

Investigating the impact of the COVID-19 pandemic on the gender productivity gap in academia

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Install and load packages

```
## install packages like so
install.packages("pacman")
rm(list = ls())
devtools::install_github("daniellnoble/orchaRd", force = TRUE)
pacman::p_load(devtools, tidyverse, metafor, patchwork, R.rsp,
  orchaRd, emmeans, ape, phytools, flextable)

## Loading required package: Matrix
## Loading required package: metadat
##
## Loading the 'metafor' package (version 3.8-1). For an
## introduction to the package please type: help(metafor)
## Loading required package: usethis
## -- Attaching packages ----- tidyverse 1.3.2 --
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## v purrr   0.3.5
## -- Conflicts ----- tidyverse_conflicts() --
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## x tidyr::pack()   masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
##
## Loading the 'orchaRd' package (version 2.0). For an
## introduction and vignette to the package please see: https://daniellnoble.github.io/orchaRd/
```

Load data

```
##
##
##
## Standardised mean difference (binary proportions)
##
## Standardised mean difference (chi-square)
##
## Standardised mean difference (f-test, unequal sample size)
##
```

```

##          Standardised mean difference (from binary proportions)
##                                     3
##          Standardised mean difference (means and sds)
##                                     6
##          Standardised mean difference (means and ses)
##                                     12
## Standardised mean difference (t-test p-value unequal sample sizes)
##                                     1
##          Standardised mean difference (two by two frequency table)
##                                     7
##          Standardised mean difference (two by two table)
##                                     70

##
## Measured Self-reported
##          92          23

##
## Biological sciences          Medicine          Multidisciplinary          Social sciences
##          17          44          15          19
##          TEMCP
##          20

##
## Other Publications Submissions
##          18          48          49

##
##          Burn-out          General productivity
##          1          11
##          Job loss          Preprints
##          1          20
##          Projects          Publications
##          1          48
##          Submissions Submissions (self-reported)
##          23          5
##          Work hours          Working papers
##          4          1

##
##
##          Ability to submit papers
##          1
##          Academic job loss
##          1
##          Academic productivity
##          1
##          Any authorship
##          13
##          Binary whether loss of research productivity
##          1
##          Corresponding authorship
##          12
##          Disruption from having to work from home
##          1
##          Effect of COVID-19 pandemic on work from home
##          1
##          First authorship
##          45
##          Hours of research per day

```

##		1
##	Last authorship	
##		17
##	Middle authorship	
##		4
##	Number of new research projects	
##		1
##	Pandemic effect on academic productivity	
##		1
##	Research hours per week	
##		1
##	Research productivity	
##		1
##	Research productivity decrease following COVID-19 relative to other gender	
##		1
##	Self reported ability to submit/complete work	
##		1
##	Self reproted adverse effect of pandemics on work perfomance	
##		1
##	self-reported loss in productivity (unability to write/research at home compared to pre-pandemic level)	
##		1
##	Self-reported productivity change on likert scale	
##		1
##	Sole authorship	
##		4
##	Whether the pandemic created low productivity (Y/N)	
##		1
##	Work productivity from home	
##		1
##	Work-productivity during pandemics: working hours, percentage of time spent on research and education	
##		1
##	Work-related burnout	
##		1

Hypothesis 1: During pandemic conditions the gender gap in academic productivity has increased.

Prediction 1a: The pandemic has increased the gender gap in productivity (as indicated by an overall negative effect size).

Looks like an overall negative effect: during pandemic conditions the gender gap in academic productivity has increased.

```
# Hierarchical mixed effect meta-analysis with all papers.
# Studies with multiple effect sizes are controlled for.
m <- rma.mv(yi, vi, random = ~1 | ID.article/ID.observation,
  data = all_data)
m

##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0022  0.0468    50    no      ID.article
## sigma^2.2  0.0136  0.1165   115    no  ID.article/ID.observation
##
## Test for Heterogeneity:
## Q(df = 114) = 4789.5722, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0700  0.0163  -4.2910  <.0001  -0.1020  -0.0380  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Forest plot produced for visual representation.
forest(m, slab = all_data$Author, xlim = c(-2, 2), ylim = c(-1,
  120), digits = 2, xlab = "Raw proportion", mlab = "Overall effect (46)")
text(-1, 122, "Author(s) and Year", pos = 2, font = 2, cex = 0.8)
text(2, 122, "Effect size [95% CI]", pos = 2, font = 2, cex = 0.8)
```

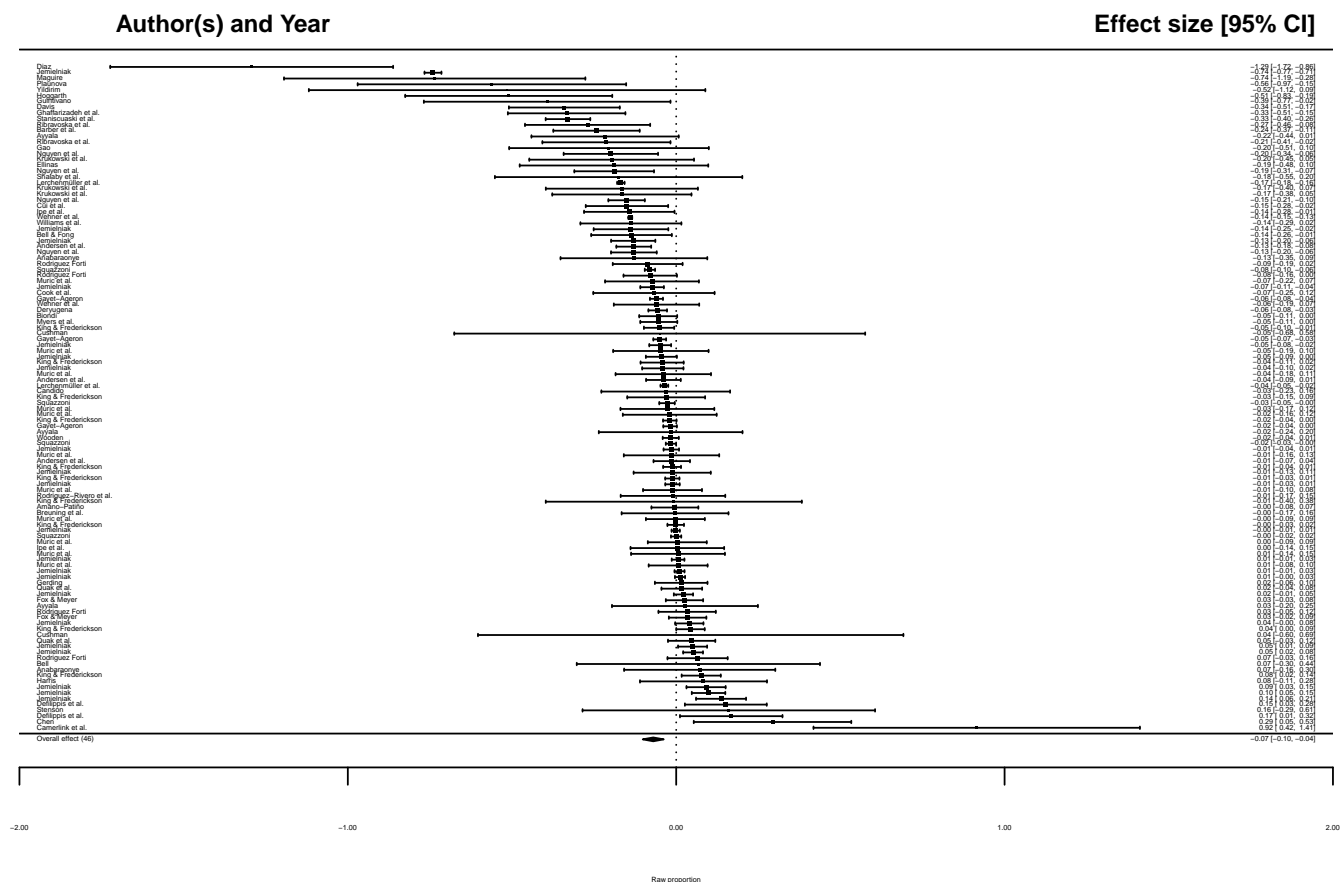
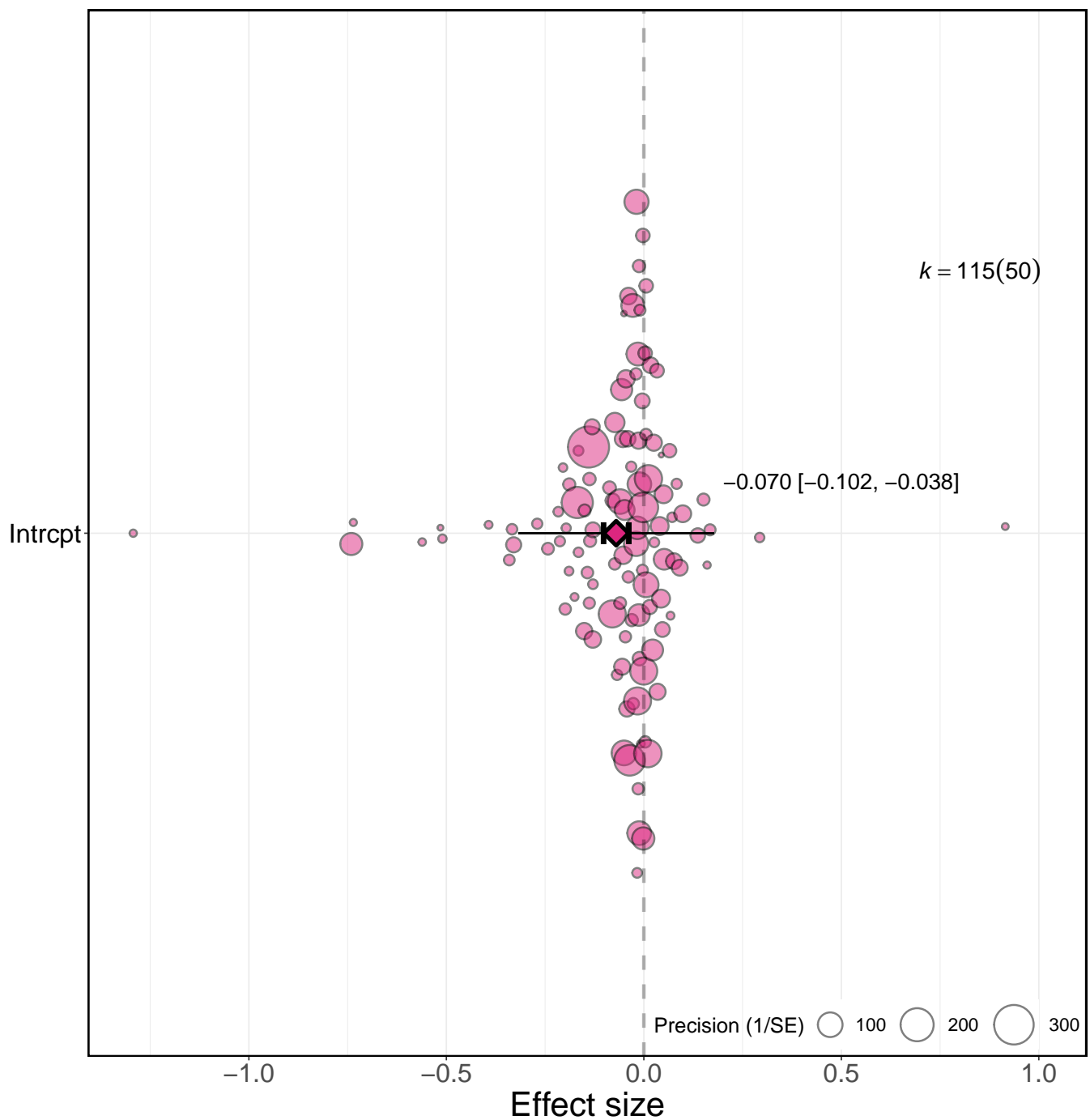


