



# Revolutionize Data Exploration with *Teal*

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# 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**

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**Providing an accurate picture of trial outcomes**

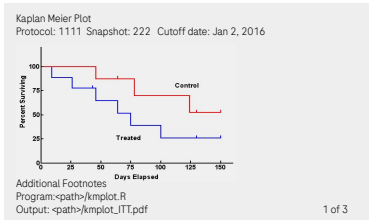
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**Managing data collection across international sites**

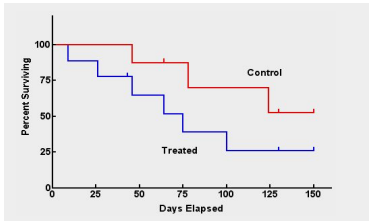


# Improve efficiency in the way we work

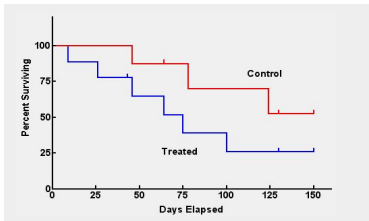
Analyzing clinical trial data requires multiple ways of presenting and interacting with our data



Per-SAP static output  
on **OS**



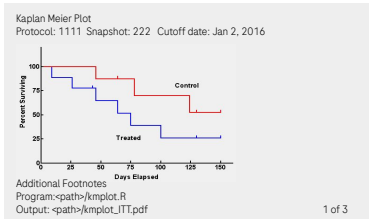
Ad-hoc analysis  
on **PFS**



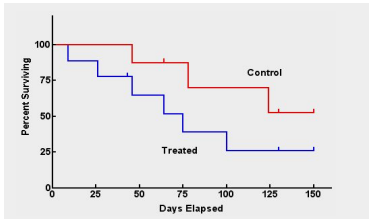
Ad-hoc analysis on **PFS**  
in **subpopulation**

# Improve efficiency in the way we work

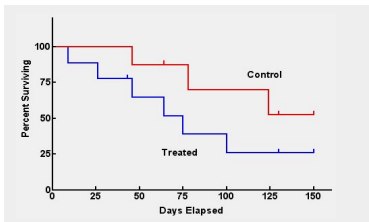
Analyzing clinical trial data requires multiple ways of presenting and interacting with our data



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 SPA

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 MMRM Binary Response ANCOVA Report previewer

Reporter

Encodings

Datasets: ADSL, ADTTE

Select Endpoint

Dataset: ADTTE

Filter by

OS Overall Survival

Analysis Variable

Select ANL

Censor Variable

Select CENS

Forest Plots by

Dataset: ADSL

Select

Select Treatment Variable

	N	Mean	95% CI
A: Dig X	134	17	4, 148
B: Placebo	134	33	2, 183
C: Combination	132	5	1, 10

Ties for Censor (Hazard Ratio): exact  
p-value Method for Censor (Hazard Ratio): log-rank

Active Filter Summary

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

Active Filter Variables

ADSL

ADTTE

Add Filter Variables

Add ADSL filter

Select variable to filter

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:

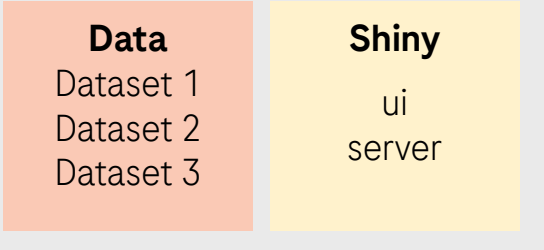
- Dynamic filtering facility
- Code reproducibility
- Reporting engine
- Many data summarization and visualizations



