

Growth

Overall

```
Multivariate Meta-Analysis Model (k = 333; method: REML)

  logLik   Deviance       AIC       BIC       AICC
-424.6146  849.2292  855.2292  866.6447  855.3024

Variance Components:

      estim    sqrt  nlevels fixed factor
sigma^2.1 0.1107  0.3327      28     no Author
sigma^2.2 0.3523  0.5935     333     no      ID

Test for Heterogeneity:
Q(df = 332) = 1014.3627, p-val < .0001

Model Results:

estimate      se     zval    pval    ci.lb    ci.ub
 0.2329  0.0822  2.8340  0.0046  0.0718  0.3940  **

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

```
> model_results <- orchard::mod_results(datag1_MA, mod = "1", at
> model_results
  name estimate    lowerCL    upperCL    lowerPR    upperPR
1 InTrcpt 0.2329253 0.07183374 0.3940168 -1.110323 1.576174
> orchard::orchard_plot(datag1_MA, mod = "1", group = "Author",
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_ml(datag1_MA)
> I2
I2_Total I2_Author      I2_ID
74.80229 17.88005  56.92224
> setwd("D:/反刍动物meta12.20")
```

species as a moderator

```
Multivariate Meta-Analysis Model (k = 333; method: REML)

  logLik   Deviance       AIC       BIC       AICC
-396.7209  793.4419  821.4419  874.2420  822.8144

Variance Components:

    estim   sqrt  nvlvs fixed factor
sigma^2.1 0.0000 0.0000     28    no Author
sigma^2.2 0.3565 0.5971    333    no      ID

Test for Residual Heterogeneity:
QE(df = 321) = 905.2875, p-val < .0001

Test of Moderators (coefficients 2:12):
QM(df = 11) = 63.3675, p-val < .0001

Model Results:

            estimate      se      zval     pval    ci.lb    ci.ub
intrcpt        0.1691  0.2126   0.7956  0.4263 -0.2476  0.5858
speciesCashmere  0.0122  0.2768   0.0440  0.9649 -0.5304  0.5547
speciesCharolais  0.5689  0.5400   1.0534  0.2921 -0.4896  1.6274
speciesH x A     0.4289  0.2427   1.7675  0.0771 -0.0467  0.9046
speciesH x N     -0.2846  0.2831  -1.0055  0.3146 -0.8394  0.2702
speciesHolstein   -0.1028  0.2198  -0.4675  0.6401 -0.5336  0.3281
speciesKarayaka   0.1042  0.2601   0.4005  0.6888 -0.4056  0.6140
speciesSaanen     0.2932  0.7281   0.4027  0.6872 -1.1338  1.7201
speciesSaint Croix -0.1050  0.3724  -0.2820  0.7779 -0.8348  0.6248
speciesSuffolk     -0.2483  0.2711  -0.9159  0.3597 -0.7797  0.2831
speciesThin-tailed  1.0840  0.3942   2.7495  0.0060  0.3113  1.8567 ** 
speciesZaraibi     1.3044  0.3191   4.0875 <.0001  0.6789  1.9299 ***

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

> res2 <- orchard::mod_results(datag_MRO, mod = "species", group = "Author")
> res2
      name   estimate    lowerCL   upperCL    lowerPR   upperPR
1     B x C  0.16914674 -0.24755070  0.5858442 -1.07310544 1.411399
2   Cashmere  0.18131657 -0.16611583  0.5287490 -1.03944672 1.402080
3   Charolais  0.73804747 -0.23494510  1.7110400 -0.78388166 2.259977
4     H x A  0.59809389  0.36871447  0.8274733 -0.59445324 1.790641
5     H x N -0.11547038 -0.48172155  0.2507808 -1.34172225 1.110781
6   Holstein  0.06637318 -0.04313936  0.1758857 -1.10901898 1.241765
7   Karayaka  0.27331373 -0.02039752  0.5670250 -0.93325994 1.479887
8     Saanen  0.46232145 -0.90243736  1.8270803 -1.33548842 2.260131
9 Saint Croix  0.06414404 -0.53500051  0.6632886 -1.25059088 1.378879
10   Suffolk -0.07915584 -0.40886642  0.2505547 -1.29499416 1.136682
11 Thin-tailed  1.25313503  0.60241040  1.9038597 -0.08589308 2.592163
12   zaraibi  1.47354583  1.00710988  1.9399818  0.21373782 2.733354
> p1<- orchard::orchard_plot(res2, mod = "species", group = "Author", xlab = ""
> p1
> ggsave('growth_species_moderator.pdf',width = 4,height = 8,p1)
```

parameter as a moderator

```
> summary(datag_MR01)

Multivariate Meta-Analysis Model (k = 333; method: REML)

  logLik Deviance      AIC      BIC      AICC
-413.2686 826.5373 848.5373 890.1255 849.3834

Variance Components:

  estim   sqrt  nvlvs fixed factor
sigma^2.1 0.1075 0.3279    28   no  Author
sigma^2.2 0.3491 0.5908   333   no     ID

Test for Residual Heterogeneity:
QE(df = 324) = 979.4239, p-val < .0001

Test of Moderators (coefficients 2:9):
QM(df = 8) = 10.5829, p-val = 0.2265

Model Results:

             estimate      se      zval      pval    ci.lb    ci.ub
intrcpt          0.4844  0.3350  1.4461  0.1481 -0.1721  1.1409
parameterADG      -0.2277  0.3312 -0.6875  0.4918 -0.8769  0.4215
parameterBCS      -0.4337  0.3619 -1.1982  0.2308 -1.1431  0.2757
parameterBirth weight -0.0954  0.4273 -0.2232  0.8234 -0.9329  0.7422
parameterDMI      -0.2638  0.3442 -0.7664  0.4434 -0.9384  0.4108
parameterFCE       -0.2900  0.3555 -0.8156  0.4147 -0.9868  0.4069
parameterHeart girth -0.1038  0.4063 -0.2556  0.7983 -0.9001  0.6924
parameterHips        0.2197  0.4303  0.5105  0.6097 -0.6238  1.0631
parameterwither height  0.2344  0.3779  0.6201  0.5352 -0.5064  0.9751

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

> res3 <- orchard::mod_results(datag_MR01, mod = "parameter", group = "Author")
> res3
  name   estimate      lowerCL      upperCL      lowerPR      upperPR
1  ADFI 0.48441202 -0.17212180 1.1409458 -0.9938106 1.962635
2   ADG 0.25668923  0.02396179 0.4894167 -1.0880291 1.601408
3    BCS 0.05073585 -0.23543978 0.3369115 -1.3042556 1.405727
4 Birth weight 0.38903841 -0.17309692 0.9511737 -1.0497463 1.827823
5      DMI 0.22061113  0.01619850 0.4250238 -1.1194970 1.560719
6      FCE 0.19442295 -0.13740392 0.5262498 -1.1709394 1.559785
7 Heart girth 0.38056277 -0.11819702 0.8793226 -1.0346639 1.795789
8      Hips 0.70409440  0.13294000 1.2752488 -0.7382380 2.146427
9 wither height 0.71877551  0.31469249 1.1228585 -0.6659224 2.103473
> p2 <- orchard::orchard_plot(res3, mod = "parameter", group = "Author", xlab = "s
> p2
> ggsave('growth_parameter_moderator.pdf', width = 4, height = 8, p2)
> |
```

additive category as a moderator

```
> datag_MR01 <- metareg(y ~ Dose, v ~ VDose, mod = "category", random = TRUE) >
> summary(datag_MR01)

Multivariate Meta-Analysis Model (k = 333; method: REML)

  logLik   Deviance       AIC       BIC       AICC
-417.2959  834.5918  846.5918  869.3681  846.8526

Variance Components:

      estim    sqrt  nlvls fixed factor
sigma^2.1  0.0908  0.3013     28    no  Author
sigma^2.2  0.3509  0.5924    333    no      ID