Figure 1

```
my_orchard(m, mod = "1", alpha = 0.5, data = all_data, whisker = 0.025,
  group = "Article.ID", xlab = "Effect size") + annotate("text",
  size = 6, y = 0.5, x = 1.06, label = paste("-0.070 [-0.102, -0.038]")) +
  scale_fill_manual(values = c("#DC267F"))
```

```
## Warning in k == TRUE && g == TRUE && k.pos == "right": 'length(x) = 2 > 1' in
## coercion to 'logical(1)'
```



```
ggsave("figure1.png", width = 10, height = 10, dpi = 300)
```

Prediction 1b: Though studies can measure the type of research productivity as by individual surveys, numbers of submissions and numbers of publications, this does not influence the gender gap increase observed during the pandemic.

```
all_data$Broad.productivity.measure[all_data$Broad.productivity.measure ==  
  "Other"] <- "Survey"
```

```
tapply(all_data$ID.observation, all_data$Broad.productivity.measure,  
  length)
```

	Publications	Submissions	Survey
##	48	49	18

```
all_data$Broad.productivity.measure.reordered <- factor(all_data$Broad.productivity.measure,
  c("Publications", "Submissions", "Survey"))
```

```
m.area <- rma.mv(yi, vi, mods = ~Broad.productivity.measure.reordered,
  random = ~1 | ID.article/ID.observation, data = all_data)
```

```
m.area
```

```
##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    50    no      ID.article
## sigma^2.2  0.0142  0.1190   115    no ID.article/ID.observation
##
## Test for Residual Heterogeneity:
## QE(df = 112) = 4751.7560, p-val < .0001
##
## Test of Moderators (coefficients 2:3):
## QM(df = 2) = 12.3488, p-val = 0.0021
##
## Model Results:
##
##              estimate      se      zval
## intrcpt          -0.0458  0.0186  -2.4599
## Broad.productivity.measure.reorderedSubmissions    0.0071  0.0268   0.2664
## Broad.productivity.measure.reorderedSurvey         -0.1469  0.0448  -3.2777
##              pval      ci.lb      ci.ub
## intrcpt          0.0139  -0.0822  -0.0093  *
## Broad.productivity.measure.reorderedSubmissions  0.7899  -0.0453   0.0596
## Broad.productivity.measure.reorderedSurvey       0.0010  -0.2347  -0.0590  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
m.area1 <- rma.mv(yi, vi, mods = ~Broad.productivity.measure.reordered -
  1, random = ~1 | ID.article/ID.observation, data = all_data)
```

```
m.area1
```

```
##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    50    no      ID.article
## sigma^2.2  0.0142  0.1190   115    no ID.article/ID.observation
##
## Test for Residual Heterogeneity:
## QE(df = 112) = 4751.7560, p-val < .0001
##
## Test of Moderators (coefficients 1:3):
## QM(df = 3) = 32.4292, p-val < .0001
##
## Model Results:
##
```

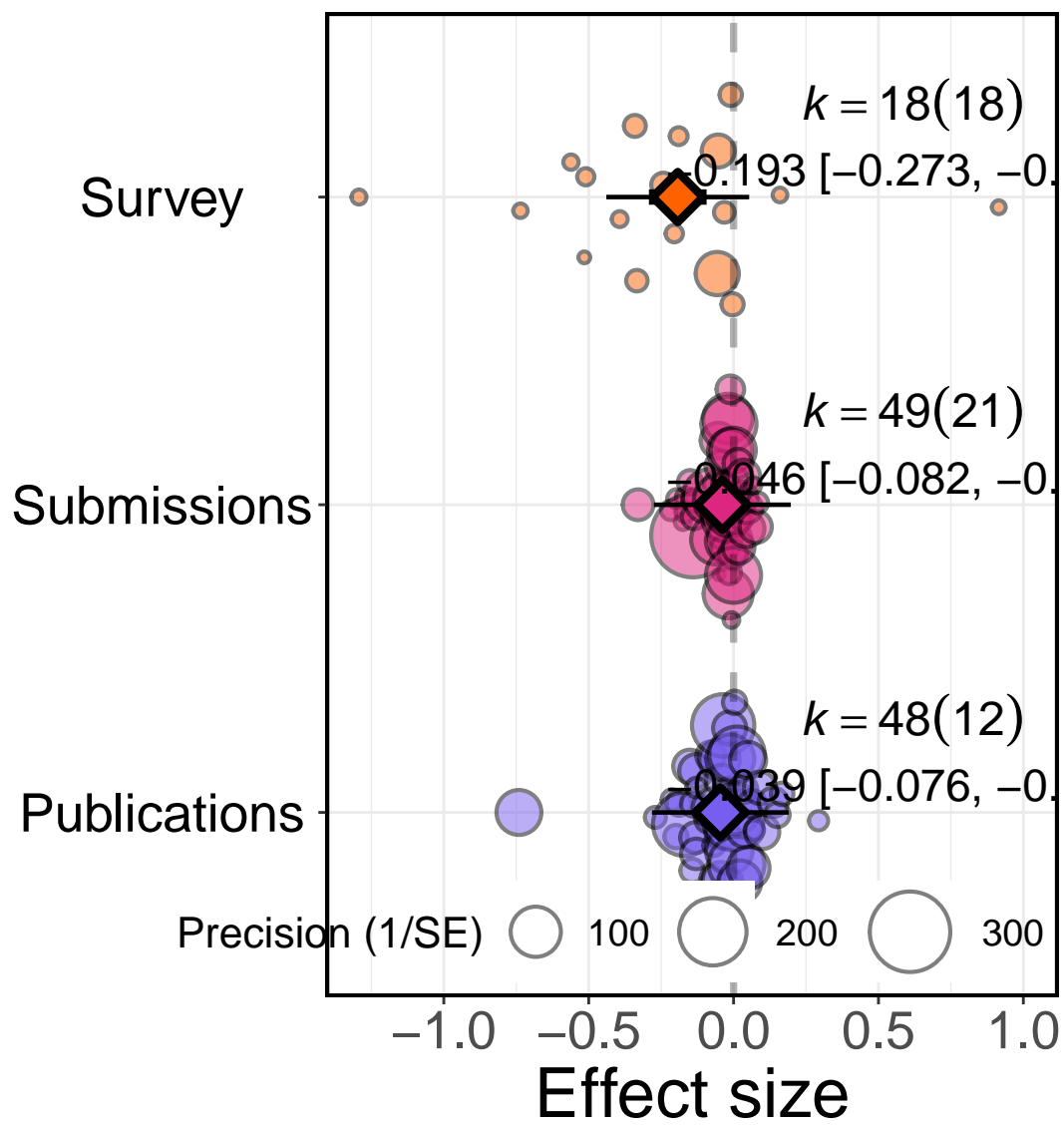
```
##
## Broad.productivity.measure.reorderedPublications    estimate    se    zval
## Broad.productivity.measure.reorderedSubmissions     -0.0386    0.0192  -2.0107
## Broad.productivity.measure.reorderedSurvey           -0.1926    0.0408  -4.7260
##
##              pval    ci.lb    ci.ub
## Broad.productivity.measure.reorderedPublications    0.0139   -0.0822  -0.0093    *
## Broad.productivity.measure.reorderedSubmissions     0.0444   -0.0763  -0.0010    *
## Broad.productivity.measure.reorderedSurvey           <.0001   -0.2725  -0.1128   ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 2

