TobriskCov analyses

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Contents

Part I

Loading packages and data

Packages

```r
# Loading packages
library(readxl)
library(haven)
library(styler)
library(tidyverse)
library(knitr)
library(kableExtra)
library(tidyr)
library(janitor)
library(gtools)
library(ggridges)
library(ggfortify)
library(tableone)
library(pollster)
library(naniar)
library(survey)
library(survival)
library(biostat3)
library(Epi)
library(lubridate)
library(mice)
library(mitools)
library(mitml)
library(Hmisc)
library(finalfit)
```

Data

```r
# Loading FinSote dataset
# As we are collaborating on different systems, as to make this work on both,
# we use:
path <- "//helfs01.thl.fi/groups4/Tobrisk_FinSote/Data and code/"
if (.Platform$OS.type == "unix") {
  path <- "/home/zzhh/mnt/groups4/Tobrisk_FinSote/Data and code/"
}
finsote2018 <- read_sas(paste0(path, "data_f181_death_covid_2022.sas7bdat"))
```

```
finsote2020 <- read_sas(paste0(path, "data_f201_death_covid.sas7bdat"))
finsote2020_dates <- read_excel(paste0(path, "FinSote2020/F201_response_dates.xlsx"))
finsote2018_vx <- read_sas(paste0(path, "data_f181_vaccination_2022.sas7bdat"))
finsote2020_vx <- read_sas(paste0(path, "data_f201_vaccination_2022.sas7bdat"))
```

Data wrangling

Data wrangling of vaccine data

We used data from the Register of Primary Health Care visits (Avohilmo) which comes directly from health service providers. Avohilmo vaccination data contains data on all vaccinations the person has taken, which includes COVID-19 vaccines but also information on other vaccines. Therefore, we cleaned the data to uniquely identify COVID-19 vaccinations. In addition, health providers enter by hand the vaccine information, making the register prone to data entry errors which need to be corrected to be able to assign the official COVID-19 vaccine name.

The listing below shows the variables in the dataset.

- gumm85id: identifier
- kaynti_alkoi_pvm: visit start date
- kaynti_loppui_pvm: visit end date
- laakeaine: ATC
- laakepakkausnro: package number
- laake_kauppanimi: commercial name
- rokote_eranro: batch number
- annos_jarjestysnro: dose order
- rokote_valmistenimi: vaccine name
- vaccine_date: vaccine date

We first combined the data on vaccine names and dates originally coming in two different variables and corrected vaccine names. We then used the ATC code for COVID-19 vaccines (lääkeaine J07BX03) to identify COVID-19 vaccines and, when the ATC was coded 0, -1 or -2, we used the batch number (eränumero) to ascertain the type of COVID-19 vaccine.

```
# Combining two variables with the same information (laake_kauppanimi and rokote_valmistenimi).
finsote_vx <- finsote2018_vx %>%
  bind_rows(finsote2020_vx) %>%
  mutate(
    vaccine_name = case_when(
      vaccine_name == "" ~ laake_kauppanimi,
      TRUE ~ vaccine_name),
    vaccine_date = case_when(
      vaccine_date == "        ." ~ NA_character_,
      TRUE ~ vaccine_date)
  )

# Check missings in vaccine_date.
sum(is.na(finsote_vx$vaccine_date))
# total 367251 rows in finsote_vx data, and 170498 have missing values
# 170498/367251 * 100% = 46.4%
```

```r
##### Batch numbers #####
Janssen <- c("21C11-04", "21C10-05", "XD955", "XD975")
Comirnaty <- c("1F1012A" , "1F1046A", "1F1053A", "1F1054A", "1F1059A", "1G044A",
               "1G047A", "1K079A", "1K081A", "1L084A", "1L085A", "31134TB",
               "8000088", "8000282", "8001016", "ACA9551", "ACB2638", "ACB3999",
               "ACC5779", "EJ6134", "EJ6790", "EJ6795", "EJ6796", "EJ6797",
               "EK9788", "EL0725", "EL1491", "EP2163", "EP2166", "ET1831",
               "ET6956", "ET7205", "EW2239", "EW2246", "EW4815", "EY3014",
               "EY7015", "FA4598", "FC0681", "FC2336", "FC3098", "FC3558",
               "FC8736", "FD0932", "FD1921", "FD4555", "FE2296", "FE3065",
               "FE7051", "FF0680", "FF2832", "FF2834", "FF3318", "FF4213",
               "FG4509", "FH0161", "FH3221", "FH4752", "FH8773", "FH9951",
               "FJ5973", "FJ8041", "FK6303", "FK9707", "FL4213", "FL4574",
               "FL5324", "FM4289", "FM7533", "FM9088", "FN1671", "FN5519",
               "FN9509", "FP8234", "FP9604", "FP9632", "FR1790", "FR3566",
               "FR9187", "PCB0003", "PCB0004", "SDCC8", "SDDC1", "SDEH4",
               "SDEU1", "SDFE2", "SDFP3", "SDHJ6")
Nuvaxovid <- c("4301MF009", "4301MF012", "4301MF015", "4302MF016", "4302MF018",
               "4302MF030")
Vaxzevria <- c("ABV3025", "ABV3374", "ABV4678", "ABV5297", "ABV5811", "ABV6096",
               "ABV7764", "ABW0891", "ABW1277", "ABW2953", "ABW9941", "ABX3502",
               "ABX3507", "NJ0138")


##### Identifying COVID-19 vaccines and managing names #####
# Split data by laakeaine (ATC classification group)
laakeaine <- split(finsote_vx, f = finsote_vx$laakeaine)
laakepakkausnro <- split(finsote_vx, f = finsote_vx$laakepakkausnro)

##### J07 #####
# Extract J07 from laakeaine
J07 <- laakeaine$J07
# Tabulate J07 by vaccine_name, 13 are named as Moderna
#  the others are not COVID-19 vaccine
table(J07$vaccine_name)
# Subset and edit names
J07 <- laakeaine$J07 %>%
  subset(vaccine_name == "Moderna") %>%
  mutate(vaccine_name = "spikevax")

##### J07BX03 #####
# Correct names by given information
J07BX03 <- laakeaine$J07BX03 %>%
  mutate(vaccine_name = case_when(
    laakepakkausnro %in% c("464201", "424981") ~ "janssen",
    laakepakkausnro %in% c("140099", "165049", "488024",
                           "516605", "545117", "072046",
                           "578912")  ~ "comirnaty",
    laakepakkausnro %in% c("152354") ~ "nuvaxovid",
    laakepakkausnro %in% c("485348", "046973") ~ "spikevax",
    laakepakkausnro %in% c("553555") ~ "vaxzevria",
    laakepakkausnro %in% c("-1") ~ "comirnaty",
    TRUE ~ vaccine_name)
```

```r
  ) %>%
  mutate(rokote_eranro = toupper(rokote_eranro) %>%
           str_replace_all(.," ",""),
         # Turn all letters in batch number to upper class
         # and remove space
         vaccine_name = tolower(vaccine_name)
         # Turn all letters in the vaccine_name to lower case
  )


# According to the package number,
# we have all vaccine names corrected in J07BX03 when the package number is not 0 (n=103024).
J07BX03_01 <- J07BX03 %>%
  subset(laakepakkausnro != 0)

# We get the rest (package number = 0, n=29591), and assign them using the batch number
J07BX03_02 <- J07BX03 %>%
  subset(laakepakkausnro == 0) %>%
  mutate(vaccine_name = case_when(rokote_eranro %in% Comirnaty ~ "comirnaty",
                                  rokote_eranro %in% Vaxzevria ~ "vaxzevria",
                                  rokote_eranro %in% Nuvaxovid ~ "nuvaxovid",
                                  rokote_eranro %in% Janssen ~ "janssen",
                                  TRUE ~ vaccine_name))

# After this procedure, we still have 5617 entries of COVID-19 vaccines without a
#harmonized name
J07BX03_03 <- J07BX03_02 %>%
  subset(!vaccine_name %in% c("comirnaty", "vaxzevria",
                              "nuvaxovid", "janssen", "spikevax")
         # select names != comirnaty, vaxzevria, nuvaxovid, janssen, spikevax
  )

# Tabulate J07BX03_03 by vaccine_name
table(J07BX03_03$vaccine_name)
# We have:
# 0: 2
# comirnaty original/omicron ba.1: 314
# comirnaty original/omicron ba.4-5: 416
# cov19 astrazeneca: 1
# cov19 moderna: 10
# covid-19 vaccine astrazeneca: 61
# covid-19 vaccine janssen: 3
# covid-19 vaccine moderna: 4792
# spikevax bivalent original/omicron ba.1: 1
# vaccine moderna: 17
# So, if a name contains string "comirnaty", it is shortened to "comirnaty";
# with "astrazeneca", we rename them to "vaxzevria";
# with "moderna" or "spikevax", we rename them to "spikevax";
# with "janssen", we rename them to "janssen";
# When name = 0, the rokote_eranro = G26761A, and it belongs to spikevax.
J07BX03_03 <- J07BX03_03 %>%
  mutate(vaccine_name = case_when(
    grepl(".*comirnaty", vaccine_name) ~ "comirnaty",
    grepl(".*astrazeneca", vaccine_name) ~ "vaxzevria",
```

```
    grepl(".*moderna|.*spikevax|0", vaccine_name) ~ "spikevax",
    grepl(".*janssen", vaccine_name) ~ "janssen"
  ))


# So, the J07BX03 should be a combination of J07BX03_01, J07BX03_02, J07BX03_03.
J07BX03_final <- bind_rows(J07BX03_01,
                           J07BX03_02 %>% subset(
                             vaccine_name %in% c("comirnaty", "vaxzevria",
                                                  "nuvaxovid", "janssen", "spikevax")),
                           J07BX03_03)

# Tabulate J07BX03_final by vaccine_name. No missing values.
table(J07BX03_final$vaccine_name, useNA = "ifany")
# We have:
# comirnaty: 106770,
# janssen: 8
# nuvaxovid: 19
# speikevax: 20958
# vaxzevria: 4860
# Names are corrected
# n(J07BX03_final) = n(J07BX03)



##### "-1" #####
# Extract -1 from laakeaine
M1 <- laakeaine$`-1`
# 10 cases in total, and 6 are named as "Covid-19 vaccine moderna"
#  the others are not COVID19 vaccine.
M1 <- M1 %>%
  subset(vaccine_name == "Covid-19 vaccine moderna") %>%
  mutate(vaccine_name = "spikevax")



##### "0" #####
# Extract 0 from laakeaine (n=61801),
#  toupper batch numbers & remove space (if exists),
#  tolower vaccine_name.
Z <- laakeaine$`0` %>%
  mutate(rokote_eranro = toupper(rokote_eranro) %>%
           str_replace_all(.," ",""),
         # Turn all letters in batch number to upper class
         # and romove space
         vaccine_name = tolower(vaccine_name)
         # Turn all letters in the vaccine_name to lower case
  )

# We first used the batch number in J07BX03_final to rename vaccine_name
Z_1 <- Z %>%
  subset(rokote_eranro %in% unique(J07BX03_final$rokote_eranro))

# Let's check the names
Z1_vxn <- unique(Z_1$vaccine_name) %>% data.frame()
# 355 different names. Let's make it simpler.
```

```r
# Find comirnaty
Z1_vxn_comirnaty <- split(Z1_vxn,
                          f = grepl(".*com|.*bnt162|.*bio|.*naty|.*pfizer",
                                    Z1_vxn$.))
Z1_vxn_comirnaty_final <- Z1_vxn_comirnaty[["TRUE"]]
# We found that vaccine_name = "comirnatycovid-19 vaccine mode" is
#  misleading, the associated batch numbers are 3004498 & FH9951.
# 3004498 is spikevax while FH9951 is comirnaty.
# Find moderna
Z1_vxn_moderna <- split(Z1_vxn_comirnaty[["FALSE"]],
                        f = grepl(".*mode|.*mod|.*spikeva|.*mocerna",
                                  Z1_vxn_comirnaty[["FALSE"]]$.))
Z1_vxn_moderna_final <- Z1_vxn_moderna[["TRUE"]]
# Find vaxzevria
Z1_vxn_vaxzevria <- split(Z1_vxn_moderna[["FALSE"]],
                          f = grepl(".*astra|.*vaxevria|.*vaxzevria|.*astar|.*az",
                                    Z1_vxn_moderna[["FALSE"]]$.))
Z1_vxn_vaxzevria_final <- Z1_vxn_vaxzevria[["TRUE"]]
# Find with string "covid" or "cov"
Z1_vxn_covid <- split(Z1_vxn_vaxzevria[["FALSE"]],
                      f = grepl(".*covid|.*cov", Z1_vxn_vaxzevria[["FALSE"]]$.))
Z1_vxn_covid_final <- Z1_vxn_covid[["TRUE"]]
# The others
Z1_vxn_others <- Z1_vxn_covid[["FALSE"]]

# Check names in Z1_vxn_covid_final
# 129 covid-19 vaccine:
#   4, 300042722, 3000489, 3001413, 300042698, spikevax
# covid-19 vaccine:
#   6, ABV3025, ABV4678, ABV6096, ABV3374,
#   ABV1277, ABW1277, vaxzevria
# covid-19 vaccine a:
#   7, ABV6096, ABW5811, ABV3374, ABW1277, ABV5811, ABV3025,
#   ABV4678, vaxzevria
# covid-19-mrna:
#   1, EL0725, comirnaty
# covid-19:
#   4, ABW1277, vaxzevria; EL0725, ET1831, comirnaty; G26761A, spikevax
# 129 covid-19 vaccin:
#   3, 3001413, 3000489, 300042722, spikevax
# covid-19 vaccines:
#   1, ABW9941, vaxzevria
# ticovac:
#   misclassified as we used keywords "cov"
# covid-19 vaccine:
#   7, ABV3025, ABW1277, ABV6096, ABV1277, ABV4678,
#   ABV5811, vaxzevria; EL1491, comirnaty
# 129 covid-19 vaci, 1:
#   3000489, spikevax
# covid rokotus käynti:
#   rokote_eranro = 0, no information related to the names,
#   mark this as "covid"
# covid-19vaccinemo:
```

```
#    1, 3001413, spikevax
# covid-19-rokotteet:
#    1, EL0725, comirnaty
# covid-19vaccineas:
#    2, ABV5811, ABV4678, vaxzevria
# covid-19 vaccine mr:
#    1, 3001940, spikevax
# * covid, covid-19:
#    1, EP2163, comirnaty
# cov-19:
#    1, 3001942, spikevax.
# covid:
#    2, ET1831, comirnaty; 3001413, spikevax.
# covid-19 vaccinemo:
#    1, 3001940, spikevax.
# covid-19vaccin:
#    1, ABV5811, vaxzevria.
# covid4:
#    1, 000227A, spikevax.
# covid-19 vacci:
#    1, ABV3374, vaxzevria.
# covid 19:
#    1, EP2163, comirnaty.
# covid1:
#    1, EP2163, comirnaty.
# covid 4:
#    1, FR9187, comirnaty.

Z_1 <- Z_1 %>%
  mutate(vaccine_name = case_when(
    grepl("EL0725|ELO725|ET1831|EL1491|EP2163|FR9187|FH9951",
          rokote_eranro) ~ "comirnaty",
    grepl("ABV3025|ABV4678|ABV6096|ABV3374|ABV1277|ABW1277|ABW5811|ABV5811|ABW9941",
          rokote_eranro) ~ "vaxzevria",
    grepl("300042722|3000489|3001413|300042698|G26761A|3001940|3001942|000227A|3004498",
          rokote_eranro) ~ "spikevax",
    TRUE ~ vaccine_name))

# Check names in Z1_vxn_others. Not all of them worth to check.
# We check 0, inf, kor1, koronarokote 1., 100.000, abv5811, 1g044a, 2005.
# 0: 29,
# V3J651V, V3J603V, W3F681V, V3H571V, V3H553V, V3H641V, V3H64, W3E392V, V3J573V,
#    W3E761V, vaxiprip
# DT374A, ditebooster
# 216043, 000185A, 000057A, 3006274, spikevax
# EJ6790, GD6799, SDCC8, FP9604, FD4555, FC0681, FA4598, EY3014, ET6956, GH9851,
#    EY7015, comirnaty
# 0000, XXXX, not covid vaccine
# and couldn't do anything to 0 as both vaccine_name & batch number = 0
# kor1", 1, 3001413, corrected in previous step
# koronarokote 1.", couldn't do anything, as rokote_eranro = 0.
# 100.000", cannot do anything, as rokote_eranro = 0.
# abv5811", rokote_eranro = ABV5811, vaxzevria
```

```r
# 1g044a", 1G044A, comirnaty
# 2005, cannot do anything, as there is not enough information

Z_1 <- Z_1 %>%
  mutate(vaccine_name = case_when(
    grepl("EJ6790|GD6799|SDCC8|FP9604|FD4555|FC0681|FA4598|EY3014|ET6956|GH9851|EY7015|1G044A",
          rokote_eranro) ~ "comirnaty",
    grepl("216043|000185A|000057A|3006274|00057A", rokote_eranro) ~ "spikevax",
    TRUE ~ vaccine_name))

# And V3J651V, V3H571V, W3F681V, V3J603V, V3H553V, V3H641V, V3H64, W3E392V, V3J573V, W3E761V,
#   DT374A, 0000, XXXX should not be in J07BX03.

Z_1_1 <- Z_1 %>%
  subset(vaccine_name %in% c("spikevax", "comirnaty", "vaxzevria"))
Z_1_2 <- Z_1 %>%
  subset(!vaccine_name %in% c("spikevax", "comirnaty", "vaxzevria")) %>%
  mutate(vaccine_name = case_when(
    .$vaccine_name %in% Z1_vxn_comirnaty_final$. ~ "comirnaty",
    .$vaccine_name %in% Z1_vxn_vaxzevria_final$. ~ "vaxzevria",
    .$vaccine_name %in% Z1_vxn_moderna_final$. ~ "spikevax",
    TRUE ~ vaccine_name))
# We found that some cases are misclassified,
# FL5324, 1F1012A, ACB3999, FL4213, FM7533, FJ8041 comirnaty
# 090F21A, spikevax
Z_1_2_1 <- Z_1_2 %>%
  subset(vaccine_name %in% c("spikevax", "comirnaty", "vaxzevria"))
Z_1_2_2 <- Z_1_2 %>%
  subset(!vaccine_name %in% c("spikevax", "comirnaty", "vaxzevria")) %>%
  mutate(vaccine_name = case_when(
    grepl("FL5324|1F1012A|ACB3999|FL4213|FM7533|FJ8041", rokote_eranro) ~ "comirnaty",
    grepl("090F21A", rokote_eranro) ~ "spikevax",
    TRUE ~ vaccine_name)) %>%
  subset(vaccine_name %in% c("comirnaty", "vaxzevria", "spikevax"))
# Get final Z1
Z1_final <- bind_rows(Z_1_1, Z_1_2_1, Z_1_2_2)

# We still need to check if we have something missing in zero
Z_2 <- Z %>%
  subset(!rokote_eranro %in% unique(J07BX03_final$rokote_eranro))
# Let's check the names
Z2_vxn <- unique(Z_2$vaccine_name) %>% data.frame()
# 1034 different names. Let's make it simpler.
# Find comirnaty
Z2_vxn_comirnaty <- split(Z2_vxn,
                          f = grepl(".*com|.*bnt162|.*bio|.*naty|.*pfizer",
                                    Z2_vxn$.))
Z2_vxn_comirnaty_final <- Z2_vxn_comirnaty[["TRUE"]]
# Find moderna
Z2_vxn_moderna <- split(Z2_vxn_comirnaty[["FALSE"]],
                        f = grepl(".*mode|.*mod|.*spikeva|.*mocerna",
                                  Z2_vxn_comirnaty[["FALSE"]]$.))
Z2_vxn_moderna_final <- Z2_vxn_moderna[["TRUE"]]
```

```r
# Find vaxzevria
Z2_vxn_vaxzevria <- split(
  Z2_vxn_moderna[["FALSE"]],
  f = grepl(".*astra|.*vaxevria|.*vaxzevria|.*astar|.*az",
            Z2_vxn_moderna[["FALSE"]]$.))
Z2_vxn_vaxzevria_final <- Z2_vxn_vaxzevria[["TRUE"]]
# Find with string "covid" or "cov"
Z2_vxn_covid <- split(Z2_vxn_vaxzevria[["FALSE"]],
                      f = grepl(".*covid|.*cov-1",
                                Z2_vxn_vaxzevria[["FALSE"]]$.))
# Use keywords: covid & cov-1 to find covid related vaccine, but there is no.
# And looking into the others, nothing related to COVID19 vaccine.
Z_2 <- Z_2 %>%
  mutate(vaccine_name = case_when(
    .$vaccine_name %in% Z2_vxn_comirnaty_final$. ~ "comirnaty",
    .$vaccine_name %in% Z2_vxn_vaxzevria_final$. ~ "vaxzevria",
    .$vaccine_name %in% Z2_vxn_moderna_final$. ~ "spikevax",
    TRUE ~ vaccine_name)) %>%
  subset(vaccine_name %in% c("comirnaty", "vaxzevria", "spikevax"))
# Get final Z
Z_final <- bind_rows(Z1_final, Z_2)


##### "-2" #####
M2 <- laakeaine$`-2` %>%
  mutate(rokote_eranro = toupper(rokote_eranro) %>%
           str_replace_all(.," ",""),
         # Turn all letters in batch number to upper class
         # and remove space
         vaccine_name = tolower(vaccine_name)
         # Turn all letters in the vaccine_name to lower case
  )


# Find out vaccines based on given information
M2 <- M2 %>%
  mutate(vaccine_name = case_when(rokote_eranro %in% Comirnaty ~ "comirnaty",
                                  rokote_eranro %in% Vaxzevria ~ "vaxzevria",
                                  rokote_eranro %in% Nuvaxovid ~ "nuvaxovid",
                                  rokote_eranro %in% Janssen ~ "janssen",
                                  TRUE ~ vaccine_name))
M2_1 <- M2 %>%
  subset(vaccine_name %in% c("comirnaty", "vaxzevria", "spikevax", "janssen",
                             "nuvaxovid"))
M2_2 <- M2 %>%
  subset(!vaccine_name %in% c("comirnaty", "vaxzevria", "spikevax", "janssen",
                              "nuvaxovid"))
# Let's check the names
M22_vxn <- unique(M2_2$vaccine_name) %>% data.frame()
# 874 obs. Continue to find comirnaty
M22_vxn_comirnaty <- split(M22_vxn,
                           f = grepl(".*com|.*bnt162|.*bio|.*naty|.*pfizer",
                                     M22_vxn$.))
M22_vxn_comirnaty_final <- M22_vxn_comirnaty[["TRUE"]]
```

```r
# Find moderna
M22_vxn_moderna <- split(M22_vxn_comirnaty[["FALSE"]],
                         f = grepl(".*mode|.*mod|.*spikeva|.*mocerna",
                                   M22_vxn_comirnaty[["FALSE"]]$.))
M22_vxn_moderna_final <- M22_vxn_moderna[["TRUE"]]
# Find vaxzevria
M22_vxn_vaxzevria <- split(
  M22_vxn_moderna[["FALSE"]],
  f = grepl(".*astra|.*vaxevria|.*vaxzevria|.*astar|.*az",
            M22_vxn_moderna[["FALSE"]]$.))
M22_vxn_vaxzevria_final <- M22_vxn_vaxzevria[["TRUE"]]
# Find with string "covid" or "cov"
M22_vxn_covid <- split(M22_vxn_vaxzevria[["FALSE"]],
                       f = grepl(".*covid|.*cov-|koron",
                                 M22_vxn_vaxzevria[["FALSE"]]$.))
M22_vxn_covid_final <- M22_vxn_covid[["TRUE"]]
M22_vxn_others <- M22_vxn_covid[["FALSE"]]
# Try to find if there is any potential cases in M22_vxn_others, but no.
# Let's check the batch number for cases in M22_vxn_covid_final
# covid-19:
#   3000489, spikevax
# covid-19 vaccine:
#   300042698, spikevax; ABV1277, vaxzevria
# covid19 vaccine:
#   300042698, spikevax
# cov-p1:
#   214003, spikevax
# covid19:
#   3001413, spikevax
# koron1:
#   300042698, spikevax
# cov-m1:
#   G26761A, spikevax
M2_2 <- M2_2 %>%
  mutate(vaccine_name = case_when(
    grepl("ABV1277", rokote_eranro) ~ "vaxzevria",
    grepl("3000489|300042698|214003|3001413|G26761A",
          rokote_eranro) ~ "vaxzevria",
    TRUE ~ vaccine_name
  )) %>%
  mutate(vaccine_name = case_when(
    .$vaccine_name %in% M22_vxn_comirnaty_final$. ~ "comirnaty",
    .$vaccine_name %in% M22_vxn_vaxzevria_final$. ~ "vaxzevria",
    .$vaccine_name %in% M22_vxn_moderna_final$. ~ "spikevax",
    TRUE ~ vaccine_name)) %>%
  subset(vaccine_name %in% c("comirnaty", "vaxzevria", "spikevax", "janssen",
                             "nuvaxovid"))
# The final M2
M2_final <- bind_rows(M2_1, M2_2)

# Combine
vaccine_com <- bind_rows(J07BX03_final, Z_final, M2_final, J07, M1)
```

```r
# Find COVID-19 vaccination in other laakeaine (Not -2, -1, 0, J07, J07BX03)
# However, when we split vaccine data by vaccine name,
#  we should remove those rokote_eranro = VO, IM, POISTETTU and 0
split_vxname <- split(
  subset(vaccine_com,
         rokote_eranro %in% c("VO", "IM", "POISTETTU", "0", "V3J651V",
                              "V3H571V", "W3F681V", "V3J603V", "V3H553V",
                              "V3H641V", "V3H64", "W3E392V", "V3J573V",
                              "W3E761V", "DT374A", "0000", "XXXX", "W3E763V",
                              "W3E39", "V3H55", "V3J65", "V3H641") == F),
  f = subset(vaccine_com,
             rokote_eranro %in% c("VO", "IM", "POISTETTU", "0", "V3J651V",
                                  "V3H571V", "W3F681V", "V3J603V", "V3H553V",
                                  "V3H641V", "V3H64", "W3E392V", "V3J573V",
                                  "W3E761V", "DT374A", "0000", "XXXX", "W3E763V",
                                  "W3E39", "V3H55", "V3J65", "V3H641") == F)$vaccine_name)

# Remove (-2, -1, 0, J07, J07BX03) from laakeaine
laakeaine_others <- laakeaine[names(laakeaine) %in% c("-2", "-1", "0", "J07", "J07BX03")] %>%
  do.call(rbind.data.frame, .) %>%
  mutate(rokote_eranro = toupper(rokote_eranro),
         rokote_eranro = str_replace_all(rokote_eranro," ",""))

# Correct vaccine name to official name
vx_others <- laakeaine_others %>%
  mutate(vaccine_name = case_when(
    rokote_eranro %in% split_vxname$comirnaty ~ "comirnaty",
    rokote_eranro %in% split_vxname$`covid-19 vaccine janssen` ~ "janssen",
    rokote_eranro %in% split_vxname$nuvaxovid ~ "nuvaxovid",
    rokote_eranro %in% split_vxname$spikevax ~ "spikevax",
    rokote_eranro %in% split_vxname$vaxzevria ~ "vaxzevria",
    TRUE ~ vaccine_name)) %>%
  subset(vaccine_name %in% names(split_vxname)) %>%
  mutate(vaccine_date = case_when(is.na(vaccine_date) ~ kaynti_alkoi_pvm,
                                  TRUE ~ vaccine_date)) %>%
  distinct(
    # Remove duplicated cases
    ., gumm85id, vaccine_date, rokote_eranro, .keep_all = T
  )


# After this final procedure,
#  we found 105 more cases of COVID-19 vaccines based on the batch number,
# Final vaccinated participants
vaccine <- bind_rows(vaccine_com, vx_others) %>%
  arrange(gumm85id, vaccine_date) %>%
  group_by(gumm85id)

##### Exploring cleaned vaccine data #####
# 1. Exploring data analysis and missing data
knitr::kable(table(vaccine$laakeaine, vaccine$vaccine_name),
             caption = "Crosstable by laakeaine and vaccine_name")
miss_var_summary(ungroup(vaccine))
```

```r
describe(vaccine)
# vaccine_date is the only variable that has missing values.

# Now, we use kaynti_alkoi_pvm to impute missing values in vaccine_date
vaccine <- vaccine  %>%
  mutate(vaccine_date = case_when(is.na(vaccine_date) ~ kaynti_alkoi_pvm,
                                  TRUE ~ vaccine_date))

# Finally, we eliminate duplicates when ID, date and batch number are equal
vaccine <- vaccine %>%
  distinct(., gumm85id, rokote_eranro, vaccine_date, .keep_all = T)

# Check the range of vaccine_date,
range(vaccine$vaccine_date)
# Finding the lower limit is not reasonable
# Find the unit with date = 20151103

# We replace the vaccine date with the visit date in this one case
vaccine %>%
  subset(vaccine_date == "20151103")
# Batch number = EW2246, kaynti_alkoi_pvm = 20210419
# Based on the batch number, we can find the range and it is 20210407 - 20210430
vaccine %>%
  subset(rokote_eranro == "EW2246" & vaccine_date != "20151103") %>%
  ungroup() %>%
  reframe(range = range(vaccine_date))

# The kaynti_alkoi_pvm falls in the interval. We can use this to fix the date.
vaccine[vaccine$vaccine_date == "20151103", ]$vaccine_date <- "20210419"
# Check the range again, the range is 20201102 - 20221128 now.
range(vaccine$vaccine_date)
# COVID-19 vaccination in Finland started on December 27, 2020.

# Restrict the study period to December 31, 2021 and December 27, 2020
# But we found that some are not in this range,
# Suggested by the vaccination team, use visit date to replace vaccine_date.
NotinRange <- vaccine %>%
  filter(vaccine_date <= "20201227") %>%
  mutate(vaccine_date = kaynti_alkoi_pvm)      # Replacement

# Now, we combine date NotinRange with the vaccine data
vaccine_final <- bind_rows(vaccine, NotinRange) %>%
  filter(vaccine_date <= "20211231" & vaccine_date >= "20201227")
# Check the range again
range(vaccine_final$vaccine_date)
# All date falls in 20201102-20211231

# We have all what we want now!
# comirnaty: 80431, janssen:3, spikevax: 12169, vaxzevria: 7102
# Total N = 99705
# nuvaxovid disappeared as dates are not in the range.

# Remove unnecessary objects from work space
```

```
rm(list = ls()[!ls() %in% c("vaccine_final", "finsote_vx", "finsote2018",
                            "finsote2020", "finsote2020_dates")])
```

Exploratory data analysis of vaccine data

```
# Frequencies by vaccine_name
knitr::kable(table(vaccine_final$vaccine_name),
            col.names = c("Vaccine name", "count"),
            caption = "Count by Vaccine Name") %>%
  kable_classic(full_width = F, position = "left")

# Check missing in vaccine_date
knitr::kable(sum(is.na(vaccine_final$vaccine_date)),
            col.names = "Missings",
            caption = "Missings in vaccine_date") %>%
  kable_classic(full_width = F, position = "left")
# After using kaynti_alkoi_pvm to replace missing values in vaccine_date
# No missings in vaccine_date

# Plotting dates distribution
vaccine_plot <- vaccine_final %>%
  mutate(vaccine_date = ymd(vaccine_date))
ggplot(vaccine_plot, aes(x = vaccine_date)) +
  geom_histogram(binwidth = 50, colour = "white")
```

Data wrangling of baseline survey data

```
# FINSOTE 2018 and 2020
# Create data id FinSote 2018 and subset with key variables
finsote2018_brief <- finsote2018 %>%
  dplyr::select(gumm85id, consent_reg, maritalstatus, educ_years, ika2,
                involvement_attend_j, smoke_cur_never, smoke_altprod_snus,
                smoke_altprod_nic_ecig, smoke_altprod_non_nic_ecig,
                smoke_altprod_nic_substitute, smoke_altprod_recipe, smoke_altprod_other,
                sukupuoli, kieliryhma, fs_shp_koodi, rg_N1, w_analysis1,
                rg_stratum1, w_expansion1) %>%
  rename(GUMM85ID = gumm85id) %>%
  rename(IKA2 = ika2) %>%
  rename(rg_N_suomi = rg_N1) %>%
  rename(w_analysis_suomi = w_analysis1) %>%
  rename(rg_stratum_suomi = rg_stratum1) %>%
  rename(w_expansion_suomi = w_expansion1) %>%
  mutate(dataid = 2018) %>%
  mutate(age_cont = IKA2) %>%
  mutate(educ_tertiles = ntile(educ_years, 3)) %>%
  filter(consent_reg == 1) #This excludes participants who didn't agree on the linkage

# Appending datasets with different data types creates problems
finsote2018_brief$sukupuoli <- as.factor(finsote2018_brief$sukupuoli)
```

```r
# Creating data id FinSote 2020 and subset with key variables
finsote2020_brief <- finsote2020 %>%
  dplyr::select(GUMM85ID, maritalstatus, educ_years, IKA2,
                involvement_attend_j, smoke_cur_never, smoke_altprod_snus,
                smoke_altprod_nic_ecig, smoke_altprod_non_nic_ecig,
                smoke_altprod_nic_substitute, sukupuoli, kieliryhma,
                fs_shp_koodi, rg_N_suomi, w_analysis_suomi,
                rg_stratum_suomi, w_expansion_suomi) %>%
  mutate(dataid = 2020) %>%
  mutate(age_cont = IKA2) %>%
  mutate(educ_tertiles = ntile(educ_years, 3))

# Appending datasets with different data types creates problems
finsote2020_brief$sukupuoli <- as.factor(finsote2020_brief$sukupuoli)

# Appending both datasets
finsote1820 <- bind_rows(finsote2018_brief, finsote2020_brief)    # dplyr works much
# better than smartbind
# print(miss_var_summary(finsote1820), n = 30)                    # now looks good

finsote1820 <- finsote1820 %>%
  mutate(mother_tongue = kieliryhma) %>%
  mutate(sex = sukupuoli)

# Checking class and levels of key variables
class(finsote1820$smoke_cur_never)   #numeric
class(finsote1820$maritalstatus)     #numeric
class(finsote1820$educ_tertiles)     #integer
class(finsote1820$sex)               #factor
class(finsote1820$mother_tongue)     #numeric

# Exposures. Tobacco use. Convert to factor, creating levels
# Smoking
finsote1820$smoking_status <- as.factor(finsote1820$smoke_cur_never)
finsote1820$smoking_status <-  recode_factor(finsote1820$smoking_status,
                                  `1` = "daily smoker",
                                  `2` = "occasional",
                                  `3` = "former smoker",
                                  `4` = "never smoker")


# Snus
finsote1820$snus_status <- as.factor(finsote1820$smoke_altprod_snus)
finsote1820$snus_status <-  recode_factor(finsote1820$snus_status,
                                  `1` = "daily user",
                                  `2` = "occasional",
                                  `3` = "former user",
                                  `4` = "never user")


# Confounders
# Marital status. Convert to factor, create categorical levels
finsote1820$maritalstatus_bin <- as.factor(finsote1820$maritalstatus)
finsote1820$maritalstatus_bin <-  recode_factor(finsote1820$maritalstatus_bin,
                                    `1` = "married or cohabiting",
```

```r
                                                   `2` = "married or cohabiting",
                                                   `3` = "separated, single or widowed",
                                                   `4` = "separated, single or widowed",
                                                   `5` = "separated, single or widowed")


# Mother tongue
finsote1820$mother_tongue <- as.factor(finsote1820$mother_tongue)
finsote1820$mother_tongue <-  recode_factor(finsote1820$mother_tongue,
                                            `1` = "finnish",
                                            `2` = "swedish",
                                            `3` = "other",
                                            `4` = "other")


# Sex. Needs no modification. 1==male and 2==female

# Years of education. Convert to factor, creating levels
finsote1820$educ_tertiles <- as.factor(finsote1820$educ_tertiles)
finsote1820$educ_tertiles <-  recode_factor(finsote1820$educ_tertiles,
                                            `1` = "lower",
                                            `2` = "medium",
                                            `3` = "high")


# Social participation
finsote1820$involvement_attend_j <- as.factor(finsote1820$involvement_attend_j)
finsote1820$involvement_attend_j <- recode_factor(finsote1820$involvement_attend_j,
                                                  `1` = "no participation",
                                                  `2` = "active",
                                                  `3` = "occasional")


# Other variables of tobacco and nicotine use for the multiple imputation
# E-cig with nicotine
finsote1820$ecig_nic_status <- as.factor(finsote1820$smoke_altprod_nic_ecig)
finsote1820$ecig_nic_status <-  recode_factor(finsote1820$ecig_nic_status,
                                              `1` = "daily user",
                                              `2` = "occasional",
                                              `3` = "former user",
                                              `4` = "never user")


# E-cig without nicotine
finsote1820$ecig_nonic_status <- as.factor(finsote1820$smoke_altprod_non_nic_ecig)
finsote1820$ecig_nonic_status <-  recode_factor(finsote1820$ecig_nonic_status,
                                                `1` = "daily user",
                                                `2` = "occasional",
                                                `3` = "former user",
                                                `4` = "never user")


# Nicotine replacement therapy
finsote1820$nrt_status <- as.factor(finsote1820$smoke_altprod_nic_substitute)
finsote1820$nrt_status <-  recode_factor(finsote1820$nrt_status,
                                         `1` = "daily user",
                                         `2` = "occasional",
                                         `3` = "former user",
                                         `4` = "never user")
```

```r
# Convert complex survey variables
finsote1820$rg_N_suomi <- as.numeric(finsote1820$rg_N_suomi)
finsote1820$rg_stratum_suomi <- as.numeric(finsote1820$rg_stratum_suomi)
finsote1820$w_analysis_suomi <- as.numeric(finsote1820$w_analysis_suomi)
finsote1820$w_expansion_suomi <- as.numeric(finsote1820$w_expansion_suomi)

# Check variable types
class(finsote1820$maritalstatus_bin) #factor
class(finsote1820$sex) #factor
class(finsote1820$rg_N_suomi) #numeric

# Dataset combining FinSote 2018 and 2020 ready

# Solving data type incompatibilities before appending
finsote1820$involvement_attend_j <- as.factor(finsote1820$involvement_attend_j)
finsote1820$educ_tertiles <- as.factor(finsote1820$educ_tertiles)

# Communicable Disease Registry
# Extract disease registry from finsote2018, finsote2020
ttr3 <- bind_rows(finsote2018 %>%
                    dplyr::select(gumm85id, sampling_date, covid) %>%
                    subset(covid == 1) %>%
                    rename(GUMM85ID = gumm85id),
                  finsote2020 %>%
                    dplyr::select(GUMM85ID, sampling_date, covid) %>%
                    subset(covid == 1))
# In total, 10 cases have missing in sampling date.
# NAs are defined as character. Use is.na() not work.
sum(ttr3$sampling_date == "NA")
# And we can't do anything except deletion.
# Limit
ttr3 <- ttr3 %>%
  subset(!sampling_date == "NA" & sampling_date <= "20211231")
```

Exploratory data analysis of survey data

```r
# Missingness
miss_var_summary(finsote1820) %>%
  print(n = length(names(finsote1820)))
```

Data wrangling of outcome and mediator varibles

We created three outcomes variables related to vaccine uptake, corresponding to the pre-registered protocol:

- have at least 1 doss (event_1dose),
- have at least 2 doses (event_2doses),
- have at least 3 doses (event_3doses),

Two outcome variables related to dose-spacing (in days):

- interval between 1st and 2nd dose (event__20weeks12),
- interval between 2nd and 3rd dose (event__7months23),

And ten outcome variables related to simulation study:

- event__sim1__1dose, event__sim2__1dose
- event__sim1__2doses, event__sim2__2doses
- event__sim1__3doses, event__sim2__3doses
- event__sim1__20weeks12, event__sim2__20weeks12
- event__sim1__7months23, event__sim2__7months23

There are two simulation studies: 1) All participants who got COVID at C1 get vaccinated; 2) All participants who got COVID at C1 not get vaccinated.

