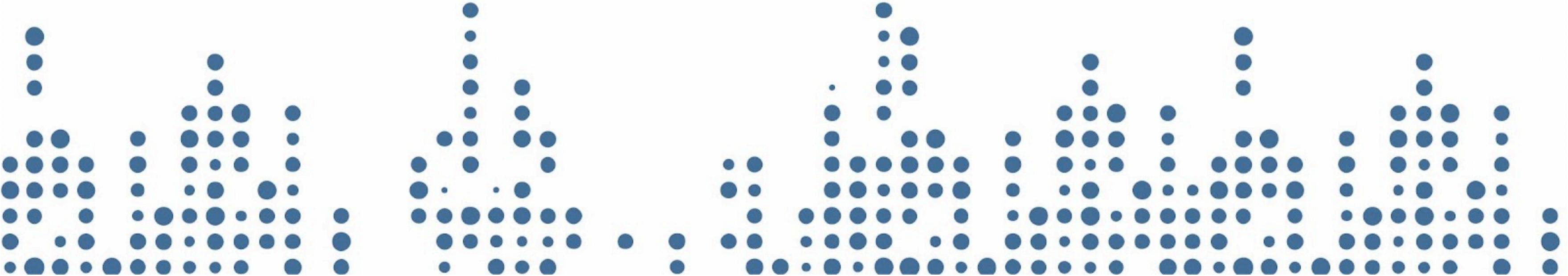


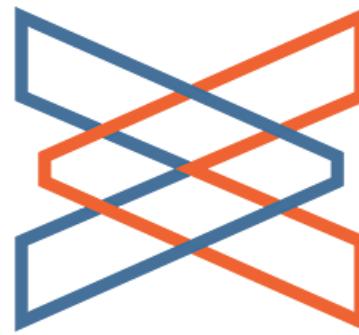


Trying Out Positron:

New IDE for Statistical Programming



Hello PharmaSUG!

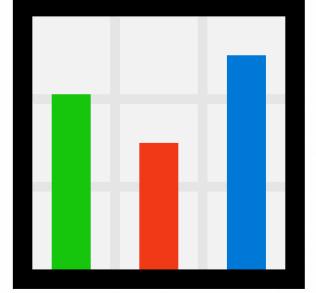


-  Phil Bowsher @philbowsher
-  youtube.com/rinpharma
-  rinpharma.com

>

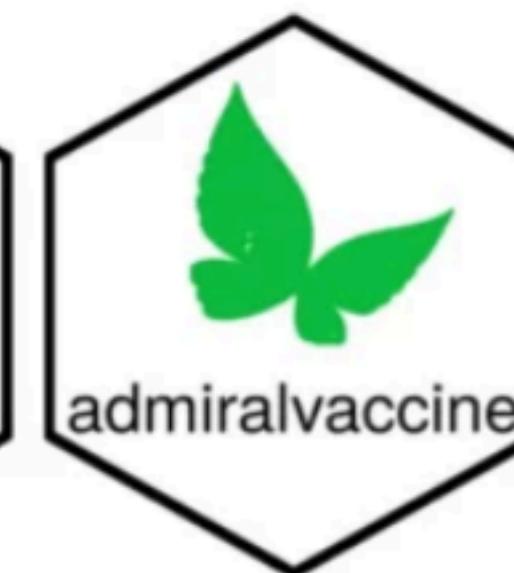


positron.posit.co



<





pharmaverse examples



Introduction

SDTM >

ADaM ▾

ADSL

ADPC

ADPPK

ADRS

ADTTE

ADVS

ADAE

ADaM > ADSL

ADSL

Introduction

This guide will show you how four pharmaverse packages, along with some from tidyverse, can be used to create an ADaM such as [ADSL](#) end-to-end, using [{pharmaversesdtm}](#) SDTM data as input.

The four packages used with a brief description of their purpose are as follows:

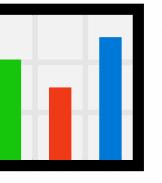
- [{metacore}](#): provides harmonized metadata/specifications object.
- [{metatools}](#): uses the provided metadata to build/enhance and check the dataset.
- [{admiral}](#): provides the ADaM derivations. (Find functions and related variables by searching [admiraldiscovery](#))
- [{xportr}](#): delivers the SAS transport file (XPT) and eSub checks.

It is important to understand [{metacore}](#) objects by reading through the above linked package site, as these are fundamental to being able to use [{metatools}](#) and [{xportr}](#). Each company may need to build a specification reader to create these objects from their source standard specification templates.

>



pharmaverse.github.io/examples/



<

Positron is...



:
a **next generation** - *a.k.a. open source!*

Positron is...



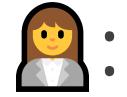
:
a next generation **data science integrated development environment (IDE)**

Positron is...



a next generation data science integrated development environment (IDE) **currently
in Public Beta**

Positron is...



:

a next generation data science integrated development environment (IDE) currently in Public Beta & **is available for free on desktop and as a Preview feature within Posit Workbench**

Welcome - phil - Positron

dev.current.posit.team/s/c1a7a6ae9dc1bb4e21043/?folder=/home/phil

New Chrome available :

Welcome - phil - Positron

SESSION HELP VIEWER CONNECTIONS

PLOTS

SESSION

SEARCH

R 4.4.1 phil

Start

Open

- New Notebook
- New File

Recent

- dashboard ~/py-shiny-templates

CONSOLE TERMINAL PROBLEMS OUTPUT PORTS DEBUG CONSOLE

R 4.4.1 ~/

You are welcome to redistribute it under certain conditions.
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.

