

# DvN\_Results

Bumblebat

12/11/2023

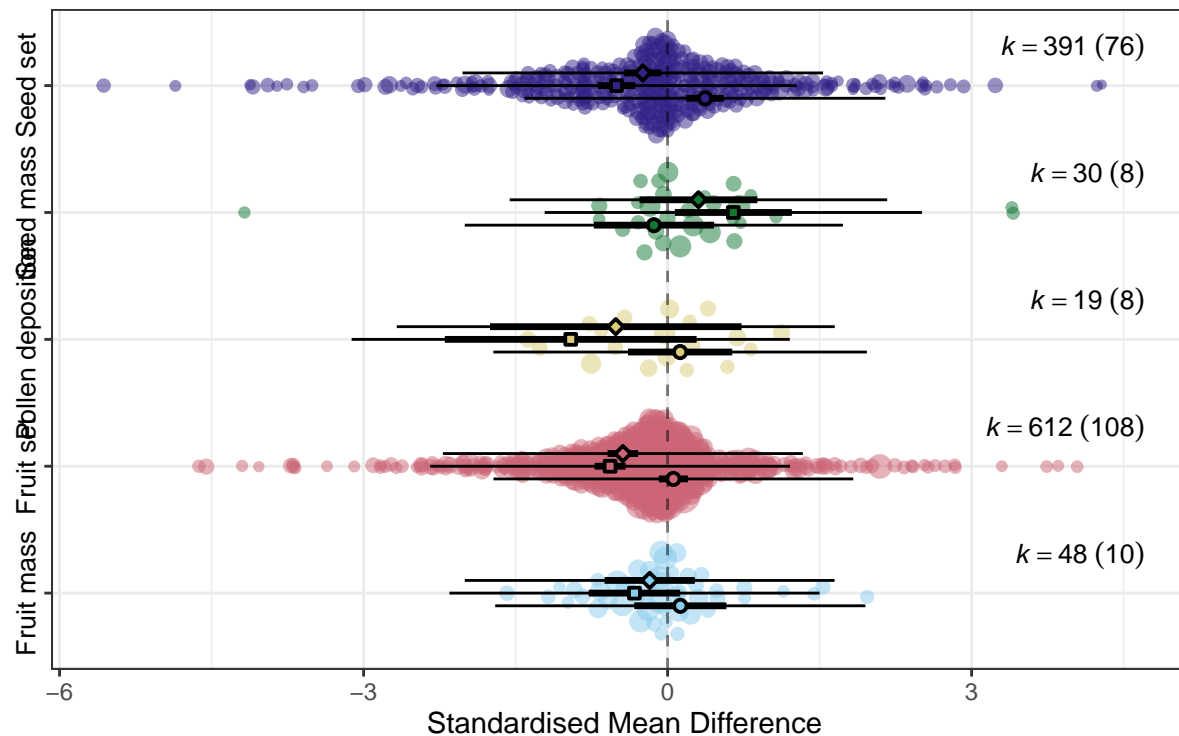
## Effect size (ES) between pollination effectiveness measures

, fig.height = 8, fig.width = 8, out.width = "8.5in"

```
##
## Multivariate Meta-Analysis Model (k = 1100; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1660  0.4074   136     no      study_ID   no
## sigma^2.2  0.6138  0.7834  1100     no      effect_ID   no
## sigma^2.3  0.0000  0.0001   140     no        phylo   yes
## sigma^2.4  0.0352  0.1877   140     no  accepted_name   no
##
## Test for Residual Heterogeneity:
## QE(df = 1085) = 12228.7017, p-val < .0001
##
## Test of Moderators (coefficients 2:15):
## QM(df = 14) = 144.0705, p-val < .0001
##
## Model Results:
##
##                                     estimate
## intrcpt                                0.1258
## treatment_effectiveness_metricfruit set -0.0685
## treatment_effectiveness_metricpollen deposition -0.0021
## treatment_effectiveness_metricseed mass -0.2611
## treatment_effectiveness_metricseed set 0.2443
## treatmentopen_day -0.4526
## treatmentopen_night -0.3025
## treatment_effectiveness_metricfruit set:treatmentopen_day -0.1721
## treatment_effectiveness_metricpollen deposition:treatmentopen_day -0.6268
## treatment_effectiveness_metricseed mass:treatmentopen_day 1.2366
## treatment_effectiveness_metricseed set:treatmentopen_day -0.4216
## treatment_effectiveness_metricfruit set:treatmentopen_night -0.1959
## treatment_effectiveness_metricpollen deposition:treatmentopen_night -0.3326
## treatment_effectiveness_metricseed mass:treatmentopen_night 0.7425
## treatment_effectiveness_metricseed set:treatmentopen_night -0.3122
##                                     se
## intrcpt 0.2321
## treatment_effectiveness_metricfruit set 0.2357
## treatment_effectiveness_metricpollen deposition 0.3490
```

## treatment_effectiveness_metricseed mass	0.3782
## treatment_effectiveness_metricseed set	0.2433
## treatmentopen_day	0.2982
## treatmentopen_night	0.2960
## treatment_effectiveness_metricfruit set:treatmentopen_day	0.3101
## treatment_effectiveness_metricpollen deposition:treatmentopen_day	0.7313
## treatment_effectiveness_metricseed mass:treatmentopen_day	0.4934
## treatment_effectiveness_metricseed set:treatmentopen_day	0.3194
## treatment_effectiveness_metricfruit set:treatmentopen_night	0.3079
## treatment_effectiveness_metricpollen deposition:treatmentopen_night	0.7298
## treatment_effectiveness_metricseed mass:treatmentopen_night	0.4938
## treatment_effectiveness_metricseed set:treatmentopen_night	0.3169
##	zval
## intrcpt	0.5420
## treatment_effectiveness_metricfruit set	-0.2908
## treatment_effectiveness_metricpollen deposition	-0.0060
## treatment_effectiveness_metricseed mass	-0.6903
## treatment_effectiveness_metricseed set	1.0044
## treatmentopen_day	-1.5178
## treatmentopen_night	-1.0220
## treatment_effectiveness_metricfruit set:treatmentopen_day	-0.5549
## treatment_effectiveness_metricpollen deposition:treatmentopen_day	-0.8571
## treatment_effectiveness_metricseed mass:treatmentopen_day	2.5063
## treatment_effectiveness_metricseed set:treatmentopen_day	-1.3201
## treatment_effectiveness_metricfruit set:treatmentopen_night	-0.6362
## treatment_effectiveness_metricpollen deposition:treatmentopen_night	-0.4558
## treatment_effectiveness_metricseed mass:treatmentopen_night	1.5036
## treatment_effectiveness_metricseed set:treatmentopen_night	-0.9850
##	pval
## intrcpt	0.5878
## treatment_effectiveness_metricfruit set	0.7712
## treatment_effectiveness_metricpollen deposition	0.9953
## treatment_effectiveness_metricseed mass	0.4900
## treatment_effectiveness_metricseed set	0.3152
## treatmentopen_day	0.1291
## treatmentopen_night	0.3068
## treatment_effectiveness_metricfruit set:treatmentopen_day	0.5789
## treatment_effectiveness_metricpollen deposition:treatmentopen_day	0.3914
## treatment_effectiveness_metricseed mass:treatmentopen_day	0.0122
## treatment_effectiveness_metricseed set:treatmentopen_day	0.1868
## treatment_effectiveness_metricfruit set:treatmentopen_night	0.5247
## treatment_effectiveness_metricpollen deposition:treatmentopen_night	0.6485
## treatment_effectiveness_metricseed mass:treatmentopen_night	0.1327
## treatment_effectiveness_metricseed set:treatmentopen_night	0.3246
##	ci.lb
## intrcpt	-0.3291
## treatment_effectiveness_metricfruit set	-0.5305
## treatment_effectiveness_metricpollen deposition	-0.6861
## treatment_effectiveness_metricseed mass	-1.0024
## treatment_effectiveness_metricseed set	-0.2324
## treatmentopen_day	-1.0370
## treatmentopen_night	-0.8827
## treatment_effectiveness_metricfruit set:treatmentopen_day	-0.7800
## treatment_effectiveness_metricpollen deposition:treatmentopen_day	-2.0601

```
## treatment_effectiveness_metricseed mass:treatmentopen_day 0.2696
## treatment_effectiveness_metricseed set:treatmentopen_day -1.0475
## treatment_effectiveness_metricfruit set:treatmentopen_night -0.7993
## treatment_effectiveness_metricpollen deposition:treatmentopen_night -1.7630
## treatment_effectiveness_metricseed mass:treatmentopen_night -0.2254
## treatment_effectiveness_metricseed set:treatmentopen_night -0.9334
## ci.ub
## intrcpt 0.5806
## treatment_effectiveness_metricfruit set 0.3934
## treatment_effectiveness_metricpollen deposition 0.6820
## treatment_effectiveness_metricseed mass 0.4802
## treatment_effectiveness_metricseed set 0.7211
## treatmentopen_day 0.1319
## treatmentopen_night 0.2777
## treatment_effectiveness_metricfruit set:treatmentopen_day 0.4358
## treatment_effectiveness_metricpollen deposition:treatmentopen_day 0.8065
## treatment_effectiveness_metricseed mass:treatmentopen_day 2.2037 *
## treatment_effectiveness_metricseed set:treatmentopen_day 0.2044
## treatment_effectiveness_metricfruit set:treatmentopen_night 0.4076
## treatment_effectiveness_metricpollen deposition:treatmentopen_night 1.0977
## treatment_effectiveness_metricseed mass:treatmentopen_night 1.7103
## treatment_effectiveness_metricseed set:treatmentopen_night 0.3090
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



COMPARISONS-1.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

Condition  $\phi$  day\_night  $\Phi$  open

## ES between exclusion treatments

##right now this chunk is redundant given above #ignore the next chunk when knitting

## ES by Env. vars

```
## **Fruit set and the environment. Order is DvN, OvD, OvN**
## Warning: 7 rows with NAs omitted from model fitting.
##
## Multivariate Meta-Analysis Model (k = 219; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.5795  0.7613   102    no      study_ID    no
## sigma^2.2  0.4187  0.6470   219    no      effect_ID    no
## sigma^2.3  0.0159  0.1262   105    no        phylo    yes
## sigma^2.4  0.3269  0.5718   105    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 216) = 3223.3170, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.3398, p-val = 0.8437
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      0.1165  0.1282  0.9085  0.3636  -0.1348  0.3677
## sDTR          0.0401  0.0963  0.4169  0.6767  -0.1485  0.2288
## sDaylength    0.0475  0.1119  0.4241  0.6715  -0.1719  0.2668
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Warning: 7 rows with NAs omitted from model fitting.
##
## Multivariate Meta-Analysis Model (k = 184; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2222  0.4714    85    no      study_ID    no
## sigma^2.2  0.0448  0.2116   184    no      effect_ID    no
## sigma^2.3  0.0888  0.2980    86    no        phylo    yes
## sigma^2.4  0.0517  0.2273    86    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 181) = 1374.2167, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.6836, p-val = 0.7105
```

```

##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.3572  0.1297  -2.7538  0.0059  -0.6113  -0.1030  **
## sDTR          0.0455  0.0618   0.7366  0.4614  -0.0756   0.1666
## sDaylength   -0.0212  0.0699  -0.3031  0.7618  -0.1582   0.1158
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Warning: 7 rows with NAs omitted from model fitting.

##
## Multivariate Meta-Analysis Model (k = 188; method: REML)
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1396  0.3736    88    no      study_ID    no
## sigma^2.2  0.0585  0.2419   188    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    88    no      phylo      yes
## sigma^2.4  0.1954  0.4420    88    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 185) = 1594.5628, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.8920, p-val = 0.6402
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.4159  0.0753  -5.5207  <.0001  -0.5636  -0.2683  ***
## sDTR          -0.0001  0.0580  -0.0017  0.9986  -0.1138   0.1136
## sDaylength   -0.0651  0.0690  -0.9430  0.3457  -0.2004   0.0702
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## **Seed set and the environment. Order is DvN, OvD, OvN**

## Warning: 3 rows with NAs omitted from model fitting.

##
## Multivariate Meta-Analysis Model (k = 132; method: REML)
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    70    no      study_ID    no
## sigma^2.2  0.1909  0.4369   132    no      effect_ID    no
## sigma^2.3  0.0000  0.0001    68    no      phylo      yes
## sigma^2.4  1.5394  1.2407    68    no  accepted_name    no
##
## Test for Residual Heterogeneity:

```

```

## QE(df = 129) = 1366.8256, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 1.1271, p-val = 0.5692
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      0.3360  0.1681  1.9990  0.0456   0.0066  0.6655  *
## sDTR         0.1322  0.1390  0.9517  0.3412  -0.1401  0.4046
## sDaylength   0.0545  0.1478  0.3684  0.7126  -0.2353  0.3442
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Warning: 3 rows with NAs omitted from model fitting.

##
## Multivariate Meta-Analysis Model (k = 122; method: REML)
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0000  0.0000    62    no      study_ID   no
## sigma^2.2  0.1454  0.3813   122    no      effect_ID   no
## sigma^2.3  0.0707  0.2660    59    no        phylo   yes
## sigma^2.4  0.4061  0.6373    59    no accepted_name   no
##
## Test for Residual Heterogeneity:
## QE(df = 119) = 803.7406, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.4775, p-val = 0.7876
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt     -0.4954  0.1532 -3.2328  0.0012  -0.7958  -0.1951  **
## sDTR        -0.0508  0.0996 -0.5098  0.6102  -0.2459   0.1444
## sDaylength  -0.0482  0.1042 -0.4625  0.6438  -0.2525   0.1561
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Warning: 3 rows with NAs omitted from model fitting.

##
## Multivariate Meta-Analysis Model (k = 128; method: REML)
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0338  0.1837    66    no      study_ID   no
## sigma^2.2  0.1128  0.3359   128    no      effect_ID   no
## sigma^2.3  0.0000  0.0001    64    no        phylo   yes
## sigma^2.4  0.7884  0.8879    64    no accepted_name   no

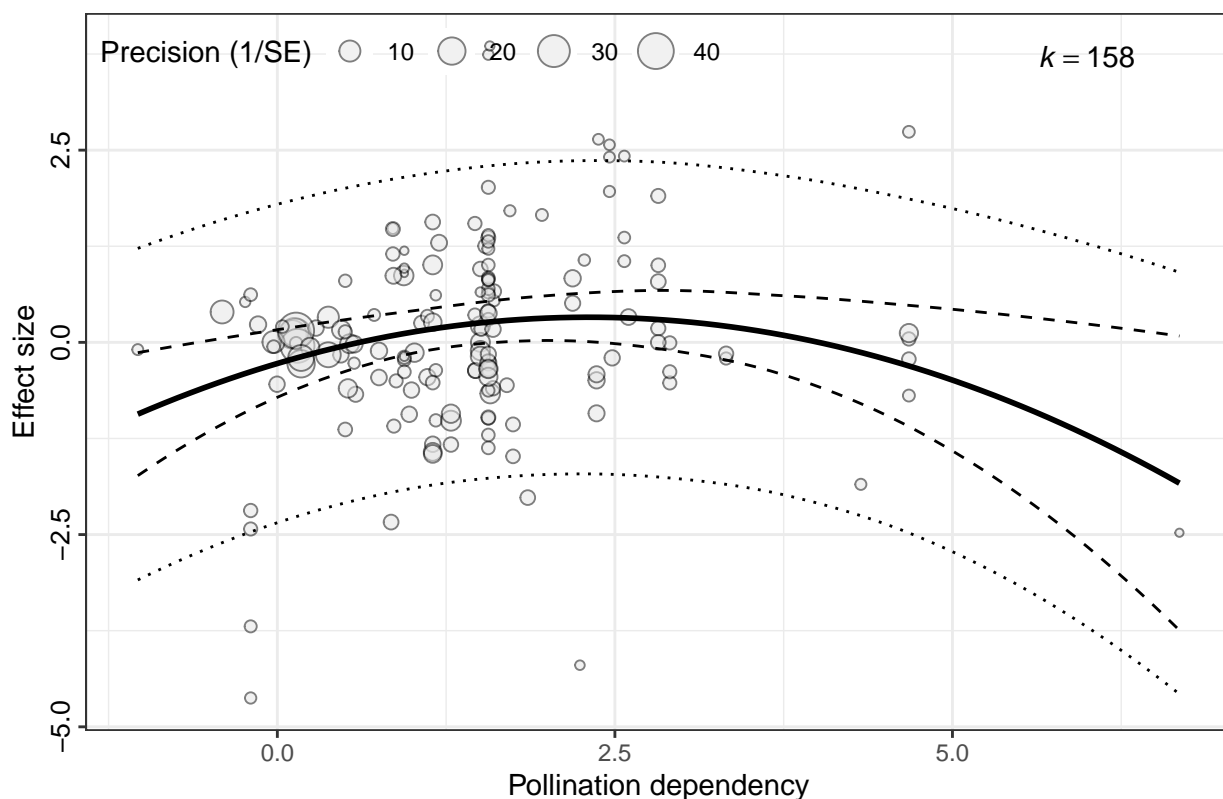
```

```
##
## Test for Residual Heterogeneity:
## QE(df = 125) = 825.1934, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 2.3171, p-val = 0.3139
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.2717  0.1292  -2.1033  0.0354  -0.5248  -0.0185  *
## sDTR           0.1295  0.1025   1.2628  0.2067  -0.0715   0.3304
## sDaylength     0.0962  0.1184   0.8126  0.4165  -0.1359   0.3284
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### ES by pollination dependency (PD) var

```
## **Fruit set and species-level pollination dependency. Order is DvN, OvD, OvN**
##
## Multivariate Meta-Analysis Model (k = 158; method: REML)
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.3835  0.6193    81    no      study_ID    no
## sigma^2.2  0.4539  0.6737   158    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    76    no        phylo    yes
## sigma^2.4  0.2187  0.4676    76    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 155) = 1828.0406, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 6.5072, p-val = 0.0386
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.2747  0.2050  -1.3399  0.1803  -0.6764   0.1271
## spp.poll.dep     0.5210  0.2142   2.4325  0.0150   0.1012   0.9408  *
## I(spp.poll.dep^2) -0.1129  0.0448  -2.5189  0.0118  -0.2007  -0.0250  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Fruit set (day vs. night)

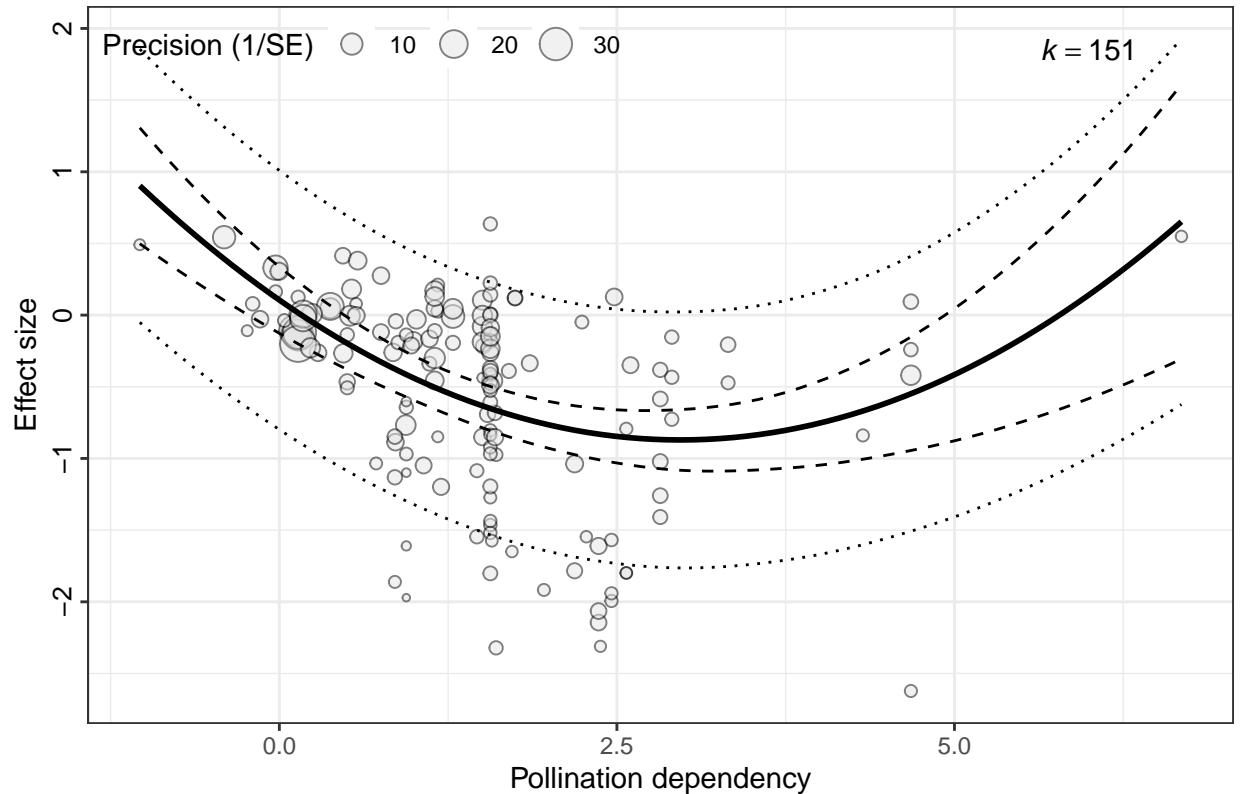


DEP-1.pdf

```
##
## Multivariate Meta-Analysis Model (k = 151; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1409  0.3754    76    no      study_ID    no
## sigma^2.2  0.0465  0.2155   151    no      effect_ID    no
## sigma^2.3  0.0090  0.0950    75    no      phylo      yes
## sigma^2.4  0.0000  0.0000    75    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 148) = 740.0655, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 37.9779, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.1052  0.1071   0.9824  0.3259  -0.1047   0.3151
## spp.poll.dep     -0.6571  0.1094  -6.0056 <.0001  -0.8715  -0.4426 ***
## I(spp.poll.dep^2)  0.1106  0.0229   4.8326 <.0001   0.0657   0.1554 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



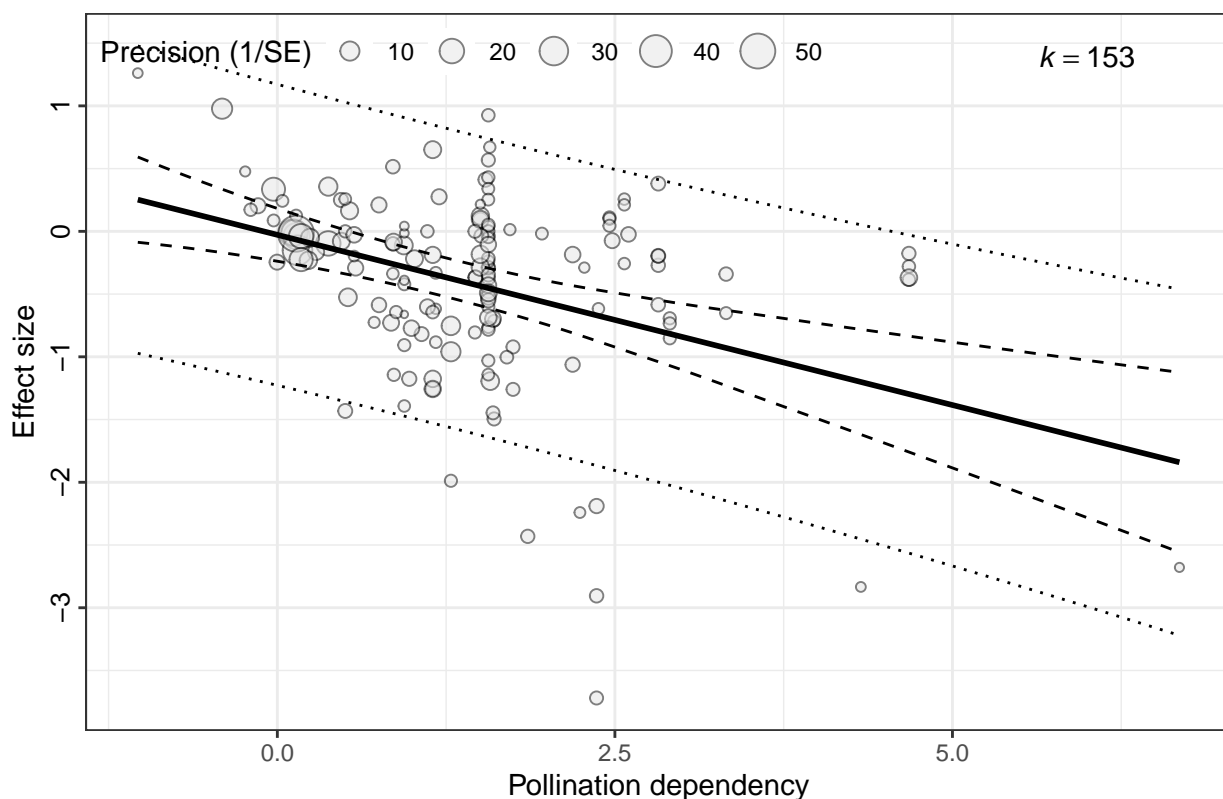
# Fruit set (open vs. day)



DEP-2.pdf

```
##
## Multivariate Meta-Analysis Model (k = 153; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0839  0.2897    78    no      study_ID    no
## sigma^2.2  0.0917  0.3027   153    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    76    no        phylo    yes
## sigma^2.4  0.1868  0.4322    76    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 151) = 1112.9203, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 17.0758, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.0279  0.1107  -0.2518  0.8012  -0.2448   0.1891
## spp.poll.dep  -0.2713  0.0657  -4.1323  <.0001  -0.4000  -0.1426 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Fruit set (open vs. night)



DEP-3.pdf

## \*\*Seed set and species-level pollination dependency. Order is DvN, OvD, OvN\*\*

##

## Multivariate Meta-Analysis Model ( $k = 59$ ; method: REML)

##

## Variance Components:

##

	estim	sqrt	nlvls	fixed	factor	R
## $\sigma^2_{.1}$	0.0000	0.0000	39	no	study_ID	no
## $\sigma^2_{.2}$	0.2384	0.4883	59	no	effect_ID	no
## $\sigma^2_{.3}$	0.1917	0.4378	36	no	phylo	yes
## $\sigma^2_{.4}$	1.6052	1.2670	36	no	accepted_name	no

##

## Test for Residual Heterogeneity:

##  $QE(df = 57) = 1081.5958$ ,  $p\text{-val} < .0001$

##

## Test of Moderators (coefficient 2):

##  $QM(df = 1) = 1.1791$ ,  $p\text{-val} = 0.2775$

##

## Model Results:

##

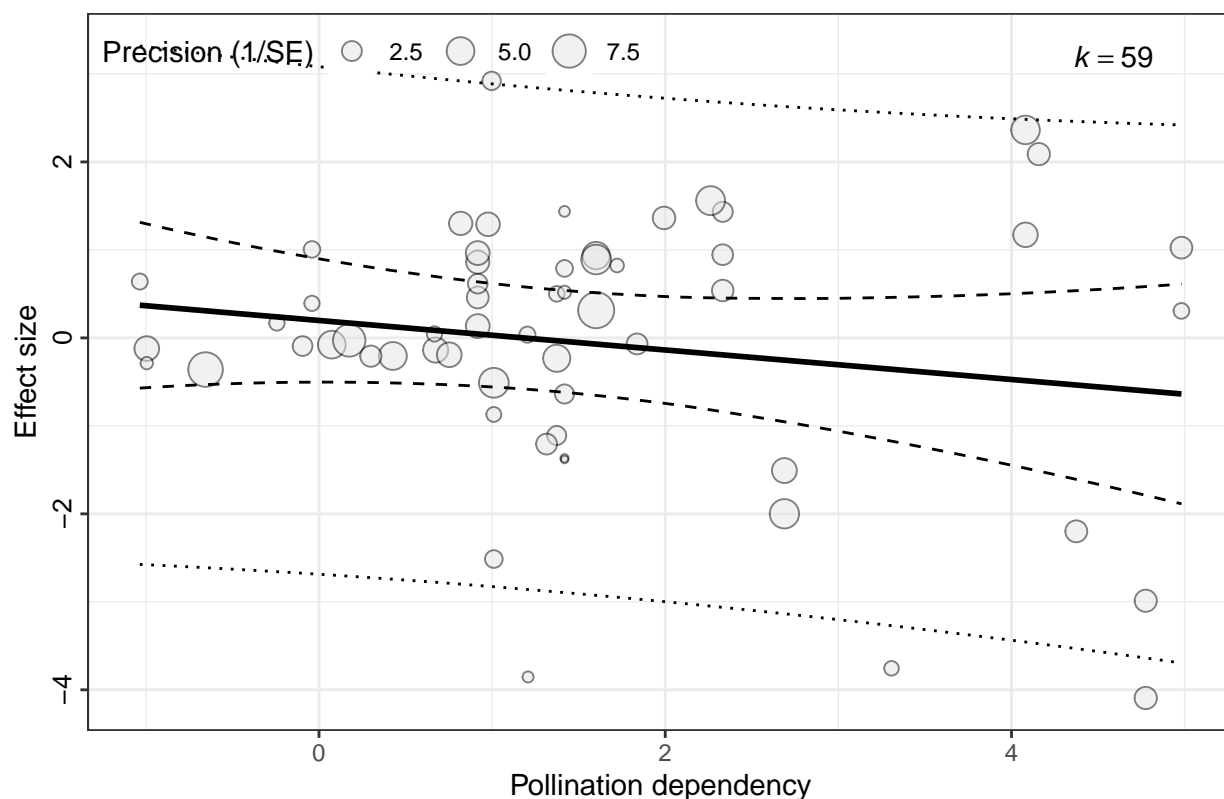
	estimate	se	zval	pval	ci.lb	ci.ub
## intrcpt	0.1980	0.3616	0.5476	0.5840	-0.5107	0.9068
## spp.poll.dep	-0.1677	0.1544	-1.0859	0.2775	-0.4704	0.1350

##

## ---

## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

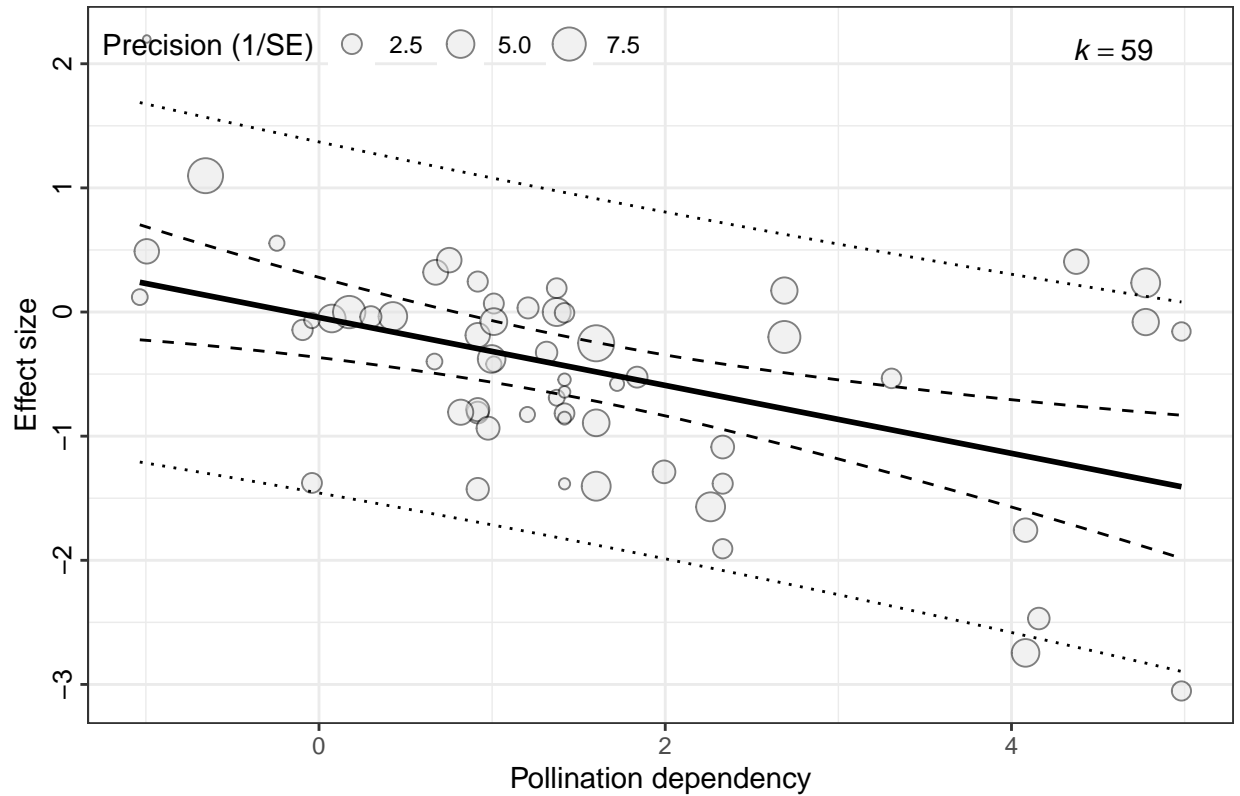
## Seed set (day vs. night)



DEP-4.pdf

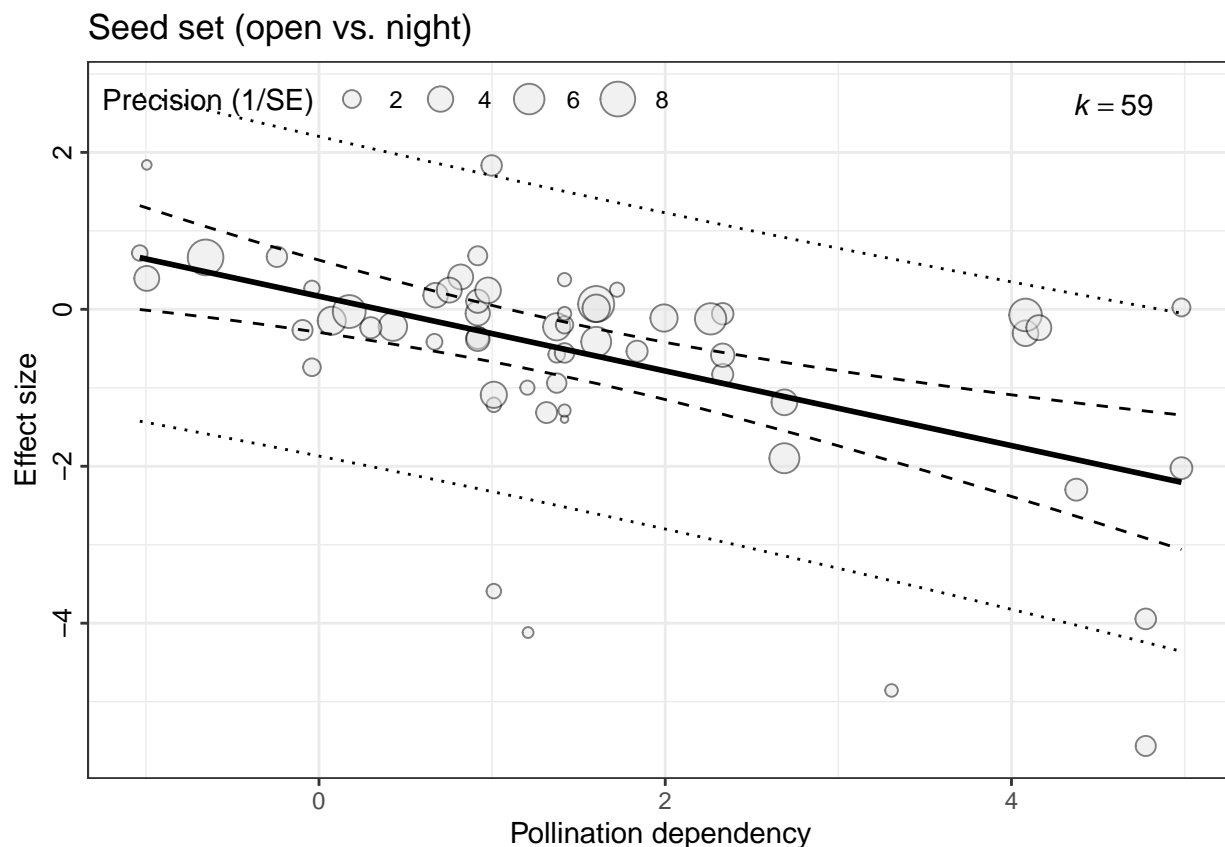
```
##
## Multivariate Meta-Analysis Model (k = 59; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000   39    no      study_ID   no
## sigma^2.2  0.2618  0.5117   59    no      effect_ID  no
## sigma^2.3  0.0000  0.0001   36    no      phylo      yes
## sigma^2.4  0.2305  0.4801   36    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 57) = 488.1021, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 12.7289, p-val = 0.0004
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.0439  0.1680  -0.2610  0.7941  -0.3732  0.2854
## spp.poll.dep  -0.2737  0.0767  -3.5678  0.0004  -0.4240  -0.1233 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Seed set (open vs. day)



