data wrangling and plots

Maggie Slein

2/22/2021

Plots

Question: How does response compare across studies and experiments?

Figure 1.

```r
#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")
```

SMD across all studies

reorder(study_id, –yi)

as.factor(experiment_id)   1   2   3
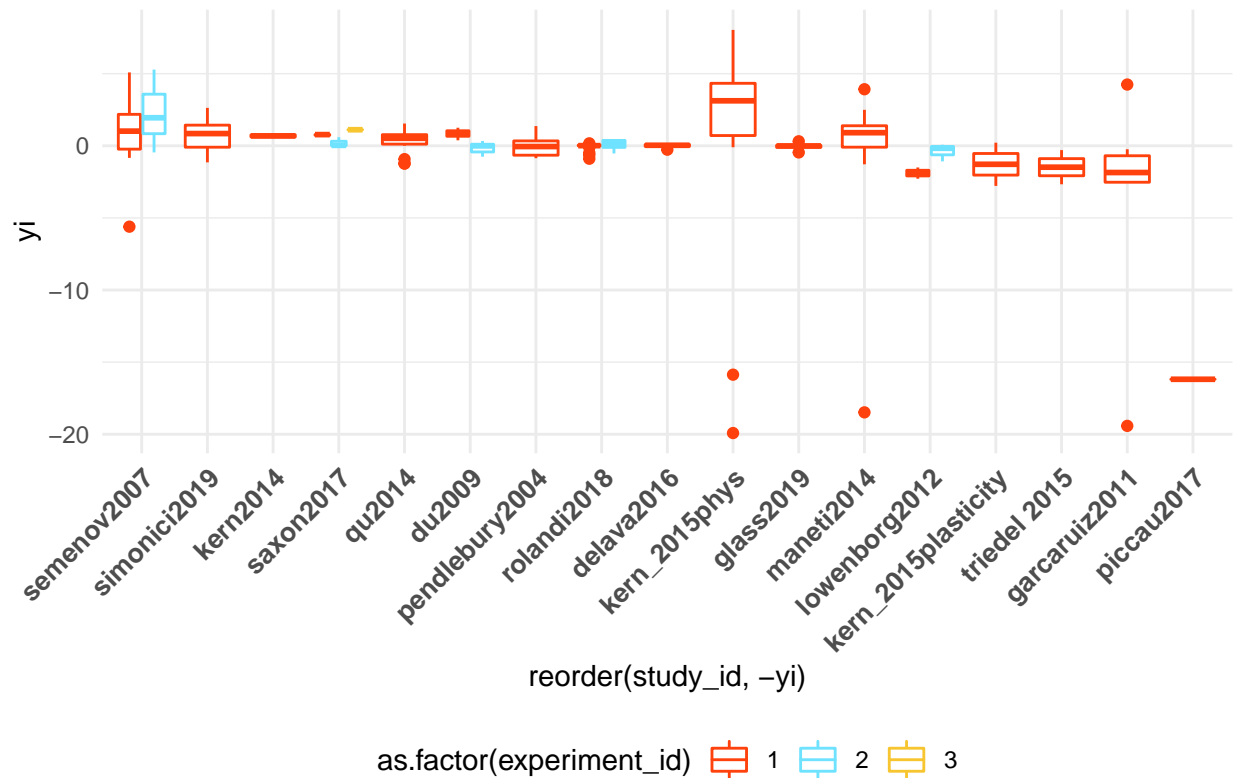
```r
#corresponding random effects model
fig1 <- rma.mv(yi, vi, data=dat_MA_ES,
            random = ~1 | experiment_id/ study_id,
               method="REML")
fig1
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt   nlvls  fixed                 factor
## sigma^2.1   0.0000  0.0007      3     no          experiment_id
## sigma^2.2  11.4486  3.3836     23     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 202) = 5614.3312, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.4951  0.7070  -0.7003  0.4837  -1.8807  0.8905
##
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
```

```
#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): 95.09%
## H^2 (unaccounted variability / sampling variability):   20.37
##
## Test for Residual Heterogeneity:
## QE(df = 186) = 3789.5783, p-val < .0001
##
## Test of Moderators (coefficients 2:17):
## QM(df = 16) = 1824.7529, 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          2.0706  0.2485    8.3316  <.0001     1.5835
## 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          2.5577  ***
## 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  ***
```
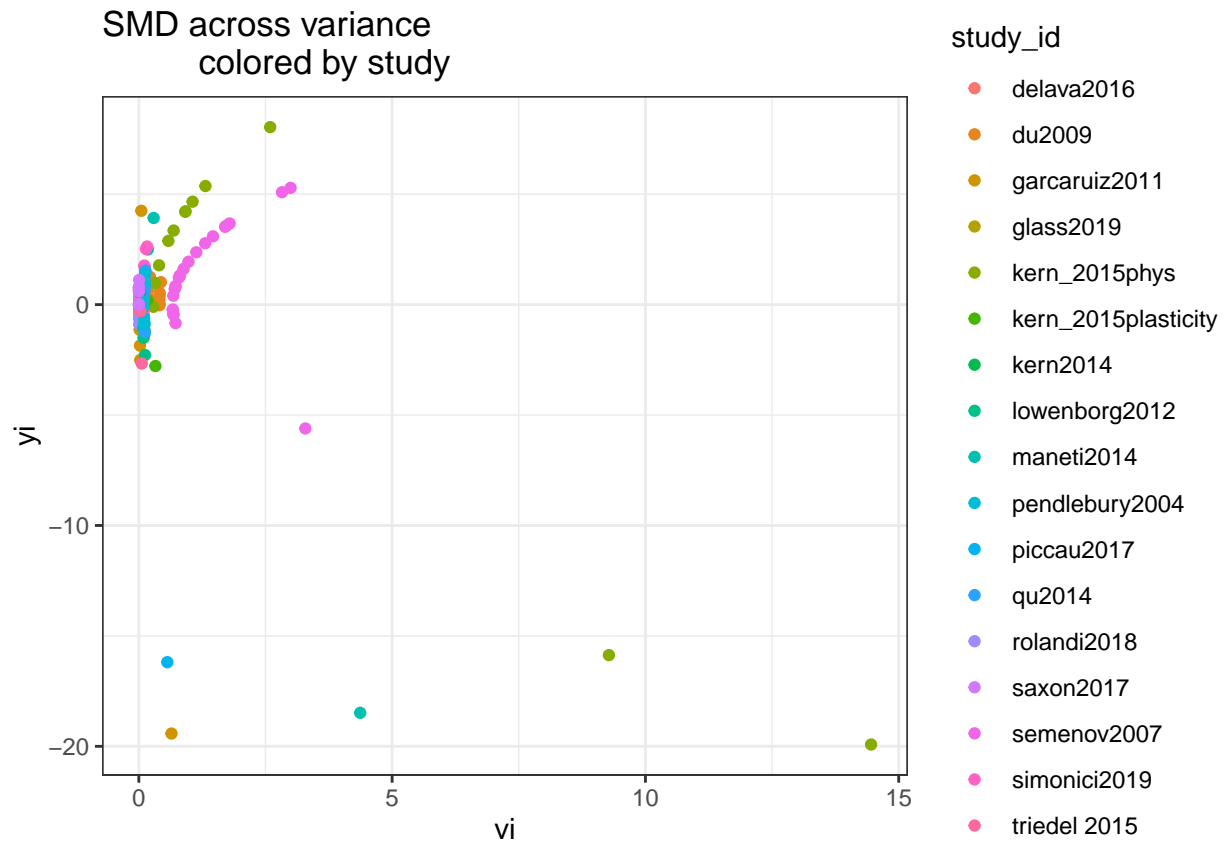
```
## study_idsimonici2019            0.7611  ***
## study_idtriedel 2015          -0.8339  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```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
## -1624.4609   3248.9218   3254.9218   3264.8466   3255.0430
##
## Variance Components:
##
##             estim    sqrt   nlvls  fixed                     factor
## sigma^2.1   0.0000  0.0007      3     no              experiment_id
## sigma^2.2  11.4486  3.3836     23     no   experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 202) = 5614.3312, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.4951  0.7070  -0.7003  0.4837  -1.8807  0.8905
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 2.

SMD across variance
colored by study

study_id
- delava2016
- du2009
- garcaruiz2011
- glass2019
- kern_2015phys
- kern_2015plasticity
- kern2014
- lowenborg2012
- maneti2014
- pendlebury2004
- piccau2017
- qu2014
- rolandi2018
- saxon2017
- semenov2007
- simonici2019
- triedel 2015

