Meta Analyses Read Me

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Contents

The aim of the meta analysis approach is to combine effects from different studies to identify an overall effect. Here, for a given trait, we consider each lab as being a study in which the effect of *Population* has been assessed via a linear mixed-effect model. However, as we are not directly interested in finding overall effects and because *Population* has 9 levels, we perform a subgroup meta analysis that allows to test for differences between populations (each population being considered as a subgroup). In a way, this is conceptually similar to performing a regression analysis to test for the effect of *Population* on a given trait.

The input data for the subgroup meta analysis consists of the estimates and standard errors obtained for *Population* in the trait- and lab-specific linear mixed-effect models. Estimates are used as populations effects, and standard errors of those estimates are used as weights — to give more or less weight to labs depending on sample size and replication level.

This approach can be used to assess differences between populations and generate compound population estimates as input data for downstream analyses. Similarly, this approach can be applied to line random coefficents extracted from the mixed-effect models (in which *Line* is a random-effect variable) to generate compound line estimates — note that we are not interested in finding differences between lines here.

1 Population differentiation and compound estimates

1.1 Input data

Linear models population estimates are located in the LinearModelsPop directory and trait sub directories. Files with identical names but different extensions contain the same data, they are just in different formats to simplify data handling and browsing.

```
## [1] "DrosEU_PhenotypingWG/LinearModelsPop/all_models_pop_estimates_list.rds"
```

```
## [2] "DrosEU_PhenotypingWG/LinearModelsPop/all_models_pop_estimates.csv"
## [3] "DrosEU_PhenotypingWG/LinearModelsPop/all_models_pop_estimates.rds"
```

Population estimates are available as a list (File 1), in which each element contains estimates for a given trait, or as a table (collapsed list, File 2 and 3). These files contain the population estimates for all the traits.

Alternatively, population estimates are available for each trait separately, for example for Viability:

```
## [1] "DrosEU_PhenotypingWG/LinearModelsPop/Viability/Via_lmers_pop_model_estimates.rds"
## [2] "DrosEU_PhenotypingWG/LinearModelsPop/Viability/Via_lmers_pop_model_estimates.txt"
```

```
# read in models estimates for a specific trait, Viability, as a table
estimates_via <- readRDS("../LinearModelsPop/Viability/Via_lmers_pop_model_estimates.rds")
print(estimates_via)
```

```
##    Model Predictor Trait             Lab Sex Population  Estimate         SE
## 1   lmer       pop   Via          Gibert  NA         AK 1.0667275 0.02967040
## 2   lmer       pop   Via          Gibert  NA         GI 0.9032921 0.03436265
## 3   lmer       pop   Via          Gibert  NA         KA 1.0249903 0.03001214
## 4   lmer       pop   Via          Gibert  NA         MA 0.9379697 0.02981620
## 5   lmer       pop   Via          Gibert  NA         MU 1.0239845 0.02993727
## 6   lmer       pop   Via          Gibert  NA         RE 0.9440023 0.03337650
## 7   lmer       pop   Via          Gibert  NA         UM 1.0162526 0.03141729
## 8   lmer       pop   Via          Gibert  NA         VA 0.9254287 0.02993727
## 9   lmer       pop   Via          Gibert  NA         YE 0.7974415 0.02993727
## 10  lmer       pop   Via           Grath  NA         AK 0.9877438 0.02906218
## 11  lmer       pop   Via           Grath  NA         MU 0.9110075 0.02857528
## 12  lmer       pop   Via           Grath  NA         RE 0.9281670 0.02857528
## 13  lmer       pop   Via         Hoedjes  NA         AK 1.0951967 0.03072596
## 14  lmer       pop   Via         Hoedjes  NA         GI 0.8938243 0.03547929
## 15  lmer       pop   Via         Hoedjes  NA         KA 1.0290781 0.03072596
## 16  lmer       pop   Via         Hoedjes  NA         MA 1.0072746 0.03072596
## 17  lmer       pop   Via         Hoedjes  NA         MU 1.0459573 0.03072596
## 18  lmer       pop   Via         Hoedjes  NA         RE 0.9154123 0.03547929
## 19  lmer       pop   Via         Hoedjes  NA         UM 0.9867874 0.03332699
## 20  lmer       pop   Via         Hoedjes  NA         VA 0.9803627 0.03072596
## 21  lmer       pop   Via         Hoedjes  NA         YE 0.8465722 0.03072596
## 22    lm       pop   Via         Schmidt  NA         AK 0.9202803 0.06392642
## 23    lm       pop   Via         Schmidt  NA         GI 0.7324057 0.07381587
## 24    lm       pop   Via         Schmidt  NA         KA 1.1336048 0.06392642
## 25    lm       pop   Via         Schmidt  NA         MA 0.9330884 0.06738436
## 26    lm       pop   Via         Schmidt  NA         MU 0.8884818 0.06392642
## 27    lm       pop   Via         Schmidt  NA         RE 0.9435455 0.07381587
## 28    lm       pop   Via         Schmidt  NA         UM 1.0235692 0.07640668
## 29    lm       pop   Via         Schmidt  NA         VA 0.8896020 0.06392642
## 30    lm       pop   Via         Schmidt  NA         YE 0.8400844 0.06392642
## 31  lmer       pop   Via StamenkovicRadak  NA         AK 0.9882281 0.03647560
## 32  lmer       pop   Via StamenkovicRadak  NA         GI 0.8928932 0.04334278
## 33  lmer       pop   Via StamenkovicRadak  NA         KA 0.9430861 0.03637479
## 34  lmer       pop   Via StamenkovicRadak  NA         MA 0.8436346 0.03651680
## 35  lmer       pop   Via StamenkovicRadak  NA         MU 1.0009710 0.03641034
## 36  lmer       pop   Via StamenkovicRadak  NA         RE 0.9176397 0.03969883
## 37  lmer       pop   Via StamenkovicRadak  NA         UM 0.8802478 0.03788400
## 38  lmer       pop   Via StamenkovicRadak  NA         VA 0.8489644 0.03647471
## 39  lmer       pop   Via StamenkovicRadak  NA         YE 0.7770819 0.03637479
## 40  lmer       pop   Via            Zwaan  NA         AK 1.0720229 0.03516694
```

```
## 41  lmer       pop   Via            Zwaan  NA         GI 0.9379069 0.04065699
## 42  lmer       pop   Via            Zwaan  NA         KA 1.0788358 0.03542601
## 43  lmer       pop   Via            Zwaan  NA         MA 1.0265446 0.03548531
## 44  lmer       pop   Via            Zwaan  NA         MU 1.0188916 0.03608115
## 45  lmer       pop   Via            Zwaan  NA         RE 0.9497071 0.03902655
## 46  lmer       pop   Via            Zwaan  NA         UM 1.1053811 0.03722279
## 47  lmer       pop   Via            Zwaan  NA         VA 1.0522722 0.03599485
## 48  lmer       pop   Via            Zwaan  NA         YE 0.8138393 0.03591688
```

