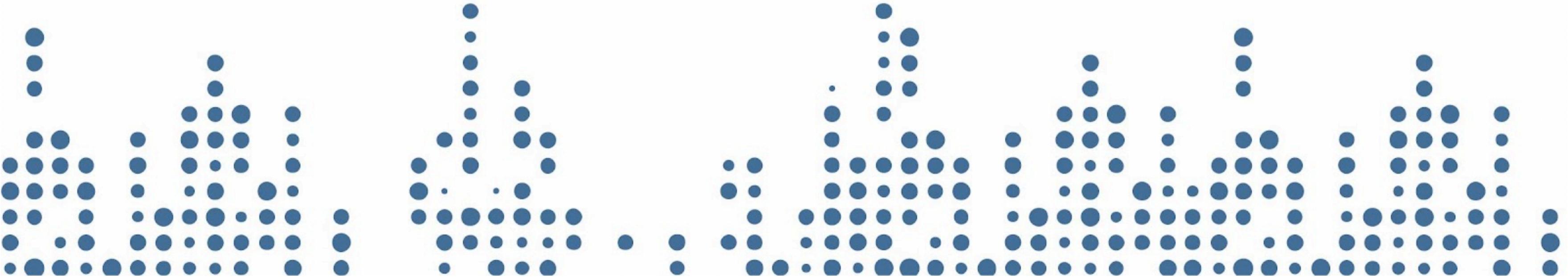


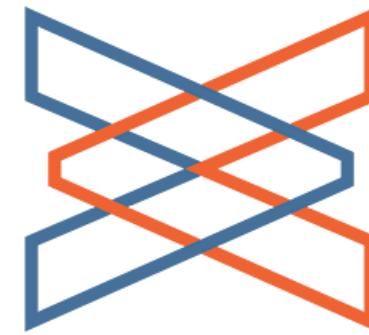


Next Generation Clinical Workflows

in R, & Python :), with Posit Team



Hello Phuse!



-  Michael Mayer @michaelmayer2
-  Aaron Jacobs @atheriel
-  Phil Bowsher @philbowsher
-  & Sumesh Kalappurakal

>

Intro, Sumesh Kalappurakal



<

First, a short survey



<https://fizz.ly/phil/survey>

Open Source Drug Development

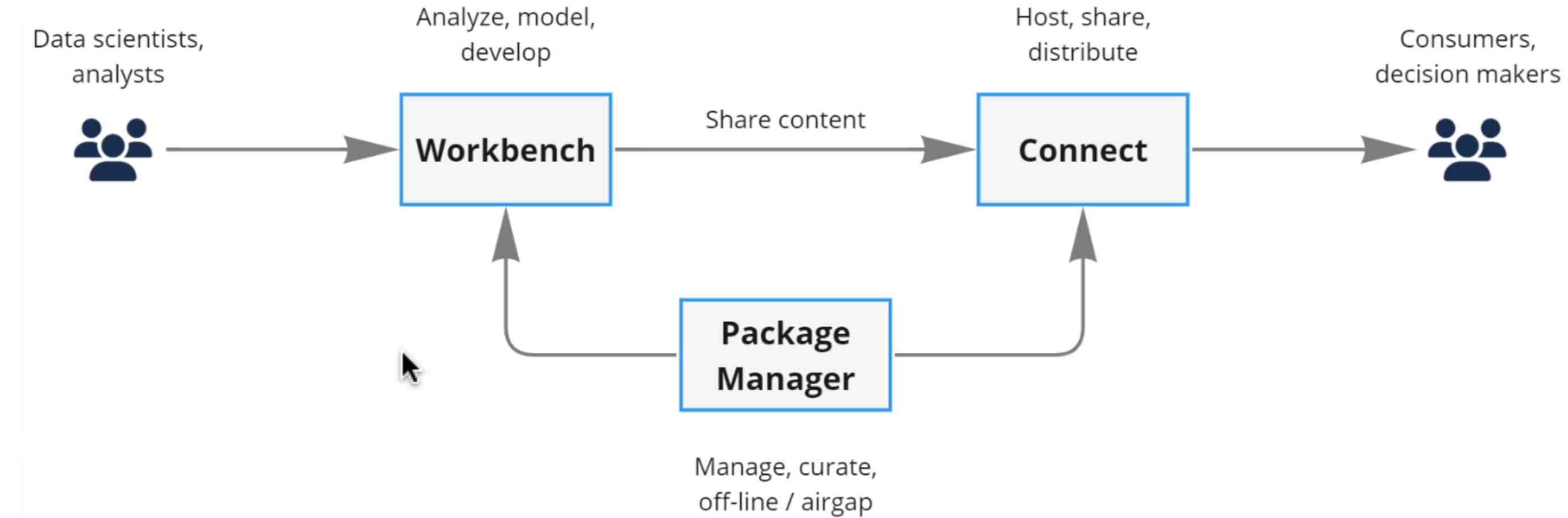
- Roche's End-to-End R Journey to Submission
- Novo Nordisk: Journey to an R-based FDA submission
- GSK's R Journey: From Pilot Projects to Enterprise Adoption
- Johnson & Johnson's Open Source Journey with R in Clinical Trials
- Increasing Number of Pharmas use R in Submissions
- Use R to generate TABLES, LISTINGS, AND FIGURES (TLFs)
- Discuss the availability of using R prior to submission & [here](#)
- Posit: Benefit Corporation

