SA Paper 1 Analysis

Contents

Prep Code

```
library(readr)
library(logistf)
library(tidyverse)
library(lubridate)
library(gtsummary)
library(gt)
library(parsedate)
library(janitor)
library(labelled)
library(parameters)
library(survival)
library(ggsurvfit)
library(table1)
library(hms)
library(readxl)
library(ggborderline)
theme_gtsummary_journal(journal = "jama")
theme_gtsummary_compact()
load(
  "~/Documents/Current_Projects/Sexual_Assault/new_SA_YNHH/Updated YNHH SA code/all_pts.RData"
)
# set TZ to east coast standard
time_zone <- "America/New_York"
#pathway went live on 7/13/21
pathway_start <- mdy("7/13/21", tz = time_zone)
#Story board notification went live on 9/8/21
sb_start <- mdy("9/8/21", tz = time_zone)
day.arrival.start <- hms::as_hms("03:00:00")
night.arrival.start <- hms::as_hms("15:00:00")
all_pts$insurance_3 <- as_factor(all_pts$insurance_3)
all_pts$insurance_3 <- relevel(all_pts$insurance_3, ref = "Public")
all_pts <- all_pts %>% mutate(
```

```
    race_eth = case_when(
      patient_ethnicity == "Hispanic or Latina/o/x" ~ "Hispanic or Latina/o/x",
      patient_race == "Black or African American" ~ "Non-Hispanic Black",
      patient_race == "White" ~ "Non-Hispanic White",
      patient_ethnicity != "Hispanic or Latina/o/x" &
        patient_race != "Black or African American" &
        patient_race != "White" ~ "Other",
      .default = patient_race
    )
  ) %>%
  mutate(
    race_eth_num = case_when(
      race_eth == "Non-Hispanic White" ~ 0,
      race_eth == "Non-Hispanic Black" ~ 1,
      race_eth == "Hispanic or Latina/o/x" ~ 3,
      race_eth == "Other" ~ 4
    )
  ) %>%
  set_value_labels(
    race_eth_num = c(
      "Non-Hispanic White" = 0,
      "Non-Hispanic Black" = 1,
      "Hispanic or Latina/o/x" = 3,
      "Other" = 4
    )
  )
all_pts$race_eth_num <- to_factor(all_pts$race_eth_num, ordered = FALSE)
all_excluded <- all_pts %>%
  mutate(exclude = case_when(age < 18 ~ 1,
                             between == 1 ~ 1,
                             sane_kit_done == 4 ~ 1,
                             exclude == 1 ~ 1)) %>%
  mutate(
    reason_to_exclude = case_when(
      age < 18 ~ 8,
      is.na(reason_to_exclude) & between == 1 ~ 7,
      is.na(reason_to_exclude) & sane_kit_done == 4 ~ 3,
      is.na(reason_to_exclude) ~ 6,
      .default = reason_to_exclude
    )
  ) %>% add_value_labels(
    reason_to_exclude = c(
      "Seen earlier" = 1 ,
      "Patient reports not being assaulted" = 2,
      "Psych" = 3,
      "not excluded" = 4,
      "Eloped" = 5,
      "NA/Not Listed" = 6,
      "Between Period" = 7,
      "Under 18 YO" = 8
    )
  ) %>% to_factor()
all_excluded <- all_excluded %>% filter(exclude == 1)
```

```
excluded_plot <-
  all_excluded %>% ggplot(aes(x = reason_to_exclude)) + geom_bar(fill = "darkred") + geom_text(stat =
                                                                                            'count
```

```
excluded_plot
```

Excluded Patients by Reason
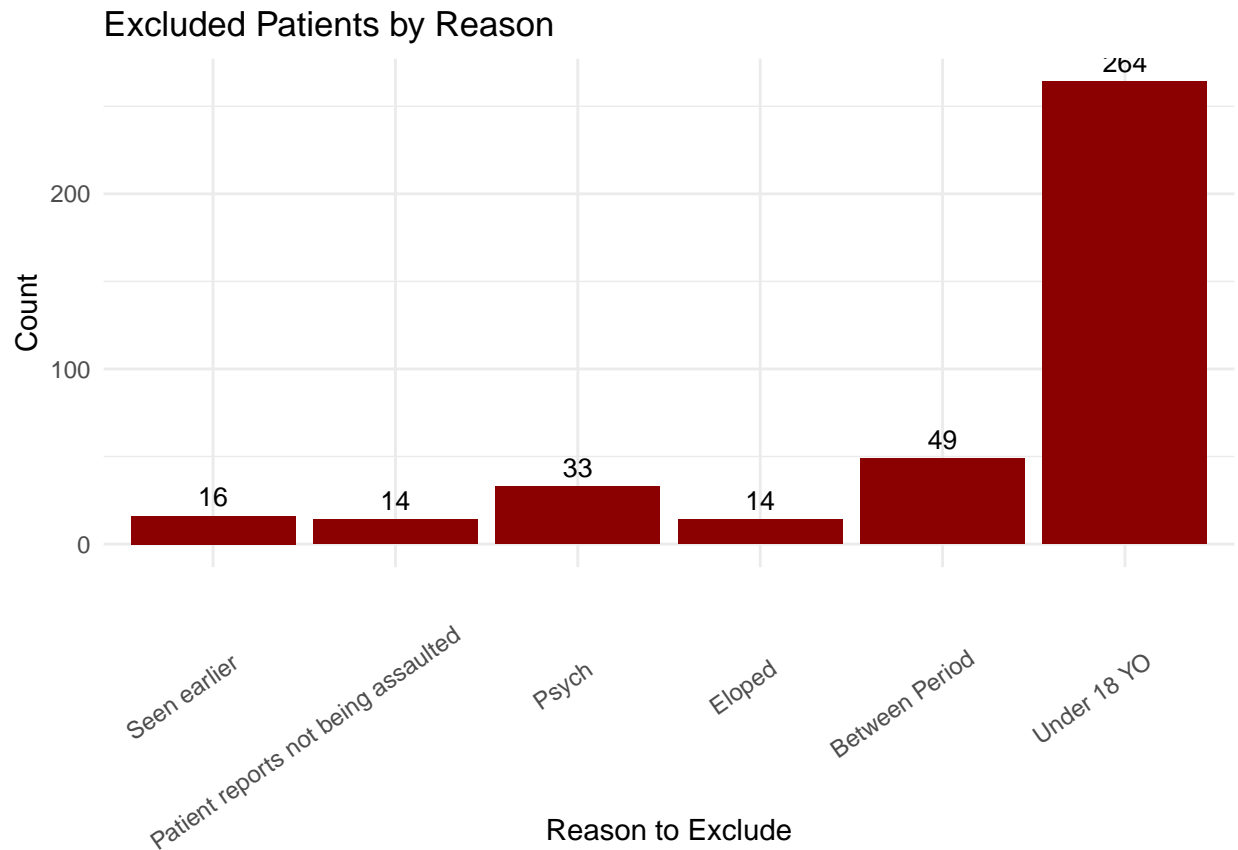

```
all_excluded %>% group_by(reason_to_exclude) %>% summarise(n = n()) %>% print()
```

```
## # A tibble: 6 x 2
##   reason_to_exclude                        n
##   <fct>                                <int>
## 1 Seen earlier                            16
## 2 Patient reports not being assaulted     14
## 3 Psych                                   33
## 4 Eloped                                  14
## 5 Between Period                          49
## 6 Under 18 YO                            264
```

```
number_of_minors <-
  all_excluded %>% filter(age < 18) #changed it so age is first exclusion criteria
number_of_minors <-
  n_distinct(number_of_minors$pat_enc_csn_id, na.rm = TRUE) %>% as.character()
cat("  ", number_of_minors, "patients under 18 YO excluded")
```

```
##    264 patients under 18 YO excluded
```

```
n_excluded <-
  all_excluded %>% filter(
    reason_to_exclude %in% c(
      "Seen earlier",
      "Patient reports not being assaulted",
      "Psych",
      "Eloped",
      "NA/Not Listed"
    )
  )
n_excluded <-
  n_distinct(n_excluded$pat_enc_csn_id, na.rm = TRUE) %>% as.character()
n_between <-
  all_excluded %>% filter(reason_to_exclude == "Between Period")
n_between <-
  n_distinct(n_between$pat_enc_csn_id, na.rm = TRUE) %>% as.character()

cat("-", n_excluded, "patients were excluded based on chart review.")
```

```
## - 77 patients were excluded based on chart review.
```

```
cat(" ",
    n_between,
    "patients who arrived between 7/13/21 and 9/8/21 were excluded")
```

```
##   49 patients who arrived between 7/13/21 and 9/8/21 were excluded
```

```
rm(n_excluded, number_of_minors, n_between)
#pre-post cohort
pp.cohort.1 <-
  all_pts %>% filter(between == 0) %>% filter(age > 17) %>% filter(is.na(exclude), sane_kit_done != 4)
#pathway v no pathway cohort
cohort.1 <-
  all_pts %>% filter(ed_arrival_date > sb_start) %>% filter(age > 17) %>% filter(is.na(exclude)) %>% mu
#pre vs no pathway cohort
pp.cohort.2 <- pp.cohort.1 %>% filter(agile_md_used_num != 1)
```

942 patient encounters from 2019-12-31 to 2022-12-24
In order of exclusion: age -> chart review -> between period

Table 1 and 2

Regression Outcomes

Primary Outcome: *Advocate Contacted*

```
advocate.regression<-function(data, exposure){
  data$advocate_offered <- as_factor(data$advocate_offered )
  data$advocate_offered <- relevel(data$advocate_offered, ref= "No Documentation of Pt Advocate")
```

