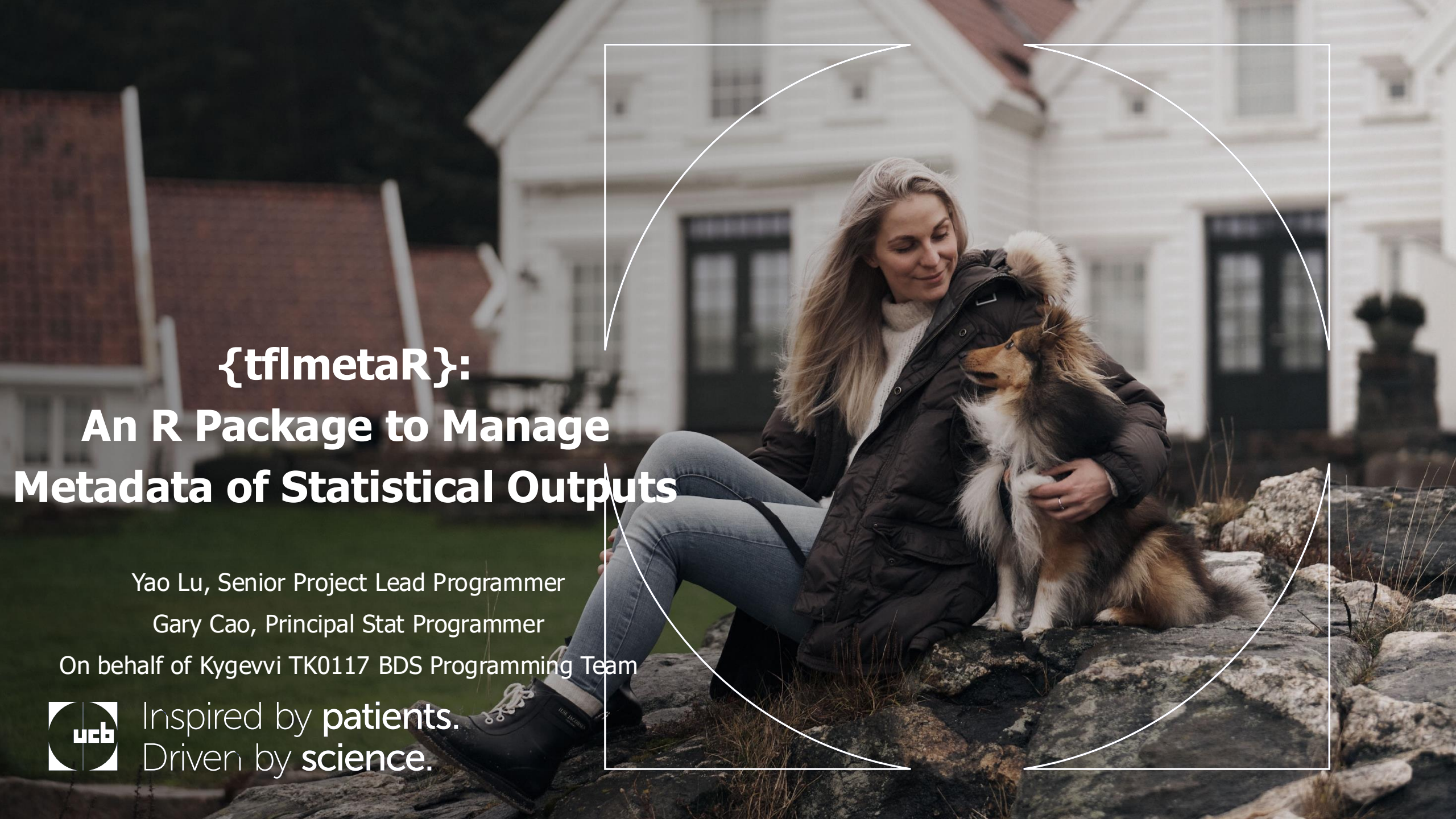




# **{tflmetaR}:** **An R Package to Manage Metadata of Statistical Outputs**

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Gary Cao, Principal Stat Programmer

On behalf of Kygevi TK0117 BDS Programming Team



Inspired by **patients.**  
Driven by **science.**

## Agenda

1. Why `{tflmetaR}` Package?
2. How to Use It
3. Examples
4. Integration With `{gridify}`
5. Conclusion



# Challenge: **R Code Mixed with Titles/Footers**

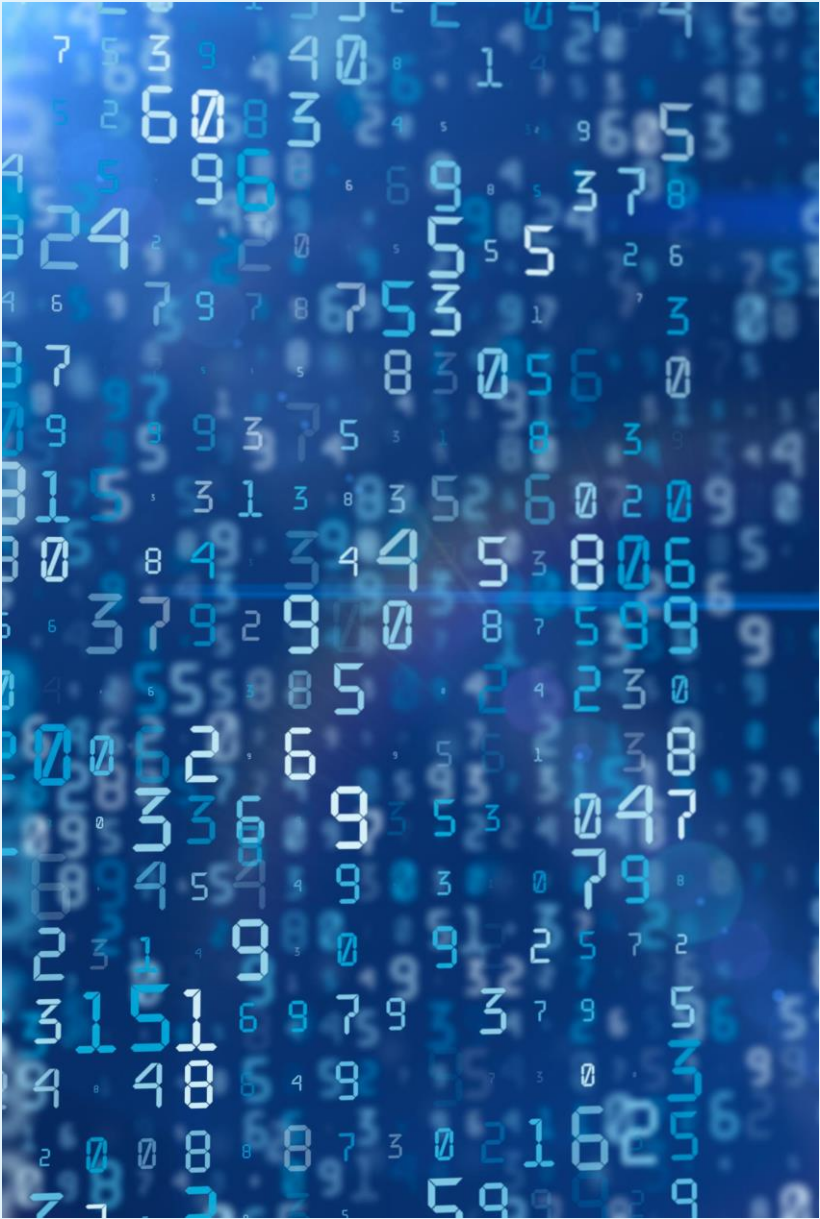
## Mixing Data Analysis Programs with Titles And Footers Metadata

```
# Analysis code
model <- lm(y ~ trt + cov1, data = adfa)
result <- summary(model)

# Hardcoded title and footnote (anti-pattern)
title <- 'Table 1: Primary Endpoint Model Summary'
footnote <- 'Note: Full analysis set; Source: Study ABC-123'

print(result)
```

- **Reduces readability and maintainability**
- **Makes updates harder because you have to edit multiple scripts**
- **Breaks the principle of separating code from metadata.**



# Problems Caused by Hardcoding Metadata in R Scripts

## Embedded Text

Hardcoding metadata mixes formatting with logic, reducing code readability and clarity.