Created case variable (when the participant infected with COVID-19):

- case__C1: those who with an incident COVID-19 case before the first dose and if whose who have not received a COVID-19 vaccine, we would consider C1 was the period between the start of the pandemic until eligibility for the first dose,
- case__C2: those who with an incident COVID-19 case after first dose,
- case__C3: those who with an incident COVID-19 case after second dose.

```
# Create event variable
# vaccine data - change vaccine_date and arrange by id and vaccine_date
Janssen <- vaccine_final %>%
  mutate(vaccine_date = ymd(vaccine_date)) %>%
  subset(vaccine_name == "janssen") %>%
  arrange(gumm85id, vaccine_date)
# Duplicate janssen participate as 1 janssen = 2 others
vaccinecc <- vaccine_final %>%
  mutate(vaccine_date = ymd(vaccine_date)) %>%
  bind_rows(Janssen) %>%
  arrange(gumm85id, vaccine_date)

# Change gumm85id to upper case
names(vaccinecc)[names(vaccinecc) == "gumm85id"] <- "GUMM85ID"

# Creates a data frame for confirmed cases
confirmed_cases <- data.frame(vaccine_name = "COVID",
                              vaccine_date = ttr3$sampling_date,
                              GUMM85ID = ttr3$GUMM85ID)

# Combines confirmed_cases with vaccine_date
# confirmed_timepoints_1: Vaccinated
confirmed_timepoints_1 <- plyr::rbind.fill(confirmed_cases, vaccinecc) %>%
  arrange(GUMM85ID, vaccine_date) %>%
  group_by(GUMM85ID) %>%
  filter(any(vaccine_name == "COVID")) %>%
  mutate(count = n()) %>%
  subset(vaccine_date >= "2020-12-27" & count > 1) %>%   # Vaccination starts
  reframe(
    case_C1 = case_when(count > 1 & first(vaccine_name) == "COVID" ~ 1,
                        TRUE ~ 0),
```

```r
    case_C2 = case_when(count >= 2 & (nth(vaccine_name, 2) == "COVID") ~ 1,
                        TRUE ~ 0),
    case_C3 = case_when(count >= 3 & (nth(vaccine_name, 3) == "COVID") ~ 1,
                        TRUE ~ 0)) %>%
  distinct()

# confirmed_timepoints_2: Not vaccinated
confirmed_timepoints_2a <- plyr::rbind.fill(confirmed_cases, vaccinecc) %>%
  arrange(GUMM85ID, vaccine_date) %>%
  group_by(GUMM85ID) %>%
  filter(any(vaccine_name == "COVID")) %>%
  mutate(count = n()) %>%
  subset(vaccine_date >= "2020-12-27" & count == 1) %>%
  distinct()

DatebyAge <- bind_rows(
  finsote2018 %>%
    subset(gumm85id %in% confirmed_timepoints_2a$GUMM85ID,
           select = c("gumm85id", "ika2")) %>%
    `colnames<-`(c("GUMM85ID", "IKA2")) %>%
    mutate(IKA2 = IKA2 + 4),
  finsote2020 %>%
    subset(GUMM85ID %in% confirmed_timepoints_2a$GUMM85ID,
           select = c("GUMM85ID", "IKA2"))) %>%
  mutate(date = case_when(IKA2 %in% 16:24 ~ "2021-06-21",
                          IKA2 %in% 25:29 ~ "2021-06-14",
                          IKA2 %in% 30:34 ~ "2021-06-07",
                          IKA2 %in% 35:39 ~ "2021-05-31",
                          IKA2 %in% 40:44 ~ "2021-05-18",
                          IKA2 %in% 45:49 ~ "2021-05-10",
                          IKA2 %in% 50:54 ~ "2021-05-03",
                          IKA2 %in% 55:59 ~ "2021-04-27",
                          IKA2 %in% 60:64 ~ "2021-04-19",
                          IKA2 %in% 65:69 ~ "2021-03-31",
                          IKA2 %in% 70:74 ~ "2021-03-09",
                          IKA2 %in% 75:79 ~ "2021-02-24",
                          IKA2 %in% 80:84 ~ "2021-02-09",
                          IKA2 %in% 85:99 ~ "2021-02-01"
  ))

# Combine confirmed_timepoints_2 and DatebyAge
confirmed_timepoints_2 <- confirmed_timepoints_2a %>%
  right_join(DatebyAge, by = "GUMM85ID") %>%
  rowwise() %>%
  reframe(case_C1 = ifelse(vaccine_date <= date, 1, 0))

# Combine confirmed_timepoints_1 and confirmed_timepoints_2
confirmed_timepoints <- plyr::rbind.fill(confirmed_timepoints_1,
                                         confirmed_timepoints_2) %>%
  replace_na(list(case_C2 = 0,
                  case_C3 = 0))

# Merge confirmed_timepoints with finsote1820 data
```

```r
finsote <- left_join(finsote1820, confirmed_timepoints, by = "GUMM85ID")

# Have at least 1 dose
dose1 <- vaccinecc %>%
  group_by(GUMM85ID) %>%
  mutate(count = n(),
         diff = difftime(vaccine_date, first(vaccine_date), units = "days"),
         diff_days = as.numeric(diff, units = "days"),
         dose_nro = row_number(),
         count = n(),
         vaccine1 = case_when(count >= 1 ~ 1,
                              TRUE ~ 0))

# Have at least 2 doses
dose2 <- vaccinecc %>%
  group_by(GUMM85ID) %>%
  mutate(count = n(),
         diff = difftime(vaccine_date, first(vaccine_date), units = "days"),
         diff_days = as.numeric(diff, units = "days"),
         dose_nro = row_number(),
         count = n(),
         vaccine2 = case_when(count >= 2 ~ 1,
                              TRUE ~ 0))

# Have 3 doses
dose3 <- vaccinecc %>%
  group_by(GUMM85ID) %>%
  mutate(count = n(),
         diff = difftime(vaccine_date, first(vaccine_date), units = "days"),
         diff_days = as.numeric(diff, units = "days"),
         dose_nro = row_number(),
         count = n(),
         vaccine3 = case_when(count >= 3 ~ 1,
                              TRUE ~ 0))

# vaccine1 in dose1, vaccine2 in dose2, vaccine3 in dose3 are the event variables.
dose1.vac <- dose1 %>%
  reframe(event_1dose = vaccine1) %>%
  distinct()
# In total 39674 have at least 1 vaccine

dose2.vac <- dose2 %>%
  reframe(event_2doses = vaccine2) %>%
  distinct()
# 38793 have at least 2 vaccines
# table(dose2.vac$event_2doses)

dose3.vac <- dose3 %>%
  reframe(event_3doses = vaccine3) %>%
  distinct()
# only 20728 have at least 3 vaccines
# table(dose3.vac$event_3doses)
```

```r
# Combine event_1dose, event_2doses & event_3doses
dose_list <- list(dose1.vac, dose2.vac, dose3.vac)
dose <- Reduce(function(x, y) merge(x, y, all = TRUE),
               dose_list,
               accumulate = FALSE)

# Combine finsote data with dose
#  and if event_2dose is missing in the register,
#  then it should 0, which means they have not taken at least 2 doses of vaccine
finsote_dose <- left_join(finsote, dose, by = "GUMM85ID") %>%
  # define event variable for simulation study
  mutate(event_sim1_1dose = case_when(case_C1 == 1 ~ 1,
                                      TRUE ~ event_1dose),
         event_sim2_1dose = case_when(case_C1 == 1 ~ 0,
                                      TRUE ~ event_1dose),
         event_sim1_2doses = case_when(case_C1 == 1 ~ 1,
                                       TRUE ~ event_2doses),
         event_sim2_2doses = case_when(case_C1 == 1 ~ 0,
                                       TRUE ~ event_2doses),
         event_sim1_3doses = case_when(case_C1 == 1 ~ 1,
                                       TRUE ~ event_3doses),
         event_sim2_3doses = case_when(case_C1 == 1 ~ 0,
                                       TRUE ~ event_3doses)) %>%
  # replace missing values by 0
  replace_na(list(case_C1 = 0,
                  case_C2 = 0,
                  case_C3 = 0,
                  event_1dose = 0,
                  event_2doses = 0,
                  event_3doses = 0,
                  event_sim1_1dose = 0,
                  event_sim2_1dose = 0,
                  event_sim1_2doses = 0,
                  event_sim2_2doses = 0,
                  event_sim1_3doses = 0,
                  event_sim2_3doses = 0))
# event variables defined!

# Define vaccine type
# vaccination records can be found in does1.vac, dose2.vac and dose3.vac
# Based on GUMM85IDs, we can find out something in vaccinecc
# Vaccine type for at least 1 dose
vaccinecc %>%
  subset(GUMM85ID %in% dose1.vac$GUMM85ID) %>%
  mutate(type1vac = case_when(first(vaccine_name) == "comirnaty" ~ "Pfizer",
                              first(vaccine_name) == "spikevax" ~ "Moderna",
                              first(vaccine_name) == "vaxzevria" ~ "Astra Zeneca")) %>%
  subset(select = c("GUMM85ID", "type1vac")) %>%
  reframe(type1vac = unique(type1vac),
          GUMM85ID = unique(GUMM85ID)) -> type.1vac

# Vaccine type for at least 2 doses
vaccinecc %>%
```

```r
    subset(GUMM85ID %in% (dose2.vac %>% subset(event_2doses == 1))$GUMM85ID) %>%
    mutate(type2vac = case_when(vaccine_name == "comirnaty" ~ "Pfizer",
                                vaccine_name == "spikevax" ~ "Moderna",
                                vaccine_name == "vaxzevria" ~ "Astra Zeneca")) %>%
  group_by(GUMM85ID) %>%
  mutate(type2vac = case_when(
    first(type2vac) %in% c("Pfizer", "Moderna") &
      nth(type2vac, 2) %in% c("Pfizer", "Moderna") ~ "both mRNA",
    first(type2vac) %in% c("Astra Zeneca") &
      nth(type2vac, 2) %in% c("Pfizer", "Moderna") ~ "Astra Zeneca + mRNA",
    first(type2vac) %in% c("Astra Zeneca") &
      nth(type2vac, 2) %in% c("Astra Zeneca") ~ "both Astra Zeneca"
  )) %>%
  reframe(type2vac = unique(type2vac),
          GUMM85ID = unique(GUMM85ID)) -> type.2vac

# Vaccine type for at least 3 doses
vaccinecc %>%
  subset(GUMM85ID %in% (dose3.vac %>% subset(event_3doses == 1))$GUMM85ID) %>%
  mutate(type3vac = case_when(vaccine_name == "comirnaty" ~ "Pfizer",
                              vaccine_name == "spikevax" ~ "Moderna",
                              vaccine_name == "vaxzevria" ~ "Astra Zeneca")) %>%
  group_by(GUMM85ID) %>%
  mutate(type3vac = case_when(
    first(type3vac) %in% c("Pfizer", "Moderna") &
      nth(type3vac, 2) %in% c("Pfizer", "Moderna") &
      nth(type3vac, 3) %in% c("Pfizer", "Moderna") ~ "3 * mRNA",
    first(type3vac) %in% c("Astra Zeneca") &
      nth(type3vac, 2) %in% c("Pfizer", "Moderna") &
      nth(type3vac, 3) %in% c("Pfizer", "Moderna") ~ "Astra Zeneca + 2 * mRNA",
    first(type3vac) %in% c("Astra Zeneca") &
      nth(type3vac, 2) %in% c("Astra Zeneca") &
      nth(type3vac, 3) %in% c("Pfizer", "Moderna") ~ "2 * Astra Zeneca + mRNA",
    first(type3vac) %in% c("Pfizer", "Moderna") &
      nth(type3vac, 2) %in% c("Astra Zeneca") &
      nth(type3vac, 3) %in% c("Pfizer", "Moderna") ~ "Astra Zeneca + 2 * mRNA"
  )) %>%
  reframe(type3vac = unique(type3vac),
          GUMM85ID = unique(GUMM85ID)) -> type.3vac

# Combine type.1vac, type.2vac & type.3vac
type_list <- list(type.1vac, type.2vac, type.3vac)
type <- Reduce(function(x, y) merge(x, y, all = TRUE),
               type_list,
               accumulate = FALSE)

# Combine finsote_dose data with type
finsote_type <- left_join(finsote_dose, type, by = "GUMM85ID")

# Count by event variables and survey year (dataid)
listVars <- c("event_1dose", "event_2doses", "event_3doses")
catVars <- c("event_1dose", "event_2doses", "event_3doses",
             "event_sim1_1dose", "event_sim2_1dose",
```

```
                "event_sim1_2doses", "event_sim2_2doses",
                "event_sim1_3doses", "event_sim2_3doses")
table1 <- CreateTableOne(listVars,
                         strata = c("dataid"),
                         factor = catVars,
                         test = FALSE,
                         data = finsote_dose)
tab1 <- print(table1,
              printToggle = FALSE,
              nospaces = TRUE,
              contDigits = 1)
kable(tab1,
      format.args = list(digits = 1,
                         nsmall = 1,
                         format))

# Count by mediator variables
tbl_case <- data.frame(case = c("before 1st dose (C1)", "After 1st and before 2nd (C2)"),
                       bind_rows(table(finsote_dose$case_C1), table(finsote_dose$case_C2)))
knitr::kable(tbl_case,
             col.names = c("case", "0", "1"),
             caption = "Count by case") %>%
  kable_classic(full_width = F, position = "left")

# By dataid
listVars <- c("case_C1", "case_C2")
catVars <- c("case_C1", "case_C2")
table_dataid <- CreateTableOne(listVars,
                               strata = c("dataid"),
                               factor = catVars,
                               test = FALSE,
                               data = finsote_dose)
tab_dataid <- print(table_dataid,
                    printToggle = FALSE,
                    nospaces = TRUE,
                    contDigits = 1)
kable(tab_dataid,
      format.args = list(digits = 1,
                         nsmall = 1,
                         format))
```

Final combinations and re-arrangements

```
# Create event variables - interval spacing.
# Interval spacing between 1st and 2nd dose
event_20weeks12 <- dose2 %>%
  group_by(GUMM85ID) %>%
  subset(dose_nro == 2) %>%
  reframe(event_20weeks12 = case_when(diff_days >= 140 ~ 1,
                                      TRUE ~ 0))

# Interval spacing between 2nd and 3rd dose
```

```r
event_7months23 <- dose2 %>%
  group_by(GUMM85ID) %>%
  subset(count >= 3) %>%
  reframe(diff_days = difftime(nth(vaccine_date, 3), nth(vaccine_date, 2), units = "days"),
          diff_days = as.numeric(diff_days)) %>%
  distinct() %>%
  reframe(GUMM85ID = GUMM85ID,
          event_7months23 = case_when(diff_days >= 210 ~ 1,
                                      TRUE ~ 0))

# Combine event_1dose, event_2doses & event_3doses
evnt_list <- list(event_20weeks12, event_7months23)
evnt <- Reduce(function(x, y) merge(x, y, all = TRUE), evnt_list, accumulate = FALSE)

# Combine finsote data with evnt
finsote_evnt <- left_join(finsote_type, evnt, by = "GUMM85ID") %>%
  mutate(event_sim1_20weeks12 = case_when(case_C1 == 1 ~ 1,
                                          TRUE ~ event_20weeks12),
         event_sim2_20weeks12 = case_when(case_C1 == 1 ~ 0,
                                          TRUE ~ event_20weeks12),
         event_sim1_7months23 = case_when(case_C1 == 1 ~ 1,
                                          TRUE ~ event_7months23),
         event_sim2_7months23 = case_when(case_C1 == 1 ~ 0,
                                          TRUE ~ event_7months23)
  ) %>%
  replace_na(list(event_20weeks12 = 0,
                  event_7months23 = 0,
                  event_sim1_20weeks12 = 0,
                  event_sim1_7months23 = 0,
                  event_sim2_20weeks12 = 0,
                  event_sim2_7months23 = 0))

# Creates a more parsimonious dataset
finsotecc <- finsote_evnt %>%
  dplyr::select(GUMM85ID, rg_N_suomi, w_analysis_suomi, rg_stratum_suomi, dataid,
                fs_shp_koodi, smoking_status, snus_status, ecig_nic_status,
                ecig_nonic_status, nrt_status, educ_tertiles, maritalstatus_bin,
                mother_tongue, involvement_attend_j, case_C1, case_C2, event_1dose,
                event_2doses, event_3doses, age_cont, sex, event_20weeks12, case_C3,
                event_7months23, event_sim1_1dose, event_sim2_1dose, event_sim1_2doses,
                event_sim2_2doses, event_sim1_3doses, event_sim2_3doses,
                event_sim1_20weeks12, event_sim2_20weeks12, event_sim1_7months23,
                event_sim2_7months23, type1vac, type2vac, type3vac)
# n = 42935

# Combines daily and occasional users
# table(finsotecc$snus_status, useNA = "ifany")
finsotecc$snus_status <- recode_factor(finsotecc$snus_status,
                                       "daily user" = "current user")
finsotecc$snus_status <- recode_factor(finsotecc$snus_status,
                                       "occasional" = "current user")

finsotecc$ecig_nic_status <- recode_factor(finsotecc$ecig_nic_status,
```

```r
                                                     "daily user" = "current user")
finsotecc$ecig_nic_status <- recode_factor(finsotecc$ecig_nic_status,
                                                     "occasional" = "current user")

finsotecc$ecig_nonic_status <- recode_factor(finsotecc$ecig_nonic_status,
                                                       "daily user" = "current user")
finsotecc$ecig_nonic_status <- recode_factor(finsotecc$ecig_nonic_status,
                                                       "occasional" = "current user")

finsotecc$nrt_status <- recode_factor(finsotecc$nrt_status,
                                              "daily user" = "current user")
finsotecc$nrt_status <- recode_factor(finsotecc$nrt_status,
                                              "occasional" = "current user")


# Create tobacco variable
finsotecc %>%
  mutate(tobacco_use = case_when(
    # Dual use
    # daily smoker & current user
    smoking_status %in% c("daily smoker") &
      snus_status %in% c("current user") ~ "Dual use",
    # occasional & current user
    smoking_status %in% c("occasional") &
      snus_status %in% c("current user") ~ "Dual use",

    # Only tobacco use
    # daily smoker and former user
    smoking_status %in% c("daily smoker") &
      snus_status %in% c("former user") ~ "only tabacco use",
    # daily smoker and never user
    smoking_status %in% c("daily smoker") &
      snus_status %in% c("never user") ~ "only tabacco use",
    # daily and NA
    smoking_status %in% c("daily smoker") &
      is.na(snus_status) ~ "only tabacco use",
    # occasional and former user
    smoking_status %in% c("occasional") &
      snus_status %in% c("former user") ~ "only tabacco use",
    # occasional and never user
    smoking_status %in% c("occasinal") &
      snus_status %in% c("never user") ~ "only tabacco use",
    # occasional and NA
    smoking_status %in% c("occassional") &
      is.na(snus_status) ~ "only tabacco use",

    # Only snus user
    # former smoker and current user
    smoking_status %in% c("former smoker") &
      snus_status %in% c("current user") ~ "only snus use",
    # never smoker and current user
    smoking_status %in% c("never smoker") &
      snus_status %in% c("current user") ~ "only snus use",
    # NA and current smoker
```

```r
    is.na(smoking_status) &
      snus_status %in% c("current user") ~ "only snus use",

    # Former tobacco use
    # former smoker and former user
    smoking_status %in% c("former smoker") &
      snus_status %in% c("former user") ~ "former tobacco use",
    # former smoker and never user
    smoking_status %in% c("former smoker") &
      snus_status %in% c("never user") ~ "former tobacco use",
    # former smoker and NA
    smoking_status %in% c("former smoker") &
      is.na(snus_status) ~ "former tobacco use",
    # never smoker and former user
    smoking_status %in% c("never smoker") &
      snus_status %in% c("former user") ~ "former tobacco use",
    # NA and former user
    is.na(smoking_status) &
      snus_status %in% c("former user") ~ "former tobacco use",

    # never tobacco use
    # never smoker and never user
    smoking_status %in% c("never smoker") &
      snus_status %in% c("never user") ~ "never tobacco use",
    # never smoker and NA
    smoking_status %in% c("never smoker") &
      is.na(snus_status) ~ "never tobacco use",
    # NA and never user
    is.na(smoking_status) &
      snus_status %in% c("never user") ~ "never tobacco use",

    # NA and NA
    TRUE ~ NA_character_) %>%
      as.factor()
  ) -> finsotecc

# Reference levels
finsotecc <- within(finsotecc,
                    smoking_status <- relevel(smoking_status, ref = "never smoker"))
finsotecc <- within(finsotecc,
                    snus_status <- relevel(snus_status, ref = 'never user'))
finsotecc <- within(finsotecc,
                    ecig_nic_status <- relevel(ecig_nic_status, ref = 'never user'))
finsotecc <- within(finsotecc,
                    ecig_nonic_status <- relevel(ecig_nonic_status, ref = 'never user'))
finsotecc <- within(finsotecc,
                    nrt_status <- relevel(nrt_status, ref = 'never user'))
finsotecc <- within(finsotecc,
                    tobacco_use <- relevel(tobacco_use, ref = 'never tobacco use'))

# Convert character to factor
finsotecc$fs_shp_koodi <- as.factor(finsotecc$fs_shp_koodi)
finsotecc$type1vac <- as.factor(finsotecc$type1vac)
```

```
finsotecc$type2vac <- as.factor(finsotecc$type2vac)
finsotecc$type3vac <- as.factor(finsotecc$type3vac)
```

Multiple imputation

We imputed the final dataset (finsotecc), which contains variables with mssing data in confounders and exposures. There are no missing data for some variables such as sex, age and mother tongue nor for any of the outcomes. We also used variables that correlate with missingness, such as the exposure to other tobacco products. We used multiple imputation with chained equations. The missing data assumption is missing at random (MAR).

We did not specify an imputation method. The package mice uses predictive mean matching as the default method. We carried out 15 imputations which we then pooled to obtain multiply imputed values. These values take the complex survey sampling into account. Specified formulas when imputing. Supposed, for example, smoking_status is predicted by dataid, fs_shp_koodi, age_cont, sex, snus_status, ecig_nic_status, ecig_nonic_status, nrt_status, educ_tertiles, maritalstatus_bin, mother_tongue, involvement_attend_j. Others, are imputed with the same logic. ecig_nic_status, ecig_nonic_status & nrt_status not included in the analysis, but use them as auxiliary information to help imputation. That is, the model is like `smoking_status ~ dataid + fs_shp_koodi + age_cont + sex + snus_status + ecig_nic_status + ecig_nonic_status + nrt_status + educ_tertiles + maritalstatus_bin + mother_tongue + involvement_attend_j`.

If not specified formulas gives the results in the slides. Tobacco and COVID-19 vaccination

The convergence plot shows that the multiple imputation process for FinSote data was successful - there is little trend and the streams mingle well.

```
# Multiple imputation
# By default, mice use Polynomial Regression for multilevel variable
#  and logreg for binary variable
# Setting up survey design (weights, strata and FPC)
finsotecc_imp <- mice(
  subset(finsotecc,
        select = c("dataid", "fs_shp_koodi", "smoking_status", "snus_status",
                   "ecig_nic_status", "ecig_nonic_status", "nrt_status",
                   "educ_tertiles", "maritalstatus_bin", "mother_tongue",
                   "involvement_attend_j", "age_cont", "sex", "tobacco_use",
                   "type1vac", "type2vac", "type3vac")),
  m = 15,
  seed = 99,
  printFlag = F)

# Check convergence
plot(finsotecc_imp,
     c("smoking_status", "snus_status"),
     main = "Convergence of Imputed data")

#
finsotecc_imp <- cbind(
  finsotecc_imp,
  subset(finsotecc,
        select = c(
          "rg_N_suomi", "w_analysis_suomi", "rg_stratum_suomi", "GUMM85ID",
```

```
            "case_C1", "case_C2", "event_1dose", "event_2doses", "event_3doses",
            "event_20weeks12", "event_7months23", "event_sim1_1dose", "case_C3",
            "event_sim2_1dose", "event_sim1_2doses", "event_sim2_2doses",
            "event_sim1_3doses", "event_sim2_3doses", "event_sim1_20weeks12",
            "event_sim2_20weeks12", "event_sim1_7months23", "event_sim2_7months23")
  )
)
```

Tables

We present descriptive tables of baseline characteristics taking the complex survey design into account.

Non-imputed

```
# Use non-imputed finsotecc
# Make survey design object
des_tbl <- svydesign(id = ~1,
                     fpc = ~rg_N_suomi,
                     weights = ~w_analysis_suomi,
                     strata = ~rg_stratum_suomi,
                     data = finsotecc)

# Table 1
knitr::kable(
  table(finsotecc$event_2doses, finsotecc$smoking_status, exclude = NULL),
  caption = "Count by event_2doses and smoking_status") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(
  table(finsotecc$smoking_status, exclude = NULL),
  caption = "Count by smoking_status",
  col.names = c("smoking_status", "count")) %>%
  kable_classic(full_width = F, position = "left")

# Count for Table 1
listVars <- c("event_1dose", "event_2doses", "event_3doses", "event_20weeks12",
              "event_7months23","case_C1", "case_C2", "case_C3",  "sex",
              "age_cont", "maritalstatus_bin", "educ_tertiles", "mother_tongue",
              "involvement_attend_j", "event_sim1_1dose", "event_sim2_1dose",
              "event_sim1_2doses", "event_sim2_2doses", "event_sim1_3doses",
              "event_sim2_3doses", "event_sim1_20weeks12",
              "event_sim2_20weeks12", "event_sim1_7months23",
              "event_sim2_7months23")
catVars <- c("event_1dose", "event_2doses", "event_3doses", "event_20weeks12",
             "event_7months23", "case_C1", "case_C2", "case_C3", "sex",
             "maritalstatus_bin", "educ_tertiles", "mother_tongue",
             "involvement_attend_j", "event_sim1_1dose", "event_sim2_1dose",
             "event_sim1_2doses", "event_sim2_2doses", "event_sim1_3doses",
             "event_sim2_3doses", "event_sim1_20weeks12",
             "event_sim2_20weeks12", "event_sim1_7months23",
```

```r
                "event_sim2_7months23")

table1 <- svyCreateTableOne(listVars,
                            strata = c("smoking_status"),
                            factor = catVars,
                            test = FALSE,
                            data = des_tbl,
                            addOverall = T)

tab1 <- print(table1,
              printToggle = FALSE,
              nospaces = TRUE,
              format = "p",
              contDigits = 1)

knitr::kable(tab1,
             format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: smoking status (Non-imputed)") %>%
  kable_classic(full_width = F, position = "left")

# Table S2 for snus
knitr::kable(
  table(finsotecc$event_2doses, finsotecc$snus_status, exclude = NULL),
  caption = "Count by event_2doses and snus_status") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(
  table(finsotecc$snus_status, exclude = NULL),
  caption = "Count by snus_status",
  col.names = c("snus_status", "count")) %>%
  kable_classic(full_width = F, position = "left")

table2 <- svyCreateTableOne(listVars,
                            strata = c("snus_status"),
                            factor = catVars,
                            test = FALSE,
                            data = des_tbl,
                            addOverall = T)
tab2 <- print(table2,
              printToggle = FALSE,
              nospaces = TRUE,
              format = "p",
              contDigits = 1)
knitr::kable(tab2,
             format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: snus status (Non-imputed)") %>%
  kable_classic(full_width = F, position = "left")

# Table 3: Tobacco use
table3 <- svyCreateTableOne(listVars,
                            strata = c("tobacco_use"),
                            factor = catVars,
                            test = FALSE,
```

```
                              data = des_tbl,
                              addOverall = T)
tab3 <- print(table3,
              printToggle = FALSE,
              nospaces = TRUE,
              format = "p",
              contDigits = 1)
knitr::kable(tab3,
             format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: Tobacco use (Non-imputed)") %>%
  kable_classic(full_width = F, position = "left")
```

Imputed

```
# Use imputed finsotecc
# Make survey design object
imp_list <- imputationList(lapply(1:finsotecc_imp$m,
                                  function(n) mice::complete(finsotecc_imp, action = n)))
des_final <- svydesign(id = ~1,
                       fpc = ~rg_N_suomi,
                       weights = ~w_analysis_suomi,
                       strata = ~rg_stratum_suomi,
                       data = imp_list,
                       nest = T)


# Table 1
table1 <- svyCreateTableOne(listVars,
                            strata = c("smoking_status"),
                            factor = catVars,
                            test = FALSE,
                            data = des_final$designs[[1]])
tab1 <- print(table1, printToggle = FALSE, nospaces = TRUE, format = "p", contDigits = 1)
knitr::kable(tab1, format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: smoking status (Imputed)") %>%
  kable_classic(full_width = F, position = "left")

# Table S2 for snus
table2 <- svyCreateTableOne(listVars,
                            strata = c("snus_status"),
                            factor = catVars,
                            test = FALSE,
                            data = subset(des_final$designs[[1]], dataid == 2020))
tab2 <- print(table2, printToggle = FALSE, nospaces = TRUE, format = "p", contDigits = 1)
knitr::kable(tab2, format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: snus status (Imputed)") %>%
  kable_classic(full_width = F, position = "left")

# Table S3 for tobacco use
table3 <- svyCreateTableOne(listVars,
                            strata = c("tobacco_use"),
                            factor = catVars,
```

```
                                 test = FALSE,
                                 data = subset(des_final$designs[[1]], dataid == 2020))
tab3 <- print(table3, printToggle = FALSE, nospaces = TRUE, format = "p", contDigits = 1)
knitr::kable(tab3, format.args = list(digits = 1, nsmall = 1, format),
             caption = "Summary table: tobacco use (Imputed)") %>%
  kable_classic(full_width = F, position = "left")
```

Information about vaccine type

```
table(finsotecc$type1vac, exclude = NULL) %>%
  kbl(caption = "Vaccine type (1 dose)") %>%
  kable_classic(full_width = F, position = "left")

table(finsotecc$type2vac, exclude = NULL) %>%
  kbl(caption = "Vaccine type (2 doses)") %>%
  kable_classic(full_width = F, position = "left")

table(finsotecc$type3vac, exclude = NULL) %>%
  kbl(caption = "Vaccine type (3 doses)") %>%
  kable_classic(full_width = F, position = "left")
```

Save

```
save(list = c("des_final", "finsotecc", "finsote2020_dates",
              "vaccinecc", "finsote_evnt", "ttr3",
              "dose2", "dose1", "dose3"), file = "TobriskCov_Data_02102023.RData")
```

End of part I

Part II

Loading packages and data

Packages

```
# Loading packages
library(readxl)
library(haven)
library(styler)
library(tidyverse)
library(knitr)
library(kableExtra)
library(tidyr)
library(janitor)
```

```
library(gtools)
library(ggridges)
library(ggfortify)
library(tableone)
library(pollster)
library(naniar)
library(survey)
library(survival)
library(biostat3)
library(Epi)
library(lubridate)
library(mice)
library(mitools)
library(mitml)
library(Hmisc)
library(finalfit)
```

Data

```
load("TobriskCov_Data_02102023.RData")
```

Testing the need for splines

We fitted a minimally adjusted model for sex and the age as a linear function or a penalized smoothing spline. We used a likelihood ratio test to compare whether using a spline provides a better fit.

