

autoslideR: an R package for slide automation

Joe Zhu¹, Bo Ci², Heng Wang², Chenkai Lv¹, Yinqi Zhao², Liming Li¹

¹PD Data sciences, Roche Shanghai

²PD Data Sciences, Genentech|Roche, South San Francisco

Abstract

As the pharmaceutical industry is becoming fast-paced and data-driven, the demand for effective presentations with a slide deck has significantly increased. The normal process of developing slides includes manually populating numbers from SAS outputs and a separate QC. The process is time-consuming, resource-intensive and error-prone. To address these issues, we created an R package, namely autoslideR, to automate the normal process of slide generation. autoslideR features a list of standard slide templates tailored for Study Results Endorsement Plan (SREP) presentation while preserving flexibility for user-customizable outputs as well as visual elements (e.g. theme). autoslideR is a compelling tool offering improved accuracy and efficiency for slide deck generation, streamlined outputs and seamless collaboration between biostatisticians and programmers.

Motivation

At Roche, BioStats give a Study Results Endorsement Plan (SREP) presentation to the senior leadership team shortly after readout of a PhIII trial for a decision of filing or not. Thus, the preparation of the SREP deck requires high quality and speed. The normal process of creating SREP deck is that BioStats manually type in the numbers from SAS outputs and a separate BioStat QCs the populated numbers. This process is time consuming, resource intensive, and error prone. Automatic slide generation is a solution to address these issues. There are a few advantages of using slide automation:

- Reduce the amount of efforts and time required when creating slides
- Reduce the risk of errors from manually typing or copying numbers from the output to slides
- Avoid unnecessary stress when creating large amounts of slide decks in a short time window, especially before SREP

Our approach

In light of the above, we have created an R package, namely “autoslideR” to automate the SREP deck creation from a set of standard (commonly used) oncology trial slide templates.

This package includes two main components:

1. Helper functions to pre-process ADaM datasets ready for the slide-generation functions
2. Slide-generation functions to produce slides varying from disposition, demographic, safety to efficacy (oncology for now).

Examples of slide templates were shown below.

Demographic table

Patient Demographics and Baseline Characteristics, Full Analysis Set



	A: Drug X (N=134)	B: Placebo (N=134)	C: Combination (N=132)	All Patients (N=400)
Sex				
F	79 (59%)	82 (61.2%)	70 (53%)	231 (57.8%)
M	55 (41%)	52 (38.8%)	62 (47%)	169 (42.2%)
Age				
Median	33.00	35.00	35.00	34.00
Min - Max	21.0 - 50.0	21.0 - 62.0	20.0 - 69.0	20.0 - 69.0
Race				
ASIAN	68 (50.7%)	67 (50%)	73 (55.3%)	208 (52%)
BLACK OR AFRICAN AMERICAN	31 (23.1%)	28 (20.9%)	32 (24.2%)	91 (22.8%)
WHITE	27 (20.1%)	26 (19.4%)	21 (15.9%)	74 (18.5%)
AMERICAN INDIAN OR ALASKA NATIVE	8 (6%)	11 (8.2%)	6 (4.5%)	25 (6.2%)
MULTIPLE	0	1 (0.7%)	0	1 (0.2%)

t_dm_slide footnote;

Patient Disposition, Full Analysis Set



	A: Drug X (N=134)	B: Placebo (N=134)	C: Combination (N=132)	All Patients (N=400)
Received Treatment	134 (100.00%)	134 (100.00%)	132 (100.00%)	400 (100.00%)
On-study Status	0 (0.0%)	2 (1.5%)	2 (1.5%)	4 (1.0%)
On Treatment	0	0	0	0
In Follow-up	0	2 (1.5%)	2 (1.5%)	4 (1%)
Discontinued the study	42 (31.3%)	40 (29.9%)	38 (28.8%)	120 (30.0%)
Adverse Event	3 (2.2%)	6 (4.5%)	5 (3.8%)	14 (3.5%)
Death	25 (18.7%)	23 (17.2%)	22 (16.7%)	70 (17.5%)
Lack Of Efficacy	2 (1.5%)	2 (1.5%)	3 (2.3%)	7 (1.8%)
Physician Decision	2 (1.5%)	3 (2.2%)	2 (1.5%)	7 (1.8%)
Protocol Violation	5 (3.7%)	3 (2.2%)	4 (3%)	12 (3%)
Withdrawal By Parent/Guardian	4 (3%)	2 (1.5%)	1 (0.8%)	7 (1.8%)
Withdrawal By Subject	1 (0.7%)	1 (0.7%)	1 (0.8%)	3 (0.8%)

t_ds footnotes:

Time to Event Summary

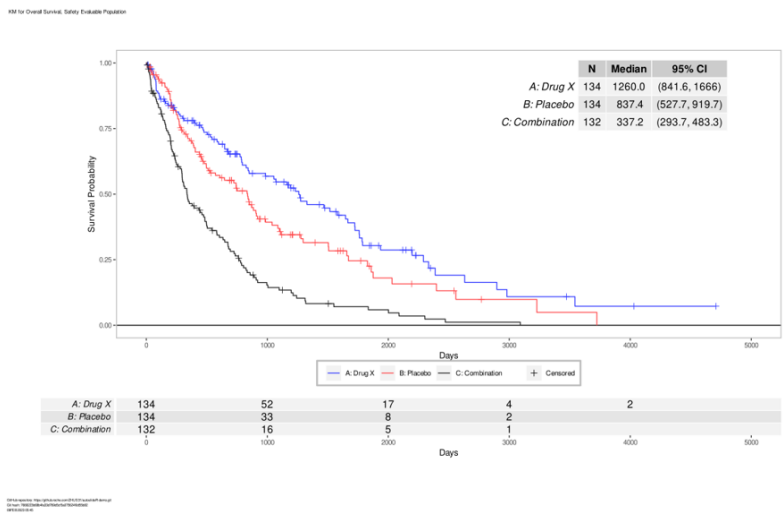
Time to Event Summary for Progression Free Survival by Investigator, Full Analysis Set