1.2 Meta analyses model

We run meta analyses trait- and sex-wise using a random-effect model since we assume that effects measured in each lab do not only deviate because of sampling error alone but also because of other sources of variance — such as lab effect.

```
# packages and function
library(meta)
library(metafor)
source("../Code/functions.R") # get makeEffects
```

```
# read in models estimates for all models as a list
estimates_list <- readRDS("../LinearModelsPop/all_models_pop_estimates_list.rds")

# meta analysis
meta_via <- metagen(data = makeEffects(estimates_list$via_lmer),
                    TE = Y,
                    seTE = SE,
                    studlab = Study,
                    fixed = FALSE,
                    random = TRUE,
                    method.tau = "REML")
```

```
# subgroup meta analysis
meta_via_sub <- update.meta(meta_via, subgroup = Population, tau.common = FALSE)
```

As discussed in early September 2022 at the "analyses task force" meeting, partial data (incomple data sets) from Posnien's lab has been removed prior to running analyses for Wing Area and Thorax Length.

Importantly meta analyses have been run for all the traits, including those that have been measured in single labs (Locomotor Activity and Egg-to-pupa Development Time) and thus for which there is no data to combine. Obviously, results from these analyses are meaningless but it allows us to keep those traits in the loop and to streamline the generation of compound estimates — they will be equal to linear model estimates in the case of the aforementioned traits. The same applies to Thorax Length males, a trait for which some populations have been measured only in one lab. *Population* subgroup meta analyses have been run for the following 33 traits / sub traits / sex combinations (only 26 of them are actually relevant):

```
##  [1] "CCRT_F_lmers"          "CCRT_M_lmers"          "CSM_F_lmers"
##  [4] "CSM_M_lmers"           "DT_A_F_lmers"          "DT_A_M_lmers"
##  [7] "DT_P_NA_lmers"         "Dia_F_glmers"          "DW_F_lmers"
## [10] "DW_M_lmers"            "Fec_F_lmers"           "HSM_F_lmers"
## [13] "HSM_M_lmers"           "LS_F_lmers"            "LS_M_lmers"
## [16] "LA_AbsPhase_B_lmers"   "LA_Activity_B_lmers"   "LA_CircPhase_B_lmers"
## [19] "LA_NDlog2_B_lmers"     "LA_Period_B_lmers"     "Pgm_T4_F_lmers"
## [22] "Pgm_T5_F_lmers"        "Pgm_T6_F_lmers"        "Pgm_Total_F_lmers"
## [25] "SR_F_lmers"            "SR_M_lmers"            "TL_F_lmers"
## [28] "TL_M_lmers"            "Via_NA_lmers"          "WA_L_F_lmers"
## [31] "WA_L_M_lmers"          "WA_R_F_lmers"          "WA_R_M_lmers"
```

Also note that glmer estimates (not lmer) were used as input for the Diapause meta analysis.

