

# philtest

## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
library(glue)
```

```
## Warning: package 'glue' was built under R version 4.0.3
```

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.4
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5      v purrr  0.3.4
## v tibble  3.1.4      v dplyr  1.0.8
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.0.1      v forcats 0.5.1
```

```
## Warning: package 'ggplot2' was built under R version 4.0.5
```

```
## Warning: package 'tibble' was built under R version 4.0.5
```

```
## Warning: package 'tidyr' was built under R version 4.0.5
```

```
## Warning: package 'readr' was built under R version 4.0.5
```

```
## Warning: package 'purrr' was built under R version 4.0.3
```

```
## Warning: package 'dplyr' was built under R version 4.0.5
```

```
## Warning: package 'stringr' was built under R version 4.0.3
```

```
## Warning: package 'forcats' was built under R version 4.0.3
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::collapse() masks glue::collapse()
## x dplyr::filter()   masks stats::filter()
## x dplyr::lag()      masks stats::lag()
```

```
library(haven)
```

```
## Warning: package 'haven' was built under R version 4.0.5
```

```
library(assertthat)
```

```
## Warning: package 'assertthat' was built under R version 4.0.3
```

```
##
```

```
## Attaching package: 'assertthat'
```

```

## The following object is masked from 'package:tibble':
##
##      has_name
library(safetyData)

## Warning: package 'safetyData' was built under R version 4.0.3
source('~/.Clinical-Tables-in-R-with-gt/data_workflow/funcs.R')

the_date <- as.character(Sys.Date())

# adsl <- read_xpt(glue("{adam_lib}/adsl.xpt"))

# Import and explore the data frame ----
adsl <- adam_adsl %>%
  filter(ITTFL == "Y") %>%
  mutate(
    RACE_DISPLAY = case_when(
      ETHNIC == 'HISPANIC OR LATINO' ~ 'Hispanic',
      RACE == 'WHITE' ~ 'Caucasian',
      RACE == 'BLACK OR AFRICAN AMERICAN' ~ 'African Descent',
      RACE == 'AMERICAN INDIAN OR ALASKA NATIVE' ~ 'Other',
    ),
    RACEN_DISPLAY = case_when(
      ETHNIC == 'HISPANIC OR LATINO' ~ 3,
      RACE == 'WHITE' ~ 1,
      RACE == 'BLACK OR AFRICAN AMERICAN' ~ 2,
      RACE == 'AMERICAN INDIAN OR ALASKA NATIVE' ~ 4,
    ),
    SEX =
      case_when(
        SEX == 'M' ~ 'Male',
        SEX == 'F' ~ 'Female'
      ),
    SEXN =
      case_when(
        SEX == 'Male' ~ 1,
        SEX == 'Female' ~ 2
      ),
    DURDSGR1N =
      case_when(
        DURDSGR1 == '<12' ~ 1,
        DURDSGR1 == '≥12' ~ 2
      ),
    DURDSGR1 = paste(DURDSGR1, 'months'),
    BMIBLGR1N =
      case_when(
        BMIBLGR1 == '<25' ~ 1,
        BMIBLGR1 == '25-<30' ~ 2,
        BMIBLGR1 == '≥30' ~ 3
      ),
    AGEGR1 = paste(AGEGR1, 'yrs')
  )