```
p1 <- my.orchard(m.area1, mod = "Broad.productivity.measure.reordered",
  group = "Article.ID", data = all_data, xlab = "Effect size",
  whisker = 0.05, transfm = "none") + annotate("text", size = 6,
  y = 0.6, x = 3.09, label = paste("-0.193 [-0.273, -0.113]")) +
  annotate("text", size = 6, y = 0.6, x = 2.09, label = paste("-0.046 [-0.082, -0.009]")) +
  annotate("text", size = 6, y = 0.6, x = 1.09, label = paste("-0.039 [-0.076, -0.001]")) +
  scale_fill_manual(values = c("#785EF0", "#DC267F", "#FE6100"))

## Warning in k == TRUE && g == TRUE && k.pos == "right": 'length(x) = 2 > 1' in
## coercion to 'logical(1)'

p1
```

```
ggsave("figure2.png")
```

```
## Saving 6 x 6 in image
```

Hypothesis 2: During pandemic conditions the gender gap in academic productivity has increased differentially across research fields.

Prediction 2a: The pandemic has increased the gender gap in academic productivity more in fields that already had a previously greater gender gap because these lacked gender-equitable support measures to prevent female academics experiencing research production setbacks.

```
all_data$Broad.research.field.reordered <- factor(all_data$Broad.research.field,
  c("TEMCP", "Biological sciences", "Medicine", "Multidisciplinary",
    "Social sciences"))

levels(all_data$Broad.research.field.reordered) <- gsub(" ",
  "\n", levels(all_data$Broad.research.field.reordered))

research_field <- metafor::rma.mv(yi = yi, V = vi, mods = ~Broad.research.field.reordered,
  random = list(~1 | Article.ID, ~1 | ID), data = all_data)
summary(research_field)

##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  44.8688  -89.7376  -75.7376  -56.8342  -74.6395
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000     50     no  Article.ID
## sigma^2.2  0.0135  0.1162    115     no           ID
##
## Test for Residual Heterogeneity:
## QE(df = 110) = 3950.1936, p-val < .0001
##
## Test of Moderators (coefficients 2:5):
## QM(df = 4) = 12.1382, p-val = 0.0164
##
## Model Results:
##
##                                     estimate      se      zval
## intrcpt                           -0.0108  0.0284  -0.3781
## Broad.research.field.reorderedBiological\nsciences    0.0171  0.0416   0.4099
## Broad.research.field.reorderedMedicine                -0.0612  0.0354  -1.7273
## Broad.research.field.reorderedMultidisciplinary        -0.1097  0.0449  -2.4452
## Broad.research.field.reorderedSocial\nsciences        -0.0816  0.0420  -1.9422
##                                     pval      ci.lb      ci.ub
## intrcpt                           0.7054  -0.0665   0.0450
## Broad.research.field.reorderedBiological\nsciences    0.6819  -0.0645   0.0986
## Broad.research.field.reorderedMedicine                0.0841  -0.1306   0.0082  .
## Broad.research.field.reorderedMultidisciplinary        0.0145  -0.1976  -0.0218  *
## Broad.research.field.reorderedSocial\nsciences        0.0521  -0.1640   0.0007  .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

research_field1 <- metafor::rma.mv(yi = yi, V = vi, mods = ~Broad.research.field.reordered -
  1, random = list(~1 | Article.ID, ~1 | ID), data = all_data)