## Maintainability

Manual updates to hardcoded metadata increase errors and inconsistencies across multiple scripts.

## Scalability and Reusability

Hardcoded metadata limits code reuse, requiring duplication and edits for new projects.



**{tflmetaR}**

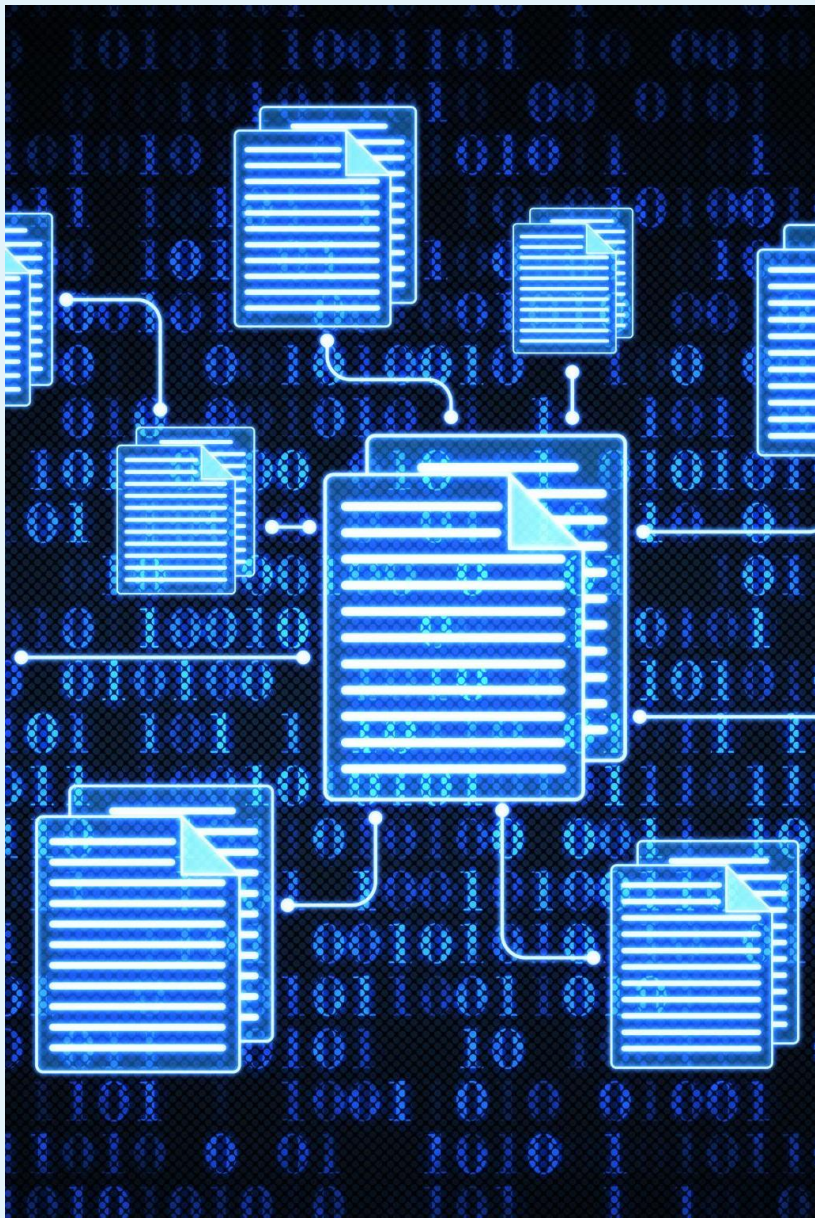


**has been inspired by the UCB SAS title macro, and was developed by the TK0117 BDS programming team to address these challenges in R programming.**



Inspired by **patients.**  
Driven by **science.**

{tflmetaR} R Package



# How {tflmetaR} Centralizes Metadata Management

## Separation of Metadata and Logic

{tflmetaR} separates metadata like titles and footnotes from analysis code, enhancing clarity and maintainability.

## Centralized Metadata Control and Single Source of Truth

All metadata is stored centrally, allowing easy and consistent updates across tables, listings, and figures.

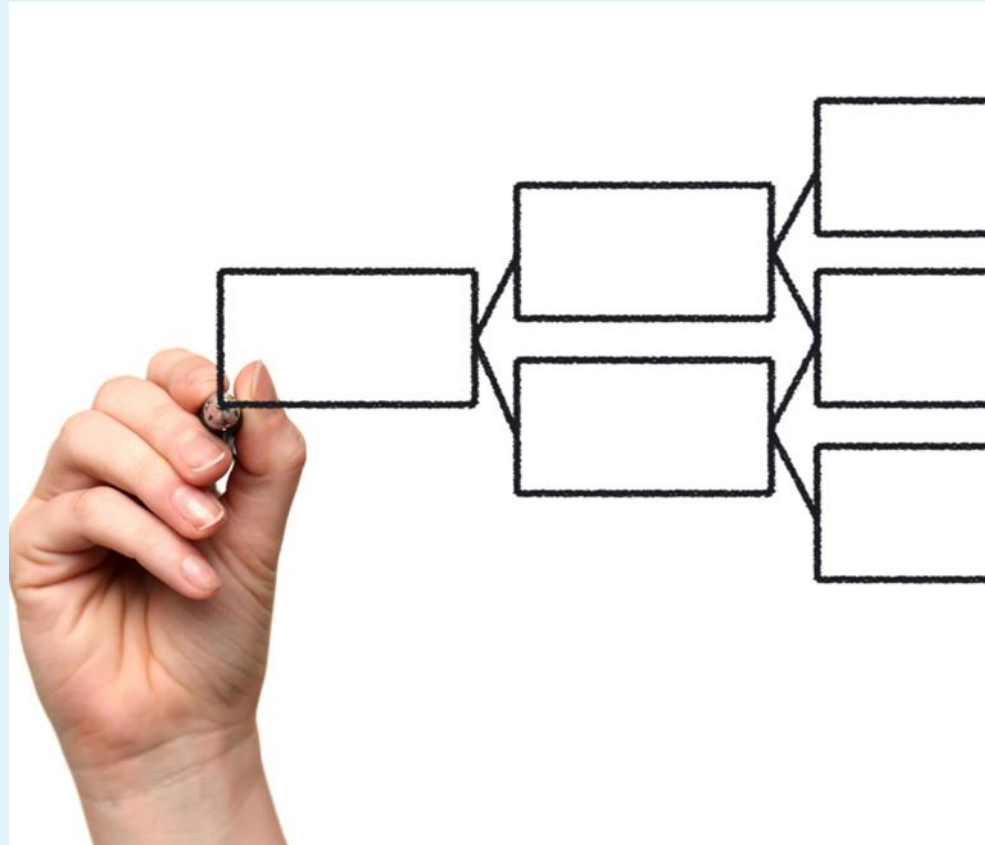
## Improved Efficiency and Metadata Version Control

The package reduces code duplication, minimizes errors, and ensures compliance with reporting standards.