Test for Residual Heterogeneity:
QE(df = 329) = 987.6506, p-val < .0001

Test of Moderators (coefficients 2:4):
QM(df = 3) = 8.2211, p-val = 0.0417

Model Results:

      estimate      se     zval    pval    ci.lb    ci.ub
intrcpt      0.5551  0.1600   3.4697  0.0005  0.2415  0.8686 *** 
categoryCattle -0.4469  0.1675  -2.6678  0.0076 -0.7752 -0.1186 ** 
categoryGoat   -0.3833  0.3008  -1.2743  0.2026 -0.9728  0.2062
categorySheep   -0.1004  0.1900  -0.5281  0.5974 -0.4729  0.2721

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

> res3 <- orchard::mod_results(datag_MR01, mod = "category", group = "Author")
> res3
  name estimate    lowerCL    upperCL    lowerPR    upperPR
1 Beef  0.5550903  0.24153258  0.8686480 -0.7847699  1.894951
2 Cattle 0.1082203 -0.07790579  0.2943464 -1.2076634  1.424104
3 Goat  0.1717866 -0.32745711  0.6710303 -1.2232587  1.566832
4 Sheep 0.4547228  0.15470690  0.7547387 -0.8820332  1.791479
> p3 <- orchard::orchard_plot(res3, mod = "category", group = "Author", xlab = "S"
> p3
> |
```

sensitivity analysis

```
> ###sensitivity analysis
> result1=rma(SMD, vsMD, data=datag1, method="REML")
> result1

Random-Effects Model (k = 333; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.4224 (SE = 0.0477)
tau (square root of estimated tau^2 value):       0.6500
I^2 (total heterogeneity / total variability):   73.04%
H^2 (total variability / sampling variability):  3.71

Test for Heterogeneity:
Q(df = 332) = 1014.3627, p-val < .0001

Model Results:

estimate      se     zval    pval    ci.lb    ci.ub
 0.2082  0.0433  4.8102  <.0001  0.1234  0.2930  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model: weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = 3.2513, df = 331, p = 0.0013
Limit Estimate (as sei -> 0): b = -0.2128 (CI: -0.4482, 0.0226)

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf
```

```
> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the left side: 0 (SE = 8.1071)

Random-Effects Model (k = 333; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.4224 (SE = 0.0477)
tau (square root of estimated tau^2 value):       0.6500
I^2 (total heterogeneity / total variability):   73.04%
H^2 (total variability / sampling variability):  3.71

Test for Heterogeneity:
Q(df = 332) = 1014.3627, p-val < .0001

Model Results:

estimate      se    zval   pval   ci.lb   ci.ub
 0.2082  0.0433  4.8102  <.0001  0.1234  0.2930  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> funnel(res.tf)
```

blood metabolites

overall

```
> summary(datab1_MA)

Multivariate Meta-Analysis Model (k = 753; method: REML)

  logLik   Deviance       AIC       BIC       AICC 
-1015.5837  2031.1673  2037.1673  2051.0355  2037.1994 

Variance Components:

            estim    sqrt  nlevs  fixed factor
sigma^2.1  0.1547  0.3933     42    no  Author
sigma^2.2  0.4226  0.6501    753    no      ID

Test for Heterogeneity:
Q(df = 752) = 3445.2512, p-val < .0001

Model Results:

estimate      se      zval      pval      ci.lb      ci.ub
  0.0311  0.0730  0.4258  0.6703  -0.1120  0.1741

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

> model_results <- orchard::mod_results(datab1_MA, mod = "1", at = 1)
> model_results
  name estimate lowerCL upperCL lowerPR upperPR
1 Intrcpt 0.03107045 -0.1119629 0.1741038 -1.464992 1.527133
> orchard::orchard_plot(datab1_MA, mod = "1", group = "Author", xlab
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_ml(datab1_MA)
> I2
  I2_Total I2_Author      I2_ID
  79.01697  21.17245  57.84452
> pp<-orchard::orchard_plot(model_results, mod = "1", xlab = "standa
", round(I2[1],2), "*\\%\\\"), color = "black", parse = TRUE, size =
+ scale_colour_manual(values = "#B1FCAC")
Scale for fill is already present.
Adding another scale for fill, which will replace the existing scale.
Scale for colour is already present.
```

species as a moderator

parameter as a moderator

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```
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 446; method: REML)

  LogLik   Deviance      AIC      BIC      AICC 
-550.6304 1101.2608 1131.2608 1192.3219 1132.4119 

Variance Components:

    estim     sqrt  nlvls fixed factor  
sigma^2.1 0.0963  0.3102     37    no Author 
sigma^2.2 0.3567  0.5973    446    no      ID  

Test for Residual Heterogeneity:
QE(df = 433) = 2150.0695, p-val < .0001

Test of Moderators (coefficients 2:13):
QM(df = 12) = 28.8032, p-val = 0.0042

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub    
intrcpt       0.0405  0.1792  0.2258  0.8213 -0.3108  0.3918    
parameterALP   -0.1278  0.2486 -0.5141  0.6072 -0.6150  0.3594    
parameterALT    0.1436  0.2213  0.6486  0.5166 -0.2902  0.5774    
parameterAST   -0.1230  0.2002 -0.6146  0.5388 -0.5153  0.2693    
parameterBetaine 0.3667  0.2771  1.3233  0.1857 -0.1764  0.9097    
parameterBHB   -0.0934  0.1973 -0.4734  0.6360 -0.4802  0.2933    
parameterBUN   -0.3683  0.1947 -1.8918  0.0585 -0.7499  0.0133    
parameterCreatinine -0.2867  0.2230 -1.2857  0.1986 -0.7236  0.1503    
parameterFibrinogen -0.0304  0.3406 -0.0894  0.9288 -0.6980  0.6371    
parameterGGT    -0.1991  0.2249 -0.8851  0.3761 -0.6399  0.2417    
parameterGlucose   0.0617  0.1871  0.3300  0.7414 -0.3049  0.4284    
parameterGSH    -0.2028  0.3702 -0.5478  0.5838 -0.9284  0.5228    
parameterIGF-1    0.7564  0.3331  2.2708  0.0232  0.1035  1.4092 *  
                                 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 +  
  
> res3 <- orchardR::mod_results(databm_MR01, mod = "parameter", group = "Author")  
> res3  
    name   estimate    lowerCL    upperCL    lowerPR    upperPR  
1    ALB  0.04047631 -0.31083475  0.39178737 -1.3246287 1.405581  
2    ALP -0.08731332 -0.50661179  0.33198516 -1.4714750 1.296848  
3    ALT  0.18403337 -0.16344863  0.53151537 -1.1800913 1.548158  
4    AST -0.08254144 -0.36166584  0.19658295 -1.4308747 1.265792  
5 Betaine 0.40713837 -0.03289481  0.84717155 -0.9834448 1.797721  
6    BHB -0.05292940 -0.25764636  0.15178755 -1.3878456 1.281987  
7    BUN -0.32783015 -0.56782158 -0.08783872 -1.6686091 1.012949  
8 Creatinine -0.24617552 -0.59883566  0.10648462 -1.6116283 1.119277  
9 Fibrinogen 0.01004151 -0.56367794  0.58376095 -1.4284460 1.448529  
10   GGT -0.15858265 -0.51636355  0.19919824 -1.5253670 1.208202  
11   Glucose 0.10219847 -0.09179456  0.29619151 -1.2311153 1.435512  
12   GSH -0.16231169 -0.82087679  0.49625340 -1.6366930 1.312070  
13   IGF-1  0.79684838  0.22809682  1.36559993 -0.6396650 2.233362  
> p2 <- orchardR::orchard_plot(res3, mod = "parameter", group = "Author", xlab = "St  
> p2
```