The results show a better fit when using penalised smoothing splines for all variables. We will thus model age using splines.

```
# Age as a linear function
agelinear <- with(des_final,
                  svyglm(event_2doses ~ factor(sex) + age_cont,
                         family = quasipoisson()))
# Age as a penalised smoothing spline
agespline <- with(des_final,
                  svyglm(event_2doses ~ factor(sex) + pspline(age_cont),
                         family = quasipoisson()))
testModels(agespline, agelinear, method = "D2")
```

Main analyses

Primary outcome - Uptake of two doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_MA_PO_Smoke <- with(des_final,
                       svyglm(event_2doses ~ factor(smoking_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_MA_PO_Smoke))

# Adjusted for age and sex
m2_MA_PO_Smoke <- with(des_final,
                       svyglm(event_2doses ~ factor(smoking_status) +
                              factor(sex) + pspline(age_cont),
                              family = quasipoisson()))
# summary(MIcombine(m2_MA_PO_Smoke))

# Adjusted for confounders
m3_MA_PO_Smoke <- with(des_final,
                       svyglm(event_2doses ~ factor(smoking_status) +
                              factor(sex) + pspline(age_cont) +
                              factor(educ_tertiles) + factor(maritalstatus_bin) +
                              factor(mother_tongue) + factor(involvement_attend_j) +
                              factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_MA_PO_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_PO_Smoke <- with(des_final,
                       svyglm(event_2doses ~ factor(smoking_status) +
                              factor(sex) + pspline(age_cont) +
                              factor(educ_tertiles) + factor(maritalstatus_bin) +
                              factor(mother_tongue) + factor(involvement_attend_j) +
                              factor(fs_shp_koodi) + factor(case_C1),
                              family = quasipoisson()))
# summary(MIcombine(m4_MA_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_PO_Smoke)),
                             confint(MIcombine(m1_MA_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_PO_Smoke)),
                             confint(MIcombine(m2_MA_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_PO_Smoke)),
                             confint(MIcombine(m3_MA_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_PO_Smoke)),
                             confint(MIcombine(m4_MA_PO_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
```

```r
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_PO_Smoke[[1]]$data)
nrow(m2_MA_PO_Smoke[[1]]$data)
nrow(m3_MA_PO_Smoke[[1]]$data)
nrow(m4_MA_PO_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_PO_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_MA_PO_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

# Remove unnecessary objects from work space
rm(list = ls()[ls() %in% c("m1_MA_PO_Smoke", "m2_MA_PO_Smoke", "m3_MA_PO_Smoke",
                           "m4_MA_PO_Smoke")])
```

Snus

```r
# Crude model
m1_MA_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                      svyglm(event_2doses ~  factor(snus_status),
                             family = quasipoisson()))
# summary(MIcombine(m1_MA_PO_Snus))

# Adjusted for age and sex
m2_MA_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                      svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                               pspline(age_cont),
                             family = quasipoisson()))
# summary(MIcombine(m2_MA_PO_Snus))

# Adjusted for confounders
m3_MA_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                      svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi),
                             family = quasipoisson()))
# summary(MIcombine(m3_MA_PO_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                      svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi) +
```

```
                                factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_MA_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_PO_Snus)),
                             confint(MIcombine(m1_MA_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_PO_Snus)),
                             confint(MIcombine(m2_MA_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_PO_Snus)),
                             confint(MIcombine(m3_MA_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_PO_Snus)),
                             confint(MIcombine(m4_MA_PO_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_PO_Snus[[1]]$data)
nrow(m2_MA_PO_Snus[[1]]$data)
nrow(m3_MA_PO_Snus[[1]]$data)
nrow(m4_MA_PO_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_PO_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_MA_PO_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

# Remove unnecessary objects from work space
rm(list = ls()[ls() %in% c("m1_MA_PO_Snus", "m2_MA_PO_Snus", "m3_MA_PO_Snus",
                           "m4_MA_PO_Snus")])
```

Tobacco use

```
# Crude model
m1_MA_PO_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(tobacco_use),
                                family = quasipoisson()))
# summary(MIcombine(m1_MA_PO_Tobacco))
```

```r
# Adjusted for age and sex
m2_MA_PO_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(tobacco_use) +
                                  factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_MA_PO_Tobacco))

# Adjusted for confounders
m3_MA_PO_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(tobacco_use) +
                                  factor(sex) + pspline(age_cont) +
                                  factor(educ_tertiles) + factor(maritalstatus_bin) +
                                  factor(mother_tongue) + factor(involvement_attend_j) +
                                  factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_MA_PO_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_PO_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(tobacco_use) +
                                  factor(sex) + pspline(age_cont) +
                                  factor(educ_tertiles) + factor(maritalstatus_bin) +
                                  factor(mother_tongue) + factor(involvement_attend_j) +
                                  factor(fs_shp_koodi) + factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_MA_PO_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_PO_Tobacco)),
                             confint(MIcombine(m1_MA_PO_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_PO_Tobacco)),
                             confint(MIcombine(m2_MA_PO_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_PO_Tobacco)),
                             confint(MIcombine(m3_MA_PO_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_PO_Tobacco)),
                             confint(MIcombine(m4_MA_PO_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_PO_Tobacco[[1]]$data)
nrow(m2_MA_PO_Tobacco[[1]]$data)
nrow(m3_MA_PO_Tobacco[[1]]$data)
```

```
nrow(m4_MA_PO_Tobacco[[1]]$data)
# n = 29192


# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_PO_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_MA_PO_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")


# Remove unnecessary objects from work space
rm(list = ls()[ls() %in% c("m1_MA_PO_Tobacco", "m2_MA_PO_Tobacco", "m3_MA_PO_Tobacco",
                           "m4_MA_PO_Tobacco")])
```

Secondary outcomes

1. Uptake of one dose of COVID-19 vaccine

1.1 Smoking

```
## Crude model
m1_MA_SO1_Smoke <- with(des_final,
                        svyglm(event_1dose ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_MA_SO1_Smoke))


# Adjusted for age and sex
m2_MA_SO1_Smoke <- with(des_final,
                        svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_MA_SO1_Smoke))


# Adjusted for confounders
m3_MA_SO1_Smoke <- with(des_final,
                        svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_MA_SO1_Smoke))


# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO1_Smoke <- with(des_final,
                        svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi) +
                               factor(case_C1),
```

```
                              family = quasipoisson())
# summary(MIcombine(m4_MA_SO1_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO1_Smoke)),
                             confint(MIcombine(m1_MA_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO1_Smoke)),
                             confint(MIcombine(m2_MA_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO1_Smoke)),
                             confint(MIcombine(m3_MA_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO1_Smoke)),
                             confint(MIcombine(m4_MA_SO1_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_SO1_Smoke[[1]]$data)
nrow(m2_MA_SO1_Smoke[[1]]$data)
nrow(m3_MA_SO1_Smoke[[1]]$data)
nrow(m4_MA_SO1_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO1_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_MA_SO1_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO1_Smoke", "m2_MA_SO1_Smoke", "m3_MA_SO1_Smoke",
                           "m4_MA_SO1_Smoke")])
```

1.2 Snus

```
# Crude model
m1_MA_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_1dose ~ factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_MA_SO1_Snus))

# Adjusted for age and sex
m2_MA_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
```

```r
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_MA_SO1_Snus))


# Adjusted for confounders
m3_MA_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_MA_SO1_Snus))


# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_MA_SO1_Snus))


# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO1_Snus)),
                              confint(MIcombine(m1_MA_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO1_Snus)),
                              confint(MIcombine(m2_MA_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO1_Snus)),
                              confint(MIcombine(m3_MA_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO1_Snus)),
                              confint(MIcombine(m4_MA_SO1_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_SO1_Snus[[1]]$data)
nrow(m2_MA_SO1_Snus[[1]]$data)
nrow(m3_MA_SO1_Snus[[1]]$data)
nrow(m4_MA_SO1_Snus[[1]]$data)
# n = 29192

# Percent attenuation
```

```r
data.frame(M3 = round(coef(MIcombine(m3_MA_SO1_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_MA_SO1_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO1_Snus", "m2_MA_SO1_Snus", "m3_MA_SO1_Snus",
                           "m4_MA_SO1_Snus")])
```

1.3 Tobacco use

```r
# Crude model
m1_MA_SO1_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(tobacco_use),
                                 family = quasipoisson()))
# summary(MIcombine(m1_MA_SO1_Tobacco))

# Adjusted for age and sex
m2_MA_SO1_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(tobacco_use) + factor(sex) +
                                 pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_MA_SO1_Tobacco))

# Adjusted for confounders
m3_MA_SO1_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(tobacco_use) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_MA_SO1_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO1_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(tobacco_use) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                 factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_MA_SO1_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO1_Tobacco)),
                             confint(MIcombine(m1_MA_SO1_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO1_Tobacco)),
                             confint(MIcombine(m2_MA_SO1_Tobacco)))), 2)[2:5,],
```

```
                caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO1_Tobacco)),
                            confint(MIcombine(m3_MA_SO1_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO1_Tobacco)),
                            confint(MIcombine(m4_MA_SO1_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_MA_SO1_Tobacco[[1]]$data)
nrow(m2_MA_SO1_Tobacco[[1]]$data)
nrow(m3_MA_SO1_Tobacco[[1]]$data)
nrow(m4_MA_SO1_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO1_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_MA_SO1_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO1_Tobacco", "m2_MA_SO1_Tobacco", "m3_MA_SO1_Tobacco",
                           "m4_MA_SO1_Tobacco")])
```

2. Uptake of three doses of COVID-19 vaccine

2.1 Smoking

```
# Crude model
m1_MA_SO2_Smoke <- with(des_final,
                        svyglm(event_3doses ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_MA_SO2_Smoke))

# Adjusted for age and sex
m2_MA_SO2_Smoke <- with(des_final,
                        svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                   pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_MA_SO2_Smoke))

# Adjusted for confounders
m3_MA_SO2_Smoke <- with(des_final,
                        svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
```

```r
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson()))
# summary(MIcombine(m3_MA_SO2_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO2_Smoke <- with(des_final,
                    svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi) +
                               factor(case_C1),
                          family = quasipoisson()))
# summary(MIcombine(m4_MA_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO2_Smoke)),
                             confint(MIcombine(m1_MA_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO2_Smoke)),
                             confint(MIcombine(m2_MA_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO2_Smoke)),
                             confint(MIcombine(m3_MA_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO2_Smoke)),
                             confint(MIcombine(m4_MA_SO2_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO2_Smoke[[1]]$data)
nrow(m2_MA_SO2_Smoke[[1]]$data)
nrow(m3_MA_SO2_Smoke[[1]]$data)
nrow(m4_MA_SO2_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO2_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_MA_SO2_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO2_Smoke", "m2_MA_SO2_Smoke", "m3_MA_SO2_Smoke",
                           "m4_MA_SO2_Smoke")])
```

2.2 Snus

```
# Crude model
m1_MA_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_3doses ~ factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_MA_SO2_Snus))

## Adjusted for age and sex
m2_MA_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_3doses ~ factor(snus_status) + factor(sex) + pspline(age_cont),
                              family = quasipoisson()))
# summary(MIcombine(m2_MA_SO2_Snus))

# Adjusted for confounders
m3_MA_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_MA_SO2_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) +
                                  factor(fs_shp_koodi) + factor(case_C1),
                              family = quasipoisson()))
# summary(MIcombine(m4_MA_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO2_Snus)),
                             confint(MIcombine(m1_MA_SO2_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO2_Snus)),
                             confint(MIcombine(m2_MA_SO2_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO2_Snus)),
                             confint(MIcombine(m3_MA_SO2_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO2_Snus)),
                             confint(MIcombine(m4_MA_SO2_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
```

```r
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO2_Snus[[1]]$data)
nrow(m2_MA_SO2_Snus[[1]]$data)
nrow(m3_MA_SO2_Snus[[1]]$data)
nrow(m4_MA_SO2_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO2_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_MA_SO2_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO2_Snus ","m2_MA_SO2_Snus", "m3_MA_SO2_Snus",
                           "m4_MA_SO2_Snus")])
```

2.3 Tobacco use

```r
# Crude model
m1_MA_SO2_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(tobacco_use),
                                 family = quasipoisson()))
# summary(MIcombine(m1_MA_SO2_Tobacco))

# Adjusted for age and sex
m2_MA_SO2_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(tobacco_use) + factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_MA_SO2_Tobacco))

# Adjusted for confounders
m3_MA_SO2_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(tobacco_use) + factor(sex) +
                                     pspline(age_cont) + factor(educ_tertiles) +
                                     factor(maritalstatus_bin) + factor(mother_tongue) +
                                     factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_MA_SO2_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO2_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(tobacco_use) + factor(sex) +
                                     pspline(age_cont) + factor(educ_tertiles) +
                                     factor(maritalstatus_bin) + factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_MA_SO2_Tobacco))
```

```r
# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO2_Tobacco)),
                            confint(MIcombine(m1_MA_SO2_Tobacco)))), 2)[2:5,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO2_Tobacco)),
                            confint(MIcombine(m2_MA_SO2_Tobacco)))), 2)[2:5,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO2_Tobacco)),
                            confint(MIcombine(m3_MA_SO2_Tobacco)))), 2)[2:5,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO2_Tobacco)),
                            confint(MIcombine(m4_MA_SO2_Tobacco)))), 2)[2:5,],
            caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO2_Tobacco[[1]]$data)
nrow(m2_MA_SO2_Tobacco[[1]]$data)
nrow(m3_MA_SO2_Tobacco[[1]]$data)
nrow(m4_MA_SO2_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO2_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_MA_SO2_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO2_Tobacco ","m2_MA_SO2_Tobacco", "m3_MA_SO2_Tobacco",
                           "m4_MA_SO2_Tobacco")])
```

3. Interval spacing between 1st and 2nd dose of COVID-19 vaccine

3.1 Smoking

```r
# Get the average days 1st - 2nd
interval1n2 <- dose2 %>%
  group_by(GUMM85ID) %>%
  subset(dose_nro == 2) %>%
  ungroup() %>%
  reframe(mean = mean(diff_days))
paste("Average interval spacing between 1st and 2nd dose of COVID-19 vaccine:", round(interval1n2, 2),

# Crude model
```

```r
m1_MA_SO3_Smoke <- with(des_final,
                        svyglm(event_20weeks12 ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_MA_SO3_Smoke))

# Adjusted for age and sex
m2_MA_SO3_Smoke <- with(des_final,
                        svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                                   pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_MA_SO3_Smoke))

# Adjusted for confounders
m3_MA_SO3_Smoke <- with(des_final,
                        svyglm(event_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_MA_SO3_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO3_Smoke <- with(des_final,
                        svyglm(event_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) + factor(involvement_
                                   factor(fs_shp_koodi) + factor(case_C1),
                               family = quasipoisson()))
# summary(MIcombine(m4_MA_SO3_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO3_Smoke)),
                             confint(MIcombine(m1_MA_SO3_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO3_Smoke)),
                             confint(MIcombine(m2_MA_SO3_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO3_Smoke)),
                             confint(MIcombine(m3_MA_SO3_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO3_Smoke)),
                             confint(MIcombine(m4_MA_SO3_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
```

```r
nrow(m1_MA_SO3_Smoke[[1]]$data)
nrow(m2_MA_SO3_Smoke[[1]]$data)
nrow(m3_MA_SO3_Smoke[[1]]$data)
nrow(m4_MA_SO3_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO3_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_MA_SO3_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO3_Smoke ","m2_MA_SO3_Smoke", "m3_MA_SO3_Smoke",
                           "m4_MA_SO3_Smoke")])
```

3.2 Snus

```r
# Crude model
m1_MA_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_20weeks12 ~ factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_MA_SO3_Snus))

# Adjusted for age and sex
m2_MA_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont),
                              family = quasipoisson()))
# summary(MIcombine(m2_MA_SO3_Snus))

# Adjusted for confounders
m3_MA_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_MA_SO3_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_20weeks12 ~ factor(snus_status) +
                                factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                factor(case_C1),
                              family = quasipoisson()))
# summary(MIcombine(m4_MA_SO3_Snus))

# Obtain main estimates
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO3_Snus)),
                             confint(MIcombine(m1_MA_SO3_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO3_Snus)),
                             confint(MIcombine(m2_MA_SO3_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO3_Snus)),
                             confint(MIcombine(m3_MA_SO3_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO3_Snus)),
                             confint(MIcombine(m4_MA_SO3_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO3_Snus[[1]]$data)
nrow(m2_MA_SO3_Snus[[1]]$data)
nrow(m3_MA_SO3_Snus[[1]]$data)
nrow(m4_MA_SO3_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO3_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_MA_SO3_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO3_Snus ","m2_MA_SO3_Snus", "m3_MA_SO3_Snus",
                           "m4_MA_SO3_Snus")])
```

3.3 Tobacco use

```r
# Crude model
m1_MA_SO3_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_20weeks12 ~ factor(tobacco_use),
                                 family = quasipoisson()))
# summary(MIcombine(m1_MA_SO3_Tobacco))

# Adjusted for age and sex
m2_MA_SO3_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_20weeks12 ~ factor(tobacco_use) + factor(sex) +
                                     pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_MA_SO3_Tobacco))
```

```r
# Adjusted for confounders
m3_MA_SO3_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_20weeks12 ~ factor(tobacco_use) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_MA_SO3_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO3_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_20weeks12 ~ factor(tobacco_use) +
                                   factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                   factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_MA_SO3_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO3_Tobacco)),
                             confint(MIcombine(m1_MA_SO3_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO3_Tobacco)),
                             confint(MIcombine(m2_MA_SO3_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO3_Tobacco)),
                             confint(MIcombine(m3_MA_SO3_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO3_Tobacco)),
                             confint(MIcombine(m4_MA_SO3_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO3_Tobacco[[1]]$data)
nrow(m2_MA_SO3_Tobacco[[1]]$data)
nrow(m3_MA_SO3_Tobacco[[1]]$data)
nrow(m4_MA_SO3_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO3_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_MA_SO3_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
```

```r
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO3_Tobacco ","m2_MA_SO3_Tobacco", "m3_MA_SO3_Tobacco",
                           "m4_MA_SO3_Tobacco")])
```

4. Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

4.1 Smoking

```r
interval2n3 <- dose2 %>%
  group_by(GUMM85ID) %>%
  subset(count >= 3) %>%
  reframe(int_days = difftime(nth(vaccine_date, 3), nth(vaccine_date, 2), units = "days"),
          int_days = as.numeric(int_days)) %>%
  distinct() %>%
  ungroup() %>%
  reframe(mean_days = mean(int_days, na.rm = T))
paste("Average interval spacing between 2nd and 3rd dose of COVID-19 vaccine:",
      round(interval2n3, 2), "days")

# Crude model
m1_MA_SO4_Smoke <- with(des_final,
                        svyglm(event_7months23 ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_MA_SO4_Smoke))

# Adjusted for age and sex
m2_MA_SO4_Smoke <- with(des_final,
                        svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                                 pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_MA_SO4_Smoke))

# Adjusted for confounders
m3_MA_SO4_Smoke <- with(des_final,
                        svyglm(event_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_MA_SO4_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO4_Smoke <- with(des_final,
                        svyglm(event_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                 factor(case_C1),
                               family = quasipoisson()))
```

```r
# summary(MIcombine(m4_MA_SO4_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO4_Smoke)),
                             confint(MIcombine(m1_MA_SO4_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO4_Smoke)),
                             confint(MIcombine(m2_MA_SO4_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO4_Smoke)),
                             confint(MIcombine(m3_MA_SO4_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO4_Smoke)),
                             confint(MIcombine(m4_MA_SO4_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO4_Smoke[[1]]$data)
nrow(m2_MA_SO4_Smoke[[1]]$data)
nrow(m3_MA_SO4_Smoke[[1]]$data)
nrow(m4_MA_SO4_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO4_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_MA_SO4_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO4_Smoke ","m2_MA_SO4_Smoke", "m3_MA_SO4_Smoke",
                           "m4_MA_SO4_Smoke")])
```

4.2 Snus

```r
# Crude model
m1_MA_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_7months23 ~ factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_MA_SO4_Snus))

# Adjusted for age and sex
m2_MA_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                       svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont),
```

```r
                                    family = quasipoisson()))
# summary(MIcombine(m2_MA_SO4_Snus))

# Adjusted for confounders
m3_MA_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                    svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                            pspline(age_cont) + factor(educ_tertiles) +
                            factor(maritalstatus_bin) + factor(mother_tongue) +
                            factor(involvement_attend_j) + factor(fs_shp_koodi),
                        family = quasipoisson()))
# summary(MIcombine(m3_MA_SO4_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                    svyglm(event_7months23 ~ factor(snus_status) +
                            factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                            factor(maritalstatus_bin) + factor(mother_tongue) +
                            factor(involvement_attend_j) + factor(fs_shp_koodi) +
                            factor(case_C1),
                        family = quasipoisson()))
# summary(MIcombine(m4_MA_SO4_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO4_Snus)),
                        confint(MIcombine(m1_MA_SO4_Snus)))), 2)[2:3,],
        caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO4_Snus)),
                        confint(MIcombine(m2_MA_SO4_Snus)))), 2)[2:3,],
        caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO4_Snus)),
                        confint(MIcombine(m3_MA_SO4_Snus)))), 2)[2:3,],
        caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO4_Snus)),
                        confint(MIcombine(m4_MA_SO4_Snus)))), 2)[2:3,],
        caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO4_Snus[[1]]$data)
nrow(m2_MA_SO4_Snus[[1]]$data)
nrow(m3_MA_SO4_Snus[[1]]$data)
nrow(m4_MA_SO4_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO4_Snus))[2:3], 4),
```

```
              M4 = round(coef(MIcombine(m4_MA_SO4_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO4_Snus ","m2_MA_SO4_Snus", "m3_MA_SO4_Snus",
                           "m4_MA_SO4_Snus")])
```

4.3 Tobacco use

```
# Crude model
m1_MA_SO4_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_7months23 ~ factor(tobacco_use),
                                 family = quasipoisson()))
# summary(MIcombine(m1_MA_SO4_Tobacco))

# Adjusted for age and sex
m2_MA_SO4_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_7months23 ~ factor(tobacco_use) + factor(sex) +
                                   pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_MA_SO4_Tobacco))

# Adjusted for confounders
m3_MA_SO4_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_7months23 ~ factor(tobacco_use) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_MA_SO4_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_MA_SO4_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                          svyglm(event_7months23 ~ factor(tobacco_use) +
                                   factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi) +
                                   factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_MA_SO4_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_MA_SO4_Tobacco)),
                             confint(MIcombine(m1_MA_SO4_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_MA_SO4_Tobacco)),
                             confint(MIcombine(m2_MA_SO4_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
```

```r
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_MA_SO4_Tobacco)),
                             confint(MIcombine(m3_MA_SO4_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_MA_SO4_Tobacco)),
                             confint(MIcombine(m4_MA_SO4_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_MA_SO4_Tobacco[[1]]$data)
nrow(m2_MA_SO4_Tobacco[[1]]$data)
nrow(m3_MA_SO4_Tobacco[[1]]$data)
nrow(m4_MA_SO4_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_MA_SO4_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_MA_SO4_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_MA_SO4_Tobacco ","m2_MA_SO4_Tobacco", "m3_MA_SO4_Tobacco",
                           "m4_MA_SO4_Tobacco")])
```

5. Simulation 1: All participants who got COVID at C1 get vaccinated

5.1 Smoking

```r
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM1_1dose_Smoke <- with(des_final,
                            svyglm(event_sim1_1dose ~ factor(smoking_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM1_1dose_Smoke))

# Adjusted for age and sex
m2_SIM1_1dose_Smoke <- with(des_final,
                            svyglm(event_sim1_1dose ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM1_1dose_Smoke))

# Adjusted for confounders
m3_SIM1_1dose_Smoke <- with(des_final,
                            svyglm(event_sim1_1dose ~ factor(smoking_status) +
```

```r
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SIM1_1dose_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_1dose_Smoke <- with(des_final,
                          svyglm(event_sim1_1dose ~ factor(smoking_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_SIM1_1dose_Smoke))


# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_1dose_Smoke)),
                        confint(MIcombine(m1_SIM1_1dose_Smoke)))), 2)[2:4,],
          caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_1dose_Smoke)),
                        confint(MIcombine(m2_SIM1_1dose_Smoke)))), 2)[2:4,],
          caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_1dose_Smoke)),
                        confint(MIcombine(m3_SIM1_1dose_Smoke)))), 2)[2:4,],
          caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_1dose_Smoke)),
                        confint(MIcombine(m4_SIM1_1dose_Smoke)))), 2)[2:4,],
          caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_1dose_Smoke[[1]]$data)
nrow(m2_SIM1_1dose_Smoke[[1]]$data)
nrow(m3_SIM1_1dose_Smoke[[1]]$data)
nrow(m4_SIM1_1dose_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_1dose_Smoke))[2:4], 4),
```

```
            M4 = round(coef(MIcombine(m4_SIM1_1dose_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_1dose_Smoke", "m2_SIM1_1dose_Smoke", "m3_SIM1_1dose_Smoke",
                           "m4_SIM1_1dose_Smoke")])



##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM1_2doses_Smoke <- with(des_final,
                             svyglm(event_sim1_2doses ~ factor(smoking_status),
                                    family = quasipoisson()))
# summary(MIcombine(m1_SIM1_2doses_Smoke))

# Adjusted for age and sex
m2_SIM1_2doses_Smoke <- with(des_final,
                             svyglm(event_sim1_2doses ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont),
                                    family = quasipoisson()))
# summary(MIcombine(m2_SIM1_2doses_Smoke))

# Adjusted for confounders
m3_SIM1_2doses_Smoke <- with(des_final,
                             svyglm(event_sim1_2doses ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                    family = quasipoisson()))
# summary(MIcombine(m3_SIM1_2doses_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_2doses_Smoke <- with(des_final,
                             svyglm(event_sim1_2doses ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi) + factor(case_C1),
                                    family = quasipoisson()))
# summary(MIcombine(m4_SIM1_2doses_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_2doses_Smoke)),
                       confint(MIcombine(m1_SIM1_2doses_Smoke)))), 2)[2:4,],
           caption = "M1: Crude model") %>%
```

```
    kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_2doses_Smoke)),
                             confint(MIcombine(m2_SIM1_2doses_Smoke))))), 2)[2:4,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_2doses_Smoke)),
                             confint(MIcombine(m3_SIM1_2doses_Smoke))))), 2)[2:4,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_2doses_Smoke)),
                             confint(MIcombine(m4_SIM1_2doses_Smoke))))), 2)[2:4,],
            caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_2doses_Smoke[[1]]$data)
nrow(m2_SIM1_2doses_Smoke[[1]]$data)
nrow(m3_SIM1_2doses_Smoke[[1]]$data)
nrow(m4_SIM1_2doses_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_2doses_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM1_2doses_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_2doses_Smoke", "m2_SIM1_2doses_Smoke", "m3_SIM1_2doses_Smoke",
                           "m4_SIM1_2doses_Smoke")])


##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM1_3doses_Smoke <- with(des_final,
                             svyglm(event_sim1_3doses ~ factor(smoking_status),
                                    family = quasipoisson()))
# summary(MIcombine(m1_SIM1_3doses_Smoke))

# Adjusted for age and sex
m2_SIM1_3doses_Smoke <- with(des_final,
                             svyglm(event_sim1_3doses ~ factor(smoking_status) +
                                        factor(sex) + pspline(age_cont),
                                    family = quasipoisson()))
# summary(MIcombine(m2_SIM1_3doses_Smoke))

# Adjusted for confounders
m3_SIM1_3doses_Smoke <- with(des_final,
                             svyglm(event_sim1_3doses ~ factor(smoking_status) +
```

```r
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SIM1_3doses_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_3doses_Smoke <- with(des_final,
                             svyglm(event_sim1_3doses ~ factor(smoking_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi) + factor(case_C1),
                                  family = quasipoisson()))
# summary(MIcombine(m4_SIM1_3doses_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_3doses_Smoke)),
                             confint(MIcombine(m1_SIM1_3doses_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_3doses_Smoke)),
                             confint(MIcombine(m2_SIM1_3doses_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_3doses_Smoke)),
                             confint(MIcombine(m3_SIM1_3doses_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_3doses_Smoke)),
                             confint(MIcombine(m4_SIM1_3doses_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_3doses_Smoke[[1]]$data)
nrow(m2_SIM1_3doses_Smoke[[1]]$data)
nrow(m3_SIM1_3doses_Smoke[[1]]$data)
nrow(m4_SIM1_3doses_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_3doses_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM1_3doses_Smoke))[2:4], 4)) %>%
```

```r
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_3doses_Smoke", "m2_SIM1_3doses_Smoke", "m3_SIM1_3doses_Smoke",
                           "m4_SIM1_3doses_Smoke")])


##### Spacing between 1st and 2nd dose #####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM1_I12_Smoke <- with(des_final,
                          svyglm(event_sim1_20weeks12 ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I12_Smoke))

# Adjusted for age and sex
m2_SIM1_I12_Smoke <- with(des_final,
                          svyglm(event_sim1_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I12_Smoke))

# Adjusted for confounders
m3_SIM1_I12_Smoke <- with(des_final,
                          svyglm(event_sim1_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
                                   factor(maritalstatus_bin) +
                                   factor(mother_tongue) +
                                   factor(involvement_attend_j) +
                                   factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I12_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_I12_Smoke <- with(des_final,
                          svyglm(event_sim1_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
                                   factor(maritalstatus_bin) +
                                   factor(mother_tongue) +
                                   factor(involvement_attend_j) +
                                   factor(fs_shp_koodi) + factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I12_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I12_Smoke)),
                       confint(MIcombine(m1_SIM1_I12_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I12_Smoke)),
                             confint(MIcombine(m2_SIM1_I12_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I12_Smoke)),
                             confint(MIcombine(m3_SIM1_I12_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I12_Smoke)),
                             confint(MIcombine(m4_SIM1_I12_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I12_Smoke[[1]]$data)
nrow(m2_SIM1_I12_Smoke[[1]]$data)
nrow(m3_SIM1_I12_Smoke[[1]]$data)
nrow(m4_SIM1_I12_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I12_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I12_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_I12_Smoke", "m2_SIM1_I12_Smoke", "m3_SIM1_I12_Smoke",
                           "m4_SIM1_I12_Smoke")])


##### Spacing between 2nd and 3rd dose #####
print("##### Spacing between 2nd and 3rd dose #####")
# Crude model
m1_SIM1_I23_Smoke <- with(des_final,
                          svyglm(event_sim1_7months23 ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I23_Smoke))

# Adjusted for age and sex
m2_SIM1_I23_Smoke <- with(des_final,
                          svyglm(event_sim1_7months23 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I23_Smoke))

# Adjusted for confounders
m3_SIM1_I23_Smoke <- with(des_final,
                          svyglm(event_sim1_7months23 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
```

```r
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I23_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_I23_Smoke <- with(des_final,
                          svyglm(event_sim1_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont) +
                                 factor(educ_tertiles) +
                                 factor(maritalstatus_bin) +
                                 factor(mother_tongue) +
                                 factor(involvement_attend_j) +
                                 factor(fs_shp_koodi) + factor(case_C1),
                             family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I23_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I23_Smoke)),
                             confint(MIcombine(m1_SIM1_I23_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I23_Smoke)),
                             confint(MIcombine(m2_SIM1_I23_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I23_Smoke)),
                             confint(MIcombine(m3_SIM1_I23_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I23_Smoke)),
                             confint(MIcombine(m4_SIM1_I23_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I23_Smoke[[1]]$data)
nrow(m2_SIM1_I23_Smoke[[1]]$data)
nrow(m3_SIM1_I23_Smoke[[1]]$data)
nrow(m4_SIM1_I23_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I23_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I23_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
```

```r
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_I23_Smoke", "m2_SIM1_I23_Smoke", "m3_SIM1_I23_Smoke",
                           "m4_SIM1_I23_Smoke")])
```

5.2 Snus

```r
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM1_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim1_1dose ~ factor(snus_status),
                                  family = quasipoisson()))
# summary(MIcombine(m1_SIM1_1dose_Snus))

# Adjusted for age and sex
m2_SIM1_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim1_1dose ~ factor(snus_status) +
                                      factor(sex) + pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SIM1_1dose_Snus))

# Adjusted for confounders
m3_SIM1_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim1_1dose ~ factor(snus_status) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SIM1_1dose_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim1_1dose ~ factor(snus_status) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi) + factor(case_C1),
                                  family = quasipoisson()))
# summary(MIcombine(m4_SIM1_1dose_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_1dose_Snus)),
                           confint(MIcombine(m1_SIM1_1dose_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_1dose_Snus)),
                             confint(MIcombine(m2_SIM1_1dose_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_1dose_Snus)),
                             confint(MIcombine(m3_SIM1_1dose_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_1dose_Snus)),
                             confint(MIcombine(m4_SIM1_1dose_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_1dose_Snus[[1]]$data)
nrow(m2_SIM1_1dose_Snus[[1]]$data)
nrow(m3_SIM1_1dose_Snus[[1]]$data)
nrow(m4_SIM1_1dose_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_1dose_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM1_1dose_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_1dose_Snus", "m2_SIM1_1dose_Snus", "m3_SIM1_1dose_Snus",
                           "m4_SIM1_1dose_Snus")])


##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM1_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_2doses ~ factor(snus_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM1_2doses_Snus))

# Adjusted for age and sex
m2_SIM1_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_2doses ~ factor(snus_status) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM1_2doses_Snus))

# Adjusted for confounders
m3_SIM1_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_2doses ~ factor(snus_status) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
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                                  factor(maritalstatus_bin) +
                                  factor(mother_tongue) +
                                  factor(involvement_attend_j) +
                                  factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SIM1_2doses_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                        svyglm(event_sim1_2doses ~ factor(snus_status) +
                               factor(sex) + pspline(age_cont) +
                               factor(educ_tertiles) +
                               factor(maritalstatus_bin) +
                               factor(mother_tongue) +
                               factor(involvement_attend_j) +
                               factor(fs_shp_koodi) + factor(case_C1),
                            family = quasipoisson()))
# summary(MIcombine(m4_SIM1_2doses_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_2doses_Snus)),
                       confint(MIcombine(m1_SIM1_2doses_Snus)))), 2)[2:3,],
          caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_2doses_Snus)),
                       confint(MIcombine(m2_SIM1_2doses_Snus)))), 2)[2:3,],
          caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_2doses_Snus)),
                       confint(MIcombine(m3_SIM1_2doses_Snus)))), 2)[2:3,],
          caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_2doses_Snus)),
                       confint(MIcombine(m4_SIM1_2doses_Snus)))), 2)[2:3,],
          caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_2doses_Snus[[1]]$data)
nrow(m2_SIM1_2doses_Snus[[1]]$data)
nrow(m3_SIM1_2doses_Snus[[1]]$data)
nrow(m4_SIM1_2doses_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_2doses_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM1_2doses_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
```

```r
    kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_2doses_Snus", "m2_SIM1_2doses_Snus", "m3_SIM1_2doses_Snus",
                           "m4_SIM1_2doses_Snus")])



##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM1_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_3doses ~ factor(snus_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM1_3doses_Snus))

# Adjusted for age and sex
m2_SIM1_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_3doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM1_3doses_Snus))

# Adjusted for confounders
m3_SIM1_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_3doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM1_3doses_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_3doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM1_3doses_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_3doses_Snus)),
                             confint(MIcombine(m1_SIM1_3doses_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_3doses_Snus)),
```

```
                              confint(MIcombine(m2_SIM1_3doses_Snus)))), 2)[2:3,],
                 caption = "M2: Adjusted for age and sex") %>%
    kable_classic(full_width = F, position = "left")


knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_3doses_Snus)),
                             confint(MIcombine(m3_SIM1_3doses_Snus)))), 2)[2:3,],
                 caption = "M3: Adjusted for confounders") %>%
    kable_classic(full_width = F, position = "left")


knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_3doses_Snus)),
                             confint(MIcombine(m4_SIM1_3doses_Snus)))), 2)[2:3,],
                 caption = "M4: Adjusted for C1") %>%
    kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_3doses_Snus[[1]]$data)
nrow(m2_SIM1_3doses_Snus[[1]]$data)
nrow(m3_SIM1_3doses_Snus[[1]]$data)
nrow(m4_SIM1_3doses_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_3doses_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM1_3doses_Snus))[2:3], 4)) %>%
    mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
    kable(caption = "Percent attenuation: M3 - M4") %>%
    kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_3doses_Snus", "m2_SIM1_3doses_Snus", "m3_SIM1_3doses_Snus",
                           "m4_SIM1_3doses_Snus")])


##### Spacing between 1st and 2nd dose ####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM1_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_20weeks12 ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I12_Snus))

