

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")
```

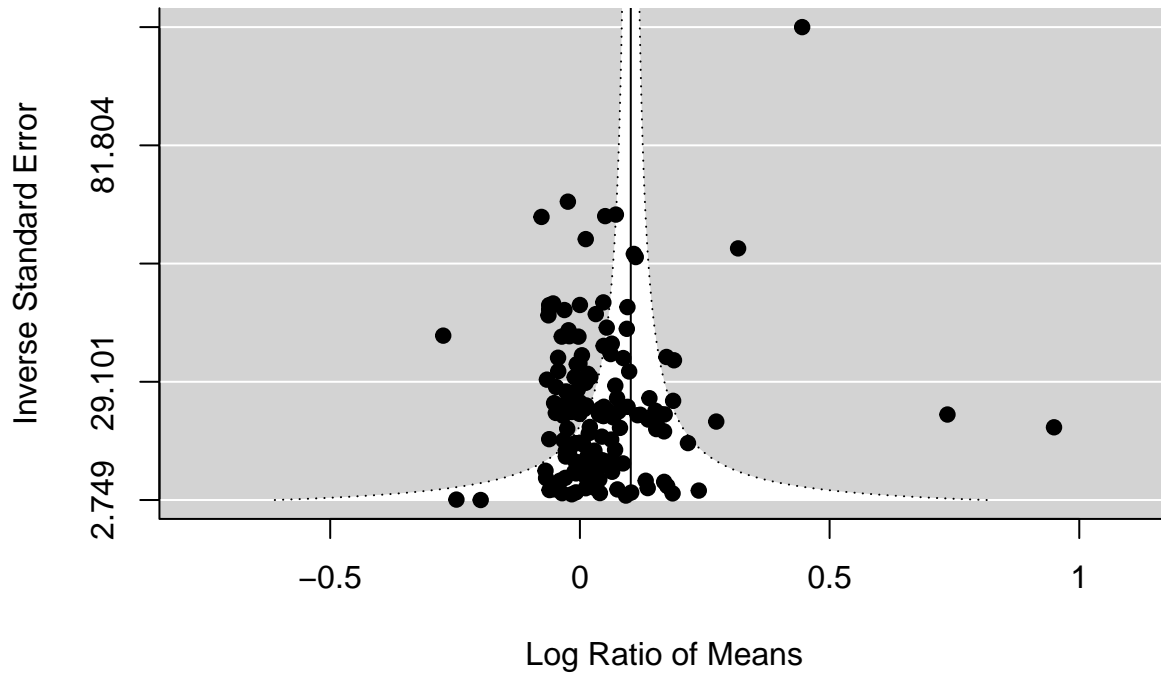
Overall analysis, not split

```
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
```

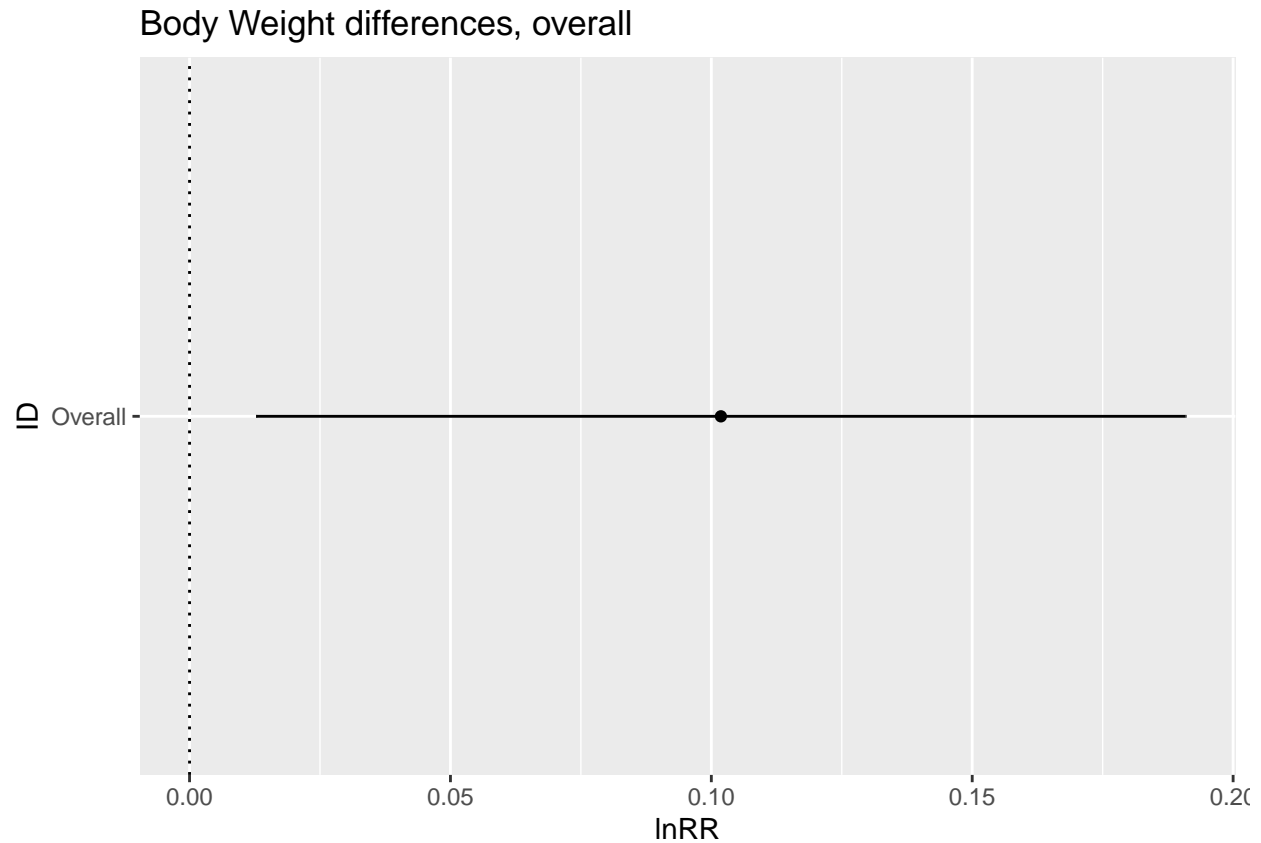
```
funnel(Body_Weight_overall,yaxis="seinv")
```



```
#Tibble of overall results
```

```
Body_Weight_overall_lnRR <- tibble(
  ID = "Overall",
  lnRR = Body_Weight_overall$b[1],
  ci.lb = Body_Weight_overall$ci.lb[1],
  ci.ub = Body_Weight_overall$ci.ub[1]
)

