data wrangling and plots

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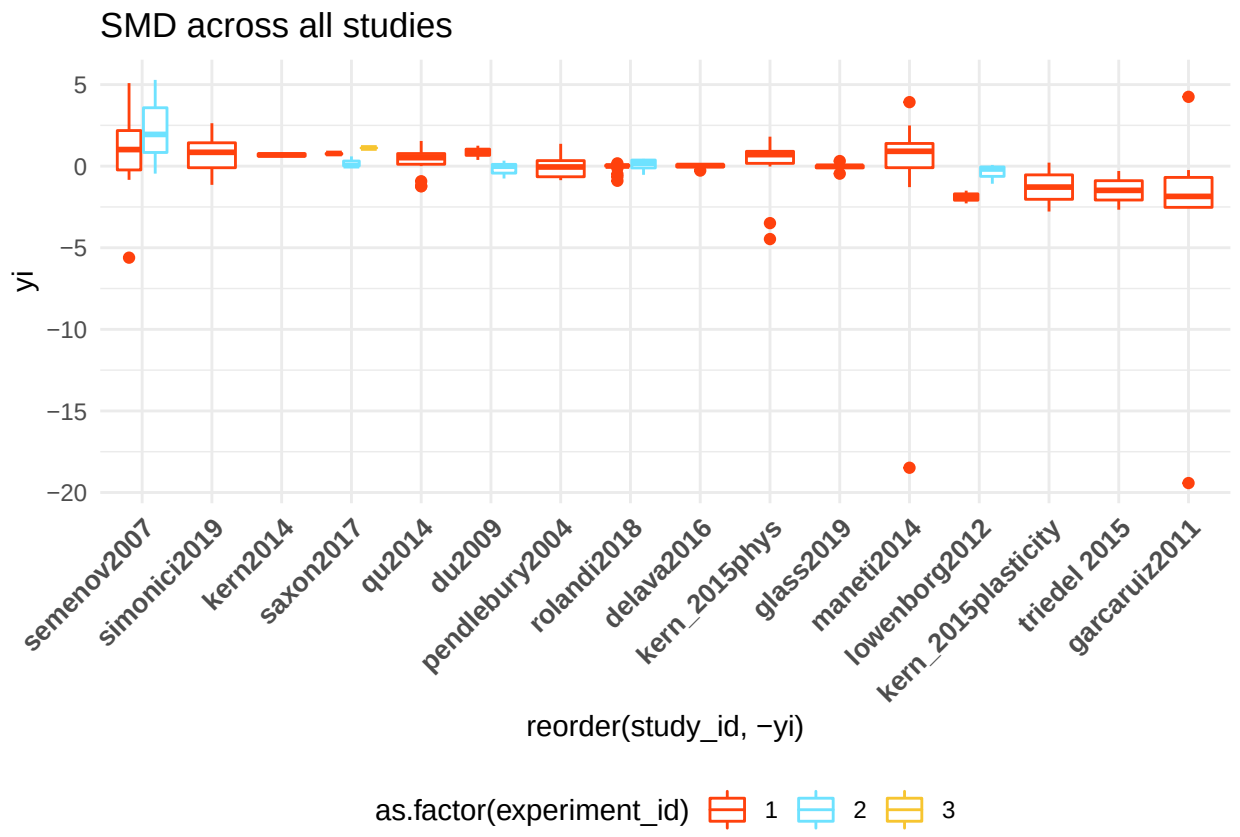
Plots

Question: How does response compare across studies and experiments?

Figure 1.

```
#SMD across all studies
ggplot(normalized, aes(x=reorder(study_id, -yi), y=yi, color = as.factor(experiment_id)))+
  geom_boxplot()+
  scale_color_tron()+
  theme_minimal()+
  theme(axis.text.x = element_text(face = "bold",
                                   size = 10, angle = 45,hjust = 1),
        legend.position = "bottom")+
  ggtitle("SMD across all studies")
```




```
#corresponding random effects model
fig1 <- rma.mv(yi, vi, data=dat_MA_ES,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig1
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0003      3     no           experiment_id
## sigma^2.2  0.5747  0.7581     22     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 201) = 6408.3572, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.1144  0.1644  0.6957  0.4866  -0.2078  0.4366
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#trying out mixed effects model
fig1me <- rma(yi, vi, data=dat_MA_ES, mods = ~study_id,
              method="FE")
fig1me
```

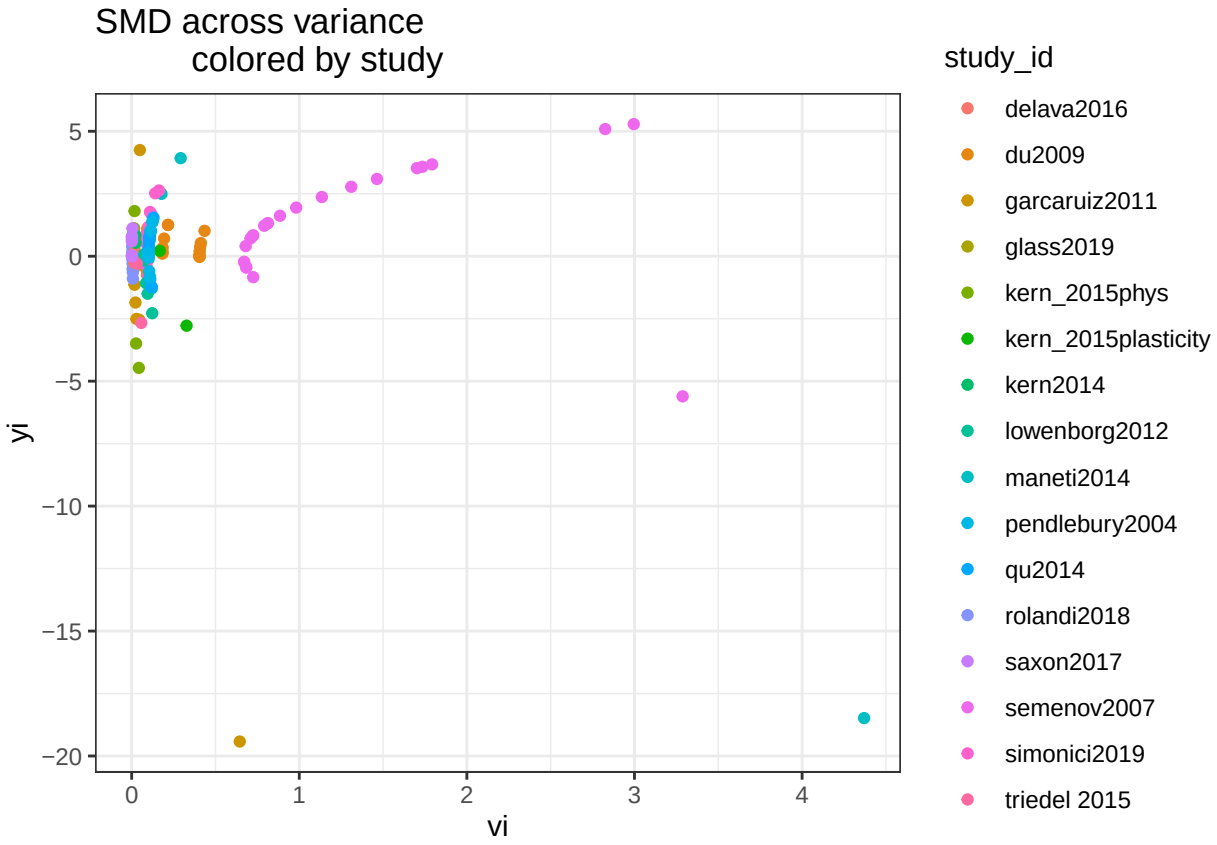
```
##
## Fixed-Effects with Moderators Model (k = 202)
##
## I^2 (residual heterogeneity / unaccounted variability): 96.33%
## H^2 (unaccounted variability / sampling variability):   27.22
##
## Test for Residual Heterogeneity:
## QE(df = 186) = 5063.4195, p-val < .0001
##
## Test of Moderators (coefficients 2:16):
## QM(df = 15) = 1344.9378, p-val < .0001
##
## Model Results:
##
##                              estimate      se      zval    pval    ci.lb
## intrcpt                        0.0006  0.0448    0.0127  0.9899  -0.0872
## study_iddu2009                 0.1754  0.0782    2.2433  0.0249   0.0222
## study_idgarcaruiz2011         -1.0855  0.0792  -13.7139  <.0001  -1.2407
## study_idglass2019             -0.0359  0.0636   -0.5638  0.5729  -0.1606
## study_idkern_2015phys          0.4404  0.0548    8.0347  <.0001   0.3330
## study_idkern_2015plasticity   -0.7988  0.3360   -2.3774  0.0174  -1.4574
## study_idkern2014               0.6921  0.1156    5.9871  <.0001   0.4655
## study_idlowenborg2012         -0.8458  0.1396   -6.0565  <.0001  -1.1195
## study_idmaneti2014             0.7240  0.1146    6.3198  <.0001   0.4995
## study_idpendlebury2004        -0.0100  0.1239   -0.0807  0.9357  -0.2529
## study_idqu2014                 0.3173  0.0858    3.6992  0.0002   0.1492
## study_idrolandi2018            0.0200  0.0467    0.4283  0.6684  -0.0716
## study_idsaxon2017              0.4966  0.0470   10.5578  <.0001   0.4044
## study_idsemenov2007            0.9931  0.2096    4.7384  <.0001   0.5823
## study_idsimonici2019           0.5785  0.0932    6.2079  <.0001   0.3958
## study_idtriedel 2015          -1.1246  0.1483   -7.5818  <.0001  -1.4153
##                                ci.ub
## intrcpt                       0.0883
## study_iddu2009                0.3287    *
## study_idgarcaruiz2011        -0.9304  ***
## study_idglass2019             0.0888
## study_idkern_2015phys         0.5479  ***
## study_idkern_2015plasticity  -0.1403    *
## study_idkern2014              0.9187  ***
## study_idlowenborg2012        -0.5721  ***
## study_idmaneti2014            0.9485  ***
## study_idpendlebury2004        0.2329
## study_idqu2014                0.4854  ***
## study_idrolandi2018           0.1116
## study_idsaxon2017             0.5888  ***
## study_idsemenov2007           1.4039  ***
## study_idsimonici2019          0.7611  ***
## study_idtriedel 2015         -0.8339  ***
```