```
##
## Call:
## lm(formula = yi ~ vi, data = dat_MA_ES)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -45.524  -0.962  -0.529   0.421  21.478
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.9781     0.3499   2.795  0.00569 **
## vi           -2.9315     0.2123 -13.805  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.783 on 201 degrees of freedom
## Multiple R-squared:  0.4867, Adjusted R-squared:  0.4842
## F-statistic: 190.6 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=as.factor(flux_range), y=yi))+
  geom_boxplot()+
  theme_bw()+
  ggtitle("SMD across flux_range")
```
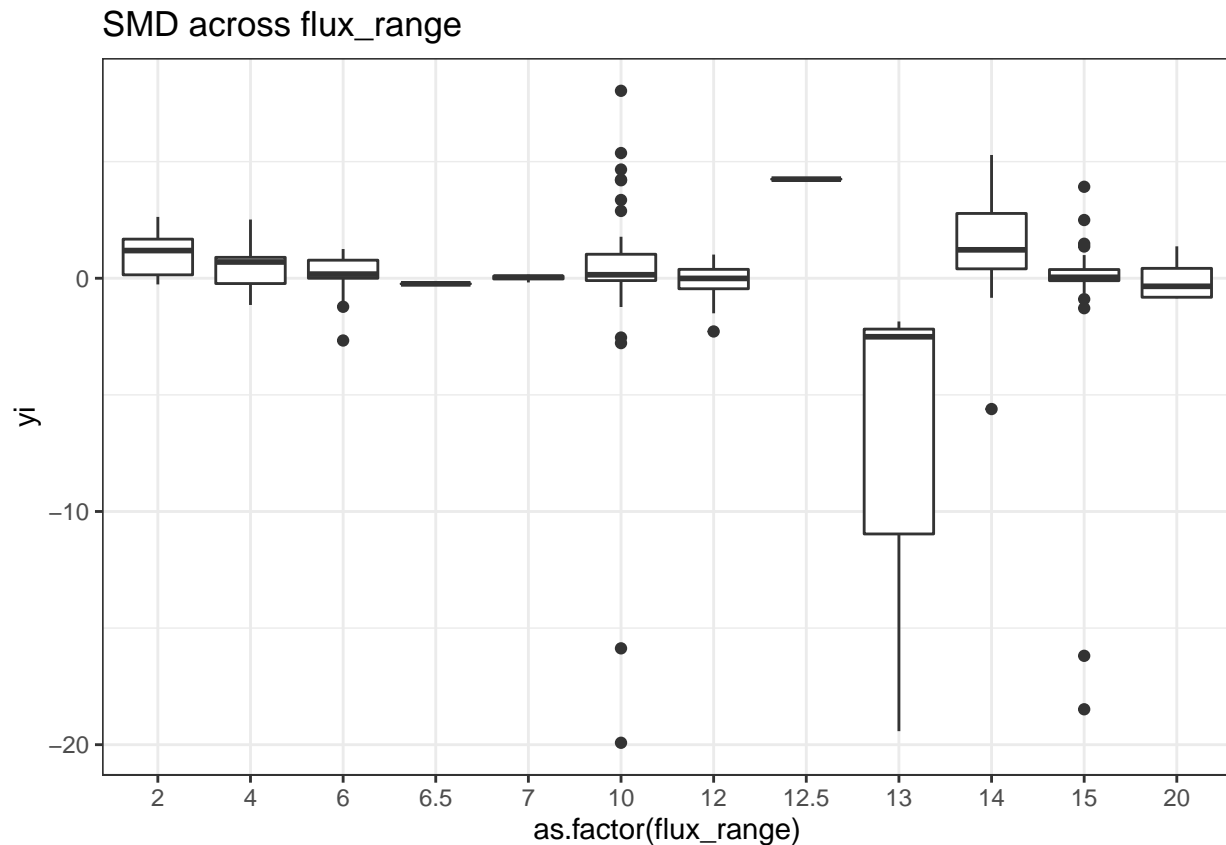


```
#random effects model including org_level as a random variable
fig7 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range,
              random = ~1 | experiment_id/ study_id,
                method="REML")
fig7
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##            estim    sqrt   nlvls   fixed             factor
## sigma^2.1  0.0000  0.0006     3     no            experiment_id
## sigma^2.2 11.1767  3.3432    23     no  experiment_id/study_id
```

```
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 5122.0123, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 18.2850, p-val < .0001
##
## Model Results:
##
##              estimate      se      zval     pval     ci.lb     ci.ub
## intrcpt       -0.0057  0.7078  -0.0081   0.9936   -1.3930    1.3816
## flux_range    -0.0466  0.0109  -4.2761   <.0001   -0.0679   -0.0252   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#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
## -82.315   0.044   0.662   1.167   8.328
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.7109     1.3490   0.527    0.599
## flux_range   -0.1001     0.1156  -0.866    0.388
##
## Residual standard error: 6.664 on 201 degrees of freedom
## Multiple R-squared:  0.003714,   Adjusted R-squared:  -0.001243
## F-statistic: 0.7493 on 1 and 201 DF,  p-value: 0.3877
```

Figure 4.

```r
# 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")
```

SMD across fluctuation ranges colored by organization level and fit with linear model
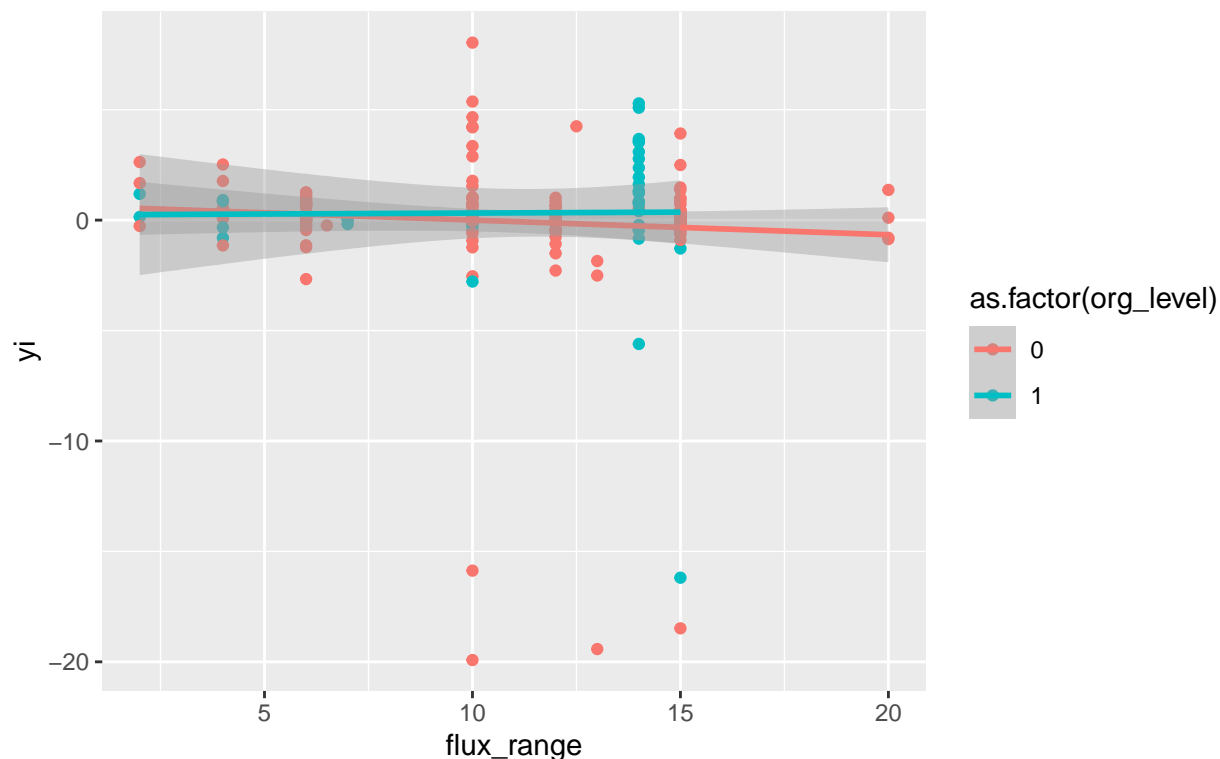

```
#random effects model including org_level as a random variable
fig8 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range + org_level,
               random = ~1 | experiment_id/ study_id,
               method="REML")
fig8
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##            estim    sqrt   nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0007      3     no             experiment_id
## sigma^2.2 10.7755  3.2826     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 200) = 5061.4557, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 45.3027, p-val < .0001
##
## Model Results:
##
##             estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt       0.0960  0.6957   0.1380  0.8903  -1.2675   1.4595
## flux_range   -0.0466  0.0109  -4.2815  <.0001  -0.0680  -0.0253  ***
```

```
## org_level      -0.4312   0.0830  -5.1961  <.0001  -0.5939  -0.2686  ***
##
## ---
## 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   0.758   1.297   8.488
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.8927     1.4984   0.596    0.552
## flux_range          -0.1343     0.1297  -1.035    0.302
## org_level           -0.6582     3.5015  -0.188    0.851
## flux_range:org_level  0.1428     0.2910   0.491    0.624
##
## Residual standard error: 6.683 on 199 degrees of freedom
## Multiple R-squared:  0.008198,   Adjusted R-squared:  -0.006754
## F-statistic: 0.5483 on 3 and 199 DF,  p-value: 0.6498
```

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")
```

