data wrangling and plots

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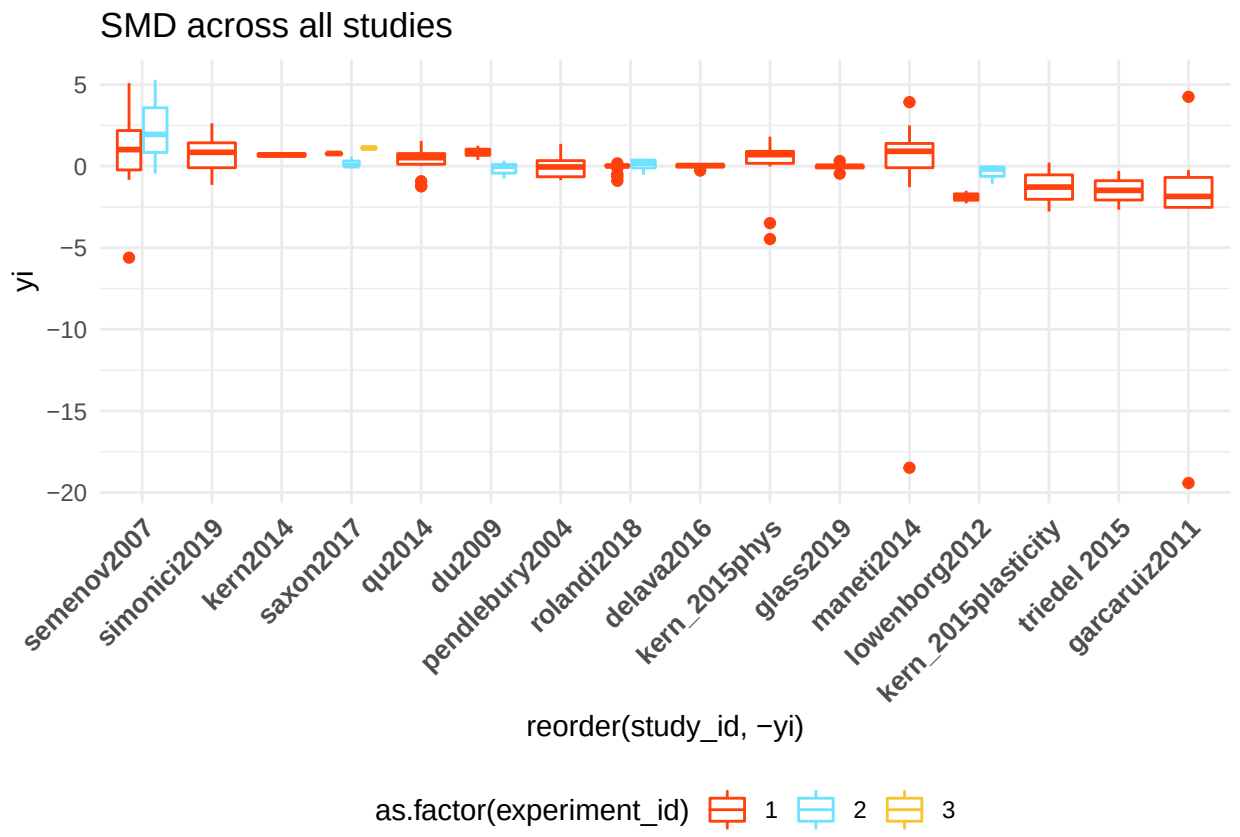
Plots

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 = 203; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                  factor
## sigma^2.1   0.0000  0.0015      3     no           experiment_id
## sigma^2.2  11.1645  3.3413     23     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 202) = 6886.4086, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.5649  0.6981  -0.8092  0.4184  -1.9331  0.8033
##
## ---
## 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
```

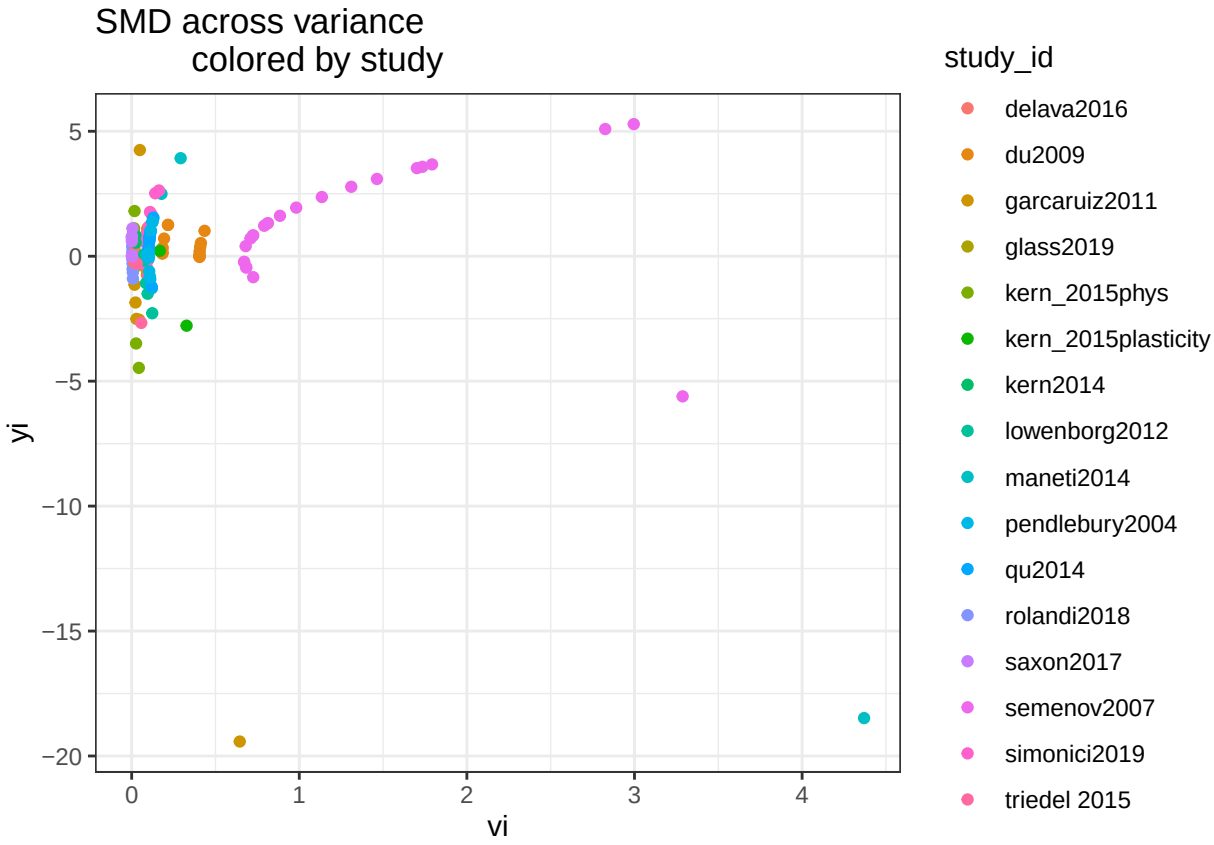
```
##
## Fixed-Effects with Moderators Model (k = 203)
##
## I^2 (residual heterogeneity / unaccounted variability): 96.33%
## H^2 (unaccounted variability / sampling variability):   27.22
##
## Test for Residual Heterogeneity:
## QE(df = 186) = 5063.4195, p-val < .0001
##
## Test of Moderators (coefficients 2:17):
## QM(df = 16) = 1822.9891, 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_idpiccau2017           -16.1904  0.7515  -21.5444  <.0001  -17.6633
## 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_idpiccau2017          -14.7175  ***
## 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
```

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

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
##     logLik    Deviance         AIC         BIC        AICc
## -2236.2768   4472.5536   4478.5536   4488.4784   4478.6748
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                 factor
## sigma^2.1   0.0000  0.0015      3     no           experiment_id
## sigma^2.2  11.1645  3.3413     23     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 202) = 6886.4086, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.5649  0.6981  -0.8092  0.4184  -1.9331  0.8033
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 2.

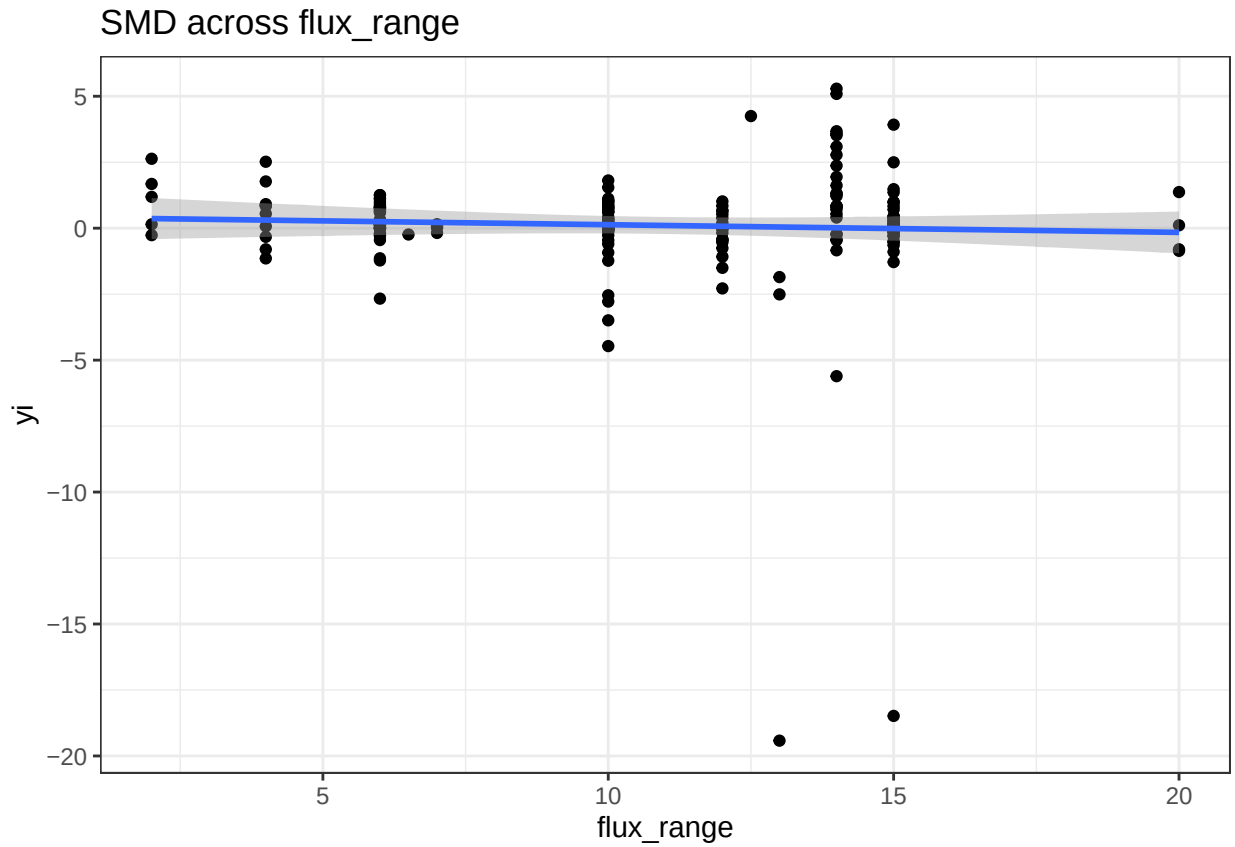