# How does {teal} work?

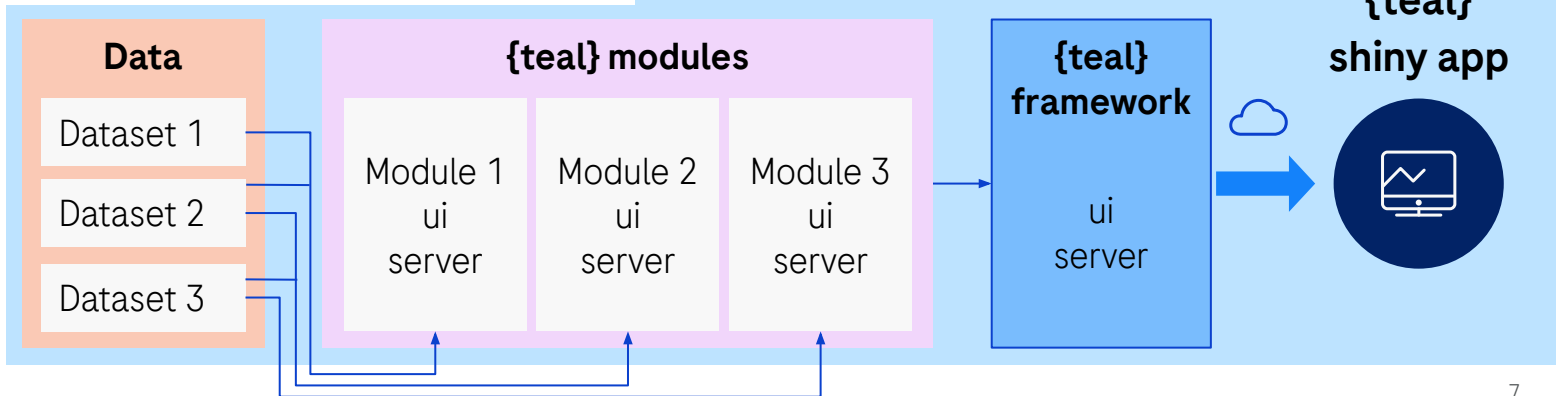


## Traditional shiny app

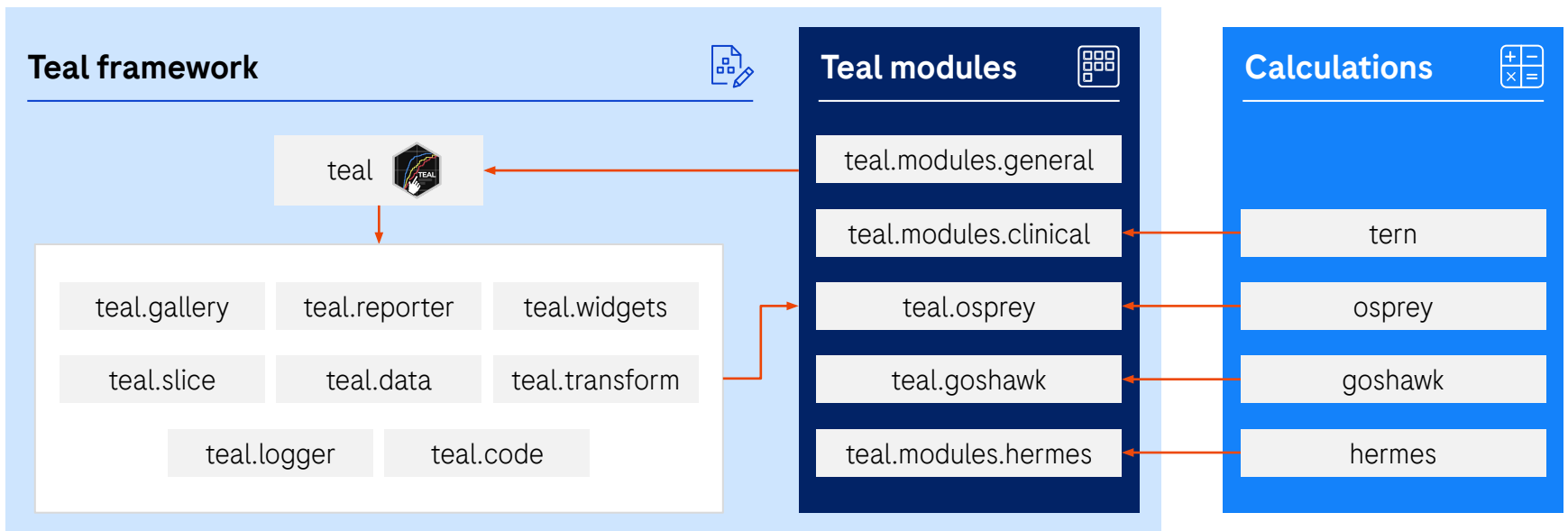
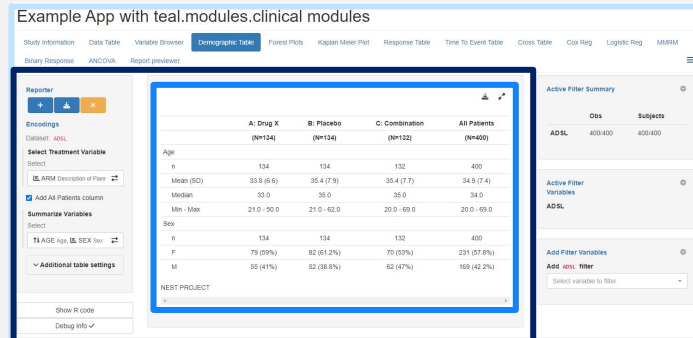


