



2024 CDISC + TMF  
US INTERCHANGE

PHOENIX/SCOTTSDALE



23-24 OCTOBER: CONFERENCE & EXPO | 21, 22, 25 OCTOBER: TRAININGS

**pharmaverse:** Disrupting the Status Quo with Collaborative  
Solutions for Common Clinical Data Flow Processes

Presented by Michael Rimler, PHUSE  
Open Source Technologies Director

# Disclaimer and Disclosures

- *The views and opinions expressed in this presentation are those of the author(s) and do not necessarily reflect the official policy or position of **CDISC**.*
- *These opinions are my own and do not necessarily reflect **GlaxoSmithKline plc's (GSK)** position or strategy.*
- *The author(s) have no real or apparent conflicts of interest to report.*



# Meet the Speaker

Michael Rimler

**Title:** Open Source Technologies Director | Head Flu/Covid Prog

**Organization:** PHUSE | GSK

Michael heads the clinical programming group for Flu/Covid Vaccines within GSK and serves as PHUSE's Open Source Technologies Director on its Board of Directors. He is a founding member of the Pharmaverse Council and has been heavily involved in pan-industry initiatives for the integration of open source technologies into clinical data analysis and reporting. He joined Ross Farrugia (Roche) to deliver the Keynote Address on this very topic at the 2024 PHUSE US Connect.

2024 PHUSE US  
Connect Keynote



# Vevox Interactive

Who is in the  
room today?

Join at:  
**vevox.app**

ID:  
**145-384-618**





# Executive Summary



- The {pharmaverse} ecosystem is
  - An evolving set of R packages
  - Enabler of clinical trial data analysis
  - Community developed and open sourced
  - Permissively licensed (free to use and modify)
- Built on pan-industry collaborative efforts



**You can benefit both as a user  
and as a contributor**



*“Ants and bees can also work together in huge numbers, but they do so in a very rigid manner and only with close relatives. Wolves and chimpanzees cooperate far more flexibly than ants, but they can do so only with small numbers of other individuals that they know intimately. Sapiens can cooperate in extremely flexible ways with countless numbers of strangers. That’s why Sapiens rule the world, whereas ants eat our leftovers and chimps are locked up in zoos and research laboratories.”*

— YUVAL NOAH HARARI, SAPIENS







*clinical reporting (CRF -  
> Submission) forms a  
small part of a large  
chain in bringing a  
treatment to patients*



*this space is not a  
source of competitive  
advantage for  
sponsors - as it is the  
treatments and  
vaccines that set them  
apart*



*thanks to CDISC we  
have industry  
standards that mean  
we face many common  
challenges with  
respect to the clinical  
data flow*



*we believe we have  
much more to gain  
(than to lose) through  
industry collaboration  
around open source  
solutions*



**ants, chimpanzees or sapiens?**

[Home](#)[GitHub](#)[YouTube](#)[Blog](#)[Examples](#)[Slack](#)[PHUSE](#)[Get Packages](#)[Contact](#)

# pharmaverse

A connected network of companies and individuals working to promote collaborative development of curated open source R packages for clinical reporting usage in pharma, in a space where previously we would only ever have worked in silos on our own closed source and often duplicative solutions.

Adopting shared solutions in this post-competitive space should ultimately ease regulatory review, resulting in bringing new treatments to patients faster.

*Disclaimer: Anyone is free to choose any selection of pharmaverse recommended software or those from any other source, as there are many different pathways available. Being listed on our site gives no endorsement of the reliability of any code, it is up to you to assess suitability for your needs. Finally, before using any open source software you should always check the license.*





