

Facilitators and barriers to COVID-19 vaccination among healthcare workers and the general population in Guinea.

Almamy Amara TOURE^{1,2}, Fodé Amara TRAORE^{3,4}, Gnoume CAMARA³, Aboubacar Sidiki MAGASSOUBA⁵, Ibrahima BARRY¹, Mohamed Lamine KOUROUMA⁴, Younoussa SYLLA¹, Naby Yaya CONTE^{1,5}, Diao CISSE⁵, Nafissatou DIOUBATÉ¹, Sidikiba SIDIBE^{6,7}, Abdoul Habib BEAVOGUI¹, Alexandre DELAMOU^{6,7}.

Authors' affiliations

1 Centre National de Formation et de Recherche en Santé Rurale de Mafèrinyah, Forécariah, Guinea. 2 Kofi Annan University of Guinea, Conakry, Guinea. 3 Faculté des Sciences et Techniques de la Santé, Université Gamal Abdel Nasser, Centre Hospitalo-Universitaire de Conakry, Service de maladies infectieuses. 4 Agence Nationale de Sécurité Sanitaire, Conakry, Guinea. 5 Centre MURAZ, Burkina Faso. 6 Department of Public Health, Faculty of Sciences and Health Techniques, Gamal Abdel Nasser University, Conakry, Guinea. 7 African Centre of Excellence in the Prevention and Control of communicable Diseases (CEA-PCMT).

```
#####Loading COVID-19 data
```

```
cvhw1 <- read.csv2("D:\\MOOC\\cvhgw11.csv")
```

```
cvhw2 <- read.csv2("D:\\MOOC\\cvhgw22.csv",stringsAsFactors = FALSE)
```

```
cvgui <- read.csv2("D:\\MOOC\\guicv-19.csv",stringsAsFactors = FALSE)
```

```
vaccine <- read.csv2("D:\\MOOC\\vaccine-gui.csv",stringsAsFactors = FALSE)
```

```
#####
```

¹ Corresponding author

Almamy Amara TOURE, Centre National de Formation et de Recherche en Santé Rurale de Maferinyah, Forecariah, Guinea, almamy@maferinyah.org

```
library(dplyr)
library(survey)
library(party)
library(gtsummary)
library(car)
library(GGally)
library(forestmodel)
library(Epi)
library(ggeffects)
library(ggparty)
library(tidyverse)
library(ggparty)
library(na.tools)
library(lubridate)
library(ComplexUpset)
library(compareGroups)
library(lubridate)
library(questionr)
```

```
#####total healthcare workers=3388
#####Recoding process
cvhw1 <- rbind(cvhw1,cvhw2)
rm(cvhw2)
cvhw1[c(3:7,10:11)] <- lapply(cvhw1[c(3:7,10:11)],factor)
#####Renaming variables names
dput(names(cvhw1))
names(cvhw1) <- c("today", "age", "gender",
                 "matstatus", "residence",
                 "education", "occupation",
                 "hmembrnum", "more18y",
```