SMD across fluctuation ranges colored by studies and fit with linear model by study
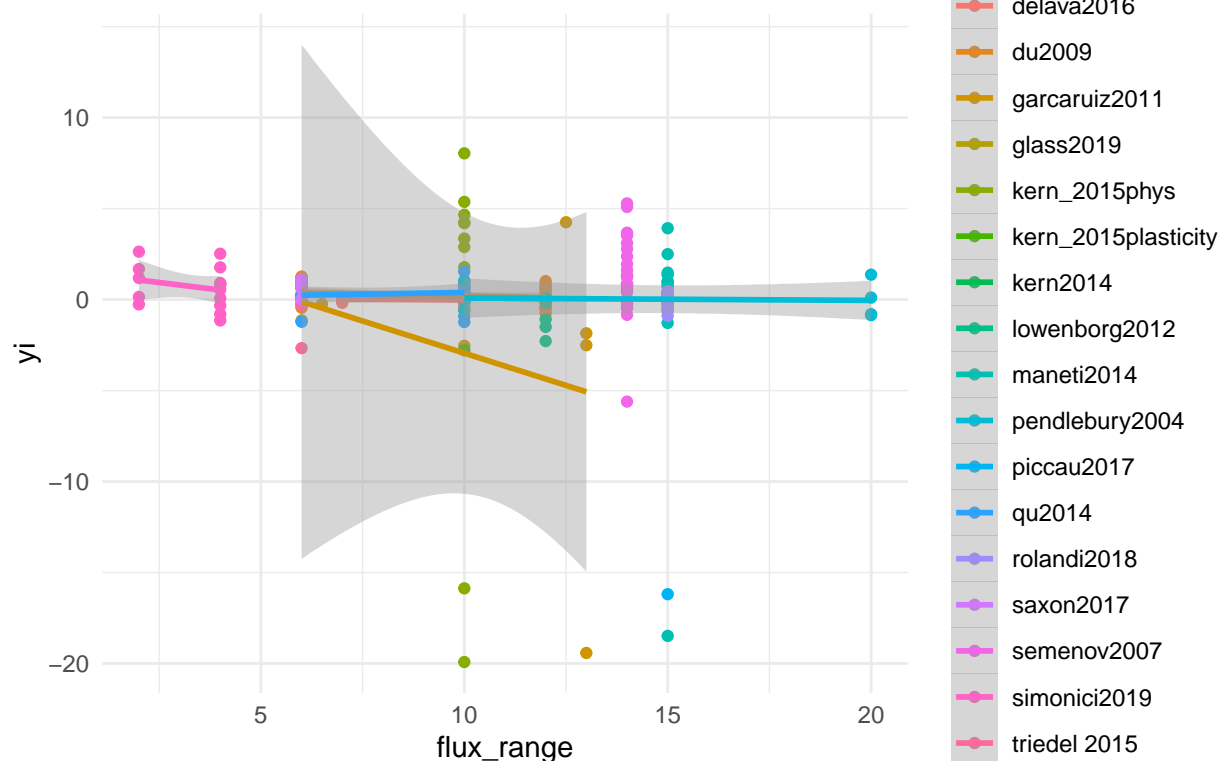
```
#random effects model including org_level as a random variable
fig9 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range + study_id,
               random = ~1 | experiment_id/ study_id,
               method="REML")
fig9
```

```
##
## 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) = 3772.5680, p-val < .0001
##
## Test of Moderators (coefficients 2:18):
## QM(df = 17) = 333.0898, 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
```

10

```
## 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             2.1396  0.8997    2.3782  0.0174     0.3763
## 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             3.9029    *
## 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
```

```r
#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   0.554  22.869
##
## Coefficients: (11 not defined because of singularities)
##                                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     0.091100  12.267945   0.007   0.9941
```

```
## flux_range                                    -0.010684    1.421326   -0.008    0.9940
## study_iddu2009                                  0.575435   12.722653    0.045    0.9640
## study_idgarcaruiz2011                          22.254823   14.894685    1.494    0.1369
## study_idglass2019                              -0.020693    3.692713   -0.006    0.9955
## study_idkern_2015phys                          -0.016487    3.481523   -0.005    0.9962
## study_idkern_2015plasticity                    -1.266498    5.222285   -0.243    0.8087
## study_idkern2014                                0.747017    9.156252    0.082    0.9351
## study_idlowenborg2012                          -0.955077    6.046902   -0.158    0.8747
## study_idmaneti2014                             -0.530046    9.639901   -0.055    0.9562
## study_idpendlebury2004                          0.119910   13.998437    0.009    0.9932
## study_idpiccau2017                            -16.120645   11.236568   -1.435    0.1531
## study_idqu2014                                 -0.077323   13.468891   -0.006    0.9954
## study_idrolandi2018                             0.087188    9.531756    0.009    0.9927
## study_idsaxon2017                               0.543332    4.729285    0.115    0.9087
## study_idsemenov2007                             1.440235    8.199783    0.176    0.8608
## study_idsimonici2019                            1.535025   13.536217    0.113    0.9098
## study_idtriedel 2015                           -1.510015    5.945833   -0.254    0.7998
## flux_range:study_iddu2009                      -0.035825    1.465069   -0.024    0.9805
## flux_range:study_idgarcaruiz2011               -3.266636    1.607803   -2.032    0.0437 *
## 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    1.483908   -0.001    0.9989
## flux_range:study_idpiccau2017                        NA          NA       NA       NA
## flux_range:study_idqu2014                       0.048564    1.573119    0.031    0.9754
## 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    2.178851   -0.121    0.9035
## flux_range:study_idtriedel 2015                      NA          NA       NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.03 on 180 degrees of freedom
## Multiple R-squared:  0.2695, Adjusted R-squared:  0.1802
## F-statistic: 3.019 on 22 and 180 DF,  p-value: 2.6e-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()+
  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)")
```
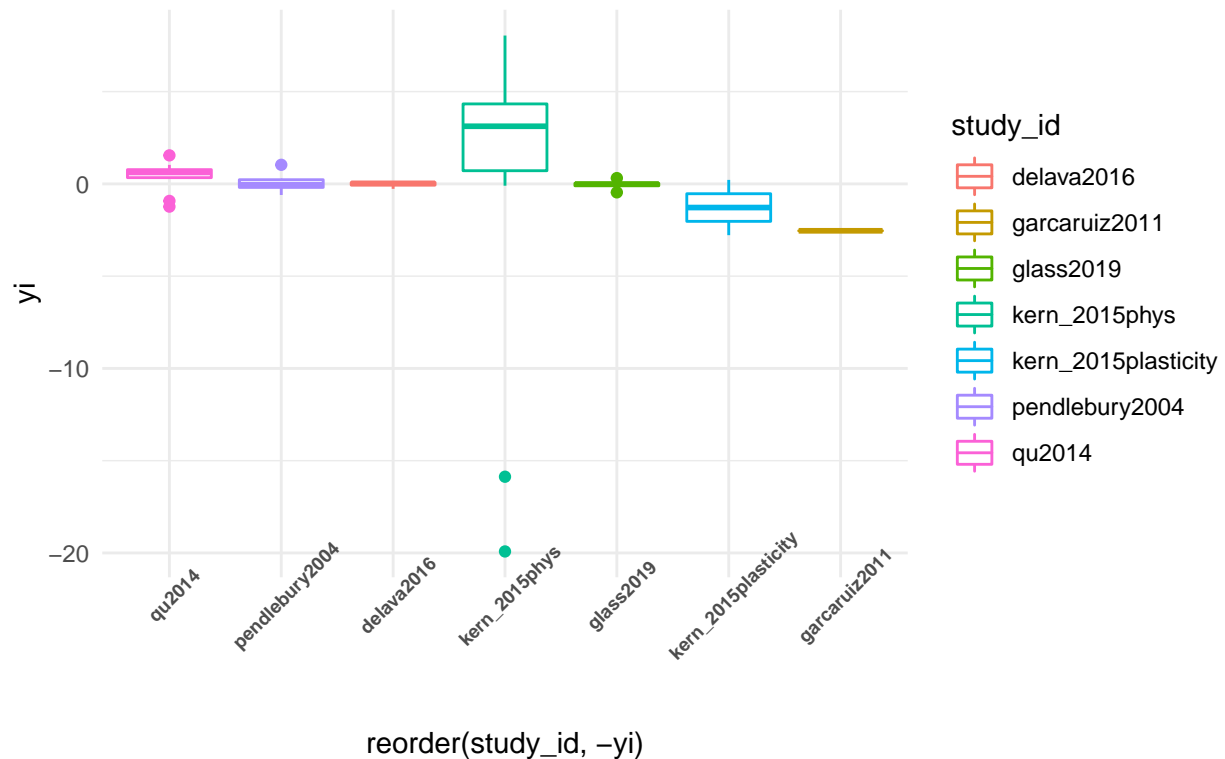
SMD across studies with the same
temperature fluctuation range (10 C)

```r
#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.
```

```r
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  1.8372  1.3554     7     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 40) = 478.3083, p-val < .0001
##
## Model Results:
##
```

```
## estimate       se      zval     pval     ci.lb    ci.ub
##   -0.1210   0.5173   -0.2338   0.8151   -1.1349   0.8930
##
## ---
## 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
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
## -19.8796  -0.0606   0.1892   1.0683   8.0766
##
## Coefficients: (1 not defined because of singularities)
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.03876    0.71869  -0.054    0.957
## flux_range        NA         NA      NA       NA
##
## Residual standard error: 4.602 on 40 degrees of freedom
```

Question how does mean temperature affect response variables?