Characteristic	Overall N = 552	Post v. Pre Post-intervention N = 252	Pre-intervention N = 300	p
Age, Median (Q1, Q3)	27 (21, 38)	27 (22, 38)	27 (21, 39)	
Female, n (%)	520 (94)	237 (94)	283 (94)	
Race, n (%)				
Non-Hispanic White	260 (47)	121 (48)	139 (46)	
Non-Hispanic Black	135 (24)	47 (19)	88 (29)	
Hispanic or Latina/o/x	118 (21)	64 (25)	54 (18)	
Other	39 (7.1)	20 (7.9)	19 (6.3)	
Presented within 120h of assault, n (%)	504 (91)	228 (90)	276 (92)	
Unknown	1	0	1	
Presented within 72h of assault, n (%)	453 (82)	200 (79)	253 (85)	
Unknown	1	0	1	
English speaking, n (%)	527 (95)	240 (95)	287 (96)	
Arrived by EMS, n (%)	215 (39)	96 (38)	119 (40)	
Diagnosis of Intoxication, n (%)	196 (36)	84 (33)	112 (37)	
Psychiatric Diagnosis, n (%)	125 (23)	41 (16)	84 (28)	
Assailant was Intimate Partner, n (%)	42 (7.6)	14 (5.6)	28 (9.3)	

[1] Wilcoxon rank sum test

[2] Pearson's Chi-squared test

Characteristic	Overall N = 552	Post v. Pre Pre-intervention N = 300	Post-int
Documentation of advocate offerred, n (%)	322 (58)	164 (55)	
PEP antibiotics ordered, n (%)	383 (69)	200 (67)	
HIV PEP ordered (if < 72h from assault, n/N Non-missing (%)	111/453 (25%)	35/253 (14%)	7
Female under 55, n (%)	492 (89)	270 (90)	
Pregnancy test ordered, n/N Non-missing (%)	362/492 (74%)	191/270 (71%)	17
Pregnancy prophalaxis ordered, n/N Non-missing (%)	204/492 (41%)	104/270 (39%)	10
ED with SANE program, n (%)	285 (52)	158 (53)	
SANE kit done, n (%)			
No	25 (4.5)	17 (5.7)	
Offered, but declined	128 (23)	62 (21)	
Outside 120 hr Window	46 (8.3)	24 (8.0)	
Yes	353 (64)	197 (66)	
Under 120 hours and SANE kit done, n/N Non-missing (%)	350/504 (69%)	195/276 (71%)	15
Has after discharge follow up, n (%)	515 (93)	273 (91)	

[1] Pearson's Chi-squared test

[2] Fisher's exact test

```r
model <-  glm(advocate_offered ~ exposure + age + race_eth_num + ipv+ intoxicated + sane_ED, family =
model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
return(model.results)
}
```

All patients

Odds of documentation of offering call to PT advocate

Characteristic	Post v. Pre OR (95% CI)[1]	p-value	Pathway v. No Pathway OR (95% CI)[1]	p-value	No Pathway v. Pre OR (95% CI)[1]	p-valu
Exposure	1.46 (1.02 to 2.10)	0.039	2.52 (1.35 to 4.76)	0.004	0.96 (0.61 to 1.50)	0.85
Age	0.99 (0.97 to 1.00)	0.12	0.99 (0.97 to 1.01)	0.31	0.99 (0.97 to 1.00)	0.12
Race and Ethnicity		0.53		0.45		0.47
Non-Hispanic White	—		—		—	
Non-Hispanic Black	0.81 (0.51 to 1.27)		1.31 (0.62 to 2.82)		0.77 (0.47 to 1.26)	
Hispanic or Latina/o/x	0.96 (0.60 to 1.54)		1.16 (0.58 to 2.33)		0.85 (0.50 to 1.46)	
Other	1.42 (0.69 to 3.06)		2.56 (0.80 to 9.97)		1.46 (0.64 to 3.52)	
Assailant was Intimate Partner	1.90 (0.95 to 3.97)	0.068	2.61 (0.72 to 12.5)	0.15	1.69 (0.82 to 3.60)	0.16
Intoxicated	0.88 (0.60 to 1.29)	0.51	0.71 (0.38 to 1.30)	0.26	0.91 (0.59 to 1.39)	0.65
ED with SANE program	2.99 (2.08 to 4.33)	<0.001	2.26 (1.21 to 4.25)	0.010	2.32 (1.53 to 3.55)	<0.001

[1] OR = Odds Ratio, CI = Confidence Interval

Unadjusted Odds of documentation of offering call to PT advocate

Characteristic	Post v. Pre OR (95% CI)[1]	p-value	Pathway v. No Pathway OR (95% CI)[1]	p-value	No Pathway v. Pre OR (95% CI)[1]	p-value
Exposure	1.39 (0.99 to 1.96)	0.056	3.48 (2.05 to 6.04)	<0.001	0.78 (0.51 to 1.18)	0.24

[1] OR = Odds Ratio, CI = Confidence Interval

```r
ua.advocate.regression<-function(data, exposure){
  data$advocate_offered <- as_factor(data$advocate_offered )
  data$advocate_offered <- relevel(data$advocate_offered, ref= "No Documentation of Pt Advocate")
  model <-  glm(advocate_offered ~ exposure, family = "binomial", data = data)
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```r
ua.tbl.reg.path.adv <-ua.advocate.regression(cohort.1, cohort.1$exposure)
ua.tbl.reg.pp.adv <-ua.advocate.regression(pp.cohort.1, pp.cohort.1$exposure)
ua.tbl.reg.prepn.adv <-ua.advocate.regression(pp.cohort.2, pp.cohort.2$exposure)
ua.tbl.all.adv <- tbl_merge(list(ua.tbl.reg.pp.adv, ua.tbl.reg.path.adv, ua.tbl.reg.prepn.adv), tab_spa
ua.tbl.all.adv
```

Unadjusted Odds of Offering to Contact Advocate

Primary Outcome: *SANE Kit*

note: restricted to pts <120 hours from assault no longer restricted to female (only 12 men) english speakers (only 11 non-english speaking)

no longer including as outcome: Method: *2-Profile penalized log-likelihood* SANE Kit Offered?

Odds of Doing SANE Kit if <120hrs

Characteristic	Post v. Pre OR (95% CI)[1]	p-value	Pathway v. No Pathway OR (95% CI)[1]	p-value	No Pathway v. Pre OR (95% CI)[1]	p-valu
Exposure	0.83 (0.56 to 1.24)	0.37	2.71 (1.37 to 5.48)	0.004	0.52 (0.31 to 0.85)	0.010
Age	0.99 (0.97 to 1.00)	0.10	0.99 (0.97 to 1.02)	0.54	0.99 (0.97 to 1.00)	0.13
Race and Ethnicity		0.18		0.94		0.12
Non-Hispanic White	—		—		—	
Non-Hispanic Black	0.67 (0.41 to 1.10)		0.90 (0.41 to 2.00)		0.61 (0.35 to 1.05)	
Hispanic or Latina/o/x	1.23 (0.73 to 2.11)		1.00 (0.47 to 2.16)		1.28 (0.70 to 2.40)	
Other	1.35 (0.59 to 3.36)		0.71 (0.23 to 2.38)		1.41 (0.54 to 4.14)	
Assailant was Intimate Partner	1.31 (0.62 to 2.96)	0.49	1.09 (0.30 to 4.53)	0.90	1.18 (0.54 to 2.73)	0.68
Intoxicated	0.49 (0.32 to 0.75)	<0.001	0.45 (0.23 to 0.87)	0.017	0.47 (0.29 to 0.76)	0.002
ED with SANE program	2.31 (1.54 to 3.51)	<0.001	1.66 (0.84 to 3.30)	0.14	1.72 (1.07 to 2.79)	0.026

[1] OR = Odds Ratio, CI = Confidence Interval

```
pp.cohort.1.u120 <- pp.cohort.1 %>% filter(under120h == TRUE) %>% mutate(sane_kit_offered = if_else(san
pp.cohort.1.u120$sane_kit_offered <- as_factor(pp.cohort.1.u120$sane_kit_offered)
pp.cohort.1.u120$sane_kit_offered <- relevel(pp.cohort.1.u120$sane_kit_offered, ref = "No")
pp.cohort.1.u120 <- pp.cohort.1 %>% filter(under120h == TRUE) %>% mutate(sane_kit_offered = if_else(san
pp.cohort.1.u120$sane_kit_offered <- as_factor(pp.cohort.1.u120$sane_kit_offered)
pp.cohort.1.u120$sane_kit_offered <- relevel(pp.cohort.1.u120$sane_kit_offered, ref = "No")
pp.cohort.2.u120 <- pp.cohort.2 %>% filter(under120h == TRUE) %>% mutate(sane_kit_offered = if_else(san
pp.cohort.2.u120$sane_kit_offered <- as_factor(pp.cohort.2.u120$sane_kit_offered)
pp.cohort.2.u120$sane_kit_offered <- relevel(pp.cohort.2.u120$sane_kit_offered, ref = "No")
path.u120 <- cohort.1 %>% filter(under120h == TRUE) %>% mutate(sane_kit_offered = if_else(sane_kit_done
path.u120$sane_kit_offered <- as_factor(path.u120$sane_kit_offered)
path.u120$sane_kit_offered <- relevel(path.u120$sane_kit_offered, ref = "No")
```

