Exploratory Data Analysis

2023-05-29

```
# Load in packages and data
library(ggplot2)
library(data.table)
library(plyr)
library(dplyr)
library(MASS)
library(RColorBrewer)
library(Hmisc)
library(ggpubr)
library(ks)
library(tidyverse)
load("Rakai_Pangea2_RCCS_pairs_household_202211XX.RData")
```

Inspect structure of the data set

```
# Determine structure of data
str(pairs_tsi)
```

```
## Classes 'data.table' and 'data.frame':   610 obs. of  19 variables:
##  $ RECIPIENT                : chr  "AID0011" "AID0023" "AID0102" "AID0110" ...
##  $ SOURCE                   : chr  "AID1640" "AID0299" "AID7619" "AID1535" ...
##  $ SEX.SOURCE               : chr  "M" "M" "M" "M" ...
##  $ SEX.RECIPIENT            : chr  "F" "F" "F" "F" ...
##  $ CL                       : Date, format: "2009-08-09" "2008-12-06" ...
##  $ IL                       : Date, format: "2010-03-07" "2009-12-09" ...
##  $ M                        : Date, format: "2011-01-18" "2011-06-09" ...
##  $ IU                       : Date, format: "2011-10-30" "2012-10-07" ...
##  $ CU                       : Date, format: "2012-04-07" "2013-07-03" ...
##  $ AGE_TRANSMISSION.SOURCE  : num  23.1 37.6 29.6 25.1 26.6 23.9 24.2 27 26.8 19.7 ...
##  $ AGE_INFECTION.RECIPIENT  : num  16.9 18.2 21 28.1 35 17.8 18.9 18.7 31.3 25.6 ...
##  $ ROUND.M                  : chr  "R014" "R014" "R012" "R012" ...
##  $ COMM.SOURCE              : chr  "fishing" "fishing" "fishing" "fishing" ...
##  $ COMM.RECIPIENT           : chr  "fishing" "fishing" "fishing" "fishing" ...
##  $ COMM_NUM.SOURCE          : int  770 771 771 38 23 40 771 602 34 772 ...
##  $ COMM_NUM.RECIPIENT       : int  770 771 771 38 23 40 771 38 34 772 ...
##  $ DATE.COLLECTION.SOURCE   : IDate, format: "2012-12-12" "2014-04-28" ...
##  $ DATE.COLLECTION.RECIPIENT: IDate, format: "2012-12-12" "2014-04-25" ...
##  $ same_hh                  : num  1 1 1 0 1 1 1 0 1 1 ...
##  - attr(*, ".internal.selfref")=<externalptr>
##  - attr(*, "sorted")= chr "RECIPIENT"
```

Description of variables:

- RECIPIENT, SOURCE - IDs for participants involved in case of HIV transmission. The recipients are all unique but sources are not.
- SEX.SOURCE, SEX.RECIPIENT - the sex of source/recipient. M for male and F for female.
- CL, IL, M, IU, CU - *UNKNOWN dates, to be completed*
- AGE_TRANSMISSION.SOURCE - Age of source of transmission.
- AGE_INFECTION.RECIPIENT - Age of recipient of transmission.
- ROUND.M - Round of survey *To be confirmed - this is the first round in which participation was recorded?*
- COMM.SOURCE, COMM.RECIPIENT - Community of source/recipient. Either 'fishing' or 'inland'.
- COMM_NUM.SOURCE, COMM_NUM.RECIPIENT - *UNKNOWN*
- DATE.COLLECTION.SOURCE, DATE.COLLECTION.RECIPIENT - *UNKNOWN*
- same_hh - whether the transmission was within the same household.

Transform data

Bin the data according to age of recipient. Divide into two data sets by household factor.

```
# Divide in 5 years age bands
age_limits <- c(15, 20, 25, 30, 35, 40, 45, 50)
age_labels <- paste0(age_limits, '-', age_limits + 5)
pairs_tsi$AGE_BAND.RECIPIENT <- cut(
    pairs_tsi$AGE_INFECTION.RECIPIENT,
    breaks = age_limits,
    labels = age_labels[1:(length(age_limits) - 1)],
    include.lowest = TRUE)

## HL: Not sure why this is here, such observations do not exist
#Exclude respondants in 'neuro' community
#pairs_tsi <- pairs_tsi[COMM.SOURCE!='neuro' & COMM.RECIPIENT!='neuro',]

# Divide in 2 datasets for transmissions within and out of HH
pairs_tsi_same_hh <- pairs_tsi[same_hh == 1,]
pairs_tsi_diff_hh <- pairs_tsi[same_hh == 0,]
```

Exploratory plots

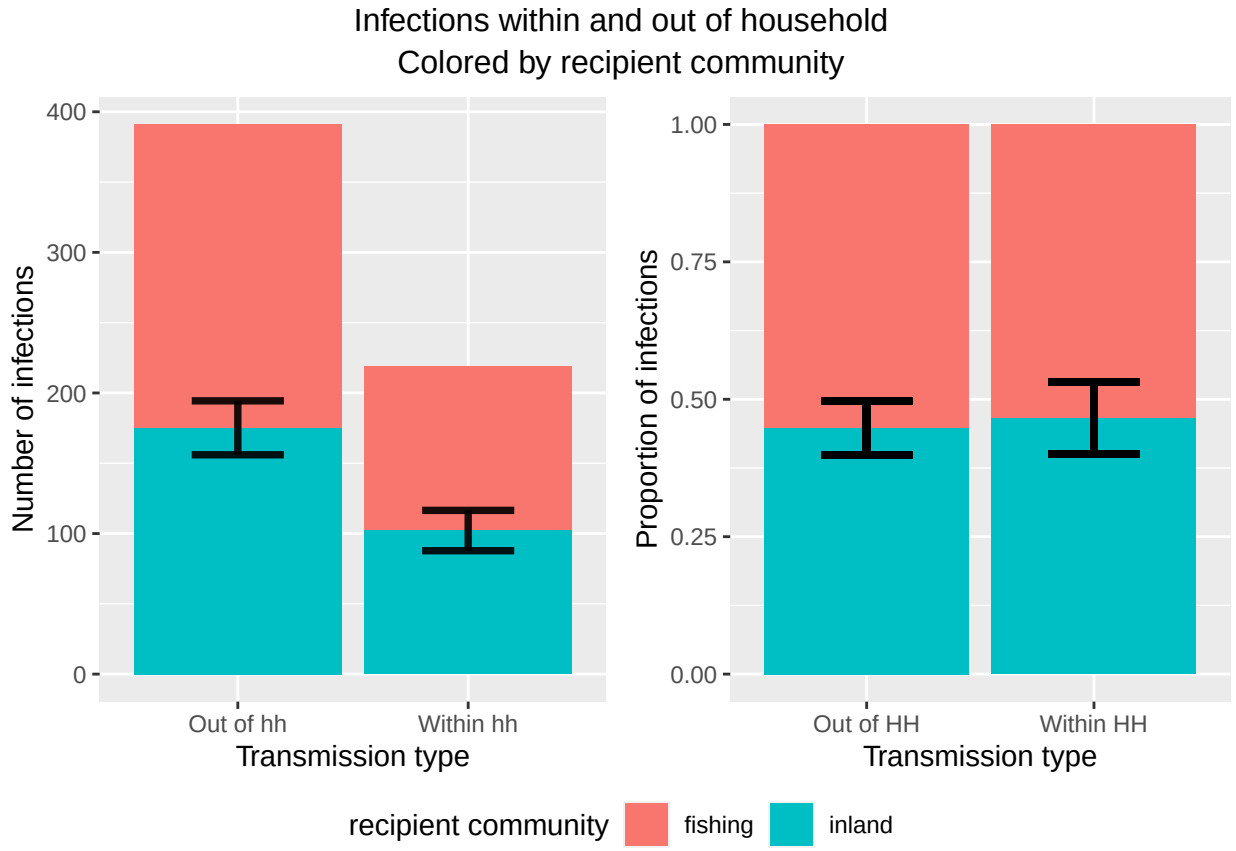
BY RECIPIENT COMMUNITY AND HOUSEHOLD FACTOR

```
# AB: it's clearer to perform operations here.
# less prone to bugs, more readable, and can focus on graphics only in ggplot snippet
p1_data <- pairs_tsi[ ,{
    N.in.inland <- sum(COMM.RECIPIENT == 'inland')
    binom.confs <- (.N*binconf(N.in.inland, .N)) |> as.list()
    names(binom.confs) <- c('BC.center', 'BC.min', 'BC.max')
    binom.confs
    }, by=same_hh]

# Plot number of counts by comm & hh factor
p1_new <- ggplot(pairs_tsi, aes(x = as.logical(same_hh),
                                fill = COMM.RECIPIENT)) +
    geom_bar() +
```

```
    geom_errorbar(data = p1_data, aes(ymin = BC.min, ymax = BC.max, fill = NA),
                  width = 0.4, colour = "black", alpha = 0.9, linewidth = 1.3) +
    labs(x='Transmission type',
        y='Number of infections',
        fill='recipient community') +
    scale_x_discrete(labels=c("Out of hh","Within hh"))
```

```
## Warning in geom_errorbar(data = p1_data, aes(ymin = BC.min, ymax = BC.max, :
## Ignoring unknown aesthetics: fill
```

```
# Plot proportions of infections by household factor
p2<-ggplot(data = pairs_tsi, aes(x = as.logical(same_hh),fill = COMM.RECIPIENT)) +
  geom_bar(position="fill") +
  labs(x='Transmission type',
    y='Proportion of infections',
    fill='Recipient community') +
  scale_x_discrete(labels=c("Out of HH","Within HH")) +
  geom_errorbar( aes(x='FALSE', ymin=binconf(nrow(pairs_tsi_diff_hh[COMM.RECIPIENT=='inland',]),nrow(pa
  geom_errorbar( aes(x='TRUE', ymin=binconf(nrow(pairs_tsi_same_hh[COMM.RECIPIENT=='inland',]),nrow(pai

# Combine above plots into one
p <- ggarrange(p1_new, p2, ncol=2, nrow=1, common.legend = TRUE,
               legend="bottom")
p2 <- annotate_figure(p, top="Colored by recipient community")
annotate_figure(p2, top="Infections within and out of household")
```



```r
# Provide summary tables of counts by comm & hh
table(as.logical(pairs_tsi$same_hh),pairs_tsi$COMM.RECIPIENT)
```

```
##
##         fishing inland
##   FALSE     216    175
##   TRUE      117    102
```

```r
# 95% confidence intervals for number of infections
cat("Fishing, Outside HH:\n")
```

```
## Fishing, Outside HH:
```

```r
binconf(216,610)*610
```

```
##  PointEst    Lower    Upper
##       216 193.4724 239.6415
```

```r
cat("Inland, Outside HH:\n")
```

```
## Inland, Outside HH:
```

```r
binconf(175,610)*610
```

```
##  PointEst    Lower    Upper
##       175 153.9719 197.6552
```

```r
cat("Fishing, Within HH:\n")
```

```
## Fishing, Within HH:
```

```r
binconf(117,610)*610
```

```
##  PointEst    Lower    Upper
##       117 99.14088 137.2122
```

