final figures for inclusion

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Question: How does response compare across studies and experiments?

Hypothesis: There should be differences across studies because of differences in experimental designs and study organism that would mean different magnitudes of response.

Initial conclusions: The studies overall are different in their responses but not owing to study_id or experiment. However, the mixed effects model does suggest some differences when you include study _id as a mod.

```
##
## Multivariate Meta-Analysis Model (k = 140; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                                factor
## sigma^2.1  0.2424  0.4924     15     no                              study_id
## sigma^2.2  0.1730  0.4159     19     no                study_id/experiment_id
## sigma^2.3  0.4156  0.6447     54     no  study_id/experiment_id/response_id
##
## Test for Heterogeneity:
## Q(df = 139) = 5373.4640, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.1453  0.1940  0.7491  0.4538  -0.2349  0.5256
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Relevant Plots

```
## `summarise()` has grouped output by 'study_id'. You can override using the `.groups` argument.
```

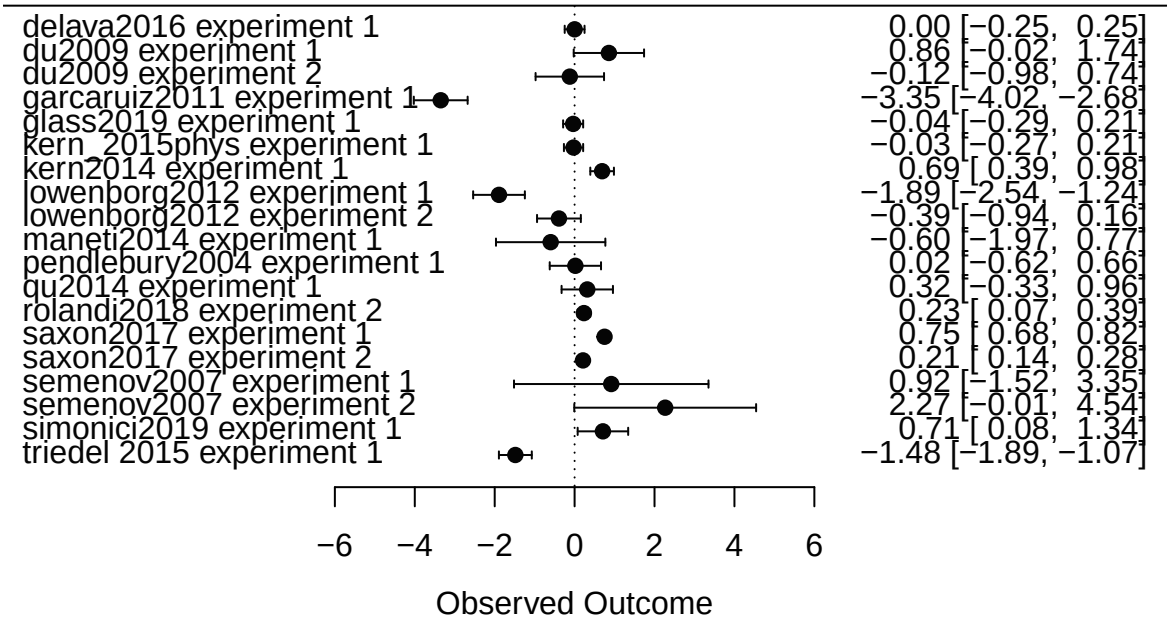

Figure 1. Forest plot broken out by study and experiment and their observed effected sizes and sampling variances.

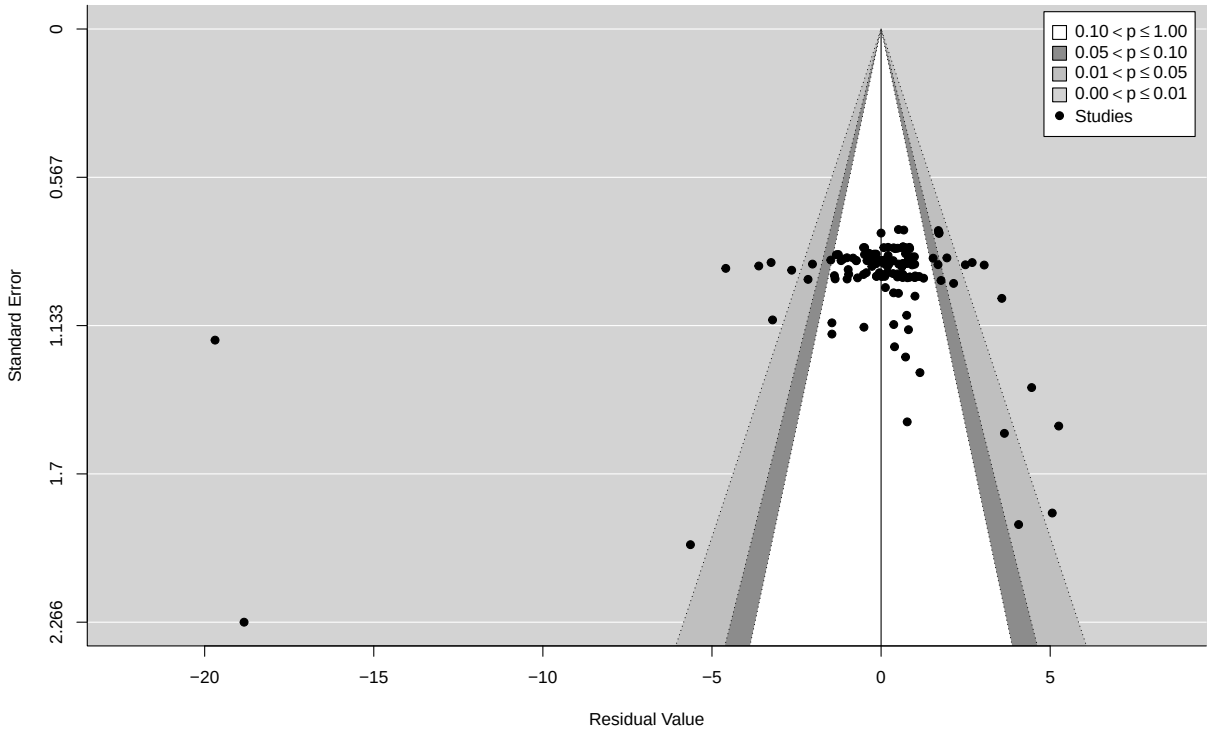

Figure 2. Well, from what I can gather, a majority of the effect sizes from our meta-analysis have a non-signficant effect size value. However, there is a population of a couple influential effect sizes that are significantly important.