"length-stay", "pregnant",
"diabetes", "hta", "obesity",
"asthma", "othallerg", "otherchrdis",
"knowd_vaccin", "vaccitypes",
"vaccin.mapi", "immunstatus",
"immuncollect", "seekcv19news",
"govradio", "private-radios",
"public-tv", "private-tv",
"social-media", "NAHS-website",
"neighborhood", "word-of-mouth",
"other-sources", "perception_peur_COVID.19.probable_attrap_COVID.19",
"perception_peur_COVID.19.arisque_COVID.19",
"perception_peur_COVID.19.possible_attrap_COVID.19",
"perception_peur_COVID.19.pense_COVID.19_grav",
"perception_peur_COVID.19.pense_COVID_19_cons_neg",
"perception_peur_COVID.19.pense_COVID.19_nuisibl",
"perception_peur_COVID.19.trepeur_COVID_19",
"perception_peur_COVID.19.penser_COVID_19_malaise",
"perception_peur_COVID.19.mains_moites_pense_COVID_19",
"perception_peur_COVID.19.peur_mourir_COVID.19",
"perception_peur_COVID.19.regarde_nouvel_COVID.19_rend_nerveu",
"perception_peur_COVID.19.nepeut_dormir_COVID.19",
"perception_peur_COVID.19.acc_rythmecard_palpitation_COVID.19",
"attitudes_croyance.prendr_vaccin_COVID.19_benefic",
"attitudes_croyance.prendr_vaccin_COVID.19_renf_immun",
"attitudes_croyance.vaccins_reserv_grpes_pers", "attitudes_croyance.vaccins_tropcher",
"attitudes_croyance.procedur_avoirvacc_laborieu",
"attitudes_croyance.peur_effet_second_vaccin",
"attitudes_croyance.appri_vaccin_donnemaladie",
"attitudes_croyance.vaccin_empecher_reproduct",
"attitudes_croyance.pas_confiance_vaccin",
"normes_subjectives.parents_amis_cons_prendr_vaccin",
"normes_subjectives.voisinage_pense_vacc_bon",
"normes_subjectives.vu_gens_commoi_vacciner",

```

"capacite.seras_mesure_avoir_vacc", "capacite.facile_avoir_vaccin",
"Intention.quete_vaccin_COVID.19", "vaccine",
"Intention.mevaccin_famill_entourage_accpt", "revenu_mensuel",
"GPS.nom_commune", "GPS.commune_gps", "GPS._commune_gps_latitude",
"GPS._commune_gps_longitude", "GPS._commune_gps_altitude",
"GPS._commune_gps_precision",
"GPS.border")

#####Recoding
#####Gender
levels(cvhw1$gender)
levels(cvhw1$gender) <- c("men", "women")
table(cvhw1$gender)

#####Residence
levels(cvhw1$residence)
levels(cvhw1$residence) <-
c("Matoto", "Ratoma", "Matam", "Dixinn", "Kaloum", "Coyah", "Kindia", "Mamou", "Kankan", "Nzerokore",
  LabÃ©", "DubrÃ©ka")
table(cvhw1$residence)
levels(cvhw1$residence) <-
c("Conakry", "Conakry", "Conakry", "Conakry", "Conakry", "Kindia", "Kindia", "Mamou", "Kankan", "Nzerokore",
  "LabÃ©", "Kindia")
table(cvhw1$residence)

#####matrimonial status
levels(cvhw1$matstatus)
levels(cvhw1$matstatus) <- c("married", "single", "single", "single")
table(cvhw1$matstatus)

#####Education
levels(cvhw1$education)
levels(cvhw1$education) <- c("second", "second", "second", "univ", "highschool")
table(cvhw1$education)

