manuscript_data_wrangling

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Acclimation Model

This data and analysis accounts for the temperatures at which organisms are reared and how their performance compares when exposed to different temperature. The results from this model has very similar results from the model I originally ran for my thesis...

```
simple_acclimation_model <- rma.mv(yi, vi, data=dat_acclim_ES,
                random = ~1 | study_id / experiment_id/ response_id,
                  method="REML")
simple_acclimation_model
```

```
##
## Multivariate Meta-Analysis Model (k = 334; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                                factor
## sigma^2.1  0.0000  0.0002     11     no                              study_id
## sigma^2.2  0.4761  0.6900     33     no                study_id/experiment_id
## sigma^2.3  0.2458  0.4958     61     no  study_id/experiment_id/response_id
##
## Test for Heterogeneity:
## Q(df = 333) = 3747.0551, p-val < .0001
##
## Model Results:
##
## estimate      se     zval    pval    ci.lb   ci.ub
##  -0.2145  0.1429  -1.5011  0.1333  -0.4946  0.0656
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
acclimation_model<-rma.mv(yi, vi, data=dat_acclim_ES, mods = ~flux_range * mean_temp_reared +
                          exp_age + size + org_level + exposure_temp,
                random = ~1 |  study_id/ experiment_id/ response_id,
                  method="REML")
```

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

```
## Warning in rma.mv(yi, vi, data = dat_acclim_ES, mods = ~flux_range *
## mean_temp_reared + : Redundant predictors dropped from the model.
```

```
acclimation_model
```

```
##
## Multivariate Meta-Analysis Model (k = 172; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.0000  0.0001      7     no                            study_id
## sigma^2.2  0.0000  0.0000     11     no               study_id/experiment_id
## sigma^2.3  0.0927  0.3045     13     no  study_id/experiment_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 165) = 806.5161, p-val < .0001
##
## Test of Moderators (coefficients 2:7):
## QM(df = 6) = 44.6988, p-val < .0001
##
## Model Results:
##
##                              estimate      se     zval    pval    ci.lb
## intrcpt                        4.8537  1.4715   3.2985  0.0010   1.9696
## flux_range                    -0.3849  0.1473  -2.6137  0.0090  -0.6736
## mean_temp_reared              -0.1570  0.0681  -2.3037  0.0212  -0.2905
## exp_age                       -0.2703  0.3888  -0.6953  0.4869  -1.0323
## size                          -0.9018  0.3697  -2.4391  0.0147  -1.6265
## exposure_temp                 -0.0038  0.0041  -0.9258  0.3545  -0.0119
## flux_range:mean_temp_reared    0.0188  0.0063   2.9944  0.0027   0.0065
##                                ci.ub
## intrcpt                       7.7377  ***
## flux_range                   -0.0963   **
## mean_temp_reared             -0.0234    *
## exp_age                       0.4917
## size                         -0.1772    *
## exposure_temp                 0.0043
## flux_range:mean_temp_reared   0.0311   **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Neglecting Acclimation

This uses the full dataset from my thesis (with more data from the additional search). Interesting that this time, mean temp is the only significant predictor?

```
simple_full_var_model <- rma.mv(yi, vi, data=dat_full_var_ES,
               random = ~1 | study_id / experiment_id/ response_id,
                 method="REML")
simple_full_var_model
```