## Integration with Pharmaverse Tools

{tflmetaR} works seamlessly with virtually all table and figure packages, e.g., Pharmaverse tools like {gridify}, supporting efficient workflows for clinical deliverables.

# {tflmetaR} in TFLs/TLGs R Scripts



## Metadata Loading

Load structured metadata file using `read_tfile()` function to access study output metadata information.

## Metadata Selection

Select relevant metadata entry for each output using unique identifiers like program name with oid or TFL number.

## Annotation Application

{tflmetaR} works with virtually all tables and figures packages and automatically applies titles, footnotes, and headers based on selected metadata.

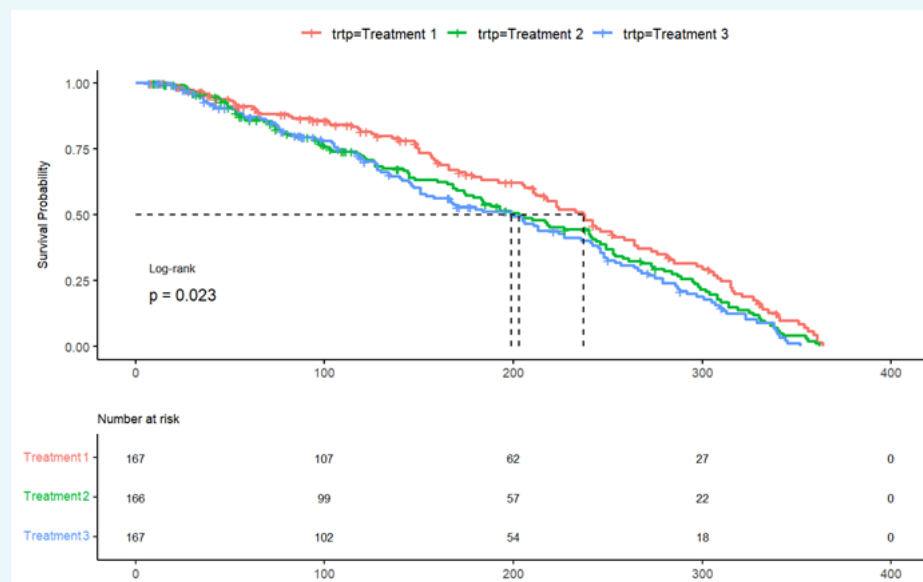
## Efficient Content Updates

Updating output annotation content is easy by editing metadata, avoiding changes in analytical code.

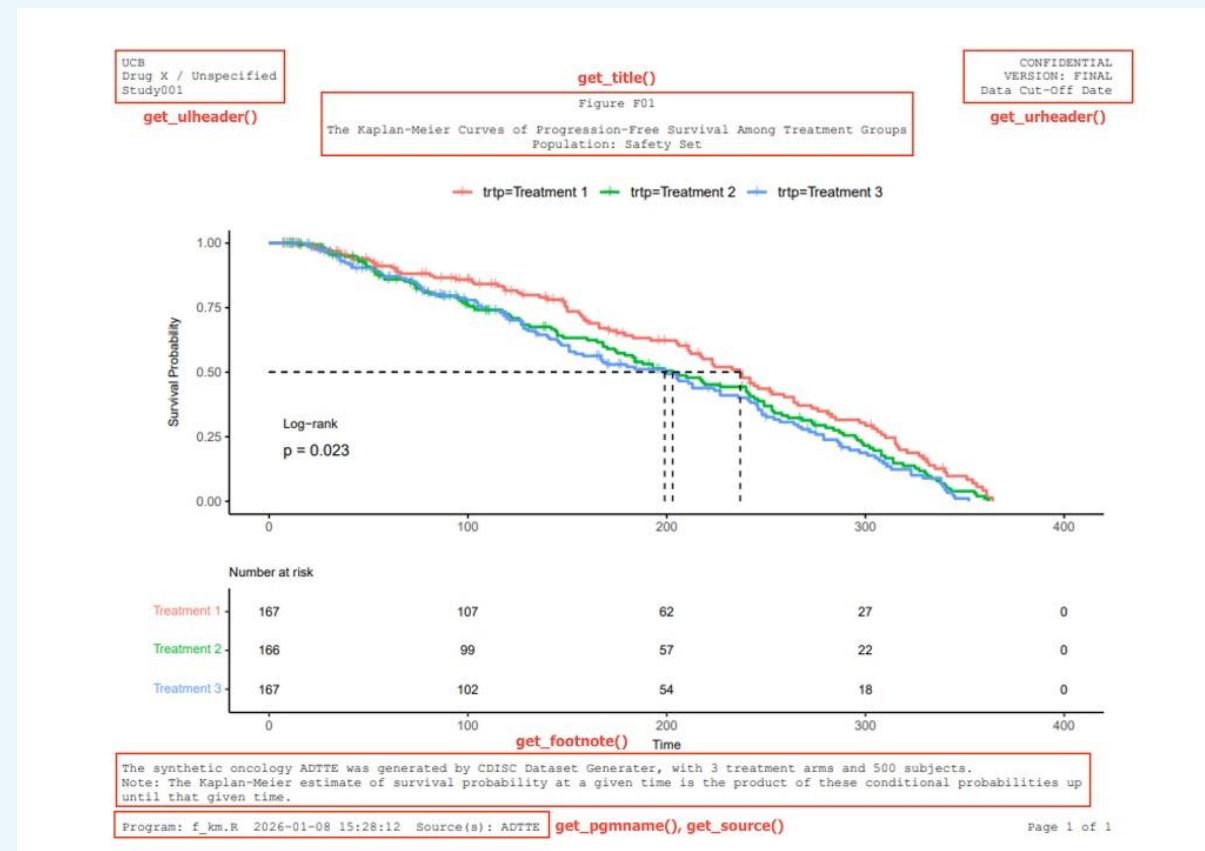
# Example: How to Use {tflmetaR}

- Design Principle: make the package small, flexible, and easy to use
- Shown below a figure annotation example
- Table annotation similar