```

```
#####occupation

levels(cvhw1$occupation)

levels(cvhw1$occupation) <-
c("hc2level","labtech","labtech","inf","inf","labtech","labtech","labtech","physician","adminwk","pharma
","midwife","midwife","internship")

table(cvhw1$occupation)

levels(cvhw1$occupation)

levels(cvhw1$occupation) <-
c("nurs.as","labtech","nurs.as","physician","medsupport","pharma","midwife","internship")

table(cvhw1$occupation)

levels(cvhw1$occupation)

levels(cvhw1$occupation) <-
c("nurs.as","labtech","physician","medsupport","medsupport","midwife","internship")

table(cvhw1$occupation)

#####Recoding continued

levels(cvhw1$`length-stay`) <- c("<6months",">=6months")

table(cvhw1$`length-stay`)

levels(cvhw1$pregnant) <- c("yes","no")

table(cvhw1$pregnant)

cvhw1[c(12:17)] <- lapply(cvhw1[c(12:17)],factor)

levels(cvhw1$hta) <- levels(cvhw1$obesity) <- levels(cvhw1$diabetes) <- levels(cvhw1$othallerg) <-
levels(cvhw1$otherchrdis) <- levels(cvhw1$sasthma)<- c("yes","no")

summary(cvhw1[c(12:17)])

#####compute score values

attach(cvhw1)

cvhw1$knowd_vaccin<- knowd_vaccin+vaccitypes+vaccin.mapi+immunstatus+immuncollect

summary(cvhw1$knowd_vaccin)

cvhw1 <- cvhw1[-c(19:22)]

cvhw1$knowd_vaccin <- cut(cvhw1$knowd_vaccin,breaks = c(5,7.286,10),include.lowest = TRUE,labels
= c("no","yes"))

table(cvhw1$knowd_vaccin)
```

```
cvhw1$percep <-  
perception_peur_COVID.19.acc_rythmecard_palpitation_COVID.19+perception_peur_COVID.19.arisqu  
e_COVID.19+perception_peur_COVID.19.mains_moites_pense_COVID_19+perception_peur_COVID.1  
9.nepeut_dormir_COVID.19+perception_peur_COVID.19.pense_COVID.19_grav+perception_peur_CO  
VID.19.pense_COVID.19_nuisibl+perception_peur_COVID.19.pense_COVID_19_cons_neg+perception  
_peur_COVID.19.penser_COVID_19_malaise+perception_peur_COVID.19.peur_mourir_COVID.19+pe  
rception_peur_COVID.19.possible_attrap_COVID.19+perception_peur_COVID.19.probable_attrap_CO  
VID.19+perception_peur_COVID.19.regarde_nouvel_COVID.19_rend_nerveu+perception_peur_COVID  
.19.trepeur_COVID_19
```

```
summary(cvhw1$percep)
```

```
cvhw1$percep <- cut(cvhw1$percep,breaks = c(13,43.6,65),include.lowest = TRUE,labels =  
c("pos","neg"))
```

```
table(cvhw1$percep)
```

```
cvhw1 <- cvhw1[-c(29:41)]
```

```
cvhw1$negatt <-  
attitudes_croyance.appri_vaccin_donnemaladie+attitudes_croyance.pas_confiance_vaccin+attitudes_croy  
ance.peur_effet_second_vaccin+attitudes_croyance.procedur_avoirvacc_laborieu+attitudes_croyance.vacc  
in_empecher_reproduct+attitudes_croyance.vaccins_reserv_grpes_pers+attitudes_croyance.vaccins_tropc  
her
```

```
summary(cvhw1$negatt)
```

```
cvhw1$negatt <- cut(cvhw1$negatt,breaks = c(7,18.25,35),include.lowest = TRUE,labels =  
c("lessneg","muchneg"))
```

```
table(cvhw1$negatt)
```

```
cvhw1$posatt <-  
attitudes_croyance.prendr_vaccin_COVID.19_benefic+attitudes_croyance.prendr_vaccin_COVID.19_ren  
f_immun
```

```
summary(cvhw1$posatt)
```

```
cvhw1$posatt <- cut(cvhw1$posatt,breaks = c(2,8.182,10),include.lowest = TRUE,labels =  
c("lesspos","muchpos"))
```

```
table(cvhw1$posatt)
```

```
cvhw1 <- cvhw1[-c(29:37)]
```

```
cvhw1$norm <-  
normes_subjectives.parents_amis_cons_prendr_vaccin+normes_subjectives.voisinage_pense_vacc_bon+n  
ormes_subjectives.vu_gens_commoi_vacciner
```

```
summary(cvhw1$norm)
```

```

cvhw1$norm <- cut(cvhw1$norm,breaks = c(3,10.61,15),include.lowest = TRUE,labels =
c("lessfav", "favor"))
table(cvhw1$norm)
cvhw1 <- cvhw1[-c(29:31)]
cvhw1$abil <- capacite.facile_avoir_vaccin+capacite.seras_mesure_avoir_vacc
summary(cvhw1$abil)
cvhw1$abil <- cut(cvhw1$abil,breaks = c(2,8,10),include.lowest = TRUE,labels = c("notabl", "able"))
table(cvhw1$abil)
cvhw1 <- cvhw1[-c(29:30)]
cvhw1$glint <- cvhw1$Intention.mevaccin_famill_entourage_accpt+Intention.quete_vaccin_COVID.19
summary(cvhw1$glint)
cvhw1$glint <- cut(cvhw1$glint,breaks = c(2,6,10),include.lowest = TRUE,labels =
c("lessint", "goodint"))
table(cvhw1$glint)
cvhw1 <- cvhw1[-c(29,31)]

#####

cvhw1$gender <- na.resample(cvhw1$gender)
levels(cvhw1$vaccine)
cvhw1$vaccine <- factor(cvhw1$vaccine)
levels(cvhw1$vaccine) <- c("no", "no", "no", "yes", "yes")
table(cvhw1$vaccine)
cvhw1$seekcv19news <- factor(cvhw1$seekcv19news)
levels(cvhw1$seekcv19news) <- c("yes", "no")
table(cvhw1$seekcv19news)

#####Imputation for income
cvhw1
set.seed(123)
cvhw1$income<-na.bootstrap(cvhw1$revenue mensuel)
cvhw1$income<-na.bootstrap(cvhw1$income)

