

# Body Weight

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## Meta-analysis Body Weight

```
load(file="Effect_Size_All_Traits.RData")
load(file="Effect_Size_All_Traits_lnCVR.RData")

Body_Weight_lnRR <- subset(Effect_Size_All_Traits, Effect_Size_All_Traits$Trait == "Body_Weight")

#Subetting (removing BOTH)

Body_Weight_lnRR_MG <- subset(Body_Weight_lnRR, Body_Weight_lnRR$Exposure_Type == "Multigenerational")

Body_Weight_lnRR_OF <- subset(Body_Weight_lnRR, Body_Weight_lnRR$Exposure_Type == "One off")
```

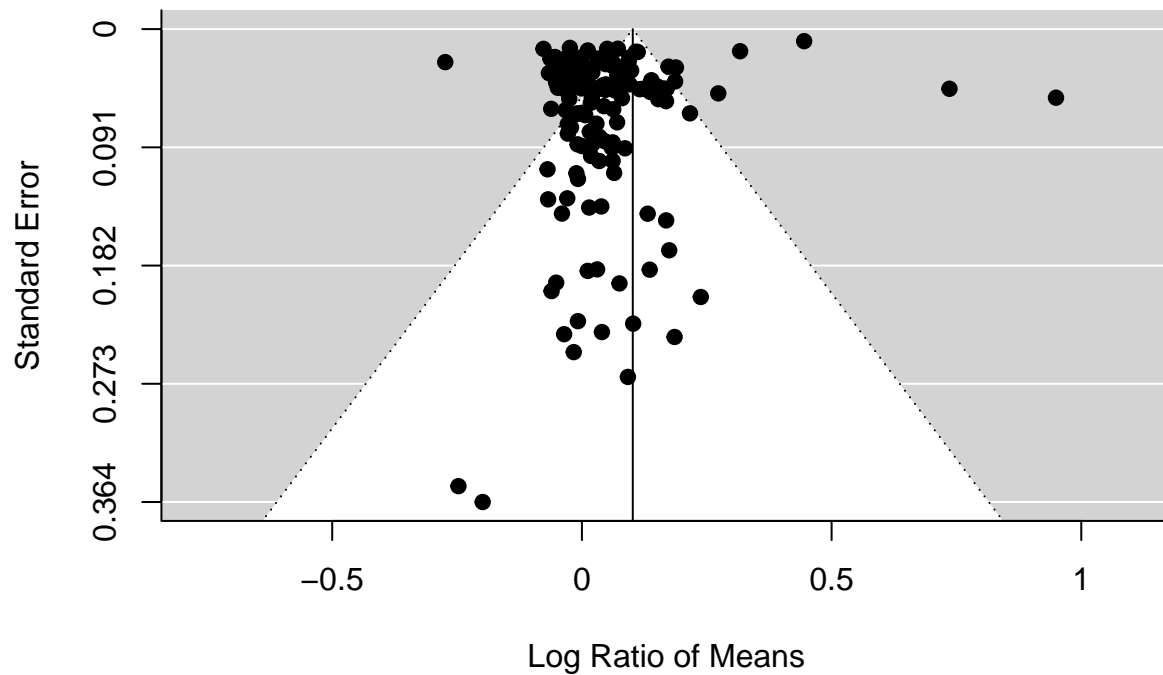
## Overall analysis, not split

```
Body_Weight_overall <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight)

summary(Body_Weight_overall)
```

```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## 112.1459 -224.2917 -216.2917 -204.3848 -216.0060
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0478  0.2187    25    no  Paper_ID
## sigma^2.2  0.0000  0.0000    72    no  Cohort_ID
## sigma^2.3  0.0039  0.0624   146    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 145) = 3213.0903, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      *
## 0.1018  0.0454  2.2412  0.0250  0.0128  0.1909
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Body_Weight_overall)
```

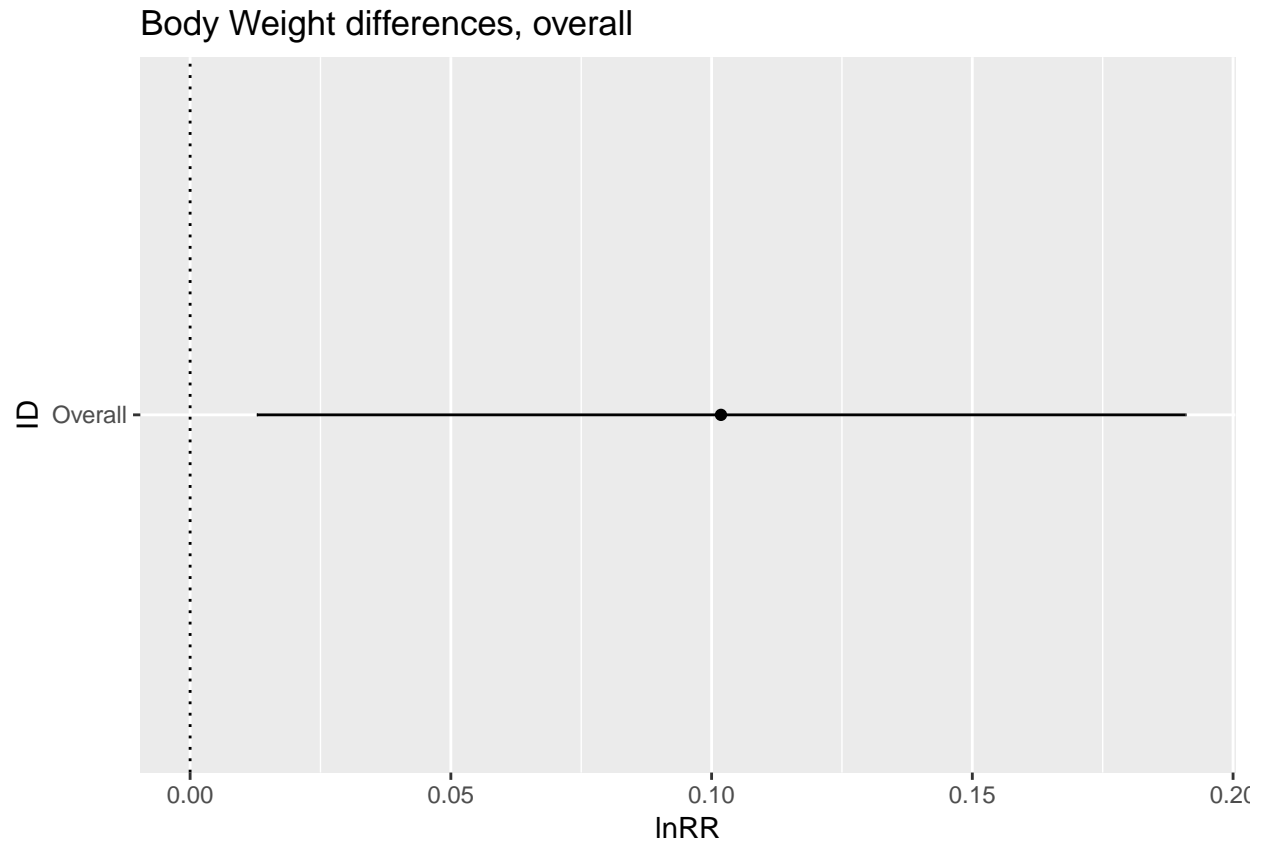


```
#Tibble of overall results
```

```
Body_Weight_overall_lnRR <- tibble(  
  ID = "Overall",  
  lnRR = 0.1018,  
  ci.lb = 0.0128,  
  ci.ub = 0.1909  
)
```

```
## Warning: `list_len()` is deprecated as of rlang 0.2.0.  
## Please use `new_list()` instead.  
## This warning is displayed once per session.
```

```
plot_BW_overall <- ggplot(Body_Weight_overall_lnRR, aes(x=ID, y=lnRR)) +  
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +  
  geom_point(aes(x = ID, y = lnRR), position = position_dodge(0.3)) +  
  geom_hline(yintercept = 0, lty = "dotted") +  
  labs(title = "Body Weight differences, overall", x = "ID", y = "lnRR") +  
  coord_flip()  
plot_BW_overall
```