```

```
get_meta(adsl)
```

```
## STUDYID Study Identifier
## USUBJID Unique Subject Identifier
## SUBJID Subject Identifier for the Study
## SITEID Study Site Identifier
## SITEGR1 Pooled Site Group 1
## ARM Description of Planned Arm
## TRT01P Planned Treatment for Period 01
## TRT01PN Planned Treatment for Period 01 (N)
## TRT01A Actual Treatment for Period 01
## TRT01AN Actual Treatment for Period 01 (N)
## TRTSDT Date of First Exposure to Treatment
## TRTEDT Date of Last Exposure to Treatment
## TRTDUR Duration of Treatment (days)
## AVGDD Avg Daily Dose (as planned)
## CUMDOSE Cumulative Dose (as planned)
## AGE Age
## AGEGR1
## AGEGR1N Pooled Age Group 1 (N)
## AGEU Age Units
## RACE Race
## RACEN Race (N)
## SEX
## ETHNIC Ethnicity
## SAFFL Safety Population Flag
## ITTFL Intent-To-Treat Population Flag
## EFFFL Efficacy Population Flag
## COMP8FL Completers of Week 8 Population Flag
## COMP16FL Completers of Week 16 Population Flag
## COMP24FL Completers of Week 24 Population Flag
## DISCONFL Did the Subject Discontinue the Study?
## DSRAEFL Discontinued due to AE?
## DTHFL Subject Died?
## BMIBL Baseline BMI (kg/m^2)
## BMIBLGR1 Pooled Baseline BMI Group 1
## HEIGHTBL Baseline Height (cm)
## WEIGHTBL Baseline Weight (kg)
## EDUCVLV Years of Education
## DISONSDT Date of Onset of Disease
## DURDIS Duration of Disease (Months)
## DURDSGR1
## VISIT1DT Date of Visit 1
## RFSTDTC Subject Reference Start Date/Time
## RFENDTC Subject Reference End Date/Time
## VISNUMEN End of Trt Visit (Vis 12 or Early Term.)
## RFENDT Date of Discontinuation/Completion
## DCDECOD Standardized Disposition Term
## DCREASCD Reason for Discontinuation
## MMSETOT MMSE Total
## RACE_DISPLAY
## RACEN_DISPLAY
## SEXN
```

```

## DURDSGR1N
## BMIBLGR1N

# Create the total values upfront for quicker summary ----
adsl_ <- adsl %>%
  bind_rows(adsl %>%
    mutate(TRT01P = 'Total',
           TRT01PN = 99))

# Get the header N's ----
header_n <- get_header_n(adsl_)

## `summarise()` has grouped output by 'TRT01P'. You can override using the
## `.groups` argument.

## Exploring Age ----

# Descriptive stats
age_1 <- adsl_ %>% desc_stats(AGE)
age_p <- adsl_ %>% aov_p(AGE ~ TRT01P) # anova

age_1 <- attach_p(age_1, age_p)

# Categorical n counts
age_2 <- adsl_ %>% sum_subgrp(AGEGR1, AGEGR1N, include.n=FALSE, header_n=header_n)

## `summarise()` has grouped output by 'TRT01PN', 'AGEGR1'. You can override using
## the `.groups` argument.

agegrp_p <- adsl_ %>% chi_p(AGEGR1, TRT01P)
age_2 <- attach_p(age_2, agegrp_p)

age <- rbind(age_1, age_2) %>%
  mutate(rowlbl1 = "Age (y)")

rm(age_1, age_2, age_p, agegrp_p)

## Exploring sex ----

sex = adsl_ %>%
  sum_subgrp(SEX, SEXN, header_n=header_n)

## `summarise()` has grouped output by 'TRT01PN', 'SEX'. You can override using the
## `.groups` argument.

sex_p <- adsl_ %>% chi_p(SEX, TRT01P)

sex <- attach_p(sex, sex_p) %>%
  mutate(rowlbl1 = 'Sex')

rm(sex_p)

## Exploring race ----

race = adsl_ %>%
  sum_subgrp(RACE_DISPLAY, RACEN_DISPLAY, header_n=header_n) %>%
  rowwise() %>%
  mutate(