Before annotation

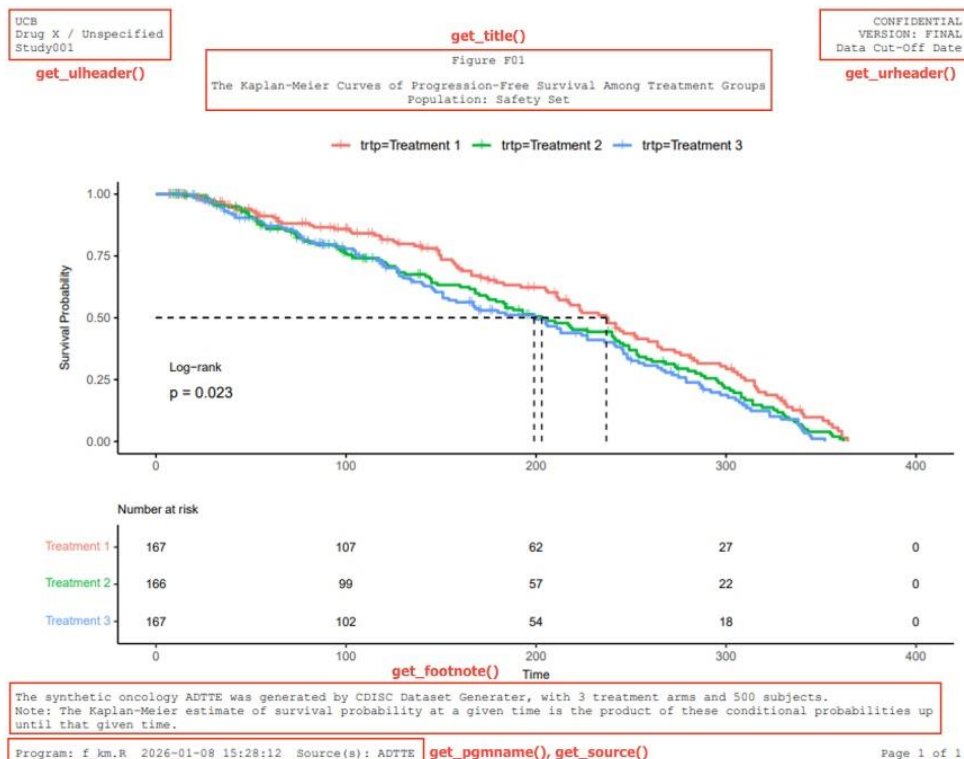


A K-M plot generated with CDISC synthetic ADTTE of oncology by {survival} and {survminer} packages



# Example: How to Use {tflmetaR} – cont'd

## Mapping of functions to annotations:



```
# read headers, titles, and footnotes excel spreadsheet
```

```
file_name <- file.path("../inst/extdata", "st_titles.xls") #titles and footer file  
title_file <- tflmetaR::read_tfile(filename = file_name, sheetname = "Sheet1")  
header_file <- tflmetaR::read_tfile(filename = file_name, sheetname = "Headr")
```

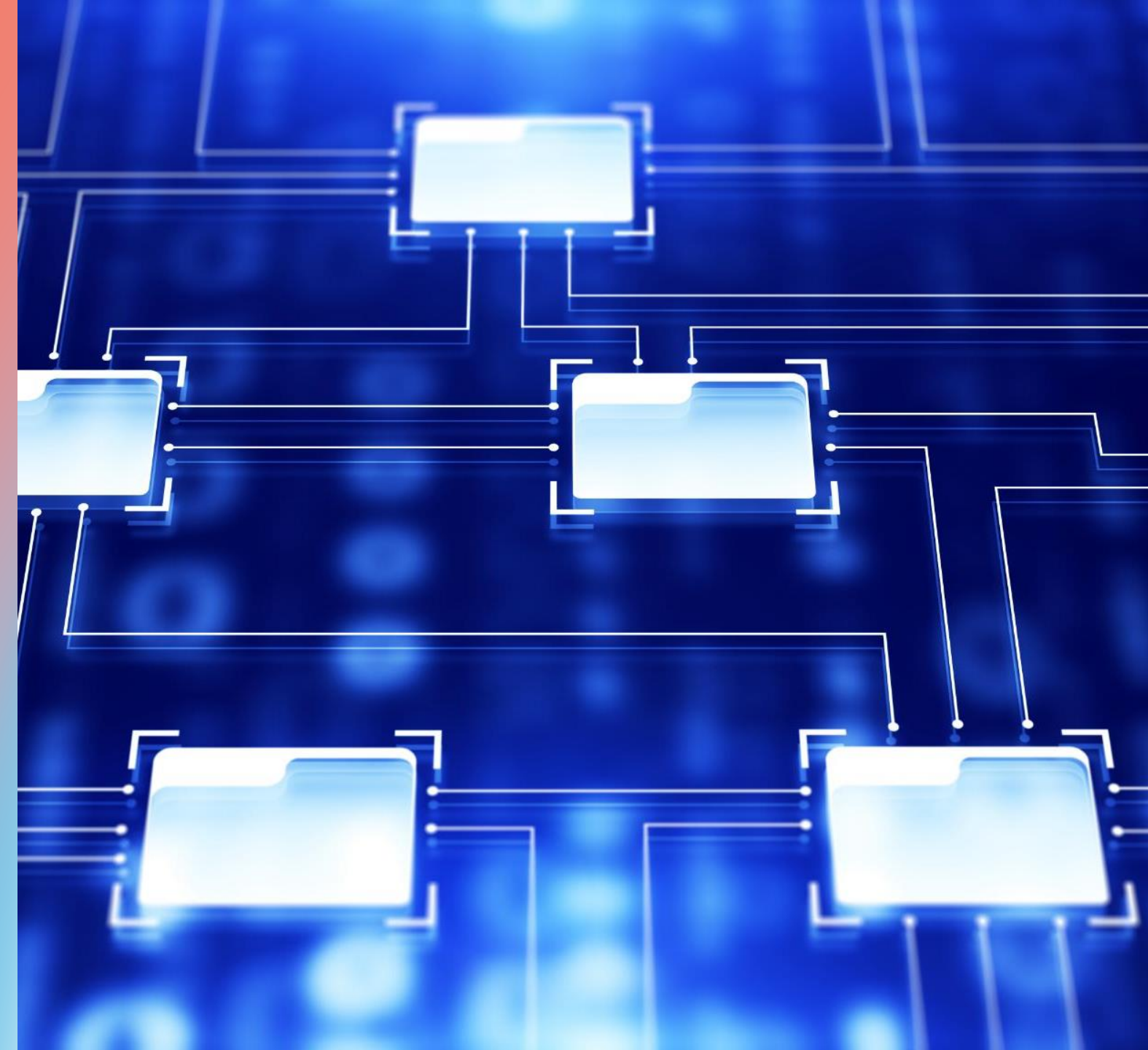
```
fig_number <- "Figure F01" #target table or figure number
```

```
ulheader <- tflmetaR::get_ulheader(header_file)[1, ]  
urheader <- tflmetaR::get_urheader(header_file)[1, ]  
titles <- tflmetaR::get_title(title_file, tnumber = fig_number)  
footnotes <- tflmetaR::get_footnote(title_file, tnumber = fig_number, add_footr_tstamp = FALSE)  
pgmname <- tflmetaR::get_pgmname(title_file, tnumber = fig_number)  
source <- tflmetaR::get_source(title_file, tnumber = fig_number)
```

```
# convert footnote list to string  
footnote_str <- paste(unlist(footnotes), collapse = "\n")
```

### Note:

- All functions return a list by default
- Multiple footers can be pasted together into a string
- Or referred to as individual element of the list



# Integration of {tflmetaR} with {gridify}

## Metadata-Driven Annotations

{tflmetaR} generates annotated components like titles, headers, and footnotes based on metadata repertoire.