“Mission: Support Open-Source Scientific Software”

Return on Investment (ROI)

- Partnerships and collaborations with external partners
- Streamlined Workflows
- Talent out of university more likely to know open-source programming languages
- Latest developments more rapidly
- Switch between languages and contexts more easily
- Time savings in creating standard TLGs
- Time savings in creating customized TLGs
- Access to free solutions to support creating a clinical submission

Posit Team Architecture



>

Sample architecture

- Slurm - good support for clinical workflows
- Programming Development: Posit Workbench with SLURM Launcher & HPC via Azure CycleCloud or AWS...Leverage elasticity of the cloud environment in Azure/AWS.
- Production Deployment: Posit Connect either in high available/load balanced Azure/AWS virtual machine setup or an EKS/AKS (Kubernetes) setup if needed to scale beyond 3-4 VMs.
- Package Governance: Posit Package Manager instance for GxP related work, also with high availability & hosted on EKS/AKS. Can be two Azure VMs if a smaller deployment. Surface R packages from internal assessment or via OpenVal.

<

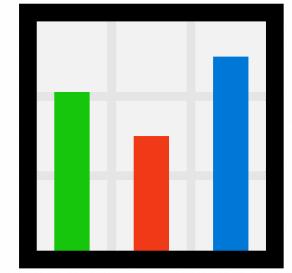
Posit Workbench:

-  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)

>

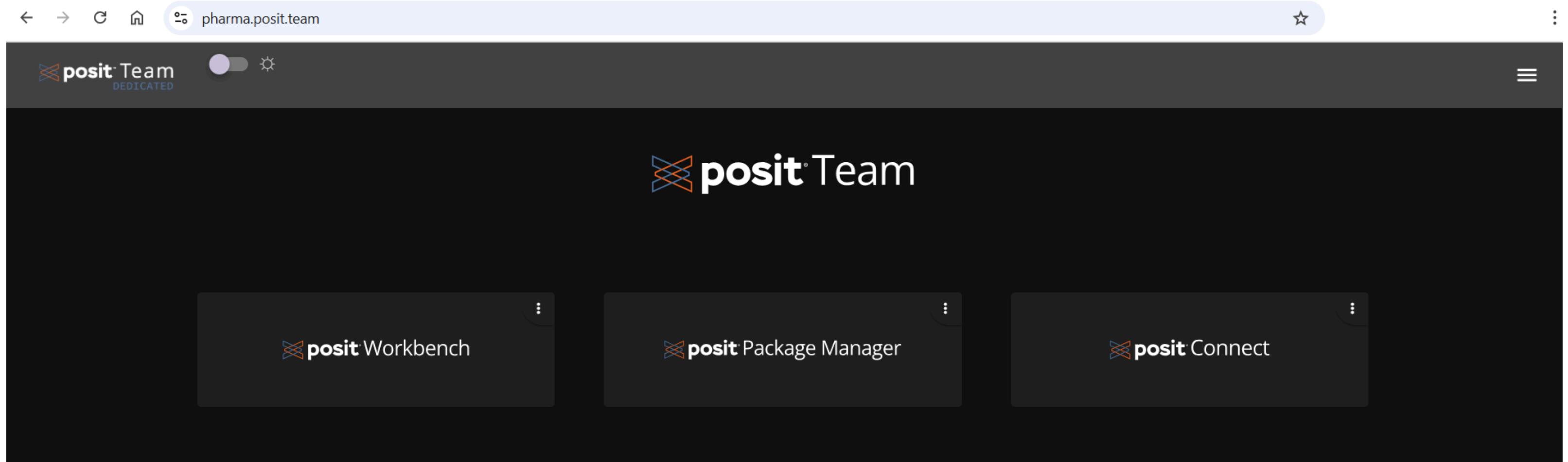


pharma.posit.team



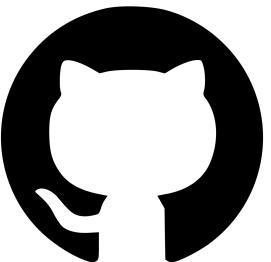
<

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

New Session

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

Session Name
RStudio Pro Session 8

Session Credentials [Edit Credentials](#)