DEP-5.pdf

```
##
## Multivariate Meta-Analysis Model (k = 59; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000   39    no      study_ID   no
## sigma^2.2  0.1920  0.4381   59    no      effect_ID  no
## sigma^2.3  0.0000  0.0001   36    no      phylo      yes
## sigma^2.4  0.8303  0.9112   36    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 57) = 495.9671, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 18.0472, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.1666  0.2397   0.6951  0.4870  -0.3031   0.6363
## spp.poll.dep    -0.4759  0.1120  -4.2482 <.0001  -0.6955  -0.2563 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



DEP-6.pdf

ES by continuous trait variables: Flower dimensions (PC1) , Plant size (PC2), and their interaction(?) (PC3)

```
## [1] 73.62
```

```
## [1] 94.8
```

```
## Phylogenetic pca
```

```
## Standard deviations:
```

```
##      PC1      PC2      PC3      PC4
## 0.15146681 0.09788505 0.09673811 0.04789623
```

```
## Loads:
```

```
##              PC1      PC2      PC3      PC4
## flower_width_midpoint_mm -0.7817083  0.5384239  0.2927808  0.115374273
## flower_length_midpoint_mm -0.9051256 -0.1198546 -0.1916796 -0.360057489
## style_length_midpoint_mm -0.7384342 -0.4756881 -0.3912048  0.274580677
## plant_height_midpoint_m   -0.2042648 -0.5624059  0.8011899 -0.008387344
```

```
## lambda:
```

```
## [1] 0.8824116
```

```
## PC1
```

```
## 51.93
```

```
## PC2
```

```
## 21.69
```

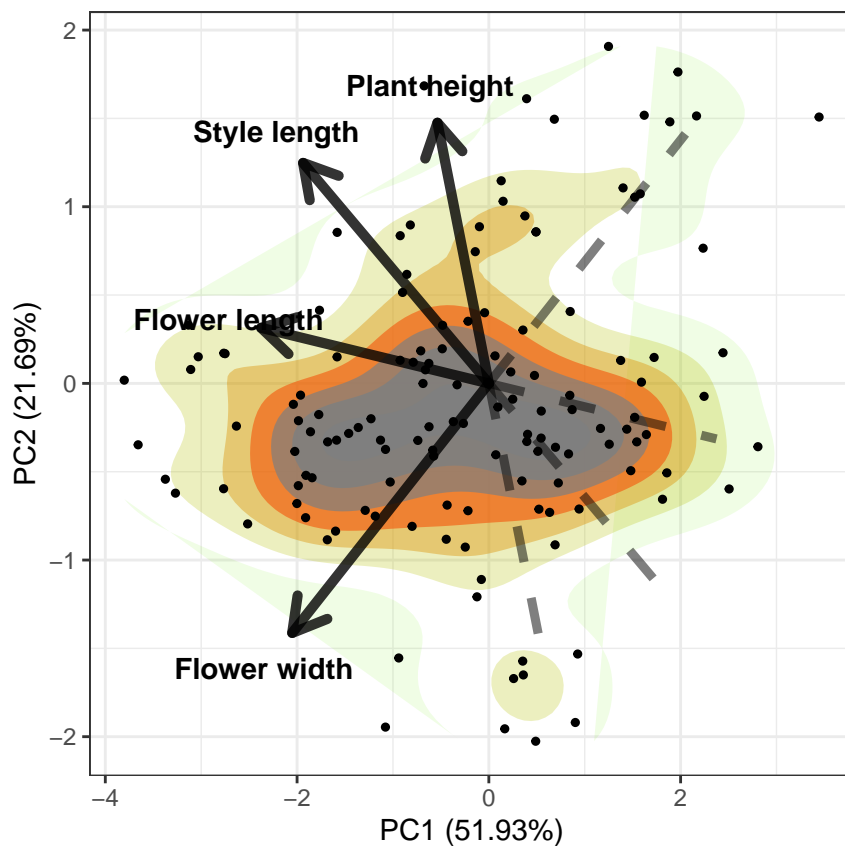
```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
```

```
## i Please use tidy evaluation idioms with `aes()``.
```

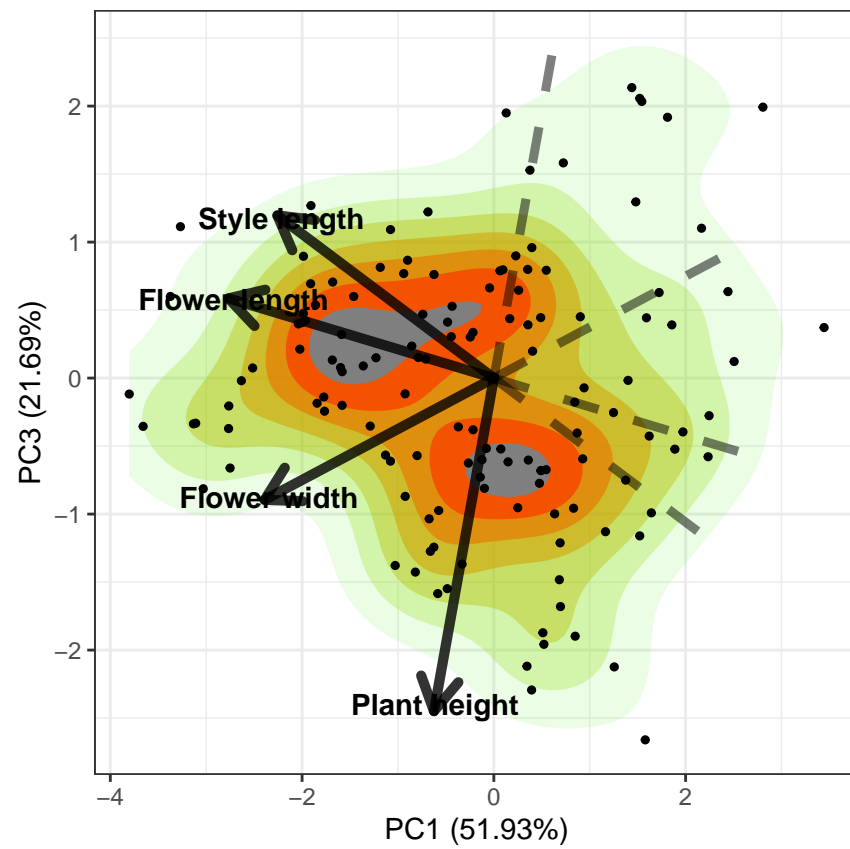
```
## i See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

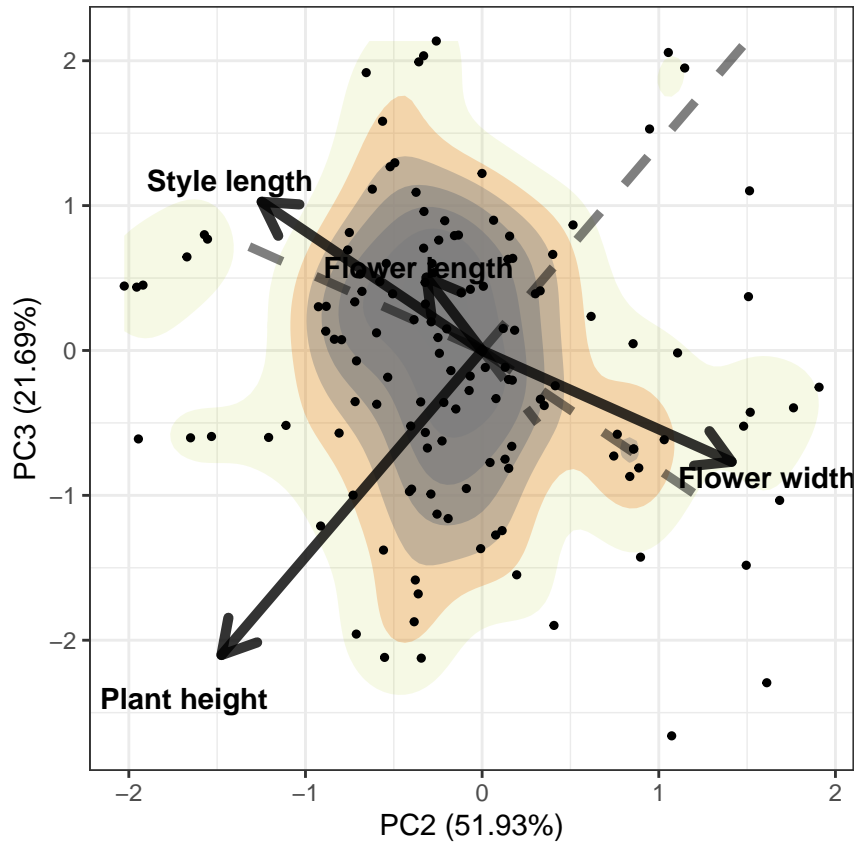
## Warning: The dot-dot notation (`..level..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(level)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```



```
## PC1
## 51.93
## PC3
## 21.18
```



```
## PC2
## 21.69
## PC3
## 21.18
```



```
## **Fruit set and continuous trait variation. Order is DvN, OvD, OvN**
```

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.5585  0.7473   107    no      study_ID    no
## sigma^2.2  0.3954  0.6288   226    no      effect_ID   no
## sigma^2.3  0.0182  0.1349   111    no        phylo    yes
## sigma^2.4  0.3539  0.5949   111    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 222) = 4246.6598, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 2.2024, p-val = 0.5315
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt    0.1200  0.1275   0.9406   0.3469   -0.1300   0.3699
## PC1       -0.0561  0.0760  -0.7381   0.4605   -0.2049   0.0928
## PC2        0.0655  0.1417   0.4621   0.6440   -0.2123   0.3432
## PC3        0.1599  0.1247   1.2829   0.1995   -0.0844   0.4043
##
```



```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

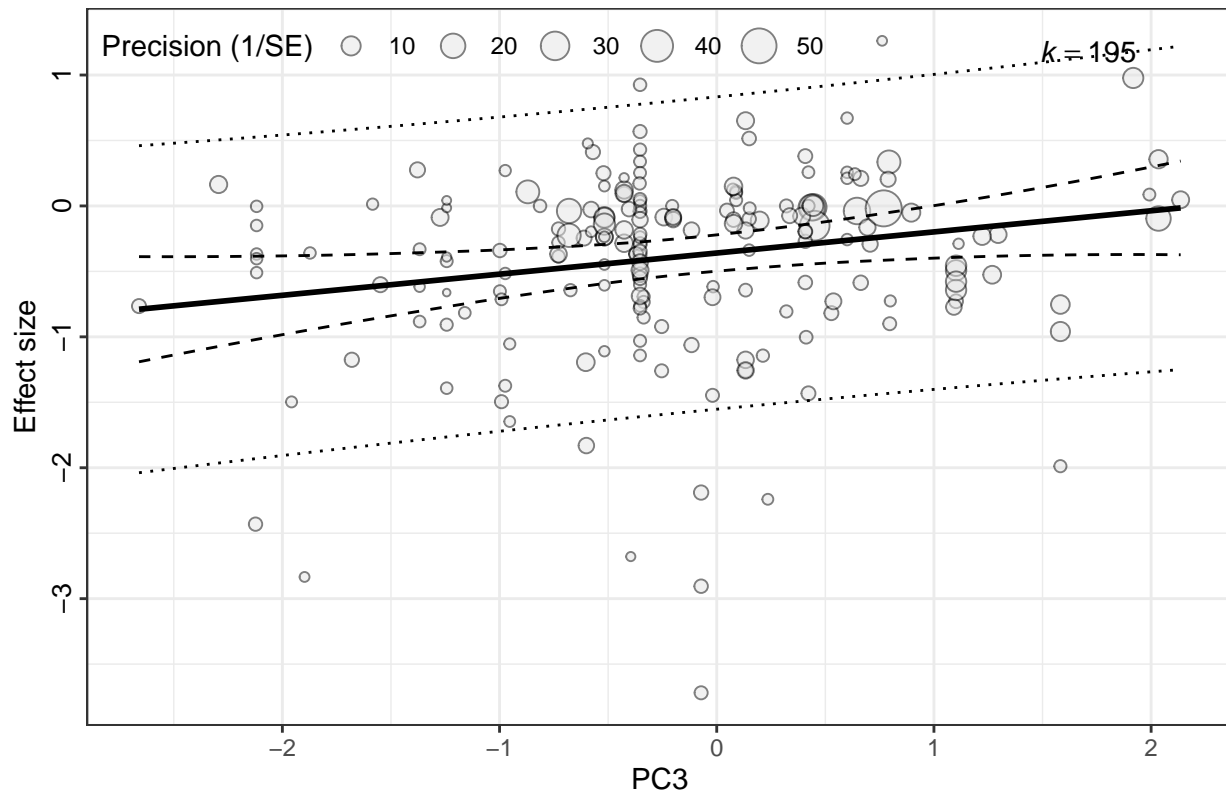
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2528  0.5028    90    no      study_ID    no
## sigma^2.2  0.0450  0.2121   191    no      effect_ID    no
## sigma^2.3  0.0664  0.2577    92    no        phylo    yes
## sigma^2.4  0.0499  0.2234    92    no accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 187) = 1668.9663, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 0.8333, p-val = 0.8415
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt  -0.3882  0.1157  -3.3545  0.0008  -0.6150  -0.1614 ***
## PC1       0.0232  0.0521  0.4447  0.6565  -0.0790  0.1253
## PC2       0.0584  0.0882  0.6621  0.5079  -0.1145  0.2312
## PC3       0.0304  0.0839  0.3628  0.7168  -0.1340  0.1949
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1134  0.3367    93    no      study_ID    no
## sigma^2.2  0.0628  0.2506   195    no      effect_ID    no
## sigma^2.3  0.0000  0.0001    94    no        phylo    yes
## sigma^2.4  0.1896  0.4355    94    no accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 191) = 1620.2365, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 6.6724, p-val = 0.0831
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt  -0.3857  0.0722  -5.3427  <.0001  -0.5272  -0.2442 ***
## PC1      -0.0574  0.0465  -1.2337  0.2173  -0.1486  0.0338
## PC2       0.0057  0.0871  0.0653  0.9480  -0.1651  0.1765
## PC3       0.1614  0.0733  2.2010  0.0277  0.0177  0.3051  *

```

```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### Fruit set (open vs. night)



```
## **Seed set and continuous trait variation. Order is DvN, OvD, OvN**
```

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
```

```
## Variance Components:
```

	estim	sqrt	nlvls	fixed	factor	R
## sigma <sup>2</sup> .1	0.0000	0.0001	72	no	study_ID	no
## sigma <sup>2</sup> .2	0.1915	0.4376	135	no	effect_ID	no
## sigma <sup>2</sup> .3	0.1324	0.3638	70	no	phylo	yes
## sigma <sup>2</sup> .4	1.4873	1.2195	70	no	accepted_name	no

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 131) = 1476.4393, p-val < .0001
```

```
## Test of Moderators (coefficients 2:4):
```

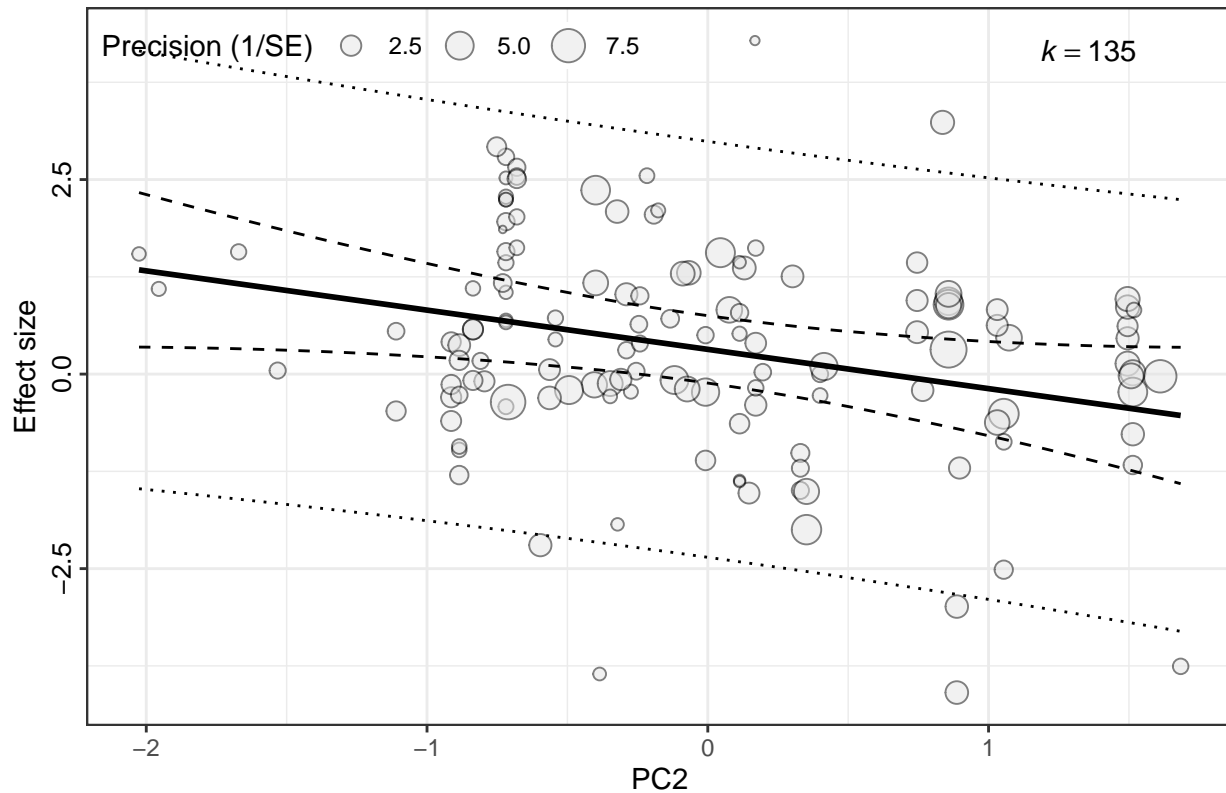
```
## QM(df = 3) = 5.1275, p-val = 0.1627
```

```
## Model Results:
```

	estimate	se	zval	pval	ci.lb	ci.ub
## intrcpt	0.3125	0.2231	1.4006	0.1613	-0.1248	0.7498
## PC1	0.0587	0.1208	0.4860	0.6270	-0.1780	0.2954

```
## PC2      -0.5045  0.2229 -2.2631  0.0236 -0.9414 -0.0676  *
## PC3      -0.1024  0.2079 -0.4924  0.6225 -0.5099  0.3052
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### Seed set (day vs. night)



```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.0000 0.0000   64    no      study_ID no
## sigma^2.2 0.1482 0.3850  125    no      effect_ID no
## sigma^2.3 0.0000 0.0001   61    no        phylo yes
## sigma^2.4 0.5193 0.7206   61    no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 121) = 896.2025, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 3.8717, p-val = 0.2757
##
## Model Results:
##
##      estimate    se    zval    pval    ci.lb    ci.ub
## intrcpt -0.4914 0.1186 -4.1451 <.0001 -0.7238 -0.2591 ***
## PC1     -0.0655 0.0775 -0.8454 0.3979 -0.2173  0.0863
```

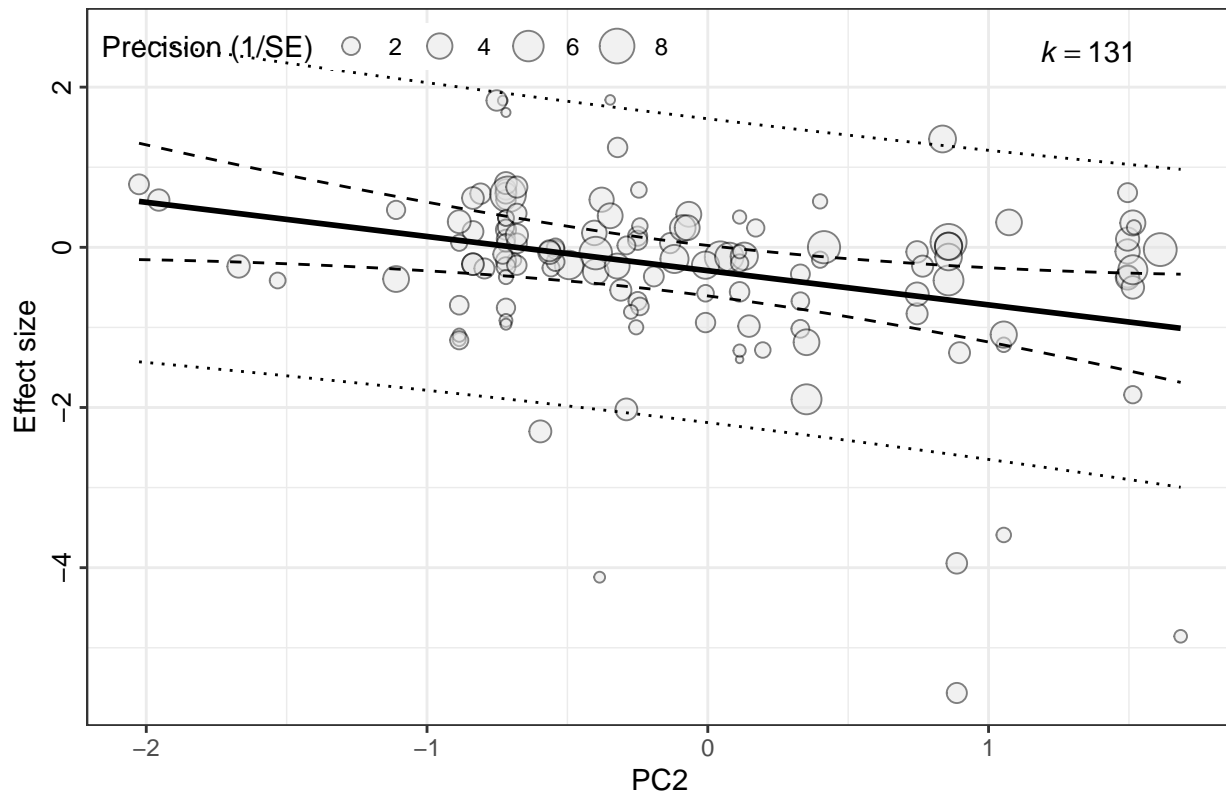
```

## PC2      0.1962  0.1505  1.3034  0.1924 -0.0988  0.4912
## PC3      0.2157  0.1292  1.6694  0.0950 -0.0375  0.4690 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0356  0.1886    68    no      study_ID  no
## sigma^2.2  0.1189  0.3449   131    no      effect_ID  no
## sigma^2.3  0.0568  0.2384    66    no      phylo     yes
## sigma^2.4  0.7001  0.8367    66    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 127) = 835.5473, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 6.9129, p-val = 0.0747
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt    -0.2645  0.1619  -1.6338  0.1023  -0.5819  0.0528
## PC1         0.0547  0.0924   0.5920  0.5538  -0.1264  0.2358
## PC2        -0.4270  0.1686  -2.5328  0.0113  -0.7575 -0.0966 *
## PC3        -0.0071  0.1505  -0.0469  0.9626  -0.3020  0.2879
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## Seed set (open vs. night)