后 20

```

Multivariate Meta-Analysis Model (k = 307; method: REML)

  logLik Deviance      AIC      BIC      AICC
-411.1577 822.3155 848.3155 896.2901 849.6062

Variance Components:

    estim   sqrt  nvlvs fixed factor
sigma^2.1 0.0000 0.0000    38    no Author
sigma^2.2 0.5166 0.7188   307    no      ID

Test for Residual Heterogeneity:
QE(df = 296) = 905.6631, p-val < .0001

Test of Moderators (coefficients 2:11):
QM(df = 10) = 105.2908, p-val < .0001

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub
intrcpt       0.0413  0.0981  0.4207  0.6740 -0.1510  0.2336
parameterInsulin 0.0108  0.1764  0.0611  0.9513 -0.3350  0.3566
parameterNEFA   -0.1466  0.1383 -1.0595  0.2894 -0.4177  0.1246
parameterOSI    -0.1844  0.3242 -0.5686  0.5696 -0.8198  0.4511
parameterP4      1.2437  0.1703  7.3033 <.0001  0.9099  1.5775 ***
parameterRQUICKI 1.7783  0.3324  5.3496 <.0001  1.1268  2.4299 ***
parametersOD    0.6115  0.4467  1.3689  0.1710 -0.2640  1.4871
parameterTAS     0.2654  0.2739  0.9689  0.3326 -0.2715  0.8022
parameterTBIL   -0.0222  0.2224 -0.1000  0.9203 -0.4581  0.4136
parameterTOS     0.3166  0.3285  0.9638  0.3352 -0.3272  0.9604
parameterTP      -0.0994  0.2226 -0.4464  0.6553 -0.5357  0.3370

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

> res3 <- orchard::mod_results(databm_MR01, mod = "parameter", group = "Author")
> res3
      name   estimate   lowerCL   upperCL   lowerPR   upperPR
1 Cholesterol 0.04128036 -0.1510299 0.23359060 -1.3805749 1.463136
2 Insulin 0.05205557 -0.2353576 0.33946879 -1.3857537 1.489865
3 NEFA -0.10530185 -0.2964659 0.08586219 -1.5270026 1.316399
4 OSI -0.14308412 -0.7487469 0.46257862 -1.6765497 1.390381
5 P4 1.28497699 1.0121830 1.55777101 -0.1499815 2.719935
6 RQUICKI 1.81960202 1.1970995 2.44210456 0.2794077 3.359796
7 SOD 0.65282790 -0.2013859 1.50704170 -0.9947067 2.300363
8 TAS 0.30664797 -0.1945528 0.80784877 -1.1886418 1.801938
9 TBIL 0.01903631 -0.3721199 0.41019256 -1.4430487 1.481121
10 TOS 0.35785873 -0.2565686 0.97228607 -1.1790896 1.894807
11 TP -0.05811206 -0.4498056 0.33358146 -1.5203408 1.404117
> p2 <- orchard::orchard_plot(res3, mod = "parameter", group = "Author", xlab =
> p2
> save('blood moderator parameter moderator_E14.ndf' width = 4 height = 8 n?1

```

additive category as a moderator

```
> databm_MR01 <- rma.mv(yi = SMD, V = vSMD, mods = ~category, random = lis
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 753; method: REML)

      logLik    Deviance        AIC        BIC        AICC
-1006.6508  2013.3016  2027.3016  2059.6234  2027.4529

Variance Components:

      estim   sqrt  nlevs  fixed factor
sigma^2.1 0.1803 0.4246     42    no  Author
sigma^2.2 0.4175 0.6461    753    no      ID

Test for Residual Heterogeneity:
QE(df = 748) = 3412.3662, p-val < .0001

Test of Moderators (coefficients 2:5):
QM(df = 4) = 6.5047, p-val = 0.1645

Model Results:

      estimate      se     zval    pval    ci.lb    ci.ub
intrcpt       -0.4263  0.2592  -1.6448  0.1000  -0.9343  0.0817
categoryBuffalo  0.0715  0.3801   0.1881  0.8508  -0.6735  0.8165
categoryCattle   0.5132  0.2510   2.0445  0.0409   0.0212  1.0052  *
categoryGoat     0.3836  0.3505   1.0944  0.2738  -0.3034  1.0705
categorySheep    0.5347  0.3188   1.6769  0.0936  -0.0903  1.1596  .

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

> res3 <- orchaRd::mod_results(databm_MR01, mod = "category", group = "Author"
> res3
  name   estimate   lowerCL   upperCL   lowerPR   upperPR
1 Beef -0.42629595 -0.9342634 0.08167146 -2.024551 1.171959
2 Buffalo -0.35479508 -0.8997600 0.19016980 -1.965191 1.255601
3 Cattle  0.08693101 -0.1029889 0.27685093 -1.440308 1.614170
4 Goat  -0.04273934 -0.5051501 0.41967141 -1.627105 1.541626
5 Sheep  0.10836054 -0.2556153 0.47233641 -1.450122 1.666843
> p2 <- orchaRd::orchard_plot(res3, mod = "category", group = "Author", xl
> p2
> |
```

sensitivity analysis

```
> ##sensitivity analysis
> result1=rma(SMD, vSMD, data=databm1, method="REML")
> result1

Random-Effects Model (k = 753; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5783 (SE = 0.0412)
tau (square root of estimated tau^2 value):      0.7605
I^2 (total heterogeneity / total variability):   79.04%
H^2 (total variability / sampling variability):  4.77

Test for Heterogeneity:
Q(df = 752) = 3445.2512, p-val < .0001

Model Results:

estimate      se     zval    pval   ci.lb   ci.ub
 0.0909  0.0327  2.7787  0.0055  0.0268  0.1550  **

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

> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> ##conduct classical Egger's test regression analysis
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model: weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -2.2330, df = 751, p = 0.0258
Limit Estimate (as sei -> 0): b =  0.2655 (CI: 0.1303, 0.4007)

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the left side: 0 (SE = 13.6299)

Random-Effects Model (k = 753; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5783 (SE = 0.0412)
tau (square root of estimated tau^2 value):      0.7605
I^2 (total heterogeneity / total variability):   79.04%
H^2 (total variability / sampling variability):  4.77

Test for Heterogeneity:
Q(df = 752) = 3445.2512, p-val < .0001
```

```
> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the left side: 0 (SE = 13.6299)

Random-Effects Model (k = 753; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5783 (SE = 0.0412)
tau (square root of estimated tau^2 value):      0.7605
I^2 (total heterogeneity / total variability):   79.04%
H^2 (total variability / sampling variability):  4.77

Test for Heterogeneity:
Q(df = 752) = 3445.2512, p-val < .0001

Model Results:

estimate      se     zval    pval   ci.lb   ci.ub
 0.0909  0.0327  2.7787  0.0055  0.0268  0.1550  **

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

> funnel(res.tf)
> ##conduct leave-one-out analysis
> le<-leave1out(result1)
```

Production

Overall

```
> Effect_size_production <- read_excel("D:/反刍动物meta12.20/product")
>
> datapp<-Effect_size_production
> datap11<-escalc(measure = "SMD", n1i = treat_n, sd1i = treat_sd,
+ data = datapp)
> datap1_MA <- rma.mv(yi = SMD, V = vsMD, random = list(~1 | Author
+ > summary(datap1_MA)

Multivariate Meta-Analysis Model (k = 425; method: REML)

      logLik   Deviance       AIC       BIC       AICC
-626.1606  1252.3212  1258.3212  1270.4705  1258.3784

Variance Components:

            estim     sqrt  nlevels  fixed  factor
sigma^2.1  0.3473  0.5893        25    no  Author
sigma^2.2  0.2671  0.5169       425    no      ID

Test for Heterogeneity:
Q(df = 424) = 1472.1765, p-val < .0001

Model Results:

estimate      se     zval    pval    ci.lb    ci.ub
  0.2805  0.1286  2.1808  0.0292  0.0284  0.5327  *
  ...
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> model_results <- orchard::mod_results(datap1_MA, mod = "1", at =
> model_results
  name estimate  lowerCL  upperCL  lowerPR  upperPR
1 Intrcpt 0.2805343 0.0284077 0.5326608 -1.27633 1.837399
> orchard::orchard_plot(datap1_MA, mod = "1", group = "Author", xla
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_ml(datap1_MA)
> I2
  I2_Total I2_Author      I2_ID
  79.54522  44.96049  34.58473
```