```

```

    rowlbl1 = "Race (Origin)",
  )

## `summarise()` has grouped output by 'TRT01PN', 'RACE_DISPLAY'. You can override
## using the `groups` argument.
race_p <- adsl %>% chi_p(RACE_DISPLAY, TRT01P)

## Warning in chisq.test(res, cats): Chi-squared approximation may be incorrect
race <- attach_p(race, race_p)

rm(race_p)

## Exploring MMSE ---
mmse <- adsl %>% desc_stats(MMSETOT) %>%
  mutate(
    rowlbl1 = 'MMSE'
  )

mmse_p <- adsl %>% aov_p(MMSETOT ~ TRT01P)

mmse <- attach_p(mmse, mmse_p)

rm(mmse_p)

## Exploring disease duration ----

# Descriptive
durdis_1 <- adsl %>% desc_stats(DURDIS)
durdis_1p <- adsl %>% aov_p(DURDIS ~ TRT01P)
durdis_1 <- attach_p(durdis_1, durdis_1p)

# Categorical
durdis_2 <- adsl %>% sum_subgrp(DURDSGR1, DURDSGR1N, include.n=FALSE, header_n=header_n)

## `summarise()` has grouped output by 'TRT01PN', 'DURDSGR1'. You can override
## using the `groups` argument.
durdis_2p <- adsl %>% chi_p(DURDSGR1, TRT01P)

## Warning in chisq.test(res, cats): Chi-squared approximation may be incorrect
durdis_2 <- attach_p(durdis_2, durdis_2p)

durdis <- durdis_1 %>%
  union(durdis_2) %>%
  mutate(
    rowlbl1 = 'Duration of disease '
  ) %>%
  pad_row()

rm(durdis_1, durdis_2, durdis_1p, durdis_2p)

## Years of education ----
educlvl <- adsl %>% desc_stats(EDUCLVL) %>%

```

```

mutate(
  rowlbl1 = 'Years of education'
)
educlvl_p <- adsl %>% aov_p(EDUCLVL ~ TRT01P)
educlvl <- attach_p(educlvl, educlvl_p)

rm(educlvl_p)

## Baseline weight ----
weightbl <- adsl %>% desc_stats(WEIGHTBL) %>%
  mutate(
    rowlbl1 = 'Baseline weight(kg)'
  )
weightbl_p <- adsl %>% aov_p(WEIGHTBL ~ TRT01P)
weightbl <- attach_p(weightbl, weightbl_p)

rm(weightbl_p)

## Baseline height ----
heightbl <- adsl %>% desc_stats(HEIGHTBL) %>%
  mutate(
    rowlbl1 = 'Baseline height(cm)'
  )
heightbl_p <- adsl %>% aov_p(HEIGHTBL ~ TRT01P)
heightbl <- attach_p(heightbl, heightbl_p)

rm(heightbl_p)

## Baseline BMI ----

# Descriptive
bmi_1 <- adsl %>% desc_stats(BMIBL)
bmi_1p <- adsl %>% aov_p(BMIBL ~ TRT01P)
bmi_1 <- attach_p(bmi_1, bmi_1p)

# Categorical
bmi_2 <- adsl %>% sum_subgrp(BMIBLGR1, BMIBLGR1N, include.n=FALSE, header_n=header_n)

## `summarise()` has grouped output by 'TRT01PN', 'BMIBLGR1'. You can override
## using the `.groups` argument.

bmi_2p <- adsl %>% chi_p(BMIBLGR1, TRT01P)
bmi_2 <- attach_p(bmi_2, bmi_2p)

bmi <- rbind(bmi_1, bmi_2) %>%
  mutate(
    rowlbl1 = 'Baseline BMI'
  )

rm(bmi_1, bmi_2, bmi_1p, bmi_2p)

## Stack together final tables ---
final <- rbind(age, sex, race, mmse, durdis, educlvl, weightbl, heightbl, bmi) %>%
  group_by(rowlbl1) %>%

```

```

mutate(ord1 = row_number()) %>%
ungroup() %>%
mutate(rowlbl1 = ifelse(ord1 == 1, rowlbl1, ""))

rm(age, sex, race, mmse, durdis, educ1vl, weightbl, heightbl, bmi)

# Make and attach column headers
header_n_v <- header_n %>% select(TRT01PN, labels) %>%
  pivot_wider(names_from = TRT01PN, values_from = labels) %>%
  mutate(
    rowlbl1 = '',
    rowlbl2 = '',
    p = 'p-value\\line [1]'
  )

final <- bind_rows(header_n_v, final) %>%
  select(rowlbl1, rowlbl2, `0`, `54`, `81`, `99`, p)

library(gt)

final %>%
  gt(groupname_col="block")