```
##
## Multivariate Meta-Analysis Model (k = 351; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.1951  0.4417     28     no                           study_id
## sigma^2.2  0.0240  0.1549     42     no               study_id/experiment_id
## sigma^2.3  0.3611  0.6009     97     no  study_id/experiment_id/response_id
##
## Test for Heterogeneity:
## Q(df = 350) = 7189.9450, p-val < .0001
##
## Model Results:
##
## estimate      se    zval    pval    ci.lb   ci.ub
##   0.1038  0.1166  0.8908  0.3730  -0.1246  0.3323
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
full_var_model <-rma.mv(yi, vi, data=dat_full_var_ES, mods = ~flux_range * mean_temp_constant +
                          exp_age + size + org_level,
                random = ~1 |  study_id/ experiment_id/ response_id,
                  method="REML")
```

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

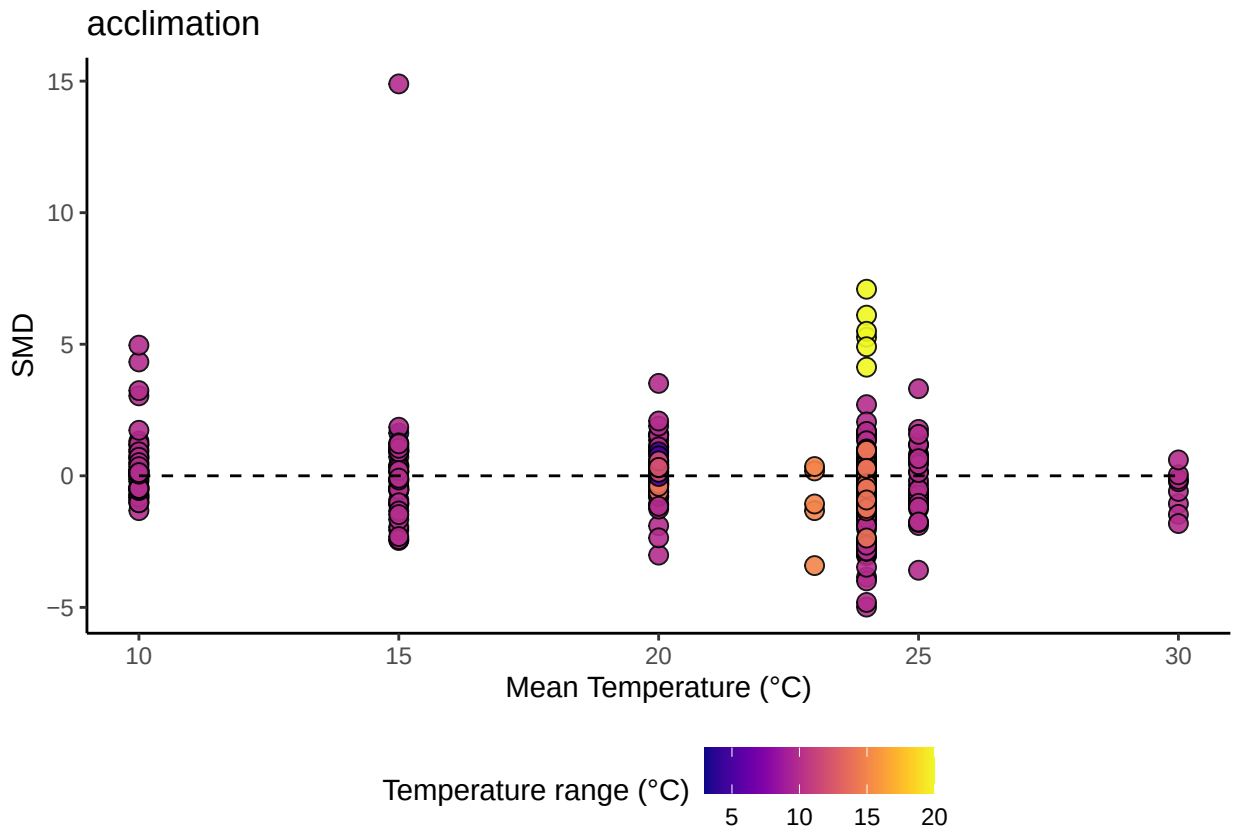
```
full_var_model
```

```
##
## Multivariate Meta-Analysis Model (k = 343; method: REML)
##
## Variance Components:
##
##             estim    sqrt  nlvls  fixed                              factor
## sigma^2.1  0.2488  0.4988     27     no                           study_id
## sigma^2.2  0.0937  0.3062     41     no               study_id/experiment_id
## sigma^2.3  0.3174  0.5634     95     no  study_id/experiment_id/response_id
##
## Test for Residual Heterogeneity:
## QE(df = 336) = 6485.2319, p-val < .0001
##
## Test of Moderators (coefficients 2:7):
## QM(df = 6) = 109.9623, p-val < .0001
##
## Model Results:
##
##                               estimate      se     zval    pval    ci.lb
## intrcpt                         1.3818  0.4545   3.0404  0.0024   0.4910
## flux_range                     -0.0274  0.0222  -1.2335  0.2174  -0.0710
## mean_temp_constant             -0.0511  0.0129  -3.9764  <.0001  -0.0763
```

```
## exp_age                           0.0699  0.0719   0.9715  0.3313  -0.0711
## size                             -0.1299  0.2169  -0.5988  0.5493  -0.5549
## org_level                        -0.2707  0.2367  -1.1439  0.2527  -0.7346
## flux_range:mean_temp_constant     0.0014  0.0010   1.3642  0.1725  -0.0006
##                                    ci.ub
## intrcpt                          2.2725   **
## flux_range                       0.0161
## mean_temp_constant              -0.0259  ***
## exp_age                          0.2109
## size                             0.2952
## org_level                        0.1931
## flux_range:mean_temp_constant    0.0033
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