Species

```
> rma.mv(yi = SMD, V = vsMD, mods = ~species, random = list(~1 | Author))
> summary(datap_MRO)

Multivariate Meta-Analysis Model (k = 425; method: REML)

  logLik Deviance      AIC      BIC      AICC
-605.3723 1210.7446 1230.7446 1271.0754 1231.2864

Variance Components:

estim     sqrt    nlvls  fixed factor
sigma^2.1 0.1635  0.4043    25     no  Author
sigma^2.2 0.2802  0.5294   425     no      ID

Test for Residual Heterogeneity:
QE(df = 417) = 1292.2152, p-val < .0001

Test of Moderators (coefficients 2:8):
QM(df = 7) = 26.5446, p-val = 0.0004

Model Results:

estimate      se      zval      pval      ci.lb      ci.ub
intrcpt       0.1319  0.4528  0.2914  0.7708 -0.7555  1.0193
speciesHolstein 0.1308  0.4685  0.2792  0.7801 -0.7874  1.0490
speciesKaran X Fries 0.3542  0.6582  0.5381  0.5905 -0.9358  1.6441
speciesMurrah   1.6394  0.6286  2.6080  0.0091  0.4073  2.8715  **
speciesRambouillet -1.5669  0.6781 -2.3108  0.0208 -2.8960 -0.2379  *
speciesSaanen    0.0082  0.5214  0.0158  0.9874 -1.0136  1.0301
speciesSurti     0.1443  0.6164  0.2341  0.8149 -1.0638  1.3524
speciesZaraibi    0.8681  0.6285  1.3812  0.1672 -0.3637  2.0999

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

> res2 <- orchard::mod_results(datap_MRO, mod = "species", group = "Author")
> res2
  name estimate      lowerCL      upperCL      lowerPR      upperPR
1 Chios  0.1319180 -0.75547809 1.0193141 -1.4466836 1.7105196
2 Holstein 0.2626967  0.02677351 0.4986199 -1.0640177 1.5894110
3 Karan X Fries 0.4860944 -0.45012831 1.4223172 -1.1204622 2.0926511
4 Murrah  1.7713225  0.91662396 2.6260210  0.2108672 3.3317778
5 Rambouillet -1.4350196 -2.42442220 -0.4456169 -3.0731370 0.2030979
6 Saanen  0.1401646 -0.36650689 0.6468362 -1.2602736 1.5406029
7 Surti   0.2762430 -0.54355817 1.0960441 -1.2653747 1.8178607
8 Zaraibi 1.0000133  0.14563852 1.8543880 -0.5602647 2.5602913
> p1<- orchard::orchard_plot(res2, mod = "species", group = "Author", xlab = "St
```

Parameter

```
Multivariate Meta-Analysis Model (k = 425; method: REML)

  logLik   Deviance      AIC      BIC      AICC
-608.1854 1216.3709 1244.3709 1300.6992 1245.4262

Variance Components:

    estim    sqrt  nvlvs fixed factor
sigma^2.1  0.3361  0.5798     25    no Author
sigma^2.2  0.2759  0.5252    425    no     ID

Test for Residual Heterogeneity:
QE(df = 413) = 1419.8147, p-val < .0001

Test of Moderators (coefficients 2:12):
QM(df = 11) = 22.7078, p-val = 0.0194

Model Results:

      estimate      se     zval    pval    ci.lb    ci.ub
intrcpt     -0.5344  0.3020  -1.7695  0.0768  -1.1264  0.0575 .
parameterMFP  0.7014  0.2941   2.3844  0.0171   0.1248  1.2779 *
parameterMFY  0.9409  0.3015   3.1208  0.0018   0.3500  1.5318 **
parameterMLP  0.8043  0.2993   2.6871  0.0072   0.2176  1.3910 **
parameterMLY  0.7301  0.3226   2.2627  0.0237   0.0977  1.3624 *
parameterMPP  0.6137  0.2926   2.0972  0.0360   0.0402  1.1873 *
parameterMPY  0.7706  0.3016   2.5548  0.0106   0.1794  1.3618 *
parameterMSP  0.5107  0.3315   1.5406  0.1234  -0.1390  1.1605
parameterMSY  0.8546  0.4509   1.8952  0.0581  -0.0292  1.7384 .
parameterMUN  0.7828  0.3215   2.4351  0.0149   0.1527  1.4128 *
parameterMY   0.9680  0.2817   3.4360  0.0006   0.4158  1.5202 ***
parametersNFP 0.6069  0.3341   1.8164  0.0693  -0.0480  1.2618 .

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

> res3 <- orchard::mod_results(datap_MR01, mod = "parameter", group = "Author"
> res3
  name      estimate    lowerCL   upperCL   lowerPR   upperPR
1 Density -0.53442000 -1.12635230 0.0575123 -2.178000 1.109160
2 MFP     0.16693286 -0.14816717 0.4820329 -1.398397 1.732263
3 MFY     0.40647771  0.07856311 0.7343923 -1.161482 1.974438
4 MLP     0.26990286 -0.07670287 0.6165086 -1.302072 1.841878
5 MLY     0.19563321 -0.20336068 0.5946271 -1.388717 1.779984
6 MPP     0.07930265 -0.23334261 0.3919479 -1.485535 1.644141
7 MPY     0.23621660 -0.08898132 0.5614145 -1.331178 1.803611
8 MSP     -0.02370860 -0.49514550 0.4477283 -1.627836 1.580418
9 MSY     0.32017412 -0.41545165 1.0557999 -1.380448 2.020796
10 MUN    0.24833636 -0.14581038 0.6424831 -1.334801 1.831473
11 MY     0.43359354  0.16606415 0.7011229 -1.122858 1.990046
12 SNFP   0.07249984 -0.40874107 0.5537407 -1.534536 1.679535
> p2 <- orchard::orchard_plot(res3, mod = "parameter", group = "Author", xlat
> p2
```

CA

```
> datap_MR01 <- rma.mv(yi = SMD, V = vSMD, mods = ~category, random =
> summary(datap_MR01)

Multivariate Meta-Analysis Model (k = 425; method: REML)

  logLik   Deviance       AIC       BIC       AICC
-618.9517 1237.9034 1249.9034 1274.1592 1250.1063

Variance Components:

      estim    sqrt  nvlvs  fixed  factor
sigma^2.1 0.3358  0.5795     25    no  Author
sigma^2.2 0.2717  0.5213    425    no      ID

Test for Residual Heterogeneity:
QE(df = 421) = 1443.7294, p-val < .0001

Test of Moderators (coefficients 2:4):
QM(df = 3) = 3.9326, p-val = 0.2688

Model Results:

      estimate      se     zval     pval    ci.lb    ci.ub
intrcpt      1.0043  0.4210   2.3856  0.0171   0.1792  1.8295 *
categoryCattle -0.7278  0.4503  -1.6163  0.1060  -1.6103  0.1548
categoryGoat   -0.8746  0.5310  -1.6469  0.0996  -1.9154  0.1662 .
categorySheep  -1.0364  0.5532  -1.8737  0.0610  -2.1206  0.0477 .

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

> res3 <- orchard::mod_results(datap_MR01, mod = "category", group =
> res3
      name  estimate  lowerCL  upperCL  lowerPR  upperPR
1 Buffalo  1.00432686  0.17919506  1.8294587 -0.7318997  2.740553
2 Cattle   0.27657076 -0.03645337  0.5895949 -1.2827958  1.835937
3 Goat    0.12974700 -0.50465120  0.7641452 -1.5243694  1.783863
4 Sheep   -0.03209806 -0.73534986  0.6711537 -1.7138243  1.649628
> p2 <- orchard::orchard_plot(res3, mod = "category", group = "Author"
. . .
```

sensitivity analysis

```
> result1

Random-Effects Model (k = 425; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5483 (SE = 0.0519)
tau (square root of estimated tau^2 value):        0.7405
I^2 (total heterogeneity / total variability):   77.63%
H^2 (total variability / sampling variability):  4.47

Test for Heterogeneity:
Q(df = 424) = 1472.1765, p-val < .0001

Model Results:

estimate      se     zval    pval   ci.lb   ci.ub
 0.3453  0.0425  8.1144  <.0001  0.2619  0.4286  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> ##conduct classical Egger's test regression analysis
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model:      weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t =  6.6735, df = 423, p < .0001
Limit Estimate (as sei -> 0):  b = -0.3901 (CI: -0.5882, -0.1920)

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the left side: 0 (SE = 10.4288)

Random-Effects Model (k = 425; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5483 (SE = 0.0519)
tau (square root of estimated tau^2 value):        0.7405
I^2 (total heterogeneity / total variability):   77.63%
H^2 (total variability / sampling variability):  4.47

Test for Heterogeneity:
Q(df = 424) = 1472.1765, p-val < .0001

Model Results:

estimate      se     zval    pval   ci.lb   ci.ub
 0.3453  0.0425  8.1144  <.0001  0.2619  0.4286  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Carcass_characteristics

Overall