```

```
cvhw1$income<-na.bootstrap(cvhw1$income)
cvhw1$income<-na.bootstrap(cvhw1$income)
cvhw1$income<-na.median(cvhw1$income)
summary(cvhw1$income)
cvhw1 <- cvhw1[-c(30)]
```

```
#####For General population
#####total healthcare workers=3388
#####Recoding process
cvpub1 <- read.csv2("D:\\MOOC\\cvpub1.csv")
cvpub2 <- read.csv2("D:\\MOOC\\cvpub2.csv")
cvpub1 <- rbind(cvpub1,cvpub2)
rm(cvpub2)
cvpub1[c(3:7,10:11,18)] <- lapply(cvpub1[c(3:7,10:11,18)],factor)
#####Renaming variables names
dput(names(cvpub1))
names(cvpub1) <- c("today", "age", "gender",
                  "matstatus", "residence",
                  "education", "occupation",
                  "hmembnum", "more18y",
                  "length-stay", "pregnant",
                  "diabetes", "hta", "obesity",
                  "asthma", "othallerg", "otherchrdis",
                  "knowd_vaccin", "seekcv19news",
                  "government-radio", "private-radios",
                  "public-tv", "private-tv",
                  "social-media", "NAHS-website",
                  "neighborhood", "word-of-mouth",
                  "other-sources", "perception_peur_COVID.19.probable_attrap_COVID.19",
```



```

      "perception_peur_COVID.19.arisque_COVID.19",
"perception_peur_COVID.19.possible_attrap_COVID.19",
      "perception_peur_COVID.19.pense_COVID.19_grav",
"perception_peur_COVID.19.pense_COVID_19_cons_neg",
      "perception_peur_COVID.19.pense_COVID.19_nuisibl",
"perception_peur_COVID.19.trepeur_COVID_19",
      "perception_peur_COVID.19.penser_COVID_19_malaise",
"perception_peur_COVID.19.mains_moites_pense_COVID_19",
      "perception_peur_COVID.19.peur_mourir_COVID.19",
"perception_peur_COVID.19.regarde_nouvel_COVID.19_rend_nerveu",
      "perception_peur_COVID.19.nepeut_dormir_COVID.19",
"perception_peur_COVID.19.acc_rythmecard_palpitation_COVID.19",
      "attitudes_croyance.prendr_vaccin_COVID.19_benefic",
"attitudes_croyance.prendr_vaccin_COVID.19_renf_immun",
      "attitudes_croyance.vaccins_reserv_grpes_pers", "attitudes_croyance.vaccins_tropcher",
      "attitudes_croyance.procedur_avoirvacc_laborieiu",
"attitudes_croyance.peur_effet_second_vaccin",
      "attitudes_croyance.appri_vaccin_donnemaladie",
"attitudes_croyance.vaccin_empecher_reproduct",
      "attitudes_croyance.pas_confiance_vaccin",
"normes_subjectives.parents_amis_cons_prendr_vaccin",
      "normes_subjectives.voisinage_pense_vacc_bon",
"normes_subjectives.vu_gens_commoi_vacciner",
      "capacite.seras_mesure_avoir_vacc", "capacite.facile_avoir_vaccin",
      "Intention.quete_vaccin_COVID.19", "vaccine",
      "Intention.mevaccin_famill_entourage_accpt", "Intention.revenu_mensuel",
      "GPS.nom_commune", "GPS.commune_gps", "GPS._commune_gps_latitude",
      "GPS._commune_gps_longitude", "GPS._commune_gps_altitude",
"GPS._commune_gps_precision",
      "GPS.border")

```

```
#####Recoding
```

```
#####Gender
```

```
levels(cvpub1$gender)
```

```
levels(cvpub1$gender) <- c("men","women")
```

```

table(cvpub1$gender)

#####Residence

levels(cvpub1$residence)

levels(cvpub1$residence) <-
c("Matoto", "Ratoma", "Matam", "Dixinn", "Kaloum", "Coyah", "Kindia", "Mamou", "Kankan", "Nzerokore", "
LabÃ©", "DubrÃ©ka")

table(cvpub1$residence)

levels(cvpub1$residence) <-
c("Conakry", "Conakry", "Conakry", "Conakry", "Conakry", "Kindia", "Kindia", "Mamou", "Kankan", "Nzerok
ore", "Mamou", "Kindia")

table(cvpub1$residence)

#####matrimonial status

levels(cvpub1$matstatus)

levels(cvpub1$matstatus) <- c("married", "single", "single", "single")

table(cvpub1$matstatus)

#####Education

levels(cvpub1$education)

levels(cvpub1$education) <- c("second", "second", "second", "univ", "highschool")

table(cvpub1$education)

#####occupation

levels(cvpub1$occupation)

levels(cvpub1$occupation) <- c("private-employee", "student", "student", "civil-servant", "civil-
servant", "freelance", "unemployed", "unemployed")

table(cvpub1$occupation)

levels(cvpub1$occupation)

#####Recoding continued

levels(cvpub1$`length-stay`) <- c("<6months", ">=6months")

table(cvpub1$`length-stay`)

levels(cvpub1$pregnant) <- c("yes", "no")

table(cvpub1$pregnant)

