0.4310 -0.1892 0.4434   
## prop 0.0770 0.2378 0.3240 0.7460 -0.3890 0.5431   
## fitnessdirect -0.4340 0.2062 -2.1048 0.0353 -0.8381 -0.0299 \*   
## fitnessindirect 0.2658 0.1620 1.6408 0.1008 -0.0517 0.5832   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Males - Fitness

MLMR\_male\_lnCVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1+deltaT+ prop +fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.0884 30.1769 44.1769 53.2477 50.0716   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0693 0.2632 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0301 0.1734 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 27) = 60.4983, p-val = 0.0002  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 11.9607, p-val = 0.0176  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1365 0.1283 1.0644 0.2871 -0.1149 0.3879   
## prop -0.3150 0.2367 -1.3310 0.1832 -0.7789 0.1489   
## fitnessdirect 0.1939 0.1906 1.0173 0.3090 -0.1797 0.5674   
## fitnessindirect 0.4254 0.1279 3.3261 0.0009 0.1747 0.6761 \*\*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR - Males - Stress

MLMR\_male\_lnVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+prop +temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -14.6031 29.2062 43.2062 52.2770 49.1009   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.2385 0.4884 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0140 0.1185 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 27) = 104.9595, p-val < .0001  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 6.3729, p-val = 0.1730  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0888 0.2004 0.4430 0.6578 -0.3040 0.4816   
## prop 0.0053 0.2474 0.0213 0.9830 -0.4796 0.4901   
## temp.rangenatural 0.2073 0.1871 1.1080 0.2679 -0.1594 0.5740   
## temp.rangestress -0.3412 0.2032 -1.6790 0.0931 -0.7395 0.0571 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Males - Stress

MLMR\_male\_lnCVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+prop +temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.6682 31.3364 45.3364 54.4072 51.2311   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0751 0.2740 14 no study   
## sigma^2.2 0.0000 0.0000 11 no spp   
## sigma^2.3 0.0360 0.1896 31 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 27) = 61.8668, p-val = 0.0001  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 9.9632, p-val = 0.0411  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1483 0.1341 1.1059 0.2688 -0.1145 0.4111   
## prop -0.4020 0.2312 -1.7389 0.0821 -0.8551 0.0511 .   
## temp.rangenatural 0.3669 0.1411 2.6010 0.0093 0.0904 0.6434 \*\*   
## temp.rangestress 0.3477 0.1631 2.1325 0.0330 0.0281 0.6673 \*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: Across all models, when we account for the slight decrease in variance resulting from effects generated with proportion data we see very little changes except for when we look at lnCVR under stress or natural temperatures. Here we see an even stronger positive mean lnCVR for both ‘stress’ and ‘natural’ coefficients that become highly significant. All other results are unchanged.

#### lnVR - Females - Fitness

MLMR\_female\_lnVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1+ deltaT+ prop +fitness, V = vi, random = list( ~1|study, ~1|obs), data = lnVR\_females)  
 summary(MLMR\_female\_lnVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -3.7321 7.4643 19.4643 23.2986 31.4643   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0000 0.0000 9 no study   
## sigma^2.2 0.0456 0.2137 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 14) = 33.4092, p-val = 0.0025  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 8.6602, p-val = 0.0702  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0783 0.0548 1.4284 0.1532 -0.0291 0.1858   
## prop 0.2837 0.2288 1.2397 0.2151 -0.1648 0.7322   
## fitnessdirect -0.1794 0.0779 -2.3023 0.0213 -0.3321 -0.0267 \*   
## fitnessindirect 0.2965 0.2240 1.3239 0.1855 -0.1425 0.7355   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Females - Fitness

MLMR\_female\_lnCVR\_T\_Fitness <- metafor::rma.mv(yi ~ -1 + deltaT+ prop + fitness, V = vi, random = list( ~1|study, ~1|obs), data = lnCVR\_females)  
 summary(MLMR\_female\_lnCVR\_T\_Fitness)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -5.3956 10.7913 22.7913 26.6256 34.7913   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.1917 0.4378 9 no study   
## sigma^2.2 0.0000 0.0000 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 14) = 39.3971, p-val = 0.0003  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 2.2513, p-val = 0.6896  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT -0.0776 0.1200 -0.6472 0.5175 -0.3128 0.1575   
## prop -0.4102 0.4211 -0.9742 0.3300 -1.2355 0.4151   
## fitnessdirect 0.2385 0.1942 1.2279 0.2195 -0.1422 0.6191   
## fitnessindirect 0.1947 0.4825 0.4035 0.6866 -0.7510 1.1404   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR - Females - Stress