```
> model_results <- orchaRd::mod_results(datab1_MA, mod = "1", at = NULL, group = "Author")
> model_results
      name   estimate    lowerCL    upperCL    lowerPR    upperPR
1 Intrcpt 0.06976242 -0.05415731 0.1936821 -0.2309301 0.370455
> orchaRd::orchard_plot(datab1_MA, mod = "1", group = "Author", xlab = "Standardised mean difference", transfm = "none", twig.size = 0.5, trunk.size = 1)
> # use i2_sn function to obtain the total I^2
> I2 <- orchaRd::i2_ml(datab1_MA)
> I2
  I2_Total   I2_Author     I2_ID
8.87560140 8.86353137 0.01207003
> setwd("C:/Users/ASUS/Desktop/反刍动物meta分析2024.12.03")
  ... orchard::orchard::model_results.mod.11" vlab "standardised
  ... ,-----,-----,
> summary(datab1_MA)

Multivariate Meta-Analysis Model (k = 167; method: REML)

      logLik   Deviance       AIC       BIC       AICC
-124.2092  248.4183  254.4183  263.7543  254.5665

Variance Components:

            estim    sqrt  nvlvs  fixed  factor
sigma^2.1  0.0195  0.1397     8      no  Author
sigma^2.2  0.0000  0.0052   167      no      ID

Test for Heterogeneity:
Q(df = 166) = 179.0483, p-val = 0.2313

Model Results:

estimate      se      zval      pval      ci.lb      ci.ub
 0.0698  0.0632  1.1034  0.2699  -0.0542  0.1937

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Species

```
> summary(datag1_MA)

Multivariate Meta-Analysis Model (k = 167; method: REML)

  logLik   Deviance      AIC      BIC      AICC 
-124.2092  248.4183  254.4183  263.7543  254.5665 

Variance Components:

            estim    sqrt  nvlvs  fixed  factor 
sigma^2.1  0.0195  0.1397     8     no  Author 
sigma^2.2  0.0000  0.0052   167     no       ID 

Test for Heterogeneity:
Q(df = 166) = 179.0483, p-val = 0.2313

Model Results:

estimate      se      zval     pval    ci.lb    ci.ub 
 0.0698  0.0632  1.1034  0.2699  -0.0542  0.1937 

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> summary(datag_MR0)

Multivariate Meta-Analysis Model (k = 167; method: REML)

  logLik   Deviance      AIC      BIC      AICC 
-115.0681  230.1363  250.1363  280.8253  251.6227 

Variance Components:

            estim    sqrt  nvlvs  fixed  factor 
sigma^2.1  0.0200  0.1413     8     no  Author 
sigma^2.2  0.0000  0.0000   167     no       ID 

Test for Residual Heterogeneity:
QE(df = 159) = 162.5755, p-val = 0.4066

Test of Moderators (coefficients 2:8):
QM(df = 7) = 10.0728, p-val = 0.1845
```

Model Results:

	estimate	se	zval	pval	ci.lb	ci.ub
intrcpt	0.1493	0.1214	1.2305	0.2185	-0.0885	0.3872
speciesCashmere	-0.1841	0.2096	-0.8785	0.3797	-0.5950	0.2267
speciesH × A	0.4069	0.2492	1.6327	0.1025	-0.0816	0.8954
speciesH × N	0.0025	0.2363	0.0107	0.9914	-0.4606	0.4657
speciesHolstein	-0.3511	0.2347	-1.4961	0.1346	-0.8110	0.1089
speciesKarayaka	-0.1797	0.2188	-0.8215	0.4113	-0.6085	0.2490
speciesSaint Croix	-0.1099	0.2009	-0.5468	0.5845	-0.5036	0.2839
speciesSuffolk	-0.1895	0.1250	-1.5168	0.1293	-0.4345	0.0554

intrcpt
speciesCashmere
speciesH × A
speciesH × N
speciesHolstein
speciesKarayaka
speciesSaint Croix
speciesSuffolk

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```
> res2 <- orchaRd::mod_results(datag_MR0, mod = "species", group = "Author")
> res2
      name   estimate    lowerCL    upperCL    lowerPR    upperPR
1     B × C  0.14932941 -0.08853189  0.3871907 -0.21577703  0.5144359
2   Cashmere -0.03481749 -0.36980089  0.3001659 -0.46948817  0.3998532
3     H × A  0.55627227  0.12958697  0.9829576  0.04756306  1.0649815
4     H × N  0.15186296 -0.24551323  0.5492391 -0.33252589  0.6362518
5   Holstein -0.20172664 -0.59534846  0.1918952 -0.68304032  0.2795870
6   Karayaka -0.03038748 -0.38710723  0.3263323 -0.48202195  0.4212470
7 Saint Croix  0.03947284 -0.27436045  0.3533061 -0.37911533  0.4580610
8   suffolk -0.04021425 -0.33400492  0.2535764 -0.44399349  0.3635650
> |
```

Parameter

```
> summary(datag_MR01)

Multivariate Meta-Analysis Model (k = 165; method: REML)

  LogLik   Deviance      AIC      BIC      AICC 
-108.3175  216.6350  242.6350  282.1153  245.2350 

Variance Components:

            estim    sqrt  nvlvs  fixed factor  
sigma^2.1  0.0320  0.1788     8     no Author  
sigma^2.2  0.0000  0.0000   165     no      ID   

Test for Residual Heterogeneity:
QE(df = 154) = 151.9062, p-val = 0.5326

Test of Moderators (coefficients 2:11):
QM(df = 10) = 24.2683, p-val = 0.0069

Model Results:

             estimate      se      zval     pval    ci.lb    ci.ub  
intrcpt        0.0233  0.1471  0.1584  0.8742 -0.2650  0.3116  
parameterDP     0.0235  0.1482  0.1584  0.8741 -0.2670  0.3140  
parameterIF     -0.3710  0.2467 -1.5038  0.1326 -0.8546  0.1125  
parameterLD     -0.3083  0.2612 -1.1802  0.2379 -0.8202  0.2037  
parameterMeat color -0.1738  0.1949 -0.8914  0.3727 -0.5558  0.2083  
parameterMeat pH  -0.1423  0.2253 -0.6317  0.5276 -0.5838  0.2992  
parametersSF    -0.2376  0.2915 -0.8152  0.4149 -0.8090  0.3337  
parametersSW    0.1188  0.1611  0.7371  0.4611 -0.1970  0.4345  
parameterVF      0.3088  0.1436  2.1505  0.0315  0.0274  0.5902  
parameterVFP     -0.1485  0.2495 -0.5955  0.5515 -0.6375  0.3404  
parameterVW      0.3208  0.2050  1.5654  0.1175 -0.0809  0.7225  

intrcpt
parameterDP
parameterIF
parameterLD
parameterMeat color
parameterMeat pH
parametersSF
parametersSW
parameterVF      *
parameterVFP
parameterVW
```

```

---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> res3 <- orchaRd::mod_results(datag_MR01, mod = "parameter", group = "Author")
> res3
      name   estimate    lowerCL    upperCL    lowerPR    upperPR
1     BFT  0.02329467 -0.26498390  0.31157323 -0.43049480  0.4770841
2     DP   0.04677703 -0.18114056  0.27469462 -0.37127414  0.4648282
3     IF  -0.34772028 -0.78463862  0.08919805 -0.90782561  0.2123850
4     LD  -0.28496630 -0.74204786  0.17211526 -0.86093844  0.2910058
5 Meat color -0.15047232 -0.44174172  0.14079708 -0.60616762  0.3052230
6 Meat pH   -0.11900917 -0.48453522  0.24651689 -0.62539799  0.3873797
7 SF    -0.21433893 -0.73099136  0.30231350 -0.83863860  0.4099607
8 SW    0.14204482 -0.06580742  0.34989707 -0.26541425  0.5495039
9 VF    0.33209598  0.12523162  0.53896034 -0.07486005  0.7390520
10 VFP   -0.12525186 -0.60361630  0.35311257 -0.71825513  0.4677514
11 VW    0.34411733  0.01483650  0.67339817 -0.13676333  0.8249980
> p2 <- orchaRd::orchard_plot(res3, mod = "parameter", group = "Author", xl
ab = "Standardised mean difference")
> |

```

additive category