## {teal} framework with modularized components

- Data agnostic
- Flexible
- Cumulative
- Collaborative
- Crowdsourcing



# {teal} Universe Products Map







## 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

- Exploring high-dimensional biomarker
- Exploring 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*

APP\_NAME

- |   |                              |
|---|------------------------------|
| <p>▶ <a href="#"><u>Exploratory analysis on general data frames</u></a></p> <hr/> | <p>▶ "exploratory"</p> <hr/> |
| <p>▶ <a href="#"><u>Safety analysis on clinical trial data</u></a></p> <hr/>      | <p>▶ "safety"</p> <hr/>      |
| <p>▶ <a href="#"><u>Efficacy analysis on clinical trial data</u></a></p>          | <p>▶ "efficacy"</p>          |



# LIVE DEMO



# {teal} Playground

## Posit Cloud Link:

- [https://posit.cloud/spaces/340990/join?access\\_code=M52ibtFP2ASLLL1MItA-dThXpPzJvRqnxdNOgejA](https://posit.cloud/spaces/340990/join?access_code=M52ibtFP2ASLLL1MItA-dThXpPzJvRqnxdNOgejA)

## Public Docker Image:

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



# Example App with teal.modules.general modules

## Header

SPA

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

### Menu with tabs

**Reporter**

Encodings

Dataset: ADSL

Reference variable

Select

AGE Age

Associated variables

Select

ARM Encodings

Association with the reference variable

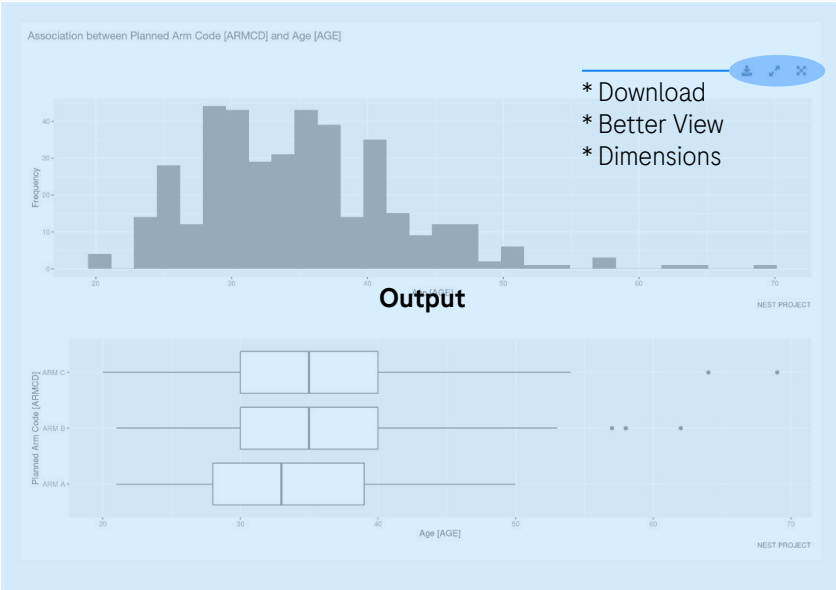
Distribution

Log transformed

Plot settings

**Reproducibility**

**Debugging**



\* Toggle Filter Panel

Active Filter Summary

	Obs	Subjects
ADSL	400/400	400/400

Active Filter Variables

**Filter Panel**

ADSL

Add Filter Variables

Add ADSL filter

Select variable to filter



# Anatomy of a teal app

## Footer

# 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

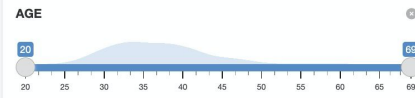
**Active Filter Variables**

**ADSL**

**RACE**

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

**AGE**



**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"))

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 Treatment")

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, fac_val) {
  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, layout.pos.row = 1))