MLMR\_female\_lnVR\_T\_stress <- metafor::rma.mv(yi ~ -1 + deltaT+ prop + temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnVR\_females)  
 summary(MLMR\_female\_lnVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -4.7937 9.5874 21.5874 25.4218 33.5874   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0000 0.0000 9 no study   
## sigma^2.2 0.0611 0.2471 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 14) = 37.2866, p-val = 0.0007  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 5.4681, p-val = 0.2425  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0255 0.0629 0.4049 0.6856 -0.0979 0.1488   
## prop 0.1272 0.2576 0.4938 0.6214 -0.3776 0.6320   
## temp.rangenatural 0.0383 0.1454 0.2635 0.7922 -0.2467 0.3233   
## temp.rangestress -0.2013 0.0994 -2.0263 0.0427 -0.3961 -0.0066 \*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Females - Stress

MLMR\_female\_lnCVR\_T\_stress <- metafor::rma.mv(yi ~ -1+deltaT+prop +temp.range, V = vi, random = list( ~1|study, ~1|obs), data = lnCVR\_females)  
 summary(MLMR\_female\_lnCVR\_T\_stress)

##   
## Multivariate Meta-Analysis Model (k = 18; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -3.7212 7.4424 19.4424 23.2768 31.4424   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor   
## sigma^2.1 0.0646 0.2541 9 no study   
## sigma^2.2 0.0000 0.0000 18 no obs   
##   
## Test for Residual Heterogeneity:  
## QE(df = 14) = 27.4320, p-val = 0.0169  
##   
## Test of Moderators (coefficients 1:4):  
## QM(df = 4) = 10.7994, p-val = 0.0289  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT -0.0179 0.0801 -0.2235 0.8231 -0.1749 0.1391   
## prop -0.2231 0.3090 -0.7219 0.4703 -0.8288 0.3826   
## temp.rangenatural -0.1008 0.1816 -0.5553 0.5787 -0.4567 0.2550   
## temp.rangestress 0.4377 0.1467 2.9833 0.0029 0.1501 0.7252 \*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: Across all models, when we account for the slight decrease in variance resulting from effects generated with proportion data we see no changes in any of the main conclusions.

### 6.2 - Adapted temperatures of the population – A discussion

Upon close reading of the research papers that were included in the meta-analysis, it is clear that study design varies a lot. More specifically, many studies are temperature manipulations on isofemale lines or lab-bred populations that have been bred and reared in the lab for many (sometimes, hundreds) of generations. These lab colonies have different temperature treatments to what would be normally encountered in nature, and to some extent, they are adapted quite well to the constant temperature conditions in which they have been bread. This means that, while temperature may affect the variance, it may also come down to which temperature treatment the population has adapted to with respect to how temperature impacts sexual selection. This means that, the relationship between temperature and its effect on sexual selection is not as simple as a linear relationship between temperature and variation in fitness, but rather it also depends on whether the temperature treatments involve a temperature for which the population is adapted to. Our analysis on the ‘magnitude’ of change in variance across temperatures gets around the above problem, but it may still be important to have a closer inspection of this problem in the future.

Given the limited sample size and the fact that so few studies reported clearly what temperature populations were adapted to (we only really know this for experimental evolution studies), it was unclear how to best deal with this issue other than to acknowledge that it exists. Additionally, it could only be dealt with for a small sample of effect sizes in our dataset. For example, for males, we could only be confident about 12 of 31 effects and only 4 of these involved a temperature that was one of the treatments. For females, we had information about 10 of 18 effects and 4 of these involved a temperature that was one of the treatments. The other treatments varied and/or it was unclear. This is further challenging to deal with given that it is unclear how temperature adaptation itself will impact the variance. We presume that this will decrease phenotypic variance as a result of stabilizing selection, but this assumption is not entirely clear.

### 6.3 - Trait dependency among effects

Given studies reported, at times, multiple traits – especially when considering indirect estimates as multiple traits were presented that could all be correlated with reproductive success (i.e., sperm motility, fertilization success). While we took the indirect estimate most closely associated with reproductive fitness where possible, at times it was not clear, and so we extracted a couple representative estimates. This induces some level of non-independence among effect sizes and so is something we should attempt to deal with.

