**This is WORK IN PROGRESS**  
**need to check xtime\_yr: stata vs. R**  
**check if edu3 results in Table 1 and 2 in the paper have any typos**

* Author: YJ Choi
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This is markdown file to reproduce analysis and results for a published paper: **Reporting sterilization as a current contraceptive method among sterilized women: lessons learned from a population with high sterilization rates, Rajasthan, India** (*Contraception*. 2019 Feb;99(2):131-136). The abstract and link to the full paper is [available here](https://www.ncbi.nlm.nih.gov/pubmed/30391289).

There are three sections in this document for: accessing public data; preparing the analysis data file (i.e., data processing/manipulation); and conducting analysis. Analysis section contains code only for reproducing results presented in the paper. The paper was prepared using **Stata** and equivalent Stata do file is available at [GitHub](https://github.com/yoonjoung/ReproResearch_Sterilization_Reporting).

"R code is shown in a gray box"

Output is in white box.

## 1. Data access

Data came from the Performance Monitoring and Accountability 2020 (PMA2020) survey conducted in Rajasthan, India, in early 2017. PMA2020 survey data are available for the public, and can be accessed here: <https://www.pma2020.org/request-access-to-datasets>. Request and download **“Round 2 (2017) Rajasthan Household/Female survey”** data. The file has been saved as **“INR2\_Rajasthan\_HHQFQ.dta”** in Stata format in a directory.

## 2. Data management

Load the downloaded public data file into “dtapublic” (If you run this markdown file on your computer, you will need to change the file path **according to your directory setting**).

suppressPackageStartupMessages(library (haven))   
dtapublic<-data.frame(read\_dta("C:/YJ/Data PMA/rawHHQFQ/INR2\_Rajasthan\_HHQFQ.dta"))

The unit of analysis is a female respondent in the survey. Since the public datafile include both household and female level observations, keep only female level observations. Then, keep only completed interviews with de facto sample. The analysis dataset, “dta”, now has 6015 observations, all de-facto women 15-49 years of age who live in the sampled households.

suppressPackageStartupMessages(library (dplyr))  
#keep only female observations (as opposed to household)  
dta<-filter(dtapublic, FQmetainstanceID!="")  
#keep only completed interviews  
dta<-filter(dta, HHQ\_result==1 & FRS\_result==1)  
#keep only defacto observations  
dta<-filter(dta, usually\_live==1)  
#check the number of observations in the analysis dataset, "dta"  
nrow(dta)

## [1] 6015

*NOTE: In the above code chunk, “dta<-filter(dta, usually\_live==1)” should have been “dta<-filter(dta, last\_night==1)”: i.e., there was an error in classifying de-factor vs. de-jure popualtion, though small (2.1% of women who completed interview, 129/6089). The correct total number of de-factor population is 6034. Revised analysis results (not presented here, but can be produced with the changed code, “dta<-filter(dta, last\_night==1)”) are very comparable with published results. In any case, YC is responsible for this error.*

Then construct variables that are used for analysis. First, create demographic and backgorund characteristics variables.

suppressPackageStartupMessages(library(car))  
  
