

eda

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```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.1      v readr      2.1.4
## v forcats    1.0.0      v stringr   1.5.0
## v ggplot2    3.4.3      v tibble    3.2.1
## v lubridate  1.9.2      v tidyr     1.3.0
## v purrr      1.0.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 4.2.3
```

```
## Loading required package: Matrix
```

```
## Warning: package 'Matrix' was built under R version 4.2.3
```

```
##
## Attaching package: 'Matrix'
##
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
library(nlme)
```

```
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:lme4':
##
##     lmList
##
## The following object is masked from 'package:dplyr':
##
##     collapse
```

```
library(lattice)
library(ggplot2)
library(forcats)
```

```
source(knitr::purl("P9185_project1.Rmd", quiet=TRUE))
```

```
## Joining with 'by = join_by(ptid, period, drug)'
## Joining with 'by = join_by(ptid, drug)'
## Joining with 'by = join_by(ptid, drug)'
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00271231 (tol = 0.002, component 1)
```

```
## 'summarise()' has grouped output by 'ptid'. You can override using the
## '.groups' argument.
## Joining with 'by = join_by(ptid, period)'
## Joining with 'by = join_by(ptid, period)'
## Joining with 'by = join_by(ptid)'
```

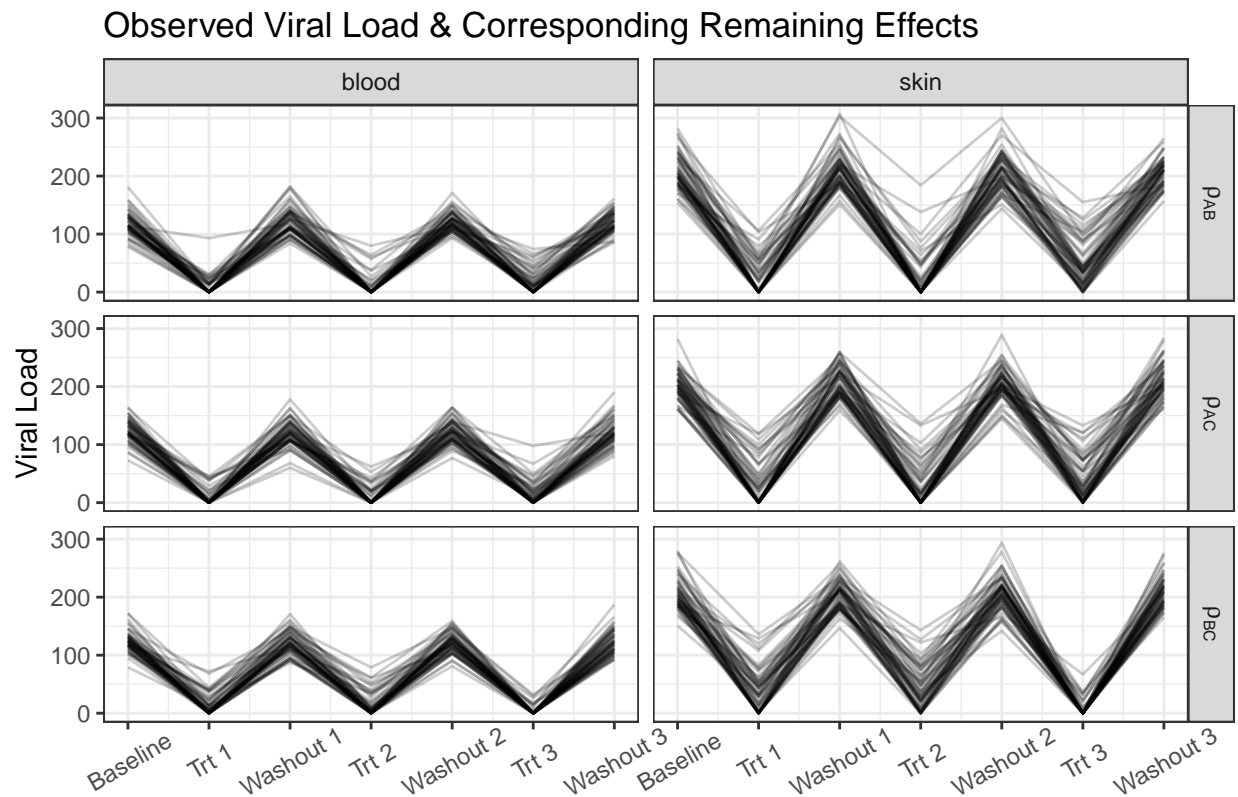
```
vload_df <- baseline.dat %>%
  pivot_longer(cols = contains("viral"), names_to = "type", values_to = "value") %>%
  mutate(obs_num = as.numeric(str_sub(type,-1,-1)),
         measure = str_sub(type,1,1),
         type = case_when(obs_num == 0 ~ "baseline",
                          obs_num %% 2 == 0 ~ "washout",
                          .default = "after"),
         period = case_when(
           obs_num <= 1 ~ 1,
           obs_num %in% c(2,3) ~ 2,
           obs_num %in% c(4,5,6) ~ 3,
           #washout in the end
           .default = 4),
         sequence = paste0(
           str_sub(period1,-1,-1),
           str_sub(period2,-1,-1),
           str_sub(period3,-1,-1))) %>%
  left_join(endpoints.AE %>%select(-week) %>% distinct(), by = c("ptid", "period", "sequence")) %>%
  mutate(measure = if_else(measure == "b", "blood", "skin")) %>%
  drop_na()
```