# How it started

Common vision of 4 individuals across 4 organizations



*support the user in this new paradigm*



*shared development and not 'solving problems in siloes'*



*Common codebase of tools / building blocks*

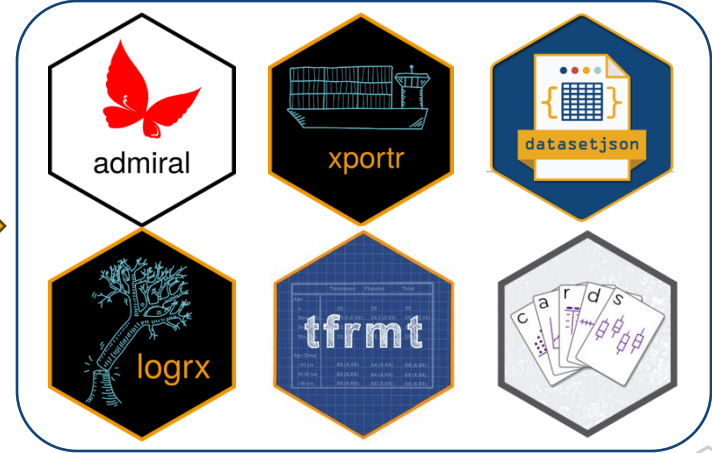
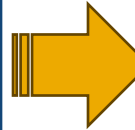
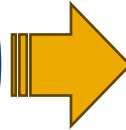
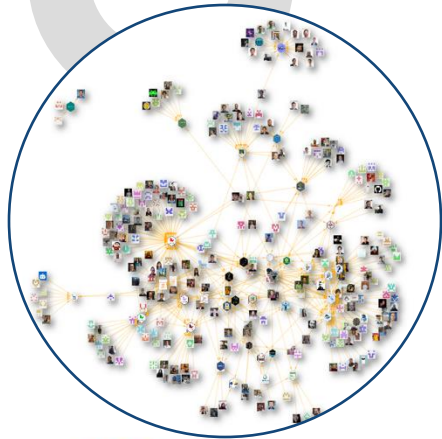


