

Meta Analyses Read Me

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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 coefficients 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	NA	AK	0.9882281	0.03647560
## 32	lmer	pop	Via StamenkovicRadak	NA	NA	GI	0.8928932	0.04334278
## 33	lmer	pop	Via StamenkovicRadak	NA	NA	KA	0.9430861	0.03637479
## 34	lmer	pop	Via StamenkovicRadak	NA	NA	MA	0.8436346	0.03651680
## 35	lmer	pop	Via StamenkovicRadak	NA	NA	MU	1.0009710	0.03641034
## 36	lmer	pop	Via StamenkovicRadak	NA	NA	RE	0.9176397	0.03969883
## 37	lmer	pop	Via StamenkovicRadak	NA	NA	UM	0.8802478	0.03788400
## 38	lmer	pop	Via StamenkovicRadak	NA	NA	VA	0.8489644	0.03647471
## 39	lmer	pop	Via StamenkovicRadak	NA	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 (incomplete data sets) from Posnien 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 not relevant 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* abbreviation (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 are shown the raw results of the Viability meta analysis (files 1 and 2):

```
# 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 phenotyping (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. Below is an example for Viability:

```
# read in population compound estimates
comp_pop_via <- readRDS("../MetaAnalyses/Viability/Via_NA_lmrs_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).

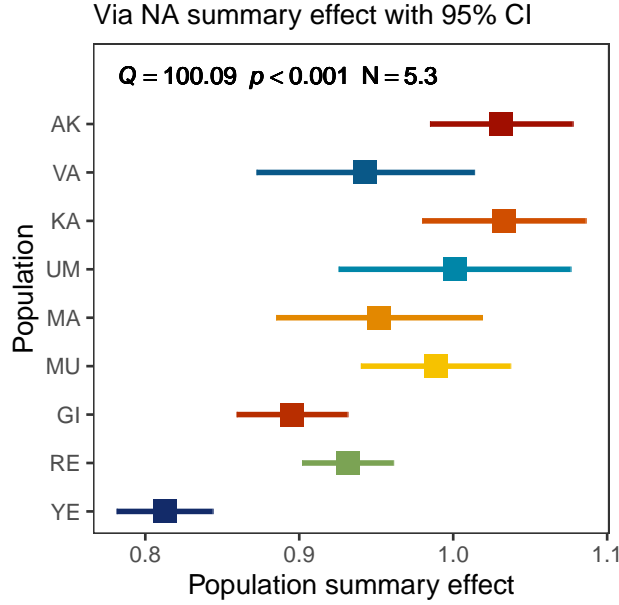


Figure 1: Subgroup meta analysis for Viability. N indicates the average number of labs that have phenotyped the different populations.

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).

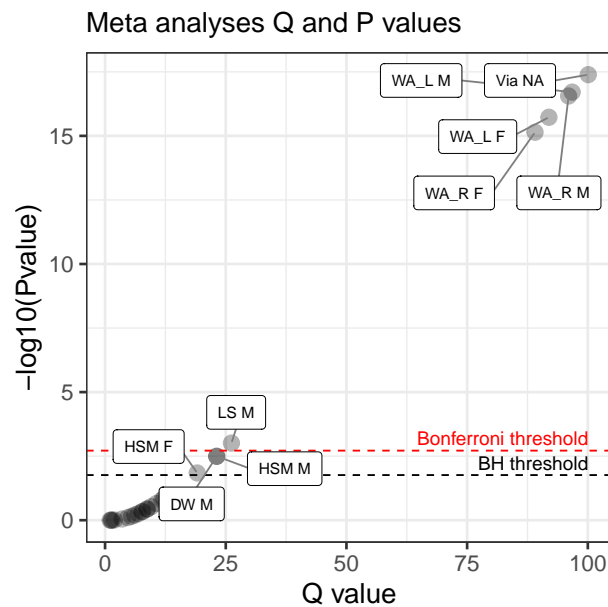


Figure 2: All meta analyses Q statistics and p values.

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).