```

```

summary(cvpub1[c(12:23)])

levels(cvpub1$knowd_vaccin) <- c("yes","no")

table(cvpub1$knowd_vaccin)

cvpub1[c(12:17)] <- lapply(cvpub1[c(12:17)],factor)

levels(cvpub1$hta) <- levels(cvpub1$obesity) <- levels(cvpub1$diabetes) <- levels(cvpub1$othallerg) <-
levels(cvpub1$otherchrdis) <- levels(cvpub1$sasthma)<- c("yes","no")

summary(cvpub1[c(12:17)])

#####Variables for recding

attach(cvpub1)

cvpub1$percep <-
perception_peur_COVID.19.acc_rythmecard_palpitation_COVID.19+perception_peur_COVID.19.arisqu
e_COVID.19+perception_peur_COVID.19.mains_moites_pense_COVID_19+perception_peur_COVID.1
9.nepeut_dormir_COVID.19+perception_peur_COVID.19.pense_COVID.19_grav+perception_peur_CO
VID.19.pense_COVID.19_nuisibl+perception_peur_COVID.19.pense_COVID_19_cons_neg+perception
_peur_COVID.19.penser_COVID_19_malaise+perception_peur_COVID.19.peur_mourir_COVID.19+pe
rception_peur_COVID.19.possible_attrap_COVID.19+perception_peur_COVID.19.probable_attrap_CO
VID.19+perception_peur_COVID.19.regarde_nouvel_COVID.19_rend_nerveu+perception_peur_COVID
.19.trepeur_COVID_19

summary(cvpub1$percep)

cvpub1$percep <- cut(cvpub1$percep,breaks = c(13,42.7,65),include.lowest = TRUE,labels =
c("pos","neg"))

table(cvpub1$percep)

cvpub1 <- cvpub1[-c(29:41)]

cvpub1$negatt <-
attitudes_croyance.appri_vaccin_donnemaladie+attitudes_croyance.pas_confiance_vaccin+attitudes_croy
ance.peur_effet_second_vaccin+attitudes_croyance.procedur_avoirvacc_laborieu+attitudes_croyance.vacc
in_empecher_reproduct+attitudes_croyance.vaccins_reserv_grpes_pers+attitudes_croyance.vaccins_tropc
her

summary(cvpub1$negatt)

cvpub1$negatt <- cut(cvpub1$negatt,breaks = c(7,19.15,35),include.lowest = TRUE,labels =
c("lessneg","muchneg"))

table(cvpub1$negatt)

```

```

cvpub1$posatt <-
attitudes_croyance.prendr_vaccin_COVID.19_benefic+attitudes_croyance.prendr_vaccin_COVID.19_ren
f_immun

summary(cvpub1$posatt)

cvpub1$posatt <- cut(cvpub1$posatt,breaks = c(2, 7.872,10),include.lowest = TRUE,labels =
c("lesspos","muchpos"))

table(cvpub1$posatt)

cvpub1 <- cvpub1[-c(29:37)]

cvpub1$norm <-
normes_subjectives.parents_amis_cons_prendr_vaccin+normes_subjectives.voisinage_pense_vacc_bon+n
ormes_subjectives.vu_gens_commoi_vacciner

summary(cvpub1$norm)

cvpub1$norm <- cut(cvpub1$norm,breaks = c(3,10.23,15),include.lowest = TRUE,labels =
c("lessfav","favor"))

table(cvpub1$norm)

cvpub1 <- cvpub1[-c(29:31)]

cvpub1$abil <- capacite.facile_avoir_vaccin+capacite.seras_mesure_avoir_vacc

summary(cvpub1$abil)

cvpub1$abil <- cut(cvpub1$abil,breaks = c(2,6.871,10),include.lowest = TRUE,labels =
c("notabl","able"))

table(cvpub1$abil)

cvpub1 <- cvpub1[-c(29:30)]

cvpub1$glint <- cvpub1$Intention.mevaccin_famill_entourage_acpt+Intention.quete_vaccin_COVID.19

summary(cvpub1$glint)

cvpub1$glint <- cut(cvpub1$glint,breaks = c(2,6.423,10),include.lowest = TRUE,labels =
c("lessint","goodint"))

table(cvpub1$glint)

cvpub1 <- cvpub1[-c(29,31)]

sapply(cvpub1, function(x)sum(is.na(x)))

cvpub1$gender <- na.resample(cvpub1$gender)

#####

levels(cvpub1$vaccine)

cvpub1$vaccine <- factor(cvpub1$vaccine)