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

```
#basic linear model
simple1<-lm(yi ~ study_id, data = dat_MA_ES)
summary(fig1)
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2202.7201   4405.4402   4411.4402   4421.3501   4411.5621
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0003      3     no           experiment_id
## sigma^2.2  0.5747  0.7581     22     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 201) = 6408.3572, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.1144  0.1644  0.6957  0.4866  -0.2078  0.4366
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 2.

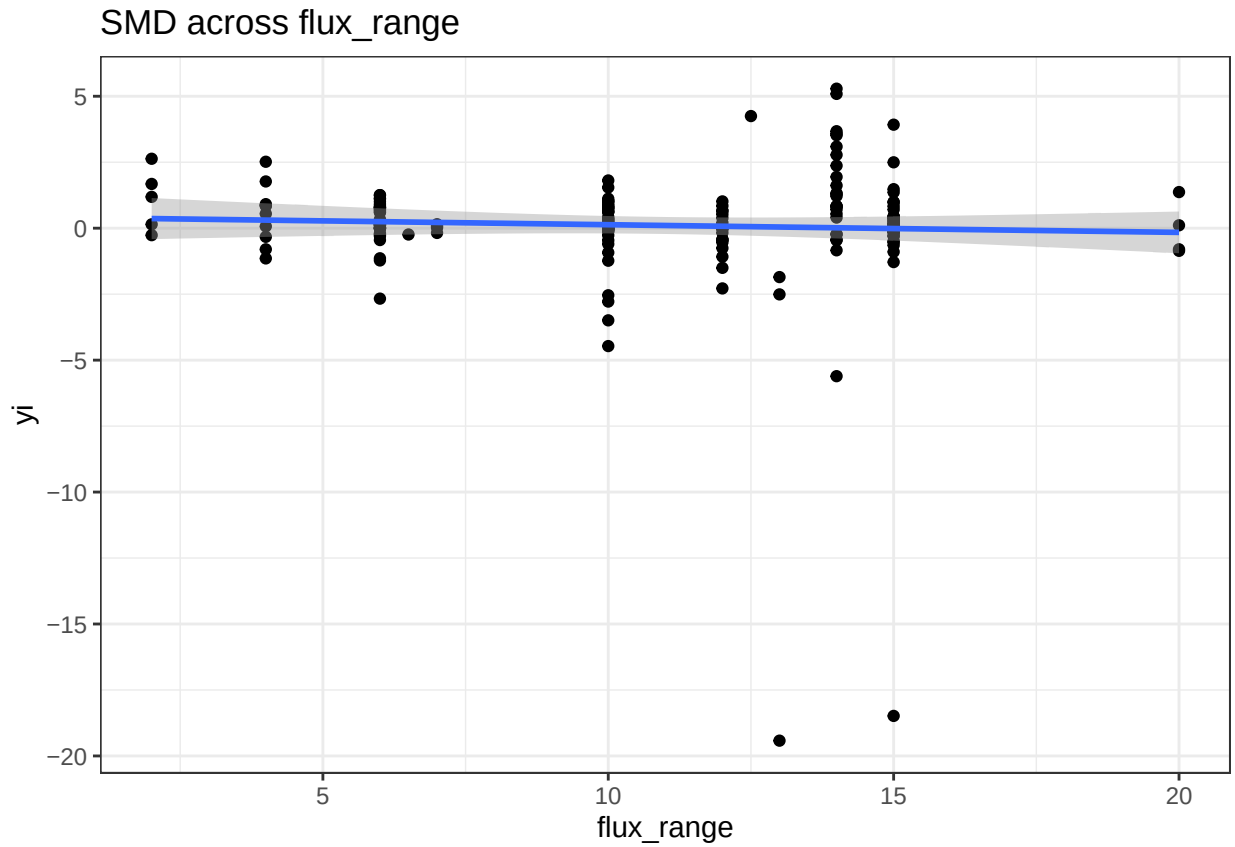



```
##
## Call:
## lm(formula = yi ~ vi, data = dat_MA_ES)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.7276  -1.1464  -0.6971   0.3935  18.8383
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.1831     0.2579   4.587 7.92e-06 ***
## vi           -4.9185     0.2349 -20.938  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.524 on 200 degrees of freedom
## Multiple R-squared:  0.6867, Adjusted R-squared:  0.6852
## F-statistic: 438.4 on 1 and 200 DF,  p-value: < 2.2e-16
```

Question: How does fluctuation amplitude affect response variables?

Figure 3.

```
# boxplots of how fluctuation range influences SMD
ggplot(normalized, aes(x=flux_range, y=yi))+
  geom_point()+
  theme_bw()+
  geom_smooth(method="lm", formula = y~x)+
  ggtitle("SMD across flux_range")
```




```
#random effects model including org_level as a random variable
fig7 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig7
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                 factor
## sigma^2.1  0.0000  0.0003      3     no          experiment_id
```

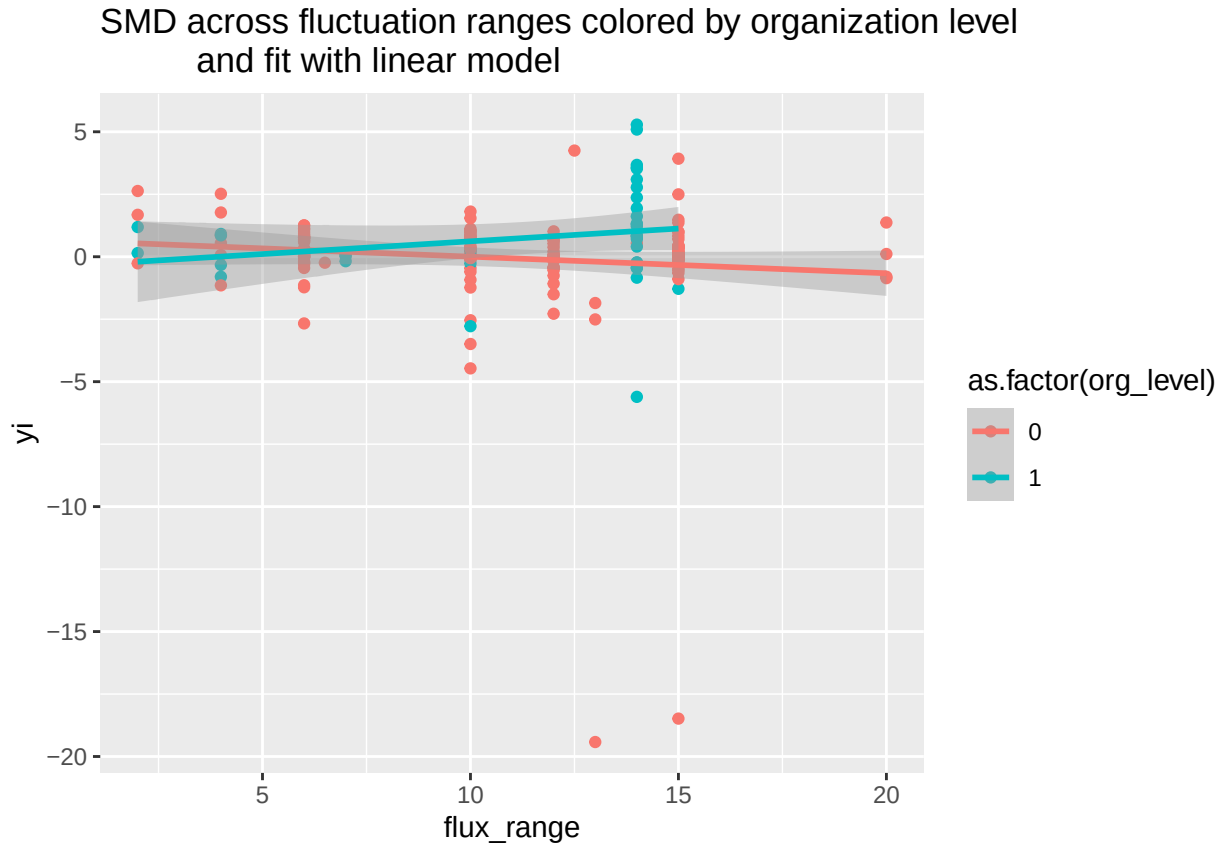
```
## sigma^2.2  0.6031  0.7766     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 5917.6127, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 16.7616, p-val < .0001
##
## Model Results:
##
##             estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt       0.5606  0.2005   2.7958  0.0052   0.1676   0.9536   **
## flux_range   -0.0435  0.0106  -4.0941  <.0001  -0.0644  -0.0227  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how flux_range affects yi
simple7<-lm(yi~flux_range, data =dat_MA_ES)
summary(simple7)
```

```
##
## Call:
## lm(formula = yi ~ flux_range, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -82.431   0.033   0.590   1.040   5.842
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.58043    1.27366   0.456    0.649
## flux_range  -0.08111    0.10932  -0.742    0.459
##
## Residual standard error: 6.287 on 200 degrees of freedom
## Multiple R-squared:  0.002745,   Adjusted R-squared:  -0.002241
## F-statistic: 0.5505 on 1 and 200 DF,  p-value: 0.459
```

Figure 4.

```
# scatterplot of standardized mean response vs flux range colored and lm fit by org level
ggplot(normalized, aes(x=flux_range, y=yi, color = as.factor(org_level)))+
  geom_point()+
  geom_smooth(method="lm", formula = y~x)+
  ggtitle("SMD across fluctuation ranges colored by organization level
          and fit with linear model")
```




```
#random effects model including org_level as a random variable
fig8 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range + org_level,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig8
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  0.6757  0.8220     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 199) = 5871.2594, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 40.7763, p-val < .0001
##
## Model Results:
##
##             estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt       0.6366  0.2093   3.0413  0.0024   0.2263   1.0468   **
## flux_range   -0.0436  0.0107  -4.0916  <.0001  -0.0645  -0.0227  ***
```

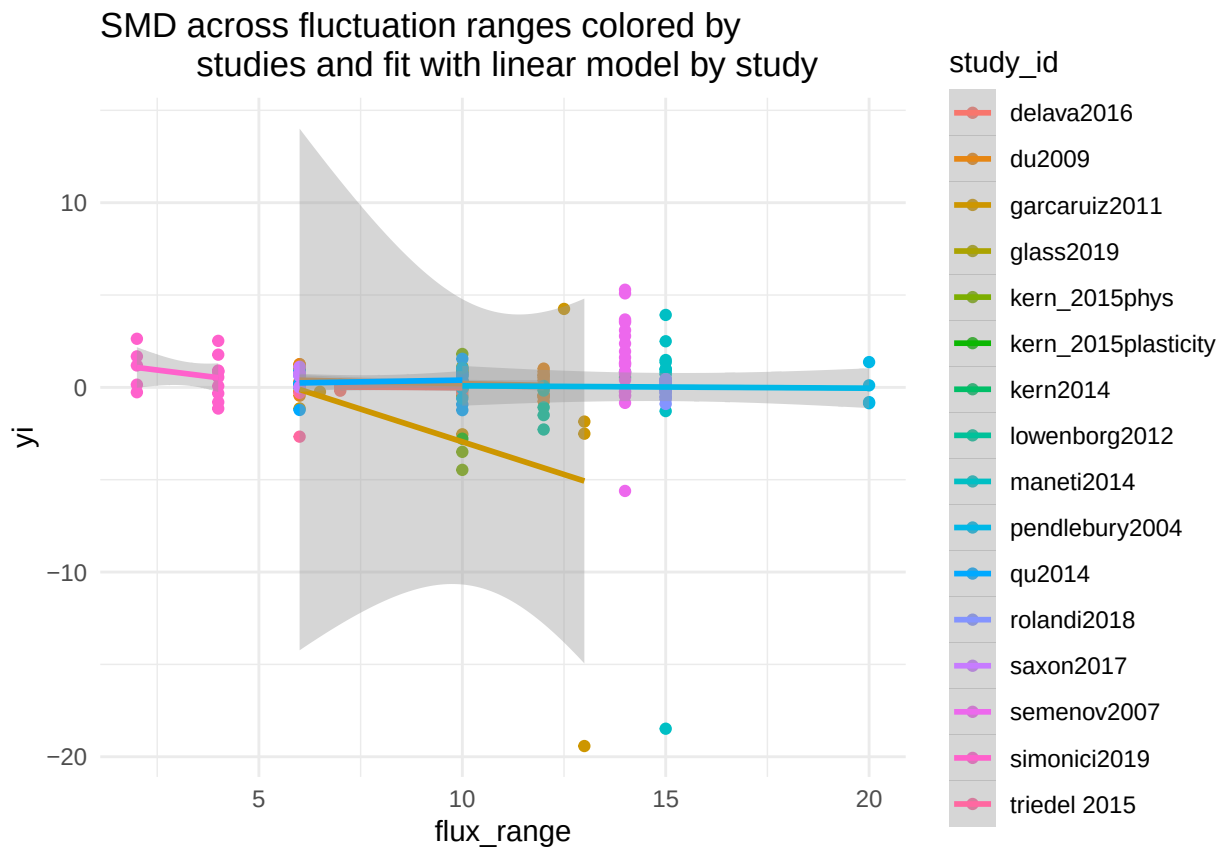
```
## org_level    -0.4010  0.0820  -4.8913  <.0001  -0.5616  -0.2403  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how flux_range and org_level affect yi
simple8<-lm(yi~flux_range*org_level, data =dat_MA_ES)
summary(simple8)
```