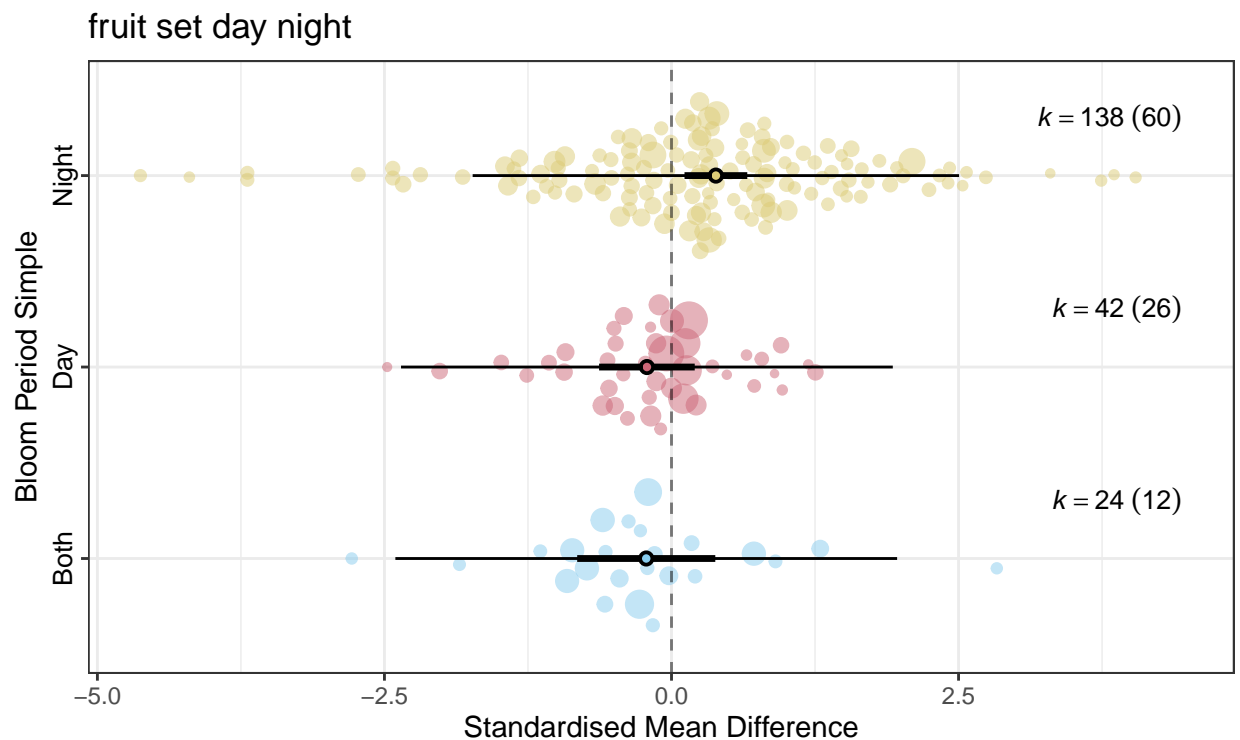
## ES by categorical traits

```
## Warning: 22 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.
## Warning: 12 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.
## Warning: 14 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.

## Warning: Redundant predictors dropped from the model.
## Warning: 8 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.
## Warning: 14 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.

## Warning: Redundant predictors dropped from the model.
## Warning: 8 rows with NAs omitted from model fitting.
## Warning: Redundant predictors dropped from the model.
##
## Multivariate Meta-Analysis Model (k = 204; method: REML)
```

```
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.4907 0.7005   94    no      study_ID  no
## sigma^2.2 0.3950 0.6285  204    no      effect_ID  no
## sigma^2.3 0.0000 0.0001   96    no        phylo  yes
## sigma^2.4 0.2628 0.5126   96    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 201) = 3654.6657, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 7.6053, p-val = 0.0223
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt             -0.2199 0.3068  -0.7168  0.4735  -0.8213  0.3815
## bloom_period_simpleday      0.0059 0.3732   0.0157  0.9874  -0.7257  0.7374
## bloom_period_simplenight    0.6065 0.3370   1.7995  0.0719  -0.0541  1.2671
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

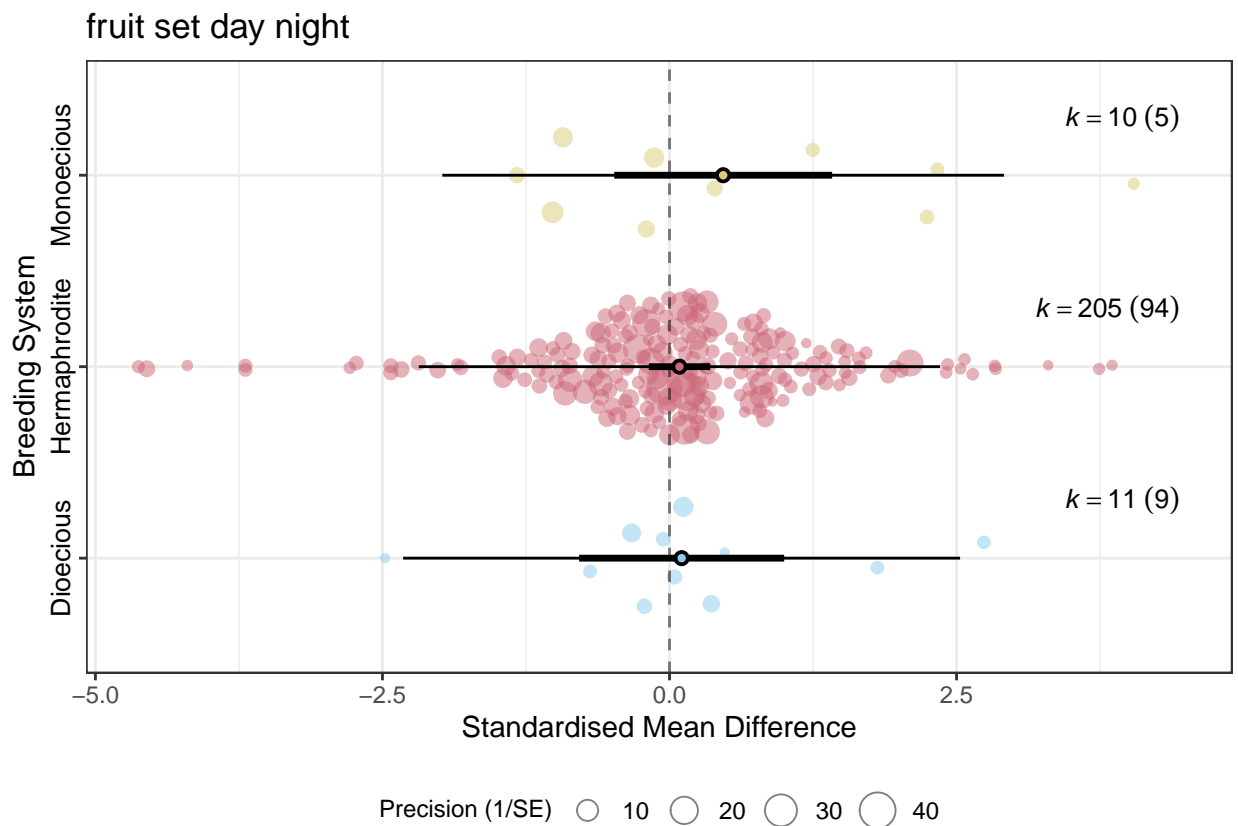


traits-1.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
```

```
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.5507 0.7421  107    no      study_ID  no
## sigma^2.2 0.4035 0.6352  226    no      effect_ID  no
## sigma^2.3 0.0302 0.1736  111    no      phylo      yes
## sigma^2.4 0.3389 0.5821  111    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 223) = 4418.1912, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.5863, p-val = 0.7459
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## intrcpt          0.1057 0.4555  0.2321  0.8165 -0.7870
## breeding_systemhermaphrodite -0.0189 0.4652 -0.0407 0.9675 -0.9307
## breeding_systemmonoecious    0.3619 0.6597  0.5486 0.5833 -0.9310
##
##      ci.ub
## intrcpt    0.9985
## breeding_systemhermaphrodite 0.8928
## breeding_systemmonoecious    1.6548
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

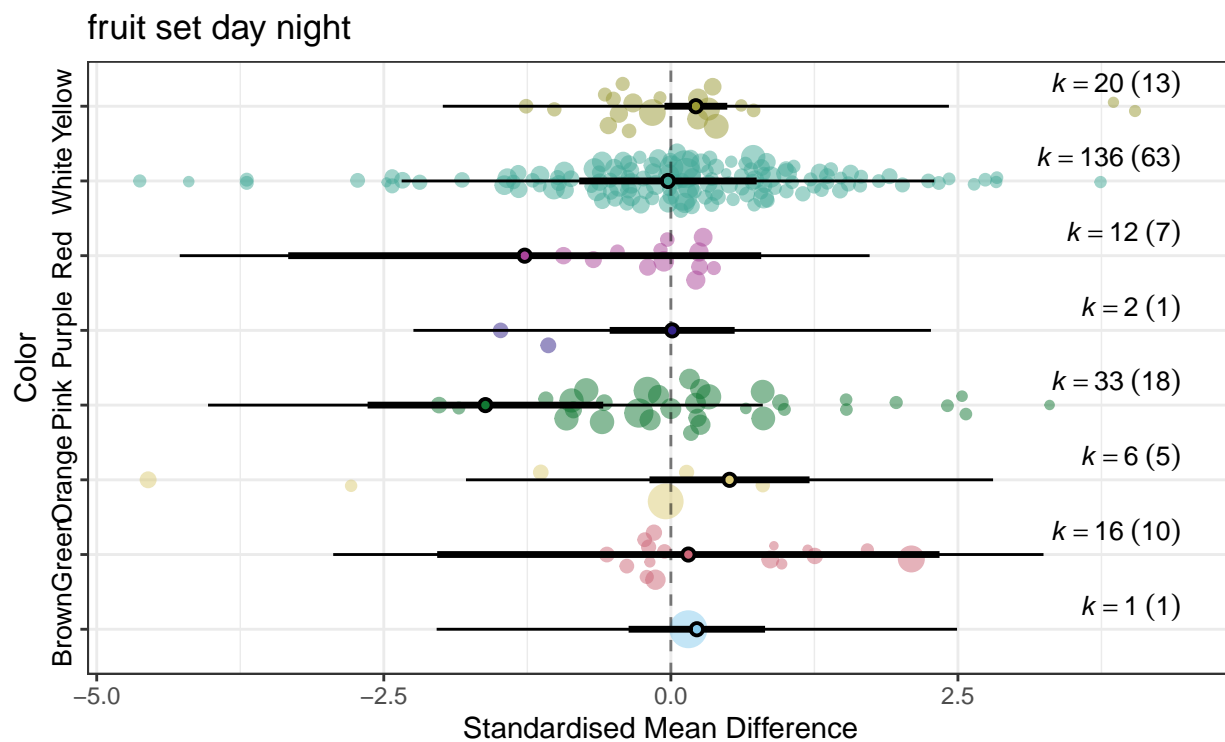


```

##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.5550  0.7450   107    no      study_ID    no
## sigma^2.2  0.3874  0.6225   226    no      effect_ID    no
## sigma^2.3  0.0000  0.0002   111    no        phylo    yes
## sigma^2.4  0.3024  0.5499   111    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 218) = 3568.0822, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 15.0707, p-val = 0.0351
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      0.2262  0.3031   0.7463  0.4555  -0.3679   0.8203
## colorbrown  -0.0739  1.1564  -0.0639  0.9491  -2.3404   2.1927
## colorgreen   0.2847  0.4526   0.6291  0.5293  -0.6023   1.1717
## colororange -1.8412  0.5975  -3.0815  0.0021  -3.0123  -0.6701  **
## colorpink   -0.2147  0.4100  -0.5238  0.6005  -1.0183   0.5889
## colorpurple -1.4991  1.0936  -1.3708  0.1704  -3.6426   0.6444
## colorred    -0.2517  0.4963  -0.5072  0.6120  -1.2244   0.7209
## colorwhite  -0.0084  0.3264  -0.0258  0.9795  -0.6482   0.6314
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```





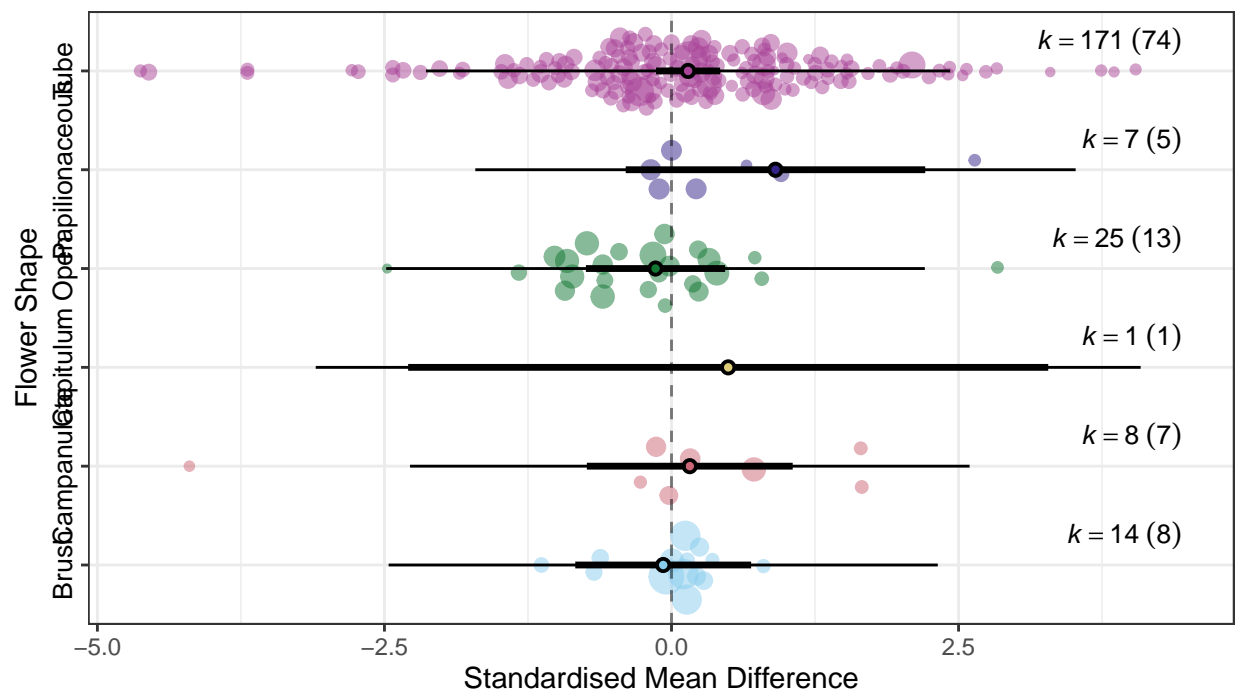
traits-3.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.5832  0.7636   107    no      study_ID    no
## sigma^2.2  0.4017  0.6338   226    no      effect_ID   no
## sigma^2.3  0.0091  0.0952   111    no        phylo    yes
## sigma^2.4  0.3424  0.5851   111    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 220) = 4146.4740, p-val < .0001
##
## Test of Moderators (coefficients 2:6):
## QM(df = 5) = 2.4092, p-val = 0.7901
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.0723  0.3907  -0.1850  0.8532  -0.8380  0.6935
## flower_shapecampanulate    0.2315  0.6005   0.3856  0.6998  -0.9454  1.4084
## flower_shapecapitulum     0.5660  1.4742   0.3839  0.7010  -2.3234  3.4555
## flower_shapeopen          -0.0670  0.4856  -0.1380  0.8903  -1.0187  0.8847
## flower_shapepapilionaceous  0.9778  0.7717   1.2671  0.2051  -0.5346  2.4902
## flower_shapetube           0.2165  0.4143   0.5227  0.6012  -0.5954  1.0285
##
## intrcpt
```

```
## flower_shapecampanulate
## flower_shapecapitulum
## flower_shapeopen
## flower_shapepapilionaceous
## flower_shapetube
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

fruit set day night



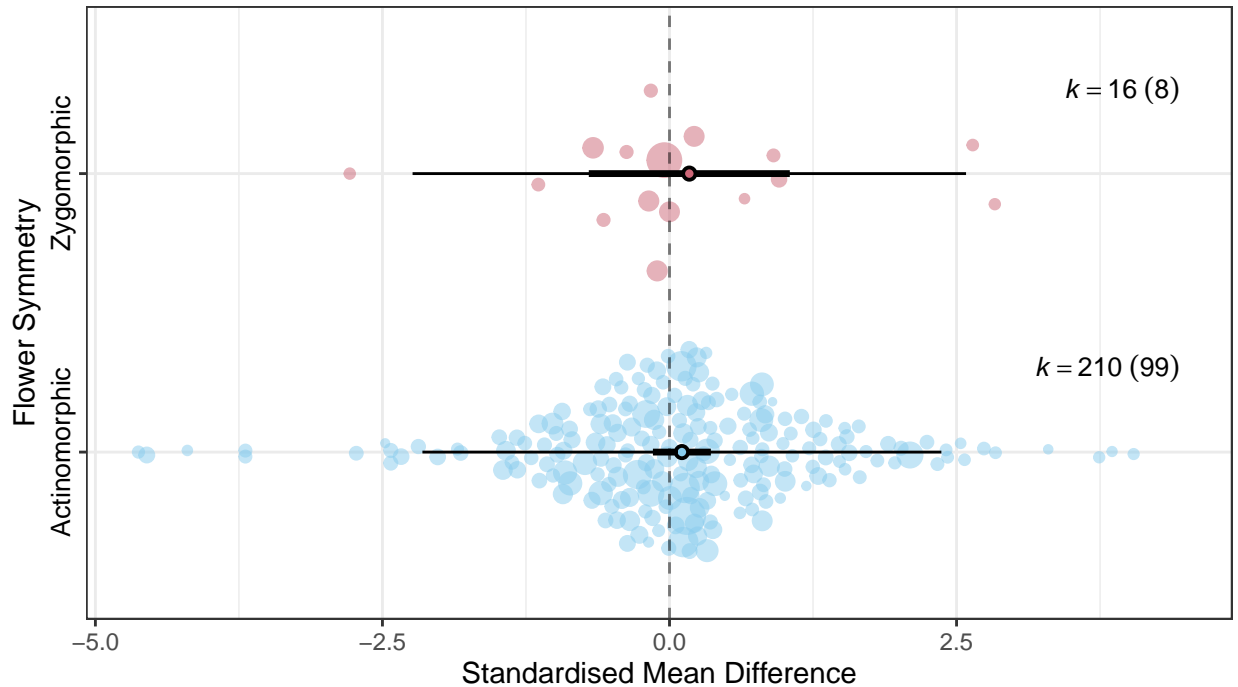
traits-4.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.5766 0.7593   107    no      study_ID no
## sigma^2.2 0.4055 0.6368   226    no      effect_ID no
## sigma^2.3 0.0214 0.1462   111    no        phylo yes
## sigma^2.4 0.3093 0.5561   111    no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 224) = 4453.1316, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0196, p-val = 0.8886
##
## Model Results:
##
```

```
##               estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          0.1079  0.1287  0.8385  0.4017  -0.1443  0.3601
## flower_symmetryzygomorphic  0.0647  0.4614  0.1401  0.8886  -0.8397  0.9690
##
## intrcpt
## flower_symmetryzygomorphic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

fruit set day night



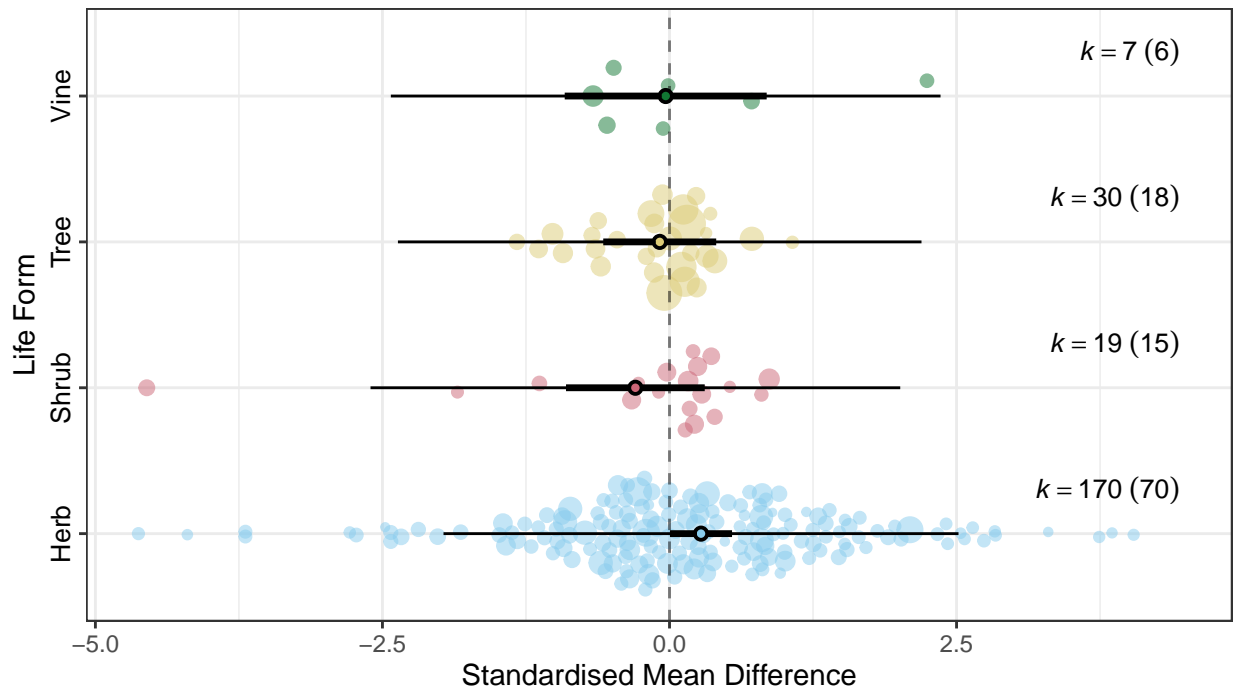
traits-5.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.5882  0.7669   107    no      study_ID   no
## sigma^2.2  0.4052  0.6365   226    no      effect_ID  no
## sigma^2.3  0.0000  0.0001   111    no        phylo   yes
## sigma^2.4  0.2968  0.5448   111    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 222) = 4458.3032, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 3.8774, p-val = 0.2750
##
## Model Results:
```

```
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.2744  0.1379   1.9893  0.0467   0.0040  0.5447  *
## life_formshrub   -0.5715  0.3377  -1.6925  0.0906  -1.2334  0.0903  .
## life_formtree    -0.3596  0.2862  -1.2564  0.2090  -0.9205  0.2013
## life_formvine    -0.3075  0.4646  -0.6620  0.5080  -1.2180  0.6030
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### fruit set day night

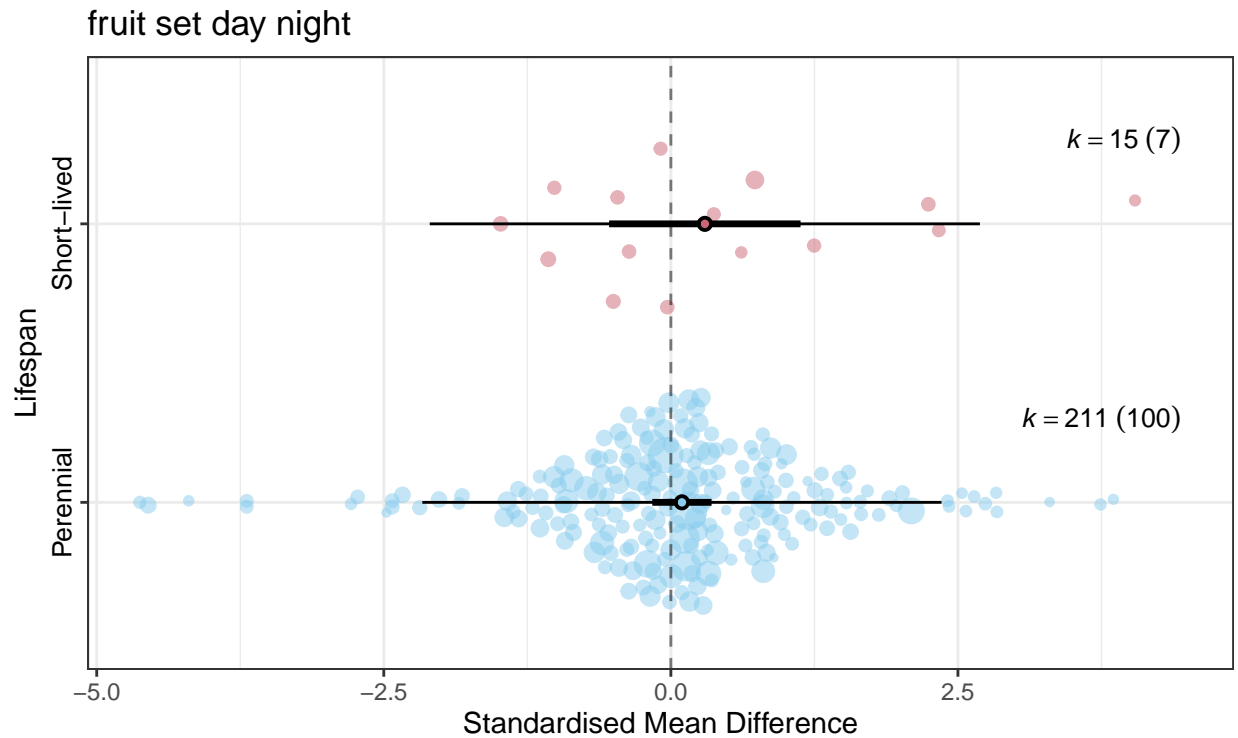


traits-6.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.5606  0.7488   107    no      study_ID    no
## sigma^2.2  0.4044  0.6360   226    no      effect_ID   no
## sigma^2.3  0.0265  0.1627   111    no        phylo   yes
## sigma^2.4  0.3215  0.5670   111    no  accepted_name   no
##
## Test for Residual Heterogeneity:
## QE(df = 224) = 4469.1626, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.2068, p-val = 0.6493
##
## Model Results:
```

```
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          0.0962  0.1316  0.7314  0.4645  -0.1616  0.3541
## lifespanshort-lived  0.1997  0.4391  0.4548  0.6493  -0.6609  1.0602
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

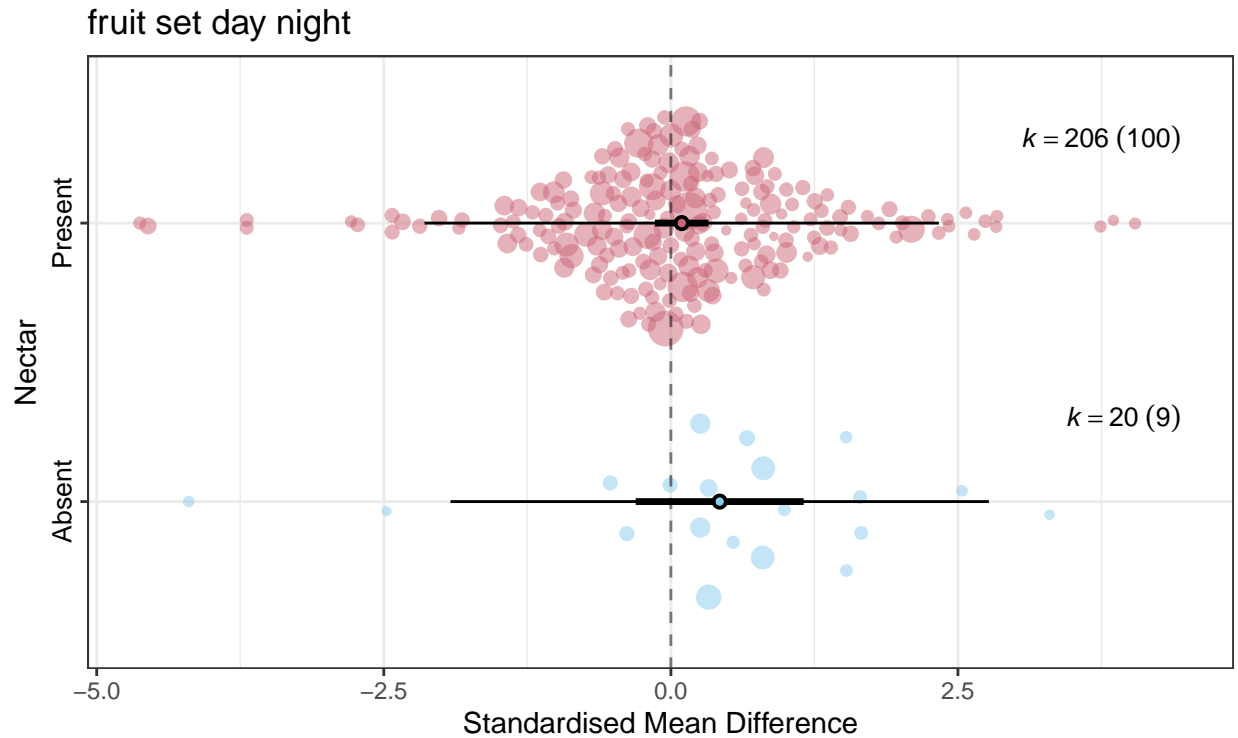


traits-7.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.6101 0.7811  107    no      study_ID no
## sigma^2.2 0.4093 0.6398  226    no      effect_ID no
## sigma^2.3 0.0092 0.0957  111    no      phylo    yes
## sigma^2.4 0.2631 0.5129  111    no  accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 224) = 4328.6464, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.7595, p-val = 0.3835
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
```

```
## intrcpt          0.4250  0.3731   1.1393  0.2546 -0.3062  1.1562
## nectarpresent   -0.3307  0.3795  -0.8715  0.3835 -1.0744  0.4130
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