# Adjusted for age and sex
m2_SIM1_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_20weeks12 ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I12_Snus))

# Adjusted for confounders
m3_SIM1_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_20weeks12 ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
```

```
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I12_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1 (all)
m4_SIM1_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                      svyglm(event_sim1_20weeks12 ~ factor(snus_status) +
                             factor(sex) + pspline(age_cont) +
                             factor(educ_tertiles) +
                             factor(maritalstatus_bin) +
                             factor(mother_tongue) +
                             factor(involvement_attend_j) +
                             factor(fs_shp_koodi) + factor(case_C1),
                          family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I12_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I12_Snus)),
                          confint(MIcombine(m1_SIM1_I12_Snus)))), 2)[2:3,],
           caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I12_Snus)),
                          confint(MIcombine(m2_SIM1_I12_Snus)))), 2)[2:3,],
           caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I12_Snus)),
                          confint(MIcombine(m3_SIM1_I12_Snus)))), 2)[2:3,],
           caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I12_Snus)),
                          confint(MIcombine(m4_SIM1_I12_Snus)))), 2)[2:3,],
           caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I12_Snus[[1]]$data)
nrow(m2_SIM1_I12_Snus[[1]]$data)
nrow(m3_SIM1_I12_Snus[[1]]$data)
nrow(m4_SIM1_I12_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I12_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I12_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")
```

```r
rm(list = ls()[ls() %in% c("m1_SIM1_I12_Snus", "m2_SIM1_I12_Snus", "m3_SIM1_I12_Snus",
                           "m4_SIM1_I12_Snus")])


##### Spacing between 2nd and 3rd dose ####
print("##### Spacing between 2nd and 3rd dose #####")
# Crude model
m1_SIM1_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_7months23 ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I23_Snus))

# Adjusted for age and sex
m2_SIM1_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_7months23 ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I23_Snus))

# Adjusted for confounders
m3_SIM1_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_7months23 ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I23_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim1_7months23 ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi) + factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I23_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I23_Snus)),
                             confint(MIcombine(m1_SIM1_I23_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I23_Snus)),
                             confint(MIcombine(m2_SIM1_I23_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
```

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```
    kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I23_Snus)),
                             confint(MIcombine(m3_SIM1_I23_Snus))))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I23_Snus)),
                             confint(MIcombine(m4_SIM1_I23_Snus))))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I23_Snus[[1]]$data)
nrow(m2_SIM1_I23_Snus[[1]]$data)
nrow(m3_SIM1_I23_Snus[[1]]$data)
nrow(m4_SIM1_I23_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I23_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I23_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_I23_Snus", "m2_SIM1_I23_Snus", "m3_SIM1_I23_Snus",
                           "m4_SIM1_I23_Snus")])
```

5.3 Tobacco

```
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM1_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim1_1dose ~ factor(tobacco_use),
                                     family = quasipoisson()))
# summary(MIcombine(m1_SIM1_1dose_Tobacco))

# Adjusted for age and sex
m2_SIM1_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim1_1dose ~ factor(tobacco_use) +
                                        factor(sex) + pspline(age_cont),
                                     family = quasipoisson()))
# summary(MIcombine(m2_SIM1_1dose_Tobacco))

# Adjusted for confounders
m3_SIM1_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim1_1dose ~ factor(tobacco_use) +
                                        factor(sex) + pspline(age_cont) +
                                        factor(educ_tertiles) +
                                        factor(maritalstatus_bin) +
```

```r
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SIM1_1dose_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim1_1dose ~ factor(tobacco_use) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                  family = quasipoisson()))
# summary(MIcombine(m4_SIM1_1dose_Tobacco))


# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_1dose_Tobacco)),
                             confint(MIcombine(m1_SIM1_1dose_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_1dose_Tobacco)),
                             confint(MIcombine(m2_SIM1_1dose_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_1dose_Tobacco)),
                             confint(MIcombine(m3_SIM1_1dose_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_1dose_Tobacco)),
                             confint(MIcombine(m4_SIM1_1dose_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_1dose_Tobacco[[1]]$data)
nrow(m2_SIM1_1dose_Tobacco[[1]]$data)
nrow(m3_SIM1_1dose_Tobacco[[1]]$data)
nrow(m4_SIM1_1dose_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_1dose_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM1_1dose_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
```

```r
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_1dose_Tobacco", "m2_SIM1_1dose_Tobacco", "m3_SIM1_1dose_Tobacco",
                           "m4_SIM1_1dose_Tobacco")])



##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM1_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_2doses ~ factor(tobacco_use),
                                      family = quasipoisson()))
# summary(MIcombine(m1_SIM1_2doses_Tobacco))

# Adjusted for age and sex
m2_SIM1_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_2doses ~ factor(tobacco_use) +
                                             factor(sex) + pspline(age_cont),
                                      family = quasipoisson()))
# summary(MIcombine(m2_SIM1_2doses_Tobacco))

# Adjusted for confounders
m3_SIM1_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_2doses ~ factor(tobacco_use) +
                                             factor(sex) + pspline(age_cont) +
                                             factor(educ_tertiles) +
                                             factor(maritalstatus_bin) +
                                             factor(mother_tongue) +
                                             factor(involvement_attend_j) +
                                             factor(fs_shp_koodi),
                                      family = quasipoisson()))
# summary(MIcombine(m3_SIM1_2doses_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_2doses ~ factor(tobacco_use) +
                                             factor(sex) + pspline(age_cont) +
                                             factor(educ_tertiles) +
                                             factor(maritalstatus_bin) +
                                             factor(mother_tongue) +
                                             factor(involvement_attend_j) +
                                             factor(fs_shp_koodi) + factor(case_C1),
                                      family = quasipoisson()))
# summary(MIcombine(m4_SIM1_2doses_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_2doses_Tobacco)),
                            confint(MIcombine(m1_SIM1_2doses_Tobacco))))), 2)[2:5,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_2doses_Tobacco)),
```

```r
                      confint(MIcombine(m2_SIM1_2doses_Tobacco)))), 2)[2:5,],
              caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")


knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_2doses_Tobacco)),
                      confint(MIcombine(m3_SIM1_2doses_Tobacco)))), 2)[2:5,],
              caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")


knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_2doses_Tobacco)),
                      confint(MIcombine(m4_SIM1_2doses_Tobacco)))), 2)[2:5,],
              caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_2doses_Tobacco[[1]]$data)
nrow(m2_SIM1_2doses_Tobacco[[1]]$data)
nrow(m3_SIM1_2doses_Tobacco[[1]]$data)
nrow(m4_SIM1_2doses_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_2doses_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM1_2doses_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_2doses_Tobacco", "m2_SIM1_2doses_Tobacco", "m3_SIM1_2doses_Tobacco"
                           "m4_SIM1_2doses_Tobacco")])


##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM1_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_3doses ~ factor(tobacco_use),
                                      family = quasipoisson()))
# summary(MIcombine(m1_SIM1_3doses_Tobacco))

# Adjusted for age and sex
m2_SIM1_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_3doses ~ factor(tobacco_use) +
                                      factor(sex) + pspline(age_cont),
                                      family = quasipoisson()))
# summary(MIcombine(m2_SIM1_3doses_Tobacco))

# Adjusted for confounders
m3_SIM1_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_3doses ~ factor(tobacco_use) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
```

```
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SIM1_3doses_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim1_3doses ~ factor(tobacco_use) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM1_3doses_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_3doses_Tobacco)),
                             confint(MIcombine(m1_SIM1_3doses_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_3doses_Tobacco)),
                             confint(MIcombine(m2_SIM1_3doses_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_3doses_Tobacco)),
                             confint(MIcombine(m3_SIM1_3doses_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_3doses_Tobacco)),
                             confint(MIcombine(m4_SIM1_3doses_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_3doses_Tobacco[[1]]$data)
nrow(m2_SIM1_3doses_Tobacco[[1]]$data)
nrow(m3_SIM1_3doses_Tobacco[[1]]$data)
nrow(m4_SIM1_3doses_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_3doses_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM1_3doses_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")
```

```r
rm(list = ls()[ls() %in% c("m1_SIM1_3doses_Tobacco", "m2_SIM1_3doses_Tobacco", "m3_SIM1_3doses_Tobacco"
                           "m4_SIM1_3doses_Tobacco")])


##### Spacing between 1st and 2nd dose ####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM1_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_20weeks12 ~ factor(tobacco_use),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I12_Tobacco))

# Adjusted for age and sex
m2_SIM1_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_20weeks12 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I12_Tobacco))

# Adjusted for confounders
m3_SIM1_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_20weeks12 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I12_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1 (all)
m4_SIM1_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_20weeks12 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I12_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I12_Tobacco)),
                             confint(MIcombine(m1_SIM1_I12_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I12_Tobacco)),
                             confint(MIcombine(m2_SIM1_I12_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
```

```r
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I12_Tobacco)),
                             confint(MIcombine(m3_SIM1_I12_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I12_Tobacco)),
                             confint(MIcombine(m4_SIM1_I12_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I12_Tobacco[[1]]$data)
nrow(m2_SIM1_I12_Tobacco[[1]]$data)
nrow(m3_SIM1_I12_Tobacco[[1]]$data)
nrow(m4_SIM1_I12_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I12_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I12_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_I12_Tobacco", "m2_SIM1_I12_Tobacco", "m3_SIM1_I12_Tobacco",
                           "m4_SIM1_I12_Tobacco")])


##### Spacing between 2nd and 3rd dose ####
print("##### Spacing between 2nd and 3rd dose #####")
# Crude model
m1_SIM1_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_7months23 ~ factor(tobacco_use),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM1_I23_Tobacco))

# Adjusted for age and sex
m2_SIM1_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_7months23 ~ factor(tobacco_use) +
                                     factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM1_I23_Tobacco))

# Adjusted for confounders
m3_SIM1_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_7months23 ~ factor(tobacco_use) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
```

```
                                    factor(fs_shp_koodi),
                                    family = quasipoisson()))
# summary(MIcombine(m3_SIM1_I23_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM1_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim1_7months23 ~ factor(tobacco_use) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
                                   factor(maritalstatus_bin) +
                                   factor(mother_tongue) +
                                   factor(involvement_attend_j) +
                                   factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM1_I23_Tobacco))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM1_I23_Tobacco)),
                             confint(MIcombine(m1_SIM1_I23_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM1_I23_Tobacco)),
                             confint(MIcombine(m2_SIM1_I23_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM1_I23_Tobacco)),
                             confint(MIcombine(m3_SIM1_I23_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM1_I23_Tobacco)),
                             confint(MIcombine(m4_SIM1_I23_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM1_I23_Tobacco[[1]]$data)
nrow(m2_SIM1_I23_Tobacco[[1]]$data)
nrow(m3_SIM1_I23_Tobacco[[1]]$data)
nrow(m4_SIM1_I23_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM1_I23_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM1_I23_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM1_I23_Tobacco", "m2_SIM1_I23_Tobacco",
```

```
                    "m3_SIM1_I23_Tobacco", "m4_SIM1_I23_Tobacco")])
```

6. Simulation 2: All participants who got COVID at C1 not get vaccinated

6.1 Smoking

```r
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM2_1dose_Smoke <- with(des_final,
                            svyglm(event_sim1_1dose ~ factor(smoking_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM2_1dose_Smoke))

# Adjusted for age and sex
m2_SIM2_1dose_Smoke <- with(des_final,
                            svyglm(event_sim2_1dose ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM2_1dose_Smoke))

# Adjusted for confounders
m3_SIM2_1dose_Smoke <- with(des_final,
                            svyglm(event_sim2_1dose ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM2_1dose_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_1dose_Smoke <- with(des_final,
                            svyglm(event_sim2_1dose ~ factor(smoking_status) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_1dose_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_1dose_Smoke)),
                             confint(MIcombine(m1_SIM2_1dose_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_1dose_Smoke)),
                             confint(MIcombine(m2_SIM2_1dose_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_1dose_Smoke)),
                             confint(MIcombine(m3_SIM2_1dose_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_1dose_Smoke)),
                             confint(MIcombine(m4_SIM2_1dose_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_1dose_Smoke[[1]]$data)
nrow(m2_SIM2_1dose_Smoke[[1]]$data)
nrow(m3_SIM2_1dose_Smoke[[1]]$data)
nrow(m4_SIM2_1dose_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_1dose_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM2_1dose_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_1dose_Smoke", "m2_SIM2_1dose_Smoke", "m3_SIM2_1dose_Smoke",
                           "m4_SIM2_1dose_Smoke")])


##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM2_2doses_Smoke <- with(des_final,
                             svyglm(event_sim2_2doses ~ factor(smoking_status),
                                    family = quasipoisson()))
# summary(MIcombine(m1_SIM2_2doses_Smoke))

# Adjusted for age and sex
m2_SIM2_2doses_Smoke <- with(des_final,
                             svyglm(event_sim2_2doses ~ factor(smoking_status) +
                                      factor(sex) + pspline(age_cont),
                                    family = quasipoisson()))
# summary(MIcombine(m2_SIM2_2doses_Smoke))

# Adjusted for confounders
m3_SIM2_2doses_Smoke <- with(des_final,
                             svyglm(event_sim2_2doses ~ factor(smoking_status) +
                                      factor(sex) + pspline(age_cont) +
                                        factor(educ_tertiles) +
```

```
                                factor(maritalstatus_bin) +
                                factor(mother_tongue) +
                                factor(involvement_attend_j) +
                                factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_SIM2_2doses_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_2doses_Smoke <- with(des_final,
                              svyglm(event_sim2_2doses ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont) +
                                factor(educ_tertiles) +
                                factor(maritalstatus_bin) +
                                factor(mother_tongue) +
                                factor(involvement_attend_j) +
                                factor(fs_shp_koodi) + factor(case_C1),
                              family = quasipoisson()))
# summary(MIcombine(m4_SIM2_2doses_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_2doses_Smoke)),
                             confint(MIcombine(m1_SIM2_2doses_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_2doses_Smoke)),
                             confint(MIcombine(m2_SIM2_2doses_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_2doses_Smoke)),
                             confint(MIcombine(m3_SIM2_2doses_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_2doses_Smoke)),
                             confint(MIcombine(m4_SIM2_2doses_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_2doses_Smoke[[1]]$data)
nrow(m2_SIM2_2doses_Smoke[[1]]$data)
nrow(m3_SIM2_2doses_Smoke[[1]]$data)
nrow(m4_SIM2_2doses_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_2doses_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM2_2doses_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
```

```r
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_2doses_Smoke", "m2_SIM2_2doses_Smoke", "m3_SIM2_2doses_Smoke",
                           "m4_SIM2_2doses_Smoke")])



##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM2_3doses_Smoke <- with(des_final,
                             svyglm(event_sim2_3doses ~ factor(smoking_status),
                                    family = quasipoisson()))
# summary(MIcombine(m1_SIM2_3doses_Smoke))

# Adjusted for age and sex
m2_SIM2_3doses_Smoke <- with(des_final,
                             svyglm(event_sim2_3doses ~ factor(smoking_status) +
                                      factor(sex) + pspline(age_cont),
                                    family = quasipoisson()))
# summary(MIcombine(m2_SIM2_3doses_Smoke))

# Adjusted for confounders
m3_SIM2_3doses_Smoke <- with(des_final,
                             svyglm(event_sim2_3doses ~ factor(smoking_status) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi),
                                    family = quasipoisson()))
# summary(MIcombine(m3_SIM2_3doses_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_3doses_Smoke <- with(des_final,
                             svyglm(event_sim2_3doses ~ factor(smoking_status) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi) + factor(case_C1),
                                    family = quasipoisson()))
# summary(MIcombine(m4_SIM2_3doses_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_3doses_Smoke)),
                       confint(MIcombine(m1_SIM2_3doses_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_3doses_Smoke)),
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                              confint(MIcombine(m2_SIM2_3doses_Smoke)))), 2)[2:4,],
              caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_3doses_Smoke)),
                              confint(MIcombine(m3_SIM2_3doses_Smoke)))), 2)[2:4,],
              caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_3doses_Smoke)),
                              confint(MIcombine(m4_SIM2_3doses_Smoke)))), 2)[2:4,],
              caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_3doses_Smoke[[1]]$data)
nrow(m2_SIM2_3doses_Smoke[[1]]$data)
nrow(m3_SIM2_3doses_Smoke[[1]]$data)
nrow(m4_SIM2_3doses_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_3doses_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM2_3doses_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_3doses_Smoke", "m2_SIM2_3doses_Smoke", "m3_SIM2_3doses_Smoke",
                           "m4_SIM2_3doses_Smoke")])


##### Spacing between 1st and 2nd dose #####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM2_I12_Smoke <- with(des_final,
                          svyglm(event_sim2_20weeks12 ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I12_Smoke))

# Adjusted for age and sex
m2_SIM2_I12_Smoke <- with(des_final,
                          svyglm(event_sim2_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I12_Smoke))

# Adjusted for confounders
m3_SIM2_I12_Smoke <- with(des_final,
                          svyglm(event_sim2_20weeks12 ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
                                   factor(maritalstatus_bin) +
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                              factor(mother_tongue) +
                              factor(involvement_attend_j) +
                              factor(fs_shp_koodi),
                           family = quasipoisson()))
# summary(MIcombine(m3_SIM2_I12_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_I12_Smoke <- with(des_final,
                   svyglm(event_sim2_20weeks12 ~ factor(smoking_status) +
                          factor(sex) + pspline(age_cont) +
                          factor(educ_tertiles) +
                          factor(maritalstatus_bin) +
                          factor(mother_tongue) +
                          factor(involvement_attend_j) +
                          factor(fs_shp_koodi) + factor(case_C1),
                       family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I12_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I12_Smoke)),
                         confint(MIcombine(m1_SIM2_I12_Smoke)))), 2)[2:4,],
          caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I12_Smoke)),
                         confint(MIcombine(m2_SIM2_I12_Smoke)))), 2)[2:4,],
          caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I12_Smoke)),
                         confint(MIcombine(m3_SIM2_I12_Smoke)))), 2)[2:4,],
          caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I12_Smoke)),
                         confint(MIcombine(m4_SIM2_I12_Smoke)))), 2)[2:4,],
          caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I12_Smoke[[1]]$data)
nrow(m2_SIM2_I12_Smoke[[1]]$data)
nrow(m3_SIM2_I12_Smoke[[1]]$data)
nrow(m4_SIM2_I12_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I12_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I12_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")
```

```r
rm(list = ls()[ls() %in% c("m1_SIM2_I12_Smoke", "m2_SIM2_I12_Smoke", "m3_SIM2_I12_Smoke",
                           "m4_SIM2_I12_Smoke")])


##### Spacing between 2nd and 3rd dose #####
print("##### Spacing between 2nd and 3rd #####")
# Crude model
m1_SIM2_I23_Smoke <- with(des_final,
                          svyglm(event_sim2_7months23 ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I23_Smoke))

# Adjusted for age and sex
m2_SIM2_I23_Smoke <- with(des_final,
                          svyglm(event_sim2_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I23_Smoke))

# Adjusted for confounders
m3_SIM2_I23_Smoke <- with(des_final,
                          svyglm(event_sim2_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont) +
                                 factor(educ_tertiles) +
                                 factor(maritalstatus_bin) +
                                 factor(mother_tongue) +
                                 factor(involvement_attend_j) +
                                 factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SIM2_I23_Smoke))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_I23_Smoke <- with(des_final,
                          svyglm(event_sim2_7months23 ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont) +
                                 factor(educ_tertiles) +
                                 factor(maritalstatus_bin) +
                                 factor(mother_tongue) +
                                 factor(involvement_attend_j) +
                                 factor(fs_shp_koodi) + factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I23_Smoke))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I23_Smoke)),
                             confint(MIcombine(m1_SIM2_I23_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I23_Smoke)),
                             confint(MIcombine(m2_SIM2_I23_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
```

```r
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I23_Smoke)),
                             confint(MIcombine(m3_SIM2_I23_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I23_Smoke)),
                             confint(MIcombine(m4_SIM2_I23_Smoke)))), 2)[2:4,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I23_Smoke[[1]]$data)
nrow(m2_SIM2_I23_Smoke[[1]]$data)
nrow(m3_SIM2_I23_Smoke[[1]]$data)
nrow(m4_SIM2_I23_Smoke[[1]]$data)
# n = 42935

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I23_Smoke))[2:4], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I23_Smoke))[2:4], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4" ) %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_I23_Smoke", "m2_SIM2_I23_Smoke", "m3_SIM2_I23_Smoke",
                           "m4_SIM2_I23_Smoke")])
```

6.2 Snus

```r
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM2_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim2_1dose ~ factor(snus_status),
                                  family = quasipoisson()))
# summary(MIcombine(m1_SIM2_1dose_Snus))

# Adjusted for age and sex
m2_SIM2_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim2_1dose ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SIM2_1dose_Snus))

# Adjusted for confounders
m3_SIM2_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim2_1dose ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
```

```r
                                 factor(mother_tongue) +
                                 factor(involvement_attend_j) +
                                 factor(fs_shp_koodi),
                            family = quasipoisson()))
# summary(MIcombine(m3_SIM2_1dose_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_1dose_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                           svyglm(event_sim2_1dose ~ factor(snus_status) +
                                    factor(sex) + pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi) + factor(case_C1),
                                 family = quasipoisson()))
# summary(MIcombine(m4_SIM2_1dose_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_1dose_Snus)),
                             confint(MIcombine(m1_SIM2_1dose_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_1dose_Snus)),
                             confint(MIcombine(m2_SIM2_1dose_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_1dose_Snus)),
                             confint(MIcombine(m3_SIM2_1dose_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_1dose_Snus)),
                             confint(MIcombine(m4_SIM2_1dose_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_1dose_Snus[[1]]$data)
nrow(m2_SIM2_1dose_Snus[[1]]$data)
nrow(m3_SIM2_1dose_Snus[[1]]$data)
nrow(m4_SIM2_1dose_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_1dose_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM2_1dose_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")
```

```r
rm(list = ls()[ls() %in% c("m1_SIM2_1dose_Snus", "m2_SIM2_1dose_Snus", "m3_SIM2_1dose_Snus",
                           "m4_SIM2_1dose_Snus")])


##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM2_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_2doses ~ factor(snus_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM2_2doses_Snus))

# Adjusted for age and sex
m2_SIM2_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_2doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM2_2doses_Snus))

# Adjusted for confounders
m3_SIM2_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_2doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM2_2doses_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_2doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_2doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_2doses_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_2doses_Snus)),
                             confint(MIcombine(m1_SIM2_2doses_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_2doses_Snus)),
                             confint(MIcombine(m2_SIM2_2doses_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
```

```r
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_2doses_Snus)),
                             confint(MIcombine(m3_SIM2_2doses_Snus))))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_2doses_Snus)),
                             confint(MIcombine(m4_SIM2_2doses_Snus))))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_2doses_Snus[[1]]$data)
nrow(m2_SIM2_2doses_Snus[[1]]$data)
nrow(m3_SIM2_2doses_Snus[[1]]$data)
nrow(m4_SIM2_2doses_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_2doses_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM2_2doses_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_2doses_Snus", "m2_SIM2_2doses_Snus", "m3_SIM2_2doses_Snus",
                           "m4_SIM2_2doses_Snus")])


##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM2_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_3doses ~ factor(snus_status),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM2_3doses_Snus))

# Adjusted for age and sex
m2_SIM2_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_3doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM2_3doses_Snus))

# Adjusted for confounders
m3_SIM2_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_3doses ~ factor(snus_status) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
```

```r
                                     factor(fs_shp_koodi),
                                     family = quasipoisson()))
# summary(MIcombine(m3_SIM2_3doses_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_3doses_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_3doses ~ factor(snus_status) +
                                   factor(sex) + pspline(age_cont) +
                                   factor(educ_tertiles) +
                                   factor(maritalstatus_bin) +
                                   factor(mother_tongue) +
                                   factor(involvement_attend_j) +
                                   factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_3doses_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_3doses_Snus)),
                             confint(MIcombine(m1_SIM2_3doses_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_3doses_Snus)),
                             confint(MIcombine(m2_SIM2_3doses_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_3doses_Snus)),
                             confint(MIcombine(m3_SIM2_3doses_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_3doses_Snus)),
                             confint(MIcombine(m4_SIM2_3doses_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_3doses_Snus[[1]]$data)
nrow(m2_SIM2_3doses_Snus[[1]]$data)
nrow(m3_SIM2_3doses_Snus[[1]]$data)
nrow(m4_SIM2_3doses_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_3doses_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM2_3doses_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_3doses_Snus", "m2_SIM2_3doses_Snus", "m3_SIM2_3doses_Snus",
```

```
                              "m4_SIM2_3doses_Snus")])


##### Spacing between 1st and 2nd dose ####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM2_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_20weeks12 ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I12_Snus))

# Adjusted for age and sex
m2_SIM2_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_20weeks12 ~ factor(snus_status) +
                                factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I12_Snus))

# Adjusted for confounders
m3_SIM2_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_20weeks12 ~ factor(snus_status) +
                                factor(sex) + pspline(age_cont) +
                                factor(educ_tertiles) +
                                factor(maritalstatus_bin) +
                                factor(mother_tongue) +
                                factor(involvement_attend_j) +
                                factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SIM2_I12_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1 (all)
m4_SIM2_I12_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_20weeks12 ~ factor(snus_status) +
                                factor(sex) + pspline(age_cont) +
                                factor(educ_tertiles) +
                                factor(maritalstatus_bin) +
                                factor(mother_tongue) +
                                factor(involvement_attend_j) +
                                factor(fs_shp_koodi) + factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I12_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I12_Snus)),
                        confint(MIcombine(m1_SIM2_I12_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I12_Snus)),
                        confint(MIcombine(m2_SIM2_I12_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I12_Snus)),
                             confint(MIcombine(m3_SIM2_I12_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I12_Snus)),
                             confint(MIcombine(m4_SIM2_I12_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I12_Snus[[1]]$data)
nrow(m2_SIM2_I12_Snus[[1]]$data)
nrow(m3_SIM2_I12_Snus[[1]]$data)
nrow(m4_SIM2_I12_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I12_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I12_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_I12_Snus", "m2_SIM2_I12_Snus", "m3_SIM2_I12_Snus",
                           "m4_SIM2_I12_Snus")])


##### Spacing between 2nd and 3rd dose ####
print("##### Spacing between 2nd and 3rd dose #####")
# Crude model
m1_SIM2_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_7months23 ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I23_Snus))

# Adjusted for age and sex
m2_SIM2_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_7months23 ~ factor(snus_status) +
                                  factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I23_Snus))

# Adjusted for confounders
m3_SIM2_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_7months23 ~ factor(snus_status) +
                                  factor(sex) + pspline(age_cont) +
                                  factor(educ_tertiles) +
                                  factor(maritalstatus_bin) +
                                  factor(mother_tongue) +
                                  factor(involvement_attend_j) +
                                  factor(fs_shp_koodi),
                                family = quasipoisson()))
```

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```r
# summary(MIcombine(m3_SIM2_I23_Snus))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_I23_Snus <- with(subset(des_final, between(age_cont, 20, 74)),
                         svyglm(event_sim2_7months23 ~ factor(snus_status) +
                                  factor(sex) + pspline(age_cont) +
                                  factor(educ_tertiles) +
                                  factor(maritalstatus_bin) +
                                  factor(mother_tongue) +
                                  factor(involvement_attend_j) +
                                  factor(fs_shp_koodi) + factor(case_C1),
                                family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I23_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I23_Snus)),
                             confint(MIcombine(m1_SIM2_I23_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I23_Snus)),
                             confint(MIcombine(m2_SIM2_I23_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I23_Snus)),
                             confint(MIcombine(m3_SIM2_I23_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I23_Snus)),
                             confint(MIcombine(m4_SIM2_I23_Snus)))), 2)[2:3,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I23_Snus[[1]]$data)
nrow(m2_SIM2_I23_Snus[[1]]$data)
nrow(m3_SIM2_I23_Snus[[1]]$data)
nrow(m4_SIM2_I23_Snus[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I23_Snus))[2:3], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I23_Snus))[2:3], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_I23_Snus", "m2_SIM2_I23_Snus", "m3_SIM2_I23_Snus",
                           "m4_SIM2_I23_Snus")])
```

6.3 Tobacco

```r
##### One dose #####
print("##### One dose #####")
# Crude model
m1_SIM2_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim2_1dose ~ factor(tobacco_use),
                                     family = quasipoisson()))
# summary(MIcombine(m1_SIM2_1dose_Tobacco))

# Adjusted for age and sex
m2_SIM2_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim2_1dose ~ factor(tobacco_use) +
                                         factor(sex) + pspline(age_cont),
                                     family = quasipoisson()))
# summary(MIcombine(m2_SIM2_1dose_Tobacco))

# Adjusted for confounders
m3_SIM2_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim2_1dose ~ factor(tobacco_use) +
                                         factor(sex) + pspline(age_cont) +
                                         factor(educ_tertiles) +
                                         factor(maritalstatus_bin) +
                                         factor(mother_tongue) +
                                         factor(involvement_attend_j) +
                                         factor(fs_shp_koodi),
                                     family = quasipoisson()))
# summary(MIcombine(m3_SIM2_1dose_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_1dose_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                              svyglm(event_sim2_1dose ~ factor(tobacco_use) +
                                         factor(sex) + pspline(age_cont) +
                                         factor(educ_tertiles) +
                                         factor(maritalstatus_bin) +
                                         factor(mother_tongue) +
                                         factor(involvement_attend_j) +
                                         factor(fs_shp_koodi) + factor(case_C1),
                                     family = quasipoisson()))
# summary(MIcombine(m4_SIM2_1dose_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_1dose_Tobacco)),
                       confint(MIcombine(m1_SIM2_1dose_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_1dose_Tobacco)),
                       confint(MIcombine(m2_SIM2_1dose_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_1dose_Tobacco)),
                            confint(MIcombine(m3_SIM2_1dose_Tobacco)))), 2)[2:5,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_1dose_Tobacco)),
                            confint(MIcombine(m4_SIM2_1dose_Tobacco)))), 2)[2:5,],
            caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_1dose_Tobacco[[1]]$data)
nrow(m2_SIM2_1dose_Tobacco[[1]]$data)
nrow(m3_SIM2_1dose_Tobacco[[1]]$data)
nrow(m4_SIM2_1dose_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_1dose_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM2_1dose_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_1dose_Tobacco", "m2_SIM2_1dose_Tobacco", "m3_SIM2_1dose_Tobacco",
                           "m4_SIM2_1dose_Tobacco")])


##### Two doses #####
print("##### Two doses #####")
# Crude model
m1_SIM2_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_2doses ~ factor(tobacco_use),
                                      family = quasipoisson()))
# summary(MIcombine(m1_SIM2_2doses_Tobacco))

# Adjusted for age and sex
m2_SIM2_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_2doses ~ factor(tobacco_use) +
                                        factor(sex) + pspline(age_cont),
                                      family = quasipoisson()))
# summary(MIcombine(m2_SIM2_2doses_Tobacco))

# Adjusted for confounders
m3_SIM2_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_2doses ~ factor(tobacco_use) +
                                        factor(sex) + pspline(age_cont) +
                                        factor(educ_tertiles) +
                                        factor(maritalstatus_bin) +
                                        factor(mother_tongue) +
                                        factor(involvement_attend_j) +
                                        factor(fs_shp_koodi),
                                      family = quasipoisson()))
```

```r
# summary(MIcombine(m3_SIM2_2doses_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_2doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_2doses ~ factor(tobacco_use) +
                                      factor(sex) + pspline(age_cont) +
                                      factor(educ_tertiles) +
                                      factor(maritalstatus_bin) +
                                      factor(mother_tongue) +
                                      factor(involvement_attend_j) +
                                      factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_2doses_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_2doses_Tobacco)),
                             confint(MIcombine(m1_SIM2_2doses_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_2doses_Tobacco)),
                             confint(MIcombine(m2_SIM2_2doses_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_2doses_Tobacco)),
                             confint(MIcombine(m3_SIM2_2doses_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_2doses_Tobacco)),
                             confint(MIcombine(m4_SIM2_2doses_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_2doses_Tobacco[[1]]$data)
nrow(m2_SIM2_2doses_Tobacco[[1]]$data)
nrow(m3_SIM2_2doses_Tobacco[[1]]$data)
nrow(m4_SIM2_2doses_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_2doses_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM2_2doses_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_2doses_Tobacco", "m2_SIM2_2doses_Tobacco", "m3_SIM2_2doses_Tobacco"
                           "m4_SIM2_2doses_Tobacco")])
```

```r
##### Three doses #####
print("##### Three doses #####")
# Crude model
m1_SIM2_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_3doses ~ factor(tobacco_use),
                                      family = quasipoisson()))
# summary(MIcombine(m1_SIM2_3doses_Tobacco))

# Adjusted for age and sex
m2_SIM2_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_3doses ~ factor(tobacco_use) +
                                          factor(sex) + pspline(age_cont),
                                      family = quasipoisson()))
# summary(MIcombine(m2_SIM2_3doses_Tobacco))

# Adjusted for confounders
m3_SIM2_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_3doses ~ factor(tobacco_use) +
                                          factor(sex) + pspline(age_cont) +
                                          factor(educ_tertiles) +
                                          factor(maritalstatus_bin) +
                                          factor(mother_tongue) +
                                          factor(involvement_attend_j) +
                                          factor(fs_shp_koodi),
                                      family = quasipoisson()))
# summary(MIcombine(m3_SIM2_3doses_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_3doses_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                               svyglm(event_sim2_3doses ~ factor(tobacco_use) +
                                          factor(sex) + pspline(age_cont) +
                                          factor(educ_tertiles) +
                                          factor(maritalstatus_bin) +
                                          factor(mother_tongue) +
                                          factor(involvement_attend_j) +
                                          factor(fs_shp_koodi) + factor(case_C1),
                                      family = quasipoisson()))
# summary(MIcombine(m4_SIM2_3doses_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_3doses_Tobacco)),
                             confint(MIcombine(m1_SIM2_3doses_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_3doses_Tobacco)),
                             confint(MIcombine(m2_SIM2_3doses_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_3doses_Tobacco)),
                             confint(MIcombine(m3_SIM2_3doses_Tobacco)))), 2)[2:5,],
```

```
                 caption = "M3: Adjusted for confounders") %>%
    kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_3doses_Tobacco)),
                             confint(MIcombine(m4_SIM2_3doses_Tobacco))))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
    kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_3doses_Tobacco[[1]]$data)
nrow(m2_SIM2_3doses_Tobacco[[1]]$data)
nrow(m3_SIM2_3doses_Tobacco[[1]]$data)
nrow(m4_SIM2_3doses_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_3doses_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM2_3doses_Tobacco))[2:5], 4)) %>%
    mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
    kable(caption = "Percent attenuation: M3 - M4") %>%
    kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_3doses_Tobacco", "m2_SIM2_3doses_Tobacco", "m3_SIM2_3doses_Tobacco"
                           "m4_SIM2_3doses_Tobacco")])


##### Spacing between 1st and 2nd dose ####
print("##### Spacing between 1st and 2nd dose #####")
# Crude model
m1_SIM2_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_20weeks12 ~ factor(tobacco_use),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I12_Tobacco))

# Adjusted for age and sex
m2_SIM2_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_20weeks12 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I12_Tobacco))

# Adjusted for confounders
m3_SIM2_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_20weeks12 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM2_I12_Tobacco))
```

```r
# Adjusted for COVID-19 cases
# Adjusted for C1 (all)
m4_SIM2_I12_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_20weeks12 ~ factor(tobacco_use) +
                                     factor(sex) + pspline(age_cont) +
                                     factor(educ_tertiles) +
                                     factor(maritalstatus_bin) +
                                     factor(mother_tongue) +
                                     factor(involvement_attend_j) +
                                     factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I12_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I12_Tobacco)),
                             confint(MIcombine(m1_SIM2_I12_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I12_Tobacco)),
                             confint(MIcombine(m2_SIM2_I12_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I12_Tobacco)),
                             confint(MIcombine(m3_SIM2_I12_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I12_Tobacco)),
                             confint(MIcombine(m4_SIM2_I12_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I12_Tobacco[[1]]$data)
nrow(m2_SIM2_I12_Tobacco[[1]]$data)
nrow(m3_SIM2_I12_Tobacco[[1]]$data)
nrow(m4_SIM2_I12_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I12_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I12_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")

rm(list = ls()[ls() %in% c("m1_SIM2_I12_Tobacco", "m2_SIM2_I12_Tobacco", "m3_SIM2_I12_Tobacco",
                           "m4_SIM2_I12_Tobacco")])