Subgroup meta analyses results

Populations summary effects with 95% CI, Q and P values and average number of labs (N)

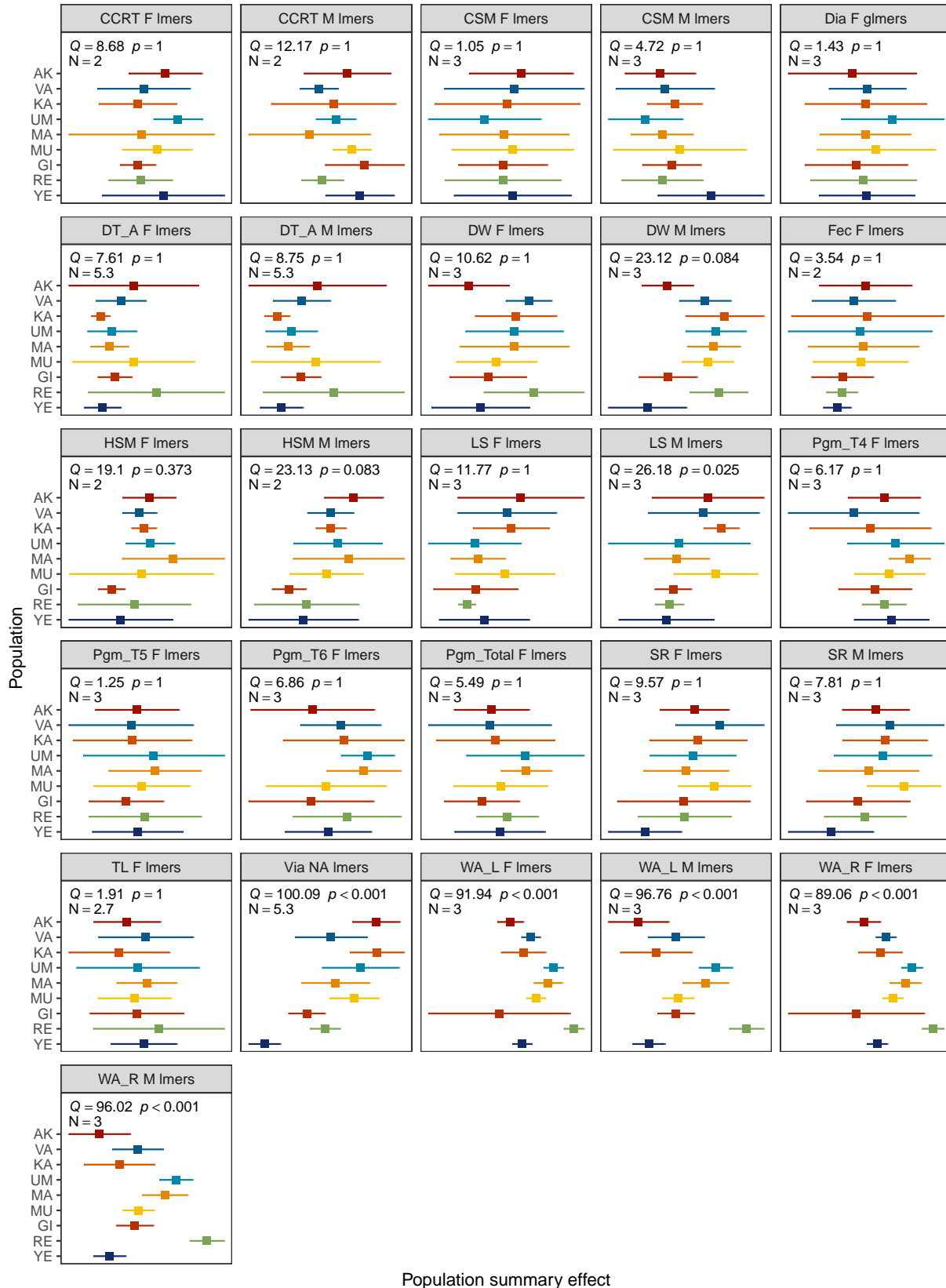


Figure 3: Meta analyses population summary effects for all 26 traits.

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 mentioned 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 (Locomotor Activity and Egg-to-pupa Development Time). In addition, even for traits involving several labs, some lines might have been measured only once. Again, results from these analyses are meaningless and should not be considered 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"
```

Note that we could not run the analysis for Locomotor Activity AbsPhase since line random coefficients are not available for that particular trait — *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 (incomplete data sets) from Posnien 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, for example 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_lmrs_line_meta_compound_random_coefs.txt"
## [2] "DrosEU_PhenotypingWG/MetaAnalyses/Viability/Via_NA_lmrs_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