1.3 Meta analyses output

All meta analyses related outputs are saved in the MetaAnalyses directory and trait sub directories. For example all the *Population* subgroup analysis files for Viability are listed below:

```
## [1] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta.rds"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta_summary.txt"
## [3] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta_summary_effect.png"
## [4] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta_summary_effect.pdf"
## [5] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta_compound_estimates.txt"
## [6] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_pop_meta_compound_estimates.rds"
```

File naming is consistent between traits. The *trait* or *sub trait* abbrevation (Via for Viability, for other traits such as Wing Area Left it will be WA_L) is followed by *sex* (NA because not available for Viability, otherwise F or M, and sometimes B when measurements were done on both sexes at the same time) and by the type of *models* the input data comes from (lmers, can also be glmers). Files with identical names but with different extensions contain the same data but are saved in different formats to facilitate both data handling and browsing. Raw results of the subgroup analysis are stored in Files 1 and 2, which are then used to extract population summary effects (compound estimates) and analysis statistics (Files 5 and 6). Files 3 and 4 are graphic representations of the subgroup analysis results.

1.3.1 Model results

Below is how subgroup meta analyses raw results look like (files 1 and 2), again for Viability:

```
# meta results for Viability
meta_via <- readRDS("../MetaAnalyses/Viability/Via_NA_lmers_pop_meta.rds")
print(meta_via)
```

```
## Number of studies combined: k = 48
##
##                                      95%-CI     z p-value
## Random effects model 0.9550 [0.9300; 0.9799] 75.03       0
##
## Quantifying heterogeneity:
##  tau^2 = 0.0062 [0.0038; 0.0107]; tau = 0.0784 [0.0618; 0.1037]
##  I^2 = 82.2% [77.1%; 86.2%]; H = 2.37 [2.09; 2.69]
##
## Test of heterogeneity:
##       Q d.f.  p-value
##  264.43   47 < 0.0001
##
## Results for subgroups (random effects model):
##                   k                  95%-CI   tau^2    tau     Q   I^2
## Population = YE   5 0.8126 [0.7814; 0.8438]       0      0  2.62  0.0%
## Population = RE   6 0.9314 [0.9019; 0.9610]       0      0  0.73  0.0%
## Population = GI   5 0.8954 [0.8594; 0.9314] <0.0001 0.0002  6.03 33.6%
## Population = MU   6 0.9886 [0.9400; 1.0371]  0.0023 0.0484 15.49 67.7%
## Population = MA   5 0.9519 [0.8850; 1.0187]  0.0043 0.0653 16.69 76.0%
## Population = UM   5 1.0009 [0.9256; 1.0762]  0.0056 0.0746 18.53 78.4%
## Population = KA   5 1.0330 [0.9799; 1.0861]  0.0022 0.0472 10.25 61.0%
## Population = VA   5 0.9429 [0.8723; 1.0136]  0.0050 0.0704 18.28 78.1%
## Population = AK   6 1.0313 [0.9849; 1.0777]  0.0020 0.0452 13.58 63.2%
##
```

```
## Test for subgroup differences (random effects model):
##                         Q d.f.  p-value
## Between groups   100.09    8 < 0.0001
##
## Details on meta-analytical method:
## - Inverse variance method
## - Restricted maximum-likelihood estimator for tau^2
## - Q-profile method for confidence interval of tau^2 and tau
```

We are mainly interested in the second part of the meta analysis output, starting from the "Results for subgroups (random effects model)" table. For each population one can extract a summary effect (compound estimate) with its 95% confidence interval as well as the number of labs that have contributed to phenoytyping (k). Differences between populations can be assessed with the Q statistic shown in the "Test for subgroup differences (random effects model)" part of the model output. In short, the Q statistic quantifies the heterogeneity between the different subgroups, the higher the Q value the greater the heterogeneity. Under the null hypothesis of no differences between subgroups, Q follows a central χ^2 distribution with degrees of freedom equal to k subgroups - 1, so one can report a p value for any observed value of Q. In the case of Viability, $Q = 100.09$ and is statistically significant ($p < 0.0001$), meaning that *Population* does have a significant effect on Viability.