## Grid-Based Layout Handling

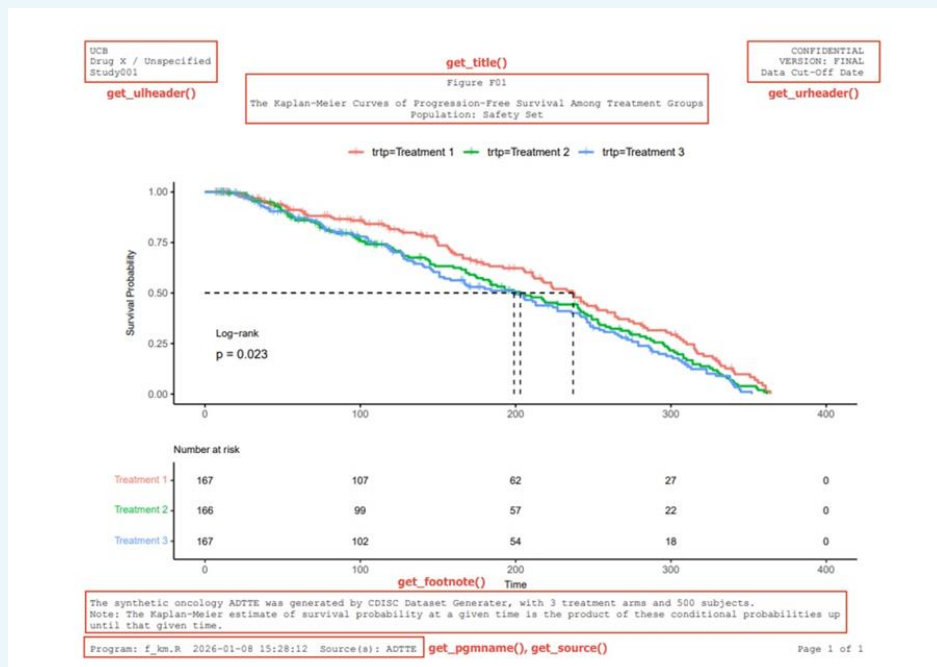
{gridify} arranges annotated components into a precise grid ensuring alignment and pagination consistency.

## Modular Integration Benefits

The modular approach supports flexible design and reproducible, scalable clinical reporting outputs.

# Integration With {gridify} Example

- {tflmetaR} and {gridify} work seamlessly together
- Code is easy to maintain and extend
- Management of annotation text become easier
- Ready for automation and standardization



```
# --- Annotate K-M plot with the titles and footers etc. produced by {tflmetaR} ----
fig2 <- gridify(
  p1,
  layout = pharma_layout_base(
    margin = grid::unit(c(0.5, 1, 0.25, 1), "inches"),
    global_gpar = grid::gpar(fontfamily = "Courier")
  )
) |>
set_cell("header_left_1", ulheader[[1]]) |>
set_cell("header_left_2", ulheader[[2]]) |>
set_cell("header_left_3", ulheader[[3]]) |>
set_cell("header_right_1", urheader[[1]]) |>
set_cell("header_right_2", urheader[[2]]) |>
set_cell("header_right_3", urheader[[3]]) |>
set_cell("output_num", titles[[1]]) |>
set_cell("title_1", "") |>
set_cell("title_2", titles[[2]]) |>
set_cell("title_3", titles[[3]]) |>
set_cell("note", footnote_str, mch = 130) |>
set_cell("footer_left", paste0("Program: ", pgmname, ".R ",
  format(Sys.time(), "%Y-%m-%d %H:%M:%S"),
  " Source(s): ", source)) |>
set_cell("footer_right", paste0("Page ", 1, " of ", 1))

gridify::export_to(fig2, "./f_surv_tflmetar.pdf")
```

Ref: <https://pharmaverse.github.io/gridify/>



# Other Functionalities

- Generate filename and bookmark of PDF output:
  - ``get_bookm()`` function looks for "bookm" column;
  - If not found or empty, use the title instead
  - Special character(s) are removed so that it can be safely used as a filename or PDF bookmark
  - Furthermore, if the length of the bookmark exceeds 128 characters, phrases are shortened using an external abbreviation lookup table stored in ``abbrev.xlsx`` file if it exists



# Other Functionalities

## Handle Non-Standard UCB Title & Footer File:

- In case an end-user reads a non-UCB standard Excel spreadsheet with different column names, a helper function `change_colname()` is provided in the package to standardize the column names.

UCB Standard title and footer spreadsheet structure (partial screenshot)

| Pgmname     | OID | Source | Population | TTL1      | TTL2             | TTL3 | BYLINE1 | BYLINE2 | BOOKM | FOOT1     | FOOT2              |
|-------------|-----|--------|------------|-----------|------------------|------|---------|---------|-------|-----------|--------------------|
| tfl example |     | ADSL   | ITT        | Table x.x | Demographic Data |      |         |         |       | Footnotes | Reference: Listing |

```
{
  "comment": "Configuration for mapping various spreadsheet headers to canonical field names used by the system.",
  "version": "1.0.0",
  "matching_rules": {
    "case_insensitive": true,
    "trim_whitespace": true,
    "normalize": [
      "collapse_spaces",
      "remove_underscores"
    ]
  },
  "canonical_fields": [
    "sample",
    "Type",
    "Pgmname",
    "OID",
    "Source",
    "Population",
    "TTL1",
    "TTL2",
    "TTL3",
    "BYLINE1",
    "BYLINE2",
    "BOOKM",
    "FOOT1",
    "FOOT2",
    "FOOT3",
    "FOOT4",
    "FOOT5",
    "FOOT6",
    "FOOT7",
    "FOOT8"
  ],
}
```

```
{
  "Pgmname": [
    "Pgmname",
    "PGMNAME",
    "pgmname",
    "Program Name",
    "Program_Name",
    "ProgramName",
    "Program",
    "Prog Name",
    "Prog_Name"
  ],
  "OID": [
    "OID",
    "oid",
    "Object ID",
    "Object_ID",
    "objectid",
    "ID (OID)"
  ],
  "Source": [
    "Source",
    "source",
    "SOURCE",
    "Data Source",
    "Data_Source",
    "datasource",
    "data source"
  ],
  "Population": [
    "Population",
    "population",
    "POPULATION",
    "Cohort",
    "Target Population",
    "Target_Population"
  ],
}
```

# Summary



Separation of Code from Data

Managing central titles, headers and footnotes repertoire

Make code easier to maintain and share

Work seamlessly with virtually all table/figure packages

Help to generate publication quality TFLs / TLGs

# Future Plan

- Modular design means easy expansion
- Implementation of support for JSON and/or XML, YAML
- Workflow automation for program execution and report generation
- Current version: 0.09
- We would appreciate your feedbacks to help us with future improvement

**Thank you!**



# Acknowledgement

- **We would like to thank UCB and BDS LT for their support**
- **Special thanks to the following people for their support and contribution to {tlfmetaR} package and to this presentation:**

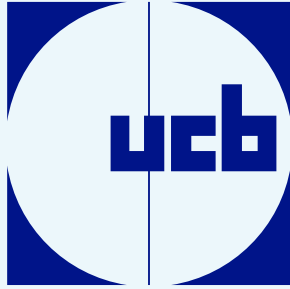
Alberto Montironi: Global Head of Programming, Visualization and Reporting

Maciej Nasinski: Tools & Standards Senior Principal Specialist

Amber Wu: Senior Statistical Programmer (FSP)

Lan Cheng: Statistical Programmer (FSP)