VARIABLES

No variables have been created.

filter

Layout: US

The screenshot displays the Positron IDE interface. The top navigation bar shows the title "Welcome - phil - Positron" and the URL "dev.current.posit.team/s/c1a7a6ae9dc1bb4e21043/?folder=/home/phil". A notification "New Chrome available :" is visible. The main workspace is titled "Welcome - phil - Positron" and includes tabs for SESSION, HELP, VIEWER, and CONNECTIONS. On the left, a sidebar features icons for file operations (New, Open, Save, Find, Refresh, Help, Settings) and a gear icon. The central area displays the Positron logo and the text "an IDE for data science". Below this are sections for "Start" (New Notebook, New File), "Open" (Open File..., Open Folder..., New Folder..., New Folder from Git...), and "Recent" (dashboard, ~/py-shiny-templates). The bottom left shows the R 4.4.1 console output, which includes the R startup message, information about natural language support, and instructions for contributors and citation. The bottom right shows the "VARIABLES" panel with a message stating "No variables have been created." The status bar at the bottom indicates "Layout: US" and shows system information like battery level (0%), signal strength (0), and Quarto version (1.5.57).

Files

Editor

Console

Environment

dev.palm.ptd.posit.it/s/062496ae9dc1b9bf79802/?folder=/home/phil

ggplot2_example.R - phil - Posit

Introducing Viewing Plots in Edi

ggplot2_example.R - phil - Positron

R 4.4.0

phil

EXPLORER

PHIL

- > .cache
- > .config
- > .duckdb
- > .ipython
- > .local
- > .positron-server
- > py-shiny-templates
- > py-shiny-templ... ●
- > quarto_example_files
- > R
- ≡ .bash_history
- \$.bash_logout
- \$.bashrc
- ❖ .gitconfig
- \$.profile
- ≡ .Renvironment
- ❸ ggplot2_example.R
- ❸ plotlyexample.R
- ❸ quarto_example.html
- ❸ quarto_example.qmd
- ❸ test app.R

CONSOLE

```
1 library(ggplot2)
2 
3 p <- ggplot(data = diamonds, aes(x = cut, fill = clarity))
4     geom_bar(position = "dodge")
5 p
```