```

```

levels(cvpub1$vaccine) <- c("no","no","no","yes","yes")
table(cvpub1$vaccine)
cvpub1$seekcv19news <- factor(cvpub1$seekcv19news)
levels(cvpub1$seekcv19news) <- c("yes","no")
table(cvpub1$seekcv19news)
set.seed(123)
summary(cvpub1$Intention.revenu_mensuel)
cvpub1$income<-na.bootstrap(cvpub1$Intention.revenu_mensuel)
cvpub1$income<-na.bootstrap(cvpub1$income)
cvpub1$income<-na.bootstrap(cvpub1$income)
cvpub1$income<-na.bootstrap(cvpub1$income)
summary(cvpub1$income)
cvpub1 <- cvpub1[-c(30)]

#####Merging datasets
#covac <- rbind(cvhw1,cvpub1)
#levels(covac$occupation)
#save.image("D:\\MOOC\\covax.RData")
#load("D:\\MOOC\\covax.RData")
summary(cvhw1$income)
summary(cvpub1$income)
table(cvhw1$hmembrnum)
cvhw1$incomem[cvhw1$income>=2000000& cvhw1$hmembrnum<=10] <- "high-inc"
cvhw1$incomem[cvhw1$income>=2000000& cvhw1$hmembrnum>10] <- "middle-inc"
cvhw1$incomem[cvhw1$income<2000000& cvhw1$hmembrnum<=10] <- "middle-inc"
cvhw1$incomem[cvhw1$income<2000000& cvhw1$hmembrnum>10] <- "low-inc"
table(cvhw1$incomem)
cvhw1$incomem <- factor(cvhw1$incomem)
summary(cvhw1$age)

```

```
cvhw1$age2 <- cut(cvhw1$age,breaks = c(18,40,75),include.lowest = TRUE,labels = c("young","adult"))
table(cvhw1$age2)
```

```
cvpub1$incomem[cvpub1$income>=2000000& cvpub1$hmembnum<=10] <- "high-inc"
cvpub1$incomem[cvpub1$income>=2000000& cvpub1$hmembnum>10] <- "middle-inc"
cvpub1$incomem[cvpub1$income<2000000& cvpub1$hmembnum<=10] <- "middle-inc"
cvpub1$incomem[cvpub1$income<2000000& cvpub1$hmembnum>10] <- "low-inc"
table(cvpub1$incomem)
```

```
summary(cvpub1$age)
```

```
cvpub1$age2 <- cut(cvpub1$age,breaks = c(18,40,80),include.lowest = TRUE,labels =
c("young","adult"))
```

```
table(cvpub1$age2)
```

```
cvpub1$incomem <- factor(cvpub1$incomem)
```

```
#####
```

```
cvpub1$hmembnum <- cut(cvpub1$hmembnum,breaks = c(1,5,10,30),include.lowest = TRUE)
```

```
table(cvpub1$hmembnum)
```

```
summary(cvpub1$more18y)
```

```
summary(cvhw1$hmembnum)
```

```
cvhw1$hmembnum <- cut(cvhw1$hmembnum,breaks = c(1,5,10,30),include.lowest = TRUE)
```

```
table(cvhw1$hmembnum)
```

```
summary(cvhw1$more18y)
```

```
#####Replacing missing for pregnant
women
```

```
cvhw1$pregnant <- na.replace(cvhw1$pregnant,.na = "notapplic")
```

```
levels(cvhw1$pregnant)
```

```
cvpub1$pregnant <- na.replace(cvpub1$pregnant,.na = "notapplic")
```

```
#####recode variables for CART
```

```
levels(cvhw1$pregnant) <- c("yes","no","no")
```

```
levels(cvpub1$pregnant) <- c("yes","no","no")
```

```

levels(cvhw1$negatt) <- c("less-negative","more-negative")
levels(cvhw1$glint) <- c("less-intend","more-intend")
levels(cvhw1$norm) <- c("less-optimist","more-optimist")
cvhw1<- rename.variable(cvhw1,"negatt","negative-attitude")
cvhw1<- rename.variable(cvhw1,"pregnant","pregnancy")
cvhw1 <- rename.variable(cvhw1,"glint","intend.to.get.vaccinated")
cvhw1 <- rename.variable(cvhw1,"knowd_vaccin","vaccine.knowledge")
levels(cvpub1$abil) <- c("not.able","able")
levels(cvpub1$norm) <- c("less-optimist","more-optimist")
cvpub1<- rename.variable(cvpub1,"abil","ability.to.get.vaccine")
cvpub1<- rename.variable(cvpub1,"norm","norms")
levels(cvpub1$glint) <- c("less-intend","more-intend")
cvpub1 <- rename.variable(cvpub1,"glint","intend.to.get.vaccinated")

```

```

#####Source of infos
analysis

```

```

#####source of news

```

```

sourcenews=colnames(cvhw1)[20:28]
cvhw1[sourcenews] = cvhw1[sourcenews] == 1
t(head(cvhw1[sourcenews], 3))

```

```

#####
##count

```

```

upset(
  cvhw1, sourcenews, width_ratio=0.1,
  n_intersections=15
)