```
##
## Family: gaussian
## Link function: identity
##
## Formula:
## yi ~ te(mean_temp_constant, flux_range, k = 7)
##
## Parametric coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.1388     0.2330   0.596    0.552
##
## Approximate significance of smooth terms:
##                                    edf Ref.df    F p-value
## te(mean_temp_constant,flux_range) 3.672  4.186 0.64   0.636
##
## R-sq.(adj) =  0.000217   Deviance explained = 2.68%
## GCV =  7.808  Scale est. = 7.5456    n = 139

## Warning: Ignoring unknown aesthetics: z
```

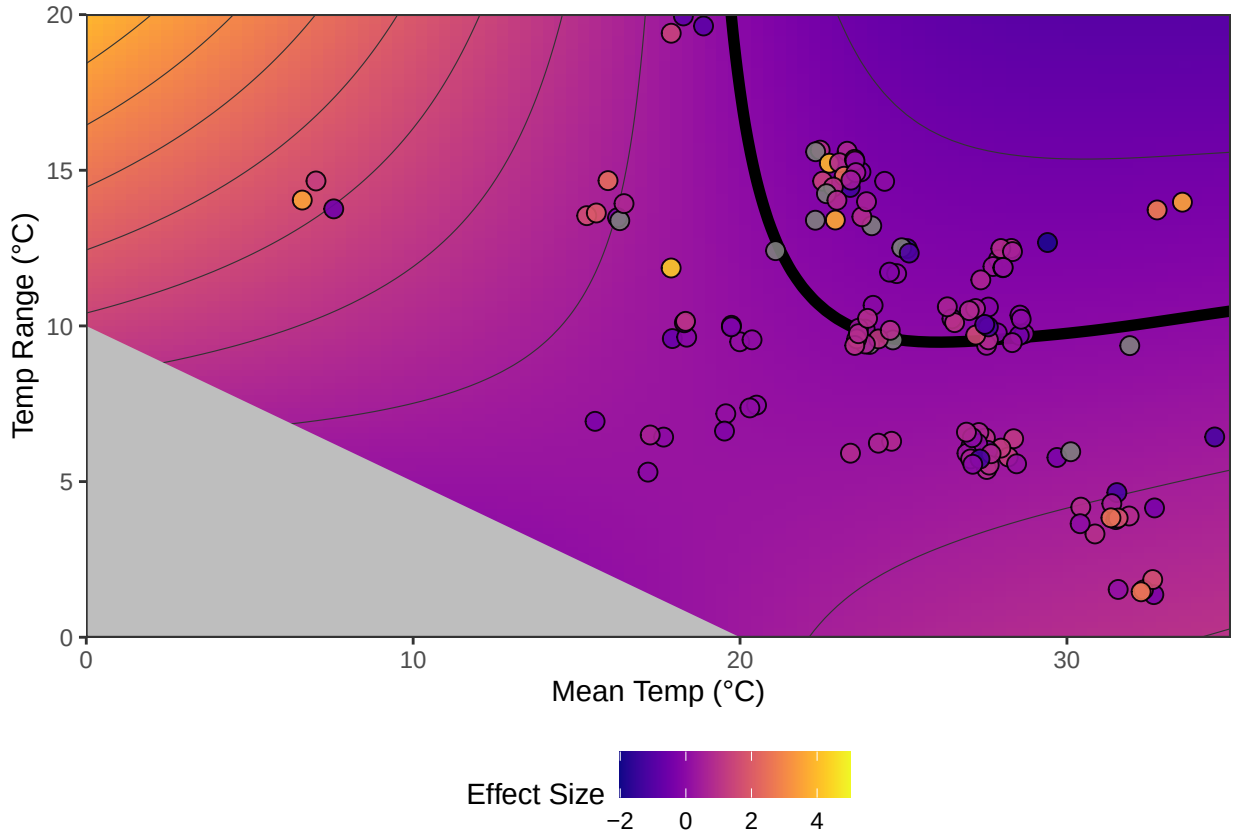

Figure 3. Contour plot of GAM generated effects sizes overlayed with raw effect sizes from the extracted dataset. Black lines denote the boundary from negative to positive effect sizes. Grey triange denotes excluded contour that lacks any raw data.

Question: How does response vary with study covariates?

Hypothesis: SMD between constant and fluctuating environments is most affected by temperature parameters (range and mean) but is also likely affected by demographic parameters (age, size, organization level)

Initial conclusions: Flux_range and mean temperature appear to be the most important contributers to variation in yi, though organization also contributes.

