PharmaSUG SDE Tokyo 2018

Automated Generation of PowerPoint Presentations Using R in Clinical Studies

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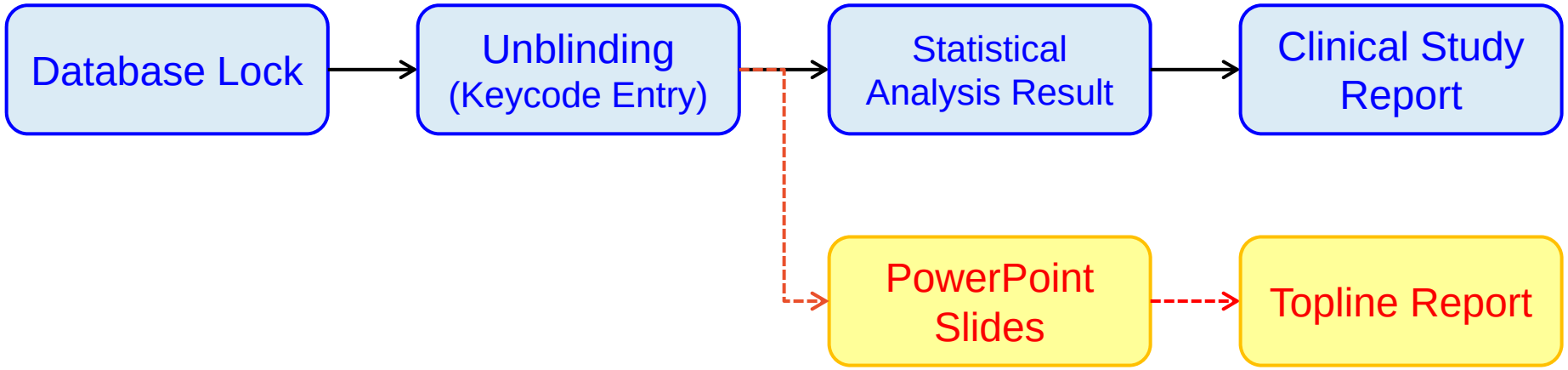
MENU

- **Introduction**
- Procedures
- Details
  - ✓ Add Texts
  - ✓ Add Figures
  - ✓ Add Tables
  - ✓ Miscellaneous
- Example:

  Automated Generation of PowerPoint Presentations from CDISC/ADaM Datasets

Closing Clinical Study



- In closing stage of a clinical study, we should provide a statistical analysis result (SAR) with tables and figures, and then create a clinical study report (CSR) based on the result.
- In the meantime, we should also create a PowerPoint slide deck (say, topline report) including a brief summary of the study and the analysis results to report our managers / directors.

Topline Report Deliverable

- **Until Now**
  - Copy contents from SAR and paste them into slides
  - Due to manual labor, the slides would have several errors (e.g., mispostings or writing errors)

- **From Now**
  - Automatically generate a PowerPoint slide deck using any software / program (e.g., R or SAS)
  - Much less errors than manually

How to Generate PowerPoint Slide Deck

- **SAS ODS Powerpoint / Layout**
  - Cannot read existing PowerPoint files
    (i.e., we cannot use any PowerPoint template)

- **R2PPT**
  - R package
  - Few functions (especially for customizing tables)
  - ActiveXObject is needed

- **ReporteRs**
  - R package
  - Many functions
  - JRA and package "rJava" are needed (i.e., a little slow)

R Package "**officer**"

- The package creates Microsoft Word and PowerPoint documents with tables and figures.

- Functions of the package can add and remove tables, figures and paragraphs of text. Slides can be added or removed.

- Like R package "ReporteRs", but this package does NOT require any installation of Microsoft products or any Java components (e.g., JRA or package "rJava").

Setup

```
> install.packages(c("dplyr", "ggplot2", "magrittr",
+   "xtable", "flextable", "officer"), dep=T)
> library(dplyr)
> library(ggplot2)
> library(magrittr)
> library(knitr)
> library(xtable)
> library(flextable)
> library(officer)
```

1. Install R
2. Install the above packages
3. Load their packages (Done!)

Example: Create PowerPoint Document

```
> myplot  <- ggplot(data=iris, aes(Sepal.Length, Sepal.Width)) +
+              geom_point()
> myppt   <- read_pptx()
> mylab <- layout_summary(myppt)[[1]]      # Slide Layout Name
> mytmp <- layout_summary(myppt)[[2]][1]   # Show Slide Master Name

> myppt <- myppt %>%
+   add_slide(layout="Title Slide", master=mytmp) %>%
+   ph_with_text(type="ctrTitle", str="Iris Data") %>%
+   ph_with_text(type="subTitle", str="Table & Figure") %>%
+   ph_with_text(type="dt",       str=format(Sys.Date())) %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Scatter Plot") %>%
+   ph_with_gg(value=myplot) %>%
+   add_slide(layout="Two Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Table") %>%
+   ph_with_table(type="body", value=iris[1:5,], index=1) %>%
+   ph_with_text(type="body", str="Iris data", index=2)
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

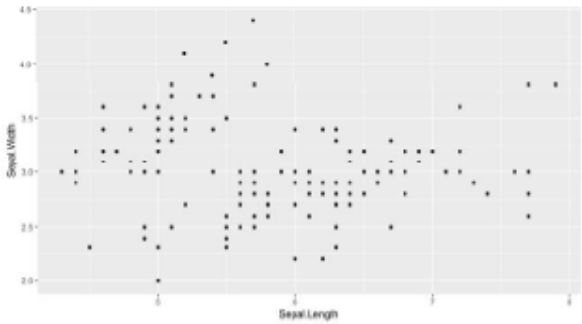
Example: Create PowerPoint Document

Iris Data

Table & Figure

2018-04-11

Scatter Plot



Table

Sepal. Length	Sepal. Width	Petal. Length	Petal. Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa

- Iris data

Example: Create WORD Document

```
> myplot <- ggplot(data=iris, aes(Sepal.Length, Sepal.Width)) +
+             geom_point()