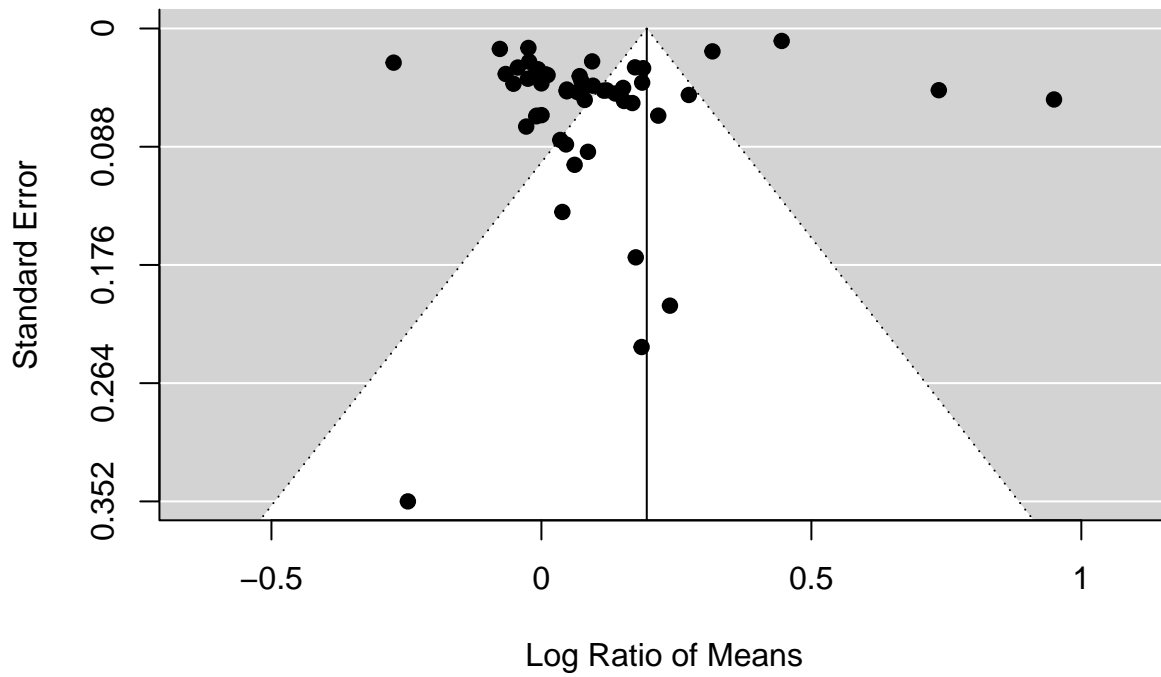
## Overall analysis when split by exposure type

```
Body_Weight_MG <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnRR)
summary(Body_Weight_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## 22.9980 -45.9960 -37.9960 -30.2687 -37.1264
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.0790 0.2811   13    no  Paper_ID
## sigma^2.2 0.0000 0.0000   24    no  Cohort_ID
## sigma^2.3 0.0080 0.0896   52    no    ES_ID
##
## Test for Heterogeneity:
## Q(df = 51) = 2529.5913, p-val < .0001
##
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.1952 0.0824 2.3691 0.0178 0.0337 0.3566 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Body_Weight_MG)
```