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
```



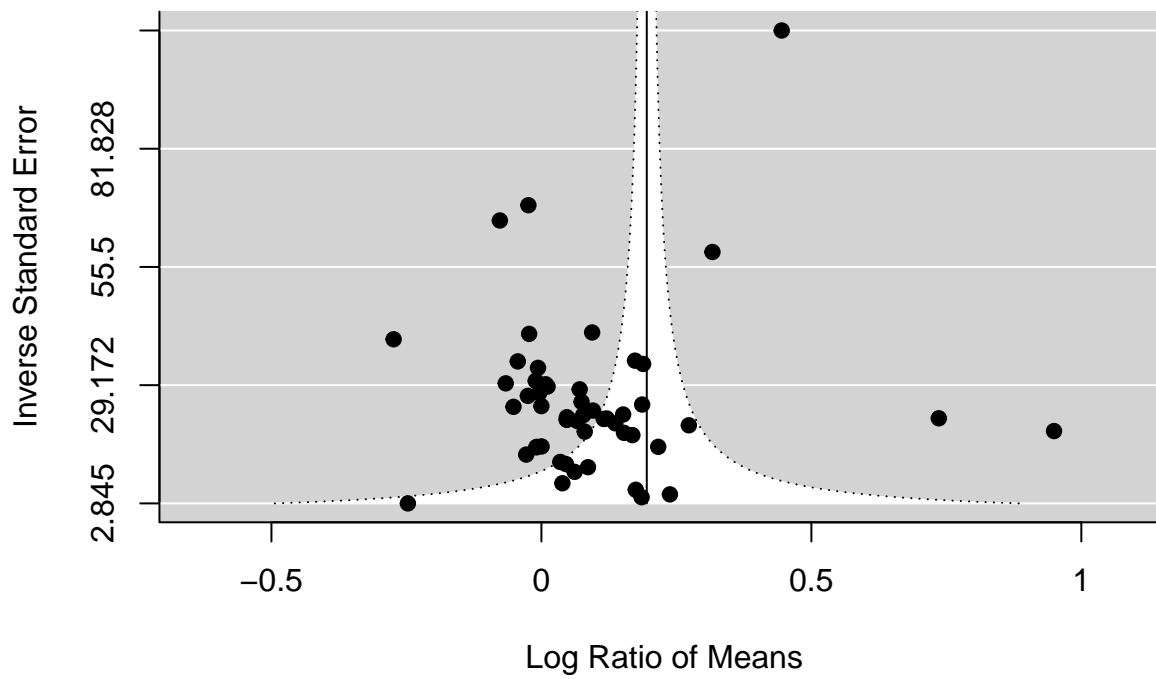
Overall analysis when split by exposure type

```
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,yaxis="seinv")
```

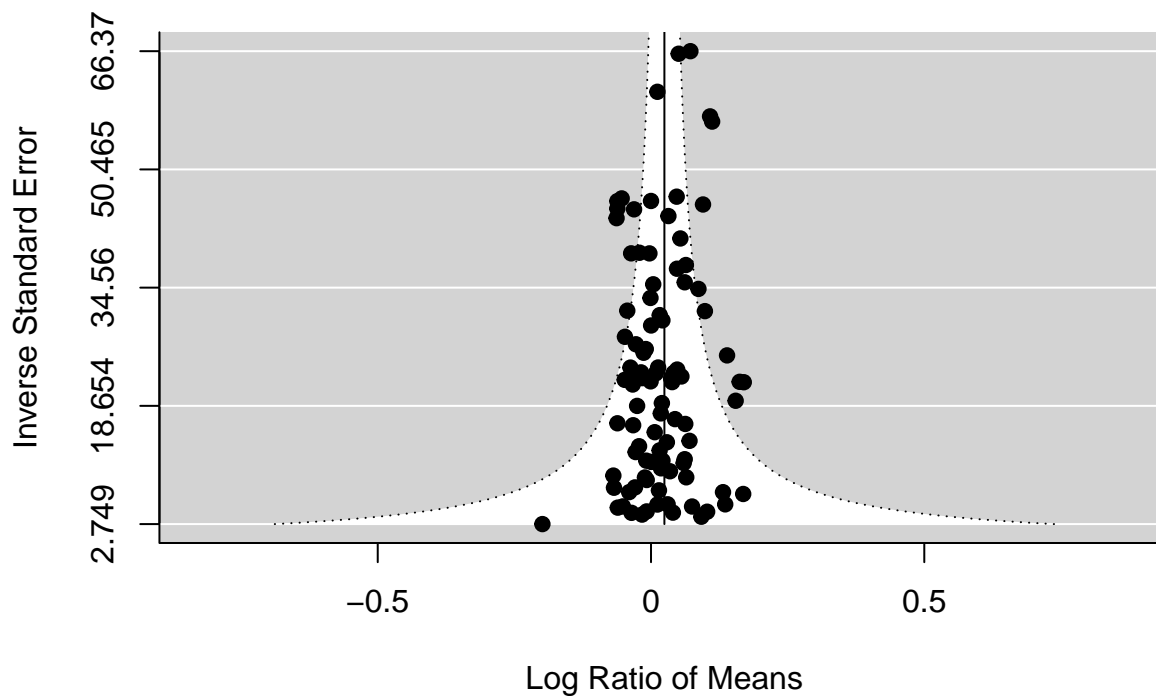


```
Body_Weight_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnR)
summary(Body_Weight_OF)
```

```
##
## 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,yaxis="seinv")
```



```
#Tibble of results
```

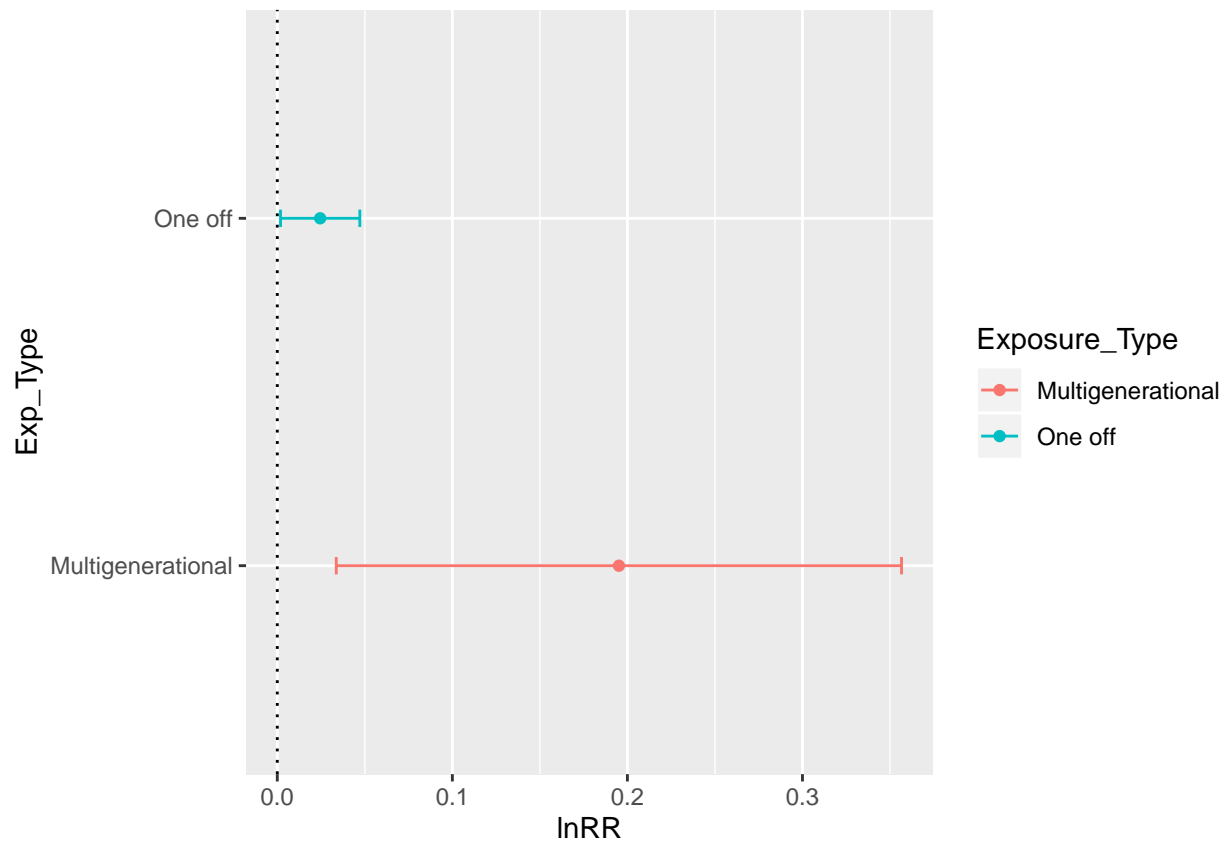
```
Body_Weight_Exp_lnRR <- tibble(
  Exposure_Type = c("Multigenerational", "One off"),
  k = c(94),
  lnRR = c(Body_Weight_MG$b[1],Body_Weight_OF$b[1]),
  ci.lb = c(Body_Weight_MG$ci.lb[1],Body_Weight_OF$ci.lb[1]),
  ci.ub = c(Body_Weight_MG$ci.ub[1],Body_Weight_OF$ci.ub[1])
)
```