##### Spacing between 2nd and 3rd dose ####
```

```r
print("##### Spacing between 2nd and 3rd dose #####")
# Crude model
m1_SIM2_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_7months23 ~ factor(tobacco_use),
                                   family = quasipoisson()))
# summary(MIcombine(m1_SIM2_I23_Tobacco))

# Adjusted for age and sex
m2_SIM2_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_7months23 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont),
                                   family = quasipoisson()))
# summary(MIcombine(m2_SIM2_I23_Tobacco))

# Adjusted for confounders
m3_SIM2_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_7months23 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi),
                                   family = quasipoisson()))
# summary(MIcombine(m3_SIM2_I23_Tobacco))

# Adjusted for COVID-19 cases
# Adjusted for C1
m4_SIM2_I23_Tobacco <- with(subset(des_final, between(age_cont, 20, 74)),
                            svyglm(event_sim2_7months23 ~ factor(tobacco_use) +
                                       factor(sex) + pspline(age_cont) +
                                       factor(educ_tertiles) +
                                       factor(maritalstatus_bin) +
                                       factor(mother_tongue) +
                                       factor(involvement_attend_j) +
                                       factor(fs_shp_koodi) + factor(case_C1),
                                   family = quasipoisson()))
# summary(MIcombine(m4_SIM2_I23_Tobacco))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SIM2_I23_Tobacco)),
                             confint(MIcombine(m1_SIM2_I23_Tobacco)))), 2)[2:5,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SIM2_I23_Tobacco)),
                             confint(MIcombine(m2_SIM2_I23_Tobacco)))), 2)[2:5,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SIM2_I23_Tobacco)),
                             confint(MIcombine(m3_SIM2_I23_Tobacco)))), 2)[2:5,],
             caption = "M3: Adjusted for confounders") %>%
```

```r
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m4_SIM2_I23_Tobacco)),
                             confint(MIcombine(m4_SIM2_I23_Tobacco)))), 2)[2:5,],
             caption = "M4: Adjusted for C1") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SIM2_I23_Tobacco[[1]]$data)
nrow(m2_SIM2_I23_Tobacco[[1]]$data)
nrow(m3_SIM2_I23_Tobacco[[1]]$data)
nrow(m4_SIM2_I23_Tobacco[[1]]$data)
# n = 29192

# Percent attenuation
data.frame(M3 = round(coef(MIcombine(m3_SIM2_I23_Tobacco))[2:5], 4),
           M4 = round(coef(MIcombine(m4_SIM2_I23_Tobacco))[2:5], 4)) %>%
  mutate("% Att" = round(100 * (M3 - M4)/M3, 4)) %>%
  kable(caption = "Percent attenuation: M3 - M4") %>%
  kable_classic(full_width = F, position = "left")
```

End of Part II

Part III

Loading packages and data

Packages

```r
# Loading packages
library(readxl)
library(haven)
library(styler)
library(tidyverse)
library(knitr)
library(kableExtra)
library(tidyr)
library(janitor)
library(gtools)
library(ggridges)
library(ggfortify)
library(tableone)
library(pollster)
library(naniar)
library(survey)
library(survival)
library(biostat3)
library(Epi)
library(lubridate)
```

```
library(mice)
library(mitools)
library(mitml)
library(Hmisc)
library(finalfit)
```

Load data and remove unused objects

```
load("TobriskCov_Data_02102023.RData")
# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Stratified analyses and testing for interactions

Stratified by sex

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_men_StrA_PO_Smoke <- with(subset(des_final, sex == 1),
                             svyglm(event_2doses ~ factor(smoking_status),
                                    family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_PO_Smoke))

m1_women_StrA_PO_Smoke <- with(subset(des_final, sex == 2),
                               svyglm(event_2doses ~ factor(smoking_status),
                                      family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_PO_Smoke))

# Adjusted for age
m2_men_StrA_PO_Smoke <- with(subset(des_final, sex == 1),
                             svyglm(event_2doses ~ factor(smoking_status) +
                                        pspline(age_cont),
                                    family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_PO_Smoke))

m2_women_StrA_PO_Smoke <- with(subset(des_final, sex == 2),
                               svyglm(event_2doses ~ factor(smoking_status) +
                                          pspline(age_cont),
                                      family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_PO_Smoke))

# Adjusted for confounders
m3_men_StrA_PO_Smoke <- with(subset(des_final, sex == 1),
                             svyglm(event_2doses ~ factor(smoking_status) +
```

```
                                        pspline(age_cont) +
                                        factor(educ_tertiles) +
                                        factor(maritalstatus_bin) +
                                        factor(mother_tongue) +
                                        factor(involvement_attend_j) +
                                        factor(fs_shp_koodi),
                                    family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_PO_Smoke))

m3_women_StrA_PO_Smoke <- with(subset(des_final, sex == 2),
                            svyglm(event_2doses ~ factor(smoking_status) +
                                    pspline(age_cont) +
                                    factor(educ_tertiles) +
                                    factor(maritalstatus_bin) +
                                    factor(mother_tongue) +
                                    factor(involvement_attend_j) +
                                    factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_PO_Smoke))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_PO_Smoke)),
                    confint(MIcombine(m1_men_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_PO_Smoke)),
                    confint(MIcombine(m1_women_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_PO_Smoke)),
                    confint(MIcombine(m2_men_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_PO_Smoke)),
                    confint(MIcombine(m2_women_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_PO_Smoke)),
                    confint(MIcombine(m3_men_StrA_PO_Smoke)))), 2)[2:4, ],
```

```
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_PO_Smoke)),
                    confint(MIcombine(m3_women_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) +
           factor(sex) + pspline(age_cont),
         family = quasipoisson()))
m2_mm_Sex_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) * factor(sex) + pspline(age_cont),
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_PO_Smoke, m2_am_Sex_StrA_PO_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) * factor(sex) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_PO_Smoke, m3_am_Sex_StrA_PO_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_men_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_PO_Snus))
m1_women_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_PO_Snus))
```

```r
# Adjusted for age
m2_men_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_PO_Snus))
m2_women_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_PO_Snus))

# Adjusted for confounders
m3_men_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi),
          family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_PO_Snus))

m3_women_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi),
          family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_PO_Snus))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_PO_Snus)),
                    confint(MIcombine(m1_men_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_PO_Snus)),
                    confint(MIcombine(m1_women_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_PO_Snus)),
                    confint(MIcombine(m2_men_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
```

```r
    round(exp(cbind(coef(MIcombine(m2_women_StrA_PO_Snus)),
                    confint(MIcombine(m2_women_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_PO_Snus)),
                    confint(MIcombine(m3_men_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_PO_Snus)),
                    confint(MIcombine(m3_women_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
m2_mm_Sex_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_PO_Snus, m2_am_Sex_StrA_PO_Snus, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),

  svyglm(event_2doses ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_PO_Snus, m3_am_Sex_StrA_PO_Snus, method = "D2")
```

Secondary outcome (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_men_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO1_Smoke))

m1_women_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO1_Smoke))

# Adjusted for age
m2_men_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO1_Smoke)

m2_women_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO1_Smoke))

# Adjusted for confounders
m3_men_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO1_Smoke))

m3_women_StrA_SO1_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO1_Smoke))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO1_Smoke)),
```

```r
                          confint(MIcombine(m1_men_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO1_Smoke)),
                    confint(MIcombine(m1_women_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_men_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_women_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_men_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_women_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
m2_mm_Sex_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO1_Smoke, m2_am_Sex_StrA_SO1_Smoke, method = "D2")
```

```r
# Adjusted for confounders
m3_am_Sex_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO1_Smoke, m3_am_Sex_StrA_SO1_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_men_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO1_Snus))

m1_women_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO1_Snus))

# Adjusted for age
m2_men_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO1_Snus))

m2_women_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO1_Snus))

# Adjusted for confounders
m3_men_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
```

```r
            family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO1_Snus))

m3_women_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO1_Snus))

# Obtain main estimates
kables(list(knitr::kable(
  round(exp(cbind(coef(MIcombine(m1_men_StrA_SO1_Snus)),
                  confint(MIcombine(m1_men_StrA_SO1_Snus)))), 2)[2:3, ],
  caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO1_Snus)),
                    confint(MIcombine(m1_women_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO1_Snus)),
                    confint(MIcombine(m2_men_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO1_Snus)),
                    confint(MIcombine(m2_women_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(knitr::kable(
  round(exp(cbind(coef(MIcombine(m3_men_StrA_SO1_Snus)),
                  confint(MIcombine(m3_men_StrA_SO1_Snus)))), 2)[2:3, ],
  caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO1_Snus)),
                    confint(MIcombine(m3_women_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()
```

```r
# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
m2_mm_Sex_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO1_Snus, m2_am_Sex_StrA_SO1_Snus, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO1_Snus, m3_am_Sex_StrA_SO1_Smoke, method = "D2")
```

Secondary outcome (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_men_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO2_Smoke))

m1_women_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO2_Smoke))

# Adjusted for age
m2_men_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 1),
```

```r
  svyglm(event_3doses ~ factor(smoking_status) +
          pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO2_Smoke))

m2_women_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_3doses ~ factor(smoking_status) +
          pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO2_Smoke))

# Adjusted for confounders
m3_men_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_3doses ~ factor(smoking_status) +
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO2_Smoke))

m3_women_StrA_SO2_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_3doses ~ factor(smoking_status) +
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO2_Smoke))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_men_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_women_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_men_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
```

```r
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_women_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_men_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_women_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) +
           factor(sex) + pspline(age_cont) ,
         family = quasipoisson()))
m2_mm_Sex_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO2_Smoke, m2_am_Sex_StrA_SO2_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO2_Smoke, m3_am_Sex_StrA_SO2_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_men_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO2_Snus))

m1_women_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO2_Snus))

# Adjusted for age
m2_men_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO2_Snus))

m2_women_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO2_Snus))

# Adjusted for confounders
m3_men_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO2_Snus))

m3_women_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO2_Snus))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO2_Snus)),
                    confint(MIcombine(m1_men_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
```

```r
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO2_Snus)),
                    confint(MIcombine(m1_women_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO2_Snus)),
                    confint(MIcombine(m2_men_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO2_Snus)),
                    confint(MIcombine(m2_women_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO2_Snus)),
                    confint(MIcombine(m3_men_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO2_Snus)),
                    confint(MIcombine(m3_women_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
m2_mm_Sex_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) * factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO2_Snus, m2_am_Sex_StrA_SO2_Snus, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_SO2_Snus <- with(
```

```
      subset(des_final, between(age_cont, 20, 74)),
      svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                pspline(age_cont) + factor(educ_tertiles) +
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(fs_shp_koodi),
            family = quasipoisson()))
m3_mm_Sex_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) * factor(sex) +
                pspline(age_cont) + factor(educ_tertiles) +
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(fs_shp_koodi),
            family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO2_Snus, m3_am_Sex_StrA_SO2_Snus, method = "D2")
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_men_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_20weeks12 ~ factor(smoking_status),
        family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO3_Smoke))

m1_women_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_20weeks12 ~ factor(smoking_status),
        family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO3_Smoke))

# Adjusted for age
m2_men_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
            pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO3_Smoke))

m2_women_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
            pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO3_Smoke))

# Adjusted for confounders
m3_men_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 1),
```

```r
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO3_Smoke))

m3_women_StrA_SO3_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO3_Smoke))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_men_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_women_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO3_Smoke)),
                    confint(MIcombine(m2_men_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO3_Smoke)),
                    confint(MIcombine(m2_women_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO3_Smoke)),
                    confint(MIcombine(m3_men_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
```

```r
knitr::kable(
  round(exp(cbind(coef(MIcombine(m3_women_StrA_SO3_Smoke)),
                  confint(MIcombine(m3_women_StrA_SO3_Smoke)))), 2)[2:4, ],
  caption = "Women") %>%
  kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           factor(sex) + pspline(age_cont) ,
         family = quasipoisson()))
m2_mm_Sex_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO3_Smoke, m2_am_Sex_StrA_SO3_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO3_Smoke, m3_am_Sex_StrA_SO3_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_men_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO3_Snus))

m1_women_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_20weeks12 ~ factor(snus_status),
```

```r
        family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO3_Snus))

# Adjusted for age
m2_men_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO3_Snus))

m2_women_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO3_Snus))

# Adjusted for confounders
m3_men_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
          factor(educ_tertiles) + factor(maritalstatus_bin) +
          factor(mother_tongue) + factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO3_Snus))

m3_women_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
          factor(educ_tertiles) + factor(maritalstatus_bin) +
          factor(mother_tongue) + factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO3_Snus))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO3_Snus)),
                  confint(MIcombine(m1_men_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO3_Snus)),
                  confint(MIcombine(m1_women_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO3_Snus)),
```

```
                confint(MIcombine(m2_men_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO3_Snus)),
                confint(MIcombine(m2_women_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO3_Snus)),
                confint(MIcombine(m3_men_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO3_Snus)),
                confint(MIcombine(m3_women_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
          pspline(age_cont) ,
        family = quasipoisson()))
m2_mm_Sex_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) * factor(sex) +
          pspline(age_cont) ,
        family = quasipoisson()))
testModels(m2_mm_Sex_StrA_SO3_Snus, m2_am_Sex_StrA_SO3_Snus, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_mm_Sex_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) * factor(sex) +
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) +
```

```
        factor(fs_shp_koodi),
        family = quasipoisson()))
testModels(m3_mm_Sex_StrA_SO3_Snus, m3_am_Sex_StrA_SO3_Snus, method = "D2")
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_men_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO4_Smoke))

m1_women_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))
# summary(MIcombine(m1_women_StrA_SO4_Smoke))

# Adjusted for age
m2_men_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO4_Smoke))

m2_women_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO4_Smoke))

# Adjusted for confounders
m3_men_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 1),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO4_Smoke))

m3_women_StrA_SO4_Smoke <- with(
  subset(des_final, sex == 2),
  svyglm(event_7months23 ~ factor(smoking_status) +
```

```
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO4_Smoke))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_men_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_women_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_men_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_women_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_men_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_men_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_women_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_women_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_StrA_SO4_Smoke <- with(
```

```
    des_final,
    svyglm(event_7months23 ~ factor(smoking_status) +
            factor(sex) + pspline(age_cont) ,
        family = quasipoisson()))
m2_mm_StrA_SO4_Smoke <- with(
    des_final,
    svyglm(event_7months23 ~ factor(smoking_status) * factor(sex) +
            pspline(age_cont) ,
        family = quasipoisson()))
testModels(m2_mm_StrA_SO4_Smoke, m2_am_StrA_SO4_Smoke, method = "D2")

# Adjusted for confounders
m3_am_StrA_SO4_Smoke <- with(
    des_final,
    svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
            pspline(age_cont) + factor(educ_tertiles) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_mm_StrA_SO4_Smoke <- with(
    des_final,
    svyglm(event_7months23 ~ factor(smoking_status) * factor(sex) +
            pspline(age_cont) + factor(educ_tertiles) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) +
            factor(fs_shp_koodi),
        family = quasipoisson()))
testModels(m3_mm_StrA_SO4_Smoke, m3_am_StrA_SO4_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_men_StrA_SO4_Snus <- with(
    subset(des_final, between(age_cont, 20, 74) & sex == 1),
    svyglm(event_7months23 ~ factor(snus_status),
        family = quasipoisson()))
# summary(MIcombine(m1_men_StrA_SO4_Snus))

m1_women_StrA_SO4_Snus <- with(
    subset(des_final, between(age_cont, 20, 74) & sex == 2),
    svyglm(event_7months23 ~ factor(snus_status),
        family = quasipoisson()))

# Adjusted for age
m2_men_StrA_SO4_Snus <- with(
    subset(des_final, between(age_cont, 20, 74) & sex == 1),
    svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont),
        family = quasipoisson()))
# summary(MIcombine(m2_men_StrA_SO4_Snus))

m2_women_StrA_SO4_Snus <- with(
    subset(des_final, between(age_cont, 20, 74) & sex == 2),
```

```r
    svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont),
           family = quasipoisson()))
# summary(MIcombine(m2_women_StrA_SO4_Snus))

# Adjusted for confounders
m3_men_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 1),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_men_StrA_SO4_Snus))

m3_women_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & sex == 2),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_women_StrA_SO4_Snus))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_men_StrA_SO4_Snus)),
                    confint(MIcombine(m1_men_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_women_StrA_SO4_Snus)),
                    confint(MIcombine(m1_women_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_men_StrA_SO4_Snus)),
                    confint(MIcombine(m2_men_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Men") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_women_StrA_SO4_Snus)),
                    confint(MIcombine(m2_women_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Women") %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
```

```r
knitr::kable(
  round(exp(cbind(coef(MIcombine(m3_men_StrA_S04_Snus)),
                  confint(MIcombine(m3_men_StrA_S04_Snus)))), 2)[2:3, ],
  caption = "Men") %>%
  kableExtra::kable_classic(full_width = T),
knitr::kable(
  round(exp(cbind(coef(MIcombine(m3_women_StrA_S04_Snus)),
                  confint(MIcombine(m3_women_StrA_S04_Snus)))), 2)[2:3, ],
  caption = "Women") %>%
  kableExtra::kable_classic(full_width = T)),
caption = "M3: Adjusted for confounders") %>%
kable_classic()

# Testing for interaction
# Adjusted for age and sex
m2_am_Sex_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) +
           factor(sex) + pspline(age_cont),
         family = quasipoisson()))
m2_mm_Sex_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) ,
         family = quasipoisson()))
testModels(m2_mm_Sex_StrA_S04_Snus, m2_am_Sex_StrA_S04_Snus, method = "D2")

# Adjusted for confounders
m3_am_Sex_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Sex_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) * factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Sex_StrA_S04_Snus, m3_am_Sex_StrA_S04_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Stratified by age

For age, we have categorized age before as 20-39, 40-59 and 60+ for smoking and 20-39, 40-59 and 60-74 for snus use.

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_2039_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_4059_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_60plus_StrA_PO_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_PO_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_4059_StrA_PO_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_60plus_StrA_PO_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
```

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        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_PO_Smoke)),
                    confint(MIcombine(m1_2039_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_PO_Smoke)),
                    confint(MIcombine(m1_4059_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_PO_Smoke)),
                    confint(MIcombine(m1_60plus_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_PO_Smoke)),
                    confint(MIcombine(m2_2039_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_PO_Smoke)),
                    confint(MIcombine(m2_4059_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_PO_Smoke)),
                    confint(MIcombine(m2_60plus_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_PO_Smoke)),
                    confint(MIcombine(m3_2039_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_PO_Smoke)),
                    confint(MIcombine(m3_4059_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
```

```r
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_PO_Smoke)),
                    confint(MIcombine(m3_60plus_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_PO_Smoke, m2_am_Age_StrA_PO_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_PO_Smoke, m3_am_Age_StrA_PO_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_2039_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
m1_4059_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
m1_60plus_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_2doses ~ factor(snus_status),
```

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        family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_4059_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_60plus_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_PO_Snus)),
                    confint(MIcombine(m1_2039_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_PO_Snus)),
                    confint(MIcombine(m1_4059_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_PO_Snus)),
```

```r
                        confint(MIcombine(m1_60plus_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_PO_Snus)),
                    confint(MIcombine(m2_2039_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_PO_Snus)),
                    confint(MIcombine(m2_4059_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_PO_Snus)),
                    confint(MIcombine(m2_60plus_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_PO_Snus)),
                    confint(MIcombine(m3_2039_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_PO_Snus)),
                    confint(MIcombine(m3_4059_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_PO_Snus)),
                    confint(MIcombine(m3_60plus_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
```

```
      svyglm(event_2doses ~ factor(snus_status) * age_cont +
             factor(sex),
           family = quasipoisson())
testModels(m2_mm_Age_StrA_PO_Snus, m2_am_Age_StrA_PO_Snus, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
             age_cont + factor(educ_tertiles) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(fs_shp_koodi),
           family = quasipoisson()))
m3_mm_Age_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) * age_cont +
             factor(educ_tertiles) + factor(sex) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(fs_shp_koodi),
           family = quasipoisson()))
testModels(m3_mm_Age_StrA_PO_Snus, m3_am_Age_StrA_PO_Snus, method = "D2")
```

Secondary outcome (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_2039_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
m1_4059_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
m1_60plus_StrA_S01_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_S01_Smoke <- with(
  subset(des_final, age_cont >= 60),
```

```r
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_4059_StrA_S01_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex)+
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_60plus_StrA_S01_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S01_Smoke)),
                    confint(MIcombine(m1_2039_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S01_Smoke)),
                    confint(MIcombine(m1_4059_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S01_Smoke)),
                    confint(MIcombine(m1_60plus_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S01_Smoke)),
                    confint(MIcombine(m2_2039_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
```

```r
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S01_Smoke)),
                    confint(MIcombine(m2_4059_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S01_Smoke)),
                    confint(MIcombine(m2_60plus_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S01_Smoke)),
                    confint(MIcombine(m3_2039_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S01_Smoke)),
                    confint(MIcombine(m3_4059_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S01_Smoke)),
                    confint(MIcombine(m3_60plus_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S01_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S01_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) * age_cont +
           factor(sex) ,
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S01_Smoke, m2_am_Age_StrA_S01_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S01_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
```

```r
m3_mm_Age_StrA_S01_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S01_Smoke, m3_am_Age_StrA_S01_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_2039_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
m1_4059_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
m1_60plus_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_4059_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
```

```r
        factor(fs_shp_koodi),
        family = quasipoisson()))
m3_60plus_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S01_Snus)),
                    confint(MIcombine(m1_2039_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S01_Snus)),
                    confint(MIcombine(m1_4059_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S01_Snus)),
                    confint(MIcombine(m1_60plus_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S01_Snus)),
                    confint(MIcombine(m2_2039_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S01_Snus)),
                    confint(MIcombine(m2_4059_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S01_Snus)),
                    confint(MIcombine(m2_60plus_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S01_Snus)),
                    confint(MIcombine(m3_2039_StrA_S01_Snus)))), 2)[2:3, ],
```

```
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S01_Snus)),
                    confint(MIcombine(m3_4059_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S01_Snus)),
                    confint(MIcombine(m3_60plus_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted age and sex
m2_am_Age_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S01_Snus, m2_am_Age_StrA_S01_Snus, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) + age_cont +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) * age_cont + factor(educ_tertiles) +
           factor(sex) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S01_Snus, m3_am_Age_StrA_S01_Snus, method = "D2")
```

Secondary outcome (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_2039_StrA_S02_Smoke <- with(
```

```r
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_4059_StrA_S02_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_60plus_StrA_S02_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S02_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_S02_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_S02_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S02_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_4059_StrA_S02_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_60plus_StrA_S02_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S02_Smoke)),
```

```
                confint(MIcombine(m1_2039_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S02_Smoke)),
                confint(MIcombine(m1_4059_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S02_Smoke)),
                confint(MIcombine(m1_60plus_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S02_Smoke)),
                confint(MIcombine(m2_2039_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S02_Smoke)),
                confint(MIcombine(m2_4059_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S02_Smoke)),
                confint(MIcombine(m2_60plus_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S02_Smoke)),
                confint(MIcombine(m3_2039_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S02_Smoke)),
                confint(MIcombine(m3_4059_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S02_Smoke)),
                confint(MIcombine(m3_60plus_StrA_S02_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()
```

```r
# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S02_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S02_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S02_Smoke, m2_am_Age_StrA_S02_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S02_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_S02_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S02_Smoke, m3_am_Age_StrA_S02_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_2039_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_4059_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_60plus_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex),
```

```r
        family = quasipoisson()))
m2_4059_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex),
        family = quasipoisson()))
m2_60plus_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex),
        family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
          factor(educ_tertiles) + factor(maritalstatus_bin) +
          factor(mother_tongue) + factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
m3_4059_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
          factor(educ_tertiles) + factor(maritalstatus_bin) +
          factor(mother_tongue) + factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
m3_60plus_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
          factor(educ_tertiles) + factor(maritalstatus_bin) +
          factor(mother_tongue) + factor(involvement_attend_j) +
          factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S02_Snus)),
                    confint(MIcombine(m1_2039_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S02_Snus)),
                    confint(MIcombine(m1_4059_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S02_Snus)),
                    confint(MIcombine(m1_60plus_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()
```

```r
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S02_Snus)),
                    confint(MIcombine(m2_2039_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S02_Snus)),
                    confint(MIcombine(m2_4059_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S02_Snus)),
                    confint(MIcombine(m2_60plus_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S02_Snus)),
                    confint(MIcombine(m3_2039_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S02_Snus)),
                    confint(MIcombine(m3_4059_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S02_Snus)),
                    confint(MIcombine(m3_60plus_StrA_S02_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S02_Snus, m2_am_Age_StrA_S02_Snus, method = "D2")

# Adjusted for confounders
```

```r
m3_am_Age_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_S02_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S02_Snus, m3_am_Age_StrA_S02_Snus, method = "D2")
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_2039_StrA_S03_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_4059_StrA_S03_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_60plus_StrA_S03_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S03_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_S03_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))
m2_60plus_StrA_S03_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S03_Smoke <- with(
```

```r
    subset(des_final, between(age_cont, 20, 39)),
    svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
             factor(educ_tertiles) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(fs_shp_koodi),
           family = quasipoisson()))
m3_4059_StrA_S03_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_60plus_StrA_S03_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S03_Smoke)),
                    confint(MIcombine(m1_2039_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S03_Smoke)),
                    confint(MIcombine(m1_4059_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S03_Smoke)),
                    confint(MIcombine(m1_60plus_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S03_Smoke)),
                    confint(MIcombine(m2_2039_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S03_Smoke)),
                    confint(MIcombine(m2_4059_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
```

```r
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S03_Smoke)),
                    confint(MIcombine(m2_60plus_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S03_Smoke)),
                    confint(MIcombine(m3_2039_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S03_Smoke)),
                    confint(MIcombine(m3_4059_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S03_Smoke)),
                    confint(MIcombine(m3_60plus_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S03_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S03_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S03_Smoke, m2_am_Age_StrA_S03_Smoke, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S03_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_S03_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
```

```
                factor(involvement_attend_j) + factor(fs_shp_koodi),
            family = quasipoisson())))
testModels(m3_mm_Age_StrA_S03_Smoke, m3_am_Age_StrA_S03_Smoke, method = "D2")
```

Snus

```
## Crude model
m1_2039_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson())))
m1_4059_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson())))
m1_60plus_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson())))

# Adjusted for age and sex
m2_2039_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex),
         family = quasipoisson())))
m2_4059_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex),
         family = quasipoisson())))
m2_60plus_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_2039_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson())))
m3_4059_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson())))
m3_60plus_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
```

```r
                  factor(educ_tertiles) + factor(maritalstatus_bin) +
                  factor(mother_tongue) + factor(involvement_attend_j) +
                  factor(fs_shp_koodi),
            family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S03_Snus)),
                    confint(MIcombine(m1_2039_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S03_Snus)),
                    confint(MIcombine(m1_4059_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S03_Snus)),
                    confint(MIcombine(m1_60plus_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S03_Snus)),
                    confint(MIcombine(m2_2039_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S03_Snus)),
                    confint(MIcombine(m2_4059_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S03_Snus)),
                    confint(MIcombine(m2_60plus_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S03_Snus)),
                    confint(MIcombine(m3_2039_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S03_Snus)),
                    confint(MIcombine(m3_4059_StrA_S03_Snus)))), 2)[2:3, ],
```

```
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S03_Snus)),
                    confint(MIcombine(m3_60plus_StrA_S03_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S03_Snus, m2_am_Age_StrA_S03_Snus, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Age_StrA_S03_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S03_Snus, m3_am_Age_StrA_S03_Snus, method = "D2")
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_2039_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_7months23 ~ factor(smoking_status),
```

```r
        family = quasipoisson()))
m1_4059_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_7months23 ~ factor(smoking_status),
        family = quasipoisson()))
m1_60plus_StrA_S04_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_7months23 ~ factor(smoking_status),
        family = quasipoisson()))

# Adjusted for sex
m2_2039_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex),
        family = quasipoisson()))
m2_4059_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex),
        family = quasipoisson()))
m2_60plus_StrA_S04_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex),
        family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
          factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_4059_StrA_S04_Smoke <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
          factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_60plus_StrA_S04_Smoke <- with(
  subset(des_final, age_cont >= 60),
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
          factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S04_Smoke)),
                    confint(MIcombine(m1_2039_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
```

```r
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S04_Smoke)),
                    confint(MIcombine(m1_4059_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S04_Smoke)),
                    confint(MIcombine(m1_60plus_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S04_Smoke)),
                    confint(MIcombine(m2_2039_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S04_Smoke)),
                    confint(MIcombine(m2_4059_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S04_Smoke)),
                    confint(MIcombine(m2_60plus_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S04_Smoke)),
                    confint(MIcombine(m3_2039_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S04_Smoke)),
                    confint(MIcombine(m3_4059_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S04_Smoke)),
                    confint(MIcombine(m3_60plus_StrA_S04_Smoke)))), 2)[2:4, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
```

```r
# Adjusted for age and sex
m2_am_Age_StrA_S04_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) + age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S04_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) * age_cont +
           factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S04_Smoke, m2_am_Age_StrA_S04_Smoke, method = "D2")

# Adjusted for confounders
m3_am_StrA_S04_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_StrA_S04_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_StrA_S04_Smoke, m3_am_StrA_S04_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_2039_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_4059_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_60plus_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_2039_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex),
         family = quasipoisson()))
m2_4059_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
```

```r
    svyglm(event_7months23 ~ factor(snus_status) + factor(sex),
        family = quasipoisson()))
m2_60plus_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
    svyglm(event_7months23 ~ factor(snus_status) + factor(sex),
        family = quasipoisson()))

# Adjusted for confounders
m3_2039_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 39)),
    svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi),
        family = quasipoisson()))
m3_4059_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 40, 59)),
    svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi),
        family = quasipoisson()))
m3_60plus_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 60, 74)),
    svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_2039_StrA_S04_Snus)),
                 confint(MIcombine(m1_2039_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_4059_StrA_S04_Snus)),
                 confint(MIcombine(m1_4059_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_60plus_StrA_S04_Snus)),
                 confint(MIcombine(m1_60plus_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_2039_StrA_S04_Snus)),
```

```r
                confint(MIcombine(m2_2039_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_4059_StrA_S04_Snus)),
                confint(MIcombine(m2_4059_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_60plus_StrA_S04_Snus)),
                confint(MIcombine(m2_60plus_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_2039_StrA_S04_Snus)),
                confint(MIcombine(m3_2039_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "20-39 years") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_4059_StrA_S04_Snus)),
                confint(MIcombine(m3_4059_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "40-59 years", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_60plus_StrA_S04_Snus)),
                confint(MIcombine(m3_60plus_StrA_S04_Snus)))), 2)[2:3, ],
    caption = "60+", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for age and sex
m2_am_Age_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) + age_cont,
         family = quasipoisson()))
m2_mm_Age_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) * age_cont + factor(sex),
         family = quasipoisson()))
testModels(m2_mm_Age_StrA_S04_Snus, m2_am_Age_StrA_S04_Snus, method = "D2")

# Adjusted for confounders
m3_am_Age_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           age_cont + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
```

```
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_mm_Age_StrA_S04_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) * age_cont +
           factor(educ_tertiles) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Age_StrA_S04_Snus, m3_am_Age_StrA_S04_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Stratified by education level

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_lower_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_medium_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_high_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_medium_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_high_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
```

```r
# Adjusted for confounders
m3_lower_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(sex) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
m3_medium_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(sex) +
          factor(fs_shp_koodi),
        family = quasipoisson()))
m3_high_StrA_PO_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(sex) +
          factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_PO_Smoke)),
                    confint(MIcombine(m1_lower_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_PO_Smoke)),
                    confint(MIcombine(m1_medium_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_PO_Smoke)),
                    confint(MIcombine(m1_high_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_PO_Smoke)),
                    confint(MIcombine(m2_lower_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_PO_Smoke)),
                    confint(MIcombine(m2_medium_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
```

```
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_PO_Smoke)),
                    confint(MIcombine(m2_high_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_PO_Smoke)),
                    confint(MIcombine(m3_lower_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_PO_Smoke)),
                    confint(MIcombine(m3_medium_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_PO_Smoke)),
                    confint(MIcombine(m3_high_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Educ_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_PO_Smoke <- with(
  des_final,
  svyglm(
    event_2doses ~ factor(smoking_status) * factor(educ_tertiles) +
      pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi),
    family = quasipoisson()))
testModels(m3_mm_Educ_StrA_PO_Smoke, m3_am_Educ_StrA_PO_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_lower_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
```

```r
      svyglm(event_2doses ~ factor(snus_status),
             family = quasipoisson()))
m1_medium_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
m1_high_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_medium_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_high_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson()))
m3_medium_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson()))
m3_high_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
```

```r
knitr::kable(
  round(exp(cbind(coef(MIcombine(m1_lower_StrA_PO_Snus)),
                  confint(MIcombine(m1_lower_StrA_PO_Snus)))), 2)[2:3, ],
  caption = "lower") %>%
  kableExtra::kable_classic(full_width = T),
knitr::kable(
  round(exp(cbind(coef(MIcombine(m1_medium_StrA_PO_Snus)),
                  confint(MIcombine(m1_medium_StrA_PO_Snus)))), 2)[2:3, ],
  caption = "medium", row.names = F) %>%
  kableExtra::kable_classic(full_width = T),
knitr::kable(
  round(exp(cbind(coef(MIcombine(m1_high_StrA_PO_Snus)),
                  confint(MIcombine(m1_high_StrA_PO_Snus)))), 2)[2:3, ],
  caption = "high", row.names = F) %>%
  kableExtra::kable_classic(full_width = T)),
caption = "M1: Crude model") %>%
kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_PO_Snus)),
                    confint(MIcombine(m2_lower_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_PO_Snus)),
                    confint(MIcombine(m2_medium_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_PO_Snus)),
                    confint(MIcombine(m2_high_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_PO_Snus)),
                    confint(MIcombine(m3_lower_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_PO_Snus)),
                    confint(MIcombine(m3_medium_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_PO_Snus)),
                    confint(MIcombine(m3_high_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
```

```
    caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for confounders
m3_am_Educ_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
          pspline(age_cont) + factor(educ_tertiles) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
m3_mm_Educ_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) * factor(educ_tertiles) +
          pspline(age_cont) + factor(sex) +
          factor(maritalstatus_bin) + factor(mother_tongue) +
          factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson()))
testModels(m3_mm_Educ_StrA_PO_Snus, m3_am_Educ_StrA_PO_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (i): Uptake of one doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_lower_StrA_SO1_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(smoking_status),
        family = quasipoisson()))
m1_medium_StrA_SO1_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(smoking_status),
        family = quasipoisson()))
m1_high_StrA_SO1_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(smoking_status),
        family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO1_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
          factor(sex),
        family = quasipoisson()))
m2_medium_StrA_SO1_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
```

```r
            factor(sex),
          family = quasipoisson()))
m2_high_StrA_S01_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
            factor(sex),
          family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_S01_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(sex) +
            factor(fs_shp_koodi),
          family = quasipoisson()))
m3_medium_StrA_S01_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(sex) +
            factor(fs_shp_koodi),
          family = quasipoisson()))
m3_high_StrA_S01_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi),
          family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_S01_Smoke)),
                    confint(MIcombine(m1_lower_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_S01_Smoke)),
                    confint(MIcombine(m1_medium_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_S01_Smoke)),
                    confint(MIcombine(m1_high_StrA_S01_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_S01_Smoke)),
```