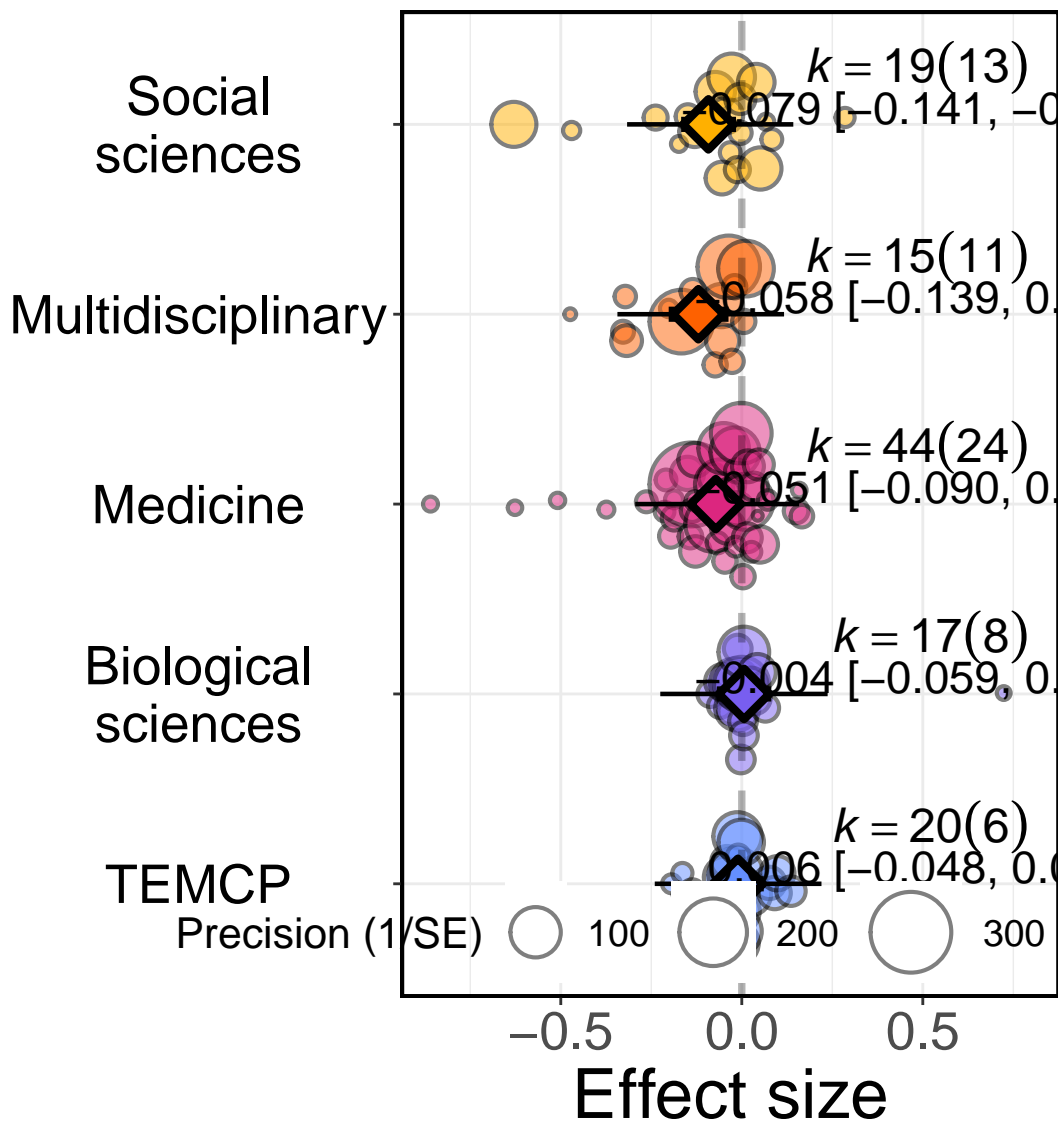
summary(research_field1)
```

```
##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  44.8688  -89.7376  -75.7376  -56.8342  -74.6395
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    50    no  Article.ID
## sigma^2.2  0.0135  0.1162   115    no           ID
##
## Test for Residual Heterogeneity:
## QE(df = 110) = 3950.1936, p-val < .0001
##
## Test of Moderators (coefficients 1:5):
## QM(df = 5) = 32.8003, p-val < .0001
##
## Model Results:
##
##                                     estimate      se      zval
## Broad.research.field.reorderedTEMCP      -0.0108  0.0284  -0.3781
## Broad.research.field.reorderedBiological\  0.0063  0.0304   0.2076
## Broad.research.field.reorderedMedicine    -0.0719  0.0211  -3.4112
## Broad.research.field.reorderedMultidisciplinary -0.1204  0.0347  -3.4727
## Broad.research.field.reorderedSocial\    -0.0924  0.0309  -2.9864
## Broad.research.field.reorderedTEMCP      0.7054 -0.0665   0.0450
## Broad.research.field.reorderedBiological\ 0.8356 -0.0532   0.0658
## Broad.research.field.reorderedMedicine    0.0006 -0.1132  -0.0306
## Broad.research.field.reorderedMultidisciplinary 0.0005 -0.1884  -0.0525
## Broad.research.field.reorderedSocial\    0.0028 -0.1530  -0.0317
##
##                                     pval      ci.lb      ci.ub
## Broad.research.field.reorderedTEMCP      0.7054 -0.0665   0.0450
## Broad.research.field.reorderedBiological\ 0.8356 -0.0532   0.0658
## Broad.research.field.reorderedMedicine    0.0006 -0.1132  -0.0306
## Broad.research.field.reorderedMultidisciplinary 0.0005 -0.1884  -0.0525
## Broad.research.field.reorderedSocial\    0.0028 -0.1530  -0.0317
##
## Broad.research.field.reorderedTEMCP
## Broad.research.field.reorderedBiological\nsciences
## Broad.research.field.reorderedMedicine      ***
## Broad.research.field.reorderedMultidisciplinary ***
## Broad.research.field.reorderedSocial\nsciences **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 3

```
my.orchard(research_field1, mod = "Broad.research.field.reordered",
  group = "Article.ID", data = all_data, whisker = 0.08, xlab = "Effect size",
  alpha = 0.5, transfm = "tanh", cb = FALSE) + annotate("text",
  size = 6, y = 0.5, x = 5.09, label = paste("-0.079 [-0.141, -0.018]")) +
  annotate("text", size = 6, y = 0.5, x = 4.09, label = paste("-0.058 [-0.139, 0.023]")) +
  annotate("text", size = 6, y = 0.5, x = 3.09, label = paste("-0.051 [-0.090, 0.012]")) +
  annotate("text", size = 6, y = 0.5, x = 2.09, label = paste("-0.004 [-0.059, 0.050]")) +
  annotate("text", size = 6, y = 0.5, x = 1.09, label = paste("0.006 [-0.048, 0.060]")) +
  scale_fill_manual(values = c("#648FFF", "#785EF0", "#DC267F",
    "#FE6100", "#FFB000"))
```

```
## Warning in k == TRUE && g == TRUE && k.pos == "right": 'length(x) = 2 > 1' in
## coercion to 'logical(1)'
```



```
ggsave("figure3.png", width = 10, height = 10, dpi = 300)
```

Prediction 2b: We predict the pandemic has increased the gender gap more for research fields of a given authorship position that already had a previously greater gender gap because less support may have been available to women to balance the effects of the pandemic.

```
all_data$nwomenprepandemic <- round(as.numeric(all_data$X..women.authors.pre.pandemic) *
  as.numeric(all_data$n.pre.pandemic), digits = 0)
```

```
## Warning: NAs introduced by coercion
```

```
## Warning: NAs introduced by coercion
```

```
all_data$nmnenprepandemic <- round(as.numeric(all_data$n.pre.pandemic) -
  as.numeric(all_data$nwomenprepandemic), digits = 0)
```

```
## Warning: NAs introduced by coercion
```

```
all_data$nwomenduringpandemic <- round(as.numeric(all_data$X..women.authors.during.pandemic) *
  as.numeric(all_data$n.during.pandemic), digits = 0)
```

```
## Warning: NAs introduced by coercion
```

```
## Warning: NAs introduced by coercion
all_data$nmenduringpandemic <- round(as.numeric(all_data$n.during.pandemic) -
  as.numeric(all_data$nwomenduringpandemic), digits = 0)

## Warning: NAs introduced by coercion
previous_bias <- metafor::rma.mv(yi = yi, V = vi, mods = ~cbind(nmenprepandemic/nwomenprepandemic),
  random = list(~1 | Article.ID, ~1 | ID), data = subset(all_data,
    all_data$Self.reported.or.measured == "Measured"))

## Warning: Rows with NAs omitted from model fitting.
# Model suggests that contrary to our prediction, the
# pandemic has increased the gender gap more for research
# fields of a given authorship position that were
# previously less biased.
summary(previous_bias)

##
## Multivariate Meta-Analysis Model (k = 84; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
##    59.7103   -119.4207   -111.4207  -101.7938  -110.9012
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000    25    no  Article.ID
## sigma^2.2  0.0110  0.1051    84    no          ID
##
## Test for Residual Heterogeneity:
## QE(df = 82) = 3373.8831, p-val < .0001
##
## Test of Moderators (coefficient 2):
## QM(df = 1) = 11.0156, p-val = 0.0009
##
## Model Results:
##
##              estimate      se      zval      pval
## intrcpt          -0.1232  0.0301  -4.0981  <.0001
## cbind(nmenprepandemic/nwomenprepandemic)  0.0389  0.0117   3.3190  0.0009
##              ci.lb    ci.ub
## intrcpt          -0.1820  -0.0643  ***
## cbind(nmenprepandemic/nwomenprepandemic)  0.0159   0.0619  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

measured_data$X..women.authors.pre.pandemic <- as.numeric(measured_data$X..women.authors.pre.pandemic)

## Warning: NAs introduced by coercion
measured_data$X..women.authors.during.pandemic <- as.numeric(measured_data$X..women.authors.during.pandemic)

## Warning: NAs introduced by coercion
measured_data <- subset(measured_data, !is.na(measured_data$X..women.authors.pre.pandemic))
measured_data <- subset(measured_data, !is.na(measured_data$X..women.authors.during.pandemic))
socialsciences <- subset(measured_data, measured_data$Broad.research.field ==
  "Social sciences")
```

```

medicine <- subset(measured_data, measured_data$Broad.research.field ==
  "Medicine")
multi <- subset(measured_data, measured_data$Broad.research.field ==
  "Multidisciplinary")
temcp <- subset(measured_data, measured_data$Broad.research.field ==
  "TEMCP technology, engineering, mathematic, chemistry and physics")
bio <- subset(measured_data, measured_data$Broad.research.field ==
  "Biological sciences")

socialsciences$X..women.authors.pre.pandemic <- as.numeric(socialsciences$X..women.authors.pre.pandemic)
socialsciences$X..women.authors.during.pandemic <- as.numeric(socialsciences$X..women.authors.during.pandemic)
mean((socialsciences$X..women.authors.pre.pandemic))

## [1] 0.3765561
mean((socialsciences$X..women.authors.during.pandemic))

## [1] 0.3581449
mean((medicine$X..women.authors.pre.pandemic))

## [1] 0.3693147
mean((medicine$X..women.authors.during.pandemic))

## [1] 0.3461209
mean((multi$X..women.authors.pre.pandemic))

## [1] 0.3916469
mean((multi$X..women.authors.during.pandemic))

## [1] 0.3669248
mean((temcp$X..women.authors.pre.pandemic))

## [1] NaN
mean((temcp$X..women.authors.during.pandemic))

## [1] NaN
mean((bio$X..women.authors.pre.pandemic))

## [1] 0.3280901
mean((bio$X..women.authors.during.pandemic))

## [1] 0.3286446
all_data$Broad.research.field.reordered.opposite <- factor(all_data$Broad.research.field,
  c("Social sciences", "Multidisciplinary", "Medicine", "Biological sciences",
    "TEMCP"))
all_data_long <- all_data
all_data_long$X..women.authors.before.pandemic <- all_data_long$X..women.authors.pre.pandemic
all_data_long$X..women.authors.before.pandemic <- as.numeric(all_data_long$X..women.authors.before.pandemic)

## Warning: NAs introduced by coercion
all_data_long$X..women.authors.during.pandemic <- as.numeric(all_data_long$X..women.authors.during.pandemic)

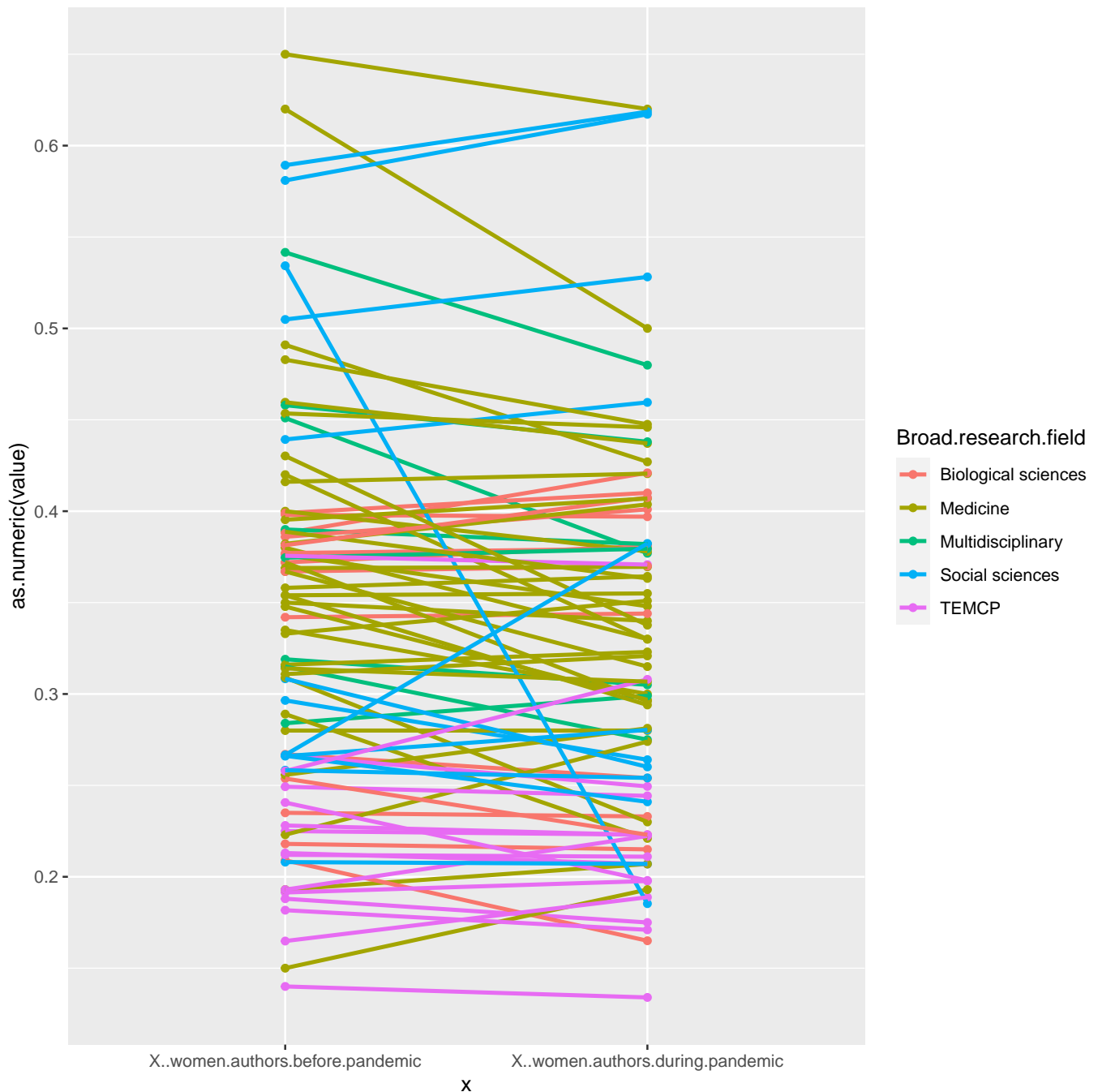
## Warning: NAs introduced by coercion