  } else {
    g_km(df = df_i, variables = variables, font_size = 8L, xlab = paste0("Time", " (", gsub("[^[:space:]]", " ", fac_val), ")")
    conf_level = 0.95,
    pval_method = "log-rank", ties = "exact"
    ), ci_ribbon = FALSE, vp = grid::viewport(layout.pos.col = 1, layout.pos.row = 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 interface. At the top, there are three buttons: a blue '+' button, a blue download icon button, and an orange 'X' button. Below these is a 'Reporter' section with a 'Report preview' tab. To the right, a 'Download the Report' form includes fields for Author (NEST), Title, Date (2023-01-29), and a dropdown for 'Choose a document type' (html\_document). Below the form are 'Download Report' and 'Reset Report' buttons. On the right side, a 'Card 1: Kaplan Meier Plot' is visible, titled 'Kaplan Meier Plot' and described as a 'Non-parametric method used to estimate the survival function from lifetime data'. It shows a 'Filter State' section with filters for dataset (ADSL), race (BLACK OR AMERICAN INDIAN, WHITE, AMERICAN INDIAN), and age (Selected range: 20,000 - 69,000). Below the filters is a 'Plot' section showing a Kaplan Meier survival plot for OS\_AGEGR1 <= v45, with survival probability on the y-axis and Time (Days) on the x-axis. The plot shows three curves for different groups: A (Black), B (White), and C (American Indian).

Below the plot, a file explorer window is open, showing a folder named 'report\_202301232356403062'. The file explorer has a search bar and a list of files:

Name	Date Modified
file15a41d15fea8f2.rds	Today at 11:56 PM
file15a41d60ef42dc.png	Today at 11:56 PM
input_20230123235640313.html	Today at 11:56 PM
input_20230123235640313.Rmd	Today at 11:56 PM

# Key Features:

## Curated sets of teal modules for targeted purposes



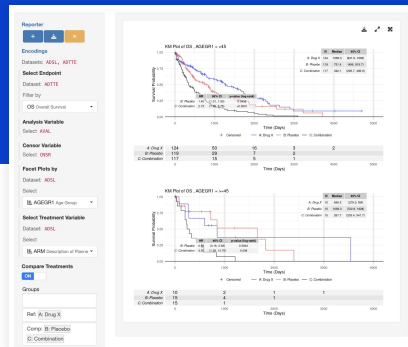
Actively developed and maintained centrally by a dedicated team



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



50+ common analysis modules available for use



**Report**

Encodings  
Dataset: ADSL  
Select Treatment Variable  
Select:  
S: ARM Description of Place

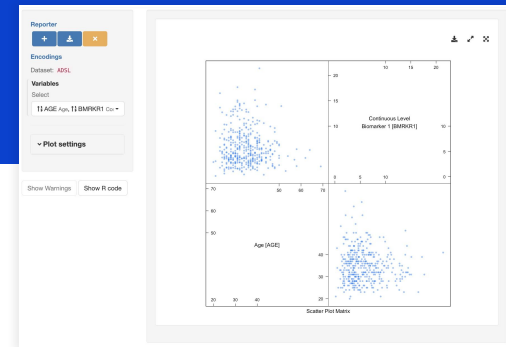
**Summary Variables**  
Select:  
T1 AGE (Age, B, SEX (Sex, L))