*Greater transparency and easier traceability*

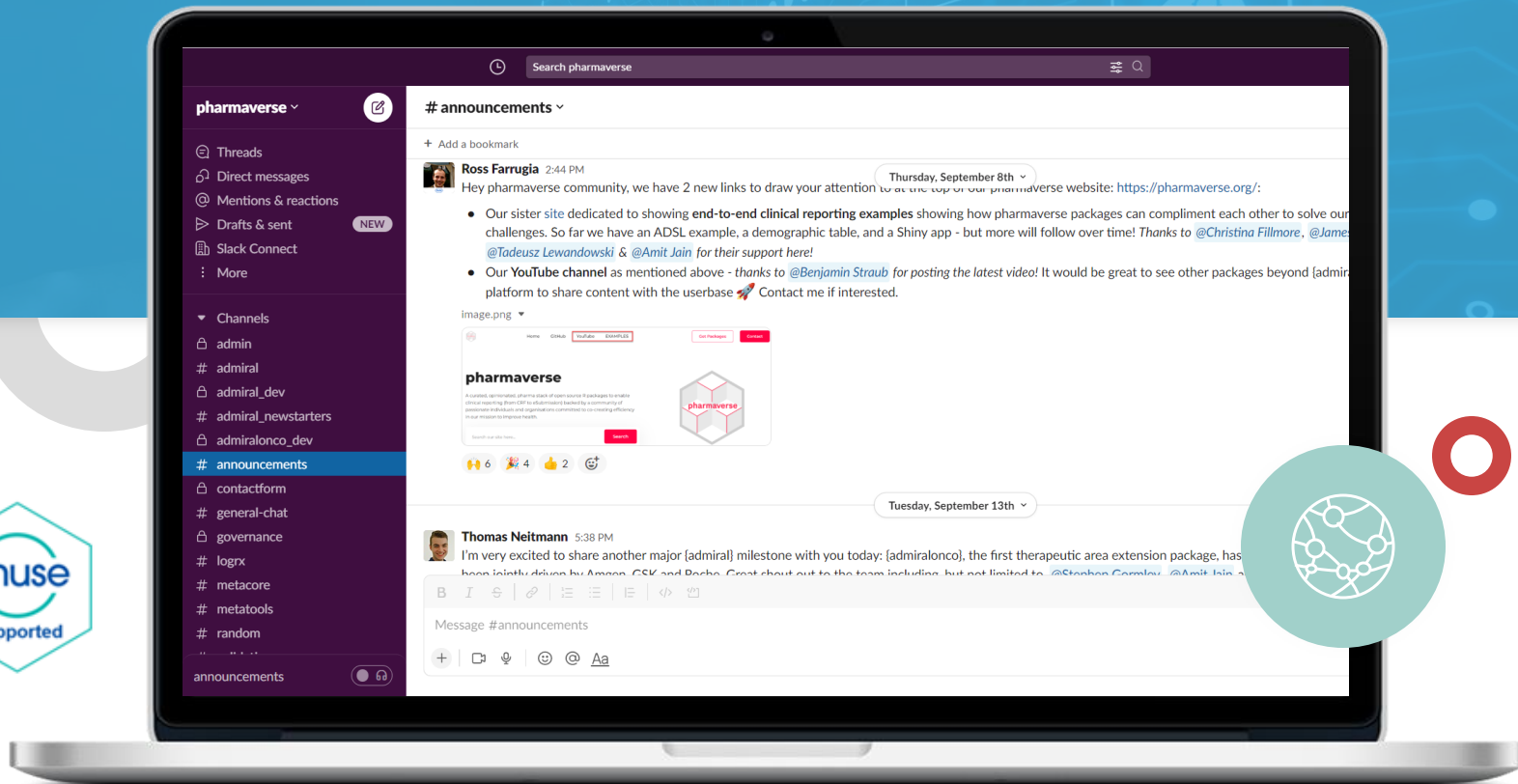


# Where are we now?

250+ Contributors → 30+ packages



# PHUSE Supported | 1300+ on Slack | 400 on LinkedIn





Contains data check functions to identify SDTM issues that are generalizable, actionable, and meaningful for analysis



Applying a datacut to SDTM



An EDC and Data Standard agnostic solution that enables development of CDISC SDTM datasets using R



Modular framework to generate ADaM via R functions relying on community contributions




























# Software Tools\*

Openly borrowed from Session 6a



Study Design	Data Collection	SDTM	ADaM	Define-XML	ARS
Open Study Builder 	odmlib 	sdtm.oak 	admiral 	OpenCST 	TLF Designer** 
Study Definitions Workbench 	ODM XML Stylesheet 	Dataset-JSON Tools 	Dataset-JSON Tools 	defineR 	cards 
BC Browser 		CORE 	carver 	odmlib 	gtsummary 
DDF SDR 		Smart Dataset Viewer 		Define XSL Stylesheet 	JMP Clinical** 

\* Examples listed – not a comprehensive listing

\*\* Open-source components expected to be available

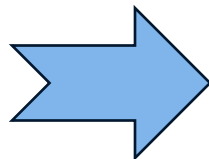


# Example 1:



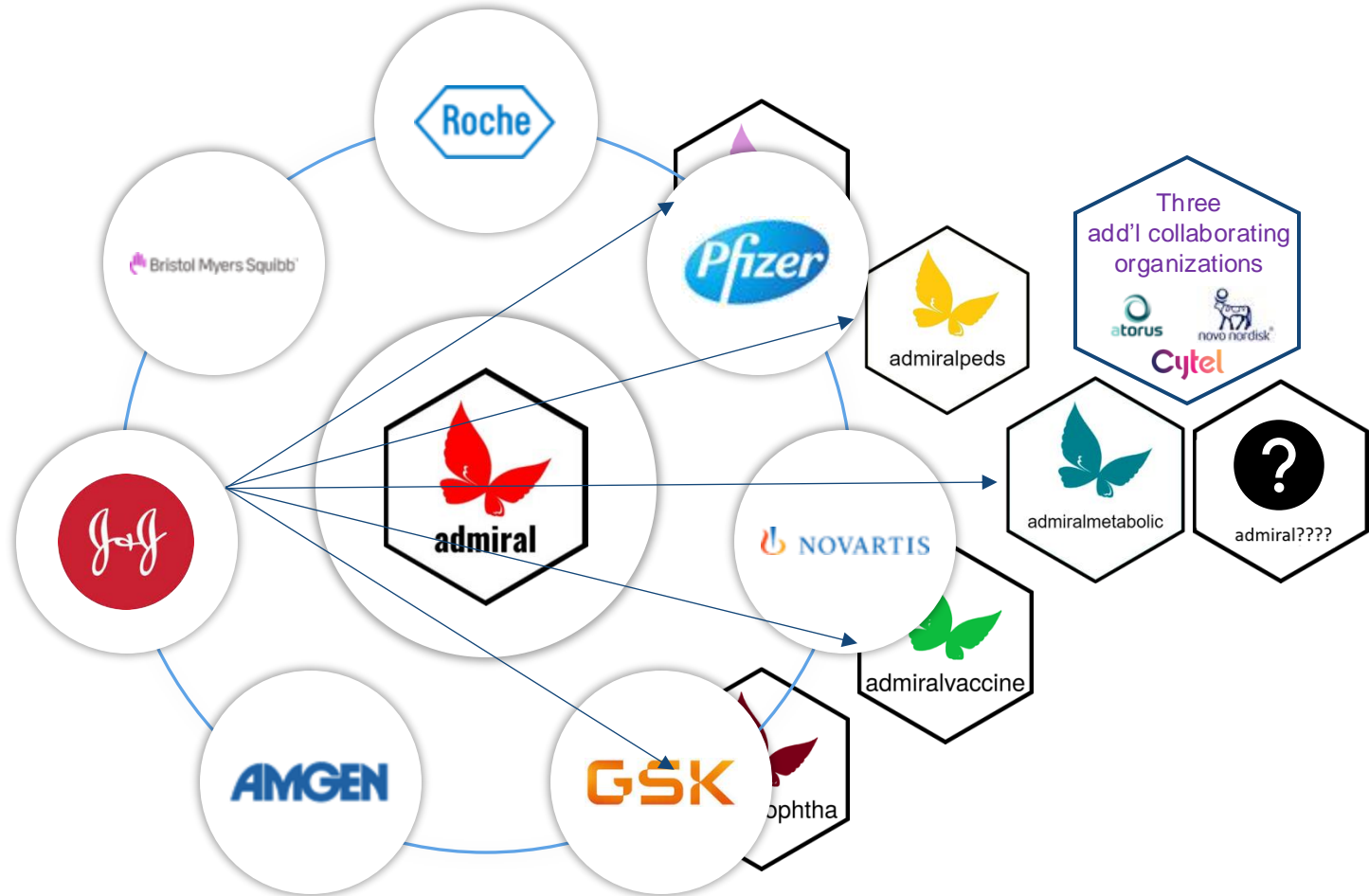
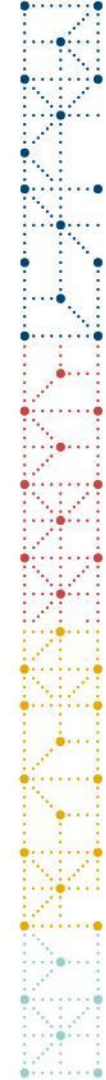
...to facilitate logging in a clinical environment with the goal of making code easily traceable and reproducible.