SANE Kit Done?

```
sane.did.reg<-function(data, exposure){
  model <-  glm(did_SANE_kit ~ exposure + age + race_eth_num + ipv+ intoxicated + sane_ED, family = "bin
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```
pp.cohort.1.u120 <- pp.cohort.1.u120 %>% mutate(did_SANE_kit = if_else(sane_kit_YN == "Yes", 1, 0))
pp.cohort.2.u120 <- pp.cohort.2.u120 %>% mutate(did_SANE_kit = if_else(sane_kit_YN == "Yes", 1, 0))
path.u120 <- path.u120 %>% mutate(did_SANE_kit = if_else(sane_kit_YN == "Yes", 1, 0))

pp.sk.did <- sane.did.reg(pp.cohort.1.u120, pp.cohort.1.u120$exposure)
prenp.sk.did <- sane.did.reg(pp.cohort.2.u120, pp.cohort.2.u120$exposure)
path.sk.did <-sane.did.reg(path.u120, path.u120$exposure)
table.reg.sk <- tbl_merge(list(pp.sk.did, path.sk.did, prenp.sk.did), tab_spanner = c("**Post v. Pre**"
table.reg.sk
```

Unadjusted Odds of Doing SANE Kit if <120hrs

Characteristic	Post v. Pre		Pathway v. No Pathway		No Pathway v. Pre	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value
Exposure	0.88 (0.60 to 1.29)	0.52	2.86 (1.62 to 5.15)	<0.001	0.53 (0.33 to 0.84)	0.007

[1] OR = Odds Ratio, CI = Confidence Interval

```r
ua.pp.sk.did <- glm(did_SANE_kit ~ exposure, family = "binomial", data = pp.cohort.1.u120) %>%
  tbl_regression(exponentiate = T)

ua.prenp.sk.did <- glm(did_SANE_kit ~ exposure, family = "binomial", data = pp.cohort.2.u120) %>%
  tbl_regression(exponentiate = T)

ua.path.sk.did <- glm(did_SANE_kit ~ exposure, family = "binomial", data = path.u120) %>%
  tbl_regression(exponentiate = T)

ua.table.reg.sk <- tbl_merge(list(ua.pp.sk.did, ua.path.sk.did, ua.prenp.sk.did), tab_spanner = c("**Pos
ua.table.reg.sk
```

Unadjusted OR for doing SAFE KIT

Secondary Outcome: *For Women =< 55 Presenting < 120 Hours*

```r
preg.test.reg<-function(data, exposure){
  model<-glm(pregnancy_test_ordered_num ~ exposure + age + race_eth_num + ipv+ intoxicated + sane_ED, fa
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}

preg.prev.reg<-function(data, exposure){
   model<-glm(prevent.preg ~ exposure + age + race_eth_num + ipv+ intoxicated + sane_ED, family = "binor
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

Pregnancy test ordered?

```r
preg.test.pp<-pp.cohort.1.u120 %>% filter(female == 1, age <= 55) %>% preg.test.reg(., .$exposure)
preg.test.prenp<-pp.cohort.2.u120 %>% filter(female == 1, age <= 55) %>% preg.test.reg(., .$exposure)
preg.test.path<-path.u120 %>% filter(female == 1, age <= 55) %>% preg.test.reg(., .$exposure)
table.reg.pregtest <- tbl_merge(list(preg.test.pp, preg.test.path, preg.test.prenp), tab_spanner = c("*
table.reg.pregtest
```

Pregnancy prophylaxis ordered?

Odds of Pregnancy Test Ordered (if =/<55 & <120 hrs)

Characteristic	Post v. Pre OR (95% CI)[1]	p-value	Pathway v. No Pathway OR (95% CI)[1]	p-value	No Pathway v. Pre OR (95% CI)[1]	p-valu
Exposure	1.41 (0.92 to 2.18)	0.12	5.38 (2.31 to 13.5)	<0.001	0.70 (0.41 to 1.20)	0.20
Age	0.98 (0.96 to 1.00)	0.056	0.98 (0.94 to 1.02)	0.35	0.98 (0.95 to 1.00)	0.10
Race and Ethnicity		0.41		0.73		0.39
Non-Hispanic White	—		—		—	
Non-Hispanic Black	1.40 (0.82 to 2.42)		1.40 (0.57 to 3.66)		1.33 (0.75 to 2.42)	
Hispanic or Latina/o/x	1.54 (0.88 to 2.79)		1.55 (0.63 to 4.10)		1.59 (0.83 to 3.16)	
Other	1.13 (0.51 to 2.74)		0.88 (0.25 to 3.59)		0.81 (0.33 to 2.08)	
Assailant was Intimate Partner	1.11 (0.52 to 2.54)	0.79	0.64 (0.17 to 2.78)	0.53	1.23 (0.55 to 2.98)	0.62
Intoxicated	0.78 (0.49 to 1.25)	0.30	0.57 (0.25 to 1.27)	0.17	0.73 (0.43 to 1.23)	0.24
ED with SANE program	0.75 (0.49 to 1.16)	0.20	0.45 (0.19 to 1.03)	0.059	0.56 (0.34 to 0.93)	0.023

[1] OR = Odds Ratio, CI = Confidence Interval

Odds of Pregnancy Prophylaxis Ordered (if =/<55 & <120 hrs)

Characteristic	Pre v. Post OR (95% CI)[1]	p-value	Pathway v. No Pathway OR (95% CI)[1]	p-value	Pre v. No Pathway OR (95% CI)[1]	p-valu
Exposure	1.25 (0.86 to 1.83)	0.25	3.23 (1.63 to 6.67)	<0.001	0.82 (0.49 to 1.36)	0.43
Age	0.98 (0.96 to 1.00)	0.10	1.00 (0.96 to 1.03)	0.92	0.97 (0.95 to 1.00)	0.027
Race and Ethnicity		0.48		0.24		0.52
Non-Hispanic White	—		—		—	
Non-Hispanic Black	1.00 (0.62 to 1.63)		1.18 (0.55 to 2.53)		1.01 (0.58 to 1.76)	
Hispanic or Latina/o/x	1.45 (0.89 to 2.38)		1.28 (0.62 to 2.66)		1.48 (0.82 to 2.68)	
Other	1.08 (0.51 to 2.28)		0.39 (0.11 to 1.21)		1.43 (0.58 to 3.47)	
Assailant was Intimate Partner	0.35 (0.14 to 0.75)	0.007	0.57 (0.14 to 2.03)	0.39	0.27 (0.09 to 0.66)	0.003
Intoxicated	1.03 (0.67 to 1.57)	0.91	0.74 (0.37 to 1.44)	0.37	1.12 (0.67 to 1.87)	0.68
ED with SANE program	1.06 (0.72 to 1.55)	0.78	0.58 (0.28 to 1.14)	0.12	0.91 (0.57 to 1.45)	0.69

[1] OR = Odds Ratio, CI = Confidence Interval

```
preg.prev.pp<-pp.cohort.1.u120 %>% filter(female == 1, age <= 55) %>% preg.prev.reg(., .$exposure)
preg.prev.prenp<-pp.cohort.2.u120 %>% filter(female == 1, age <= 55) %>% preg.prev.reg(., .$exposure)
preg.prev.path<-path.u120 %>% filter(female == 1, age <= 55) %>% preg.prev.reg(., .$exposure)
table.reg.pregprev <- tbl_merge(list(preg.prev.pp, preg.prev.path, preg.prev.prenp), tab_spanner = c("*
table.reg.pregprev
```

```
ua.preg.test.reg<-function(data, exposure){
  model<-glm(pregnancy_test_ordered_num ~ exposure, family = "binomial", data = data)
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}

ua.preg.prev.reg<-function(data, exposure){
   model<-glm(prevent.preg ~ exposure, family = "binomial", data = data)
```

Unadjusted Odds of Pregnancy Test Ordered (if =/<55 & <120 hrs)

Characteristic	Post v. Pre		Pathway v. No Pathway		No Pathway v. Pre	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value
Exposure	1.43 (0.94 to 2.20)	0.10	3.32 (1.68 to 6.87)	<0.001	0.85 (0.52 to 1.40)	0.51

[1] OR = Odds Ratio, CI = Confidence Interval

Unadjusted Odds of Pregnancy Prophylaxis Ordered (if =/<55 & <120 hrs)

Characteristic	Pre v. Post		Pathway v. No Pathway		Pre v. No Pathway	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value
Exposure	1.33 (0.92 to 1.94)	0.13	2.31 (1.33 to 4.07)	0.003	0.86 (0.53 to 1.38)	0.54

[1] OR = Odds Ratio, CI = Confidence Interval

```
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

Unadjusted Outcomes: Pregnancy Test and Prevention   *Unadjusted* Pregnancy test ordered?

```
ua.preg.test.pp<-pp.cohort.1.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.test.reg(., .$exposure)
ua.preg.test.prenp<-pp.cohort.2.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.test.reg(., .$exposu
ua.preg.test.path<-path.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.test.reg(., .$exposure)
ua.table.reg.pregtest <- tbl_merge(list(ua.preg.test.pp, ua.preg.test.path, ua.preg.test.prenp), tab_spa
ua.table.reg.pregtest
```

Unadjusted Pregnancy prophylaxis ordered?

```
ua.preg.prev.pp<-pp.cohort.1.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.prev.reg(., .$exposure)
ua.preg.prev.prenp<-pp.cohort.2.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.prev.reg(., .$exposu
ua.preg.prev.path<-path.u120 %>% filter(female == 1, age <= 55) %>% ua.preg.prev.reg(., .$exposure)
ua.table.reg.pregprev <- tbl_merge(list(ua.preg.prev.pp, ua.preg.prev.path, ua.preg.prev.prenp), tab_spa
ua.table.reg.pregprev
```