```
##
## Call:
## lm(formula = yi ~ vi, data = dat_MA_ES)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.4410  -1.0808  -0.6359   0.4524  18.9554
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.1163     0.2675   4.173 4.48e-05 ***
## vi           -4.9353     0.2441 -20.219  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.662 on 201 degrees of freedom
## Multiple R-squared:  0.6704, Adjusted R-squared:  0.6688
## F-statistic: 408.8 on 1 and 201 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 = 203; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                 factor
## sigma^2.1   0.0000  0.0005      3     no          experiment_id
```

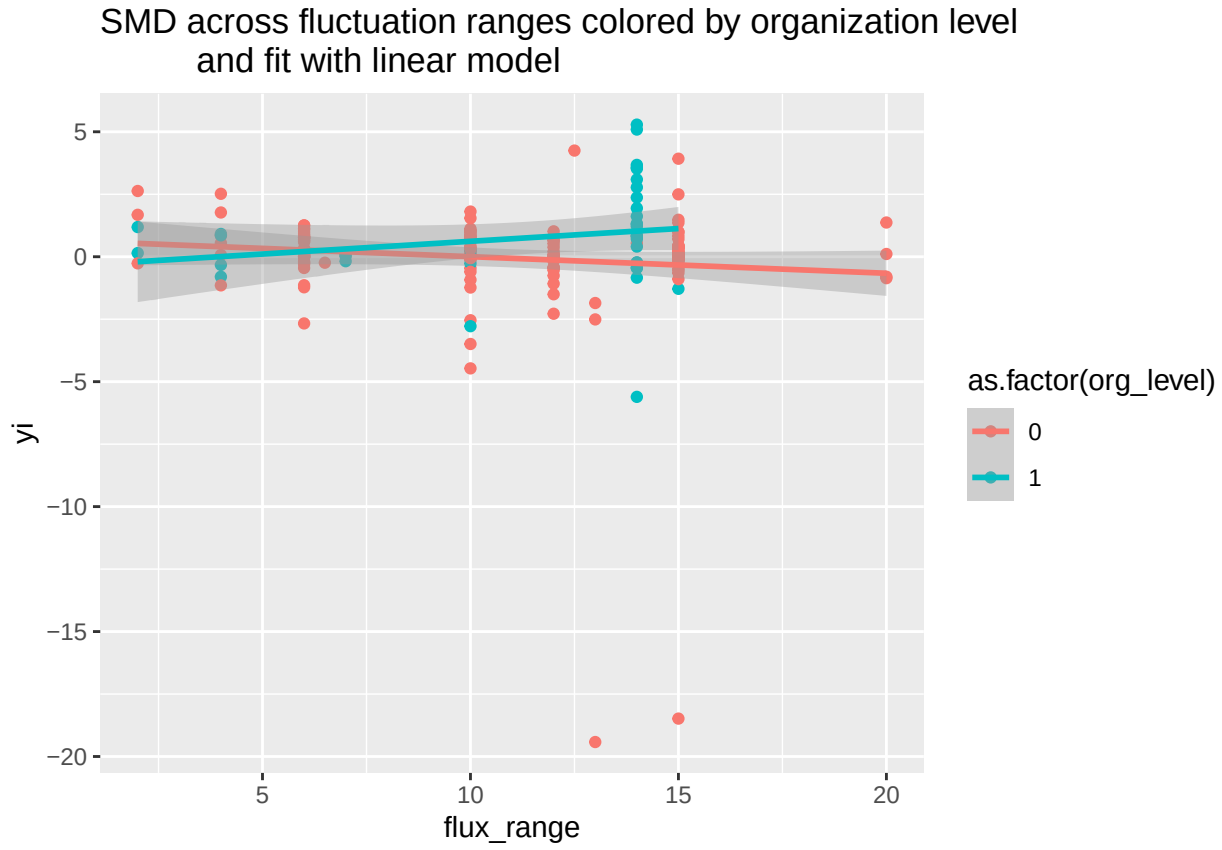
```
## sigma^2.2  10.8960  3.3009     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 6383.8992, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 18.2908, p-val < .0001
##
## Model Results:
##
##             estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt      -0.0755  0.6991  -0.1080  0.9140  -1.4456   1.2947
## flux_range   -0.0466  0.0109  -4.2768  <.0001  -0.0679  -0.0252  ***
##
## ---
## 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
## -82.316   0.044   0.656   1.147   5.976
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.7115     1.2885   0.552    0.581
## flux_range   -0.1001     0.1104  -0.906    0.366
##
## Residual standard error: 6.366 on 201 degrees of freedom
## Multiple R-squared:  0.004071,   Adjusted R-squared:  -0.0008838
## F-statistic: 0.8216 on 1 and 201 DF,  p-value: 0.3658
```

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 = 203; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                  factor
## sigma^2.1   0.0000  0.0012      3     no           experiment_id
## sigma^2.2  10.5105  3.2420     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 6318.2410, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 45.2966, p-val < .0001
##
## Model Results:
##
##             estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt       0.0262  0.6873   0.0381  0.9696  -1.3208   1.3732
## flux_range   -0.0466  0.0109  -4.2821  <.0001  -0.0680  -0.0253  ***
```