Inspired by **patients.**  
Driven by **science.**

## Q & A

Introduction to {tflmetaR} Package

# Programming Environment: SAS vs R

|                                         | UCB SAS Standard Model                                                                                                           | R (TK0117 Pilot Approach)                                                                                                                                                                                                                                                 |
|-----------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Platform                                | SAS 9.4 for Windows (enterprise software)                                                                                        | RStudio within UCB ValidatedR and migrated to <b>UCB RVIS SPAdA</b> (Jan2026)                                                                                                                                                                                             |
| Environment Control and Reproducibility | <ul style="list-style-type: none"><li>▪ System-level control by SAS</li><li>▪ Same SAS version ensures reproducibility</li></ul> | <ul style="list-style-type: none"><li>▪ Study-level environment isolation using <b>{renv}</b></li><li>▪ <code>renv.lock</code> stores exact dependency names and versions</li><li>▪ <code>renv::restore()</code> enables environment rebuilt on another machine</li></ul> |
| Program Structure                       | Individual .sas programs                                                                                                         | Structured <b>R Project</b> (.Rproj)                                                                                                                                                                                                                                      |
| Reusable Components                     | Centralized macro libraries                                                                                                      | <ul style="list-style-type: none"><li>▪ Custom package <b>{tflmetaR}</b></li><li>▪ Modular scripts (<b>config.R</b>, <b>report.R</b>)</li></ul>                                                                                                                           |
| Folder Structure                        | UCB standard SAS directories                                                                                                     | <ul style="list-style-type: none"><li>▪ Same SAS-style folder structure maintained</li><li>▪ Enable parallel R/SAS programming and validation</li></ul>                                                                                                                   |

**TK0117 R pilot maintained the same controls and standards used in SAS, while using different environment control approaches.**

# Programming Workflow: SAS vs R

|                                          | UCB SAS Standard Model | R (TK0117 Pilot Approach)                                                                                                                                                                                 |
|------------------------------------------|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>File Paths &amp; Global Variables</b> | Macro %SPATH, %CENTRAL | Centralized configuration script ( <a href="#">config.R</a> )                                                                                                                                             |
| <b>Validation</b>                        | PROC COMPARE           | <a href="#">{arsenal}</a> for dataset comparison                                                                                                                                                          |
| <b>Dataset Export</b>                    | Data step + PROC COPY  | <a href="#">{haven}</a> for XPT export                                                                                                                                                                    |
| <b>Table and Listing Formatting</b>      | PROC REPORT            | Reporting framework ( <a href="#">report.R</a> )                                                                                                                                                          |
| <b>Titles &amp; Footnotes</b>            | %sm_titles macro       | Custom package <a href="#">{tflmetaR}</a>                                                                                                                                                                 |
| <b>PDF rendering</b>                     | %pdf_rtf macro         | Reporting framework ( <a href="#">report.R</a> ) <ul style="list-style-type: none"> <li>Generates submission-ready PDF output</li> <li>Implemented UCB SCHSTYLE formatting to match SAS output</li> </ul> |
| <b>Logging</b>                           | Standard SAS log       | Structured logging within R script ( <a href="#">config.R</a> )                                                                                                                                           |
| <b>Batch Execution</b>                   | Window batch (.bat)    | <a href="#">R CMD BATCH</a> execution using {tools}                                                                                                                                                       |

**TK0117 demonstrates that core SAS programming functions can be implemented in R while maintaining submission standards and validation traceability.**

# TK0117 Study-Level Environment Control: {renv}

## What {renv} Provides

- Project-level environment isolation for each study
- Enables study-level environment control and reproducibility
- Prevents cross-study impact from package updates

## How the Environment Is Reproduced

- renv.lock stores exact package names and versions
- Environment rebuilt on another machine using `renv::restore()` and the **renv.lock** snapshot.



```
{
  "R": {
    "Version": "4.4.3",
    "Repositories": [
      {
        "Name": "CRAN",
        "URL": "https://uarm-01-repo.dir.ucb-group.com/repository/r-rvis_curated_repo"
      }
    ]
  },
  "Packages": {
    "DBI": {
      "Package": "DBI",
      "Version": "1.2.3",
      "Source": "Repository",
      "Title": "R Database Interface",
      "Date": "2024-06-02",
      "Authors@R": "c( person(\"R Special Interest Group on Databases (R-SIG-DB)\", r",
      "Description": "A database interface definition for communication between R and",
      "License": "LGPL (>= 2.1)",
      "URL": "https://dbi.r-dbi.org, https://github.com/r-dbi/DBI",
      "BugReports": "https://github.com/r-dbi/DBI/issues",
      "Depends": [
        "methods",
        "R (>= 3.0.0)"
      ],
      "Suggests": [
        "arrow",
        "blob",
        "covr",
        "DBItest",
        "dbplyr",
        "downlit",
        "dplyr",
        "glue",
        "hms",
        "knitr",
        "magrittr",
```

# TK0117 Reporting Framework (report.R)

## Purpose

- Converts raw datasets into formatted tables
- Generates submission-ready PDF outputs consistent with UCB standards
- Integrates metadata within the same workflow via `{tflmetaR}`

## Key Characteristics

- Modular and reusable across reports
- Self-contained (minimal external dependencies)
- Lightweight with low memory footprint and CPU usage

## Core Functions

- `report(df, ...)`

UCB  
MT1621 / TK2d  
TK0117

Version: FINAL  
Confidential  
Data Cut-off: 13 Jan 2026

Table 2.1  
Demographics  
Analysis Population: ES

| Variable                              | Statistic | All Participants (N=20) |
|---------------------------------------|-----------|-------------------------|
| Birth Year                            | n         | 20                      |
|                                       | Mean      | 1998.2                  |
|                                       | SD        | 18.1                    |
|                                       | Median    | 2004.0                  |
|                                       | Q1, Q3    | 1997.8, 2008.2          |
|                                       | Min, Max  | 1942, 2015              |
| Birth Year                            |           |                         |
|                                       | <2000     | n (%)                   |
|                                       | >=2000    | n (%)                   |
| Missing                               | n (%)     | 0                       |
| Age of Tk2d symptom onset (years) [a] | n         | 18                      |
|                                       | Mean      | 7.454                   |
|                                       | SD        | 12.929                  |
|                                       | Median    | 2.535                   |
|                                       | Q1, Q3    | 1.241, 4.015            |
|                                       | Min, Max  | 0.33, 45.08             |

ES=Enrolled Set, Max=maximum, Min=minimum, Q1=the first quartile, Q3=the third quartile, SD=standard deviation.  
TK2d=Thymidine Kinase 2 deficiency.  
[a] Age of TK2d Symptom Onset is calculated using Date of TK2d Symptom Onset - Date of birth. If calculated age is not available, collected age is used.  
Reference Listings: 3.1, 3.2, 3.3, 3.4 and 3.7

Generated from t\_dm.R on 2026-02-11 23:01:54 Data Source(s): ADL

Page 1 of 3

# TK0117 Log File Generation: Audit Traceability

## Purpose

- A logging approach that combines full, SAS-like execution transparency with structured metadata traceability for audit and compliance.