- Create a log for the execution of an R script
- Why?
  - We've come to expect them
  - GxP (reproducibility, traceability)
  - Enable debugging
- What? `axecute()`
  - Provide an overview of what happened
  - Document the environment of execution



```
-----
logrx Metadata
-----
This log was generated using logrx 0.1.0
logrx package version: 0.1.0
logrx build: local
logrx link to repository: https://github.com/atorus-research/logrx
-----
User and File Information
-----
User: rstudio-user
File Name: adsl.R
File Path: /cloud/project/data-raw
-----
Session Information
-----
- Session info -----
setting value
version R version 4.1.3 (2022-03-10)
os Ubuntu 20.04.4 LTS
system x86_64, linux-gnu
ui RStudio
language (EN)
collate C.UTF-8
ctype C.UTF-8
tz UTC
date 2022-06-02
rstudio 2022.02.2+485.pro2 Prairie Trillium (server)
pandoc NA

- Packages -----
package * version date (UTC) lib source
admiral * 0.7.0 2022-05-31 [1] RSPM (R 4.1.0)
admiral.test * 0.2.0 2022-05-30 [1] RSPM (R 4.1.0)
assertthat 0.2.1 2019-03-21 [1] RSPM (R 4.1.0)
bslib 0.3.1 2021-10-06 [1] RSPM (R 4.1.0)
cachem 1.0.6 2021-08-19 [1] RSPM (R 4.1.0)
cli 3.3.0 2022-04-25 [1] RSPM (R 4.1.0)
crayon 1.5.1 2022-03-26 [1] RSPM (R 4.1.0)
DBI 1.1.2 2021-12-20 [1] RSPM (R 4.1.0)
diffdf * 1.0.4 2020-03-17 [1] RSPM (R 4.1.0)
digest 0.6.29 2021-12-01 [1] RSPM (R 4.1.0)
dplyr * 1.0.9 2022-04-28 [1] RSPM (R 4.1.0)
ellipsis 0.3.2 2021-04-29 [1] RSPM (R 4.1.0)
fansl 1.0.3 2022-03-24 [1] RSPM (R 4.1.0)
fontaine 1.1.0 2021-03-25 [1] RSPM (R 4.1.0)
```



## Example 3: {diffdf}

...to enable detailed comparison of two data.frames.