```
#with interaction term
full_rf_model<-rma.mv(yi, vi, data=dat_MA_ES, mods = ~flux_range * mean_temp_constant +
                        exp_age + size + org_level + resp_type,
                random = ~1 |  study_id/ experiment_id/ response_id,
                  method="REML")
full_rf_model
```

```
##
## Multivariate Meta-Analysis Model (k = 140; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0013  0.0363     15     no                            study_id
## sigma^2.2  0.5014  0.7081     19     no                study_id/experiment_id
## sigma^2.3  0.3450  0.5874     54     no  study_id/experiment_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 132) = 4892.9150, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 191.3722, p-val < .0001
##
## Model Results:
##
##                                estimate      se     zval    pval    ci.lb
## intrcpt                          0.8826  0.9494   0.9297  0.3525  -0.9781
## flux_range                       0.2753  0.0489   5.6300  <.0001   0.1794
## mean_temp_constant               0.0176  0.0184   0.9581  0.3380  -0.0184
## exp_age                         -0.5517  0.4023  -1.3715  0.1702  -1.3401
## size                            -0.3275  0.2869  -1.1415  0.2537  -0.8898
## org_level                       -0.6456  0.3315  -1.9475  0.0515  -1.2954
## resp_typetrait                   0.6099  0.3811   1.6002  0.1096  -0.1371
## flux_range:mean_temp_constant   -0.0137  0.0020  -6.7644  <.0001  -0.0177
##                                  ci.ub
## intrcpt                         2.7433
## flux_range                      0.3711  ***
## mean_temp_constant              0.0536
## exp_age                         0.2367
## size                            0.2348
## org_level                       0.0041    .
## resp_typetrait                  1.3568
## flux_range:mean_temp_constant  -0.0097  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#separate model with thermal history trait as a mod
full_rf_thermal<-rma.mv(yi, vi, data=dat_MA_ES, mods =
                          ~flux_range * mean_temp_constant + stressful,
                random = ~1 | experiment_id/ study_id/ response_id,
                  method="REML")
```

```
## Warning in rma.mv(yi, vi, data = dat_MA_ES, mods = ~flux_range *
## mean_temp_constant + : Rows with NAs omitted from model fitting.
```

```r
full_rf_thermal
```

```
##
## Multivariate Meta-Analysis Model (k = 132; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0000  0.0001      2     no                       experiment_id
## sigma^2.2  0.6219  0.7886     18     no                experiment_id/study_id
## sigma^2.3  0.4191  0.6474     53     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 127) = 2874.4152, p-val < .0001
##
## Test of Moderators (coefficients 2:5):
## QM(df = 4) = 6.4225, p-val = 0.1697
##
## Model Results:
##
##                                estimate      se     zval    pval    ci.lb
## intrcpt                         -2.2157  1.2026  -1.8425  0.0654  -4.5727
## flux_range                       0.0845  0.0780   1.0833  0.2787  -0.0684
## mean_temp_constant               0.1040  0.0480   2.1665  0.0303   0.0099
## stressfuly                      -0.0688  0.0934  -0.7366  0.4614  -0.2519
## flux_range:mean_temp_constant   -0.0040  0.0032  -1.2535  0.2100  -0.0102
##                                 ci.ub
## intrcpt                        0.1413   .
## flux_range                     0.2373
## mean_temp_constant             0.1980   *
## stressfuly                     0.1143
## flux_range:mean_temp_constant  0.0022
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#absolute yi model
absolute_model<-rma.mv(abs(yi), vi, data=dat_MA_ES, mods =
                          ~flux_range * mean_temp_constant +
                        exp_age + size + org_level + resp_type,
                random = ~1 | experiment_id/ study_id/ response_id,
                  method="REML")
absolute_model
```