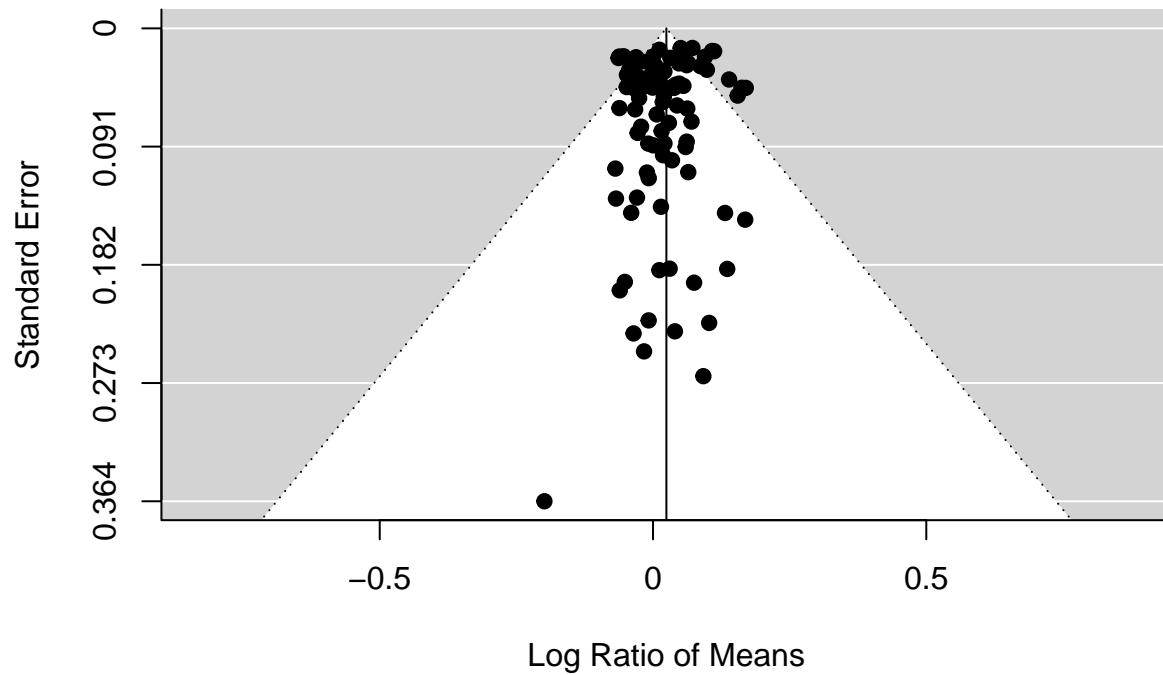


```
Body_Weight_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnR)
summary(Body_Weight_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## 124.3442 -248.6885 -240.6885 -230.5581 -240.2339
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0012 0.0348    16    no  Paper_ID
## sigma^2.2 0.0000 0.0000    50    no  Cohort_ID
## sigma^2.3 0.0006 0.0248    94    no    ES_ID
```

```
##
## Test for Heterogeneity:
## Q(df = 93) = 236.3106, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.0245 0.0116 2.1197 0.0340 0.0018 0.0471 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(Body_Weight_OF)
```



```
#Tibble of results

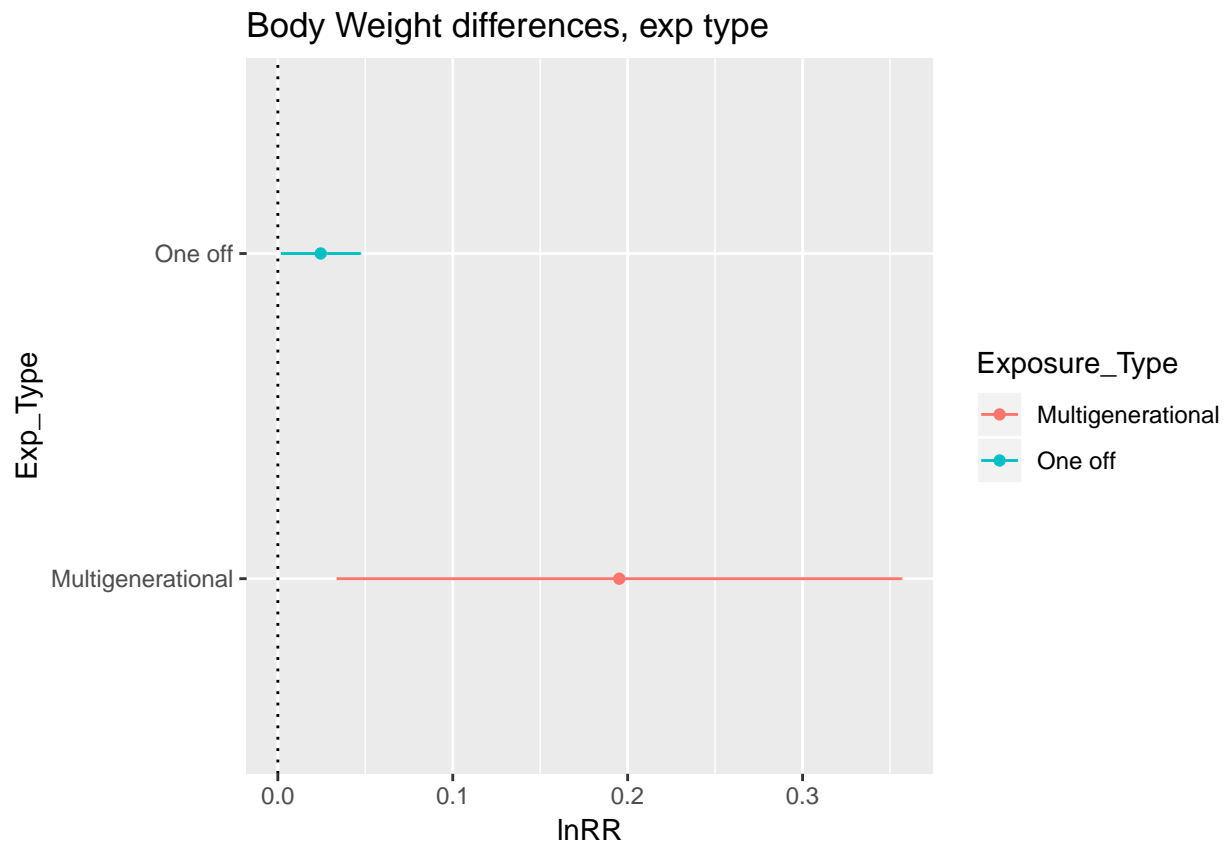
Body_Weight_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  k = c(52,94),
  lnRR = c(0.1952, 0.0245),
  ci.lb = c(0.0337, 0.0018),
  ci.ub = c(0.3566, 0.0471)
)

Body_Weight_Exp_lnRR
```

```
## # A tibble: 2 x 5
##   Exposure_Type      k  lnRR  ci.lb  ci.ub
##   <chr>          <dbl> <dbl> <dbl> <dbl>
## 1 Multigenerational    52 0.195  0.0337 0.357
## 2 One off              94 0.0245 0.0018 0.0471
```

*#Plotting when split by exp type*

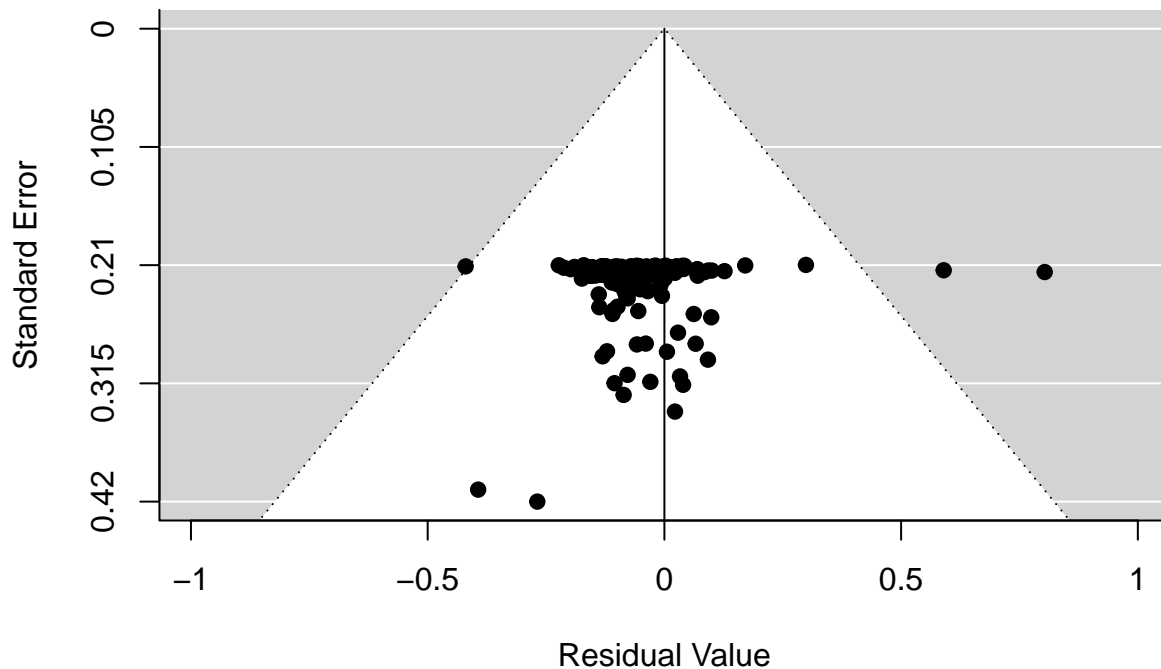
```
plot_BW_exp_type <- ggplot(Body_Weight_Exp_lnRR, aes(x=Exposure_Type, y=lnRR, colour = Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(title = "Body Weight differences, exp type", x = "Exp_Type", y = "lnRR") +
  coord_flip()
plot_BW_exp_type
```