R 4.4.0

or

```
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

SESSION

HELP

VIEWER

CONNECTIONS

VARIABLES

R 4.4.0

VALUES

p [data = [53940 rows x 10 columns] <tbl_df>, l... gg

PLOTS

Fit Auto

Output

count

clarity

- I1
- SI2
- SI1
- VVS2
- VVS1
- VV52
- VVS1
- IF

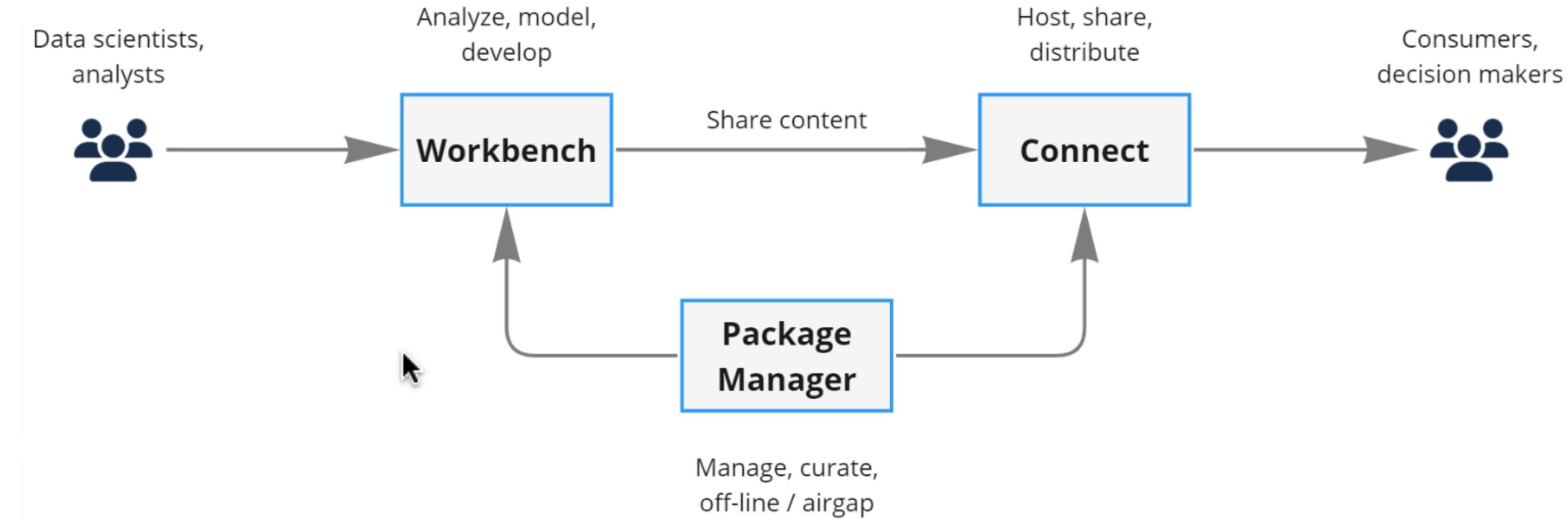
Fair Good Very Good Premium Ideal

Ln 5, Col 2 (121 selected) Spaces: 2 UTF-8 LF R Layout: US

Posit Workbench:

-  Server Based Environment
- Provides Various IDEs (RStudio, Positron etc.)
- Compute is in the Server or Cloud Based Environment (AWS, Azure etc.)
-  Managed by the Organization (Or Posit Team Dedicated)

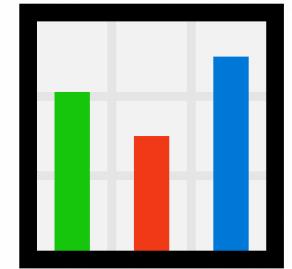
Posit Team Architecture



>

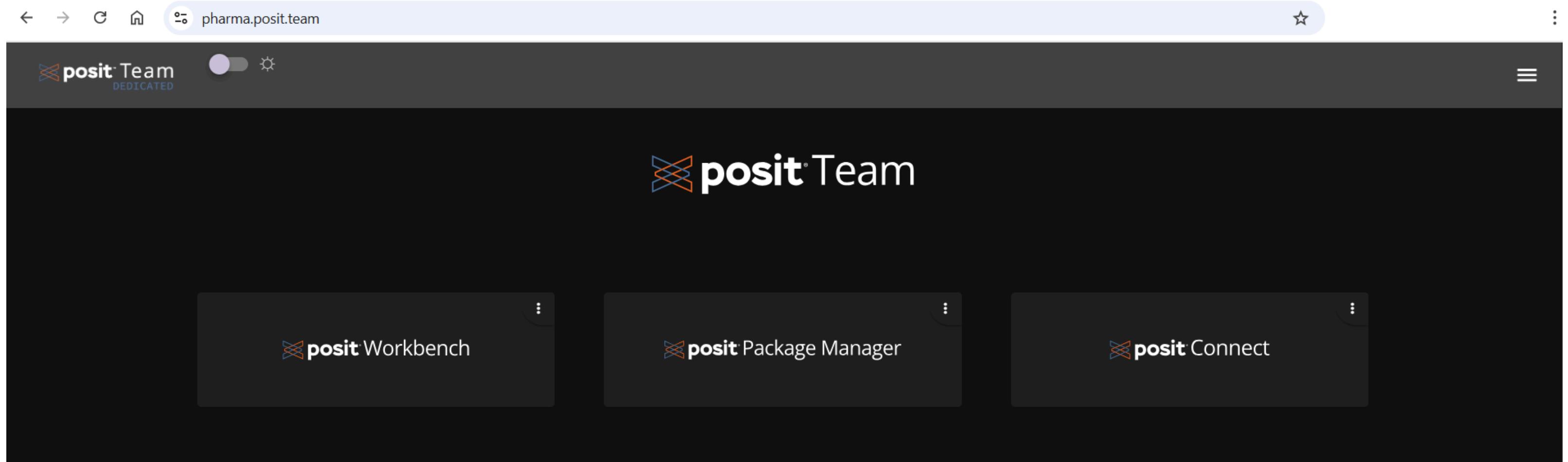


pharma.posit.team



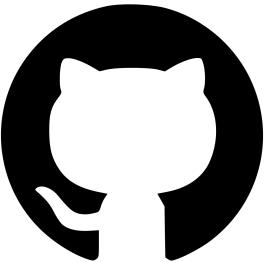
<

pharma.posit.team



Posit Workbench

-  Click “Sign in with OpenID”
-  Click “New user? Register”
- Make sure to include both First Name and last initial



- OR, click
- Sign in to GitHub

CREATE // Rename // EDIT

New Session

Jupyter Notebook JupyterLab **Positron Pro** Preview RStudio Pro VS Code

Session Name
Phil's Positron

Session Credentials Edit Credentials

Posit AWS POSIT_SOFTWARE_PBC_DEV

Cluster Options

When selecting a memory amount, use at least 4 GB

Resource Profile
Large

CPUs Memory (GB)
4 7.81

Image
rstudio-workbench-preview:dev-jammy-2024.12.1-563.pro2 (default) Edit

Join session when ready Notify when ready

Cancel Start Session

In workbench...

-  Select “New Session”
-  Click “Positron”
- In cluster Options, Select a Large Resource Profile
- Click “Start Session”



Sessions

+ New Session

Create a new session

+ New Session

Projects

typst-css

~/typst-css

LAST USED: 10/7/2024

quarto-website-test

~/quarto-website-test

LAST USED: 9/24/2024



test_ws

~/test_ws

LAST USED: 9/24/2024

test123

~/test123

LAST USED: 9/24/2024

>



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



<

> Clone Repo

Follow these steps:



Start



New Notebook



New File



New Console



New Project

Help

[Positron Documentation](#)

[Positron Community](#)

[Report a bug](#)

Open

- Open File...
- Open Folder...
- New Folder...
- New Folder from Git...

[Open a new folder from Git.](#)

Recent

- [Open-Source-Drug-Development-ADAM-TLGs-Interactivity-...](#)
- [phil /home](#)
- [py-shiny-templates ~](#)

New Folder from Git

Git repository URL

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

Create folder as subfolder of

</home/phil/pharmaverse>

[Browse...](#)

Open in a new window

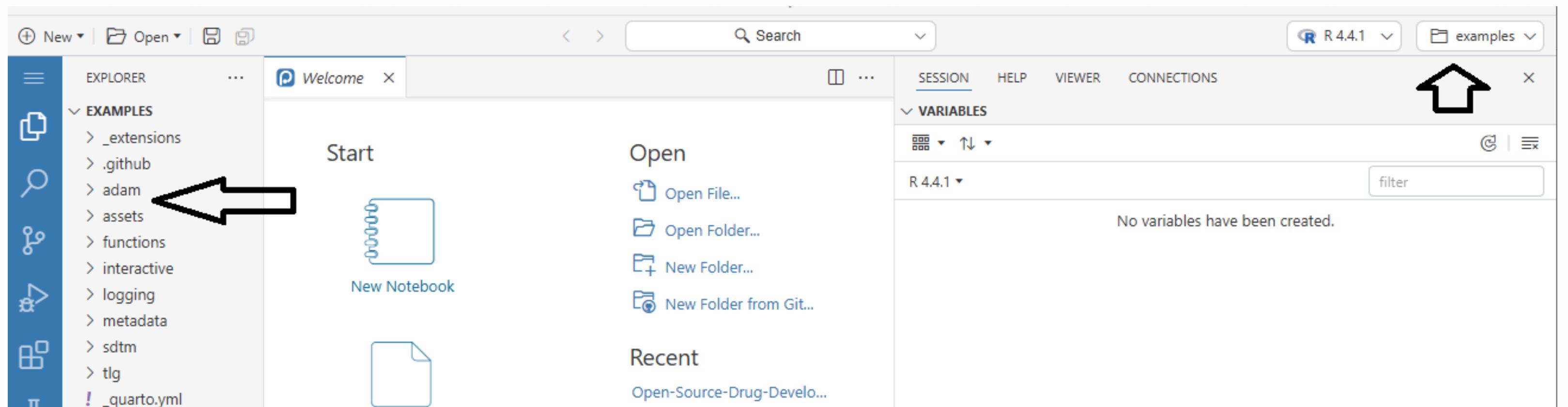
[OK](#)

[Cancel](#)



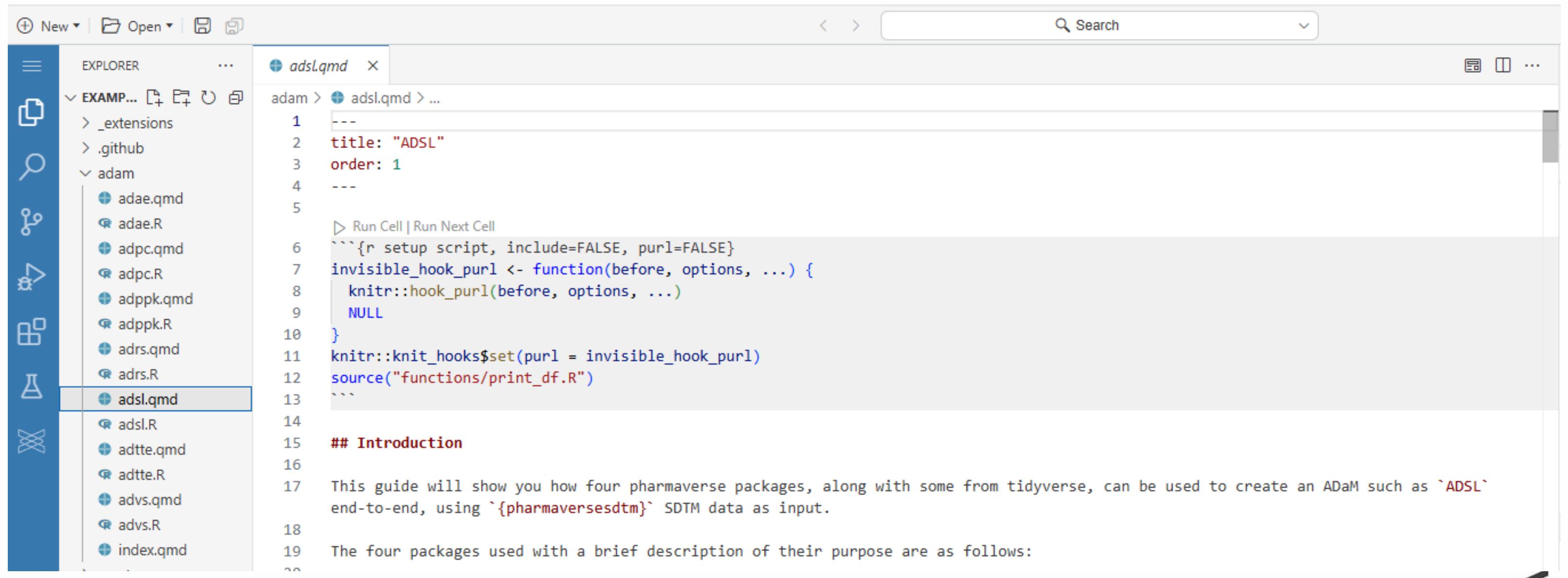
Open Folder

Open the “adam” folder as seen here:



Open ADSL

Open the adsl.qmd file as below:



The screenshot shows a code editor interface with a sidebar and a main editor area. The sidebar on the left has icons for New, Open, Save, and other file operations. Below these are sections for EXAMP... (with _extensions and .github), adam (with adae.qmd, adae.R, adpc.qmd, adpc.R, adppk.qmd, adppk.R, adrs.qmd, adrs.R), and a selected item adsl.qmd. The main editor area shows the content of the adsl.qmd file. The code is a QMD (Quarto Markdown Document) file. It includes R code for setting up a script, defining an invisible hook for purl, and sourceing a function. It also contains a section titled "## Introduction" and a paragraph explaining the purpose of the document.