```

> summary(datag_MR01)

Multivariate Meta-Analysis Model (k = 167; method: REML)

  logLik Deviance      AIC      BIC      AICC
-121.3262 242.6523 254.6523 273.2148 255.1908

Variance Components:

            estim   sqrt  nlvls fixed factor
sigma^2.1 0.0395 0.1987      8    no Author
sigma^2.2 0.0000 0.0000    167    no     ID

Test for Residual Heterogeneity:
QE(df = 163) = 176.5673, p-val = 0.2212

Test of Moderators (coefficients 2:4):
QM(df = 3) = 2.7230, p-val = 0.4363

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub
intrcpt       0.1910  0.1266  1.5089  0.1313 -0.0571  0.4390
categoryCattle -0.0348  0.2182 -0.1596  0.8732 -0.4624  0.3928
categoryGoat   -0.2258  0.2544 -0.8875  0.3748 -0.7244  0.2728
categorySheep  -0.1708  0.1135 -1.5057  0.1321 -0.3932  0.0515

---
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```

```

> res3 <- orcharD::mod_results(datag_MR01, mod = "category", group = "Author")
> res3
      name   estimate    lowerCL   upperCL   lowerPR   upperPR
1  Beef  0.19096373 -0.05708307  0.4390105 -0.2706873  0.6526147
2 Cattle 0.15615405 -0.19213698  0.5044451 -0.3662453  0.6785534
3 Goat -0.03481749 -0.46734909  0.3977141 -0.6167780  0.5471430
4 Sheep 0.02011688 -0.18812062  0.2283544 -0.4214228  0.4616566
> |

```

sensitivity analysis

```

> #####
> ###sensitivity analysis
> result1=rma(SMD, vsMD, data=datag1, method="REML")
> result1

Random-Effects Model (k = 167; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.0064 (SE = 0.0181)
tau (square root of estimated tau^2 value):       0.0799
I^2 (total heterogeneity / total variability):   3.09%
H^2 (total variability / sampling variability):  1.03

Test for Heterogeneity:
Q(df = 166) = 179.0483, p-val = 0.2313

Model Results:

estimate      se     zval    pval    ci.lb    ci.ub
 0.0437  0.0355  1.2296  0.2189 -0.0259  0.1133

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model: weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -1.5891, df = 165, p = 0.1139
Limit Estimate (as sei -> 0): b = 0.2092 (CI: -0.0061, 0.4245)

> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model: weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -1.5891, df = 165, p = 0.1139
Limit Estimate (as sei -> 0): b = 0.2092 (CI: -0.0061, 0.4245)

```

```
> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the right side: 25 (SE = 8.4274)

Random-Effects Model (k = 192; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.0473 (SE = 0.0251)
tau (square root of estimated tau^2 value):      0.2176
I^2 (total heterogeneity / total variability):   18.40%
H^2 (total variability / sampling variability):  1.23

Test for Heterogeneity:
Q(df = 191) = 269.0435, p-val = 0.0002

Model Results:

estimate      se     zval    pval    ci.lb    ci.ub
 0.1415  0.0381  3.7144  0.0002  0.0668  0.2162  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Liver_composition

Overall

```
> datam1_MA <- rma.mv(yi = SMD, V = VSMD, random = list(~1 | Author))
> summary(datam1_MA)

Multivariate Meta-Analysis Model (k = 211; method: REML)

logLik Deviance      AIC      BIC      AICC
-195.4029 390.8057 396.8057 406.8470 396.9222

Variance Components:

          estim   sqrt  nvlvs fixed factor
sigma^2.1 0.2631 0.5129     27    no Author
sigma^2.2 0.0328 0.1812    211    no      ID

Test for Heterogeneity:
Q(df = 210) = 417.0065, p-val < .0001

Model Results:

estimate      se      zval      pval      ci.lb      ci.ub
 0.0560  0.1095  0.5114  0.6091 -0.1586  0.2706

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

> model_results <- orchardD::mod_results(datam1_MA, mod = "1", at
> model_results
  name estimate      lowerCL      upperCL      lowerPR      upperPR
1 InTrcpt 0.05600011 -0.1586113  0.2706115 -1.031615  1.143615
> orchardD::orchard_plot(datam1_MA, mod = "1", group = "Author", x
> # use i2_sn function to obtain the total I^2
> I2 <- orchardD::i2_ml(datam1_MA)
> pp<-orchardD::orchard_plot(model_results, mod = "1", xlab = "Sta
", round(I2[1],2), "*\\%\\\"), color = "black", parse = TRUE, size
+   scale_colour_manual(values = "#78D3AC")
scale for f11 is already present
```

species as a moderator

parameter as a moderator

```
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 211; method: REML)

  LogLik   Deviance      AIC      BIC      AICC
-183.8499  367.6998  385.6998  415.5629  386.6276

Variance Components:

            estim    sqrt  nvlvs fixed factor
sigma^2.1  0.2475  0.4975     27    no Author
sigma^2.2  0.0298  0.1725    211    no      ID

Test for Residual Heterogeneity:
QE(df = 204) = 403.2829, p-val < .0001

Test of Moderators (coefficients 2:7):
QM(df = 6) = 17.3533, p-val = 0.0081

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub
intrcpt     -0.0124  0.1334  -0.0931  0.9258  -0.2740  0.2491
parameterHDL  0.0776  0.1940   0.3998  0.6893  -0.3026  0.4578
parameterLDL  0.3024  0.1932   1.5649  0.1176  -0.0763  0.6811
parameterPC   0.3444  0.1361   2.5312  0.0114   0.0777  0.6111 *
parameterTAG  -0.1048  0.1249  -0.8392  0.4013  -0.3497  0.1400
parameterTAGp  0.0121  0.1373   0.0884  0.9295  -0.2570  0.2813
parameterVLDL  0.4360  0.2363   1.8448  0.0651  -0.0272  0.8992 .

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

> res3 <- orchard::mod_results(databm_MR01, mod = "parameter", group = "Author")
> res3
  name      estimate     lowerCL     upperCL     lowerPR     upperPR
1  FAD -0.0124273942 -0.273969153  0.2491144 -1.0771652  1.0523104
2  HDL  0.0651326847 -0.291206330  0.4214717 -1.0267647  1.1570301
3  LDL  0.2899574625 -0.064703870  0.6446188 -0.8013936  1.3813085
4  PC   0.3319616606  0.006527174  0.6573961 -0.7502445  1.4141678
5  TAG  -0.1172771875 -0.366075936  0.1315216 -1.1789567  0.9444023
6  TAGp -0.0002824608 -0.304388870  0.3038239 -1.0762672  1.0757023
7  VLDL  0.4235608852 -0.012419266  0.8595410 -0.6968592  1.5439810
> p2 <- orchard::orchard_plot(res3, mod = "parameter", group = "Author", x1
> p2
> ggsave('liver composition_parameter_moderator.pdf', width = 4, height = 8, p2
~ |
```

additive category

```
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 211; method: REML)

  logLik   Deviance      AIC      BIC      AICC
-194.7161  389.4322  401.4322  421.4285  401.8522

Variance Components:

  estim    sqrt  nlevels fixed factor
sigma^2.1 0.2579  0.5079     26   no  Author
sigma^2.2 0.0478  0.2186    211   no     ID

Test for Residual Heterogeneity:
QE(df = 207) = 406.4009, p-val < .0001

Test of Moderators (coefficients 2:4):
QM(df = 3) = 1.7006, p-val = 0.6368

Model Results:

  estimate      se     zval    pval    ci.lb    ci.ub
intcpt       0.1747  0.2998  0.5828  0.5600 -0.4128  0.7622
categoryBuffalo 0.2744  0.6055  0.4531  0.6505 -0.9124  1.4612
categoryCattle -0.0723  0.2969 -0.2435  0.8077 -0.6543  0.5097
categorySheep -0.3597  0.3911 -0.9198  0.3577 -1.1263  0.4068