```

```

#####adding
percent

```

```

upset(
  cvhw1,

```

```

sourcenews,
base_annotatons=list(
  'Intersection size'=intersection_size(
    text_colors=c(
      on_background='brown', on_bar='yellow'
    )
  )
)
+ annotate(
  geom='text', x=Inf, y=Inf,
  label=paste("Total:", nrow(cvhw1)),
  vjust=1, hjust=1
)
+ ylab('Intersection size')
),
min_size=10,
width_ratio=0.2,
n_intersections=15
)
#####For General
Population
sourcenews=colnames(cvpub1)[20:28]

cvpub1[sourcenews] = cvpub1[sourcenews] == 1
t(head(cvpub1[sourcenews], 3))
#####count
upset(
  cvpub1, sourcenews, width_ratio=0.2,
  n_intersections=15
)

```



```
#####adding percent
```

```
upset(  
  cvpub1,  
  sourcenews,  
  base_annotations=list(  
    'Intersection size'=intersection_size(  
      text_colors=c(  
        on_background='brown', on_bar='yellow'  
      )  
    )  
  )  
  + annotate(  
    geom='text', x=Inf, y=Inf,  
    label=paste('Total:', nrow(cvpub1)),  
    vjust=1, hjust=1  
  )  
  + ylab('Intersection size')  
),  
min_size=10,  
width_ratio=0.2,  
n_intersections=15  
)
```

```
#####Descriptive  
Analysis
```

```
cvhw11 <- cvhw1[-c(1,5,20:28,30:36,43)]
```

```
#####Making graph for those vaccinated
```

```
library(lessR)  
par(mfrow=c(1,2))  
rm(vaccine)  
tabbb1 <- BarChart(vaccine,data = cvhw11 ,fill="black", color="black", trans=.8, values_color="black",  
sort = "+")
```

```
#####
```

```
#####
```

```
tabb1 <- tbl_summary(cvhw11)
```

```
table2 <-
```

```
tbl_summary(
```

```
  cvhw11,
```

```
  by = vaccine, # split table by group
```

```
  missing = "no" # don't list missing data separately
```

```
) %>%
```

```
add_n() %>% # add column with total number of non-missing observations
```

```
add_p() %>% # test for a difference between groups
```

```
modify_header(label = "***Variable**") %>% # update the column header
```

```
bold_labels()
```

```
table2
```

```
#####
```

```
cvpub11 <- cvpub1[-c(1,5,20:28,30:36,43)]
```

```
#####making graph
```

```
tabb2<- BarChart(vaccine,data = cvpub11 ,fill="blue", color="black", trans=.8, values_color="black",sort = "+")
```

```
tabb2 <- tbl_summary(cvpub11)
```

```
table3 <-
```

```
tbl_summary(
```

```
  cvpub11,
```

```
  by = vaccine, # split table by group
```

```
  missing = "no" # don't list missing data separately
```

```
) %>%
```

```
add_n() %>% # add column with total number of non-missing observations
```

```
add_p() %>% # test for a difference between groups
```

```
modify_header(label = "***Variable**") %>% # update the column header
```

```
bold_labels()
```

```
table3
```

```
#####Merging descriptive table
```

```
tbl_merge(tbls = list(tab1, tab2)) %>%
```

```
  modify_spanning_header(everything() ~ NA_character_)
```

```
#####Univariate data
```

```
tbl_merge(tbls = list(table2, table3)) %>%
```

```
  modify_spanning_header(everything() ~ NA_character_)
```

```
#####Multivariate analysis
```

```
cvhw11 <- cvhw11[-(1)]
```

```
cvhw11$vaccine <- relevel(cvhw11$vaccine,ref = "no")
```

```
levels(cvhw11$vaccine) <- c("0","1")
```

```
cvhw11$vaccine <- relevel(cvhw11$vaccine,ref = "0")
```

```
tab1 <- glm(vaccine~.,family = binomial(link = "logit"),data = cvhw11)
```

```
tab2 <- step(tab1)
```

```
#####Model fit tools/Quality of the model healthcare workers
```

```
library(blorr)
```

```
blr_model_fit_stats(tab2)
```

```
#####confusion matrix
```

```
blr_confusion_matrix(tab2, cutoff = 0.5)
```

```
#####Goodness of fit Lemeshow
```

```
blr_test_hosmer_lemeshow(tab2)
```

```
#####ROC Curve
```

```
tab2 %>%
```

```
  blr_gains_table() %>%
```

```
  blr_roc_curve()
```

```
##### Gains tables
```

```
tab2 %>%  
  blr_gains_table() %>%  
  blr_roc_curve()
```

```
#####KS chart should be big as (>=0.3)
```

```
tab2 %>%  
  blr_gains_table() %>%  
  blr_ks_chart()
```

```
#####Lorenz curve
```

```
blr_lorenz_curve(tab2)
```

```
#####Model  
Evaluation
```

```
##### ROC curve
```

```
ROC(form=vaccine ~ gender + matstatus + education + occupation + `length-stay` +  
  diabetes + knowd_vaccin + seekcv19news + percep + negatt +  
  posatt + norm + glint + incomem + age2,plot="ROC",data = cvhw11)
```

```
#####coefficients significance
```

```
anova(tab2, test = "Chisq")
```

```
#####model assessment
```

```
with(tab2,pchisq(null.deviance-deviance,df.null-df.residual,lower.tail = F))
```

```
#####multicollinearity
```

```
vif(tab2)#####no collinearity
```

```
#####Building with gtsummary
```

```
tab2 <- tbl_regression(tab2,exponentiate = TRUE)
```

```
tab2
```

```
#####Mulivariate analysis For  
population
```

```
cvpub11 <- cvpub11[-(1)]
```

```

cvpub1$vaccine <- relevel(cvpub1$vaccine,ref = "yes")
tab3 <- glm(vaccine~.,family = binomial(link = "logit"),data = cvpub1)
tab4 <- step(tab3)
#####Confusion matrix/ Quality of the model population
blr_model_fit_stats(tab4)
#####confusion matrix
blr_confusion_matrix(tab4, cutoff = 0.5)
#####Goodness of fit Lemeshow
blr_test_hosmer_lemeshow(tab4)

#####ROC Curve
tab4 %>%
  blr_gains_table() %>%
  blr_roc_curve()

##### Gains tables
tab4 %>%
  blr_gains_table() %>%
  blr_roc_curve()

#####KS chart should be big as (>=0.3)
tab4 %>%
  blr_gains_table() %>%
  blr_ks_chart()

#####Lorenz curve
blr_lorenz_curve(tab4)

#####Model Evaluation
##### ROC curve