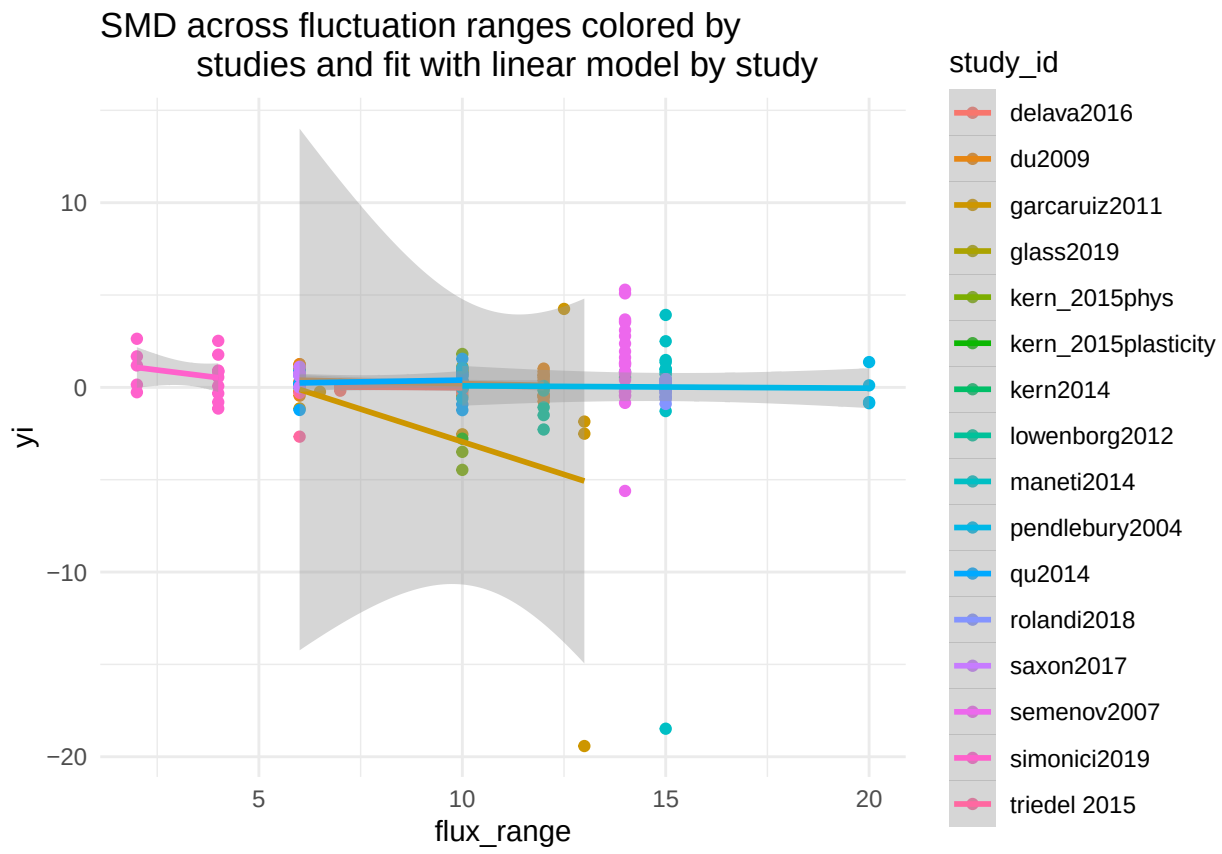
```
## org_level    -0.4311  0.0830  -5.1950  <.0001  -0.5938  -0.2685  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#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  -0.047   0.757   1.243   5.043
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0.8933     1.4309   0.624    0.533
## flux_range             -0.1343     0.1239  -1.084    0.280
## org_level              -0.6589     3.3438  -0.197    0.844
## flux_range:org_level    0.1428     0.2779   0.514    0.608
##
## Residual standard error: 6.382 on 199 degrees of freedom
## Multiple R-squared:  0.008982,   Adjusted R-squared:  -0.005958
## F-statistic: 0.6012 on 3 and 199 DF,  p-value: 0.615
```

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 = 203; 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     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 185) = 5046.4092, p-val < .0001
##
## Test of Moderators (coefficients 2:18):
## QM(df = 17) = 322.5804, p-val < .0001
##
## 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_idpiccau2017           -15.8917  1.1477  -13.8471  <.0001  -18.1410
## 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_idpiccau2017          -13.6423  ***
## 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
```

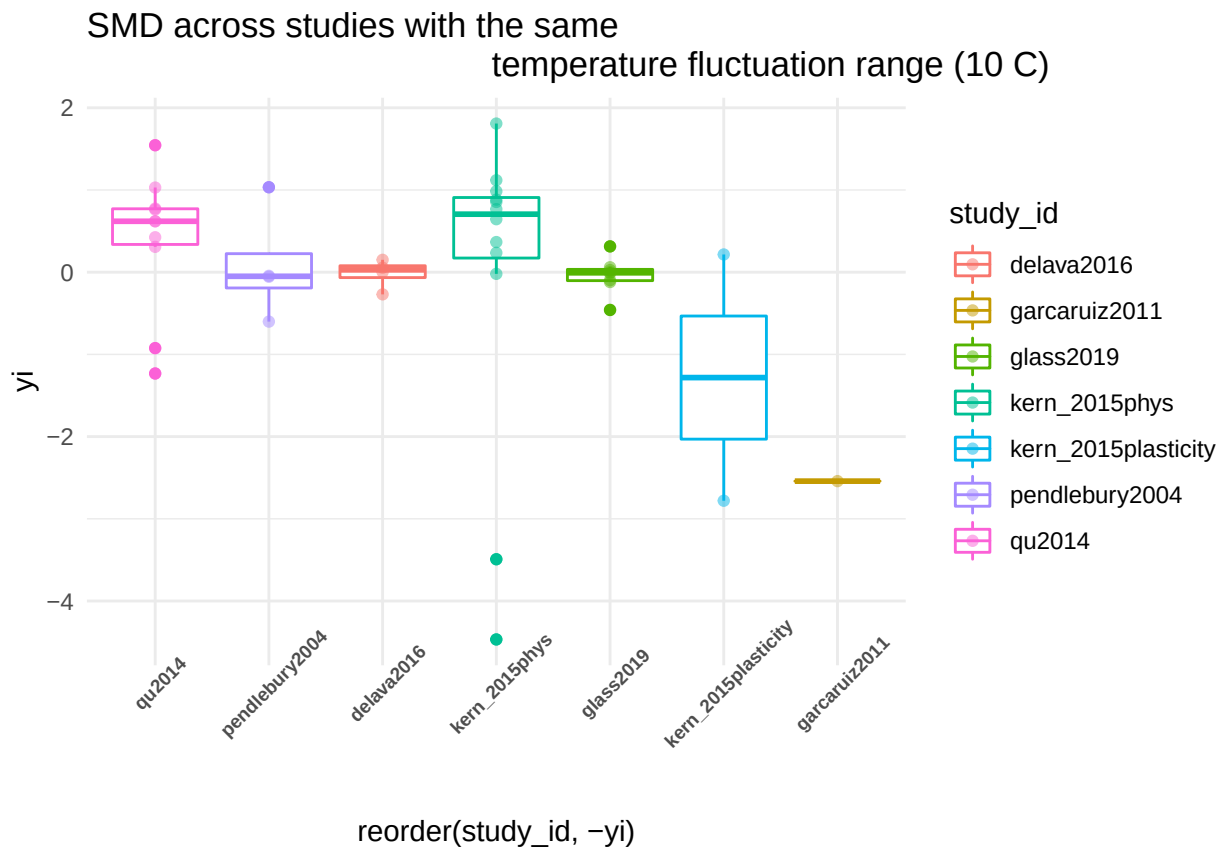
```
#simple linear model looking at how flux_range and study_id affect yi
simple9<-lm(yi~flux_range*study_id, data =dat_MA_ES)
summary(simple9)
```