```r
                     confint(MIcombine(m2_lower_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_medium_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_high_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO1_Smoke)),
                               confint(MIcombine(m3_lower_StrA_SO1_Smoke)))), 2)[2:4, ],
               caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_medium_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_high_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for confounders
m3_am_Educ_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(
    event_1dose ~ factor(smoking_status) * factor(educ_tertiles) +
      pspline(age_cont) + factor(sex) +
      factor(maritalstatus_bin) + factor(mother_tongue) +
      factor(involvement_attend_j) + factor(fs_shp_koodi),
    family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO1_Smoke, m3_am_Educ_StrA_SO1_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_lower_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
m1_medium_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
m1_high_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_medium_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_high_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
```

```r
          factor(fs_shp_koodi),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_S01_Snus)),
                    confint(MIcombine(m1_lower_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_S01_Snus)),
                    confint(MIcombine(m1_medium_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_S01_Snus)),
                    confint(MIcombine(m1_high_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_S01_Snus)),
                    confint(MIcombine(m2_lower_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_S01_Snus)),
                    confint(MIcombine(m2_medium_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_S01_Snus)),
                    confint(MIcombine(m2_high_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_S01_Snus)),
                    confint(MIcombine(m3_lower_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_S01_Snus)),
                    confint(MIcombine(m3_medium_StrA_S01_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
```

```
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO1_Snus)),
                    confint(MIcombine(m3_high_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for confounders
# am for additive model; mm for multiplicative model
m3_am_Educ_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) * factor(educ_tertiles) +
           pspline(age_cont) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO1_Snus, m3_am_Educ_StrA_SO1_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_lower_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_medium_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_high_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO2_Smoke <- with(
```

```r
    subset(des_final, educ_tertiles == "lower"),
    svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
             factor(sex),
           family = quasipoisson())))
m2_medium_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))
m2_high_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_lower_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_3doses ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson())))
m3_medium_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson())))
m3_high_StrA_SO2_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_lower_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_medium_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_high_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
```

```r
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_lower_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_medium_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_high_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_lower_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_medium_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_high_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Educ_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson())))
m3_mm_Educ_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(
    event_3doses ~ factor(smoking_status) * factor(educ_tertiles) +
```

```
        factor(sex) + factor(maritalstatus_bin) +
        factor(mother_tongue) + factor(involvement_attend_j) +
        factor(fs_shp_koodi),
    family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO2_Smoke, m3_am_Educ_StrA_SO2_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_lower_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_medium_StrA_SO2_Snus <- with(
  subset(des_final,between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_high_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson()))
m3_medium_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
```

```r
        factor(sex),
        family = quasipoisson()))
m3_high_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO2_Snus)),
                    confint(MIcombine(m1_lower_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO2_Snus)),
                    confint(MIcombine(m1_medium_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_SO2_Snus)),
                    confint(MIcombine(m1_high_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_SO2_Snus)),
                    confint(MIcombine(m2_lower_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO2_Snus)),
                    confint(MIcombine(m2_medium_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO2_Snus)),
                    confint(MIcombine(m2_high_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO2_Snus)),
                    confint(MIcombine(m3_lower_StrA_SO2_Snus)))), 2)[2:3, ],
```

```r
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO2_Snus)),
                    confint(MIcombine(m3_medium_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO2_Snus)),
                    confint(MIcombine(m3_high_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for confounders
m3_am_Educ_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) * factor(educ_tertiles) +
           factor(sex) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO2_Snus, m3_am_Educ_StrA_SO2_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_lower_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_medium_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_high_StrA_SO3_Smoke <- with(
```

```r
    subset(des_final, educ_tertiles == "high"),
    svyglm(event_20weeks12 ~ factor(smoking_status),
           family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_medium_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(maritalstatus_bin) +
           factor(mother_tongue) +  factor(involvement_attend_j) +
           factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_high_StrA_SO3_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(sex) + factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_lower_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO3_Smoke)),
```

```
                  confint(MIcombine(m1_medium_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_S03_Smoke)),
                  confint(MIcombine(m1_high_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_S03_Smoke)),
                  confint(MIcombine(m2_lower_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_S03_Smoke)),
                  confint(MIcombine(m2_medium_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_S03_Smoke)),
                  confint(MIcombine(m2_high_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_S03_Smoke)),
                  confint(MIcombine(m3_lower_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_S03_Smoke)),
                  confint(MIcombine(m3_medium_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_S03_Smoke)),
                  confint(MIcombine(m3_high_StrA_S03_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Educ_StrA_S03_Smoke <- with(
  des_final,
```

```
    svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) * factor(educ_tertiles)+
           pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO3_Smoke, m3_am_Educ_StrA_SO3_Smoke, method = "D2")
```

Snus

```
# Crude model
m1_lower_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
m1_medium_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
m1_high_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
```

```r
              factor(involvement_attend_j) + factor(fs_shp_koodi) +
              factor(sex),
         family = quasipoisson()))
m3_medium_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
              factor(maritalstatus_bin) + factor(mother_tongue) +
              factor(involvement_attend_j) + factor(fs_shp_koodi) +
              factor(sex),
         family = quasipoisson()))
m3_high_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
              factor(maritalstatus_bin) + factor(mother_tongue) +
              factor(involvement_attend_j) + factor(fs_shp_koodi) +
              factor(sex),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO3_Snus)),
                    confint(MIcombine(m1_lower_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO3_Snus)),
                    confint(MIcombine(m1_medium_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_SO3_Snus)),
                    confint(MIcombine(m1_high_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_SO3_Snus)),
                    confint(MIcombine(m2_lower_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO3_Snus)),
                    confint(MIcombine(m2_medium_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO3_Snus)),
                    confint(MIcombine(m2_high_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
```

```
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO3_Snus)),
                    confint(MIcombine(m3_lower_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO3_Snus)),
                    confint(MIcombine(m3_medium_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO3_Snus)),
                    confint(MIcombine(m3_high_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for confounders
m3_am_Educ_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_20weeks12 ~ factor(snus_status) * factor(educ_tertiles) +
           pspline(age_cont) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO3_Snus, m3_am_Educ_StrA_SO3_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_lower_StrA_SO4_Smoke <- with(
```

```r
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))
m1_medium_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))
m1_high_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_lower_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "lower"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_medium_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "medium"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
m3_high_StrA_SO4_Smoke <- with(
  subset(des_final, educ_tertiles == "high"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi),
         family = quasipoisson()))

# Obtain main estimates
```

```r
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_lower_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_medium_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_high_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_lower_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_medium_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_high_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_lower_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_medium_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_high_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "high", row.names = F) %>%
```

```r
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()


# Testing for interaction
# Adjust confounders
m3_am_Educ_StrA_SO4_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
           factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO4_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) * factor(educ_tertiles) +
           factor(sex) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO4_Smoke, m3_am_Educ_StrA_SO4_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_lower_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_medium_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_high_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_lower_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_medium_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_high_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
```

```
      svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
             factor(sex),
           family = quasipoisson())))

# Adjusted for confounders
m3_lower_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "lower"),
    svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson())))
m3_medium_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "medium"),
    svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson())))
m3_high_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & educ_tertiles == "high"),
    svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(sex),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_lower_StrA_SO4_Snus)),
                    confint(MIcombine(m1_lower_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_medium_StrA_SO4_Snus)),
                    confint(MIcombine(m1_medium_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_high_StrA_SO4_Snus)),
                    confint(MIcombine(m1_high_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_lower_StrA_SO4_Snus)),
                    confint(MIcombine(m2_lower_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
```

```r
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_medium_StrA_SO4_Snus)),
                    confint(MIcombine(m2_medium_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_high_StrA_SO4_Snus)),
                    confint(MIcombine(m2_high_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_lower_StrA_SO4_Snus)),
                    confint(MIcombine(m3_lower_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "lower") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_medium_StrA_SO4_Snus)),
                    confint(MIcombine(m3_medium_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "medium", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_high_StrA_SO4_Snus)),
                    confint(MIcombine(m3_high_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "high", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Test for interaction
# Adjusted for confounders
m3_am_Educ_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Educ_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) * factor(educ_tertiles) +
           pspline(age_cont) + factor(sex) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
testModels(m3_mm_Educ_StrA_SO4_Snus, m3_am_Educ_StrA_SO4_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Stratified by vaccine type

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_am_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_2doses ~ factor(smoking_status),
       family = quasipoisson()))
m1_aa_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(smoking_status),
       family = quasipoisson()))
m1_mm_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(smoking_status),
       family = quasipoisson()))

# Adjusted for age and sex
m2_am_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
       family = quasipoisson()))
m2_aa_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
       family = quasipoisson()))
m2_mm_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
       family = quasipoisson()))

# Adjusted for confounders
m3_am_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
       family = quasipoisson()))
m3_aa_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
       family = quasipoisson()))
```

```r
m3_mm_StrA_PO_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_am_StrA_PO_Smoke)),
                    confint(MIcombine(m1_am_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aa_StrA_PO_Smoke)),
                    confint(MIcombine(m1_aa_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mm_StrA_PO_Smoke)),
                    confint(MIcombine(m1_mm_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_am_StrA_PO_Smoke)),
                    confint(MIcombine(m2_am_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aa_StrA_PO_Smoke)),
                    confint(MIcombine(m2_aa_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mm_StrA_PO_Smoke)),
                    confint(MIcombine(m2_mm_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_am_StrA_PO_Smoke)),
                    confint(MIcombine(m3_am_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
```

```r
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aa_StrA_PO_Smoke)),
                    confint(MIcombine(m3_aa_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mm_StrA_PO_Smoke)),
                    confint(MIcombine(m3_mm_StrA_PO_Smoke)))), 2)[2:4, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type2_StrA_PO_Smoke <- with(
  des_final,
  svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(type2vac) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type2_StrA_PO_Smoke <- with(
  des_final,
  svyglm(
    event_2doses ~ factor(smoking_status) * factor(type2vac) +
      pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi)+ factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type2_StrA_PO_Smoke, m3_am_Type2_StrA_PO_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_am_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
m1_aa_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))
m1_mm_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_am_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
```

```r
  svyglm(event_2doses ~ factor(snus_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson())))
m2_aa_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(snus_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson())))
m2_mm_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(snus_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_am_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))
m3_aa_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))
m3_mm_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_2doses ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_am_StrA_PO_Snus)),
                    confint(MIcombine(m1_am_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aa_StrA_PO_Snus)),
                    confint(MIcombine(m1_aa_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mm_StrA_PO_Snus)),
                    confint(MIcombine(m1_mm_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
```

```r
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_am_StrA_PO_Snus)),
                    confint(MIcombine(m2_am_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aa_StrA_PO_Snus)),
                    confint(MIcombine(m2_aa_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mm_StrA_PO_Snus)),
                    confint(MIcombine(m2_mm_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_am_StrA_PO_Snus)),
                    confint(MIcombine(m3_am_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aa_StrA_PO_Snus)),
                    confint(MIcombine(m3_aa_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mm_StrA_PO_Snus)),
                    confint(MIcombine(m3_mm_StrA_PO_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(type2vac) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type_StrA_PO_Snus <- with(
```

```
    subset(des_final, between(age_cont, 20, 74)),
  svyglm(
    event_2doses ~ factor(snus_status) * factor(type2vac) +
      pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi)+ factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_PO_Snus, m3_am_Type_StrA_PO_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (i): Uptake of one doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_az_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
m1_md_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Moderna"),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))
m1_pz_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_az_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_md_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Moderna"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_pz_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_az_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
```

```
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(sex) +
                factor(fs_shp_koodi) + factor(educ_tertiles),
            family = quasipoisson()))
m3_md_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Moderna"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(sex) +
                factor(fs_shp_koodi) + factor(educ_tertiles),
            family = quasipoisson()))
m3_pz_StrA_SO1_Smoke <- with(
  subset(des_final, type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(smoking_status) + pspline(age_cont) +
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
                factor(educ_tertiles),
            family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_az_StrA_SO1_Smoke)),
                    confint(MIcombine(m1_az_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_md_StrA_SO1_Smoke)),
                    confint(MIcombine(m1_md_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_pz_StrA_SO1_Smoke)),
                    confint(MIcombine(m1_pz_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_az_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_az_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_md_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_md_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_pz_StrA_SO1_Smoke)),
                    confint(MIcombine(m2_pz_StrA_SO1_Smoke)))), 2)[2:4, ],
```

```r
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_az_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_az_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_md_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_md_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_pz_StrA_SO1_Smoke)),
                    confint(MIcombine(m3_pz_StrA_SO1_Smoke)))), 2)[2:4, ],
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for confounders
m3_am_Type_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(type1vac) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Type_StrA_SO1_Smoke <- with(
  des_final,
  svyglm(
    event_1dose ~ factor(smoking_status) * factor(type1vac) +
      factor(educ_tertiles) + pspline(age_cont) + factor(sex) +
      factor(maritalstatus_bin) + factor(mother_tongue) +
      factor(involvement_attend_j) + factor(fs_shp_koodi),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO1_Smoke, m3_am_Type_StrA_SO1_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_az_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson()))
m1_md_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Moderna"),
```

```r
      svyglm(event_1dose ~ factor(snus_status),
             family = quasipoisson())))
m1_pz_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson())))

# Adjusted for age and sex
m2_az_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))
m2_md_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Moderna"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))
m2_pz_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_az_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Astra Zeneca"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))
m3_md_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Moderna"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))
m3_pz_StrA_S01_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type1vac == "Pfizer"),
  svyglm(event_1dose ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_az_StrA_S01_Snus)),
                    confint(MIcombine(m1_az_StrA_S01_Snus))))), 2)[2:3, ],
    caption = "Astra Zeneca") %>%
```

```r
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_md_StrA_SO1_Snus)),
                    confint(MIcombine(m1_md_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_pz_StrA_SO1_Snus)),
                    confint(MIcombine(m1_pz_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_az_StrA_SO1_Snus)),
                    confint(MIcombine(m2_az_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_md_StrA_SO1_Snus)),
                    confint(MIcombine(m2_md_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_pz_StrA_SO1_Snus)),
                    confint(MIcombine(m2_pz_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age") %>%
  kable_classic()

kables(list(
  knitr::kable(round(exp(cbind(coef(MIcombine(m3_az_StrA_SO1_Snus)),
                              confint(MIcombine(m3_az_StrA_SO1_Snus)))), 2)[2:3, ],
             caption = "Astra Zeneca") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_md_StrA_SO1_Snus)),
                    confint(MIcombine(m3_md_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Moderna", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_pz_StrA_SO1_Snus)),
                    confint(MIcombine(m3_pz_StrA_SO1_Snus)))), 2)[2:3, ],
    caption = "Pfizer", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjusted for confounders
```

```r
m3_am_Type_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(type1vac) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
m3_mm_Type_StrA_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(
    event_1dose ~ factor(snus_status) * factor(type1vac) +
      factor(educ_tertiles) + pspline(age_cont) + factor(sex) +
      factor(maritalstatus_bin) + factor(mother_tongue) +
      factor(involvement_attend_j) + factor(fs_shp_koodi),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO1_Snus, m3_am_Type_StrA_SO1_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_aam_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_mmm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))
m1_amm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_3doses ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_aam_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_mmm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_amm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
```

```r
    svyglm(event_3doses ~ factor(smoking_status) + pspline(age_cont) +
             factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_aam_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(smoking_status) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
             factor(educ_tertiles),
         family = quasipoisson())))
m3_mmm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(smoking_status) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
             factor(educ_tertiles),
         family = quasipoisson())))
m3_amm_StrA_SO2_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_3doses ~ factor(smoking_status) +
             factor(maritalstatus_bin) + factor(mother_tongue) +
             factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
             factor(educ_tertiles),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aam_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_aam_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mmm_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_mmm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_amm_StrA_SO2_Smoke)),
                    confint(MIcombine(m1_amm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aam_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_aam_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
```

```r
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mmm_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_mmm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_amm_StrA_SO2_Smoke)),
                    confint(MIcombine(m2_amm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aam_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_aam_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mmm_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_mmm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_amm_StrA_SO2_Smoke)),
                    confint(MIcombine(m3_amm_StrA_SO2_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
           factor(type3vac) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson())))
m3_mm_Type_StrA_SO2_Smoke <- with(
  des_final,
  svyglm(
    event_3doses ~ factor(smoking_status) * factor(type3vac) +
      factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi) + factor(educ_tertiles),
    family = quasipoisson())))
testModels(m3_mm_Type_StrA_SO2_Smoke, m3_am_Type_StrA_SO2_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_aam_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_mmm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
m1_amm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_aam_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_mmm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_amm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_aam_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_3doses ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_mmm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_amm_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_3doses ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
```

```r
        factor(educ_tertiles),
        family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aam_StrA_SO2_Snus)),
                    confint(MIcombine(m1_aam_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mmm_StrA_SO2_Snus)),
                    confint(MIcombine(m1_mmm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_amm_StrA_SO2_Snus)),
                    confint(MIcombine(m1_amm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aam_StrA_SO2_Snus)),
                    confint(MIcombine(m2_aam_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mmm_StrA_SO2_Snus)),
                    confint(MIcombine(m2_mmm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_amm_StrA_SO2_Snus)),
                    confint(MIcombine(m2_amm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aam_StrA_SO2_Snus)),
                    confint(MIcombine(m3_aam_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mmm_StrA_SO2_Snus)),
                    confint(MIcombine(m3_mmm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
```

```r
knitr::kable(
  round(exp(cbind(coef(MIcombine(m3_amm_StrA_SO2_Snus)),
                  confint(MIcombine(m3_amm_StrA_SO2_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           factor(educ_tertiles) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type_StrA_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(
    event_3doses ~ factor(snus_status) * factor(educ_tertiles) +
      factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi) + factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO2_Snus, m3_am_Type_StrA_SO2_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_am_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_aa_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))
m1_mm_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_am_StrA_SO3_Smoke <- with(
```

```r
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_aa_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_mm_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status) +
           pspline(age_cont) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_am_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_aa_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_StrA_SO3_Smoke <- with(
  subset(des_final, type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(smoking_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_am_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_am_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aa_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_aa_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mm_StrA_SO3_Smoke)),
                    confint(MIcombine(m1_mm_StrA_SO3_Smoke)))), 2)[2:4, ],
```

```
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_am_StrA_SO3_Smoke)),
                    confint(MIcombine(m2_am_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aa_StrA_SO3_Smoke)),
                    confint(MIcombine(m2_aa_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mm_StrA_SO3_Smoke)),
                    confint(MIcombine(m2_mm_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_am_StrA_SO3_Smoke)),
                    confint(MIcombine(m3_am_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aa_StrA_SO3_Smoke)),
                    confint(MIcombine(m3_aa_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mm_StrA_SO3_Smoke)),
                    confint(MIcombine(m3_mm_StrA_SO3_Smoke)))), 2)[2:4, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
           pspline(age_cont) + factor(type1vac) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
```

```r
m3_mm_Type_StrA_SO3_Smoke <- with(
  des_final,
  svyglm(
    event_20weeks12 ~ factor(smoking_status) * factor(type1vac) +
      pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi)+ factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO3_Smoke, m3_am_Type_StrA_SO3_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_am_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
m1_aa_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
m1_mm_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_am_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_aa_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) + factor(sex),
         family = quasipoisson()))
m2_mm_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) + factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
m3_am_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "Astra Zeneca + mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_aa_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both Astra Zeneca"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
```

```
            factor(involvement_attend_j) + factor(sex) +
            factor(fs_shp_koodi) + factor(educ_tertiles),
          family = quasipoisson()))
m3_mm_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type2vac == "both mRNA"),
  svyglm(event_20weeks12 ~ factor(snus_status) + pspline(age_cont) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(sex) +
            factor(fs_shp_koodi) + factor(educ_tertiles),
          family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_am_StrA_SO3_Snus)),
                    confint(MIcombine(m1_am_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aa_StrA_SO3_Snus)),
                    confint(MIcombine(m1_aa_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mm_StrA_SO3_Snus)),
                    confint(MIcombine(m1_mm_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_am_StrA_SO3_Snus)),
                    confint(MIcombine(m2_am_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aa_StrA_SO3_Snus)),
                    confint(MIcombine(m2_aa_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mm_StrA_SO3_Snus)),
                    confint(MIcombine(m2_mm_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_am_StrA_SO3_Snus)),
```

```
                confint(MIcombine(m3_am_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aa_StrA_SO3_Snus)),
                confint(MIcombine(m3_aa_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both Astra Zeneca", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mm_StrA_SO3_Snus)),
                confint(MIcombine(m3_mm_StrA_SO3_Snus)))), 2)[2:3, ],
    caption = "both mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(type2vac) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type_StrA_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(
    event_2doses ~ factor(snus_status) * factor(type2vac) +
      pspline(age_cont) + factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi)+ factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO3_Snus, m3_am_Type_StrA_SO3_Snus, method = "D2")

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final")])
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_aam_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson()))
m1_mmm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
```

```r
      svyglm(event_7months23 ~ factor(smoking_status),
             family = quasipoisson())))
m1_amm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status),
         family = quasipoisson())))

# Adjusted for age and sex
m2_aam_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))
m2_mmm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))
m2_amm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson())))

# Adjusted for confounders
m3_aam_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson())))
m3_mmm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "3 * mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson())))
m3_amm_StrA_SO4_Smoke <- with(
  subset(des_final, type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(smoking_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson())))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aam_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_aam_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
```

```r
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mmm_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_mmm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_amm_StrA_SO4_Smoke)),
                    confint(MIcombine(m1_amm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aam_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_aam_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mmm_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_mmm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_amm_StrA_SO4_Smoke)),
                    confint(MIcombine(m2_amm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aam_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_aam_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mmm_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_mmm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_amm_StrA_SO4_Smoke)),
                    confint(MIcombine(m3_amm_StrA_SO4_Smoke)))), 2)[2:4, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
```

```r
# Adjust confounders
m3_am_Type_StrA_SO4_Smoke <- with(
  des_final,
  svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
           factor(type3vac) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type_StrA_SO4_Smoke <- with(
  des_final,
  svyglm(
    event_7months23 ~ factor(smoking_status) * factor(type3vac) +
      factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi) + factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type_StrA_SO4_Smoke, m3_am_Type_StrA_SO4_Smoke, method = "D2")
```

Snus

```r
# Crude model
m1_aam_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_mmm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
m1_amm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))

# Adjusted for age and sex
m2_aam_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_mmm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))
m2_amm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) + pspline(age_cont) +
           factor(sex),
         family = quasipoisson()))

# Adjusted for confounders
```

```
m3_aam_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "2 * Astra Zeneca + mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_mmm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "3 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))
m3_amm_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & type3vac == "Astra Zeneca + 2 * mRNA"),
  svyglm(event_7months23 ~ factor(snus_status) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(sex) + factor(fs_shp_koodi) +
           factor(educ_tertiles),
         family = quasipoisson()))

# Obtain main estimates
kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_aam_StrA_SO4_Snus)),
                    confint(MIcombine(m1_aam_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_mmm_StrA_SO4_Snus)),
                    confint(MIcombine(m1_mmm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m1_amm_StrA_SO4_Snus)),
                    confint(MIcombine(m1_amm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M1: Crude model") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_aam_StrA_SO4_Snus)),
                    confint(MIcombine(m2_aam_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_mmm_StrA_SO4_Snus)),
                    confint(MIcombine(m2_mmm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
```

```r
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m2_amm_StrA_SO4_Snus)),
                    confint(MIcombine(m2_amm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M2: Adjusted for age and sex") %>%
  kable_classic()

kables(list(
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_aam_StrA_SO4_Snus)),
                    confint(MIcombine(m3_aam_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "2 * Astra Zeneca + mRNA") %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_mmm_StrA_SO4_Snus)),
                    confint(MIcombine(m3_mmm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "3 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T),
  knitr::kable(
    round(exp(cbind(coef(MIcombine(m3_amm_StrA_SO4_Snus)),
                    confint(MIcombine(m3_amm_StrA_SO4_Snus)))), 2)[2:3, ],
    caption = "Astra Zeneca + 2 * mRNA", row.names = F) %>%
    kableExtra::kable_classic(full_width = T)),
  caption = "M3: Adjusted for confounders") %>%
  kable_classic()

# Testing for interaction
# Adjust confounders
m3_am_Type_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           factor(type3vac) + factor(maritalstatus_bin) +
           factor(mother_tongue) + factor(involvement_attend_j) +
           factor(fs_shp_koodi) + factor(educ_tertiles),
         family = quasipoisson()))
m3_mm_Type3_StrA_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74)),
  svyglm(
    event_7months23 ~ factor(snus_status) * factor(type3vac) +
      factor(sex) + factor(maritalstatus_bin) +
      factor(mother_tongue) + factor(involvement_attend_j) +
      factor(fs_shp_koodi) + factor(educ_tertiles),
    family = quasipoisson()))
testModels(m3_mm_Type3_StrA_SO4_Snus, m3_am_Type_StrA_SO4_Snus, method = "D2")
```

End of Part III

Part IV

Loading packages and data

Packages

```r
# Loading packages
library(readxl)
library(haven)
library(styler)
library(tidyverse)
library(knitr)
library(kableExtra)
library(tidyr)
library(janitor)
library(gtools)
library(ggridges)
library(ggfortify)
library(tableone)
library(pollster)
library(naniar)
library(survey)
library(survival)
library(biostat3)
library(Epi)
library(lubridate)
library(mice)
library(mitools)
library(mitml)
library(Hmisc)
library(finalfit)
```

Data and remove unused objects

```r
load("TobriskCov_Data_25092023.RData")
# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                            "vaccinecc", "finsote_evnt", "ttr3",
                            "dose2", "dose1", "dose3")])
```

Sensitivity analyses

i) Complete case analysis

This sensitivity analysis replicates the main analysis but removing participants with missing values in any variable.

```
# Remove rows with missing values in any columns of the
finsote_compl <- finsotecc %>%
  subset(select = -c(36:39)) %>%
  na.omit()
# Make survey design object
des_compl <- svydesign(id = ~1,
                       fpc = ~rg_N_suomi,
                       weights = ~w_analysis_suomi,
                       strata = ~rg_stratum_suomi,
                       data = finsote_compl)
```

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_CCA_PO_Smoke <- svyglm(event_2doses ~ factor(smoking_status),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m1_CCA_PO_Smoke)

# Adjusted for age and sex
m2_CCA_PO_Smoke <- svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                            pspline(age_cont),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m2_CCA_PO_Smoke)

# Adjusted for confounders
m3_CCA_PO_Smoke <- svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                            pspline(age_cont) + factor(educ_tertiles) +
                            factor(maritalstatus_bin) + factor(mother_tongue) +
                            factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m3_CCA_PO_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_PO_Smoke)[2:4, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_PO_Smoke)[2:4, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_PO_Smoke)[2:4, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
```

```
nrow(m1_CCA_PO_Smoke$model[1])
nrow(m2_CCA_PO_Smoke$model[1])
nrow(m3_CCA_PO_Smoke$model[1])
# n = 26800
```

Snus

```
# Crude model
m1_CCA_PO_Snus <- svyglm(event_2doses ~ factor(snus_status),
                         family = quasipoisson(),
                         design = des_compl)
# summary(m1_CCA_PO_Snus)

# Adjusted for age and sex
m2_CCA_PO_Snus <- svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                             pspline(age_cont),
                         family = quasipoisson(),
                         design = des_compl)
# summary(m2_CCA_PO_Snus)

# Adjusted for confounders
m3_CCA_PO_Snus <- svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                             pspline(age_cont) + factor(educ_tertiles) +
                             factor(maritalstatus_bin) + factor(mother_tongue) +
                             factor(involvement_attend_j) + factor(fs_shp_koodi),
                         family = quasipoisson(),
                         design = des_compl)
# summary(m3_CCA_PO_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_PO_Snus)[2:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_PO_Snus)[2:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_PO_Snus)[2:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_PO_Snus$model[1])
nrow(m2_CCA_PO_Snus$model[1])
nrow(m3_CCA_PO_Snus$model[1])
# n = 26800
```

Secondary outcome (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_CCA_SO1_Smoke <- svyglm(event_1dose ~ factor(smoking_status),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m1_CCA_SO1_Smoke)

# Adjusted for age and sex
m2_CCA_SO1_Smoke <- svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m2_CCA_SO1_Smoke)

# Adjusted for confounders
m3_CCA_SO1_Smoke <- svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m3_CCA_SO1_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO1_Smoke)[2:4, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO1_Smoke)[2:4, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO1_Smoke)[2:4, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO1_Smoke$model[1])
nrow(m2_CCA_SO1_Smoke$model[1])
nrow(m3_CCA_SO1_Smoke$model[1])
# n = 26800
```

Snus

```
# Crude model
m1_CCA_SO1_Snus <- svyglm(event_1dose ~ factor(snus_status),
                          family = quasipoisson(),
                          design = des_compl)
```

```r
# summary(m1_CCA_SO1_Snus)

# Adjusted for age and sex
m2_CCA_SO1_Snus <- svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m2_CCA_SO1_Snus)

# Adjusted for confounders
m3_CCA_SO1_Snus <- svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont) + factor(educ_tertiles) +
                              factor(maritalstatus_bin) + factor(mother_tongue) +
                              factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m3_CCA_SO1_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO1_Snus)[2:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO1_Snus)[2:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO1_Snus)[2:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO1_Snus$model[1])
nrow(m2_CCA_SO1_Snus$model[1])
nrow(m3_CCA_SO1_Snus$model[1])
# n = 26800
```

Secondary outcome (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_CCA_SO2_Smoke <- svyglm(event_3doses ~ factor(smoking_status),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m1_CCA_SO2_Smoke)

# Adjusted for age and sex
m2_CCA_SO2_Smoke <- svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont),
                           family = quasipoisson(),
                           design = des_compl)
```

```
# summary(m2_CCA_SO2_Smoke)

# Adjusted for confounders
m3_CCA_SO2_Smoke <- svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                               pspline(age_cont) + factor(educ_tertiles) +
                               factor(maritalstatus_bin) + factor(mother_tongue) +
                               factor(involvement_attend_j) + factor(fs_shp_koodi),
                            family = quasipoisson(),
                            design = des_compl)
# summary(m3_CCA_SO2_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO2_Smoke)[2:4, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO2_Smoke)[2:4, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO2_Smoke)[2:4, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO2_Smoke$model[1])
nrow(m2_CCA_SO2_Smoke$model[1])
nrow(m3_CCA_SO2_Smoke$model[1])
# n = 26800
```

Snus

```
# Crude model
m1_CCA_SO2_Snus <- svyglm(event_3doses ~ factor(snus_status),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m1_CCA_SO2_Snus)

# Adjusted for age and sex
m2_CCA_SO2_Snus <- svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m2_CCA_SO2_Snus)

# Adjusted for confounders
m3_CCA_SO2_Snus <- svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont) + factor(educ_tertiles) +
                              factor(maritalstatus_bin) + factor(mother_tongue) +
                              factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson(),
                          design = des_compl)
```

```r
# summary(m3_CCA_SO2_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO2_Snus)[2:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")
kable(round(ci.exp(m2_CCA_SO2_Snus)[2:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
kable(round(ci.exp(m3_CCA_SO2_Snus)[2:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO2_Snus$model[1])
nrow(m2_CCA_SO2_Snus$model[1])
nrow(m3_CCA_SO2_Snus$model[1])
# n = 26800
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_CCA_SO3_Smoke <- svyglm(event_20weeks12 ~ factor(smoking_status),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m1_CCA_SO3_Smoke)

# Adjusted for age and sex
m2_CCA_SO3_Smoke <- svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                             pspline(age_cont),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m2_CCA_SO3_Smoke)

# Adjusted for confounders
m3_CCA_SO3_Smoke <- svyglm(event_20weeks12 ~ factor(smoking_status) +
                             factor(sex) + pspline(age_cont) +
                             factor(educ_tertiles) + factor(maritalstatus_bin) +
                             factor(mother_tongue) + factor(involvement_attend_j) +
                             factor(fs_shp_koodi),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m3_CCA_SO3_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO3_Smoke)[2:4, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")
```

```r
kable(round(ci.exp(m2_CCA_SO3_Smoke)[2:4, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO3_Smoke)[2:4, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO3_Smoke$model[1])
nrow(m2_CCA_SO3_Smoke$model[1])
nrow(m3_CCA_SO3_Smoke$model[1])
# n = 26800
```

Snus

```r
# Crude model
m1_CCA_SO3_Snus <- svyglm(event_20weeks12 ~ factor(snus_status),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m1_CCA_SO3_Snus)

# Adjusted for age and sex
m2_CCA_SO3_Snus <- svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                            pspline(age_cont),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m2_CCA_SO3_Snus)

# Adjusted for confounders
m3_CCA_SO3_Snus <- svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                            pspline(age_cont) + factor(educ_tertiles) +
                            factor(maritalstatus_bin) + factor(mother_tongue) +
                            factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m3_CCA_SO3_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO3_Snus)[2:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO3_Snus)[2:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO3_Snus)[2:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")
```

```
# Check the estimates are on the same sample
nrow(m1_CCA_SO3_Snus$model[1])
nrow(m2_CCA_SO3_Snus$model[1])
nrow(m3_CCA_SO3_Snus$model[1])
# n = 26800
```

Secondary outcome (iv): Interval spacing between 2nd and 3nd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_CCA_SO4_Smoke <- svyglm(event_7months23 ~ factor(smoking_status),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m1_smoking_intvl12_compl)

# Adjusted for age and sex
m2_CCA_SO4_Smoke <- svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                             pspline(age_cont),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m2_CCA_SO4_Smoke)

# Adjusted for confounders
m3_CCA_SO4_Smoke <- svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                             pspline(age_cont) + factor(educ_tertiles) +
                             factor(maritalstatus_bin) + factor(mother_tongue) +
                             factor(involvement_attend_j) + factor(fs_shp_koodi),
                           family = quasipoisson(),
                           design = des_compl)
# summary(m3_CCA_SO4_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO4_Smoke)[2:4, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO4_Smoke)[2:4, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO4_Smoke)[2:4, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO4_Smoke$model[1])
nrow(m2_CCA_SO4_Smoke$model[1])
nrow(m3_CCA_SO4_Smoke$model[1])
# n = 26800
```

Snus

```r
# Crude model
m1_CCA_SO4_Snus <- svyglm(event_7months23 ~ factor(snus_status),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m1_CCA_SO3_Snus)

# Adjusted for age and sex
m2_CCA_SO4_Snus <- svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                            pspline(age_cont),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m2_CCA_SO4_Snus)

# Adjusted for confounders
m3_CCA_SO4_Snus <- svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                            pspline(age_cont) + factor(educ_tertiles) +
                            factor(maritalstatus_bin) + factor(mother_tongue) +
                            factor(involvement_attend_j) + factor(fs_shp_koodi),
                          family = quasipoisson(),
                          design = des_compl)
# summary(m3_CCA_SO4_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_CCA_SO4_Snus)[2:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_CCA_SO4_Snus)[2:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_CCA_SO4_Snus)[2:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_CCA_SO4_Snus$model[1])
nrow(m2_CCA_SO4_Snus$model[1])
nrow(m3_CCA_SO4_Snus$model[1])
# n = 26800

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                            "vaccinecc", "finsote_evnt", "ttr3",
                            "dose2", "dose1", "dose3")])
```

ii) Exclude participants who participated in FinSote after Dec 27, 2020

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# participated after 2020-12-27
IDs <- finsote2020_dates %>%
  subset(date <= "2020-12-27") %>%
  reframe(GUMM85ID)

# Crude model
m1_SA2_PO_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA2_PO_Smoke))

# Adjusted for age and sex
m2_SA2_PO_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA2_PO_Smoke))

# Adjusted for confounders
m3_SA2_PO_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA2_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_PO_Smoke)),
                             confint(MIcombine(m1_SA2_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_PO_Smoke)),
                             confint(MIcombine(m2_SA2_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_PO_Smoke)),
                             confint(MIcombine(m3_SA2_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA2_PO_Smoke[[1]]$data)
nrow(m2_SA2_PO_Smoke[[1]]$data)
```

```r
nrow(m3_SA2_PO_Smoke[[1]]$data)
# n = 24412
```