```
##
## Call:
## lm(formula = yi ~ flux_range * org_level, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -82.053  -0.088   0.714   1.236   5.043
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0.8933     1.4089   0.634    0.527
## flux_range             -0.1343     0.1220  -1.101    0.272
## org_level              -1.2959     3.3009  -0.393    0.695
## flux_range:org_level    0.2363     0.2759   0.856    0.393
##
## Residual standard error: 6.284 on 198 degrees of freedom
## Multiple R-squared:  0.01376,    Adjusted R-squared:  -0.001188
## F-statistic: 0.9205 on 3 and 198 DF,  p-value: 0.4319
```

Figure 5.

```
#scatterplot of standardized mean difference across flux range colored by study fit with lm
ggplot(normalized, aes(x=flux_range, y=yi, color = study_id))+
  geom_point()+
  geom_smooth(method="lm", formula = y~x)+
  theme_minimal()+
  ggtitle("SMD across fluctuation ranges colored by
          studies and fit with linear model by study")
```




```
#random effects model including org_level as a random variable
fig9 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range + study_id,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig9
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  0.3737  0.6113     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 185) = 5046.4092, p-val < .0001
##
## Test of Moderators (coefficients 2:17):
## QM(df = 16) = 43.9663, p-val = 0.0002
##
## Model Results:
##
##                              estimate      se     zval    pval    ci.lb
## intrcpt                        0.3911  0.6199   0.6309  0.5281  -0.8239
## flux_range                    -0.0459  0.0109  -4.2133  <.0001  -0.0673
```

```
## study_iddu2009                 0.3311  0.7530   0.4397  0.6602  -1.1447
## study_idgarcaruiz2011         -1.0411  0.8682  -1.1992  0.2305  -2.7427
## study_idglass2019              0.0331  0.8670   0.0382  0.9696  -1.6662
## study_idkern_2015phys          0.5094  0.8664   0.5880  0.5566  -1.1887
## study_idkern_2015plasticity   -0.7299  0.9276  -0.7868  0.4314  -2.5480
## study_idkern2014               0.9448  0.8742   1.0807  0.2798  -0.7687
## study_idlowenborg2012         -0.9177  0.7640  -1.2013  0.2296  -2.4151
## study_idmaneti2014             1.0227  0.8749   1.1689  0.2424  -0.6921
## study_idpendlebury2004         0.2829  0.8761   0.3229  0.7467  -1.4342
## study_idqu2014                 0.2923  0.8688   0.3365  0.7365  -1.4104
## study_idrolandi2018            0.3188  0.7535   0.4231  0.6722  -1.1579
## study_idsaxon2017              0.5722  0.7082   0.8079  0.4192  -0.8160
## study_idsemenov2007            1.3393  0.7816   1.7134  0.0866  -0.1927
## study_idsimonici2019           0.3429  0.8713   0.3936  0.6939  -1.3648
## study_idtriedel 2015          -1.2394  0.8775  -1.4124  0.1578  -2.9594
##                                ci.ub
## intrcpt                       1.6060
## flux_range                   -0.0246  ***
## study_iddu2009                1.8068
## study_idgarcaruiz2011         0.6605
## study_idglass2019             1.7323
## study_idkern_2015phys         2.2075
## study_idkern_2015plasticity   1.0883
## study_idkern2014              2.6583
## study_idlowenborg2012         0.5796
## study_idmaneti2014            2.7375
## study_idpendlebury2004        2.0000
## study_idqu2014                1.9950
## study_idrolandi2018           1.7956
## study_idsaxon2017             1.9603
## study_idsemenov2007           2.8712    .
## study_idsimonici2019          2.0506
## study_idtriedel 2015          0.4805
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

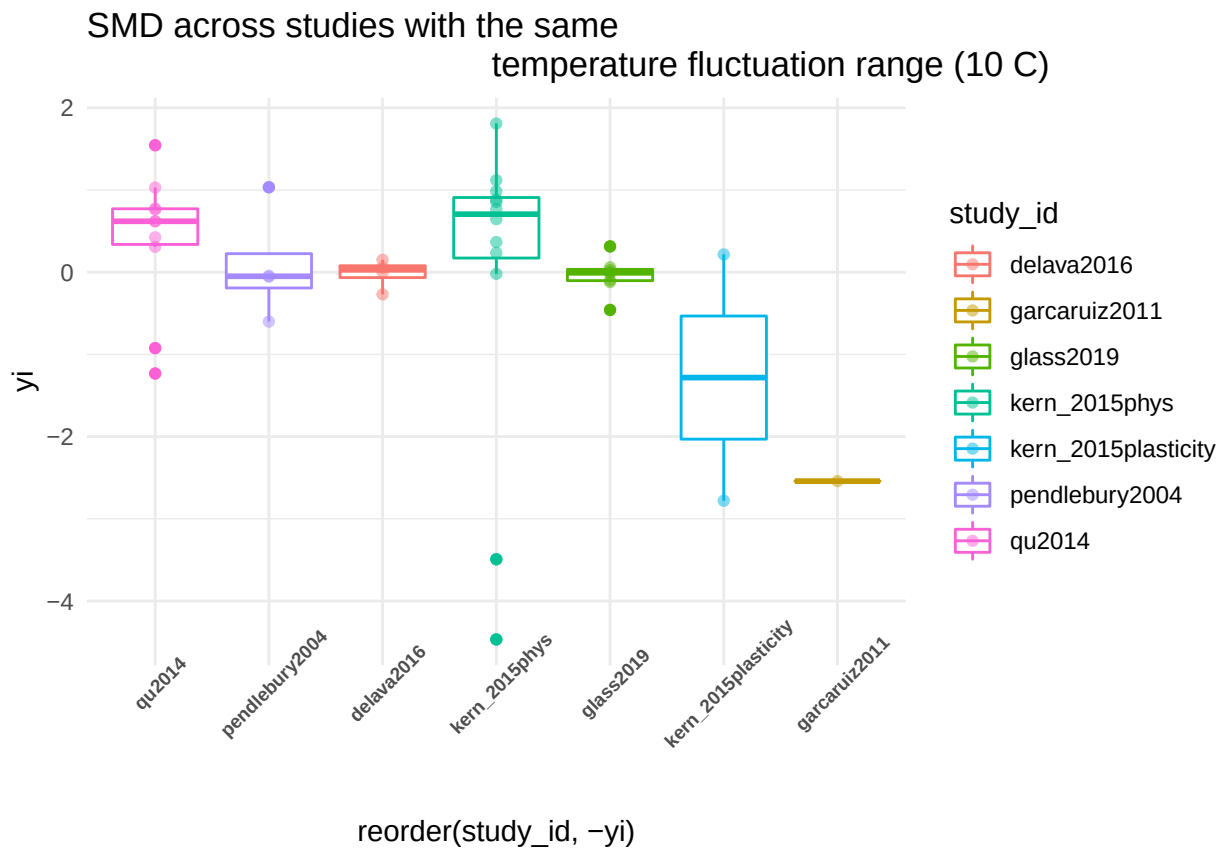
```
#simple linear model looking at how flux_range and study_id affect yi
simple9<-lm(yi~flux_range*study_id, data =dat_MA_ES)
summary(simple9)
```

```
##
## Call:
## lm(formula = yi ~ flux_range * study_id, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -62.646  -0.318   0.036   0.541  22.869
##
## Coefficients: (10 not defined because of singularities)
##                                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)                         0.091100  11.511151   0.008   0.9937
## flux_range                         -0.010684   1.333646  -0.008   0.9936
## study_iddu2009                      0.575435  11.937810   0.048   0.9616
```

```
## study_idgarcaruiz2011                  22.254823  13.975852   1.592   0.1131
## study_idglass2019                      -0.020693   3.464914  -0.006   0.9952
## study_idkern_2015phys                  -0.010713   3.266753  -0.003   0.9974
## study_idkern_2015plasticity            -1.266498   4.900129  -0.258   0.7963
## study_idkern2014                        0.747017   8.591415   0.087   0.9308
## study_idlowenborg2012                  -0.955077   5.673877  -0.168   0.8665
## study_idmaneti2014                     -0.530046   9.045229  -0.059   0.9533
## study_idpendlebury2004                  0.119910  13.134892   0.009   0.9927
## study_idqu2014                         -0.077323  12.638013  -0.006   0.9951
## study_idrolandi2018                     0.087188   8.943754   0.010   0.9922
## study_idsaxon2017                       0.543332   4.437542   0.122   0.9027
## study_idsemenov2007                     1.440235   7.693949   0.187   0.8517
## study_idsimonici2019                    1.535025  12.701186   0.121   0.9039
## study_idtriedel 2015                   -1.510015   5.579042  -0.271   0.7870
## flux_range:study_iddu2009              -0.035825   1.374691  -0.026   0.9792
## flux_range:study_idgarcaruiz2011       -3.266636   1.508620  -2.165   0.0317 *
## flux_range:study_idglass2019                 NA         NA      NA       NA
## flux_range:study_idkern_2015phys             NA         NA      NA       NA
## flux_range:study_idkern_2015plasticity       NA         NA      NA       NA
## flux_range:study_idkern2014                  NA         NA      NA       NA
## flux_range:study_idlowenborg2012             NA         NA      NA       NA
## flux_range:study_idmaneti2014                NA         NA      NA       NA
## flux_range:study_idpendlebury2004      -0.002104   1.392368  -0.002   0.9988
## flux_range:study_idqu2014               0.048564   1.476076   0.033   0.9738
## flux_range:study_idrolandi2018               NA         NA      NA       NA
## flux_range:study_idsaxon2017                 NA         NA      NA       NA
## flux_range:study_idsemenov2007               NA         NA      NA       NA
## flux_range:study_idsimonici2019        -0.264625   2.044441  -0.129   0.8972
## flux_range:study_idtriedel 2015              NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.658 on 180 degrees of freedom
## Multiple R-squared:  0.273,  Adjusted R-squared:  0.1882
## F-statistic: 3.219 on 21 and 180 DF,  p-value: 1.148e-05
```