```
1 ---  
2 title: "ADSL"  
3 order: 1  
4 ---  
5  
6 ```{r setup script, include=FALSE, purl=FALSE}  
7 invisible_hook_purl <- function(before, options, ...){  
8   knitr::hook_purl(before, options, ...)  
9   NULL  
10 }  
11 knitr::knit_hooks$set(purl = invisible_hook_purl)  
12 source("functions/print_df.R")  
13 ```  
14  
15 ## Introduction  
16  
17 This guide will show you how four pharmaverse packages, along with some from tidyverse, can be used to create an ADaM such as `ADSL` end-to-end, using `pharmaversesdtm` SDTM data as input.  
18  
19 The four packages used with a brief description of their purpose are as follows:  
20
```

>

Run ADSL

Run the Quarto code chunks using the “Run/Play” button. Continue running the chunks all the way through the Quarto document to generate the adsl dataset:

The screenshot shows the RStudio interface with the Quarto document 'adsl.qmd' open. The left sidebar displays the project structure under 'EXAMPLES'. The main pane shows the Quarto code with two arrows pointing to the 'Run Cell' button in the code editor. The right sidebar shows the generated datasets: 'adsl' (306 rows x 51 columns), 'adsl_cat' (306 rows x 19 columns), 'adsl_ct' (306 rows x 20 columns), 'adsl_cust' (306 rows x 19 columns), 'adsl_preds' (306 rows x 17 columns), 'adsl_raw' (306 rows x 29 columns), and 'ae' (1191 rows x 35 columns). A large black arrow points from the 'Run Cell' button to the generated datasets.