agebreaks<-c(15,20,25,30,35,40,45,50)  
agelabels<-c("15-19","20-24","25-29","30-34","35-39","40-44","45-49")  
dta<-mutate(dta,  
 #Sampling weight  
 xweight=FQweight/1000000,   
 #Age  
 xage=FQ\_age,  
 xagegroup5=cut(FQ\_age, breaks=agebreaks, right = FALSE,   
 labels = agelabels),  
 xagegroup5\_3=xagegroup5=="25-29",  
 xagegroup5\_4=xagegroup5=="30-34",  
 xagegroup5\_5=xagegroup5=="35-39",  
 xagegroup5\_6=xagegroup5=="40-44",  
 xagegroup5\_7=xagegroup5=="45-49",  
 #Marital status  
 xunion =(FQmarital\_status==1 | FQmarital\_status==2),  
 xmarried=(FQmarital\_status==1),  
 #Sexual activity   
 xsa=( (last\_time\_sex==1 & last\_time\_sex\_value<=30 & last\_time\_sex\_value>=0)   
 | (last\_time\_sex==2 & last\_time\_sex\_value<=4 & last\_time\_sex\_value>=0)   
 | (last\_time\_sex==3 & last\_time\_sex\_value<=1 & last\_time\_sex\_value>=0) ),   
 xsa = ifelse(is.na(xsa), 0, xsa),  
 #residential area  
 xurban = ur==1,  
 #Household wealth   
 xwealth5= wealthquintile,  
 xpoor = wealthquintile==1,  
 xrich = wealthquintile==5,  
 #education   
 school = ifelse(school<0, NA, school),  
 xedu3 =cut(school, breaks=c(0,1,3,5), right=FALSE,  
 labels = c("None", "Primary", ">Secondary") ),  
 xedupri =cut(school, breaks=c(0,1,5), right=FALSE,   
 labels = c("<Primary", ">= Primary" ) ),  
 xedusec =cut(school, breaks=c(0,3,5), right=FALSE,   
 labels = c("<Secondary", ">=Secondary") ),  
 #caste  
 caste = ifelse(caste<0, NA, caste),  
 xcaste\_sc = caste==1,  
 xcaste\_st = caste==2,  
 xcaste\_obc = caste==3,  
 xcaste4 =cut(caste, breaks=c(1,2,3,4,5), right=FALSE,  
 labels = c("SC", "ST", "OBC", "General") ),  
 #Religion   
 xhindu = religion==1,  
 xreligion=cut(religion, breaks=c(1,2,3,100), right = FALSE,   
 labels = c("Hindu", "Muslim", "Other") )   
)

suppressPackageStartupMessages(library(Hmisc))  
  
label(dta$xagegroup5)<-"5-year age group"  
label(dta$xunion)<-"currently in union"  
label(dta$xmarried)<-"currently married"  
label(dta$xsa)<-"sexual activity in the last 30 days"  
label(dta$xurban)<-"living in urban"  
label(dta$xwealth5)<-"household wealth quintile"   
label(dta$xpoor)<-"household wealth quintile: lowest"   
label(dta$xrich)<-"household wealth quintile: highest"  
label(dta$xedu3)<-"3-category education"   
label(dta$xedupri)<-"attended primary school or higher"  
label(dta$xedusec)<-"attended secondary school or higher"  
label(dta$xcaste4)<-"4-category caste"   
label(dta$xreligion)<-"religion"

Next, construct variables regarding contraception, including sterilization.

suppressPackageStartupMessages(library(lubridate))  
suppressPackageStartupMessages(library(dplyr))  
  
dta<-mutate(dta,   
 #using any, modern, and female sterilization   
 xuseany=current\_user==1,  
 xusemodern=current\_methodnum>=2 & current\_methodnum<30,  
 xusest=current\_methodnum==1,  
 #F Sterilization spontanously reported  
 xst\_report = femalester==1,   
 xst\_report = ifelse(is.na(xst\_report), 0, xst\_report),  
 #F sterilization reported only when probed  
 xst\_probe = sterilization\_probe ==1,  
 xst\_probe = ifelse(is.na(xst\_probe), 0, xst\_probe),  
 #F sterilization overall   
 xsteril = xst\_report==1 | xst\_probe==1,  
 # prep variables to calculate times since sterilization   
 # xinterview\_cmc "timing of interview (CMC)"   
 xinterview\_mo = month(FQdoi\_correctedSIF),  
 xinterview\_yr = year(FQdoi\_correctedSIF),  
 xinterview\_cmc = 12\*(xinterview\_yr - 1900) + xinterview\_mo,  
 # xbegin\_cmc "timing of start using methods (CMC)"   
 xbegin\_mo = month(begin\_usingSIF),  
 xbegin\_yr = year(begin\_usingSIF),  
 xbegin\_cmc = 12\*(xbegin\_yr - 1900) + xbegin\_mo,  
 # time since start   
 xtime=xinterview\_cmc - xbegin\_cmc,   
 xtime = ifelse(xsteril==FALSE, NA, xtime),  
 xtime\_yr = round((xtime/12), 0),  
 xtime\_yr5=cut(xtime\_yr,   
 breaks=c(0, 5, 10, 15, 20, 30),   
 right = FALSE,   
 labels = c("0-4","5-9","10-14","15-19",">=20")),   
 xtime\_yr5\_2=xtime\_yr5=="5-9",  
 xtime\_yr5\_3=xtime\_yr5=="10-14",  
 xtime\_yr5\_4=xtime\_yr5=="15-19",  
 xtime\_yr5\_5=xtime\_yr5==">=20"  
)

suppressPackageStartupMessages(library(Hmisc))  
  