Figure 6.

```
#looking at yi across studies with the same temperature range (10 C)
ggplot(common_range, aes(y=yi, x=reorder(study_id, -yi), color = study_id))+
  geom_boxplot()+
  geom_point(alpha = 0.5)+
  theme_minimal()+
  theme(axis.text.x = element_text(face = "bold",
                                   size = 7, angle = 45))+
                                   ggtitle("SMD across studies with the same
                                           temperature fluctuation range (10 C)")
```




```
#random effects model within subset data
fig12 <- rma.mv(yi, vi, data=common_range,
                random = ~1 | experiment_id/ study_id,
                  method="REML")
```

```
## Warning in rma.mv(yi, vi, data = common_range, random = ~1 | experiment_id/
## study_id, : Single-level factor(s) found in 'random' argument. Corresponding
## 'sigma2' value(s) fixed to 0.
```

```
fig12
```

```
##
## Multivariate Meta-Analysis Model (k = 41; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                 factor
## sigma^2.1  0.0000  0.0000      1    yes          experiment_id
## sigma^2.2  1.0453  1.0224      7     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 40) = 1793.3191, p-val < .0001
##
## Model Results:
##
```

```
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.3405  0.3914  -0.8699  0.3843  -1.1078  0.4267
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

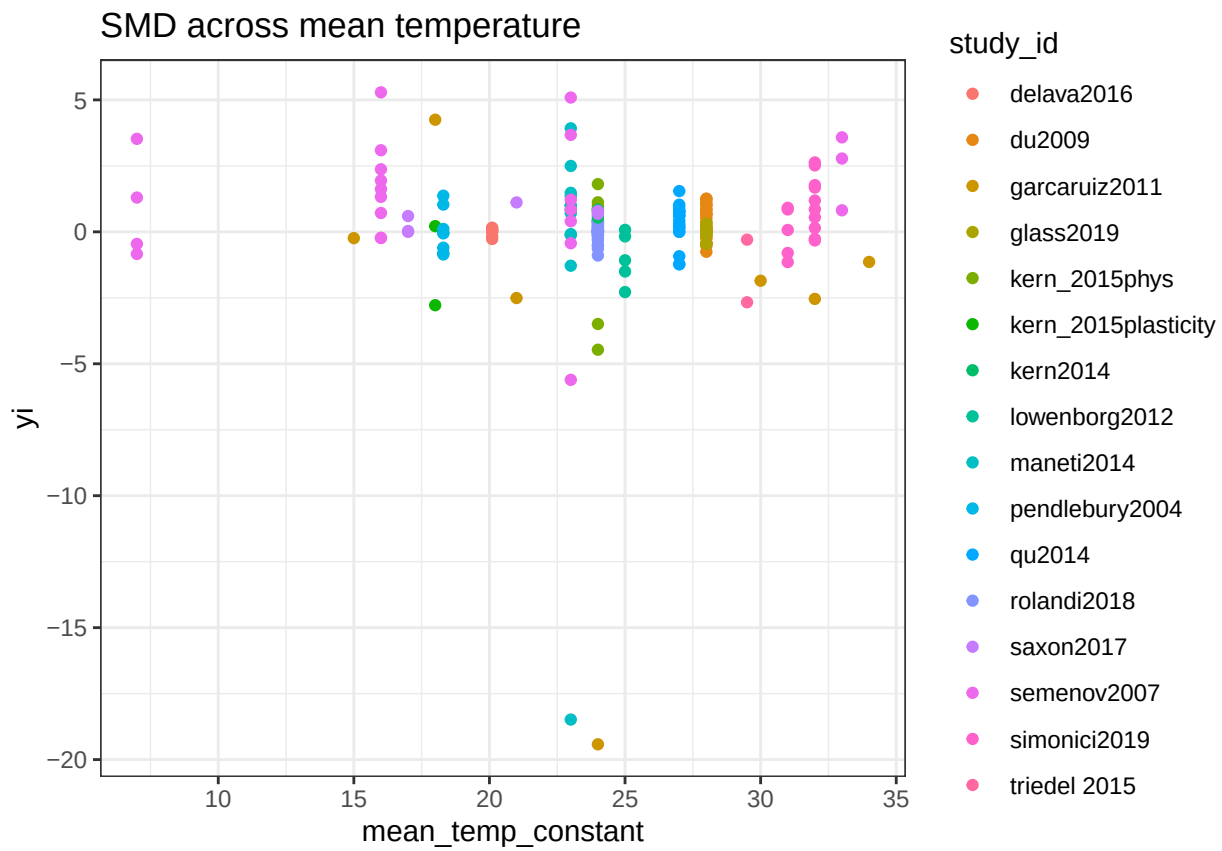
```
#simple linear model looking at how flux_range affects yi within subset data
simple12<-lm(yi~flux_range, data =common_range)
summary(simple12)
```

```
##
## Call:
## lm(formula = yi ~ flux_range, data = common_range)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.4306 -0.0600  0.1875  0.7992  1.8452
##
## Coefficients: (1 not defined because of singularities)
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.03707    0.19822  -0.187    0.853
## flux_range        NA         NA      NA       NA
##
## Residual standard error: 1.269 on 40 degrees of freedom
```

Question how does mean temperature affect response variables?

Figure 7.

```
# scatterplot of how mean temperature influences SMD
ggplot(normalized, aes(x=mean_temp_constant, y=yi, color = study_id))+
  geom_point()+
  theme_bw()+
  ggtitle("SMD across mean temperature")
```




```
#random effects model including org_level as a random variable
fig6 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~mean_temp_constant,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig6
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                 factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  0.5761  0.7590     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 6375.5756, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 115.3401, p-val < .0001
##
## Model Results:
##
##                    estimate      se      zval    pval    ci.lb    ci.ub
## intrcpt              2.1506  0.2511    8.5655  <.0001   1.6585   2.6426  ***
## mean_temp_constant  -0.0858  0.0080  -10.7397  <.0001  -0.1014  -0.0701  ***
```

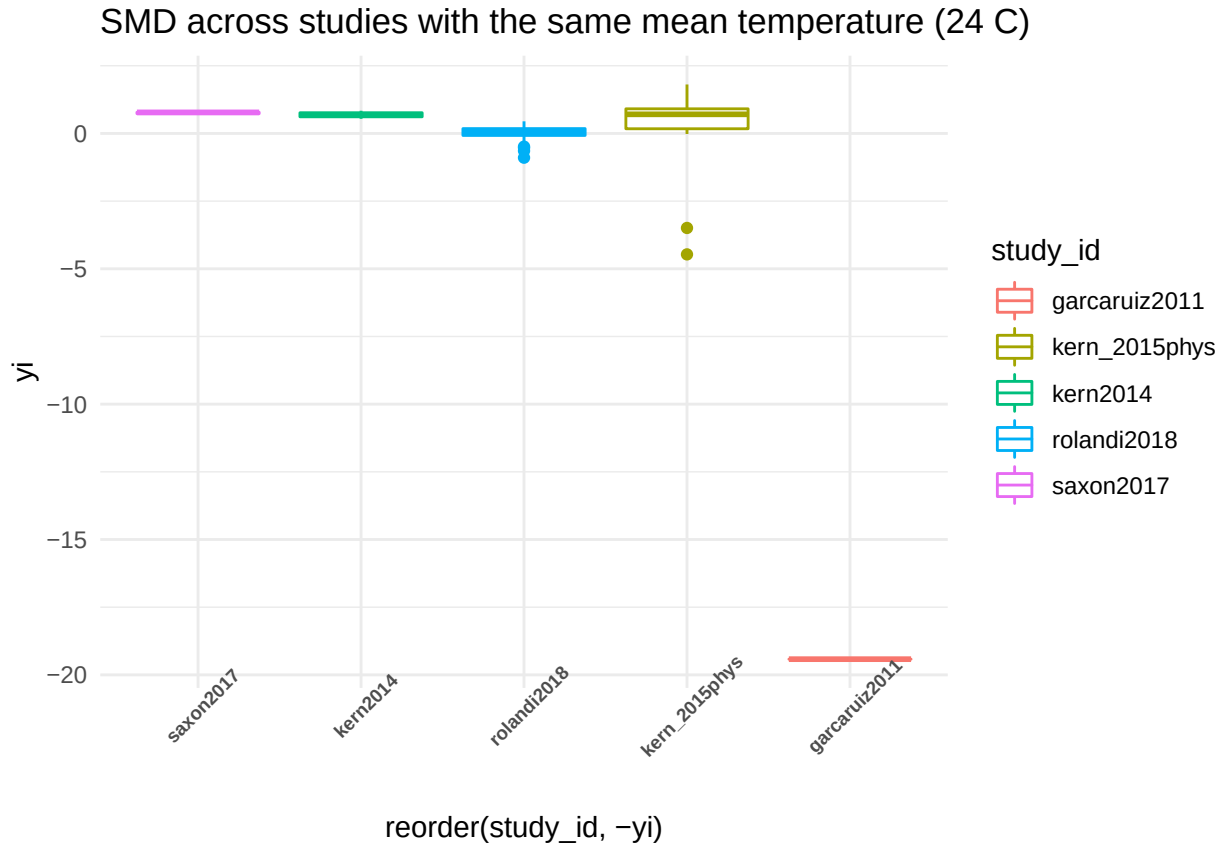
```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how mean_temp_constant affects yi
simple6<-lm(yi~mean_temp_constant, data =dat_MA_ES)
summary(simple6)
```

```
##
## Call:
## lm(formula = yi ~ mean_temp_constant, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -82.457   0.076   0.507   1.148   5.303
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          1.13630    2.31046   0.492    0.623
## mean_temp_constant -0.05869    0.09229  -0.636    0.526
##
## Residual standard error: 6.289 on 200 degrees of freedom
## Multiple R-squared:  0.002018,   Adjusted R-squared:  -0.002972
## F-statistic: 0.4044 on 1 and 200 DF,  p-value: 0.5256
```

Figure 8.