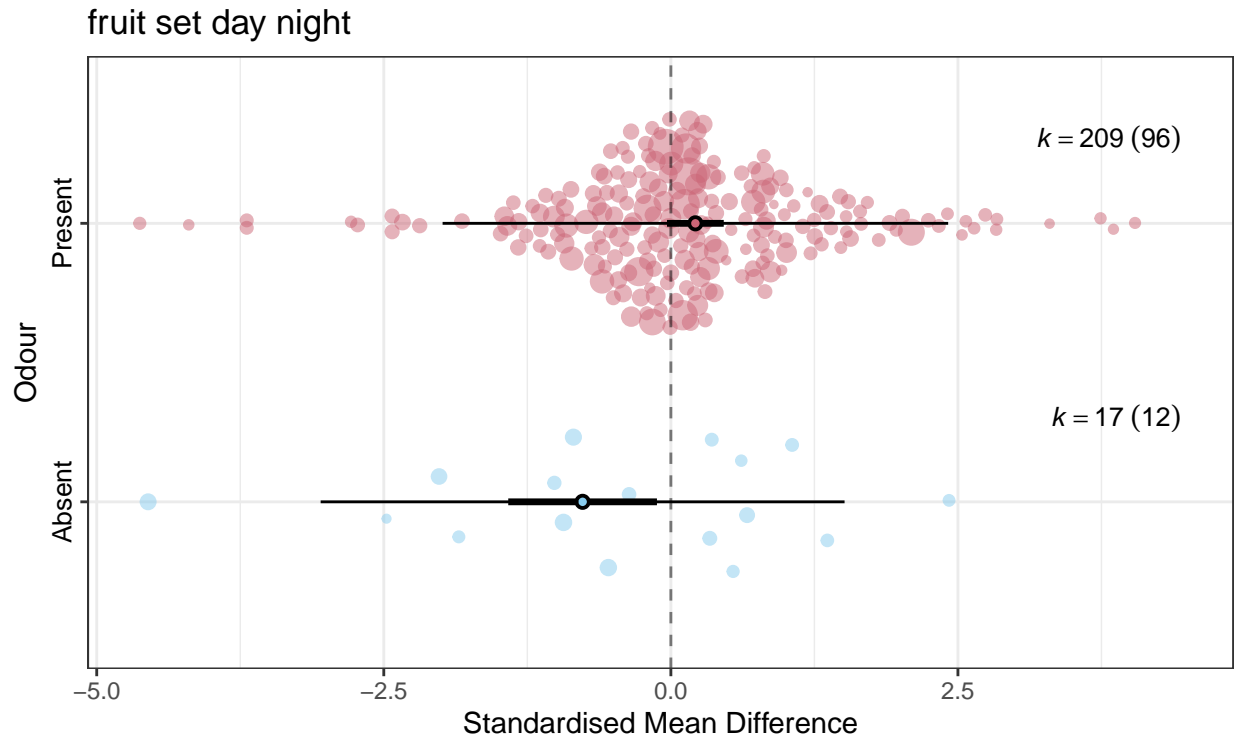


traits-8.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 226; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.5757 0.7587   107    no      study_ID  no
## sigma^2.2 0.3904 0.6248   226    no      effect_ID  no
## sigma^2.3 0.0199 0.1409   111    no        phylo  yes
## sigma^2.4 0.2598 0.5097   111    no accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 224) = 4352.8716, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 8.2198, p-val = 0.0041
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      -0.7686  0.3304 -2.3263  0.0200 -1.4162 -0.1210  *
## odourpresent   0.9823  0.3426  2.8670  0.0041  0.3108  1.6538  **
```

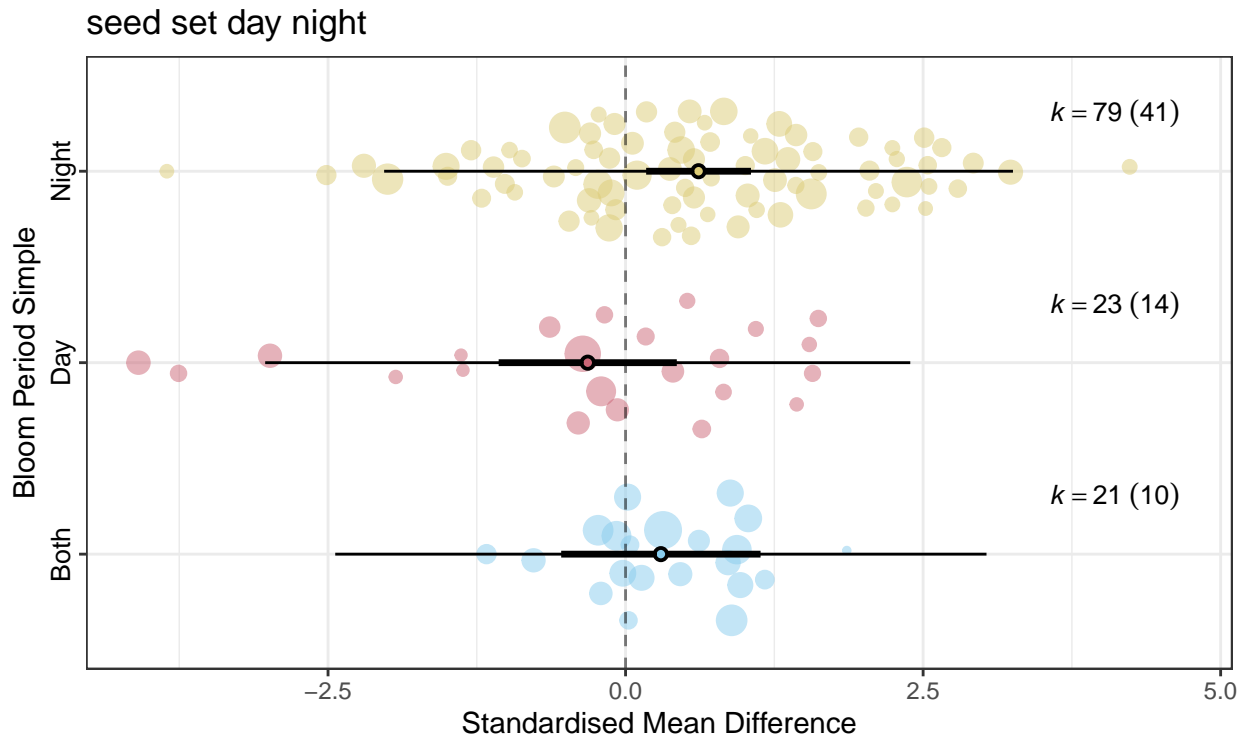
```
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-9.pdf Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40

```
##
## Multivariate Meta-Analysis Model (k = 123; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.0000 0.0000   63    no      study_ID  no
## sigma^2.2 0.1667 0.4083  123    no      effect_ID  no
## sigma^2.3 0.0000 0.0002   61    no      phylo    yes
## sigma^2.4 1.5994 1.2647   61    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 120) = 1331.5610, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 4.4458, p-val = 0.1083
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt           0.2967 0.4273   0.6942 0.4875   -0.5409  1.1342
## bloom_period_simpleday -0.6147 0.5731  -1.0726 0.2835   -1.7378  0.5085
## bloom_period_simplenight 0.3166 0.4828   0.6558 0.5119   -0.6296  1.2629
##
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



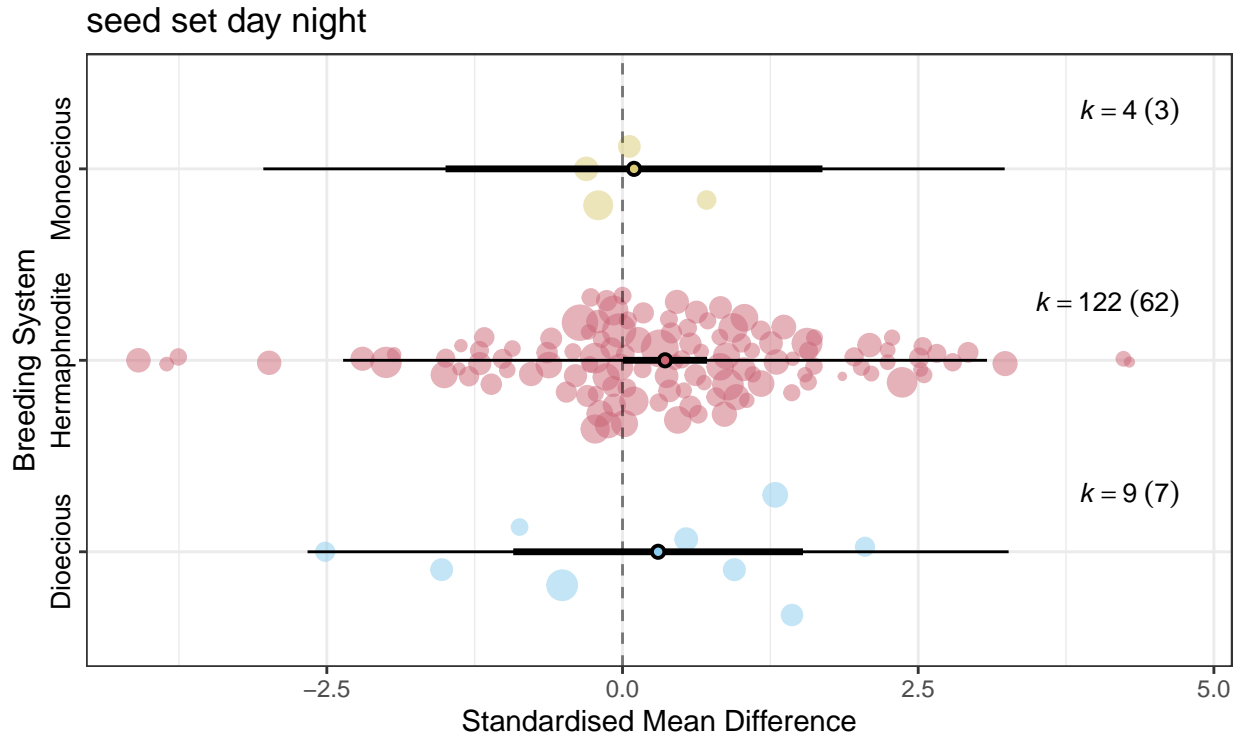
traits-10.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    72    no      study_ID    no
## sigma^2.2  0.1891  0.4349   135    no      effect_ID    no
## sigma^2.3  0.0000  0.0002    70    no      phylo      yes
## sigma^2.4  1.7067  1.3064    70    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 132) = 1555.7539, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.1045, p-val = 0.9491
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## intrcpt          0.3010  0.6250   0.4816  0.6301  -0.9240
## breeding_systemhermaphrodite  0.0588  0.6508   0.0904  0.9280  -1.2168
## breeding_systemmonoecious  -0.2038  1.0255  -0.1988  0.8425  -2.2138
##      ci.ub
## intrcpt          1.5260
```



```
## breeding_systemhermaphrodite 1.3344
## breeding_systemmonoecious 1.8061
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

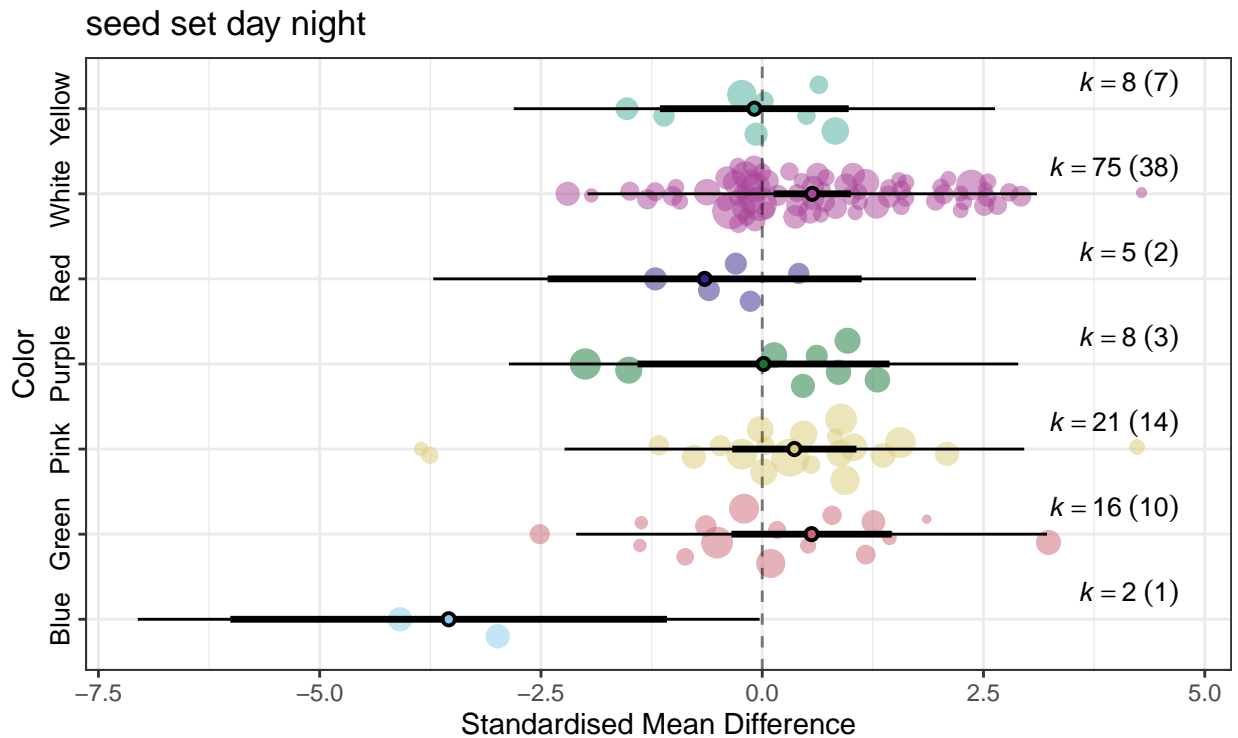


traits-11.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.0000 0.0000   72    no      study_ID no
## sigma^2.2 0.1913 0.4374  135    no      effect_ID no
## sigma^2.3 0.0000 0.0001   70    no        phylo yes
## sigma^2.4 1.4365 1.1985   70    no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 128) = 1192.2179, p-val < .0001
##
## Test of Moderators (coefficients 2:7):
## QM(df = 6) = 12.7831, p-val = 0.0466
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt    -3.5427  1.2587  -2.8145  0.0049   -6.0098   -1.0757  **
## colorgreen  4.1002  1.3408   3.0581  0.0022   1.4723   6.7282  **
```

```
## colorpink      3.9058  1.3086  2.9846  0.0028  1.3409  6.4706  **
## colorpurple    3.5577  1.4532  2.4481  0.0144  0.7094  6.4060  *
## colorred       2.8922  1.5504  1.8654  0.0621 -0.1466  5.9309  .
## colorwhite     4.1077  1.2782  3.2136  0.0013  1.6024  6.6130  **
## coloryellow    3.4536  1.3713  2.5185  0.0118  0.7659  6.1413  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

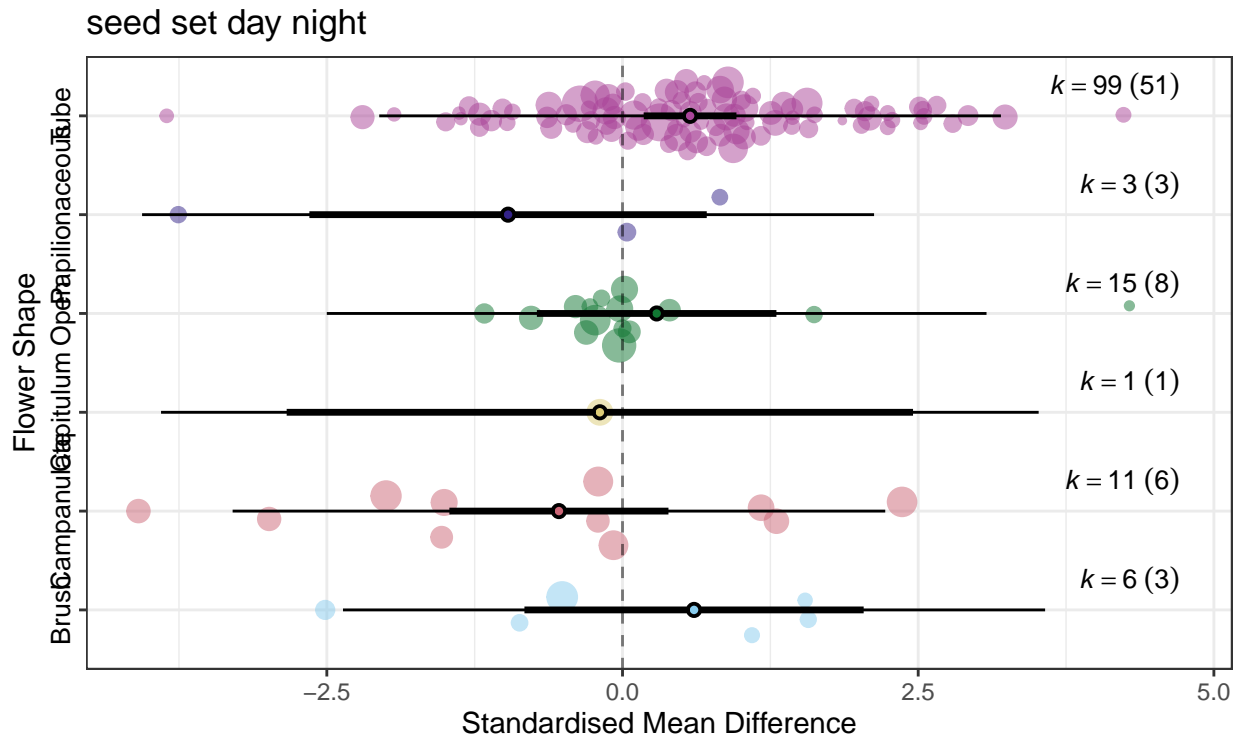


traits-12.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0001   72    no    study_ID  no
## sigma^2.2  0.1893  0.4351  135    no    effect_ID  no
## sigma^2.3  0.0000  0.0000   70    no      phylo  yes
## sigma^2.4  1.5689  1.2525   70    no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 129) = 1382.7733, p-val < .0001
##
## Test of Moderators (coefficients 2:6):
## QM(df = 5) = 7.4118, p-val = 0.1918
##
## Model Results:
##
```

```
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt              0.6048  0.7317   0.8266  0.4085  -0.8293  2.0389
## flower_shapecampanulate -1.1425  0.8710  -1.3117  0.1896  -2.8495  0.5646
## flower_shapecapitulum  -0.7964  1.5364  -0.5183  0.6042  -3.8077  2.2149
## flower_shapeopen       -0.3162  0.8957  -0.3530  0.7241  -2.0717  1.4394
## flower_shapepapilionaceous -1.5725  1.1269  -1.3954  0.1629  -3.7812  0.6362
## flower_shapetube       -0.0335  0.7585  -0.0442  0.9648  -1.5201  1.4531
##
## intrcpt
## flower_shapecampanulate
## flower_shapecapitulum
## flower_shapeopen
## flower_shapepapilionaceous
## flower_shapetube
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

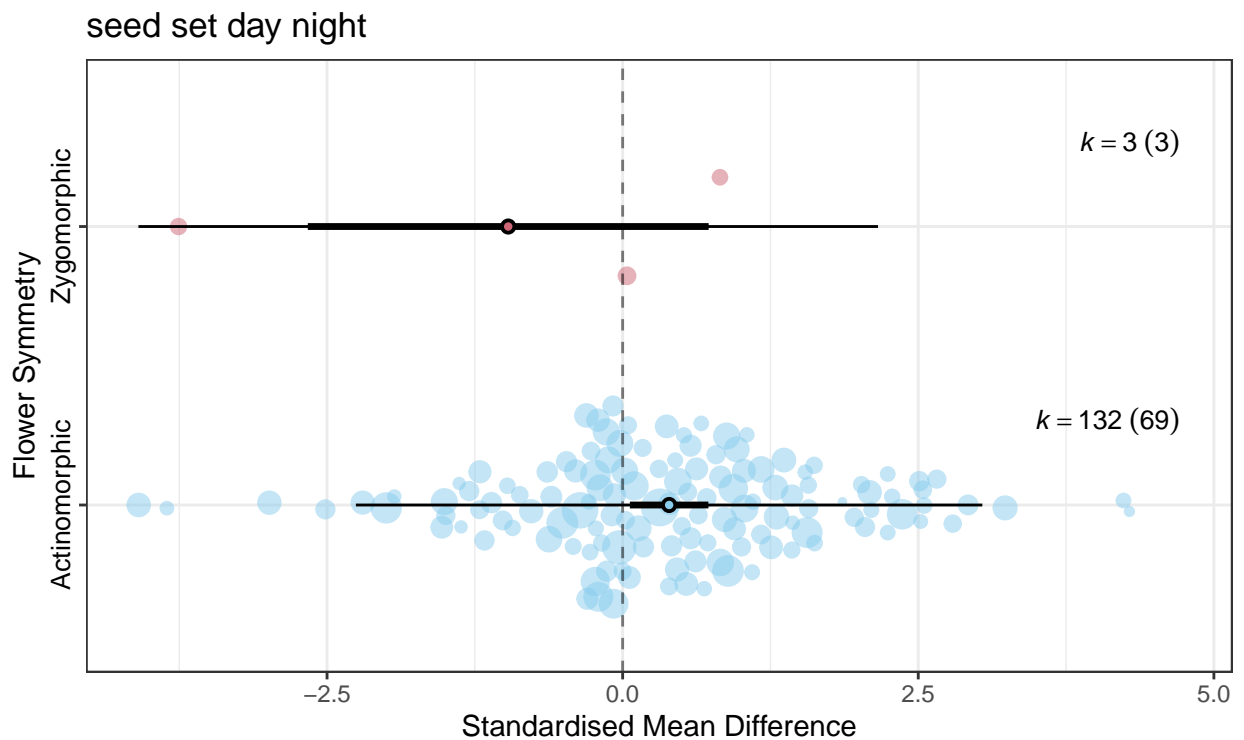


traits-13.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    72    no      study_ID   no
## sigma^2.2  0.1886  0.4343   135    no      effect_ID   no
## sigma^2.3  0.0000  0.0001    70    no        phylo   yes
## sigma^2.4  1.6093  1.2686    70    no  accepted_name   no
```

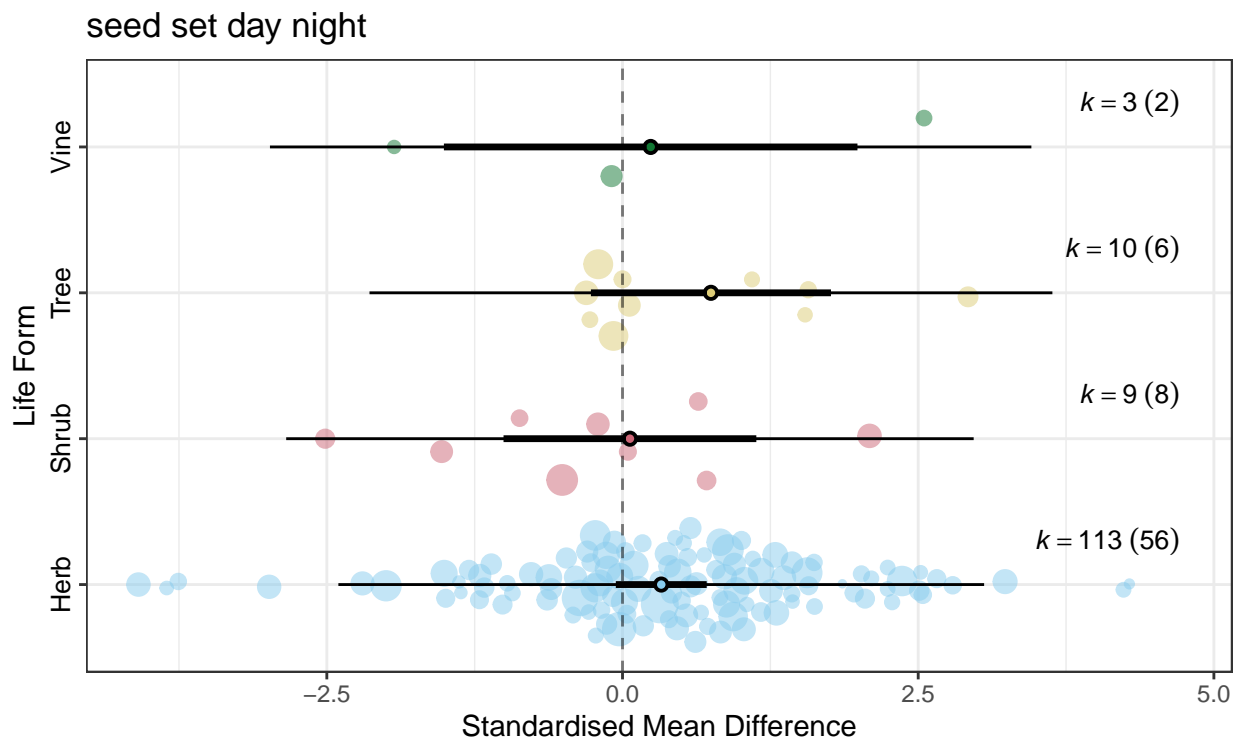
```
##
## Test for Residual Heterogeneity:
## QE(df = 133) = 1554.4200, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 2.3843, p-val = 0.1226
##
## Model Results:
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt              0.3930  0.1693   2.3217  0.0202   0.0612   0.7248
## flower_symmetryzygomorphic -1.3607  0.8812  -1.5441  0.1226  -3.0877   0.3664
##
## intrcpt              *
## flower_symmetryzygomorphic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-14.pdf

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0000    72    no    study_ID  no
## sigma^2.2  0.1898  0.4357   135    no    effect_ID  no
## sigma^2.3  0.0000  0.0006    70    no     phylo   yes
```

```
## sigma^2.4  1.7117  1.3083    70    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 131) = 1547.2042, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 0.8951, p-val = 0.8266
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.3275  0.1960  1.6708  0.0948  -0.0567  0.7117 .
## life_formshrub   -0.2648  0.5794  -0.4570  0.6477  -1.4004  0.8708
## life_formtree     0.4201  0.5536  0.7589  0.4479  -0.6650  1.5052
## life_formvine    -0.0895  0.9133  -0.0980  0.9219  -1.8795  1.7005
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

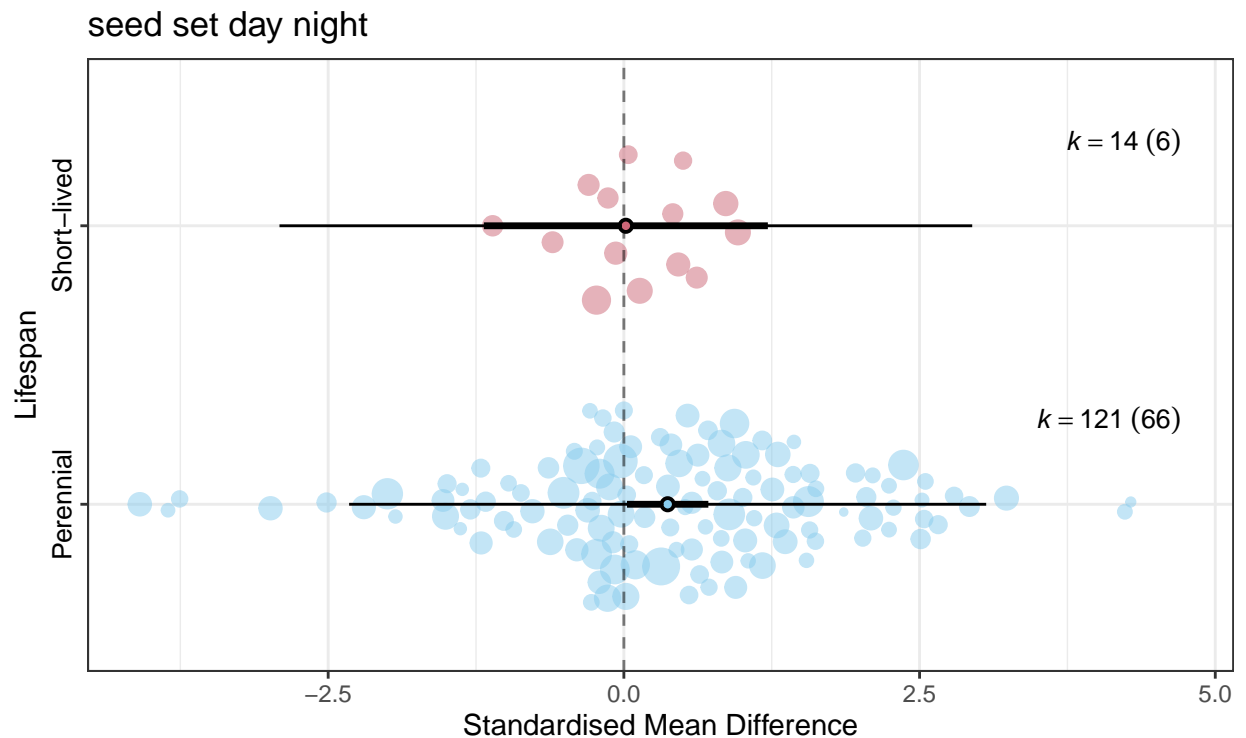


traits-15.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    72    no      study_ID   no
## sigma^2.2  0.1887  0.4344   135    no      effect_ID  no
## sigma^2.3  0.0000  0.0001    70    no        phylo  yes
```

```
## sigma^2.4  1.6685  1.2917    70    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 133) = 1563.2943, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.3080, p-val = 0.5789
##
## Model Results:
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt           0.3703  0.1755   2.1103  0.0348   0.0264   0.7142  *
## lifespanshort-lived -0.3537  0.6373  -0.5550  0.5789  -1.6027   0.8954
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

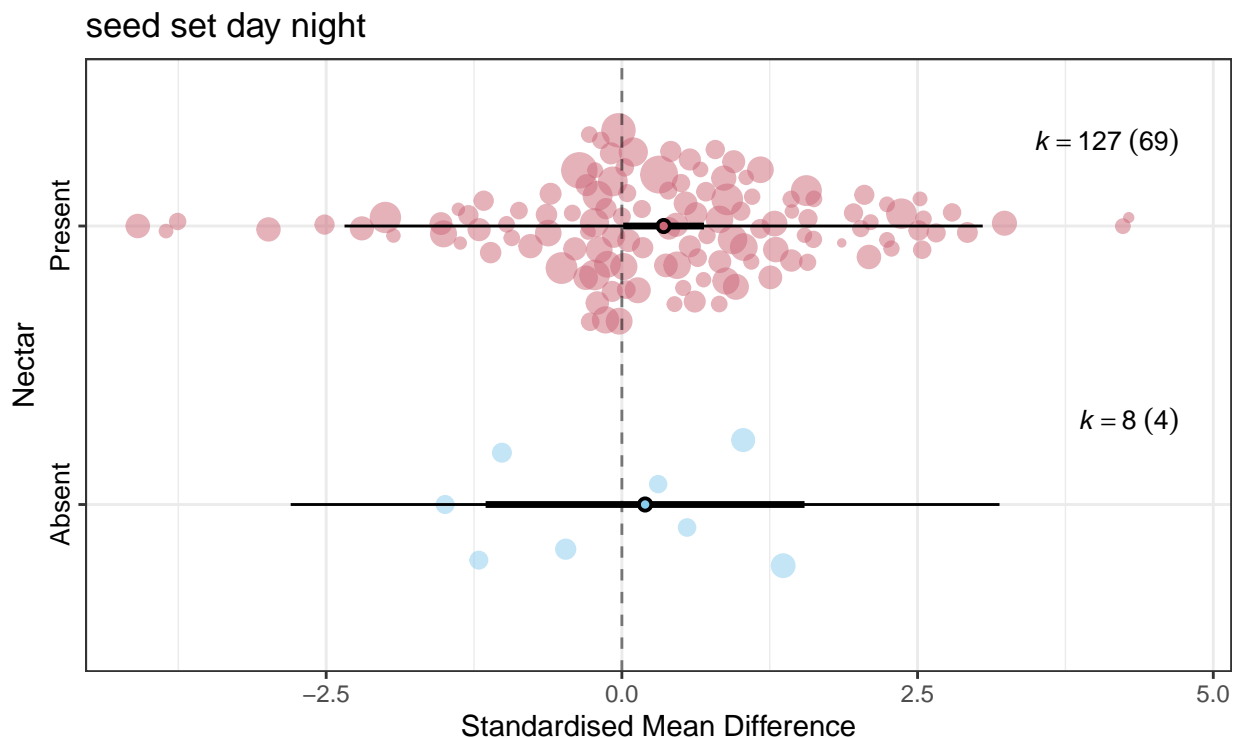


traits-16.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0000    72    no    study_ID  no
## sigma^2.2  0.1891  0.4348   135    no    effect_ID  no
## sigma^2.3  0.0000  0.0002    70    no     phylo  yes
## sigma^2.4  1.6752  1.2943    70    no accepted_name  no
##
```

```
## Test for Residual Heterogeneity:
## QE(df = 133) = 1563.5459, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0488, p-val = 0.8252
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt         0.1963  0.6879  0.2854  0.7754  -1.1519  1.5445
## nectarpresent    0.1567  0.7096  0.2208  0.8252  -1.2341  1.5475
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

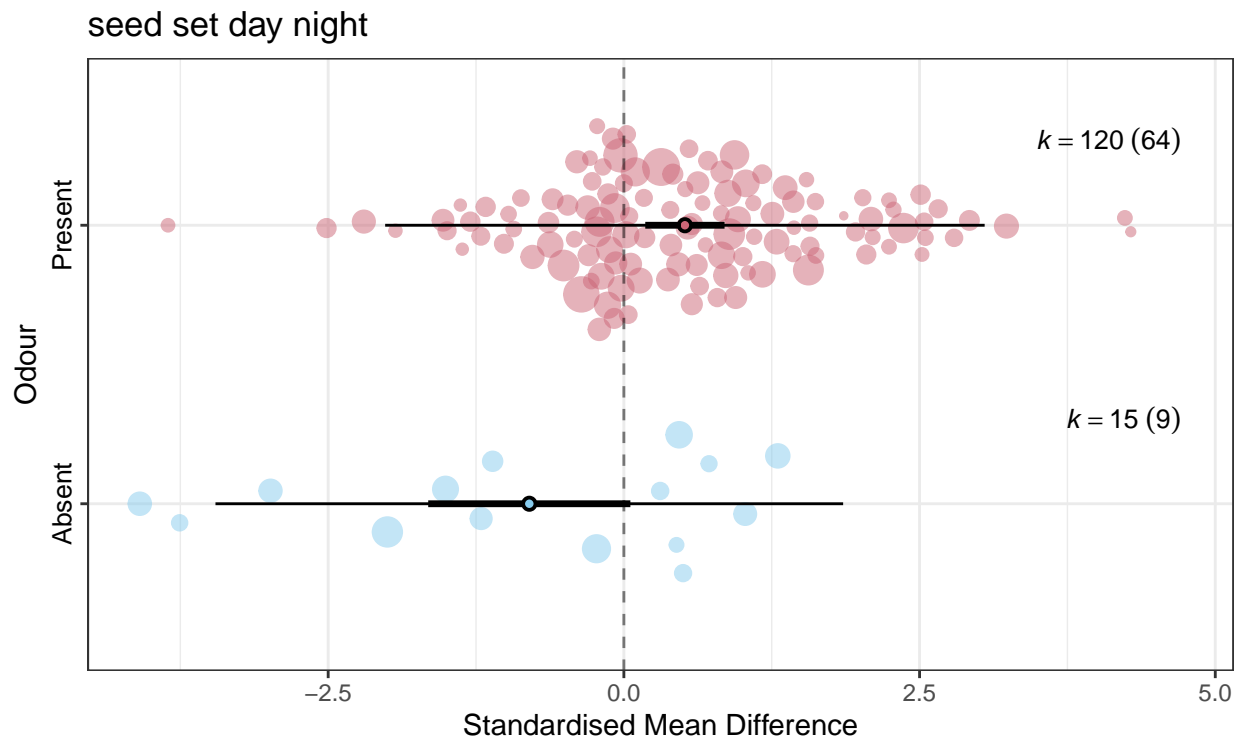


traits-17.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 135; method: REML)
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0000    72    no      study_ID  no
## sigma^2.2  0.1907  0.4367   135    no      effect_ID  no
## sigma^2.3  0.0000  0.0001    70    no        phylo  yes
## sigma^2.4  1.4519  1.2050    70    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 133) = 1320.5970, p-val < .0001
```

```
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 7.8891, p-val = 0.0050
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      -0.7996  0.4361 -1.8336  0.0667  -1.6542   0.0551  .
## odourpresent   1.3155  0.4684  2.8088  0.0050   0.3976   2.2335  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



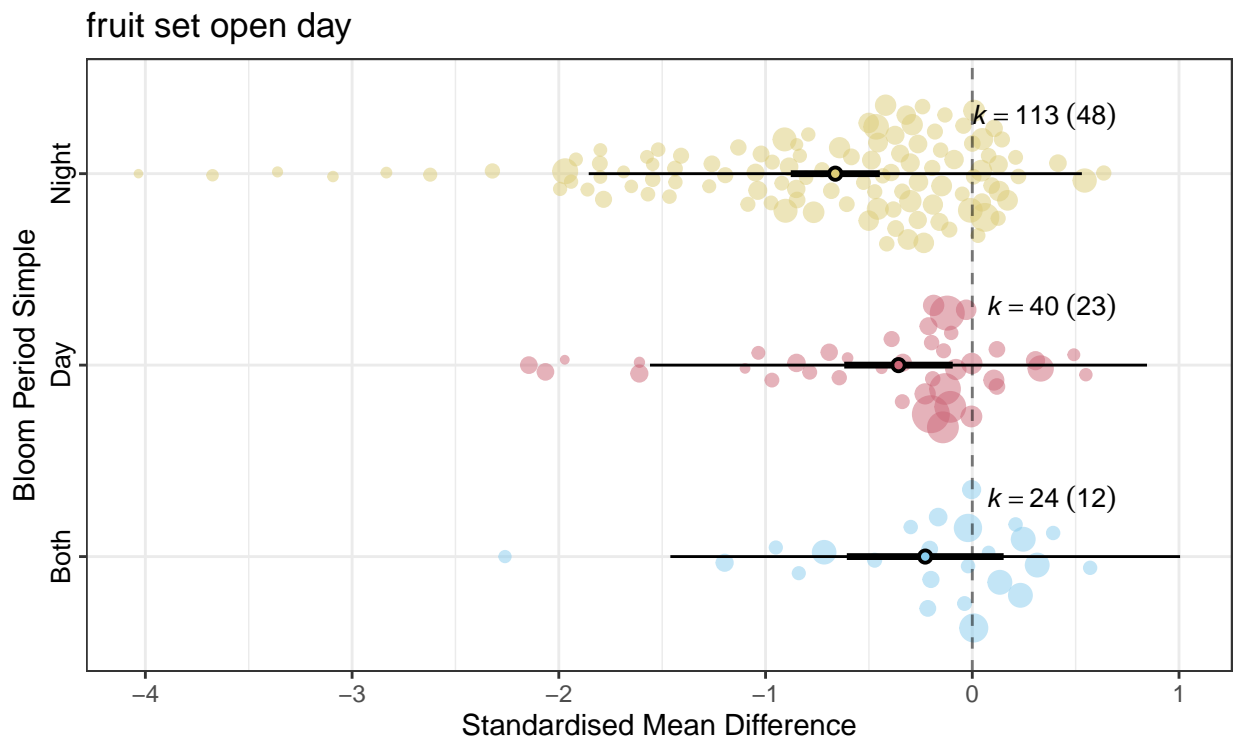
traits-18.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 177; method: REML)
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.2415  0.4914    80    no    study_ID  no
## sigma^2.2  0.0460  0.2145   177    no    effect_ID  no
## sigma^2.3  0.0162  0.1275    81    no    phylo    yes
## sigma^2.4  0.0545  0.2334    81    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 174) = 1728.7685, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
```



```
## QM(df = 2) = 6.5498, p-val = 0.0378
##
## Model Results:
##
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.2276  0.1935  -1.1762  0.2395  -0.6069   0.1517
## bloom_period_simpleday -0.1293  0.2270  -0.5698  0.5688  -0.5743   0.3156
## bloom_period_simplenight -0.4350  0.2136  -2.0370  0.0417  -0.8536  -0.0164
##
## intrcpt
## bloom_period_simpleday
## bloom_period_simplenight  *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

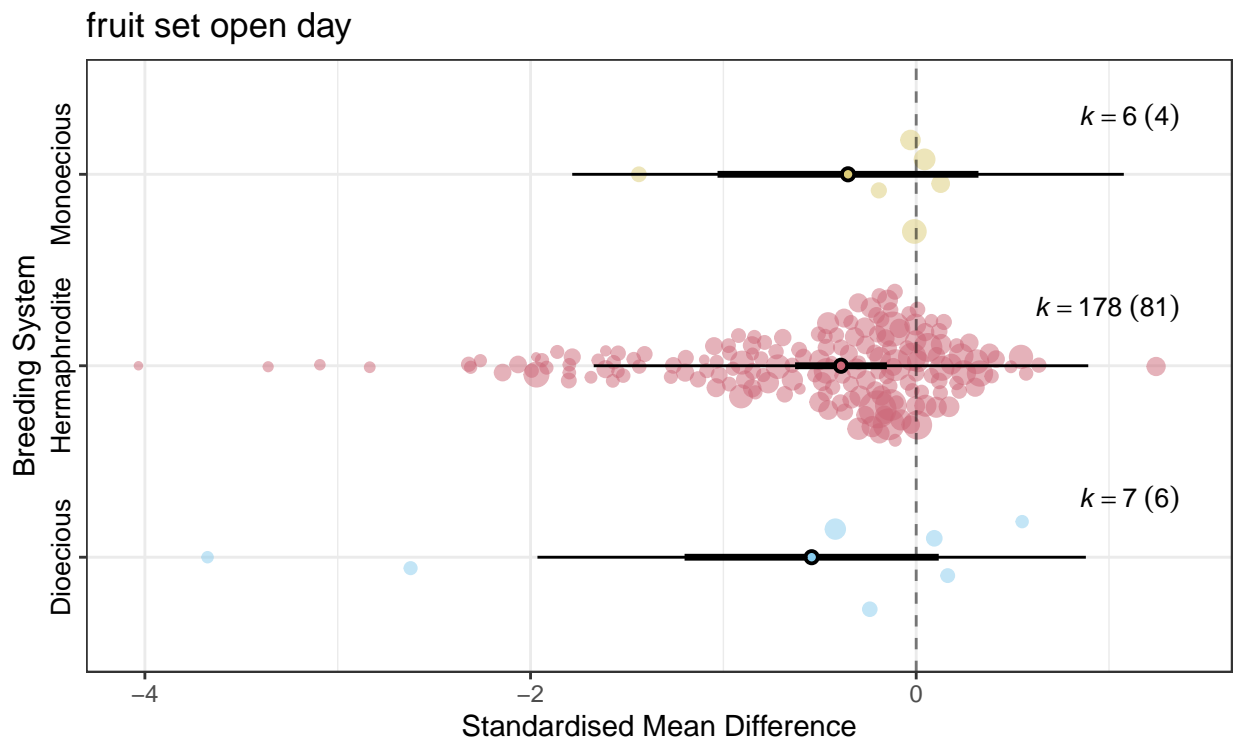


traits-19.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2425  0.4924    90    no      study_ID  no
## sigma^2.2  0.0443  0.2105   191    no      effect_ID  no
## sigma^2.3  0.0748  0.2735    92    no        phylo  yes
## sigma^2.4  0.0517  0.2275    92    no  accepted_name  no
##
## Test for Residual Heterogeneity:
```

```
## QE(df = 188) = 2073.3395, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.2284, p-val = 0.8921
##
## Model Results:
##
##               estimate      se    zval    pval    ci.lb
## intrcpt          -0.5421  0.3363 -1.6122  0.1069 -1.2012
## breeding_systemhermaphrodite  0.1521  0.3297  0.4614  0.6445 -0.4942
## breeding_systemmonoecious    0.1885  0.4678  0.4030  0.6869 -0.7283
##               ci.ub
## intrcpt          0.1169
## breeding_systemhermaphrodite  0.7984
## breeding_systemmonoecious    1.1054
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

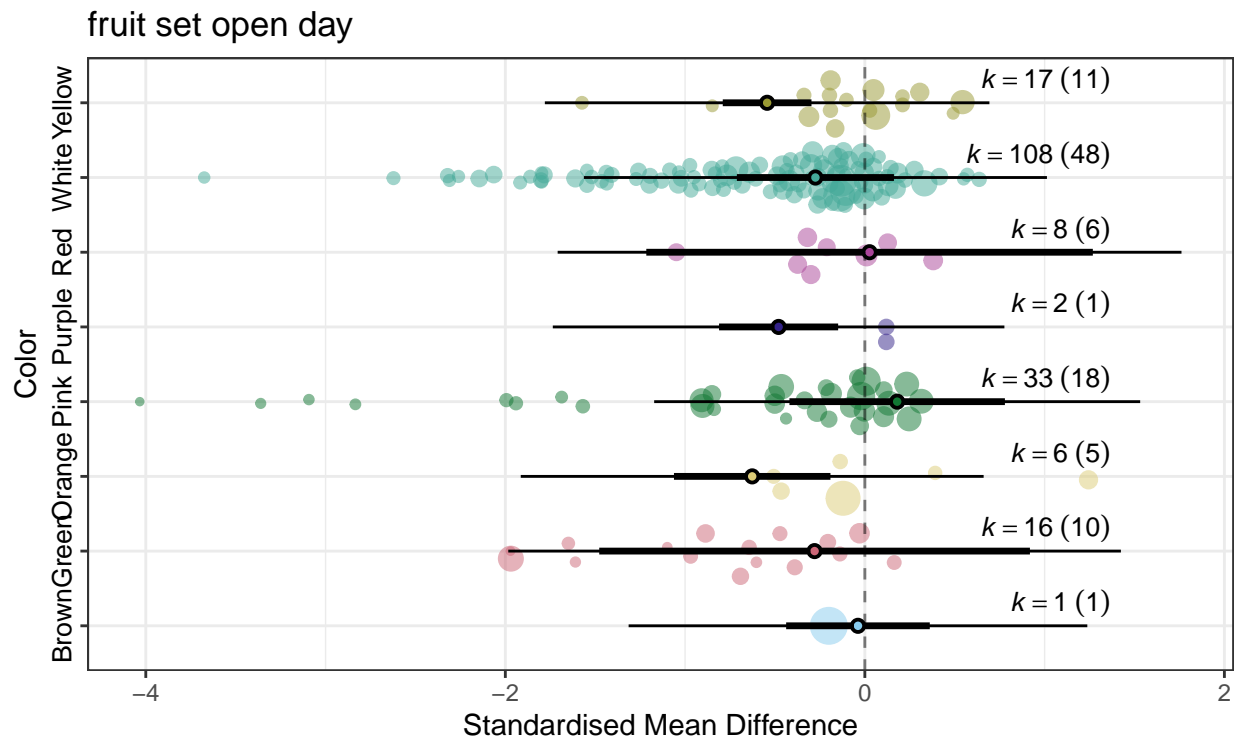


traits-20.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.2446  0.4946   90    no    study_ID no
## sigma^2.2  0.0406  0.2015  191    no    effect_ID no
## sigma^2.3  0.0534  0.2311   92    no    phylo    yes
```

```
## sigma^2.4 0.0435 0.2087 92 no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 183) = 1575.6790, p-val < .0001
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 13.5614, p-val = 0.0596
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.0383 0.2038 -0.1879 0.8509 -0.4378 0.3612
## colorbrown    -0.2413 0.6332 -0.3812 0.7031 -1.4823 0.9997
## colorgreen    -0.5884 0.2576 -2.2839 0.0224 -1.0934 -0.0835 *
## colororange    0.2181 0.3525 0.6188 0.5360 -0.4727 0.9090
## colorpink     -0.4415 0.2403 -1.8372 0.0662 -0.9124 0.0295 .
## colorpurple    0.0646 0.6592 0.0980 0.9220 -1.2274 1.3565
## colorred      -0.2368 0.2809 -0.8427 0.3994 -0.7874 0.3139
## colorwhite    -0.5053 0.2071 -2.4398 0.0147 -0.9112 -0.0994 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-21.pdf

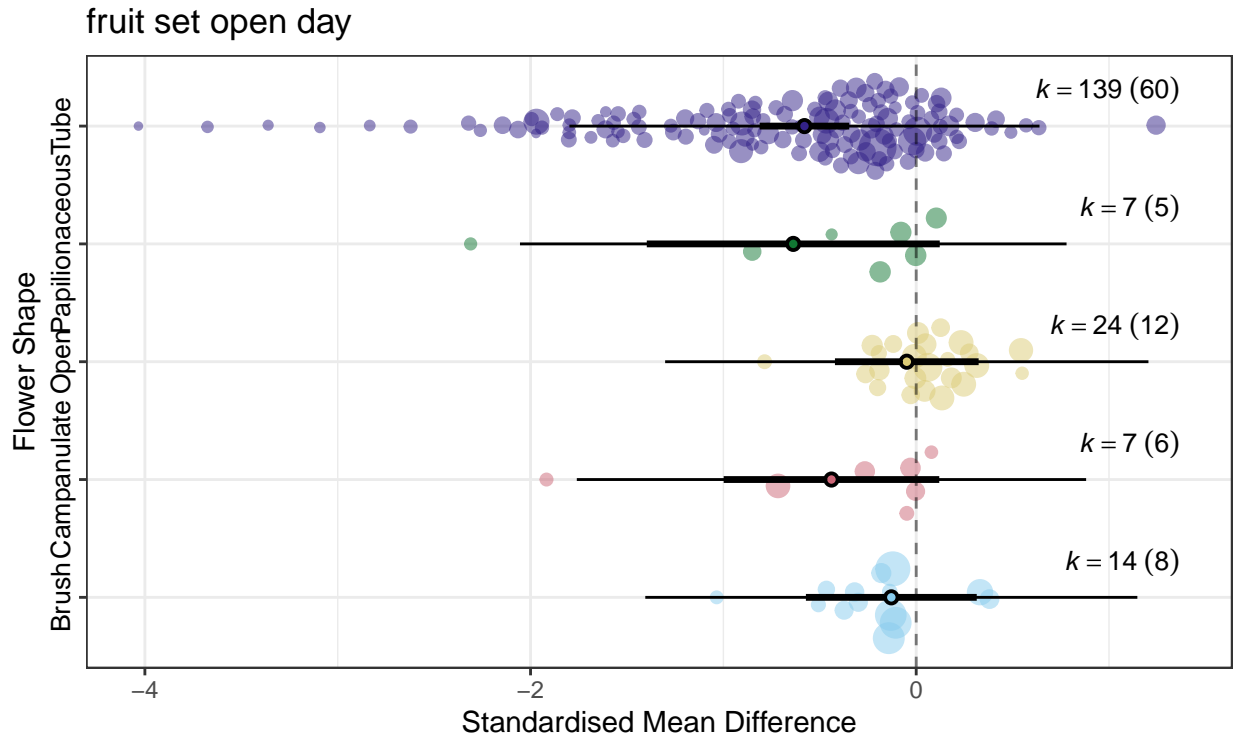
Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
```

```

##          estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1 0.2352  0.4850    90    no      study_ID  no
## sigma^2.2 0.0451  0.2124   191    no      effect_ID  no
## sigma^2.3 0.0334  0.1828    92    no        phylo  yes
## sigma^2.4 0.0590  0.2429    92    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 186) = 1658.2381, p-val < .0001
##
## Test of Moderators (coefficients 2:5):
## QM(df = 4) = 7.8454, p-val = 0.0974
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          -0.1290  0.2260  -0.5706  0.5682  -0.5720  0.3140
## flower_shapecampanulate -0.3104  0.3556  -0.8731  0.3826  -1.0073  0.3865
## flower_shapeopen         0.0802  0.2712   0.2956  0.7675  -0.4514  0.6117
## flower_shapepapilionaceous -0.5085  0.4479  -1.1353  0.2562  -1.3864  0.3694
## flower_shapetube        -0.4505  0.2465  -1.8280  0.0675  -0.9336  0.0325
##
## intrcpt
## flower_shapecampanulate
## flower_shapeopen
## flower_shapepapilionaceous
## flower_shapetube      .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

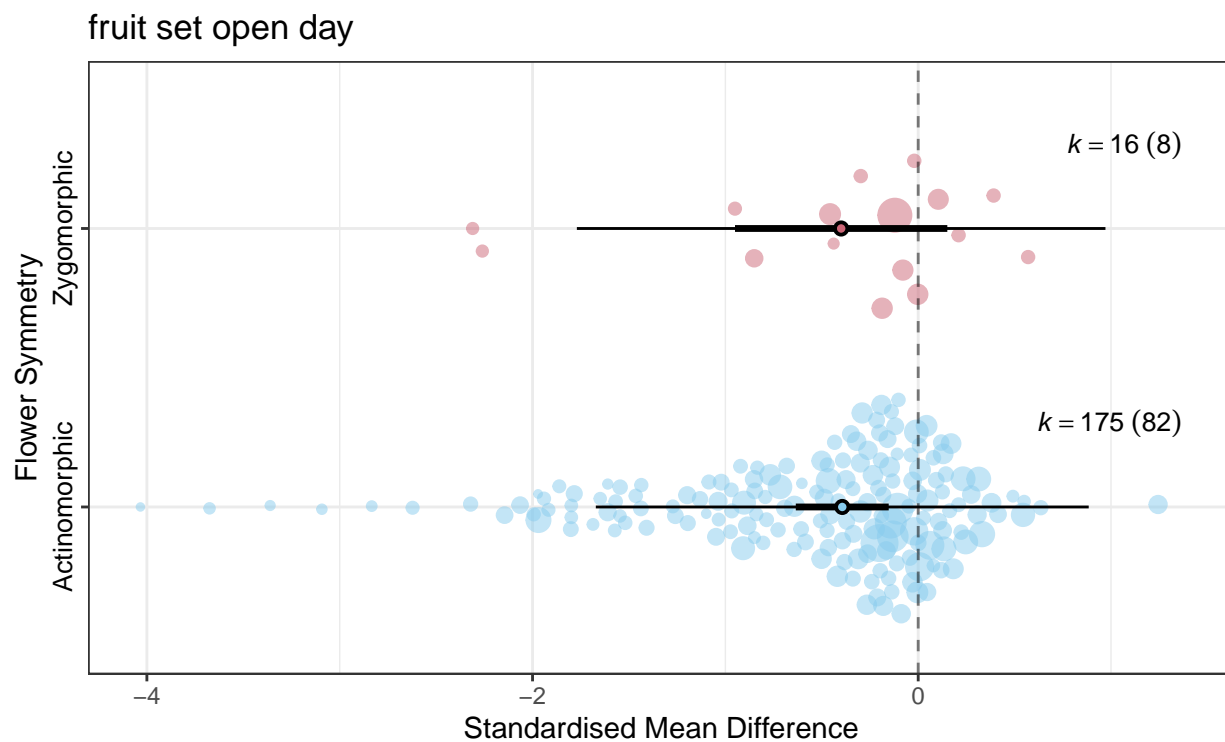
```