label(dta$xuseany)<-"currently using any methods, reported"   
label(dta$xusemodern)<-"curretnly using modern methods, reported"   
label(dta$xusest)<-"currently using sterilization, reported"  
  
label(dta$xst\_report)<-"sterilized, reported"  
label(dta$xst\_probe)<-"sterilized, reported when only probed"  
label(dta$xsteril)<-"sterilized"  
label(dta$xinterview\_cmc)<-"time of interview (CMC)"   
label(dta$xbegin\_cmc)<-"time when started the method (CMC)"  
label(dta$xtime)<-"time since method adoption (month)"   
label(dta$xtime\_yr)<-"time since method adoption (year)"   
label(dta$xtime\_yr5)<-"5-year category since method adoption"

## 3. Data analysis

There are three tables in results. All estimates (e.g., proportion, odds ratio) were adjusted for survey sample design, since PMA2020 household surveys are sample surveys (see details regarding the sample design [here](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6084342/) and [here](https://www.pma2020.org/sampling-overview)). The number of observations in all tables is unweighted number.

### Table 1

[Table 1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6367562/table/t0005/?report=objectonly) presents study population characteristics: overall and by sterilization status.

suppressPackageStartupMessages(library(survey))  
suppressPackageStartupMessages(library(dplyr))  
  
dta2<-dta%>% filter(!is.na(dta$xweight))  
dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dta2,  
 strata = ~ur,   
 weights = ~xweight)  
  
# Distribution of background characterisics among the study sample (second column in Table 1)   
round(svymean( ~ xage, dtaw), 1)  
 mysvymean<-svymean( ~ xage, dtaw)  
 round(confint(mysvymean), 1)  
round(prop.table(svytable(~ xmarried, dtaw))\*100, 1)  
round(prop.table(svytable(~ xsa, dtaw))\*100, 1)  
round(prop.table(svytable(~ xurban, dtaw))\*100, 1)  
round(prop.table(svytable(~ xwealth5, dtaw))\*100, 1)  
round(prop.table(svytable(~ xedu3, dtaw))\*100, 1)  
round(prop.table(svytable(~ xcaste4, dtaw))\*100, 1)  
round(prop.table(svytable(~ xreligion, dtaw))\*100, 1)

*Note: There were 55 cases (last\_night!=1, due to the error mentioned above!) that have missing xweight. In Stata, these cases are excluded in calculation, but R needs no mising weights for “surveydesign”. Thus, those cases are dropped here (see the code line for “dta2” above) to be consistent with the STATA results. Technically, we could have replaced missing values with the cluster-specific weight values. But, that was not done for the paper.*

# level of strilization   
table(dta$xsteril)  
round(prop.table(svytable(~ xsteril, dtaw))\*100, 1)  
  
# Distribution of background characterisics among those NOT sterilized (third column in Table 1)   
dtaneverst<-dta2%>% filter(dta2$xsteril==FALSE)   
nrow(dtaneverst)  
  
dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dtaneverst,  
 strata = ~ur,   
 weights = ~xweight)  
  
round(svymean( ~ xage, dtaw), 1)  
 mysvymean<-svymean( ~ xage, dtaw)  
 round(confint(mysvymean), 1)  
round(prop.table(svytable(~ xmarried, dtaw))\*100, 1)  
round(prop.table(svytable(~ xsa, dtaw))\*100, 1)  
round(prop.table(svytable(~ xurban, dtaw))\*100, 1)  
round(prop.table(svytable(~ xwealth5, dtaw))\*100, 1)  
round(prop.table(svytable(~ xedu3, dtaw))\*100, 1)  
round(prop.table(svytable(~ xcaste4, dtaw))\*100, 1)  
round(prop.table(svytable(~ xreligion, dtaw))\*100, 1)

# Distribution of background characterisics among those EVER sterilized (fourth column in Table 1)   
  
dtaeverst<-dta2%>% filter(dta2$xsteril==TRUE)   
nrow(dtaeverst)  
  
dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dtaeverst,  
 strata = ~ur,   
 weights = ~xweight)  
  
round(svymean( ~ xage, dtaw), 1)  
 mysvymean<-svymean( ~ xage, dtaw)  
 round(confint(mysvymean), 1)  
round(prop.table(svytable(~ xmarried, dtaw))\*100, 1)  
round(prop.table(svytable(~ xsa, dtaw))\*100, 1)  
round(prop.table(svytable(~ xurban, dtaw))\*100, 1)  
round(prop.table(svytable(~ xwealth5, dtaw))\*100, 1)  
round(prop.table(svytable(~ xedu3, dtaw))\*100, 1)  
round(prop.table(svytable(~ xcaste4, dtaw))\*100, 1)  
round(prop.table(svytable(~ xreligion, dtaw))\*100, 1)  
round(prop.table(svytable(~ xtime\_yr5, dtaw))\*100, 1)