▼ Additional table settings

Show H code  
Delete Info

	A: Drug 0	B: Placebo	C: Combination	All Patients
	(N=124)	(N=124)	(N=124)	(N=372)
Age	134	134	132	400
Mean (SD)	33.8 (6.6)	35.4 (7.8)	34.4 (7.7)	34.9 (7.4)
Median	23.0	23.0	23.0	23.0
Min - Max	21.0 - 92.0	21.0 - 92.0	22.0 - 90.0	20.0 - 99.0
Sex				
n	124	124	120	400
F	79 (63%)	80 (64%)	70 (58%)	231 (57%)
M	50 (41%)	42 (34%)	50 (42%)	169 (42%)
Race				
n	124	124	120	400
ASIAN	68 (55.7%)	47 (38%)	51 (42.5%)	206 (51%)
BLACK OR AFRICAN AMERICAN	31 (25.1%)	28 (23.4%)	32 (26.7%)	91 (22.8%)
WHITE	27 (22.1%)	36 (29.8%)	21 (17.6%)	76 (19.4%)
AMERICAN INDIAN OR ALASKA NATIVE	8 (6.5%)	11 (9.2%)	6 (5.0%)	25 (6.2%)
PACIFIC ISLANDER	0	1 (0.7%)	0	1 (0.2%)
NATIVE HAWAIIAN OR OTHER PACIFIC ISLANDER	0	1 (0.7%)	0	1 (0.2%)
OTHER	0	0	0	0
UNKNOWN	0	0	0	0

NEST PROJECT



# Key Features: teal bootstrap theme

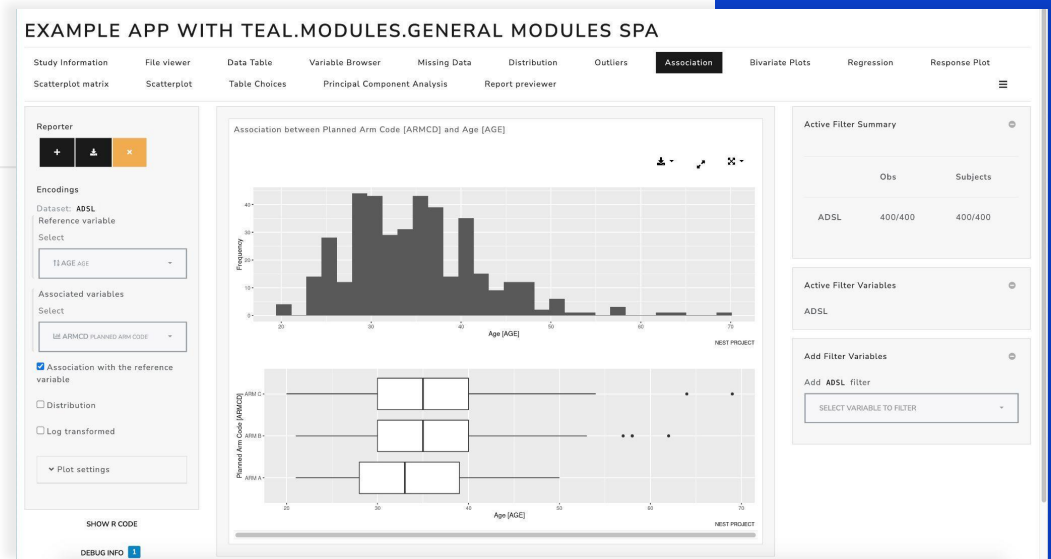


Customize the look of your teal app, powered by bslib



Custom and real-live theming

- <https://insightengineering.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!



