

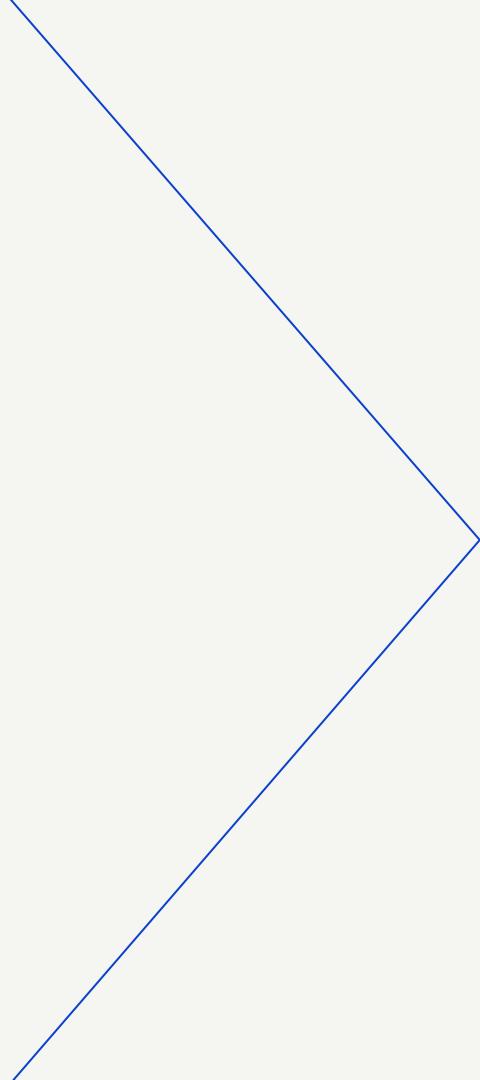


# Revolutionize Data Exploration with *Teal*

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August 29, 2023  
@ useR China

# Agenda

- 
1. Introduction to teal framework
  2. teal-verse product map
  3. Example app demo
  4. Additional resources



# Product Development Data Sciences

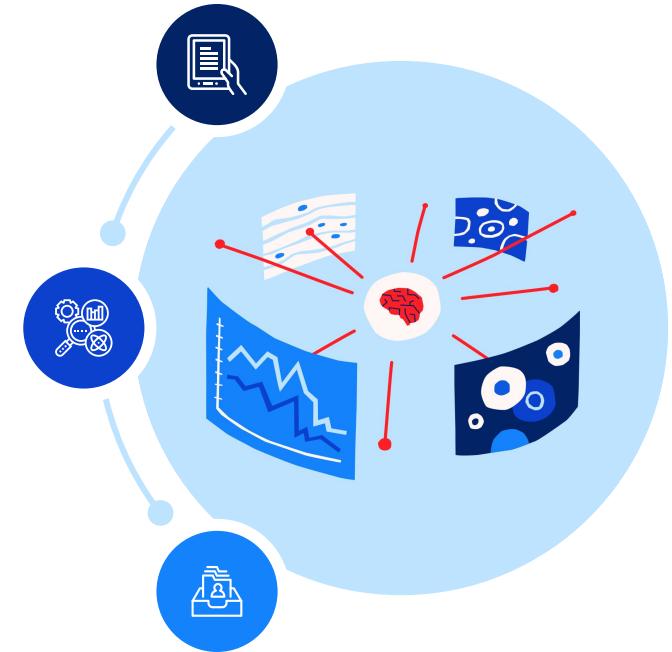


Main task:  
reporting  
clinical trials

Summarising safety and  
efficacy data

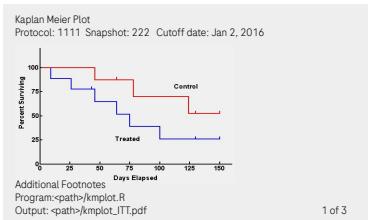
Providing an accurate  
picture of trial outcomes

Managing data collection  
across international sites

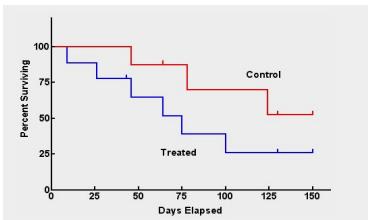


# Improve efficiency in the way we work

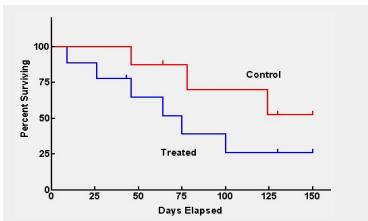
Analyzing clinical trial data requires multiple ways of presenting and interacting with our data



