Gender and international diversity improves equity in peer review: R Notebook

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This notebook documents the analysis of the dataset on peer review outcomes by eLife. Due to the sensitive nature of the data, it is not all made public. However, a sample dataset with all identifying information such as name and instution has been supplied. If you are using this data, run the first, and the third code blocks, skipping the second.

Setup

The first step is to set up the environment. We import all the required pacakges and setup our custom ggplot theme. We also define here a simple function that is used to convert p-balues to a series of astericks, and another function that capitalizes the first letter of a word, used for capitalizing place names.

```r
library(ggplot2)
library(dplyr)
library(readr)
library(readxl)
library(gridExtra)
library(grid)
library(tidyr)

theme_dakota <- function () {
    theme_bw(base_size=10, base_family="Times") %+replace%
        theme(
            strip.background = element_blank(),
            strip.text = element_text(face = "bold"),
            plot.title = element_text(size = 11, face = "bold"),
            axis.text.x = element_text(size = 9, margin = margin(t = 5, b = 5)),
            legend.title = element_blank(),
            legend.position = "bottom"
        )
}

# converts a provided p-value into a representation that is easier to visualize
sig2ast <- function(p) { ifelse(p <= 0.0001, "****",
                                ifelse(p <= 0.001, "***",
                                       ifelse(p <= 0.01, "**",
                                              ifelse(p <= 0.05, "*",
                                                     ifelse(p < 0.1, ".", "ns")
                                              )
                                       )
                                )
                          )
}

# I copied the below function from a stack overflow question. It should capitalize the first letter of
# https://stackoverflow.com/questions/6364783/capitalize-the-first-letter-of-both-words-in-a-two-word-s
simpleCap <- function(x) {
  s <- strsplit(x, " ")[[1]]
  paste(toupper(substring(s, 1,1)), substring(s, 2),
      sep="", collapse=" ")
}
```

Data import and manipulation

Next we import the data. This version of the dataset was compiled from a seried of excel files provided by elife. Several pre-processing steps are not shown here, but are instead in the other R scipt present in this project. Due to the sensitive nature of this data, it has not been made public. Two datasets are created, one representing some basic characteristics of the people at elife, including all types of people and authors, and another dataset containing metadata and outcomes data for all the manuscripts at elife. For the person-level dataset, we simply compile the unique instances of people appearing in the dataset and place them into a dataframe. The manuscript metadata requires additional work. We perform several manupulations and add new variables in order to make analysis easier throughout the document.

1. Disambiguate country names and add continent categories
2. Convert all cases of null-gender assignment to a value of "UNK", or "Unknown". Typically, NA assignments occur when an author is missing (as is the case for reviewer 4, when there are only three reviewers, or for a last author when the manuscript was rejected during initial submission), or when some error occured during the assignment process (no name was matched during the assignment.
3. Convert all vairbales relating to gender to be a factor with three levels.
4. Flag the data if no decision has been made for the initial submission, which tends to be the case when they were submitted close our date cutoff.
5. Flag the data if no decision has been made for the full submission, which usuall occurs when the manuscript is pending decision or revisions during our date cutoff.
6. Flag the data if an appeal has been made at any stage of the review process.
7. Flag the data if it has been encouraged during the initial decision phase.
8. Flag the data if it has been submitted and accepted as a full submission
9. Flag the data if there are potential inconsistencies in how names are present. For example, in some full submissions there is no first author present, but there is a last author present. The assumption is that a first author and last author should always be present, even if they are the same person.
10. Add variables containing a list of all full submission decisions made on each document
11. Add variables for the time spent for reviewers to deliberate each part of the revision process
12. Identify the stage in which the final decision was made
13. Count the number of reviewers invovled in reviewing the full submission
14. Count the number of male and number of female reviewers
15. Create a categorical variable representing the composition of the reviewer team as being all male, all female, or mixed-gender
16. Create an adjusted composition of the reviewer team, this time excluding the BRE, if they are also listed as a reviewer
17. Count the number of revisions that the manuscript went through
18. Create variables representing country homophily between each type of authorship and any member of the reviewer team
19. Remove potentially sensitive information, such as individual names, institutions, countries, submission dates, etc.

```
# Load the main eLife data file
elife <- read_excel("~/Dropbox/eLife/data/elife_datafile.xlsx")

# Load the country infomration .csv file, which was manually created and available along with this file
country_mapping <- read_csv("~/Dropbox/eLife/data/elife_countries.csv")
```

```
# Get a single list of all the peer reviewers, which presently are represented as separate variables on
# is ugly and can be improved, but it is simple and works, so I won't bother changing it
reviewer1 <- elife[, c("reviewer1_name", "reviewer1_gender", "reviewer1_institution", "reviewer1_countr
reviewer1 <- reviewer1[with(reviewer1, !is.na(reviewer1_name)), ]
colnames(reviewer1) <- c("reviewer_name", "reviewer_gender", "reviewer_institution", "reviewer_country"

reviewer2 <- elife[, c("reviewer2_name", "reviewer2_gender", "reviewer2_institution", "reviewer2_countr
reviewer2 <- reviewer2[with(reviewer2, !is.na(reviewer2_name)), ]
colnames(reviewer2) <- c("reviewer_name", "reviewer_gender", "reviewer_institution", "reviewer_country"

reviewer3 <- elife[, c("reviewer3_name", "reviewer3_gender", "reviewer3_institution", "reviewer3_countr
reviewer3 <- reviewer2[with(reviewer3, !is.na(reviewer3_name)), ]
colnames(reviewer3) <- c("reviewer_name", "reviewer_gender", "reviewer_institution", "reviewer_country"

reviewer4 <- elife[, c("reviewer4_name", "reviewer4_gender", "reviewer4_institution", "reviewer4_countr
reviewer4 <- reviewer2[with(reviewer4, !is.na(reviewer4_name)), ]
colnames(reviewer4) <- c("reviewer_name", "reviewer_gender", "reviewer_institution", "reviewer_country"

reviewers <- rbind(reviewer1, reviewer2, reviewer3, reviewer4)

# proportion of reviewers by gender compared to proportions of author by gender
bres <- elife[, c("bre_gender", "bre_name", "bre_country")]
peer_reviewers <- reviewers[, c("reviewer_gender", "reviewer_name", "reviewer_country")]
editors <- elife[, c("se_gender", "se_name", "se_country")]
names(editors) <- c("gender", "name", "country")
names(bres) <- c("gender", "name", "country")
names(peer_reviewers) <- c("gender", "name", "country")

revs <- as.data.frame(rbind(bres, editors, peer_reviewers))
revs$type <- "Gatekeeper"
revs <- revs[!is.na(revs$country), ]

# now we add the authors
ca_authors <- elife[, c("ca_gender", "ca_name", "ca_country")]
names(ca_authors) <- c("gender", "name", "country")
ca_authors$type <- "Corr. Author"

fa_authors <- elife[, c("fa_gender", "fa_name", "fa_country")]
names(fa_authors) <- c("gender", "name", "country")
fa_authors$type <- "First Author"

la_authors <- elife[, c("la_gender", "la_name", "la_country")]
names(la_authors) <- c("gender", "name", "country")
la_authors$type <- "Last Author"

# combine all these variables into a single data frame
people <- as.data.frame(rbind(revs, ca_authors, fa_authors, la_authors))
people <- people[!duplicated(people[, c("name", "country", "type")]), ]
people <- people[!is.na(people$name), ]

# Adjust the levels of the gender factor, limit to "Male/Female/UNK", the matching algorithm will assig
people$gender = with(people, relevel(factor(ifelse(gender %in% c("M", "F"), gender,
                                                                  ifelse(!is.na(name), "UNK", NA)), leve
```

```
# Now lets map the continent values onto this dataframe
people <- people %>%
  mutate(country = tolower(country)) %>%
  left_join(country_mapping, by = c("country" = "Country")) %>%
    mutate(
      country = Mapping,
      continent = Continent
    ) %>%
  select(-Mapping, -Continent, -name, -country)


# Moving on, lets begin to work with the manuscript data.
elife <- elife %>%
  # This group_by is needed to make the mutate functions work propoerly
  group_by(MSNO) %>%
  # these vairbales need to be converted to lowercase for the next step...
  mutate(
    ca_country = tolower(ca_country),
    la_country = tolower(la_country),
    fa_country = tolower(fa_country),
    bre_country = tolower(bre_country),
    se_country = tolower(se_country),
    reviewer1_country = tolower(reviewer1_country),
    reviewer2_country = tolower(reviewer2_country),
    reviewer3_country = tolower(reviewer3_country),
    reviewer4_country = tolower(reviewer4_country)
  ) %>%
  # This series of left_joins + mutates + selects is ugly, but it seems one of the most straightforward
  # each of the author and reviewer types.
  left_join(country_mapping, by = c("ca_country" = "Country")) %>%
  mutate(
    ca_country = Mapping,
    ca_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("la_country" = "Country")) %>%
  mutate(
    la_country = Mapping,
    la_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("fa_country" = "Country")) %>%
  mutate(
    fa_country = Mapping,
    fa_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("se_country" = "Country")) %>%
  mutate(
    se_country = Mapping,
    se_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("bre_country" = "Country")) %>%
  mutate(
    bre_country = Mapping,
    bre_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("reviewer1_country" = "Country")) %>%
  mutate(
    reviewer1_country = Mapping,
    reviewer1_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("reviewer2_country" = "Country")) %>%
  mutate(
    reviewer2_country = Mapping,
    reviewer2_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("reviewer3_country" = "Country")) %>%
  mutate(
    reviewer3_country = Mapping,
    reviewer3_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  left_join(country_mapping, by = c("reviewer4_country" = "Country")) %>%
  mutate(
    reviewer4_country = Mapping,
    reviewer4_continent = Continent
  ) %>%
  select(-Mapping, -Continent) %>%
  # Now I will turn towards the other variables that we will be working with.
  mutate(
    # convert NA assignments in gender assignment to a value of "Unknown" as well as setup factor level
    ca_gender = relevel(factor(ifelse(ca_gender %in% c("M", "F"), ca_gender, ifelse(!is.na(ca_name), "U
    fa_gender = relevel(factor(ifelse(fa_gender %in% c("M", "F"), fa_gender, ifelse(!is.na(fa_name), "U
    la_gender = relevel(factor(ifelse(la_gender %in% c("M", "F"), la_gender, ifelse(!is.na(la_name), "U
    se_gender = relevel(factor(ifelse(se_gender %in% c("M", "F"), se_gender, ifelse(!is.na(se_name), "U
    bre_gender = relevel(factor(ifelse(se_gender %in% c("M", "F"), bre_gender, ifelse(!is.na(bre_name),
                               levels = c("M", "F", "UNK")), ref = "F"),
    reviewer1_gender = relevel(factor(ifelse(reviewer1_gender %in% c("M", "F"), reviewer1_gender, ifels
                                      levels = c("M", "F", "UNK")), ref = "F"),
    reviewer2_gender = relevel(factor(ifelse(reviewer2_gender %in% c("M", "F"), reviewer2_gender, ifels
                                      levels = c("M", "F", "UNK")), ref = "F"),
    reviewer3_gender = relevel(factor(ifelse(reviewer3_gender %in% c("M", "F"), reviewer3_gender, ifels
                                      levels = c("M", "F", "UNK")), ref = "F"),
    reviewer4_gender = relevel(factor(ifelse(reviewer4_gender %in% c("M", "F"), reviewer4_gender, ifels
                                      levels = c("M", "F", "UNK")), ref = "F"),

    submission_year = as.numeric(format(as.Date(initial_submission_time), "%Y")),
    # Flag the data if there is an initial submission but no decision has been made
    initial_decision_made = !is.na(initial_decision),

    # Flag is the manuscript had a full submission
```

```r
    has_full_submission = !is.na(full_submission_date),

    # Flag data if full submission has been submitted, but no decision has been made (ie: still in revi
    full_decision_made = !is.na(full_submission_date) & last(na.omit(c(full_decision, rev1_decision, re

    # Flag the data if it was appealed at any state during its process
    appealed_any_stage = any(c(appeal_state1, appeal_state2, appeal_state3) == 4) & any(!is.na(c(appeal_

    # Flag the data if the initial decision of the manuscript was encouraged
    encouraged = initial_decision_made & initial_decision == "Encourage",

    # Flag the data if the full submission was eventually accepted
    accepted = full_decision_made & any(c(full_decision, rev1_decision, rev2_decision) == "Accept", na.

    # Flag whether a final decision of accept or reject has been passed
    final_decision_made = any(c(full_decision, rev1_decision, rev2_decision) %in% c("Accept", "Reject")

    # Flag data if there are potential inconsistencies with the naming, ie: no last name for a full sub
    #name_inconsistency = full_decision_made & ((!is.na(la_name) & is.na(elife$fa_name)) | ((is.na(la_n

    # This is a list of all the full decisions made (first decision or full submission + subsequent rev
    full_decisions = list(na.omit(c(full_decision, rev1_decision, rev2_decision))),

    # Add variables related to how long it takes to go through the review process
    deltatime_rev1 = as.Date(rev1_decision_date) - as.Date(rev1_submission_date),
    deltatime_rev2 = as.Date(rev2_decision_date) - as.Date(rev2_submission_date),

    # Store the final stage of the full-submission process in which the final decision was amde
    final_decision_stage = ifelse(full_decision_made, c("Full", "Rev1", "Rev2")[grep("Accept|Reject", u

    # Calculat the total amount of time spent deliberating revision decisions
    revision_time = ifelse(final_decision_stage == "Full", NA,
                           ifelse(final_decision_stage == "Rev1", deltatime_rev1,
                                  deltatime_rev1 + deltatime_rev2)),

    # Calculate total amount of time spent deliberating decisions from first full submittion to the fin
    deltatime_final = ifelse(final_decision_stage == "Full", deltatime_full_submission_decision,
                             ifelse(final_decision_stage == "Rev1", deltatime_rev1 + deltatime_full_subm
                                    deltatime_rev2 + deltatime_rev1 + deltatime_full_submission_decisio

    # just some simple boolean values for whether or not the full submission and decision dates are NA-
    #!has_full_submission = is.na(full_submission_date),
    full_decision_date_isNA = is.na(full_decision_date),


    # Now add variables relating to the composition of the reviewer team
    # Quality of list variables-list of the names, countries, and genders of reviewers
    reviewer_names = list(tolower(na.omit(c(bre_name, reviewer1_name, reviewer2_name, reviewer3_name, re
    reviewer_genders = list(na.omit(c(bre_gender, reviewer1_gender, reviewer2_gender, reviewer3_gender,
    reviewer_countries = list(tolower(na.omit(c(bre_country, reviewer1_country, reviewer2_country, revi
    reviewer_continents = list(tolower(na.omit(c(bre_continent, reviewer1_continent, reviewer2_continent

    reviewer_names_nobre = list(tolower(na.omit(c(reviewer1_name, reviewer2_name, reviewer3_name, revie
    reviewer_genders_nobre = list(na.omit(c(reviewer1_gender, reviewer2_gender, reviewer3_gender, revie

    # Number of reviewers in the team
    num_reviewers = length(unlist(reviewer_names)),
    num_reviewers_nobre = length(unlist(reviewer_names_nobre)),

    # Number of reviewers on the team identified as female
    num_female_reviewers = sum(unlist(reviewer_genders) == 1),
    # NUmber of reviewers on the team identified as male
    num_male_reviewers = sum(unlist(reviewer_genders) == 2),

    num_female_reviewers_nobre = sum(unlist(reviewer_genders_nobre) == 1),
    # NUmber of reviewers on the team identified as male
    num_male_reviewers_nobre = sum(unlist(reviewer_genders_nobre) == 2),

    # Composition: three variables indicaitng whether all have a gender identified as male, all have a
    # of at least one male and one female reviewer on the team
    composition = factor(ifelse(is.na(full_submission_date), NA,
                                ifelse(all(unlist(reviewer_genders) == 2), "All Men",
                                       ifelse(all(unlist(reviewer_genders) == 1), "All Women",
                                              ifelse(any(unlist(reviewer_genders) == 1) & any(unlist(re
                                                     "Uncertain"
                                                     )
                                              )
                                       )
                                ) # end first ifelse
                         , levels = c("All Men", "All Women", "Mixed", "Uncertain")), # end factor
    # Number of revisions
    num_revisions = length(unlist(full_decisions)) - 1,
    # The corresponding author is from the same country as at least one reviewer
    ca_country_homophily = !is.na(ca_country) & tolower(ca_country) %in% unlist(reviewer_countries),
    # The last author is from the same country as at least one reviewer
    la_country_homophily = !is.na(la_country) & tolower(la_country) %in% unlist(reviewer_countries),
    # The first author is from the same country as at least one reviewer
    fa_country_homophily = !is.na(fa_country) & tolower(fa_country) %in% unlist(reviewer_countries),

    # The corresponding author is from the same country as at least one reviewer
    ca_continent_homophily = !is.na(ca_continent) & tolower(ca_continent) %in% unlist(reviewer_continen
    # The last author is from the same country as at least one reviewer
    la_continent_homophily = !is.na(la_continent) & tolower(la_continent) %in% unlist(reviewer_continen
    # The first author is from the same country as at least one reviewer
    fa_continent_homophily = !is.na(fa_continent) & tolower(fa_continent) %in% unlist(reviewer_continen

    # The BRE is also listed as a reviewer
    bre_is_reviewer = tolower(bre_name) %in% unlist(reviewer_names_nobre),

    ca_bre_country_homophily = bre_country == ca_country,

    ca_bre_continent_homophily = bre_continent == ca_continent,

    # A short series of variables specifying if the first and last authors are the same, or if the CA i
    ca_is_first = tolower(ca_name) == tolower(fa_name),
    ca_is_last = tolower(ca_name) == tolower(la_name),
    single_authored = tolower(fa_name) == tolower(la_name),

    # this just cleans up a poorly named variable earlier in the preprocessing step
    submission_type = type.x,

    # Recalculate the composition, but this time justed for the BRE
    num_female_reviewers_adj = ifelse(bre_is_reviewer == T & bre_gender == "F", num_female_reviewers_no
    num_male_reviewers_adj = ifelse(bre_is_reviewer ==T & bre_gender == "M", num_male_reviewers_nobre -
    num_reviewers_adj = ifelse(bre_is_reviewer, num_reviewers_nobre - 1, num_reviewers_nobre),
    composition_adj = ifelse(!has_full_submission, NA,
                             ifelse(num_male_reviewers_adj > 0 & num_female_reviewers_adj > 0, "Mixed",
                                    ifelse(num_male_reviewers_adj == num_reviewers_adj, "All Men",
                                           ifelse(num_female_reviewers_adj == num_reviewers_adj, "All W
                                                  )
                                       )
                                )
                  )
  )
```

Lets calculate some basic things, before we anonymize the data, like number of unique co-authors, etc.