Snus

```r
# Crude model
m1_SA2_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_2doses ~  factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA2_PO_Snus))

# Adjusted for age and sex
m2_SA2_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA2_PO_Snus))

# Adjusted for confounders
m3_SA2_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_SA2_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_PO_Snus)),
                             confint(MIcombine(m1_SA2_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_PO_Snus)),
                             confint(MIcombine(m2_SA2_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_PO_Snus)),
                             confint(MIcombine(m3_SA2_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA2_PO_Snus[[1]]$data)
nrow(m2_SA2_PO_Snus[[1]]$data)
nrow(m3_SA2_PO_Snus[[1]]$data)
# n = 15806
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA2_SO1_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO1_Smoke))

## Adjusted for age and sex
m2_SA2_SO1_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO1_Smoke))

# Adjusted for confounders
m3_SA2_SO1_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont) + factor(educ_tertiles) +
                                    factor(maritalstatus_bin) + factor(mother_tongue) +
                                    factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO1_Smoke)),
                             confint(MIcombine(m1_SA2_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO1_Smoke)),
                             confint(MIcombine(m2_SA2_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO1_Smoke)),
                             confint(MIcombine(m3_SA2_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA2_SO1_Smoke[[1]]$data)
nrow(m2_SA2_SO1_Smoke[[1]]$data)
nrow(m3_SA2_SO1_Smoke[[1]]$data)
# n = 24412
```

Snus

```r
# Crude model
m1_SA2_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
```

```
      svyglm(event_1dose ~ factor(snus_status),
             family = quasipoisson())))
# summary(MIcombine(m1_SA2_SO1_Snus))


# Adjusted for age and sex
m2_SA2_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
              pspline(age_cont),
             family = quasipoisson())))
# summary(MIcombine(m2_SA2_SO1_Snus))


# Adjusted for confounders
m3_SA2_SO1_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
              pspline(age_cont) + factor(educ_tertiles) +
              factor(maritalstatus_bin) + factor(mother_tongue) +
              factor(involvement_attend_j) + factor(fs_shp_koodi),
             family = quasipoisson())))
# summary(MIcombine(m3_SA2_SO1_Snus))


# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO1_Snus)),
                             confint(MIcombine(m1_SA2_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO1_Snus)),
                             confint(MIcombine(m2_SA2_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO1_Snus)),
                             confint(MIcombine(m3_SA2_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA2_SO1_Snus[[1]]$data)
nrow(m2_SA2_SO1_Snus[[1]]$data)
nrow(m3_SA2_SO1_Snus[[1]]$data)
# n = 15806
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA2_SO2_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                          svyglm(event_3doses ~ factor(smoking_status),
                                 family = quasipoisson())))
```

```r
# summary(MIcombine(m1_SA2_SO2_Smoke))

# Adjusted for age and sex
m2_SA2_SO2_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO2_Smoke))

## Adjusted for confounders
m3_SA2_SO2_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO2_Smoke)),
                             confint(MIcombine(m1_SA2_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO2_Smoke)),
                             confint(MIcombine(m2_SA2_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO2_Smoke)),
                             confint(MIcombine(m3_SA2_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA2_SO2_Smoke[[1]]$data)
nrow(m2_SA2_SO2_Smoke[[1]]$data)
nrow(m3_SA2_SO2_Smoke[[1]]$data)
# n = 24412
```

Snus

```r
## Crude model
m1_SA2_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO2_Snus))

## Adjusted for age and sex
m2_SA2_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) + pspline(age_cont),
         family = quasipoisson()))
```

```
# summary(MIcombine(m2_SA2_SO2_Snus))

# Adjusted for confounders
m3_SA2_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO2_Snus)),
                            confint(MIcombine(m1_SA2_SO2_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO2_Snus)),
                            confint(MIcombine(m2_SA2_SO2_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO2_Snus)),
                            confint(MIcombine(m3_SA2_SO2_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA2_SO2_Snus[[1]]$data)
nrow(m2_SA2_SO2_Snus[[1]]$data)
nrow(m3_SA2_SO2_Snus[[1]]$data)
# n = 15806
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA2_SO3_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO3_Smoke))

# Adjusted for age and sex
m2_SA2_SO3_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO3_Smoke))
```

```r
# Adjusted for confounders
m3_SA2_SO3_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                         family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO3_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO3_Smoke)),
                       confint(MIcombine(m1_SA2_SO3_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO3_Smoke)),
                       confint(MIcombine(m2_SA2_SO3_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO3_Smoke)),
                       confint(MIcombine(m3_SA2_SO3_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA2_SO3_Smoke[[1]]$data)
nrow(m2_SA2_SO3_Smoke[[1]]$data)
nrow(m3_SA2_SO3_Smoke[[1]]$data)
# n = 24412
```

Snus

```r
# Crude model
m1_SA2_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO3_Snus))

# Adjusted for age and sex
m2_SA2_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO3_Snus))

# Adjusted for confounders
m3_SA2_SO3_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
```

```
        svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
               pspline(age_cont) + factor(educ_tertiles) +
               factor(maritalstatus_bin) + factor(mother_tongue) +
               factor(involvement_attend_j) + factor(fs_shp_koodi),
           family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO3_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO3_Snus)),
                             confint(MIcombine(m1_SA2_SO3_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO3_Snus)),
                             confint(MIcombine(m2_SA2_SO3_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO3_Snus)),
                             confint(MIcombine(m3_SA2_SO3_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA2_SO3_Snus[[1]]$data)
nrow(m2_SA2_SO3_Snus[[1]]$data)
nrow(m3_SA2_SO3_Snus[[1]]$data)
# n = 15806
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA2_SO4_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO4_Smoke))

# Adjusted for age and sex
m2_SA2_SO4_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO4_Smoke))

# Adjusted for confounders
m3_SA2_SO4_Smoke <- with(subset(des_final, GUMM85ID %in% IDs$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status) +
                                    factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
```

```
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                           family = quasipoisson()))
# summary(MIcombine(m3_SA2_SO4_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO4_Smoke)),
                              confint(MIcombine(m1_SA2_SO4_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO4_Smoke)),
                              confint(MIcombine(m2_SA2_SO4_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO4_Smoke)),
                              confint(MIcombine(m3_SA2_SO4_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA2_SO4_Smoke[[1]]$data)
nrow(m2_SA2_SO4_Smoke[[1]]$data)
nrow(m3_SA2_SO4_Smoke[[1]]$data)
# n = 24412
```

Snus

```
# Crude model
m1_SA2_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA2_SO4_Snus))

# Adjusted for age and sex
m2_SA2_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA2_SO4_Snus))

# Adjusted for confounders
m3_SA2_SO4_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & GUMM85ID %in% IDs$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
```

```r
# summary(MIcombine(m3_SA2_SO4_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA2_SO4_Snus)),
                             confint(MIcombine(m1_SA2_SO4_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA2_SO4_Snus)),
                             confint(MIcombine(m2_SA2_SO4_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA2_SO4_Snus)),
                             confint(MIcombine(m3_SA2_SO4_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA2_SO4_Snus[[1]]$data)
nrow(m2_SA2_SO4_Snus[[1]]$data)
nrow(m3_SA2_SO4_Snus[[1]]$data)
# n = 15806

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                            "vaccinecc", "finsote_evnt", "ttr3",
                            "dose2", "dose1", "dose3")])
```

iii) Count and exclude participants who have received a vaccination dose prior to February 8, 2021, when the data collection of FinSote 2020 ended

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Count based on vaccinecc data
Count_before8Feb <- vaccinecc %>%
  subset(vaccine_date < "2021-02-08") %>%
  reframe(GUMM85ID = unique(GUMM85ID)) %>%
  count()
paste(
  "Number of participants who have received a vaccintion dose prior to 8th Feb, 2021:",
  Count_before8Feb)

IDs_before8Feb <- vaccinecc %>%
  subset(vaccine_date < "2021-02-08") %>%
  reframe(GUMM85ID = unique(GUMM85ID))

# Crude model
m1_SA3_PO_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
```

```
                        svyglm(event_2doses ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA3_PO_Smoke))

# Adjusted for age and sex
m2_SA3_PO_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA3_PO_Smoke))

# Adjusted for confounders
m3_SA3_PO_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA3_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_PO_Smoke)),
                        confint(MIcombine(m1_SA3_PO_Smoke)))), 2)[2:4,],
            caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_PO_Smoke)),
                        confint(MIcombine(m2_SA3_PO_Smoke)))), 2)[2:4,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_PO_Smoke)),
                        confint(MIcombine(m3_SA3_PO_Smoke)))), 2)[2:4,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA3_PO_Smoke[[1]]$data)
nrow(m2_SA3_PO_Smoke[[1]]$data)
nrow(m3_SA3_PO_Smoke[[1]]$data)
# n = 41032
```

Snus

```
# Crude model
m1_SA3_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_2doses ~  factor(snus_status),
        family = quasipoisson()))
# summary(MIcombine(m1_SA3_PO_Snus))

# Adjusted for age and sex
```

```r
m2_SA3_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA3_PO_Snus))


# Adjusted for confounders
m3_SA3_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_SA3_PO_Snus))


# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_PO_Snus)),
                             confint(MIcombine(m1_SA3_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_PO_Snus)),
                             confint(MIcombine(m2_SA3_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_PO_Snus)),
                             confint(MIcombine(m3_SA3_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")


# Checking the estimates are on the same sample
nrow(m1_SA3_PO_Snus[[1]]$data)
nrow(m2_SA3_PO_Snus[[1]]$data)
nrow(m3_SA3_PO_Snus[[1]]$data)
# n = 28241
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA3_SO1_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA3_SO1_Smoke))

## Adjusted for age and sex
m2_SA3_SO1_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
```

```
                          svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                     pspline(age_cont),
                                 family = quasipoisson())))
# summary(MIcombine(m2_SA3_SO1_Smoke))


# Adjusted for confounders
m3_SA3_SO1_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                          svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                     pspline(age_cont) + factor(educ_tertiles) +
                                     factor(maritalstatus_bin) + factor(mother_tongue) +
                                     factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson())))
# summary(MIcombine(m3_SA3_SO1_Smoke))


# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO1_Smoke)),
                              confint(MIcombine(m1_SA3_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO1_Smoke)),
                              confint(MIcombine(m2_SA3_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO1_Smoke)),
                              confint(MIcombine(m3_SA3_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA3_SO1_Smoke[[1]]$data)
nrow(m2_SA3_SO1_Smoke[[1]]$data)
nrow(m3_SA3_SO1_Smoke[[1]]$data)
# n = 41032
```

Snus

```
# Crude model
m1_SA3_SO1_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_1dose ~ factor(snus_status),
         family = quasipoisson())))
# summary(MIcombine(m1_SA3_SO1_Snus))

# Adjusted for age and sex
m2_SA3_SO1_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
```

```r
        family = quasipoisson()))
# summary(MIcombine(m2_SA3_SO1_Snus))

# Adjusted for confounders
m3_SA3_SO1_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & ! GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_SA3_SO1_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO1_Snus)),
                             confint(MIcombine(m1_SA3_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO1_Snus)),
                             confint(MIcombine(m2_SA3_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO1_Snus)),
                             confint(MIcombine(m3_SA3_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA3_SO1_Snus[[1]]$data)
nrow(m2_SA3_SO1_Snus[[1]]$data)
nrow(m3_SA3_SO1_Snus[[1]]$data)
# n = 28241
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA3_SO2_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA3_SO2_Smoke))

# Adjusted for age and sex
m2_SA3_SO2_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
```

```
# summary(MIcombine(m2_SA3_SO2_Smoke))

## Adjusted for confounders
m3_SA3_SO2_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson())))
# summary(MIcombine(m3_SA3_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO2_Smoke)),
                             confint(MIcombine(m1_SA3_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO2_Smoke)),
                             confint(MIcombine(m2_SA3_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO2_Smoke)),
                             confint(MIcombine(m3_SA3_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA3_SO2_Smoke[[1]]$data)
nrow(m2_SA3_SO2_Smoke[[1]]$data)
nrow(m3_SA3_SO2_Smoke[[1]]$data)
# n = 41032
```

Snus

```
## Crude model
m1_SA3_SO2_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_3doses ~ factor(snus_status),
         family = quasipoisson())))
# summary(MIcombine(m1_SA3_SO2_Snus))

## Adjusted for age and sex
m2_SA3_SO2_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_3doses ~ factor(snus_status) + factor(sex) + pspline(age_cont),
         family = quasipoisson())))
# summary(MIcombine(m2_SA3_SO2_Snus))

# Adjusted for confounders
m3_SA3_SO2_Snus <- with(
```

```
     subset(des_final,
            between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
     svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
            pspline(age_cont) + factor(educ_tertiles) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson())))
# summary(MIcombine(m3_SA3_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO2_Snus)),
                            confint(MIcombine(m1_SA3_SO2_Snus)))), 2)[2:3,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO2_Snus)),
                            confint(MIcombine(m2_SA3_SO2_Snus)))), 2)[2:3,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO2_Snus)),
                            confint(MIcombine(m3_SA3_SO2_Snus)))), 2)[2:3,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA3_SO2_Snus[[1]]$data)
nrow(m2_SA3_SO2_Snus[[1]]$data)
nrow(m3_SA3_SO2_Snus[[1]]$data)
# n = 28241
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA3_SO3_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                        svyglm(event_20weeks12 ~ factor(smoking_status),
                                family = quasipoisson())))
# summary(MIcombine(m1_SA3_SO3_Smoke))

# Adjusted for age and sex
m2_SA3_SO3_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                        svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson())))
# summary(MIcombine(m2_SA3_SO3_Smoke))

# Adjusted for confounders
m3_SA3_SO3_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
```

```
                  svyglm(event_20weeks12 ~ factor(smoking_status) +
                         factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                         factor(maritalstatus_bin) + factor(mother_tongue) +
                         factor(involvement_attend_j) + factor(fs_shp_koodi),
                       family = quasipoisson()))
# summary(MIcombine(m3_SA3_SO3_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO3_Smoke)),
                             confint(MIcombine(m1_SA3_SO3_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO3_Smoke)),
                             confint(MIcombine(m2_SA3_SO3_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO3_Smoke)),
                             confint(MIcombine(m3_SA3_SO3_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA3_SO3_Smoke[[1]]$data)
nrow(m2_SA3_SO3_Smoke[[1]]$data)
nrow(m3_SA3_SO3_Smoke[[1]]$data)
# n = 41032
```

Snus

```
# Crude model
m1_SA3_SO3_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_20weeks12 ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA3_SO3_Snus))

# Adjusted for age and sex
m2_SA3_SO3_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA3_SO3_Snus))

# Adjusted for confounders
m3_SA3_SO3_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
```

```r
    svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
            pspline(age_cont) + factor(educ_tertiles) +
            factor(maritalstatus_bin) + factor(mother_tongue) +
            factor(involvement_attend_j) + factor(fs_shp_koodi),
        family = quasipoisson())))
# summary(MIcombine(m3_SA3_SO3_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO3_Snus)),
                        confint(MIcombine(m1_SA3_SO3_Snus)))), 2)[2:3,],
        caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO3_Snus)),
                        confint(MIcombine(m2_SA3_SO3_Snus)))), 2)[2:3,],
        caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO3_Snus)),
                        confint(MIcombine(m3_SA3_SO3_Snus)))), 2)[2:3,],
        caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA3_SO3_Snus[[1]]$data)
nrow(m2_SA3_SO3_Snus[[1]]$data)
nrow(m3_SA3_SO3_Snus[[1]]$data)
# n = 28241
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA3_SO4_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                    svyglm(event_7months23 ~ factor(smoking_status),
                            family = quasipoisson()))
# summary(MIcombine(m1_SA3_SO4_Smoke))

# Adjusted for age and sex
m2_SA3_SO4_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                    svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                            pspline(age_cont),
                            family = quasipoisson()))
# summary(MIcombine(m2_SA3_SO4_Smoke))

# Adjusted for confounders
m3_SA3_SO4_Smoke <- with(subset(des_final, !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
                    svyglm(event_7months23 ~ factor(smoking_status) +
                            factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
```

```
                                    factor(maritalstatus_bin) + factor(mother_tongue) +
                                    factor(involvement_attend_j) + factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_SA3_SO4_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO4_Smoke)),
                              confint(MIcombine(m1_SA3_SO4_Smoke)))), 2)[2:4,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO4_Smoke)),
                              confint(MIcombine(m2_SA3_SO4_Smoke)))), 2)[2:4,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO4_Smoke)),
                              confint(MIcombine(m3_SA3_SO4_Smoke)))), 2)[2:4,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA3_SO4_Smoke[[1]]$data)
nrow(m2_SA3_SO4_Smoke[[1]]$data)
nrow(m3_SA3_SO4_Smoke[[1]]$data)
# n = 41032
```

Snus

```
# Crude model
m1_SA3_SO4_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA3_SO4_Snus))

# Adjusted for age and sex
m2_SA3_SO4_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA3_SO4_Snus))

# Adjusted for confounders
m3_SA3_SO4_Snus <- with(
  subset(des_final,
         between(age_cont, 20, 74) & !GUMM85ID %in% IDs_before8Feb$GUMM85ID),
  svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
```

```
                factor(maritalstatus_bin) + factor(mother_tongue) +
                factor(involvement_attend_j) + factor(fs_shp_koodi),
            family = quasipoisson()))
# summary(MIcombine(m3_SA3_SO4_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA3_SO4_Snus)),
                            confint(MIcombine(m1_SA3_SO4_Snus)))), 2)[2:3,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA3_SO4_Snus)),
                            confint(MIcombine(m2_SA3_SO4_Snus)))), 2)[2:3,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA3_SO4_Snus)),
                            confint(MIcombine(m3_SA3_SO4_Snus)))), 2)[2:3,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA3_SO4_Snus[[1]]$data)
nrow(m2_SA3_SO4_Snus[[1]]$data)
nrow(m3_SA3_SO4_Snus[[1]]$data)
# n = 28241

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                            "vaccinecc", "finsote_evnt", "ttr3",
                            "dose2", "dose1", "dose3")])
```

iv) Same estimates as the main analyses, but restricting the follow-up time to when vaccination coverage reached 60% and 80%

Vaccination coverage reached 60%

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```
# Find 2nd dose in vaccinecc data
Find2nddose <- vaccinecc %>%
  group_by(GUMM85ID) %>%
  arrange(vaccine_date) %>%
  filter(row_number() == 2)

# Combine Find2nddose with finsote_evnt data
# Get cumulative percentage and subset prop <=0.6
IDs_60 <- finsote_evnt %>%
  left_join(Find2nddose, by = "GUMM85ID")  %>%
```

```r
    arrange(vaccine_date) %>%
    mutate(prop = cumsum(event_2doses)/sum(!is.na(event_2doses))) %>%
    subset(prop <= 0.6) %>%
    reframe(GUMM85ID)


# Update design object
des_60 <- update(des_final,
                event_2doses = case_when(
                  GUMM85ID %in% IDs_60$GUMM85ID ~ event_2doses,
                  TRUE ~ 0),
                event_1dose = case_when(
                  GUMM85ID %in% IDs_60$GUMM85ID ~ event_1dose,
                  TRUE ~ 0),
                event_3doses = case_when(
                  GUMM85ID %in% IDs_60$GUMM85ID ~ event_3doses,
                  TRUE ~ 0))


# Crude model
m1_SA4.1_PO_Smoke <- with(des_60,
                          svyglm(event_2doses ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_PO_Smoke))

# Adjusted for age and sex
m2_SA4.1_PO_Smoke <- with(des_60,
                          svyglm(event_2doses ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_PO_Smoke))

# Adjusted for confounders
m3_SA4.1_PO_Smoke <- with(des_60,
                          svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_PO_Smoke)),
                             confint(MIcombine(m1_SA4.1_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_PO_Smoke)),
                             confint(MIcombine(m2_SA4.1_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_PO_Smoke)),
                             confint(MIcombine(m3_SA4.1_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
```

```
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA4.1_PO_Smoke[[1]]$data)
nrow(m2_SA4.1_PO_Smoke[[1]]$data)
nrow(m3_SA4.1_PO_Smoke[[1]]$data)
# n = 42935
```

Snus

```
# Crude model
m1_SA4.1_PO_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_PO_Snus))

# Adjusted for age and sex
m2_SA4.1_PO_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_PO_Snus))

# Adjusted for confounders
m3_SA4.1_PO_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                         svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_PO_Snus)),
                            confint(MIcombine(m1_SA4.1_PO_Snus)))), 2)[2:3,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_PO_Snus)),
                            confint(MIcombine(m2_SA4.1_PO_Snus)))), 2)[2:3,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_PO_Snus)),
                            confint(MIcombine(m3_SA4.1_PO_Snus)))), 2)[2:3,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.1_PO_Snus[[1]]$data)
nrow(m2_SA4.1_PO_Snus[[1]]$data)
```

```
nrow(m3_SA4.1_PO_Snus[[1]]$data)
# n = 19501
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA4.1_SO1_Smoke <- with(des_60,
                           svyglm(event_1dose ~ factor(smoking_status),
                                  family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_SO1_Smoke))

## Adjusted for age and sex
m2_SA4.1_SO1_Smoke <- with(des_60,
                           svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_SO1_Smoke))

# Adjusted for confounders
m3_SA4.1_SO1_Smoke <- with(des_60,
                           svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont) + factor(educ_tertiles) +
                                    factor(maritalstatus_bin) + factor(mother_tongue) +
                                    factor(involvement_attend_j) + factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_SO1_Smoke)),
                             confint(MIcombine(m1_SA4.1_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_SO1_Smoke)),
                             confint(MIcombine(m2_SA4.1_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_SO1_Smoke)),
                             confint(MIcombine(m3_SA4.1_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.1_SO1_Smoke[[1]]$data)
nrow(m2_SA4.1_SO1_Smoke[[1]]$data)
nrow(m3_SA4.1_SO1_Smoke[[1]]$data)
# n = 27977
```

Snus

```r
# Crude model
m1_SA4.1_SO1_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_SO1_Snus))

# Adjusted for age and sex
m2_SA4.1_SO1_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                     pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_SO1_Snus))

# Adjusted for confounders
m3_SA4.1_SO1_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                     pspline(age_cont) + factor(educ_tertiles) +
                                     factor(maritalstatus_bin) + factor(mother_tongue) +
                                     factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_SO1_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_SO1_Snus)),
                             confint(MIcombine(m1_SA4.1_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_SO1_Snus)),
                             confint(MIcombine(m2_SA4.1_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_SO1_Snus)),
                             confint(MIcombine(m3_SA4.1_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.1_SO1_Snus[[1]]$data)
nrow(m2_SA4.1_SO1_Snus[[1]]$data)
nrow(m3_SA4.1_SO1_Snus[[1]]$data)
# n = 19501
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA4.1_SO2_Smoke <- with(des_60,
                           svyglm(event_3doses ~ factor(smoking_status),
                                  family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_SO2_Smoke))

# Adjusted for age and sex
m2_SA4.1_SO2_Smoke <- with(des_60,
                           svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                     pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_SO2_Smoke))

## Adjusted for confounders
m3_SA4.1_SO2_Smoke <- with(des_60,
                           svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                     pspline(age_cont) + factor(educ_tertiles) +
                                     factor(maritalstatus_bin) + factor(mother_tongue) +
                                     factor(involvement_attend_j) + factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_SO2_Smoke)),
                             confint(MIcombine(m1_SA4.1_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_SO2_Smoke)),
                             confint(MIcombine(m2_SA4.1_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_SO2_Smoke)),
                             confint(MIcombine(m3_SA4.1_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA4.1_SO2_Smoke[[1]]$data)
nrow(m2_SA4.1_SO2_Smoke[[1]]$data)
nrow(m3_SA4.1_SO2_Smoke[[1]]$data)
# n = 42935
```

Snus

```r
## Crude model
m1_SA4.1_SO2_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.1_SO2_Snus))

## Adjusted for age and sex
```

```r
m2_SA4.1_SO2_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.1_SO2_Snus))

# Adjusted for confounders
m3_SA4.1_SO2_Snus <- with(subset(des_60, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.1_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.1_SO2_Snus)),
                       confint(MIcombine(m1_SA4.1_SO2_Snus)))), 2)[2:3,],
        caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.1_SO2_Snus)),
                       confint(MIcombine(m2_SA4.1_SO2_Snus)))), 2)[2:3,],
        caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.1_SO2_Snus)),
                       confint(MIcombine(m3_SA4.1_SO2_Snus)))), 2)[2:3,],
        caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.1_SO2_Snus[[1]]$data)
nrow(m2_SA4.1_SO2_Snus[[1]]$data)
nrow(m3_SA4.1_SO2_Snus[[1]]$data)
# n = 19501
```

Vaccination coverage reached 80%

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Combine Findfirstdose with finsoto_evnt data
# Get cumulative precentage and subset prop <= 0.8
IDs_80 <- finsote_evnt %>%
  left_join(Find2nddose, by = "GUMM85ID") %>%
  arrange(vaccine_date) %>%
  mutate(prop = cumsum(event_2doses)/sum(!is.na(event_2doses))) %>%
  subset(prop <= 0.8) %>%
  reframe(GUMM85ID)
```

```r
# update design object
des_80 <- update(des_final,
                 event_2doses = case_when(
                   GUMM85ID %in% IDs_80$GUMM85ID ~ event_2doses,
                   TRUE ~ 0),
                 event_1dose = case_when(
                   GUMM85ID %in% IDs_80$GUMM85ID ~ event_1dose,
                   TRUE ~ 0),
                 event_3doses = case_when(
                   GUMM85ID %in% IDs_80$GUMM85ID ~ event_3doses,
                   TRUE ~ 0))


# Crude model
m1_SA4.2_PO_Smoke <- with(des_80,
                          svyglm(event_2doses ~ factor(smoking_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_PO_Smoke))

# Adjusted for age and sex
m2_SA4.2_PO_Smoke <- with(des_80,
                          svyglm(event_2doses ~ factor(smoking_status) +
                                   factor(sex) + pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.2_PO_Smoke))

# Adjusted for confounders
m3_SA4.2_PO_Smoke <- with(des_80,
                          svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_PO_Smoke)),
                             confint(MIcombine(m1_SA4.2_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_PO_Smoke)),
                             confint(MIcombine(m2_SA4.2_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_PO_Smoke)),
                             confint(MIcombine(m3_SA4.2_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA4.2_PO_Smoke[[1]]$data)
nrow(m2_SA4.2_PO_Smoke[[1]]$data)
```

```
nrow(m3_SA4.2_PO_Smoke[[1]]$data)
# n = 37180
```

Snus

```
# Crude model
m1_SA4.2_PO_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_2doses ~ factor(snus_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_PO_Snus))

# Adjusted for age and sex
m2_SA4.2_PO_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.2_PO_Snus))

# Adjusted for confounders
m3_SA4.2_PO_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_PO_Snus)),
                             confint(MIcombine(m1_SA4.2_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_PO_Snus)),
                             confint(MIcombine(m2_SA4.2_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_PO_Snus)),
                             confint(MIcombine(m3_SA4.2_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.2_PO_Snus[[1]]$data)
nrow(m2_SA4.2_PO_Snus[[1]]$data)
nrow(m3_SA4.2_PO_Snus[[1]]$data)
# n = 25342
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA4.2_SO1_Smoke <- with(des_80,
                           svyglm(event_1dose ~ factor(smoking_status),
                                  family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_SO1_Smoke))

## Adjusted for age and sex
m2_SA4.2_SO1_Smoke <- with(des_80,
                           svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                      pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SA4.2_SO1_Smoke))

# Adjusted for confounders
m3_SA4.2_SO1_Smoke <- with(des_80,
                           svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                      pspline(age_cont) + factor(educ_tertiles) +
                                      factor(maritalstatus_bin) + factor(mother_tongue) +
                                      factor(involvement_attend_j) + factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_SO1_Smoke)),
                             confint(MIcombine(m1_SA4.2_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_SO1_Smoke)),
                             confint(MIcombine(m2_SA4.2_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_SO1_Smoke)),
                             confint(MIcombine(m3_SA4.2_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.2_SO1_Smoke[[1]]$data)
nrow(m2_SA4.2_SO1_Smoke[[1]]$data)
nrow(m3_SA4.2_SO1_Smoke[[1]]$data)
# n = 37180
```

Snus

```r
# Crude model
m1_SA4.2_SO1_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_SO1_Snus))

# Adjusted for age and sex
m2_SA4.2_SO1_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont),
                                 family = quasipoisson()))
# summary(MIcombine(m2_SA4.2_SO1_Snus))

# Adjusted for confounders
m3_SA4.2_SO1_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_SO1_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_SO1_Snus)),
                             confint(MIcombine(m1_SA4.2_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_SO1_Snus)),
                             confint(MIcombine(m2_SA4.2_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_SO1_Snus)),
                             confint(MIcombine(m3_SA4.2_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.2_SO1_Snus[[1]]$data)
nrow(m2_SA4.2_SO1_Snus[[1]]$data)
nrow(m3_SA4.2_SO1_Snus[[1]]$data)
# n = 25342
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA4.2_SO2_Smoke <- with(des_80,
                           svyglm(event_3doses ~ factor(smoking_status),
```

```
                                  family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_SO2_Smoke))

# Adjusted for age and sex
m2_SA4.2_SO2_Smoke <- with(des_80,
                           svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                  family = quasipoisson()))
# summary(MIcombine(m2_SA4.2_SO2_Smoke))

## Adjusted for confounders
m3_SA4.2_SO2_Smoke <- with(des_80,
                           svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_SO2_Smoke)),
                             confint(MIcombine(m1_SA4.2_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_SO2_Smoke)),
                             confint(MIcombine(m2_SA4.2_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_SO2_Smoke)),
                             confint(MIcombine(m3_SA4.2_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA4.2_SO2_Smoke[[1]]$data)
nrow(m2_SA4.2_SO2_Smoke[[1]]$data)
nrow(m3_SA4.2_SO2_Smoke[[1]]$data)
# n = 37180
```

Snus

```
## Crude model
m1_SA4.2_SO2_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status),
                                 family = quasipoisson()))
# summary(MIcombine(m1_SA4.2_SO2_Snus))

## Adjusted for age and sex
m2_SA4.2_SO2_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont),
                                 family = quasipoisson()))
```

```r
# summary(MIcombine(m2_SA4.2_SO2_Snus))

# Adjusted for confounders
m3_SA4.2_SO2_Snus <- with(subset(des_80, between(age_cont, 20, 74)),
                          svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                                 family = quasipoisson()))
# summary(MIcombine(m3_SA4.2_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA4.2_SO2_Snus)),
                             confint(MIcombine(m1_SA4.2_SO2_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA4.2_SO2_Snus)),
                             confint(MIcombine(m2_SA4.2_SO2_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA4.2_SO2_Snus)),
                             confint(MIcombine(m3_SA4.2_SO2_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA4.2_SO2_Snus[[1]]$data)
nrow(m2_SA4.2_SO2_Snus[[1]]$data)
nrow(m3_SA4.2_SO2_Snus[[1]]$data)
# n = 25342

# Remove unnecessary objects from work space.
rm(list=ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                          "vaccinecc", "finsote_evnt", "ttr3",
                          "dose2", "dose1", "dose3")])
```

v) Restricts analysis to prospectively collected data to examine information bias

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA5_PO_Smoke <- with(subset(des_final, dataid == 2018),
                        svyglm(event_2doses ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA5_PO_Smoke))

# Adjusted for age and sex
```

```r
m2_SA5_PO_Smoke <- with(subset(des_final, dataid == 2018),
                        svyglm(event_2doses ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA5_PO_Smoke))

# Adjusted for confounders
m3_SA5_PO_Smoke <- with(subset(des_final, dataid == 2018),
                        svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA5_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_PO_Smoke)),
                         confint(MIcombine(m1_SA5_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_PO_Smoke)),
                         confint(MIcombine(m2_SA5_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_PO_Smoke)),
                         confint(MIcombine(m3_SA5_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA5_PO_Smoke[[1]]$data)
nrow(m2_SA5_PO_Smoke[[1]]$data)
nrow(m3_SA5_PO_Smoke[[1]]$data)
# n = 14736
```

Snus

```r
# Crude model
m1_SA5_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_2doses ~  factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_SA5_PO_Snus))

# Adjusted for age and sex
m2_SA5_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont),
                              family = quasipoisson()))
# summary(MIcombine(m2_SA5_PO_Snus))
```

```
# Adjusted for confounders
m3_SA5_PO_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
                              pspline(age_cont) + factor(educ_tertiles) +
                              factor(maritalstatus_bin) + factor(mother_tongue) +
                              factor(involvement_attend_j) + factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_SA5_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_PO_Snus)),
                             confint(MIcombine(m1_SA5_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_PO_Snus)),
                             confint(MIcombine(m2_SA5_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_PO_Snus)),
                             confint(MIcombine(m3_SA5_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA5_PO_Snus[[1]]$data)
nrow(m2_SA5_PO_Snus[[1]]$data)
nrow(m3_SA5_PO_Snus[[1]]$data)
# n = 10912
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA5_SO1_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_1dose ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO1_Smoke))

# Adjusted for age and sex
m2_SA5_SO1_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO1_Smoke))

# Adjusted for confounders
m3_SA5_SO1_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
```

```
                                    factor(maritalstatus_bin) + factor(mother_tongue) +
                                    factor(involvement_attend_j) + factor(fs_shp_koodi),
                                  family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO1_Smoke)),
                            confint(MIcombine(m1_SA5_SO1_Smoke)))), 2)[2:4,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO1_Smoke)),
                            confint(MIcombine(m2_SA5_SO1_Smoke)))), 2)[2:4,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO1_Smoke)),
                            confint(MIcombine(m3_SA5_SO1_Smoke)))), 2)[2:4,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA5_SO1_Smoke[[1]]$data)
nrow(m2_SA5_SO1_Smoke[[1]]$data)
nrow(m3_SA5_SO1_Smoke[[1]]$data)
# n = 14736
```

Snus

```
# Crude model
m1_SA5_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_1dose ~ factor(snus_status),
                              family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO1_Snus))

# Adjusted for age and sex
m2_SA5_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont),
                              family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO1_Snus))

# Adjusted for confounders
m3_SA5_SO1_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                       svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                              family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO1_Snus))

# Obtain main estimates
```

```
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO1_Snus)),
                             confint(MIcombine(m1_SA5_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO1_Snus)),
                             confint(MIcombine(m2_SA5_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO1_Snus)),
                             confint(MIcombine(m3_SA5_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA5_SO1_Snus[[1]]$data)
nrow(m2_SA5_SO1_Snus[[1]]$data)
nrow(m3_SA5_SO1_Snus[[1]]$data)
# n = 10912
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA5_SO2_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_3doses ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO2_Smoke))

# Adjusted for age and sex
m2_SA5_SO2_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO2_Smoke))

## Adjusted for confounders
m3_SA5_SO2_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO2_Smoke)),
                             confint(MIcombine(m1_SA5_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")
```

```
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO2_Smoke)),
                             confint(MIcombine(m2_SA5_SO2_Smoke))))), 2)[2:4,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO2_Smoke)),
                             confint(MIcombine(m3_SA5_SO2_Smoke))))), 2)[2:4,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA5_SO2_Smoke[[1]]$data)
nrow(m2_SA5_SO2_Smoke[[1]]$data)
nrow(m3_SA5_SO2_Smoke[[1]]$data)
# n = 14736
```