```
## Warning in left_join(., endpoints.AE %>% select(-week) %>% distinct(), by = c("ptid", : Detected an
## i Row 37 of 'x' matches multiple rows in 'y'.
## i Row 1 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
## "many-to-many"' to silence this warning.
```

```
vload_df$seq2 = factor(vload_df$seq2)
```

```
levels(vload_df$seq2) <- c("0" = 'rho[AB]', "1" = 'rho[AC]', "2" = 'rho[BC]')
```

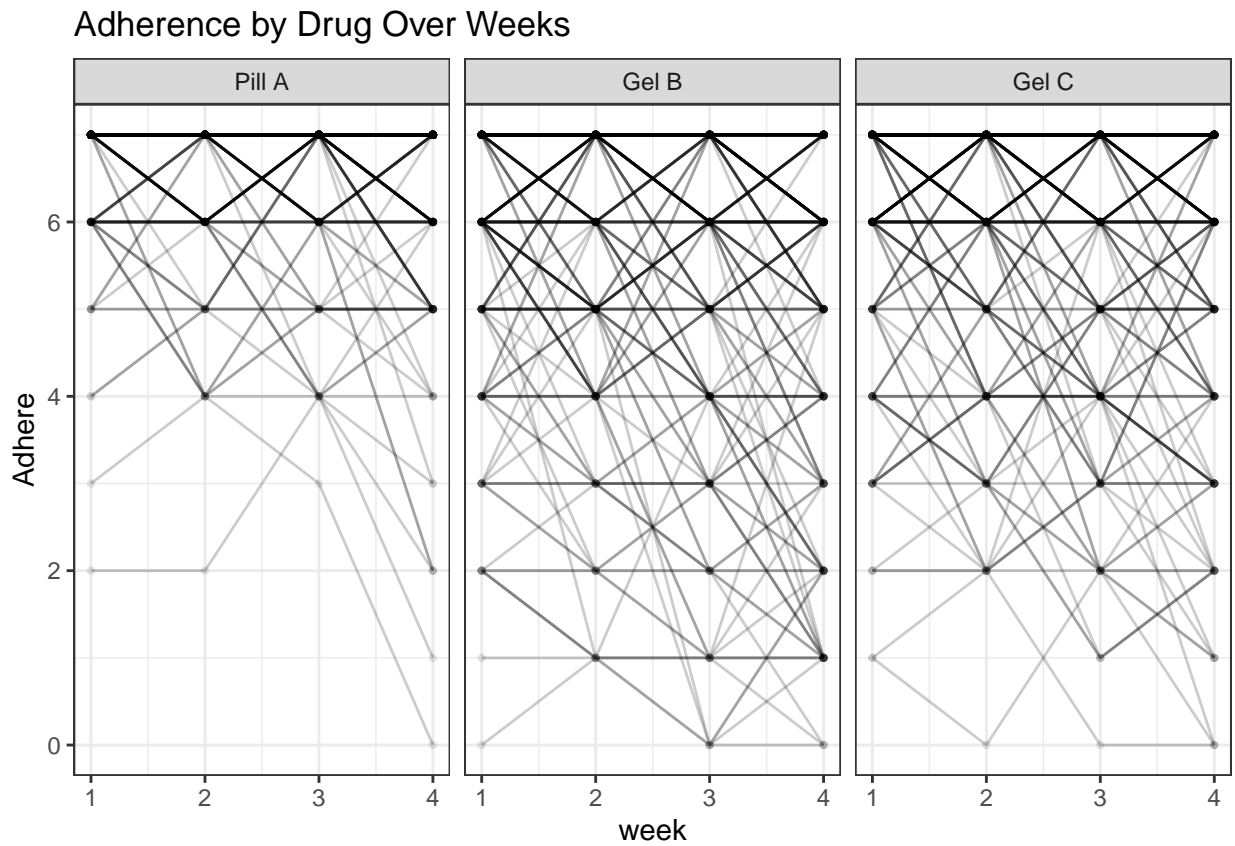
```
# maybe not including washout 3
vload_df %>%
  ggplot(aes(x = obs_num, y = value, group = ptid)) +
  geom_line(alpha = 0.2, linewidth = 0.5) +
  facet_grid(seq2~measure, labeller = label_parsed) +
  theme_bw() +
  ylab("Viral Load") +
  xlab("") +
  scale_x_continuous(breaks = seq(0, 6),
    labels = c("0" = "Baseline", "1" = "Trt 1",
      "2" = "Washout 1", "3" = "Trt 2",
      "4" = "Washout 2", "5" = "Trt 3",
      "6" = "Washout 3")) +
  theme(axis.text.x = element_text(angle = 30, vjust = 0.7)) +
  ggtitle("Observed Viral Load & Corresponding Remaining Effects")
```