1.3.2 Compound population estimates

Compound population estimates (population summary effects) and their 95% confidence intervals were extracted from the meta analyses results and stored in Files 5 and 6. This is how those files look like for Viability:

```
# read in population compound estimates
comp_pop_via <- readRDS("../MetaAnalyses/Viability/Via_NA_lmers_pop_meta_compound_estimates.rds")
print(select(comp_pop_via, -c(Models, Sex, SE, N_lab_av))) # for clarity
```

```
##   Trait Population  Estimate     LLEst     ULEst        Q            P N_lab
## 1   Via         YE 0.8125780 0.7813953 0.8437606 100.0945 4.083404e-18     5
## 2   Via         RE 0.9314387 0.9018622 0.9610153 100.0945 4.083404e-18     6
## 3   Via         GI 0.8953657 0.8593534 0.9313780 100.0945 4.083404e-18     5
## 4   Via         MU 0.9885519 0.9400152 1.0370886 100.0945 4.083404e-18     6
## 5   Via         MA 0.9518613 0.8850298 1.0186928 100.0945 4.083404e-18     5
## 6   Via         UM 1.0009199 0.9255974 1.0762424 100.0945 4.083404e-18     5
## 7   Via         KA 1.0329804 0.9798800 1.0860809 100.0945 4.083404e-18     5
## 8   Via         VA 0.9429267 0.8722642 1.0135892 100.0945 4.083404e-18     5
## 9   Via         AK 1.0312744 0.9848986 1.0776502 100.0945 4.083404e-18     6
```

1.3.3 Visualisation of the meta analyses results

Results can be represented with a simplified forest plot (Files 3 and 4) where population summary effects (compound estimates) and populations are represented on x and y axis, respectively (Figure 1). Figure 1 below shows results for Viability.

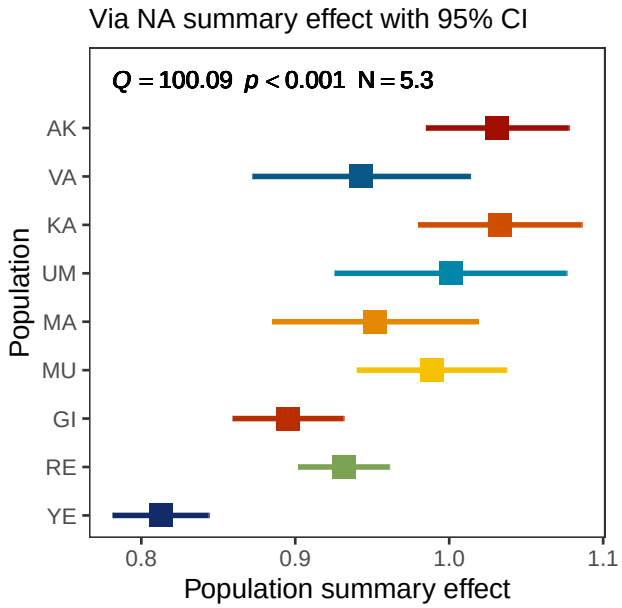

Figure 1: Subgroup meta analysis for Viability. N indicates the average number of labs that have phenotyped the different populations.

1.3.4 Compiled data for all traits

Compiled population compound estimates, meta analyses statistics and composite figures for all traits are available in the MetaAnalyses directory:

```
## [1] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_compound_estimates_list.rds"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_compound_estimates.csv"
## [3] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_compound_estimates.rds"
## [4] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_pvalues.csv"
## [5] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_pvalues.pdf"
## [6] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_pvalues.rds"
## [7] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_summary_effect.pdf"
## [8] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_pop_meta_summary_effect.png"
```