```
adsl.qmd X Data: adsl
adam > adsl.qmd > Start Building Derivations > Grouping Variables > (code cell)
29 ## Programming Flow
40
41 ## Load Data and Required pharmaverse Packages {#loaddata}
42
43 The first step is to load our pharmaverse packages and input data.
44 D Run Cell | Run Next Cell | Run Above
45 `r setup_message=FALSE, warning=FALSE, results='hold'
46 li Execute the code in this cell
47 library(metatools)
48 library(pharmaversesdtm)
49 library(admiral)
50 library(xportr)
51 library(dplyr)
52 library(tidyr)
```

> adsl	[306 rows x 51 columns] <tbl_df>	
> adsl_cat	[306 rows x 19 columns] <tbl_df>	
> adsl_ct	[306 rows x 20 columns] <tbl_df>	
> adsl_cust	[306 rows x 19 columns] <tbl_df>	
> adsl_preds	[306 rows x 17 columns] <tbl_df>	
> adsl_raw	[306 rows x 29 columns] <tbl_df>	
> ae	[1191 rows x 35 columns] <tbl_df>	

<

Follow the same steps but for ADAE...

- 🧑 Users can use the adsl, ae, and ex datasets from the pharmaverseadam R package
- Or use the created ADSL data
- Run the chunks in the Quarto document to create our final ADAE dataset

>

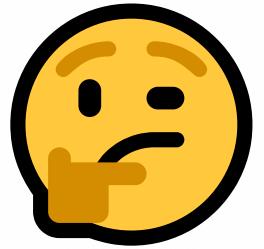
```
1 library(pharmaverseadam)
2 adae <- adae
```

<

>



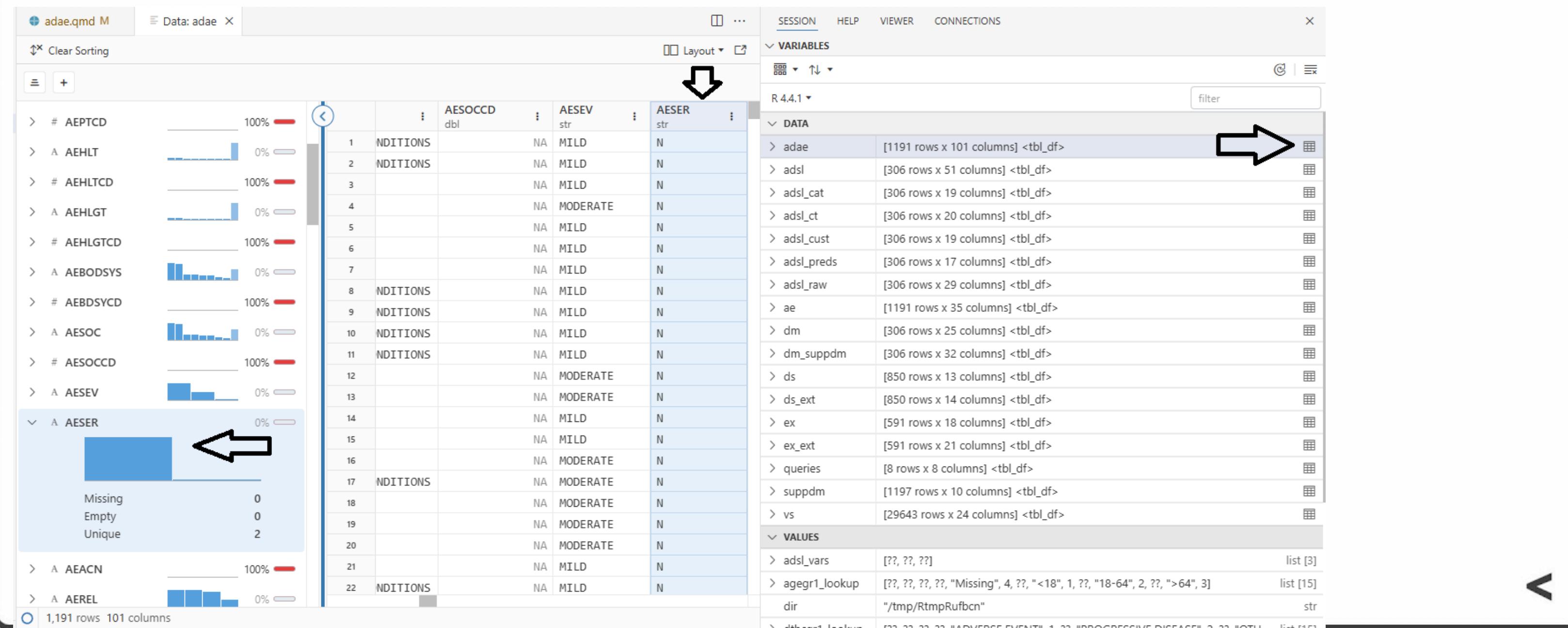
How do I see the data? (



<

Review ADAE:

We will review the adae dataset by clicking on the the dataset icon on the right side of name as in:



>

Using GenAI in Positron

We will use generative artificial intelligence (GenAI) to create an app with Shiny for R:

- 🧑 Create the Shiny app with the ellmer R package
- Positron Assistant to provide LLM integration within Positron
- We will use the Anthropic Claude model

<

AI - Productivity

olympic-analysis.R — positron-assistant-demo

New Open ⌂ ⌂ Search R 4.4.3 positron-assistant-demo

CHAT 

Positron Assistant

Positron Assistant is an AI coding companion designed to accelerate and enhance your data science projects.

Click on or type @ to work with Chat Participants in Positron Assistant.

Click on # or type # to add context, such as files to your Positron Assistant chat.

Type / to use predefined quick commands such as /help or /quattro.

The [Positron Assistant User Guide](#) explains the possibilities and capabilities of Positron Assistant.

Always verify results. AI assistants can sometimes produce incorrect code.

olympic-analysis.R ...