Figure 7.

```r
# boxplots of how mean temperature influences SMD
ggplot(normalized, aes(x=as.factor(mean_temp_constant), y=yi))+
  geom_boxplot()+
  theme_bw()+
  ggtitle("SMD across mean temperature")
```

SMD across mean temperature
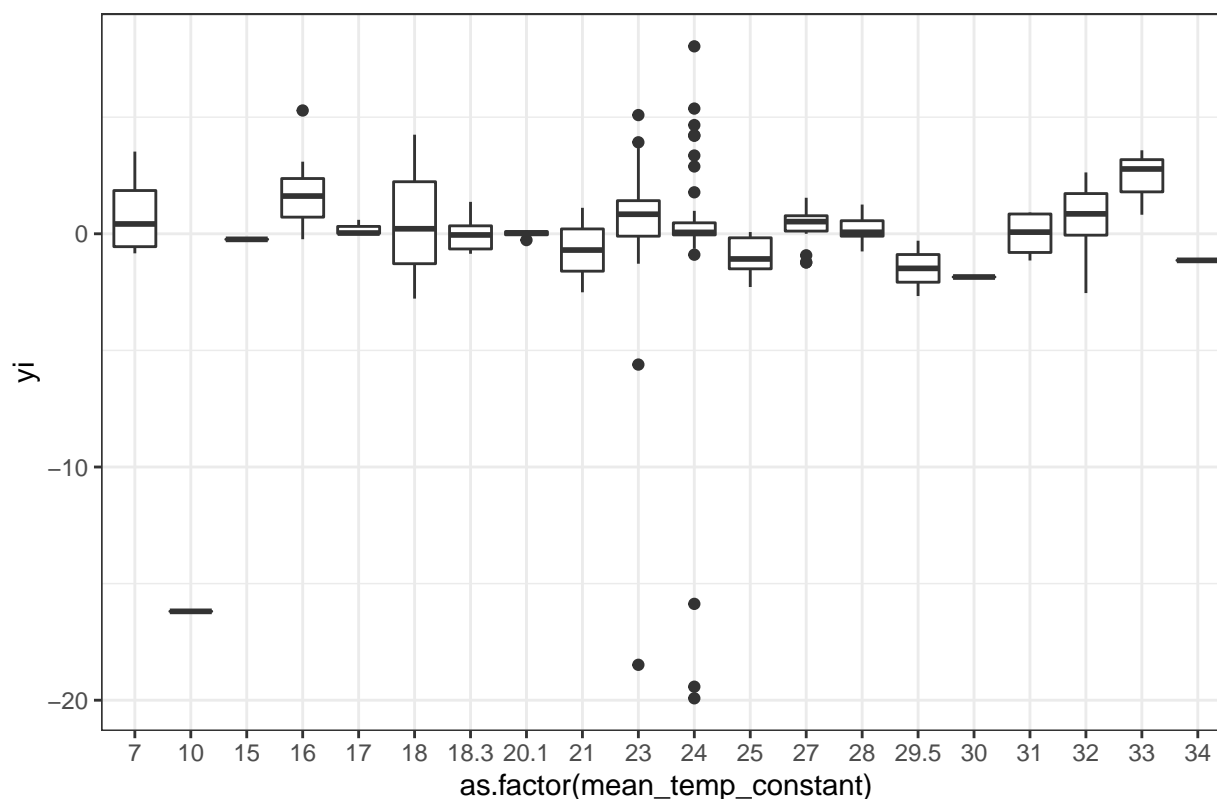

```r
#random effects model including org_level as a random variable
fig6 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~mean_temp_constant,
               random = ~1 | experiment_id/ study_id,
               method="REML")
fig6
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                factor
## sigma^2.1  0.0000  0.0006      3     no           experiment_id
## sigma^2.2 13.1747  3.6297     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 5585.5672, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 112.3797, p-val < .0001
##
## Model Results:
##
##                    estimate      se     zval     pval    ci.lb    ci.ub
## intrcpt              1.4917  0.7811   1.9098   0.0562  -0.0392   3.0226    .
## mean_temp_constant  -0.0863  0.0081 -10.6009   <.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   0.217   0.512   1.238   8.418
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.171402   2.393869  -0.072    0.943
## mean_temp_constant -0.008692   0.095824  -0.091    0.928
##
## Residual standard error: 6.677 on 201 degrees of freedom
## Multiple R-squared:  4.093e-05,  Adjusted R-squared:  -0.004934
## F-statistic: 0.008227 on 1 and 201 DF,  p-value: 0.9278
```

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)")
```

SMD across studies with the same mean temperature (24 C)
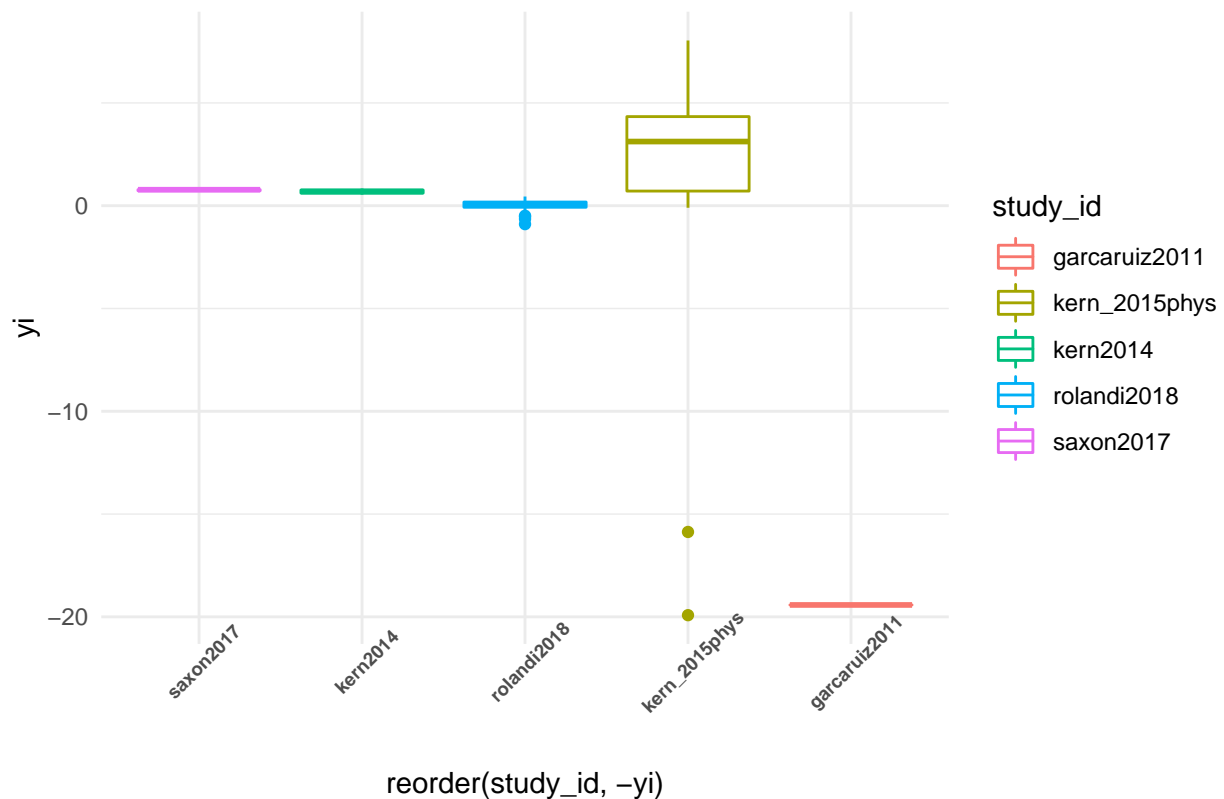

```r
#random effects model within subset data
fig13 <- rma.mv(yi, vi, data=common_temp,
                random = ~1 | experiment_id/ study_id,
                method="REML")
fig13
```

```
##
## Multivariate Meta-Analysis Model (k = 56; method: REML)
##
## Variance Components:
##
##                estim    sqrt  nlvls  fixed                    factor
## sigma^2.1     0.0000  0.0024      2     no              experiment_id
## sigma^2.2    67.1521  8.1946      6     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 55) = 2146.3005, p-val < .0001
##
## Model Results:
##
## estimate       se     zval     pval    ci.lb    ci.ub
##  -2.6186   3.3484  -0.7820   0.4342  -9.1814   3.9442
##
## ---
## 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
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
## -19.6416   0.2290   0.3368   0.7468   8.3146
##
## Coefficients: (1 not defined because of singularities)
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         -0.2767     0.6247  -0.443    0.659
## mean_temp_constant       NA         NA      NA       NA
##
## Residual standard error: 4.675 on 55 degrees of freedom
```

Question: How does genus affect response?

Figure 9.

```
#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)")
```

SMD across studies with the same study genus (Drosophila)
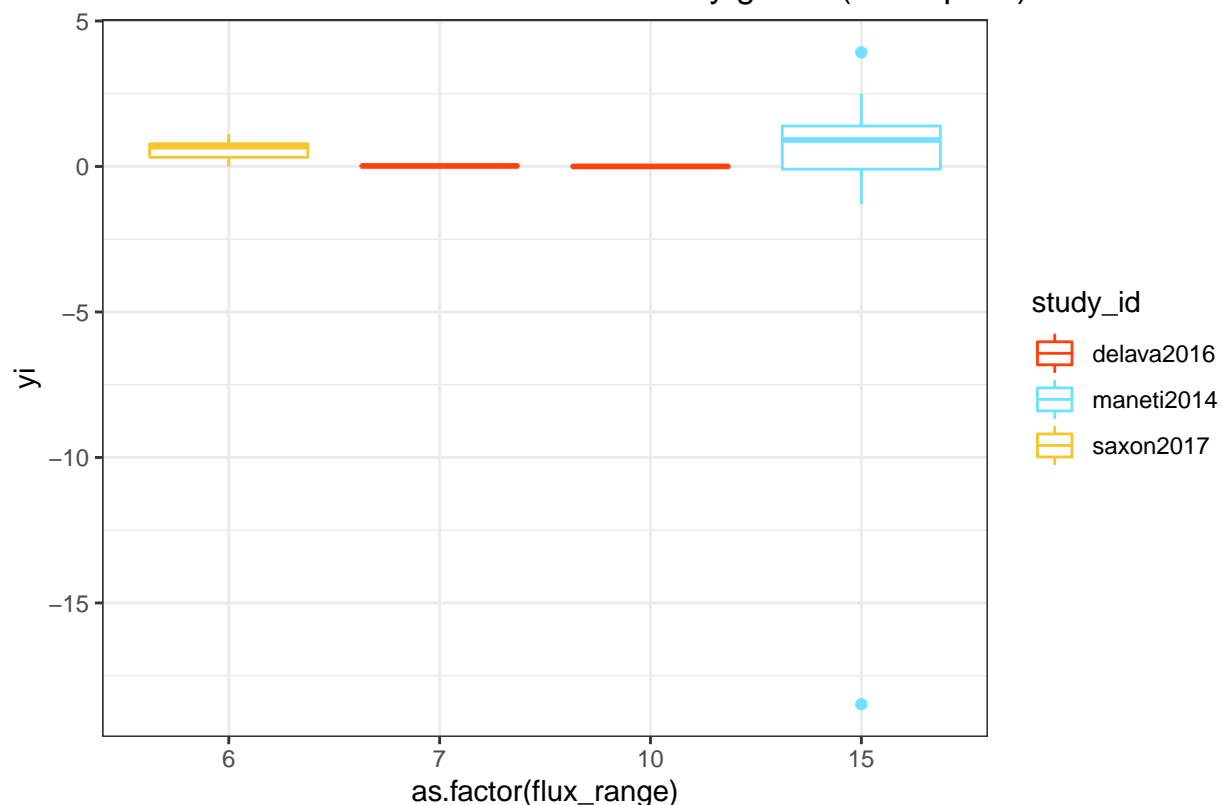