AWS Databricks Workspace POSIT_SOFTWARE_PBC_DEV

Cluster Options

Resource Profile
Medium

CPUs Memory (GB)
2 3.91

Image
rstudio-workbench:ubuntu2204-2024.12.1--f806238 (default) [Edit](#)

Join session when ready Notify when ready

[Cancel](#) **Start Session**

>

Options for using Docker images

There are three options for using Docker images:

- Option A) Using one of the default rstudio/workbench-session images
- Option B) Extending one of the rstudio/workbench-session images
- Option C) Building a custom rstudio/workbench-session image

<

In workbench...

-  Select “New Session”
-  Click “RStudio Pro”
- Click “Start Session”

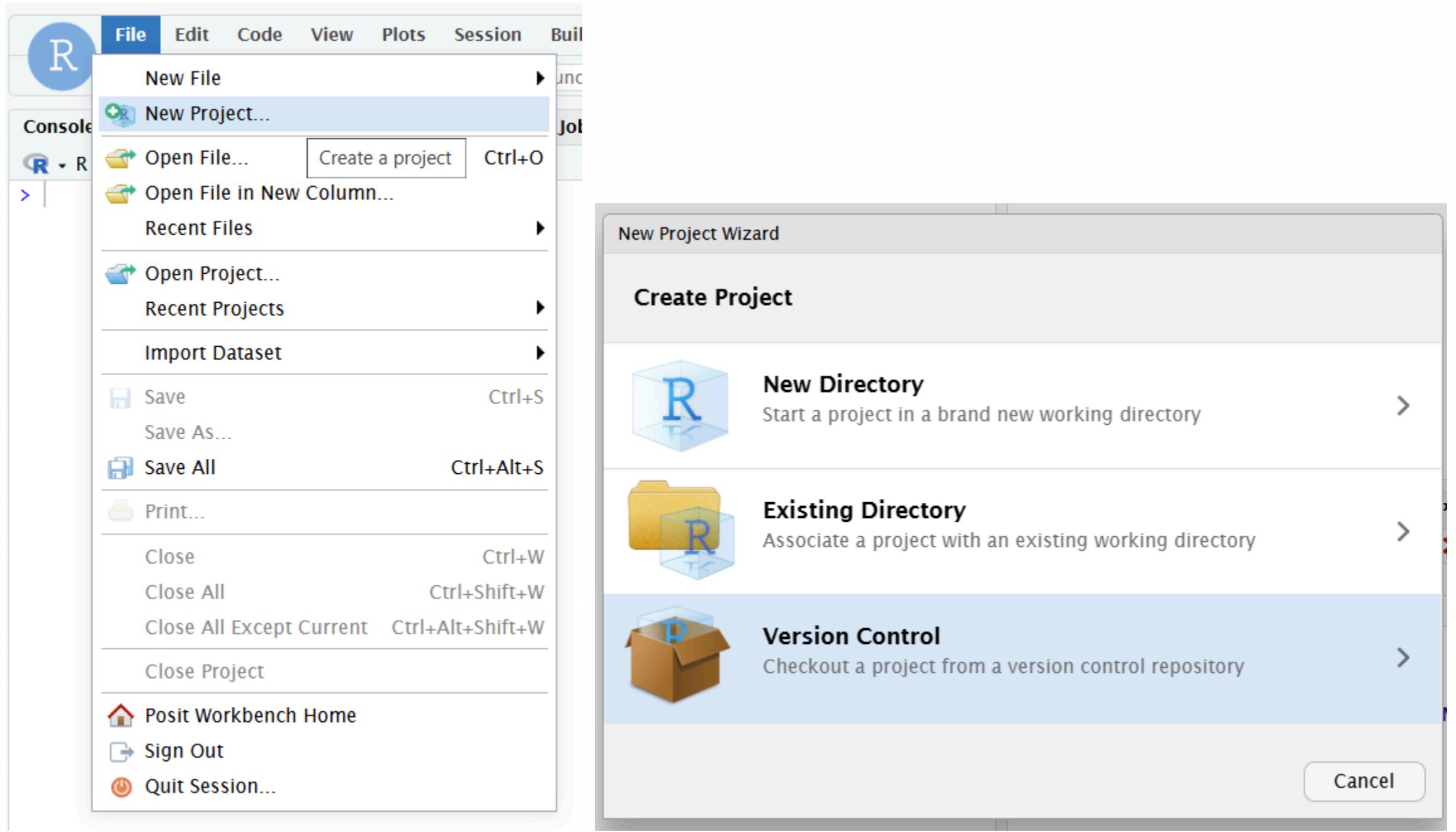
>

 <https://github.com/philibowsher/Open-Source-Drug-Development-ADAM-TLGs-Interactivity-with-R> 