```
Body_Weight_Exp_lnRR
```

```
## # A tibble: 2 x 5
##   Exposure_Type      k  lnRR   ci.lb ci.ub
##   <chr>          <dbl> <dbl>   <dbl> <dbl>
## 1 Multigenerational    94 0.195  0.0337 0.357
## 2 One off              94 0.0245 0.00185 0.0471
```

#Plotting when split by exp type

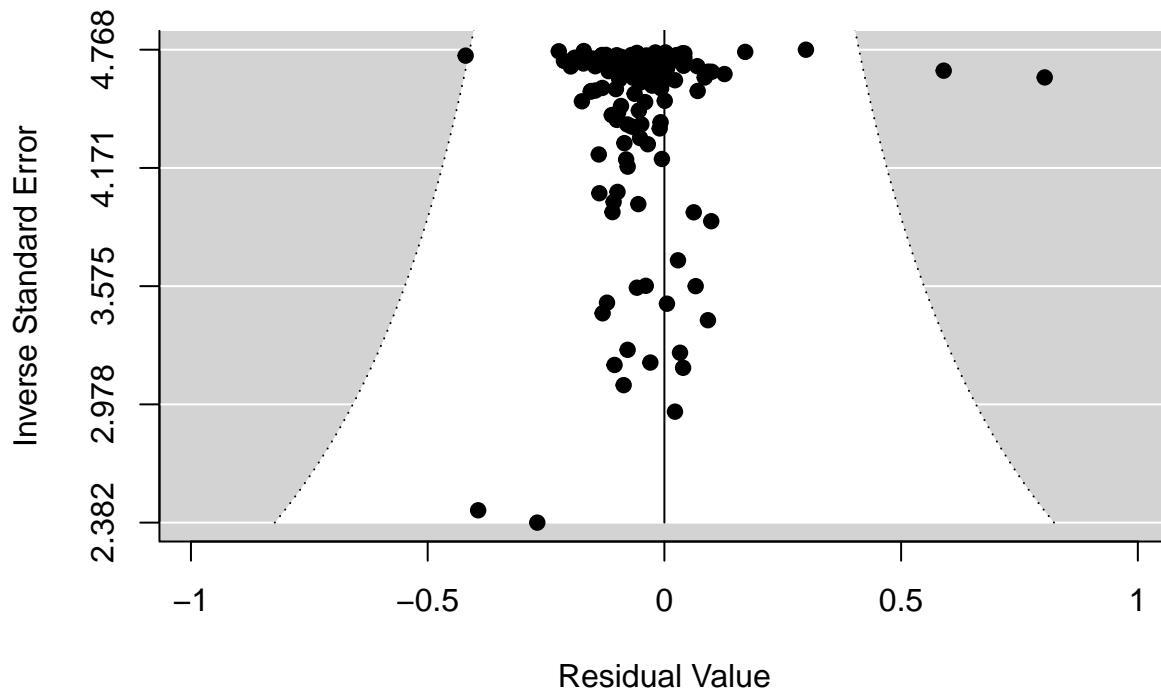
```
plot_BW_exp_type <- ggplot(Body_Weight_Exp_lnRR, aes(x=Exposure_Type, y=lnRR, colour = Exposure_Type)) +
  geom_errorbar(aes(ymin=ci.lb, ymax=ci.ub), width = 0.05, position = position_dodge(0.3)) +
  geom_point(aes(x = Exposure_Type, y = lnRR), position = position_dodge(0.3)) +
  geom_hline(yintercept = 0, lty = "dotted") +
  labs(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 (coefficients 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
```

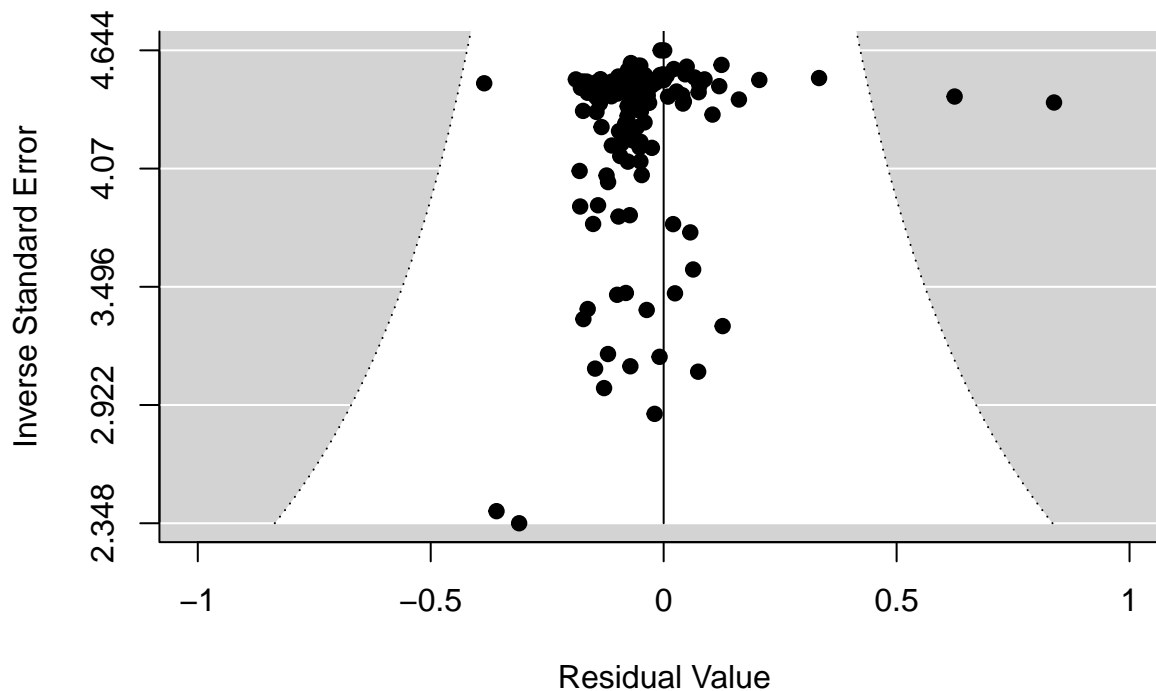