Secondary Outcome: *HIV PEP*

```
hiv.pep.reg<-function(data, exposure){
  model<-glm(hiv_pep_kit_ordered_num ~ exposure + age + race_eth_num + ipv + intoxicated + sane_ED, fami
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```
pathway.u72 <- cohort.1 %>% filter(u72 == 1)
pp.u72 <- pp.cohort.1 %>% filter(u72 == 1)
prenp.u72 <- pp.cohort.2 %>% filter(u72 == 1)
```

Odds of Receiving HIV PEP if Presented to ED <72 Hours Since Assault

Characteristic	Pre v. Post		Pathway v. No Pathway		Pre v. No Pathway	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p
Exposure	3.85 (2.42 to 6.22)	<0.001	8.70 (3.93 to 20.7)	<0.001	0.86 (0.41 to 1.73)	
Age	0.98 (0.95 to 1.00)	0.022	0.99 (0.96 to 1.01)	0.32	0.98 (0.95 to 1.01)	
Race and Ethnicity		0.91		0.49		
Non-Hispanic White	—		—		—	
Non-Hispanic Black	1.15 (0.64 to 2.05)		1.54 (0.64 to 3.69)		1.37 (0.63 to 2.94)	
Hispanic or Latina/o/x	1.22 (0.68 to 2.17)		0.95 (0.42 to 2.16)		1.19 (0.50 to 2.68)	
Other	1.04 (0.39 to 2.52)		0.52 (0.13 to 1.93)		1.01 (0.22 to 3.39)	
Assailant was Intimate Partner	0.37 (0.08 to 1.12)	0.081	0.74 (0.13 to 3.72)	0.71	0.00 (0.00 to 10,725,108)	
Intoxicated	0.93 (0.56 to 1.53)	0.78	0.57 (0.27 to 1.17)	0.13	0.78 (0.37 to 1.58)	
ED with SANE program	1.62 (1.01 to 2.61)	0.043	1.39 (0.65 to 2.92)	0.39	0.63 (0.31 to 1.22)	

[1] OR = Odds Ratio, CI = Confidence Interval

Unadjusted Odds of Receiving HIV PEP if Presented to ED <72 Hours Since Assault

Characteristic	Pre v. Post		Pathway v. No Pathway		Pre v. No Pathway	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value
Exposure	3.82 (2.43 to 6.08)	<0.001	8.51 (4.34 to 17.7)	<0.001	1.02 (0.50 to 1.99)	0.94

[1] OR = Odds Ratio, CI = Confidence Interval

```
tbl.pep.pp <- hiv.pep.reg(pp.u72, pp.u72$exposure)
tbl.pep.path <- hiv.pep.reg(pathway.u72, pathway.u72$exposure)
#### WARNING. Non-convirgence for no path vs pre. has to do with zero cell in ipv variable. does it mat
tbl.pep.prenp <- hiv.pep.reg(prenp.u72, prenp.u72$exposure)
tbl.pep.hiv <- tbl_merge(list(tbl.pep.pp, tbl.pep.path, tbl.pep.prenp), tab_spanner = c("**Pre v. Post**
tbl.pep.hiv
```

```
ua.hiv.pep.reg<-function(data, exposure){
  model<-glm(hiv_pep_kit_ordered_num ~ exposure, family = "binomial", data = data)
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```
ua.tbl.pep.pp <- ua.hiv.pep.reg(pp.u72, pp.u72$exposure)
ua.tbl.pep.path <- ua.hiv.pep.reg(pathway.u72, pathway.u72$exposure)
ua.tbl.pep.prenp <- ua.hiv.pep.reg(prenp.u72, prenp.u72$exposure)
ua.tbl.pep.hiv <- tbl_merge(list(ua.tbl.pep.pp, ua.tbl.pep.path, ua.tbl.pep.prenp), tab_spanner = c("**
ua.tbl.pep.hiv
```

Unadjusted OR for HIV PEP

Odds of Ordering Antibiotics

Characteristic	Post v. Pre OR (95% CI)[1]	Post v. Pre p-value	Pathway v. No Pathway OR (95% CI)[1]	Pathway v. No Pathway p-value	No Pathway v. Pre OR (95% CI)[1]	No Pathway v. Pre p-valu
Exposure	1.28 (0.87 to 1.88)	0.21	5.26 (2.54 to 11.4)	<0.001	0.75 (0.47 to 1.20)	0.23
Age	0.97 (0.96 to 0.99)	<0.001	0.98 (0.96 to 1.00)	0.078	0.97 (0.96 to 0.99)	<0.001
Race and Ethnicity		0.47		0.050		0.49
Non-Hispanic White	—		—		—	
Non-Hispanic Black	1.13 (0.70 to 1.84)		1.62 (0.69 to 4.07)		1.14 (0.68 to 1.92)	
Hispanic or Latina/o/x	1.34 (0.81 to 2.28)		0.86 (0.40 to 1.90)		1.55 (0.87 to 2.85)	
Other	0.73 (0.35 to 1.56)		0.26 (0.08 to 0.81)		0.91 (0.39 to 2.22)	
Assailant was Intimate Partner	0.32 (0.16 to 0.61)	<0.001	0.25 (0.07 to 0.85)	0.026	0.33 (0.16 to 0.67)	0.002
Intoxicated	0.78 (0.52 to 1.16)	0.21	0.57 (0.29 to 1.10)	0.094	0.77 (0.49 to 1.20)	0.25
ED with SANE program	1.38 (0.94 to 2.03)	0.10	0.69 (0.33 to 1.39)	0.30	1.18 (0.76 to 1.85)	0.46

[1] OR = Odds Ratio, CI = Confidence Interval

Secondary Outcome: *ABX given*

refers to any abx given, not looking at correct med/dosage

```
abx.pep.reg<-function(data, exposure){
  model<-glm(abx_given ~ exposure + age + race_eth_num + ipv + intoxicated + sane_ED, family = "binomial
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```
tbl.reg.path.abx <-abx.pep.reg(cohort.1, cohort.1$exposure)
tbl.reg.pp.abx <-abx.pep.reg(pp.cohort.1, pp.cohort.1$exposure)
tbl.reg.prepn.abx <-abx.pep.reg(pp.cohort.2, pp.cohort.2$exposure)
tbl.all.abx <- tbl_merge(list(tbl.reg.pp.abx, tbl.reg.path.abx, tbl.reg.prepn.abx), tab_spanner = c("**
tbl.all.abx
```

```
ua.abx.pep.reg<-function(data, exposure){
  model<-glm(abx_given ~ exposure, family = "binomial", data = data)
  model.results <- tbl_regression(model, exponentiate = TRUE) %>% add_global_p()
  return(model.results)
}
```

```
ua.tbl.reg.path.abx <-ua.abx.pep.reg(cohort.1, cohort.1$exposure)
ua.tbl.reg.pp.abx <-ua.abx.pep.reg(pp.cohort.1, pp.cohort.1$exposure)
ua.tbl.reg.prepn.abx <-ua.abx.pep.reg(pp.cohort.2, pp.cohort.2$exposure)
ua.tbl.all.abx <- tbl_merge(list(ua.tbl.reg.pp.abx, ua.tbl.reg.path.abx, ua.tbl.reg.prepn.abx), tab_spar
ua.tbl.all.abx
```

Unadjusted OR for abx admin

Unadjusted Odds of Ordering Antibiotics

Characteristic	Post v. Pre		Pathway v. No Pathway		No Pathway v. Pre	
	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value	OR (95% CI)[1]	p-value
Exposure	1.33 (0.92 to 1.92)	0.13	3.53 (1.97 to 6.53)	<0.001	0.77 (0.50 to 1.18)	0.23

[1] OR = Odds Ratio, CI = Confidence Interval

Tertiary Outcome: *Follow Up at Discharge?*

note: removed outcome on 8/22/24

Restricted to YSC and SRC

```
#create cohort restricted to YSC and SRC (SAFE program sites)

SAFE_Site_Cohort <- pp.cohort.1 %>%
  filter(sane_ED == 1)
SAFE_Site_Cohort_u120 <- SAFE_Site_Cohort %>%
   mutate(did_SANE_kit = if_else(sane_kit_YN == "Yes", 1, 0)) %>%
  filter(under120h == TRUE) #383 patients u120 at SAFE sites
SAFE_Site_Cohort_u120.f <- SAFE_Site_Cohort_u120 %>% filter(female_u55 == 1)
SAFE_Site_Cohort_u72 <- SAFE_Site_Cohort %>% filter(u72 == 1)
# number of patients who had pathway used
SAFE_Site_Cohort %>% filter(agile_md_used_num == 1) %>% nrow() %>% print()
```

```
## [1] 95
```

```
SAFE_Site_Cohort_u120 %>% filter(agile_md_used_num == 1) %>% nrow() %>% print()
```

```
## [1] 89
```

```
# SAFE Kit Done; restricted to u120
reg.ss.sk.did <-  glm(did_SANE_kit ~ exposure + age + race_eth_num + ipv+ intoxicated, family = "binomi
tbl.reg.ss.sk.did <- tbl_regression(reg.ss.sk.did, exponentiate = TRUE) %>% add_global_p() %>% as_gt()
tbl.reg.ss.sk.did
```

```
# advocate offered

  SAFE_Site_Cohort$advocate_offered <- as_factor(SAFE_Site_Cohort$advocate_offered )
  SAFE_Site_Cohort$advocate_offered <- relevel(SAFE_Site_Cohort$advocate_offered, ref= "No Documentation
  reg.ss.adv <-  glm(advocate_offered ~ exposure + age + race_eth_num + ipv+ intoxicated, family = "bin
  tbl.reg.ss.adv <- tbl_regression(reg.ss.adv, exponentiate = TRUE) %>% add_global_p() %>% as_gt() %>%
  tbl.reg.ss.adv
```

```
# pregnancy test ordered
  reg.ss.preg <-glm(pregnancy_test_ordered_num ~ exposure + age + race_eth_num + ipv+ intoxicated, fam
  tbl.reg.ss.preg <- tbl_regression(reg.ss.preg, exponentiate = TRUE) %>% add_global_p() %>% as_gt() %>
  tbl.reg.ss.preg
```