```r
#random effects model including org_level as a random variable
fig10 <- rma.mv(yi, vi, data=drosophila, mods = ~flux_range + study_id,
                random = ~1 | experiment_id/ study_id,
                method="REML")
fig10
```

```
## 
## 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")
```

SMD across genuses colored by body size
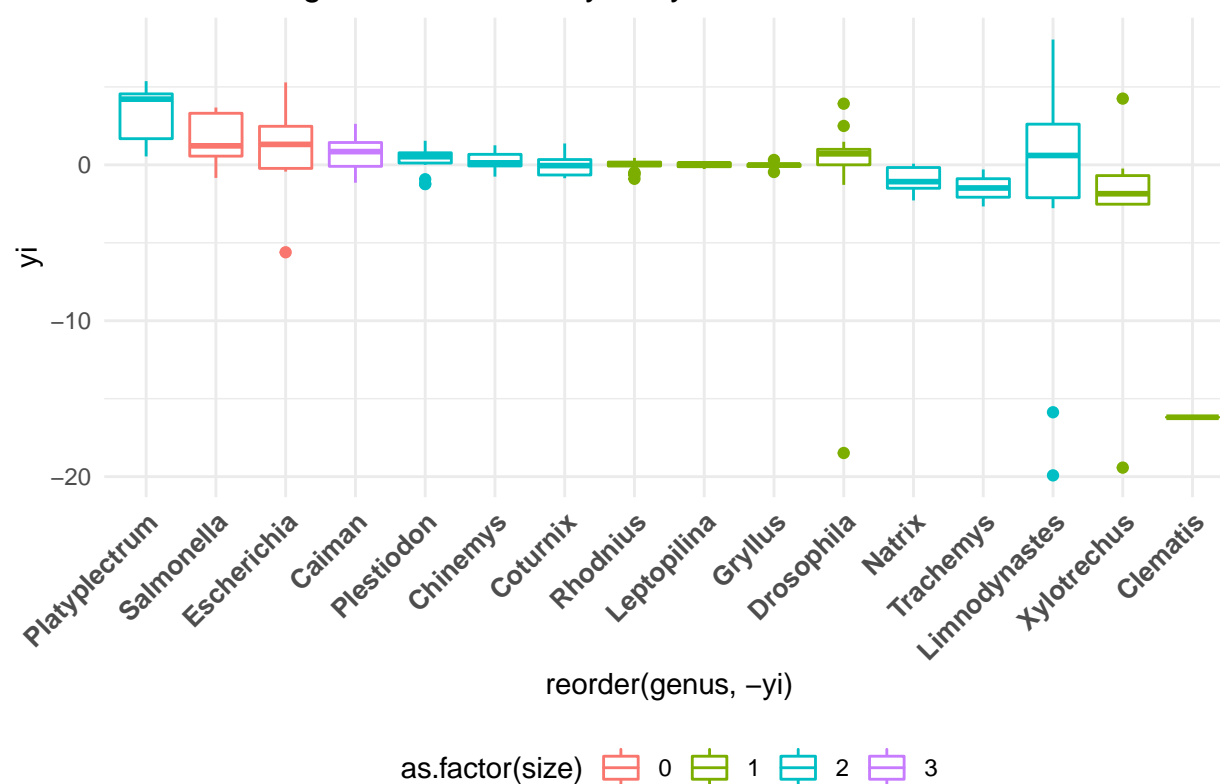

```
#random effects model including genus as a random variable
fig11 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~genus,
            random = ~1 | experiment_id/ study_id,
              method="REML")
fig11
```

```
##
## 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  0.8920  0.9445     23     no  experiment_id/study_id
##
## Test for Residual Heterogeneity:
## QE(df = 187) = 3871.5222, p-val < .0001
##
## Test of Moderators (coefficients 2:16):
## QM(df = 15) = 217.8816, p-val < .0001
##
## Model Results:
##
##                  estimate      se     zval    pval    ci.lb    ci.ub
## intrcpt            0.5791  0.9480   0.6108  0.5413  -1.2790   2.4371
## genusChinemys     -0.2569  1.1615  -0.2211  0.8250  -2.5334   2.0197
```

```
## genusClematis          -16.7689   1.5341  -10.9306  <.0001  -19.7757  -13.7620  ***
## genusCoturnix            -0.5885   1.3432   -0.4381  0.6613   -3.2211    2.0441
## genusDrosophila          -0.0185   1.0383   -0.0179  0.9858   -2.0536    2.0165
## genusEscherichia          0.5687   1.2012    0.4735  0.6359   -1.7855    2.9230
## genusGryllus             -0.6144   1.3390   -0.4588  0.6464   -3.2387    2.0100
## genusLeptopilina         -0.0365   1.0419   -0.0351  0.9720   -2.0786    2.0055
## genusLimnodynastes       -1.0945   1.1257   -0.9723  0.3309   -3.3008    1.1118
## genusNatrix              -1.6709   1.1681   -1.4304  0.1526   -3.9604    0.6186
## genusPlatyplectrum        1.6995   1.1435    1.4863  0.1372   -0.5416    3.9407
## genusPlestiodon          -0.2612   1.3402   -0.1949  0.8455   -2.8879    2.3655
## genusRhodnius            -0.5584   1.1597   -0.4815  0.6302   -2.8314    1.7146
## genusSalmonella           0.4783   1.1953    0.4001  0.6890   -1.8645    2.8211
## genusTrachemys           -1.7031   1.3456   -1.2656  0.2057   -4.3405    0.9343
## genusXylotrechus         -1.6640   1.3398   -1.2420  0.2142   -4.2899    0.9619
##
## ---
## 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  -0.301   0.067   0.765  17.544
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.7084     1.5951   0.444  0.65746
## genusChinemys       -0.4605     1.9331  -0.238  0.81198
## genusClematis      -16.8982     6.3803  -2.648  0.00878 **
## genusCoturnix       -0.6892     2.7046  -0.255  0.79913
## genusDrosophila     -0.8597     2.0884  -0.412  0.68106
## genusEscherichia     0.4926     2.3926   0.206  0.83712
## genusGryllus        -0.7449     2.7046  -0.275  0.78331
## genusLeptopilina    -0.7115     2.9841  -0.238  0.81181
## genusLimnodynastes  -2.8493     2.5220  -1.130  0.26002
## genusNatrix         -1.7006     3.1902  -0.533  0.59461
## genusPlatyplectrum   2.5973     2.9841   0.870  0.38520
## genusPlestiodon     -0.3916     2.1101  -0.186  0.85297
## genusRhodnius       -0.6904     1.8838  -0.366  0.71441
## genusSalmonella      0.8706     2.4523   0.355  0.72299
## genusTrachemys      -2.1914     4.6504  -0.471  0.63802
## genusXylotrechus   -14.0034     2.7046  -5.178 5.77e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.178 on 187 degrees of freedom
## Multiple R-squared:  0.2035, Adjusted R-squared:  0.1396
## F-statistic: 3.186 on 15 and 187 DF,  p-value: 0.0001102
```

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")
```