```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
```

```

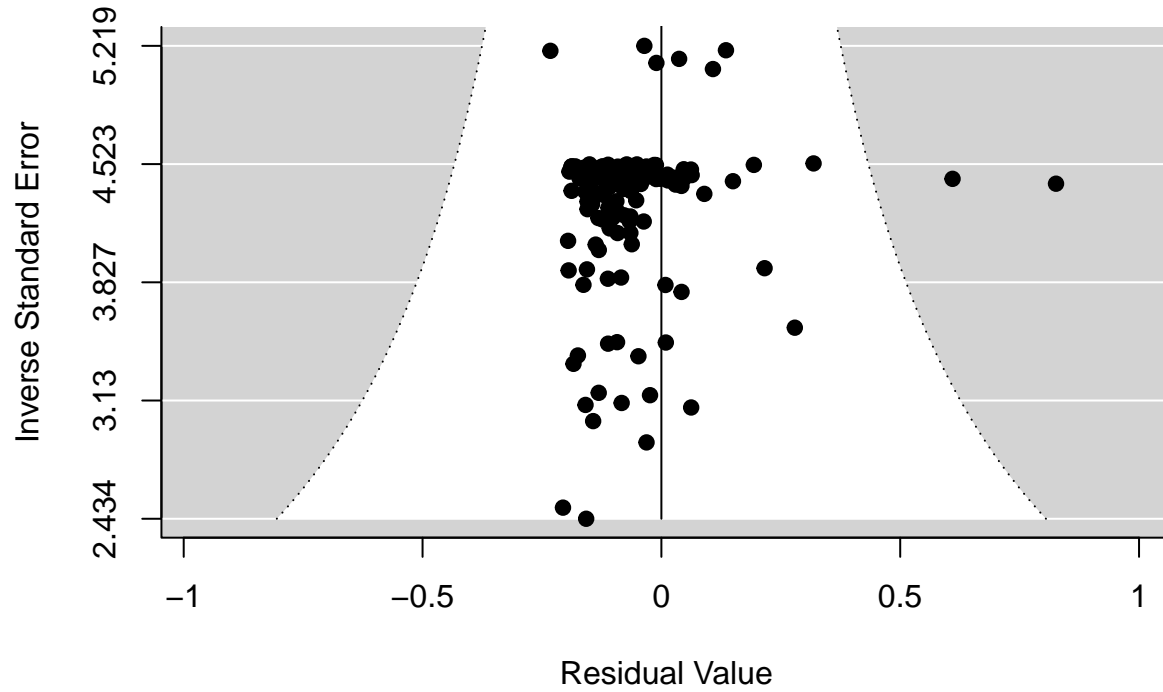
## 112.5935 -225.1869 -213.1869 -195.4098 -212.5693
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0474  0.2178    25     no   Paper_ID
## sigma^2.2  0.0000  0.0000    72     no   Cohort_ID
## sigma^2.3  0.0038  0.0616   146     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 143) = 3179.4121, p-val < .0001
##
## Test of Moderators (coefficients 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

```

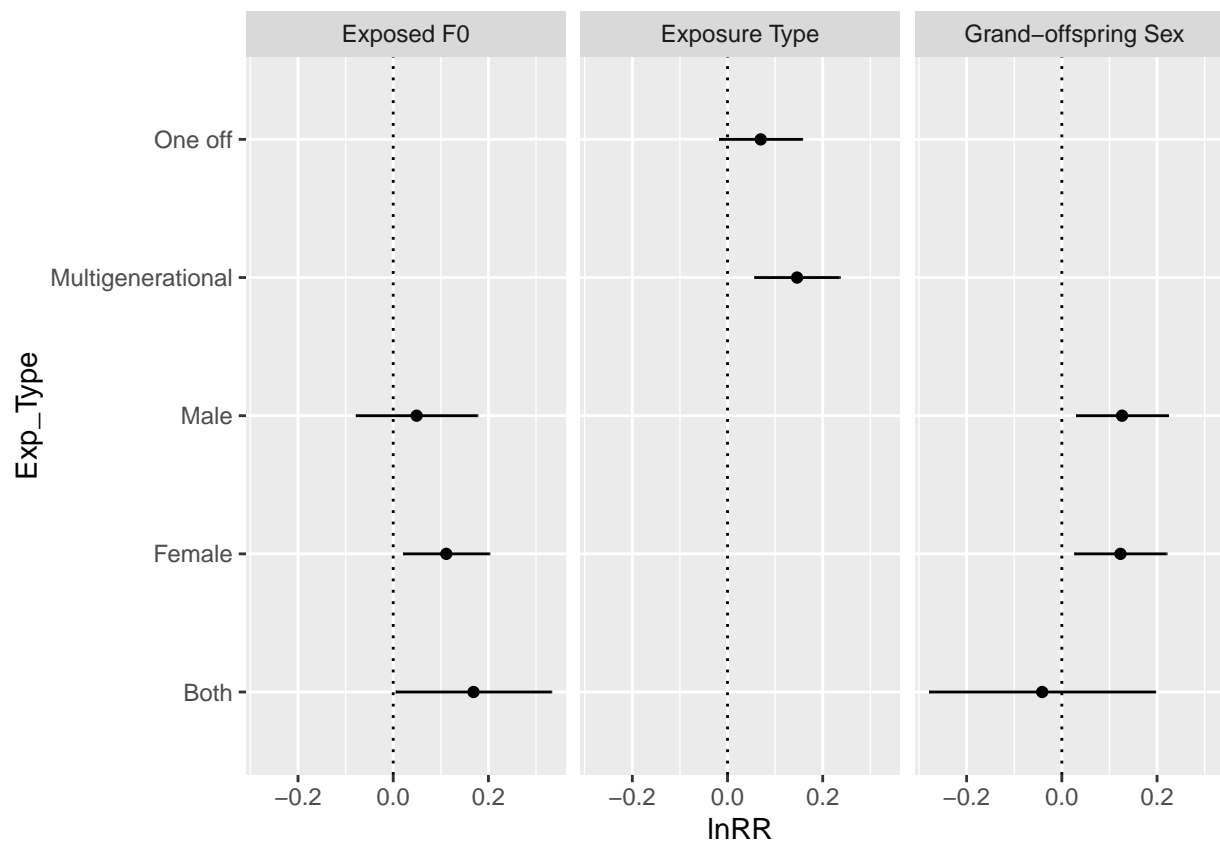