```

```

ROC(form=vaccine ~ education + occupation + more18y + `length-stay` +
    hta + obesity + otherchrdis + knowd_vaccin + percep + `negative-attitude` +
    posatt + norm + abil + `intend.to.get.vaccinated` + age2,plot="ROC",data = cvpub11)
#####coefficients significance
anova(tab4, test = "Chisq")
#####model assessment
with(tab4,pchisq(null.deviance-deviance,df.null-df.residual,lower.tail = F))

#####multicollinearity
vif(tab4)#####no collinearity
tab4<- tbl_regression(tab4,exponentiate = TRUE)

#####Merging Multivariate
analysis
tbl_merge(tbls = list(tab2, tab4)) %>%
  modify_spanning_header(everything() ~ NA_character_)

#####Using tree
decision
#A) For Healthcareworkers
tab10 <- ctree(vaccine ~ matstatus + occupation +education +pregnancy +
  vaccine.knowledge + seekcv19news + `negative-attitude` + norm + intend.to.get.vaccinated +
  incomem + age2,cvhw11)

nid <- nodeids(tab10)
iid <- nid[!(nid %in% nodeids(tab10, terminal = TRUE))]
(pval <- unlist(nodeapply(tab10, ids = iid,
  FUN = function(n) info_node(n)$p.value)))

myttnc2 <- nodeprune(tab10, ids = iid[pval > 1e-5])

```

```

plot(myttnc2)
tab10 <- as.constparty(myttnc2)

#####Using###ggtree
ggparty(myttnc2) +
  geom_edge() +
  geom_edge_label() +
  geom_node_splitvar() +
  geom_node_plot(gglist = list(geom_bar(aes(x = "", fill = vaccine),
                                position = position_fill()),
                              xlab("")),
                # draw only one label for each axis
                shared_axis_labels = TRUE,
                # draw line between tree and legend
                legend_separator = TRUE
  )
#####For population
tab11 <- ctree(vaccine ~ education + `length-stay` +
              pregnant + hta + obesity + otherchrdis + knowd_vaccin + percep +
              negatt + posatt + norms + ability.to.get.vaccine + intend.to.get.vaccinated + age2,cvpub11)

nid <- nodeids(tab11)
iid <- nid[!(nid %in% nodeids(tab11, terminal = TRUE))]
(pval <- unlist(nodeapply(tab11, ids = iid,
                        FUN = function(n) info_node(n)$p.value)))

myttnc3 <- nodeprune(tab11, ids = iid[pval > 1e-5])

plot(myttnc3)
tab11 <- as.constparty(myttnc3)

```

```
tab11 <- as.constparty(tab11)
```

```
#####Using  
###ggtree
```

```
ggparty(tab11) +  
  geom_edge() +  
  geom_edge_label() +  
  geom_node_splitvar() +  
  geom_node_plot(gglist = list(geom_bar(aes(x = "", fill = vaccine),  
    position = position_fill()),  
    xlab("")),  
  # draw only one label for each axis  
  shared_axis_labels = TRUE,  
  # draw line between tree and legend  
  legend_separator = TRUE  
)
```