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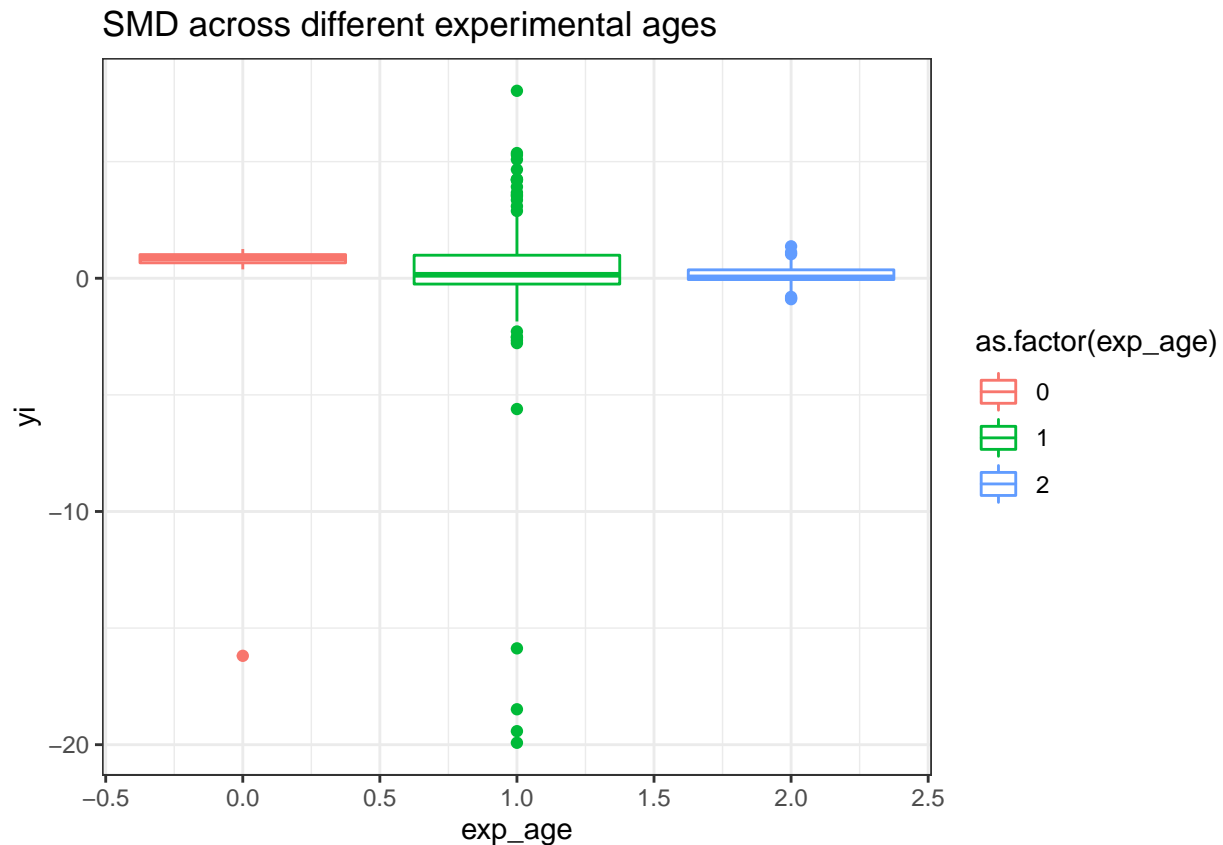
```
#random effects model including exp_age as a random variable
fig3 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~exp_age,
               random = ~1 | experiment_id/ study_id,
                 method="REML")
fig3
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                  factor
## sigma^2.1  0.0000  0.0002      3     no           experiment_id
## sigma^2.2  9.7610  3.1243     23     no  experiment_id/study_id
```

```
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 5524.6959, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 4.8667, p-val = 0.0274
##
## Model Results:
##
##          estimate       se     zval     pval    ci.lb     ci.ub
## intrcpt   -3.5084   1.5160  -2.3142   0.0207  -6.4798   -0.5371    *
## exp_age    2.5642   1.1624   2.2061   0.0274   0.2861    4.8424    *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#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
## -82.432   0.032   0.473   1.324   8.511
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.9220     1.1476  -0.803    0.423
## exp_age        0.4491     0.8752   0.513    0.608
##
## Residual standard error: 6.672 on 201 degrees of freedom
## Multiple R-squared:  0.001308,   Adjusted R-squared:  -0.00366
## F-statistic: 0.2633 on 1 and 201 DF,  p-value: 0.6084
```

Figure 12.

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

Variance across different experimental ages
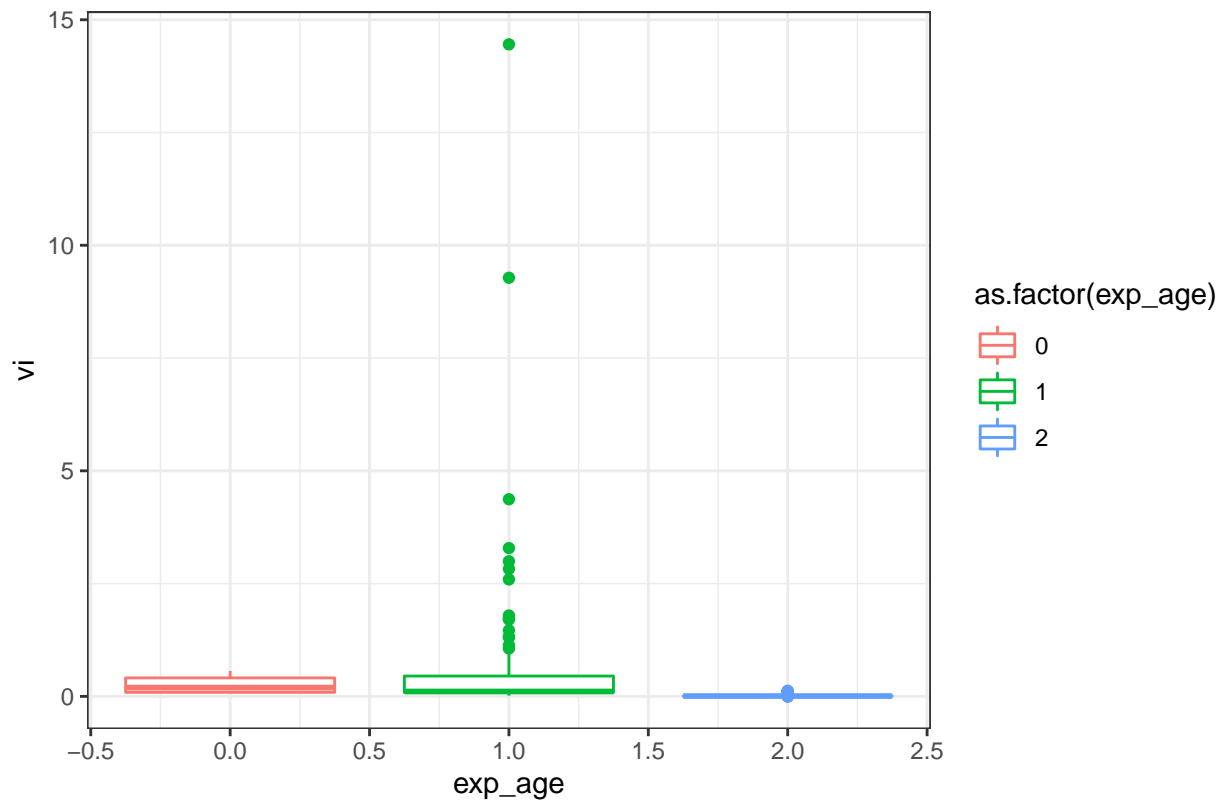

```r
count(normalized, exp_age)
```

```
##   exp_age   n
## 1       0  13
## 2       1 136
## 3       2  53
```

```r
#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
## -0.7998 -0.4468 -0.3512 -0.1753 13.9209
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.8859     0.2713   3.265  0.00129 **
## exp_age      -0.3518     0.2069  -1.700  0.09067 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 1.578 on 201 degrees of freedom
## Multiple R-squared:  0.01418,    Adjusted R-squared:  0.009271
## F-statistic:  2.89 on 1 and 201 DF,  p-value: 0.09067
```

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")
```
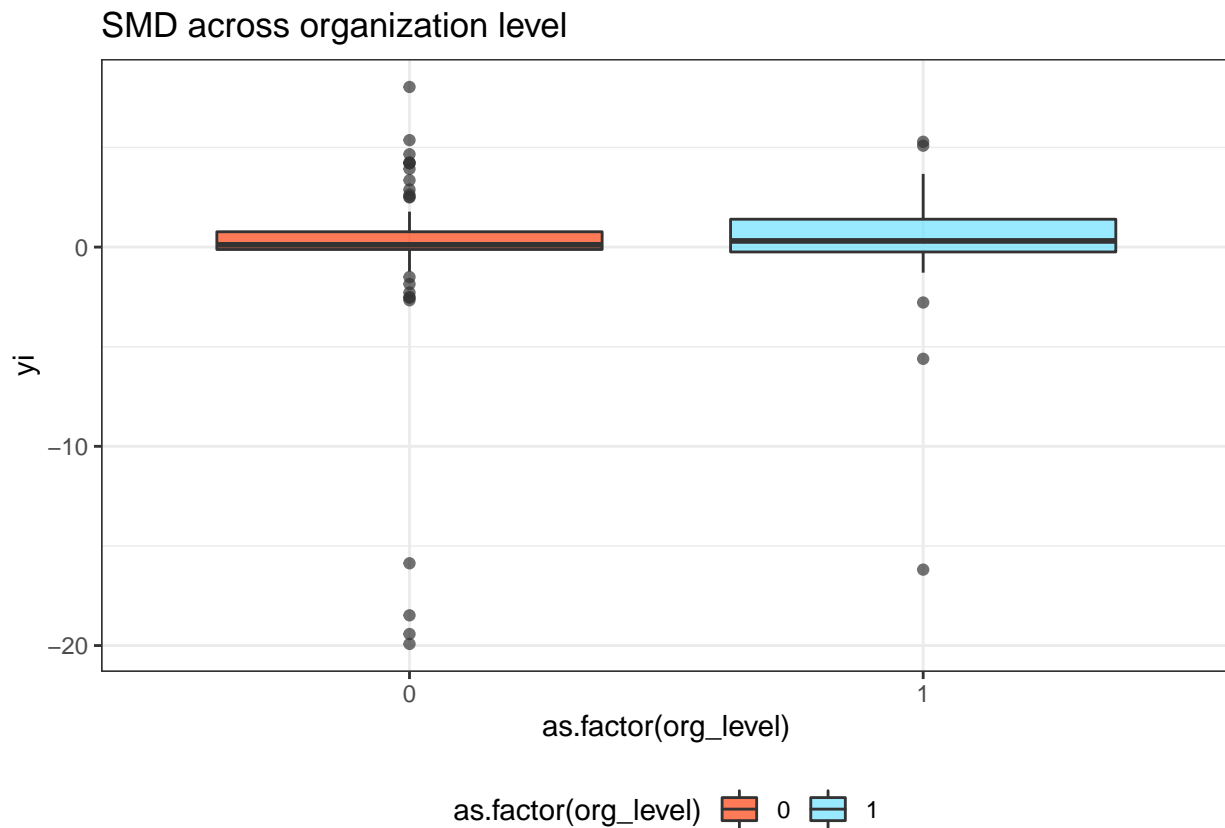