Odds of Doing SAFE Kit (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	1.06 (0.58 to 1.93)	0.86
Age	1.01 (0.98 to 1.04)	0.46
Race and Ethnicity		0.62
Non-Hispanic White	—	
Non-Hispanic Black	0.79 (0.40 to 1.57)	
Hispanic or Latina/o/x	1.07 (0.48 to 2.48)	
Other	2.00 (0.50 to 13.4)	
Assailant was Intimate Partner	1.41 (0.43 to 6.38)	0.60
Intoxicated	0.37 (0.19 to 0.69)	0.002

[1] OR = Odds Ratio, CI = Confidence Interval

Odds of Offering Advocate (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	1.69 (0.99 to 2.91)	0.053
Age	1.01 (0.99 to 1.04)	0.42
Race and Ethnicity		0.78
Non-Hispanic White	—	
Non-Hispanic Black	0.89 (0.48 to 1.64)	
Hispanic or Latina/o/x	1.03 (0.50 to 2.18)	
Other	0.59 (0.20 to 1.78)	
Assailant was Intimate Partner	2.91 (0.94 to 12.8)	0.066
Intoxicated	1.06 (0.60 to 1.88)	0.83

[1] OR = Odds Ratio, CI = Confidence Interval

Odds of Ordering Pregnancy Test (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	1.95 (1.07 to 3.64)	0.030
Age	0.98 (0.95 to 1.01)	0.27
Race and Ethnicity		0.25
Non-Hispanic White	—	
Non-Hispanic Black	2.02 (0.99 to 4.24)	
Hispanic or Latina/o/x	1.13 (0.53 to 2.47)	
Other	1.70 (0.53 to 6.61)	
Assailant was Intimate Partner	0.90 (0.31 to 2.87)	0.86
Intoxicated	0.83 (0.43 to 1.61)	0.58

[1] OR = Odds Ratio, CI = Confidence Interval

```r
# EC ordered
  reg.ss.ec<-glm(prevent.preg ~ exposure + age + race_eth_num + ipv+ intoxicated, family = "binomial", 
  tbl.reg.ss.ec <- tbl_regression(reg.ss.ec, exponentiate = TRUE) %>% add_global_p() %>% as_gt() %>% tal
  tbl.reg.ss.ec
```

Odds of Ordering Emergency Contraception (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	1.22 (0.71 to 2.09)	0.47
Age	0.98 (0.95 to 1.01)	0.19
Race and Ethnicity		0.72
Non-Hispanic White	—	
Non-Hispanic Black	0.92 (0.48 to 1.74)	
Hispanic or Latina/o/x	1.30 (0.64 to 2.63)	
Other	1.46 (0.50 to 4.31)	
Assailant was Intimate Partner	0.55 (0.17 to 1.57)	0.27
Intoxicated	0.99 (0.54 to 1.82)	0.98

[1] OR = Odds Ratio, CI = Confidence Interval

Odds of Ordering HIV PEP (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	9.73 (4.92 to 20.4)	<0.001
Age	0.96 (0.93 to 0.99)	0.009
Race and Ethnicity		0.98
Non-Hispanic White	—	
Non-Hispanic Black	1.03 (0.47 to 2.27)	
Hispanic or Latina/o/x	0.94 (0.39 to 2.21)	
Other	0.75 (0.17 to 2.94)	
Assailant was Intimate Partner	0.43 (0.06 to 1.93)	0.29
Intoxicated	0.86 (0.42 to 1.77)	0.69

[1] OR = Odds Ratio, CI = Confidence Interval

```
# HIV Prophylaxis ordered
  reg.ss.hiv <-glm(hiv_pep_kit_ordered_num ~ exposure + age + race_eth_num + ipv + intoxicated, family =
  tbl.reg.ss.hiv <- tbl_regression(reg.ss.hiv, exponentiate = TRUE) %>% add_global_p() %>% as_gt() %>%
  tbl.reg.ss.hiv
```

```
# Abx ordered
  reg.ss.abx <-glm(abx_given ~ exposure + age + race_eth_num + ipv + intoxicated, family = "binomial",
  tbl.reg.ss.abx <- tbl_regression(reg.ss.abx, exponentiate = TRUE) %>% add_global_p() %>% as_gt() %>%
  tbl.reg.ss.abx
```

Graphs

Updated CI Graph

```
OR_Data<- read_excel("~/Documents/Current_Projects/Sexual_Assault/new_SA_YNHH/Updated YNHH SA code/OR_Ta
OR_Data <- OR_Data %>%  mutate(Measure = fct_relevel(Measure, "Antibiotics Ordered", "HIV Prophylaxis O
FinalArrowMsg = "Less likely                          OR                          More likely"
TitleStr <-  paste("Association Between", sep = " ", collapse = NULL)
TitleStr <- paste(TitleStr,'Exposure and ED Outcome Measures', sep = " ", collapse = NULL)
```

Odds of Ordering Antibiotics (Restricted to YSC/SRC)

Characteristic	OR (95% CI)[1]	p-value
Exposure	1.45 (0.84 to 2.55)	0.18
Age	0.97 (0.95 to 1.0)	0.016
Race and Ethnicity		0.82
Non-Hispanic White	—	
Non-Hispanic Black	1.09 (0.59 to 2.06)	
Hispanic or Latina/o/x	0.94 (0.45 to 2.00)	
Other	1.77 (0.52 to 8.20)	
Assailant was Intimate Partner	0.52 (0.20 to 1.34)	0.17
Intoxicated	0.88 (0.50 to 1.56)	0.67

[1] OR = Odds Ratio, CI = Confidence Interval

```
pd <- position_dodge(width = 0.6)
 p <- ggplot(OR_Data, aes(OR, Measure, group = Exposure))
 CI_Log_Graph <- p + geom_point(position = pd, aes(shape=Exposure, color=Exposure)) + geom_errorbarh(ae
   theme(
     plot.title = element_text(size=15),
     axis.title.x = element_text(size=13),
     axis.title.y = element_text(size=14),
     plot.caption = element_text(hjust = 0, face= "italic",size=10),
     axis.line.x = element_line(arrow = grid::arrow(length = unit(0.3, "cm"),ends = "both")),
     axis.text.y = element_text(size=12),
     axis.text.x = element_text(size=10),
     legend.text=element_text(size=12),
     legend.title = element_text(size = 14),
     legend.key.height=unit(1, "cm")
   ) +
   geom_vline(xintercept = 1)  +
   scale_x_log10() +
   labs(caption = "Note: Horizontal lines are 95% confidence intervals")+
   ggtitle(TitleStr) + theme(plot.title = element_text(hjust = 0.5))+
   guides(color = guide_legend(reverse=TRUE),shape =guide_legend(reverse=TRUE))
CI_Log_Graph
```

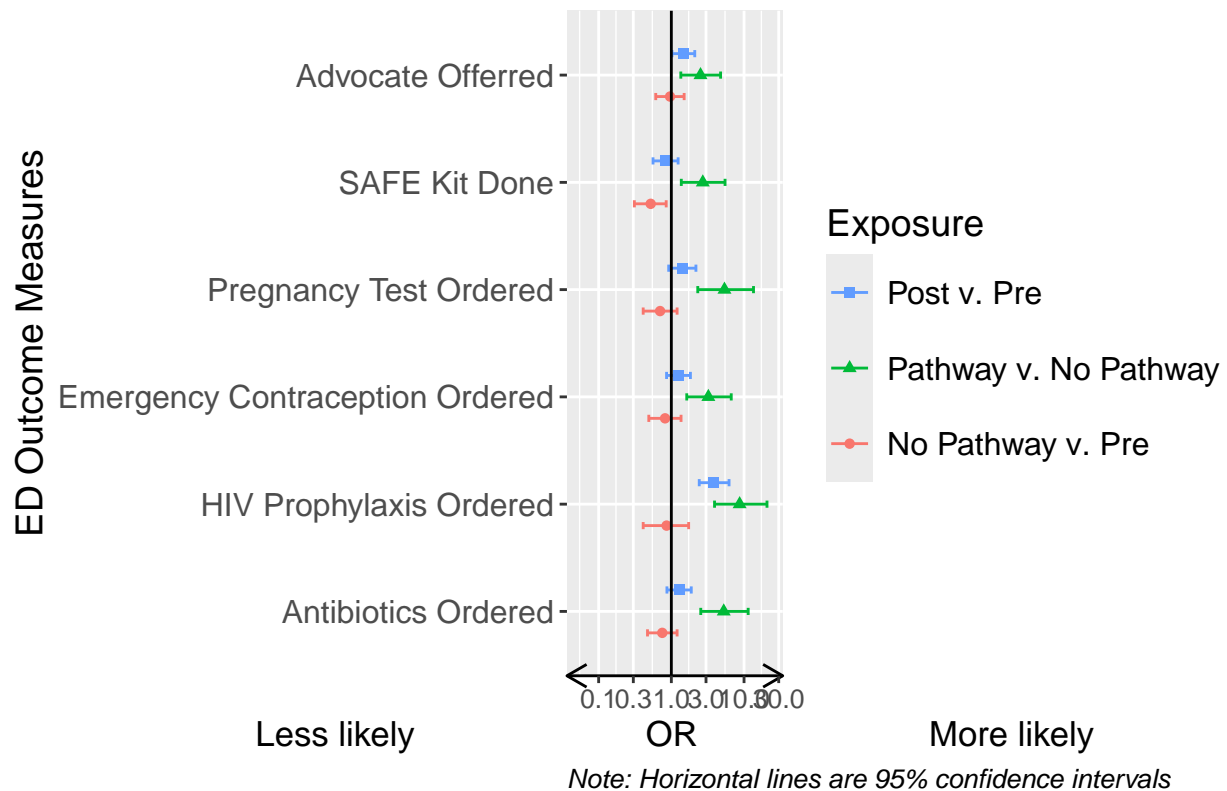## Association Between Exposure and ED Outcome Measures