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

> res3 <- orchard::mod_results(databm_MR01, mod = "category", group = "Author")
> res3
  name  estimate lowerCL upperCL lowerPR upperPR
1 Beef  0.1747114 -0.4127996 0.7622224 -1.058010 1.407433
2 Buffalo 0.4490671 -0.5821052 1.4802394 -1.046844 1.944978
3 Cattle 0.1024166 -0.1511576 0.3559908 -1.010568 1.215401
4 Sheep -0.1850381 -0.6774311 0.3073550 -1.375368 1.005292
> p2 <- orchard::orchard_plot(res3, mod = "category", group = "Author", xlab = "Standa
> p2
```

sensitivity analysis

```
> ####sensitivity analysis
> result1=rma(SMD, vSMD, data=databm1, method="REML")
> result1

Random-Effects Model (k = 211; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.1356 (SE = 0.0303)
tau (square root of estimated tau^2 value):      0.3682
I^2 (total heterogeneity / total variability):   46.17%
H^2 (total variability / sampling variability):  1.86

Test for Heterogeneity:
Q(df = 210) = 417.0065, p-val < .0001

Model Results:

estimate      se    zval   pval   ci.lb   ci.ub
 0.1359  0.0393  3.4534  0.0006  0.0588  0.2130  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> ##conduct classical Egger's test regression analysis
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model:      weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -0.8140, df = 209, p = 0.4165
Limit Estimate (as sei -> 0):   b =  0.2378 (CI: 0.0042, 0.4714)
```

```
> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> ##conduct classical Egger's test regression analysis
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model:      weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -0.8140, df = 209, p = 0.4165
Limit Estimate (as sei -> 0):   b =  0.2378 (CI: 0.0042, 0.4714)

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the right side: 37 (SE = 9.5050)

Random-Effects Model (k = 248; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.2967 (SE = 0.0448)
tau (square root of estimated tau^2 value):       0.5447
I^2 (total heterogeneity / total variability):   63.83%
H^2 (total variability / sampling variability):  2.76

Test for Heterogeneity:
Q(df = 247) = 624.3958, p-val < .0001

Model Results:

estimate      se    zval   pval   ci.lb   ci.ub
 0.2929  0.0453  6.4607  <.0001  0.2041  0.3818  ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Immunity

Overall

```
> data11_MA <- rma.mv(y1 = SMD, V = VSMD, random = list(~1 | Author))
> summary(data11_MA)

Multivariate Meta-Analysis Model (k = 111; method: REML)

  logLik   Deviance      AIC      BIC      AICC
-149.4577  298.9155  304.9155  313.0169  305.1419

Variance Components:

            estim    sqrt  nvlvs  fixed factor
sigma^2.1  0.0726  0.2695     20     no  Author
sigma^2.2  0.4165  0.6454    107     no      ID

Test for Heterogeneity:
Q(df = 110) = 404.8266, p-val < .0001

Model Results:

estimate      se      zval     pval    ci.lb    ci.ub
-0.2904  0.1095  -2.6526  0.0080  -0.5050  -0.0758  **

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

> model_results <- orchaRd::mod_results(data11_MA, mod = "1", at =
> model_results
  name estimate    lowerCL      upperCL    lowerPR      upperPR
1 Intrcpt -0.2903995 -0.5049729 -0.07582618 -1.677898 1.097099
  ...
```

species as a moderator

```

Multivariate Meta-Analysis Model (k = 101; method: REML)

logLik Deviance      AIC      BIC      AICC
-128.4121  256.8243  264.8243  275.2047  265.2498

Variance Components:

          estim   sqrt  nvlvs fixed factor
sigma^2.1 0.1469  0.3833    18     no Author
sigma^2.2 0.4042  0.6357   101     no     ID

Test for Residual Heterogeneity:
QE(df = 99) = 335.8587, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 2.9674, p-val = 0.0850

Model Results:

           estimate      se     zval    pval    ci.lb    ci.ub
intrcpt     -0.1240  0.1633  -0.7593  0.4477  -0.4440  0.1961
speciesSurti -0.5241  0.3042  -1.7226  0.0850  -1.1204  0.0722  .

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

> res2 <- orchard::mod_results(databm_MRO, mod = "species", group = "Author")
> res2
  name  estimate  lowerCL  upperCL  lowerPR  upperPR
1 Holstein -0.1239804 -0.4440248  0.1960640 -1.613726 1.3657652
2 Surti    -0.6480664 -1.1512043 -0.1449285 -2.187567 0.8914339
> p1<- orchard::orchard_plot(res2, mod = "species", group = "Author", xlab =
> p1
> ggsave('immunity_species_moderator.pdf',width = 4,height = 8,p1)
>

```

parameter as a moderator

```
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 111; method: REML)

  LogLik Deviance      AIC      BIC      AICC
-139.9398 279.8796 297.8796 321.6791 299.7945

Variance Components:

    estim   sqrt  nlvls fixed factor
sigma^2.1 0.0811 0.2847     20    no Author
sigma^2.2 0.4278 0.6541    107    no     ID

Test for Residual Heterogeneity:
QE(df = 104) = 380.6610, p-val < .0001

Test of Moderators (coefficients 2:7):
QM(df = 6) = 8.1770, p-val = 0.2254

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub
intrcpt     -0.3202  0.1611  -1.9881  0.0468  -0.6359  -0.0045 *
parameterIgG  0.0829  0.4047   0.2048  0.8377  -0.7104  0.8762
parameterLBP  -0.2693  0.3055  -0.8814  0.3781  -0.8681  0.3295
parameterLeukocyte  0.4819  0.3681   1.3090  0.1905  -0.2396  1.2035
parametersAA  -0.2517  0.3943  -0.6384  0.5232  -1.0246  0.5211
parametersCS  0.5161  0.2973   1.7361  0.0825  -0.0665  1.0988
parameterTNF $\alpha$  -0.2965  0.3128  -0.9479  0.3432  -0.9095  0.3165

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

> res3 <- orchard::mod_results(databm_MR01, mod = "parameter", group = "Author")
> res3
  name   estimate    lowerCL    upperCL    lowerPR    upperPR
1 Haptoglobin -0.3202060 -0.6358815 -0.004530535 -1.753533 1.1131208
2 IgG -0.2373243 -1.0447099  0.570061342 -1.851835 1.3771869
3 LBP -0.5894866 -1.1327995 -0.046173634 -2.089475 0.9105014
4 Leukocyte  0.1617061 -0.4879024  0.811314641 -1.379970 1.7033825
5 SAA -0.5719538 -1.2798456  0.135937870 -2.139080 0.9951727
6 SCS 0.1958996 -0.3476989  0.739498078 -1.304192 1.6959910
7 TNF $\alpha$  -0.6166913 -1.1611392 -0.072243371 -2.117091 0.8837081
> p2 <- orchard::orchard_plot(res3, mod = "parameter", group = "Author", xlab = "Standardise"
> p2
> ggsave('immunity_parameter_moderator.pdf', width = 4, height = 8, p2)
> |
```

additive category

```
> summary(databm_MR01)

Multivariate Meta-Analysis Model (k = 111; method: REML)

  logLik Deviance      AIC      BIC      AICC
-146.6967 293.3934 301.3934 312.1588 301.7780

Variance Components:

            estim   sqrt  nvlvs fixed factor
sigma^2.1  0.1841 0.4290    20     no Author
sigma^2.2  0.3850 0.6205   107     no      ID

Test for Residual Heterogeneity:
QE(df = 109) = 404.6908, p-val < .0001

Test of Moderators (coefficient 2):
QM(df = 1) = 3.6920, p-val = 0.0547

Model Results:

            estimate      se     zval    pval    ci.lb    ci.ub
intrcpt     -0.7899  0.2623  -3.0111  0.0026  -1.3040  -0.2757  **
categoryCattle  0.5852  0.3046   1.9215  0.0547  -0.0117  1.1822  .
```

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

> res3 <- orchard::mod_results(databm_MR01, mod = "category", group = "Author"
> res3
 name estimate lowerCL upperCL lowerPR upperPR
1 Buffalo -0.7898805 -1.3040267 -0.2757343 -2.355241 0.7754797
2 Cattle -0.2046546 -0.5214487 0.1121396 -1.716728 1.3074184
> p2 <- orchard::orchard_plot(res3, mod = "category", group = "Author", xlab :
> p2
> ggsave('immunity_category_moderator.pdf', width = 10, height = 12, p2)
> ggsave('immunity_category_moderator.pdf', width = 4, height = 8, p2)
`|
```

## sensitivity analysis