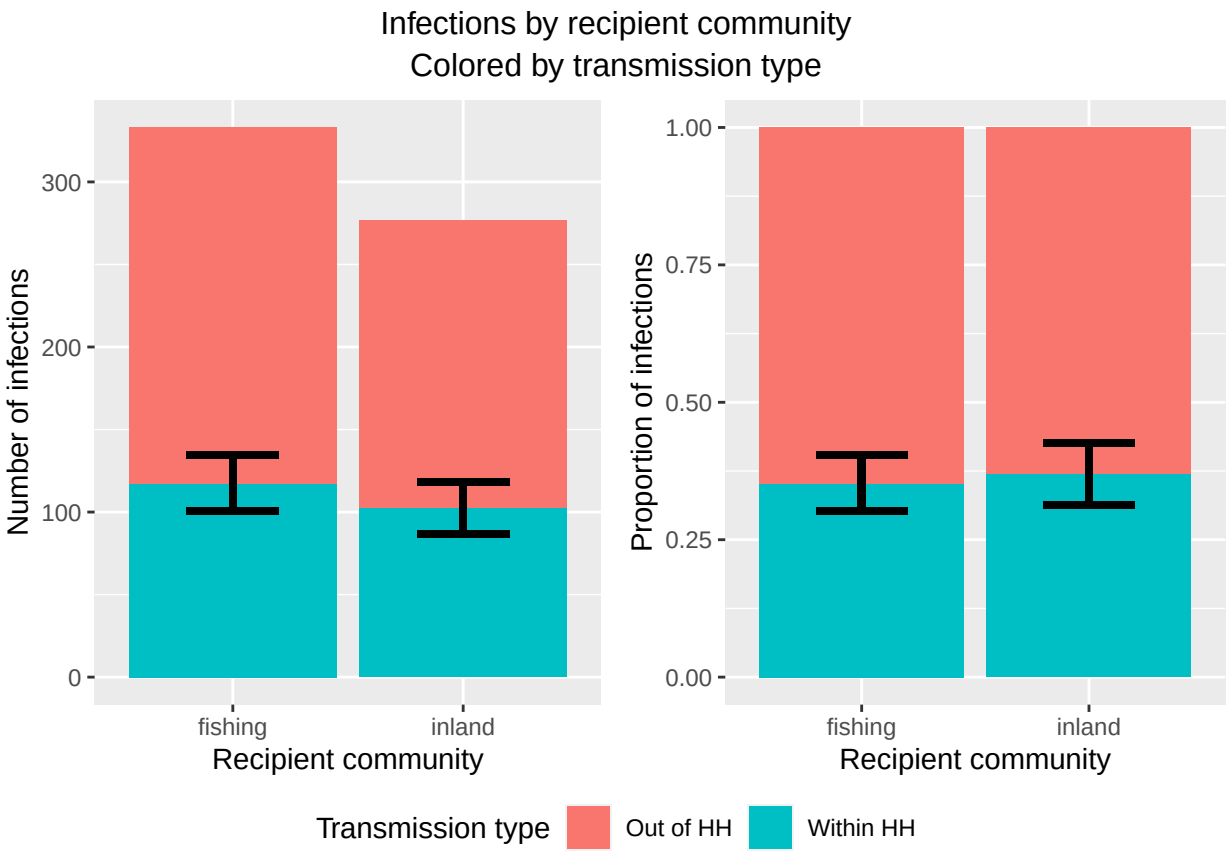
```r
cat("Inland, Within HH:\n")
```

```
## Inland, Within HH:
```

```r
binconf(102,610)*610
```