> mydoc  <- read_docx() %>%
+   body_add_par(value="Table of contents", style="heading 1") %>%
+   body_add_toc(level=2) %>%
+   body_add_break() %>%
+   body_add_par(value="Iris Data", style="heading 1") %>%
+   body_add_par(value="Table", style="heading 2") %>%
+   body_add_par("Sepal.Length vs. Sepal.Width", style="Normal") %>%
+   body_add_table(value=iris[1:5,], style="table_template" ) %>%
+   body_add_par(value="Scatter Plot", style="heading 2") %>%
+   body_add_gg(value=myplot, style="centered")
> print(mydoc, target="c:/temp/sample.docx")
[1] "c:/temp/sample.docx"
```

Example: Create WORD Document

1. Table of contents

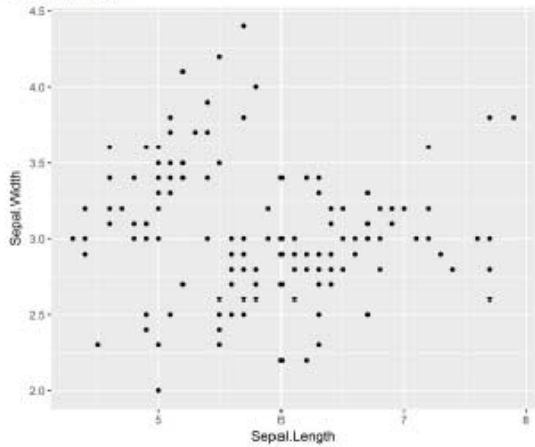
2. Iris Data

2.1. Table

Sepal.Length vs. Sepal.Width

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa

2.2. Scatter Plot



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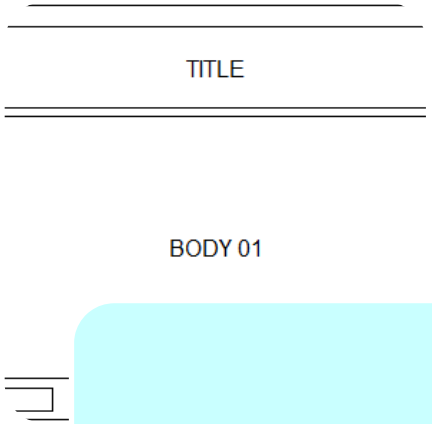
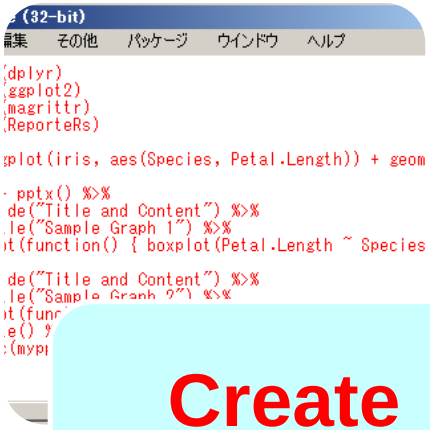
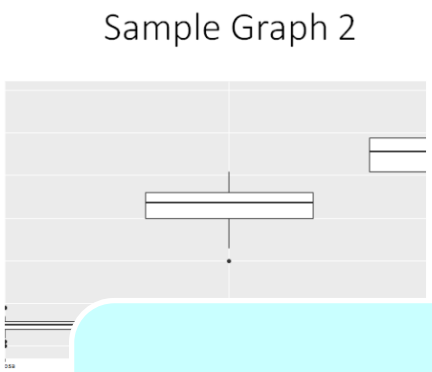
Procedures



Preparation



Create Contents & Slides



Write PowerPoint File

1. Preparation

- Open a connection to a PowerPoint file <u>without</u> an existing PowerPoint file

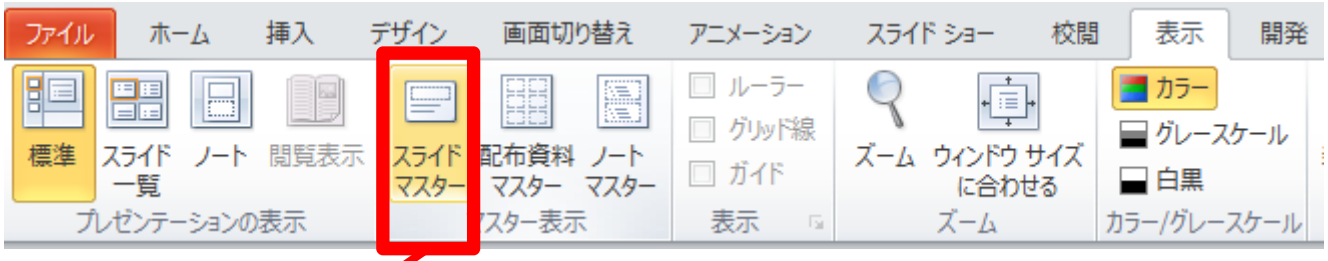
```
> myppt   <- read_pptx()                          # Create PowerPoint Object
> ( mylab <- layout_summary(myppt)[[1]] )         # Show Slide Layout Name
[1] "Title Slide"       "Title and Content" "Section Header"
[4] "Two Content"       "Comparison"        "Title Only"
[7] "Blank"
> ( mytmp <- layout_summary(myppt)[[2]][1] ) # Show Slide Master Name
[1] "Office Theme"
> myppt %>%
+   layout_properties(layout="Title and Content", master=mytmp)%>%
+   kable(digits=2)                               # Show Slide Properties

|   |master_name  |name              |type   |id |ph_label                    | offx| offy|   cx|   cy|
|:--|:------------|:-----------------|:------|:--|:--------------------------|----:|----:|----:|----:|
|5  |Office Theme |Title and Content |body   |3  |Content Placeholder 2      | 0.50| 1.75| 9.00| 4.95|
|10 |Office Theme |Title and Content |dt     |4  |Date Placeholder 3         | 0.50| 6.95| 2.33| 0.40|
|21 |Office Theme |Title and Content |ftr    |5  |Footer Placeholder 4       | 3.42| 6.95| 3.17| 0.40|
|25 |Office Theme |Title and Content |sldNum |6  |Slide Number Placeholder 5 | 7.17| 6.95| 2.33| 0.40|
|31 |Office Theme |Title and Content |title  |2  |Title 1                    | 0.50| 0.30| 9.00| 1.25|
```

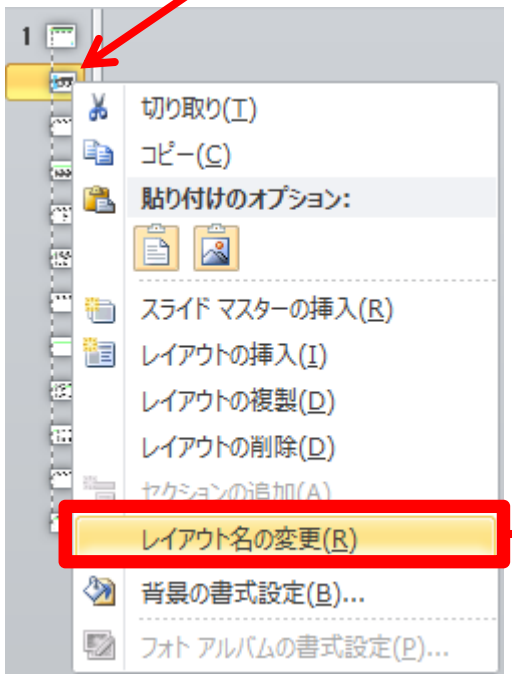
1. Preparation

- Open a connection to a PowerPoint file with an existing PowerPoint file (e.g., C:¥temp¥nds.pptx)

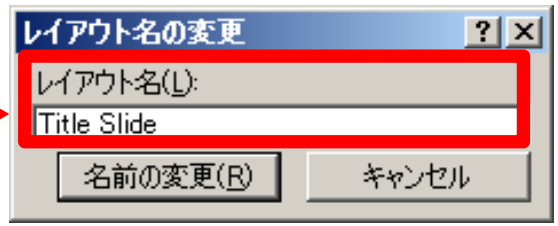
```
> myppt   <- read_pptx("C:/temp/nds.pptx")   # Create PowerPoint Object
> ( mylab <- layout_summary(myppt)[[1]] )    # Show Slide Layout Name
 [1] "Title Slide"             "Title and Vertical Text"
 [3] "Vertical Title and Text" "Title and Content"
 [5] "Section Header"          "Two Content"
 [7] "Comparison"              "Title Only"
 [9] "Blank"                   "Content with Caption"
[11] "Figure with Caption"
> ( mytmp <- layout_summary(myppt)[[2]][1] ) # Show Slide Master Name
[1] "Slide Template"
> for (i in 1:length(mylab)) {
+   layout_properties(myppt, mylab[i], master=mytmp) %>% kable(digits=2) %>% print()
+ }

|   |master_name    |name        |type     |id   |ph_label     | offx| offy|   cx|   cy|
|:--|:--------------|:-----------|:--------|:----|:------------|----:|----:|----:|----:|
|1  |Slide Template |Title Slide |body     |8223 |AutoShape 31 | 0.36| 2.59| 0.48| 0.42|
|2  |Slide Template |Title Slide |body     |8227 |AutoShape 35 | 0.36| 1.16| 0.48| 0.42|
|3  |Slide Template |Title Slide |body     |8224 |AutoShape 32 | 0.36| 0.44| 0.48| 0.42|