traits-22.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

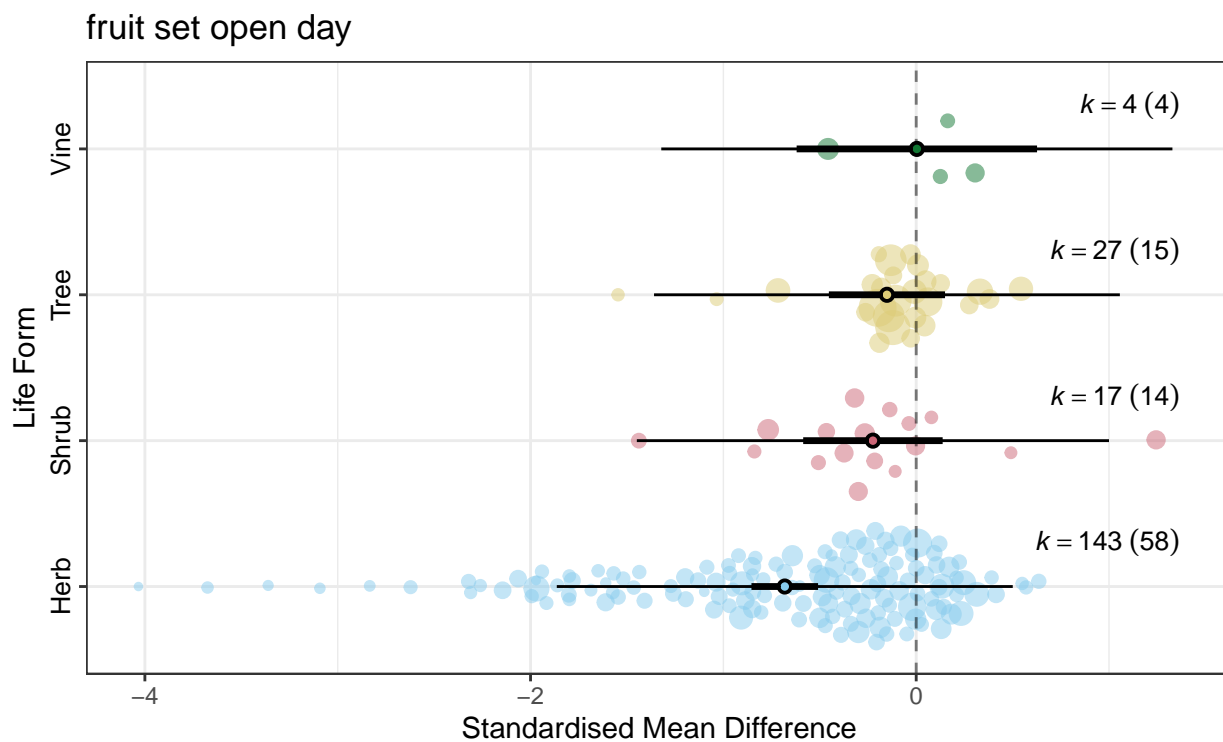
```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2421  0.4920    90    no      study_ID  no
## sigma^2.2  0.0440  0.2098   191    no      effect_ID  no
## sigma^2.3  0.0744  0.2728    92    no        phylo  yes
## sigma^2.4  0.0496  0.2228    92    no accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 189) = 2081.0430, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0004, p-val = 0.9841
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          -0.3938  0.1229  -3.2034  0.0014  -0.6347  -0.1528
## flower_symmetryzygomorphic -0.0057  0.2888  -0.0199  0.9841  -0.5717   0.5602
##
## intrcpt                **
## flower_symmetryzygomorphic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-23.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

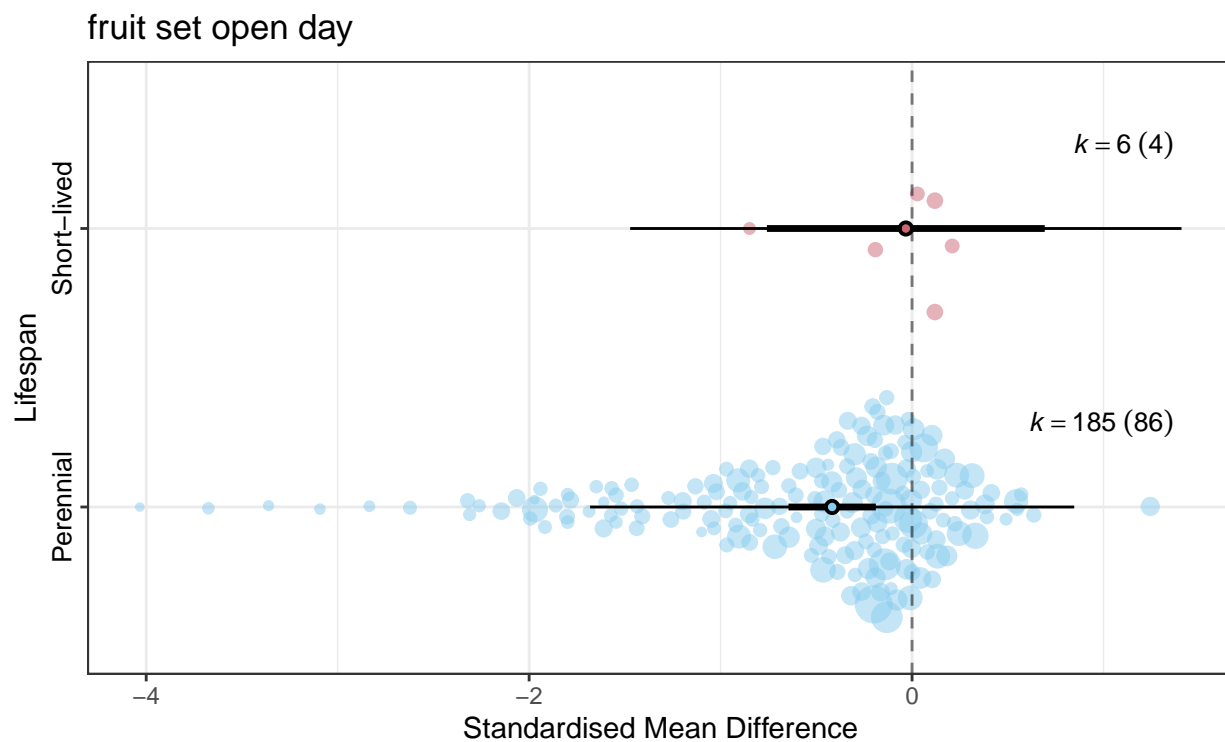
```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2472  0.4972    90    no      study_ID  no
## sigma^2.2  0.0447  0.2115   191    no      effect_ID  no
## sigma^2.3  0.0009  0.0307    92    no        phylo  yes
## sigma^2.4  0.0633  0.2516    92    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 187) = 1917.2403, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 13.5814, p-val = 0.0035
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.6816  0.0881  -7.7337  <.0001  -0.8543  -0.5088  ***
## life_formshrub  0.4572  0.2041   2.2404  0.0251   0.0572   0.8572   *
## life_formtree   0.5299  0.1768   2.9969  0.0027   0.1834   0.8765  **
## life_formvine   0.6849  0.3298   2.0767  0.0378   0.0385   1.3314   *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-24.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2416  0.4915    90    no      study_ID  no
## sigma^2.2  0.0441  0.2099   191    no      effect_ID  no
## sigma^2.3  0.0678  0.2604    92    no        phylo  yes
## sigma^2.4  0.0491  0.2216    92    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 189) = 2085.5968, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.0744, p-val = 0.3000
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.4173  0.1164  -3.5840  0.0003  -0.6454  -0.1891 ***
## lifespanshort-lived  0.3848  0.3712  1.0365  0.3000  -0.3428  1.1123
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

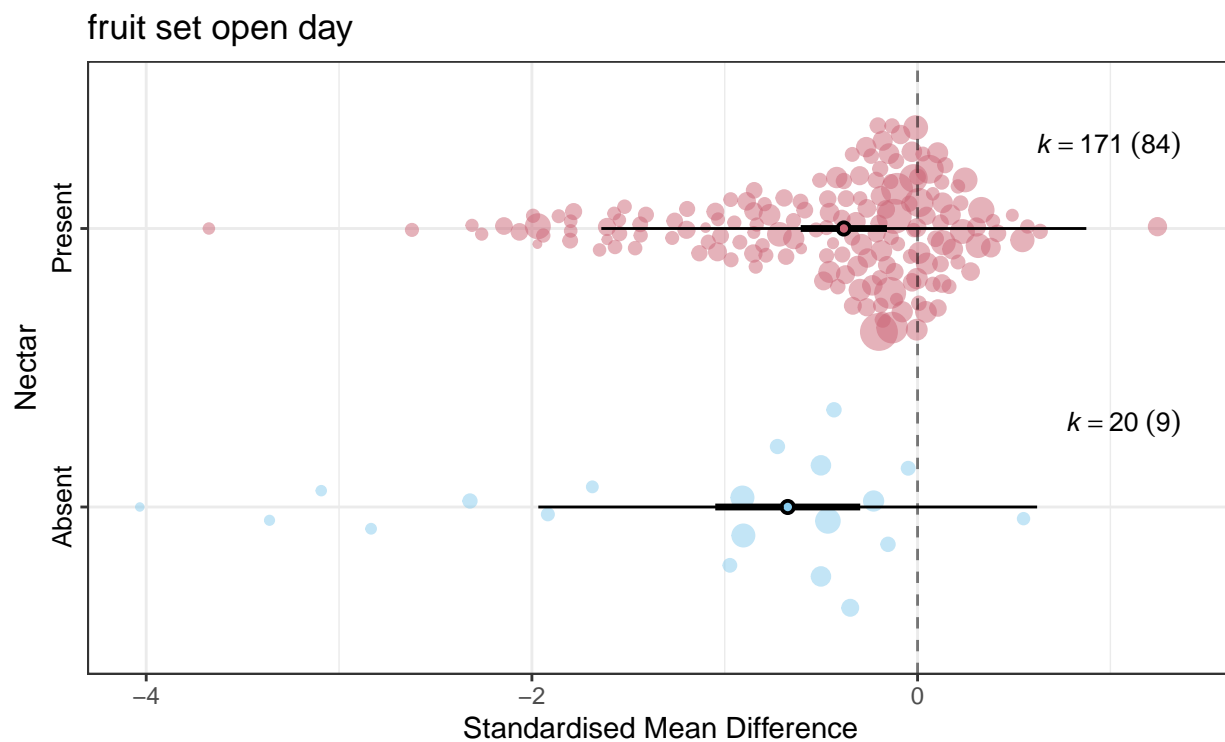


traits-25.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2583  0.5083    90    no      study_ID  no
## sigma^2.2  0.0486  0.2204   191    no      effect_ID  no
## sigma^2.3  0.0664  0.2577    92    no        phylo  yes
## sigma^2.4  0.0254  0.1593    92    no accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 189) = 1946.7422, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 3.1698, p-val = 0.0750
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.6733  0.1917  -3.5113  0.0004  -1.0491  -0.2975  ***
## nectarpresent  0.2909  0.1634   1.7804  0.0750  -0.0293   0.6111   .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

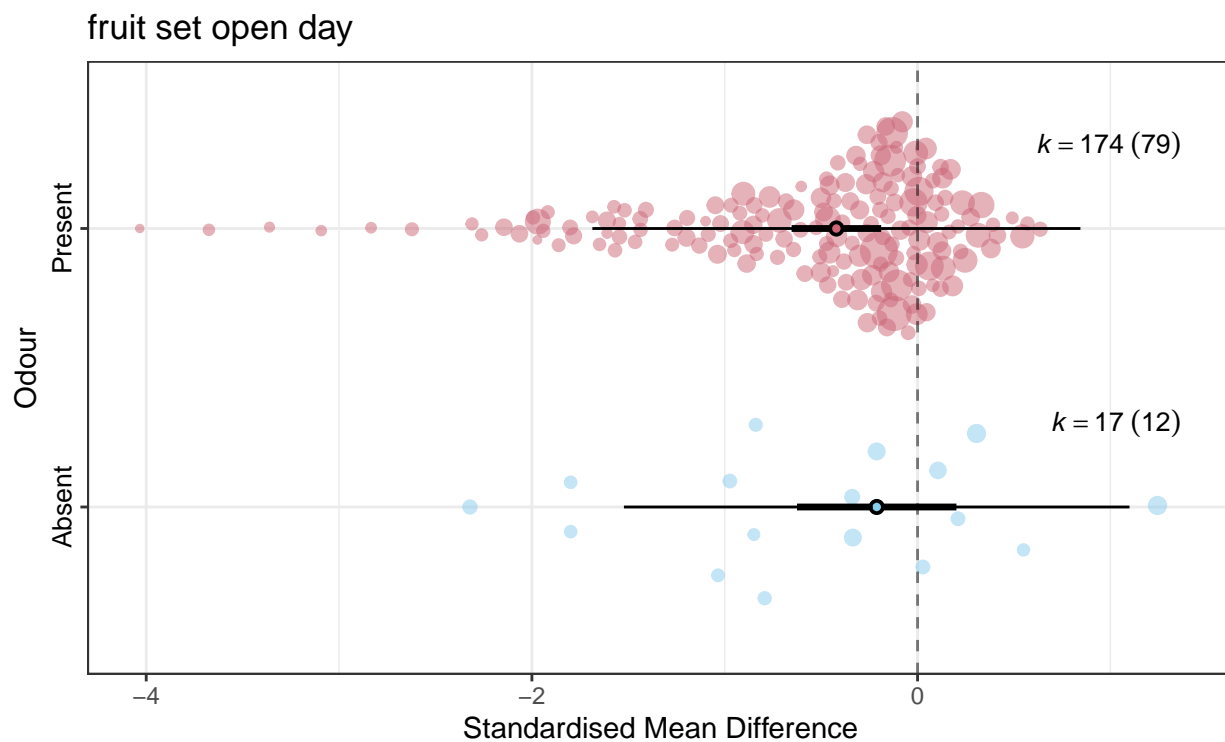




traits-26.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 191; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.2389  0.4887    90    no      study_ID    no
## sigma^2.2  0.0437  0.2091   191    no      effect_ID    no
## sigma^2.3  0.0704  0.2654    92    no        phylo    yes
## sigma^2.4  0.0499  0.2233    92    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 189) = 2083.3875, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.0888, p-val = 0.2967
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.2119  0.2109  -1.0046  0.3151  -0.6252  0.2015
## odourpresent  -0.2092  0.2004  -1.0434  0.2967  -0.6020  0.1837
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