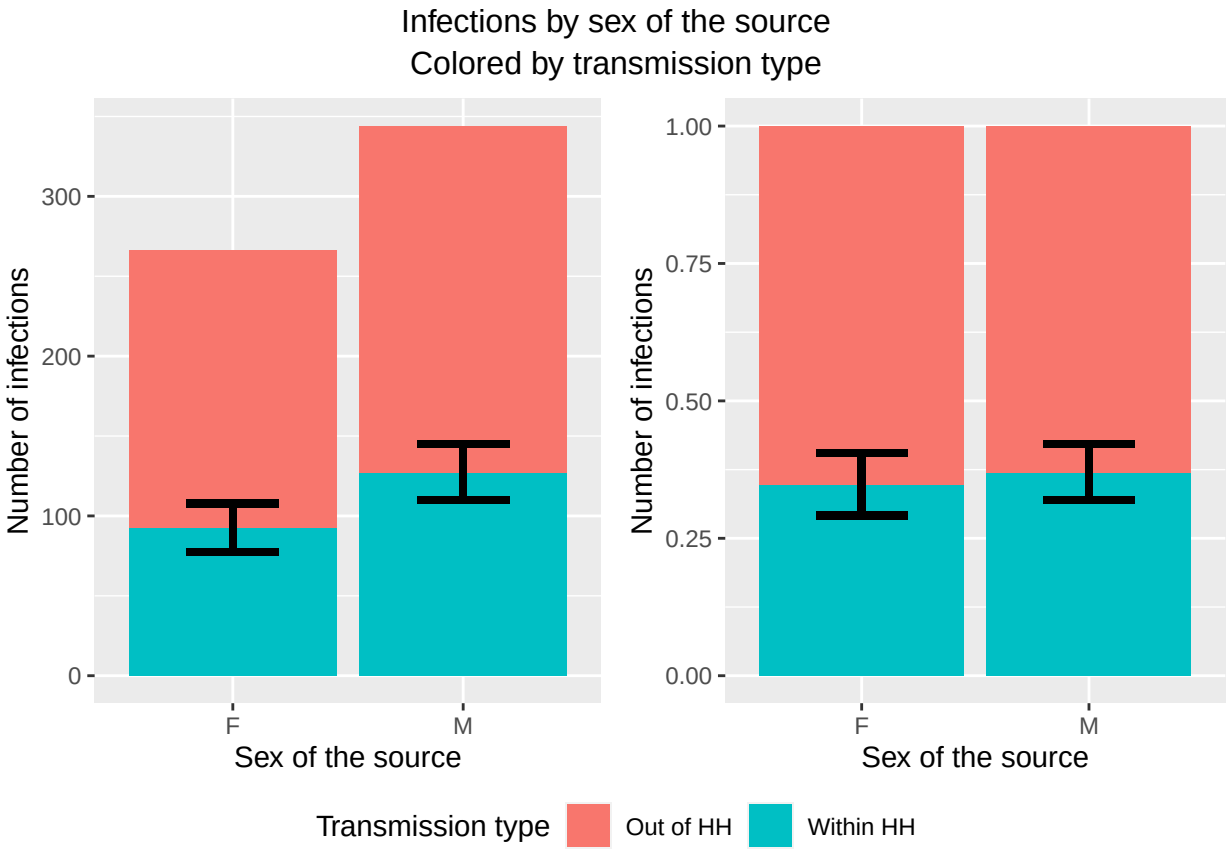
```
##  PointEst    Lower    Upper
##       102 85.21819 121.3226
```

```
# Same as above but flipped hh and comm (x axis vs fill colour)
p3<-ggplot(data = pairs_tsi, aes(x = COMM.RECIPIENT,fill = as.logical(same_hh))) +
  geom_bar()+
  labs(x='Recipient community',
       y='Number of infections',
       fill='Transmission type') +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  geom_errorbar( aes(x='fishing', ymin=binconf(nrow(pairs_tsi_same_hh[COMM.RECIPIENT=='fishing',]),nrow
  geom_errorbar( aes(x='inland', ymin=binconf(nrow(pairs_tsi_same_hh[COMM.RECIPIENT=='inland',]),nrow(pa



p4<-ggplot(data = pairs_tsi, aes(x = COMM.RECIPIENT,fill = as.logical(same_hh))) +
  geom_bar(position='fill')+
  labs(x='Recipient community',
       y='Proportion of infections',
       fill='Transmission type') +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  geom_errorbar( aes(x='fishing', ymin=binconf(nrow(pairs_tsi_same_hh[COMM.RECIPIENT=='fishing',]),nrow
  geom_errorbar( aes(x='inland', ymin=binconf(nrow(pairs_tsi_same_hh[COMM.RECIPIENT=='inland',]),nrow(pa

p <- ggarrange(p3, p4, ncol=2, nrow=1, common.legend = TRUE, legend="bottom")
p2<-annotate_figure(p, top="Colored by transmission type")
annotate_figure(p2, top="Infections by recipient community")
```

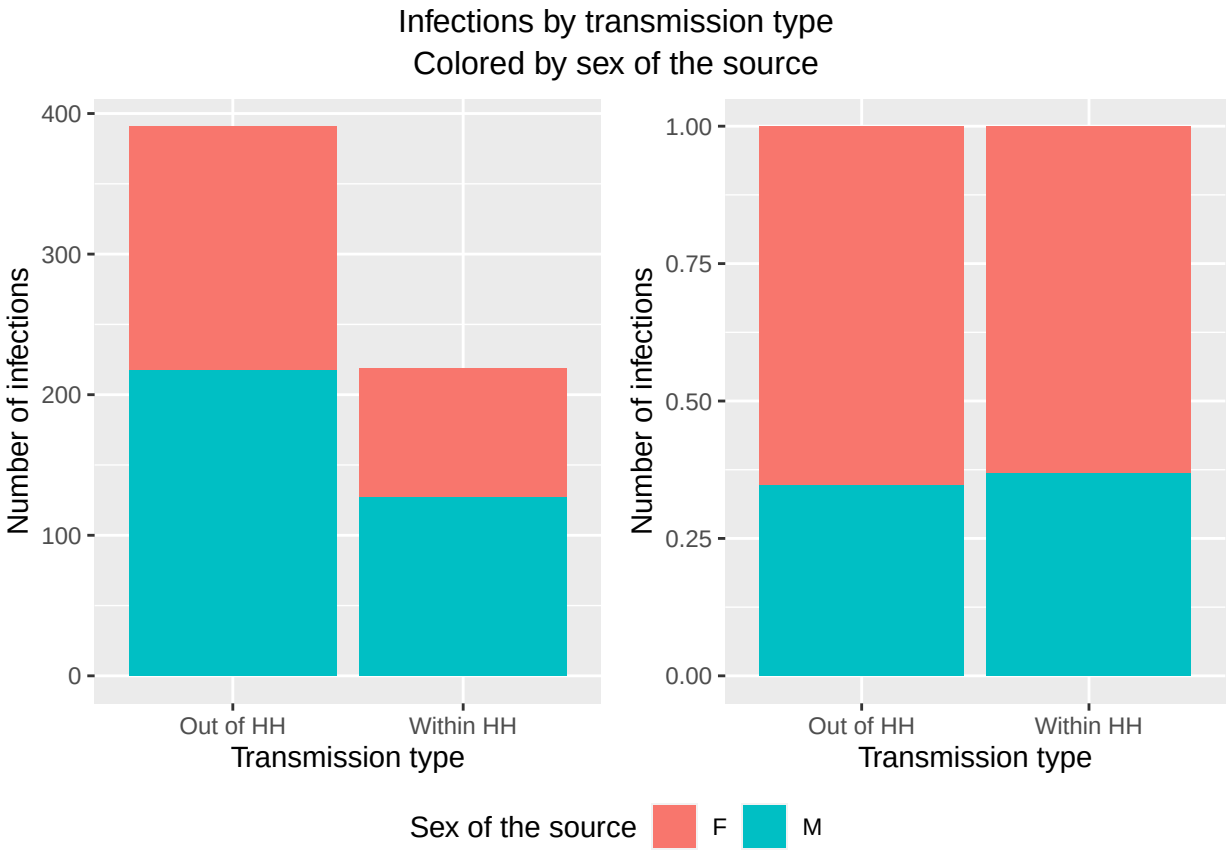


BY SEX AND HOUSEHOLD FACTOR

```
p1<-ggplot(data = pairs_tsi, aes(x = SEX.SOURCE,fill = as.logical(same_hh))) +
  geom_bar()+
  labs(x='Sex of the source',
    y='Number of infections',
    fill='Transmission type') +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  geom_errorbar( aes(x='F', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi[SEX.S
  geom_errorbar( aes(x='M', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi[SEX.S

p2<-ggplot(data = pairs_tsi, aes(x = SEX.SOURCE,fill = as.logical(same_hh))) +
  geom_bar(position = "fill")+
  labs(x='Sex of the source',
       y='Number of infections',
       fill='Transmission type') +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  geom_errorbar( aes(x='F', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi[SEX.S
  geom_errorbar( aes(x='M', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi[SEX.S

p<-ggarrange(p1, p2, ncol=2, nrow=1, common.legend = TRUE, legend="bottom")
p2<-annotate_figure(p, top="Colored by transmission type")
annotate_figure(p2, top="Infections by sex of the source")
```