Note: Horizontal lines are 95% confidence intervals
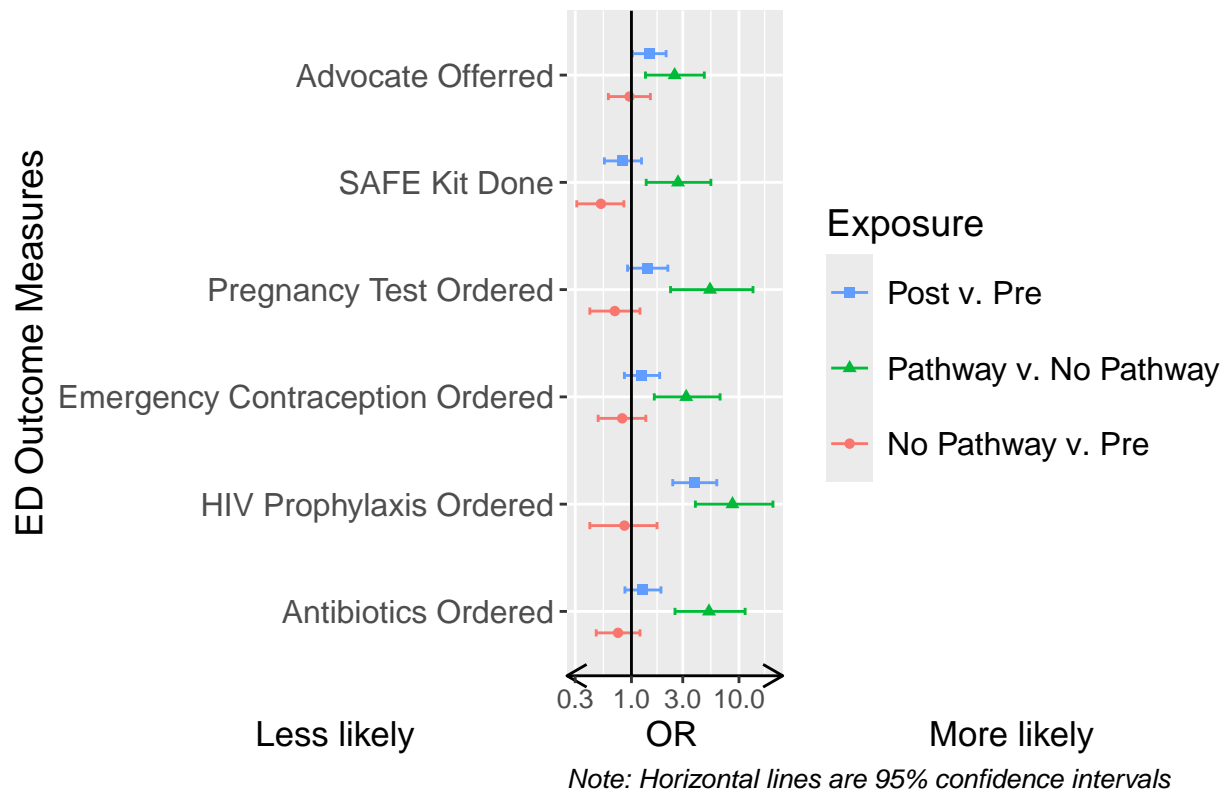
```
CI_Log_Graph + scale_x_log10(limits = c(0.05, 25), n.breaks = 6)
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```

## Association Between Exposure and ED Outcome Measures

Note: Horizontal lines are 95% confidence intervals

```r
CI_Graph <- p + geom_point(position = pd,aes(shape=Exposure, color=Exposure)) + geom_errorbarh(aes(xma
  theme(
    plot.title = element_text(size=15),
    axis.title.x = element_text(size=12, vjust = -.05),
    axis.title.y = element_text(size=14),
    plot.caption = element_text(hjust = 0, face= "italic",size=10),
    axis.line.x = element_line(arrow = grid::arrow(length = unit(0.3, "cm"),ends = "both")),
    axis.text.y = element_text(size=12),
    axis.text.x = element_text(size=11),
    legend.text=element_text(size=12),
    legend.title = element_text(size = 14),
    legend.key.height=unit(1, "cm")
  ) +
  geom_vline(xintercept = 1)  +
  labs(caption = "Note: Horizontal lines are 95% confidence intervals")+
  ggtitle(TitleStr) + theme(plot.title = element_text(hjust = 0.5)) +
  guides(color = guide_legend(reverse=TRUE),shape =guide_legend(reverse=TRUE))

CI_Graph
```

Association Between Exposure and ED Outcome Measures

*Note: Horizontal lines are 95% confidence intervals*
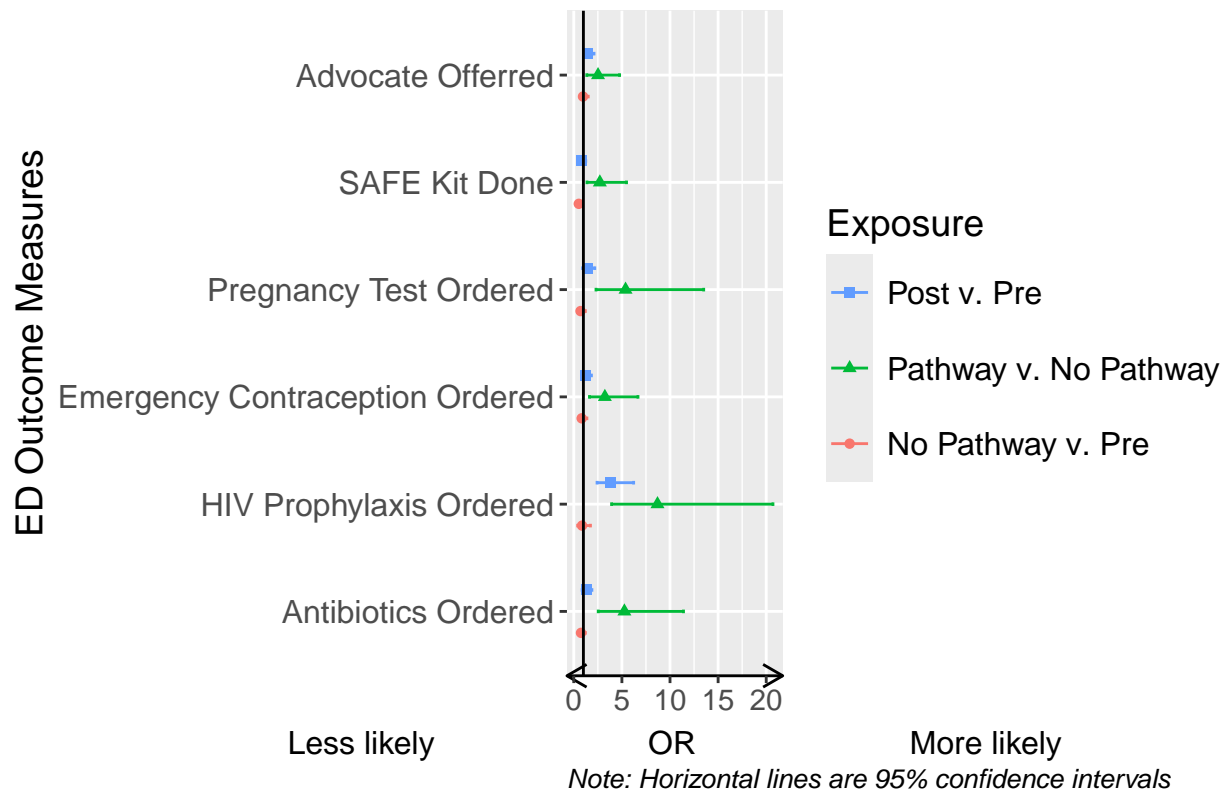
CI Graph for Post V. Pre for SAFE Sites (defined as YSC or SRC discharge)

```
SAFE_SITE_OR_Data <- read_excel("~/Documents/Current_Projects/Sexual_Assault/new_SA_YNHH/Updated YNHH S

ggplot(SAFE_SITE_OR_Data, aes(OR, Measure)) + geom_errorbar(aes(xmax = UCI, xmin = LCI), color = "blue"
```

```
## Warning in geom_errorbar(aes(xmax = UCI, xmin = LCI), color = "blue", height =
## 0.1): Ignoring unknown parameters: 'height'
```

