Script 2b

Descriptive stats at each time interval

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Objective

To describe the demographic characteristics and disease status of the analysis cohort at each study assessment interval.

Analysis notes

Definitions of missingness

Data were regarded as **missing** when *pain in the last week* data were not present for one or more of weeks 0, 12, 24, 36, 48. Data also were classified as **missing** when there were inconsistencies in the data across the variables collected within a week.

Definition of data inconsistencies

Pain was defined as *pain in the last week* being 'Yes', and *pain at its worst* being > 0. These two measurements were then the "gatekeeper" measurements, such that the two measurements both had to be positive ('Yes' and '> 0', respectively) in order for there to be any entries for *site of pain* and *site of worst pain.* Were the data were inconsistent (e.g., when there was no *pain in the last week* and *pain at its worst* $= 0$, but there were entries for *site of pain* and *site of worst pain*), then the *site of pain* and *site of worst pain* entries were marked as **inconsistent**.

Data also were considered **inconsistent** when *pain in the last week* = 'Yes', but *site of worst pain* = 'None'.

Lastly, data were considered **inconsistent** when *site of worst pain* was not listed as one of the pain locations for a given measurement week.

For analysis purposes, missing data in the *site of pain* columns were changed to **'No'** (pain not present in the site). This approach was conservative, but we believed that the approach would have the least effect on the outcome, while still retaining as many participants as possible.

Import data

```
df <- read_rds('data-cleaned/data-ADVANCE.rds') %>%
    select(ranid, interval_name, pain_in_the_last_week,
           cd4_cells.ul, viral_load_cp.ml,
           general_health, any_missing, interval_numeric)
```

First look

```
head(df)
```

```
## # A tibble: 6 x 8
##   ranid interval_name pain_in_the_las… cd4_cells.ul viral_load_cp.ml
##   <chr> <ord>         <chr>                   <dbl>            <dbl>
## 1 01-0… 0 weeks       No                        642              641
## 2 01-0… 12 weeks      No                         NA               50
## 3 01-0… 24 weeks      No                        525               50
## 4 01-0… 36 weeks      No                         NA               50
## 5 01-0… 48 weeks      No                        668               50
## 6 01-0… 0 weeks       No                        241             3851
## # … with 3 more variables: general_health <dbl>, any_missing <chr>,
## #   interval_numeric <dbl>
```

```
glimpse(df)
```

```
## Observations: 5,265
## Variables: 8
## $ ranid                 <chr> "01-0001", "01-0001", "01-0001", "01-0001"…
## $ interval_name         <ord> 0 weeks, 12 weeks, 24 weeks, 36 weeks, 48 …
## $ pain_in_the_last_week <chr> "No", "No", "No", "No", "No", "No", "Yes",…
## $ cd4_cells.ul          <dbl> 642, NA, 525, NA, 668, 241, NA, 364, NA, 4…
## $ viral_load_cp.ml      <dbl> 641, 50, 50, 50, 50, 3851, 50, 50, 50, 50,…
## $ general_health        <dbl> 4, 4, 5, 5, 4, 3, 5, 3, 3, 3, 4, 5, 5, 5, …
## $ any_missing           <chr> "No", "No", "No", "No", "No", "No", "No", …
## $ interval_numeric      <dbl> 0, 12, 24, 36, 48, 0, 12, 24, 36, 48, 0, 1…
```

Basic clean

```
# Clean and process data
df %<>%
    filter(any_missing == 'No') %>%
    select(-any_missing)
```

Quick tabulation

Analysis data set for the period 0 to 48 weeks

```
# Tabulate data
xtabs(~interval_name, data = df)
```

```
## interval_name
##  0 weeks 12 weeks 24 weeks 36 weeks 48 weeks
##      787      787      787      787      787
```