All meta analyses main statistics are compiled in a single table (Files 4 and 6). P values were corrected for multiple testing using Bonferroni and Benjamini Hochberg procedures (For Bonferroni n= 26 which corresponds to the number of "relevant" meta analyses that have been performed, see above). As mentioned earlier in the document, statistics for Locomotor Activity, Egg-to-pupa Development Time and Thorax Length in males should not be considered and have been filtered out from this table, leaving results for only 26 traits.

```
# meta compiled statistics
meta_stats <- readRDS("../MetaAnalyses/all_models_pop_meta_pvalues.rds")
print(meta_stats %>% mutate_at(vars(contains(c("P", "Q"))), round, 3))
```

```
##    Models     Trait Sex       Q     P Min_lab Max_lab P_bonf  P_bh
## 1   lmers      CCRT   F   8.685 0.370       2       2  1.000 0.641
## 2   lmers      CCRT   M  12.169 0.144       2       2  1.000 0.374
## 3   lmers       CSM   F   1.051 0.998       3       3  1.000 0.998
## 4   lmers       CSM   M   4.721 0.787       3       3  1.000 0.974
## 5   lmers      DT_A   F   7.608 0.473       5       6  1.000 0.723
## 6   lmers      DT_A   M   8.746 0.364       5       6  1.000 0.641
## 7  glmers       Dia   F   1.434 0.994       3       3  1.000 0.998
```

```
## 8   lmers        DW   F  10.624 0.224       3       3  1.000 0.485
## 9   lmers        DW   M  23.121 0.003       3       3  0.084 0.010
## 10  lmers       Fec   F   3.535 0.896       2       2  1.000 0.998
## 11  lmers       HSM   F  19.097 0.014       2       2  0.373 0.041
## 12  lmers       HSM   M  23.133 0.003       2       2  0.083 0.010
## 13  lmers        LS   F  11.773 0.162       3       3  1.000 0.382
## 14  lmers        LS   M  26.180 0.001       3       3  0.025 0.004
## 15  lmers    Pgm_T4   F   6.170 0.628       3       3  1.000 0.860
## 16  lmers    Pgm_T5   F   1.254 0.996       3       3  1.000 0.998
## 17  lmers    Pgm_T6   F   6.855 0.552       3       3  1.000 0.798
## 18  lmers Pgm_Total   F   5.491 0.704       3       3  1.000 0.915
## 19  lmers        SR   F   9.567 0.297       3       3  1.000 0.594
## 20  lmers        SR   M   7.813 0.452       3       3  1.000 0.723
## 21  lmers        TL   F   1.912 0.984       2       3  1.000 0.998
## 22  lmers       Via  NA 100.095 0.000       5       6  0.000 0.000
## 23  lmers      WA_L   F  91.941 0.000       3       3  0.000 0.000
## 24  lmers      WA_L   M  96.760 0.000       3       3  0.000 0.000
## 25  lmers      WA_R   F  89.065 0.000       3       3  0.000 0.000
## 26  lmers      WA_R   M  96.017 0.000       3       3  0.000 0.000
```

Statistics such as Q and p values for all traits can be visualised on a single graph (File 5 and Figure 2).

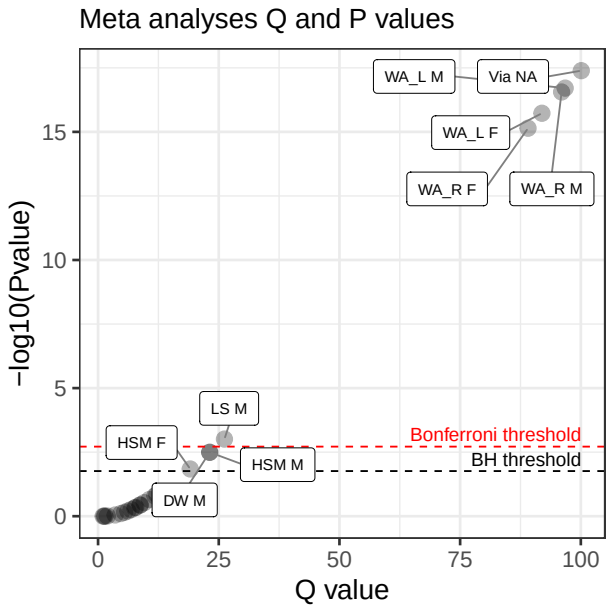

Figure 2: All meta analyses Q statistics and p values.