```
1 #| label: load-packages
2 library(tidyverse)
3 library(gt)
4
5 olympics_full <- read_csv("data/olympics.csv")
6
7 #| label: prep-data
8 olympics <- olympics_full |>
9   filter(!is.na(medal)) |>
10  separate_wider_delim(
11    cols = team,
12    names = c("team", "suffix"),
13    delim = "-",
14  )
```

SESSION CONNECTIONS HELP VIEWER ... X

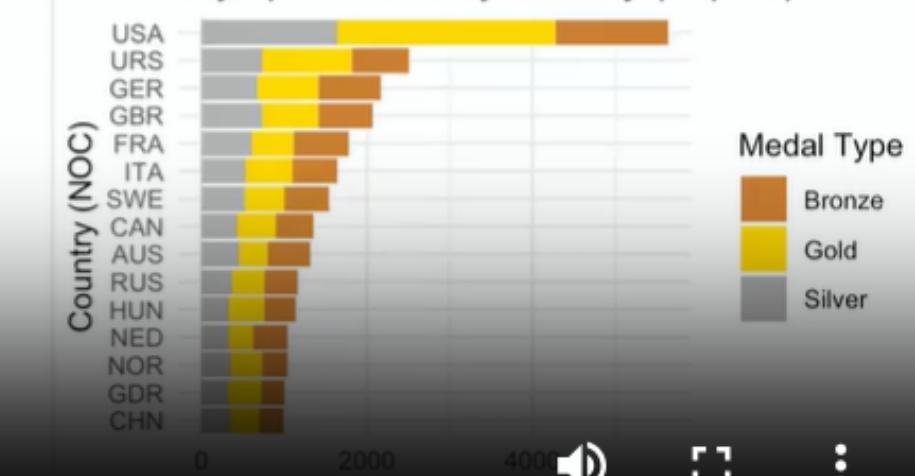
VARIABLES

R 4.4.3 DATA

	olympics_data	[271116 rows x 15 columns] <data.fr...
> id	15 15 16 17 17 20 20 29 37 ...	int [271116]
> name	"Arvo Ossian Aaltonen" "Ar...	str [271116]
> sex	"M" "M" "M" "M" "M" "M" ...	str [271116]
> age	30 30 28 28 32 20 22 22 2...	int [271116]
> height	NA NA 184 175 175 176 176...	int [271116]
> weight	NA NA 85 64 64 85 85 NA...	dbl [271116]
> team	"Finland" "Finland" "Finlan..."	str [271116]

PLOTS

Olympic Medals by Country (Top 15)



Country (NOC)

Medal Type

Bronze

Gold

Silver

0 2000 4000 Number of Medals

0:00 / 0:42 ⏪ ⏴

Positron-Assistant

>

```
1 library(ellmer)
2
3 chat <- chat_claude()
4
5 chat$chat("using the adae R dataset here in my session, help me create a simple Shiny app. Add sections in the app th
```

<

Use GenAI

This code will be executed in Positron as below:

The screenshot shows the Posit RStudio interface. The top navigation bar includes tabs for 'adae.qmd M', 'ellmer_app.R U', 'shiny_adae.R U', and 'adsl.R'. The main area displays R code and its output. A large black arrow points from the text 'using the adae R dataset here in my session, help me create a simple Shiny app.' to the 'DATA' panel on the right. Another large black arrow points from the 'library(ellmer)' line to the 'CONSOLE' tab at the bottom. A third black arrow points from the 'library(dplyr)' line to the 'DATA' panel. The 'DATA' panel lists various datasets: adae, ads1, ads1_cat, ads1_ct, ads1_cust, ads1_preds, ads1_raw, ae, dm, dm_suppdm, ds, ds_ext, ex, ex_ext, suppdm, vs. The 'VALUES' and 'PLOTS' panels are also visible.

```
adae.qmd M ellmer_app.R U shiny_adae.R U adsl.R ... SESSION HELP VIEWER CONNECTIONS X
adam > ellmer_app.R ...
1 library(ellmer)
2 chat <- chat_claude()
3
4 chat$chat("using the adae R dataset here in my session, help me create a simple Shiny app. Add sections in the app that explains what kind of dataset it is")
Here's an enhanced Shiny app for the adae dataset that includes informational sections:
```r
library(shiny)
library(ggplot2)
library(dplyr)

UI portion
ui <- fluidPage(
 titlePanel("ADAE (Adverse Events Analysis Dataset) Explorer"),

 # Information Section
 wellPanel(
 h3("About this Dataset"),
 p("ADAE is a standard analysis dataset for Adverse Events in clinical trials.
 It contains information about adverse events reported during the study."),
 h4("Key Variables:")
)
)
```