[Show Properties for All Templates]
```

1. Preparation - Note for Japanese User





- It is recommended that each layout name should be in English, when using an existing PowerPoint file as default.

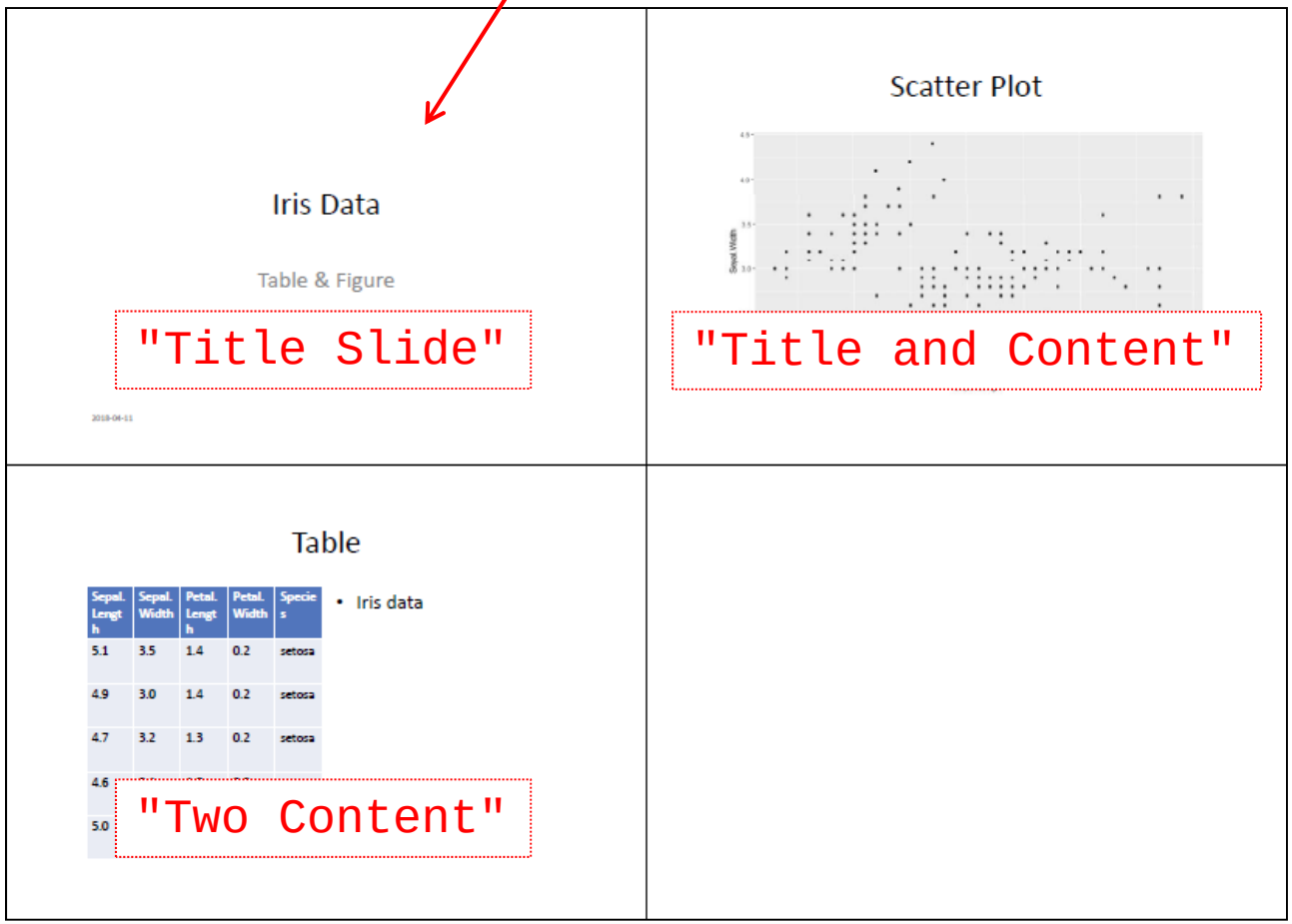


2. Create Contents and Slides

```
> myplot <- ggplot(data=iris, aes(Sepal.Length, Sepal.Width)) + geom_point()

> myppt  <- myppt %>%
+
+   # Add "Title Slide" using an argument of "layout"
+   add_slide(layout="Title Slide", master=mytmp) %>%
+   ph_with_text(type="ctrTitle", str="Iris Data") %>%
+   ph_with_text(type="subTitle", str="Table & Figure") %>%
+   ph_with_text(type="dt",       str=format(Sys.Date())) %>%
+
+   # Slide for Scatter Plot
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Scatter Plot") %>%
+   ph_with_gg(value=myplot) %>%
+
+   # Slide for Text and Table
+   add_slide(layout="Two Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Table") %>%
+   ph_with_table(type="body", value=iris[1:5,], index=1) %>%
+   ph_with_text(type="body", str="Iris data", index=2)
```

3. Write PowerPoint File

```
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```



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Add Texts

- Function ph_with_text() is used to add texts to a slide without any format.
  - **"type"** argument: placeholder type
  - **"index"** argument: placeholder index for "Two Content" slide

```
> myppt <- read_pptx()
> mylab <- layout_summary(myppt)[[1]]
> mytmp <- layout_summary(myppt)[[2]][1]

> myppt <- myppt %>%
+   add_slide(layout="Two Content", master=mytmp) %>%
+   ph_with_text(type="title", str="A title") %>%
+   ph_with_text(type="ftr",   str="A footnote") %>%
+   ph_with_text(type="dt",    str=format(Sys.Date())) %>%
+   ph_with_text(type="body",  str="A first text",  index=1) %>%
+   ph_with_text(type="body",  str="A second text", index=2)
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

Add Texts

A title

- A first text
- A second text

2018-04-12

A footnote

Add Texts

- Function ph_with_ul() is used to add unordered lists to a slide with some format.
  - **"type"** argument: placeholder type
  - **"index"** argument: placeholder index for "Two Content" slide
  - **"str_list"** argument: list of texts
  - **"level_list"** argument: list of levels
  - **"style=fp_text(...)"** argument: text style ("font.size=0" to use the default size)
- The functions of ph_add_par() and ph_add_text() can be used to add texts more.

```
> myppt <- read_pptx()
> mytmp <- layout_summary(myppt)[[2]][1]
> myppt <- myppt %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="A title") %>%
+   ph_with_ul(type="body", level_list=c(1,2), str_list=c("aaa","bbb"),
+     style=fp_text(font.size=0, color="red")) %>%
+     ph_add_par(type="body", level=3) %>%
+     ph_add_text(type="body", str="ccc", style=fp_text(color="blue"))
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

Add Texts

A title

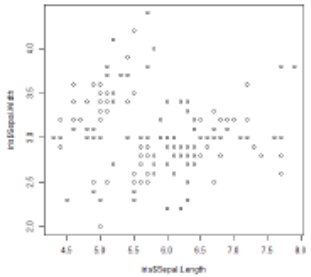
- aaa
  - bbb
    - ccc

Add Figures (image file / ggplot object)

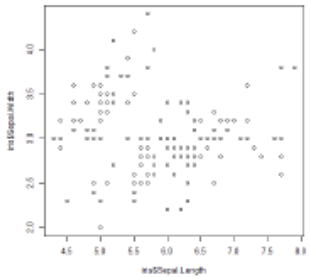
```
> png("C:/temp/myplot.png")
> plot(iris$Sepal.Length, iris$Sepal.Width)
> dev.off()
null device
          1
> myplot <- ggplot(data=iris, aes(Sepal.Length, Sepal.Width)) + geom_point()
> myppt  <- read_pptx()
> mytmp  <- layout_summary(myppt)[[2]][1]
> myppt <- myppt %>%
+   # Add Plot by ph_with_img()
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Scatter Plot by plot()") %>%
+   ph_with_img(type="body", src="C:/temp/myplot.png", width=5, height=5) %>%
+
+   # Add Plot by ph_with_img_at()
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Scatter Plot by plot()") %>%
+   ph_with_img_at(src="C:/temp/myplot.png", left=2, top=2, width=5, height=5) %>%
+
+   # Add Plot by ph_with_gg()
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Scatter Plot by ggplot()") %>%
+   ph_with_gg(value=myplot)> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

Add Figures (image file / ggplot object)

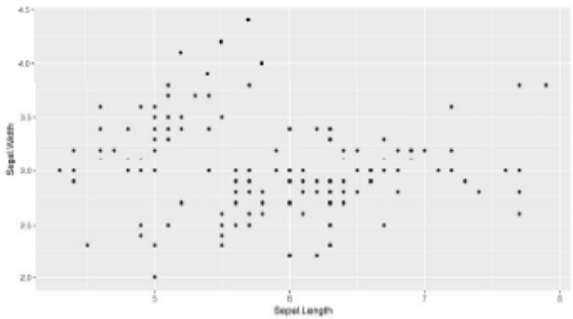
Scatter Plot by plot()



Scatter Plot by plot()



Scatter Plot by ggplot()



Add Tables

- Two functions of ph_with_table() and ph_with_table_at() are used to add a table into a slide

```
> myppt  <- read_pptx()
> mytmp  <- layout_summary(myppt)[[2]][1]

> myppt <- myppt %>%
+   add_slide(layout="Two Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Table 1") %>%
+   ph_with_table(type="body", value=iris[1:5,], index=1) %>%
+   ph_with_text(type="body", str="Iris data", index=2) %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Table 2") %>%
+   ph_with_table_at(value=iris[1:5,], left=1, top=2, width=8, height=5)
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

Add Tables

Table 1

Sepal. Length	Sepal. Width	Petal. Length	Petal. Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa

- Iris data

Table 2

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa

- There is no function to customize table in the "officer" package
- Next, "flextable" package will be introduced to customize