Per-SAP static output  
on **OS**



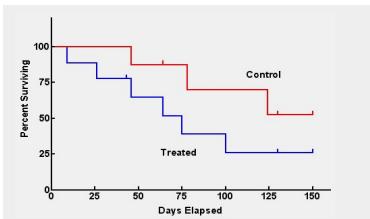
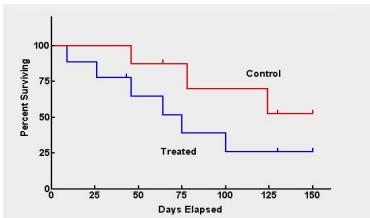
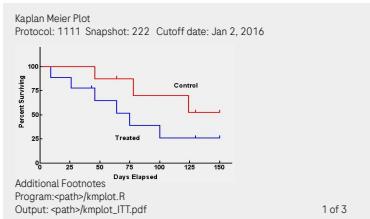
Ad-hoc analysis  
on **PFS**



Ad-hoc analysis on **PFS**  
in **subpopulation**

# Improve efficiency in the way we work

Analyzing clinical trial data requires multiple ways of presenting and interacting with our data



Per-SAP static output  
on OS

Ad-hoc analysis  
on PFS

Ad-hoc analysis on PFS  
in subpopulation

Example App with teal.modules.clinical modules

Study Information Data Table Variable Browser Demographic Table Forest Plots Response Table Time to Event Table Cross Table Cox Reg Logistic Reg MMRM Binary Response ANCOVA Report previewer

Reporter +   
 Encodings Datasets: ADSL, ADTTE  
Select Endpoint Dataset: ADTTE  
Filter by OS Overall Survival  
Analysis Variable Select AVE  
Censor Variable Select OSAS  
Facet Plots by Dataset: ADSL  
Select - Nothing selected -  
Select Treatment Variable

Active Filter Summary

	Obs	Subjects
ADSL	400/400	400/400
ADTTE	2000/2000	400/400

Active Filter Variables ADSL ADTTE

Building scalable exploratory R-shiny web-apps

# What is {teal}?



A Rshiny-based interactive data exploration framework



Modularized and standardized building blocks



Collection of specialized R packages

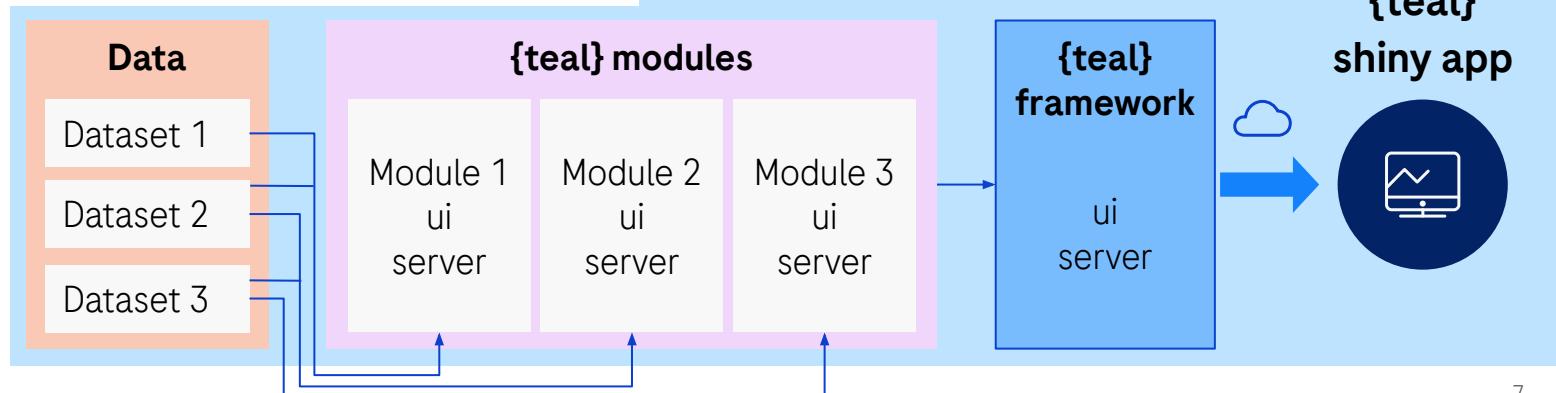
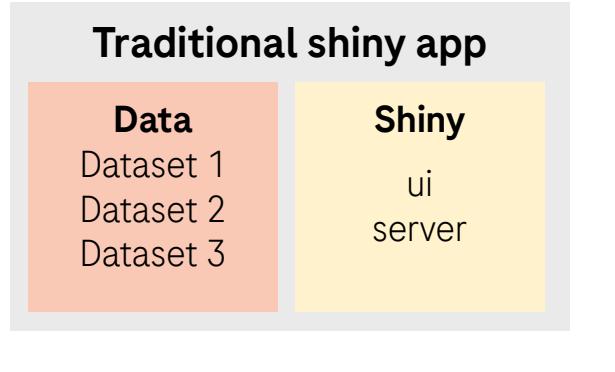