## R CMD BATCH as the execution driver

- Produces a full, SAS-like execution log
- Code and output interleaved line-by-line
- Warnings and errors appear inline with the code executed

## Config.R provides custom metadata logging

- Environment Information
- File Information
- Session Information
- Global Variables
- Program start / end time

## Compliance Strength

- Answers: "What happened, line by line?"
- Answers: "Who ran what, when, where, and how?"

```
t_dm.Rout - Notepad
File Edit Format View Help
-----
Environment Information
-----
[2026-02-11 23:01:44] [config.R] USER: e643795
[2026-02-11 23:01:44] [config.R] HOME: /home/e643795
[2026-02-11 23:01:44] [config.R] R_HOME: /opt/R/4.4.3/lib/R
[2026-02-11 23:01:44] [config.R] R_LIBS_USER: /Biocdm/Products/MT1621/TK0117/gsp/final/programs/tfls/ren
[2026-02-11 23:01:44] [config.R] LANG: en_GB.UTF-8
-----
File Information
-----
[2026-02-11 23:01:44] [config.R] Execution mode detected: CMD BATCH
[2026-02-11 23:01:44] [config.R] Args: /opt/R/4.4.3/lib/R/bin/exec/R -f t_dm.R --restore --save --no-read
[2026-02-11 23:01:44] [config.R] File name: t_dm.R
-----
Session Information
-----
[2026-02-11 23:01:44] [config.R] R version: R version 4.4.3 (2025-02-28)
[2026-02-11 23:01:44] [config.R] Platform: x86_64-pc-linux-gnu
[2026-02-11 23:01:44] [config.R] Locale: LC_CTYPE=en_GB.UTF-8;LC_NUMERIC=C;LC_TIME=en_GB.UTF-8;LC_COLLAT
[2026-02-11 23:01:44] [config.R] Attached packages:
[2026-02-11 23:01:44] [config.R]   - haven 2.5.5
[2026-02-11 23:01:44] [config.R]   - rstudioapi 0.17.1
[2026-02-11 23:01:44] [config.R] Loaded (not attached) packages:
[2026-02-11 23:01:44] [config.R]   - compiler 4.4.3
[2026-02-11 23:01:44] [config.R]   - magrittr 2.0.4
[2026-02-11 23:01:44] [config.R]   - cli 3.6.5
[2026-02-11 23:01:44] [config.R]   - hms 1.1.3
[2026-02-11 23:01:44] [config.R]   - tools 4.4.3
[2026-02-11 23:01:44] [config.R]   - pillar 1.11.1
[2026-02-11 23:01:44] [config.R]   - glue 1.8.0
[2026-02-11 23:01:44] [config.R]   - tibble 3.3.0
[2026-02-11 23:01:44] [config.R]   - vctrs 0.6.5
[2026-02-11 23:01:44] [config.R]   - forcats 1.0.1
[2026-02-11 23:01:44] [config.R]   - lifecycle 1.0.4
[2026-02-11 23:01:44] [config.R]   - pkgconfig 2.0.3
[2026-02-11 23:01:44] [config.R]   - rlang 1.1.6
[2026-02-11 23:01:44] [config.R]   - renv 1.1.5
-----
Global Variables
-----
[2026-02-11 23:01:44] [config.R] g_ranpath: /Biocdm/Products/MT1621/TK0117/gsp/final/
[2026-02-11 23:01:44] [config.R] g_anapath: /Biocdm/Products/MT1621/TK0117/gsp/final/programs
[2026-02-11 23:01:44] [config.R] g_pdfpath: /Biocdm/Products/MT1621/TK0117/gsp/final/tfls
[2026-02-11 23:01:44] [config.R] g_data: /Biocdm/Products/MT1621/TK0117/gsp/final/data/adam/
```

# TK0117 Log File Generation: Error Handling

## Controlled Execution

- Execution stops immediately upon error
- Prevents silent continuation after failure

## Enhanced Debugging Traceability

- Errors displayed inline at point of failure
- Full backtrace available for root-cause analysis

## Syntax

- `tools::Rcmdr("BATCH --no-save demo.R")`

Compare with summary-style logging: `{logrx}`

| Errors and Warnings                                                         |                                            |
|-----------------------------------------------------------------------------|--------------------------------------------|
| Errors:                                                                     | In argument: `SDV_BRTHY = case_when(...)`. |
| Warnings:                                                                   |                                            |
| Messages, Output, and Result                                                |                                            |
| Messages:                                                                   |                                            |
| File Information                                                            |                                            |
| [2026-02-10 20:50:07] [config.R] Execution mode detected: logrx             |                                            |
| [2026-02-10 20:50:07] [config.R] File name: t_dm.R//Biocdm/Products/MT1621/ |                                            |

Enhance  
debugging  
traceability

```
t_dm.Rout - Notepad
File Edit Format View Help
> df <- ads1 |>
+   filter(ESFL == 'Y') |>
+   mutate(
+     SDV_BRTHY = case_when(
+       BRTHS1FL == "Y" ~ ifelse(!is_na_or_empty(BRTHDTC), as.numeric(s
+       BRTHS2FL == "Y" ~ ifelse(!is.na(BRCLDT), lubridate::year(BRCL
+       TRUE ~ ifelse(!is_na_or_empty(BRTHDTC), as.numeric(
+     ),
+     SDV_GENCONF = case_when(
+       GENCS1FL == "Y" ~ GENCONF,
+       GENCS2FL == "Y" ~ GENCCL,
+       TRUE ~ GENCONF
+     )
+   ) |>
+   select(USUBJID, starts_with("SDV_"))
Error in `mutate()` :
  In argument: `SDV_BRTHY = case_when(...)` .
Caused by error in `case_when()` :
  ! `..1 (left)` must be a logical vector, not a character vector.
Backtrace:
  1. └─dplyr::select(...)
  2. └─dplyr::mutate(...)
  3. └─dplyr::mutate.data.frame(...)
  4.   └─dplyr::mutate_cols(.data, dplyr_quosures(...), by)
  5.     └─base::withCallingHandlers(...)
  6.       └─dplyr::mutate_col(dots[[i]], data, mask, new_columns)
  7.         └─mask$eval_all_mutate(quo)
  8.           └─dplyr (local) eval()
  9.             └─dplyr::case_when(...)
 10.               └─dplyr::vec_case_when(...)
 11.                 └─dplyr::check_logical(condition, arg = condition_arg, call
 12.                   └─dplyr::stop_input_type(...)
 13.                     └─rlang::abort(message, ..., call = call, arg = arg)
> proc.time()
  user system elapsed
 2.523   0.922  26.747
```

# TK0117 Custom Package: {tflmetaR}

## What is {tflmetaR}?

**{tflmetaR}** is a custom R package developed by the DoxTM team. It reads and extracts headers, titles and footnotes from an external Excel metadata file (st\_titles.xls), and automates their annotation in TFL outputs.