```
#looking at yi across studies with the same mean temperature (24 C)
ggplot(common_temp, aes(y=yi, x=reorder(study_id, -yi), color = study_id))+
  geom_boxplot()+
  theme_minimal()+
  theme(axis.text.x = element_text(face = "bold",
                                   size = 7, angle = 45))+
  ggtitle("SMD across studies with the same mean temperature (24 C)")
```




```
#random effects model within subset data
fig13 <- rma.mv(yi, vi, data=common_temp,
                random = ~1 | experiment_id/ study_id,
                  method="REML")
fig13
```

```
##
## Multivariate Meta-Analysis Model (k = 56; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                  factor
## sigma^2.1   0.0000  0.0052      2     no           experiment_id
## sigma^2.2  64.5106  8.0318      6     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 55) = 3403.3975, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -2.8890  3.2818  -0.8803  0.3787  -9.3211  3.5431
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

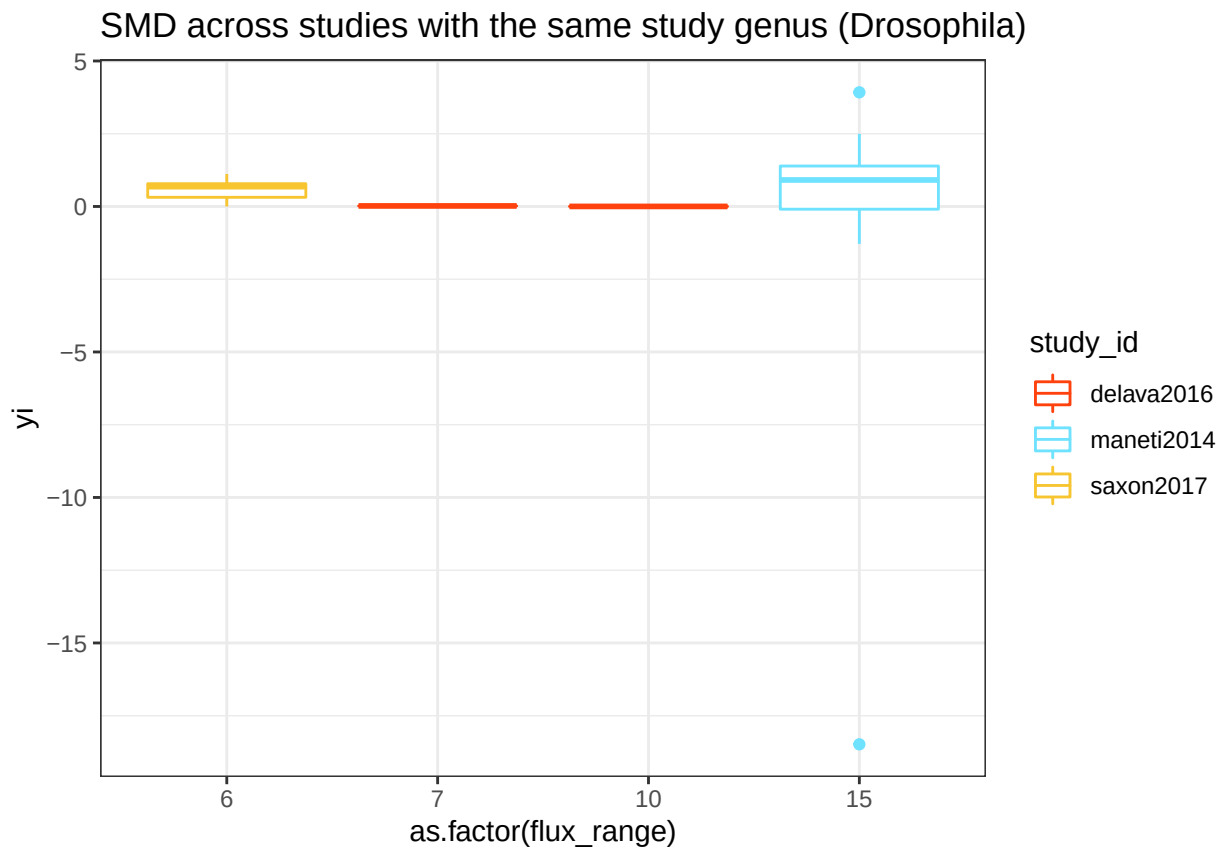
```r
#simple linear model looking at how flux_range affects yi within subset data
simple13<-lm(yi~mean_temp_constant, data =common_temp)
summary(simple13)
```

```
##
## Call:
## lm(formula = yi ~ mean_temp_constant, data = common_temp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.1451   0.2517   0.3356   0.7096   2.0837
##
## Coefficients: (1 not defined because of singularities)
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -0.2755     0.3690  -0.747    0.458
## mean_temp_constant       NA         NA      NA       NA
##
## Residual standard error: 2.761 on 55 degrees of freedom
```

Question: How does genus affect response?

Figure 9.

```r
#trying to look at drosophila response across studies
ggplot(drosophila, aes(y=yi, x=as.factor(flux_range), color = study_id))+
  geom_boxplot()+
  scale_color_tron()+
  theme_bw()+
  ggtitle("SMD across studies with the same study genus (Drosophila)")
```




```
#random effects model including org_level as a random variable
fig10 <- rma.mv(yi, vi, data=drosophila, mods = ~flux_range + study_id,
                random = ~1 | experiment_id/ study_id,
                  method="REML")
fig10
```

```
##
## Multivariate Meta-Analysis Model (k = 21; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                 factor
## sigma^2.1  0.1034  0.3216      3     no           experiment_id
## sigma^2.2  0.1034  0.3216      5     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 17) = 798.4274, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 3.2667, p-val = 0.3523
##
## Model Results:
##
##                    estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt              0.0259  0.6614   0.0392  0.9687  -1.2704  1.3223
## flux_range          -0.0055  0.0596  -0.0922  0.9265  -0.1224  0.1114
```

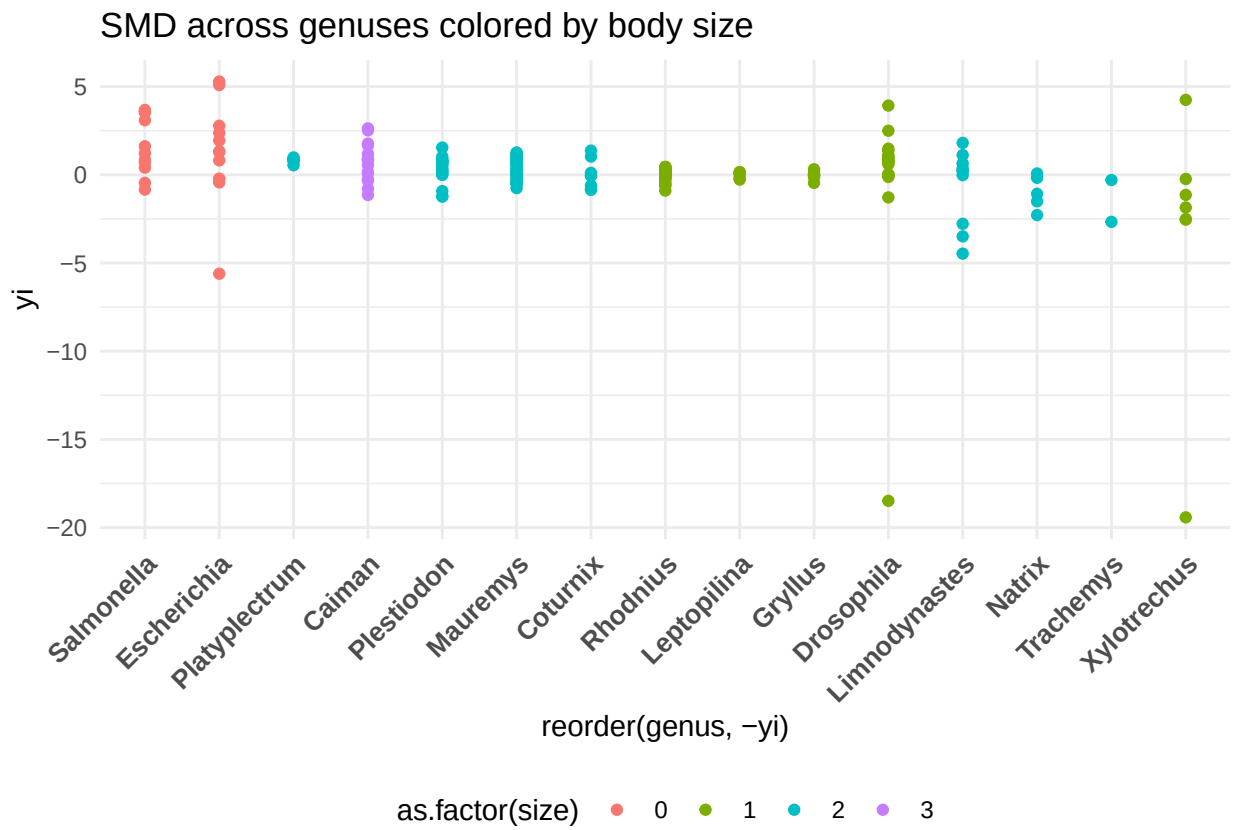
```
## study_idmaneti2014    0.7499  0.6134   1.2226  0.2215  -0.4523  1.9521
## study_idsaxon2017     0.6933  0.4505   1.5389  0.1238  -0.1897  1.5763
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how flux_range and study_id affect yi in drosphila specific studies
simple10<-lm(yi~flux_range + study_id, data =drosophila)
summary(simple10)
```

```
##
## Call:
## lm(formula = yi ~ flux_range + study_id, data = drosophila)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.8832   0.0000   0.4773   1.5850   4.5217
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.057126  18.951260   0.003    0.998
## flux_range         -0.005498   2.195634  -0.003    0.998
## study_idmaneti2014 -0.573860  14.708290  -0.039    0.969
## study_idsaxon2017   0.546191   6.638973   0.082    0.935
##
## Residual standard error: 4.658 on 17 degrees of freedom
## Multiple R-squared:  0.01628,    Adjusted R-squared:  -0.1573
## F-statistic: 0.09381 on 3 and 17 DF,  p-value: 0.9624
```

Figure 10.

```
#boxplots of SMD across different genuses colored by body size
ggplot(normalized, aes(y=yi, x= reorder(genus, -yi), color = as.factor(size)))+
  geom_point()+
  theme_minimal()+
  ggtitle("SMD across genuses colored by body size")+
  theme(axis.text.x = element_text(face = "bold",
                                   size = 10, angle = 45,hjust = 1),
        legend.position = "bottom")
```




```
#random effects model including genus as a random variable
fig11 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~size,
                random = ~1 | experiment_id/ study_id,
                  method="REML")
fig11
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  0.5536  0.7441     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 6384.8965, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 2.1661, p-val = 0.1411
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt    0.6043  0.3699   1.6337  0.1023  -0.1207  1.3293
## size      -0.3348  0.2275  -1.4718  0.1411  -0.7807  0.1111
```