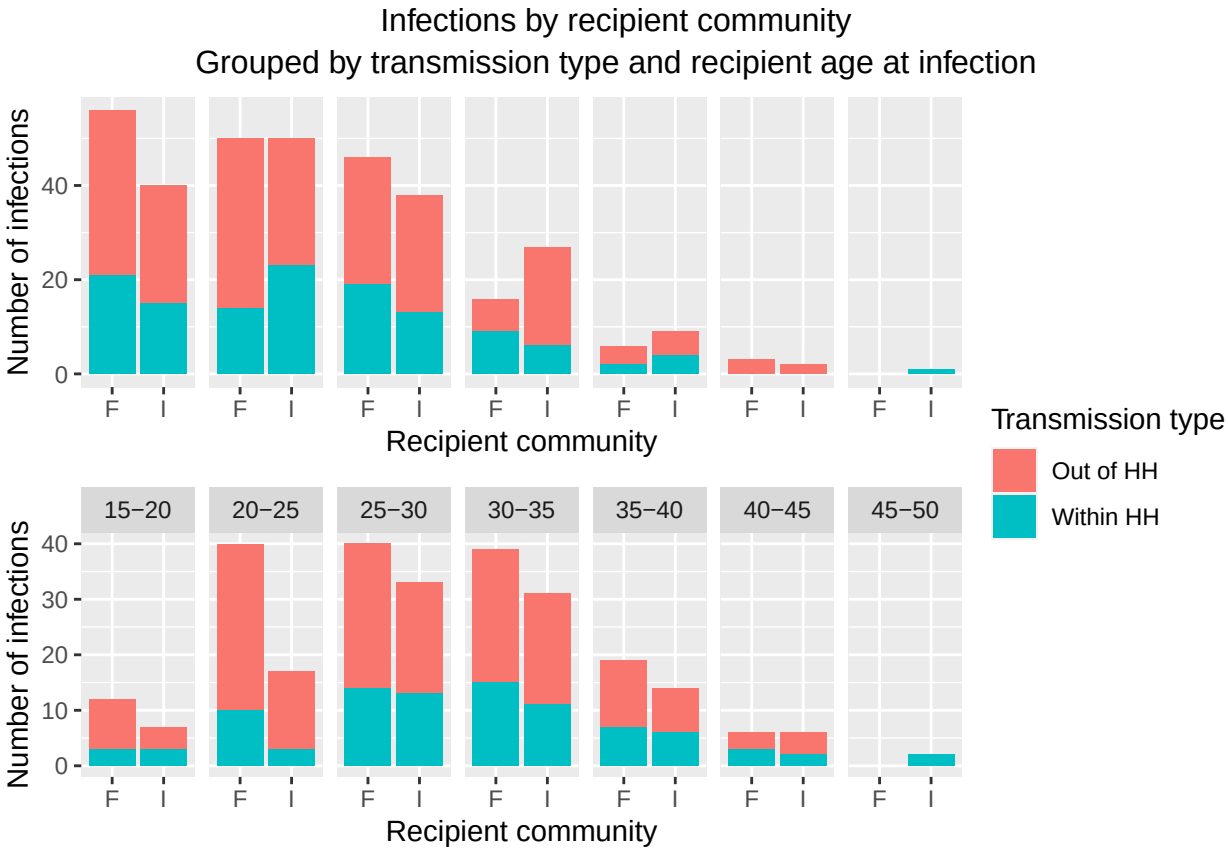


```r
#### Other way around:
p1<-ggplot(data = pairs_tsi, aes(x = as.logical(same_hh),fill = SEX.SOURCE)) +
  geom_bar()+
  labs(x='Transmission type',
       y='Number of infections',
       fill='Sex of the source') +
  scale_x_discrete(labels=c("Out of HH","Within HH"))
  #geom_errorbar( aes(x='F', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi[SEX.
  #geom_errorbar( aes(x='M', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi[SEX.

p2<-ggplot(data = pairs_tsi, aes(x = SEX.SOURCE,fill = as.logical(same_hh))) +
  geom_bar(position="fill") +
  labs(x='Transmission type',
       y='Number of infections',
       fill='Sex of the source') +
  scale_x_discrete(labels=c("Out of HH","Within HH"))
  #geom_errorbar( aes(x='F', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi[SEX.
  #geom_errorbar( aes(x='M', ymin=binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi[SEX.

p<-ggarrange(p1, p2, ncol=2, nrow=1, common.legend = TRUE, legend="bottom")
p2<-annotate_figure(p, top="Colored by sex of the source")
annotate_figure(p2, top="Infections by transmission type")
```



BY AGE BAND

```
p1<-ggplot(data = pairs_tsi[is.na(AGE_BAND.RECIPIENT)==FALSE & SEX.RECIPIENT=='F',], aes(fill = as.logi
  geom_bar()+
  labs(fill='Transmission type',
       y='Number of infections',
       x='Recipient community')+
  facet_grid(.~ AGE_BAND.RECIPIENT, scales="free_y") +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  scale_x_discrete(labels=c('F','I')) +
  theme(strip.text = element_blank()) +
  theme(legend.position='bottom')

p2<-ggplot(data = pairs_tsi[is.na(AGE_BAND.RECIPIENT)==FALSE & SEX.RECIPIENT=='M',], aes(fill = as.logi
  geom_bar()+
  labs(fill='Transmission type',
       y='Number of infections',
       x='Recipient community')+
  facet_grid(.~ AGE_BAND.RECIPIENT, scales="free_y") +
  scale_x_discrete(labels=c('F','I')) +
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  theme(legend.position='bottom')

p<-ggarrange(p1, p2, ncol=1, nrow=2, common.legend = TRUE, legend="right")
p2<-annotate_figure(p, top="Grouped by transmission type and recipient age at infection")
annotate_figure(p2, top="Infections by recipient community")
```



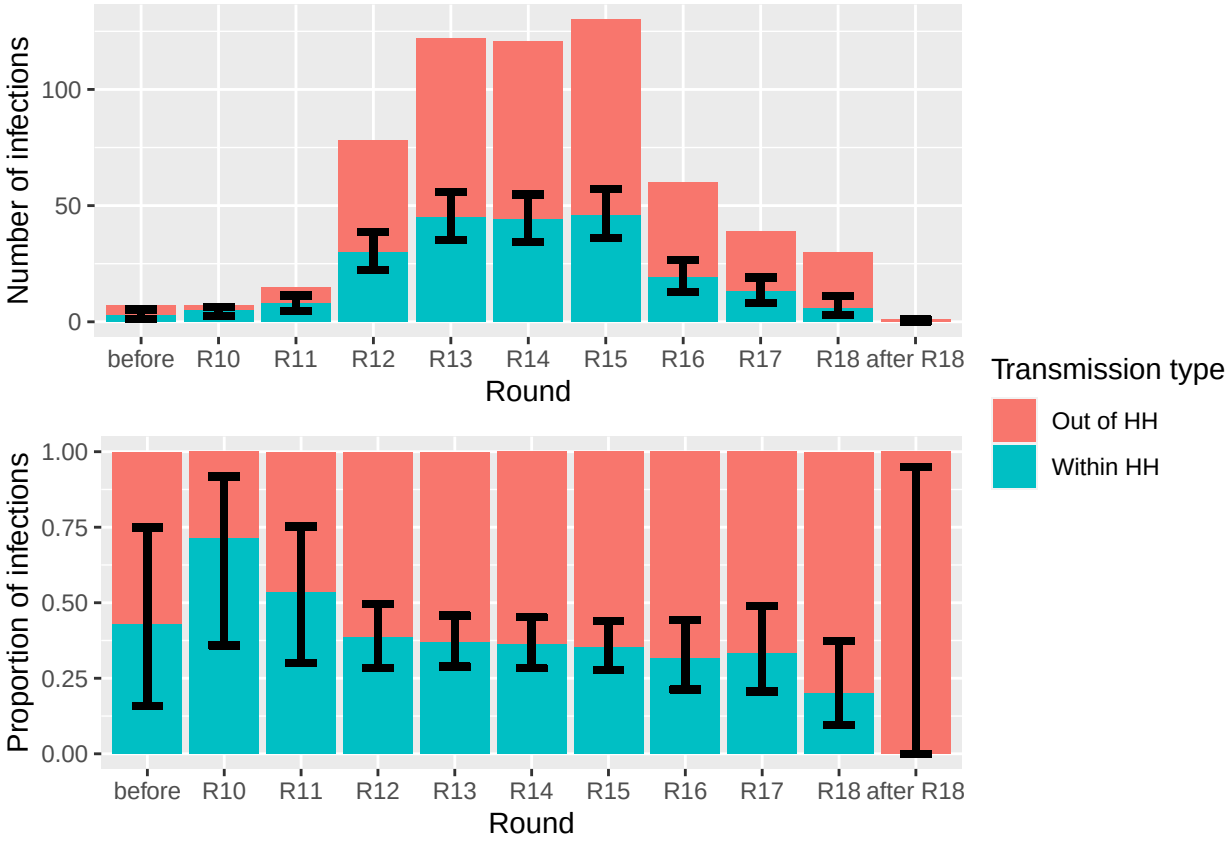
By round

```
tmp<-pairs_tsi
tmp[is.na(ROUND.M)==TRUE,]$M
```

```
## [1] "2000-04-09" "2002-08-24" "2003-03-06" "2018-11-17" "2002-08-29"
## [6] "2002-10-07" "2001-05-06" "2002-06-14"
```

```
tmp[is.na(ROUND.M)==TRUE & year(M)<=2003,]$ROUND.M<-'before R10'
tmp[is.na(ROUND.M)==TRUE & year(M)>=2018,]$ROUND.M<-'after R18'
pairs_tsi<-tmp
pairs_tsi$ROUND.M<-factor(pairs_tsi$ROUND.M,levels=c('before R10','R010','R011','R012','R013','R014','R
pairs_tsi_same_hh<-pairs_tsi[same_hh==1,]
pairs_tsi_diff_hh<-pairs_tsi[same_hh==0,]

p2<-ggplot(data = pairs_tsi, aes(x = ROUND.M ,fill = as.logical(same_hh))) +
  geom_bar(position="fill")+
  labs(x='Round',
       y='Proportion of infections',
       fill='Same HH') +
  geom_errorbar( aes(x='before R10', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='before R10',]),nrow(
  geom_errorbar( aes(x='R010', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R010',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R011', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R011',]),nrow(pairs_tsi[ROU
```

```
  geom_errorbar( aes(x='R012', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R012',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R013', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R013',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R014', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R014',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R015', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R015',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R016', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R016',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R017', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R017',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R018', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R018',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='after R18', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='after R18',]),nrow(pai
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  scale_x_discrete(labels=c("before","R10",'R11','R12','R13','R14','R15','R16','R17','R18','after R18'))


p1<-ggplot(data = pairs_tsi, aes(x = ROUND.M,fill = as.logical(same_hh))) +
  geom_bar()+
  labs(x='Round',
       y='Number of infections',
       fill='Transmission type')+
  geom_errorbar( aes(x='before R10', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='before R10',]),nrow(p
  geom_errorbar( aes(x='R010', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R010',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R011', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R011',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R012', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R012',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R013', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R013',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R014', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R014',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R015', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R015',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R016', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R016',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R017', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R017',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='R018', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='R018',]),nrow(pairs_tsi[ROU
  geom_errorbar( aes(x='after R18', ymin=binconf(nrow(pairs_tsi_same_hh[ROUND.M=='after R18',]),nrow(pai
  scale_fill_discrete(labels=c("Out of HH","Within HH")) +
  scale_x_discrete(labels=c("before","R10",'R11','R12','R13','R14','R15','R16','R17','R18','after R18'))

ggarrange(p1, p2, ncol=1, nrow=2, common.legend = TRUE, legend="right")
```