Add Tables - "flextable" Object

- A "flextable" ("flex"ible "table") is an object for reporting table from data.frame
- A "flextable" is containing three parts below*, header rows, body rows and footer rows

header part	row 1 - cell from 1 to 5				
	row 2 - cell from 1 to 2		row 2 cell from 3 to 5		
	row 3 cell 1	row 3 cell 2	row 3 cell 3	row 3 cell 4	row 3 cell 5
body part	data[1,1]	data[1,2]	data[1,3]	data[1,4]	data[1,5]
	data[2,1]	data[2,2]	data[2,3]	data[2,4]	data[2,5]
	...	...	...	...	...
	data[n,1]	data[n,2]	data[n,3]	data[n,4]	data[n,5]
footer part	*Grouped footer 1.1*		*Grouped footer 1.2*		
	Grouped footer 2.1				

* : https://davidgohel.github.io/flextable/articles/overview.html

Add Tables - "flextable" Object

- Both flextable() and regulartable() functions produce a flextable. The first one is resource consuming.

```
> myft <- regulartable(iris[49:52,c(5,1,2)]) # Create "flextable" object
> myft <- theme_booktabs(myft)               # Change "flextable" theme
> myft <- autofit(myft)                      # Adjust Cell Width and Height
>
> myppt  <- read_pptx()
> mytmp  <- layout_summary(myppt)[[2]][1]
> myppt  <- myppt %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_flextable(myft, type="body")
> print(myppt, target="c:/temp/sample.pptx")
[1] "c:/temp/sample.pptx"
```

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

Add Tables - "flextable" Object
Select Columns and Change Theme

- **"col_keys"** argument selects displayed columns (blank columns are added if some column names are not in the list of this argument)
- Several functions are defined to change theme of tables

```
> myft1 <- regulartable(iris[49:52,],
+             col_keys=c("Species","XXX","Sepal.Length","Sepal.Width"))
> myft2 <- theme_booktabs(myft1)
> myft3 <- theme_box(myft1)
> myft4 <- theme_tron(myft1)
> myft5 <- theme_tron_legacy(myft1)
> myft6 <- theme_vanilla(myft1)
> myft7 <- theme_zebra(myft1)
> myft8 <- empty_blanks(myft7)   # Set Blank Columns as Transparent
```

myft1

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

myft3

Species		Sepal.Length	Sepal.Width
setosa		5.300	3.700
setosa		5.000	3.300
versicolor		7.000	3.200
versicolor		6.400	3.200

myft8

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

Add Tables - "flextable" Object
Merge Cells

- Three functions of merge_h(**i=rows**), merge_v(**j=columns**), and merge_at(**i=rows**, **j=columns**) merge rows, columns and cells.
- The merge_none() function deletes all merging information.

```
> myft  <- regulartable(iris[49:52,],
+            col_keys=c("Species","Sepal.Length","Sepal.Width"))
> myft1 <- merge_v(myft, j=c(1,3))
> myft1
> myft2 <- merge_v(myft, ~ Species)
> myft2
```

myft1

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
	5.000	3.300
versicolor	7.000	3.200
	6.400	

myft2

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
	5.000	3.300
versicolor	7.000	3.200
	6.400	3.200

Add Tables - "flextable" Object
Change Labels and Add Headers

- The set_header_labels() function replaces column labels of the bottom row of the header.
- The add_header() and add_footer() functions add a header and a footer, respectively.

```
> myft  <- regulartable(iris[49:52,],
+            col_keys=c("Species","Sepal.Length","Sepal.Width"))
> myft1 <- set_header_labels(myft, Species = "Species",
+            Sepal.Length="Length", Sepal.Width="Width") %>%
+          theme_vanilla()
> myft2 <- add_header(myft1, Species = "Species",
+            Sepal.Length="Sepal", Sepal.Width="Sepal", top=T) %>%
+          theme_vanilla() %>% autofit() %>%
+          merge_h(part="header") %>% merge_v(part="header") %>%
+          add_footer(Species="This is a footnote." ) %>%
+          merge_at(i=1, j=1:3, part="footer")
```

myft1

Species	Length	Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

myft2

Species	Sepal	
	Length	Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

This is a footnote.

Add Tables - "flextable" Object
Adjust Cell Widths and Heights

- The autofit() function adjusts automatically cell widths and heights.
- Three functions of width(), height(), and height_all() adjust manually cell widths and heights, respectively.

```
> myft  <- regulartable(iris[49:52,],
+             col_keys=c("Species","Sepal.Length","Sepal.Width"))
> myft1 <- autofit(myft)
> myft2 <- width(myft, j=~ Species, width=2) %>%
+          height_all(height=0.5) %>%
+          height(i=2, height=1)
```

myft1

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

myft2

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

Add Tables - "flextable" Object Formatting

- The several functions below modify formatting properties of a flextable.
- The **"part"** argument should be "all", "body", "header" and "footer".

```
> myft1 <- regulartable(iris[49:52,],
+             col_keys=c("Species","Sepal.Length","Sepal.Width"))
> myft2 <- align(myft1, align="center", part="all") %>%       # Text Alignment
+          bg(bg="cyan", part="body") %>%                      # Background Color
+          bold(part="header") %>%                             # Bold
+          color(color="red", part="header") %>%               # Font Color
+          font(j="Species", fontname="Arial") %>%             # Font
+          fontsize(part="all", size=14) %>%                   # Font Size
+          italic(i=~ Sepal.Length>6,                          # Conditional format
+                 j=~ Sepal.Length+Sepal.Width, italic=T) %>% # Italic
+          padding(padding=3, part="all") # Padding(space around a text in a cell)
```

myft1

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

myft2

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	*7.000*	*3.200*
versicolor	*6.400*	*3.200*

Add Tables - "flextable" Object Borders

- The several functions below change properties of the horizontal or vertical borders for a flextable.

```
> # Create Border Properties Objects
> b0 <- fp_border(color="white", style="none")
> b1 <- fp_border(color="blue", style="solid", width=1)
> b2 <- fp_border(color="red", style="dotted", width=2) # style="dashed" is available

> myft  <- regulartable(iris[49:52,],
+            col_keys=c("Species","Sepal.Length","Sepal.Width")) %>%
+          add_footer(Species="This is a footnote." ) %>%
+          merge_at(i=1, j=1:3, part="footer")
> myft1 <- border_remove(myft)                          # Remove All Borders
> myft2 <- hline(myft1, border=b1) %>%                  # Set horizontal lines
+          hline_top(border=b2, part="body") %>%        # Set first horizontal line
+          hline_bottom(border=b0, part="footer") %>%   # Set last horizontal line
+          vline(border=b1, part="header") %>%          # Set vertical lines
+          vline_left(border=b0, part="footer") %>%     # Set first vertical line
+          vline_right(border=b0, part="footer")        # Set last vertical line
```

Add Tables - "flextable" Object Borders

- The functions of border_inner_h(), border_inner_v() and border_outer() are useful to apply a border to inner/outer cells of one or all parts of a flextable if the border design is simple.

```
myft3 <- border_inner_h(myft1, border=b1, part="all") %>%
         border_inner_v(border=b2, part="all") %>%
         border_outer(border=b3, part="all")
```

myft1

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

This is a footnote.

myft2

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

This is a footnote.

myft3

Species	Sepal.Length	Sepal.Width
setosa	5.300	3.700
setosa	5.000	3.300
versicolor	7.000	3.200
versicolor	6.400	3.200

This is a footnote.

Miscellaneous: Some Objects for Properties

- **Create Border properties object**

```
fp_border(color="black", style="solid", width=1)
```

- **Create Text formatting properties object**

```
fp_text(color="black", font.size=10, bold=FALSE, italic=FALSE,
        underlined=FALSE, font.family="Arial", vertical.align="baseline",
        shading.color="transparent")
```

- **Create Cell formatting object**

```
fp_cell(border=fp_border(width=0), border.bottom, border.left, border.top,
       border.right, vertical.align="center", margin=0, margin.bottom,
       margin.top, margin.left, margin.right, background.color="transparent",
       text.direction="lrtb") # "lrtb"(left to right top to bottom),"tbrl","btlr"
```

```
> b     <- fp_border(color="white", style="none")
> myft  <- regulartable(iris[49:52,],
+            col_keys=c("Species","Sepal.Length","Sepal.Width"))
> myft1 <- border_inner_h(myft, border=b, part="all") %>%
+          border_inner_v(border=b, part="all")
> b     <- update(b, color="blue", style="solid", width=1)
> myft2 <- border_outer(myft1, border=b, part="all")
```


There is another function "fp_par" for creating paragraph formatting properties.