#### Running meta-analysis (Overall with moderators, and then overall split by exposure type with moderators)

```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.0424 0.2060   25    no   Paper_ID
```

```
## sigma^2.2  0.0000  0.0000    72    no Cohort_ID
## sigma^2.3  0.0036  0.0597   146    no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 144) = 2765.9019, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 13.5325, p-val = 0.0012
##
## Model Results:
##
##               estimate      se   zval   pval   ci.lb
## Exposure_TypeMultigenerational  0.1461  0.0457  3.1978  0.0014  0.0566
## Exposure_TypeOne off            0.0697  0.0444  1.5696  0.1165 -0.0173
##               ci.ub
## Exposure_TypeMultigenerational 0.2356 **
## Exposure_TypeOne off          0.1568
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



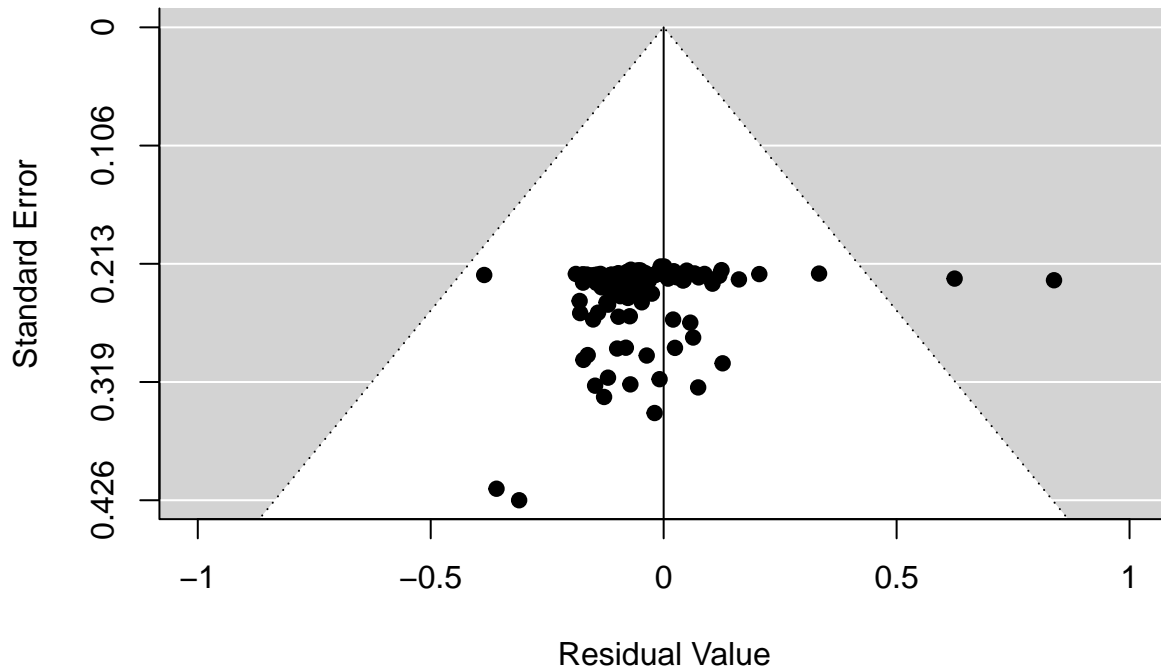
```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
```

```

## 112.5935 -225.1869 -213.1869 -195.4098 -212.5693
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0474  0.2178    25     no    Paper_ID
## sigma^2.2 0.0000  0.0000    72     no    Cohort_ID
## sigma^2.3 0.0038  0.0616   146     no      ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 143) = 3179.4121, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 9.9721, p-val = 0.0188
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb    ci.ub
## F0_Parent_ExposedBoth      0.1687  0.0833  2.0246  0.0429   0.0054  0.3319
## F0_Parent_ExposedFemale     0.1115  0.0462  2.4151  0.0157   0.0210  0.2020
## F0_Parent_ExposedMale       0.0492  0.0651  0.7549  0.4503  -0.0785  0.1768
##
## F0_Parent_ExposedBoth      *
## F0_Parent_ExposedFemale     *
## F0_Parent_ExposedMale
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