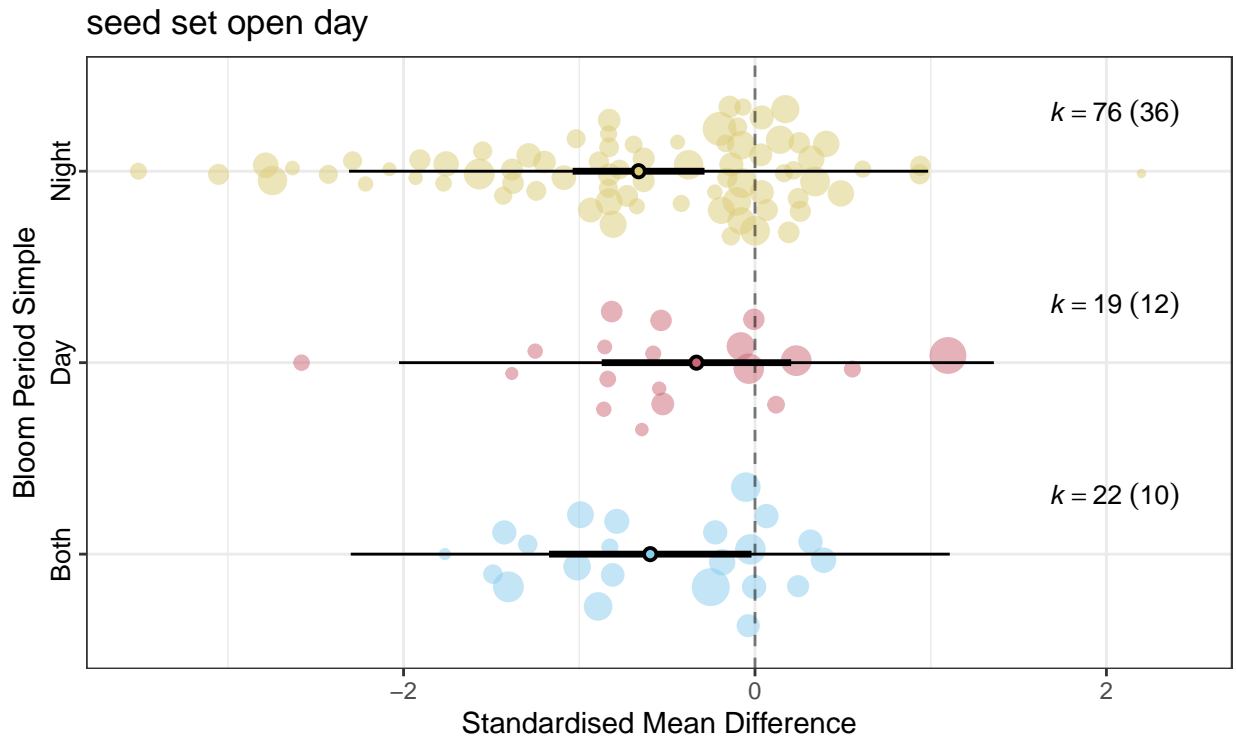


traits-27.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30

```
##
## Multivariate Meta-Analysis Model (k = 117; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    57    no      study_ID    no
## sigma^2.2  0.1439  0.3794   117    no      effect_ID    no
## sigma^2.3  0.0721  0.2685    54    no        phylo    yes
## sigma^2.4  0.4540  0.6738    54    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 114) = 765.7035, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 1.1199, p-val = 0.5712
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.5960  0.2939  -2.0281  0.0426  -1.1720  -0.0200
## bloom_period_simpleday      0.2628  0.3806   0.6905  0.4899  -0.4832   1.0088
## bloom_period_simplenight  -0.0664  0.3156  -0.2104  0.8334  -0.6850   0.5522
##
## intrcpt          *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

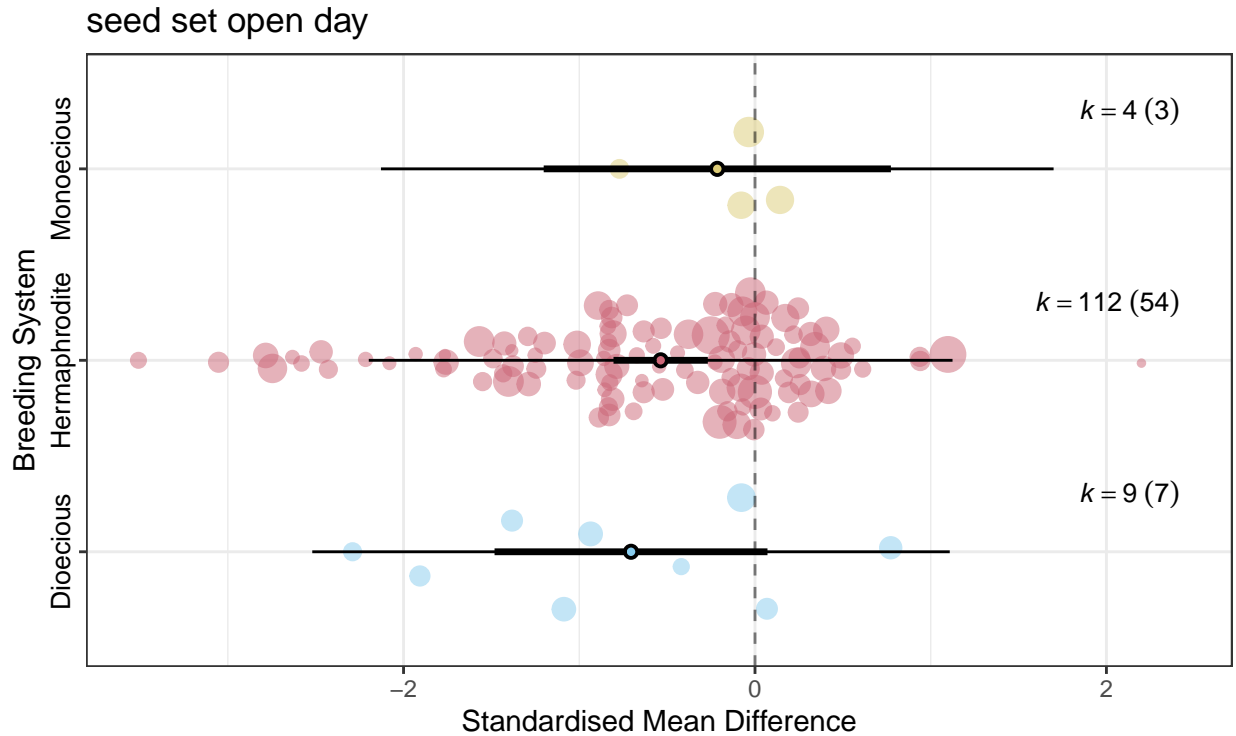


traits-28.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    64    no      study_ID    no
## sigma^2.2  0.1461  0.3822   125    no      effect_ID    no
## sigma^2.3  0.0252  0.1587    61    no      phylo      yes
## sigma^2.4  0.5282  0.7268    61    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 122) = 929.3696, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.5970, p-val = 0.7419
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb
## intrcpt      -0.7055  0.3963  -1.7804  0.0750  -1.4822
## breeding_systemhermaphrodite  0.1687  0.4098  0.4118  0.6805  -0.6344
## breeding_systemmonoecious    0.4910  0.6367  0.7712  0.4406  -0.7569
##      ci.ub
## intrcpt      0.0711 .
```

```
## breeding_systemhermaphrodite 0.9718
## breeding_systemmonoecious 1.7389
##
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-29.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0000  0.0000   64    no      study_ID  no
## sigma^2.2  0.1446  0.3802  125    no      effect_ID  no
## sigma^2.3  0.0703  0.2652   61    no        phylo  yes
## sigma^2.4  0.5412  0.7357   61    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 118) = 906.1191, p-val < .0001
##
## Test of Moderators (coefficients 2:7):
## QM(df = 6) = 1.5216, p-val = 0.9580
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      0.1716  0.8341   0.2057  0.8370  -1.4633  1.8064
## colorgreen  -0.7954  0.9046  -0.8793  0.3792  -2.5684  0.9775
```

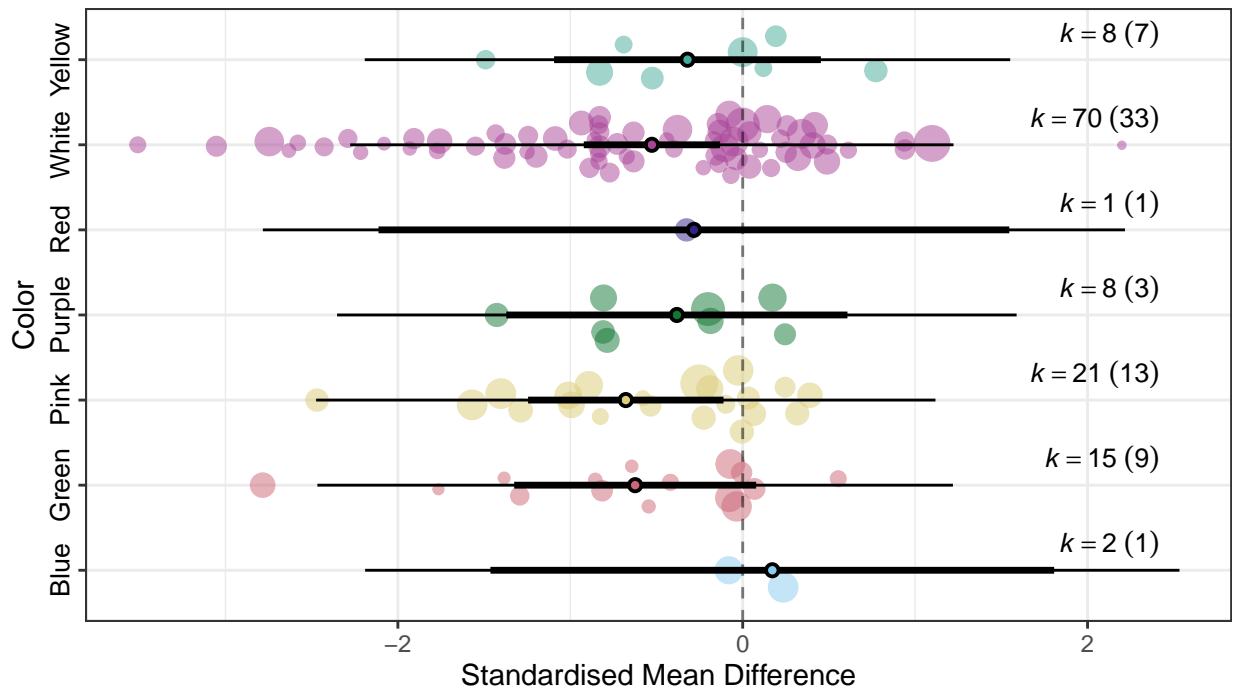
```
## colorpink      -0.8498  0.8712  -0.9754  0.3294  -2.5572  0.8577
## colorpurple    -0.5536  0.9303  -0.5951  0.5518  -2.3770  1.2698
## colorred       -0.4547  1.2508  -0.3635  0.7162  -2.9063  1.9969
## colorwhite     -0.6986  0.8435  -0.8282  0.4075  -2.3518  0.9546
## coloryellow    -0.4919  0.9168  -0.5366  0.5916  -2.2889  1.3050
```

```
##
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

seed set open day



traits-30.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
```

```
## Multivariate Meta-Analysis Model (k = 125; method: REML)
```

```
##
```

```
## Variance Components:
```

```
##
```

```
##      estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0000  0.0000   64    no      study_ID no
## sigma^2.2  0.1451  0.3810  125    no      effect_ID no
## sigma^2.3  0.0478  0.2185   61    no        phylo yes
## sigma^2.4  0.5009  0.7077   61    no  accepted_name no
```

```
##
```

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 119) = 894.7931, p-val < .0001
```

```
##
```

```
## Test of Moderators (coefficients 2:6):
```

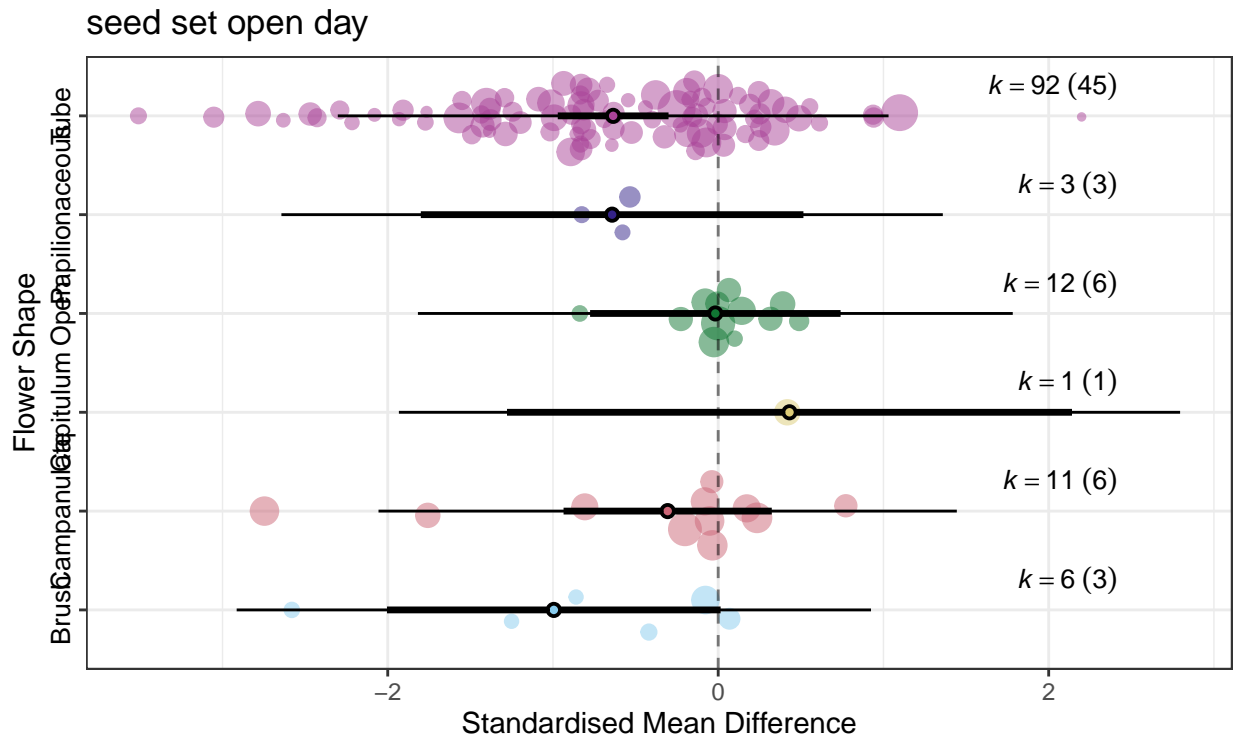
```
## QM(df = 5) = 4.8000, p-val = 0.4408
```

```
##
```

```
## Model Results:
```

```
##
```

```
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.9948  0.5150  -1.9315  0.0534  -2.0043  0.0147
## flower_shapecampanulate    0.6889  0.5990   1.1500  0.2501  -0.4852  1.8630
## flower_shapecapitulum     1.4262  1.0090   1.4135  0.1575  -0.5514  3.4037
## flower_shapeopen          0.9775  0.6369   1.5346  0.1249  -0.2709  2.2258
## flower_shapepapilionaceous  0.3527  0.7757   0.4547  0.6493  -1.1676  1.8730
## flower_shapetube          0.3590  0.5372   0.6683  0.5039  -0.6939  1.4119
##
## intrcpt
## flower_shapecampanulate
## flower_shapecapitulum
## flower_shapeopen
## flower_shapepapilionaceous
## flower_shapetube
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

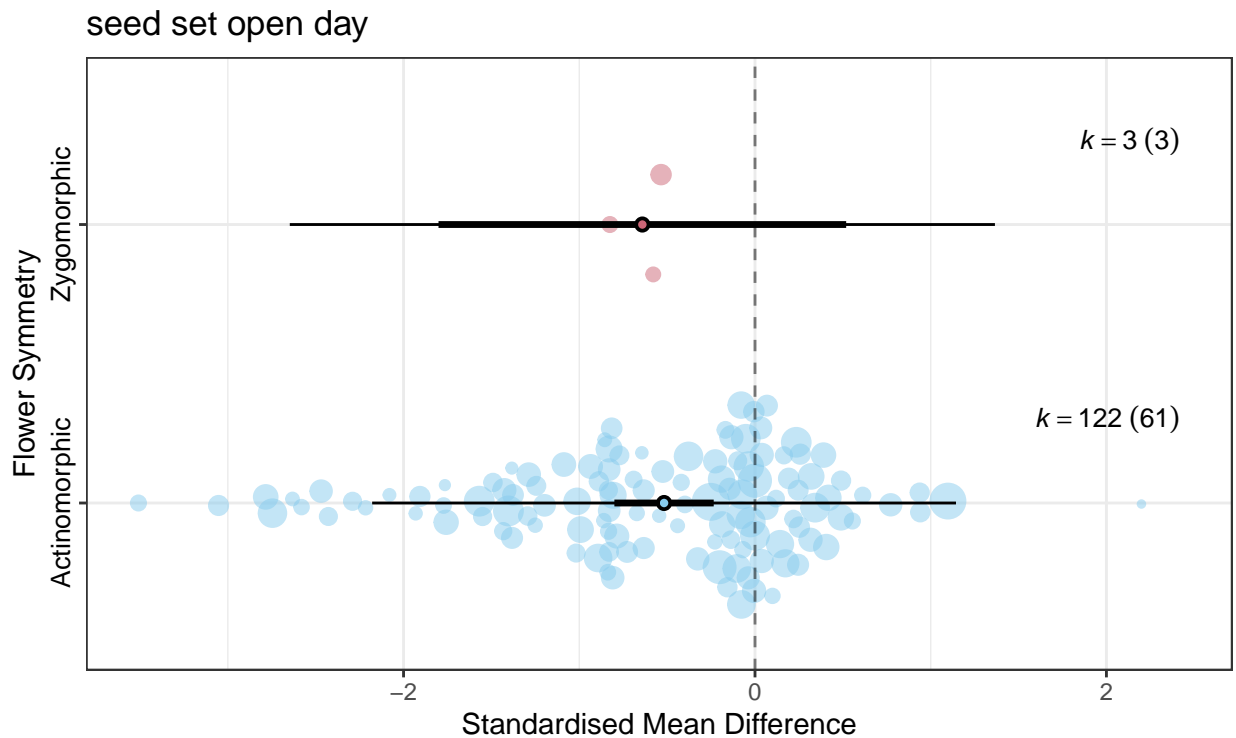


traits-31.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    64    no      study_ID  no
## sigma^2.2  0.1457  0.3817   125    no      effect_ID  no
## sigma^2.3  0.0504  0.2244    61    no        phylo  yes
## sigma^2.4  0.5016  0.7083    61    no accepted_name  no
```

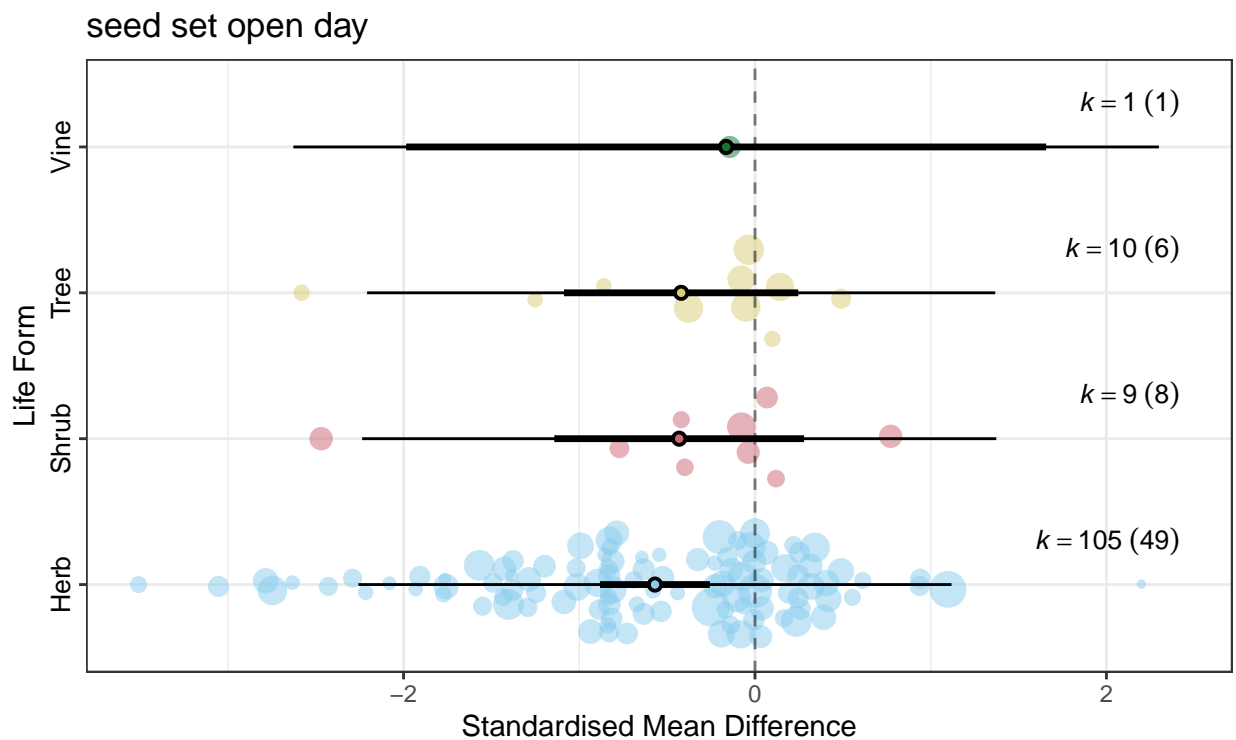
```
##
## Test for Residual Heterogeneity:
## QE(df = 123) = 940.4992, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0422, p-val = 0.8372
##
## Model Results:
##
##               estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          -0.5174  0.1442  -3.5880  0.0003  -0.8001  -0.2348
## flower_symmetryzygomorphic -0.1236  0.6013  -0.2055  0.8372  -1.3021   1.0549
##
## intrcpt          ***
## flower_symmetryzygomorphic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-32.pdf

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0000   64    no    study_ID  no
## sigma^2.2  0.1466  0.3828  125    no    effect_ID  no
## sigma^2.3  0.0448  0.2117   61    no    phylo     yes
```

```
## sigma^2.4  0.5246  0.7243    61    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 121) = 932.5164, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 0.4045, p-val = 0.9393
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt        -0.5692  0.1595  -3.5687  0.0004  -0.8818  -0.2566 ***
## life_formshrub   0.1379  0.3847   0.3584  0.7200  -0.6161   0.8919
## life_formtree    0.1490  0.3658   0.4075  0.6836  -0.5678   0.8659
## life_formvine    0.4051  0.9368   0.4324  0.6654  -1.4310   2.2412
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



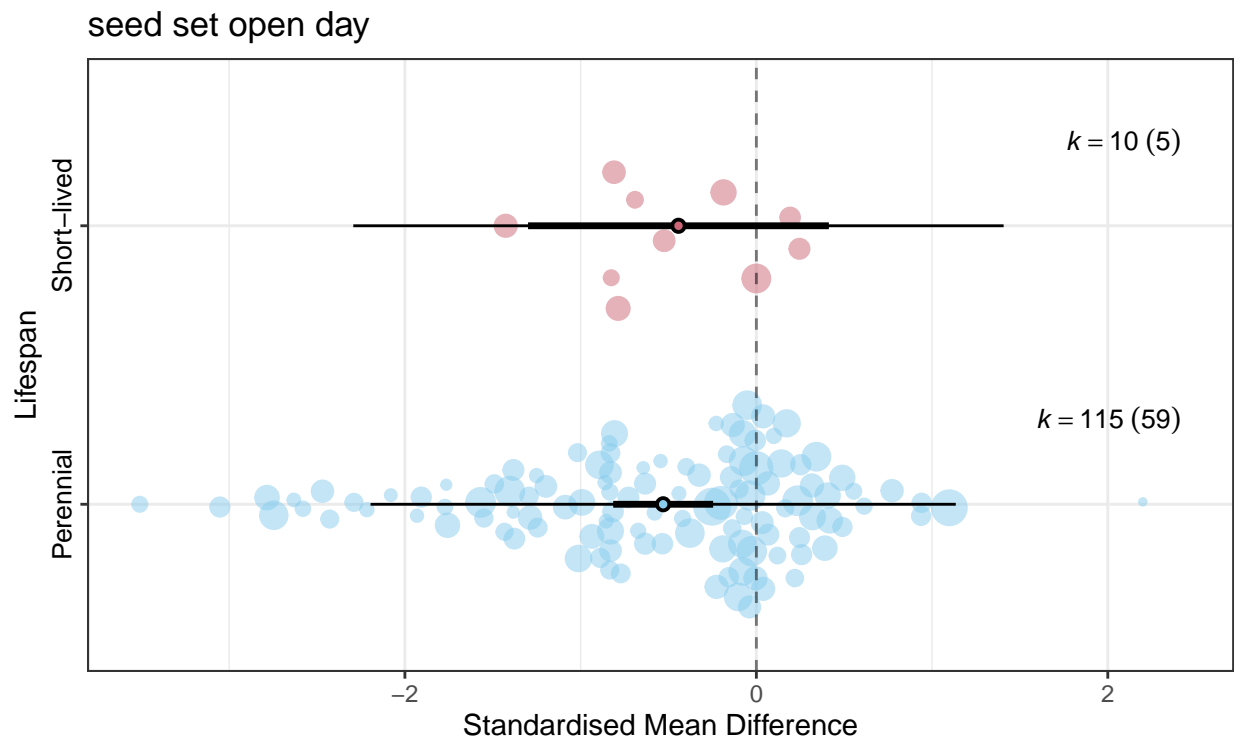
traits-33.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed  factor  R
## sigma^2.1 0.0000 0.0000   64    no  study_ID no
## sigma^2.2 0.1449 0.3807  125    no  effect_ID no
## sigma^2.3 0.0486 0.2205   61    no   phylo  yes
```



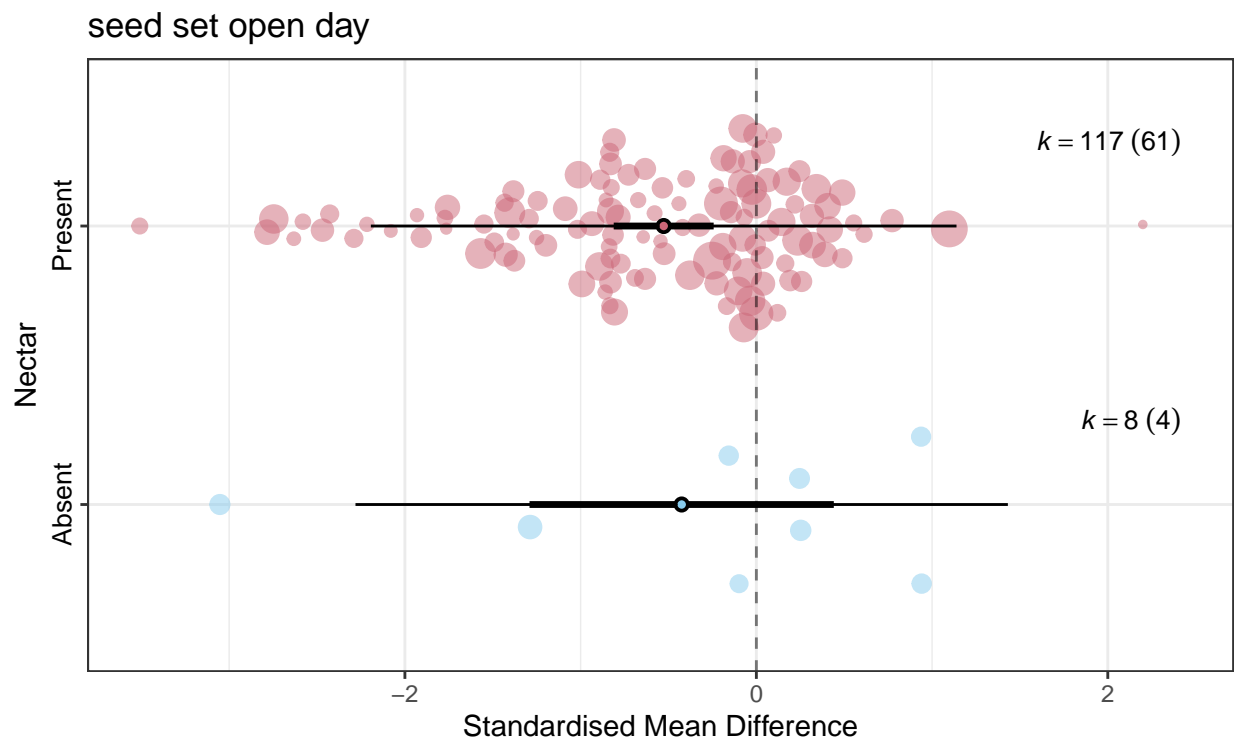
```
## sigma^2.4 0.5071 0.7121 61 no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 123) = 941.0240, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0379, p-val = 0.8456
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.5303 0.1451 -3.6554 0.0003 -0.8146 -0.2460 ***
## lifespanshort-lived 0.0871 0.4470 0.1948 0.8456 -0.7890 0.9631
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-34.pdf

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1 0.0000 0.0000   64    no      study_ID   no
## sigma^2.2 0.1454 0.3813  125    no      effect_ID   no
## sigma^2.3 0.0533 0.2308   61    no      phylo      yes
## sigma^2.4 0.5031 0.7093   61    no  accepted_name   no
##
```

```
## Test for Residual Heterogeneity:
## QE(df = 123) = 940.8048, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0540, p-val = 0.8162
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      -0.4250  0.4417  -0.9620  0.3360  -1.2908  0.4408
## nectarpresent -0.1023  0.4404  -0.2324  0.8162  -0.9655  0.7608
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

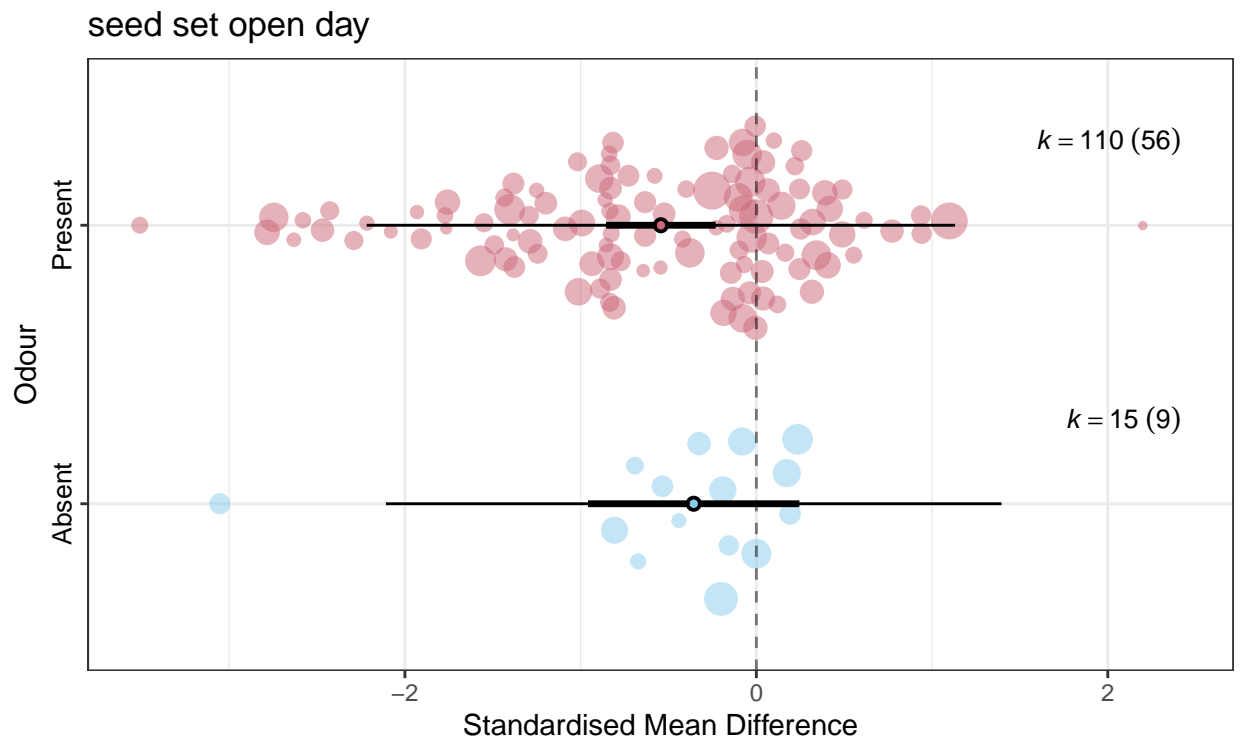


traits-35.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 125; method: REML)
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.0000  0.0000    64    no    study_ID  no
## sigma^2.2  0.1452  0.3810   125    no    effect_ID  no
## sigma^2.3  0.0726  0.2695    61    no    phylo     yes
## sigma^2.4  0.4866  0.6975    61    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 123) = 934.1544, p-val < .0001
```

```
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.3553, p-val = 0.5511
##
## Model Results:
##
##          estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      -0.3564  0.3068  -1.1619  0.2453  -0.9577  0.2448
## odourpresent  -0.1869  0.3135  -0.5961  0.5511  -0.8013  0.4276
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