Miscellaneous: Slide selection and manipulation

- Four functions of add_slide(), remove_slide(), on_slide() and ph_remove() are used to select and manipulate a slide/content

```
> myppt <- read_pptx()
> mylab <- layout_summary(myppt)[[1]]
> mytmp <- layout_summary(myppt)[[2]][1]
> myppt <- myppt %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   add_slide(layout="Title Only",        master=mytmp) %>%
+   add_slide(layout="Two Content",       master=mytmp)       # Create 3 slides
> myppt <- myppt %>% remove_slide(index=1)                    # Remove Slide #1
> myppt <- myppt %>%
+   on_slide(index=1) %>%                                     # Focus on #1
+   ph_with_text(type="title", str="Dummy Title") %>%         # Add a text
+   on_slide(index=2) %>%                                     # Focus on #2
+   ph_with_table(type="body", value=iris[1:5,], index=1) %>% # Add a table
+   ph_with_text(type="body", str="Iris data", index=2) %>%   # Add a text
+   on_slide(index=1) %>%                                     # Focus on #1
+   ph_remove(type="title")                                   # Remove title
> print(myppt, target="c:/temp/sample.pptx")
```

Miscellaneous: "xtable" Object

- The xtable_to_flextable() function gets a flextable from a xtable object (e.g., a xtable object converted from a lm.object)

```
> result  <- lm(Sepal.Length ~ Species, data=iris)
> mytable <- xtable(summary(result)$coefficients)
> myft1   <- xtable_to_flextable(mytable,
+             hline.after=c(-1,0,1,nrow(mytable)))
> mytable <- table(sample(LETTERS[1:3],10, rep=T))
> myft2   <- xtable_to_flextable(xtable(mytable)) %>%
+            set_header_labels(rowname="Char.", V1="Freq.") %>% autofit()
```

myft1

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	5.01	0.07	68.76	0.00
Speciesversicolor	0.93	0.10	9.03	0.00
Speciesvirginica	1.58	0.10	15.37	0.00

myft2

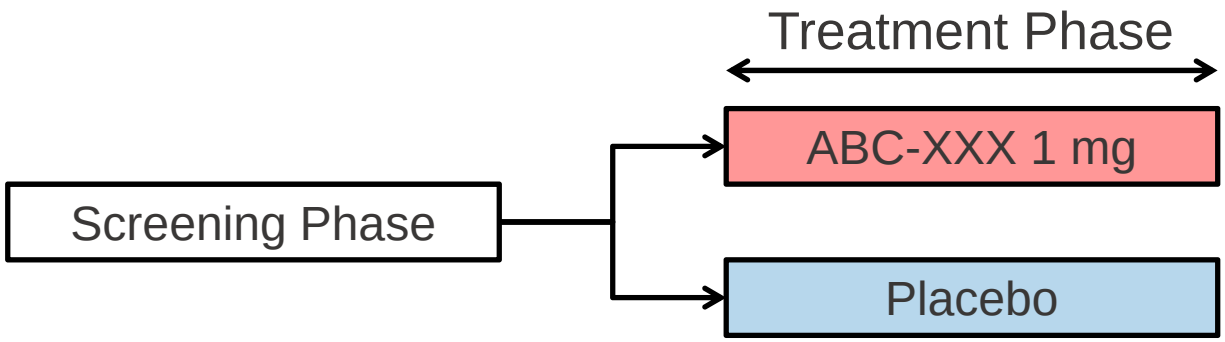
Char.	Freq.
A	5
B	1
C	4

MENU

- Introduction
- Procedures
- Details
  - ✓ Add Texts
  - ✓ Add Figures
  - ✓ Add Tables
  - ✓ Miscellaneous
- **Example:**

  Automated Generation of PowerPoint Presentations from CDISC/ADaM Datasets

A Virtual Clinical Study



Target Population:	Subjects with history of gastric ulcer (GU)
Treatment:	ABC-XXX 1 mg or Placebo
Primary Endpoint:	Time to recurrence of GU
Secondary Endpoint:	Time to occurrence of duodenal ulcer (DU)
Other Endpoints:	Proportion of GU recurrence, Proportion of DU occurrence, Treatment-emergent adverse event (TEAE)
Demography / Baseline Characteristics:	Age, Gender, BMI, Helicobacter Pylori test, Caffeine consumption, Alcohol consumption, Smoking status
ADaM Datasets:	ADSL, ADTTE, ADAE (simple for illustrative purposes)

ADSL

Variable	Type	Label
STUDYID	Char	Study Identifier
USUBJID	Char	Unique Subject Identifier
SUBJID	Char	Subject Identifier for the Study
SITEID	Char	Study Site Identifier
AGE	Num	Age
AGEU	Char	Age Units
AGEGR1	Char	Pooled Age Group 1
AGEGR1N	Num	Pooled Age Group 1 (N)
SEX	Char	Sex
RACE	Char	Race
BMIBL	Num	Baseline Body Mass Index (kg/m2)
BMIGR1	Char	Pooled Baseline BMI (kg/m2) Group 1
BMIGR1N	Num	Pooled Baseline BMI (kg/m2) Group 1 (N)
ALCOHOL	Char	Consumption of Alcohol
CAFFEINE	Char	Consumption of Caffeine
HPYLORI	Char	Helicobacter Pylori Infection
TOBACCO	Char	Consumption of Tobacco
FASFL	Char	Full Analysis Set Population Flag
PPROTFL	Char	Per-Protocol Population Flag
SAFFL	Char	Safety Population Flag
COMPLFL	Char	Completers Population Flag
RANDFL	Char	Randomized Population Flag
ARM	Char	Description of Planned Arm
ACTARM	Char	Description of Actual Arm
TRT01P	Char	Planned Treatment for Period 01
TRT01PN	Num	Planned Treatment for Period 01 (N)
TRT01A	Char	Actual Treatment for Period 01
TRT01AN	Num	Actual Treatment for Period 01 (N)

- **TRTP** : ABC-XXX, Placebo
- **RANDFL** : Y, N
- **AGE** : Age (years)
- **AGEGR1** :
  Min<= - <65, 65<= - <=Max
- **SEX** : M (Male), F (Female)
- **BMIBL** : Baseline BMI (kg/m^2)
- **BMIGR1** :
  Min<= - <25.0, 25.0<= - <=Max
- **HPYLORI** : Negative, Positive
- **CAFFEINE** : No, Yes
- **ALCOHOL** : No, Yes
- **TOBACCO** : No, Yes

ADTTE

Variable	Type	Label
STUDYID	Char	Study Identifier
USUBJID	Char	Unique Subject Identifier
SUBJID	Char	Subject Identifier for the Study
SITEID	Char	Study Site Identifier
AGE	Num	Age
AGEU	Char	Age Units
AGEGR1	Char	Pooled Age Group 1
AGEGR1N	Num	Pooled Age Group 1 (N)
SEX	Char	Sex
RACE	Char	Race
BMIBL	Num	Baseline Body Mass Index (kg/m2)
BMIGR1	Char	Pooled Baseline BMI (kg/m2) Group 1
BMIGR1N	Num	Pooled Baseline BMI (kg/m2) Group 1 (N)
ALCOHOL	Char	Consumption of Alcohol
CAFFEINE	Char	Consumption of Caffeine
HPYLORI	Char	Helicobacter Pylori Infection
TOBACCO	Char	Consumption of Tobacco
FASFL	Char	Full Analysis Set Population Flag
PPROTFL	Char	Per-Protocol Population Flag
SAFFL	Char	Safety Population Flag
COMPLFL	Char	Completers Population Flag
RANDFL	Char	Randomized Population Flag
ARM	Char	Description of Planned Arm
ACTARM	Char	Description of Actual Arm
TRTP	Char	Planned Treatment
TRTPN	Num	Planned Treatment (N)
TRTA	Char	Actual Treatment
TRTAN	Num	Actual Treatment (N)

Variable	Type	Label
ASEQ	Num	Analysis Sequence Number
ADT	Num	Analysis Date
PARAM	Char	Parameter
PARAMCD	Char	Parameter Code
PARAMN	Num	Parameter (N)
AVAL	Num	Analysis Value
STARTDT	Num	Time to Event Origin Date for Subject
CNSR	Num	Censor

- **TRTP** : ABC-XXX, Placebo
- **FASFL** : Y, N
- **PPROTFL** : Y, N
- **PARAMCD** : GU (Gastric ulcer),
  DU (Duodenal ulcer)
- **AVAL** : Time to Event/Censor (days)
- **CNSR** : 0 (Event), 1 (Censor)
- **Covariates/Subgroups** :
  AGE, SEX, BMIBL, HPYLORI,
  CAFFEINE, ALCOHOL, TOBACCO