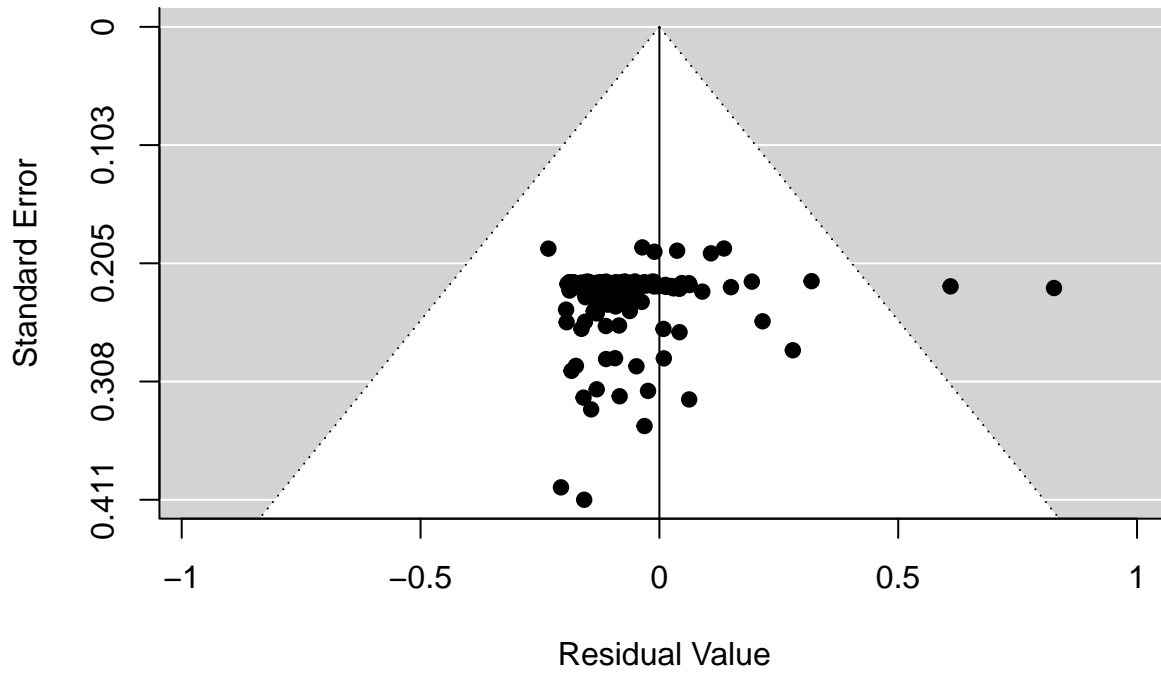
```



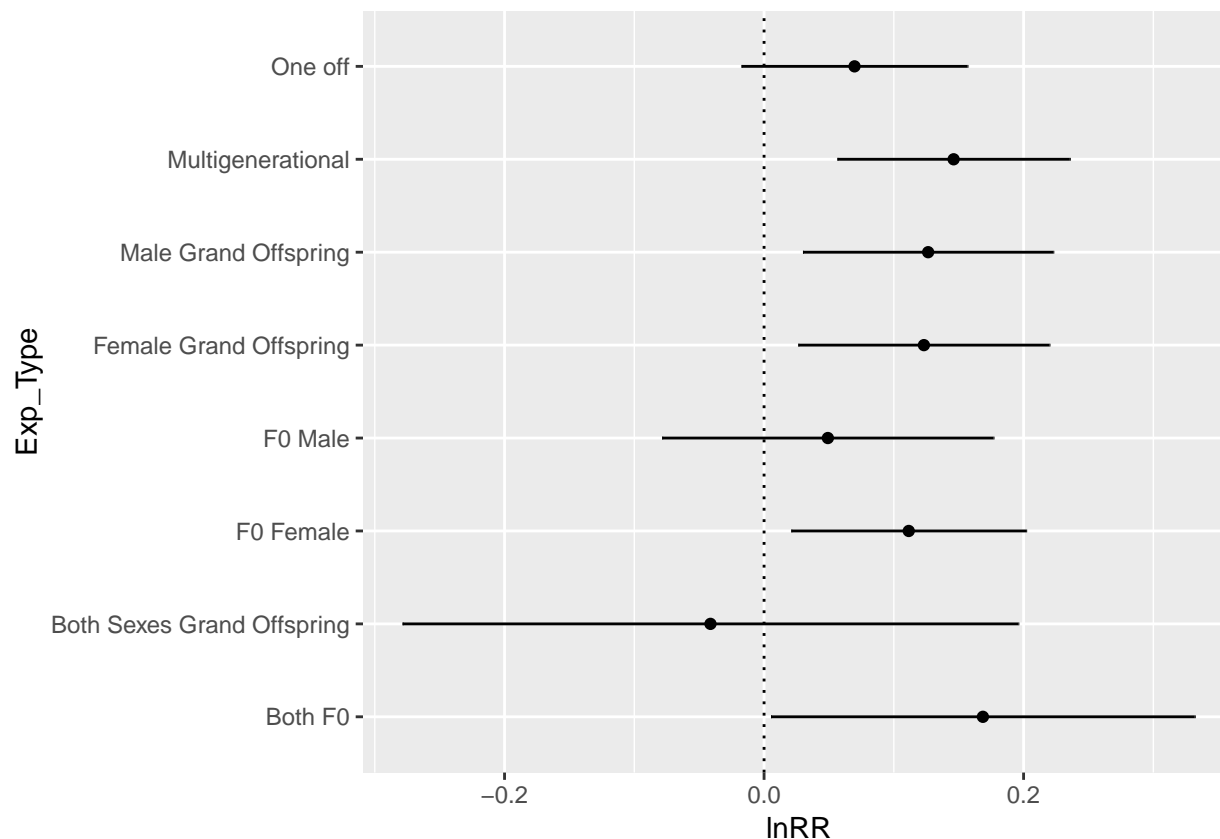


```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## 111.4842 -222.9684 -210.9684 -193.1914 -210.3508
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor
## sigma^2.1 0.0472 0.2173   25    no  Paper_ID
## sigma^2.2 0.0000 0.0000   72    no  Cohort_ID
## sigma^2.3 0.0039 0.0627  146    no    ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 143) = 2943.1372, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 6.7456, p-val = 0.0805
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexBoth      -0.0413 0.1211 -0.3411 0.7330 -0.2786 0.1960
## SexFemale      0.1232 0.0494 2.4950 0.0126 0.0264 0.2200 *
## SexMale       0.1265 0.0492 2.5694 0.0102 0.0300 0.2229 *
##
```

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



```
## # A tibble: 8 x 4
##   ID                lnRR    ci.lb ci.ub
##   <chr>             <dbl>   <dbl> <dbl>
## 1 Multigenerational 0.146  0.0566 0.236
## 2 One off           0.0697 -0.0173 0.157
## 3 Both F0           0.169  0.00539 0.332
## 4 F0 Female         0.112  0.0210 0.202
## 5 F0 Male           0.0492 -0.0785 0.177
## 6 Both Sexes Grand Offspring -0.0413 -0.279 0.196
## 7 Female Grand Offspring 0.123  0.0264 0.220
## 8 Male Grand Offspring 0.126  0.0300 0.223
```



*#splitting by exposure type*

```
Body_Weight_MG_F0 <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID
```

```
## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.
```

```
Body_Weight_MG_F0
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0840  0.2898   13    no    Paper_ID
## sigma^2.2  0.0000  0.0000   24    no    Cohort_ID
## sigma^2.3  0.0080  0.0893   52    no      ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 50) = 2501.2015, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 5.7273, p-val = 0.0571
##
```

```
## Model Results:
```

```
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## F0_Parent_ExposedFemale    0.2197  0.0928  2.3677  0.0179    0.0378  0.4015
## F0_Parent_ExposedMale      0.0723  0.2076  0.3482  0.7277   -0.3345  0.4791
##
## F0_Parent_ExposedFemale *
## F0_Parent_ExposedMale
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Body_Weight_OF_F0 <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID,
```

```
Body_Weight_OF_F0
```

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
```

```
##
## Variance Components:
```

```
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0012  0.0343    16     no    Paper_ID
## sigma^2.2  0.0000  0.0000    50     no    Cohort_ID
## sigma^2.3  0.0005  0.0222    94     no      ES_ID
```

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 91) = 215.2181, p-val < .0001
```

```
##
```

```
## Test of Moderators (coefficient(s) 1:3):
```

```
## QM(df = 3) = 16.3788, p-val = 0.0009
```

```
##
```

```
## Model Results:
```

```
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## F0_Parent_ExposedBoth      0.1409  0.0417  3.3810  0.0007    0.0592  0.2226
## F0_Parent_ExposedFemale    0.0296  0.0131  2.2541  0.0242    0.0039  0.0553
## F0_Parent_ExposedMale      0.0025  0.0200  0.1234  0.9018   -0.0367  0.0417
##
## F0_Parent_ExposedBoth      ***
## F0_Parent_ExposedFemale    *
## F0_Parent_ExposedMale
##
```

```
## ---
```

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

```
Body_Weight_MG_Sex <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), d
```