```
#not really plotting observed rhos, just facet by seq2
#maybe need to change facet titles
```

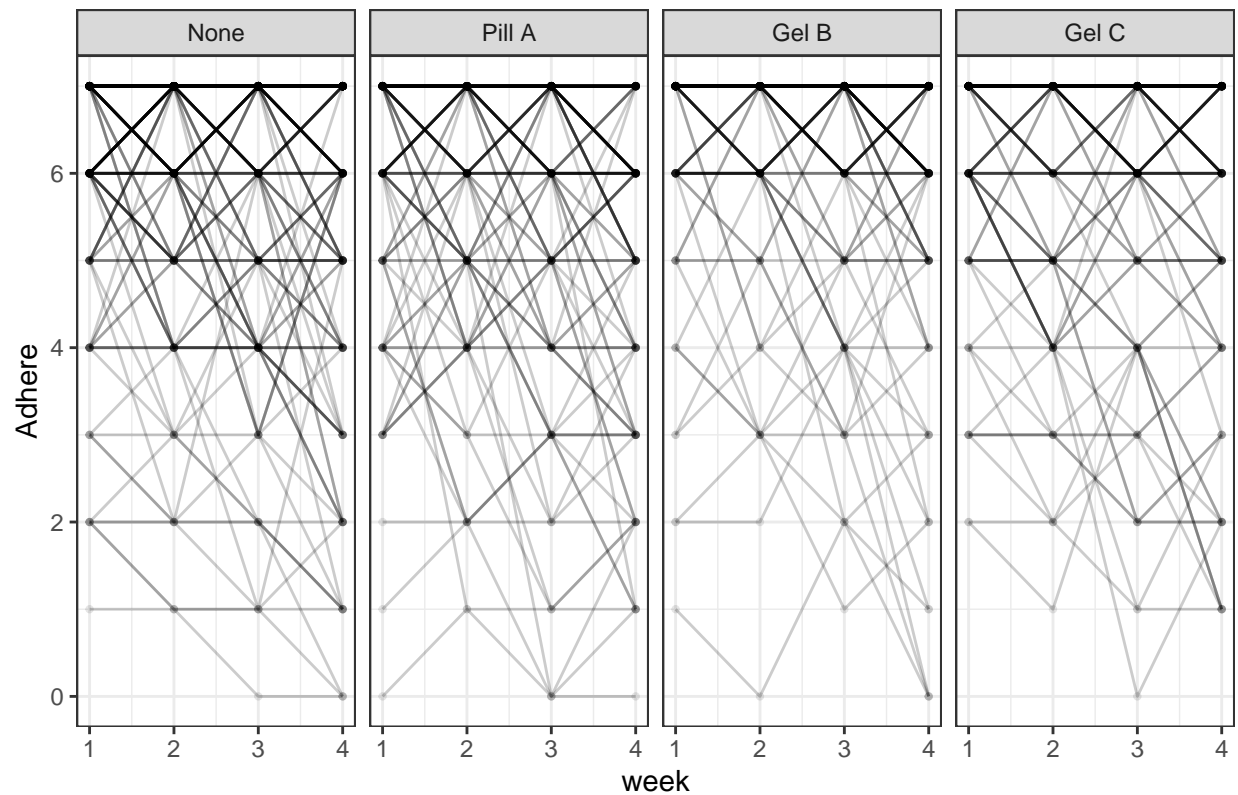
```
endpoints.Adhere %>%
  # each line is adherence of a drug taken by a subject
  ggplot(aes(x = week, y = Adhere, group = interaction(ptid, drug))) +
  geom_line(alpha = 0.2) +
  geom_point(alpha = 0.1, size = 0.8) +
  facet_grid(.~drug) +
```