```
##
## Multivariate Meta-Analysis Model (k = 146; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
## 111.4842 -222.9684 -210.9684 -193.1914 -210.3508
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0472  0.2173   25    no  Paper_ID
## 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 (coefficients 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 5
##   ID      Mod      lnRR    ci.lb ci.ub
##   <chr>    <chr>    <dbl>  <dbl> <dbl>
## 1 Multigenerational Exposure Type  0.146  0.0566 0.236
## 2 One off    Exposure Type  0.0697 -0.0173 0.157
## 3 Both      Exposed F0    0.169  0.00539 0.332
## 4 Female    Exposed F0    0.112  0.0210 0.202
## 5 Male      Exposed F0    0.0492 -0.0785 0.177
## 6 Both      Grand-offspring Sex -0.0413 -0.279 0.196
## 7 Female    Grand-offspring Sex 0.123  0.0264 0.220
## 8 Male      Grand-offspring Sex 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 (coefficients 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 (coefficients 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
```

```
k_exp <- Body_Weight_lnRR_OF %>% group_by(F0_Parent_Exposed) %>% count()
k_exp
```

```
## # A tibble: 3 x 2
## # Groups:   F0_Parent_Exposed [3]
##   F0_Parent_Exposed     n
##   <fct>              <int>
```

```
## 1 Both          2
## 2 Female        75
## 3 Male          17
```

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

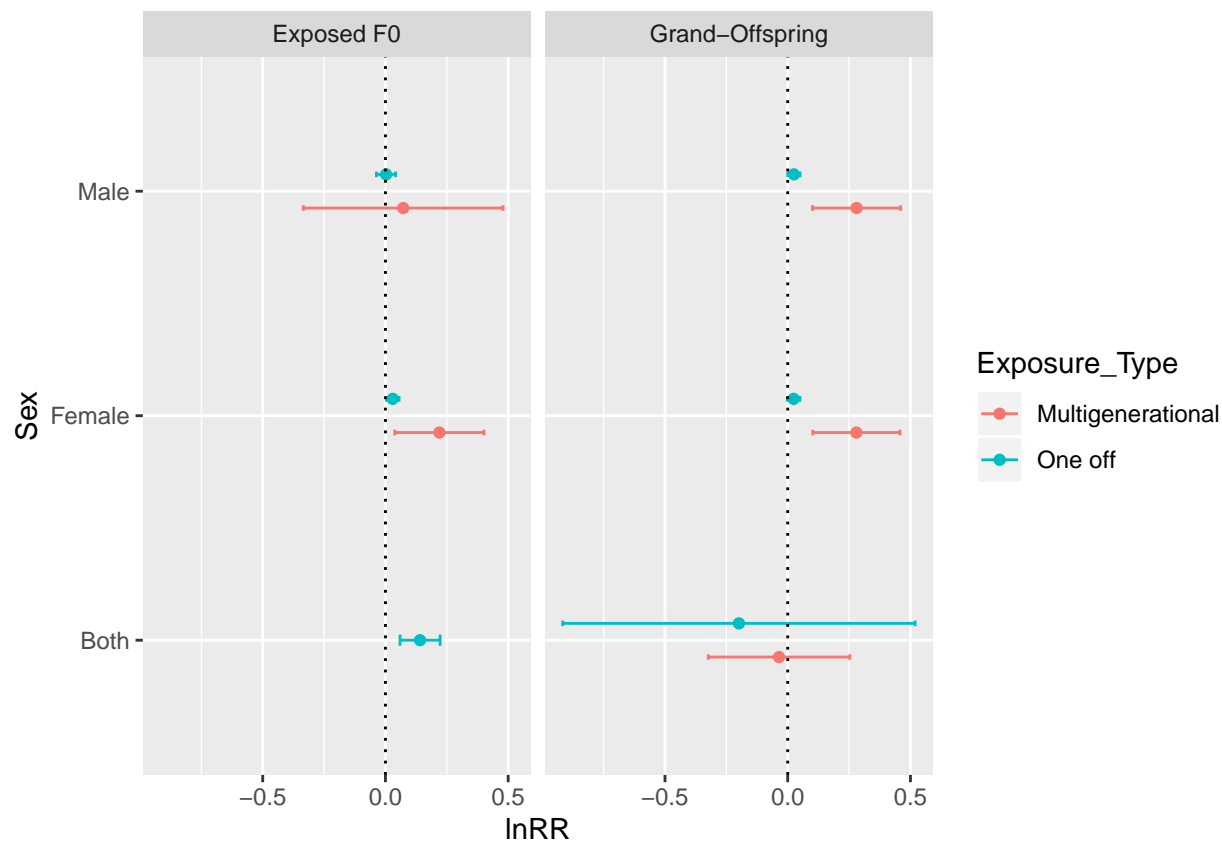
```
Body_Weight_MG_Sex
```

```
##
## 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 (coefficients 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
##
```

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)

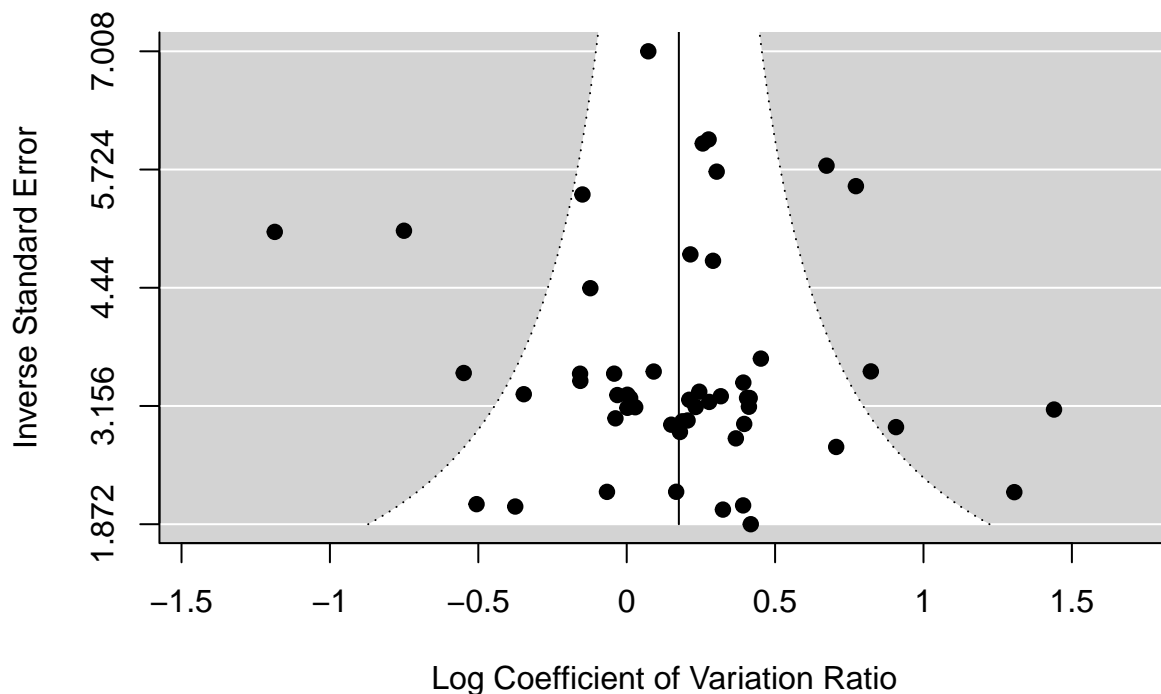
```
# Modelling all traits with no mods MG (lnCVR)
Body_Weight_lnCVR_Omods_MG <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnCVR_Omods_MG)