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

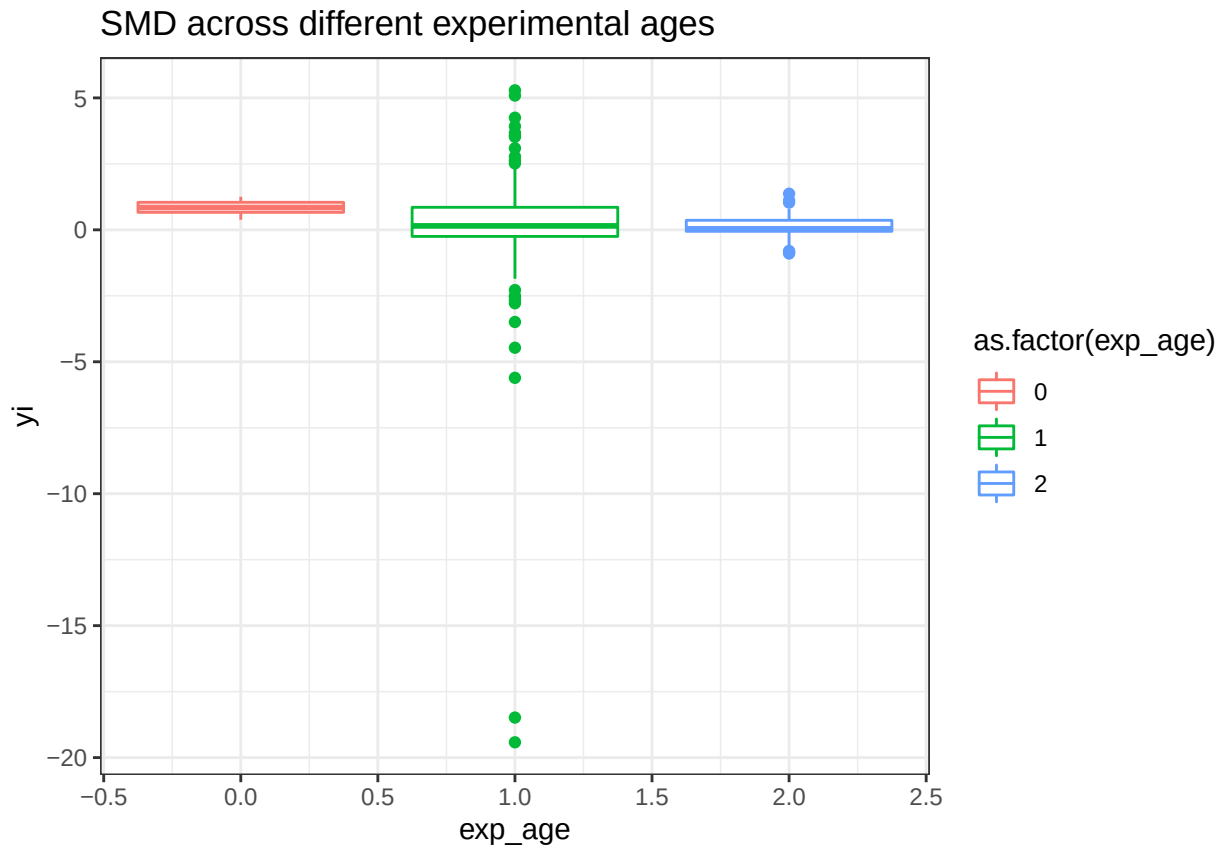
```
#simple linear model looking at how genus affects yi
simple11<-lm(yi~genus, data =dat_MA_ES)
summary(simple11)
```

```
##
## Call:
## lm(formula = yi ~ genus, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -69.610  -0.275   0.060   0.612  17.544
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)           0.7084     1.5173   0.467    0.641
## genusCoturnix        -0.6892     2.5727  -0.268    0.789
## genusDrosophila      -0.8597     1.9866  -0.433    0.666
## genusEscherichia      0.4926     2.2759   0.216    0.829
## genusGryllus         -0.7449     2.5727  -0.290    0.772
## genusLeptopilina     -0.7115     2.8386  -0.251    0.802
## genusLimnodynastes   -1.3455     2.3990  -0.561    0.576
## genusMauremys        -0.4605     1.8388  -0.250    0.803
## genusNatrix          -1.7006     3.0345  -0.560    0.576
## genusPlatyplectrum    0.1025     2.8386   0.036    0.971
## genusPlestiodon      -0.3916     2.0072  -0.195    0.846
## genusRhodnius        -0.6904     1.7919  -0.385    0.700
## genusSalmonella       0.8706     2.3327   0.373    0.709
## genusTrachemys       -2.1914     4.4236  -0.495    0.621
## genusXylotrechus    -14.0034     2.5727  -5.443 1.63e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.876 on 187 degrees of freedom
## Multiple R-squared:  0.1854, Adjusted R-squared:  0.1244
## F-statistic: 3.039 on 14 and 187 DF,  p-value: 0.0003013
```

Question how does scale (life or org level) affect response?

Figure 11.

```
#boxplot
ggplot(normalized, aes(x=exp_age, y=yi, color = as.factor(exp_age)))+
  geom_boxplot()+
  theme_bw()+
  ggtitle("SMD across different experimental ages")
```




```
#random effects model including exp_age as a random variable
fig3 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~exp_age,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig3
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0003      3     no           experiment_id
## sigma^2.2  0.6027  0.7763     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 6391.6365, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.1280, p-val = 0.7206
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb   ci.ub
## intrcpt   -0.0283  0.4325  -0.0653  0.9479  -0.8760  0.8195
## exp_age    0.1155  0.3229   0.3577  0.7206  -0.5173  0.7483
```

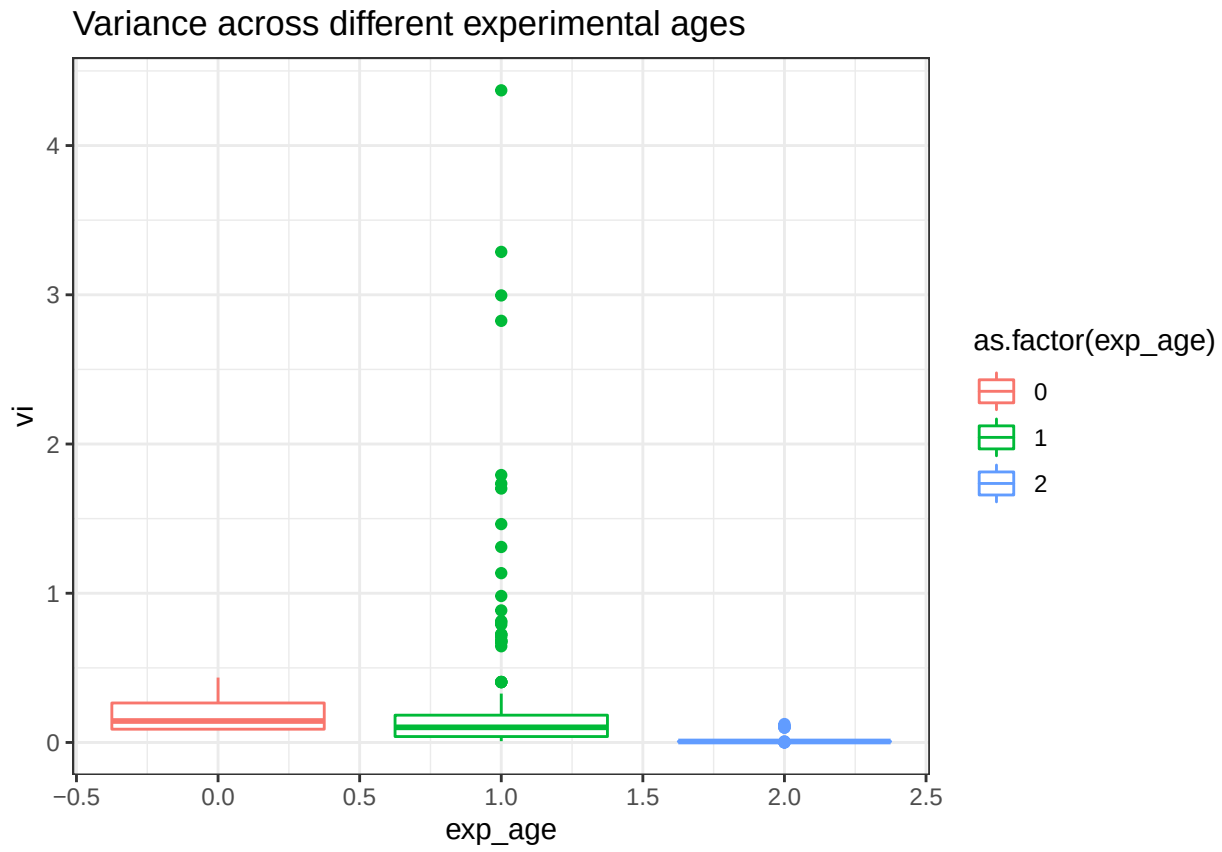
```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how exp_age affects yi
simple3<-lm(yi~exp_age, data =dat_MA_ES)
summary(simple3)
```

```
##
## Call:
## lm(formula = yi ~ exp_age, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -82.574   0.109   0.406   1.140   5.618
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.4559     1.0991  -0.415    0.679
## exp_age       0.1248     0.8362   0.149    0.881
##
## Residual standard error: 6.295 on 200 degrees of freedom
## Multiple R-squared:  0.0001114,  Adjusted R-squared:  -0.004888
## F-statistic: 0.02228 on 1 and 200 DF,  p-value: 0.8815
```

Figure 12.

```
ggplot(normalized, aes(x=exp_age, y=vi, color = as.factor(exp_age)))+
  geom_boxplot()+
  theme_bw()+
  ggtitle("Variance across different experimental ages")
```




```
count(normalized, exp_age)
```

```
##   exp_age   n
## 1       0  12
## 2       1 136
## 3       2  53
```