Initial Submissions and General Info

Number of initial submissions

```
dim(elife)[1]
```

```
## [1] 23879
```

Distribution of manuscript types

```
table(elife$type.x)
```

```
##
##    RA    RE    SR    TR
## 20945     6  2186   742
```

Distribution of manuscript types, as %

```
prop.table(table(elife$type.x))
```

```
##
##           RA           RE           SR           TR
## 0.8771305331 0.0002512668 0.0915448721 0.0310733280
```

Review outcome of initial submissions to eLife

```
outcomes <- elife %>%
  mutate(outcome = ifelse(!initial_decision_made, "No Decision Yet", ifelse(encouraged, "Encouraged", "
```

```r
table(outcomes$outcome)
```

```
## 
##       Encouraged No Decision Yet        Rejected 
##             7112             147           16620 
```

Gender dsitirbution of distinct corresponding authors of initial submissions to eLife

```r
# get distint corresondign authros on first submissions
ca_authors <- elife %>%
  mutate(ca_name = tolower(ca_name)) %>%
  group_by(ca_name, ca_country) %>%
  filter(row_number() == 1)

table(ca_authors$ca_gender)
```

```
## 
##     F     M   UNK 
##  4803 11968  1447 
```

National distribution of distinct corresonding authors of initial submissions

```r
t <- table(ca_authors$ca_country)
t[order(-t)]
```

```
## 
##          united states        united kingdom               germany 
##                   6431                  1853                  1601 
##                  china                france                 japan 
##                   1156                   913                   658 
##                 canada                 italy                 spain 
##                    580                   444                   443 
##                  india           switzerland             australia 
##                    380                   377                   361 
##            netherlands                israel                sweden 
##                    345                   326                   254 
##            south korea               belgium                taiwan 
##                    228                   185                   162 
##              singapore               austria               denmark 
##                    159                   138                   118 
##               portugal               finland                brazil 
##                     99                    91                    84 
##                 poland        czech republic             argentina 
##                     71                    61                    56 
##                 norway             hong kong                russia 
##                     55                    53                    51 
##                hungary               ireland           new zealand 
##                     49                    42                    35 
##                  chile                mexico          south africa 
##                     31                    28                    28 
##                 greece                  iran          saudi arabia 
##                     24                    23                    22 
##               estonia                 kenya              thailand 
##                    14                    12                    11 
##                turkey              slovenia  united arab emirates 
##                    10                     9                     8 
##              colombia              malaysia               croatia 
##                     7                     6                     5 
##                 qatar                 egypt                 macau 
##                     5                     4                     4 
##            madagascar                  peru           puerto rico 
##                     4                     4                     4 
##               romania               ukraine             indonesia 
##                     4                     4                     3 
##                  iraq               nigeria             sri lanka 
##                     3                     3                     3 
##               uruguay               vietnam            bangladesh 
##                     3                     3                     2 
##      french polynesia                 ghana               lebanon 
##                     2                     2                     2 
##            luxembourg                malawi                monaco 
##                     2                     2                     2 
##                 nepal serbia and montenegro              slovakia 
##                     2                     2                     2 
##             venezuela            antarctica          burkina faso 
##                     2                     1                     1 
##              cambodia            costa rica                cyprus 
##                     1                     1                     1 
##              ethiopia                  fiji         french guiana 
##                     1                     1                     1 
##                 gabon               iceland                kuwait 
##                     1                     1                     1 
##             lithuania            mozambique                  oman 
##                     1                     1                     1 
##              pakistan           philippines               reunion 
##                     1                     1                     1 
##              tanzania                uganda                 yemen 
##                     1                     1                     1
```

Gender distibution of distinct senior editors of initial submissions

```
# get distint corresondign authros on first submissions
se_authors <- elife %>%
  mutate(se_name = tolower(se_name)) %>%
  group_by(se_name, se_country) %>%
  filter(row_number() == 1)

table(se_authors$se_gender)
```

```
## 
##   F   M UNK 
##  15  42   0
```

National distribution of distinct senior editors of initial submissions

```
t <- table(se_authors$se_country)
t[order(-t)]
```

```
##
##  united states united kingdom        germany         canada          china
##             32              7              6              3              2
##    switzerland          india         israel          japan    netherlands
##              2              1              1              1              1
##          spain
##              1
```

Full Submissions

Total number of full submissions

```
full <- elife %>%
  filter(has_full_submission)

dim(full)[1]
```

```
## [1] 7193
```

Final decision outcomes for full submissions

```
outcomes <- full %>%
  mutate(outcome = ifelse(!final_decision_made, "No Decision Yet", ifelse(accepted, "Accepted", "Rejecte

table(outcomes$outcome)
```

```
##
##        Accepted No Decision Yet        Rejected
##            3426             602            3165
```

First full decision outcomes for full submissions

```
table(ifelse(is.na(full$full_decision), "No Decision", full$full_decision))
```

```
##
##      Accept No Decision      Reject      Revise
##          54         217        3155        3767
```

First revision review outcomes for full submissions

```
rev1 <- full %>% filter(!is.na(rev1_submission_date))
table(ifelse(is.na(rev1$rev1_decision), "No Decision", rev1$rev1_decision))
```

```
##
##      Accept No Decision      Reject      Revise
##        2545          47         473        1005
```

Second revision review outcomes for full submissions

```
rev2 <- full %>% filter(!is.na(rev2_submission_date))
table(ifelse(is.na(rev2$rev2_decision), "No Decision", rev2$rev2_decision))
```

```
##
##      Accept No Decision      Reject      Revise
##         827           5          67         125
```

Number of distinct corresponding authors in full submissions at eLife

```
ca_authors <- full %>%
  filter(!is.na(ca_name)) %>%
  mutate(ca_name = tolower(ca_name)) %>%
  group_by(ca_name, ca_country) %>%
  filter(row_number() == 1)

dim(ca_authors)[1]
```

```
## [1] 5695
```

Gender distirbution of distinct correpsonding authors on full submissions at eLife

```
table(ca_authors$ca_gender)
```

```
##
##    F    M  UNK
## 1419 3829  447
```

Number of distinct first authors on full submissions at eLife

```
fa_authors <- full %>%
  filter(!is.na(fa_name)) %>%
  mutate(fa_name = tolower(fa_name)) %>%
  group_by(fa_name, fa_country) %>%
  filter(row_number() == 1)

dim(fa_authors)[1]
```

```
## [1] 6692
```

Gender distirbution of distinct first authors on full submissions at eLife

```
table(fa_authors$fa_gender)
```

```
##
##    F    M  UNK
## 2252 3820  620
```

Number of distinct last authors on full submissions at eLife

```r
la_authors <- full %>%
  filter(!is.na(la_name)) %>%
  mutate(la_name = tolower(la_name)) %>%
  group_by(la_name, la_country) %>%
  filter(row_number() == 1)

dim(la_authors)[1]
```

```
## [1] 5581
```

Gender distirbution of distinct last authors on full submissions at eLife

```r
table(la_authors$la_gender)
```

```
##
##    F    M  UNK
## 1241 3908  432
```

Gender distirbution of distinct last authors on full submissions at eLife, as %

```r
prop.table(table(la_authors$la_gender))
```

```
##
##          F          M        UNK
## 0.22236158 0.70023293 0.07740548
```

Number of distinct gatekeepers involved in processing full submissions at eLife, includes senior editors, reviewing editors, and invited peer reviewers

```r
gatekeepers <- people %>% filter(type == "Gatekeeper")
dim(gatekeepers)[1]
```

```
## [1] 6669
```

Gender distirbution of distinct gatekeepers involved in processing full submissions at eLife, includes senior editors, reviewing editors, and invited peer reviewers

```r
table(gatekeepers$gender)
```

```
##
##    F    M  UNK
## 1372 4934  363
```

Gender distirbution of distinct gatekeepers involved in processing full submissions at eLife, includes senior editors, reviewing editors, and invited peer reviewers as %

```
prop.table(table(gatekeepers$gender))
```

```
##
##          F          M        UNK
## 0.20572800 0.73984106 0.05443095
```

Continent distirbution of distinct gatekeepers involved in processing full submissions at eLife, includes senior editors, reviewing editors, and invited peer reviewers

```
table(gatekeepers$continent)
```

```
##
##        Africa          Asia        Europe North America       Oceania
##            17           379          2161          3992            98
## South America
##            22
```

Proportion of full submissions for which the correposnding author was also the last author

```
sum(full$ca_name == full$fa_name, na.rm = T) / dim(full)[1]
```

```
## [1] 0.2649798
```

Proportion of full submissions for which the correposnding author was also the last author

```
sum(tolower(full$ca_name) == tolower(full$la_name), na.rm = T) / dim(full)[1]
```

```
## [1] 0.7115251
```

Number of full submissions that were appealed

```
table(full$appealed_any_stage)
```

```
##
## FALSE  TRUE
##  6574   619
```

Average number of revisions before final acceptance of full submissions at eLife

```
# In this case, "0" means
f <- full %>% filter(accepted)
mean(f$num_revisions, na.rm = T)
```

```
## [1] 1.225628
```

Proportion of full submissions for which the correpsonding auhtor is from the same country as the first author

```
sum(full$ca_country == full$fa_country, na.rm = T) / dim(full)[1]
```

```
## [1] 0.9414709
```

Proportion of full submissions for which the correpsonding auhtor is from the same country as the last author

```
sum(full$ca_country == full$la_country, na.rm = T) / dim(full)[1]
```

```
## [1] 0.9446684
```

Table SI.2

```
gatekeepers <- subset(people, type == "Gatekeeper")
#table(gatekeepers$continent)
editors <- subset(editors, !duplicated(name, country))
reviewers <- subset(reviewers, !duplicated(reviewer_name, reviewer_country))
bres <- subset(bres, !duplicated(name, country))


t1 <- data.frame(table(editors$country), prop.table(table(editors$country)))
t2 <- data.frame(table(reviewers$reviewer_country), prop.table(table(reviewers$reviewer_country)))
t3 <- data.frame(table(bres$country), prop.table(table(bres$country)))

all_data <- t2 %>%
  left_join(t3, by = "Var1") %>%
  left_join(t1, by = "Var1") %>%
  select(-Var1.1.x, -Var1.1.y, -Var1.1)


names(all_data) <- c("country", "rev.freq", "rev.prop", "bre.freq", "bre.prop", "se.freq", "se.prop")

ord <- with(all_data, order(-se.freq, -bre.freq))

all_data <- all_data[ord, ]

write.csv(all_data, file = "tables/table_SI2.csv")

all_data
```

```
##                       country rev.freq     rev.prop bre.freq    bre.prop
## 55              United States     3648 0.5594234013      536 0.620370370
## 54             United Kingdom      707 0.1084189541       88 0.101851852
## 18                    Germany      469 0.0719214844       69 0.079861111
## 8                      Canada      249 0.0381843276       22 0.025462963
## 48                Switzerland      166 0.0254562184       19 0.021990741
## 10                      China       61 0.0093543935       10 0.011574074
## 25                     Israel       89 0.0136482135       19 0.021990741
## 34                Netherlands      114 0.0174819813       11 0.012731481
## 46                      Spain       78 0.0119613556       10 0.011574074
## 27                      Japan      128 0.0196288913        9 0.010416667
## 23                      India       20 0.0030670143        6 0.006944444
## 16                     France      245 0.0375709247       21 0.024305556
## 4                   Australia       87 0.0133415120        7 0.008101852
## 45               South Africa       12 0.0018402086        5 0.005787037
## 5                     Austria       49 0.0075141849        4 0.004629630
## 6                     Belgium       37 0.0056739764        3 0.003472222
## 15                    Finland       26 0.0039871185        3 0.003472222
## 26                      Italy       60 0.0092010428        3 0.003472222
## 43                  Singapore       33 0.0050605735        3 0.003472222
## 51                   Thailand        4 0.0006134029        3 0.003472222
## 13                    Denmark       30 0.0046005214        2 0.002314815
## 29 Korea (South), Republic of        9 0.0013801564        2 0.002314815
## 14                    Estonia        1 0.0001533507        1 0.001157407
## 20                  Hong Kong        3 0.0004600521        1 0.001157407
## 21                    Hungary        7 0.0010734550        1 0.001157407
## 24                    Ireland        6 0.0009201043        1 0.001157407
## 28                      Kenya        2 0.0003067014        1 0.001157407
## 32                     Mexico        7 0.0010734550        1 0.001157407
## 35                New Zealand       10 0.0015335071        1 0.001157407
## 37                     Poland        9 0.0013801564        1 0.001157407
## 47                     Sweden       53 0.0081275878        1 0.001157407
## 1                     Albania        1 0.0001533507       NA          NA
## 2                     Andorra        1 0.0001533507       NA          NA
## 3                   Argentina       10 0.0015335071       NA          NA
## 7                      Brazil        5 0.0007667536       NA          NA
## 9                       Chile        5 0.0007667536       NA          NA
## 11                    Croatia        2 0.0003067014       NA          NA
## 12             Czech Republic        5 0.0007667536       NA          NA
## 17              French Guiana        1 0.0001533507       NA          NA
## 19                     Greece        8 0.0012268057       NA          NA
## 22                    Iceland        1 0.0001533507       NA          NA
## 30                 Madagascar        1 0.0001533507       NA          NA
## 31                   Malaysia        1 0.0001533507       NA          NA
## 33                     Monaco        1 0.0001533507       NA          NA
## 36                     Norway       11 0.0016868578       NA          NA
## 38                   Portugal       25 0.0038337678       NA          NA
## 39                Puerto Rico        2 0.0003067014       NA          NA
## 40          Republic of Korea        8 0.0012268057       NA          NA
## 41         Russian Federation        1 0.0001533507       NA          NA
## 42               Saudi Arabia        1 0.0001533507       NA          NA
## 44                   Slovenia        1 0.0001533507       NA          NA
## 49                     Taiwan        4 0.0006134029       NA          NA
## 50  Taiwan, Republic of China        2 0.0003067014       NA          NA
## 52                     Turkey        1 0.0001533507       NA          NA
## 53       United Arab Emirates        1 0.0001533507       NA          NA
## 56                    Uruguay        1 0.0001533507       NA          NA
## 57                        USA        1 0.0001533507       NA          NA
## 58                    Vietnam        1 0.0001533507       NA          NA
##    se.freq    se.prop
## 55      32 0.56140351
## 54       7 0.12280702
## 18       6 0.10526316
## 8        3 0.05263158
## 48       2 0.03508772
## 10       2 0.03508772
## 25       1 0.01754386
## 34       1 0.01754386
## 46       1 0.01754386
## 27       1 0.01754386
## 23       1 0.01754386
## 16      NA         NA
## 4       NA         NA
## 45      NA         NA
## 5       NA         NA
## 6       NA         NA
## 15      NA         NA
## 26      NA         NA
## 43      NA         NA
## 51      NA         NA
## 13      NA         NA
## 29      NA         NA
## 14      NA         NA
## 20      NA         NA
## 21      NA         NA
## 24      NA         NA
## 28      NA         NA
## 32      NA         NA
## 35      NA         NA
## 37      NA         NA
## 47      NA         NA
## 1       NA         NA
## 2       NA         NA
## 3       NA         NA
## 7       NA         NA
## 9       NA         NA
## 11      NA         NA
## 12      NA         NA
## 17      NA         NA
## 19      NA         NA
## 22      NA         NA
## 30      NA         NA
## 31      NA         NA
## 33      NA         NA
## 36      NA         NA
## 38      NA         NA
## 39      NA         NA
## 40      NA         NA
## 41      NA         NA
## 42      NA         NA
## 44      NA         NA
## 49      NA         NA
## 50      NA         NA
## 52      NA         NA
## 53      NA         NA
## 56      NA         NA
## 57      NA         NA
## 58      NA         NA
```

Anonymize and save date

```
# Get rid of these temporary variables
bres <- peer_reviewers <- editors <- revs <- ca_authors <- fa_authors <- la_authors <-  NULL
reviewer1 <- reviewer2 <- reviewer3 <- reviewer4 <- reviewers <- NULL

elife <-elife %>%
  # Now lets remove any identifying information, ie: names and institutions. We also remove country/con
  # We also remove all dates and times, because thees could probably be used to identify information ab
  # Also, lets remove variables that we will not prefently be working with, just to keep the table clea
  select(-c(ca_name, la_name, fa_name,  se_name, bre_name, reviewer1_name, reviewer2_name, reviewer3_nam
         ca_institution, la_institution, fa_institution, se_institution, bre_institution,
         reviewer1_institution, reviewer2_institution, reviewer3_institution, reviewer4_institution,
         se_country, bre_country, se_continent, reviewer1_country, reviewer2_country, reviewer3_country
         initial_submission_time, full_submission_date, rev1_submission_date, rev2_submission_date,
         initial_decision_time, full_decision_date, rev1_decision_date, rev2_decision_date, submission_r
         deltatime_initial_submission_decision, deltatime_full_submission_decision, deltatime_initial_su
         deltatime_rev1,    deltatime_rev2, revision_time,  deltatime_final,
         prop_male_reviewers, prop_female_reviewers, appeal_state1, appeal_state2, appeal_state3, type.r
         reviewer_names, reviewer_countries, reviewer_continents, reviewer_genders, full_decisions,
         reviewer_names_nobre, reviewer_genders_nobre))

# write this file as output, so that future analysis can start from this file as a checkpoint
write.csv(elife, "formatted_data/formatted_elife.csv")

write.csv(people, "formatted_data/elife_people.csv")

# clean the namespace
country_mapping <- NULL
```

Checkpoint

Here we load the data that was manipulated in the previous code chunk. Skip to here if the original (non-anonymized) data is not available.