```
##
## Call:
## lm(formula = yi ~ flux_range * study_id, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -62.646  -0.307   0.035   0.539  22.869
##
## Coefficients: (11 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_idpiccau2017                       -16.120645  10.543399  -1.529   0.1280
## 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_idpiccau2017                   NA         NA      NA       NA
## 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:  0.2953, Adjusted R-squared:  0.2092
## F-statistic: 3.429 on 22 and 180 DF,  p-value: 2.439e-06
```

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
```

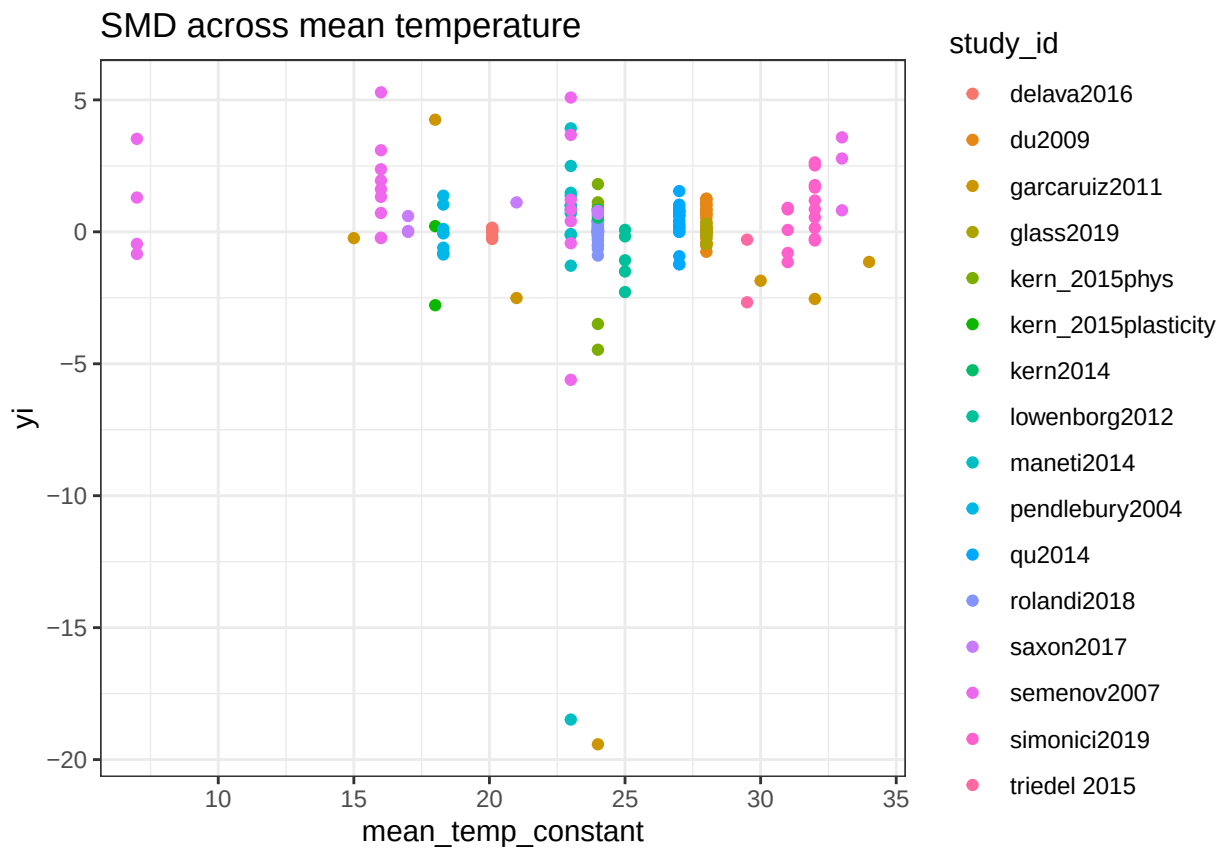
```
#simple linear model looking at how flux_range affects yi within subset data
simple12<-lm(yi~flux_range, data =common_range)
summary(simple12)
```

```
##
## 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 = 203; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                  factor
## sigma^2.1   0.0000  0.0008      3     no           experiment_id
## sigma^2.2  12.8795  3.5888     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 6863.7808, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 112.3388, p-val < .0001
##
## Model Results:
##
##                     estimate      se      zval    pval    ci.lb    ci.ub
## intrcpt               1.4214  0.7728    1.8393  0.0659  -0.0932   2.9359    .
## mean_temp_constant   -0.0863  0.0081  -10.5990  <.0001  -0.1022  -0.0703  ***
```

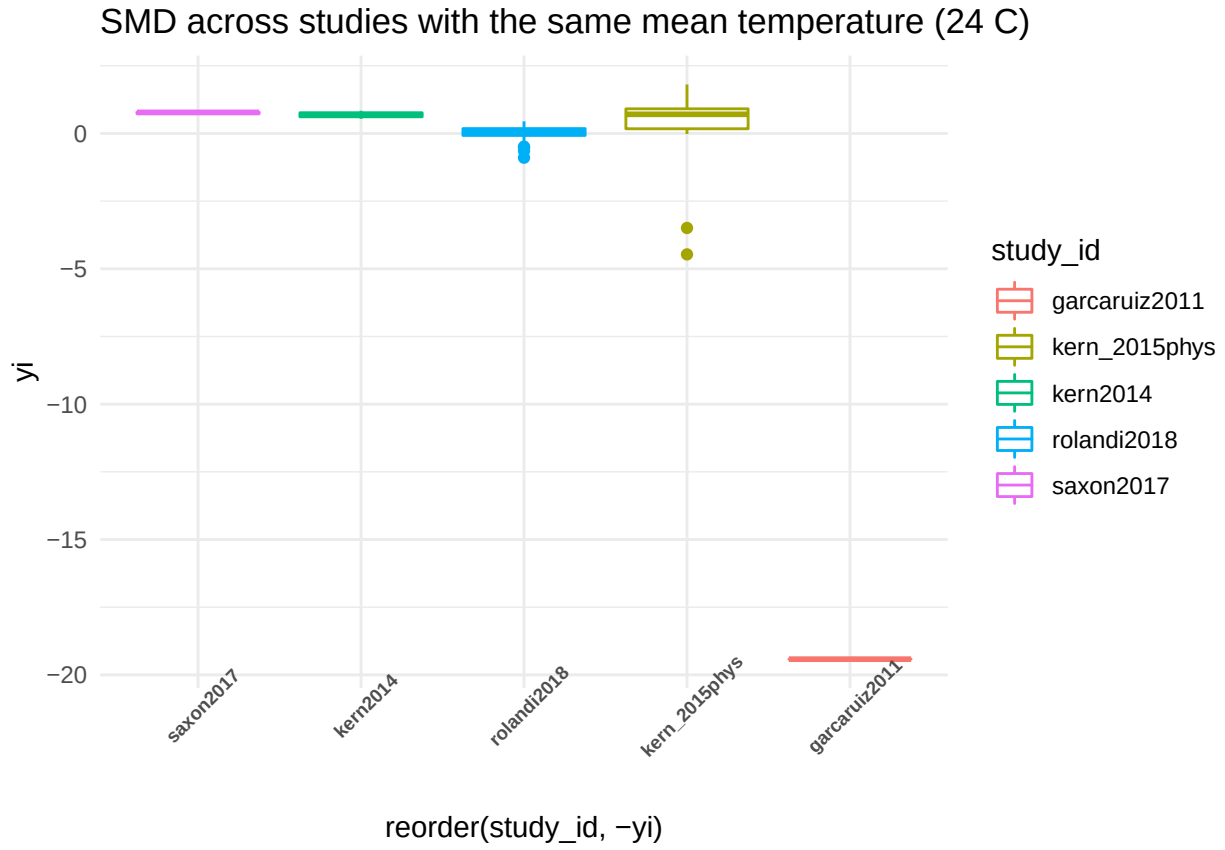
```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#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
## -82.499   0.216   0.511   1.180   5.597
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.170886   2.286937  -0.075    0.941
## mean_temp_constant -0.008699   0.091544  -0.095    0.924
##
## Residual standard error: 6.378 on 201 degrees of freedom
## Multiple R-squared:  4.492e-05,  Adjusted R-squared:  -0.00493
## F-statistic: 0.00903 on 1 and 201 DF,  p-value: 0.9244
```