```
> result1=rma(SMD, vSMD, data=databm1, method="REML")
> result1

Random-Effects Model (k = 111; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5514 (SE = 0.0974)
tau (square root of estimated tau^2 value): 0.7426
I^2 (total heterogeneity / total variability): 78.89%
H^2 (total variability / sampling variability): 4.74

Test for Heterogeneity:
Q(df = 110) = 404.8266, p-val < .0001

Model Results:

estimate se zval pval ci.lb ci.ub
-0.2273 0.0809 -2.8106 0.0049 -0.3858 -0.0688 **

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

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the right side: 0 (SE = 4.7364)

Random-Effects Model (k = 111; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0.5514 (SE = 0.0974)
tau (square root of estimated tau^2 value): 0.7426
I^2 (total heterogeneity / total variability): 78.89%
H^2 (total variability / sampling variability): 4.74

Test for Heterogeneity:
Q(df = 110) = 404.8266, p-val < .0001

Model Results:

estimate se zval pval ci.lb ci.ub
-0.2273 0.0809 -2.8106 0.0049 -0.3858 -0.0688 **

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

# Gene expression

## Overall

```

> summary(dataim1_MA)

Multivariate Meta-Analysis Model (k = 345; method: REML)

 logLik deviance AIC BIC AICC
-126.9994 253.9989 259.9989 271.5208 260.0695

Variance Components:

 estim sqrt nlvls fixed factor
sigma^2.1 0.0585 0.2418 7 no Author
sigma^2.2 0.0000 0.0000 345 no ID

Test for Heterogeneity:
Q(df = 344) = 188.9716, p-val = 1.0000

Model Results:

estimate se zval pval ci.lb ci.ub
-0.0448 0.1003 -0.4471 0.6548 -0.2413 0.1517

signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> model_results <- orchardD::mod_results(dataim1_MA, mod = "1", at
> model_results
 name estimate lowerCL upperCL lowerPR upperPR
1 Intrcpt -0.04482693 -0.2413445 0.1516907 -0.5579417 0.4682879
> orchardD::orchard_plot(dataim1_MA, mod = "1", group = "Author",
"ID", "S.E.", "Z-value", "P-value", "CI-LB", "CI-UB")

```

## Species

```
> summary(databm_MRO)

Multivariate Meta-Analysis Model (k = 345; method: REML)

 logLik Deviance AIC BIC AICC
-126.3340 252.6680 260.6680 276.0190 260.7864

Variance Components:

 estim sqrt nlvls fixed factor
sigma^2.1 0.0705 0.2656 7 no Author
sigma^2.2 0.0000 0.0000 345 no ID

Test for Residual Heterogeneity:
QE(df = 343) = 188.6161, p-val = 1.0000

Test of Moderators (coefficient 2):
QM(df = 1) = 0.0447, p-val = 0.8325

Model Results:

 estimate se zval pval ci.lb ci.ub
intrcpt -0.0349 0.1165 -0.2997 0.7644 -0.2631 0.1933
speciessaanen -0.0685 0.3240 -0.2115 0.8325 -0.7036 0.5666

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

> res2 <- orchard::mod_results(databm_MRO, mod = "species", group =
> res2
 name estimate lowerCL upperCL lowerPR upperPR
1 Holstein -0.03490341 -0.2631486 0.1933417 -0.6033131 0.5335063
2 Saanen -0.10343279 -0.6961233 0.4892577 -0.8922774 0.6854118
> p1<- orchard::orchard_plot(res2, mod = "species", group = "Author")
```

## parameter as a moderator

```
Multivariate Meta-Analysis Model (k = 345; method: REML)

 logLik Deviance AIC BIC AICC
-119.5053 239.0106 261.0106 302.9988 261.8254

Variance Components:

 estim sqrt nvlvs fixed factor
sigma^2.1 0.0373 0.1931 7 no Author
sigma^2.2 0.0000 0.0000 345 no ID

Test for Residual Heterogeneity:
QE(df = 336) = 168.9219, p-val = 1.0000

Test of Moderators (coefficients 2:9):
QM(df = 8) = 12.1160, p-val = 0.1461

Model Results:

 estimate se zval pval ci.lb ci.ut
intrcpt -0.0772 0.1572 -0.4910 0.6234 -0.3854 0.2310
parameterApoptosis 0.0448 0.1831 0.2448 0.8066 -0.3141 0.4038
parameterCarbohydrate Metabolism 0.1061 0.2367 0.4485 0.6538 -0.3577 0.5700
parameterCholine Metabolism 0.1811 0.2224 0.8142 0.4155 -0.2548 0.6171
parameterEnergy Metabolism -0.1225 0.1672 -0.7325 0.4639 -0.4503 0.2053
parameterImmunity -0.0661 0.1551 -0.4263 0.6699 -0.3701 0.2379
parameterLipid Metabolism 0.1371 0.1426 0.9616 0.3363 -0.1424 0.4166
parameterMethylation 0.1711 0.1510 1.1332 0.2571 -0.1248 0.4670
parameterOxidative Stress -0.1233 0.1590 -0.7758 0.4379 -0.4349 0.1883

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

> res3 <- orchaRd::mod_results(databm_MR01, mod = "parameter", group = "Author")
> res3
 name estimate lowerCL upperCL lowerPR upperPR
1 Amino Acid Metabolism -0.07721187 -0.3854108 0.23098702 -0.5652905 0.4108667
2 Apoptosis -0.03238409 -0.3138628 0.24909462 -0.5040455 0.4392773
3 Carbohydrate Metabolism 0.02892656 -0.3686174 0.42647048 -0.5199590 0.5778121
4 Choline Metabolism 0.10389956 -0.3052062 0.51300535 -0.4534170 0.6612161
5 Energy Metabolism -0.19970385 -0.4325845 0.03317680 -0.6440771 0.2446694
6 Immunity -0.14332633 -0.3372517 0.05059904 -0.5685806 0.2819280
7 Lipid Metabolism 0.05989959 -0.1439556 0.26375482 -0.3699738 0.4897730
8 Methylation 0.09386282 -0.1279858 0.31571147 -0.3448296 0.5325552
9 Oxidative Stress -0.20055053 -0.4417090 0.04060794 -0.6493173 0.2482162
```

## 敏感性分析

```
> ###sensitivity analysis
> result1=rma(SMD, VSMD, data=dataim1, method="REML")
> result1

Random-Effects Model (k = 345; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0 (SE = 0.0153)
tau (square root of estimated tau^2 value): 0
I^2 (total heterogeneity / total variability): 0.00%
H^2 (total variability / sampling variability): 1.00

Test for Heterogeneity:
Q(df = 344) = 188.9716, p-val = 1.0000

Model Results:

estimate se zval pval ci.lb ci.ub
-0.0185 0.0243 -0.7590 0.4479 -0.0662 0.0292

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

```

> inf<-influence(result1)
> plot(inf)#red points indicates outliers
> ##conduct classical Egger's test regression analysis
> regtest(result1, model="lm")

Regression Test for Funnel Plot Asymmetry

Model: weighted regression with multiplicative dispersion
Predictor: standard error

Test for Funnel Plot Asymmetry: t = -0.6380, df = 343, p = 0.5239
Limit Estimate (as sei -> 0): b = 0.1039 (CI: -0.2751, 0.4830)

> ## conduct trim and fill analysis
> res.tf <- trimfill(result1)
> res.tf

Estimated number of missing studies on the right side: 0 (SE = 10.5593)

Random-Effects Model (k = 345; tau^2 estimator: REML)

tau^2 (estimated amount of total heterogeneity): 0 (SE = 0.0153)
tau (square root of estimated tau^2 value): 0
I^2 (total heterogeneity / total variability): 0.00%
H^2 (total variability / sampling variability): 1.00

Test for Heterogeneity:
Q(df = 344) = 188.9716, p-val = 1.0000

Model Results:

estimate se zval pval ci.lb ci.ub
-0.0185 0.0243 -0.7590 0.4479 -0.0662 0.0292

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

> funnel(res.tf)
>

```