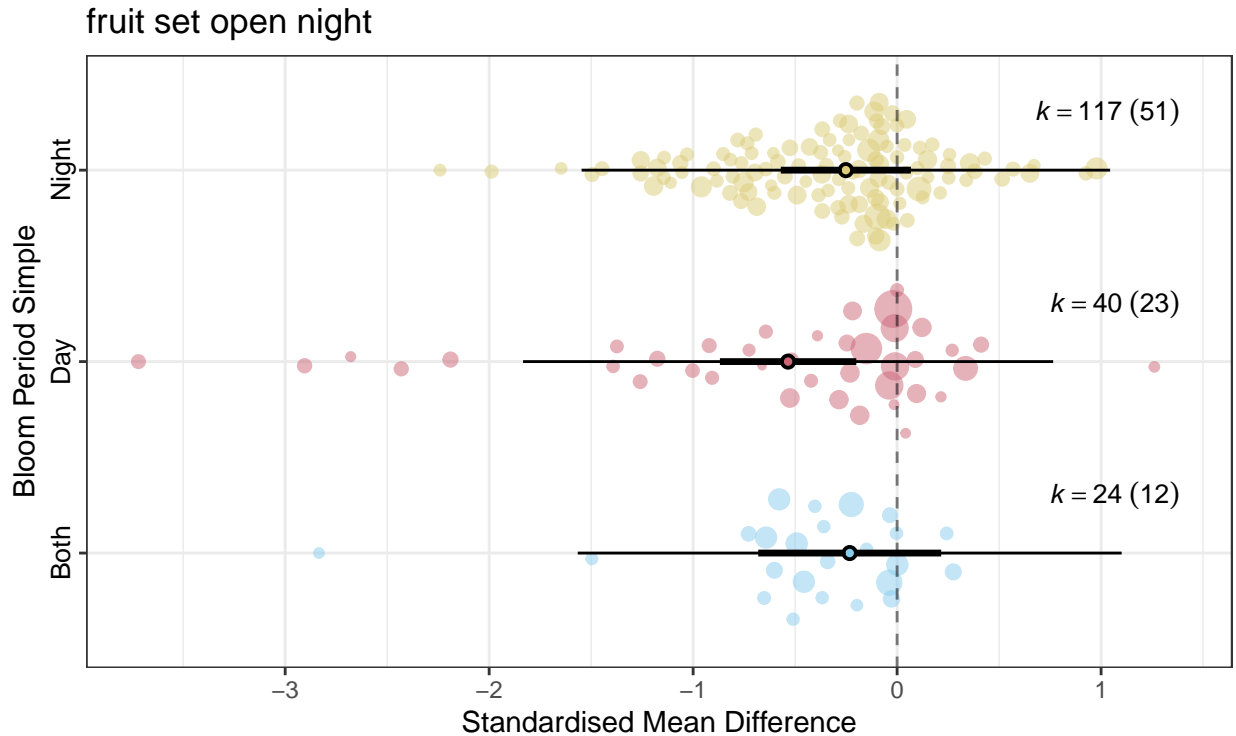


traits-36.pdf

Precision (1/SE) ○ 2.5 ○ 5.0 ○ 7.5

```
##
## Multivariate Meta-Analysis Model (k = 181; method: REML)
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0710  0.2664    83    no      study_ID  no
## sigma^2.2  0.0624  0.2497   181    no      effect_ID  no
## sigma^2.3  0.1107  0.3327    83    no        phylo  yes
## sigma^2.4  0.1664  0.4079    83    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 178) = 1484.5188, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
```

```
## QM(df = 2) = 3.1097, p-val = 0.2112
##
## Model Results:
##
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.2325  0.2288  -1.0160  0.3096  -0.6809  0.2160
## bloom_period_simpleday -0.3019  0.2373  -1.2722  0.2033  -0.7670  0.1632
## bloom_period_simplenight -0.0188  0.2290  -0.0822  0.9345  -0.4677  0.4300
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

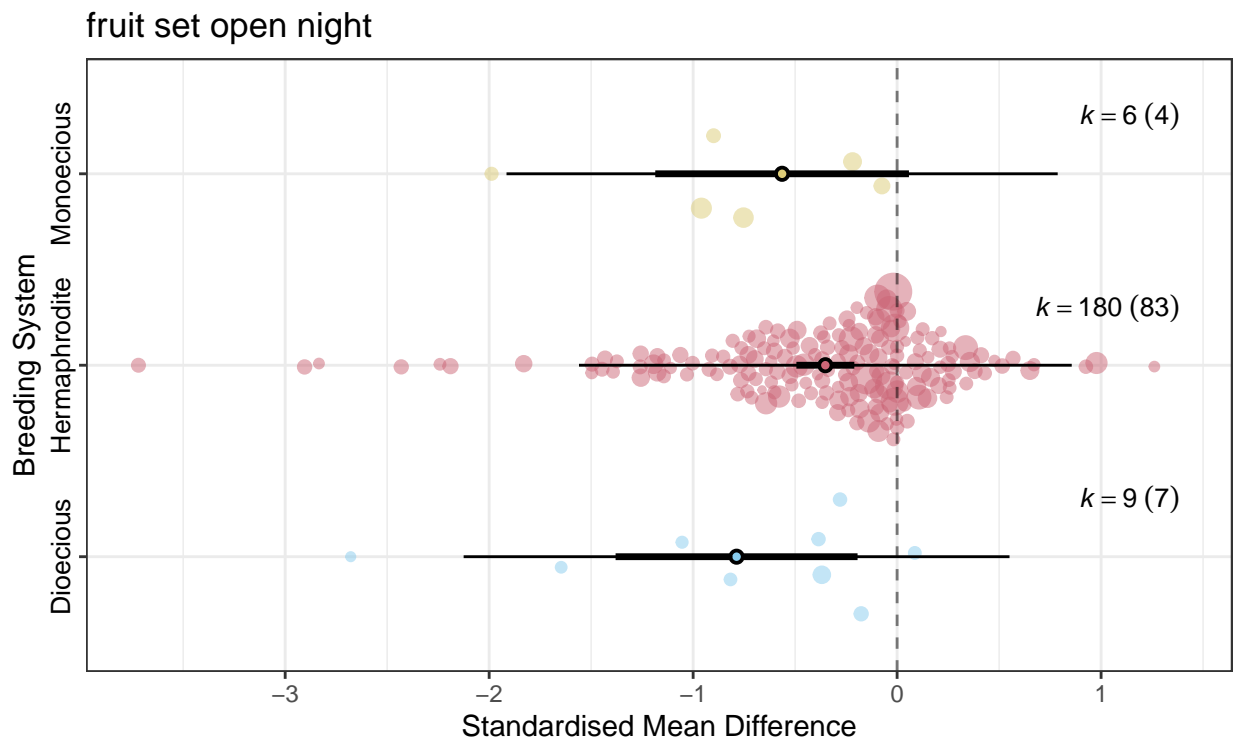


traits-37.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1358  0.3685    93    no      study_ID    no
## sigma^2.2  0.0623  0.2497   195    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    94    no        phylo    yes
## sigma^2.4  0.1764  0.4200    94    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 192) = 1595.5584, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 2.3094, p-val = 0.3152
```

```
##
## Model Results:
##
##               estimate      se    zval    pval    ci.lb
## intrcpt          -0.7870  0.3026 -2.6005  0.0093 -1.3801
## breeding_systemhermaphrodite  0.4352  0.3102  1.4031  0.1606 -0.1727
## breeding_systemmonoecious    0.2232  0.4385  0.5090  0.6107 -0.6362
##               ci.ub
## intrcpt          -0.1938  **
## breeding_systemhermaphrodite  1.0431
## breeding_systemmonoecious    1.0825
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

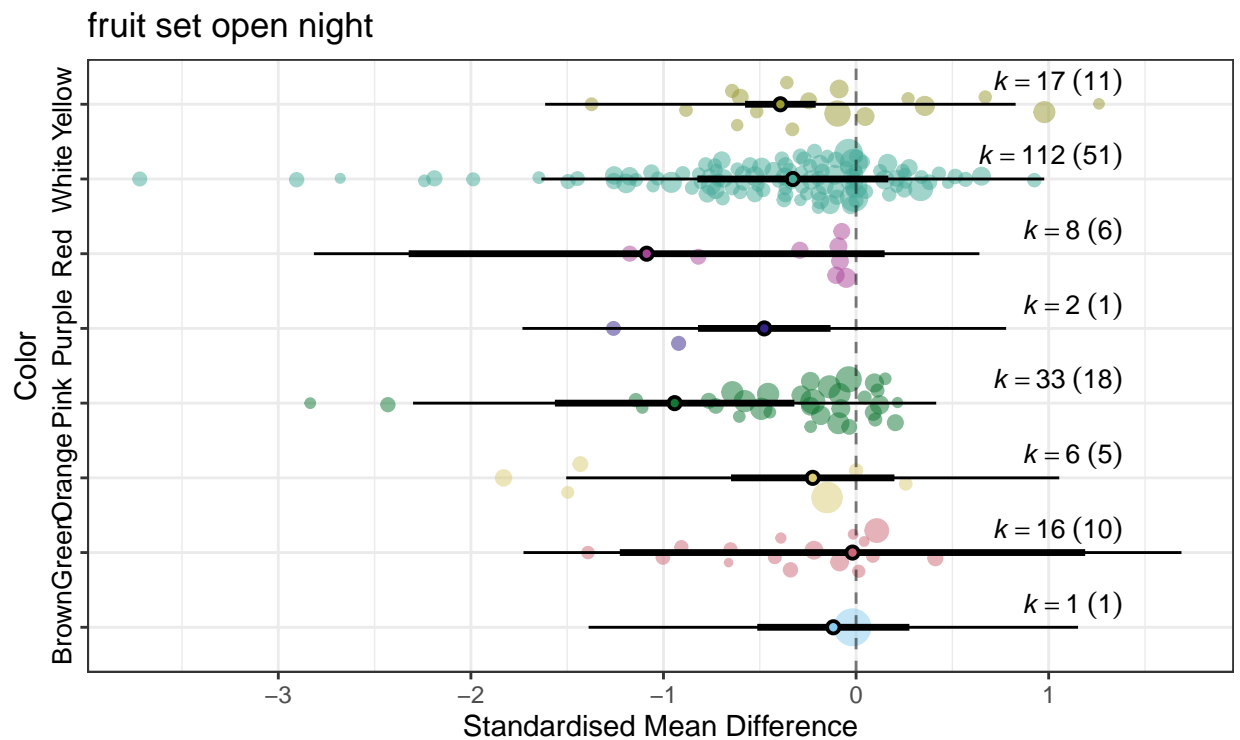


traits-38.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor    R
## sigma^2.1  0.1250  0.3536   93    no    study_ID  no
## sigma^2.2  0.0616  0.2482  195    no    effect_ID  no
## sigma^2.3  0.0000  0.0001   94    no      phylo  yes
## sigma^2.4  0.1930  0.4394   94    no accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 187) = 1539.1085, p-val < .0001
```

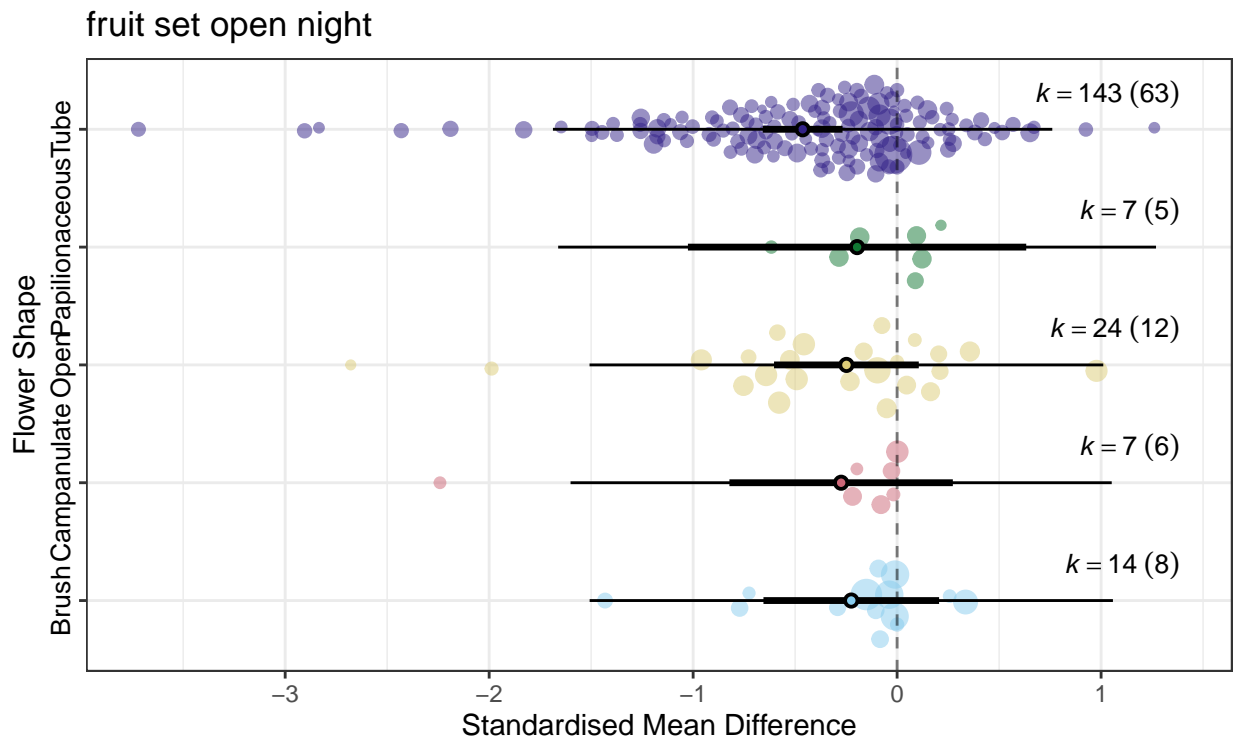
```
##
## Test of Moderators (coefficients 2:8):
## QM(df = 7) = 7.3596, p-val = 0.3924
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.1182  0.2015  -0.5866  0.5575  -0.5132  0.2767
## colorbrown     0.0996  0.6485   0.1536  0.8779  -1.1715  1.3707
## colorgreen    -0.1069  0.2914  -0.3669  0.7137  -0.6780  0.4642
## colororange   -0.8239  0.3729  -2.2098  0.0271  -1.5547 -0.0931 *
## colorpink     -0.3584  0.2670  -1.3423  0.1795  -0.8818  0.1649
## colorpurple   -0.9693  0.6619  -1.4645  0.1431  -2.2665  0.3279
## colorred      -0.2102  0.3231  -0.6507  0.5152  -0.8435  0.4230
## colorwhite    -0.2748  0.2200  -1.2490  0.2117  -0.7061  0.1564
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-39.pdf

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1218  0.3490    93    no      study_ID    no
## sigma^2.2  0.0635  0.2520   195    no      effect_ID    no
## sigma^2.3  0.0117  0.1082    94    no        phylo    yes
```

```
## sigma^2.4 0.1830 0.4278 94 no accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 190) = 1648.9390, p-val < .0001
##
## Test of Moderators (coefficients 2:5):
## QM(df = 4) = 2.1214, p-val = 0.7134
##
## Model Results:
##
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.2247  0.2197  -1.0228  0.3064  -0.6553  0.2059
## flower_shapecampanulate -0.0497  0.3527  -0.1410  0.8879  -0.7410  0.6416
## flower_shapeopen    -0.0238  0.2761  -0.0864  0.9312  -0.5649  0.5172
## flower_shapepapilionaceous 0.0285  0.4766   0.0598  0.9523  -0.9057  0.9627
## flower_shapetube    -0.2385  0.2382  -1.0014  0.3167  -0.7053  0.2283
##
## intrcpt
## flower_shapecampanulate
## flower_shapeopen
## flower_shapepapilionaceous
## flower_shapetube
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

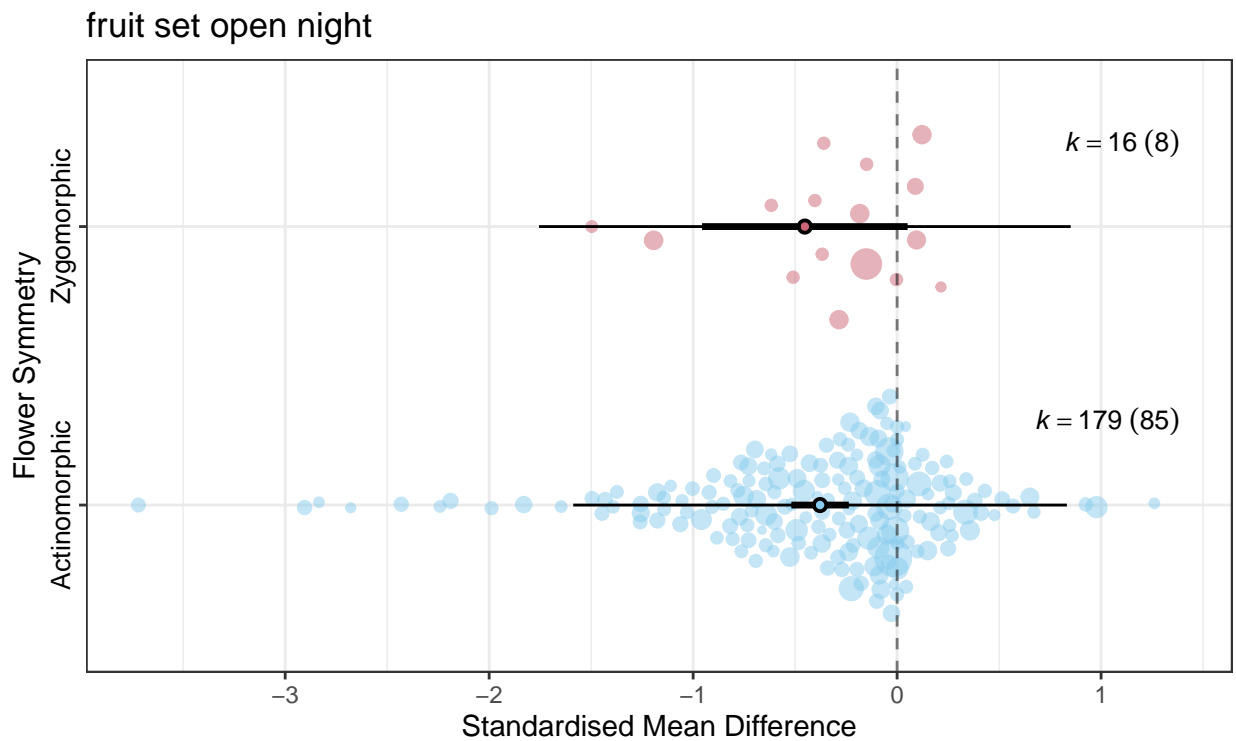


traits-40.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
```

```
##
## Variance Components:
##
##      estim  sqrt  nlvls  fixed      factor  R
## sigma^2.1 0.1379 0.3714   93    no      study_ID  no
## sigma^2.2 0.0619 0.2489  195    no      effect_ID  no
## sigma^2.3 0.0000 0.0000   94    no        phylo  yes
## sigma^2.4 0.1762 0.4197   94    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 193) = 1694.5303, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.0782, p-val = 0.7798
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          -0.3777  0.0718 -5.2589 <.0001  -0.5184  -0.2369
## flower_symmetryzygomorphic -0.0746  0.2669 -0.2796  0.7798  -0.5978   0.4485
##
## intrcpt          ***
## flower_symmetryzygomorphic
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



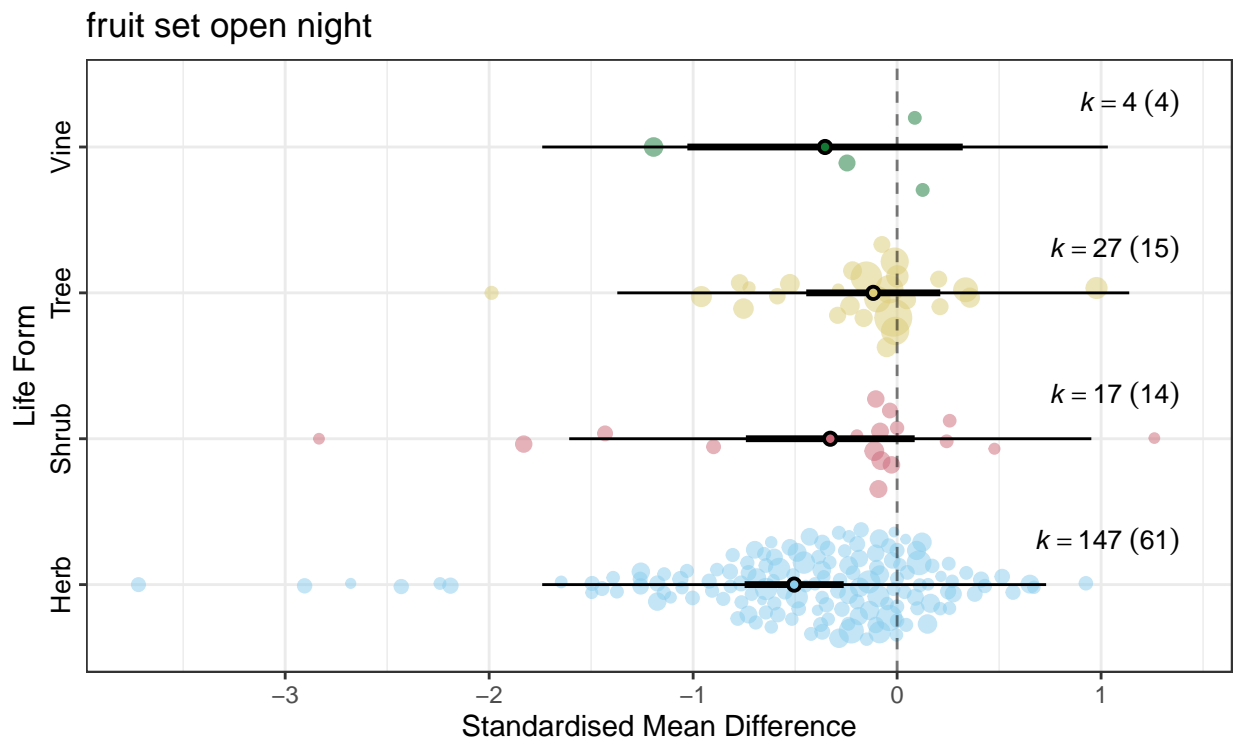
traits-41.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

##



```
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1047  0.3235    93    no      study_ID  no
## sigma^2.2  0.0653  0.2555   195    no      effect_ID  no
## sigma^2.3  0.0363  0.1906    94    no        phylo  yes
## sigma^2.4  0.1756  0.4190    94    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 191) = 1481.6811, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 3.8563, p-val = 0.2774
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.5047  0.1239  -4.0729  <.0001  -0.7476  -0.2618  ***
## life_formshrub  0.1771  0.2315   0.7649  0.4444  -0.2767   0.6309
## life_formtree   0.3878  0.1982   1.9568  0.0504  -0.0006   0.7762  .
## life_formvine   0.1514  0.3582   0.4227  0.6725  -0.5507   0.8536
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

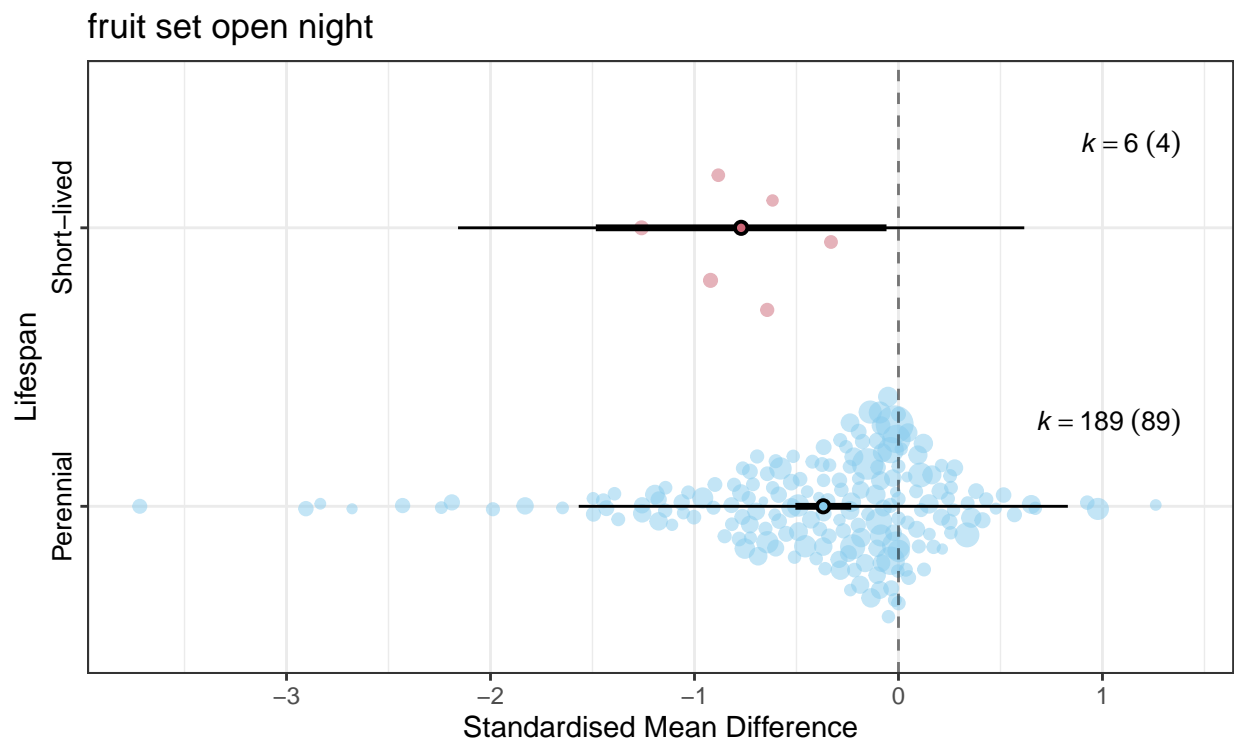


traits-42.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

##

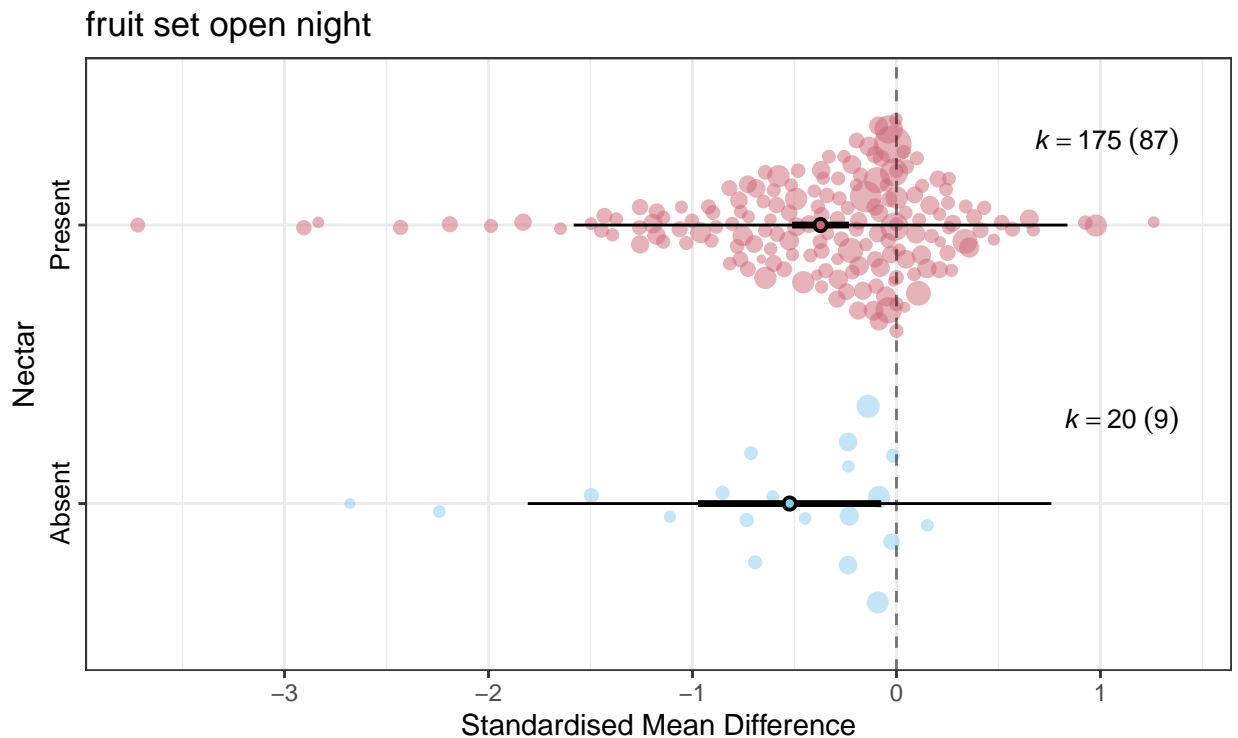
```
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1367  0.3697    93    no      study_ID  no
## sigma^2.2  0.0624  0.2497   195    no      effect_ID  no
## sigma^2.3  0.0000  0.0001    94    no        phylo  yes
## sigma^2.4  0.1702  0.4126    94    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 193) = 1677.1891, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 1.1828, p-val = 0.2768
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.3686  0.0698  -5.2784  <.0001  -0.5055  -0.2317  ***
## lifespanshort-lived  -0.4026  0.3702  -1.0876  0.2768  -1.1282   0.3230
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



traits-43.pdf

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
```

```
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1225  0.3499    93    no      study_ID    no
## sigma^2.2  0.0635  0.2520   195    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    94    no        phylo    yes
## sigma^2.4  0.1903  0.4362    94    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 193) = 1694.9802, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.4136, p-val = 0.5202
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.5239  0.2293  -2.2849  0.0223  -0.9732  -0.0745  *
## nectarpresent   0.1517  0.2359   0.6431  0.5202  -0.3107   0.6142
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

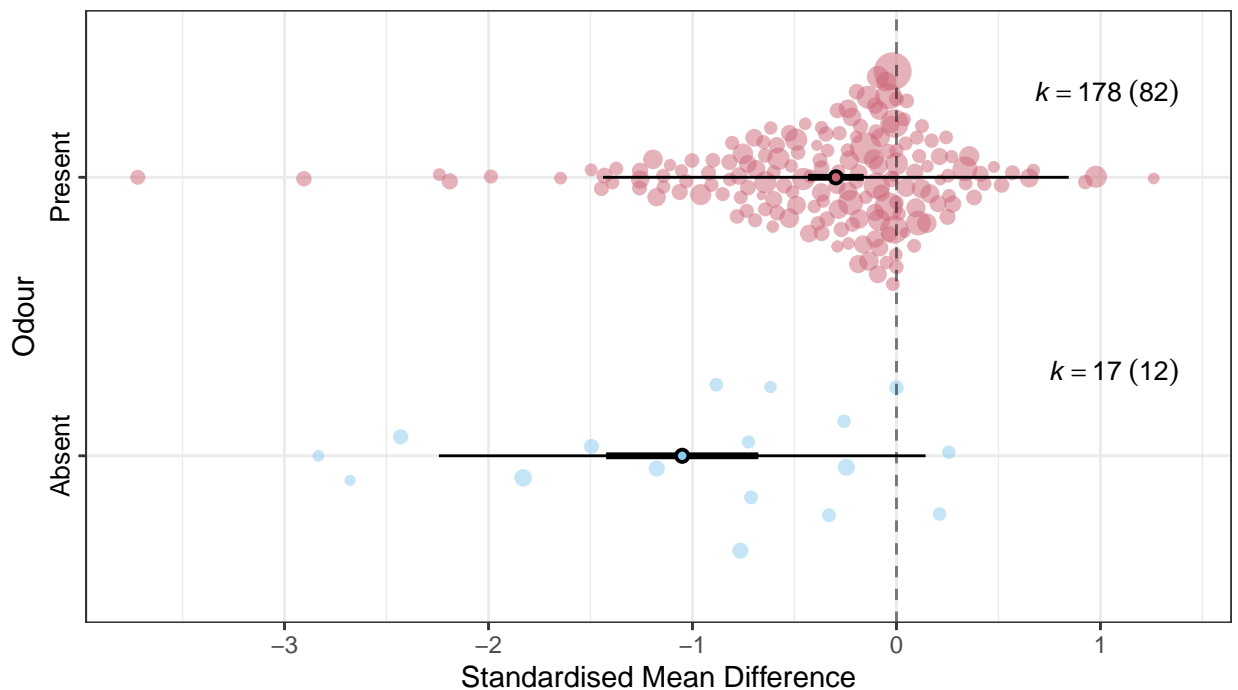


traits-44.pdf

