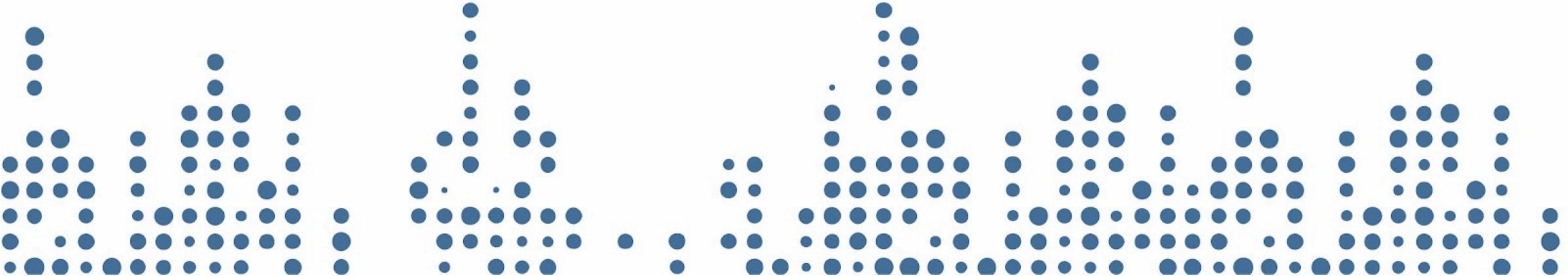




Positron: Overview for Pharma

Phil Bowsher | 2025 March 17



Hello!

< hi Phuse >

Hello!

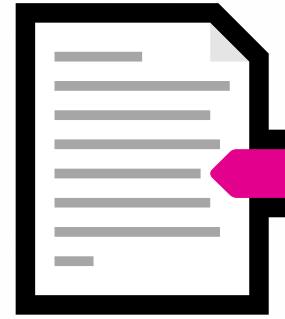


 @philbowsher

 youtube.com/rinpharma

 rinpharma.com

>



positron.posit.co



<

Positron is...



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

Positron is...



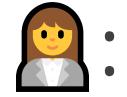
:
a next generation **data science integrated development environment (IDE)**

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 window has a header "Welcome - phil - Positron" with tabs for SESSION, HELP, VIEWER, and CONNECTIONS. On the left, there's a sidebar with icons for file operations (New, Open, Save, etc.) and a search bar. Below the sidebar, the Positron logo and the text "an IDE for data science" are displayed. The central area is divided into sections: "Start" (with "New Notebook" and "New File" buttons), "Open" (with "Open File...", "Open Folder...", "New Folder...", and "New Folder from Git..."), and "Recent" (listing "dashboard ~/py-shiny-templates"). At the bottom, there are tabs for CONSOLE, TERMINAL, PROBLEMS, OUTPUT, PORTS, and DEBUG CONSOLE. The CONSOLE tab is active, showing the R 4.4.1 startup message: "You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details." It also mentions natural language support and provides information about contributors and citations. The right side of the interface includes a "VARIABLES" section which currently displays "No variables have been created." with a "filter" button. The bottom status bar shows "main* Quarto: 1.5.57" and "Layout: US".

Posit Workbench:

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

CREATE // Rename // EDIT

New Session

Jupyter Notebook JupyterLab Positron Pro 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

Next-Gen Statistical Computing Environments (SCE)

- Enabling shift to open-source data science with language-agnostic frameworks
- Blend tools like parquet, git, & Docker
- Future where clinical reporting SCEs are generalized into data science SCEs
- Support incoming new-hires with experience in open source (R, Python etc.)
- And other drug development use-cases like Real-World Evidence
- **Data science toolbox of various languages**
- Connect to data platforms (Databricks, Snowflake etc.)...
- Where ETL & data ingestion processes are often in Python



>

Session credentials & connections to databases / datastores
Databricks, Snowflake, Amazon S3 Cloud Storage, DuckDB etc

<

>

**Positron is an 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 ⌂

Positron has data-science centric features of RStudio like...

