

Create an AE Table with gt Package in R

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ABSTRACT

We will use the gt package in R to create an AE table with system organ class and preferred term.

INTRODUCTION

We will use two made-up datasets ADSL and ADAE. In the datasets there are two treatments, placebo and active. In the AE table, we will display columns for placebo and active, and a total column.

We will use the gt package in R to produce the AE table. See the reference [1] and [2] for more details about the gt package.

The datasets, R program and output in this paper are available in reference [3].

THE DETAILS

We will need four packages in the R program:

- use the haven package to read the SAS datasets
- use the summarise function from the package dplyr to count the distinct values of a variable
- use the spread function from the package tidyr to transpose a dataset
- use the gt package to create the table in HTML format.

This is the R program ae.R.

```
library(haven)
library(dplyr)
library(tidyr)
library(gt)

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

adsl <- read_sas("C:\\ae\\adsl.sas7bdat")
adae <- read_sas("C:\\ae\\adae.sas7bdat")

# create adsl4 with treatment variable grp

adsl1 <- adsl[(adsl$trt01p=='Placebo' & adsl$SAFFL=='Y'), ]
adsl1$grp <- 'grp1'
```

```

adsl2 <- adsl[(adsl$trt01p=='Active' & adsl$SAFFL=='Y'), ]
adsl2$grp <- 'grp2'

adsl3 <- rbind(adsl1, adsl2)
adsl3$grp <- 'grp3'

adsl4 <- rbind(adsl1, adsl2, adsl3)

# create adae4 with treatment variable grp

adae1 <- adae[(adae$trt01p=='Placebo' & adae$SAFFL=='Y' & adae$TRTEMFL=='Y'),
]
adae1$grp <- 'grp1'

adae2 <- adae[(adae$trt01p=='Active' & adae$SAFFL=='Y' & adae$TRTEMFL=='Y'),
]
adae2$grp <- 'grp2'

adae3 <- rbind(adae1, adae2)
adae3$grp <- 'grp3'

adae4 <- rbind(adae1, adae2, adae3)

# get the big N in column headers from adsl4
bign <- table(group=adsl4$grp)

# get the number of subjects with at least one TEAE

group_by_grp <-
  adae4 %>%
  group_by(grp) %>%
  summarise(unique_subj = n_distinct(USUBJID))

# get the count by System Organ class

group_by_grp1 <-
  adae4 %>%
  group_by(grp, AEBODSYS) %>%

```

```

summarise(unique_subj = n_distinct(USUBJID))

# get the count by preferred term

group_by_grp2 <-
  adae4 %>%
  group_by(grp, AEBODSYS, AEDECOD) %>%
  summarise(unique_subj = n_distinct(USUBJID))

# do the transpose

a1 <- spread(group_by_grp, grp, unique_subj)
a2 <- spread(group_by_grp1, grp, unique_subj)
a3 <- spread(group_by_grp2, grp, unique_subj)

a1$term <- "Subjects with at least one TEAE"
a1$AEBODSYS <- " "
a2$term <- a2$AEBODSYS
a3$term <- a3$AEDECOD

a1 <- a1[c("AEBODSYS", "term", "grp1", "grp2", "grp3")]
a2 <- a2[c("AEBODSYS", "term", "grp1", "grp2", "grp3")]
a3 <- a3[c("AEBODSYS", "term", "grp1", "grp2", "grp3")]

final <- rbind(a1, a2, a3)

#sort the ae data by AEBODSYS and descending order in the total column
df <-final[order(final$AEBODSYS, -final$grp3),]

#create the final data df for reporting

df$perc1 <- 100*df$grp1/bign[1]
df$perc1 <- format(round(df$perc1, 1), nsmall = 1)
df$grp1_c <- paste(df$grp1, "(", df$perc1, ")")
df$grp1_c <- ifelse(is.na(df$grp1),"0", df$grp1_c)

```

```

df$perc2 <- 100*df$grp2/bign[2]
df$perc2 <- format(round(df$perc2, 1), nsmall = 1)
df$grp2_c <- paste(df$grp2, "(", df$perc2, ")")
df$grp2_c <- ifelse(is.na(df$grp2),"0", df$grp2_c)

df$perc3 <- 100*df$grp3/bign[3]
df$perc3 <- format(round(df$perc3, 1), nsmall = 1)
df$grp3_c <- paste(df$grp3, "(", df$perc3, ")")
df$grp3_c <- ifelse(is.na(df$grp3),"0", df$grp3_c)

df <- df[c("AEBODSYS", "term", "grp1_c","grp2_c","grp3_c")]

# use gt to do the reporting
tab_html <- df %>%
  gt() %>%

  tab_header(
    title = "Table 14.3.1 Treatment Emergent Adverse Events by System Organ
Class and Preferred Term",
    subtitle = "Safety Population"
  ) %>%
  tab_source_note(
    source_note = "Note: TEAE is defined to be the AEs with start date >=
first dose date and <= last dose date + 30."
  ) %>%
  tab_source_note(
    source_note = "System organ class is in light gray. The table is sorted
by system organ class and descending order in the total column."
  ) %>%

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

  cols_label(
    term = html("System Organ Class <br> Preferred Term"),
    grp1_c = html(paste("Placebo <br> (N=", bign[1], ")")),
    grp2_c = html(paste("Active <br> (N=", bign[2], ")")),
    grp3_c = html(paste("Total <br> (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",
) %>%

tab_style(
  style = list(
    cell_fill(color = "#D3D3D3")
  ),
  locations = cells_body(

    rows = AEBODSYS==term
  )
) %>%

cols_hide(
  columns = c(AEBODSYS)
)

# output the HTML table

tab_html %>%
  gtsave("teae_soc_pt.html", path = "C:\\\\ae" )

```

The table created with this R program is shown in display 1. As the author is not able to add indentation to the rows for preferred terms, the rows for system organ class are displayed in light gray.

Table 14.3.1 Treatment Emergent Adverse Events by System Organ Class and Preferred Term

Safety Population			
System Organ Class Preferred Term	Placebo (N= 4)	Active (N= 4)	Total (N= 8)
Subjects with at least one TEAE	4 (100.0)	4 (100.0)	8 (100.0)
Blood and lymphatic system disorders	0	1 (25.0)	1 (12.5)
Lymphopenia	0	1 (25.0)	1 (12.5)
Eye disorders	0	1 (25.0)	1 (12.5)
Eye disorder	0	1 (25.0)	1 (12.5)
Gastrointestinal disorders	4 (100.0)	4 (100.0)	8 (100.0)
Diarrhoea	3 (75.0)	4 (100.0)	7 (87.5)
Nausea	4 (100.0)	2 (50.0)	6 (75.0)
Vomiting	1 (25.0)	3 (75.0)	4 (50.0)
Abdominal pain	0	1 (25.0)	1 (12.5)
Dyspepsia	1 (25.0)	0	1 (12.5)

Display 1. AE Table in HTML Format, Created with gt Package in R**CONCLUSION**

The package gt is a powerful tool to create tables.

REFERENCES

[1] Some detailed discussion about gt package, available at:

https://aosmith16.github.io/spring-r-topics/slides/week04_gt_tables.html#1

[2] Presentation by Rich Iannone, available at:

<https://www.youtube.com/watch?v=h1KAjSfSbmK&t=872s>

[3] the datasets, R program and output in this paper are available at:

<https://github.com/hengweiliu2020/create-table-with-gt>

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