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
```

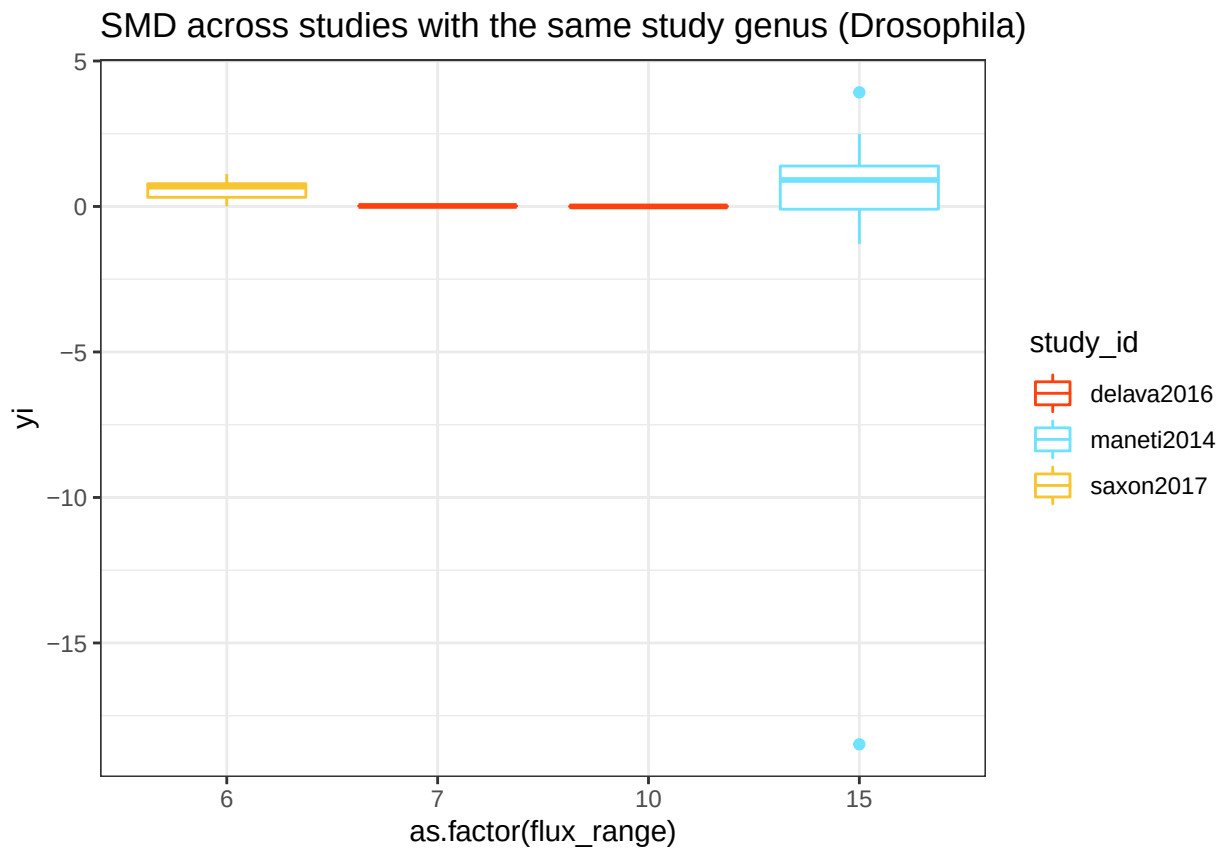
```r
#simple linear model looking at how flux_range affects yi within subset data
simple13<-lm(yi~mean_temp_constant, data =common_temp)
summary(simple13)
```

```
##
## 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
```

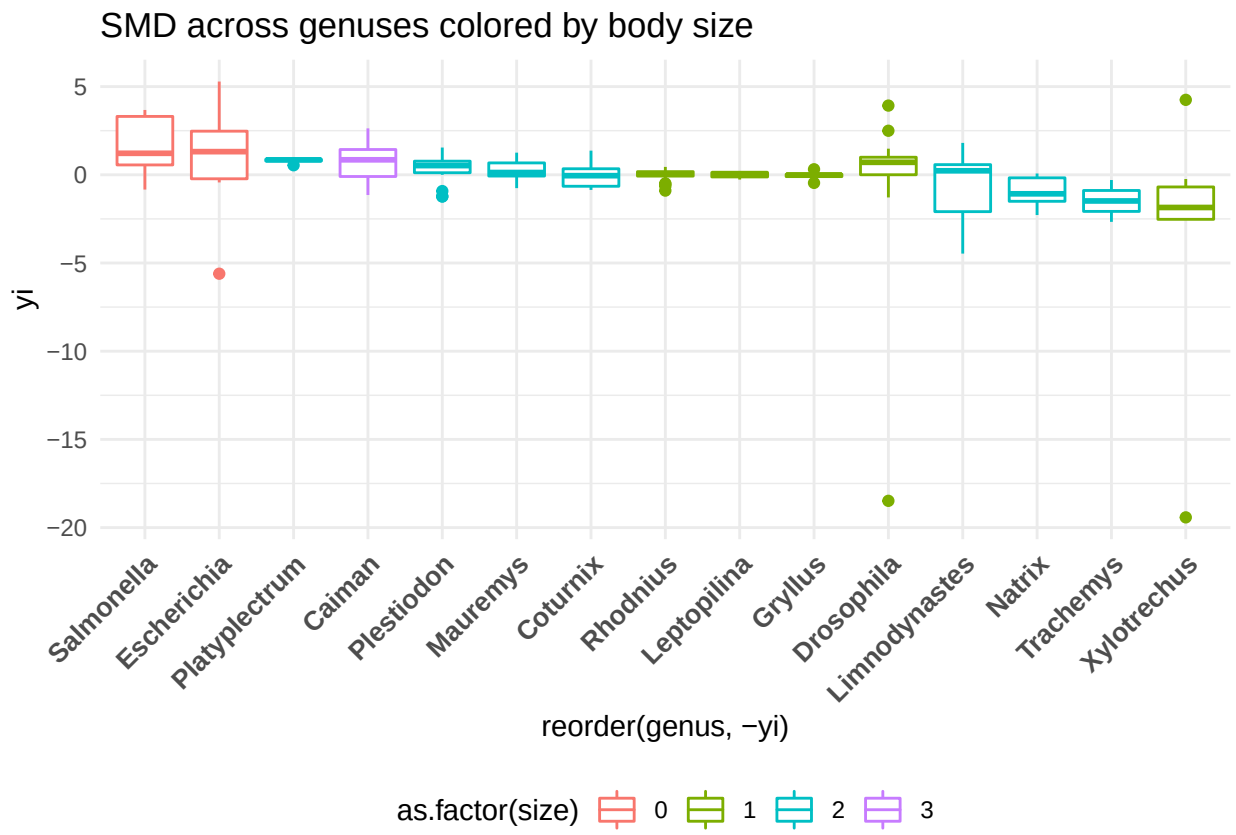
```
## study_idmaneti2014    0.7499  0.6134   1.2226  0.2215  -0.4523  1.9521
## study_idsaxon2017     0.6933  0.4505   1.5389  0.1238  -0.1897  1.5763
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#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_boxplot()+
  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 = ~genus,
                random = ~1 | experiment_id/ study_id,
                  method="REML")
fig11
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                 factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  0.2888  0.5374     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 187) = 4957.0842, p-val < .0001
##
## Test of Moderators (coefficients 2:16):
## QM(df = 15) = 487.2880, p-val < .0001
##
## Model Results:
##
##                    estimate      se      zval    pval     ci.lb     ci.ub
## intrcpt              0.5791  0.5436    1.0653  0.2868   -0.4863    1.6445
## genusClematis      -16.7689  1.0710  -15.6574  <.0001  -18.8679  -14.6698  ***
```