CONSOLE TERMINAL PROBLEMS OUTPUT PORTS DEBUG CONSOLE — □ □

R 4.4.1 ~ /pharmaverse/examples

> chat\$chat("using the adae R dataset here in my session, help me create a simple Shiny app. Add sections in the app that explains what kind of dataset it is")
Here's an enhanced Shiny app for the adae dataset that includes informational sections:
```r
library(shiny)
library(ggplot2)
library(dplyr)

UI portion
ui <- fluidPage(
 titlePanel("ADAE (Adverse Events Analysis Dataset) Explorer"),

 # Information Section
 wellPanel(
 h3("About this Dataset"),
 p("ADAE is a standard analysis dataset for Adverse Events in clinical trials.
 It contains information about adverse events reported during the study."),
 h4("Key Variables:")
)
)

SESSION HELP VIEWER CONNECTIONS X

VARIABLES

R 4.4.1 filter

DATA

| Object | Type |
|------------|------------------------------------|
| adae | [1191 rows x 113 columns] <tbl_df> |
| ads1 | [306 rows x 51 columns] <tbl_df> |
| ads1_cat | [306 rows x 19 columns] <tbl_df> |
| ads1_ct | [306 rows x 20 columns] <tbl_df> |
| ads1_cust | [306 rows x 19 columns] <tbl_df> |
| ads1_preds | [306 rows x 17 columns] <tbl_df> |
| ads1_raw | [306 rows x 29 columns] <tbl_df> |
| ae | [1191 rows x 35 columns] <tbl_df> |
| dm | [306 rows x 25 columns] <tbl_df> |
| dm_suppdm | [306 rows x 32 columns] <tbl_df> |
| ds | [850 rows x 13 columns] <tbl_df> |
| ds_ext | [850 rows x 14 columns] <tbl_df> |
| ex | [591 rows x 18 columns] <tbl_df> |
| ex_ext | [591 rows x 21 columns] <tbl_df> |
| suppdm | [1197 rows x 10 columns] <tbl_df> |
| vs | [29643 rows x 24 columns] <tbl_df> |

VALUES

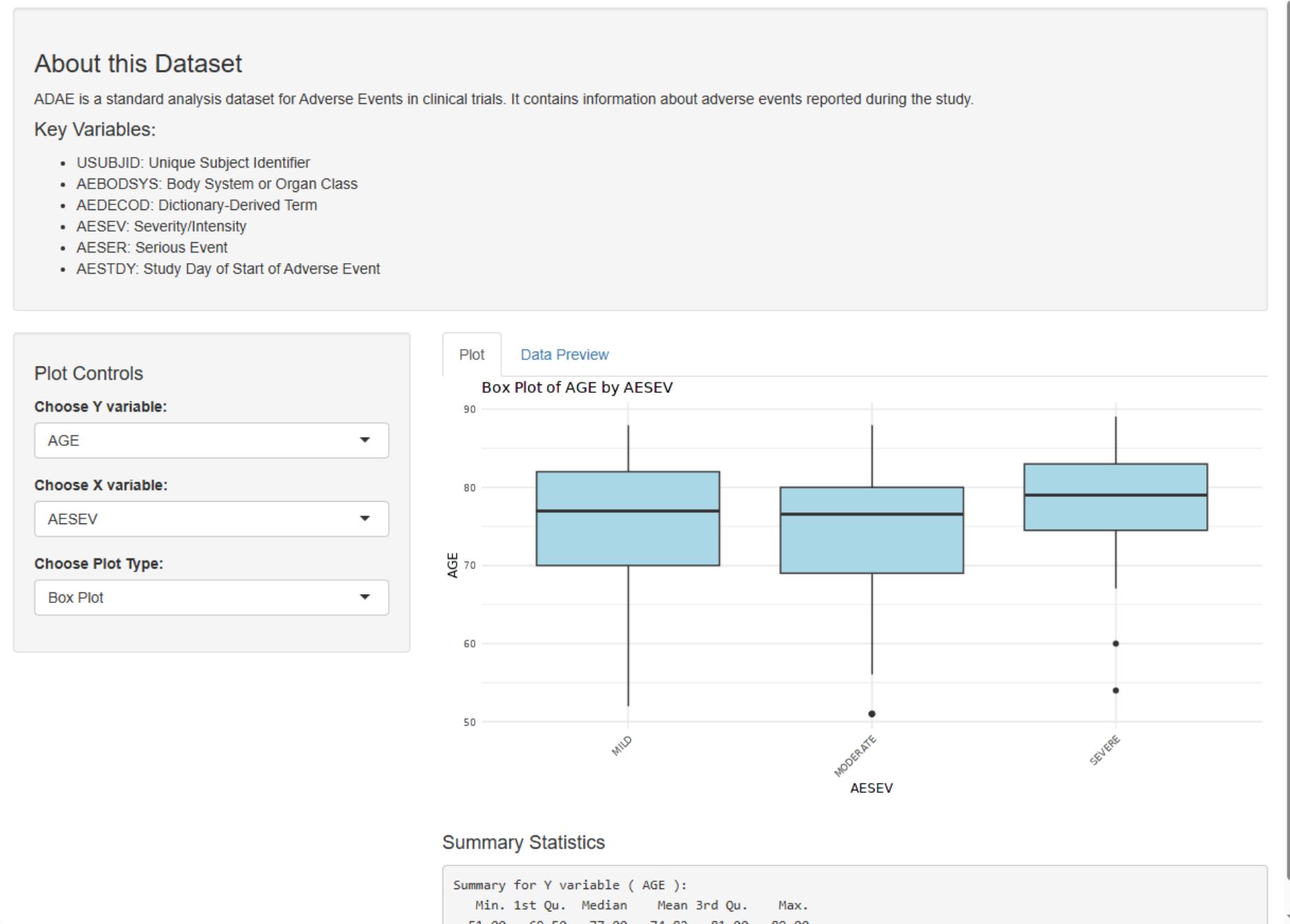
| Object | Type |
|---------------|---|
| ads1_vars | list [3] |
| agegr1_lookup | list [15] |
| chat | {chat, chat_async, clone, extract_data, extract_data_async, ... Chat} |

PLOTS

GenAI Shiny App

This will generate the following Shiny app!

ADAE (Adverse Events Analysis Dataset) Explorer



>



Agents



<

Run Databot Example in Positron

 <https://github.com/jcheng5/databot>

 `pak::pak("jcheng5/databot")`

 `databot::chat()`

 `adae`



Hi! I'm here to help you with your data analysis tasks in R. Here are some things I can help you with:

1. [Let's explore what data is currently loaded in the R session](#)
2. [Could you help me analyze a specific dataset?](#)
3. [I'd like to create some visualizations of my data](#)
4. [Could you help me create a reproducible report of my analysis?](#)

Of course, these are just suggestions - I'm happy to help with any other data analysis, manipulation, or visualization tasks you have in mind. What would you like to work on?

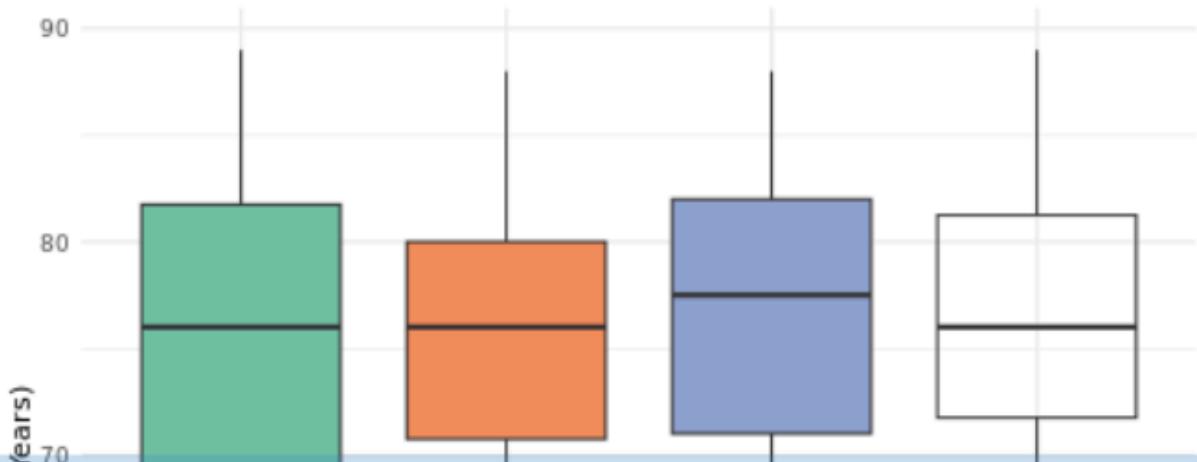


I'll create some visualizations to help us understand the age distribution across treatment arms using ggplot2.