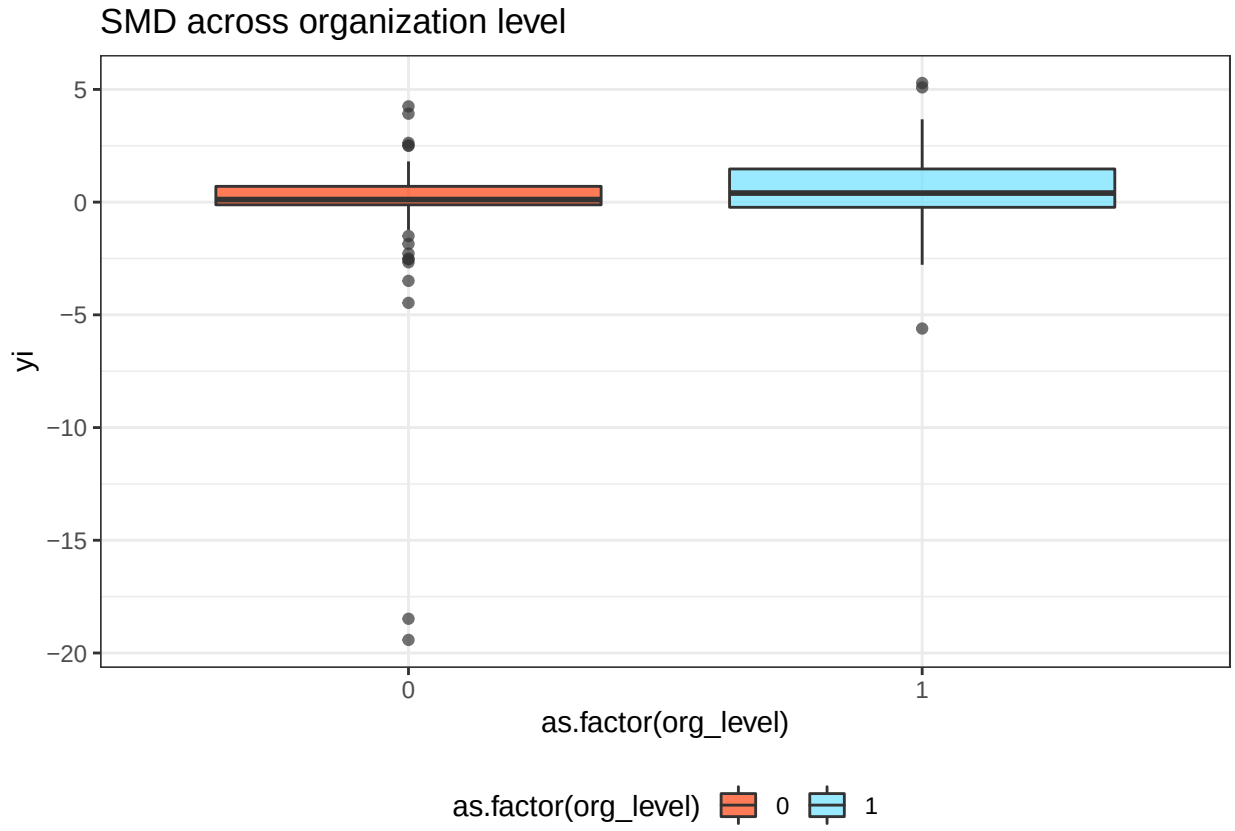
```
#simple linear model looking at how exp_age affects vi
simple4<-lm(vi~ exp_age, data =dat_MA_ES)
summary(simple4)
```

```
##
## Call:
## lm(formula = vi ~ exp_age, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5074 -0.2694 -0.2289 -0.1032 12.7336
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5936     0.1838   3.229  0.00145 **
## exp_age      -0.2418     0.1398  -1.729  0.08536 .
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
##
## Residual standard error: 1.053 on 200 degrees of freedom
## Multiple R-squared:  0.01473,    Adjusted R-squared:  0.0098
## F-statistic: 2.989 on 1 and 200 DF,  p-value: 0.08536
```

Figure 13.

```
#boxplot of SMD across levels of organization
ggplot(normalized, aes(x=as.factor(org_level), y=yi, fill=as.factor(org_level)))+
  geom_boxplot(alpha =0.7)+
  scale_fill_tron()+
  theme_bw()+
  theme(legend.position = "bottom")+
  ggtitle("SMD across organization level")
```




```
#random effects model including org_level as a random variable
fig5 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~org_level,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig5
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
```

```
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0003      3     no           experiment_id
## sigma^2.2  0.6417  0.8011     22     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 6387.9383, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 23.9377, p-val < .0001
##
## Model Results:
##
##            estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt      0.1890  0.1741   1.0856  0.2777  -0.1522   0.5302
## org_level   -0.4008  0.0819  -4.8926  <.0001  -0.5614  -0.2403  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#simple linear model looking at how org_level affects yi
simple5<-lm(yi~org_level, data =dat_MA_ES)
summary(simple5)
```

```
##
## Call:
## lm(formula = yi ~ org_level, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -82.345   0.103   0.607   1.223   4.809
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.5598     0.4914  -1.139    0.256
## org_level     1.3158     1.1184   1.177    0.241
##
## Residual standard error: 6.274 on 200 degrees of freedom
## Multiple R-squared:  0.006874,   Adjusted R-squared:  0.001908
## F-statistic: 1.384 on 1 and 200 DF,  p-value: 0.2408
```

Question: How does response variable affect response?

Figure 14.

```
#full random effects model looking at all the responses in the entire dataset
response_variable_mod <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~resp_def,
               random = ~1 | experiment_id/ study_id/ response_id,
                 method="REML")
response_variable_mod
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0000  0.0006      3     no                       experiment_id
## sigma^2.2  0.7207  0.8489     22     no                 experiment_id/study_id
## sigma^2.3  0.0366  0.1913     57     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 156) = 4319.5235, p-val < .0001
##
## Test of Moderators (coefficients 2:46):
## QM(df = 45) = 225.7261, p-val < .0001
##
## Model Results:
##
##                                                          estimate      se
## intrcpt                                                    0.3899  0.5166
## resp_defaquatic speed                                     -1.4687  1.0533
## resp_defaverage cumulative number of eggs laid per female -0.2757  1.0122
## resp_defaverage number of eggs laid per female            -0.4628  1.0122
## resp_defbody (centroid) size                              -0.0128  0.8984
## resp_defbody length                                       -0.1800  0.3808
## resp_defbody mass                                          0.0850  0.3733
## resp_defcarapace height                                    0.1119  0.5218
## resp_defcarapace width                                     0.1797  0.5223
## resp_defdaily energy expenditure                          -0.9579  1.0249
## resp_defdays to first slough                              -2.6718  1.0709
## resp_defdessication tolerance                             -0.7060  0.8906
## resp_defdevelopment time                                  -0.2640  0.7713
## resp_defdevelopment to stages 35-37                       -1.4180  0.4312
## resp_defdevelopmental time                                 0.0554  0.8396
## resp_defdistance covered                                  -0.5621  1.0483
## resp_defegg mass                                           0.1754  1.0253
## resp_defegg to adult viability                            -2.4873  0.8883
## resp_deffore-limb length                                   0.8910  0.4270
## resp_defhatching success                                   0.0392  1.0276
## resp_defhead length                                        0.2518  0.4203
## resp_defhead width                                         0.5433  0.4210
## resp_defhind-limb length                                   0.3872  0.4194
## resp_defincubation period                                 -0.0271  1.0266
## resp_defincubation time                                   -1.8923  1.0581
## resp_definfestation rate                                  -0.3500  0.7712
## resp_defmass                                               1.0584  1.0323
## resp_defmaximal length                                    -1.4584  0.4277
## resp_defoffspring per mating                               0.0835  0.7296
## resp_defovary mass, dry                                   -0.4085  1.0140
## resp_defoxidative damage                                  -0.6869  1.0270
## resp_defpercent females                                   -0.1973  1.0265
## resp_defproductivity                                      -0.9955  0.8882
## resp_defrate of change                                     1.1321  1.0681
## resp_defsnout-vent length                                  0.6062  0.4218
```

```
## resp_defsprint speed                                          -0.6694  0.4196
## resp_defstartvation tolerance                                 -1.4144  0.8873
## resp_defsuccess of parasitism                                 -0.6387  0.7713
## resp_defsurvival                                              -0.4057  0.7342
## resp_defTAC                                                   -3.0590  1.0399
## resp_deftail length                                            0.1884  0.3749
## resp_defterrestrial speed                                     -0.3156  1.0482
## resp_deftestes mass, dry                                      -0.4427  1.0141
## resp_deftotal length                                           0.3417  1.0302
## resp_deftotal offspring                                        0.1470  0.7297
## resp_defwing centroid                                          0.4437  0.7212
##                                                                 zval    pval
## intrcpt                                                       0.7548  0.4504
## resp_defaquatic speed                                        -1.3944  0.1632
## resp_defaverage cumulative number of eggs laid per female    -0.2723  0.7854
## resp_defaverage number of eggs laid per female               -0.4573  0.6475
## resp_defbody (centroid) size                                 -0.0142  0.9886
## resp_defbody length                                          -0.4727  0.6365
## resp_defbody mass                                             0.2278  0.8198
## resp_defcarapace height                                       0.2145  0.8302
## resp_defcarapace width                                        0.3440  0.7308
## resp_defdaily energy expenditure                             -0.9346  0.3500
## resp_defdays to first slough                                 -2.4950  0.0126
## resp_defdessication tolerance                                -0.7928  0.4279
## resp_defdevelopment time                                     -0.3423  0.7322
## resp_defdevelopment to stages 35-37                          -3.2889  0.0010
## resp_defdevelopmental time                                    0.0660  0.9474
## resp_defdistance covered                                     -0.5362  0.5918
## resp_defegg mass                                              0.1711  0.8641
## resp_defegg to adult viability                               -2.7999  0.0051
## resp_deffore-limb length                                      2.0868  0.0369
## resp_defhatching success                                      0.0382  0.9696
## resp_defhead length                                           0.5992  0.5490
## resp_defhead width                                            1.2905  0.1969
## resp_defhind-limb length                                      0.9232  0.3559
## resp_defincubation period                                    -0.0264  0.9790
## resp_defincubation time                                      -1.7885  0.0737
## resp_definfestation rate                                     -0.4538  0.6500
## resp_defmass                                                  1.0253  0.3052
## resp_defmaximal length                                       -3.4097  0.0007
## resp_defoffspring per mating                                  0.1145  0.9088
## resp_defovary mass, dry                                      -0.4029  0.6870
## resp_defoxidative damage                                     -0.6688  0.5036
## resp_defpercent females                                      -0.1922  0.8476
## resp_defproductivity                                         -1.1208  0.2624
## resp_defrate of change                                        1.0599  0.2892
## resp_defsnout-vent length                                     1.4371  0.1507
## resp_defsprint speed                                         -1.5953  0.1106
## resp_defstartvation tolerance                                -1.5940  0.1109
## resp_defsuccess of parasitism                                -0.8281  0.4076
## resp_defsurvival                                             -0.5525  0.5806
## resp_defTAC                                                  -2.9415  0.0033
## resp_deftail length                                           0.5026  0.6153
## resp_defterrestrial speed                                    -0.3011  0.7633
```

```
## resp_deftestes mass, dry                                        -0.4365  0.6625
## resp_deftotal length                                             0.3317  0.7401
## resp_deftotal offspring                                          0.2015  0.8403
## resp_defwing centroid                                            0.6152  0.5384
##                                                                    ci.lb   ci.ub
## intrcpt                                                         -0.6226  1.4025
## resp_defaquatic speed                                           -3.5331  0.5957
## resp_defaverage cumulative number of eggs laid per female       -2.2595  1.7082
## resp_defaverage number of eggs laid per female                  -2.4466  1.5210
## resp_defbody (centroid) size                                    -1.7737  1.7481
## resp_defbody length                                             -0.9263  0.5663
## resp_defbody mass                                               -0.6465  0.8166
## resp_defcarapace height                                         -0.9108  1.1346
## resp_defcarapace width                                          -0.8441  1.2035
## resp_defdaily energy expenditure                                -2.9667  1.0509
## resp_defdays to first slough                                    -4.7708 -0.5729
## resp_defdessication tolerance                                   -2.4515  1.0394
## resp_defdevelopment time                                        -1.7756  1.2477
## resp_defdevelopment to stages 35-37                             -2.2631 -0.5730
## resp_defdevelopmental time                                      -1.5901  1.7010
## resp_defdistance covered                                        -2.6167  1.4925
## resp_defegg mass                                                -1.8341  2.1850
## resp_defegg to adult viability                                  -4.2284 -0.7462
## resp_deffore-limb length                                         0.0541  1.7279
## resp_defhatching success                                        -1.9748  2.0533
## resp_defhead length                                             -0.5719  1.0756
## resp_defhead width                                              -0.2819  1.3686
## resp_defhind-limb length                                        -0.4349  1.2092
## resp_defincubation period                                       -2.0392  1.9851
## resp_defincubation time                                         -3.9661  0.1815
## resp_definfestation rate                                        -1.8616  1.1616
## resp_defmass                                                    -0.9649  3.0818
## resp_defmaximal length                                          -2.2967 -0.6201
## resp_defoffspring per mating                                    -1.3465  1.5136
## resp_defovary mass, dry                                         -2.3959  1.5788
## resp_defoxidative damage                                        -2.6999  1.3261
## resp_defpercent females                                         -2.2092  1.8147
## resp_defproductivity                                            -2.7364  0.7454
## resp_defrate of change                                          -0.9614  3.2255
## resp_defsnout-vent length                                       -0.2205  1.4330
## resp_defsprint speed                                            -1.4918  0.1530
## resp_defstartvation tolerance                                   -3.1535  0.3247
## resp_defsuccess of parasitism                                   -2.1504  0.8730
## resp_defsurvival                                                -1.8447  1.0333
## resp_defTAC                                                     -5.0973 -1.0208
## resp_deftail length                                             -0.5464  0.9233
## resp_defterrestrial speed                                       -2.3700  1.7388
## resp_deftestes mass, dry                                        -2.4302  1.5448
## resp_deftotal length                                            -1.6774  2.3608
## resp_deftotal offspring                                         -1.2831  1.5771
## resp_defwing centroid                                           -0.9698  1.8572
##
## intrcpt
## resp_defaquatic speed
```

```
## resp_defaverage cumulative number of eggs laid per female
## resp_defaverage number of eggs laid per female
## resp_defbody (centroid) size
## resp_defbody length
## resp_defbody mass
## resp_defcarapace height
## resp_defcarapace width
## resp_defdaily energy expenditure
## resp_defdays to first slough                                  *
## resp_defdessication tolerance
## resp_defdevelopment time
## resp_defdevelopment to stages 35-37                          **
## resp_defdevelopmental time
## resp_defdistance covered
## resp_defegg mass
## resp_defegg to adult viability                               **
## resp_deffore-limb length                                      *
## resp_defhatching success
## resp_defhead length
## resp_defhead width
## resp_defhind-limb length
## resp_defincubation period
## resp_defincubation time                                       .
## resp_definfestation rate
## resp_defmass
## resp_defmaximal length                                      ***
## resp_defoffspring per mating
## resp_defovary mass, dry
## resp_defoxidative damage
## resp_defpercent females
## resp_defproductivity
## resp_defrate of change
## resp_defsnout-vent length
## resp_defsprint speed
## resp_defstartvation tolerance
## resp_defsuccess of parasitism
## resp_defsurvival
## resp_defTAC                                                  **
## resp_deftail length
## resp_defterrestrial speed
## resp_deftestes mass, dry
## resp_deftotal length
## resp_deftotal offspring
## resp_defwing centroid
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

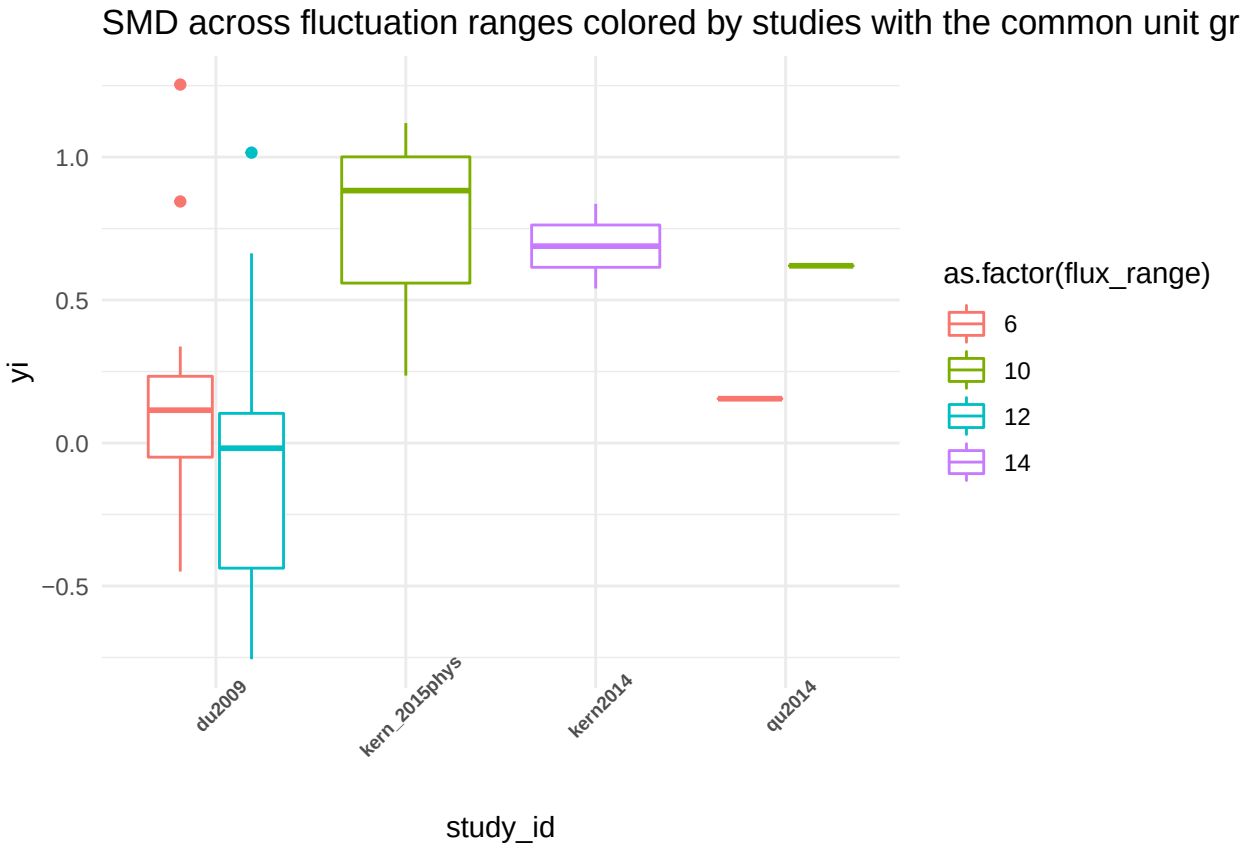
```
#full random effects model looking at all the response units in the entire dataset
response_units_mod <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~resp_units,
               random = ~1 | experiment_id/ study_id /response_id,
                 method="REML")
response_units_mod
```