Compiled compound population estimates for all traits are available both as a list (File 1) or a table (collapsed list, Files 2 and 3).

```
# population compoud estimates as list
comp_pop_list <- readRDS("../MetaAnalyses/all_models_pop_meta_compound_estimates_list.rds")
lapply(comp_pop_list, function(x) select(x, -c(Models, SE, N_lab_av))) %>% head(4)
```

```
## $CCRT_F_lmers_pop_meta_compound_estimates
##   Trait Sex Population Estimate    LLEst    ULEst        Q         P N_lab
## 1  CCRT   F         YE 1686.687 1276.713 2096.660 8.684978 0.3695636     2
## 2  CCRT   F         RE 1534.213 1319.867 1748.560 8.684978 0.3695636     2
```

```
## 3  CCRT   F         GI 1516.612 1397.093 1636.132 8.684978 0.3695636     2
## 4  CCRT   F         MU 1646.321 1411.554 1881.087 8.684978 0.3695636     2
## 5  CCRT   F         MA 1541.103 1052.333 2029.872 8.684978 0.3695636     2
## 6  CCRT   F         UM 1786.288 1622.238 1950.338 8.684978 0.3695636     2
## 7  CCRT   F         KA 1515.422 1254.197 1776.647 8.684978 0.3695636     2
## 8  CCRT   F         VA 1556.032 1243.886 1868.179 8.684978 0.3695636     2
## 9  CCRT   F         AK 1701.556 1455.533 1947.580 8.684978 0.3695636     2
##
## $CCRT_M_lmers_pop_meta_compound_estimates
##   Trait Sex Population Estimate    LLEst    ULEst        Q         P N_lab
## 1  CCRT   M         YE 1729.246 1558.606 1899.886 12.16904 0.1438195     2
## 2  CCRT   M         RE 1542.950 1437.879 1648.021 12.16904 0.1438195     2
## 3  CCRT   M         GI 1752.887 1556.901 1948.872 12.16904 0.1438195     2
## 4  CCRT   M         MU 1690.640 1595.557 1785.724 12.16904 0.1438195     2
## 5  CCRT   M         MA 1479.440 1176.635 1782.246 12.16904 0.1438195     2
## 6  CCRT   M         UM 1610.294 1511.261 1709.327 12.16904 0.1438195     2
## 7  CCRT   M         KA 1598.621 1289.433 1907.809 12.16904 0.1438195     2
## 8  CCRT   M         VA 1526.679 1431.565 1621.793 12.16904 0.1438195     2
## 9  CCRT   M         AK 1666.717 1451.398 1882.035 12.16904 0.1438195     2
##
## $CSM_F_lmers_pop_meta_compound_estimates
##   Trait Sex Population Estimate     LLEst    ULEst        Q        P N_lab
## 1   CSM   F         YE 1.155249 0.8953922 1.415107 1.051165 0.997904     3
## 2   CSM   F         RE 1.112459 0.8547746 1.370143 1.051165 0.997904     3
## 3   CSM   F         GI 1.112156 0.9147955 1.309516 1.051165 0.997904     3
## 4   CSM   F         MU 1.155516 0.8849492 1.426083 1.051165 0.997904     3
## 5   CSM   F         MA 1.117443 0.8297335 1.405152 1.051165 0.997904     3
## 6   CSM   F         UM 1.031687 0.7821792 1.281194 1.051165 0.997904     3
## 7   CSM   F         KA 1.131730 0.8100121 1.453447 1.051165 0.997904     3
## 8   CSM   F         VA 1.161708 0.8518418 1.471574 1.051165 0.997904     3
## 9   CSM   F         AK 1.193219 0.9625454 1.423892 1.051165 0.997904     3
##
## $CSM_M_lmers_pop_meta_compound_estimates
##   Trait Sex Population  Estimate     LLEst    ULEst        Q         P N_lab
## 1   CSM   M         YE 1.1867956 0.9915225 1.382069 4.720664 0.7869719     3
## 2   CSM   M         RE 1.0080916 0.8588830 1.157300 4.720664 0.7869719     3
## 3   CSM   M         GI 1.0431651 0.9349974 1.151333 4.720664 0.7869719     3
## 4   CSM   M         MU 1.0725449 0.8275978 1.317492 4.720664 0.7869719     3
## 5   CSM   M         MA 1.0075638 0.8929595 1.122168 4.720664 0.7869719     3
## 6   CSM   M         UM 0.9466504 0.8097001 1.083601 4.720664 0.7869719     3
## 7   CSM   M         KA 1.0541057 0.9523560 1.155855 4.720664 0.7869719     3
## 8   CSM   M         VA 1.0186589 0.8371505 1.200167 4.720664 0.7869719     3
## 9   CSM   M         AK 1.0007472 0.8707303 1.130764 4.720664 0.7869719     3
```

Finally population summary effects for all traits can be visualized with a composite figure of all the meta analyses results (Files 7 and 8, Figure 3).