```
theme_bw() +
ggtitle("Adherence by Drug Over Weeks")
```



```
endpoints.Adhere %>%
  ggplot(aes(x = week, y = Adhere, group = interaction(ptid, drug))) +
  geom_line(alpha = 0.2) +
  geom_point(alpha = 0.1, size = 0.8) +
  facet_grid(.~factor(drug_lag, levels=c('None', 'Pill A', 'Gel B', 'Gel C')))+
  theme_bw() +
  ggtitle("Adherence by Remaining Effects Over Weeks")
```

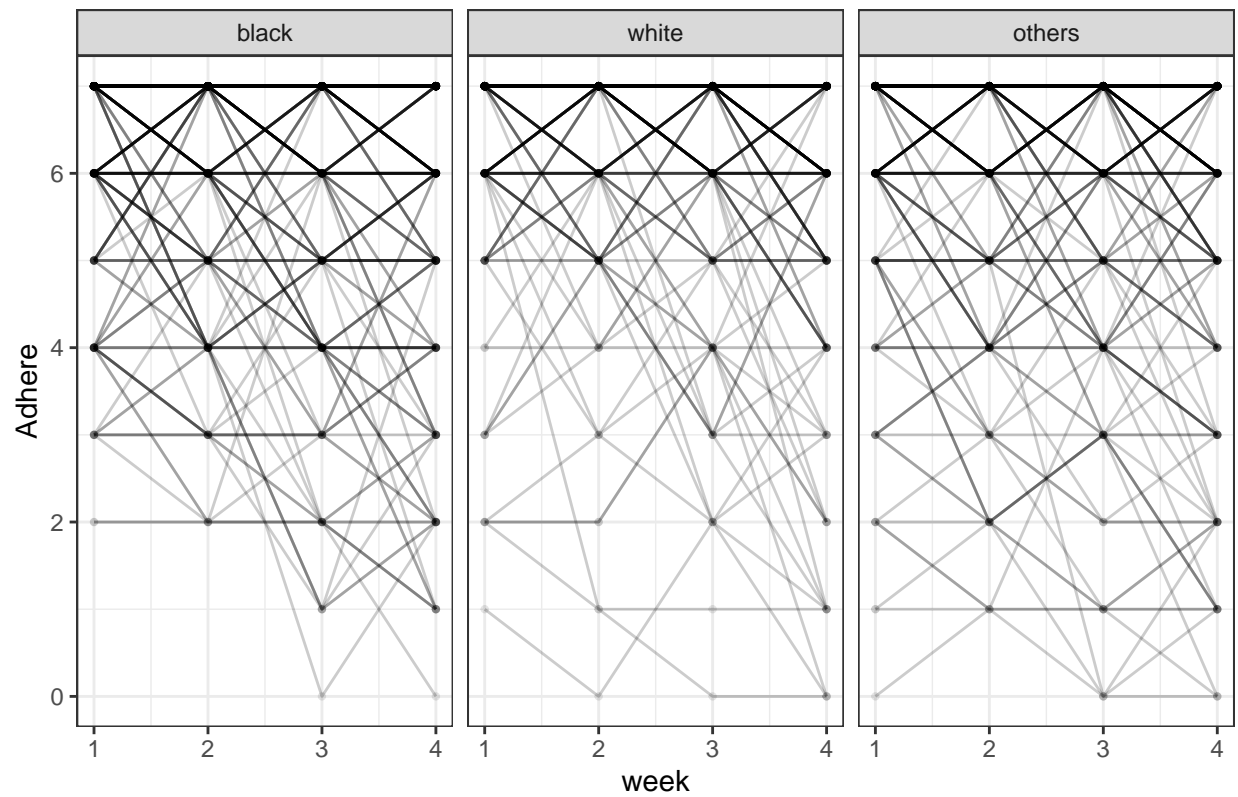
Adherence by Remaining Effects Over Weeks



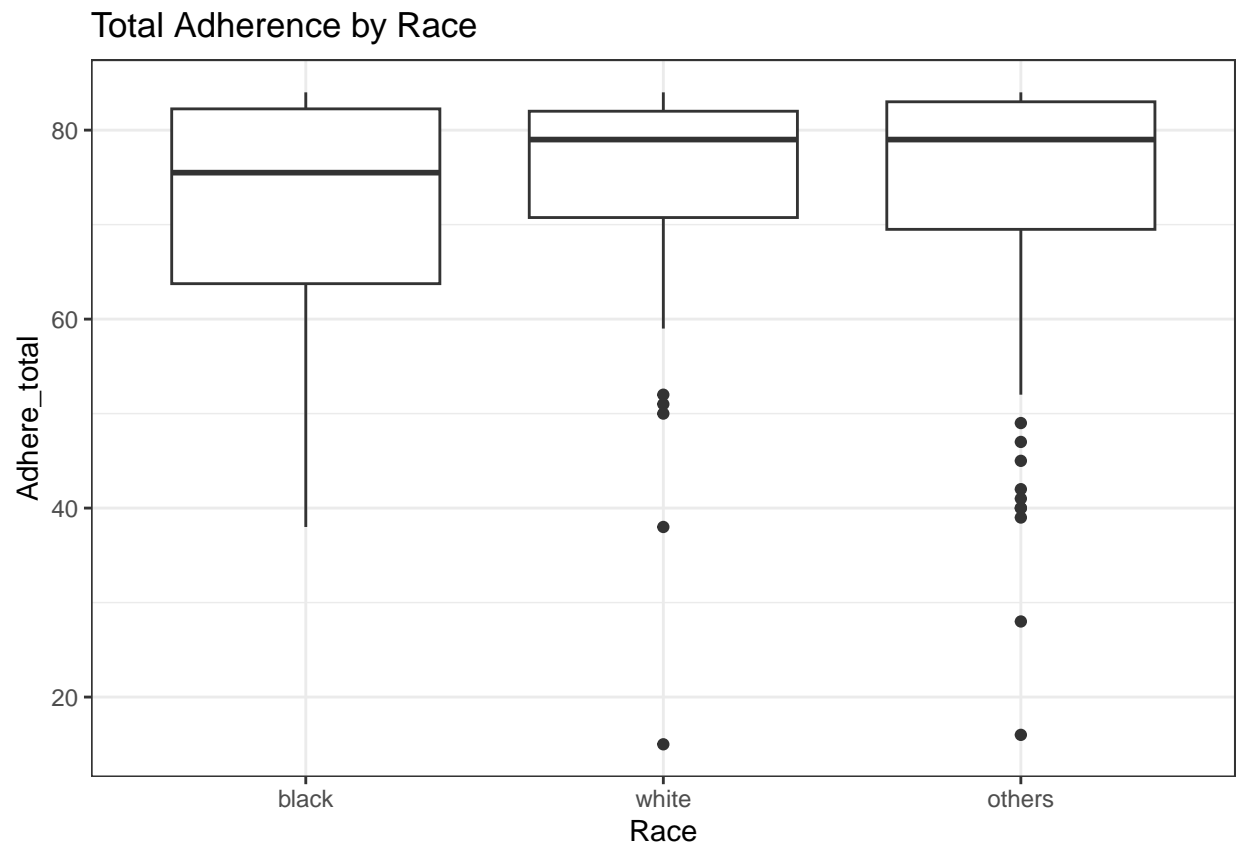
```
Adhere.demo.week <- left_join(Adhere.demo, endpoints.Adhere, by = "ptid")
```