```
#random effects model including org_level as a random variable
fig5 <- rma.mv(yi, vi, data=dat_MA_ES, mods = ~org_level,
              random = ~1 | experiment_id/ study_id,
                method="REML")
fig5
```

```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
```

```
## 
## Variance Components:
## 
##             estim    sqrt   nlvls  fixed                    factor
## sigma^2.1   0.0000  0.0005      3     no           experiment_id
## sigma^2.2  11.0340  3.3217     23     no  experiment_id/study_id
## 
## Test for Residual Heterogeneity:
## QE(df = 201) = 5584.5912, p-val < .0001
## 
## Test of Moderators (coefficient 2):
## QM(df = 1) = 26.9530, p-val < .0001
## 
## Model Results:
## 
##             estimate      se     zval    pval     ci.lb    ci.ub
## intrcpt      -0.3940  0.6944  -0.5675  0.5704   -1.7549   0.9669
## org_level    -0.4309  0.0830  -5.1916  <.0001   -0.5935  -0.2682  ***
## 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#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   0.132   0.620   1.304   8.598
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.5602     0.5222  -1.073    0.285
## org_level      0.8926     1.1764   0.759    0.449
## 
## Residual standard error: 6.667 on 201 degrees of freedom
## Multiple R-squared:  0.002856,   Adjusted R-squared:  -0.002105
## F-statistic: 0.5756 on 1 and 201 DF,  p-value: 0.4489
```

Question: How does response variable affect response?

Figure 14.

```r
#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  0.0005      3     no                          experiment_id
## sigma^2.2  1.1317  1.0638     23     no                 experiment_id/study_id
## sigma^2.3  0.0494  0.2222     58     no  experiment_id/study_id/response_id
## 
## Test for Residual Heterogeneity:
## QE(df = 156) = 3362.1739, p-val < .0001
## 
## Test of Moderators (coefficients 2:47):
## QM(df = 46) = 301.2288, p-val < .0001
## 
## Model Results:
## 
##                                                        estimate      se
## intrcpt                                                  0.7651  0.6179
## resp_defaquatic speed                                   -1.8439  1.2838
## resp_defaverage cumulative number of eggs laid per female  -0.6509  1.2503
## resp_defaverage number of eggs laid per female          -0.8380  1.2503
## resp_defbody (centroid) size                            -0.4839  1.0727
## resp_defbody length                                     -0.8167  0.6643
## resp_defbody mass                                        0.0207  0.4261
## resp_defcarapace height                                  0.0186  0.5831
## resp_defcarapace width                                   0.0864  0.5836
## resp_defdaily energy expenditure                        -1.3331  1.2606
## resp_defdays to first slough                            -3.0470  1.2983
## resp_defdessication tolerance                           -1.1771  1.0661
## resp_defdevelopment time                                -0.6439  0.9320
## resp_defdevelopment to stages 35-37                     -1.2264  1.1748
## resp_defdevelopmental time                              -0.2328  1.0174
## resp_defdistance covered                                -0.9373  1.2797
## resp_defegg mass                                        -0.1998  1.2609
## resp_defegg to adult viability                          -2.9584  1.0642
## resp_deffore-limb length                                 0.8910  0.4560
## resp_defgermination                                    -16.9549  1.4579
## resp_defhatching success                                -0.3360  1.2628
## resp_defhead length                                      0.2518  0.4497
## resp_defhead width                                       0.5433  0.4504
## resp_defhind-limb length                                 0.3872  0.4489
## resp_defincubation period                               -0.4023  1.2620
## resp_defincubation time                                 -2.2675  1.2877
## resp_definfestation rate                                -0.7299  0.9319
## resp_defmass                                             0.6832  1.2667
## resp_defmaximal length                                  -1.4584  0.4567
## resp_defoffspring per mating                            -0.2905  0.8904
## resp_defovary mass, dry                                 -0.7837  1.2517
## resp_defoxidative damage                                -1.0621  1.2624
## resp_defpercent females                                 -0.5725  1.2619
## resp_defproductivity                                    -1.4666  1.0641
## resp_defrate of change                                   0.7569  1.2960
```

```
## resp_defsnout-vent length                                     0.6062  0.4512
## resp_defsprint speed                                          -0.6694  0.4491
## resp_defstartvation tolerance                                 -1.8855  1.0634
## resp_defsuccess of parasitism                                 -1.0187  0.9320
## resp_defsurvival                                              -0.7856  0.8919
## resp_defTAC                                                   -3.4342  1.2729
## resp_deftail length                                            0.2805  0.4301
## resp_defterrestrial speed                                     -0.6908  1.2796
## resp_deftestes mass, dry                                      -0.8179  1.2518
## resp_deftotal length                                          -0.0335  1.2649
## resp_deftotal offspring                                       -0.2270  0.8904
## resp_defwing centroid                                          0.0686  0.8811
##                                                                  zval    pval
## intrcpt                                                        1.2383  0.2156
## resp_defaquatic speed                                         -1.4363  0.1509
## resp_defaverage cumulative number of eggs laid per female     -0.5206  0.6027
## resp_defaverage number of eggs laid per female                -0.6703  0.5027
## resp_defbody (centroid) size                                  -0.4511  0.6519
## resp_defbody length                                           -1.2294  0.2189
## resp_defbody mass                                              0.0485  0.9613
## resp_defcarapace height                                        0.0319  0.9745
## resp_defcarapace width                                         0.1481  0.8823
## resp_defdaily energy expenditure                              -1.0575  0.2903
## resp_defdays to first slough                                  -2.3470  0.0189
## resp_defdessication tolerance                                 -1.1042  0.2695
## resp_defdevelopment time                                      -0.6909  0.4896
## resp_defdevelopment to stages 35-37                           -1.0439  0.2965
## resp_defdevelopmental time                                    -0.2288  0.8190
## resp_defdistance covered                                      -0.7325  0.4639
## resp_defegg mass                                              -0.1584  0.8741
## resp_defegg to adult viability                                -2.7799  0.0054
## resp_deffore-limb length                                       1.9540  0.0507
## resp_defgermination                                          -11.6294  <.0001
## resp_defhatching success                                      -0.2661  0.7902
## resp_defhead length                                            0.5600  0.5755
## resp_defhead width                                             1.2063  0.2277
## resp_defhind-limb length                                       0.8625  0.3884
## resp_defincubation period                                     -0.3188  0.7499
## resp_defincubation time                                       -1.7609  0.0783
## resp_definfestation rate                                      -0.7833  0.4335
## resp_defmass                                                   0.5394  0.5896
## resp_defmaximal length                                        -3.1935  0.0014
## resp_defoffspring per mating                                  -0.3263  0.7442
## resp_defovary mass, dry                                       -0.6261  0.5312
## resp_defoxidative damage                                      -0.8414  0.4002
## resp_defpercent females                                       -0.4536  0.6501
## resp_defproductivity                                          -1.3782  0.1681
## resp_defrate of change                                         0.5840  0.5592
## resp_defsnout-vent length                                      1.3437  0.1791
## resp_defsprint speed                                          -1.4906  0.1361
## resp_defstartvation tolerance                                 -1.7731  0.0762
## resp_defsuccess of parasitism                                 -1.0930  0.2744
## resp_defsurvival                                              -0.8808  0.3784
## resp_defTAC                                                   -2.6980  0.0070
```

```
## resp_deftail length                                            0.6522   0.5142
## resp_defterrestrial speed                                      -0.5399   0.5893
## resp_deftestes mass, dry                                       -0.6533   0.5135
## resp_deftotal length                                           -0.0265   0.9789
## resp_deftotal offspring                                        -0.2550   0.7987
## resp_defwing centroid                                           0.0779   0.9379
##                                                                   ci.lb      ci.ub
## intrcpt                                                        -0.4459     1.9762
## resp_defaquatic speed                                          -4.3601     0.6723
## resp_defaverage cumulative number of eggs laid per female      -3.1014     1.7997
## resp_defaverage number of eggs laid per female                 -3.2885     1.6125
## resp_defbody (centroid) size                                   -2.5863     1.6185
## resp_defbody length                                            -2.1188     0.4853
## resp_defbody mass                                              -0.8146     0.8559
## resp_defcarapace height                                        -1.1242     1.1614
## resp_defcarapace width                                         -1.0573     1.2301
## resp_defdaily energy expenditure                               -3.8039     1.1377
## resp_defdays to first slough                                   -5.5916    -0.5024
## resp_defdessication tolerance                                  -3.2666     0.9123
## resp_defdevelopment time                                       -2.4705     1.1827
## resp_defdevelopment to stages 35-37                            -3.5288     1.0761
## resp_defdevelopmental time                                     -2.2267     1.7612
## resp_defdistance covered                                       -3.4455     1.5708
## resp_defegg mass                                               -2.6712     2.2716
## resp_defegg to adult viability                                 -5.0442    -0.8725
## resp_deffore-limb length                                       -0.0027     1.7847
## resp_defgermination                                           -19.8124   -14.0974
## resp_defhatching success                                       -2.8111     2.1391
## resp_defhead length                                            -0.6296     1.1333
## resp_defhead width                                             -0.3395     1.4262
## resp_defhind-limb length                                       -0.4927     1.2670
## resp_defincubation period                                      -2.8758     2.0712
## resp_defincubation time                                        -4.7914     0.2564
## resp_definfestation rate                                       -2.5565     1.0966
## resp_defmass                                                   -1.7994     3.1659
## resp_defmaximal length                                         -2.3535    -0.5633
## resp_defoffspring per mating                                   -2.0356     1.4546
## resp_defovary mass, dry                                        -3.2371     1.6696
## resp_defoxidative damage                                       -3.5363     1.4121
## resp_defpercent females                                        -3.0458     1.9009
## resp_defproductivity                                           -3.5523     0.6191
## resp_defrate of change                                         -1.7833     3.2970
## resp_defsnout-vent length                                      -0.2781     1.4905
## resp_defsprint speed                                           -1.5496     0.2108
## resp_defstartvation tolerance                                  -3.9696     0.1987
## resp_defsuccess of parasitism                                  -2.8453     0.8080
## resp_defsurvival                                               -2.5336     0.9625
## resp_defTAC                                                    -5.9290    -0.9394
## resp_deftail length                                            -0.5625     1.1236
## resp_defterrestrial speed                                      -3.1988     1.8172
## resp_deftestes mass, dry                                       -3.2714     1.6356
## resp_deftotal length                                           -2.5126     2.4457
## resp_deftotal offspring                                        -1.9722     1.5181
## resp_defwing centroid                                          -1.6583     1.7955
```