Streamlines creation of web-apps that offers:

- Dynamic filtering facility
- Code reproducibility
- Reporting engine
- Many data summarization and visualizations

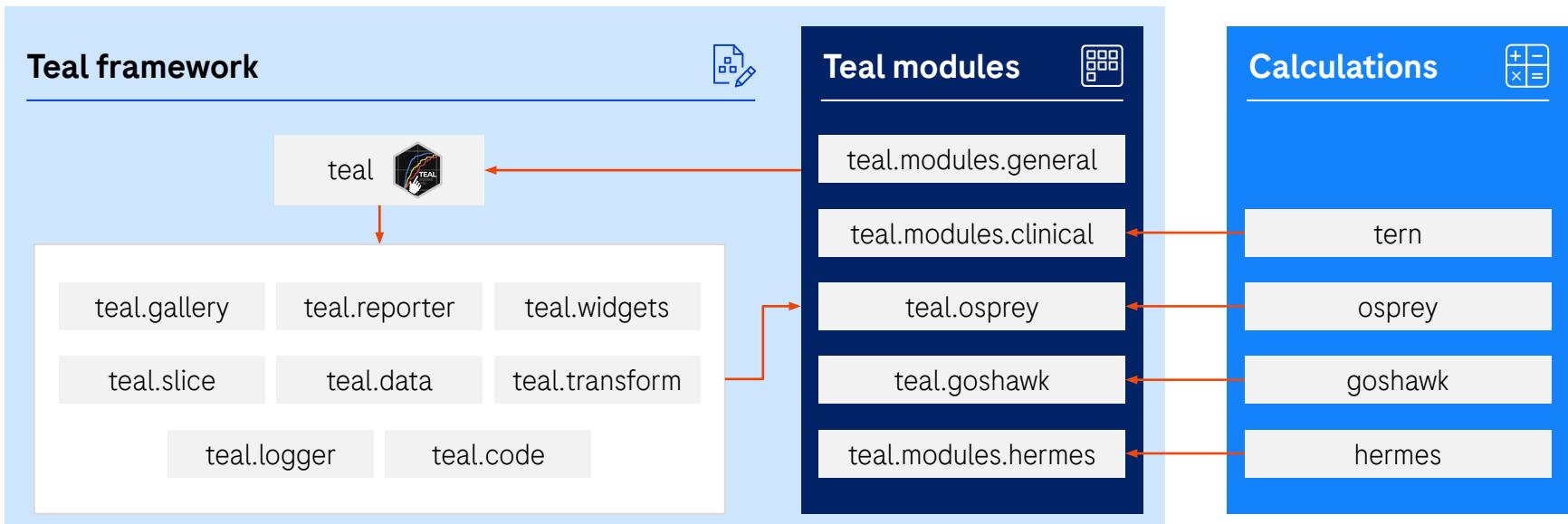


# How does {teal} work?



# {teal} Universe Products Map

The screenshot shows a software application window titled "Example App with teal.modules.clinical modules". The interface includes a top navigation bar with links like "Study Information", "Data Table", "Variable Browser", "Demographic Table", "Forest Plots", "Kaplan Meier Plot", "Response Table", "Time To Event Table", "Cross Table", "Cox Reg", "Logistic Reg", and "MMRM". Below the navigation is a toolbar with icons for "Report", "Encodings", "Dataset: ADSL", "Select Treatment Variable", "ARM Description of Prior", "Add All Patients column", "Summarize Variables", "Additional table settings", "Show R code", and "Debug Info". The main content area displays a table titled "Demographic Table" comparing four groups: A: Drug X (N=134), B: Placebo (N=134), C: Combination (N=132), and All Patients (N=400). The table includes columns for Age, Sex, and various statistical measures like Mean, Median, and Min-Max. On the right side of the interface, there are sections for "Active Filter Summary" (ADS L, 400/400), "Active Filter Variables" (ADS L), and "Add Filter Variables" (ADS L, filter selected). At the bottom, there's a "NEST PROJECT" section.