Analysis

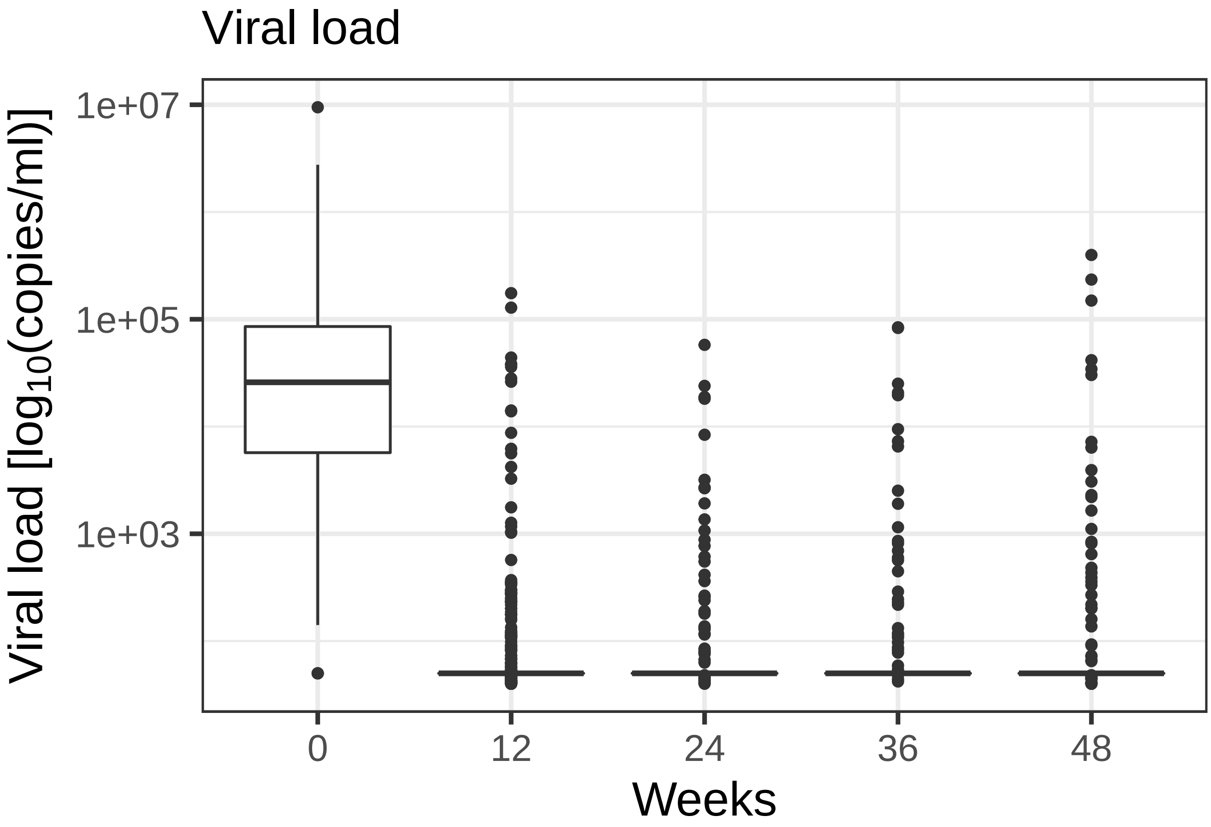
Viral load

```
# Tabulate data
df %>%
  select(interval_name, viral_load_cp.ml) %>%
  group_by(interval_name) %>%
  skim_to_wide() %>%
  select(-type, -variable) %>%
  skimr::kable(caption = '5-number summary of viral load (copies/ml)')
```

interval_name	missing	complete	n	mean	sd	p0	p25	p50	p75	p100
0 weeks	0	787	787	98611.6	386719.99	50	5704.5	25853	85574	9475772
12 weeks	3	784	787	793.27	8367.89	40	50	50	50	175168
24 weeks	2	785	787	236.82	2438.64	40	50	50	50	57754
36 weeks	9	778	787	391.53	4466.29	42	50	50	50	84167
48 weeks	9	778	787	1232.53	17517.81	40	50	50	50	4e+05

```
# Plot data
df %>%
  ggplot(data = .) +
  aes(x = factor(interval_numeric),
      y = viral_load_cp.ml) +
  geom_boxplot() +
  scale_y_log10() +
  labs(subtitle = 'Viral load',
       y = expression('Viral load [log'[10]*'(copies/ml)]'),
       x = 'Weeks')
```

```
## Warning: Removed 23 rows containing non-finite values (stat_boxplot).
```