```
Body_Weight_MG_Sex
```

```
##
```

```
## Multivariate Meta-Analysis Model (k = 52; method: REML)
```

```
##
```

```
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0671  0.2590    13     no   Paper_ID
## sigma^2.2  0.0000  0.0000    24     no   Cohort_ID
## sigma^2.3  0.0082  0.0906    52     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 49) = 1925.4486, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 9.8604, p-val = 0.0198
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexBoth      -0.0353  0.1472  -0.2398  0.8104  -0.3238  0.2532
## SexFemale      0.2799  0.0907   3.0866  0.0020   0.1021  0.4576 **
## SexMale       0.2805  0.0917   3.0600  0.0022   0.1008  0.4602 **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Body_Weight_OF_Sex <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), d
```

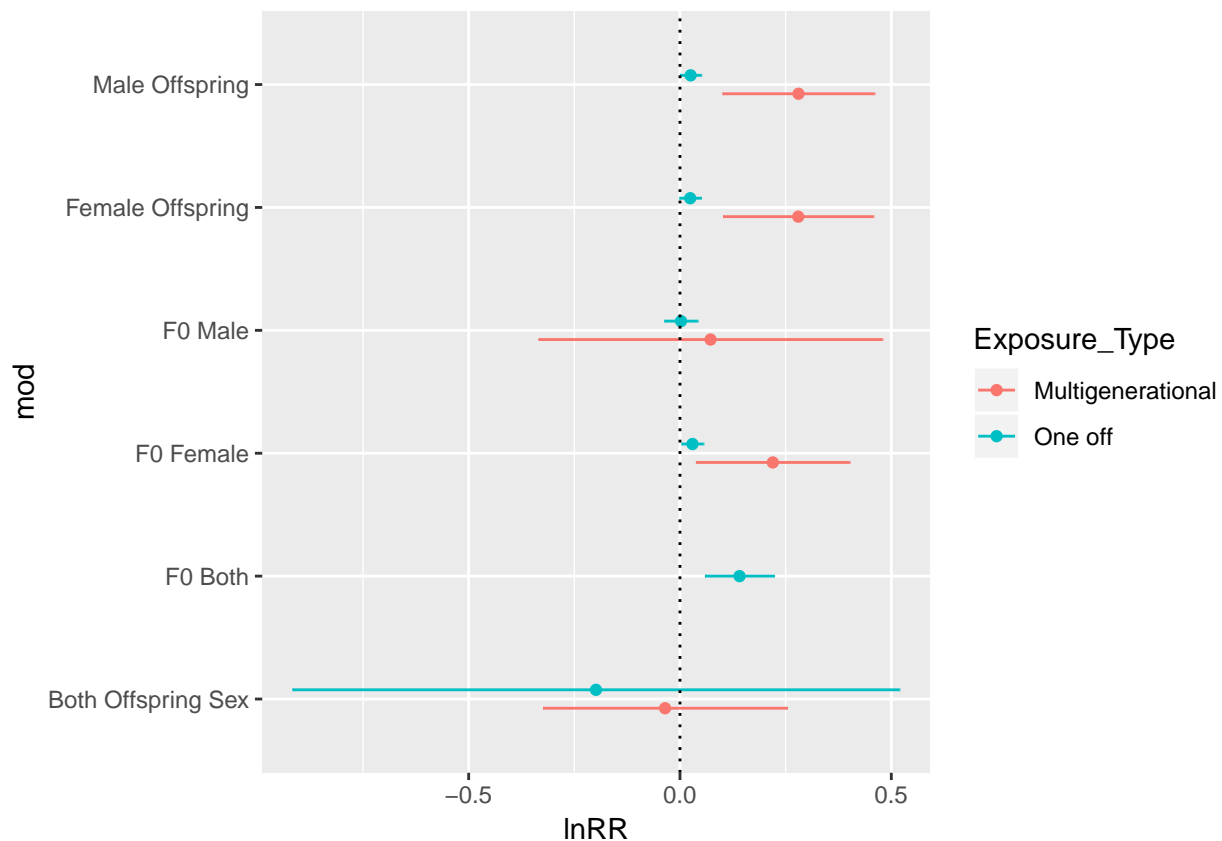
```
Body_Weight_OF_Sex
```

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0012  0.0349    16     no   Paper_ID
## sigma^2.2  0.0000  0.0000    50     no   Cohort_ID
## sigma^2.3  0.0006  0.0253    94     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 91) = 227.5944, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 4.8352, p-val = 0.1843
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexBoth      -0.1987  0.3663  -0.5425  0.5875  -0.9166  0.5192
## SexFemale      0.0242  0.0130   1.8656  0.0621  -0.0012  0.0496 .
## SexMale       0.0252  0.0128   1.9738  0.0484   0.0002  0.0502 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Overall_Exp_mods_lnRR <- tibble(
  Exposure_Type = c("Multigenerational","Multigenerational", "One off", "One off", "One off", "Multigen
mod = c("F0 Female","F0 Male", "F0 Both", "F0 Female", "F0 Male","Both Offspring Sex","Female Offsprin
lnRR = c(0.2197,0.0723,0.1409,0.0296,0.0025,-0.0353,0.2799,0.2805,-0.1987,0.0242,0.0252),
ci.lb = c(0.0378,-0.3345,0.0592,0.0039,-0.0367,-0.3238,0.1021,0.1008,-0.9166,-0.0012,0.0002),
ci.ub = c(0.4015,0.4791,0.2226,0.0553,0.0417,0.2532,0.4576,0.4602,0.5192,0.0496,0.0502)
)

plot_lnRR_overall_mods_exp <- ggplot(Overall_Exp_mods_lnRR, aes(x=mod, y=lnRR, colour=Exposure_Type))+
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = mod, y = lnRR), position = position_dodge(0.3))+
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(x = "mod", y = "lnRR") +
  coord_flip()

plot_lnRR_overall_mods_exp
```



### Meta-analysis overall results (lnCVR)

#### 4. Calculating effect sizes (Done)

We calculated our effect sizes (lnCVR) for our complete data set (all traits).

## 5. Running meta-analysis for body weight lnCVR

## All Data (lnCVR)

```
# Modelling all traits with no mods MG (lnCVR)
```

```
Body_Weight_lnCVR_Omods_MG <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnCVR_Omods_MG)
```

```
summary(Body_Weight_lnCVR_Omods_MG)
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -32.8293  65.6585   73.6585   81.3858   74.5281
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    13    no   Paper_ID
## sigma^2.2  0.0000  0.0000    24    no   Cohort_ID
## sigma^2.3  0.1314  0.3624    52    no     ES_ID
##
## Test for Heterogeneity:
## Q(df = 51) = 151.9554, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.1757  0.0653  2.6889  0.0072  0.0476  0.3038  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Modelling all traits with no mods OF (lnCVR)
```

```
Body_Weight_lnCVR_Omods_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnCVR_Omods_OF)
```

```
summary(Body_Weight_lnCVR_Omods_OF)
```

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -73.1775 146.3549 154.3549 164.4853 154.8095
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0343  0.1852    16    no   Paper_ID
## sigma^2.2  0.0000  0.0000    50    no   Cohort_ID
## sigma^2.3  0.1358  0.3685    94    no     ES_ID
##
## Test for Heterogeneity:
```