## Teal Framework R Packages

- [teal](#): shiny-based interactive exploration framework for analyzing data.
- [teal.gallery](#): gallery of sample teal apps.
- [teal.widgets](#): shiny components used within teal.
- [teal.reporter](#): allows teal applications to generate reports.
- [teal.slice](#): provides a filtering panel to allow subset of data.
- [teal.data](#): creating and loading the data needed for teal applications.
- [teal.code](#): handles reproducibility of outputs.
- [teal.transform](#): standardizes extracting and merging data
- [teal.logger](#): standardizes logging within teal framework.

## Teal Modules R Packages



- [teal.modules.general](#): general analysis modules for exploring any data types
- [teal.modules.clinical](#): modules for analyzing CDISC data and clinical trial reporting with [tern](#) R package
- [teal.osprey](#): modules for analyzing and reporting early-phase clinical trial data with [osprey](#) R package
- [teal.goshawk](#): modules for analyzing and visualizing biomarker data with [goshawk](#) R package
- [teal.modules.hermes](#): modules for analyzing and visualizing RNAseq data with [hermes](#) R package

# Application of {teal} in clinical trial



## Clinical trial reporting

- QCing of clinical trial reporting outputs
- Trial monitoring
- Ad-hoc & exploratory analyses
- Content generation to support internal strategic decision meetings
- Complement study milestone events
- Pooled data analysis



## Outside of trial reporting setting

- Explorating high-dimensional biomarker
- Explorating real-world data off-label use
- Data quality monitoring
- Operations analytics

# Demo Apps via {teal} Gallery

<https://insightsengineering.github.io/teal.gallery/demo.html>

## Links on shinyapps.io

- | > | <u>Exploratory analysis on general data frames</u> | > | <u>APP_NAME</u> |
|---|--|---|-----------------|
|   |  |   | "exploratory"   |
| > | <u>Safety analysis on clinical trial data</u>      | > | "safety"        |
| > | <u>Efficacy analysis on clinical trial data</u>    | > | "efficacy"      |



# LIVE DEMO



# {teal} Playground

Posit Cloud Link:

- [https://posit.cloud/spaces/340990/join?access\\_code=M52ibtFP2ASLLL1MltA-dThXpPzJvRqnxdNOgejA](https://posit.cloud/spaces/340990/join?access_code=M52ibtFP2ASLLL1MltA-dThXpPzJvRqnxdNOgejA)

Public Docker Image:

- [https://github.com/insightsengineering/ci-images/pkgs/container/rstudio\\_4.3.1\\_bioc\\_3.17](https://github.com/insightsengineering/ci-images/pkgs/container/rstudio_4.3.1_bioc_3.17)





# Anatomy of a teal app

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## Example App with teal.modules.general modules

**Header**

Study Information File viewer Data Table Variable Browser Missing Data Distribution Outliers Association **Menu with tabs** Response Plot Scatterplot matrix Scatterplot Table Choices Principal Component Analysis Report previewer SPA

**Reporter**

Dataset: ADSL

Reference variable Select AGE Age

Associated variables Select ARM Encodings

Association with the reference variable

Distribution

Log transformed

Plot settings

**Reproducibility Debugging**

Source: test\_gallery package  
Pdt6448 Token:70820724

**Figure**

Association between Planned Arm Code [ARMCD] and Age [AGE]

Frequency

Output

Planned Arm Code [ARMCD]

Age [AGE]

\* Download \* Better View \* Dimensions

**Footer**

\* Toggle Filter Panel

Active Filter Summary

Obs Subjects

ADSL 400/400 400/400

Active Filter Variable Filter Panel

ADSL

Add Filter Variables

Add ADSL filter

Select variable to filter

# Key Features: Filter Panel



Ability to subset your dataset



Out of the box from teal framework



Active filter summary



Pre-defined filter state

Active Filter Summary

	Obs	Subjects
ADSL	400/400	400/400
ADTTE	1600/1600	400/400

Active Filter Variables

ADSL

RACE

ASIAN (208), BLACK OR AFRICAN AMERICAN (91), WHITE (74), AI

AGE

20 25 30 35 40 45 50 55 60 65 69 89

ADTTE

PARAMCD Parameter Code

- CRSD (400)
- EFS (400)
- OS (400)
- PFS (400)