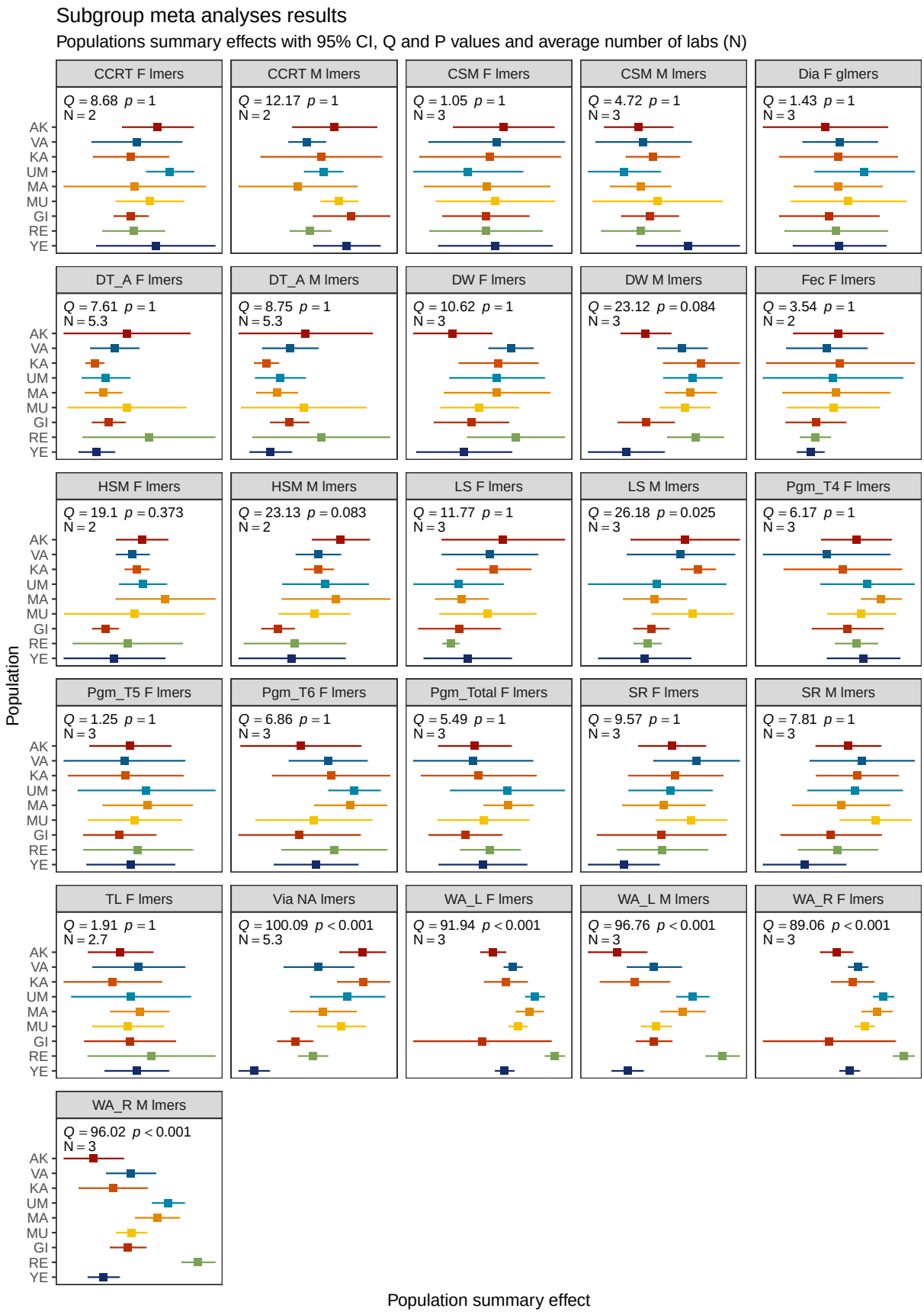

Figure 3: Meta analyses results.

2 Compound line estimates

The meta analysis approach described for *Population* has also been used to generate line compound estimates.

2.1 Input data

Compiled line random coefficients extracted from the linear models outputs:

```
## [1] "DrosEU_PhenotypingWG/LinearModelsPop/all_models_line_random_coefs.csv"
```

Trait-specific line random coefficients extracted from the linear models outputs, for example for Viability:

```
## [1] "DrosEU_PhenotypingWG/LinearModelsPop/Viability/Via_lmers_line_random_coefs.rds"
## [2] "DrosEU_PhenotypingWG/LinearModelsPop/Viability/Via_lmers_line_random_coefs.txt"
```

2.2 Meta analyses model

The only difference with the *Population* subgroup meta analyses is that here subgroups are defined by the *Line* variable.

Importantly, as previously mentionned in the *Population* meta analyses section, meta analyses for *Line* have been run for all the traits, including those that have been measured in single labs (such as Locomotor Activity and Egg-to-pupa Development Time) and for which there is no data to combine. In addition, even for traits involving several labs, some lines might have been measured only once. Obviously, results from these analyses are meaningless but it allows us to keep those traits in the loop and to streamline the generation of compound estimates. *Line* subgroup meta analyses have been run for the following 32 traits to generate line compound estimates:

```
##  [1] "CCRT_F_lmers"         "CCRT_M_lmers"         "CSM_F_lmers"
##  [4] "CSM_M_lmers"          "DT_A_F_lmers"         "DT_A_M_lmers"
##  [7] "DT_P_NA_lmers"        "Dia_F_glmers"         "DW_F_lmers"
## [10] "DW_M_lmers"           "Fec_F_lmers"          "HSM_F_lmers"
## [13] "HSM_M_lmers"          "LS_F_lmers"           "LS_M_lmers"
## [16] "LA_Activity_B_lmers" "LA_CircPhase_B_lmers" "LA_NDlog2_B_lmers"
## [19] "LA_Period_B_lmers"    "Pgm_T4_F_lmers"       "Pgm_T5_F_lmers"
## [22] "Pgm_T6_F_lmers"       "Pgm_Total_F_lmers"    "SR_F_lmers"
## [25] "SR_M_lmers"           "TL_F_lmers"           "TL_M_lmers"
## [28] "Via_NA_lmers"         "WA_L_F_lmers"         "WA_L_M_lmers"
## [31] "WA_R_F_lmers"         "WA_R_M_lmers"
```

However, for Locomotor Activity AbsPhase, no analysis could be run since line random coefficients are not available — *Line* could not be included as a random-effect factor in the linear model. For Diapause, we ran the meta analysis using the glmer models estimates only.