```
Adhere.demo.week %>%
  ggplot(aes(x = week, y = Adhere, group = interaction(ptid, drug))) +
  geom_line(alpha = 0.2) +
  geom_point(alpha = 0.1, size = 0.8) +
  facet_grid(.~factor(race, levels=c('black', 'white', 'others')))+
  theme_bw() +
  ggtitle("Adherence by Race Over Weeks")
```

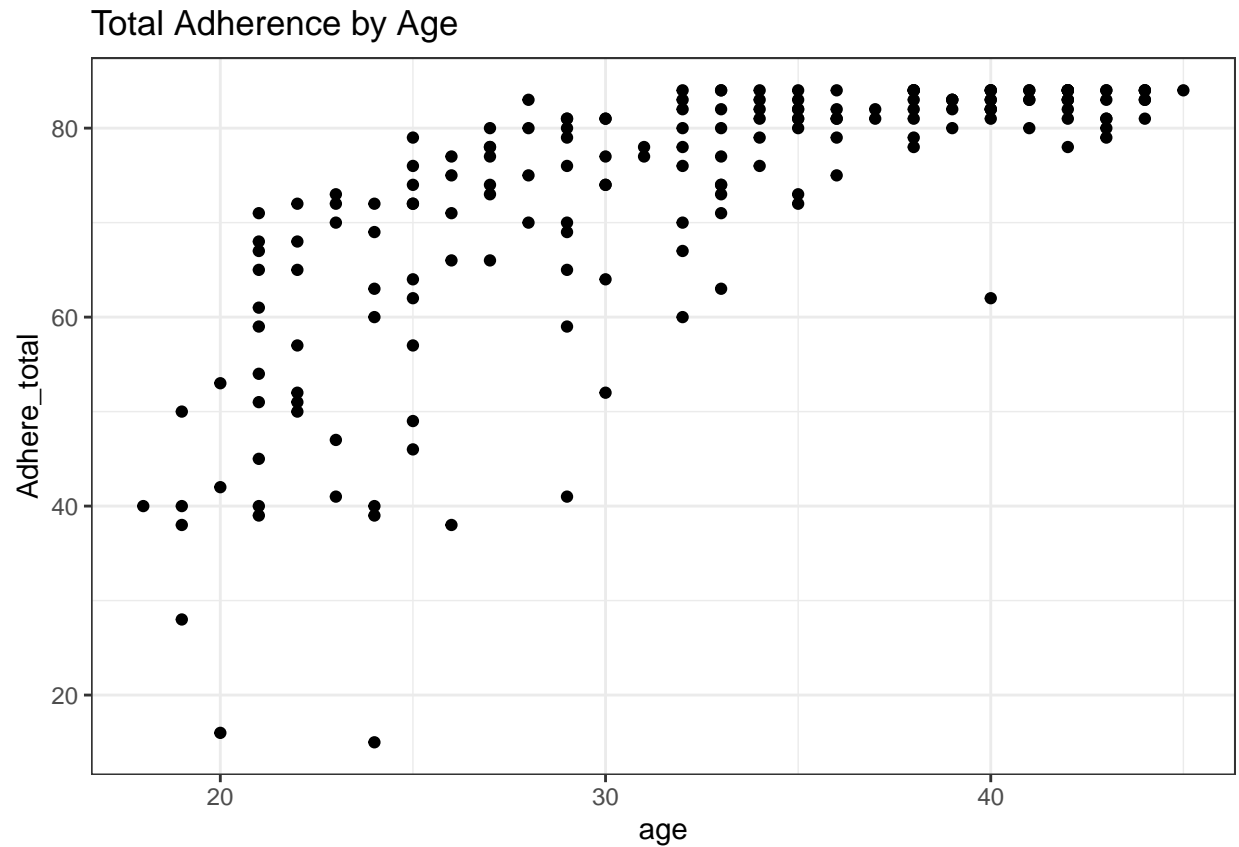
Adherence by Race Over Weeks



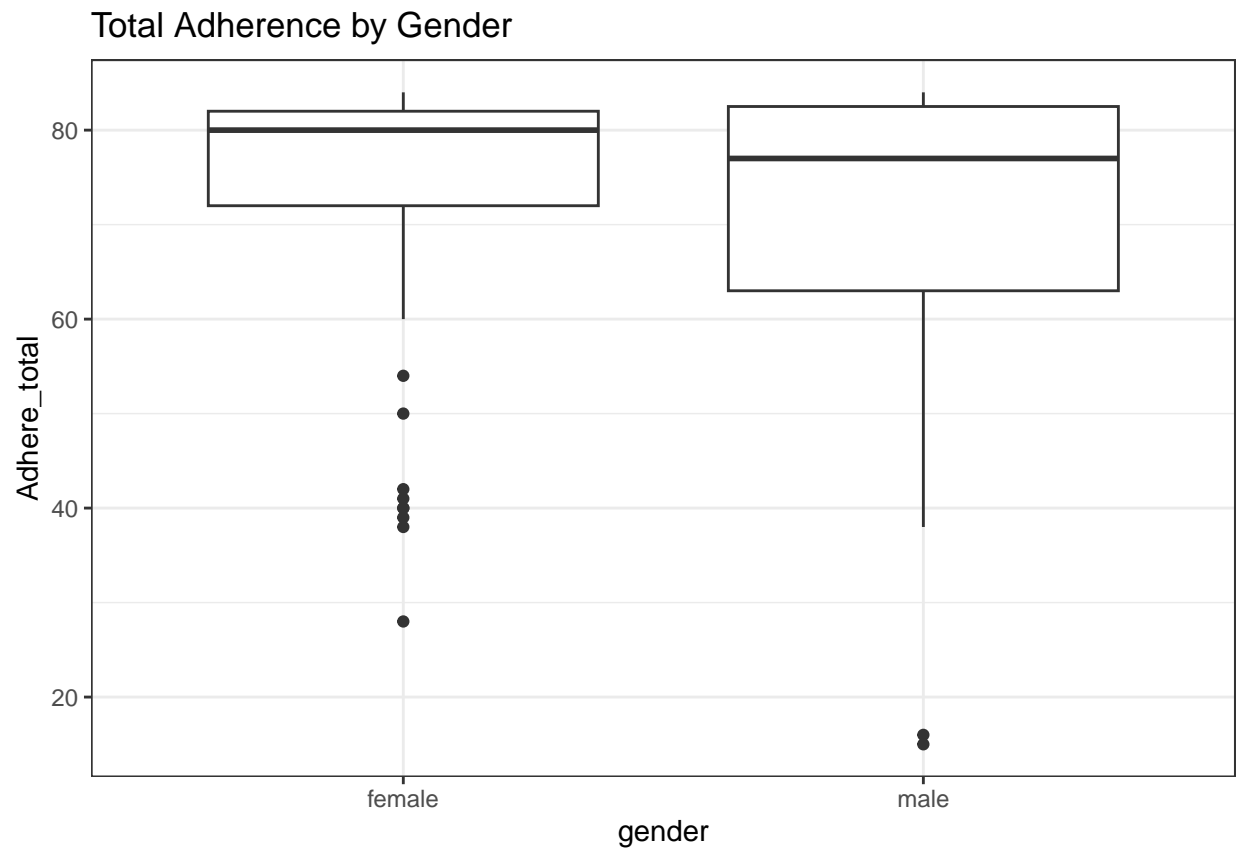