	B: Placebo (N=134)	A: Drug X (N=134)	C: Combination (N=132)
Patients with event (%)	90 (67.2%)	86 (64.2%)	92 (69.7%)
Median (mon, 95% CI)	19.7 (13.3, 25.2)	16.9 (12.8, 19)	12.3 (8.4, 14.9)
Stratified HR (95% CI)		1.04 (0.77, 1.41)	1.42 (1.05, 1.93)
p-value (log-rank)		0.8068	0.0239
6 mon event free rate (%)	77.8	77.3	67.7
95% CI	(70.59, 85.10)	(69.83, 84.71)	(59.42, 75.99)
12 mon event free rate (%)	62.7	62.8	50.2
95% CI	(53.97, 71.42)	(54.04, 71.63)	(41.00, 59.32)

Kaplan–Meier (KM) plot

KM for Overall Survival, Safety Evaluable Population



Objective Response Rate (ORR) table

ORR table



	A: Drug X	B: Placebo	C: Combination
	(N=134)	(N=134)	(N=132)
ORR (%)	100 (74.6%)	84 (62.7%)	81 (61.4%)
95% CI (Wilson, without correction)	(66.2, 81.6)	(53.9, 70.8)	(52.5, 69.6)
CR (%)	60 (44.8%)	47 (35.1%)	57 (43.2%)
PR (%)	40 (29.9%)	37 (27.6%)	24 (18.2%)
SD (%)	9 (6.7%)	22 (16.4%)	13 (9.8%)
PD (%)	24 (17.9%)	16 (11.9%)	33 (25%)
ORR difference		-11.94	-13.26

95% CI (Wilson, without correction)
t_orr_slide footnotes;

Most Common AEs with System Organ Class with Incidence Rate of at Least 10%

Most Common AEs (Incidence Rate of at Least 10%), Safety Evaluable Population (cont.)

MedDRA System Organ Class	A: Drug X	B: Placebo	C: Combination
MedDRA Preferred Term N (%)	(N=134)	(N=134)	(N=132)
cl C.2			
dcd C.2.1.2.1	28 (20.9%)	36 (26.9%)	48 (36.4%)
cl D.1			
dcd D.1.1.1.1	42 (31.3%)	32 (23.9%)	46 (34.8%)
dcd D.1.1.4.2	38 (28.4%)	34 (25.4%)	40 (30.3%)
cl D.2			
dcd D.2.1.5.3	37 (27.6%)	46 (34.3%)	50 (37.9%)

t_ae_pt_soc_slide footnote

Most Common AEs with System Organ Class with Incidence Rate of at Least 10% (with a different slide theme)

Most Common AEs (Incidence Rate of at Least 10%), Safety Evaluable Population (cont.)

MedDRA System Organ Class	A: Drug X	B: Placebo	C: Combination
MedDRA Preferred Term N (%)	(N=134)	(N=134)	(N=132)
cl C.2			
dcd C.2.1.2.1	28 (20.9%)	36 (26.9%)	48 (36.4%)
cl D.1			
dcd D.1.1.1.1	42 (31.3%)	32 (23.9%)	46 (34.8%)
dcd D.1.1.4.2	38 (28.4%)	34 (25.4%)	40 (30.3%)
cl D.2			
dcd D.2.1.5.3	37 (27.6%)	46 (34.3%)	50 (37.9%)

t_ae_pt_soc_slide footnote

To create a slide, the users need to have the following three files:

1. A **filter** yaml file to clarify the filters to be used in the slide-generation process, e.g. filters of safety evaluable population and overall survival parameter in the adtte.
2. A **specification** yaml file to clarify the requirements of each slide, e.g. the title, the table template to use, the treatment groups to involve and the filters.
3. An R file to pre-process datasets and call the specification yaml file to produce the desired sides.

For all the above three files, we have prepared example files that users could start with for their own projects.

Technical advantage

The autoslideR has a relatively mature machinery to render powerpoints - converting a rtable [Becker G, Waddell A (2023)] object to flextable object and then to powerpoint. The process is independent from the built-in standard templates. This means that the users can create their customized templates to fit various needs of their projects following the workflow. Moreover, these new templates could be incorporated into the package template library as a community effort to expand the capability of autoslideR.

Next steps and future uses

So far, the package mainly focuses on key slides of the oncology SREP deck, but we have been working with study teams to expand features to enable more slide templates (e.g. concordance analysis and summary of non-protocol therapies) and promote it to broader indications (e.g. neuroscience).

We would like to vision this package to become a part of the next-generation tools to support future SREP presentations and facilitate the slide generation of other decision making meetings.

Reference

Becker G, Waddell A (2023). `_rtables: Reporting Tables_`. R package version 0.6.1, <<https://CRAN.R-project.org/package=rtables>>

Zhu J, Sabanés Bové D, Stoilova J, Wang H, Collin F, Waddell A, Rucki P, Liao C, Li J (2023). `_tern: Create Common TLGs Used in Clinical Trials_`. R package version 0.8.4, <<https://CRAN.R-project.org/package=tern>>

Contact information

Joe Zhu
Roche
joe.zhu@roche.com

Bo Ci
Genentech
cib1@gene.com

Heng Wang
Genentech
wang.heng@gene.com

Chenkai Lv
Roche
chenkai.lv@roche.com

Yinqi Zhao
Genentech
zhaoy143@gene.com

Liming Li
Roche
liming.li@roche.com