```
## 
## 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,
```

31

```
                random = ~1 | experiment_id/ study_id /response_id,
                method="REML")
response_units_mod
```
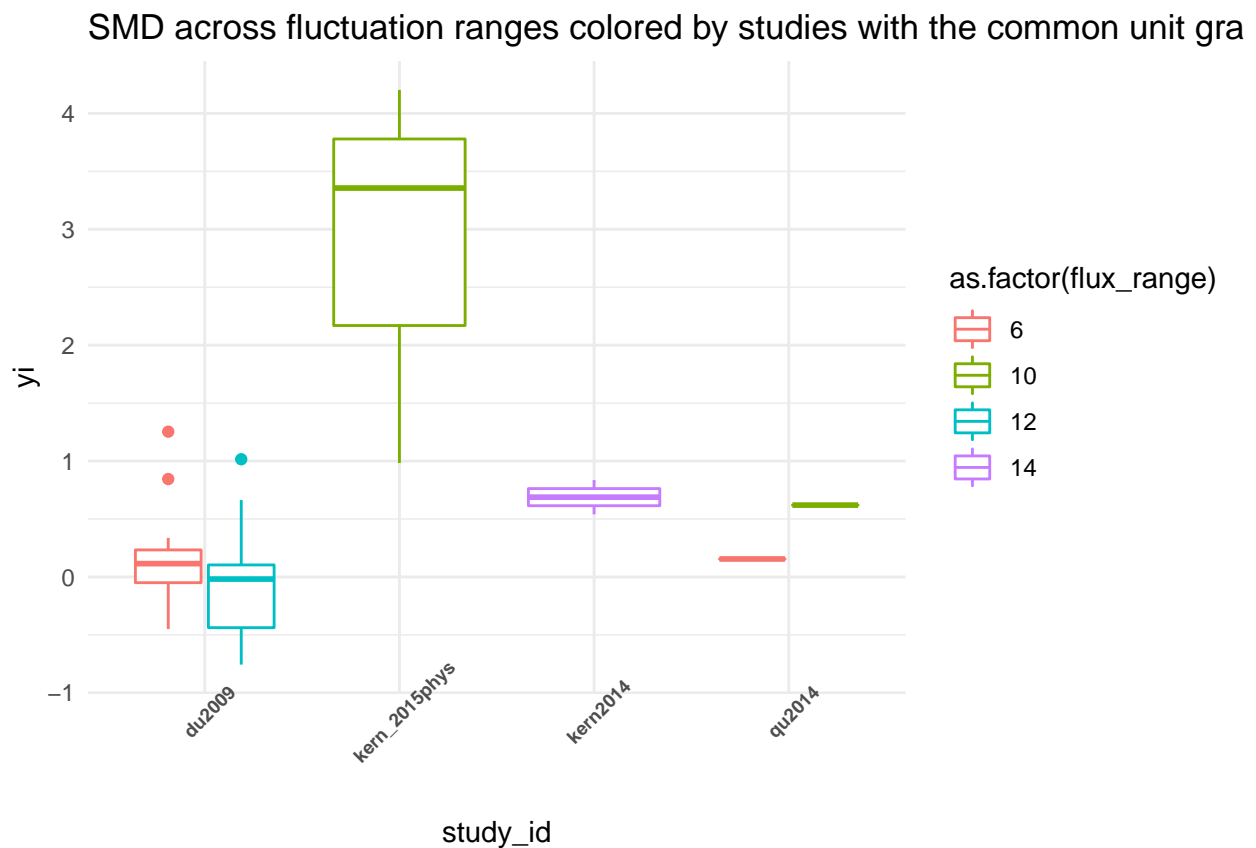
```
##
## Multivariate Meta-Analysis Model (k = 203; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                          factor
## sigma^2.1  0.0000  0.0004      3     no                   experiment_id
## sigma^2.2 13.2323  3.6376     23     no          experiment_id/study_id
## sigma^2.3  0.1505  0.3880     58     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 183) = 4135.6068, p-val < .0001
##
## Test of Moderators (coefficients 2:20):
## QM(df = 19) = 53.7881, p-val < .0001
##
## Model Results:
##
##                                          estimate       se     zval     pval
## intrcpt                                    1.5220   3.6742   0.4142   0.6787
## resp_unitsCFU * g dry weight manure^-1    -0.8243   5.1911  -0.1588   0.8738
## resp_unitscm                              -2.7028   3.8344  -0.7049   0.4809
## resp_unitsdays                            -2.7310   3.8135  -0.7161   0.4739
## resp_unitseggs laid                       -1.5013   4.4935  -0.3341   0.7383
## resp_unitsg                               -1.8582   3.8095  -0.4878   0.6257
## resp_unitskJ *day^-1 *kg^-1               -2.9796   3.8520  -0.7735   0.4392
## resp_unitsm                               -3.2358   3.8333  -0.8441   0.3986
## resp_unitsm * s^-1                        -3.0503   3.8323  -0.7959   0.4261
## resp_unitsmg                              -1.5573   5.1850  -0.3003   0.7639
## resp_unitsmm                              -1.7160   3.8152  -0.4498   0.6529
## resp_unitsnmol CHE / mgww                 -1.8189   5.1878  -0.3506   0.7259
## resp_unitsoffspring per mating            -1.0426   4.2440  -0.2457   0.8059
## resp_unitsoffspring/female                -2.6804   3.8516  -0.6959   0.4865
## resp_unitspercent                         -3.3689   3.8119  -0.8838   0.3768
## resp_unitspixels                          -1.6977   3.8539  -0.4405   0.6596
## resp_unitstime to  death (hour)           -2.7500   3.8383  -0.7165   0.4737
## resp_unitstotal offspring                 -0.9791   4.2440  -0.2307   0.8175
## resp_unitsuM Trolox Equivalents/ mgww     -4.1911   5.1903  -0.8075   0.4194
## resp_unitswing centroid                   -0.6880   4.2381  -0.1623   0.8710
##                                             ci.lb    ci.ub
## intrcpt                                   -5.6793   8.7232
## resp_unitsCFU * g dry weight manure^-1   -10.9987   9.3502
## resp_unitscm                             -10.2181   4.8125
## resp_unitsdays                           -10.2053   4.7433
## resp_unitseggs laid                      -10.3083   7.3057
## resp_unitsg                               -9.3247   5.6083
## resp_unitskJ *day^-1 *kg^-1              -10.5293   4.5701
## resp_unitsm                              -10.7490   4.2773
## resp_unitsm * s^-1                       -10.5613   4.4608
```

```
## resp_unitsmg                              -11.7197   8.6052
## resp_unitsmm                               -9.1937   5.7618
## resp_unitsnmol CHE / mgww                 -11.9868   8.3489
## resp_unitsoffspring per mating            -9.3607   7.2755
## resp_unitsoffspring/female               -10.2294   4.8685
## resp_unitspercent                        -10.8401   4.1024
## resp_unitspixels                          -9.2513   5.8559
## resp_unitstime to  death (hour)          -10.2730   4.7730
## resp_unitstotal offspring                 -9.2973   7.3390
## resp_unitsuM Trolox Equivalents/ mgww    -14.3640   5.9818
## resp_unitswing centroid                   -8.9945   7.6185
##
## ---
## 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")
```


SMD across fluctuation ranges colored by studies with the common unit gra

```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  0.4301  0.6558      2     no            experiment_id
## sigma^2.2  0.4115  0.6415      5     no  experiment_id/study_id
##
## Test for Heterogeneity:
## Q(df = 30) = 112.7702, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.4964  0.5770  0.8603  0.3896  -0.6345  1.6273
##
## ---
## 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
## -1.86411 -0.28023 -0.05915  0.19022  1.35561
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)            0.05915    0.13247   0.447    0.659
## study_idkern_2015phys  2.78814    0.39742   7.016 1.53e-07 ***
## study_idkern2014       0.62940    0.47764   1.318    0.199
## study_idqu2014         0.32825    0.47764   0.687    0.498
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.649 on 27 degrees of freedom
## Multiple R-squared:  0.6478, Adjusted R-squared:  0.6087
## F-statistic: 16.56 on 3 and 27 DF,  p-value: 2.655e-06
```