```

```
all_data_long <- pivot_longer(all_data_long, c(X..women.authors.before.pandemic,
  X..women.authors.during.pandemic), names_to = "Period")

# This plot shows the above model about how previous gender
# bias influence gender bias during the pandemic
ggplot(all_data_long, aes(x = factor(Period), y = as.numeric(value),
  color = factor(Broad.research.field), group = ID)) + geom_point(position = position_jitter(width = 0))
  geom_smooth(method = "lm", se = FALSE) + labs(x = "x", color = "Broad.research.field")

## `geom_smooth()` using formula 'y ~ x'
## Warning: Removed 62 rows containing non-finite values (stat_smooth).
## Warning: Removed 62 rows containing missing values (geom_point).
```



```
all_data_long$Period[all_data_long$Period == "X..women.authors.before.pandemic"] <- "Before pandemic"
all_data_long$Period[all_data_long$Period == "X..women.authors.during.pandemic"] <- "During pandemic"
all_data_long$"Broad research field" <- all_data_long$Broad.research.field.reordered
```

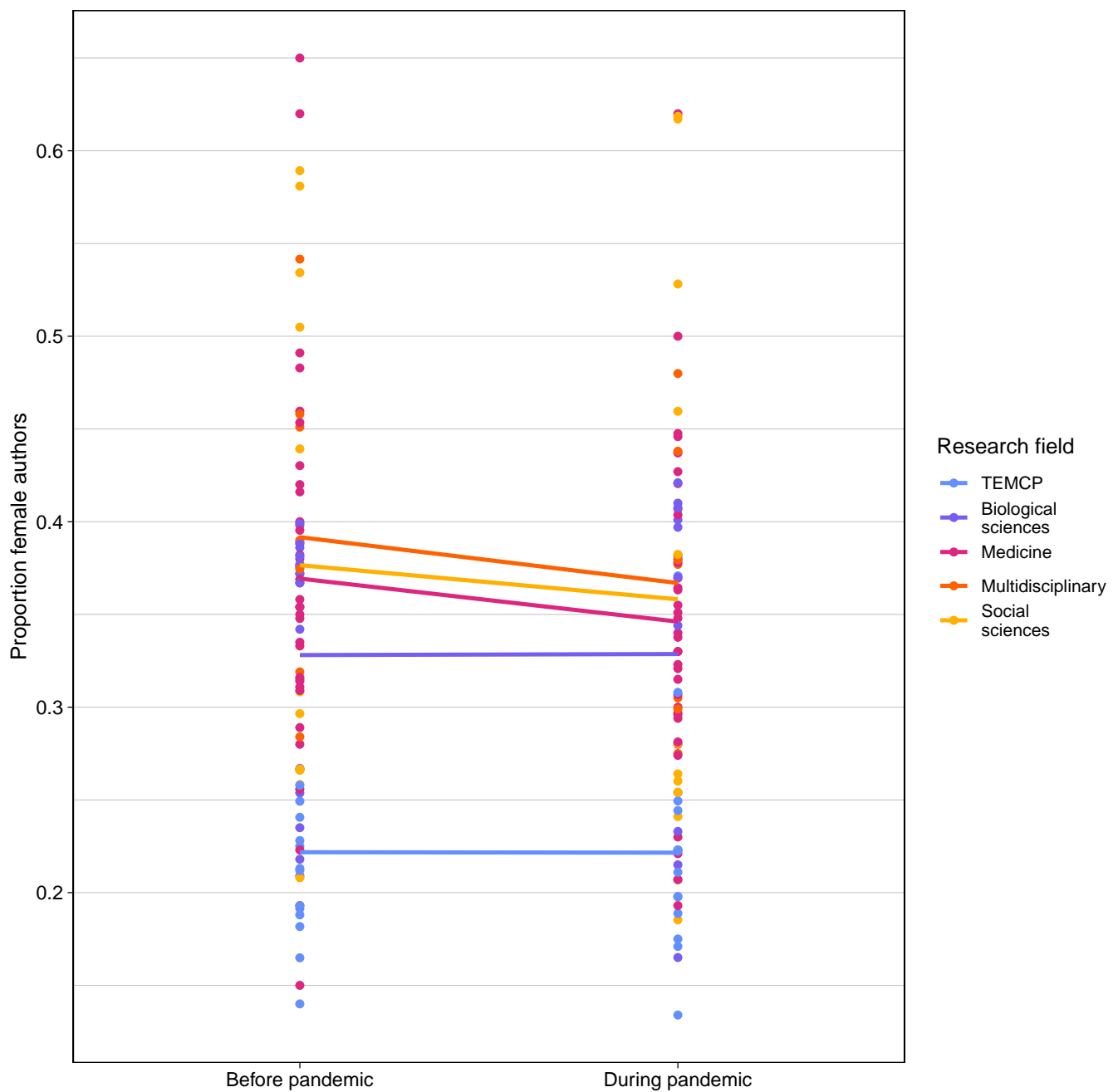
Figure 4

```
ggplot(all_data_long, aes(x = factor(Period), y = as.numeric(value),
  color = factor(Broad.research.field.reordered), group = Broad.research.field.reordered)) +
  geom_point(position = position_jitter(width = 0)) + geom_smooth(method = "lm",
  se = FALSE) + labs(color = "Research field") + labs(x = "",
  y = "Proportion female authors") + theme_linedraw() + theme(panel.grid.major.x = element_blank(),
  panel.grid.major = element_line(size = 0.1, linetype = "solid",
  colour = "gray"), panel.grid.minor = element_line(size = 0.1,
  linetype = "solid", colour = "gray")) + theme(axis.text = element_text(size = 10)) +
  scale_color_manual(values = c("#648FFF", "#785EF0", "#DC267F",
  "#FE6100", "#FFB000"))
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning: Removed 62 rows containing non-finite values (stat_smooth).
```

```
## Warning: Removed 62 rows containing missing values (geom_point).
```

```
ggsave("figure4.png", width = 5, height = 5, dpi = 300)
```

```
## `geom_smooth()` using formula 'y ~ x'
```

```
## Warning: Removed 62 rows containing non-finite values (stat_smooth).
```

```
## Removed 62 rows containing missing values (geom_point).
```