```
library(ggplot2)
library(tidyverse)

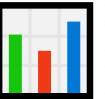
# Create a boxplot
ggplot(adsl_raw, aes(x = ARM, y = AGE, fill = ARM)) +
  geom_boxplot() +
  theme_minimal() +
  labs(title = "Age Distribution by Treatment Arm",
       x = "Treatment Arm",
       y = "Age (Years)") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        legend.position = "none") +
  scale_fill_brewer(palette = "Set2")
```

Age Distribution by Treatment Arm



Enter a message...

>

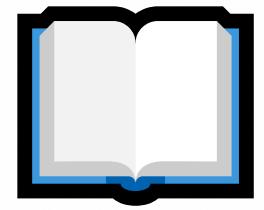
Could you help me create a reproducible report of my analysis? 

<

>



But how do I Share this?



<

Deploy to Connect

The screenshot illustrates the process of deploying a Shiny application using the Posit Publisher extension in a Jupyter Notebook.

Code Editor:

```
1 import seaborn as sns
2 from faicons import icon_svg
3
4 # Import data from shared.py
5 from shared import app_dir, df
6 from shiny import App, reactive, render, ui
7
8 app_ui = ui.page_sidebar(
9     ui.sidebar(
10         ui.input_slider("mass", "Mass", 2000, 6000),
11         ui.input_checkbox_group(
12             "species",
13             "Species",
14             ["Adelie", "Gentoo", "Chinstrap"],
15             selected=["Adelie", "Gentoo", "Chinstrap"]
16     ),
```

Terminal:

```
phil@session-062496ae9dc1b9bf79802-phil---phils-positron-k4
4xm-5vkxn:~/py-shiny-templates/dashboard$ /opt/python/3.12.
4/bin/python -m shiny run --port 35875 --reload --autoreload
d-port 44271 /home/phil/py-shiny-templates/dashboard/app-co
re.py
```

Deployment:

A large black arrow points upwards from the code editor towards the "Deploy with Posit Publisher" button in the toolbar.

Dashboard Preview:

The right side of the interface shows the "Penguins dashboard" with "Filter controls". It includes a slider for "Mass" ranging from 2,000 to 6,000, currently set at 33. Below it is a checkbox group for "Species" with three options: Adelie, Gentoo, and Chinstrap, all of which are checked.

>

Positron

Extensible, polyglot tool

<

← → ⌂ ⌂ dev.current posit.team/s/c1a7a6ae9dc1bb4e21043/?folder=/home/phil/py-shiny-templates/dashboard ⌂ New Chrome available ⌂

app-core.py - dashboard - Positron

EXPLORER DASHB... app-core.py < > Search SESSION HELP VIEWER CONNECTIONS PLOTS

app-core.py > ...

```
1 import seaborn as sns
2 from faicons import icon_svg
3
4 # Import data from shared.py
5 from shared import app_dir, df
6 from shiny import App, reactive, render, ui
7
8 app_ui = ui.page_sidebar(
9     ui.sidebar(
10         ui.input_slider("mass", "Mass", 2000, 6000, 6000),
11         ui.input_checkbox_group(
12             "species",
13             "Species",
14             ["Adelie", "Gentoo", "Chinstrap"],
15             selected=["Adelie", "Gentoo", "Chinstrap"],
16         ),
17         title="Filter controls".
```

CONSOLE TERMINAL PROBLEMS OUTPUT PORTS ...

Python 3.12.6 (Global) ~ /py-shiny-templates/dashboard

```
Python 3.12.6 (Global) started.
Python 3.12.6 (main, Oct 18 2024, 15:31:59) [GCC 11.4.0]
Type 'copyright', 'credits' or 'license' for more information
IPython 8.31.0 -- An enhanced Interactive Python. Type '?' for help.
>>>
```

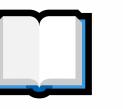
VARIABLES

No variables have been created.

filter

Posit Workbench ⌂ 0 △ 0 ⌂ 0 Ln 3, Col 1 Spaces: 4 UTF-8 LF {} Python Layout: US ⌂

>

 Familiar environment for reproducible authoring & publishing 

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GenAI in Pharma 2024



GENAI IN PHARMA



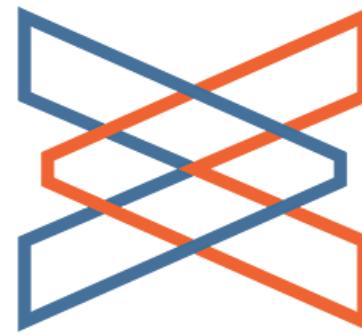
Done!

/Q: What do sharks order at McDonald's? A: A quarter\
\ flounder with cheese. /

\
\

/ " " - . _
. . ' - ,
: : ' ' ,
; ; * ' .
' * () ' .
\ \ .

Thank you!



@philbowsher

▶ youtube.com/rinpharma

🔗 rinpharma.com