<

Clone Repo

Follow these steps:





Clone Repo

Follow these steps:

New Project Wizard

Back Create Project from Version Control

Git
Clone a project from a Git repository

SVN
Checkout a project from a Subversion repository

Cancel

New Project Wizard

Back Clone Git Repository

+ **G**

Repository URL:
`Drug-Development-ADAM-TLGs-Interactivity-with-R`

Project directory name:
`Open-Source-Drug-Development-ADAM-TLGs-Intera`

Create project as subdirectory of:
`~`

R version 4.4.1 ▾ Open in new session

Create Project Cancel

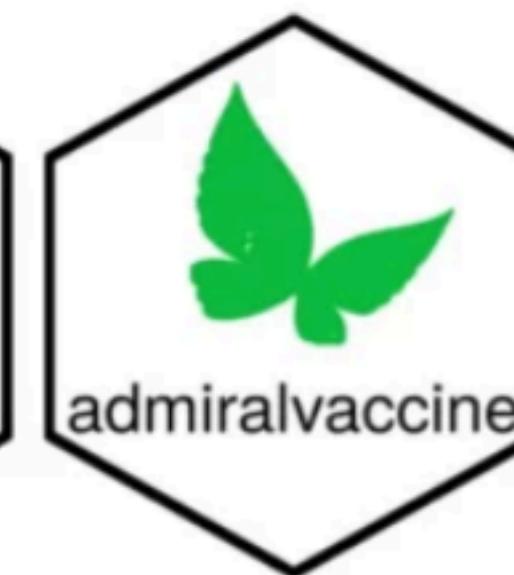






Creating ADaM Subject-Level Analysis Datasets (ADSL) with the Pharmaverse

 **posit**[™]



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.

Run ADSL Example

-  Open-Source-Drug-Development-ADAM-TLGs-Interactivity-with-R
-  Part 1 - ADAM
-  adam
-  adsl.qmd



Where do the R packages come from??



R Packages Used For Clinical Trials Reporting

- R Validation Hub's Risk-Based Approach
- Qualification information is here
- Sharing Packages with Posit Package Manager
- Custom Package Metadata

pharma.posit.team

← → ⌂ ⌂ pkg.pharma.posit.team/client/#/ ⭐ ⋮

Metadata Services and Feature Improvements! Learn more in [What's New](#).

X

 posit Package Manager

≡

Welcome to Posit Package Manager

The best way to discover and install R and Python packages

 Repository: cran ▾

 Packages in the cran repository

 SETUP

4 repositories

28,974 CRAN packages

668,813 PyPI packages

473 monthly package downloads

← → ⌂(pkg.pharma.posit.team/client/#/repos/cran/packages/admiral/overview?search=admiral#package-details) ⭐ ⋮

Metadata Services and Feature Improvements! Learn more in [What's New](#).

X

posit Package Manager Repository: cran admiral SETUP ☰

R packages in cran 8 of 8

admiral	1.2.0
ADaM in R Asset Library	
admiral.test	0.7.0
Test Data for the 'admiral' Package	
admiraldev	1.2.0
Utility Functions and Development Tools for the Admiral Package Family	
admiralmetabolic	0.1.0
Metabolism Extension Package for ADaM in 'R' Asset Library	
admiralonco	1.2.0
Oncology Extension Package for ADaM in 'R' Asset Library	
admiralophtha	1.2.0
ADaM in R Asset Library - Ophthalmology	
admiralpeds	0.2.0
Pediatrics Extension Package for ADaM in 'R' Asset Library	

admiral ADaM in R Asset Library

Overview Readme

A toolbox for programming Clinical Data Interchange Standards Consortium (CDISC) compliant Analysis Data Model (ADaM) datasets in R. ADaM datasets are a mandatory part of any New Drug or Biologics License Application submitted to the United States Food and Drug Administration (FDA). Analysis derivations are implemented in accordance with the "Analysis Data Model Implementation Guide" (CDISC Analysis Data Model Team, 2021, <<https://www.cdisc.org/standards/foundational/adam>>).