```
## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```

CI Graph for Post V. Pre for SAFE Sites
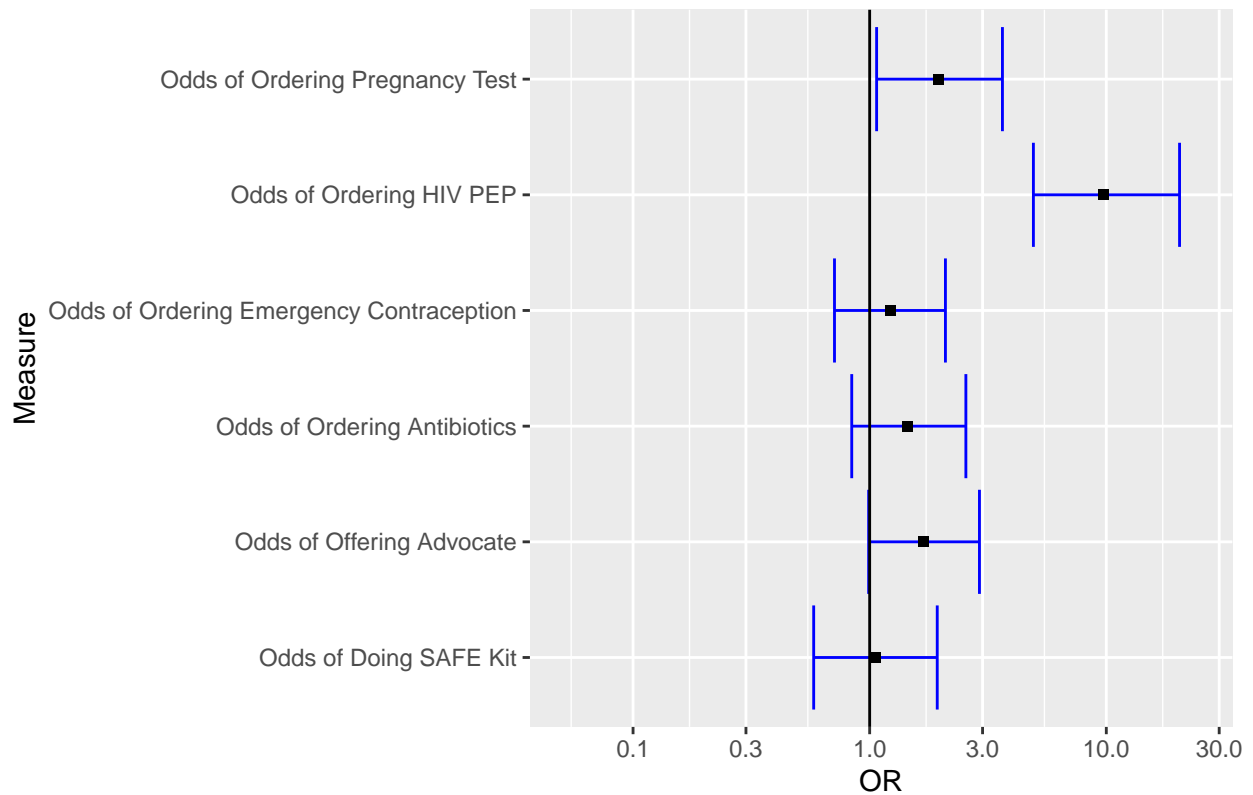
Percent pathway, sane kit done and advocate offered over time

```r
month_line_df <-
  pp.cohort.1 %>% mutate(
    month = ceiling_date(arrive_dt, unit = "month"),
    advocate = case_when(
      advocate_offered == "Advocate Offered" ~ 1,
      advocate_offered == "No Documentation of Pt Advocate" ~ 0,
      .default = NA
    ),
    did_SANE_kit = case_when(
      under120h == TRUE & sane_kit_done == 1 ~ 1,
      under120h == TRUE & sane_kit_done != 1 ~ 0,
      .default = NA
    ),
) %>%
  group_by(month) %>% summarise(
    Percent_Advocate = mean(advocate),
    Percent_Pathway = mean(agile_md_used_num, na.rm = FALSE),
    Percent_Sane = mean(did_SANE_kit, na.rm = TRUE)
) %>% gather(key = "Metric", value = "Percent", -month) %>% filter(Percent !=0) %>% mutate(Metric = f

month_line_df %>% ggplot(aes(x = month, y = Percent, color = Metric)) + geom_point() + geom_path() + sca
```
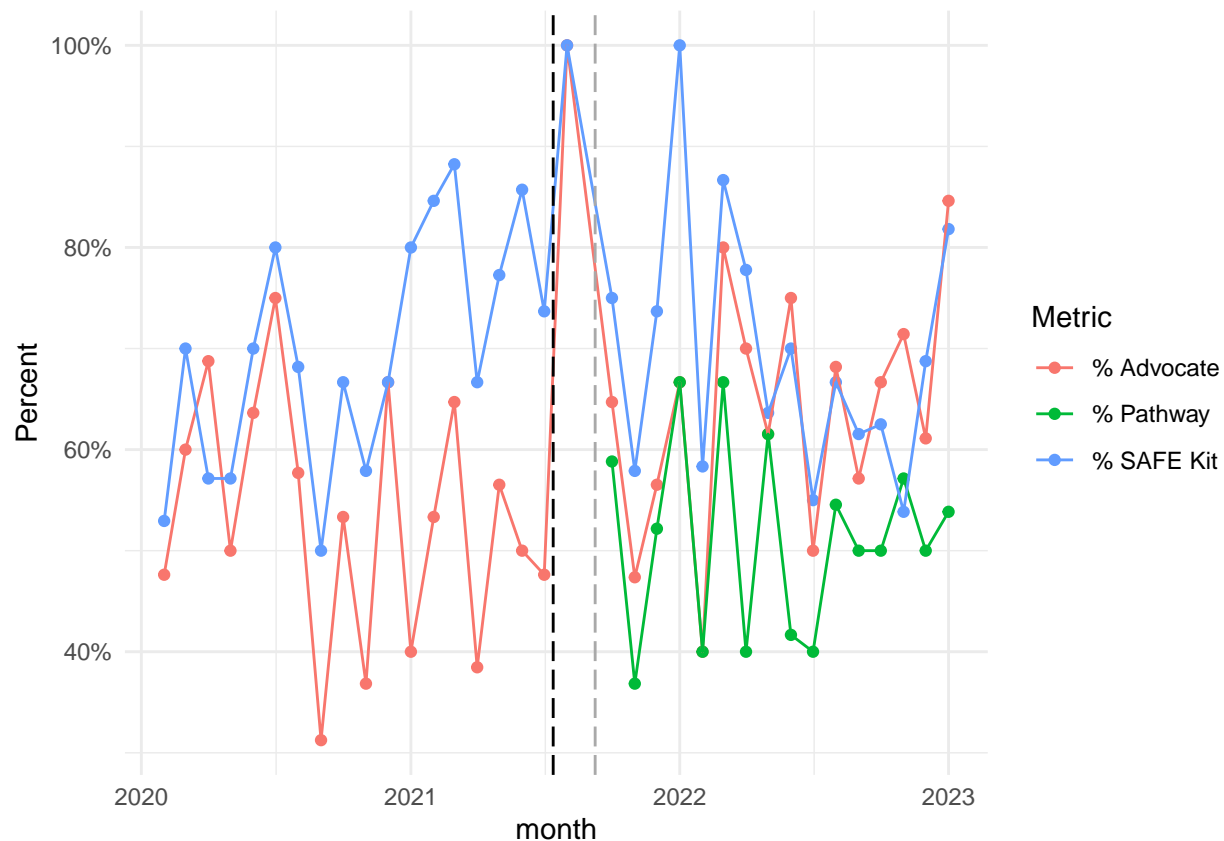
```r
quarter_line_df <-
  pp.cohort.1 %>% mutate(
    quarter = ceiling_date(arrive_dt, unit = "quarter"),
    advocate = case_when(
      advocate_offered == "Advocate Offered" ~ 1,
      advocate_offered == "No Documentation of Pt Advocate" ~ 0,
      .default = NA
    ),
    did_SANE_kit = case_when(
      under120h == TRUE & sane_kit_done == 1 ~ 1,
      under120h == TRUE & sane_kit_done != 1 ~ 0,
      .default = NA
    )) %>%
  group_by(quarter) %>% summarise(
    Percent_Advocate = mean(advocate),
    Percent_Pathway = mean(agile_md_used_num),
    Percent_Sane = mean(did_SANE_kit, na.rm = TRUE)
  ) %>% gather(key = "Metric", value = "Percent", -quarter) %>% filter(Percent !=0) %>% mutate(Metric =

quarter_percent_plot<- quarter_line_df %>% ggplot(aes(x = quarter, y = Percent, color = Metric)) + geom_
quarter_percent_plot + xlab("Quarter")
```
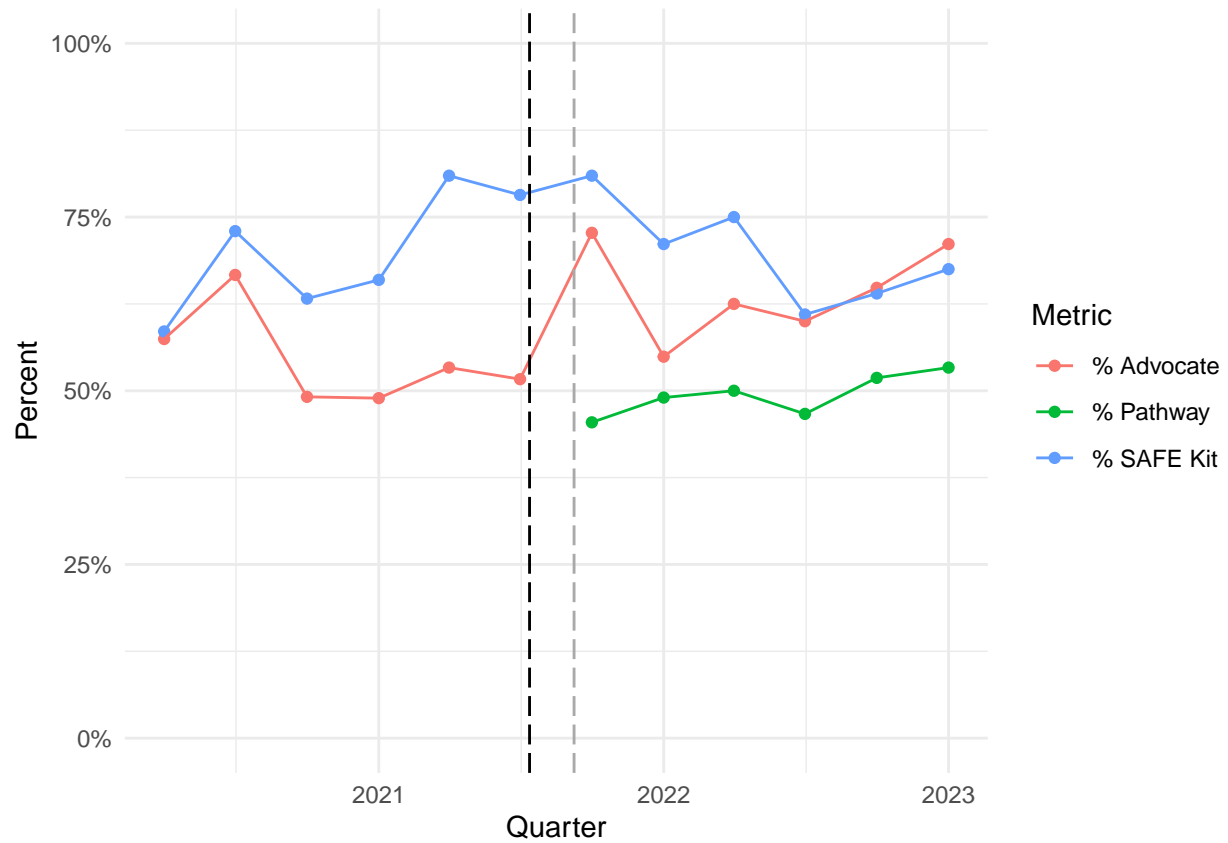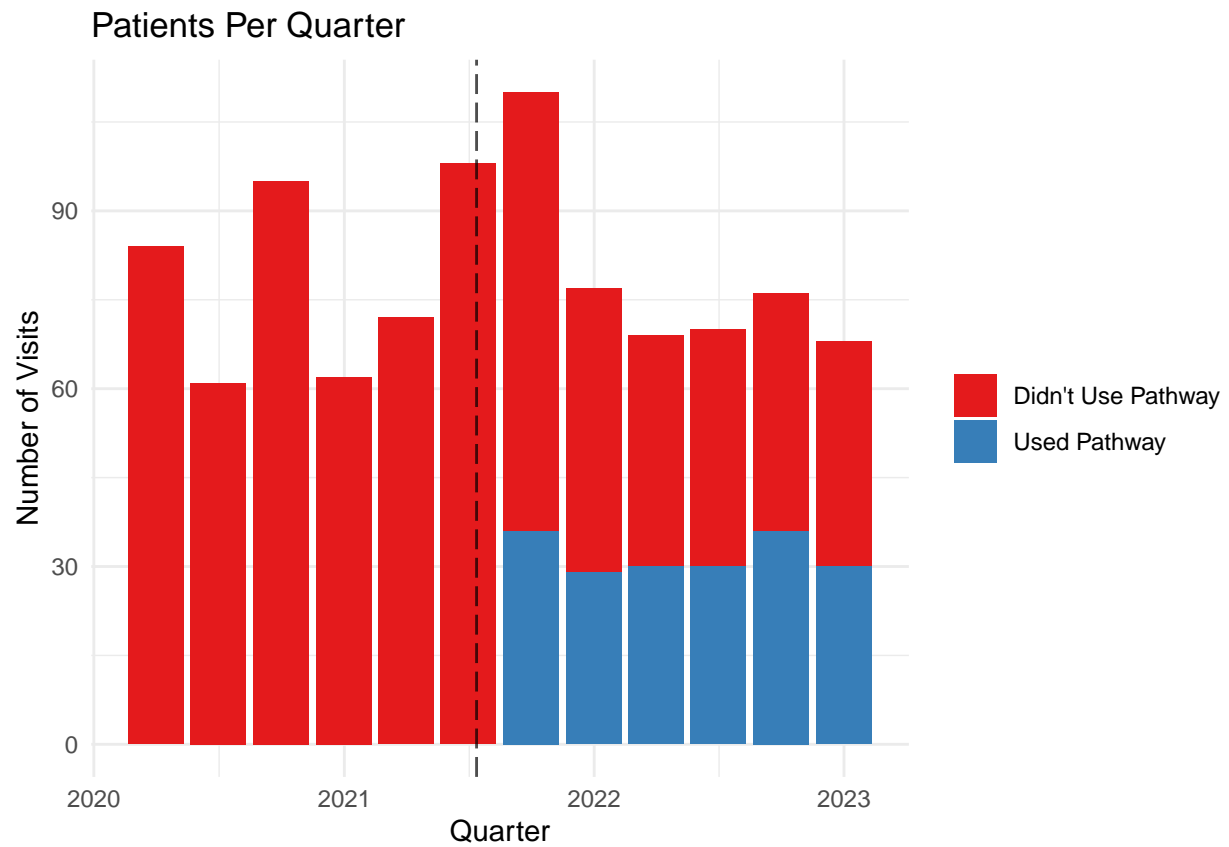
Percent pathway utilization over time

```
time_graph_1 <- all_pts %>% mutate(month = ceiling_date(arrive_dt, "month")) %>% ggplot() + geom_bar(map
time_graph_1
```