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
```

```
funnel(Body_Weight_lnCVR_0mods_MG,yaxis="seinv")
```

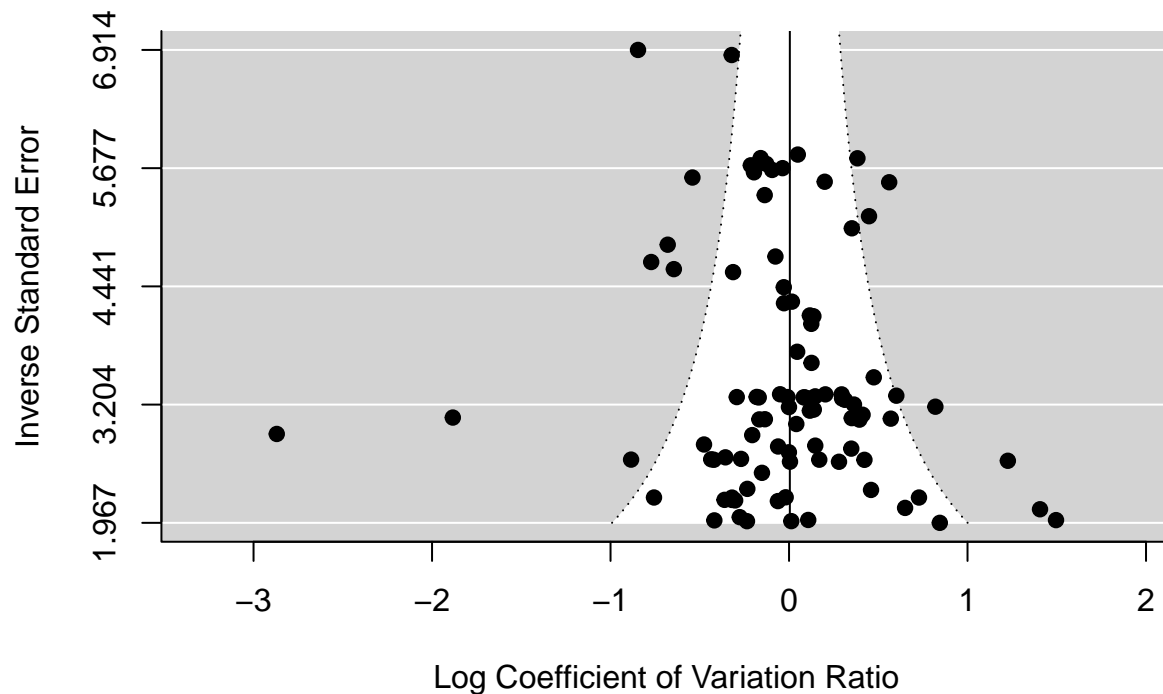


```
# Modelling all traits with no mods OF (lnCVR)
Body_Weight_lnCVR_0mods_OF <- rma.mv(yi, vi, random = list(~1|Paper_ID,~1|Cohort_ID,~1|ES_ID), data=Body_Weight_lnCVR_0mods_MG)
summary(Body_Weight_lnCVR_0mods_OF)
```



```
##
## 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
```

```
funnel(Body_Weight_lnCVR_0mods_OF,yaxis="seinv")
```



```
#Tibble of results
```

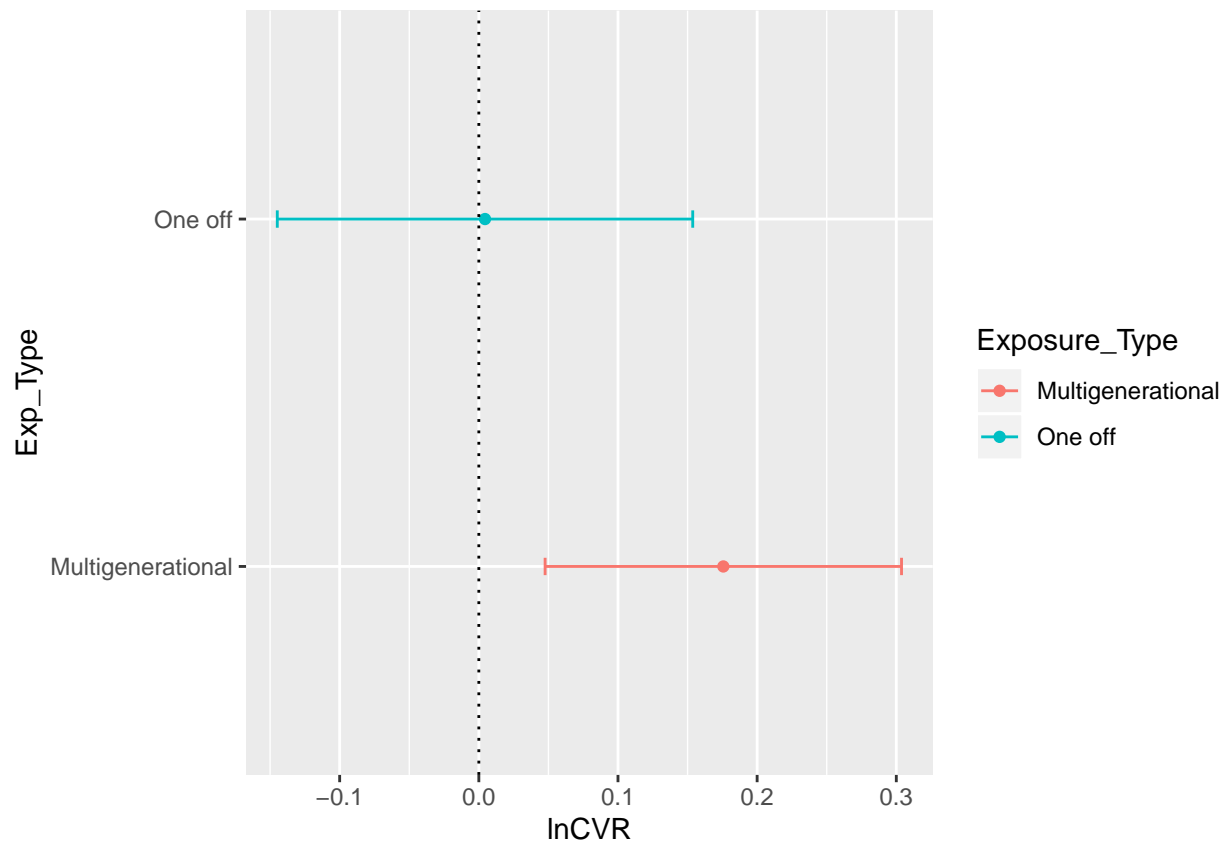
```
Body_Weight_Exp_lnCVR <- tibble(  
  Exposure_Type = c("Multigenerational", "One off"),  
  lnCVR = c(Body_Weight_lnCVR_Omods_MG$b[1], Body_Weight_lnCVR_Omods_OF$b[1]),  
  ci.lb = c(Body_Weight_lnCVR_Omods_MG$ci.lb[1], Body_Weight_lnCVR_Omods_OF$ci.lb[1]),  
  ci.ub = c(Body_Weight_lnCVR_Omods_MG$ci.ub[1], Body_Weight_lnCVR_Omods_OF$ci.ub[1])  
)
```