Snus

```
## Crude model
m1_SA5_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_3doses ~ factor(snus_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO2_Snus))

## Adjusted for age and sex
m2_SA5_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO2_Snus))

# Adjusted for confounders
m3_SA5_SO2_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO2_Snus)),
                             confint(MIcombine(m1_SA5_SO2_Snus))))), 2)[2:3,],
            caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO2_Snus)),
                             confint(MIcombine(m2_SA5_SO2_Snus))))), 2)[2:3,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")
```

```
knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO2_Snus)),
                             confint(MIcombine(m3_SA5_SO2_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA5_SO2_Snus[[1]]$data)
nrow(m2_SA5_SO2_Snus[[1]]$data)
nrow(m3_SA5_SO2_Snus[[1]]$data)
# n = 10912
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA5_SO3_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_20weeks12 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO3_Smoke))

# Adjusted for age and sex
m2_SA5_SO3_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO3_Smoke))

# Adjusted for confounders
m3_SA5_SO3_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_20weeks12 ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO3_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO3_Smoke)),
                             confint(MIcombine(m1_SA5_SO3_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO3_Smoke)),
                             confint(MIcombine(m2_SA5_SO3_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO3_Smoke)),
                             confint(MIcombine(m3_SA5_SO3_Smoke)))), 2)[2:4,],
```

```
                     caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA5_SO3_Smoke[[1]]$data)
nrow(m2_SA5_SO3_Smoke[[1]]$data)
nrow(m3_SA5_SO3_Smoke[[1]]$data)
# n = 14736
```

Snus

```
# Crude model
m1_SA5_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_20weeks12 ~ factor(snus_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO3_Snus))

# Adjusted for age and sex
m2_SA5_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO3_Snus))

# Adjusted for confounders
m3_SA5_SO3_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO3_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO3_Snus)),
                             confint(MIcombine(m1_SA5_SO3_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO3_Snus)),
                             confint(MIcombine(m2_SA5_SO3_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO3_Snus)),
                             confint(MIcombine(m3_SA5_SO3_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA5_SO3_Snus[[1]]$data)
nrow(m2_SA5_SO3_Snus[[1]]$data)
```

```
nrow(m3_SA5_SO3_Snus[[1]]$data)
# n = 10912
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA5_SO4_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_7months23 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO4_Smoke))

# Adjusted for age and sex
m2_SA5_SO4_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                                    pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO4_Smoke))

# Adjusted for confounders
m3_SA5_SO4_Smoke <- with(subset(des_final, dataid == 2018),
                         svyglm(event_7months23 ~ factor(smoking_status) +
                                    factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                    factor(maritalstatus_bin) + factor(mother_tongue) +
                                    factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO4_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO4_Smoke)),
                             confint(MIcombine(m1_SA5_SO4_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO4_Smoke)),
                             confint(MIcombine(m2_SA5_SO4_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO4_Smoke)),
                             confint(MIcombine(m3_SA5_SO4_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA5_SO4_Smoke[[1]]$data)
nrow(m2_SA5_SO4_Smoke[[1]]$data)
nrow(m3_SA5_SO4_Smoke[[1]]$data)
# n = 14736
```

Snus

```r
# Crude model
m1_SA5_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_7months23 ~ factor(snus_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA5_SO4_Snus))

# Adjusted for age and sex
m2_SA5_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA5_SO4_Snus))

# Adjusted for confounders
m3_SA5_SO4_Snus <- with(subset(des_final, between(age_cont, 20, 74) & dataid == 2018),
                        svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                                   pspline(age_cont) + factor(educ_tertiles) +
                                   factor(maritalstatus_bin) + factor(mother_tongue) +
                                   factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA5_SO4_Snus))

# Obtains main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA5_SO4_Snus)),
                             confint(MIcombine(m1_SA5_SO4_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA5_SO4_Snus)),
                             confint(MIcombine(m2_SA5_SO4_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA5_SO4_Snus)),
                             confint(MIcombine(m3_SA5_SO4_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA5_SO4_Snus[[1]]$data)
nrow(m2_SA5_SO4_Snus[[1]]$data)
nrow(m3_SA5_SO4_Snus[[1]]$data)
# n = 10912

# Remove unnecessary objects from work space.
rm(list=ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                          "vaccinecc", "finsote_evnt", "ttr3",
                          "dose2", "dose1", "dose3")])
```

vi) Excluding everyone who has had a COVID-19 infection

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA6_PO_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA6_PO_Smoke))

# Adjusted for age and sex
m2_SA6_PO_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) +
                                 factor(sex) + pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA6_PO_Smoke))

# Adjusted for confounders
m3_SA6_PO_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_2doses ~ factor(smoking_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA6_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_PO_Smoke)),
                             confint(MIcombine(m1_SA6_PO_Smoke)))), 2)[2:4,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_PO_Smoke)),
                             confint(MIcombine(m2_SA6_PO_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_PO_Smoke)),
                             confint(MIcombine(m3_SA6_PO_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA6_PO_Smoke[[1]]$data)
nrow(m2_SA6_PO_Smoke[[1]]$data)
nrow(m3_SA6_PO_Smoke[[1]]$data)
# n = 42117
```

Snus

```r
# Crude model
m1_SA6_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
  svyglm(event_2doses ~  factor(snus_status),
         family = quasipoisson()))
# summary(MIcombine(m1_SA6_PO_Snus))

# Adjusted for age and sex
m2_SA6_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont),
         family = quasipoisson()))
# summary(MIcombine(m2_SA6_PO_Snus))

# Adjusted for confounders
m3_SA6_PO_Snus <- with(
  subset(des_final, between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
  svyglm(event_2doses ~ factor(snus_status) + factor(sex) +
           pspline(age_cont) + factor(educ_tertiles) +
           factor(maritalstatus_bin) + factor(mother_tongue) +
           factor(involvement_attend_j) + factor(fs_shp_koodi),
         family = quasipoisson()))
# summary(MIcombine(m3_SA6_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_PO_Snus)),
                             confint(MIcombine(m1_SA6_PO_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_PO_Snus)),
                             confint(MIcombine(m2_SA6_PO_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_PO_Snus)),
                             confint(MIcombine(m3_SA6_PO_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA6_PO_Snus[[1]]$data)
nrow(m2_SA6_PO_Snus[[1]]$data)
nrow(m3_SA6_PO_Snus[[1]]$data)
# n = 28479
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA6_SO1_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO1_Smoke))

## Adjusted for age and sex
m2_SA6_SO1_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO1_Smoke))

# Adjusted for confounders
m3_SA6_SO1_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO1_Smoke)),
                             confint(MIcombine(m1_SA6_SO1_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO1_Smoke)),
                             confint(MIcombine(m2_SA6_SO1_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO1_Smoke)),
                             confint(MIcombine(m3_SA6_SO1_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA6_SO1_Smoke[[1]]$data)
nrow(m2_SA6_SO1_Smoke[[1]]$data)
nrow(m3_SA6_SO1_Smoke[[1]]$data)
# n = 42117
```

Snus

```r
# Crude model
m1_SA6_SO1_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(snus_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO1_Snus))

# Adjusted for age and sex
m2_SA6_SO1_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO1_Snus))

# Adjusted for confounders
m3_SA6_SO1_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_1dose ~ factor(snus_status) + factor(sex) +
                                 pspline(age_cont) + factor(educ_tertiles) +
                                 factor(maritalstatus_bin) + factor(mother_tongue) +
                                 factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO1_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO1_Snus)),
                             confint(MIcombine(m1_SA6_SO1_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO1_Snus)),
                             confint(MIcombine(m2_SA6_SO1_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO1_Snus)),
                             confint(MIcombine(m3_SA6_SO1_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA6_SO1_Snus[[1]]$data)
nrow(m2_SA6_SO1_Snus[[1]]$data)
nrow(m3_SA6_SO1_Snus[[1]]$data)
# n = 28479
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA6_SO2_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO2_Smoke))

# Adjusted for age and sex
m2_SA6_SO2_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO2_Smoke))

## Adjusted for confounders
m3_SA6_SO2_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(smoking_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO2_Smoke)),
                             confint(MIcombine(m1_SA6_SO2_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO2_Smoke)),
                             confint(MIcombine(m2_SA6_SO2_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO2_Smoke)),
                             confint(MIcombine(m3_SA6_SO2_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA6_SO2_Smoke[[1]]$data)
nrow(m2_SA6_SO2_Smoke[[1]]$data)
nrow(m3_SA6_SO2_Smoke[[1]]$data)
# n = 42117
```

Snus

```
## Crude model
m1_SA6_SO2_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(snus_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO2_Snus))

## Adjusted for age and sex
m2_SA6_SO2_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO2_Snus))

# Adjusted for confounders
m3_SA6_SO2_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_3doses ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO2_Snus)),
                             confint(MIcombine(m1_SA6_SO2_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO2_Snus)),
                             confint(MIcombine(m2_SA6_SO2_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO2_Snus)),
                             confint(MIcombine(m3_SA6_SO2_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA6_SO2_Snus[[1]]$data)
nrow(m2_SA6_SO2_Snus[[1]]$data)
nrow(m3_SA6_SO2_Snus[[1]]$data)
# n = 28479
```

Secondary outcome (iii): Interval spacing between 1st and 2nd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA6_SO3_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO3_Smoke))

# Adjusted for age and sex
m2_SA6_SO3_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO3_Smoke))

# Adjusted for confounders
m3_SA6_SO3_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_20weeks12 ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO3_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO3_Smoke)),
                             confint(MIcombine(m1_SA6_SO3_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO3_Smoke)),
                             confint(MIcombine(m2_SA6_SO3_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO3_Smoke)),
                             confint(MIcombine(m3_SA6_SO3_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Checking the estimates are on the same sample
nrow(m1_SA6_SO3_Smoke[[1]]$data)
nrow(m2_SA6_SO3_Smoke[[1]]$data)
nrow(m3_SA6_SO3_Smoke[[1]]$data)
# n = 42117
```

Snus

```r
# Crude model
m1_SA6_SO3_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_20weeks12 ~ factor(snus_status),
                               family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO3_Snus))

# Adjusted for age and sex
m2_SA6_SO3_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont),
                               family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO3_Snus))

# Adjusted for confounders
m3_SA6_SO3_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & ! GUMM85ID %in% ttr3$GUMM85ID),
                        svyglm(event_20weeks12 ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                               family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO3_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO3_Snus)),
                             confint(MIcombine(m1_SA6_SO3_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO3_Snus)),
                             confint(MIcombine(m2_SA6_SO3_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO3_Snus)),
                             confint(MIcombine(m3_SA6_SO3_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA6_SO3_Snus[[1]]$data)
nrow(m2_SA6_SO3_Snus[[1]]$data)
nrow(m3_SA6_SO3_Snus[[1]]$data)
# n = 28479
```

Secondary outcome (iv): Interval spacing between 2nd and 3rd dose of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA6_SO4_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status),
                                family = quasipoisson()))
# summary(MIcombine(m1_SA6_SO4_Smoke))

# Adjusted for age and sex
m2_SA6_SO4_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status) + factor(sex) +
                                pspline(age_cont),
                                family = quasipoisson()))
# summary(MIcombine(m2_SA6_SO4_Smoke))

# Adjusted for confounders
m3_SA6_SO4_Smoke <- with(subset(des_final, ! GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(smoking_status) +
                                factor(sex) + pspline(age_cont) + factor(educ_tertiles) +
                                factor(maritalstatus_bin) + factor(mother_tongue) +
                                factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson()))
# summary(MIcombine(m3_SA6_SO4_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO4_Smoke)),
                             confint(MIcombine(m1_SA6_SO4_Smoke)))), 2)[2:4,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO4_Smoke)),
                             confint(MIcombine(m2_SA6_SO4_Smoke)))), 2)[2:4,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO4_Smoke)),
                             confint(MIcombine(m3_SA6_SO4_Smoke)))), 2)[2:4,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA6_SO4_Smoke[[1]]$data)
nrow(m2_SA6_SO4_Smoke[[1]]$data)
nrow(m3_SA6_SO4_Smoke[[1]]$data)
# n = 42117
```

Snus

```r
# Crude model
m1_SA6_SO4_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & !GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(snus_status),
                                family = quasipoisson())))
# summary(MIcombine(m1_SA6_SO4_Snus))

# Adjusted for age and sex
m2_SA6_SO4_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & !GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont),
                                family = quasipoisson())))
# summary(MIcombine(m2_SA6_SO4_Snus))

# Adjusted for confounders
m3_SA6_SO4_Snus <- with(subset(des_final,
                               between(age_cont, 20, 74) & !GUMM85ID %in% ttr3$GUMM85ID),
                         svyglm(event_7months23 ~ factor(snus_status) + factor(sex) +
                                  pspline(age_cont) + factor(educ_tertiles) +
                                  factor(maritalstatus_bin) + factor(mother_tongue) +
                                  factor(involvement_attend_j) + factor(fs_shp_koodi),
                                family = quasipoisson())))
# summary(MIcombine(m3_SA6_SO4_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA6_SO4_Snus)),
                             confint(MIcombine(m1_SA6_SO4_Snus)))), 2)[2:3,],
             caption = "M1: Crude model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA6_SO4_Snus)),
                             confint(MIcombine(m2_SA6_SO4_Snus)))), 2)[2:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA6_SO4_Snus)),
                             confint(MIcombine(m3_SA6_SO4_Snus)))), 2)[2:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA6_SO4_Snus[[1]]$data)
nrow(m2_SA6_SO4_Snus[[1]]$data)
nrow(m3_SA6_SO4_Snus[[1]]$data)
# n = 28479

# Remove unnecessary objects from work space.
rm(list = ls()[!ls() %in% c("des_final", "finsotecc", "finsote2020_dates",
                            "vaccinecc", "finsote_evnt", "ttr3",
                            "dose2", "dose1", "dose3")])
```

vii) Cox proportional hazards model and assumption tested on complete case analysis

Exploratory survival analysis

```r
# Compute time differences
# Uptake at least 2 doses
dose2.time <- dose2 %>%
  mutate(time2 = difftime(vaccine_date, "2020-12-27", units = "days") %>%
           as.numeric(., unit = "days")) %>%
  subset(vaccine2 == 1 & dose_nro == 2) %>%
  subset(select = c("GUMM85ID", "time2"))

# at least 1 dose
dose1.time <- dose1 %>%
  mutate(time1 = difftime(vaccine_date, "2020-12-27", units = "days") %>%
           as.numeric(., unit = "days")) %>%
  subset(vaccine1 == 1 & dose_nro == 1) %>%
  subset(select = c("GUMM85ID", "time1"))

# 3 doses
dose3.time <- dose3 %>%
  mutate(time3 = difftime(vaccine_date, "2020-12-27", units = "days") %>%
           as.numeric(., unit = "days")) %>%
  subset(vaccine3 == 1 & dose_nro == 3) %>%
  subset(select = c("GUMM85ID", "time3"))

# Connect time to finsotecc data
# fill missing with 1, 0 is not allow when using tmerge in later step
findosecc <- finsotecc %>%
  left_join(dose2.time, by = "GUMM85ID") %>%
  left_join(dose1.time, by = "GUMM85ID") %>%
  left_join(dose3.time, by = "GUMM85ID") %>%
  replace_na(list(time2 = 0,
                  time1 = 0,
                  time3 = 0)) %>%
  mutate(age_start = case_when(dataid == 2018 ~ age_cont + 2,
                               TRUE ~ age_cont),
         age_stop = case_when(dataid == 2020 ~ age_cont + 1,
                              dataid == 2018 ~ age_start + 1))

##### Primary outcome: 2 doses #####
print("##### Primary outcome: 2 doses #####")
# KM
# NULL
survRate(Surv(time2, event_2doses) ~ 1, data = findosecc)
KMfit_PO_NULL <- survfit(Surv(time2, event_2doses) ~ 1, data = findosecc)
autoplot(KMfit_PO_NULL) + ggtitle("Primary outcome: NULL")
# Smoke
survRate(Surv(time2, event_2doses) ~ smoking_status, data = findosecc)
KMfit_PO_Smoke <- survfit(Surv(time2, event_2doses) ~ smoking_status, data = findosecc)
autoplot(KMfit_PO_Smoke) + ggtitle("Primary outcome: Smoke")
# Snus
```

```r
survRate(Surv(time2, event_2doses) ~ snus_status, data = findosecc)
KMfit_PO_Snus <- survfit(Surv(time2, event_2doses) ~ snus_status, data = findosecc)
autoplot(KMfit_PO_Snus) + ggtitle("Primary outcome: Snus")


# Log rank tests
# Smoke
logrank_PO_Smoke <- survdiff(Surv(time2, event_2doses) ~ smoking_status, data = findosecc)
logrank_PO_Smoke
# Snus
logrank_PO_Snus <- survdiff(Surv(time2, event_2doses) ~ snus_status, data = findosecc)
logrank_PO_Snus


##### Secondary outcome (i): 1 dose #####
print("##### Secondary outcome (i): 1 dose #####")
# KM
# NULL
survRate(Surv(time1, event_1dose) ~ 1, data = findosecc)
KMfit_SO1_NULL <- survfit(Surv(time1, event_1dose) ~ 1, data = findosecc)
autoplot(KMfit_SO1_NULL) + ggtitle("Secondary outcome (i): NULL")
# Smoke
survRate(Surv(time1, event_1dose) ~ smoking_status, data = findosecc)
KMfit_SO1_Smoke <- survfit(Surv(time1, event_1dose) ~ smoking_status, data = findosecc)
autoplot(KMfit_SO1_Smoke) + ggtitle("Secondary outcome (i): Smoke")
# Snus
survRate(Surv(time1, event_1dose) ~ snus_status, data = findosecc)
KMfit_SO1_Snus <- survfit(Surv(time1, event_1dose) ~ snus_status, data = findosecc)
autoplot(KMfit_SO1_Snus) + ggtitle("Secondary outcome (i): Snus")


# Log rank tests
# Smoke
logrank_SO1_Smoke <- survdiff(Surv(time1, event_1dose) ~ smoking_status, data = findosecc)
logrank_SO1_Smoke
# Snus
logrank_SO1_Snus <- survdiff(Surv(time1, event_1dose) ~ snus_status, data = findosecc)
logrank_SO1_Snus


##### Secondary outcome (ii): 3 doses #####
print("##### Secondary outcome (i): 3 doses #####")
# KM
# NULL
survRate(Surv(time3, event_3doses) ~ 1, data = findosecc)
KMfit_SO2_NULL <- survfit(Surv(time3, event_3doses) ~ 1, data = findosecc)
autoplot(KMfit_SO2_NULL) + ggtitle("Secondary outcome (ii): NULL")
# Smoke
survRate(Surv(time3, event_3doses) ~ smoking_status, data = findosecc)
KMfit_SO2_Smoke <- survfit(Surv(time3, event_3doses) ~ smoking_status, data = findosecc)
autoplot(KMfit_SO2_Smoke) + ggtitle("Secondary outcome (ii): Smoke")
# Snus
survRate(Surv(time3, event_3doses) ~ snus_status, data = findosecc)
KMfit_SO2_Snus <- survfit(Surv(time3, event_3doses) ~ snus_status, data = findosecc)
autoplot(KMfit_SO2_Snus) + ggtitle("Secondary outcome (ii): Snus")
```

```
# Log rank tests
# Smoke
logrank_SO2_Smoke <- survdiff(Surv(time3, event_3doses) ~ smoking_status, data = findosecc)
logrank_SO2_Smoke
# Snus
logrank_SO2_Snus <- survdiff(Surv(time3, event_3doses) ~ snus_status, data = findosecc)
logrank_SO2_Snus
```

Cox proportional hazard models

We ran Cox proportional hazard models using the same models and data as in main analyses. Some models run into singular fit problems and thus, to obtain a coefficient, we modeled the variables as linear predictors instead of using penalized smoothing splines.

Imputation

```
# Imputation
cox_imp <- mice(subset(findosecc,
                        select = c("dataid", "fs_shp_koodi", "smoking_status", "snus_status",
                                   "ecig_nic_status", "ecig_nonic_status", "nrt_status",
                                   "educ_tertiles", "maritalstatus_bin", "mother_tongue",
                                   "involvement_attend_j", "age_cont", "sex")),
                 m = 15,
                 seed = 100,
                 printFlag = F)

cox_imp <- cbind(
  cox_imp,
  subset(findosecc,
         select = c(
           "rg_N_suomi", "w_analysis_suomi", "rg_stratum_suomi", "GUMM85ID",
           "case_C1", "case_C2", "event_1dose", "event_2doses", "event_3doses",
           "event_20weeks12", "event_7months23", "event_sim1_1dose", "case_C3",
           "event_sim2_1dose", "event_sim1_2doses", "event_sim2_2doses",
           "event_sim1_3doses", "event_sim2_3doses", "event_sim1_20weeks12",
           "event_sim2_20weeks12", "event_sim1_7months23", "event_sim2_7months23",
           "time2", "time1", "time3", "age_start", "age_stop")
  )
)

# Convert to a design object
findosecc_list <- imputationList(lapply(1:cox_imp$m,
                                        function(n) mice::complete(cox_imp, action = n)))
des_findosecc_imp <- svydesign(id = ~1,
                               fpc = ~rg_N_suomi,
                               weights = ~w_analysis_suomi,
                               strata = ~rg_stratum_suomi,
                               data = findosecc_list)
```

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA7.1_PO_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status)))
# summary(MIcombine(m1_SA7.1_PO_Smoke))

# Adjusted for age and sex
m2_SA7.1_PO_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_PO_Smoke))

# Adjusted for confounders
m3_SA7.1_PO_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status) + factor(sex) +
            factor(educ_tertiles) + factor(maritalstatus_bin) +
            factor(mother_tongue) + factor(involvement_attend_j) +
            factor(fs_shp_koodi)))
# summary(MIcombine(m3_SA7.1_PO_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_PO_Smoke)),
                             confint(MIcombine(m1_SA7.1_PO_Smoke)))), 2)[1:3,],
            caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_PO_Smoke)),
                             confint(MIcombine(m2_SA7.1_PO_Smoke)))), 2)[1:3,],
            caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_PO_Smoke)),
                             confint(MIcombine(m3_SA7.1_PO_Smoke)))), 2)[1:3,],
            caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA7.1_PO_Smoke[[1]]$y)
nrow(m2_SA7.1_PO_Smoke[[1]]$y)
nrow(m3_SA7.1_PO_Smoke[[1]]$y)
# n = 42935
```

Snus

```r
# Crude model
m1_SA7.1_PO_Snus <- with(
```

```
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(snus_status)))
# summary(MIcombine(m1_SA7.1_PO_Snus))

# Adjusted for age and sex
m2_SA7.1_PO_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(snus_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_PO_Snus))

# Adjusted for confounders
m3_SA7.1_PO_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_2doses) ~ factor(snus_status) + factor(sex) +
             factor(educ_tertiles) + factor(maritalstatus_bin) +
             factor(mother_tongue) + factor(involvement_attend_j) +
             factor(fs_shp_koodi)))
# summary(MIcombine(m3_SA7.1_PO_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_PO_Snus)),
                             confint(MIcombine(m1_SA7.1_PO_Snus)))), 2)[1:2,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_PO_Snus)),
                             confint(MIcombine(m2_SA7.1_PO_Snus)))), 2)[1:2,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_PO_Snus)),
                             confint(MIcombine(m3_SA7.1_PO_Snus)))), 2)[1:2,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA7.1_PO_Snus[[1]]$y)
nrow(m2_SA7.1_PO_Snus[[1]]$y)
nrow(m3_SA7.1_PO_Snus[[1]]$y)
# n = 29192
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA7.1_SO1_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status)))
# summary(MIcombine(m1_SA7.1_SO1_Smoke))

# Adjusted for age and sex
```

```r
m2_SA7.1_SO1_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_SO1_Smoke))

# Adjusted for confounders
m3_SA7.1_SO1_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status) + factor(sex) +
             factor(educ_tertiles) + factor(maritalstatus_bin) +
             factor(mother_tongue) + factor(involvement_attend_j) +
             factor(fs_shp_koodi)))
# summary(MIcombine(m3_SA7.1_SO1_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_SO1_Smoke)),
                             confint(MIcombine(m1_SA7.1_SO1_Smoke)))), 2)[1:3,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_SO1_Smoke)),
                             confint(MIcombine(m2_SA7.1_SO1_Smoke)))), 2)[1:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_SO1_Smoke)),
                             confint(MIcombine(m3_SA7.1_SO1_Smoke)))), 2)[1:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")


# Check the estimates are on the same sample
nrow(m1_SA7.1_SO1_Smoke[[1]]$y)
nrow(m2_SA7.1_SO1_Smoke[[1]]$y)
nrow(m3_SA7.1_SO1_Smoke[[1]]$y)
# n = 42935
```

Snus

```r
# Crude model
m1_SA7.1_SO1_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(snus_status)))
# summary(MIcombine(m1_SA7.1_SO1_Snus))

# Adjusted for age and sex
m2_SA7.1_SO1_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(snus_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_SO1_Snus))

# Adjusted for confounders
```

```
m3_SA7.1_S01_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_1dose) ~ factor(snus_status) + factor(sex) +
             factor(educ_tertiles) + factor(maritalstatus_bin) +
             factor(mother_tongue) + factor(involvement_attend_j) +
             factor(fs_shp_koodi)))
# summary(MIcombine(m3_SA7.1_S01_Snus))

knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_S01_Snus)),
                            confint(MIcombine(m1_SA7.1_S01_Snus)))), 2)[1:2,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_S01_Snus)),
                            confint(MIcombine(m2_SA7.1_S01_Snus)))), 2)[1:2,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_S01_Snus)),
                            confint(MIcombine(m3_SA7.1_S01_Snus)))), 2)[1:2,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA7.1_S01_Snus[[1]]$y)
nrow(m2_SA7.1_S01_Snus[[1]]$y)
nrow(m3_SA7.1_S01_Snus[[1]]$y)
# n = 29192
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA7.1_S02_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status)))
# summary(MIcombine(m1_SA7.1_S02_Smoke))

# Adjusted for age and sex
m2_SA7.1_S02_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_S02_Smoke))

# Adjusted for confounders
m3_SA7.1_S02_Smoke <- with(
  des_findosecc_imp,
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status) + factor(sex) +
             factor(educ_tertiles) + factor(maritalstatus_bin) +
             factor(mother_tongue) + factor(involvement_attend_j) +
             factor(fs_shp_koodi)))
```

273

```
# summary(MIcombine(m3_SA7.1_SO2_Smoke))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_SO2_Smoke)),
                             confint(MIcombine(m1_SA7.1_SO2_Smoke)))), 2)[1:3,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_SO2_Smoke)),
                             confint(MIcombine(m2_SA7.1_SO2_Smoke)))), 2)[1:3,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_SO2_Smoke)),
                             confint(MIcombine(m3_SA7.1_SO2_Smoke)))), 2)[1:3,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA7.1_SO2_Smoke[[1]]$y)
nrow(m2_SA7.1_SO2_Smoke[[1]]$y)
nrow(m3_SA7.1_SO2_Smoke[[1]]$y)
# n = 42935
```

Snus

```
# Crude model
m1_SA7.1_SO2_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(snus_status)))
# summary(MIcombine(m1_SA7.1_SO2_Snus))

# Adjusted for age and sex
m2_SA7.1_SO2_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(snus_status) + factor(sex)))
# summary(MIcombine(m2_SA7.1_SO2_Snus))

# Adjusted for confounders
m3_SA7.1_SO2_Snus <- with(
  subset(des_findosecc_imp, between(age_cont, 20, 74)),
  svycoxph(Surv(age_start, age_stop, event_3doses) ~ factor(snus_status) + factor(sex) +
             factor(educ_tertiles) + factor(maritalstatus_bin) +
             factor(mother_tongue) + factor(involvement_attend_j) +
             factor(fs_shp_koodi)))
# summary(MIcombine(m3_SA7.1_SO2_Snus))

# Obtain main estimates
knitr::kable(round(exp(cbind(coef(MIcombine(m1_SA7.1_SO2_Snus)),
                             confint(MIcombine(m1_SA7.1_SO2_Snus)))), 2)[1:2,],
             caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")
```

```r
knitr::kable(round(exp(cbind(coef(MIcombine(m2_SA7.1_SO2_Snus)),
                             confint(MIcombine(m2_SA7.1_SO2_Snus)))), 2)[1:2,],
             caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

knitr::kable(round(exp(cbind(coef(MIcombine(m3_SA7.1_SO2_Snus)),
                             confint(MIcombine(m3_SA7.1_SO2_Snus)))), 2)[1:2,],
             caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
nrow(m1_SA7.1_SO2_Snus[[1]]$y)
nrow(m2_SA7.1_SO2_Snus[[1]]$y)
nrow(m3_SA7.1_SO2_Snus[[1]]$y)
# n = 29192
```

Without imputation

```r
# Set up a design object
# In order to make them models comparable, filter data based on confounders.
des_findosecc_nonimp <- svydesign(id = ~1,
                                  fpc = ~rg_N_suomi,
                                  weights = ~w_analysis_suomi,
                                  strata = ~rg_stratum_suomi,
                                  data = findosecc %>%
                                    filter(
                                      complete.cases(
                                        educ_tertiles, maritalstatus_bin, mother_tongue,
                                        involvement_attend_j, fs_shp_koodi
                                      )
                                    )
)
```

Primary outcome: Uptake of two doses of COVID-19 vaccine

Smoking

```r
# Crude model
m1_SA7.2_PO_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status),
  design = des_findosecc_nonimp)
# summary(m1_SA7.2_PO_Smoke)

# Adjusted for age and sex
m2_SA7.2_PO_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status) + factor(sex),
  design = des_findosecc_nonimp)
# summary(m2_SA7.2_PO_Smoke)
```

```r
# Adjusted for confounders
m3_SA7.2_PO_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(smoking_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
    factor(fs_shp_koodi),
  design = des_findosecc_nonimp)
# summary(m3_SA7.2_PO_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_PO_Smoke)[1:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_SA7.2_PO_Smoke)[1:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_PO_Smoke)[1:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_PO_Smoke$n
m2_SA7.2_PO_Smoke$n
m3_SA7.2_PO_Smoke$n
# n = 39344

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_PO_Smoke <- cox.zph(m3_SA7.2_PO_Smoke)
plot(cox.zph(cox.zph.m3_SA7.2_PO_Smoke), df = 2)
cox.zph.m3_SA7.2_PO_Smoke
```

Snus

```r
# Crude model
m1_SA7.2_PO_Snus <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(snus_status),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m1_SA7.2_PO_Snus)

# Adjusted for age and sex
m2_SA7.2_PO_Snus <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(snus_status) + factor(sex),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m2_SA7.2_PO_Snus)

# Adjusted for confounders
m3_SA7.2_PO_Snus <- svycoxph(
  Surv(age_start, age_stop, event_2doses) ~ factor(snus_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
```

```
      factor(fs_shp_koodi),
    design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m3_SA7.2_PO_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_PO_Snus)[1:2, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_SA7.2_PO_Snus)[1:2, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_PO_Snus)[1:2, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_PO_Snus$n
m2_SA7.2_PO_Snus$n
m3_SA7.2_PO_Snus$n
# n = 27486

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_PO_Snus <- cox.zph(m3_SA7.2_PO_Snus)
plot(cox.zph(m3_SA7.2_PO_Snus), df = 2)
m3_SA7.2_PO_Snus
```

Secondary outcomes (i): Uptake of one dose of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA7.2_SO1_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status),
  design = des_findosecc_nonimp)
# summary(m1_SA7.2_SO1_Smoke)

# Adjusted for age and sex
m2_SA7.2_SO1_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status) + factor(sex),
  design = des_findosecc_nonimp)
# summary(m2_SA7.2_SO1_Smoke)

# Adjusted for confounders
m3_SA7.2_SO1_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(smoking_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
    factor(fs_shp_koodi),
  design = des_findosecc_nonimp)
```

```
# summary(m3_SA7.2_SO1_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_SO1_Smoke)[1:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_SA7.2_SO1_Smoke)[1:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_SO1_Smoke)[1:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_SO1_Smoke$n
m2_SA7.2_SO1_Smoke$n
m3_SA7.2_SO1_Smoke$n
# n = 39344

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_SO1_Smoke <- cox.zph(m3_SA7.2_SO1_Smoke)
plot(cox.zph(m3_SA7.2_SO1_Smoke), df = 2)
m3_SA7.2_SO1_Smoke
```

Snus

```
# Crude model
m1_SA7.2_SO1_Snus <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(snus_status),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m1_SA7.2_SO1_Snus)

# Adjusted for age and sex
m2_SA7.2_SO1_Snus <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(snus_status) + factor(sex),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m2_SA7.2_SO1_Snus)

# Adjusted for confounders
m3_SA7.2_SO1_Snus <- svycoxph(
  Surv(age_start, age_stop, event_1dose) ~ factor(snus_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
    factor(fs_shp_koodi),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m3_SA7.2_SO1_Snus))

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_SO1_Snus)[1:2, ], 2),
      caption = "M1: Crude Model") %>%
```

```
    kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_SA7.2_S01_Snus)[1:2, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_S01_Snus)[1:2, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_S01_Snus$n
m2_SA7.2_S01_Snus$n
m3_SA7.2_S01_Snus$n
# n = 27486

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_S01_Snus <- cox.zph(m3_SA7.2_S01_Snus)
plot(cox.zph(m3_SA7.2_S01_Snus), df = 2)
m3_SA7.2_S01_Snus
```

Secondary outcomes (ii): Uptake of three doses of COVID-19 vaccine

Smoking

```
# Crude model
m1_SA7.2_S02_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status),
  design = des_findosecc_nonimp)
# summary(m1_SA7.2_S02_Smoke)

# Adjusted for age and sex
m2_SA7.2_S02_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status) + factor(sex),
  design = des_findosecc_nonimp)
# summary(m2_SA7.2_S02_Smoke)

# Adjusted for confounders
m3_SA7.2_S02_Smoke <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(smoking_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
    factor(fs_shp_koodi),
  design = des_findosecc_nonimp)
# summary(m3_SA7.2_S02_Smoke)

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_S02_Smoke)[1:3, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")
```

```
kable(round(ci.exp(m2_SA7.2_SO2_Smoke)[1:3, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_SO2_Smoke)[1:3, ], 2),
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_SO2_Smoke$n
m2_SA7.2_SO2_Smoke$n
m3_SA7.2_SO2_Smoke$n
# n = 39344

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_SO2_Smoke <- cox.zph(m3_SA7.2_SO2_Smoke)
plot(cox.zph(m3_SA7.2_SO2_Smoke), df = 2)
m3_SA7.2_SO2_Smoke
```

Snus

```
# Crude model
m1_SA7.2_SO2_Snus <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(snus_status),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m1_SA7.2_SO2_Snus)

# Adjusted for age and sex
m2_SA7.2_SO2_Snus <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(snus_status) + factor(sex),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m2_SA7.2_SO2_Snus)

# Adjusted for confounders
m3_SA7.2_SO2_Snus <- svycoxph(
  Surv(age_start, age_stop, event_3doses) ~ factor(snus_status) + factor(sex) +
    factor(educ_tertiles) + factor(maritalstatus_bin) +
    factor(mother_tongue) + factor(involvement_attend_j) +
    factor(fs_shp_koodi),
  design = subset(des_findosecc_nonimp, between(age_cont, 20, 74)))
# summary(m3_SA7.2_SO2_Snus)

# Obtain main estimates
kable(round(ci.exp(m1_SA7.2_SO2_Snus)[1:2, ], 2),
      caption = "M1: Crude Model") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m2_SA7.2_SO2_Snus)[1:2, ], 2),
      caption = "M2: Adjusted for age and sex") %>%
  kable_classic(full_width = F, position = "left")

kable(round(ci.exp(m3_SA7.2_SO2_Snus)[1:2, ], 2),
```

```
      caption = "M3: Adjusted for confounders") %>%
  kable_classic(full_width = F, position = "left")

# Check the estimates are on the same sample
m1_SA7.2_SO2_Snus$n
m2_SA7.2_SO2_Snus$n
m3_SA7.2_SO2_Snus$n
# n = 27486

# Check proportional hazard assumption in final models
cox.zph.m3_SA7.2_SO2_Snus <- cox.zph(m3_SA7.2_SO2_Snus)
plot(cox.zph(m3_SA7.2_SO2_Snus), df = 2)
m3_SA7.2_SO2_Snus
```

Save image

```
save.image("TobriskCov_Data_Cox.RData")
```

End of Part IV

End of scripts

Please contact me if you find errors or have any feedback on the code at sebastian.penafajuri@thl.fi or @spenafajuri (Twitter).