ADAE

Variable	Type	Label
STUDYID	Char	Study Identifier
USUBJID	Char	Unique Subject Identifier
SUBJID	Char	Subject Identifier for the Study
SITEID	Char	Study Site Identifier
AGE	Num	Age
AGEU	Char	Age Units
AGEGR1	Char	Pooled Age Group 1
AGEGR1N	Num	Pooled Age Group 1 (N)
SEX	Char	Sex
RACE	Char	Race
BMIBL	Num	Baseline Body Mass Index (kg/m2)
BMIGR1	Char	Pooled Baseline BMI (kg/m2) Group 1
BMIGR1N	Num	Pooled Baseline BMI (kg/m2) Group 1 (N)
ALCOHOL	Char	Consumption of Alcohol
CAFFEINE	Char	Consumption of Caffeine
HPYLORI	Char	Helicobacter Pylori Infection
TOBACCO	Char	Consumption of Tobacco
FASFL	Char	Full Analysis Set Population Flag
PPROTFL	Char	Per-Protocol Population Flag
SAFFL	Char	Safety Population Flag
COMPLFL	Char	Completers Population Flag
RANDFL	Char	Randomized Population Flag
TRTP	Char	Planned Treatment
TRTPN	Num	Planned Treatment (N)
TRTA	Char	Actual Treatment
TRTAN	Num	Actual Treatment (N)
AESEQ	Num	Sequence Number
AETERM	Char	Reported Term for the Adverse Event

Variable	Type	Label
AEDECOD	Char	Dictionary-Derived Term
AEBODSYS	Char	Body System or Organ Class
TRTEMFL	Char	Treatment Emergent Analysis Flag
AESTDTC	Num	Start Date/Time of Adverse Event
AESTDY	Num	Study Day of Start of Adverse Event
AEENDTC	Num	End Date/Time of Adverse Event
AESEV	Char	Severity/Intensity
ASEV	Char	Analysis Severity/Intensity
ASEVN	Num	Analysis Severity/Intensity (N)
AEBDSYCD	Num	Body System or Organ Class Code
AESER	Char	Serious Event
AEREL	Char	Causality
AREL	Char	Analysis Causality
ARELN	Num	Analysis Causality (N)
AEPTCD	Num	Preferred Term Code
AOCCFL	Char	1st Occurrence within Subject Flag
AOCCPFL	Char	1st Occurrence of Preferred Term Flag
AOCCSFL	Char	1st Occurrence of SOC Flag

- **TRTA** : ABC-XXX, Placebo
- **TRTEMFL** : Y (TEAE), N (PTE)
- **AEDECOD** : PT Name
- **AESER** : Y (SAE), N (Non-SAE)
- **AREL** : Not Related, Related
- **ASEV** : Mild, Moderate, Severe

Analytical Methods for Primary Endpoint

- **Primary Analysis**

  The cumulative incidences and the two-sided 95% confidence intervals (CIs) will be provided by treatment group using the Kaplan-Meier method.
  A log-rank test will be used to test for treatment differences.

  – Tables for the cumulative incidences with 95% CIs
  – Kaplan-Meier Plot
  – Using FAS

- **Other Analysis**

  – Sensitivity Analysis (the same as above, but using PPS)
  – Covariate Adjusted Analysis (Cox regression model with treatment and each demographic data as covariate)
  – Subgroup Analysis

Purpose

- Automatically generate a PowerPoint slide deck using R
- The slides will include below:
  - Summary table of Demographics and Baseline Characteristics [Randomized Set, ADSL]
  - Table and Figure of Analysis Result for Primary Endpoint [FAS and PPS, ADTTE]
  - Table and Figure of Analysis Result for Secondary Endpoint [FAS, ADTTE]
  - Tables for Other Efficacy Endpoints [FAS, ADTTE]
  - Covariate Adjusted Analysis [FAS, ADTTE]
  - Subgroup Analysis [FAS, ADTTE]
  - Tables and Figures of TEAE, Drug-related TEAE, TEAE by Intensity and SAE [Safety Analysis Set, ADAE and ADSL]

R Program (1/3)

- Execute the following R program after reading the data, definition of R functions, creating R variables (omitted)

```
> # For Page Number
> myPageNumber <- 0
> pageNum <- function (x) {
+   if (missing(x)) { myPageNumber <<- myPageNumber+1; return(as.character(myPageNumber)) }
+   else            { myPageNumber <<- x;              return(as.character(myPageNumber)) }
+ }
> # Create Slides
> myppt <- read_pptx("C:/temp/nds.pptx")
> mytmp <- layout_summary(myppt)[[2]][1]
> myppt <- myppt %>%
+   add_slide(layout="Title Slide", master=mytmp) %>%
+   ph_with_text(type="ctrTitle", str="ABC-XXX Phase 3 Study") %>%
+   ph_with_text(type="subTitle", str="Flash Result") %>%
+   ph_with_text(type="ftr",       str=format(Sys.Date())) %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Demographics and Baseline Characteristics") %>%
+   ph_with_flextable_at(value=DEMOG_TABLE1, left=0.5, top=1.3) %>%
+   ph_with_text(type="sldNum", str=pageNum(2)) %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Demographics and Baseline Characteristics") %>%
+   ph_with_flextable_at(value=DEMOG_TABLE2, left=0.5, top=1.3) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Cumulative Incidence of GU [FAS]") %>%
+   ph_with_gg_at(value=kmplot(T1), width=9, height=5, left=0.5, top=2) %>%
+   ph_with_ul(type="body", level_list=1, str_list=T1$pot, style=fp_text(font.size=24, color=T1$col)) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%
```

R Program (2/3)

```
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Life Table of GU [FAS]") %>%
+   ph_with_flextable_at(value=T1$table, left=0.5, top=1.3) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Cumulative Incidence of GU [PPS]") %>%
+   ph_with_gg_at(value=kmplot(T2), width=9, height=5, left=0.5, top=2) %>%
+   ph_with_ul(type="body", level_list=1, str_list=T2$pot, style=fp_text(font.size=24, color=T2$col)) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Life Table of GU [PPS]") %>%
+   ph_with_flextable_at(value=T2$table, left=0.5, top=1.3) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Cumulative Incidence of DU [FAS]") %>%
+   ph_with_gg_at(value=kmplot(T3), width=9, height=5, left=0.5, top=2) %>%
+   ph_with_ul(type="body", level_list=1, str_list=T3$pot, style=fp_text(font.size=24, color=T3$col)) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Life Table of DU [FAS]") %>%
+   ph_with_flextable_at(value=T3$table, left=0.5, top=1.3) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Proportion of GU/DU [FAS]") %>%
+   ph_with_ul(type="body", level_list=1, str_list=ADDITIONAL$pot1,
+     style=fp_text(font.size=20, color=ADDITIONAL$col1)) %>%
+   ph_add_par(type="body", level=1) %>%
+   ph_add_text(type="body", str=ADDITIONAL$pot2,
+     style=fp_text(font.size=20, color=ADDITIONAL$col2)) %>%
+   ph_with_flextable_at(value=ADDITIONAL$table1, left=0.5, top=2.4) %>%
+   ph_with_flextable_at(value=ADDITIONAL$table2, left=0.5, top=5.2) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%
```

R Program (3/3)

```
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Covariate Adjusted Analysis") %>%
+   ph_with_img_at(src="C:/temp/adj.bmp", left=0.4, top=1.1, width=9, height=6) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Subgroup Analysis") %>%
+   ph_with_img_at(src="C:/temp/sub.bmp", left=0.4, top=1.1, width=9, height=6) %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="All TEAEs") %>%
+   ph_with_img_at(src="C:/temp/teae1.bmp", left=0.4, top=1.1, width=9, height=6) %>%
+   ph_with_text(type="dt", str="TEAE: Treatment Emergent Adverse Event") %>%
+   ph_with_text(type="sldNum", str=pageNum()) %>%

+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="Drug-related TEAEs") %>%
+   ph_with_img_at(src="C:/temp/teae2.bmp", left=0.4, top=1.1, width=9, height=6) %>%
+   ph_with_text(type="dt", str="TEAE: Treatment Emergent Adverse Event") %>%
+   ph_with_text(type="sldNum", str=pageNum())

> for (i in 1:length(INT_TABLE)) {
+   myppt <- myppt %>%
+     add_slide(layout="Title and Content", master=mytmp) %>%
+     ph_with_text(type="title", str="Intensity of TEAEs") %>%
+     ph_with_flextable_at(value=INT_TABLE[[i]], left=0.5, top=1.3) %>%
+     ph_with_text(type="dt", str="TEAE: Treatment Emergent Adverse Event") %>%
+     ph_with_text(type="sldNum", str=pageNum())
+ }

> myppt <- myppt %>%
+   add_slide(layout="Title and Content", master=mytmp) %>%
+   ph_with_text(type="title", str="SAEs") %>%
+   ph_with_img_at(src="C:/temp/teae3.bmp", left=0.4, top=1.1, width=9, height=6) %>%
+   ph_with_text(type="sldNum", str=pageNum())
> print(myppt, target="c:/temp/result.pptx")
```