```
## genusCoturnix        -0.5885  0.7731   -0.7612  0.4465   -2.1037    0.9267
## genusDrosophila      -0.0186  0.5952   -0.0312  0.9751   -1.1851    1.1480
## genusEscherichia      0.5307  0.7317    0.7252  0.4683   -0.9035    1.9649
## genusGryllus         -0.6144  0.7657   -0.8023  0.4224   -2.1151    0.8864
## genusLeptopilina     -0.0465  0.6013   -0.0773  0.9384   -1.2250    1.1320
## genusLimnodynastes   -0.7919  0.6358   -1.2455  0.2130   -2.0382    0.4543
## genusMauremys        -0.2598  0.6666   -0.3898  0.6967   -1.5662    1.0466
## genusNatrix          -1.6507  0.6779   -2.4351  0.0149   -2.9793   -0.3221    *
## genusPlatyplectrum   -0.0106  0.6357   -0.0167  0.9867   -1.2566    1.2353
## genusPlestiodon      -0.2612  0.7679   -0.3401  0.7337   -1.7662    1.2438
## genusRhodnius        -0.5584  0.6634   -0.8417  0.4000   -1.8585    0.7418
## genusSalmonella       0.4786  0.7238    0.6612  0.5085   -0.9401    1.8972
## genusTrachemys       -1.7031  0.7774   -2.1909  0.0285   -3.2267   -0.1795    *
## genusXylotrechus     -1.6640  0.7672   -2.1690  0.0301   -3.1676   -0.1604    *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

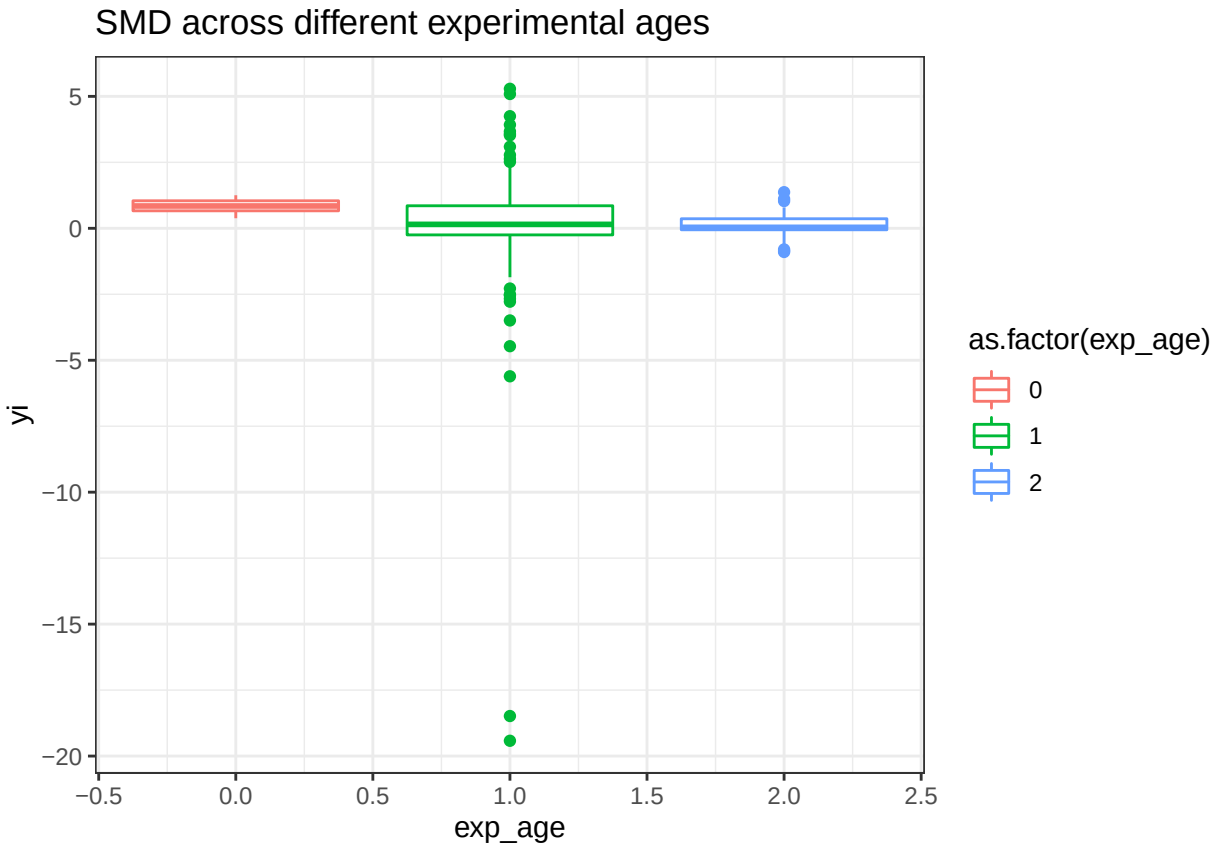
```
#simple linear model looking at how genus affects yi
simple11<-lm(yi~genus, data =dat_MA_ES)
summary(simple11)
```

```
##
## Call:
## lm(formula = yi ~ genus, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -69.610  -0.274   0.057   0.608  17.544
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.7084     1.5173   0.467  0.64111
## genusClematis      -16.8982     6.0691  -2.784  0.00592 **
## genusCoturnix       -0.6892     2.5727  -0.268  0.78907
## genusDrosophila     -0.8597     1.9866  -0.433  0.66568
## genusEscherichia     0.4926     2.2759   0.216  0.82890
## genusGryllus        -0.7449     2.5727  -0.290  0.77250
## genusLeptopilina    -0.7115     2.8386  -0.251  0.80235
## genusLimnodynastes  -1.3455     2.3990  -0.561  0.57558
## genusMauremys       -0.4605     1.8388  -0.250  0.80254
## genusNatrix         -1.7006     3.0345  -0.560  0.57587
## genusPlatyplectrum   0.1025     2.8386   0.036  0.97123
## genusPlestiodon     -0.3916     2.0072  -0.195  0.84552
## genusRhodnius       -0.6904     1.7919  -0.385  0.70046
## genusSalmonella      0.8706     2.3327   0.373  0.70942
## genusTrachemys      -2.1914     4.4236  -0.495  0.62090
## 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:  0.2104, Adjusted R-squared:  0.147
## F-statistic: 3.321 on 15 and 187 DF,  p-value: 6.022e-05
```