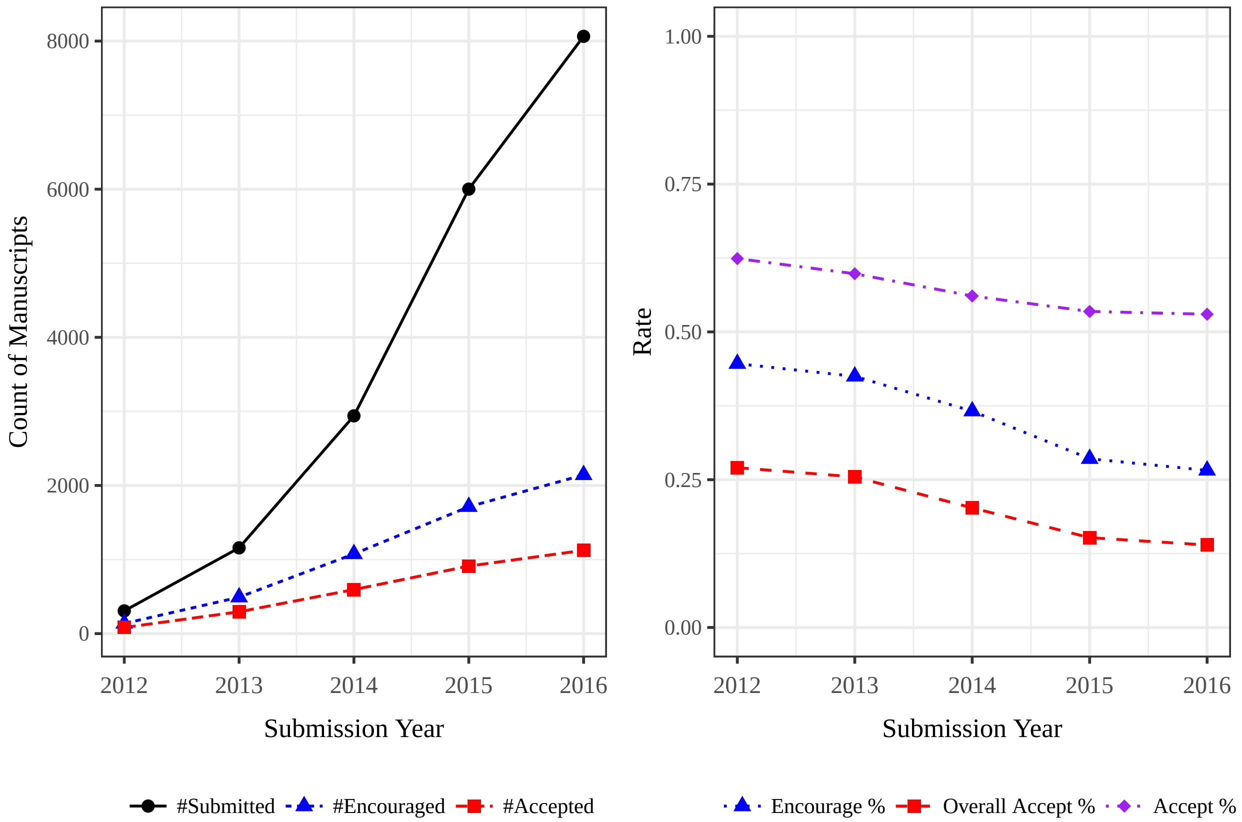
```
elife <- read.csv("formatted_data/formatted_elife.csv")
```

Figure 2

Note: Figure 1 wa smade in an external program, *RawGraphics*, and so does not appear in this notebook.

> Figure 2. Left: Yearly count of initial submissions, encouraged initial submissions, and accepted full submissions to eLife between 2012 and 2016; Right: encourage rate of initial submissions, overall accept rate of initial submissions, and accept rate of full submissions between 2012 and 2016. Submissions during the year of 2017 were not included because we do not have sufficient data for full lifecycle of these manuscripts.

```
d1 <- elife %>%
  group_by(submission_year) %>%
  summarize(
        paper_count = n(),
        accept_count = sum(accepted == TRUE, na.rm = T),
        encourage_count = sum(encouraged == TRUE, na.rm = T)
  ) %>%
  gather(measure_key, value = measurement, paper_count, encourage_count, accept_count) %>%
  mutate(measure_key = factor(measure_key, levels = c("paper_count", "encourage_count", "accept_count")
  filter(submission_year != "2017")


p1 <- d1 %>%
  ggplot(aes(x = submission_year, y = measurement, linetype = measure_key, color = measure_key, shape =
  geom_line() +
  geom_point(size = 2) +
  theme_dakota() +
  labs(
    x = "Submission Year",
    y = "Count of Manuscripts"
  ) +
  scale_color_manual(labels = c("accept_count" = "#Accepted", "encourage_count" = "#Encouraged", "paper_
  scale_shape_discrete(labels = c("accept_count" = "#Accepted", "encourage_count" = "#Encouraged", "pape
  scale_linetype_discrete(labels = c("accept_count" = "#Accepted", "encourage_count" = "#Encouraged", "


d2 <- elife %>%
  group_by(submission_year) %>%
  summarize(
        paper_count = n(),
        accept_count = sum(accepted == TRUE, na.rm = T),
        encourage_count = sum(encouraged == TRUE, na.rm = T),
        encourage_rate = encourage_count / paper_count,
        accept_rate = accept_count / paper_count,
        encourage_accept_rate = accept_count / sum(!is.na(full_decision_made) & full_decision_made)
  ) %>%
  gather(measure_key, value = measurement, encourage_rate, accept_rate, encourage_accept_rate) %>%
  mutate(
    measure_key = factor(measure_key, levels = c("encourage_rate", "accept_rate", "encourage_accept_rat
  ) %>%
  filter(submission_year < 2017)

p2 <- d2 %>%
  ggplot(aes(x = submission_year, y = measurement, linetype = measure_key, color = measure_key, shape =
  geom_line() +
  geom_point(size = 2) +
  ylim(0, 1) +
  theme_dakota() +
  labs(
    x = "Submission Year",
    y = "Rate"
  ) +
  scale_color_manual(labels = c("accept_rate" = "Overall Accept %", "encourage_rate" = "Encourage %", "
                     values = c("blue", "red", "purple")) +
  scale_shape_manual(labels = c("accept_rate" = "Overall Accept %", "encourage_rate" = "Encourage %", "
                     values = c(17, 15, 18)) +
  scale_linetype_manual(labels = c("accept_rate" = "Overall Accept %", "encourage_rate" = "Encourage %"
                        values = c("dotted", "dashed", "dotdash"))

fig2 <- grid.arrange(p1, p2, ncol = 2)
```



```
ggsave("figures/main/fig_2.png", plot = fig2, height = 4, width = 7)

write.csv(d1, "formatted_data/figure2_leftpanel_data.csv")
write.csv(d2, "formatted_data/figure2_rightpanel_data.csv")
```

Data to construct figure 2, right panel, including enocurage, overall accept, and accept rates

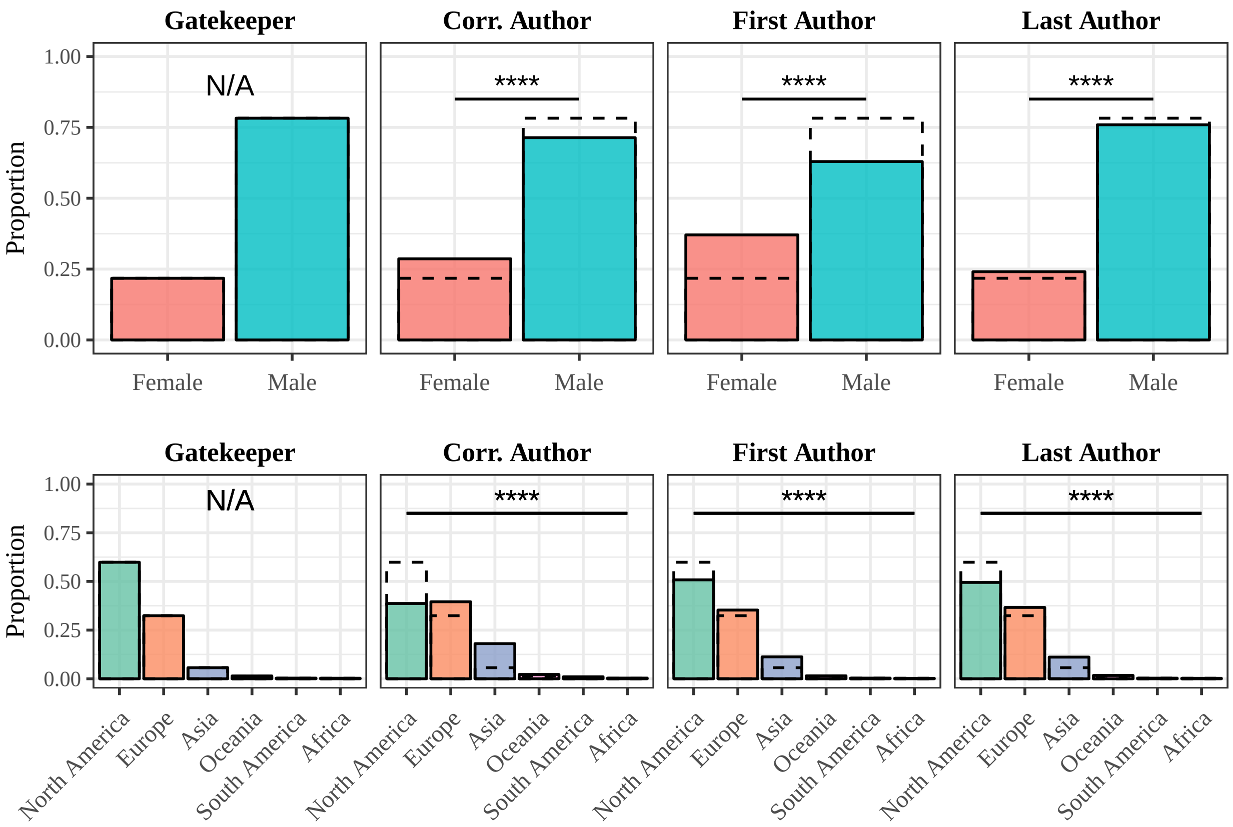
```
d2 %>%
  spread(measure_key, measurement) %>%
  rename(
    overall_accept_rate = accept_rate,
    accept_rate = encourage_accept_rate
    )
```

```
## # A tibble: 5 x 7
##   submission_year paper_count accept_count encourage_count encourage_rate
## *           <int>       <int>        <int>           <int>          <dbl>
## 1            2012         307           83             137      0.4462541
## 2            2013        1158          295             492      0.4248705
## 3            2014        2940          595            1076      0.3659864
## 4            2015        6001          912            1713      0.2854524
## 5            2016        8064         1125            2143      0.2657490
## # ... with 2 more variables: overall_accept_rate <dbl>, accept_rate <dbl>
```

Figure 3

Figure 3. Top: proportion of identified men and women in the populations of distinct gatekeepers (senior editors, reviewing editors, and peer reviewers) and of the populations of distinct corresponding authors, first authors, and last authors; percentages exclude those for whom gender could be identified. Bottom: proportion of people with national affiliations within each of six continents in the population of distinct gatekeepers, and for the population of distinct corresponding, first, and last authors. Black dashed lines overlaid on authorship graphs indicate the proportion of gatekeepers within that gendered or continental category. Asterisks indicate the significance level of X2 tests of independence comparing the frequency of gender or continents between gatekeepers and each authorship type. "*****" = p < 0.0001; "ns" = p > 0.05.

```r
# Now lets get the significance levels...
s <- subset(people, type == "Corr. Author" | type == "Gatekeeper" )
t <- t(table(s$gender, s$type))
corr <- chisq.test(t[1, 1:2], p = prop.table(t[2, 1:2]))


s <- subset(people, type == "First Author" | type == "Gatekeeper" )
t <- t(table(s$gender, s$type))
first <- chisq.test(t[1, 1:2], p = prop.table(t[2, 1:2]))


s <- subset(people, type == "Last Author" | type == "Gatekeeper" )
t <- t(table(s$gender, s$type))
last <- chisq.test(t[2, 1:2], p = prop.table(t[1, 1:2]))

sig_df <- data.frame(type = rep(c("Gatekeeper", "Corr. Author", "First Author", "Last Author"), 1),
                     gender = rep(c("Male", "Female"), 2),
                     sig = c("N/A", sig2ast(corr$p.value), sig2ast(first$p.value), sig2ast(last$p.value

gender_sig_list <- list("Corresponding Author" = corr, "First Author" = first, "Last Author" = last)


expected <- people %>%
  filter(gender %in% c("M", "F")) %>%
  mutate(gender = ifelse(gender == "M", "Male", "Female")) %>%
  filter(type == "Gatekeeper") %>%
  mutate(total = n()) %>%
  group_by(type, gender) %>%
  summarize(
    expected_prop = n() / total[1]
  ) %>%
  ungroup() %>%
  select(-type)


p1 <- people %>%
  filter(gender %in% c("M", "F")) %>%
  mutate(gender = ifelse(gender == "M", "Male", "Female")) %>%
  group_by(type) %>%
  mutate(total = n()) %>%
  group_by(type, gender) %>%
  summarize(
    prop = n() / total[1]
  ) %>%
  ungroup() %>%
  left_join(expected, by = "gender") %>%
  left_join(sig_df, by = c("gender", "type")) %>%
  mutate(
    type = factor(type, levels = c("Gatekeeper", "Corr. Author", "First Author", "Last Author"))
  ) %>%
  # start ggplot
  ggplot(aes(x = gender, y = prop, fill = gender)) +
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  geom_bar(stat = "identity", aes(y = expected_prop), alpha = 0, color = "black", fill = "white", size =
  #geom_text(aes(label = paste0(round(prop, 3) * 100, "%"), y = 0.1), size = 3) +
  geom_text(aes(label = sig, x = 1.5, y = 0.9)) +
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.85, 1.1), yend = ifelse(sig != "N/A", 0.8
  facet_wrap(~type, nrow = 1) +
  theme_dakota() +
  ylim(c(0, 1)) +
  theme(
    axis.title.x = element_blank(),
    legend.position = "right"
  ) +
  labs(y = "Proportion") +
  guides(fill = F)

s <- subset(people, continent != "Antarctica" & (type == "Corr. Author" | type == "Gatekeeper" ))
t <- t(table(s$continent, s$type))
corr <- chisq.test(t[1, ], p = prop.table(t[2, ]))

s <- subset(people, continent != "Antarctica" & (type == "First Author" | type == "Gatekeeper" ))
t <- t(table(s$continent, s$type))
first <- chisq.test(t[1, ], p = prop.table(t[2, ]))

s <- subset(people, continent != "Antarctica" & (type == "Last Author" | type == "Gatekeeper" ))
t <- t(table(s$continent, s$type))
last <- chisq.test(t[2, ], p = prop.table(t[1, ]))

sig_df <- data.frame(type = rep(c("Gatekeeper", "Corr. Author", "First Author", "Last Author"), 3),
                     continent = rep(c("Africa", "Asia", "Europe", "North America", "Oceania", "South Am
                     sig = c("N/A", sig2ast(corr$p.value), sig2ast(first$p.value), sig2ast(last$p.value

continent_sig_list <- list("Corresponding Author" = corr, "First Author" = first, "Last Author" = last)

# Now we should repeat this graph, except this time for the continental representation
expected <- people %>%
  filter(type == "Gatekeeper") %>%
  mutate(total = n()) %>%
  filter(continent != "Antarctica") %>%
  group_by(type, continent) %>%
  summarize(
    expected_prop = n() / total[1]
  ) %>%
  ungroup() %>%
  select(-type)


p2 <- people %>%
  group_by(type) %>%
  mutate(total = n()) %>%
  filter(continent != "Antarctica") %>%
  group_by(type, continent) %>%
  summarize(
    prop = n() / total[1]
  ) %>%
  ungroup() %>%
  left_join(expected, by = "continent") %>%
  left_join(sig_df, by = c("continent", "type")) %>%
  mutate(
    type = factor(type, levels = c("Gatekeeper", "Corr. Author", "First Author", "Last Author")),
    continent = reorder(continent, -prop)
  ) %>%
  # start ggplot
  ggplot(aes(x = continent, y = prop, fill = continent)) +
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  geom_bar(stat = "identity", aes(y = expected_prop), alpha = 0, color = "black", fill = "white", size =
  #geom_text(aes(label = paste0(round(prop, 3) * 100, "%"), y = 0.05), size = 2) +
  geom_text(aes(label = sig, x = 3.5, y = 0.92)) +
  geom_segment(aes(x = 1, xend = 6, y = ifelse(sig != "N/A", 0.85, 1.1), yend = ifelse(sig != "N/A", 0.8
  facet_wrap(~type, nrow = 1) +
  theme_dakota() +
  ylim(c(0, 1)) +
  guides(fill = F) +
  theme(
    axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1),
    axis.title.x = element_blank()
  ) +
  labs(y = "Proportion") +
  scale_fill_brewer(palette = "Set2")

fig3 <- grid.arrange(p1, p2)
```



```r
ggsave("figures/main/fig_3.png", plot = fig3, height = 5, width = 7)
```

And below are the explicit results of the significaince tests used in the previous graphs to compare the actual proportion of male/female authors with the expected proportion given the population of gatekeepers.

```r
fig3_top_sig_table <- data.frame(
  authorship = c("Corresponding", "First", "Last"),
  p.value = sapply(gender_sig_list, function(x) x$p.value),
  n = sapply(gender_sig_list, function(x) sum(x$observed)),
  statistic = sapply(gender_sig_list, function(x) x$statistic),
  df = sapply(gender_sig_list, function(x) x$parameter)
)

rownames(fig3_top_sig_table) <- NULL
fig3_top_sig_table
```

```
##      authorship       p.value     n statistic df
## 1 Corresponding 3.002259e-103 16776 465.53476  1
## 2         First 1.877701e-184  6088 838.90516  1
## 3          Last  5.413785e-05  5163  16.29741  1
```

And the same for the content-level tests

```r
fig3_bottom_sig_table <- data.frame(
  continent = c("Corresponding", "First", "Last"),
  p.value = sapply(continent_sig_list, function(x) x$p.value),
  n = sapply(continent_sig_list, function(x) sum(x$observed)),
  statistic = sapply(continent_sig_list, function(x) x$statistic),
  df = sapply(continent_sig_list, function(x) x$parameter)
)
```

```
rownames(fig3_bottom_sig_table) <- NULL
fig3_bottom_sig_table
```

```
##       continent       p.value     n statistic df
## 1 Corresponding  0.000000e+00 18193 6908.6581  5
## 2         First 1.271975e-101  6671  480.5294  5
## 3          Last  2.237163e-90  5565  428.4003  5
```

Frequencies of author and gatekeeper genders at eLife

```
people %>%
  group_by(type) %>%
  mutate(total = n()) %>%
  group_by(type, gender) %>%
  summarize(
    freq = n(),
    prop = freq / total[1]
    )
```

```
## # A tibble: 12 x 4
## # Groups:   type [?]
##            type gender  freq       prop
##           <chr> <fctr> <int>      <dbl>
##  1 Corr. Author      F  4803 0.26356802
##  2 Corr. Author      M 11973 0.65702683
##  3 Corr. Author    UNK  1447 0.07940515
##  4 First Author      F  2257 0.33646392
##  5 First Author      M  3831 0.57110912
##  6 First Author    UNK   620 0.09242695
##  7   Gatekeeper      F  1372 0.20572800
##  8   Gatekeeper      M  4934 0.73984106
##  9   Gatekeeper    UNK   363 0.05443095
## 10  Last Author      F  1243 0.22216265
## 11  Last Author      M  3920 0.70062556
## 12  Last Author    UNK   432 0.07721180
```

Frequencies of author and gatekepeer continental affilaitions at eLife

```
people %>%
  group_by(type) %>%
  mutate(total = n()) %>%
  group_by(type, continent) %>%
  summarize(
    freq = n(),
    prop = freq / total[1]
    )
```

```
## # A tibble: 29 x 4
## # Groups:   type [?]
##            type     continent  freq         prop
##           <chr>         <chr> <int>        <dbl>
##  1 Corr. Author        Africa    62 3.402294e-03
##  2 Corr. Author    Antarctica     1 5.487571e-05
##  3 Corr. Author          Asia  3288 1.804313e-01
##  4 Corr. Author        Europe  7211 3.957087e-01
##  5 Corr. Author North America  7045 3.865994e-01
##  6 Corr. Author       Oceania   399 2.189541e-02
##  7 Corr. Author South America   188 1.031663e-02
##  8 Corr. Author          <NA>    29 1.591395e-03
##  9 First Author        Africa    14 2.087060e-03
## 10 First Author    Antarctica     1 1.490757e-04
## # ... with 19 more rows
```