Finally partial data (incomple data sets) from Posnien's lab has been removed prior to running analyses for Wing Area and Thorax Length, to match what has been done in the *Population* meta analyses.

2.3 Meta analyses output

We are not interested in testing for differences between lines, we just want to extract line summary effects (compound estimates), so there is not much to be shown here. However analyses raw results are still available for each trait. Below are listed the files for Viability:

```
## [1] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_line_meta.rds"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_line_meta_summary.txt"
```

2.3.1 Compound line estimates

Compound line estimates (line summary effects) and their 95% confidence intervals were extracted from the meta analyses raw results for each trait. Below are listed the files for Viability:

```
## [1] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_line_meta_compound_random_coefs.txt"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmers_line_meta_compound_random_coefs.rds"
```

2.3.2 Compiled data for all traits

Line compound estimates for all traits have been exported as a list, table and wide table:

```
## [1] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_line_meta_compound_random_coefs_list.rds"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_line_meta_compound_random_coefs_wide.csv"
## [3] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_line_meta_compound_random_coefs.csv"
## [4] "DrosEU_PhenotypingWG/MetaAnalyses/all_models_line_meta_compound_random_coefs.rds"
```

```
# wide table, showing the first 30 lines and first 6 traits
lc_wide <- read.csv("all_models_line_meta_compound_random_coefs_wide.csv")
print(lc_wide[1:30, 1:8])
```

```
##    Population Line   CCRT_F   CCRT_M     CSM_F     CSM_M   DT_A_F   DT_A_M
## 1          YE YE11 1740.780 1830.576 1.3275626 1.1963985 235.4732 239.1486
## 2          YE YE13 1781.789 1656.551 1.2260388 1.1584263 226.7726 230.1101
## 3          YE YE14 1671.897 1657.121 0.9824461 0.9996533 225.1444 225.8184
## 4          YE YE15 1362.911 1652.729 1.3303449 1.3056244 225.2086 229.9096
## 5          YE YE19 1472.411 1779.762 1.2675460 1.3026688 222.2045 228.1961
## 6          YE YE20 1591.951 1699.021 1.2331000 1.0773738 224.5176 228.0411
## 7          YE YE21 1708.447 1633.441 1.1147023 1.0346458 226.4920 230.5008
## 8          YE YE22 1709.371 1695.337 1.2396333 1.2872839 223.4337 229.7819
## 9          YE YE23 1795.400 2016.186 1.1905514 1.3088599 223.6788 231.6504
## 10         YE YE24 1558.838 1623.848 1.1327469 0.9871201 232.5192 236.5691
## 11         YE YE26 1569.518 1611.529 1.1926895 1.1862068 227.5662 236.6907
## 12         YE YE27 1457.183 1784.242 1.0717561 1.1570583 225.6873 228.6688
## 13         YE YE33 1755.847 1694.216 1.1405096 1.2280582 229.6328 236.8524
## 14         YE YE40 1766.915 1696.542 1.1166134 1.3257893 224.3934 228.0587
## 15         YE YE41 1491.782 1676.064 1.4380061 1.2233844 225.2077 230.6798
## 16         YE YE48 1833.330 1720.081 1.0947795 1.1352451 228.0689 235.2367
## 17         YE YE49 1823.436 1752.562 1.1594867 1.2124204 223.7138 229.4629
## 18         YE YE51 1950.524 1764.231 1.2221075 1.1895328 220.0692 223.3028
## 19         YE YE69 1695.839 1654.898 1.3872745 1.2657438 226.4956 232.2970
## 20         YE YE80 1507.935 1596.565 1.1894775 1.0502805 225.6099 228.7259
## 21         RE  RE1 1557.270 1383.196 1.0422795 0.9619523 228.3596 231.5537
## 22         RE RE10 1547.911 1481.723 1.0745103 1.0957891 236.0361 238.7644
## 23         RE RE11 1634.018 1546.893 1.1358114 1.0272604 240.6573 243.7958
## 24         RE RE12 1565.845 1539.496 1.1796471 1.0565322 229.2855 232.3166
## 25         RE RE13 1591.331 1572.867 1.1839831 1.0236077 244.7395 244.3921
## 26         RE RE15 1779.343 1607.090 1.2057720 1.0500683 228.0661 234.9629
## 27         RE RE16 1459.590 1620.195 1.1933715 0.9722350 230.1908 233.7513
## 28         RE RE17 1637.078 1602.437 1.0334030 0.8595064 239.9727 245.6674
## 29         RE RE18 1362.157 1564.137 1.3186600 1.0768863 231.5852 233.2652
## 30         RE  RE2 1438.888 1548.444 1.1429690 0.9627394 238.0246 243.6389
```