

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	nlvls	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	**

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_m1(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	nlvls	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_MK01)
```

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	nlvls	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
parameterwithr 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	withr 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 <- rma.mv(yi ~ 0, x = 0, mod = "category", random = "ID", data = datag_MR01)
> 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)
> 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      nlvls      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 = "Stand: ",
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_m1(datab1_MA)
> I2
      I2_Total I2_Author      I2_ID
79.01697 21.17245 57.84452
> pp<-orchard::orchard_plot(model_results, mod = "1", xlab = "Stand: ",
", round(I2[1],2), "%\\%\\\"", color = "black", parse = TRUE, size = 12,
+ scale_colour_manual(values = "#B1FCA3")
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

前 20

```
> 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 ' ' 1

> res3 <- orchard::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 <- orchard::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	nlvls	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
> ggsave('blood_moderator_parameter_moderator_E14.pdf' width = 4 height = 8 n2)
```

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	nlvls	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 = "Aut")
> 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", x1)
> p2
> |
```

sensitivity analysis

```
> ##sensitivity analysis
> result1=rma(SMD, vSMD, data=datam1, 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 se1 -> 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
> datapl1<-escalc(measure = "SMD", nli = treat_n, sdli = treat_sd,
data = datapp)
> datapl1_MA <- rma.mv(yi = SMD, V = vSMD, random = list(~1 | Author
> summary(datapl1_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	nlvls	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(datapl1_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(datapl1_MA, mod = "1", group = "Author", xla
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_m1(datapl1_MA)
> I2
      I2_Total I2_Author      I2_ID
79.54522    44.96049    34.58473
```

Species

```
vr[,data = datapij]
> datapij_MRO <- rma.mv(yi = SMD, V = VSMD, mods = ~species, random = list(~1 | Au
> summary(datapij_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(datapij_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	nlvls	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", xlab = "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	nlvls	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"
. _2
```

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",transform = "none", twig.size = 0.5, trunk.size = 1)
> # use i2_sn function to obtain the total I^2
> I2 <- orchaRd::i2_m1(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_plot(model_results, mod = "1", xlab = "Standardised mean difference", ylab = "I-squared", main = "Forest plot", legend = TRUE)
> 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	nlvls	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	nlvls	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	nlvls	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 x A	0.4069	0.2492	1.6327	0.1025	-0.0816	0.8954
speciesH x 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 x A
speciesH x 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 x 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 x A	0.55627227	0.12958697	0.9829576	0.04756306	1.0649815
4	H x 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	nlvls	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
parametersF	-0.2376	0.2915	-0.8152	0.4149	-0.8090	0.3337
parametersW	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
parametersF
parametersW
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", xlab = "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

```

> ##sensivity 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; tau² estimator: REML)

tau² (estimated amount of total heterogeneity): 0.0473 (SE = 0.0251)
 tau (square root of estimated tau² value): 0.2176
 I² (total heterogeneity / total variability): 18.40%
 H² (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	nlvls	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 <- orchard::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
> orchard::orchard_plot(datam1_MA, mod = "1", group = "Author", x
> # use i2_sn function to obtain the total I^2
> I2 <- orchard::i2_m1(datam1_MA)
> pp<-orchard::orchard_plot(model_results, mod = "1", xlab = "Sta
", round(I2[1],2), "%\\%", color = "black", parse = TRUE, size
+   scale_colour_manual(values = "#78D3AC")
scale for fill 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  nlvls  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 = "Aut
> 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  nlvls  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
intrcpt          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=datam1, 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 $se_i \rightarrow 0$): $b = 0.2378$ (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 ($k = 248$; τ^2 estimator: REML)

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

Test for Heterogeneity:
 $Q(df = 247) = 624.3958$, $p\text{-val} < .0001$

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  nlvls  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
1 orchard::orchard::mod_results(data11_MA, mod = "1", at = "Author" ...
```

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	nlvls	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
speciesurti	-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_MR0, 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 .
parameterTNFα  -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      TNFα -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  nlvls  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 = "Category")
> 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=datam1, 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 <- orchard::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
> orchard::orchard_plot(dataim1_MA, mod = "1", group = "Author",
  "use_df = FALSE" to check the exact fit
```

Species

```

> summary(databm_MR0)

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_MR0, 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
> pl<- 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	nlvls	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.ub
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 $se_i \rightarrow 0$): $b = 0.1039$ (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 ($k = 345$; τ^2 estimator: REML)

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

Test for Heterogeneity:
 $Q(df = 344) = 188.9716$, $p\text{-val} = 1.0000$

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)
> |

```