INSTALL CODE

install.packages('admiral')

Copy

VERSION

1.2.0

METADATA

▶ 0 METADATA

SECURITY

▶ 0 VULNERABILITIES

ABOUT

<https://pharmaverse.github.io/admiral/>, <https://github.com/pharmaverse/admiral>

IMPORTS

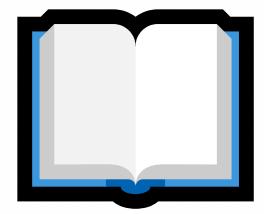
1 DEPENDS

Run TLG Example

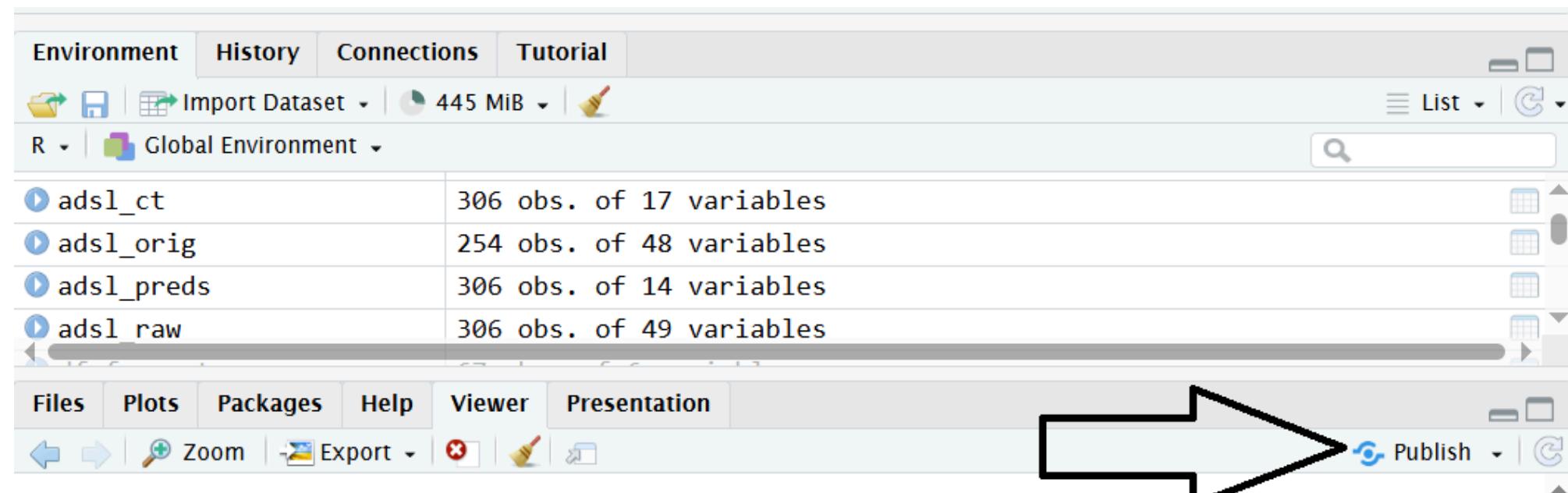
-  Open-Source-Drug-Development-ADAM-TLGs-Interactivity-with-R
-  Part 3 - TLGs
-  gtsummary
-  cdisc_tbl_14-2.01.R



But how do I Share this?



Deploy to Connect



The screenshot shows the RStudio interface with the Global Environment tab selected. It lists four datasets: `ads1_ct`, `ads1_orig`, `ads1_preds`, and `ads1_raw`. A large black arrow points from the RStudio interface down to the table caption.

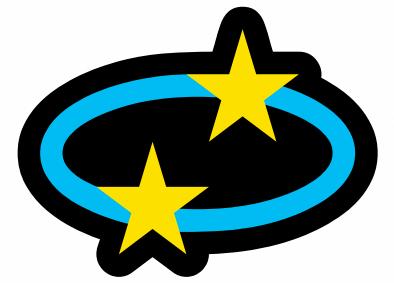
Table 14-2.01
Summary of Demographic and Baseline Characteristics

	Xanomeline			Total (N=254)	p-value ¹
	Placebo (N=86)	Low Dose (N=84)	High Dose (N=84)		
Age (y)					0.593
N Non-missing	86	84	84	254	
Mean	75.2	75.7	74.4	75.1	
SD	8.59	8.29	7.89	8.25	
Median	76.0	77.5	76.0	77.0	
Min	52.0	51.0	56.0	51.0	
Max	89.0	88.0	88.0	89.0	

>



Future Topics



<

GenAI Options in Workbench

- GenAI UI & capabilities planned to be built directly within Positron for the future
- [ellmer](#) for R
- [chatlas](#) for Python

CONSOLE TERMINAL PROBLEMS 5 OUTPUT PORTS DEBUG CONSOLE

R 4.4.0 ~/

```
Here is the revised Shiny app code:

```r
library(shiny)
library(ggplot2)
library(plotly)
library(dplyr)
library(pharmaverseadam)

Load the ADAM adverse events dataset from the pharmaverseadam package
adae <- adae