```
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          0.00444 -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 = 0.05, 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(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
## -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 (coefficients 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
```

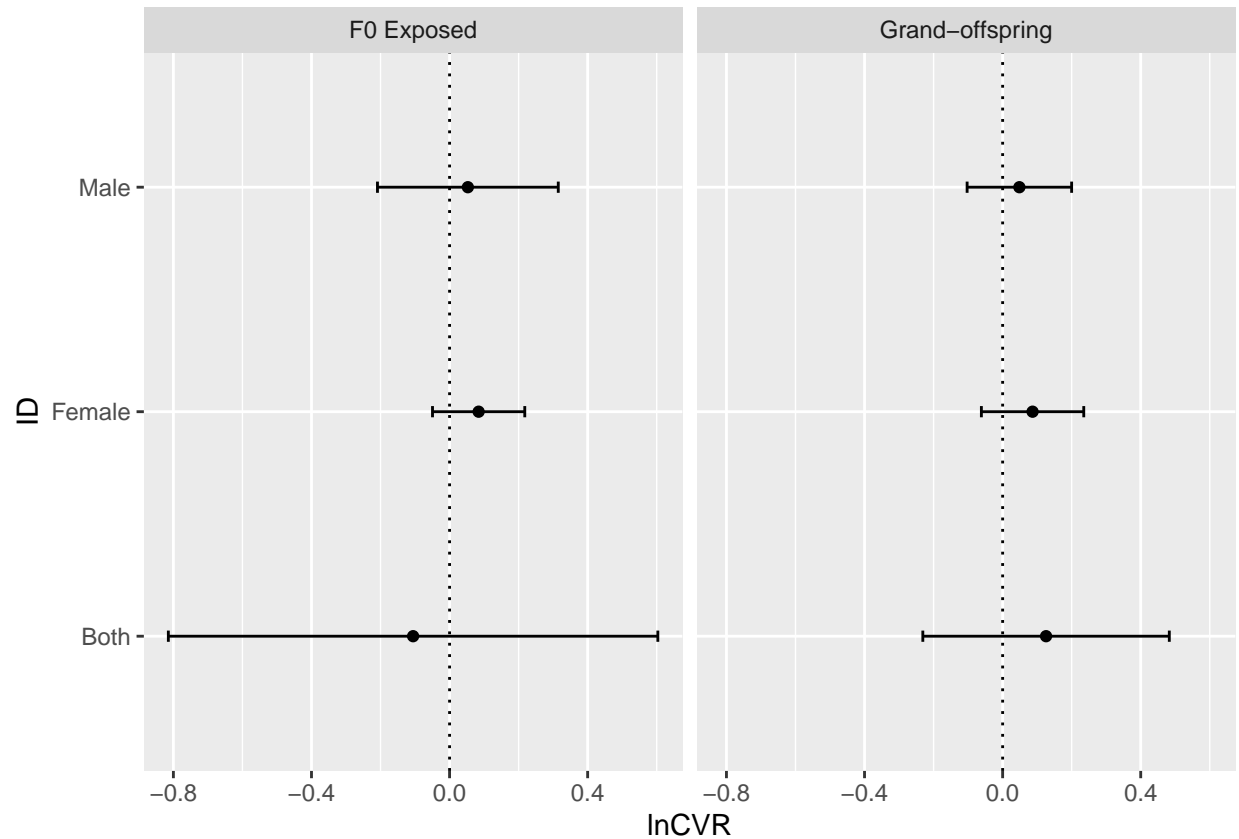
```

##                               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 (coefficients 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: 6 x 5
##   ID      Mod      lnCVR      ci.lb ci.ub
##   <chr> <chr>      <dbl>   <dbl> <dbl>
## 1 Both   F0 Exposed   -0.106 -0.815  0.603
## 2 Female F0 Exposed    0.0842 -0.0494  0.218
## 3 Male   F0 Exposed    0.0530 -0.209  0.315
## 4 Both   Grand-offspring  0.126  -0.231  0.483
## 5 Female Grand-offspring  0.0867 -0.0616  0.235
## 6 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))
```

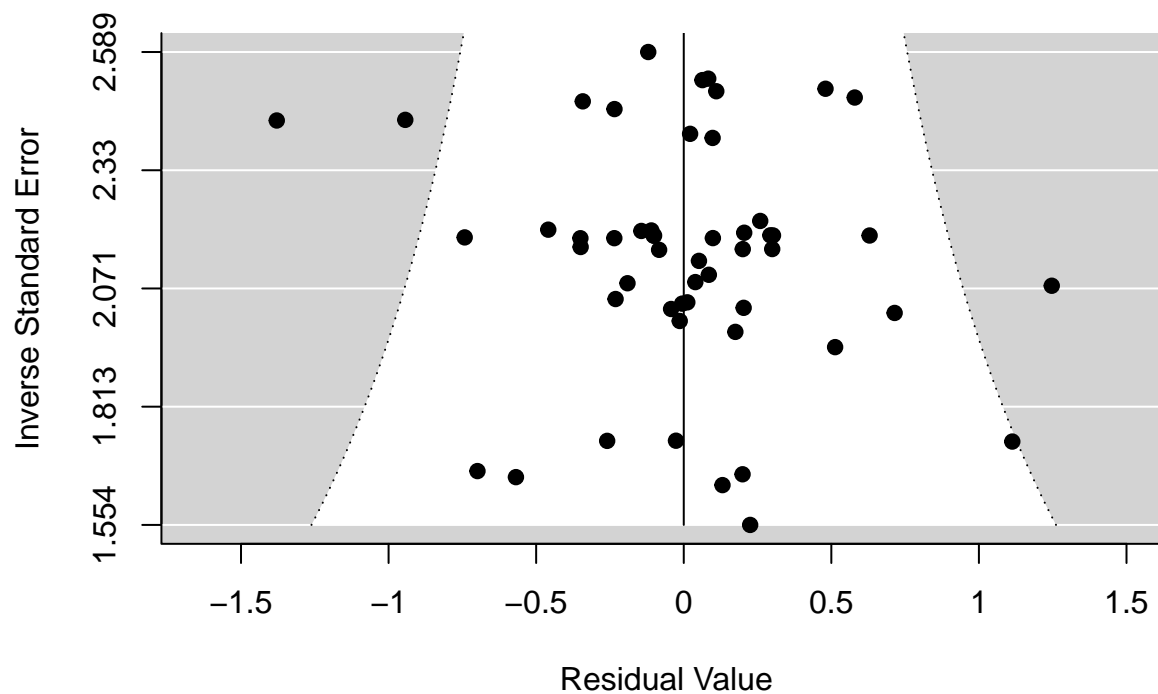
```
## Warning in rma.mv(yi, vi, mods = ~F0_Parent_Exposed - 1, random = list(~1
## | : Redundant predictors dropped from the model.
```