BY AGE OF THE SOURCE AND RECIPIENT

```
p1<-ggplot(data = pairs_tsi[SEX.SOURCE=='M',], aes(x = AGE_INFECTION.RECIPIENT,y=AGE_TRANSMISSION.SOURCE
  geom_point(size=1)+
  geom_abline(intercept=0,slope=1,color='black')+
  geom_smooth(data=pairs_tsi_diff_hh[SEX.SOURCE=='M',],color='red',size=1,se=FALSE)+
  geom_smooth(data=pairs_tsi_same_hh[SEX.SOURCE=='M',],color='blue',size=1,se=FALSE)+
  xlim(15,50)+
  ylim(15,50)+
  labs(title='                    M to F',
       x='Age at transmission of the recipient',
       y='Age at transmission of the source',
       color='Transmission type')+
  scale_color_manual(values=c("red", "blue"),labels=c('Out of household','Within household'))
```

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

```
p2<-ggplot(data = pairs_tsi[SEX.SOURCE=='F',], aes(x = AGE_INFECTION.RECIPIENT,y=AGE_TRANSMISSION.SOURCE
  geom_point(size=1)+
```

```
  geom_abline(intercept=0,slope=1,color='black')+
  geom_smooth(data=pairs_tsi_diff_hh[SEX.SOURCE=='F',],color='red',size=1,se=FALSE)+
  geom_smooth(data=pairs_tsi_same_hh[SEX.SOURCE=='F',],color='blue',size=1,se=FALSE)+
  xlim(15,50)+
  ylim(15,50)+
  labs(title='                    F to M',
       x='Age at transmission of the recipient',
       y='Age at transmission of the source',
       color='Transmission type')+
  scale_color_manual(values=c("red", "blue"),labels=c('Out of household','Within household'))
p3<-ggarrange(p1, p2, ncol=2, nrow=1, common.legend = TRUE, legend="bottom")
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

```
annotate_figure(p3, top="Infections by age")
```


```
################   SOURCE AGE   ###################
med.fac = ddply(pairs_tsi, .(SEX.SOURCE, same_hh), function(.d)
data.frame(x=median(.d$AGE_TRANSMISSION.SOURCE)))
```

```
p1<-ggplot(data = pairs_tsi, aes(x = AGE_TRANSMISSION.SOURCE,color=as.logical(same_hh))) +
  geom_density(alpha=.2)+#, fill="#FF6666")+
  labs(title='Histogram of the age at transmission of sources',
       x='Age at transmission',
       color='Transmission type') +
  scale_color_manual(values=c("red", "blue"),labels=c('Out of household','Within household')) +
  facet_grid(.~ SEX.SOURCE, scales="free_y") +
  geom_vline(data=med.fac[c(1,3),], aes(xintercept=x),color="red", linetype="dashed", size=.5)+
  geom_vline(data=med.fac[c(2,4),], aes(xintercept=x),color="blue", linetype="dashed", size=.5)+
  theme(legend.position='bottom')

#Double check:
median(pairs_tsi_diff_hh[SEX.SOURCE=='M',]$AGE_TRANSMISSION.SOURCE)
```

```
## [1] 28.3
```

```
median(pairs_tsi_same_hh[SEX.SOURCE=='M',]$AGE_TRANSMISSION.SOURCE)
```

```
## [1] 28.4
```

```
median(pairs_tsi_diff_hh[SEX.SOURCE=='F',]$AGE_TRANSMISSION.SOURCE)
```

```
## [1] 25.3
```

```
median(pairs_tsi_same_hh[SEX.SOURCE=='F',]$AGE_TRANSMISSION.SOURCE)
```

```
## [1] 25.3
```

```
################   RECIPIENT AGE   ###################
med.fac = ddply(pairs_tsi, .(SEX.RECIPIENT, same_hh), function(.d)
  data.frame(x=median(.d$AGE_INFECTION.RECIPIENT)))
p2<-ggplot(data = pairs_tsi, aes(x = AGE_INFECTION.RECIPIENT,color=as.logical(same_hh))) +
  geom_density(alpha=.2)+
  labs(title='Histogram of the age at transmission of recipients',
       x='Age at transmission ',
       color='Transmission type') +
  scale_color_manual(values=c("red", "blue"),labels=c('Out of household','Within household')) +
  facet_grid(.~ SEX.RECIPIENT, scales="free_y") +
  geom_vline(data=med.fac[c(1,3),], aes(xintercept=x),color="red", linetype="dashed", size=.5)+
  geom_vline(data=med.fac[c(2,4),], aes(xintercept=x),color="blue", linetype="dashed", size=.5)+
  theme(legend.position='bottom')

#Double check:
median(pairs_tsi_diff_hh[SEX.RECIPIENT=='M',]$AGE_INFECTION.RECIPIENT)
```