```
## Q(df = 93) = 297.4432, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## 0.0044 0.0762 0.0583 0.9535 -0.1448 0.1537
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*#Tibble of results*

```
Body_Weight_Exp_lnCVR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  lnCVR = c(0.1757, 0.0044),
  ci.lb = c(0.0476, -0.1448),
  ci.ub = c(0.3038, 0.1537)
)
```

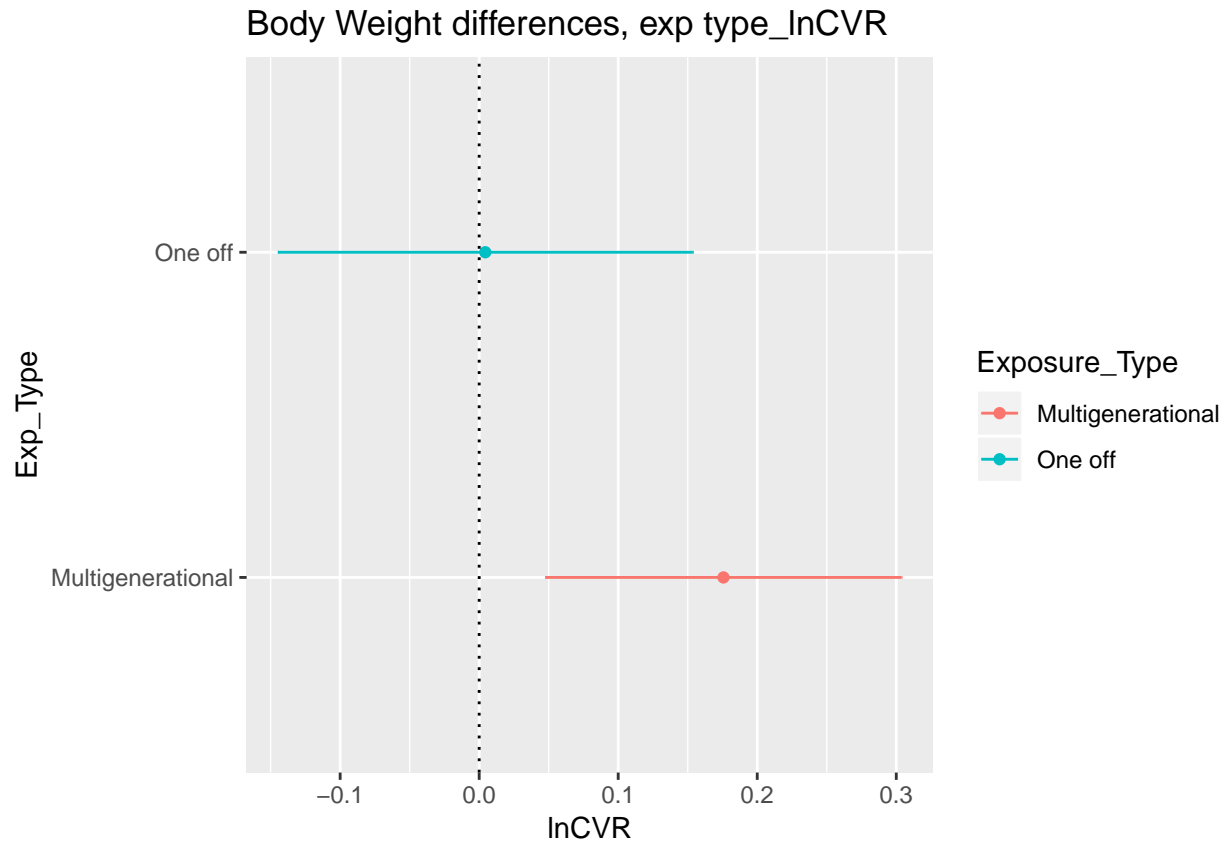
Body\_Weight\_Exp\_lnCVR

```
## # A tibble: 2 x 4
##   Exposure_Type      lnCVR    ci.lb ci.ub
##   <chr>          <dbl>    <dbl> <dbl>
## 1 Multigenerational 0.176    0.0476 0.304
## 2 One off          0.0044 -0.145  0.154
```

*#Plotting when split by exp type*

```
plot_BW_exp_type_lnCVR <- ggplot(Body_Weight_Exp_lnCVR, aes(x=Exposure_Type, y=lnCVR, colour = Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnCVR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(title = "Body Weight differences, exp type_lnCVR", x = "Exp_Type", y = "lnCVR") +
  coord_flip()
plot_BW_exp_type_lnCVR
```





#### Running meta-analysis (Overall with moderators)

```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -106.9560    213.9121    223.9121    238.7611    224.3468
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0214  0.1462    25     no   Paper_ID
## sigma^2.2  0.0000  0.0000    72     no   Cohort_ID
## sigma^2.3  0.1355  0.3681   146     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 144) = 449.3985, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 4.1249, p-val = 0.1271
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb
## Exposure_TypeMultigenerational    0.1703  0.0840  2.0270  0.0427  0.0056
## Exposure_TypeOne off              0.0049  0.0676  0.0731  0.9417 -0.1276
##              ci.ub
```

```

## Exposure_TypeMultigenerational 0.3350 *
## Exposure_TypeOne off 0.1374
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

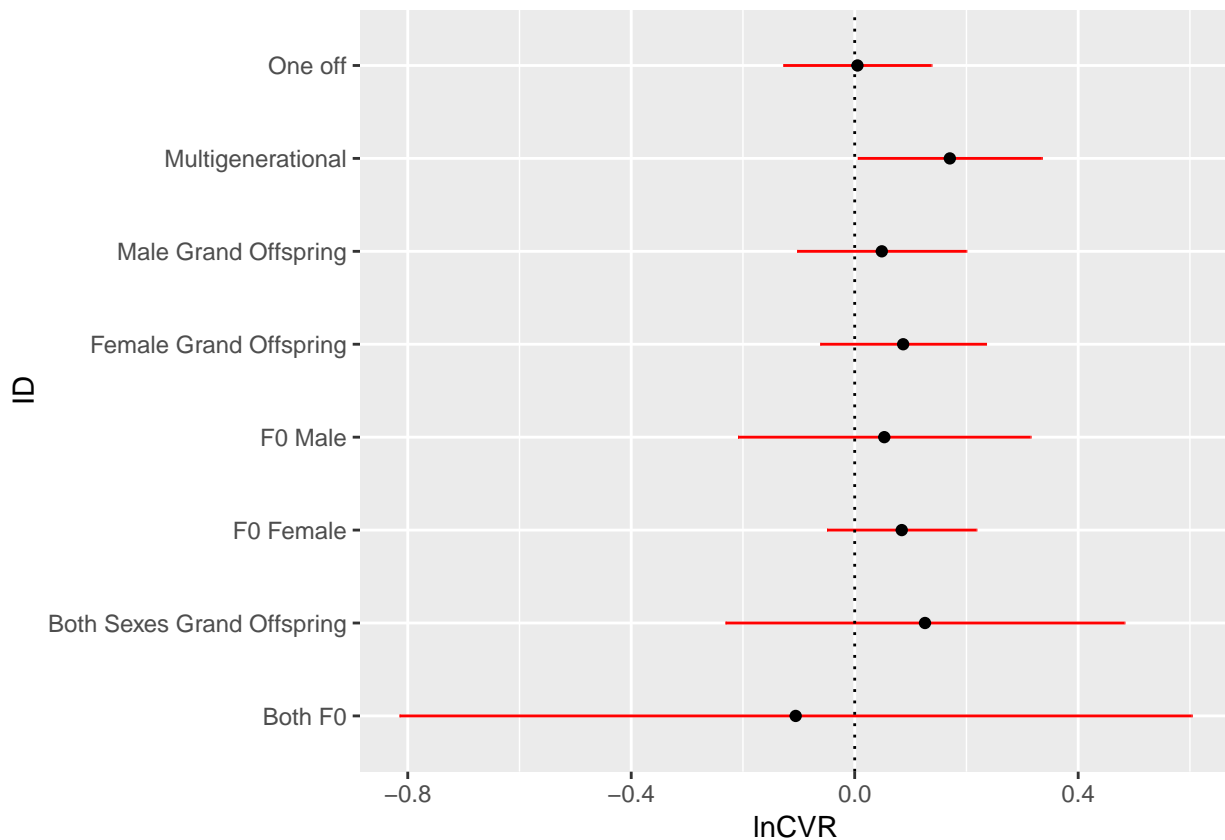
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -107.6256   215.2511   227.2511   245.0282   227.8688
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0353 0.1878    25    no   Paper_ID
## sigma^2.2 0.0000 0.0000    72    no   Cohort_ID
## sigma^2.3 0.1343 0.3665   146    no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 143) = 470.3490, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 1.8106, p-val = 0.6126
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## F0_Parent_ExposedBoth -0.1056 0.3617 -0.2920 0.7703 -0.8146
## F0_Parent_ExposedFemale 0.0842 0.0682 1.2350 0.2168 -0.0494
## F0_Parent_ExposedMale 0.0530 0.1336 0.3967 0.6916 -0.2089
##
##      ci.ub
## F0_Parent_ExposedBoth 0.6033
## F0_Parent_ExposedFemale 0.2178
## F0_Parent_ExposedMale 0.3149
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -107.7785   215.5571   227.5571   245.3342   228.1747
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1 0.0316 0.1777    25    no   Paper_ID
## sigma^2.2 0.0000 0.0000    72    no   Cohort_ID
## sigma^2.3 0.1354 0.3680   146    no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 143) = 457.5484, p-val < .0001