For females, all effect sizes were independent samples of individuals. For males, there were approximately 8 effect sizes that were dependent in some form. To account for this non-independence, we can estimate a correlation matrix and include this as the residual level to account for this dependency. Part of the problem here is simply that we don’t know the exact correlation among these effect sizes exactly to properly address this issue, but in all cases these are sperm traits that were done on the same sample and so presumably have a moderate to high correlation with each other. We will assume for now that they have a correlation (on average) of about 0.70 and generate a residual correlation matrix to just simply test this out:

First, lets generate a correlation matrix. Its so few studies that we’ll just do this by hand for now, but there are easier methods for more complicated problems

# Create a matrix the same size as observations. lnVR and lnCVR are the same in terms of what is dependent, so we can do this with one dataset  
 R <- diag(nrow(lnVR\_males))  
 R[c(8,9), c(9,8)] <- 0.7  
 R[c(10,11), c(11,10)] <- 0.7  
 R[c(19,20), c(20,19)] <- 0.7  
 R[c(21,22), c(22,21)] <- 0.7  
 diag(R) <- 1  
 rownames(R) <- colnames(R) <- rownames(lnVR\_males)

Now that we have the matrix with the relevant off-diagonals set to a correlation of 0.7, we can fit this at the residual level to account for non-independence and test if it impacts the inferences drawn from our main conclusions:

#### lnVR - Males - Fitness

MLMR\_male\_lnVR\_T\_Fitness\_R <- metafor::rma.mv(yi ~ -1 + deltaT+fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(obs = R), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_Fitness\_R)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -14.5667 29.1335 41.1335 49.1267 45.1335   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.1186 0.3443 14 no study no   
## sigma^2.2 0.0164 0.1281 11 no spp no   
## sigma^2.3 0.0216 0.1471 31 no obs yes   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 85.9664, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 9.8758, p-val = 0.0197  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1298 0.1565 0.8295 0.4068 -0.1769 0.4366   
## fitnessdirect -0.3950 0.1722 -2.2943 0.0218 -0.7325 -0.0576 \*   
## fitnessindirect 0.2803 0.1551 1.8069 0.0708 -0.0237 0.5844 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Males - Fitness

MLMR\_male\_lnCVR\_T\_Fitness\_R <- metafor::rma.mv(yi ~ -1+deltaT+fitness, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(obs = R), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_Fitness\_R)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -16.3982 32.7964 44.7964 52.7897 48.7964   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.1046 0.3234 14 no study no   
## sigma^2.2 0.0000 0.0000 11 no spp no   
## sigma^2.3 0.0000 0.0000 31 no obs yes   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 67.3331, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 9.3309, p-val = 0.0252  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1030 0.1373 0.7502 0.4531 -0.1661 0.3721   
## fitnessdirect 0.0573 0.1646 0.3481 0.7278 -0.2653 0.3799   
## fitnessindirect 0.4024 0.1353 2.9735 0.0029 0.1372 0.6676 \*\*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnVR - Males - Stress

MLMR\_male\_lnVR\_T\_stress\_R <- metafor::rma.mv(yi ~ -1 + deltaT+temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(obs = R), data = lnVR\_males)  
 summary(MLMR\_male\_lnVR\_T\_stress\_R)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -15.1140 30.2280 42.2280 50.2212 46.2280   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.2300 0.4796 14 no study no   
## sigma^2.2 0.0000 0.0000 11 no spp no   
## sigma^2.3 0.0075 0.0867 31 no obs yes   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 108.1396, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 6.7088, p-val = 0.0818  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.0878 0.1953 0.4497 0.6529 -0.2949 0.4705   
## temp.rangenatural 0.2097 0.1759 1.1921 0.2332 -0.1351 0.5546   
## temp.rangestress -0.3399 0.1820 -1.8672 0.0619 -0.6967 0.0169 .   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### lnCVR - Males - Stress

MLMR\_male\_lnCVR\_T\_stress\_R <- metafor::rma.mv(yi ~ -1 + deltaT+temp.range, V = vi, random = list( ~1|study, ~1|spp, ~1|obs), R = list(obs = R), data = lnCVR\_males)  
 summary(MLMR\_male\_lnCVR\_T\_stress\_R)