Add Filter Variables

Add **ADSL** filter

Select variable to filter

Add **ADTTE** filter

Select variable to filter

# Key Features:

## Show R Code



Reproducible code when you see the desired output in analysis



Include any filters added



Include library ( ) calls

Show R code

```

## and might have omitted this step for some reason. Please reach
## out to the app developer for details.

# ADSL MD5 hash at the time of analysis: 01965f31841821489767446baaff0ad2
# ADTTE MD5 hash at the time of analysis: af41fb660390618275fbcba67c82a563

ADTTE <- dplyr::inner_join(x = ADTTE, y = ADSL[, c("STUDYID", "USUBJID"), drop = FALSE], by = c("STUDYID", "USUBJID"))

# Description of Planned Analysis
ANL_1 <- ADTTE %>% dplyr::select(STUDYID, USUBJID, PARAMCD, AVAL, CNSR, AVALU)
ANL_2 <- ADSL %>% dplyr::select(STUDYID, USUBJID, ARM, STRATA1, AGEGR1)
ANL_3 <- ADTTE %>%
  dplyr::filter(PARAMCD == "OS") %>%
  dplyr::select(STUDYID, USUBJID, PARAMCD)
ANL <- ANL_1
ANL <- dplyr::inner_join(ANL, ANL_2, by = c("STUDYID", "USUBJID"))
ANL <- dplyr::inner_join(ANL, ANL_3, by = c("STUDYID", "USUBJID", "PARAMCD"))
ANL <- ANL %>% formatters::var_relabel(AVAL = "Analysis Value", CNSR = "Censor", ARM = "Description of Planned Analysis")

anl <- ANL %>%
  dplyr::filter(ARM %in% c("A: Drug X", "B: Placebo", "C: Combination")) %>%
  dplyr::mutate(ARM = stats::relevel(ARM, ref = "A: Drug X")) %>%
  dplyr::mutate(ARM = droplevels(ARM)) %>%
  dplyr::mutate(is_event = CNSR == 0)
variables <- list(tte = "AVAL", is_event = "is_event", arm = "ARM", strat = "STRATA1")
grid::grid.newpage()
lyt <- grid::grid.layout(nrow = nlevels(ANL$AGEGR1), ncol = 1) %>%
  grid::viewport(layout = .)
grid::pushViewport()
result <- mapply(df = split(anl, f = anl$AGEGR1), nrow = seq_along(levels(anl$AGEGR1)), FUN = function(df_i, r) {
  if (nrow(df_i) == 0) {
    grid::grid.text("No data found for a given facet value.", x = 0.5, y = 0.5, vp = grid::viewport(layout.pos.col = 1))
  } else {
    g_km(df = df_i, variables = variables, font_size = 8L, xlab = paste0("Time", " (", gsub("(^|[[:space:]])", "", r), ")"),
        conf_level = 0.95,
        pval_method = "log-rank", ties = "exact"
      ), ci_ribbon = FALSE, vp = grid::viewport(layout.pos.row = nrow_i, layout.pos.col = 1), draw = TRUE)
  }
}, SIMPLIFY = FALSE)
km_grobs <- tern::stack_grobs(grobs = result)
km_grobs

```

[Copy to Clipboard](#)
[Dismiss](#)

# Key Features: teal Reporter



Create a report for your analysis



Zip file that contains:

- .Rmd
- .rds
- .png
- And the requested report type  
(html, pdf, or ppt)