```
##
## Multivariate Meta-Analysis Model (k = 195; method: REML)
##
## Variance Components:
##
```

```
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1 0.1405  0.3748    93    no      study_ID    no
## sigma^2.2 0.0581  0.2411   195    no      effect_ID   no
## sigma^2.3 0.0000  0.0000    94    no        phylo   yes
## sigma^2.4 0.1357  0.3684    94    no  accepted_name   no
##
## Test for Residual Heterogeneity:
## QE(df = 193) = 1576.5178, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 14.0198, p-val = 0.0002
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt       -1.0504  0.1904  -5.5178  <.0001  -1.4234  -0.6773  ***
## odourpresent    0.7533  0.2012   3.7443  0.0002   0.3590   1.1477  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### fruit set open night

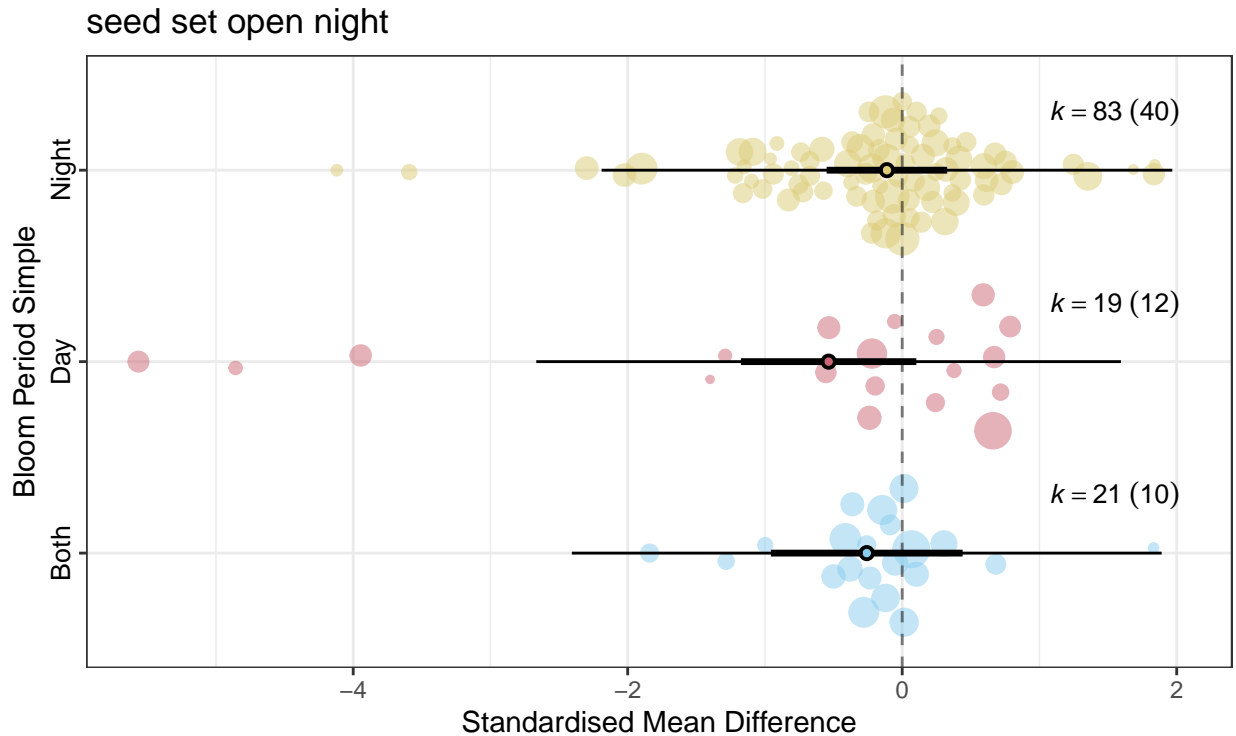


traits-45.pdf

Precision (1/SE) ○ 10 ○ 20 ○ 30 ○ 40 ○ 50

```
##
## Multivariate Meta-Analysis Model (k = 123; method: REML)
##
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1 0.0493  0.2221    61    no      study_ID    no
```

```
## sigma^2.2  0.1177  0.3431    123    no    effect_ID    no
## sigma^2.3  0.0838  0.2895     59    no          phylo  yes
## sigma^2.4  0.8238  0.9077     59    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 120) = 861.2056, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 1.3034, p-val = 0.5212
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.2582  0.3564  -0.7245  0.4688  -0.9567  0.4403
## bloom_period_simpleday -0.2779  0.4616  -0.6021  0.5471  -1.1825  0.6267
## bloom_period_simplenight  0.1468  0.3877   0.3786  0.7050  -0.6132  0.9068
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

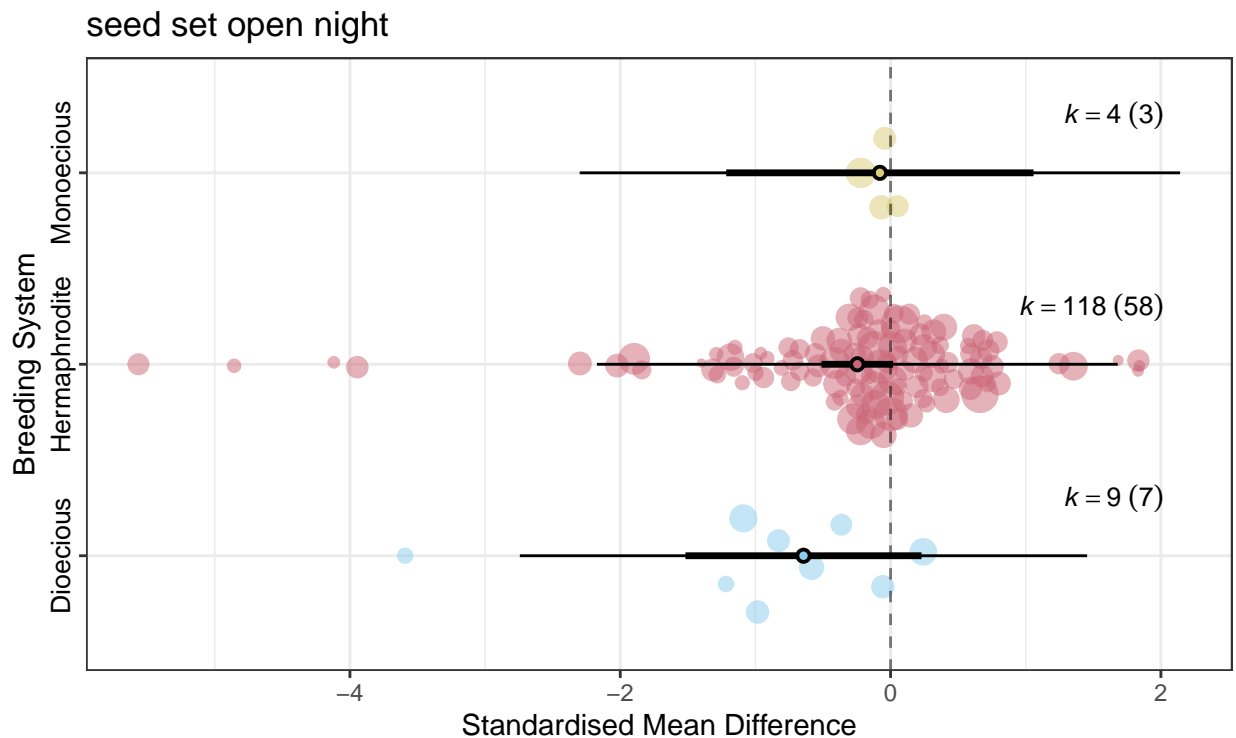


traits-46.pdf

Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0567  0.2382    68    no      study_ID    no
## sigma^2.2  0.1152  0.3394   131    no      effect_ID    no
```

```
## sigma^2.3  0.0000  0.0001    66    no          phylo  yes
## sigma^2.4  0.7759  0.8808    66    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 128) = 863.1431, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 0.8461, p-val = 0.6550
##
## Model Results:
##
##              estimate      se    zval    pval    ci.lb
## intrcpt          -0.6444  0.4455 -1.4466  0.1480 -1.5176
## breeding_systemhermaphrodite  0.3984  0.4656  0.8557  0.3922 -0.5141
## breeding_systemmonoecious    0.5653  0.7314  0.7730  0.4395 -0.8681
##              ci.ub
## intrcpt          0.2287
## breeding_systemhermaphrodite  1.3108
## breeding_systemmonoecious    1.9988
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



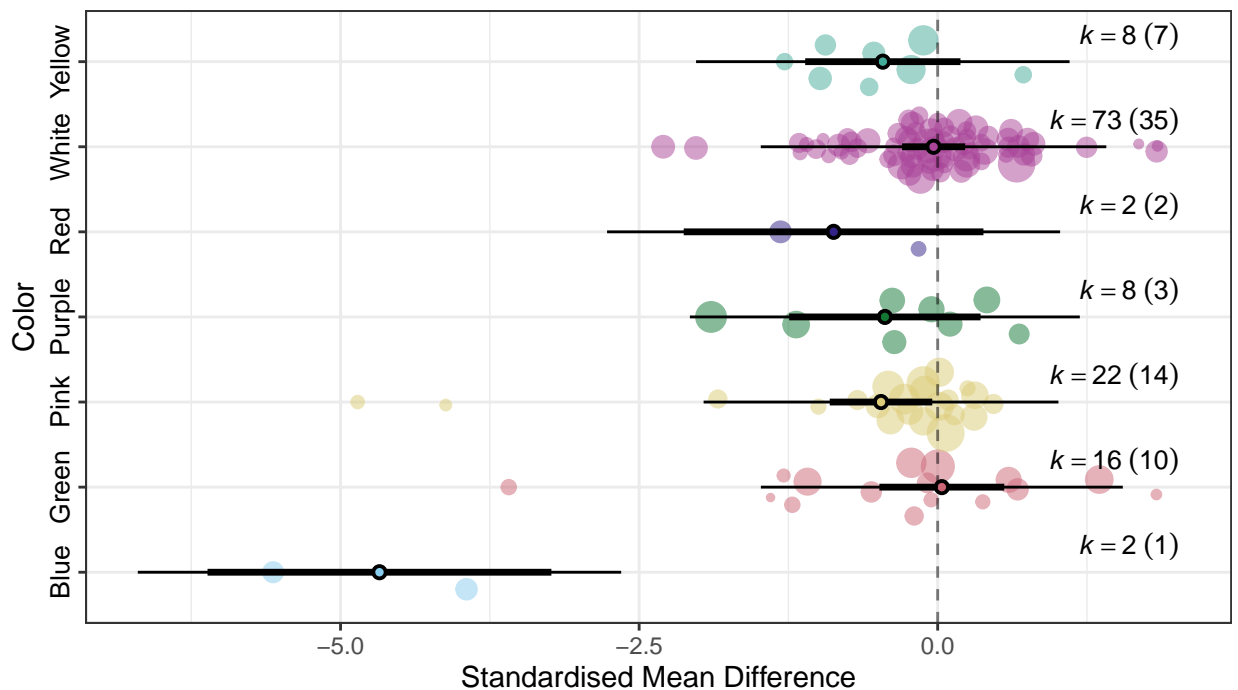
traits-47.pdf

Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
```

```
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1 0.0236  0.1537   68    no      study_ID   no
## sigma^2.2 0.1250  0.3536  131    no      effect_ID  no
## sigma^2.3 0.0000  0.0000   66    no      phylo     yes
## sigma^2.4 0.3779  0.6147   66    no  accepted_name no
##
## Test for Residual Heterogeneity:
## QE(df = 124) = 538.0494, p-val < .0001
##
## Test of Moderators (coefficients 2:7):
## QM(df = 6) = 42.6448, p-val < .0001
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -4.6742  0.7345  -6.3635 <.0001  -6.1139  -3.2346 ***
## colorgreen    4.7091  0.7815   6.0257 <.0001   3.1774   6.2408 ***
## colorpink     4.1998  0.7665   5.4793 <.0001   2.6975   5.7020 ***
## colorpurple   4.2320  0.8314   5.0903 <.0001   2.6025   5.8615 ***
## colorred      3.8026  0.9744   3.9025 <.0001   1.8928   5.7124 ***
## colorwhite    4.6396  0.7456   6.2222 <.0001   3.1781   6.1010 ***
## coloryellow   4.2149  0.8059   5.2297 <.0001   2.6352   5.7945 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### seed set open night



traits-48.pdf

Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
```

```

##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0164  0.1282    68    no      study_ID  no
## sigma^2.2  0.1199  0.3462   131    no      effect_ID  no
## sigma^2.3  0.0000  0.0001    66    no        phylo  yes
## sigma^2.4  0.7339  0.8567    66    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 125) = 752.4157, p-val < .0001
##
## Test of Moderators (coefficients 2:6):
## QM(df = 5) = 10.4621, p-val = 0.0632
##
## Model Results:
##
##              estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt              -0.1888  0.4961  -0.3805  0.7036  -1.1611  0.7836
## flower_shapecampanulate -0.7729  0.6012  -1.2856  0.1986  -1.9512  0.4054
## flower_shapecapitulum   0.4332  1.0878   0.3983  0.6904  -1.6989  2.5654
## flower_shapeopen        0.1487  0.6571   0.2263  0.8209  -1.1391  1.4366
## flower_shapepapilionaceous -1.5759  0.8487  -1.8569  0.0633  -3.2392  0.0875
## flower_shapetube        0.0650  0.5170   0.1258  0.8999  -0.9483  1.0784
##
## intrcpt
## flower_shapecampanulate
## flower_shapecapitulum
## flower_shapeopen
## flower_shapepapilionaceous .
## flower_shapetube
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

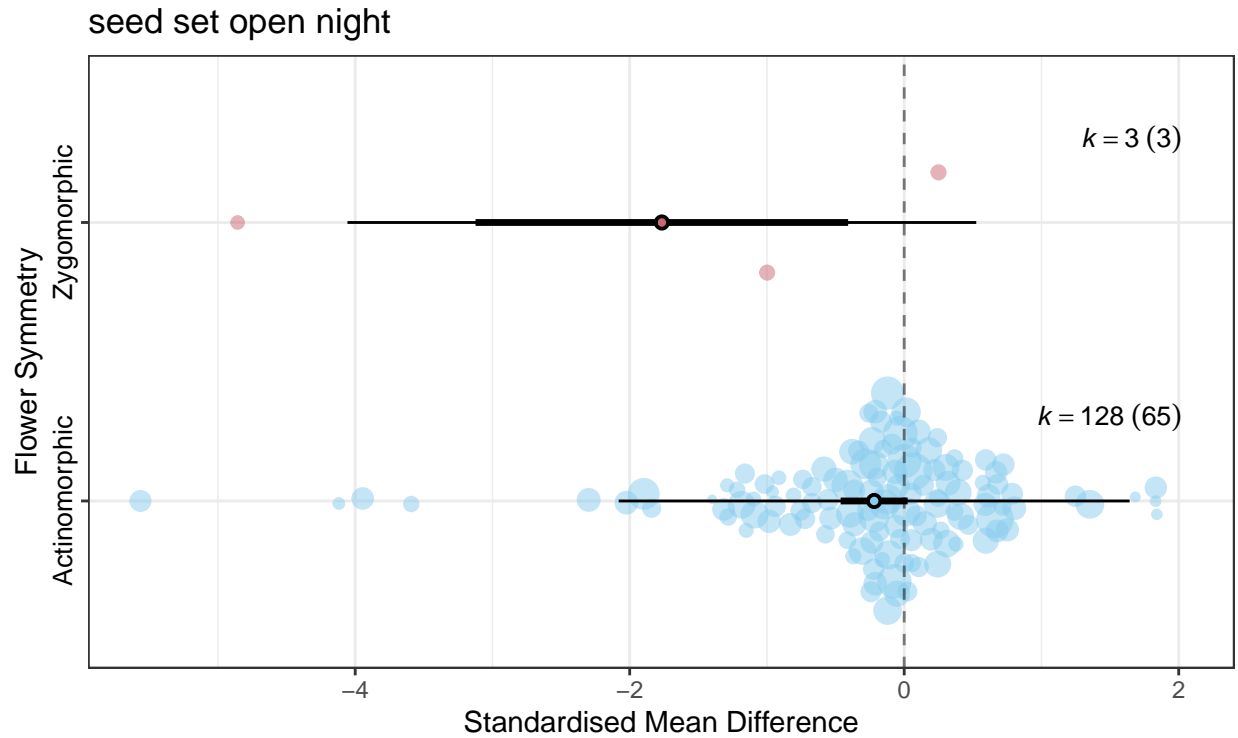


A forest plot showing the Standardised Mean Difference (SMD) for various values of  $k$ . The x-axis represents the SMD, ranging from -4 to 2, with a vertical dashed line at 0. The y-axis lists the  $k$  values and their corresponding sample sizes in parentheses:  $k = 100$  (49),  $k = 3$  (3),  $k = 10$  (6),  $k = 1$  (1),  $k = 11$  (6), and  $k = 6$  (3). Each point represents the SMD estimate, and the horizontal line represents the 95% confidence interval. The estimates for  $k = 100$  and  $k = 11$  are positive, while the others are negative or near zero.

$k$	Sample Size	Standardised Mean Difference (approx.)	95% CI (approx.)
100	49	0.0	[-0.5, 0.5]
3	3	-1.8	[-3.2, -0.4]
10	6	-0.2	[-1.0, 0.6]
1	1	0.3	[-1.5, 2.1]
11	6	-0.8	[-1.8, 0.2]
6	3	-0.2	[-1.0, 0.6]

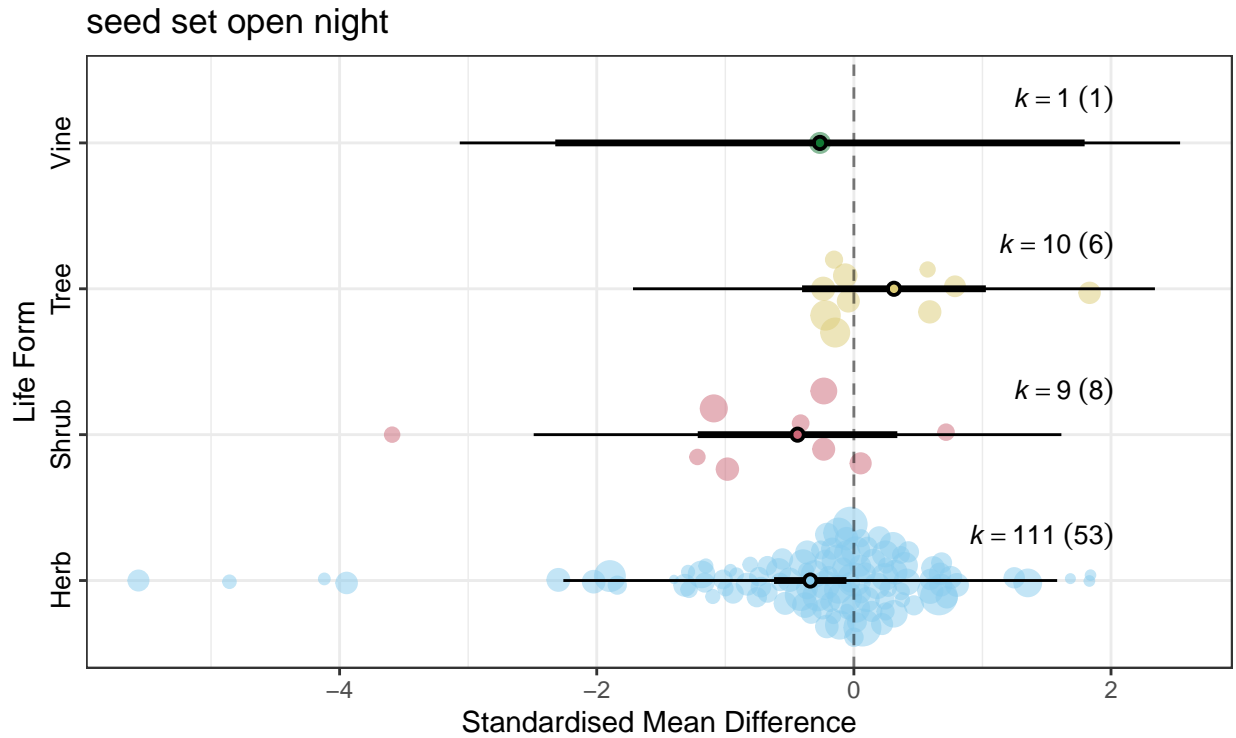
Precision (1/SE)    ○ 2    ○ 4    ○ 6    ○ 8

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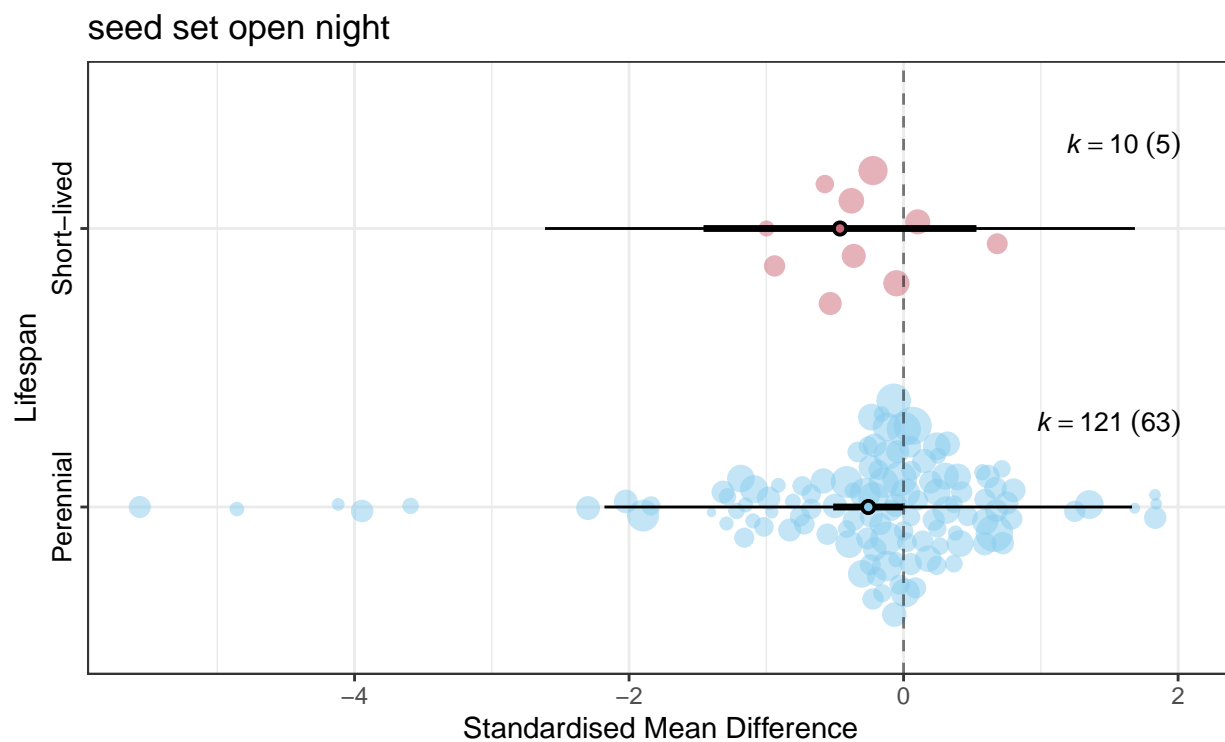
```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0463  0.2152    68    no      study_ID    no
## sigma^2.2  0.1146  0.3385   131    no      effect_ID    no
## sigma^2.3  0.0000  0.0001    66    no        phylo    yes
## sigma^2.4  0.7787  0.8824    66    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 127) = 859.0307, p-val < .0001
##
## Test of Moderators (coefficients 2:4):
## QM(df = 3) = 2.9582, p-val = 0.3981
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.3394  0.1436  -2.3637  0.0181  -0.6208  -0.0580  *
## life_formshrub -0.0989  0.4212  -0.2348  0.8144  -0.9244  0.7266
## life_formtree  0.6511  0.3920  1.6612  0.0967  -0.1171  1.4194  .
## life_formvine  0.0754  1.0601  0.0711  0.9433  -2.0024  2.1532
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

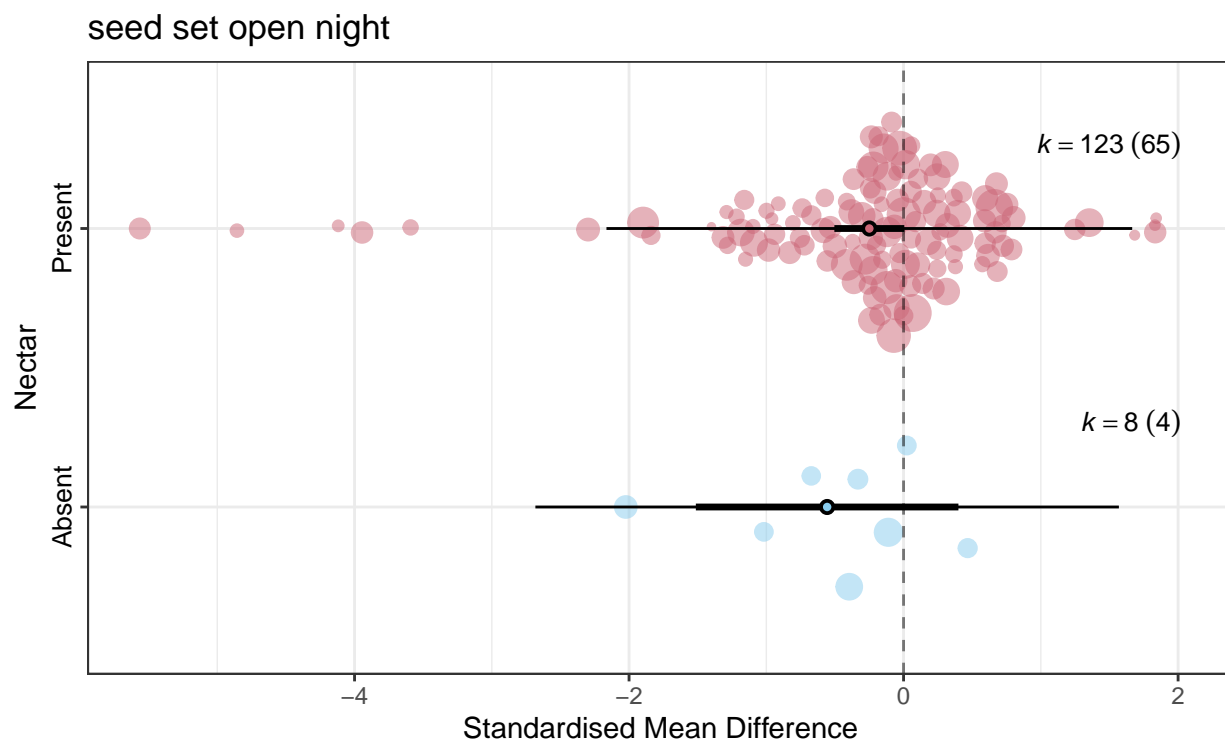
```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0561  0.2368    68    no      study_ID   no
## sigma^2.2  0.1127  0.3357   131    no      effect_ID  no
## sigma^2.3  0.0000  0.0001    66    no        phylo   yes
## sigma^2.4  0.7758  0.8808    66    no  accepted_name  no
##
## Test for Residual Heterogeneity:
## QE(df = 129) = 880.6905, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.1546, p-val = 0.6942
##
## Model Results:
##
##      estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt      -0.2573  0.1302 -1.9763  0.0481 -0.5125 -0.0021 *
## lifespanshort-lived -0.2059  0.5237 -0.3932  0.6942 -1.2324  0.8205
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

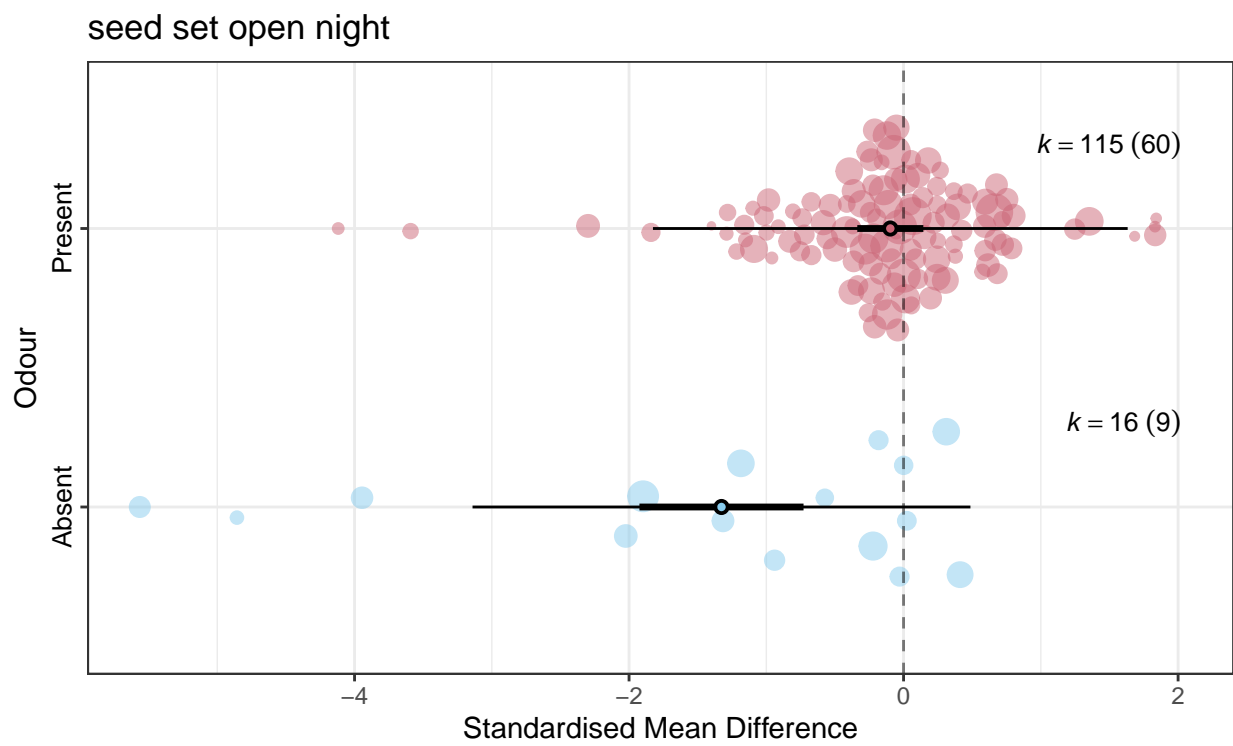
```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0596  0.2442    68    no      study_ID    no
## sigma^2.2  0.1115  0.3339   131    no      effect_ID   no
## sigma^2.3  0.0000  0.0001    66    no        phylo    yes
## sigma^2.4  0.7668  0.8756    66    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 129) = 873.9259, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 0.3715, p-val = 0.5422
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.5569  0.4881  -1.1410  0.2539  -1.5134  0.3997
## nectarpresent   0.3074  0.5044   0.6095  0.5422  -0.6811  1.2960
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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Precision (1/SE) ○ 2 ○ 4 ○ 6 ○ 8

```
##
## Multivariate Meta-Analysis Model (k = 131; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0267  0.1633    68    no      study_ID    no
## sigma^2.2  0.1151  0.3392   131    no      effect_ID    no
## sigma^2.3  0.0000  0.0000    66    no        phylo    yes
## sigma^2.4  0.6216  0.7884    66    no  accepted_name    no
##
## Test for Residual Heterogeneity:
## QE(df = 129) = 708.6974, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 14.0329, p-val = 0.0002
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -1.3266  0.3050  -4.3501  <.0001  -1.9243  -0.7289  ***
## odourpresent   1.2300  0.3283   3.7461  0.0002   0.5864   1.8735  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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