```

```
##
## Test of Moderators (coefficient(s) 1:3):
## QM(df = 3) = 1.8278, p-val = 0.6089
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## SexBoth      0.1258  0.1821  0.6909  0.4896  -0.2312  0.4828
## SexFemale    0.0867  0.0757  1.1463  0.2517  -0.0616  0.2350
## SexMale      0.0485  0.0772  0.6281  0.5299  -0.1029  0.1999
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## # A tibble: 8 x 4
##   ID                lnCVR      ci.lb ci.ub
##   <chr>              <dbl>    <dbl> <dbl>
## 1 Multigenerational    0.170    0.00563 0.335
## 2 One off              0.00494 -0.128  0.137
## 3 Both F0             -0.106   -0.815  0.603
## 4 F0 Female            0.0842  -0.0494 0.218
## 5 F0 Male              0.0530  -0.209  0.315
## 6 Both Sexes Grand Offspring 0.126   -0.231 0.483
## 7 Female Grand Offspring 0.0867  -0.0616 0.235
## 8 Male Grand Offspring  0.0485  -0.103  0.200
```



```
# Meta-regression when split by exposure type
```

```
Body_Weight_MG_F0_lnCVR <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID))
```

```
## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.
```

```
Body_Weight_MG_F0_lnCVR
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    13     no   Paper_ID
## sigma^2.2  0.0000  0.0000    24     no  Cohort_ID
## sigma^2.3  0.1344  0.3665    52     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 50) = 151.4427, p-val < .0001
##
## Test of Moderators (coefficient(s) 1:2):
## QM(df = 2) = 7.3958, p-val = 0.0248
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## F0_Parent_ExposedFemale    0.1930  0.0741  2.6040  0.0092    0.0477  0.3383
## F0_Parent_ExposedMale     0.1122  0.1430  0.7842  0.4329   -0.1682  0.3925
##
## F0_Parent_ExposedFemale **
## F0_Parent_ExposedMale
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Body_Weight_OF_F0_lnCVR <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID))
```

```
Body_Weight_OF_F0_lnCVR
```

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0378  0.1943    16     no   Paper_ID
## sigma^2.2  0.0000  0.0000    50     no  Cohort_ID
## sigma^2.3  0.1397  0.3737    94     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 91) = 294.4327, p-val < .0001
##
```

```
## Test of Moderators (coefficient(s) 1:3):
```

```
## QM(df = 3) = 0.2087, p-val = 0.9762
```

```
##
```

```
## Model Results:
```

```
##
```

	estimate	se	zval	pval	ci.lb
## F0_Parent_ExposedBoth	-0.1228	0.3705	-0.3314	0.7403	-0.8491
## F0_Parent_ExposedFemale	-0.0000	0.0889	-0.0003	0.9997	-0.1743
## F0_Parent_ExposedMale	0.0387	0.1543	0.2505	0.8022	-0.2637

	ci.ub
## F0_Parent_ExposedBoth	0.6035
## F0_Parent_ExposedFemale	0.1742
## F0_Parent_ExposedMale	0.3410

```
##
```

```
## ---
```

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

```
Body_Weight_MG_Sex_lnCVR <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_
```

```
Body_Weight_MG_Sex_lnCVR
```

```
##
```

```
## Multivariate Meta-Analysis Model (k = 52; method: REML)
```

```
##
```

```
## Variance Components:
```

```
##
```

	estim	sqrt	nlvls	fixed	factor
## sigma^2.1	0.0000	0.0000	13	no	Paper_ID
## sigma^2.2	0.0000	0.0000	24	no	Cohort_ID
## sigma^2.3	0.1294	0.3597	52	no	ES_ID

```
##
```

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 49) = 141.8454, p-val < .0001
```

```
##
```

```
## Test of Moderators (coefficient(s) 1:3):
```

```
## QM(df = 3) = 9.5637, p-val = 0.0227
```

```
##
```

```
## Model Results:
```

```
##
```

	estimate	se	zval	pval	ci.lb	ci.ub
## SexBoth	0.2032	0.1529	1.3284	0.1840	-0.0966	0.5029
## SexFemale	0.2676	0.0973	2.7500	0.0060	0.0769	0.4583
## SexMale	0.0518	0.1066	0.4865	0.6266	-0.1570	0.2607

```
##
```

```
## ---
```

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

```
Body_Weight_OF_Sex_lnCVR <- rma.mv(yi, vi, mods = ~Sex-1, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_
```

```
Body_Weight_OF_Sex_lnCVR
```

```
##
```

```
## Multivariate Meta-Analysis Model (k = 94; method: REML)
```