Output Slides (1/5)

ABC-XXX Phase 3 Study

Flash Result

2018-04-17

Demographics and Baseline Characteristics

Variable	Group	N	Mean	S.D.	Min.	Q1	Median	Q3	Max.
Age (years)	ABC-XXX	100	53.5	14.47	30.000	40.00	53.500	66.00	79.000
	Placebo	100	53.5	14.52	30.000	40.00	53.000	66.25	79.000
	Total	200	53.5	14.46	30.000	40.00	53.000	66.00	79.000
BMI (kg/m^2)	ABC-XXX	100	27.26	5.590	18.000	22.575	26.950	32.100	37.400
	Placebo	100	27.77	5.701	18.200	22.700	27.850	33.200	37.800
	Total	200	27.51	5.637	18.000	22.675	27.500	32.450	37.800

2

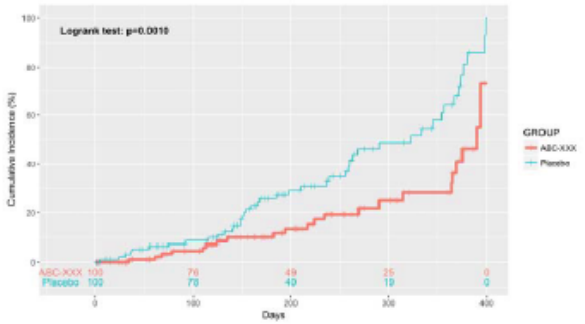
Demographics and Baseline Characteristics

Variable	Category	ABC-XXX [n=100]	Placebo [n=100]	Total [n=200]
Age (years)	Min<= - <65	72 (72.0)	70 (70.0)	142
	65<= - <=Max	28 (28.0)	30 (30.0)	58
Alcohol Consumption	Yes	31 (31.0)	24 (24.0)	55
	No	69 (69.0)	76 (76.0)	145
BMI (kg/m^2)	Min<= - <25.0	39 (39.0)	37 (37.0)	76
	25.0<= - <=Max	61 (61.0)	63 (63.0)	124
Caffeine Consumption	Yes	38 (38.0)	32 (32.0)	70
	No	62 (62.0)	68 (68.0)	130
H. pylori Infection	Positive	46 (46.0)	45 (45.0)	91
	Negative	54 (54.0)	55 (55.0)	109
Gender	Male	52 (52.0)	61 (61.0)	113
	Female	48 (48.0)	39 (39.0)	87
Tobacco Consumption	Yes	18 (18.0)	21 (21.0)	39
	No	82 (82.0)	79 (79.0)	161

3

Cumulative Incidence of GU [FAS]

- Superiority of ABC-XXX to Placebo was confirmed.



4

Output Slides (2/5)

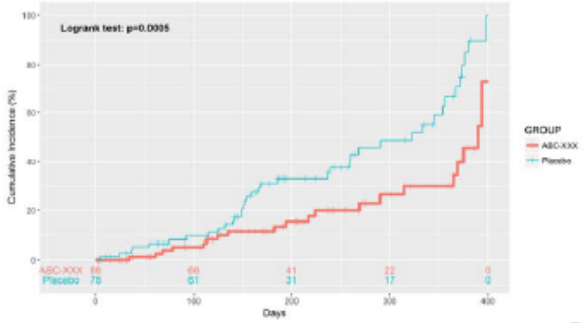
Life Table of GU [FAS]

Group	Time	At Risk	Event	Censor	%	95% CI	
						Lower	Upper
ABC-XXX	0	100	0	0	0.0	0.0	0.0
	100	76	4	20	4.6	0.2	9.0
	200	49	10	41	13.4	5.5	21.3
	300	25	15	60	24.9	13.1	36.7
	400	0	23	77	73.2	49.9	96.5
Placebo	0	100	0	0	0.0	0.0	0.0
	100	78	8	14	8.7	2.9	14.4
	200	40	23	37	29.0	18.8	39.2
	300	19	32	49	49.0	35.5	62.4
	400	0	44	56	100.0	100.0	100.0

5

Cumulative Incidence of GU [PPS]

- Superiority of ABC-XXX to Placebo was confirmed.



6

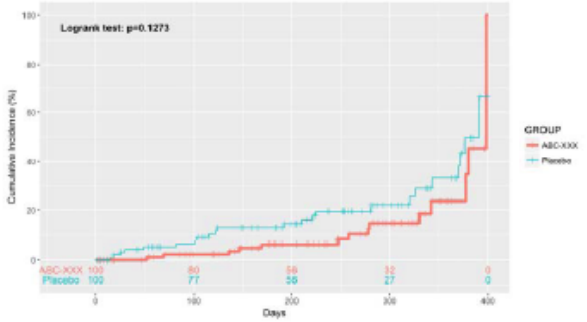
Life Table of GU [PPS]

Group	Time	At Risk	Event	Censor	%	95% CI	
						Lower	Upper
ABC-XXX	0	88	0	0	0.0	0.0	0.0
	100	66	4	18	5.3	0.2	10.3
	200	41	10	37	15.4	6.4	24.4
	300	22	14	52	26.4	13.5	39.2
	400	0	21	67	72.9	49.1	96.6
Placebo	0	78	0	0	0.0	0.0	0.0
	100	61	7	10	9.7	2.9	16.5
	200	31	21	26	32.7	21.1	44.4
	300	17	27	34	46.9	34.5	63.4
	400	0	38	40	100.0	100.0	100.0

7

Cumulative Incidence of DU [FAS]

- Superiority of ABC-XXX to Placebo was not confirmed.



8

Output Slides (3/5)

Life Table of DU [FAS]

Group	Time	At Risk	Event	Censor	%	95% CI Lower	95% CI Upper
ABC-XXX	0	100	0	0	0.0	0.0	0.0
	100	80	2	18	2.2	0.0	5.3
	200	56	5	39	6.3	0.9	11.8
	300	32	9	59	14.7	5.4	24.0
	400	0	14	86	100.0	100.0	100.0
Placebo	0	100	0	0	0.0	0.0	0.0
	100	77	6	17	6.6	1.5	11.6
	200	56	12	32	14.4	6.8	22.0
	300	27	16	57	22.1	12.0	32.2
	400	0	23	77	66.4	36.5	96.3

9

Proportion of GU/DU [FAS]

- The difference in proportions of GU was statistically significant.
- The difference in proportions of DU was not statistically significant.

Test	Group	Yes (%)	No	Total	95% CI Lower	95% CI Upper
GU	ABC-XXX	23 (23.0)	77	100	15.2	32.8
	Placebo	44 (44.0)	56	100	34.1	54.3
DU	ABC-XXX	14 (14.0)	86	100	7.9	22.4
	Placebo	23 (23.0)	77	100	15.2	32.5

Test	Group	Diff.	95% CI Lower	95% CI Upper	Chi-square Test Chisq.	DF	p-value
GU	ABC-XXX - Placebo	-21.0	-33.8	-8.2	8.978	1	0.0027
DU	ABC-XXX - Placebo	-9.0	-19.7	1.7	2.122	1	0.1452

10

Covariate Adjusted Analysis

Covariate	HR	95% LCL	95% UCL
Overall	0.44	0.26	0.73
Age	0.44	0.26	0.73
Gender	0.43	0.26	0.73
BMI	0.45	0.27	0.75
H. pylori Infection	0.44	0.26	0.73
Caffeine Consumption	0.44	0.26	0.73
Alcohol Consumption	0.43	0.26	0.72
Tobacco Consumption	0.44	0.26	0.73