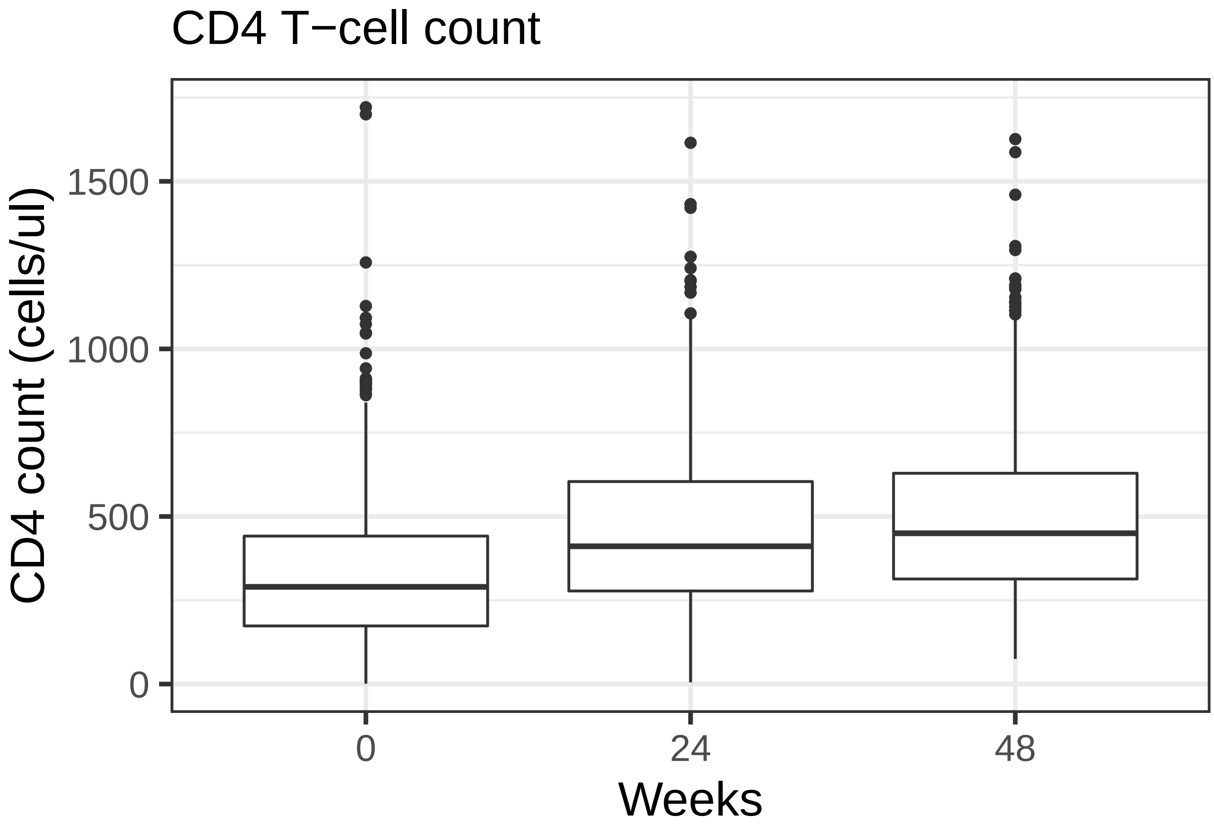
CD4 T-cell count

```r
# Tabulate data
df %>%
  filter(interval_numeric %in% c(0, 24, 48)) %>%
  select(interval_name, cd4_cells.ul) %>%
  group_by(interval_name) %>%
  skim_to_wide() %>%
  select(-type, -variable) %>%
  skimr::kable(caption = '5-number summary of CD4 T-cell count (cells/ul)')
```

interval_name	missing	complete	n	mean	sd	p0	p25	p50	p75	p100
0 weeks	0	787	787	333.25	224.05	1	173.5	290	441.5	1721
24 weeks	11	776	787	452.76	237.42	5	277.75	411	604.25	1615
48 weeks	16	771	787	489.88	246.61	75	313.5	450	629	1626

```r
# Plot data
df %>%
  filter(interval_numeric %in% c(0, 24, 48)) %>%
  ggplot(data = .) +
  aes(x = factor(interval_numeric),
      y = cd4_cells.ul) +
  geom_boxplot() +
  labs(subtitle = 'CD4 T-cell count',
       y = 'CD4 count (cells/ul)',
       x = 'Weeks')
```

```
## Warning: Removed 27 rows containing non-finite values (stat_boxplot).
```