Data preprocessing: Summarizing the adverse events
ae_summary <- adae %>%
 filter(!is.na(AEBODSYS)) %>%
 group_by(AEBODSYS) %>%
 summarise(Count = n(), .groups = "drop")

Define UI
ui <- fluidPage(
 titlePanel("Adverse Events Plot"),
 plotlyOutput("aePlot")
)

Define Server
server <- function(input, output) {
 output$aePlot <- renderPlotly({
 gg <- ggplot(ae_summary, aes(x = reorder(AEBODSYS, -Count), y = Count)) +
 geom_bar(stat = "identity", fill = "steelblue") +
 labs(x = "Adverse Event Body System", y = "Count of Adverse Events") +
 theme_minimal() +
 coord_flip()

 ggplotly(gg)
 })
}

Run the app
shinyApp(ui, server)
```

```

Build chatbot-powered AI Apps in Shiny

- Shiny Assistant
- AI Tools for R, Shiny, and Pharma
- jcheng.shinyapps.io/elmer-assistant/
- Databot: Data exploration assistant for R
- Joe Cheng - Summer is Coming: AI for R, Shiny, and Pharma

Summer is Coming x Restaurant tipping x 127.0.0.1:6502 x 127.0.0.1:6503 x pharma-sidebot/app.R at dev x +

127.0.0.1:6502

AGE , AGEGR1 (Pooled Age Group 1), AGEGR1N (Pooled Age Group 1< (N)), and AGEU (Age Units).

2. **Race:** Represented by the columns RACE and RACEN (Race (N)).

3. **Sex:** Represented by the column SEX.

4. **Ethnicity:** Represented by the column ETHNIC.

5. **Baseline BMI, Height, and Weight:** Represented by the columns BMIBL (Baseline BMI), BMIBLGR1 (Pooled Baseline BMI Group 1), HEIGHTBL (Baseline Height), and WEIGHTBL (Baseline Weight).

6. **Years of Education:** Represented by the column EDUCLVL .

These variables help describe various demographic characteristics of the subjects in the study.

Show only subjects of age 70 or greater

SELECT * FROM anl WHERE AGE >=

I've filtered the dashboard to show only subjects who are 70 years of age or older.

Enter a message... ↑

Subjects of Age 70 or Greater

SELECT * FROM anl WHERE AGE >= 70

Subjects
194/254

| ARM | Shown | Total |
|-----------------------|-------|-------|
| Placebo | 64 | 86 |
| Xanomelaine High Dose | 64 | 84 |
| Xanomelaine Low Dose | 66 | 84 |

KM plot for Time to First Dermatologic Event

Survival Probability (%)

Time (Months)

TRT01A — Placebo — Xanomelaine Low Dose — Xanomelaine High Dose

The shaded areas are 95% CI of the survival probability for each group
2024-10-29 10:22:23.012869

Joe Cheng

Run Databot Example in RStudio

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

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

 `databot::chat()`

 `adsl_raw`



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?