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 = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0004      3     no           experiment_id
## sigma^2.2  9.3934  3.0649     23     no  experiment_id/study_id
```

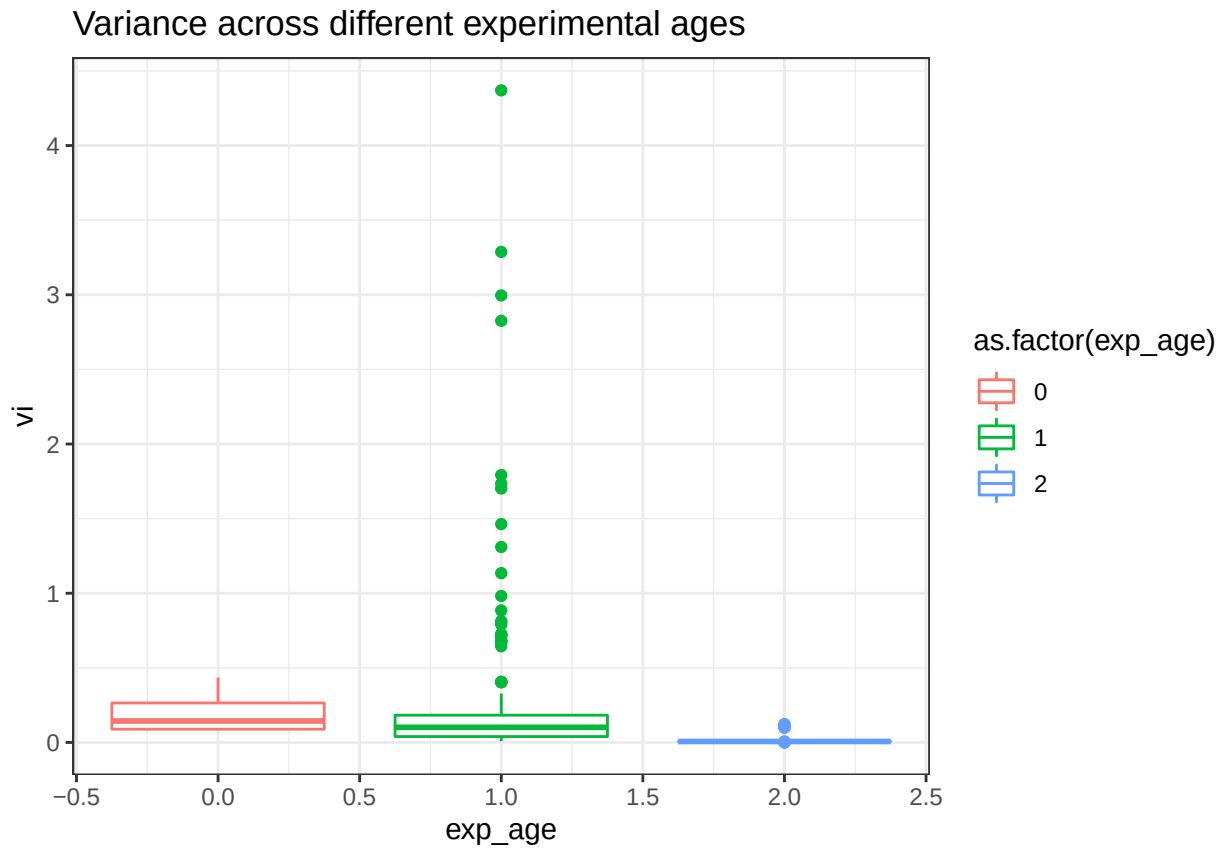
```
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 6860.5383, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 5.1960, p-val = 0.0226
##
## Model Results:
##
##          estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt   -3.6196  1.4875  -2.4333  0.0150  -6.5350  -0.7041  *
## exp_age    2.5997  1.1405   2.2795  0.0226   0.3644   4.8350  *
##
## ---
## 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
## -82.433   0.032   0.472   1.306   5.759
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.9213     1.0963  -0.840    0.402
## exp_age       0.4489     0.8361   0.537    0.592
##
## Residual standard error: 6.374 on 201 degrees of freedom
## Multiple R-squared:  0.001432,   Adjusted R-squared:  -0.003536
## F-statistic: 0.2882 on 1 and 201 DF,  p-value: 0.5919
```

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
```

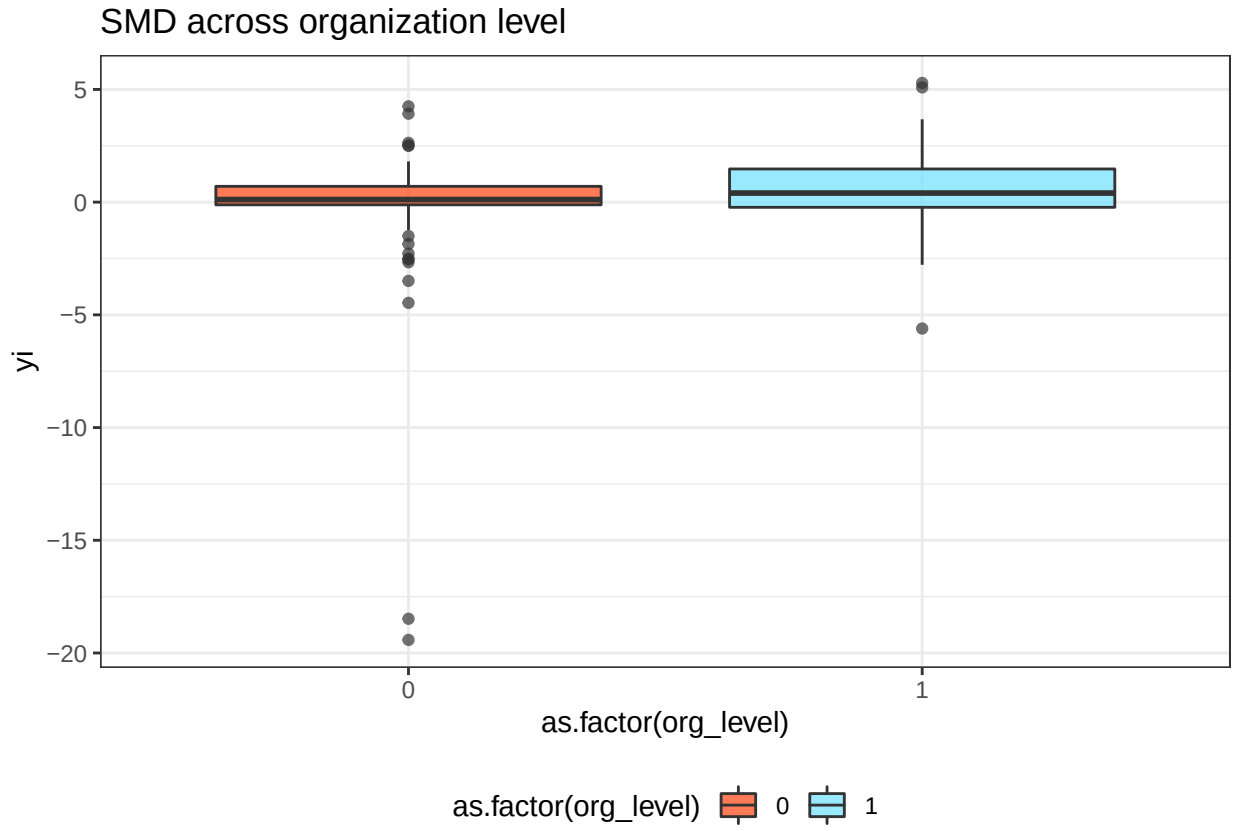
```
#simple linear model looking at how exp_age affects vi
simple4<-lm(vi~ exp_age, data =dat_MA_ES)
summary(simple4)
```

```
##
## Call:
## lm(formula = vi ~ exp_age, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5065 -0.2682 -0.2284 -0.1036 12.7339
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.5927     0.1806   3.281  0.00122 **
## exp_age      -0.2412     0.1378  -1.751  0.08155 .
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
##
## Residual standard error: 1.05 on 201 degrees of freedom
## Multiple R-squared:  0.01502,    Adjusted R-squared:  0.01012
## F-statistic: 3.064 on 1 and 201 DF,  p-value: 0.08155
```

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 = 203; method: REML)
```

```
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                  factor
## sigma^2.1   0.0000  0.0006      3     no           experiment_id
## sigma^2.2  10.7655  3.2811     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 6852.7599, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 26.9418, p-val < .0001
##
## Model Results:
##
##            estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt     -0.4639  0.6858  -0.6764  0.4988  -1.8081   0.8803
## org_level   -0.4308  0.0830  -5.1906  <.0001  -0.5934  -0.2681  ***
##
## ---
## 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   0.131   0.620   1.254   4.954
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.5598     0.4988  -1.122    0.263
## org_level     0.8921     1.1237   0.794    0.428
##
## Residual standard error: 6.369 on 201 degrees of freedom
## Multiple R-squared:  0.003126,   Adjusted R-squared:  -0.001834
## F-statistic: 0.6303 on 1 and 201 DF,  p-value: 0.4282
```

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 = 203; 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     23     no                 experiment_id/study_id
## sigma^2.3  0.0366  0.1913     58     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 156) = 4319.5235, p-val < .0001
##
## Test of Moderators (coefficients 2:47):
## QM(df = 46) = 421.7530, 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_defgermination                                    -16.5797  1.2597
## 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_defgermination                                            -13.1616  <.0001
## 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_defgermination                                        -19.0487  -14.1108
## 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_defgermination                                         ***
## 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
```