General health

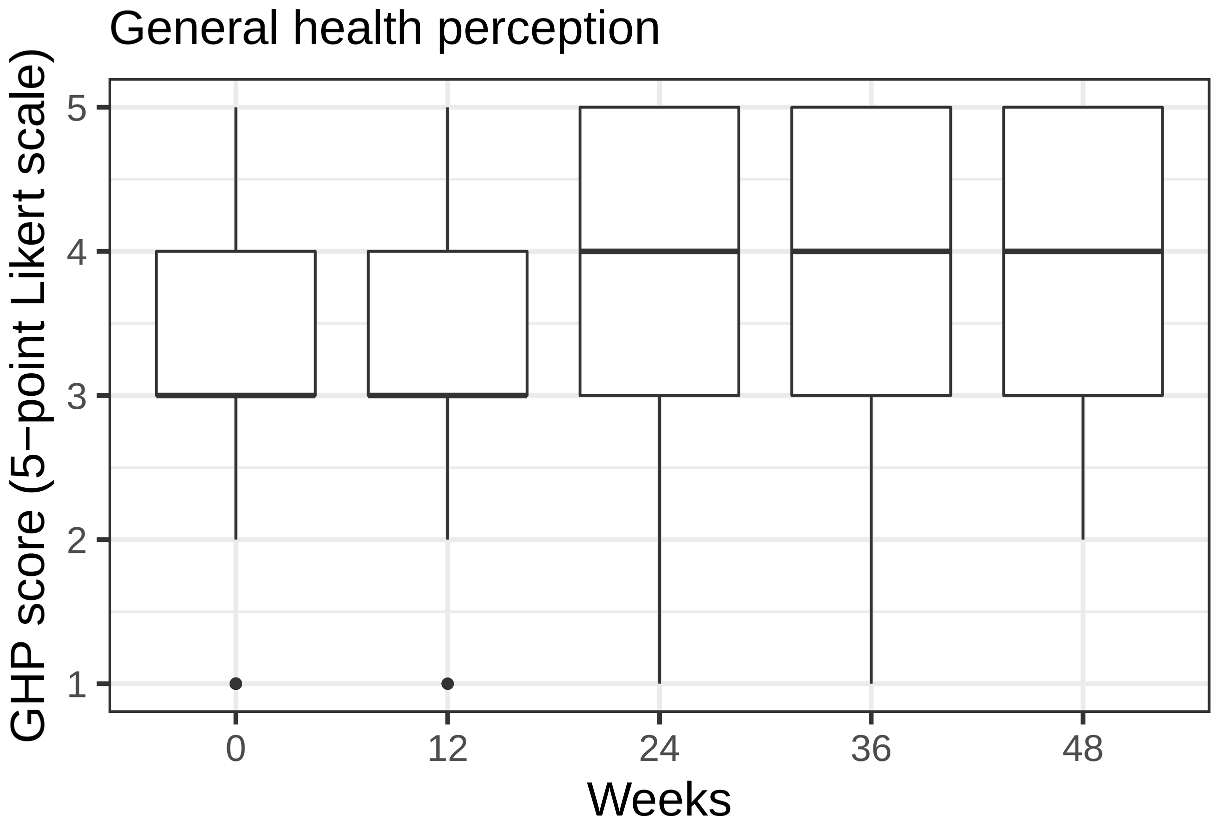
Rating of perceived health status on a 5-point Likert scale (1 = poor, 5 = excellent).

```
# Tabulate data
df %>%
  select(interval_name, general_health) %>%
  group_by(interval_name) %>%
  skim_to_wide() %>%
  select(-type, -variable) %>%
  skimr::kable(caption = '5-number summary of the general health score')
```

interval_name	missing	complete	n	mean	sd	p0	p25	p50	p75	p100
0 weeks	4	783	787	3.45	0.82	1	3	3	4	5
12 weeks	1	786	787	3.65	0.8	1	3	3	4	5
24 weeks	0	787	787	3.76	0.87	1	3	4	5	5
36 weeks	1	786	787	3.81	0.89	1	3	4	5	5
48 weeks	2	785	787	3.9	0.93	2	3	4	5	5

```
# Plot data
df %>%
  ggplot(data = .) +
  aes(x = factor(interval_numeric),
      y = general_health) +
  geom_boxplot() +
  labs(subtitle = 'General health perception',
       y = 'GHP score (5-point Likert scale)',
       x = 'Weeks')
```

```
## Warning: Removed 8 rows containing non-finite values (stat_boxplot).
```



Session information

```
sessionInfo()
```

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Mojave 10.14.6
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] skimr_1.0.7     magrittr_1.5    forcats_0.4.0   stringr_1.4.0
##  [5] dplyr_0.8.3     purrr_0.3.3     readr_1.3.1     tidyr_1.0.0
##  [9] tibble_2.1.3    ggplot2_3.2.1   tidyverse_1.2.1
##
## loaded via a namespace (and not attached):
##  [1] tidyselect_0.2.5 xfun_0.10        haven_2.1.1      lattice_0.20-38
##  [5] colorspace_1.4-1 vctrs_0.2.0      generics_0.0.2   htmltools_0.4.0
##  [9] yaml_2.2.0       utf8_1.1.4       rlang_0.4.2      pillar_1.4.2
## [13] glue_1.3.1       withr_2.1.2      modelr_0.1.5     readxl_1.3.1
## [17] lifecycle_0.1.0  munsell_0.5.0    gtable_0.3.0     cellranger_1.1.0
## [21] rvest_0.3.4      evaluate_0.14    labeling_0.3     knitr_1.25
## [25] fansi_0.4.0      highr_0.8        broom_0.5.2      Rcpp_1.0.3
## [29] scales_1.0.0     backports_1.1.5  jsonlite_1.6     hms_0.5.1
## [33] digest_0.6.23    stringi_1.4.3    grid_3.6.1       cli_2.0.0
## [37] tools_3.6.1      lazyeval_0.2.2   crayon_1.3.4     pkgconfig_2.0.3
## [41] zeallot_0.1.0    xml2_1.2.2       lubridate_1.7.4  assertthat_0.2.1
## [45] rmarkdown_1.16   httr_1.4.1       rstudioapi_0.10  R6_2.4.1
## [49] nlme_3.1-141     compiler_3.6.1
```