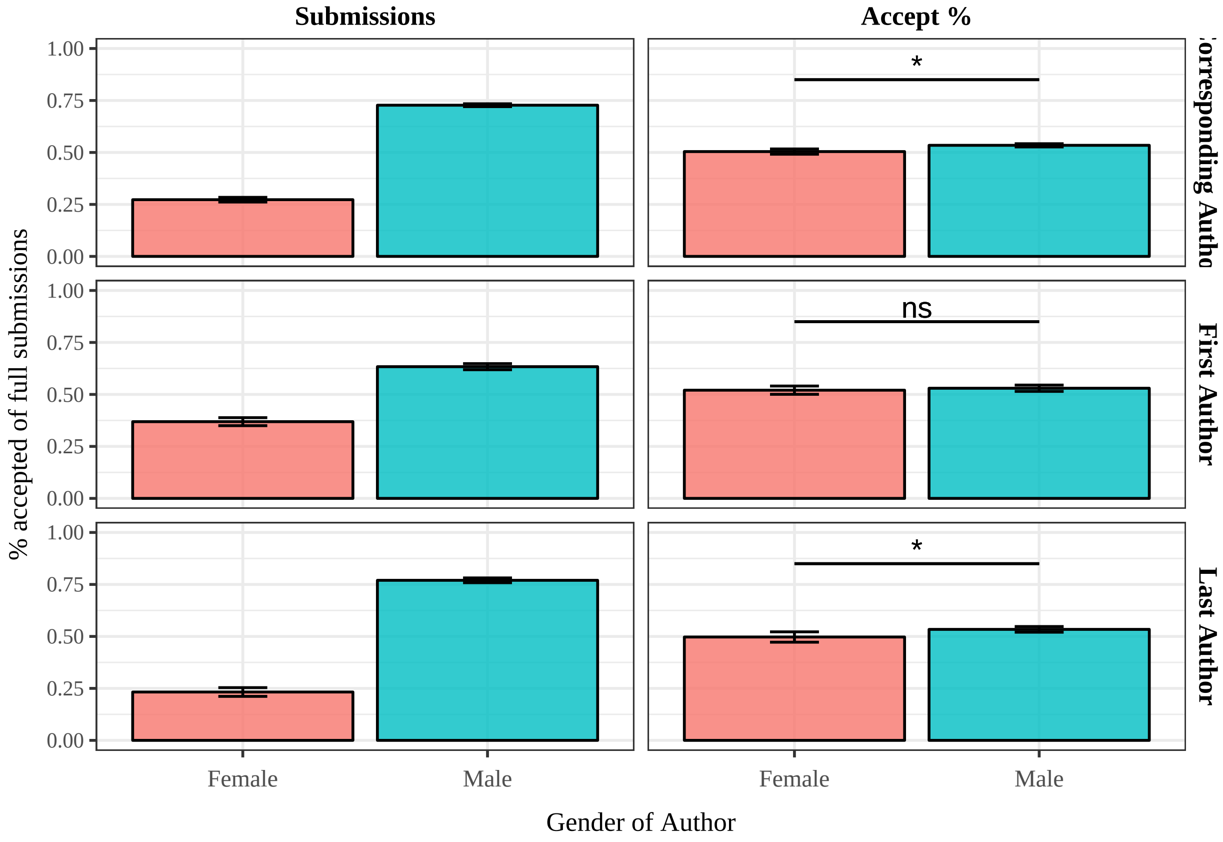
Figure 4

> Figure 4. Percentage of full submissions that were accepted, shown by the gender of the corresponding author, first author, and last author. Authors whose gender is unknown are excluded from analysis. See Figure SI.2 for an extension of this figure including submission rates, encourage rates, and overall acceptance races. Vertical error bars indicate 95th confidence intervals of the proportion of submitted, encouraged, and accepted initial and full submissions. Asterisks indicate significance level of X2 tests of independence of frequency of encourage and acceptance by gender; "*" = p < 0.05; "ns" = p > 0.05.

Note: There is a lot of extra code with this figure, because this figure originally showed informastion for submission rates and encourage and acceptance rates of initial submissions. Now we only show acceptance rates of full submissions. See figure SI.### for the expanded figure.

```r
# First, I'll go through and run all the tests to get signif. values. I toyed around with ways to do th
# manual method is perhaps the simplest

# First, test the encourage rate diffs
s <- subset(elife, initial_decision_made)
t <- table("ca_gender" = s$ca_gender, "encouraged" = s$encouraged)[1:2,]
ca_encouraged <- chisq.test(t[, 1:2])

# Difference in acceptance rates by gender of corresponding author
s <- subset(elife, initial_decision_made & (!has_full_submission | full_decision_made))
t <- table("ca_gender" = s$ca_gender, "accepted" = s$accepted)[1:2,]
ca_accepted <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of corresponding author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("ca_gender" = s$ca_gender, "accepted" = s$accepted)[1:2,]
ca_ea <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of first author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("fa_gender" = s$fa_gender, "accepted" = s$accepted)[1:2,]
fa_ea <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of last author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("la_gender" = s$la_gender, "accepted" = s$accepted)[1:2,]
la_ea <- chisq.test(t[, 1:2])

# Now we use the results of these tests to construct a table
```

```
measurements <- c(rep("submit_rate", 3), rep("encourage_rate", 3), rep("accept_rate", 3), rep("encourag
author <- rep(c("ca_gender", "fa_gender", "la_gender"), 4)

sig <- c("N/A", "N/A", "N/A", # submit rates, all NA since we don't really compare this
         sig2ast(ca_encouraged$p.value), "N/A", "N/A", # encourage rate
         sig2ast(ca_accepted$p.value), "N/A", "N/A",
         sig2ast(ca_ea$p.value), sig2ast(fa_ea$p.value), sig2ast(la_ea$p.value)
         )
sig_df <- data.frame(measure_key = factor(measurements), author_key = factor(author), sig = sig)

# Now lets save these test results for later
sig_list <- list("Corresponding author enc. rate" = ca_encouraged,
                   "Corresponding author acc. rate" = ca_accepted,
                   "Corresponding author enc-acc rate" = ca_ea,
                   "First author enc-acc rate" = fa_ea,
                   "last author enc-acc rate" = la_ea)



data_fig4 <- elife %>%
  filter(initial_decision_made) %>%
  gather(author_key, value = gender, ca_gender, la_gender, fa_gender) %>%
  filter(gender %in% c('M', 'F')) %>%
  group_by(author_key) %>%
  mutate(
    # if not ocnsidering the corr. author, then the count is all full submissions, ie: for when a submi
    total_papers = ifelse(author_key == "ca_gender", n(), sum(has_full_submission))
    )%>%
  group_by(author_key, gender) %>%
  summarize(
        paper_count = n(),
        accept_count = sum(accepted == TRUE, na.rm = T),
        encourage_count = sum(encouraged == TRUE),
        encourage_rate = ifelse(author_key[1] == "ca_gender", encourage_count / n(), NA),
        # this accept rate is the number of accepted papers / number of initial + full submissions
        accept_rate = ifelse(author_key[1] == "ca_gender", accept_count / sum(!has_full_submission | ful
        submit_rate = n() / total_papers[1],
        # this is the number of accepted papers divided by all papers
        encourage_accept_rate = accept_count / sum(has_full_submission & full_decision_made, na.rm = T)
  ) %>%
  ungroup() %>%
  gather(measure_key, value = measurement, submit_rate, encourage_accept_rate) %>%
  left_join(sig_df, by = c("measure_key", "author_key")) %>%
  mutate(
    author_key = factor(author_key,
                        levels = c("ca_gender", "fa_gender", "la_gender"),
                        labels = c("ca_gender" = "Corresponding Author", "fa_gender" = "First Author",
                        ),
    measure_key = factor(measure_key,
                         labels = c("submit_rate" = "Submissions", "encourage_rate" = "Enc %", "accept_
                         levels = c("submit_rate", "encourage_rate", "accept_rate", "encourage_accept_ra
    gender = ifelse(gender == "F", "Female", "Male"),
    standard_error = 1.96 * sqrt( (measurement * (1 - measurement)) / paper_count),
    lower = measurement - standard_error,
    upper = measurement + standard_error
  )


fig4 <- data_fig4 %>%
  ggplot(aes(x = gender, y = measurement, color = factor(gender), shape = factor(gender), fill = factor
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2, color = "black") +
  geom_text(aes(x = 1.5, y = 0.92, label = ifelse(measure_key == "Submissions", "", as.character(sig)))
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.85, 1.1), yend = ifelse(sig != "N/A", 0.8
  facet_grid(author_key ~ measure_key) +
  coord_cartesian(ylim = c(0, 1)) +
  theme_dakota() +
  guides(fill = F) +
  labs(
    x = "Gender of Author",
    y = "% accepted of full submissions"
  )

fig4
```



```
ggsave("figures/main/fig_4.png", plot = fig4, height = 5, width = 7)
```

Signif. test results for figure 4

```
fig4_sig_table <- data.frame(
  test = names(sig_list),
  p.value = sapply(sig_list, function(x) x$p.value),
  n = sapply(sig_list, function(x) sum(x$observed)),
  statistic = sapply(sig_list, function(x) x$statistic),
  df = sapply(sig_list, function(x) x$parameter)
)

rownames(fig4_sig_table)<- NULL
fig4_sig_table
```

```
##                                 test     p.value     n  statistic df
## 1    Corresponding author enc. rate 0.005739427 21846  7.6303466  1
## 2    Corresponding author acc. rate 0.001199540 21222 10.4910521  1
## 3 Corresponding author enc-acc rate 0.042796113  6014  4.1034377  1
## 4         First author enc-acc rate 0.504719617  5914  0.4449987  1
## 5          last author enc-acc rate 0.017358230  6036  5.6597870  1
```

Data used to produce figure 4

```
data_fig4 %>%
  select(-sig, -lower, -upper, -standard_error) %>%
  spread(measure_key, measurement)
```

```
## # A tibble: 6 x 9
##             author_key gender paper_count accept_count encourage_count
## *               <fctr>  <chr>       <int>        <int>           <int>
## 1 Corresponding Author Female        5959          790            1705
## 2 Corresponding Author   Male       15887         2376            4853
## 3         First Author Female        2409         1142            2356
## 4         First Author   Male        4136         1971            4045
## 5          Last Author Female        1549          695            1515
## 6          Last Author   Male        5128         2476            5014
## # ... with 4 more variables: encourage_rate <dbl>, accept_rate <dbl>,
## #   Submissions <dbl>, `Accept %` <dbl>
```

Gender distirbution of gender-identified authors on full submissions at eLife, at manuscript level, includes duplicate authors

```
full <- elife %>%
  filter(has_full_submission)
```

Of correpsonding authors

```
full %>%
  filter(ca_gender %in% c("M", "F")) %>%
  group_by(ca_gender) %>%
  summarize(
    freq = n(),
    prop = freq / dim(full)[1]
  )
```

```
## # A tibble: 2 x 3
##   ca_gender  freq      prop
##      <fctr> <int>     <dbl>
## 1          F  1725 0.2398165
## 2          M  4913 0.6830252
```

First authors…

```
full %>%
  filter(fa_gender %in% c("M", "F")) %>%
  group_by(fa_gender) %>%
  summarize(
    freq = n(),
    prop = freq / dim(full)[1]
  )
```

```
## # A tibble: 2 x 3
##   fa_gender  freq      prop
##      <fctr> <int>     <dbl>
## 1          F  2404 0.3342138
## 2          M  4125 0.5734742
```

And last authors

```
full %>%
  filter(la_gender %in% c("M", "F")) %>%
  group_by(la_gender) %>%
  summarize(
    freq = n(),
    prop = freq / dim(full)[1]
  )
```

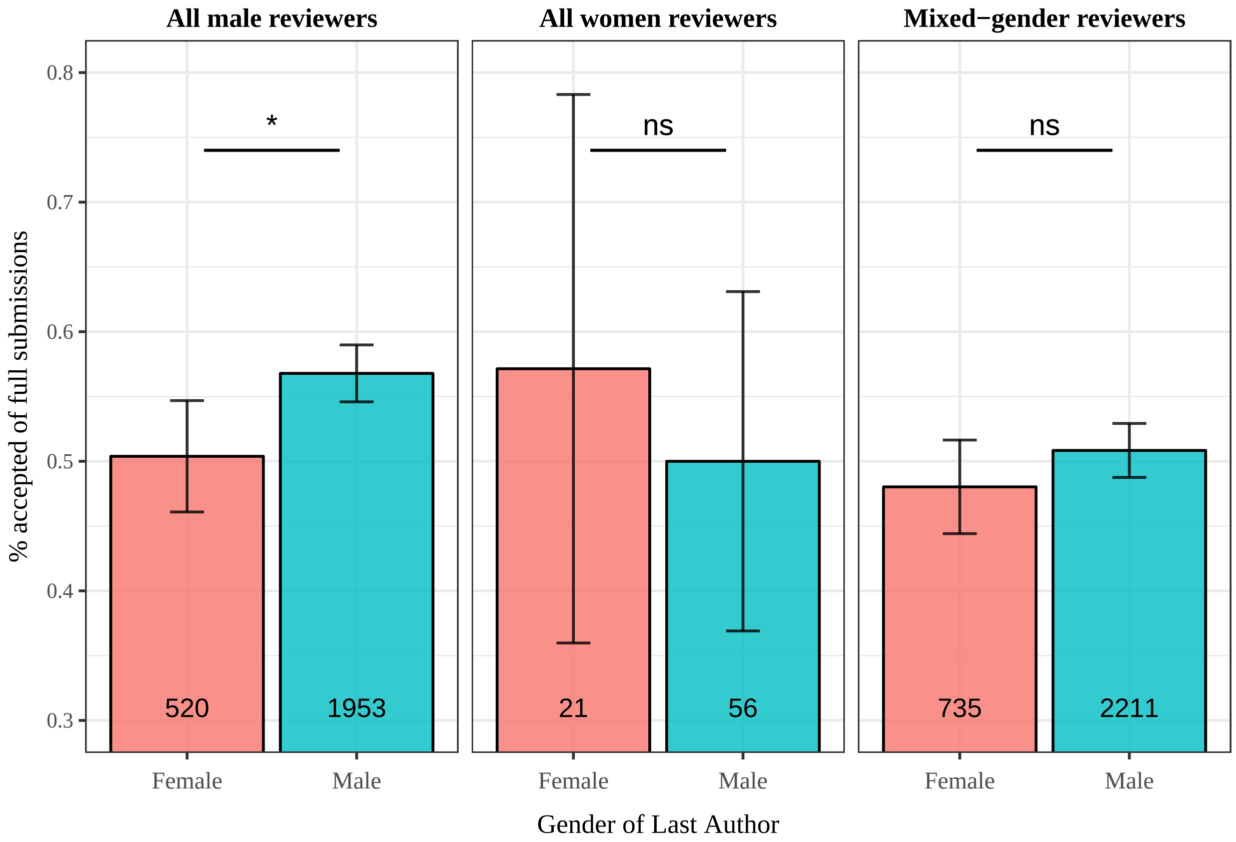
```
## # A tibble: 2 x 3
##   la_gender  freq      prop
##      <fctr> <int>     <dbl>
## 1          F  1547 0.2150702
## 2          M  5114 0.7109690
```

Figure 5

Figure 5. Percentage of full submissions that were accepted, shown by the gender of the last author, and divided by the gender composition of the peer reviewers. Text at the base of each bar indicate the number full submissions within each category of reviewer team and authorship gender. Vertical error bars indicate 95th percentile confidence intervals of the proportion of accepted full submissions. For the composition category of "All women reviewers", error bars extend beyond scale of figure; see Figure SI.3 to see the error interval. Asterisks indicate significance level of X2 tests of independence on frequency of acceptance by gender of author given each team composition; "ns" indicates no observed statistical significance. "*" = $p < 0.05$; "ns" = $p > 0.05$.

Note: As with figure 4, we ultimately decided to simplify this figure, and so there is some excess code. The expanded code can be found in figure SI.###.

```
sig_list <- list()
for(comp in c("All Men", "All Women", "Mixed", "Uncertain")) {
  for(gender_var in c("ca_gender", "fa_gender", "la_gender")) {
    if (!is.na(comp)) {
      sub <- subset(elife, initial_decision_made & full_decision_made & composition == comp)[, c("accep
      t <- t(table(sub))[1:2,]
      test = chisq.test(t)
      test$n = dim(sub)[1]
      sig_list[length(sig_list) + 1] <- list(test)
    }
  }
}

sig_df <- data.frame(composition = c(rep("All Men", 3), rep("All Women", 3), rep("Mixed", 3), rep("Unce
                     author_key = rep(c("ca_gender", "fa_gender", "la_gender"), 4),
                     sig = sapply(sig_list, function(test) { sig2ast(test$p.value)})
)


data_fig5 <- elife %>%
  filter(initial_decision_made & full_decision_made & !is.na(composition)) %>%
  mutate(total_submissions = n()) %>%
  gather(author_key, value = gender, la_gender) %>%
  filter(gender %in% c("M", "F")) %>%
  group_by(composition, author_key, gender) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE),
    acceptance_rate = sum(accepted == TRUE) / paper_count,
    standard_error = 1.96 * sqrt( (acceptance_rate * (1 - acceptance_rate)) / paper_count),
    lower = acceptance_rate - standard_error,
    upper = acceptance_rate + standard_error
  ) %>%
  ungroup() %>%
  left_join(sig_df, by = c("composition", "author_key")) %>%
  mutate(
    author_key = factor(author_key,
                        levels = c("ca_gender", "fa_gender", "la_gender"),
                        labels = c("ca_gender" = "Corresponding", "fa_gender" = "First", "la_gender" =
    ,
    gender = ifelse(gender == "M", "Male", "Female"),
    composition = factor(composition, labels = c("All Men" = "All male reviewers", "All Women" = "All w
  ) %>%
  filter(composition != "Uncertain")


fig5 <- data_fig5 %>%
  ggplot(aes(x = gender, y = acceptance_rate, fill = gender)) +
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  geom_text(aes(y = 0.31, label = paper_count), size = 3.5, color = "black") +
  #geom_text(aes(y = 0.1, label = paste0(round(acceptance_rate, 3) * 100, "%")), size = 2.5, color = "b
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2, color = "black", alpha = 0.8) +
  geom_text(aes(x = 1.5, y = 0.76, label = sig), color = "black") +
  #geom_text(aes(x = gender, y = 0.1, label = round(acceptance_rate, 3) * 100 ), color = "black") +
  geom_segment(aes(x = 1.1, xend = 1.9, y = ifelse(sig != "N/A", 0.74, 1.1), yend = ifelse(sig != "N/A"
  facet_wrap( ~composition) +
  coord_cartesian(ylim = c(0.30, 0.8)) +
  theme_dakota() +
  guides(fill = F) +
  labs(y = "% accepted of full submissions",
       x = "Gender of Last Author"
  )

fig5
```



```
ggsave("figures/main/fig_5.png", plot = fig5, height = 5, width = 7)
```