Hypothesis 3: Pandemic conditions made it difficult for women to lead research, rather than support research.

Prediction 3: We predict the pandemic has increased the gender gap more in first and last, rather than middle authorship positions as female academics have been more limited in undertaking leading research roles, but not supportive research roles in pandemic conditions.

Note: Only 3 effect sizes from 2 studies that use middle authorship makes it difficult to test this.

```
measured_data$Specific.productivity.measure[measured_data$Specific.productivity.measure ==
  "Sole authorship"] <- "Last authorship"

measured_data$Specific.productivity.measure.reordered <- factor(measured_data$Specific.productivity.measure,
  c("Last authorship", "Middle authorship", "First authorship",
    "Corresponding authorship", "Any authorship"))

levels(measured_data$Specific.productivity.measure.reordered) <- gsub(" ",
  "\\n", levels(measured_data$Specific.productivity.measure.reordered))

# Models
authorship_position <- metafor::rma.mv(yi = yi, V = vi, mods = ~Specific.productivity.measure.reordered,
  random = list(~1 | Article.ID, ~1 | ID), data = measured_data)

summary(authorship_position)

##
## Multivariate Meta-Analysis Model (k = 84; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
##  51.1354 -102.2708  -88.2708  -71.6847  -86.6934
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed    factor
## sigma^2.1  0.0000  0.0000   25    no  Article.ID
## sigma^2.2  0.0132  0.1150   84    no         ID
##
## Test for Residual Heterogeneity:
## QE(df = 79) = 3776.9941, p-val < .0001
##
## Test of Moderators (coefficients 2:5):
## QM(df = 4) = 0.2786, p-val = 0.9912
##
## Model Results:
##
##                                     estimate
## intrcpt                           -0.0343
## Specific.productivity.measure.reorderedMiddle\nauthorship -0.0112
## Specific.productivity.measure.reorderedFirst\nauthorship    0.0033
## Specific.productivity.measure.reorderedCorresponding\nauthorship 0.0181
## Specific.productivity.measure.reorderedAny\nauthorship      -0.0123
##                                     se
## intrcpt                        0.0292
## Specific.productivity.measure.reorderedMiddle\nauthorship 0.0737
## Specific.productivity.measure.reorderedFirst\nauthorship 0.0349
## Specific.productivity.measure.reorderedCorresponding\nauthorship 0.0564
## Specific.productivity.measure.reorderedAny\nauthorship 0.0504
```

```

##                                                                 zval
## intrcpt                                                         -1.1745
## Specific.productivity.measure.reorderedMiddle\nauthorship      -0.1521
## Specific.productivity.measure.reorderedFirst\nauthorship       0.0934
## Specific.productivity.measure.reorderedCorresponding\nauthorship 0.3219
## Specific.productivity.measure.reorderedAny\nauthorship          -0.2442
##                                                                 pval
## intrcpt                                                         0.2402
## Specific.productivity.measure.reorderedMiddle\nauthorship      0.8791
## Specific.productivity.measure.reorderedFirst\nauthorship       0.9256
## Specific.productivity.measure.reorderedCorresponding\nauthorship 0.7475
## Specific.productivity.measure.reorderedAny\nauthorship          0.8071
##                                                                 ci.lb
## intrcpt                                                         -0.0916
## Specific.productivity.measure.reorderedMiddle\nauthorship      -0.1558
## Specific.productivity.measure.reorderedFirst\nauthorship       -0.0651
## Specific.productivity.measure.reorderedCorresponding\nauthorship -0.0924
## Specific.productivity.measure.reorderedAny\nauthorship          -0.1112
##                                                                 ci.ub
## intrcpt                                                         0.0230
## Specific.productivity.measure.reorderedMiddle\nauthorship      0.1333
## Specific.productivity.measure.reorderedFirst\nauthorship       0.0716
## Specific.productivity.measure.reorderedCorresponding\nauthorship 0.1287
## Specific.productivity.measure.reorderedAny\nauthorship          0.0865
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

authorship_position1 <- metafor::rma.mv(yi = yi, V = vi, mods = ~Specific.productivity.measure.reordered -
  1, random = list(~1 | Article.ID, ~1 | ID), data = measured_data)

summary(authorship_position1)

##
## Multivariate Meta-Analysis Model (k = 84; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
##    51.1354  -102.2708   -88.2708   -71.6847   -86.6934
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000    25    no  Article.ID
## sigma^2.2  0.0132  0.1150    84    no          ID
##
## Test for Residual Heterogeneity:
## QE(df = 79) = 3776.9941, p-val < .0001
##
## Test of Moderators (coefficients 1:5):
## QM(df = 5) = 5.9053, p-val = 0.3155
##
## Model Results:
##
##                                                                 estimate
## Specific.productivity.measure.reorderedLast\nauthorship      -0.0343
## Specific.productivity.measure.reorderedMiddle\nauthorship     -0.0456
## Specific.productivity.measure.reorderedFirst\nauthorship      -0.0311

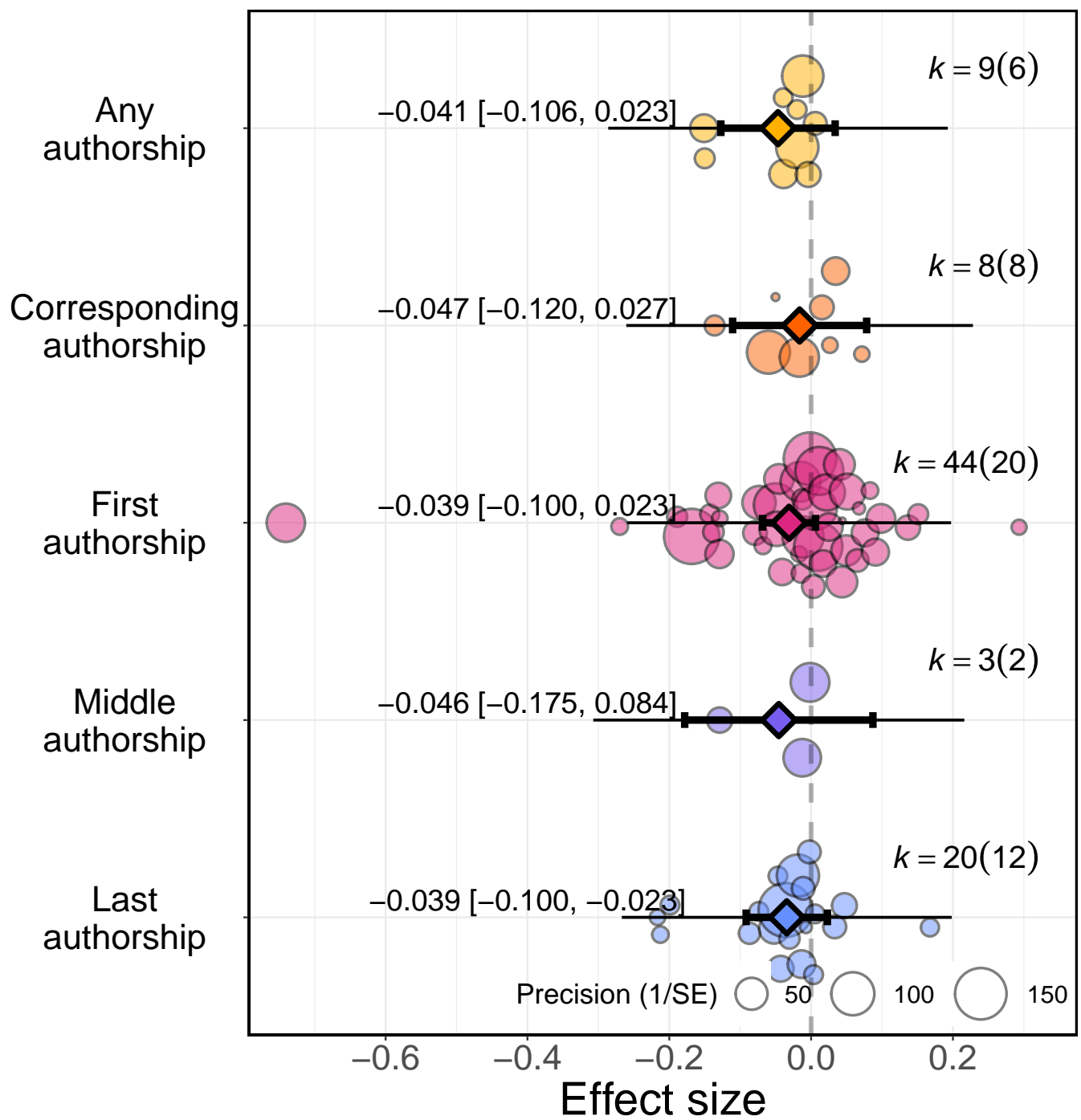
```

```
## Specific.productivity.measure.reorderedCorresponding\authorship -0.0162
## Specific.productivity.measure.reorderedAny\authorship -0.0467
## se
## Specific.productivity.measure.reorderedLast\authorship 0.0292
## Specific.productivity.measure.reorderedMiddle\authorship 0.0677
## Specific.productivity.measure.reorderedFirst\authorship 0.0190
## Specific.productivity.measure.reorderedCorresponding\authorship 0.0482
## Specific.productivity.measure.reorderedAny\authorship 0.0411
## zval
## Specific.productivity.measure.reorderedLast\authorship -1.1745
## Specific.productivity.measure.reorderedMiddle\authorship -0.6729
## Specific.productivity.measure.reorderedFirst\authorship -1.6346
## Specific.productivity.measure.reorderedCorresponding\authorship -0.3358
## Specific.productivity.measure.reorderedAny\authorship -1.1350
## pval
## Specific.productivity.measure.reorderedLast\authorship 0.2402
## Specific.productivity.measure.reorderedMiddle\authorship 0.5010
## Specific.productivity.measure.reorderedFirst\authorship 0.1021
## Specific.productivity.measure.reorderedCorresponding\authorship 0.7370
## Specific.productivity.measure.reorderedAny\authorship 0.2564
## ci.lb
## Specific.productivity.measure.reorderedLast\authorship -0.0916
## Specific.productivity.measure.reorderedMiddle\authorship -0.1783
## Specific.productivity.measure.reorderedFirst\authorship -0.0683
## Specific.productivity.measure.reorderedCorresponding\authorship -0.1107
## Specific.productivity.measure.reorderedAny\authorship -0.1272
## ci.ub
## Specific.productivity.measure.reorderedLast\authorship 0.0230
## Specific.productivity.measure.reorderedMiddle\authorship 0.0871
## Specific.productivity.measure.reorderedFirst\authorship 0.0062
## Specific.productivity.measure.reorderedCorresponding\authorship 0.0783
## Specific.productivity.measure.reorderedAny\authorship 0.0339
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Figure 5

