eda

Fanyu, Ryan, Serena

2024-02-19

```
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
```

```r
library(lattice)
library(ggplot2)
```

```r
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)`
```

```r
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.
```

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

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

```r
# 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 & Remaining Effects")
```


Observed Viral Load & Remaining Effects