Signif. test resutls for figure 5

```
names(sig_list) <- c("Reviewers all Men - Corresponding", "Reviewers all Men - First", "Reviewers all Me
                     "Reviewers all Women - Corresponding", "Reviewers all Women - First", "Reviewers al
                     "Mixed Gender Reviewers - Corresponding", "Mixed Gender Reviewers - First", "Mixed
                     "Uncertain Composition - Corresponding", "Uncertain Composition - First", "Uncertai

fig4_sig_table <- data.frame(
  composition = sapply(strsplit(names(sig_list), " - "), function(x) x[1]),
  authorship = sapply(strsplit(names(sig_list), " - "), function(x) x[2]),
  n = sapply(sig_list, function(x) sum(x$observed)),
  df = sapply(sig_list, function(x) x$parameter),
  statistic = sapply(sig_list, function(x) x$statistic),
  p.value = sapply(sig_list, function(x) x$p.value)
)

rownames(fig4_sig_table) <- NULL
fig4_sig_table
```

```
##                  composition    authorship    n df   statistic    p.value
## 1       Reviewers all Men Corresponding 2473  1 4.67111748 0.03067396
## 2       Reviewers all Men         First 2443  1 0.18348567 0.66839467
## 3       Reviewers all Men          Last 2473  1 6.55182123 0.01047769
## 4     Reviewers all Women Corresponding   75  1 2.60643930 0.10643049
## 5     Reviewers all Women         First   71  1 0.17354928 0.67697652
## 6     Reviewers all Women          Last   77  1 0.09158925 0.76216640
## 7  Mixed Gender Reviewers Corresponding 2928  1 1.37835803 0.24038103
## 8  Mixed Gender Reviewers         First 2870  1 0.00000000 1.00000000
## 9  Mixed Gender Reviewers          Last 2946  1 1.63111443 0.20154898
## 10  Uncertain Composition Corresponding  538  1 0.09738538 0.75499013
## 11  Uncertain Composition         First  530  1 1.01590767 0.31349169
## 12  Uncertain Composition          Last  540  1 0.53894969 0.46286834
```

Data used to produce figure 5

```
data_fig5 %>%
  select(-standard_error, -lower, -upper, -sig, -author_key)
```

```
## # A tibble: 6 x 5
##              composition gender paper_count accept_count acceptance_rate
##                   <fctr>  <chr>       <int>        <int>           <dbl>
## 1     All male reviewers Female         520          262       0.5038462
## 2     All male reviewers   Male        1953         1109       0.5678443
## 3    All women reviewers Female          21           12       0.5714286
## 4    All women reviewers   Male          56           28       0.5000000
## 5 Mixed-gender reviewers Female         735          353       0.4802721
## 6 Mixed-gender reviewers   Male        2211         1124       0.5083673
```

Number of full submissions

```
full <- elife %>% filter(has_full_submission)
dim(full)[1]
```

```
## [1] 7193
```

Number of full submissions for which a final decision of accept or reject was made

```
table(full$final_decision_made)
```

```
##
## FALSE  TRUE
##   602  6591
```

Reviewer team composition for full submissions with a final decision

```
full_final <- full %>% filter(final_decision_made)
table(full_final$composition)
```

```
##
##   All Men All Women     Mixed Uncertain
##      2697        81      3226       587
```

As %

```
prop.table(table(full_final$composition))
```

```
##
##    All Men  All Women      Mixed  Uncertain
## 0.40919436 0.01228949 0.48945532 0.08906084
```

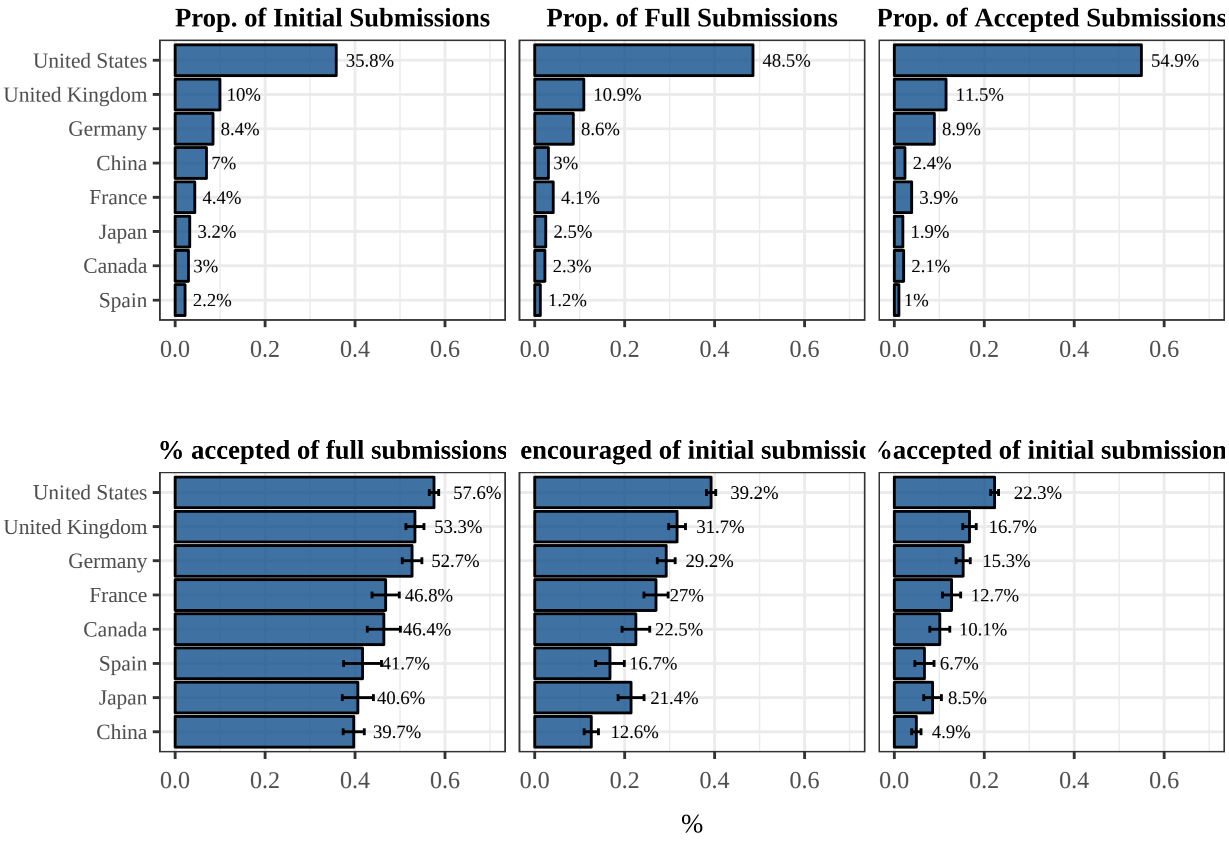
Figure 6

Figure 6. Top: proportion of all initial submissions, encouraged initial submissions, and accepted full submissions comprised by the national affiliation of the corresponding author for the top eight most prolific countries in terms of initial submissions. Bottom: Encourage rate of initial submissions, acceptance rate of initial submissions, and acceptance rate of full submissions by national affiliation of the corresponding author for the top eight more prolific countries in terms of initial submissions. Error bars on bottom panel indicate standard error of proportion of encouraged initial submissions and accepted initial and full submissions for each country. This same graph with the top 16 most prolific nations can be found in Figure SI.4

```
# Its easiest and most efficient to calculate these total values outside of the dplyr chain below
total_submissions <- length(unique(elife$MSNO))
total_full_submissions <- sum(!elife$full_decision_date_isNA, na.rm = T)
total_encouraged <- with(elife, sum(initial_decision_made & encouraged, na.rm = T))
total_accepted <- with(elife, sum(full_decision_made & accepted == T, na.rm = T))

# Firs the first plot, this one will show the proportion that each countrie constitutes the total numbe
data_fig5_p1 <- elife %>%
  filter(initial_decision_made & (full_decision_made | full_decision_date_isNA) & !is.na(ca_country)) %
  mutate(ca_country = factor(sapply(as.character(ca_country), simpleCap))) %>% # capitalize first lette
  group_by(ca_country) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_count = sum(encouraged == TRUE, na.rm = T),
    full_submissions = sum(has_full_submission),
    prop_of_full =  full_submissions / total_full_submissions,
    prop_of_initial = paper_count / total_submissions,
    prop_of_encouraged = encourage_count / total_encouraged,
    prop_of_accepted = accept_count / total_accepted
  ) %>%
  group_by(ca_country) %>%
  mutate(totals = sum(paper_count)) %>%
  ungroup() %>%
  top_n(8, totals) %>%
  gather(prop_key, value = prop, prop_of_initial, prop_of_full, prop_of_accepted) %>%
  mutate(prop_key = factor(prop_key,
                           levels = c("prop_of_initial", "prop_of_full", "prop_of_accepted"),
                           labels = c("prop_of_initial" = "Prop. of Initial Submissions",
                                      "prop_of_full" = "Prop. of Full Submissions",
                                      "prop_of_accepted" = "Prop. of Accepted Submissions")),
         ca_country = reorder(ca_country, paper_count)
  )
```

```
p1 <- data_fig5_p1 %>%
  # Start ggplot
  ggplot(aes(x = ca_country, y = prop)) +
  geom_bar(stat = "identity", color = "black", alpha = 0.8, fill = "dodgerblue4", position = position_d
  geom_text(aes(y = prop, label = paste0(round(prop, 3) * 100, "%")), size = 2.5, hjust = -0.2, family
  scale_y_continuous(limits = c(0, 1)) +
  facet_wrap(~prop_key, labeller = labeller(key = labels)) +
  theme_dakota() +
  coord_flip() +
  ylim(0, 0.7) +
  labs(y = "") +
  theme(
    strip.background = element_blank(),
    text = element_text(size = 10, family = "Times"),
    plot.title = element_text(size = 12),
    strip.text = element_text(face = "bold"),
    axis.title.y = element_blank()
  )


data_fig5_p2 <- elife %>%
  filter(initial_decision_made & (full_decision_made | full_decision_date_isNA) & !is.na(ca_country)) %
  mutate(ca_country = factor(sapply(as.character(ca_country), simpleCap))) %>% # capitalize first lette
  group_by(ca_country) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_count = sum(encouraged == TRUE, na.rm = T),
    encourage_rate = encourage_count / paper_count,
    accept_rate = accept_count / sum(!has_full_submission | full_decision_made, na.rm = T),
    encourage_accept_rate = accept_count / sum(has_full_submission & full_decision_made, na.rm = T)
  ) %>%
  group_by(ca_country) %>%
  mutate(totals = sum(paper_count)) %>%
  ungroup() %>%
  top_n(8, totals) %>%
  mutate(
    ca_country = reorder(ca_country, encourage_accept_rate)
  ) %>%
  gather(measure_key, value = measurement, encourage_rate, accept_rate, encourage_accept_rate) %>%
  mutate(measure_key = factor(measure_key,
                         levels = c("encourage_accept_rate", "encourage_rate", "accept_rate"),
                         labels = c("encourage_accept_rate" = "% accepted of full submissions",
                                    "encourage_rate" = "% encouraged of initial submissions",
                                    "accept_rate" = "%accepted of initial submissions"
                                    ))
  ) %>%
  group_by(measure_key) %>%
  mutate(
    se = 1.96 * sqrt(measurement * (1 - measurement) / paper_count),
    lower = measurement - se,
    upper = measurement + se
  )
```

```
p2 <- data_fig5_p2 %>%
  ggplot(aes(x = ca_country, y = measurement)) +
  geom_bar(stat = "identity", color = "black", fill = "dodgerblue4", alpha = 0.8) +
  geom_text(aes(y = measurement, label = paste0(round(measurement, 3) * 100, "%")), size = 2.5, hjust =
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2) +
  facet_wrap(~measure_key, labeller = labeller(key = labels)) +
  theme_dakota() +
  labs(y = "%") +
  coord_flip() +
  ylim(0, 0.7) +
  theme(
    axis.title.y = element_blank()
  )

fig6 <- grid.arrange(p1, p2)
```



```
ggsave("figures/main/fig_6.png", plot = fig6, height = 7, width = 8)
```

Data to produce figure 5, the top panel

```
data_table <- data_fig5_p1 %>%
  spread(prop_key, prop)

data_table
```

```
## # A tibble: 8 x 10
##       ca_country paper_count accept_count encourage_count full_submissions
## *         <fctr>       <int>        <int>           <int>            <int>
## 1          Spain         526           35              88               87
## 2         Canada         707           71             159              158
## 3          Japan         775           65             166              171
## 4         France        1042          132             281              287
## 5          China        1662           81             209              212
## 6        Germany        2011          305             588              598
## 7 United Kingdom        2379          394             753              761
## 8  United States        8553         1882            3354             3383
## # ... with 5 more variables: prop_of_encouraged <dbl>, totals <int>,
## #   `Prop. of Initial Submissions` <dbl>, `Prop. of Full
## #   Submissions` <dbl>, `Prop. of Accepted Submissions` <dbl>
```

Proportion of intiial submissions constituted by top 8 counties

```
sum(data_table$`Prop. of Initial Submissions`)
```

```
## [1] 0.7393526
```

Proportion of full submissions constituted by top 8 counties

```
sum(data_table$`Prop. of Full Submissions`)
```

```
## [1] 0.8115048
```

Proportion of accepted submissions constituted by top 8 counties

```
sum(data_table$`Prop. of Accepted Submissions`)
```

```
## [1] 0.8654407
```

Data used to produce figure 5, bottom panel

```
data_table <- data_fig5_p2 %>%
  select(-se, -lower, -upper)

data_table
```

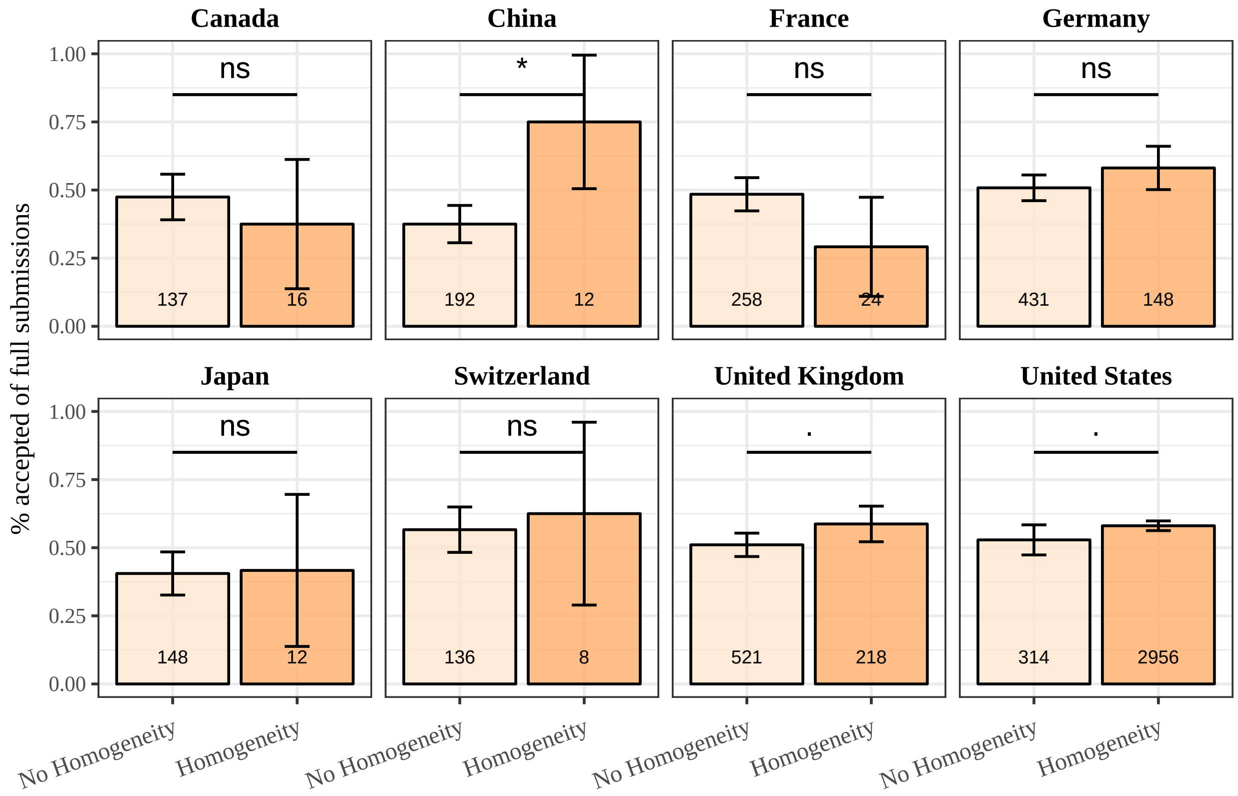
```
## # A tibble: 24 x 7
## # Groups:   measure_key [3]
##        ca_country paper_count accept_count encourage_count totals
##            <fctr>       <int>        <int>           <int>  <int>
##  1         Canada         707           71             159    707
##  2          China        1662           81             209   1662
##  3         France        1042          132             281   1042
##  4        Germany        2011          305             588   2011
##  5          Japan         775           65             166    775
##  6          Spain         526           35              88    526
##  7 United Kingdom        2379          394             753   2379
##  8  United States        8553         1882            3354   8553
##  9         Canada         707           71             159    707
## 10          China        1662           81             209   1662
## # ... with 14 more rows, and 2 more variables: measure_key <fctr>,
## #   measurement <dbl>
```

Figure 7

Figure 7. Left: acceptance rate of full submissions compared between presence and absence of homogeneity between the national affiliation of the corresponding author and of at least one. Difference is shown comparing the results for all submissions (top), for all submissions that do not have corresponding authors from the U.S. (middle), and for all submissions that do not have a corresponding author from the U.S., U.K., or Germany (bottom). Right: acceptance rate of full submissions by national homogeneity, shown by individual countries. Included here are the top eight most prolific countries in terms of number of initial submissions. For both panels: vertical error bars indicate 95th percentile confidence intervals for the proportion of accepted full submissions. Values at the base of each bar indicate the number of observations within that combination of country and homophily variables. Asterisks indicate significance level of X2 tests of independence comparing frequency of accepted full submissions between presence and absence of homophily and within each country. “*****” $= p < 0.0001$; “***” $= p < 0.01$”; “*“ $= p < 0.05$; “.” $= p < 0.1$; “ns” $= p > 0.05$.