```
## [1] 28.15
```

```
median(pairs_tsi_same_hh[SEX.RECIPIENT=='M',]$AGE_INFECTION.RECIPIENT)
```

```
## [1] 30.15
```

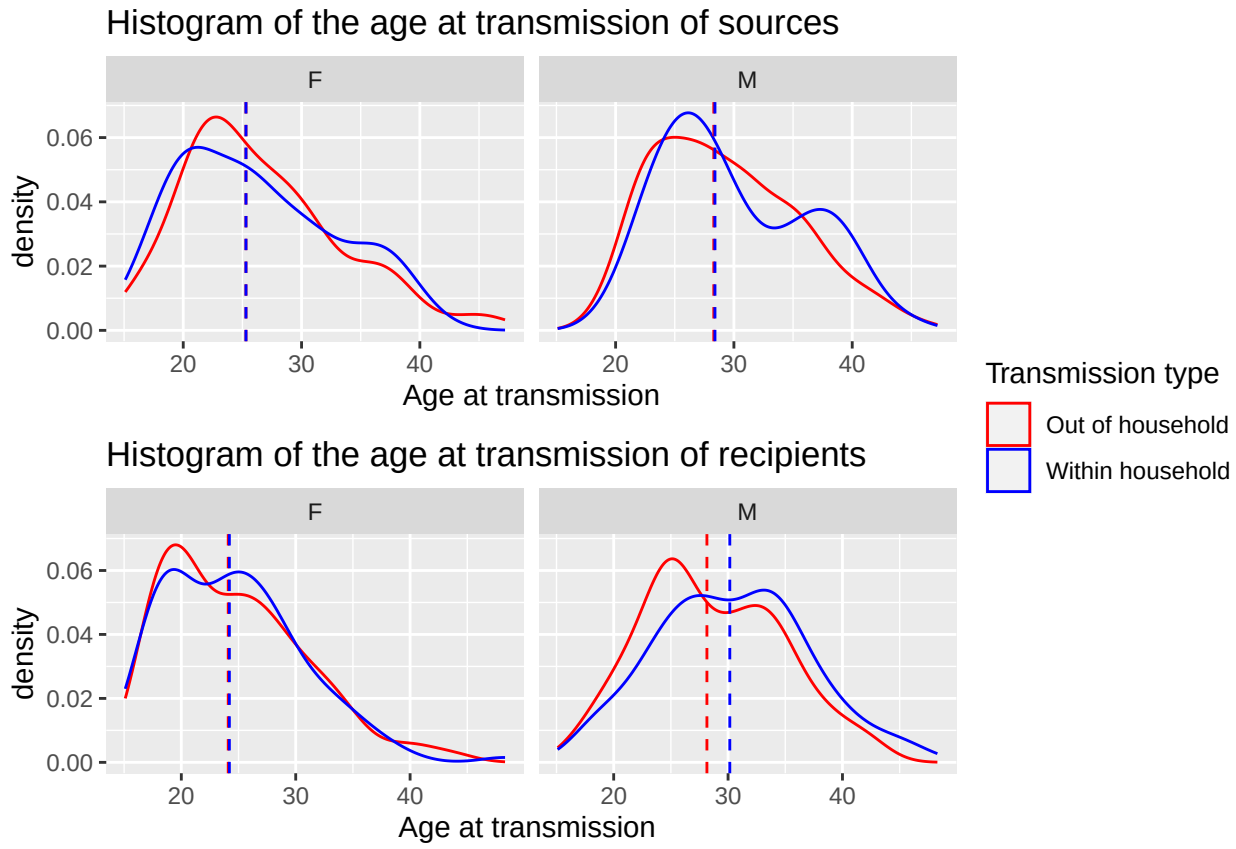
```
median(pairs_tsi_diff_hh[SEX.RECIPIENT=='F',]$AGE_INFECTION.RECIPIENT)
```

```
## [1] 24.1
```

```
median(pairs_tsi_same_hh[SEX.RECIPIENT=='F',]$AGE_INFECTION.RECIPIENT)
```

```
## [1] 24.2
```

```
ggarrange(p1, p2, ncol=1, nrow=2, common.legend = TRUE, legend="right")
```



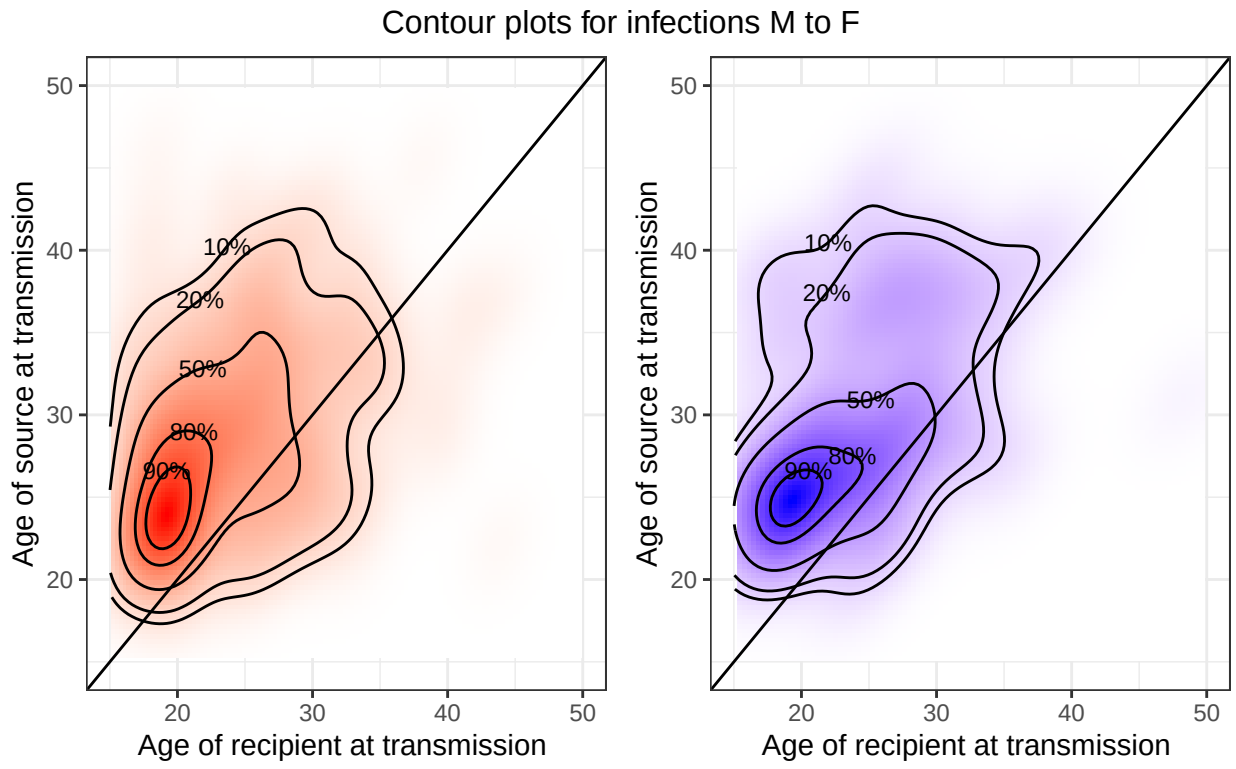

```
###############  2-D KERNEL DENISTY ESTIMATION: ############################
set.seed(1001)

#DIFFERENT HH, M to F
d <- matrix(c(pairs_tsi[as.logical(same_hh)==0 & SEX.SOURCE=='M', ]$AGE_INFECTION.RECIPIENT, pairs_tsi[a
  magrittr::set_colnames(c("x", "y")) %>%
  as_tibble()
```

```r
kd<-ks::kde(d, compute.cont=TRUE, h=0.2)
get_contour <- function(kd_out=kd, prob="5%") {
  contour_95 <- with(kd_out, contourLines(x=eval.points[[1]], y=eval.points[[2]],
                                          z=estimate, levels=cont[prob])[[1]])
  as_tibble(contour_95) %>%
    mutate(prob = prob)
}

dat_out <- map_dfr(c("10%", "20%", "50%" ,"80%", "90%"), ~get_contour(kd, .)) %>%
  group_by(prob) %>%
  mutate(n_val = 1:n()) %>%
  ungroup()

## clean kde output
kd_df <- expand_grid(x=kd$eval.points[[1]], y=kd$eval.points[[2]]) %>%
  mutate(z = c(kd$estimate %>% t))

p1<-ggplot(data=kd_df, aes(x, y)) +
  geom_tile(aes(fill=z)) +
  geom_path(aes(x, y, group = prob),
            data=dat_out, colour = I("black")) +
  geom_text(aes(label = prob), data =
              filter(dat_out, (prob%in% c("10%") & n_val==100 | prob%in% c("20%") & n_val==80) | prob%in
            colour = I("black"), size =I(3))+
  xlim(15,50)+
  ylim(15,50)+
  geom_abline(intercept=0,slope=1,color='black')+
  scale_fill_gradient(low = "white", high = "red") +
  labs(x='Age of recipient at transmission ',
       y='Age of source at transmission') +
  theme_bw() +
  theme(legend.position = "none")