```

rowlbl1	rowlbl2	0	54	81
Age (y)		Placebo\line (N=86)	Xanomeline\line Low Dose\line (N=84)	Xanomeline\line
	n	86	84	84
	Mean	75.2	75.7	74.4
	SD	8.59	8.29	7.89
	Median	76.0	77.5	76.0
	Min	52.0	51.0	56.0
	Max	89.0	88.0	88.0
	<65 yrs	14 ( 16%)	8 ( 10%)	11 ( 13%)
	65-80 yrs	42 ( 49%)	47 ( 56%)	55 ( 65%)
	>80 yrs	30 ( 35%)	29 ( 35%)	18 ( 21%)
Sex	n	86	84	84
	Male	33 ( 38%)	34 ( 40%)	44 ( 52%)
	Female	53 ( 62%)	50 ( 60%)	40 ( 48%)
Race (Origin)	n	86	84	84
	Caucasian	75 ( 87%)	72 ( 86%)	71 ( 85%)
	African Descent	8 ( 9%)	6 ( 7%)	9 ( 11%)
	Hispanic	3 ( 3%)	6 ( 7%)	3 ( 4%)
	Other	0	0	1 ( 1%)
MMSE	n	86	84	84
	Mean	18.0	17.9	18.5
	SD	4.27	4.22	4.16
	Median	19.5	18.0	20.0
	Min	10.0	10.0	10.0
	Max	23.0	24.0	24.0

Duration of disease	n	86	84	84
	Mean	42.6	48.7	40.5
	SD	30.24	29.58	24.69
	Median	35.3	40.2	36.0
	Min	7.2	7.8	2.2
	Max	183.1	130.8	135.0
	<12 months	5 ( 6%)	3 ( 4%)	4 ( 5%)
	>=12 months	81 ( 94%)	81 ( 96%)	80 ( 95%)
Years of education	n	86	84	84
	Mean	12.6	13.2	12.5
	SD	2.95	4.15	2.92
	Median	12.0	12.0	12.0
	Min	6.0	3.0	6.0
	Max	21.0	24.0	20.0
Baseline weight(kg)	n	86	83	84
	Mean	62.8	67.3	70.0
	SD	12.77	14.12	14.65
	Median	60.5	64.9	69.2
	Min	34.0	45.4	41.7
	Max	86.2	106.1	108.0
Baseline height(cm)	n	86	84	84
	Mean	162.6	163.4	165.8
	SD	11.52	10.42	10.13
	Median	162.6	162.6	165.1
	Min	137.2	135.9	146.1
	Max	185.4	195.6	190.5
Baseline BMI	n	86	83	84
	Mean	23.6	25.1	25.3
	SD	3.67	4.27	4.16
	Median	23.4	24.3	24.8
	Min	15.1	17.7	13.7
	Max	33.3	40.1	34.5
	<25	59 ( 69%)	47 ( 56%)	44 ( 52%)
	25-<30	21 ( 24%)	27 ( 32%)	28 ( 33%)
	>=30	6 ( 7%)	10 ( 12%)	12 ( 14%)

```

# use gt to do the reporting
tab_html <- final %>%
  gt(groupname_col="block") %>%

  tab_header(
    title = "Table 14.2.0",
    subtitle = "Summary of Demographic and Baseline Characteristics"
  ) %>%

  tab_source_note(

```



```

    source_note = "[1]: P-values are results of ANOVA treatment group comparison for continuous variable"
  ) %>%

  tab_source_note(
    source_note = paste('Program Source: 14-2.01.R Executed:
(Draft)', the_date)) %>%

# cols_label(
# catlabel= " ",
# GroupA = paste0("Group A (N=", bign[1], ")"),
# GroupB = paste0("Group B (N=", bign[2], ")"),
# GroupC = paste0("Group C (N=", bign[3], ")")) %>%

  tab_options(
    table.border.top.color = "white",
    heading.border.bottom.color = "black",
    table.border.bottom.color = "white",
    table_body.border.bottom.color = "black",
    table_body.hlines.color = "white",
    row_group.border.bottom.color = "white",
    row_group.border.top.color = "white",
    column_labels.border.top.color = "black",
    column_labels.border.bottom.color = "black",) %>%

  cols_align(
    align = "left")

```