Note: this figure is constructed in multiple parts

```r
countries <- c("canada", "china", "france", "germany", "japan", "switzerland", "united kingdom", "unite
sig_list <- list()
for (country in countries) {
  s <- subset(elife, full_decision_made == T & has_full_submission & ca_country == country)
  t <- table(s$ca_country_homophily, s$accepted)
  test = chisq.test(t[, 1:2])
  sig_list[length(sig_list) + 1] <- list(country = test)
}

sig_df <- data.frame(
  ca_country = countries,
  sig = sapply(sig_list, function(l) {sig2ast(l$p.value) })
)

fig7.A <- elife %>%
  filter(full_decision_made & has_full_submission & ca_country %in% countries) %>%
  group_by(ca_country, ca_country_homophily) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_accept_rate = accept_count / paper_count,
    se = 1.96 * sqrt( (encourage_accept_rate * (1 - encourage_accept_rate)) / paper_count),
    lower = encourage_accept_rate - se,
    upper = encourage_accept_rate + se,
    upper = ifelse(upper > 1, 1, upper)
  ) %>%
  group_by(ca_country) %>%
  mutate(totals = sum(paper_count)) %>%
  ungroup() %>%
  left_join(sig_df) %>%
  #top_n(16, totals) %>% # 8 countries, 3 authorship types per country, therefore first 24 rows
  mutate(ca_country = factor(sapply(as.character(ca_country), simpleCap))) %>%
  # Start ggplot
  ggplot(aes(x = ca_country_homophily, y = encourage_accept_rate, fill = ca_country_homophily)) +
  geom_bar(stat = "identity", position = position_dodge(), color = "black", alpha = 0.8) +
  geom_errorbar(aes(ymin = lower, ymax = upper), color = "black", width = 0.2) +
  geom_text(aes(label = paper_count, y = 0.1), size = 2.5) +
  geom_text(aes(label = sig, x = 1.5, y = 0.95)) +
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.85, 1.1), yend = ifelse(sig != "N/A", 0.8
  facet_wrap(~ca_country, nrow = 2, ncol = 4) +
  ylim(0, 1) +
  theme_dakota() +
  guides(fill = FALSE) +
  scale_fill_brewer(palette = "Oranges", labels = c("No Homogeneity", "Homogeneity")) +
  scale_x_discrete(labels = c("No Homogeneity", "Homogeneity")) +
  labs(
    x = "",
    y = "% accepted of full submissions"
  ) +
  theme(
    axis.text.x = element_text(angle = 20, vjust = 1, hjust = 1)
  )

fig7.A
```

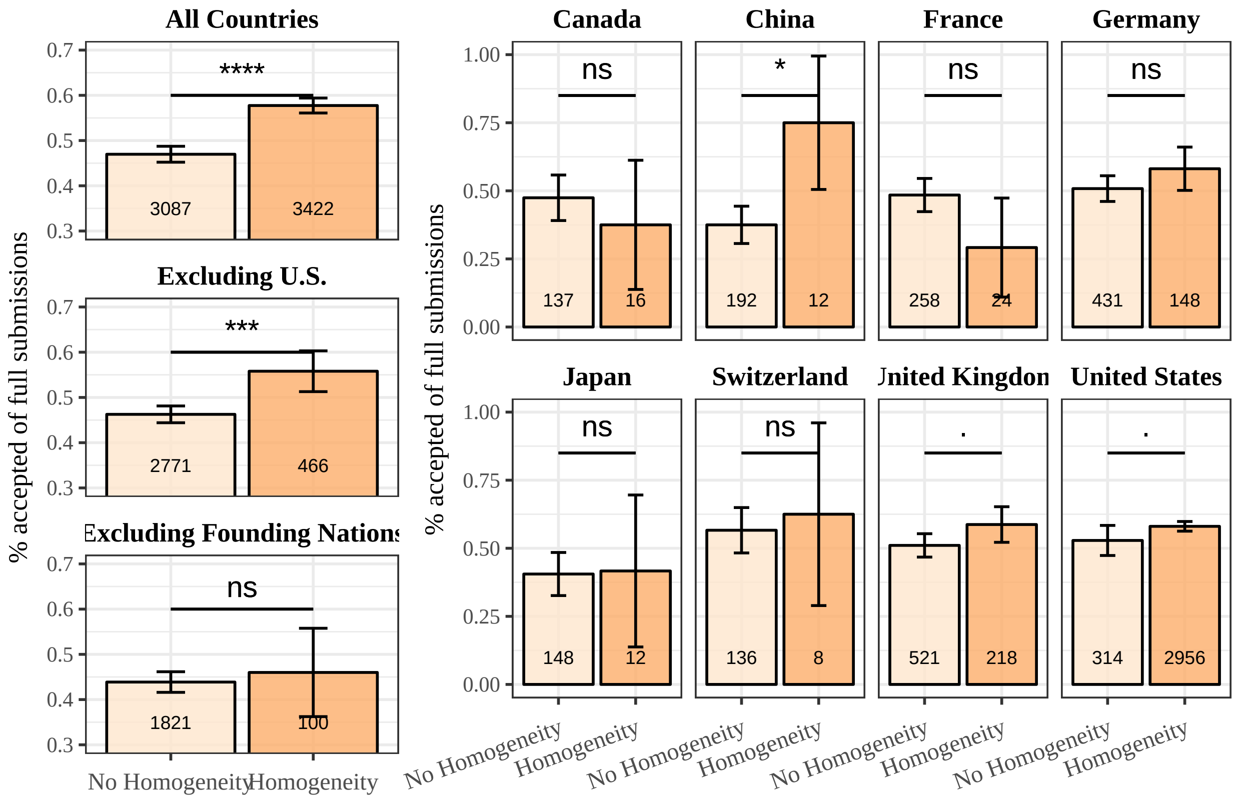


And here are the results from the tests used in the graph above

```
fig7_sig_table <- data.frame(
  country = countries,
  p.value = sapply(sig_list, function(x) x$p.value),
  n = sapply(sig_list, function(x) sum(x$observed)),
  statistic = sapply(sig_list, function(x) x$statistic),
  df = sapply(sig_list, function(x) x$parameter)
)

rownames(fig7_sig_table) <- NULL
fig7_sig_table
```

```
##          country    p.value    n    statistic df
## 1         canada 0.62417406  153 2.400444e-01  1
## 2          china 0.02311008  204 5.160212e+00  1
## 3         france 0.11026576  282 2.550408e+00  1
## 4        germany 0.15032115  579 2.068989e+00  1
## 5          japan 1.00000000  160 0.000000e+00  1
## 6    switzerland 1.00000000  144 1.608755e-30  1
## 7 united kingdom 0.06836581  739 3.321827e+00  1
## 8  united states 0.08774438 3270 2.915276e+00  1
```

```
# Get the data, all countries included
d1 <- elife %>%
  filter(full_decision_made & has_full_submission)

# exclude United States
d2 <- elife %>%
  filter(full_decision_made & has_full_submission) %>%
  filter(ca_country != "united states")

# Excluding all founding countries: U.S., U.K., and Germany
d3 <- elife %>%
  filter(full_decision_made & has_full_submission) %>%
  filter(!ca_country %in% c("united states", "united kingdom", "germany"))


# we also need to get the statistical test infomration for each
t1 <- chisq.test(table(d1$ca_country_homophily, d1$accepted))
t2 <- chisq.test(table(d2$ca_country_homophily, d2$accepted))
t3 <- chisq.test(table(d3$ca_country_homophily, d3$accepted))
sig_list <- list(t1, t2, t3)

sig_df <- data.frame(
  type = c("all", "no us", "no founder"),
  sig = sapply(sig_list, function(l) {sig2ast(l$p.value) })
)

d1.summ <- d1 %>%
  group_by(ca_country_homophily) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_accept_rate = accept_count / paper_count,
    se = 1.96 * sqrt( (encourage_accept_rate * (1 - encourage_accept_rate)) / paper_count),
    lower = encourage_accept_rate - se,
    upper = encourage_accept_rate + se,
    upper = ifelse(upper > 1, 1, upper),
    type = "all"
  )

d2.summ <- d2 %>%
  group_by(ca_country_homophily) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_accept_rate = accept_count / paper_count,
    se = 1.96 * sqrt( (encourage_accept_rate * (1 - encourage_accept_rate)) / paper_count),
    lower = encourage_accept_rate - se,
    upper = encourage_accept_rate + se,
    upper = ifelse(upper > 1, 1, upper),
    type = "no us"
  )

d3.summ <- d3 %>%
  group_by(ca_country_homophily) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_accept_rate = accept_count / paper_count,
    se = 1.96 * sqrt( (encourage_accept_rate * (1 - encourage_accept_rate)) / paper_count),
    lower = encourage_accept_rate - se,
    upper = encourage_accept_rate + se,
    upper = ifelse(upper > 1, 1, upper),
    type = "no founder"
  )

fig7.B <- d1.summ %>%
  union(d2.summ) %>%
  union(d3.summ) %>%
  left_join(sig_df, by = "type") %>%
  mutate(type = factor(type,
                       levels = c("all", "no us", "no founder"),
                       labels = c("All Countries", "Excluding U.S.", "Excluding Founding Nations")
                       )
         ) %>%
  ggplot(aes(x = ca_country_homophily, y = encourage_accept_rate, fill = ca_country_homophily)) +
  geom_bar(stat = "identity", position = position_dodge(), color = "black", alpha = 0.8) +
  geom_errorbar(aes(ymin = lower, ymax = upper), color = "black", width = 0.2) +
  geom_text(aes(label = paper_count, y = 0.35), size = 2.5) +
  geom_text(aes(label = sig, x = 1.5, y = 0.65)) +
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.6, 1.1), yend = ifelse(sig != "N/A", 0.6
  facet_wrap(~type, nrow = 3) +
  coord_cartesian(ylim = c(0.3, 0.7)) +
  theme_dakota() +
  guides(fill = FALSE) +
  scale_fill_brewer(palette = "Oranges", labels = c("No Homogeneity", "Homogeneity")) +
  scale_x_discrete(labels = c("No Homogeneity", "Homogeneity")) +
  labs(
    x = "",
    y = "% accepted of full submissions"
  )

fig7 <- grid.arrange(fig7.B, fig7.A, ncol = 2, widths = 1:2)
```



```
ggsave("figures/main/fig_7.png", plot = fig7, height = 4, width = 7)
```

```
fig7.B_sig_table <- data.frame(
  type   = c("all", "no us", "no founer"),
  p.value = sapply(sig_list, function(x) x$p.value),
  n = sapply(sig_list, function(x) sum(x$observed)),
  statistic = sapply(sig_list, function(x) x$statistic),
  df = sapply(sig_list, function(x) x$parameter)
)

rownames(fig7.B_sig_table) <- NULL
fig7.B_sig_table
```

```
##        type      p.value    n   statistic df
## 1       all 4.434496e-18 6509 75.11780295  1
## 2     no us 1.695054e-04 3237 14.14212248  1
## 3 no founer 7.543076e-01 1921  0.09794679  1
```

Presence of author-reviewer national homogeny by country of correposnding author

```
full <- elife %>%
  filter(has_full_submission) %>%
  group_by(ca_country) %>%
  summarize(
    submissions = n(),
    prop_homogeny = sum(ca_country_homophily, na.rm = T) / submissions
  ) %>%
  arrange(-prop_homogeny)

full
```

```
## # A tibble: 54 x 3
##        ca_country submissions prop_homogeny
##            <fctr>       <int>         <dbl>
##  1  united states        3605    0.90513176
##  2 united kingdom         803    0.29763387
##  3        germany         641    0.25273011
##  4         canada         176    0.11363636
##  5    south korea          45    0.11111111
##  6   south africa          11    0.09090909
##  7         france         310    0.07741935
##  8          japan         184    0.07608696
##  9      australia         101    0.06930693
## 10          china         233    0.06437768
## # ... with 44 more rows
```

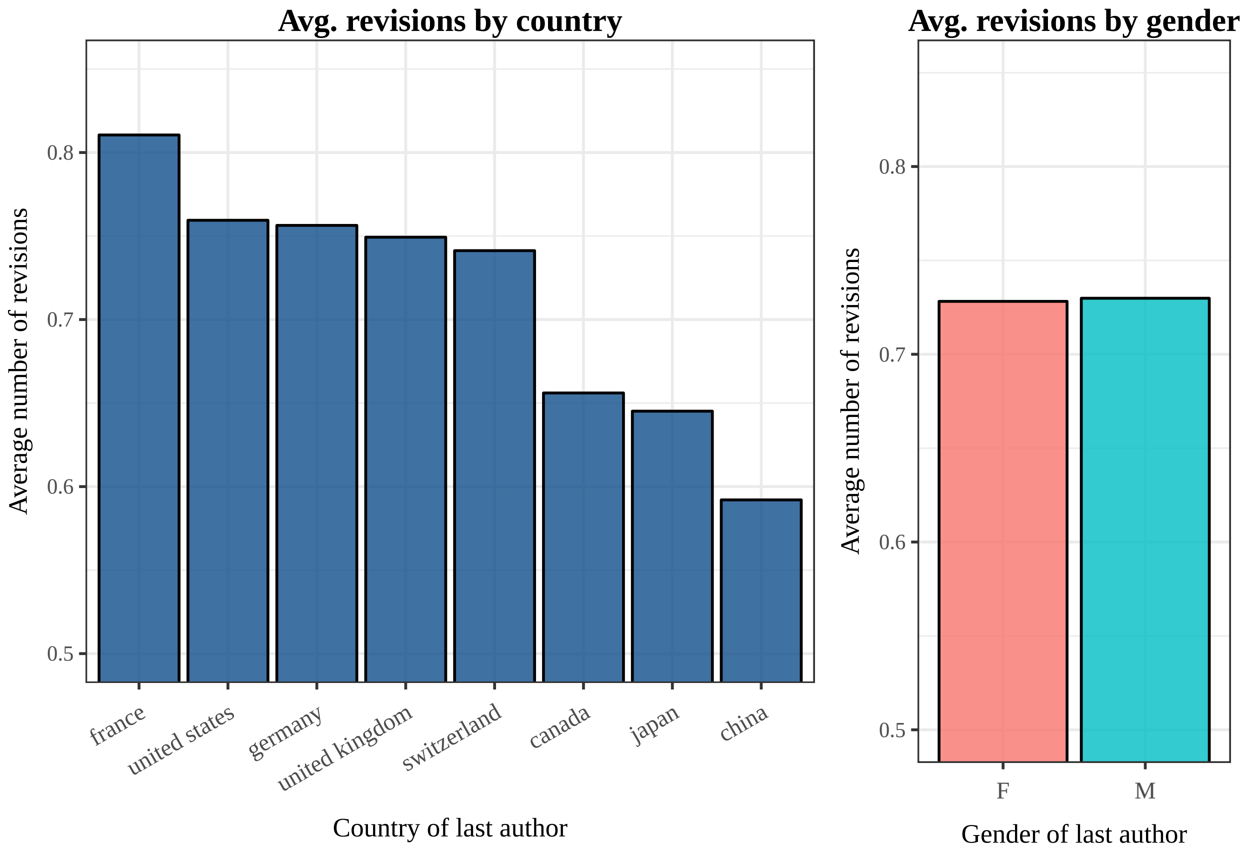
Supp. Materials

Figure SI.1

Figure SI.1 Average number of revisions a full submissions undergoes before a final decision of accept or reject is made. In this case, zero revisions occurs when a full submission is accepted or rejected without a request for any revisions. The dataset records at maximum two revisions, though only a small number of manuscripts remain in revision after two submissions (see figure 1). For this figure, we only include manuscripts for which a final decision is made after zero, one, or two revisions. The left panel shows differences in the average number of revisions by the country of the last author. The right shows the average revisions by the gender of the last author.

```
fig_SI.1.A <- elife %>%
  filter(full_decision_made & has_full_submission & la_country %in% countries) %>%
  group_by(la_country) %>%
  summarize(
    avg_revisions = mean(num_revisions)
  ) %>%
  ggplot(aes(x = reorder(la_country, -avg_revisions), y = avg_revisions)) +
  geom_bar(stat = "identity", fill = "dodgerblue4", alpha = 0.8, color = "black") +
  theme_dakota() +
  labs(x = "Country of last author",
       y = "Average number of revisions",
       title = "Avg. revisions by country") +
  coord_cartesian(ylim = c(0.5, 0.85)) +
  theme(
    plot.title = element_text(size = 12, margin = margin(0, 0, 2, 0)),
    axis.text.x = element_text(angle = 30, hjust = 1, vjust = 1)
        )
```

```
fig_SI.1.B <- elife %>%
  filter(full_decision_made & has_full_submission & la_gender %in% c("M", "F")) %>%
  group_by(la_gender) %>%
  summarize(
    avg_revisions = mean(num_revisions)
  ) %>%
  ggplot(aes(x = la_gender, y = avg_revisions, fill = la_gender)) +
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  theme_dakota() +
  labs(x = "Gender of last author",
       y = "Average number of revisions",
       title = "Avg. revisions by gender") +
  guides(fill = FALSE) +
  coord_cartesian(ylim = c(0.5, 0.85)) +
  theme(plot.title = element_text(size = 12, margin = margin(0, 0, 2, 0)))

fig_SI.1 <- grid.arrange(fig_SI.1.A, fig_SI.1.B, widths = 2:1)
```



```
fig_SI.1
```

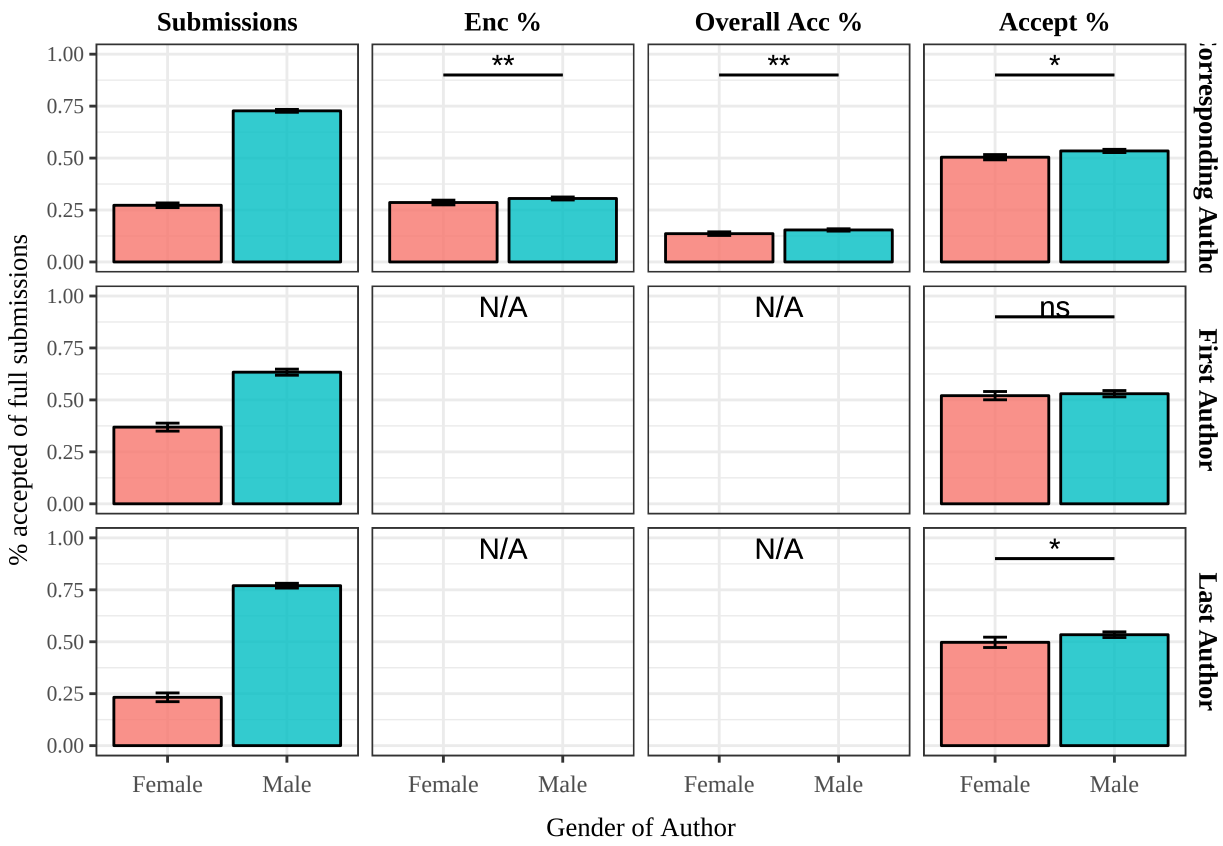
```
## TableGrob (1 x 2) "arrange": 2 grobs
##   z     cells    name           grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
```

```r
ggsave("figures/supp/fig_SI1.png", plot = fig_SI.1, height = 4, width = 7)
```