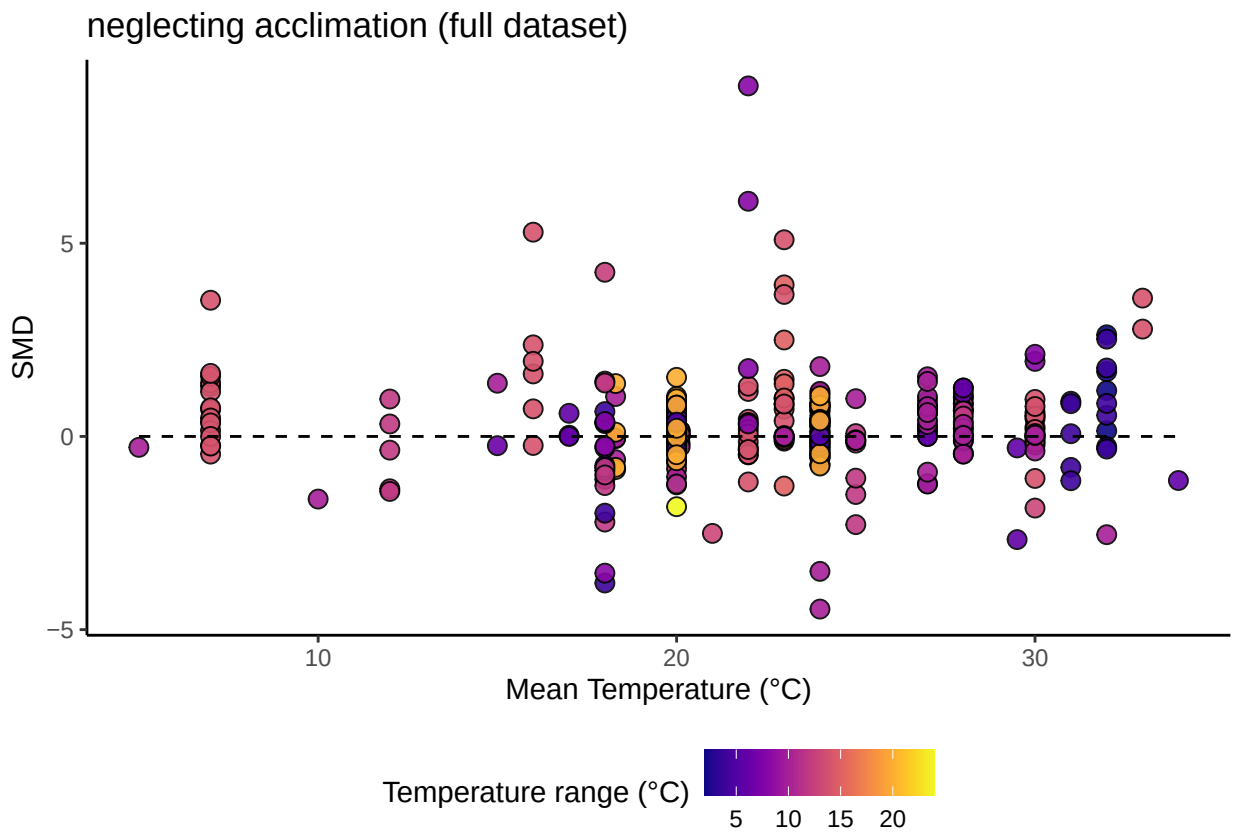
```
dat_acclim_ES %>%
  filter(yi > -5) %>%
ggplot(aes(x=mean_temp_reared, y = yi, fill=flux_range))+
  geom_point(alpha = 0.9, pch=21,size=3,colour="black", width = 0.7, height = 0.7)+
  scale_fill_viridis('Temperature range (°C)', option = "C")+
  theme_classic()+
  xlab("Mean Temperature (°C)")+
  ylab("SMD")+
  geom_line(y=0, linetype = "dashed")+
  theme(legend.position="bottom")+
  ggtitle("acclimation")
```

```
## Warning: Ignoring unknown parameters: width, height
```




```
dat_full_var_ES %>%
  filter(yi > -5) %>%
ggplot(aes(x=mean_temp_constant, y = yi, fill=flux_range))+
  geom_point(alpha = 0.9, pch=21,size=3,colour="black", width = 0.7, height = 0.7)+
  scale_fill_viridis('Temperature range (°C)', option = "C")+
  theme_classic()+
  xlab("Mean Temperature (°C)")+
  ylab("SMD")+
  geom_line(y=0, linetype = "dashed")+
  theme(legend.position="bottom")+
  ggtitle("neglecting acclimation (full dataset)")
```

```
## Warning: Ignoring unknown parameters: width, height
```


neglecting acclimation (full dataset)
SMD
5
0
−5
10
20
30
Mean Temperature (°C)
Temperature range (°C)
5
10
15
20