### Table 2

[Table 2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6367562/table/t0010/?report=objectonly) shows, among women who are sterilized, the percentage whoreported sterilization as a current contraceptive method by background characteristics. The research question here is

dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dtaeverst,  
 strata = ~ur,   
 weights = ~xweight)  
  
svyby(~xst\_report, ~xmarried, dtaw, svymean)  
svyby(~xst\_report, ~ xsa, dtaw, svymean)  
svyby(~xst\_report, ~ xurban, dtaw, svymean)  
svyby(~xst\_report, ~ xwealth5, dtaw, svymean)  
svyby(~xst\_report, ~ xedu3, dtaw, svymean)  
svyby(~xst\_report, ~ xcaste4, dtaw, svymean)  
svyby(~xst\_report, ~ xreligion, dtaw, svymean)  
svyby(~xst\_report, ~ xtime\_yr5, dtaw, svymean)

### Table 3

Fnally, [Table 3](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6367562/table/t0015/?report=objectonly) presents differential odds of reporting sterilization as a current contraceptive method by background characteristics, among women who are sterilized. The table shows both bivariate and multivariable logistic regression analyses results.

First, bivariate regression by each covariate:

dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dtaeverst,  
 strata = ~ur,   
 weights = ~xweight)  
  
mysvyglm<-svyglm(xst\_report ~ xmarried, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 # Odds ratio, 95% confidence interval, and p-value  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xmarriedTRUE 1.89 1.11 3.24 0.021

mysvyglm<-svyglm(xst\_report ~ xsa, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xsa 1.09 0.73 1.63 0.659

mysvyglm<-svyglm(xst\_report ~ xurban, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xurbanTRUE 0.85 0.44 1.63 0.631

mysvyglm<-svyglm(xst\_report ~ xedupri, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xedupri>= Primary 1.05 0.73 1.52 0.779

mysvyglm<-svyglm(xst\_report ~ xpoor+xrich, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xpoorTRUE 0.61 0.36 1.02 0.059  
xrichTRUE 1.14 0.72 1.79 0.585

mysvyglm<-svyglm(xst\_report ~ xcaste\_sc+xcaste\_st+xcaste\_obc, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xcaste\_scTRUE 1.72 0.96 3.11 0.072  
xcaste\_stTRUE 1.94 0.88 4.26 0.103  
xcaste\_obcTRUE 2.14 1.25 3.67 0.006

mysvyglm<-svyglm(xst\_report ~ xhindu, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xhinduTRUE 1.07 0.54 2.13 0.841

mysvyglm<-svyglm(xst\_report ~ xtime\_yr5\_2+xtime\_yr5\_3+xtime\_yr5\_4+xtime\_yr5\_5, dtaw, family=binomial)  
 summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
 confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
 summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
 cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xtime\_yr5\_2TRUE 0.84 0.60 1.17 0.297  
xtime\_yr5\_3TRUE 0.86 0.57 1.28 0.459  
xtime\_yr5\_4TRUE 1.22 0.79 1.89 0.367  
xtime\_yr5\_5TRUE 1.48 0.75 2.94 0.261

Multivariable regression:

dtaw <- svydesign(ids = ~ EA\_ID,  
 data = dtaeverst,  
 strata = ~ur,   
 weights = ~xweight)  
  
mysvyglm<-svyglm(xst\_report ~   
 xagegroup5\_3+xagegroup5\_4+xagegroup5\_5+xagegroup5\_6+xagegroup5\_7+  
 xmarried+xsa+xurban+xedupri+xpoor+xrich+  
 xcaste\_sc+xcaste\_st+xcaste\_obc+xhindu+  
 xtime\_yr5\_2+xtime\_yr5\_3+xtime\_yr5\_4+xtime\_yr5\_5,  
 dtaw, family=binomial)  
#Overall summary   
summary(mysvyglm)