Figure SI.2

Figure SI.2. Proportion of initial submissions, encourage rate, overall accept rate, and accept rate of full submissions by the gender of the corresponding author, first author, and last author. Gender metadata is unavailable for first and last authors of initial submissions that were never submitted as full submissions, therefore these cells remain blank. Authors whose gender is unknown are excluded from analysis. Vertical error bars indicate 95th confidence intervals of the proportion of submitted, encouraged, and accepted initial and full submissions. Asterisks indicate significance level of X2 tests of independence of frequency of encourage and acceptance by gender; “*” = $p < 0.05$; “ns” = $p > 0.05$.

```r
# First, test the encourage rate diffs
s <- subset(elife, initial_decision_made)
t <- table("ca_gender" = s$ca_gender, "encouraged" = s$encouraged)[1:2,]
ca_encouraged <- chisq.test(t[, 1:2])

# Difference in acceptance rates by gender of corresponding author
s <- subset(elife, initial_decision_made & (!has_full_submission | full_decision_made))
t <- table("ca_gender" = s$ca_gender, "encouraged" = s$accepted)[1:2,]
ca_accepted <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of corresponding author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("ca_gender" = s$ca_gender, "accepted" = s$accepted)[1:2,]
ca_ea <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of first author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("fa_gender" = s$fa_gender, "accepted" = s$accepted)[1:2,]
fa_ea <- chisq.test(t[, 1:2])

# Difference in encourage-acceptance rates by gender of last author
s <- subset(elife, initial_decision_made & full_decision_made)
t <- table("la_gender" = s$la_gender, "accepted" = s$accepted)[1:2,]
la_ea <- chisq.test(t[, 1:2])

# Now we use the results of these tests to construct a table
measurements <- c(rep("submit_rate", 3), rep("encourage_rate", 3), rep("accept_rate", 3), rep("encourag
author <- rep(c("ca_gender", "fa_gender", "la_gender"), 4)

sig <- c("N/A", "N/A", "N/A", # submit rates, all NA since we don't really compare this
         sig2ast(ca_encouraged$p.value), "N/A", "N/A", # encourage rate
         sig2ast(ca_accepted$p.value), "N/A", "N/A",
         sig2ast(ca_ea$p.value), sig2ast(fa_ea$p.value), sig2ast(la_ea$p.value)
         )
sig_df <- data.frame(measure_key = factor(measurements), author_key = factor(author), sig = sig)

# Now lets save these test results for later
sig_list <- list("Corresponding author enc. rate" = ca_encouraged,
                 "Corresponding author acc. rate" = ca_accepted,
                 "Corresponding author enc-acc rate" = ca_ea,
                   "First author enc-acc rate" = fa_ea,
                   "last author enc-acc rate" = la_ea)


fig_SI.2 <- elife %>%
  filter(initial_decision_made) %>%
  gather(author_key, value = gender, ca_gender, la_gender, fa_gender) %>%
  filter(gender %in% c('M', 'F')) %>%
  group_by(author_key) %>%
  mutate(
    # if not ocnsidering the corr. author, then the count is all full submissions, ie: for when a submi
    total_papers = ifelse(author_key == "ca_gender", n(), sum(has_full_submission))
    )%>%
  group_by(author_key, gender) %>%
  summarize(
        paper_count = n(),
        accept_count = sum(accepted == TRUE, na.rm = T),
        encourage_count = sum(encouraged == TRUE),
        encourage_rate = ifelse(author_key[1] == "ca_gender", encourage_count / n(), NA),
        # this accept rate is the number of accepted papers / number of initial + full submissions
        accept_rate = ifelse(author_key[1] == "ca_gender", accept_count / sum(!has_full_submission | ful
        submit_rate = n() / total_papers[1],
        # this is the number of accepted papers divided by all papers
        encourage_accept_rate = accept_count / sum(has_full_submission & full_decision_made, na.rm = T)
  ) %>%
  ungroup() %>%
  gather(measure_key, value = measurement, submit_rate, encourage_rate, accept_rate, encourage_accept_ra
  left_join(sig_df, by = c("measure_key", "author_key")) %>%
  mutate(
    author_key = factor(author_key,
                        levels = c("ca_gender", "fa_gender", "la_gender"),
                        labels = c("ca_gender" = "Corresponding Author", "fa_gender" = "First Author",
                        ),
    measure_key = factor(measure_key,
                         labels = c("submit_rate" = "Submissions", "encourage_rate" = "Enc %", "accept_
                         levels = c("submit_rate", "encourage_rate", "accept_rate", "encourage_accept_ra
    gender = ifelse(gender == "F", "Female", "Male"),
    standard_error = 1.96 * sqrt( (measurement * (1 - measurement)) / paper_count),
    lower = measurement - standard_error,
    upper = measurement + standard_error
  ) %>%
  ggplot(aes(x = gender, y = measurement, color = factor(gender), shape = factor(gender), fill = factor
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  #geom_text(aes(y = 0.08, label = paper_count), size = 2.5, color = "black") +
  #geom_text(aes(x = gender, y = 0.1, label = round(measurement, 3) * 100 ), color = "black") +
  #facet_grid(measure_key ~ author_key) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2, color = "black") +
  geom_text(aes(x = 1.5, y = 0.95, label = ifelse(measure_key == "Submissions", "", as.character(sig)))
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.90, 1.1), yend = ifelse(sig != "N/A", 0.9
  facet_grid(author_key ~ measure_key) +
  coord_cartesian(ylim = c(0, 1)) +
  theme_dakota() +
  guides(fill = F) +
  labs(
    x = "Gender of Author",
    y = "% accepted of full submissions"
  )

fig_SI.2
```

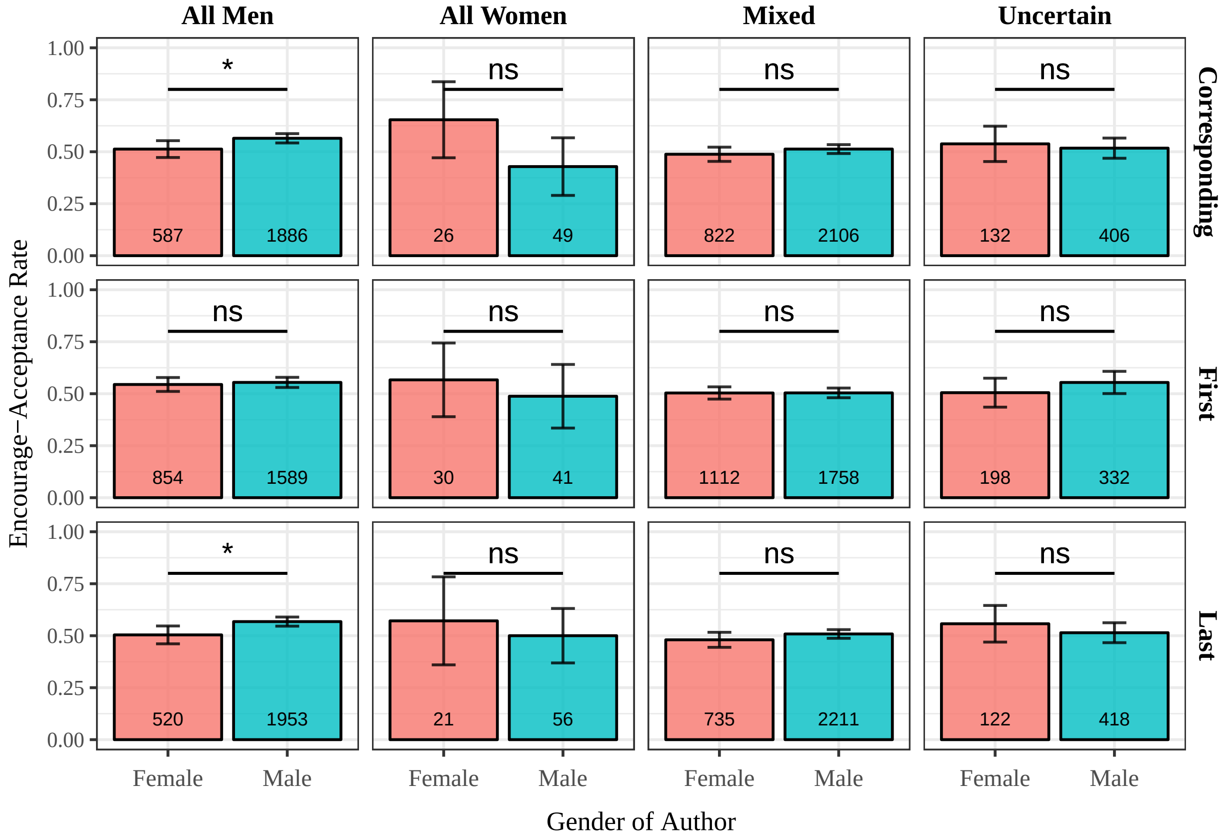


```
ggsave("figures/supp/fig_SI2.png", plot = fig_SI.2, height = 4, width = 7)
```

Figure SI.3

Figure SI.3. Percentage of full submissions that were accepted, shown by the gender of the corresponding, first, and last author, and by the gender composition of the peer reviewers. Text at the base of each bar indicate the number full submissions within each category of reviewer team and authorship gender. Vertical error bars indicate 95th percentile confidence intervals of the proportion of accepted full submissions. Asterisks indicate significance level of X2 tests of independence on frequency of acceptance by gender of author given each team composition; “ns” indicates no observed statistical significance. “*“ = p < 0.05; “ns” = p > 0.05.

```
sig_list <- list()
for(comp in c("All Men", "All Women", "Mixed", "Uncertain")) {
  for(gender_var in c("ca_gender", "fa_gender", "la_gender")) {
    if (!is.na(comp)) {
      sub <- subset(elife, initial_decision_made & full_decision_made & composition == comp)[, c("accep
      t <- t(table(sub))[1:2,]
      test = chisq.test(t)
      test$n = dim(sub)[1]
      sig_list[length(sig_list) + 1] <- list(test)
    }
  }
}

sig_df <- data.frame(composition = c(rep("All Men", 3), rep("All Women", 3), rep("Mixed", 3), rep("Unce
                     author_key = rep(c("ca_gender", "fa_gender", "la_gender"), 4),
                     sig = sapply(sig_list, function(test) { sig2ast(test$p.value)})
)

fig_SI.3 <- elife %>%
  filter(initial_decision_made & full_decision_made & !is.na(composition)) %>%
  mutate(total_submissions = n()) %>%
  gather(author_key, value = gender, ca_gender, fa_gender, la_gender) %>%
  filter(gender %in% c("M", "F")) %>%
  group_by(composition, author_key, gender) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE),
    acceptance_rate = sum(accepted == TRUE) / paper_count,
    standard_error = 1.96 * sqrt( (acceptance_rate * (1 - acceptance_rate)) / paper_count),
    lower = acceptance_rate - standard_error,
    upper = acceptance_rate + standard_error
  ) %>%
  ungroup() %>%
  left_join(sig_df, by = c("composition", "author_key")) %>%
  mutate(
    author_key = factor(author_key,
                        levels = c("ca_gender", "fa_gender", "la_gender"),
                        labels = c("ca_gender" = "Corresponding", "fa_gender" = "First", "la_gender" =
    ,
    gender = ifelse(gender == "M", "Male", "Female")
  ) %>%
  # Start ggplot
  ggplot(aes(x = gender, y = acceptance_rate, fill = gender)) +
  geom_bar(stat = "identity", alpha = 0.8, color = "black") +
  geom_text(aes(y = 0.1, label = paper_count), size = 2.5, color = "black") +
  #geom_text(aes(y = 0.1, label = paste0(round(acceptance_rate, 3) * 100, "%")), size = 2.5, color = "b
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2, color = "black", alpha = 0.8) +
  geom_text(aes(x = 1.5, y = 0.90, label = sig), color = "black") +
  #geom_text(aes(x = gender, y = 0.1, label = round(acceptance_rate, 3) * 100 ), color = "black") +
  geom_segment(aes(x = 1, xend = 2, y = ifelse(sig != "N/A", 0.8, 1.1), yend = ifelse(sig != "N/A", 0.8
  facet_grid(author_key ~ composition) +
  ylim(0, 1) +
  theme_dakota() +
  guides(fill = F) +
  labs(y = "Encourage-Acceptance Rate",
       x = "Gender of Author"
  )

fig_SI.3
```

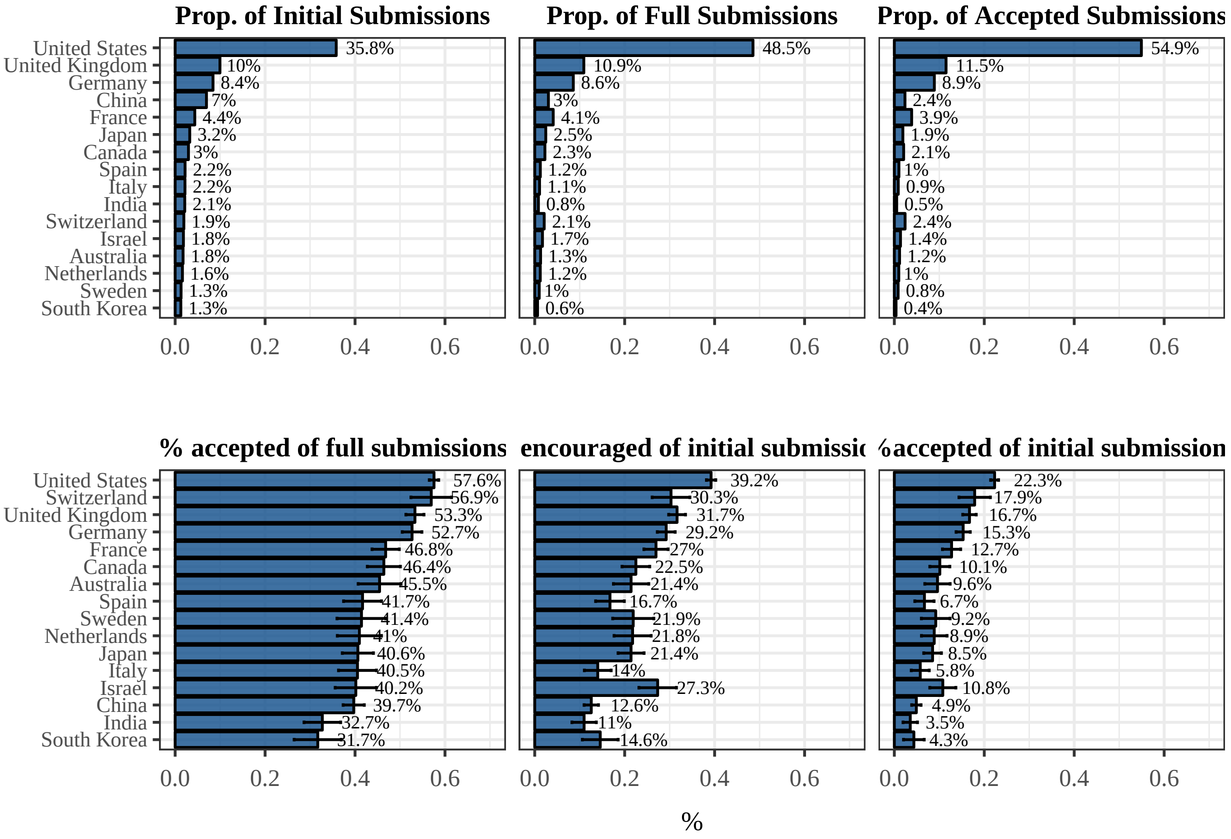


```r
ggsave("figures/supp/fig_SI2.png", plot = fig_SI.2, height = 4, width = 7)
```