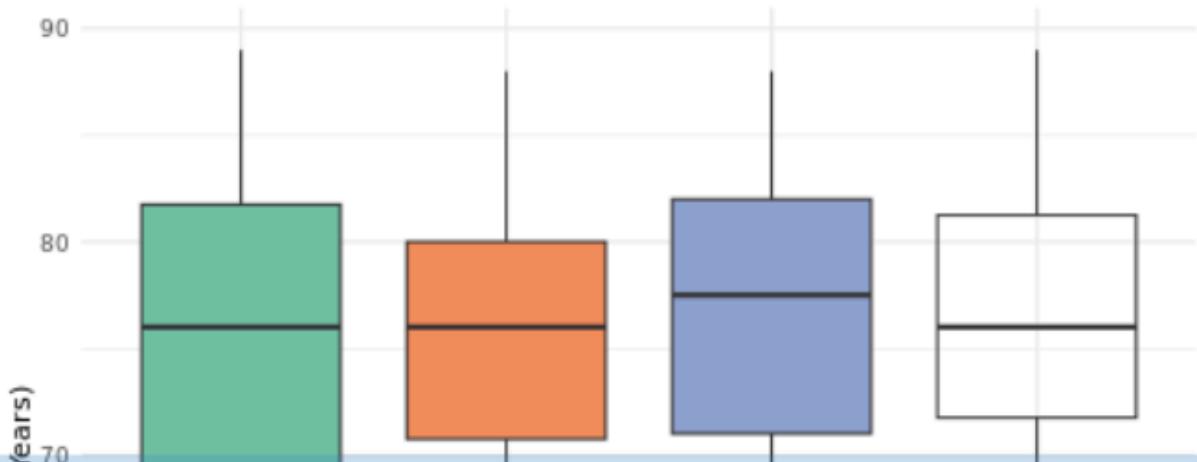


I'll create some visualizations to help us understand the age distribution across treatment arms using ggplot2.

```
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? 

<

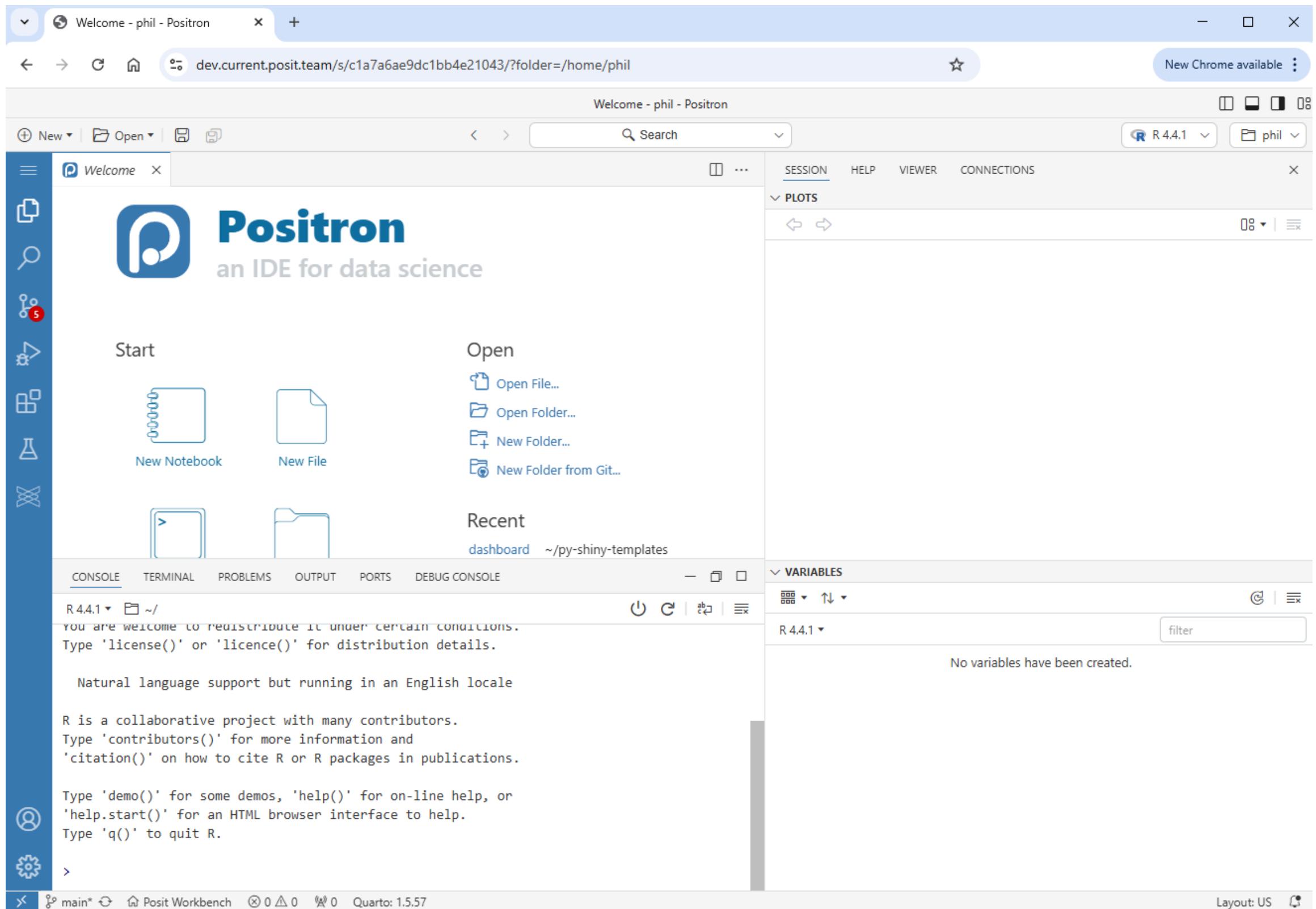
>

Positron

Extensible, polyglot tool

<

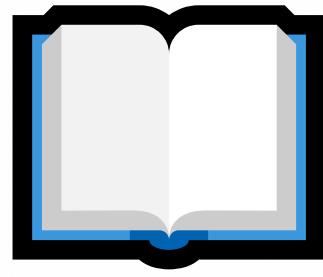
Currently in Public Beta!



>



Shiny for Python



<

← → ⌂ ⌂ 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

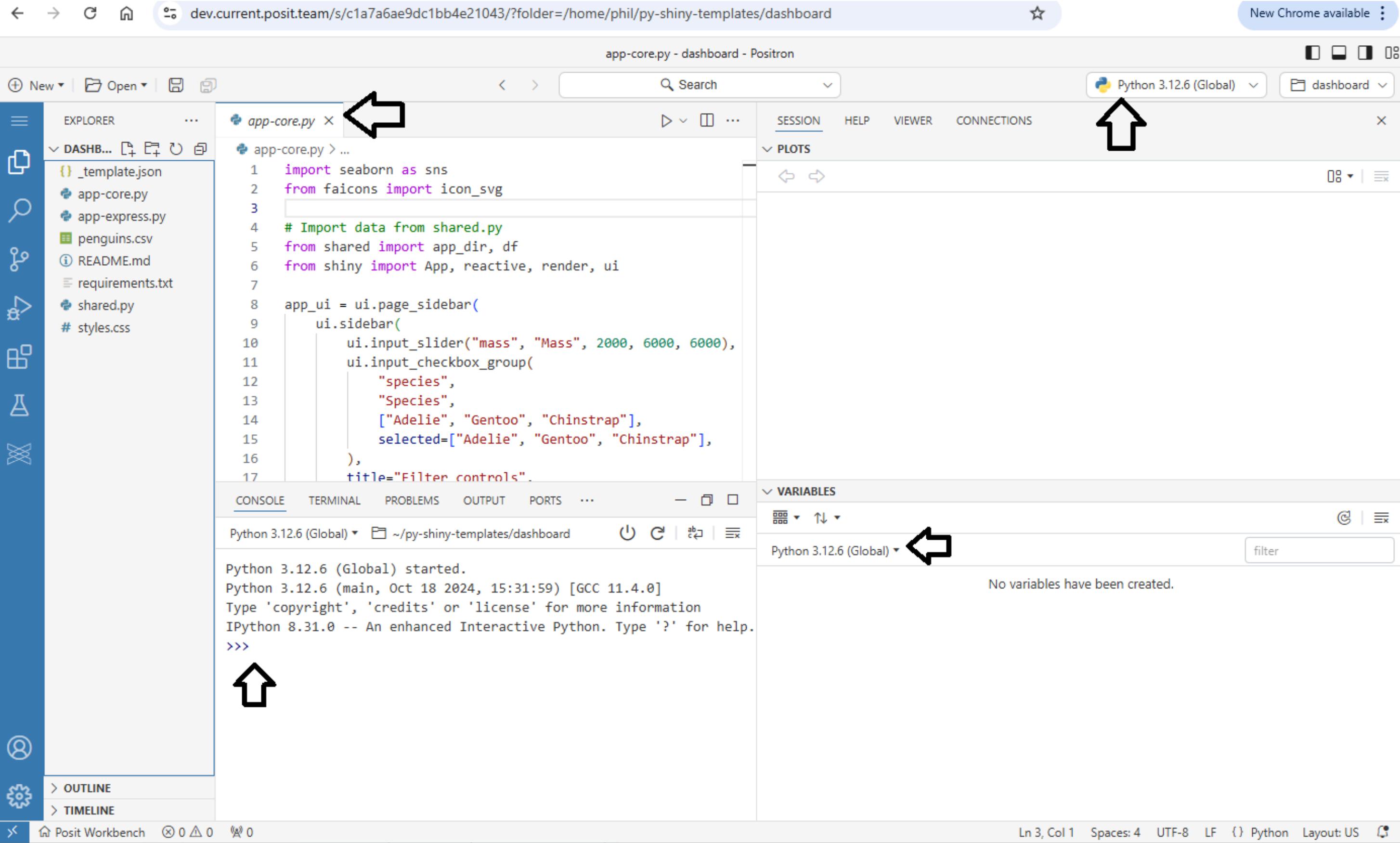
```
Python 3.12.6 (Global) started.
Python 3.12.6 (main, Oct 18 2024, 15:31:59) [GCC 11.4.0]
Type 'copyright', 'credits' or 'license' for more information
IPython 8.31.0 -- An enhanced Interactive Python. Type '?' for help.
>>>
```

VARIABLES

Python 3.12.6 (Global) filter

No variables have been created.

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

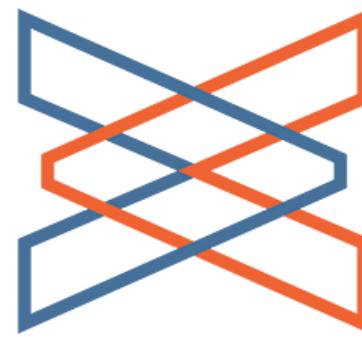


Done!

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



Thank you!



@philbowsher

▶ youtube.com/rinpharma

🔗 rinpharma.com