```
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 (coefficients 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
```

```
funnel(Body_Weight_MG_F0_lnCVR,yaxis="seinv")
```

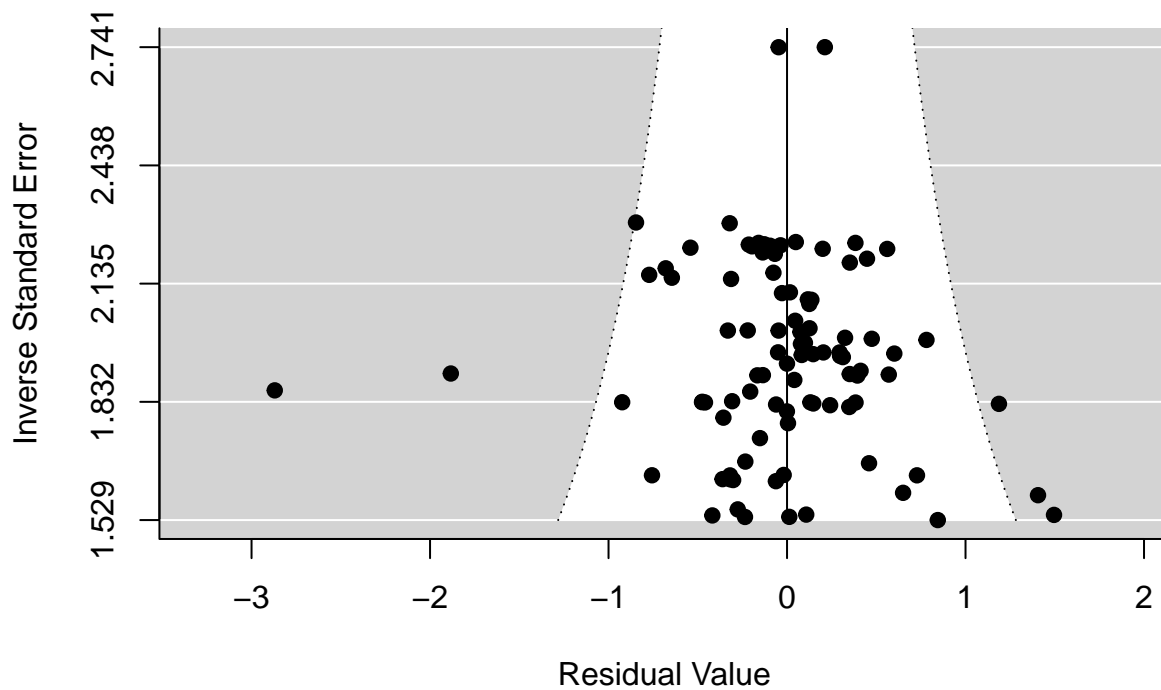


```
Body_Weight_OF_F0_lnCVR <- rma.mv(yi, vi, mods = ~F0_Parent_Exposed-1, random = list(~1|Paper_ID,~1|Cohort_ID))
Body_Weight_OF_F0_lnCVR
```

```
##
## 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 (coefficients 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
```

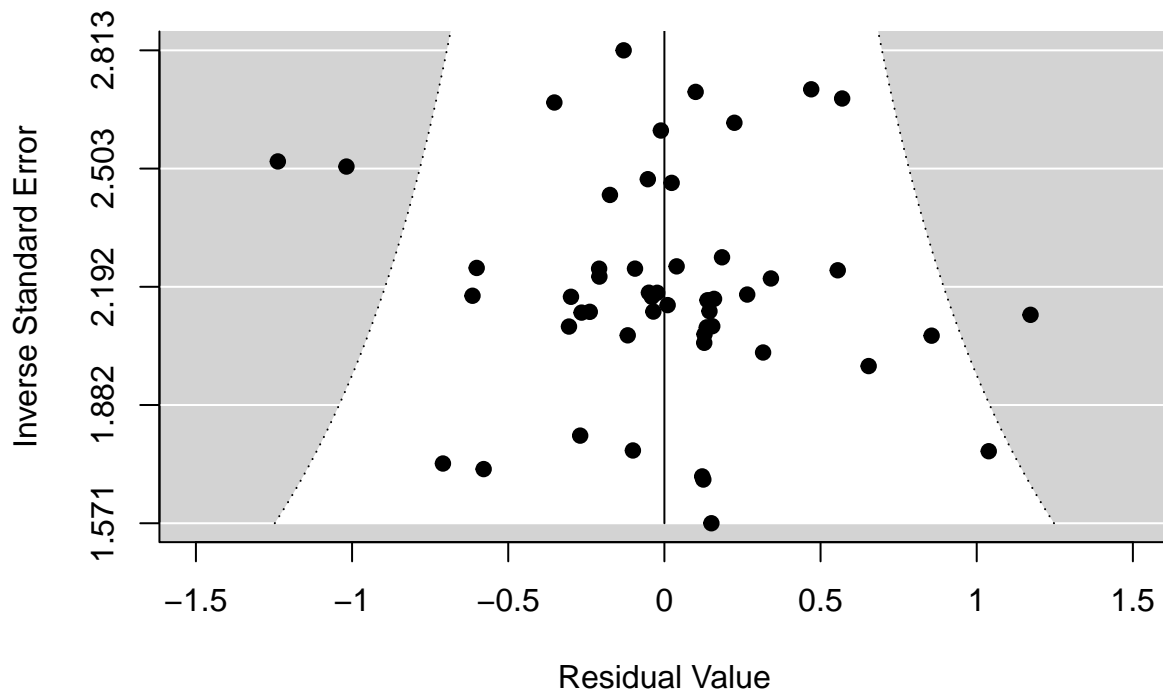
```
funnel(Body_Weight_OF_F0_lnCVR,yaxis="seinv")
```



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

```
funnel(Body_Weight_MG_Sex_lnCVR,yaxis="seinv")
```

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

```
##
## Multivariate Meta-Analysis Model (k = 94; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0357  0.1891    16     no   Paper_ID
## sigma^2.2  0.0000  0.0000    50     no   Cohort_ID
## sigma^2.3  0.1394  0.3734    94     no     ES_ID
##
## Test for Residual Heterogeneity:
## QE(df = 91) = 296.9085, p-val < .0001
##
## Test of Moderators (coefficients 1:3):
## QM(df = 3) = 0.4697, p-val = 0.9255
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## SexBoth      -0.2760  0.6470  -0.4266  0.6696  -1.5441  0.9920
## SexFemale     -0.0174  0.0930  -0.1872  0.8515  -0.1997  0.1648
```

```
funnel(Body_Weight_OF_Sex_lnCVR, yaxis="seinv")
```