```
##
## Multivariate Meta-Analysis Model (k = 140; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0071  0.0840      2     no                       experiment_id
## sigma^2.2  0.0868  0.2946     19     no                 experiment_id/study_id
## sigma^2.3  0.4000  0.6324     54     no  experiment_id/study_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 132) = 3282.6803, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 110.0220, p-val < .0001
##
## Model Results:
##
##                                estimate      se     zval    pval    ci.lb
## intrcpt                         -1.7984  0.7576  -2.3737  0.0176  -3.2834
## flux_range                       0.2593  0.0483   5.3688  <.0001   0.1646
## mean_temp_constant               0.0698  0.0181   3.8501  0.0001   0.0343
## exp_age                         -0.2533  0.2595  -0.9762  0.3290  -0.7619
## size                            -0.0057  0.1911  -0.0300  0.9761  -0.3803
## org_level                       -0.2847  0.3048  -0.9343  0.3502  -0.8820
## resp_typetrait                   0.2684  0.3535   0.7592  0.4477  -0.4244
## flux_range:mean_temp_constant   -0.0064  0.0020  -3.2064  0.0013  -0.0104
##                                  ci.ub
## intrcpt                         -0.3135    *
## flux_range                       0.3539  ***
## mean_temp_constant               0.1054  ***
## exp_age                          0.2553
## size                             0.3688
## org_level                        0.3126
## resp_typetrait                   0.9611
## flux_range:mean_temp_constant   -0.0025   **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Relevant plots

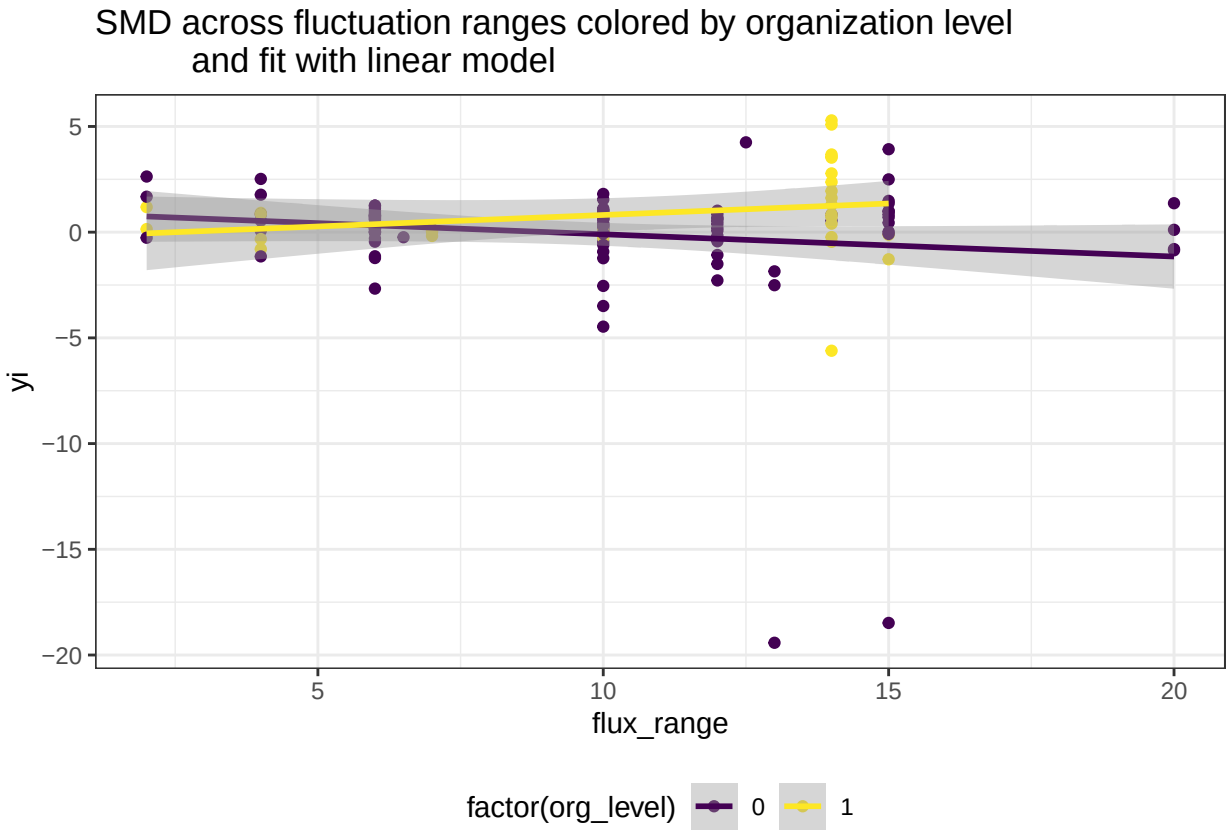

Figure 4. We can also see that there a difference in effect size in organization level responses across fluctuation range. Population level reponses trended positively across fluctuation ranges, while organism level responses trended negatively across fluctuation ranges.