#SAME HH, M to F
d <- matrix(c(pairs_tsi[as.logical(same_hh)==1 & SEX.SOURCE=='M', ]$AGE_INFECTION.RECIPIENT, pairs_tsi[a
  magrittr::set_colnames(c("x", "y")) %>%
  as_tibble()

kd<-ks::kde(d, compute.cont=TRUE, h=0.2)
get_contour <- function(kd_out=kd, prob="5%") {
  contour_95 <- with(kd_out, contourLines(x=eval.points[[1]], y=eval.points[[2]],
                                          z=estimate, levels=cont[prob])[[1]])
  as_tibble(contour_95) %>%
    mutate(prob = prob)
}

dat_out <- map_dfr(c("10%", "20%","50%","80%", "90%"), ~get_contour(kd, .)) %>%
  group_by(prob) %>%
  mutate(n_val = 1:n()) %>%
  ungroup()

## clean kde output
```

```
kd_df <- expand_grid(x=kd$eval.points[[1]], y=kd$eval.points[[2]]) %>%
  mutate(z = c(kd$estimate %>% t))

p2<-ggplot(data=kd_df, aes(x, y)) +
  geom_tile(aes(fill=z)) +
  geom_path(aes(x, y, group = prob),
            data=dat_out, colour = I("black")) +
  geom_text(aes(label = prob), data =
              filter(dat_out, (prob%in% c("10%") & n_val==100 | prob%in% c("20%") & n_val==80) | prob%in
            colour = I("black"), size =I(3))+
  xlim(15,50)+
  ylim(15,50)+
  geom_abline(intercept=0,slope=1,color='black')+
  scale_fill_gradient(low = "white", high = "blue") +
  labs(x='Age of recipient at transmission ',
       y='Age of source at transmission') +
  theme_bw() +
  theme(legend.position = "none")
p3<-ggarrange(p1,p2,ncol=2,nrow=1)
```

```
## Warning: Removed 8527 rows containing missing values (‘geom_tile()‘).

## Warning: Removed 60 rows containing missing values (‘geom_path()‘).

## Warning: Removed 10153 rows containing missing values (‘geom_tile()‘).

## Warning: Removed 76 rows containing missing values (‘geom_path()‘).
```

```
annotate_figure(p3,bottom=('Red: Out of household \nBlue: Within household'), top='Contour plots for in
```



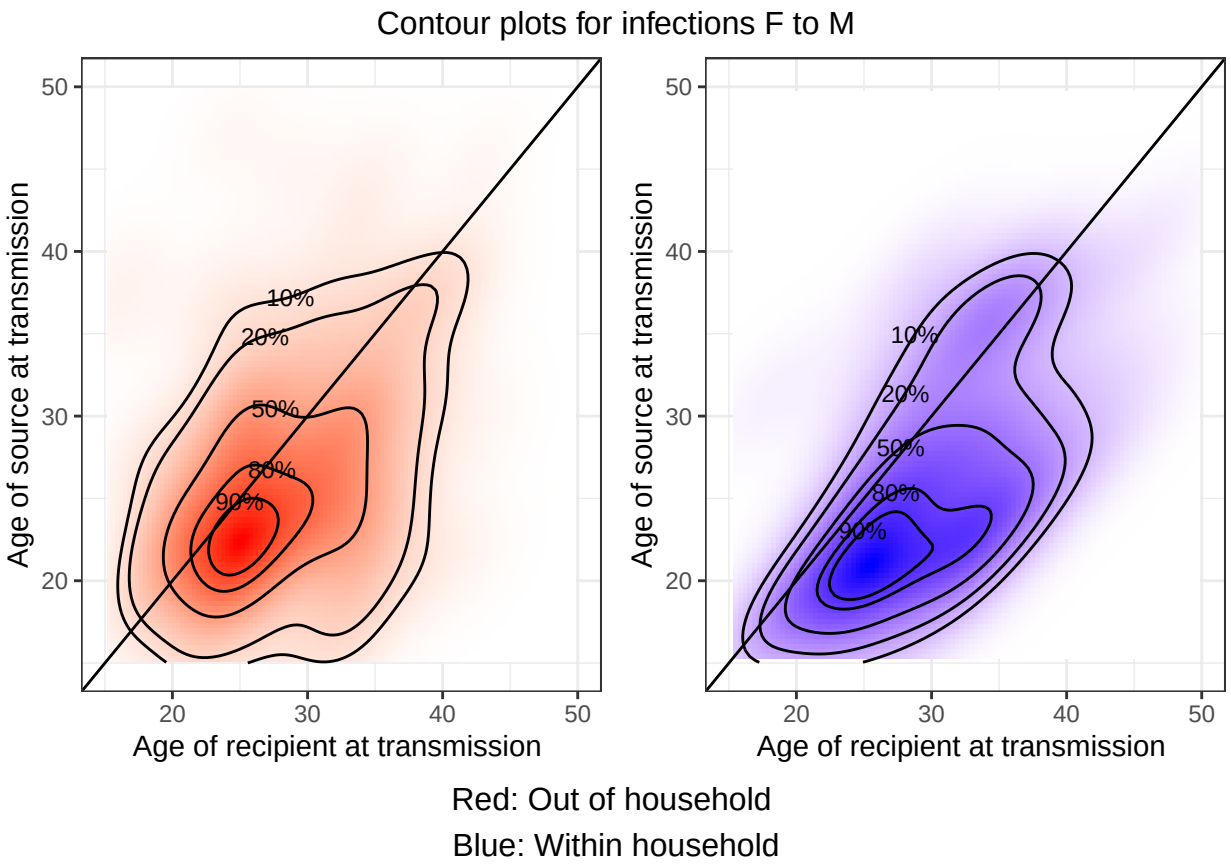

```
#DIFFERENT HH, F to M
d <- matrix(c(pairs_tsi[as.logical(same_hh)==0 & SEX.SOURCE=='F', ]$AGE_INFECTION.RECIPIENT, pairs_tsi[a
  magrittr::set_colnames(c("x", "y")) %>%
  as_tibble()

kd<-ks::kde(d, compute.cont=TRUE, h=0.2)
get_contour <- function(kd_out=kd, prob="5%") {
  contour_95 <- with(kd_out, contourLines(x=eval.points[[1]], y=eval.points[[2]],
                                          z=estimate, levels=cont[prob])[[1]])
  as_tibble(contour_95) %>%
    mutate(prob = prob)
}

dat_out <- map_dfr(c("10%", "20%","50%","80%", "90%"), ~get_contour(kd, .)) %>%
  group_by(prob) %>%
  mutate(n_val = 1:n()) %>%
  ungroup()

## clean kde output
kd_df <- expand_grid(x=kd$eval.points[[1]], y=kd$eval.points[[2]]) %>%
  mutate(z = c(kd$estimate %>% t))

p1<-ggplot(data=kd_df, aes(x, y)) +
  geom_tile(aes(fill=z)) +
  geom_path(aes(x, y, group = prob),
            data=dat_out, colour = I("black")) +
```

```
  geom_text(aes(label = prob), data =
              filter(dat_out, (prob%in% c("10%") & n_val==100 | prob%in% c("20%") & n_val==80) | prob%in
            colour = I("black"), size =I(3))+
  xlim(15,50)+
  ylim(15,50)+
  geom_abline(intercept=0,slope=1,color='black')+
  scale_fill_gradient(low = "white", high = "red") +
  labs(x='Age of recipient at transmission ',
       y='Age of source at transmission') +
  theme_bw() +
  theme(legend.position = "none")