```
##
## Multivariate Meta-Analysis Model (k = 202; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0000  0.0002      3     no                       experiment_id
## sigma^2.2  0.3046  0.5519     22     no                 experiment_id/study_id
## sigma^2.3  0.0792  0.2815     57     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 182) = 4638.5585, p-val < .0001
##
## Test of Moderators (coefficients 2:20):
## QM(df = 19) = 115.6956, p-val < .0001
##
## Model Results:
##
##                                        estimate      se     zval    pval
## intrcpt                                  1.5220  0.7075   2.1511  0.0315
## resp_unitsCFU * g dry weight manure^-1   -0.8243  0.9746  -0.8457  0.3977
## resp_unitscm                             -1.6458  0.8200  -2.0072  0.0447
## resp_unitsdays                           -2.0189  0.7423  -2.7198  0.0065
## resp_unitseggs laid                      -1.5013  0.8323  -1.8038  0.0713
## resp_unitsg                              -0.8991  0.7390  -1.2167  0.2237
## resp_unitskJ *day^-1 *kg^-1              -2.0473  0.8426  -2.4298  0.0151
## resp_unitsm                              -2.2524  0.7962  -2.8291  0.0047
## resp_unitsm * s^-1                       -2.0425  0.7880  -2.5920  0.0095
## resp_unitsmg                             -1.5573  0.9415  -1.6540  0.0981
## resp_unitsmm                             -0.7526  0.7436  -1.0121  0.3115
## resp_unitsnmol CHE / mgww                -1.8189  0.9566  -1.9014  0.0572
## resp_unitsoffspring per mating           -1.0710  0.8082  -1.3251  0.1851
## resp_unitsoffspring/female               -1.3423  0.8573  -1.5657  0.1174
## resp_unitspercent                        -2.2337  0.7478  -2.9869  0.0028
## resp_unitspixels                         -0.3595  0.8678  -0.4143  0.6787
## resp_unitstime to  death (hour)          -1.4145  0.8177  -1.7298  0.0837
## resp_unitstotal offspring                -1.0076  0.8083  -1.2466  0.2125
## resp_unitsuM Trolox Equivalents/ mgww    -4.1911  0.9705  -4.3186  <.0001
## resp_unitswing centroid                  -0.6888  0.7933  -0.8682  0.3853
##                                           ci.lb    ci.ub
## intrcpt                                  0.1352   2.9087    *
## resp_unitsCFU * g dry weight manure^-1  -2.7344   1.0859
## resp_unitscm                            -3.2530  -0.0387    *
## resp_unitsdays                          -3.4737  -0.5640   **
## resp_unitseggs laid                     -3.1326   0.1300    .
## resp_unitsg                             -2.3474   0.5493
## resp_unitskJ *day^-1 *kg^-1             -3.6988  -0.3959    *
## resp_unitsm                             -3.8129  -0.6920   **
## resp_unitsm * s^-1                      -3.5869  -0.4980   **
## resp_unitsmg                            -3.4027   0.2881    .
## resp_unitsmm                            -2.2100   0.7049
## resp_unitsnmol CHE / mgww               -3.6939   0.0560    .
## resp_unitsoffspring per mating          -2.6552   0.5131
## resp_unitsoffspring/female              -3.0225   0.3380
```

```
## resp_unitspercent                        -3.6994  -0.7680   **
## resp_unitspixels                         -2.0605   1.3414
## resp_unitstime to  death (hour)          -3.0171   0.1882    .
## resp_unitstotal offspring                -2.5917   0.5766
## resp_unitsuM Trolox Equivalents/ mgww    -6.0931  -2.2890  ***
## resp_unitswing centroid                  -2.2437   0.8661
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leftover/excluded plots

```
#plot across studies with common response variable body mass
ggplot(common_unit_g, aes(y=yi, color=as.factor(flux_range), x = study_id))+
  geom_boxplot()+
  theme_minimal()+
  theme(axis.text.x = element_text(face = "bold",
                                   size = 7, angle = 45))+
  ggtitle("SMD across fluctuation ranges colored by studies with the common unit grams")
```




```
#random effects model within subset data
fig14 <- rma.mv(yi, vi, data=common_unit_g,
                random = ~1 | experiment_id/ study_id,
```

```
                  method="REML")
fig14
#simple linear model looking at how flux_range affects yi within subset data
simple14<-lm(yi~study_id, data =common_unit_g)
summary(simple14)
```