```
my.orchard(authorship_position, mod = "Specific.productivity.measure.reordered",
  group = "Article.ID", data = measured_data, whisker = 0.08,
  xlab = "Effect size", alpha = 0.5) + annotate("text", size = 6,
  y = -0.4, x = 1.09, label = paste("-0.039 [-0.100, -0.023]")) +
  annotate("text", size = 6, y = -0.4, x = 2.09, label = paste("-0.046 [-0.175, 0.084]")) +
  annotate("text", size = 6, y = -0.4, x = 3.09, label = paste("-0.039 [-0.100, 0.023]")) +
  annotate("text", size = 6, y = -0.4, x = 4.09, label = paste("-0.047 [-0.120, 0.027]")) +
  annotate("text", size = 6, y = -0.4, x = 5.09, label = paste("-0.041 [-0.106, 0.023]")) +
  scale_fill_manual(values = c("#648FFF", "#785EF0", "#DC267F",
    "#FE6100", "#FFB000"))

## Warning in k == TRUE && g == TRUE && k.pos == "right": 'length(x) = 2 > 1' in
## coercion to 'logical(1)'
```



```
ggsave("figure5.png")
```

```
## Saving 9 x 9 in image
```

Heterogeneity test

```
##                I2_Total                I2_ID.article
##                98.20614                13.63583
## I2_ID.article/ID.observation
##                84.57031

##                I2_Total                I2_ID.article
##                98.206                13.636
## I2_ID.article/ID.observation
##                84.570

##                I2_Total                I2_ID.article
##                98.891445006                0.000000019
##                I2_ID.observation        I2_Self.reported.or.measured
##                49.840640483                49.050804504
## I2_Specific.productivity.measure        I2_Broad.productivity.measure
##                0.000000000                0.000000000
```

Publication bias

Figure 6

Funnel plots.

```
par(mfrow = c(1, 2))
meta_measured <- rma.mv(yi = yi, V = vi, data = as.data.frame(measured_data))
f1 <- funnel(meta_measured, level = c(90, 95, 99), shade = c("white",
  "gray", "darkgray"), yaxis = "seinv", xlab = "Effect size",
  ylab = "Precision (1/SE)", digits = c(1, 0), xlim = c(-1.5,
    1.5), ylim = c(1, 180), legend = TRUE, back = "white",
  hlines = "white", main = "a) Survey response")
```

f1