```
Adhere.demo %>%
  ggplot(aes(y = Adhere_total, x = factor(race, levels=c('black','white','others'))))+
  geom_boxplot()+
  theme_bw()+
  xlab("Race")+
  ggtitle("Total Adherence by Race")
```



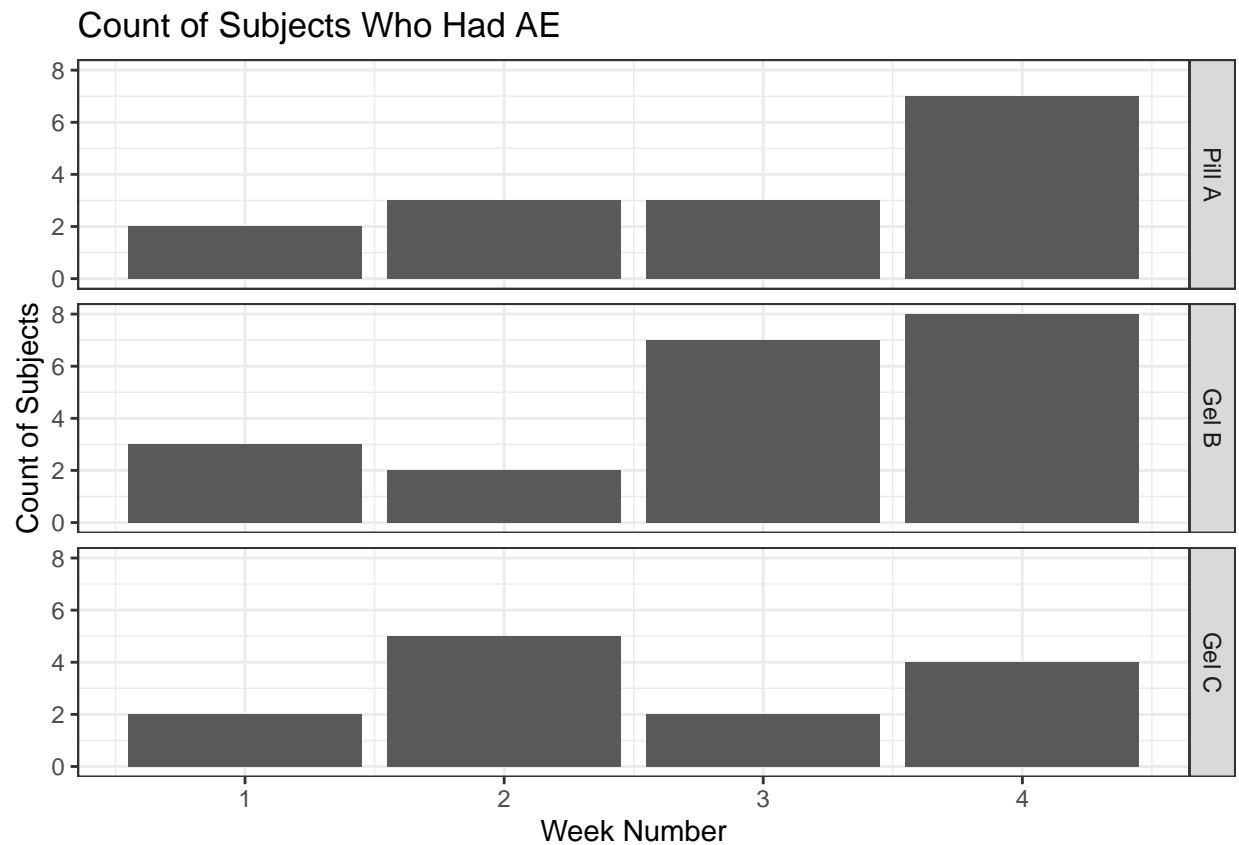
```
Adhere.demo %>%  
  ggplot(aes(y = Adhere_total, x = age))+  
  geom_point()+  
  theme_bw()+  
  ggtitle("Total Adherence by Age")
```