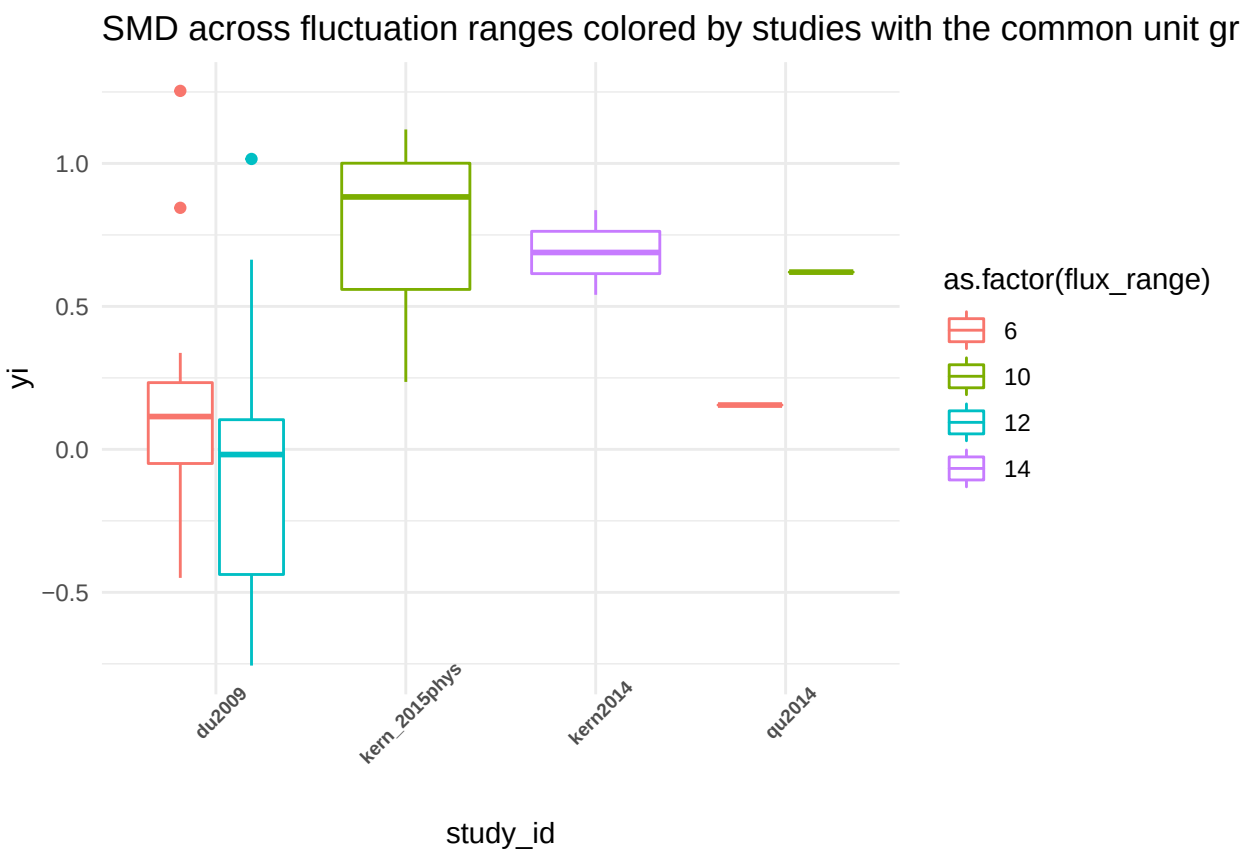
```
#full random effects model looking at all the response units in the entire dataset
response_units_mod <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~resp_units,
```

```
               random = ~1 | experiment_id/ study_id /response_id,
                 method="REML")
response_units_mod
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##              estim    sqrt  nlvls  fixed                              factor
## sigma^2.1   0.0000  0.0010      3     no                       experiment_id
## sigma^2.2  12.7637  3.5726     23     no                 experiment_id/study_id
## sigma^2.3   0.1127  0.3357     58     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 183) = 5100.4215, p-val < .0001
##
## Test of Moderators (coefficients 2:20):
## QM(df = 19) = 77.1912, p-val < .0001
##
## Model Results:
##
##                                       estimate      se     zval    pval
## intrcpt                                 1.5220  3.6046   0.4222  0.6729
## resp_unitsCFU * g dry weight manure^-1  -0.8243  5.0926  -0.1619  0.8714
## resp_unitscm                            -2.8677  3.7556  -0.7636  0.4451
## resp_unitsdays                          -3.0170  3.7349  -0.8078  0.4192
## resp_unitseggs laid                     -1.5013  4.4081  -0.3406  0.7334
## resp_unitsg                             -1.8742  3.7345  -0.5019  0.6158
## resp_unitskJ *day^-1 *kg^-1             -2.9976  3.7687  -0.7954  0.4264
## resp_unitsm                             -3.2515  3.7523  -0.8665  0.3862
## resp_unitsm * s^-1                      -3.0594  3.7513  -0.8156  0.4148
## resp_unitsmg                            -1.5573  5.0864  -0.3062  0.7595
## resp_unitsmm                            -1.7278  3.7363  -0.4624  0.6438
## resp_unitsnmol CHE / mgww               -1.8189  5.0892  -0.3574  0.7208
## resp_unitsoffspring per mating          -1.0423  4.1622  -0.2504  0.8023
## resp_unitsoffspring/female              -2.8275  3.7693  -0.7501  0.4532
## resp_unitspercent                       -3.5402  3.7363  -0.9475  0.3434
## resp_unitspixels                        -1.8448  3.7717  -0.4891  0.6248
## resp_unitstime to  death (hour)         -2.8982  3.7583  -0.7711  0.4406
## resp_unitstotal offspring               -0.9788  4.1622  -0.2352  0.8141
## resp_unitsuM Trolox Equivalents/ mgww   -4.1911  5.0918  -0.8231  0.4105
## resp_unitswing centroid                 -0.6880  4.1577  -0.1655  0.8686
##                                          ci.lb   ci.ub
## intrcpt                                 -5.5429  8.5869
## resp_unitsCFU * g dry weight manure^-1  -10.8056  9.1571
## resp_unitscm                            -10.2285  4.4931
## resp_unitsdays                          -10.3373  4.3034
## resp_unitseggs laid                     -10.1410  7.1385
## resp_unitsg                              -9.1937  5.4453
## resp_unitskJ *day^-1 *kg^-1             -10.3842  4.3890
## resp_unitsm                             -10.6058  4.1028
## resp_unitsm * s^-1                      -10.4119  4.2931
```

```
## resp_unitsmg                              -11.5265  8.4119
## resp_unitsmm                               -9.0508  5.5953
## resp_unitsnmol CHE / mgww                 -11.7936  8.1557
## resp_unitsoffspring per mating             -9.2001  7.1155
## resp_unitsoffspring/female                -10.2152  4.5603
## resp_unitspercent                         -10.8632  3.7829
## resp_unitspixels                           -9.2372  5.5477
## resp_unitstime to  death (hour)           -10.2643  4.4679
## resp_unitstotal offspring                  -9.1366  7.1789
## resp_unitsuM Trolox Equivalents/ mgww     -14.1709  5.7888
## resp_unitswing centroid                    -8.8368  7.4609
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#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")
```




```r
#random effects model within subset data
fig14 <- rma.mv(yi, vi, data=common_unit_g,
```

```
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig14
```

```
##
## Multivariate Meta-Analysis Model (k = 31; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.4274  0.6537      2     no           experiment_id
## sigma^2.2  0.0000  0.0000      5     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 30) = 153.8790, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.2455  0.4647  0.5284  0.5972  -0.6652  1.1562
##
## ---
## 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
simple14<-lm(yi~study_id, data =common_unit_g)
summary(simple14)
```

```
##
## Call:
## lm(formula = yi ~ study_id, data = common_unit_g)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.81541 -0.28023 -0.05915  0.14639  1.19456
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0.05915    0.09796   0.604   0.5510
## study_idkern_2015phys   0.68669    0.29389   2.337   0.0271 *
## study_idkern2014        0.62940    0.35321   1.782   0.0860 .
## study_idqu2014          0.32825    0.35321   0.929   0.3610
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4799 on 27 degrees of freedom
## Multiple R-squared:  0.2352, Adjusted R-squared:  0.1502
## F-statistic: 2.768 on 3 and 27 DF,  p-value: 0.06101
```