##   
## Multivariate Meta-Analysis Model (k = 31; method: REML)  
##   
## logLik Deviance AIC BIC AICc   
## -17.2146 34.4291 46.4291 54.4224 50.4291   
##   
## Variance Components:  
##   
## estim sqrt nlvls fixed factor R   
## sigma^2.1 0.1112 0.3335 14 no study no   
## sigma^2.2 0.0612 0.2475 11 no spp no   
## sigma^2.3 0.0000 0.0000 31 no obs yes   
##   
## Test for Residual Heterogeneity:  
## QE(df = 28) = 73.0902, p-val < .0001  
##   
## Test of Moderators (coefficients 1:3):  
## QM(df = 3) = 4.0148, p-val = 0.2599  
##   
## Model Results:  
##   
## estimate se zval pval ci.lb ci.ub   
## deltaT 0.1260 0.1679 0.7503 0.4530 -0.2030 0.4550   
## temp.rangenatural 0.3026 0.1628 1.8585 0.0631 -0.0165 0.6218 .   
## temp.rangestress 0.1277 0.1801 0.7090 0.4783 -0.2253 0.4807   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

**Conclusions**: For the most part, these sensitivity analyses show that including the dependency among effects at the residual level does not impact any of the results

# 7.0 - Session Information

**R version 3.6.0 (2019-04-26)**

**Platform:** x86\_64-apple-darwin15.6.0 (64-bit)

**locale:** en\_AU.UTF-8||en\_AU.UTF-8||en\_AU.UTF-8||C||en\_AU.UTF-8||en\_AU.UTF-8

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

**other attached packages:** *pander(v.0.6.3)*, *bindrcpp(v.0.2.2)*, *metaAidR(v.0.0.0.9000)*, *psych(v.1.9.12.31)*, *gridExtra(v.2.3)*, *rmarkdown(v.2.1)*, *kableExtra(v.1.1.0)*, *magrittr(v.1.5)*, *rotl(v.3.0.10)*, *forcats(v.0.5.0)*, *stringr(v.1.4.0)*, *dplyr(v.0.8.5)*, *purrr(v.0.3.4)*, *readr(v.1.3.1)*, *tidyr(v.1.0.3)*, *tibble(v.3.0.1)*, *ggplot2(v.3.3.0)*, *tidyverse(v.1.3.0)*, *MCMCglmm(v.2.29)*, *ape(v.5.3)*, *coda(v.0.19-3)*, *metafor(v.2.4-0)* and *Matrix(v.1.2-18)*

**loaded via a namespace (and not attached):** *httr(v.1.4.1)*, *jsonlite(v.1.6.1)*, *viridisLite(v.0.3.0)*, *modelr(v.0.1.7)*, *assertthat(v.0.2.1)*, *tensorA(v.0.36.1)*, *cellranger(v.1.1.0)*, *yaml(v.2.2.1)*, *progress(v.1.2.2)*, *pillar(v.1.4.4)*, *backports(v.1.1.6)*, *lattice(v.0.20-41)*, *glue(v.1.4.0)*, *digest(v.0.6.25)*, *rvest(v.0.3.5)*, *colorspace(v.1.4-1)*, *htmltools(v.0.4.0)*, *XML(v.3.99-0.3)*, *pkgconfig(v.2.0.3)*, *rncl(v.0.8.4)*, *broom(v.0.5.6)*, *haven(v.2.2.0)*, *bookdown(v.0.18)*, *corpcor(v.1.6.9)*, *scales(v.1.1.1)*, *webshot(v.0.5.2)*, *cubature(v.2.0.4)*, *farver(v.2.0.3)*, *generics(v.0.0.2)*, *ellipsis(v.0.3.0)*, *pacman(v.0.5.1)*, *withr(v.2.2.0)*, *mnormt(v.1.5-7)*, *cli(v.2.0.2)*, *crayon(v.1.3.4)*, *readxl(v.1.3.1)*, *evaluate(v.0.14)*, *fs(v.1.4.1)*, *fansi(v.0.4.1)*, *nlme(v.3.1-147)*, *xml2(v.1.3.2)*, *tools(v.3.6.0)*, *prettyunits(v.1.1.1)*, *hms(v.0.5.3)*, *lifecycle(v.0.2.0)*, *munsell(v.0.5.0)*, *reprex(v.0.3.0)*, *compiler(v.3.6.0)*, *rlang(v.0.4.6)*, *grid(v.3.6.0)*, *rstudioapi(v.0.11)*, *labeling(v.0.3)*, *codetools(v.0.2-16)*, *gtable(v.0.3.0)*, *rentrez(v.1.2.2)*, *DBI(v.1.1.0)*, *R6(v.2.4.1)*, *lubridate(v.1.7.8)*, *knitr(v.1.28)*, *bindr(v.0.1.1)*, *stringi(v.1.4.6)*, *parallel(v.3.6.0)*, *Rcpp(v.1.0.4.6)*, *vctrs(v.0.3.0)*, *dbplyr(v.1.4.3)*, *tidyselect(v.1.1.0)* and *xfun(v.0.13)*