```
Adhere.demo %>%  
  mutate(gender = if_else(gender == 0, "male", "female"))%>%  
  ggplot(aes(y = Adhere_total, x = gender))+  
  geom_boxplot()+  
  theme_bw()+  
  ggtitle("Total Adherence by Gender")
```

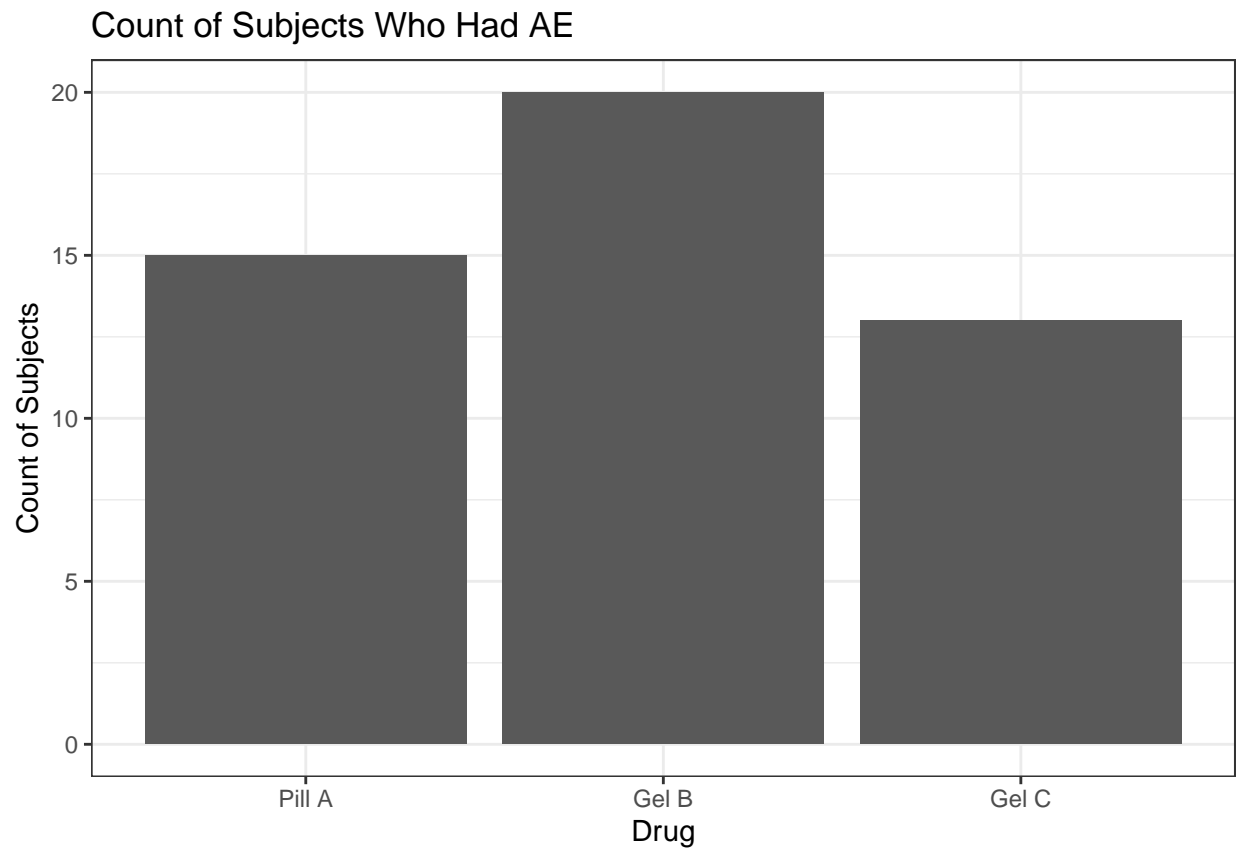



```
endpoints.AE %>%  
  filter(AE ==1) %>%  
  group_by(drug, week) %>%  
  ggplot(aes(x=week))+  
  geom_bar()+  
  facet_grid(factor(drug, levels=c('Pill A', 'Gel B', 'Gel C'))~.)+  
  theme_bw()+  
  ylab("Count of Subjects")+  
  xlab("Week Number")+  
  ggtitle("Count of Subjects Who Had AE")
```



it's a balanced design, so can compare count value

```
endpoints.AE %>%
  filter(AE ==1) %>%
  ggplot(aes(x=factor(drug, levels=c('Pill A', 'Gel B', 'Gel C')))) +
  geom_bar() +
  theme_bw() +
  ylab("Count of Subjects") +
  xlab("Drug") +
  ggtitle("Count of Subjects Who Had AE")
```



```
endpoints.AE %>%  
  filter(AE ==1) %>%  
  ggplot(aes(x=factor(drug_lag, levels=c('None', 'Pill A', 'Gel B', 'Gel C'))))+  
  geom_bar()+  
  theme_bw()+  
  ylab("Count of Subjects")+  
  xlab("Previous Drug Taken")+  
  ggtitle("Count of Subjects Who Had AE")
```