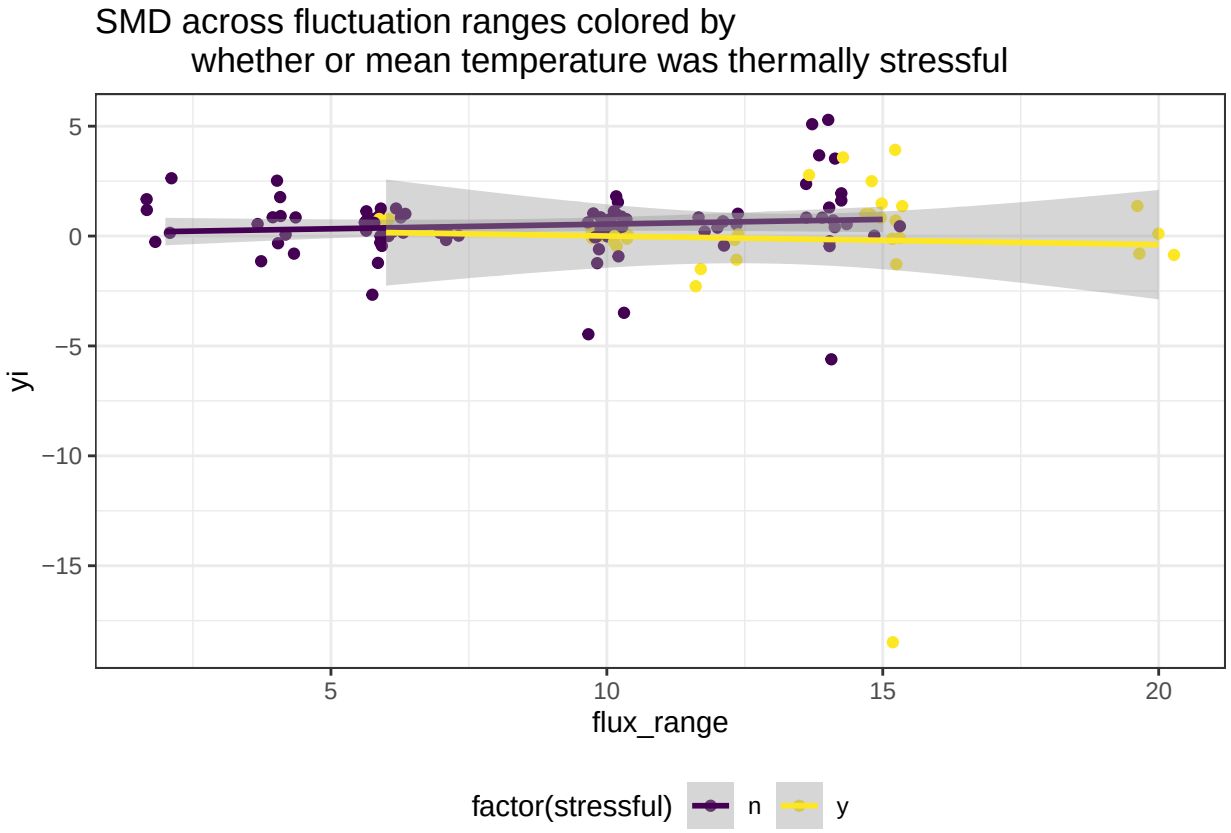

Figure 5. When we consider where the temperatures in the fluctuation range reach thermally stressful levels, there is a small difference between responses to stressful temperatures (negative) and non-stressful temperatures (positive).