The screenshot displays the teal Reporter application interface. At the top, there are three large buttons: a blue '+' button, a blue download icon button, and an orange 'X' button. Below these are sections for 'Report previewer' and 'Download the Report'. The 'Report previewer' shows a 'Kaplan Meier Plot' card, which is described as a non-parametric method used to estimate the survival function from lifetime data. It includes filter settings for 'RACE' (Selected values: ASIAN, Include missing values: FALSE), 'AGE' (Selected values: 24-49yrs - 50-69yrs, Include missing values: FALSE), and 'ADTTE' (Selected values: OSDD EFS OS, Include missing values: FALSE). The plot itself shows survival probability over time (0 to 5000 days) for four groups: A (Drug A), B (Placebo), C (Combination), and D (Drug X). The 'Download the Report' section allows selecting 'Author' (NEST), 'Title' (Report), 'Date' (2023-01-23), and 'Choose a document type' (HTML\_document). Buttons for 'Download Report' and 'Reset Report X' are also present. To the right of the previewer is a 'Card 1: Kaplan Meier Plot' panel with detailed filter settings. Below these panels is a 'Plot' section showing the Kaplan Meier survival curve. At the bottom of the interface is a file browser window titled 'report\_202301232356403062'. The browser lists files: 'file15a41d15fea8f2.rds', 'file15a41d60ef42dc.png', 'input\_20230123235640313.html', and 'input\_20230123235640313.Rmd'. All files were modified 'Today at 11:56 PM'.

# Key Features:

## Curated sets of teal modules for targeted purposes



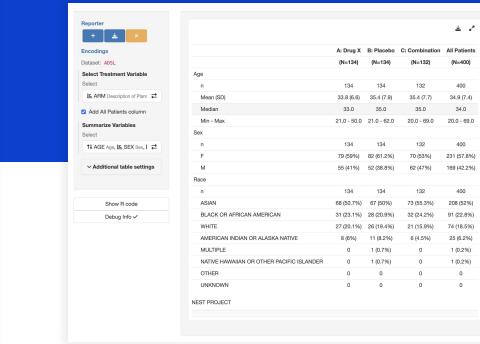
Actively developed and maintained centrally by a dedicated team



Purposefully designed, e.g. for clinical trials reporting or biomarker analysis



50+ common analysis modules available for use



# Key Features: teal bootstrap theme

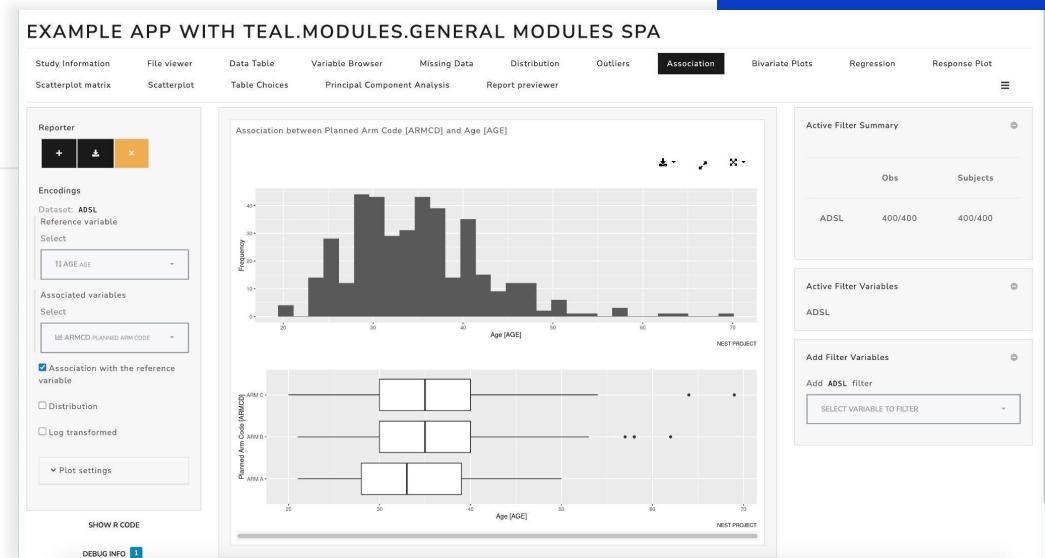


Customize the look of your teal app, powered by bslib



Custom and real-live theming

- <https://insightsengineering.github.io/teal/main/articles/teal-bs-themes.html>



# Additional Resources



{teal} is part of pharmaverse:  
<https://pharmaverse.org/>



More information about support:  
<https://pharmaverse.org/support/>



Slack channel [#teal](#) under  
pharmaverse workspace



Upcoming course on Coursera  
["Hands On Clinical Reporting Using R"](#)  
in Q4 2023

## Support Packages

For all [pharmaverse packages](#) we recommend to use the following for support and communications between user and developer communities:

-  **Slack** - for informal discussions, Q&A and building user community
-  **GitHub Issues** - for direct feedback, enhancement requests or raising bugs

# Collaborating on {teal}



We are looking for collaborators to develop this framework further!