Patients Per Month
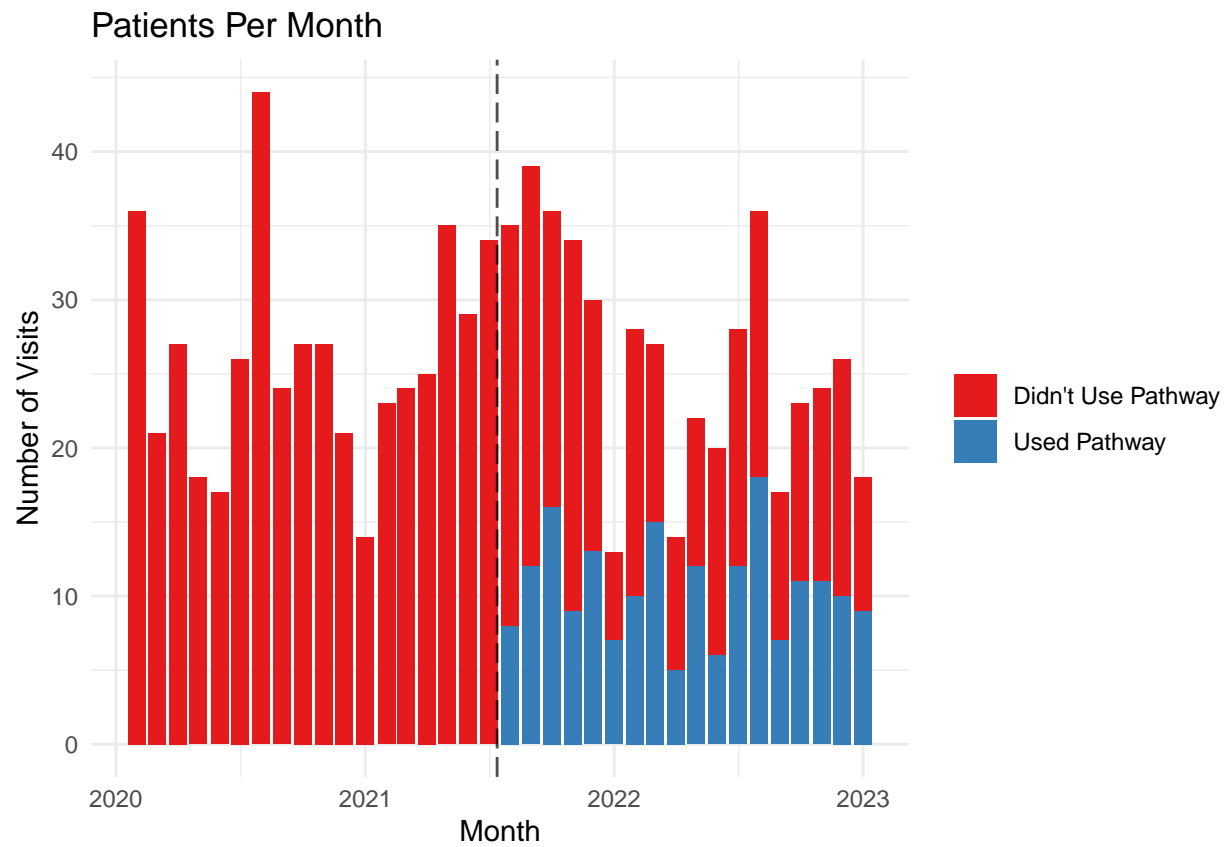

```
time_graph_2 <- all_pts %>% mutate(quarter = ceiling_date(arrive_dt, "quarter")) %>% ggplot() + geom_bar
time_graph_2
```

Patients Per Quarter

OR Graph

no longer using