#SAME HH, F to M
d <- matrix(c(pairs_tsi[as.logical(same_hh)==1 & SEX.SOURCE=='F', ]$AGE_INFECTION.RECIPIENT, pairs_tsi[a
  magrittr::set_colnames(c("x", "y")) %>%
  as_tibble()

kd<-ks::kde(d, compute.cont=TRUE, h=0.2)
get_contour <- function(kd_out=kd, prob="5%") {
  contour_95 <- with(kd_out, contourLines(x=eval.points[[1]], y=eval.points[[2]],
                                          z=estimate, levels=cont[prob])[[1]])
  as_tibble(contour_95) %>%
    mutate(prob = prob)
}

dat_out <- map_dfr(c("10%", "20%","50%","80%", "90%"), ~get_contour(kd, .)) %>%
  group_by(prob) %>%
  mutate(n_val = 1:n()) %>%
  ungroup()

## clean kde output
kd_df <- expand_grid(x=kd$eval.points[[1]], y=kd$eval.points[[2]]) %>%
  mutate(z = c(kd$estimate %>% t))

p2<-ggplot(data=kd_df, aes(x, y)) +
  geom_tile(aes(fill=z)) +
  geom_path(aes(x, y, group = prob),
            data=dat_out, colour = I("black")) +
  geom_text(aes(label = prob), data =
              filter(dat_out, (prob%in% c("10%") & n_val==100 | prob%in% c("20%") & n_val==80) | prob%in
            colour = I("black"), size =I(3))+
  xlim(15,50)+
  ylim(15,50)+
  geom_abline(intercept=0,slope=1,color='black')+
  scale_fill_gradient(low = "white", high = "blue") +
  labs(x='Age of recipient at transmission ',
       y='Age of source at transmission') +
  theme_bw() +
  theme(legend.position = "none")
p3<-ggarrange(p1,p2,ncol=2,nrow=1)
```

```
## Warning: Removed 10956 rows containing missing values (‘geom_tile()‘).
```

```
## Warning: Removed 11713 rows containing missing values (`geom_tile()`).
```

```
annotate_figure(p3,bottom=('Red: Out of household \nBlue: Within household'), top='Contour plots for in
```




```
#For the table
nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',])
```

```
## [1] 127
```

```
nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',])
```

```
## [1] 92
```

```
nrow(pairs_tsi_diff_hh[SEX.SOURCE=='M',])
```

```
## [1] 217
```

```
nrow(pairs_tsi_diff_hh[SEX.SOURCE=='F',])
```

```
## [1] 174
```

```
binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi))*nrow(pairs_tsi)
```

```
##  PointEst    Lower    Upper
##       127 108.4895 147.7383
```

```
binconf(nrow(pairs_tsi_same_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi))*nrow(pairs_tsi)
```

```
##  PointEst    Lower    Upper
##        92 76.01214 110.6538
```

```
binconf(nrow(pairs_tsi_diff_hh[SEX.SOURCE=='M',]),nrow(pairs_tsi))*nrow(pairs_tsi)
```

```
##  PointEst    Lower    Upper
##       217 194.4423 240.6591
```

```
binconf(nrow(pairs_tsi_diff_hh[SEX.SOURCE=='F',]),nrow(pairs_tsi))*nrow(pairs_tsi)
```

```
##  PointEst    Lower    Upper
##       174 153.0154 196.6243
```

Further summary statistics

```
# Convert strings to factors
pairs_tsi[,SEX.SOURCE:=as.factor(SEX.SOURCE)]
pairs_tsi[,SEX.RECIPIENT:=as.factor(SEX.RECIPIENT)]
pairs_tsi[,ROUND.M:=as.factor(ROUND.M)]
pairs_tsi[,COMM.SOURCE:=as.factor(COMM.SOURCE)]
pairs_tsi[,COMM.RECIPIENT:=as.factor(COMM.RECIPIENT)]
pairs_tsi[,same_hh:=as.factor(same_hh)]

# Return summary of data set
summary(pairs_tsi)
```

```
##   RECIPIENT            SOURCE          SEX.SOURCE SEX.RECIPIENT
##  Length:610         Length:610         F:266      F:344
##  Class :character   Class :character   M:344      M:266
##  Mode  :character   Mode  :character
##
##
##
##
##        CL                   IL                   M
##  Min.   :1998-11-20   Min.   :2000-01-17   Min.   :2000-04-09
##  1st Qu.:2006-07-21   1st Qu.:2007-08-22   1st Qu.:2009-01-18
##  Median :2009-11-18   Median :2010-05-29   Median :2011-03-12
##  Mean   :2009-08-02   Mean   :2010-04-15   Mean   :2011-03-18
##  3rd Qu.:2012-05-09   3rd Qu.:2012-07-20   3rd Qu.:2013-01-18
##  Max.   :2018-08-06   Max.   :2018-09-14   Max.   :2018-11-17
```

```
##
##        IU                   CU             AGE_TRANSMISSION.SOURCE
##  Min.   :2000-06-28   Min.   :2000-08-13   Min.   :15.10
##  1st Qu.:2010-06-14   1st Qu.:2011-03-07   1st Qu.:23.10
##  Median :2011-09-23   Median :2012-02-09   Median :27.10
##  Mean   :2012-01-07   Mean   :2012-06-25   Mean   :28.22
##  3rd Qu.:2013-07-17   3rd Qu.:2013-11-21   3rd Qu.:32.60
##  Max.   :2019-01-20   Max.   :2019-02-28   Max.   :47.20
##
##  AGE_INFECTION.RECIPIENT    ROUND.M     COMM.SOURCE  COMM.RECIPIENT
##  Min.   :15.10           R015   :130   fishing:326   fishing:333
##  1st Qu.:21.20           R013   :122   inland :284   inland :277
##  Median :25.75           R014   :121
##  Mean   :26.66           R012   : 78
##  3rd Qu.:31.40           R016   : 60
##  Max.   :48.30           R017   : 39
##                          (Other): 60
##  COMM_NUM.SOURCE COMM_NUM.RECIPIENT DATE.COLLECTION.SOURCE
##  Min.   :  2.0   Min.   :  0.0      Min.   :2010-01-20
##  1st Qu.: 38.0   1st Qu.: 38.0      1st Qu.:2011-12-02
##  Median : 40.0   Median : 39.0      Median :2012-04-29
##  Mean   :285.6   Mean   :286.3      Mean   :2012-10-28
##  3rd Qu.:770.0   3rd Qu.:770.0      3rd Qu.:2013-01-20
##  Max.   :776.0   Max.   :776.0      Max.   :2019-05-14
##
##  DATE.COLLECTION.RECIPIENT same_hh AGE_BAND.RECIPIENT
##  Min.   :2010-02-08        0:391   15-20:115
##  1st Qu.:2012-02-07        1:219   20-25:157
##  Median :2012-10-14                25-30:157
##  Mean   :2013-08-20                30-35:113
##  3rd Qu.:2014-11-21                35-40: 48
##  Max.   :2019-05-17                40-45: 17
##                                    45-50:  3
```

```
# Perform chisq tests of independence
chisq.test(pairs_tsi$same_hh, pairs_tsi$SEX.SOURCE)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  pairs_tsi$same_hh and pairs_tsi$SEX.SOURCE
## X-squared = 0.26043, df = 1, p-value = 0.6098
```

```
chisq.test(pairs_tsi$same_hh, pairs_tsi$COMM.SOURCE)
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  pairs_tsi$same_hh and pairs_tsi$COMM.SOURCE
## X-squared = 0.0083285, df = 1, p-value = 0.9273
```

```r
# Plot infections by community (source) and within-household
n_obs <- pairs_tsi[, .N]
data_comm_hh <- pairs_tsi[, .(count = .N), by = .(COMM.SOURCE, same_hh)]

p1_data <- pairs_tsi[ , {
    N.in.inland <- sum(COMM.RECIPIENT == 'inland')
    binom.confs <- (.N*binconf(N.in.inland, .N)) |> as.list()
    names(binom.confs) <- c('BC.center', 'BC.min', 'BC.max')
    binom.confs
}, by=same_hh]

p <- ggplot(data_comm_hh, aes(fill = COMM.SOURCE, y = count, x = same_hh)) +
  geom_bar(position = "stack", stat = "identity") +
  geom_errorbar(data = data_comm_hh[, COMM.SOURCE == "inland"],
                aes(ymin = BC.min, ymax = BC.max, fill = NA), width=0.4,
                colour="black", alpha=0.9, linewidth=1.3) +
  labs(x='transmission type',
       y='number of infections',
       fill='recipient community') +
    scale_x_discrete(labels=c("out of hh","within hh"))

print(p)
```