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Subgroup Analysis

Subgroup	Category	HR	95% LCL	95% UCL
Overall		0.44	0.26	0.73
Age	Min<= - <65	0.42	0.23	0.76
Age	65<= - <=Max	0.55	0.21	1.46
Gender	Male	0.32	0.14	0.7
Gender	Female	0.59	0.29	1.24
BMI	Min<= - <25	0.25	0.09	0.69
BMI	25<= - <=Max	0.49	0.26	0.93
H. pylori Infection	Positive	0.44	0.21	0.92
H. pylori Infection	Negative	0.39	0.19	0.83
Caffeine Consumption	Yes	0.44	0.18	1.08
Caffeine Consumption	No	0.41	0.22	0.77
Alcohol Consumption	Yes	0.61	0.25	1.49
Alcohol Consumption	No	0.33	0.17	0.65
Tobacco Consumption	Yes	0.14	0.03	0.63
Tobacco Consumption	No	0.55	0.31	0.98

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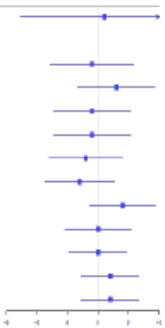
Output Slides (4/5)

All TEAEs

PT Name	ABC-XXX n (%)	Placebo n (%)	Difference
Subjects with Any TEAEs	43 (43.0)	42 (42.0)	1.0%
HEADACHE	6 (6.0)	7 (7.0)	-1.0%
CONSTIPATION	7 (7.0)	4 (4.0)	3.0%
SWELLING FACE	5 (5.0)	6 (6.0)	-1.0%
VOMITING	5 (5.0)	6 (6.0)	-1.0%
ABDOMINAL PAIN	4 (4.0)	6 (6.0)	-2.0%
LIVER FUNCTION TEST ABNORMAL	3 (3.0)	6 (6.0)	-3.0%
ARRHYTHMIA	6 (6.0)	2 (2.0)	4.0%
NAUSEA	4 (4.0)	4 (4.0)	0.0%
DIZZINESS	3 (3.0)	3 (3.0)	0.0%
INFLUENZA	4 (4.0)	2 (2.0)	2.0%
UPPER RESPIRATORY TRACT INFECTION	4 (4.0)	2 (2.0)	2.0%

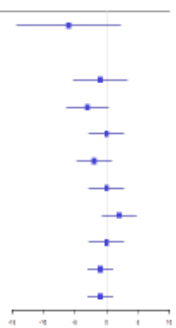


TEAE: Treatment Emergent Adverse Event

13

Drug-related TEAEs

PT Name	ABC-XXX n (%)	Placebo n (%)	Difference
Subjects with Any TEAEs	7 (7.0)	13 (13.0)	-6.0%
ABDOMINAL PAIN	2 (2.0)	3 (3.0)	-1.0%
LIVER FUNCTION TEST ABNORMAL	0 (0.0)	3 (3.0)	-3.0%
ARRHYTHMIA	1 (1.0)	1 (1.0)	0.0%
DIZZINESS	0 (0.0)	2 (2.0)	-2.0%
HEADACHE	1 (1.0)	1 (1.0)	0.0%
INFLUENZA	2 (2.0)	0 (0.0)	2.0%
NAUSEA	1 (1.0)	1 (1.0)	0.0%
CONSTIPATION	0 (0.0)	1 (1.0)	-1.0%
VOMITING	0 (0.0)	1 (1.0)	-1.0%



TEAE: Treatment Emergent Adverse Event

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Intensity of TEAEs

PT Name	Intensity	ABC-XXX [n=100]	Placebo [n=100]
Subjects with Any TEAEs	Overall	43 (43.0)	42 (42.0)
	Mild	23 (23.0)	21 (21.0)
	Moderate	15 (15.0)	19 (19.0)
	Severe	5 (5.0)	2 (2.0)
HEADACHE	Overall	6 (6.0)	7 (7.0)
	Mild	4 (4.0)	3 (3.0)
	Moderate	1 (1.0)	4 (4.0)
	Severe	1 (1.0)	0 (0.0)
CONSTIPATION	Overall	7 (7.0)	4 (4.0)
	Mild	5 (5.0)	3 (3.0)
	Moderate	1 (1.0)	1 (1.0)
	Severe	1 (1.0)	0 (0.0)
SWELLING FACE	Overall	5 (5.0)	6 (6.0)
	Mild	2 (2.0)	4 (4.0)
	Moderate	2 (2.0)	2 (2.0)
	Severe	1 (1.0)	0 (0.0)
VOMITING	Overall	5 (5.0)	6 (6.0)
	Mild	1 (1.0)	4 (4.0)
	Moderate	3 (3.0)	2 (2.0)
	Severe	1 (1.0)	0 (0.0)

TEAE: Treatment Emergent Adverse Event

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Intensity of TEAEs

PT Name	Intensity	ABC-XXX [n=100]	Placebo [n=100]
Subjects with Any TEAEs	Overall	43 (43.0)	42 (42.0)
	Mild	23 (23.0)	21 (21.0)
	Moderate	15 (15.0)	19 (19.0)
	Severe	5 (5.0)	2 (2.0)
ABDOMINAL PAIN	Overall	4 (4.0)	6 (6.0)
	Mild	3 (3.0)	4 (4.0)
	Moderate	1 (1.0)	1 (1.0)
	Severe	0 (0.0)	1 (1.0)
LIVER FUNCTION TEST ABNORMAL	Overall	3 (3.0)	6 (6.0)
	Mild	1 (1.0)	2 (2.0)
	Moderate	1 (1.0)	3 (3.0)
	Severe	1 (1.0)	1 (1.0)
ARRHYTHMIA	Overall	6 (6.0)	2 (2.0)
	Mild	5 (5.0)	0 (0.0)
	Moderate	1 (1.0)	2 (2.0)
	Severe	0 (0.0)	0 (0.0)
NAUSEA	Overall	4 (4.0)	4 (4.0)
	Mild	3 (3.0)	3 (3.0)
	Moderate	1 (1.0)	1 (1.0)
	Severe	0 (0.0)	0 (0.0)

TEAE: Treatment Emergent Adverse Event

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Output Slides (5/5)

Intensity of TEAEs

PT Name	Intensity	ABC-XXX [n=100]	Placebo [n=100]
Subjects with Any TEAEs	Overall	43 (43.0)	42 (42.0)
	Mild	23 (23.0)	21 (21.0)
	Moderate	15 (15.0)	19 (19.0)
	Severe	5 (5.0)	2 (2.0)
DIZZINESS	Overall	3 (3.0)	3 (3.0)
	Mild	2 (2.0)	1 (1.0)
	Moderate	1 (1.0)	2 (2.0)
	Severe	0 (0.0)	0 (0.0)
INFLUENZA	Overall	4 (4.0)	2 (2.0)
	Mild	1 (1.0)	1 (1.0)
	Moderate	3 (3.0)	1 (1.0)
	Severe	0 (0.0)	0 (0.0)
UPPER RESPIRATORY TRACT INFECTION	Overall	4 (4.0)	2 (2.0)
	Mild	1 (1.0)	2 (2.0)
	Moderate	2 (2.0)	0 (0.0)
	Severe	1 (1.0)	0 (0.0)

TEAE: Treatment Emergent Adverse Event

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SAEs

PT Name	ABC-XXX n (%)	Placebo n (%)	Difference
Subjects with Any TEAEs	4 (4.0)	1 (1.0)	3.0%
NAUSEA	1 (1.0)	1 (1.0)	0.0%
ARRHYTHMIA	1 (1.0)	0 (0.0)	1.0%
DIZZINESS	1 (1.0)	0 (0.0)	1.0%
VOMITING	1 (1.0)	0 (0.0)	1.0%

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MENU

- Introduction
- Procedures
- Details
  - ✓ Add Texts
  - ✓ Add Figures
  - ✓ Add Tables
  - ✓ Miscellaneous
- Example:

  Automated Generation of PowerPoint Presentations from CDISC/ADaM Datasets

References

- **The R Project**
  https://www.r-project.org/

- **officer by David Gohel**
  CRAN: https://cran.r-project.org/web/packages/officer/index.html
  Github: https://davidgohel.github.io/officer/index.html

- **flextable by David Gohel**
  CRAN: https://cran.r-project.org/web/packages/flextable/index.html
  Github: https://davidgohel.github.io/flextable/index.html

- **ReporteRs by David Gohel**
  CRAN: https://cran.r-project.org/web/packages/ReporteRs/index.html
  Github: http://davidgohel.github.io/ReporteRs/index.html

- **Crafting a PowerPoint Presentation with R by Len Kiefer**
  http://lenkiefer.com/2017/09/23/crafting-a-powerpoint-presentation-with-r/

- **Analysis Data Model Implementation Guide Version 1.1**
  https://www.cdisc.org/standards/foundational/adam

Thank you for your attention!

Takeda Pharmaceutical Company, Ltd.