Call:  
svyglm(formula = xst\_report ~ xagegroup5\_3 + xagegroup5\_4 + xagegroup5\_5 +   
 xagegroup5\_6 + xagegroup5\_7 + xmarried + xsa + xurban + xedupri +   
 xpoor + xrich + xcaste\_sc + xcaste\_st + xcaste\_obc + xhindu +   
 xtime\_yr5\_2 + xtime\_yr5\_3 + xtime\_yr5\_4 + xtime\_yr5\_5, design = dtaw,   
 family = binomial)  
  
Survey design:  
svydesign(ids = ~EA\_ID, data = dtaeverst, strata = ~ur, weights = ~xweight)  
  
Coefficients:  
 Estimate Std. Error t value Pr(>|t|)   
(Intercept) -0.04989 0.59587 -0.084 0.93341   
xagegroup5\_3TRUE 0.01351 0.32671 0.041 0.96708   
xagegroup5\_4TRUE -0.11505 0.30056 -0.383 0.70252   
xagegroup5\_5TRUE -0.16946 0.34889 -0.486 0.62802   
xagegroup5\_6TRUE -0.13805 0.37776 -0.365 0.71539   
xagegroup5\_7TRUE -0.16236 0.43067 -0.377 0.70682   
xmarriedTRUE 0.80993 0.32869 2.464 0.01509 \*   
xsa 0.02227 0.25792 0.086 0.93135   
xurbanTRUE -0.27209 0.33449 -0.813 0.41751   
xedupri>= Primary 0.06537 0.16050 0.407 0.68447   
xpoorTRUE -0.61629 0.26449 -2.330 0.02140 \*   
xrichTRUE 0.25741 0.19467 1.322 0.18850   
xcaste\_scTRUE 0.68876 0.27956 2.464 0.01511 \*   
xcaste\_stTRUE 0.81330 0.38487 2.113 0.03657 \*   
xcaste\_obcTRUE 0.82758 0.27496 3.010 0.00316 \*\*  
xhinduTRUE 0.06942 0.37437 0.185 0.85319   
xtime\_yr5\_2TRUE -0.09980 0.18546 -0.538 0.59146   
xtime\_yr5\_3TRUE -0.04611 0.26953 -0.171 0.86445   
xtime\_yr5\_4TRUE 0.27244 0.30942 0.880 0.38028   
xtime\_yr5\_5TRUE 0.44248 0.44180 1.002 0.31850   
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
  
(Dispersion parameter for binomial family taken to be 0.9984464)  
  
Number of Fisher Scoring iterations: 4

summaryexp<-round(as.data.frame(exp(summary(mysvyglm)$coef)), 2)  
confint <-round(as.data.frame(exp(confint(mysvyglm))), 2)  
summary <-round(as.data.frame(summary(mysvyglm)$coef), 3)  
  
# Odds ratio, 95% confidence interval, and p-value  
cbind(summaryexp[,1], confint[,1:2], summary[,4])[-1,]

summaryexp[, 1] 2.5 % 97.5 % summary[, 4]  
xagegroup5\_3TRUE 1.01 0.53 1.92 0.967  
xagegroup5\_4TRUE 0.89 0.49 1.61 0.703  
xagegroup5\_5TRUE 0.84 0.43 1.67 0.628  
xagegroup5\_6TRUE 0.87 0.42 1.83 0.715  
xagegroup5\_7TRUE 0.85 0.37 1.98 0.707  
xmarriedTRUE 2.25 1.18 4.28 0.015  
xsa 1.02 0.62 1.70 0.931  
xurbanTRUE 0.76 0.40 1.47 0.418  
xedupri>= Primary 1.07 0.78 1.46 0.684  
xpoorTRUE 0.54 0.32 0.91 0.021  
xrichTRUE 1.29 0.88 1.89 0.188  
xcaste\_scTRUE 1.99 1.15 3.44 0.015  
xcaste\_stTRUE 2.26 1.06 4.80 0.037  
xcaste\_obcTRUE 2.29 1.33 3.92 0.003  
xhinduTRUE 1.07 0.51 2.23 0.853  
xtime\_yr5\_2TRUE 0.91 0.63 1.30 0.591  
xtime\_yr5\_3TRUE 0.95 0.56 1.62 0.864  
xtime\_yr5\_4TRUE 1.31 0.72 2.41 0.380  
xtime\_yr5\_5TRUE 1.56 0.65 3.70 0.319