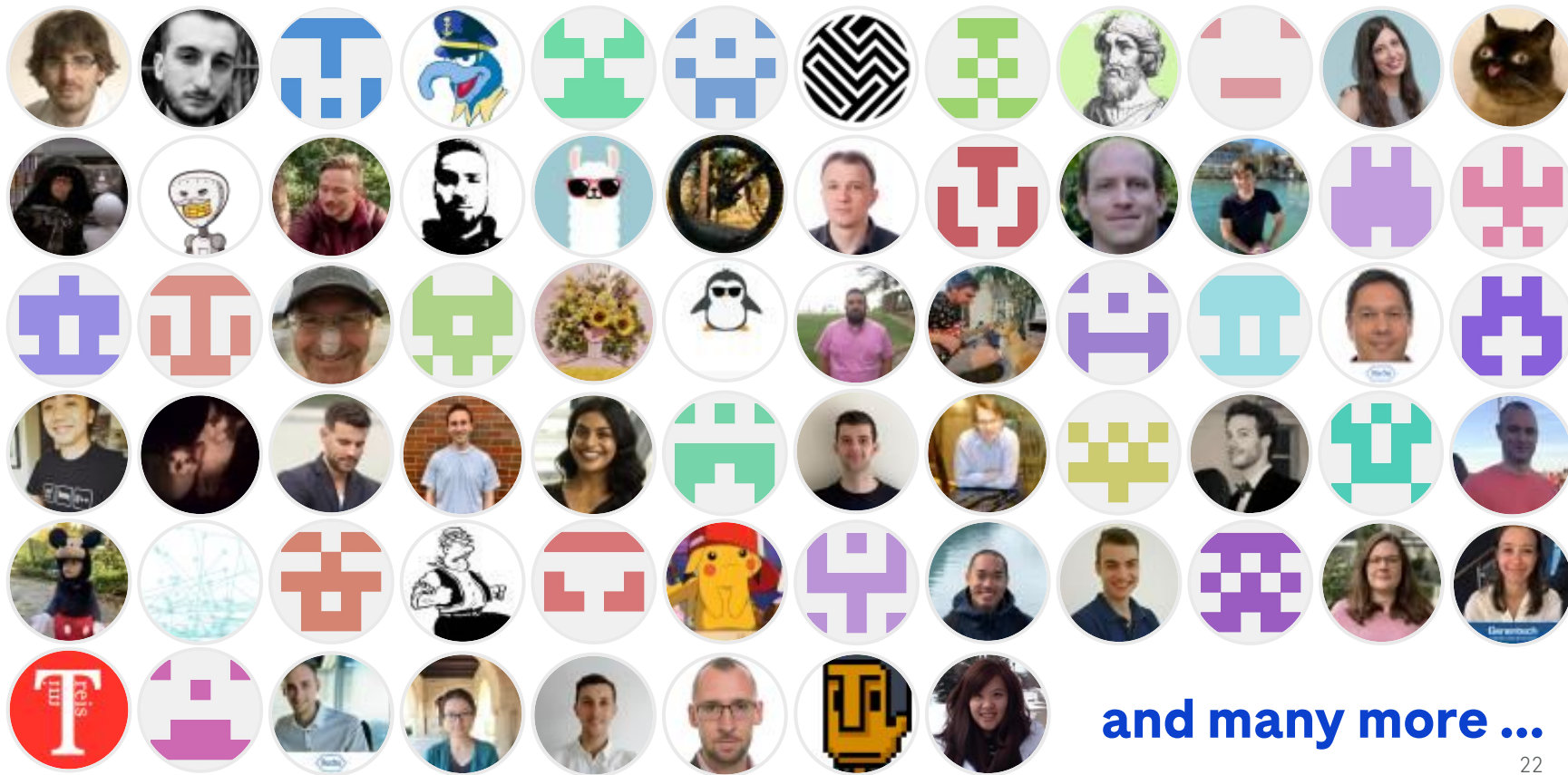
If you're an individual, please contribute on GitHub and join us via [pharmaverse](#) Slack [#teal](#) channel



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*