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If you're an individual, please contribute on GitHub and join us via [pharmaverse](#) Slack [#teal](#) channel

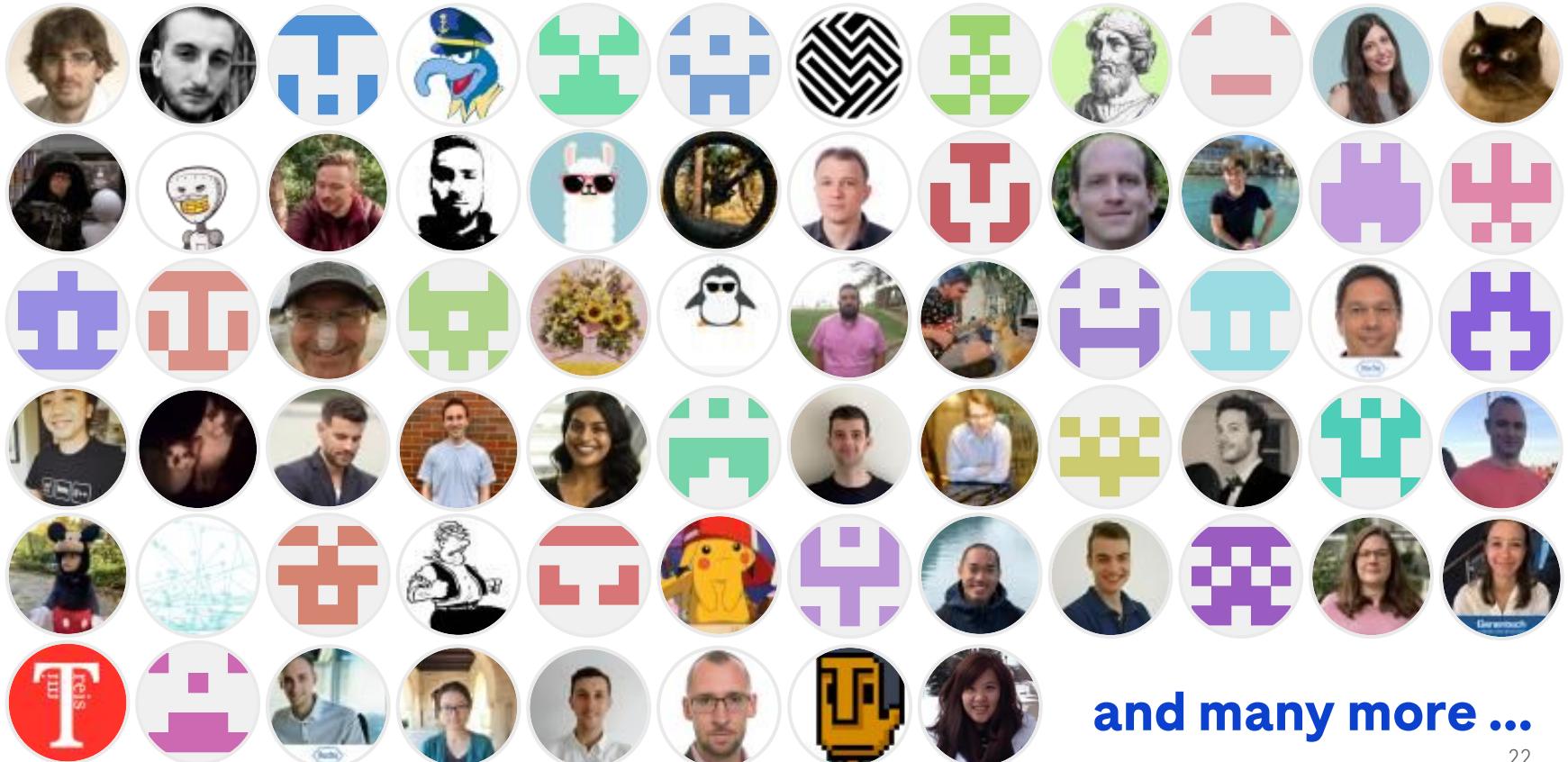


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If you're an organization wanting to adopt {teal} and co-develop, please get in touch with our Product Owner [chendi.liao@roche.com](mailto:chendi.liao@roche.com)



# Acknowledgement



and many more ...

*Doing now what patients need next*