- Used as 'PROC COMPARE' for QC using R
- Why?  
“Whilst many packages exist for informing you if there are differences between data.frames, none provide as much detail on what and where those differences are as diffdf does!”
- What?
  - Checking for differences in values, attributes, classes, column names, number of observations
  - Matching rows by key/id variables
  - Fuzzy comparisons
  - Extracting datasets of different rows

```
test_data2 <- test_data
test_data2 <- test_data2[,-6]
diffdf(test_data , test_data2 , suppress_warnings = T)
#> Differences found between the objects!
#>
#> A summary is given below.
#>
#> There are columns in BASE that are not in COMPARE !!
#> All rows are shown in table below
#>
#> =====
#>   COLUMNS
#>   -----
#>   DATE
#>   -----
#>
#> There are rows in BASE that are not in COMPARE !!
#> All rows are shown in table below
#>
#> =====
#>   ..ROWNUMBER..
#>   -----
#>
#>   29
#>   30
#>   -----
#>
#> Not all Values Compared Between Objects
#> All rows are shown in table below
#>
#> =====
#>   Variable  No of Differences
#>   -----
#>   GROUP1      1
#>   -----
#>
#>
#> All rows are shown in table below
#>
#> =====
#>   VARIABLE  ..ROWNUMBER..  BASE  COMPARE
#>   -----
#>   GROUP1      5          1      6
#>   -----
```

# CDISC Open Source Alliance (COSA)

- Several packages are part of both Pharmaverse and COSA
  - datasetjson R package born out of initial Dataset JSON hackathon
  - Built through collaboration between Atorus and J&J
- Additional support from COSA for packages such as admiral
  - Orchestration of hackathons
  - Supporting additional R package projects like sdtm.oak
  - Embracing open-source packages for CDISC activities within pharmaverse



# Posit webinar: Submission Experience



datacutr



sdtm.oak



admiral



admiralonco



METATOOLS



metacore



xportr



rtables

listings

chevzon

team



pkglite



# Imagine a world where...



*every company (large & small), charity, academic group etc all have access to FREE solutions to support creating a clinical submission*



*regulators receive more consistent data submission packages delivered using trusted code, thus speeding up approval times and patient access*



*less resource intensive clinical reporting leads to individual data science talents being freed to help generate new scientific insights*



*our regulatory pathways are revolutionised opening the doors for paperless submissions via interactive tools*



***we achieve all of the above TOGETHER (as Sapiens)!***



# HMW Enable and Automate?





## How might you help?



What features of packages...

- ...do you like?
- ...would you like added?
- ...would you like improved?



Raise issues



Engage in Issue discussions



Upvote Issues or comments



Pull request updates



What are your thoughts on pharmaverse at the moment?

***R you ready?***



# useful links...



[pharmaverse.council@phuse.global](mailto:pharmaverse.council@phuse.global)



**slack channel:**

<https://pharmaverse.slack.com/>



*join*



**website:**

<https://pharmaverse.org/>



**examples:**

<https://pharmaverse.github.io/examples/>



**Michael Rimler**

*Open Source Technologies Director, PHUSE  
Director, Vx Prog, Head Flu/Covid, GSK  
[michael.rimler@phuse.global](mailto:michael.rimler@phuse.global)*



**pharmaverse blog:**

<https://pharmaverse.github.io/blog/>



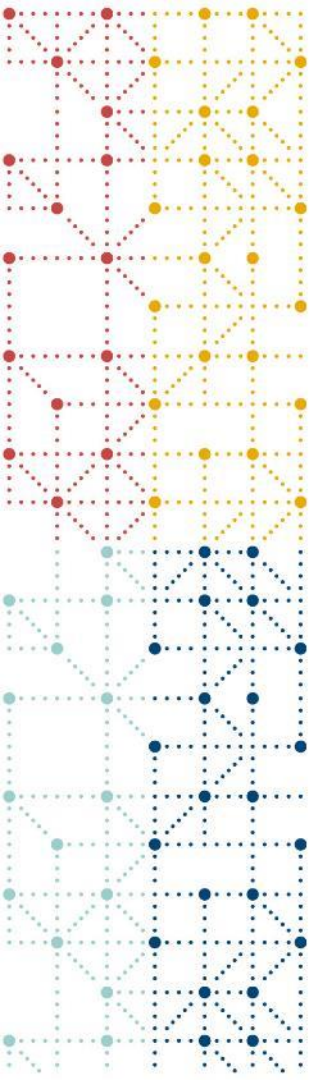
**youtube:**

<https://www.youtube.com/channel/UCxQFEv8HNqM01DXzdQLCy6Q>



**linkedin:**

<https://www.linkedin.com/groups/9126149/>



**Thank You!**

**cdisc**