```
##          x          y slab
## 1 -0.7407 76.028592    1
## 2 -0.2699 10.283082    2
## 3 -0.2166  8.739376    3
## 4 -0.2125 10.051901    4
## 5 -0.1990 13.633547    5
## 6 -0.1889 16.160594    6
## 7 -0.1685 174.077656    7
## 8 -0.1511 35.333263    8
## 9 -0.1500 15.625000    9
## 10 -0.1429 14.236408   10
## 11 -0.1377 17.246507   11
## 12 -0.1361 15.971914   12
## 13 -0.1309 29.123469   13
## 14 -0.1292 36.961064   14
## 15 -0.1289 28.182994   15
## 16 -0.1288  8.772267   16
## 17 -0.0869 18.433375   17
## 18 -0.0791 24.112141   18
## 19 -0.0737 13.719241   19
## 20 -0.0734 54.717566   20
## 21 -0.0678 10.613702   21
## 22 -0.0601 99.014754   22
## 23 -0.0522 42.524326   23
```

## 24	-0.0502	3.132688	24
## 25	-0.0502	100.503782	25
## 26	-0.0487	59.028134	26
## 27	-0.0467	13.492586	27
## 28	-0.0452	41.558582	28
## 29	-0.0429	29.880715	29
## 30	-0.0408	31.204324	30
## 31	-0.0393	13.492586	31
## 32	-0.0389	37.190400	32
## 33	-0.0360	166.666667	33
## 34	-0.0305	16.536269	34
## 35	-0.0268	13.719241	35
## 36	-0.0197	13.719241	36
## 37	-0.0195	95.782629	37
## 38	-0.0186	94.915800	38
## 39	-0.0169	8.960056	39
## 40	-0.0166	80.064077	40
## 41	-0.0149	83.333333	41
## 42	-0.0143	13.493815	42
## 43	-0.0135	35.333263	43
## 44	-0.0125	72.168784	44
## 45	-0.0122	16.694514	45
## 46	-0.0118	90.535746	46
## 47	-0.0113	89.442719	47
## 48	-0.0112	21.853030	48
## 49	-0.0073	5.026776	49
## 50	-0.0040	27.451403	50
## 51	-0.0025	21.853030	51
## 52	-0.0015	77.849894	52
## 53	-0.0015	156.173762	53
## 54	0.0033	21.853030	54
## 55	0.0035	13.749033	55
## 56	0.0055	13.719241	56
## 57	0.0057	101.534617	57
## 58	0.0059	21.853030	58
## 59	0.0101	129.099445	59
## 60	0.0116	127.000127	60
## 61	0.0152	24.477769	61
## 62	0.0170	31.654447	62
## 63	0.0221	66.964953	63
## 64	0.0252	34.503278	64
## 65	0.0266	8.823339	65
## 66	0.0333	22.456323	66
## 67	0.0347	34.340141	67
## 68	0.0399	45.596075	68
## 69	0.0435	45.314325	69
## 70	0.0441	3.025958	70
## 71	0.0470	27.216553	71
## 72	0.0499	44.280744	72
## 73	0.0514	64.956980	73
## 74	0.0651	21.398025	74
## 75	0.0675	5.291968	75
## 76	0.0716	8.515960	76
## 77	0.0762	32.915401	77
## 78	0.0831	10.137797	78
## 79	0.0909	32.897585	79

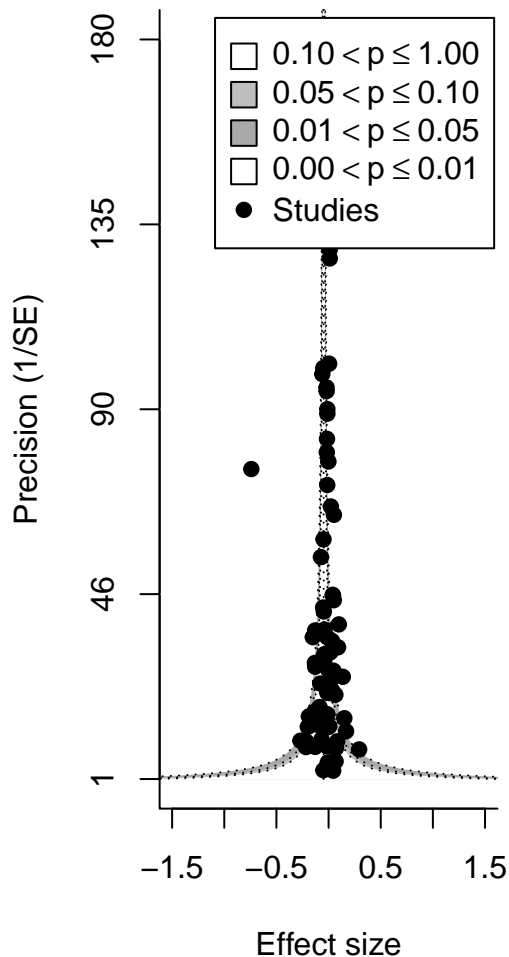
```
## 80 0.0985 38.433122 80
## 81 0.1366 25.751310 81
## 82 0.1511 15.723193 82
## 83 0.1676 12.559009 83
## 84 0.2933 8.172324 84
```

```
ggsave("figure6a.png")
```

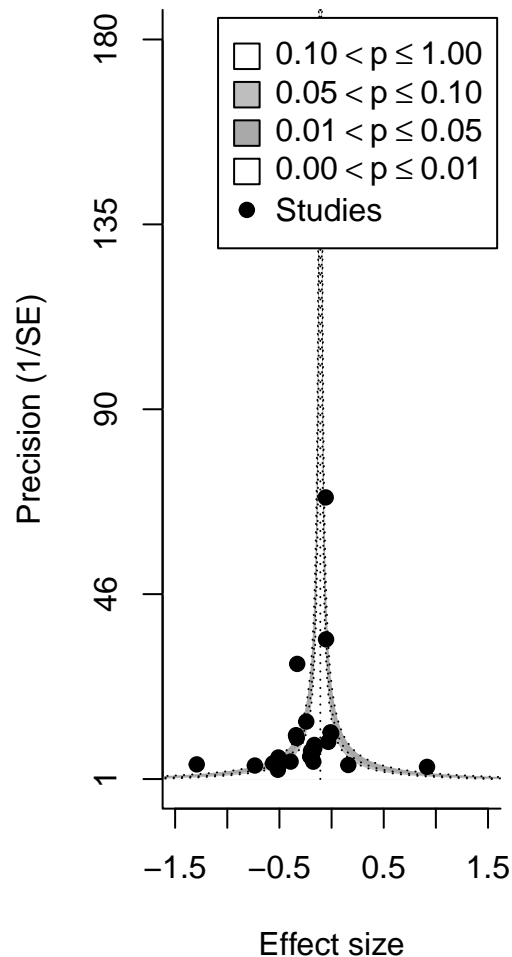
```
## Saving 6 x 6 in image
```

```
selfreported_data <- subset(all_data, all_data$Self.reported.or.measured ==
  "Self-reported")
meta_selfreported <- rma.mv(yi = yi, V = vi, data = as.data.frame(selfreported_data))
f2 <- funnel(meta_selfreported, level = c(90, 95, 99), shade = c("white",
  "gray", "darkgray"), yaxis = "seinv", xlab = "Effect size",
  ylab = "Precision (1/SE)", digits = c(1, 0), xlim = c(-1.5,
  1.5), ylim = c(1, 180), legend = TRUE, back = "white",
  hlines = "white", main = "b) Article output")
```

a) Survey response



b) Article output



```
f2
```

```
##      x      y slab
## 1 -1.2928000 4.550676 1
## 2 -0.7355000 4.271788 2
## 3 -0.5612000 4.794633 3
```



```
## 4 -0.5150000 3.246753 4
## 5 -0.5100000 6.216579 5
## 6 -0.3930000 5.219958 6
## 7 -0.3407000 11.610651 7
## 8 -0.3337000 10.953356 8
## 9 -0.3296000 28.867513 9
## 10 -0.2427000 14.907120 10
## 11 -0.2046802 6.448692 11
## 12 -0.1966000 7.814408 12
## 13 -0.1895000 6.827410 13
## 14 -0.1754000 5.202832 14
## 15 -0.1655000 8.463642 15
## 16 -0.1655000 9.248957 16
## 17 -0.0563000 69.171446 17
## 18 -0.0530000 34.813499 18
## 19 -0.0319000 10.000000 19
## 20 -0.0098000 12.309149 20
## 21 -0.0035000 12.047318 21
## 22 0.1602000 4.400805 22
## 23 0.9151000 3.943615 23
```

```
ggsave("figure6b.png")
```

```
## Saving 6 x 6 in image
```

Multilevel meta-regression test for publication bias. Significant positive slope would suggest small-study effects (small-studies with larger effect sizes being published that skew my meta-analysis) .

```
# Application of Equation 24 from the main manuscript of
# Nakagawa et. al 2021
```

```
# Note that we are removing the intercept in this model
# (using '-1') because the intercept is not of interest at
# this point. Instead we prefer to see the slopes of the
# continues moderators and the estimates of all the levels
# of the categorical moderator 'CaptivityC'. Note that
# whether or not the intercept is removed, it does not
# change the conclusions of the small-study effects test or
# the decline effects test.
```

```
publication.bias.model.r.all.se <- rma.mv(yi, vi, mods = ~Variance.as.standard.error +
  Self.reported.or.measured - 1, random = list(~1 | ID.article/ID.observation),
  data = all_data)
```

```
summary(publication.bias.model.r.all.se)
```

```
##
## Multivariate Meta-Analysis Model (k = 115; method: REML)
##
##      logLik    Deviance      AIC      BIC      AICc
##    51.6769 -103.3538  -93.3538  -79.7613  -92.7877
##
## Variance Components:
##
##      estim    sqrt  nlvls  fixed      factor
## sigma^2.1  0.0000  0.0000   50    no      ID.article
## sigma^2.2  0.0130  0.1141  115    no  ID.article/ID.observation
##
```

```

## Test for Residual Heterogeneity:
## QE(df = 112) = 4688.7755, p-val < .0001
##
## Test of Moderators (coefficients 1:3):
## QM(df = 3) = 41.5100, p-val < .0001
##
## Model Results:
##
##               estimate      se      zval      pval
## Variance.as.standard.error    -0.2643  0.3047  -0.8674  0.3857
## Self.reported.or.measuredMeasured    -0.0253  0.0178  -1.4159  0.1568
## Self.reported.or.measuredSelf-reported    -0.1731  0.0463  -3.7380  0.0002
##               ci.lb      ci.ub
## Variance.as.standard.error    -0.8616  0.3329
## Self.reported.or.measuredMeasured    -0.0603  0.0097
## Self.reported.or.measuredSelf-reported    -0.2638  -0.0823  ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```