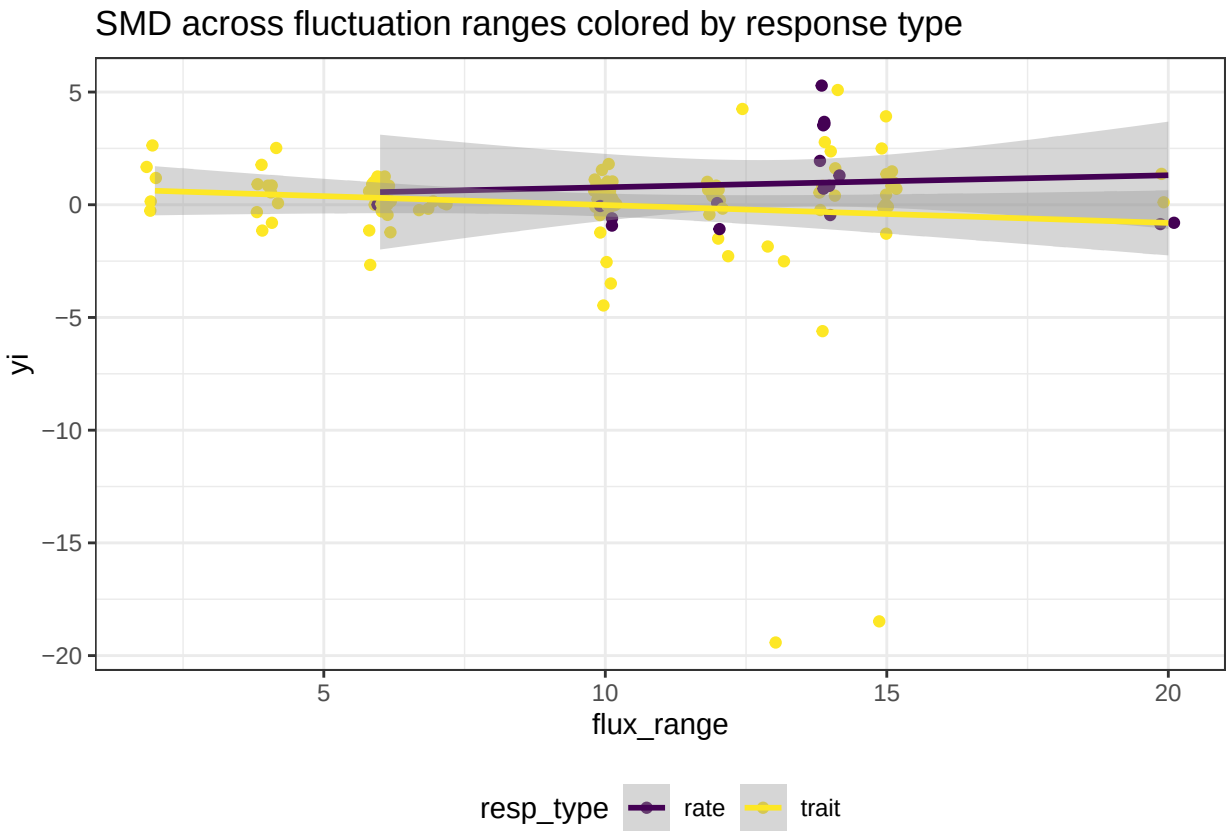

Figure 6. We cab see that the ranges at which traits are measured is much wider than rates, however, there appears to a minorly negative trend in effect sizes as traits increase in fluctuation range. The opposite is true for rates. Great way to show that there is a lack of information on rates in the collected dataset.

Running questions:

- How do all the different models sound? Does it make sense to have these different models?
- Do the figures match up with the story/questions associated with them?
- Jittering versus standard plotting for the regression plots? _____
  Supplementary Plots/Code

```
## 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.
```