## Why using {tflmetaR}

### Eliminates hardcoding

- Headers/titles/footnotes are no longer embedded in each program
- Reduces manual edits and QC burden

### Centralized content control

- All headers/titles/footnotes info live in a single Excel file
- One change updates all related outputs instantly

### Modular code design

- TFL programs hence remain lightweight and focus on data manipulation
- The {tflmetaR} + report.R automates headers/titles/footnotes generation for TFL outputs
- Promotes reusability and simplifies debugging

# Demo: demo.R

```
11 # Set up -----
12 # Always include the following two lines at the beginning of your script.
13 rm(list = ls())
14 source("config.R")
15
16
17 # Load your R Packages -----
18 library(tidyverse)
19
20 # Load ADSL
21 adsl <- readRDS(file = file.path(g_ad, "adsl.rds"))
22
23 # Some global variables:
24 g_pgmname # current program name
25 g_qc      # data directory for PROD
26 g_qc_v    # data directory for VAL
27 g_pdfpath # PDF output directory
28
29 # Modify Data -----
30 df <- adsl %>%
31   # filter(ESFL == 'Y') %>%
32   select(USUBJID, SITEID, AGEGR2N, BRTHDTC, COUNTRY, AGEONS, AGELKA, AGEDTH) %>%
33   # replace NA with empty string
34   mutate(across(where(is.character), ~replace_na(., ""))) %>%
35   arrange(USUBJID)
36
37 # Save data in both RDS and XPT formats to the g_qc directory -----
38 saveRDS(df, file=file.path(g_qc, "demo.rds"))
39 haven::write_xpt(df, path=file.path(g_qc, "demo.xpt"), version=5)
```

demo.R

demo.Rout - Notepad

File Edit Format View Help

demo.Rout

R version 3.6.2 (2019-12-12) -- "Dark and Stormy Night"  
Copyright (C) 2019 The R Foundation for Statistical Computing  
Platform: x86\_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.  
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Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.

```
>
> # Set up -----
> # Always include the following two lines at the beginning of your script.
> rm(list = ls())
> source("config.R")
[2025-07-07 02:38:15] [INFO] [config.R] ===== Session Info =====
[2025-07-07 02:38:15] [INFO] [config.R] R version: R version 3.6.2 (2019-12-12)
[2025-07-07 02:38:15] [INFO] [config.R] Platform: x86_64-pc-linux-gnu (64-bit)
[2025-07-07 02:38:15] [INFO] [config.R] Locale: LC_CTYPE=en_US.UTF-8;LC_NUMERIC=C;LC_
[2025-07-07 02:38:15] [INFO] [config.R] Attached packages:
[2025-07-07 02:38:15] [INFO] [config.R]   - haven 2.4.3
[2025-07-07 02:38:15] [INFO] [config.R]   - rstudioapi 0.13
[2025-07-07 02:38:15] [INFO] [config.R]   - futile.logger 1.4.3
[2025-07-07 02:38:15] [INFO] [config.R] ===== Environment Info =====
[2025-07-07 02:38:15] [INFO] [config.R] USER: e643795
[2025-07-07 02:38:15] [INFO] [config.R] HOME: /home/E643795
[2025-07-07 02:38:15] [INFO] [config.R] R_HOME: /opt/software/R-3.6.2/lib64/R
[2025-07-07 02:38:15] [INFO] [config.R] R_LIBS_USER: ~/R/x86_64-pc-linux-gnu-librai
[2025-07-07 02:38:15] [INFO] [config.R] LANG: en_US.UTF-8
[2025-07-07 02:38:15] [INFO] [config.R] RSTUDIO: 1
[2025-07-07 02:38:15] [INFO] [config.R] ===== Global Variables =====
[2025-07-07 02:38:15] [INFO] [config.R] g_ranpath: /Biocdm/Products/MT1621/TK0117/
[2025-07-07 02:38:15] [INFO] [config.R] g_anapath: /Biocdm/Products/MT1621/TK0117/
[2025-07-07 02:38:15] [INFO] [config.R] g_pdfpath: /Biocdm/Products/MT1621/TK0117/
[2025-07-07 02:38:15] [INFO] [config.R] g_sd: /Biocdm/Products/MT1621/TK0117/gsp/d
[2025-07-07 02:38:15] [INFO] [config.R] g_qc: /Biocdm/Products/MT1621/TK0117/gsp/d
[2025-07-07 02:38:15] [INFO] [config.R] g_qc_v: /Biocdm/Products/MT1621/TK0117/gsp/
```



# Demo: demo.R (cont.)

```
demo.Rout - Notepad
File Edit Format View Help
> source("report.R")

> # Use function report(df, col_names, col_widths) to create PDF file.
> # The PDF file will be created in the g_pdfpath directory, with a filename
> # automatically generated by concatenating TTL1 and TTL2.
>
> col_names <- c("Subject ID",
+               "Site ID",
+               "Date of Birth\n(YYYY-MM)",
+               "Country",
+               "Age of Onset\n(Year)",
+               "Age of Last Known\nAlive (Year)",
+               "Age of Death\n(Year)")
>
> # If 'col_width' is not specified, all column widths are evenly distributed.
> # In our example, 'USUBJID' is truncated in the generated PDF because it was not
> # allocated sufficient space.
> report(df, col_names=col_names)
[2025-07-07 02:38:19] [INFO] [report.R] TFL program: demo.R, total_pages: 5
[2025-07-07 02:38:19] [INFO] [report.R] Left header: [UCB, MT1621 / TK2d, TK0117]
[2025-07-07 02:38:19] [INFO] [report.R] Right header: [CONFIDENTIAL, DRAFT - FOR INTERNAL USE ONLY]
[2025-07-07 02:38:19] [INFO] [report.R] Titles: [Demo Listing, Summary of Participant Disposition, Analysis Population: All Potential Participants]
[2025-07-07 02:38:19] [INFO] [report.R] Footnotes: [ES=Enrolled Set, SDV=Source Data Verification, TK2d=Thymidine Kinase 2 deficiency., Note: First Participant]
[2025-07-07 02:38:19] [INFO] [report.R] Start to create PDF output: /Biocdm/Products/MT1621/TK0117/gsp/dem1/tfls/Demo Listing Summary of Participant Disposition
[2025-07-07 02:38:19] [INFO] [report.R] Drawing page 1 ...
[2025-07-07 02:38:20] [INFO] [report.R] Drawing page 2 ...
[2025-07-07 02:38:20] [INFO] [report.R] Drawing page 3 ...
[2025-07-07 02:38:21] [INFO] [report.R] Drawing page 4 ...
[2025-07-07 02:38:22] [INFO] [report.R] Drawing page 5 ...
[2025-07-07 02:38:22] [INFO] [report.R] Created PDF output: /Biocdm/Products/MT1621/TK0117/gsp/dem1/tfls/Demo Listing Summary of Participant Disposition.pdf
```

demo.Rout

```
40 # Create PDF output -----
41 source("report.R")
42
43 # Use function report(df, col_names, col_widths) to create PDF file.
44 # The PDF file will be created in the g_pdfpath directory, with a filename
45 # automatically generated by concatenating TTL1 and TTL2.
46 col_names <- c("Subject ID",
47               "Site ID",
48               "Age\nCategory",
49               "Date of Birth\n(YYYY-MM)",
50               "Country",
51               "Age of Onset\n(Year)",
52               "Age of Last\nKnown Alive\n(Year)",
53               "Age of Death\n(Year)")
54
55 # If 'col_width' is not specified, all column widths are evenly distributed.
56 # In our example, 'USUBJID' is truncated in the generated PDF because it was not
57 # allocated sufficient space.
58 report(df, col_names=col_names)
59
60 # allocate more space to 'USUBJID'
61 col_widths <- c(1.4, 0.8, 0.8, 1.4, 1, 1, 1, 1)
62
63 # When specifying both col_names and col_widths, make sure they have the same
64 # length, as each column name maps one-to-one with a corresponding column width.
65 report(df, col_names=col_names, col_widths=col_widths)
```

demo.R