Figure SI.4

Figure SI.4 Top: proportion of all initial submissions, encouraged initial submissions, and accepted full submissions comprised by the national affiliation of the corresponding author for the top sixteen most prolific countries in terms of initial submissions. Bottom: acceptance rate of full submissions, encourage rate of full submissions, and overall accept rate of full submissions by national affiliation of the corresponding author for the top eight more prolific countries in terms of initial submissions. Error bars on bottom panel indicate standard error of proportion of encouraged initial submissions and accepted initial and full submissions for each country.

```r
# Its easiest and most efficient to calculate these total values outside of the dplyr chain below
total_submissions <- length(unique(elife$MSNO))
total_full_submissions <- sum(!elife$full_decision_date_isNA, na.rm = T)
total_encouraged <- with(elife, sum(initial_decision_made & encouraged, na.rm = T))
total_accepted <- with(elife, sum(full_decision_made & accepted == T, na.rm = T))

# Firs the first plot, this one will show the proportion that each countrie constitutes the total numbe
p1 <- elife %>%
  filter(initial_decision_made & (full_decision_made | full_decision_date_isNA) & !is.na(ca_country)) %
  mutate(ca_country = factor(sapply(as.character(ca_country), simpleCap))) %>% # capitalize first lette
  group_by(ca_country) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_count = sum(encouraged == TRUE, na.rm = T),
    full_submissions = sum(has_full_submission),
    prop_of_full =  full_submissions / total_full_submissions,
    prop_of_initial = paper_count / total_submissions,
    prop_of_encouraged = encourage_count / total_encouraged,
    prop_of_accepted = accept_count / total_accepted
  ) %>%
  group_by(ca_country) %>%
  mutate(totals = sum(paper_count)) %>%
  ungroup() %>%
  top_n(16, totals) %>%
  gather(prop_key, value = prop, prop_of_initial, prop_of_full, prop_of_accepted) %>%
  mutate(prop_key = factor(prop_key,
                           levels = c("prop_of_initial", "prop_of_full", "prop_of_accepted"),
                           labels = c("prop_of_initial" = "Prop. of Initial Submissions",
                                      "prop_of_full" = "Prop. of Full Submissions",
                                      "prop_of_accepted" = "Prop. of Accepted Submissions")),
         ca_country = reorder(ca_country, paper_count)
  ) %>%
  # Start ggplot
  ggplot(aes(x = ca_country, y = prop)) +
  geom_bar(stat = "identity", color = "black", alpha = 0.8, fill = "dodgerblue4", position = position_d
  geom_text(aes(y = prop, label = paste0(round(prop, 3) * 100, "%")), size = 2.5, hjust = -0.2, family =
  scale_y_continuous(limits = c(0, 1)) +
  facet_wrap(~prop_key, labeller = labeller(key = labels)) +
  theme_dakota() +
  coord_flip() +
  ylim(0, 0.7) +
  labs(y = "") +
  theme(
    strip.background = element_blank(),
    text = element_text(size = 10, family = "Times"),
    plot.title = element_text(size = 12),
    strip.text = element_text(face = "bold"),
    axis.title.y = element_blank()
  )


p2 <- elife %>%
  filter(initial_decision_made & (full_decision_made | full_decision_date_isNA) & !is.na(ca_country)) %
  mutate(ca_country = factor(sapply(as.character(ca_country), simpleCap))) %>% # capitalize first lette
  group_by(ca_country) %>%
  summarize(
    paper_count = n(),
    accept_count = sum(accepted == TRUE, na.rm = T),
    encourage_count = sum(encouraged == TRUE, na.rm = T),
    encourage_rate = encourage_count / paper_count,
    accept_rate = accept_count / sum(!has_full_submission | full_decision_made, na.rm = T),
    encourage_accept_rate = accept_count / sum(has_full_submission & full_decision_made, na.rm = T)
  ) %>%
  group_by(ca_country) %>%
  mutate(totals = sum(paper_count)) %>%
  ungroup() %>%
  top_n(16, totals) %>%
  mutate(
    ca_country = reorder(ca_country, encourage_accept_rate)
  ) %>%
  gather(measure_key, value = measurement, encourage_rate, accept_rate, encourage_accept_rate) %>%
  mutate(measure_key = factor(measure_key,
                           levels = c("encourage_accept_rate", "encourage_rate", "accept_rate"),
                           labels = c("encourage_accept_rate" = "% accepted of full submissions",
                                      "encourage_rate" = "% encouraged of initial submissions",
                                      "accept_rate" = "%accepted of initial submissions"
                                      ))
  ) %>%
  group_by(measure_key) %>%
  mutate(
    se = 1.96 * sqrt(measurement * (1 - measurement) / paper_count),
    lower = measurement - se,
    upper = measurement + se
  ) %>%
  ggplot(aes(x = ca_country, y = measurement)) +
  geom_bar(stat = "identity", color = "black", fill = "dodgerblue4", alpha = 0.8) +
  geom_text(aes(y = measurement, label = paste0(round(measurement, 3) * 100, "%")), size = 2.5, hjust =
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2) +
  facet_wrap(~measure_key, labeller = labeller(key = labels)) +
  theme_dakota() +
  labs(y = "%") +
  coord_flip() +
  ylim(0, 0.7) +
  theme(
    axis.title.y = element_blank()
  )

fig_SI.4 <- grid.arrange(p1, p2)
```

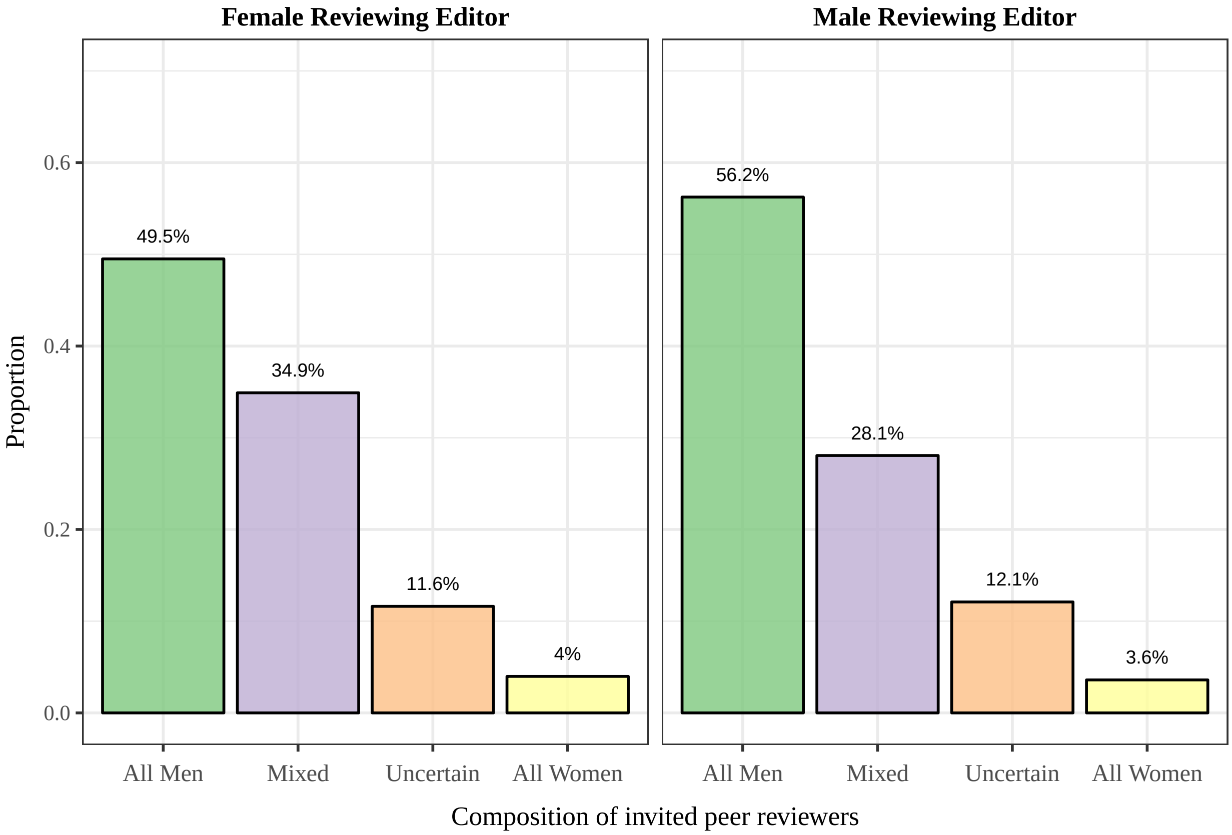


```
ggsave("figures/supp/fig_SI3.png", plot = fig_SI.3, height = 4, width = 7)
```

Figure SI.5

Figure SI.5. Proportion of peer reviewer team's gender compositions by gender of the reviewing editor. Compositions are determined while excluding the reviewing editor from team membership, if they are listed as a peer reviewer.

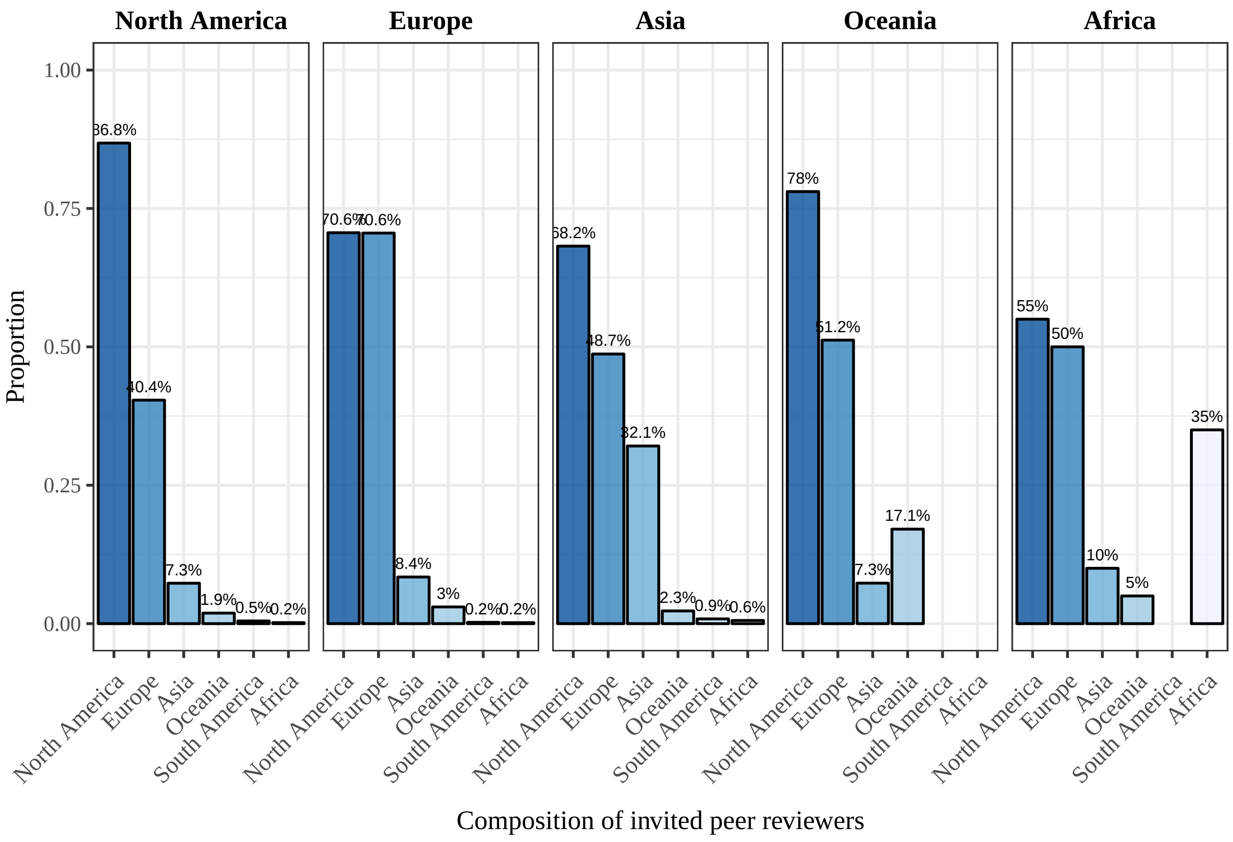
```
fig_SI.5 <- elife %>%
  filter(bre_gender %in% c("M", "F")) %>%
  mutate(
    bre_gender = ifelse(bre_gender == "M", "Male Reviewing Editor", "Female Reviewing Editor")
    ) %>%
  group_by(bre_gender) %>%
  mutate(total = n()) %>%
  group_by(composition_adj, bre_gender) %>%
  summarize(
    prop = n() / total[1]
  ) %>%
  ungroup() %>%
  mutate(
    composition_adj = reorder(composition_adj, -prop)
  ) %>%
  #arrange(prop) %>%
  ggplot(aes(x = composition_adj, y = prop, fill = composition_adj)) +
  geom_bar(stat = "identity", color = "black", alpha = 0.8) +
  facet_wrap(~bre_gender) +
  geom_text(aes(label = paste0(round(prop, 3) * 100, "%"), y = prop + 0.025), size = 2.5) +
  theme_dakota() +
  scale_fill_brewer(palette = "Accent") +
  guides(fill = F) +
  ylim(0, 0.7) +
  labs(y = "Proportion",
       x = "Composition of invited peer reviewers"
       )

fig_SI.5
```



```
ggsave("figures/supp/fig_SI5.png", plot = fig_SI.5, height = 4, width = 7)
```

Figure SI.6

```
fig_SI.6 <- elife %>%
  filter(has_full_submission & full_decision_made & !is.na(bre_continent)) %>%
  group_by(MSNO) %>%
  mutate(
    num_africa = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer4_
    contains_africa = ifelse(bre_is_reviewer & bre_continent == "Africa", num_africa > 1, num_africa >
    num_asia = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer4_c
    contains_asia = ifelse(bre_is_reviewer & bre_continent == "Asia", num_asia > 1, num_asia > 0),
    num_na = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer4_con
    contains_na = ifelse(bre_is_reviewer & bre_continent == "North America", num_na > 1, num_na > 0),
    num_eu = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer4_con
    contains_eu = ifelse(bre_is_reviewer & bre_continent == "Europe", num_eu > 1, num_eu > 0),
    num_sa = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer4_con
    contains_sa = ifelse(bre_is_reviewer & bre_continent == "South America", num_sa > 1, num_sa > 0),
    num_oceania = sum(na.omit(c(reviewer1_continent, reviewer2_continent, reviewer3_continent, reviewer
    contains_oceania = ifelse(bre_is_reviewer & bre_continent == "Oceania", num_oceania > 1, num_oceani
  ) %>%
  group_by(bre_continent) %>%
  mutate(total = n()) %>%
  gather(contains_key, contains, contains_africa, contains_asia, contains_na, contains_eu, contains_sa,
  group_by(contains_key, contains, bre_continent) %>%
  summarize(
    prop = n() / total[1]
  ) %>%
  ungroup() %>%
  mutate(
    bre_continent = factor(bre_continent, levels = c("North America", "Europe", "Asia", "Oceania", "Sou
    contains_key = factor(contains_key,
                          levels = c("contains_na", "contains_eu", "contains_asia", "contains_oceania",
                          labels = c("contains_na" = "North America", "contains_eu" = "Europe",
                                     "contains_asia" = "Asia", "contains_oceania" = "Oceania",
                                     "contains_sa" = "South America", "contains_africa" = "Africa"))
  ) %>%
  filter(contains == T) %>%
  ggplot(aes(x = contains_key, y = prop, fill = contains_key)) +
  geom_bar(stat = "identity", color = "black", alpha = 0.8) +
  facet_wrap(~bre_continent, ncol = 6) +
  geom_text(aes(label = paste0(round(prop, 3) * 100, "%"), y = prop + 0.025), size = 2) +
  theme_dakota() +
  scale_fill_brewer(palette = "Blues", direction = -1) +
  ylim(0, 1.0) +
   guides(fill = F) +
  theme(
    axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1)
  ) +
  labs(y = "Proportion",
       x = "Composition of invited peer reviewers"
       )


fig_SI.6
```

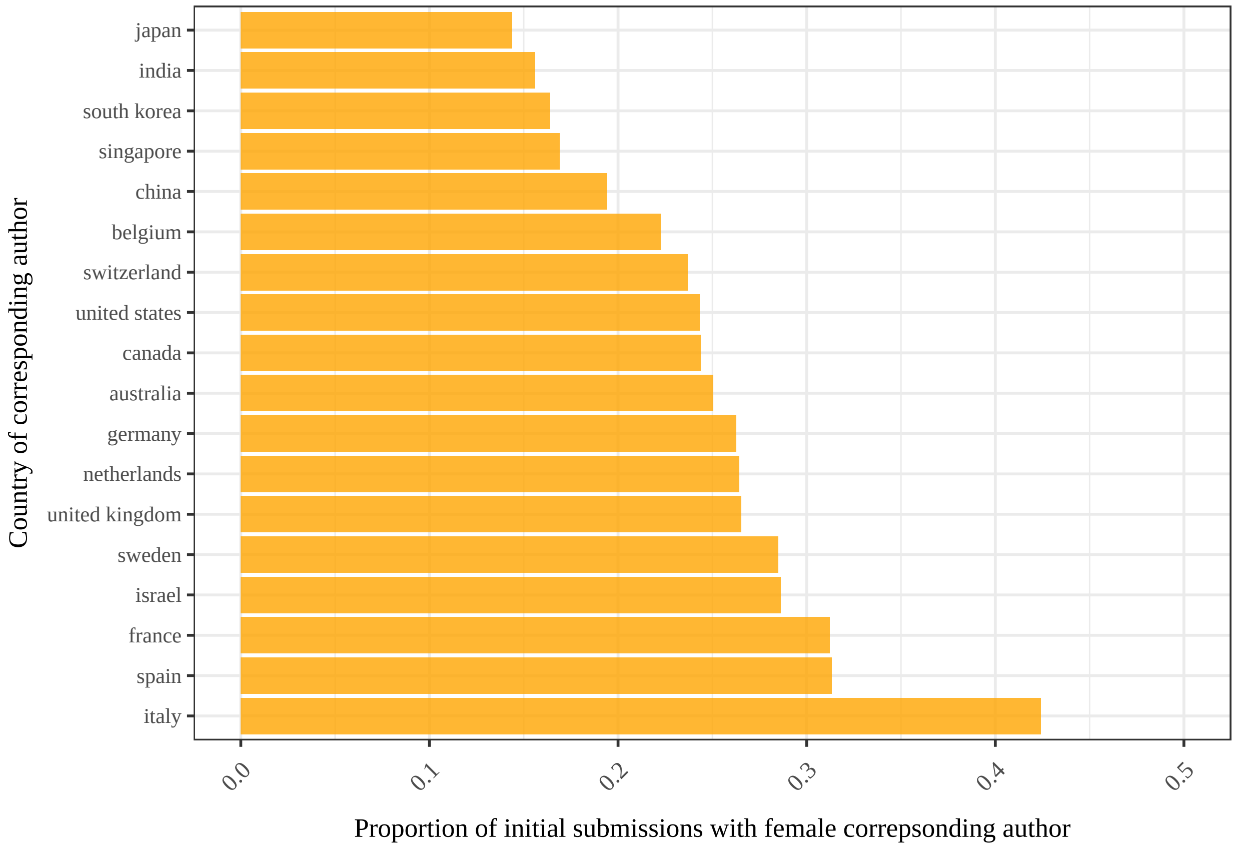


```
ggsave("figures/supp/fig_SI6.png", plot = fig_SI.6, height = 4, width = 7)
```

Figure SI.7

Figure SI.7. Proportion of initial submissions with a female corresponding author by the country of the corresponding author. Includes only countries with at least 200 initial submissions to eLife between 2012 and 2017.

```
fig_SI.7 <- elife %>%
  group_by(ca_country) %>%
  mutate(total = n()) %>%
  filter(total > 200) %>%
  filter(ca_gender == "F") %>%
  group_by(ca_country) %>%
  summarize(
    prop = n() / total[1]
  ) %>%
  #group_by(ca_gender) %>%
  mutate(
    ca_country = reorder(ca_country, -prop)
  ) %>%
  ggplot(aes(x = ca_country, y = prop)) +
  geom_bar(stat = "identity", alpha = 0.8, fill = "orange") +
  ylim(0, 0.5) +
  coord_flip() +
  theme_dakota() +
  theme(
    axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1)
  ) +
  labs(x = "Country of corresponding author",
       y = "Proportion of initial submissions with female correpsonding author") +
  scale_fill_discrete(labels = c("F" = "Female", "M" = "Male"))

fig_SI.7
```



```
ggsave("figures/supp/fig_SI7.png", plot = fig_SI.7, height = 4, width = 7)
```