- UI & capabilities to help data scientists be more productive
- **Batteries included** experience for doing data science
- Positron **core** is shared among all languages
- Key items like a *dedicated console, data explorer, plots pane, & output viewer*
- Project-oriented workflow & initialize **version control** or run git init via a terminal
- Plus: offers an advanced **Data Explorer**

>



4-Pane Data Science



<

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

VALUES

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

PLOTS

Output

clarity

- I1
- SI2
- SI1
- VVS2
- VVS1
- VVVS2
- VVVS1
- IF

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

2 year = 2013 × and month >= 2 × + 2

+ Add Filter

Hide Filters

Clear Filters 1

> # dep_time 2% 0% 0%

> # sched_dep_ti... 0% 2% 2%

> # dep_delay 2% 2% 2%

> # arr_time 2% 2% 2%

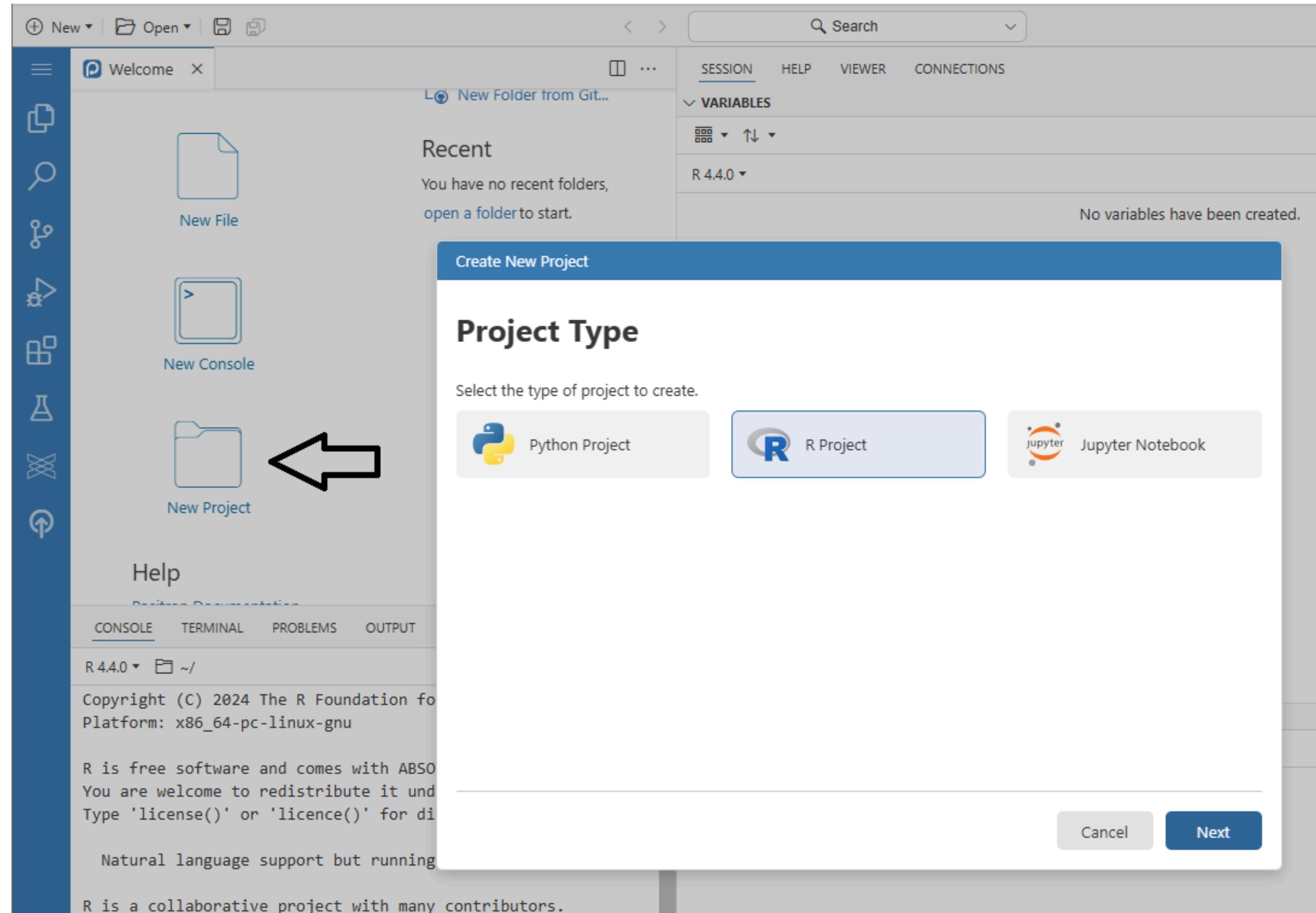
Showing 309,772 rows (91.98% of 336,776 total) 19 columns 3

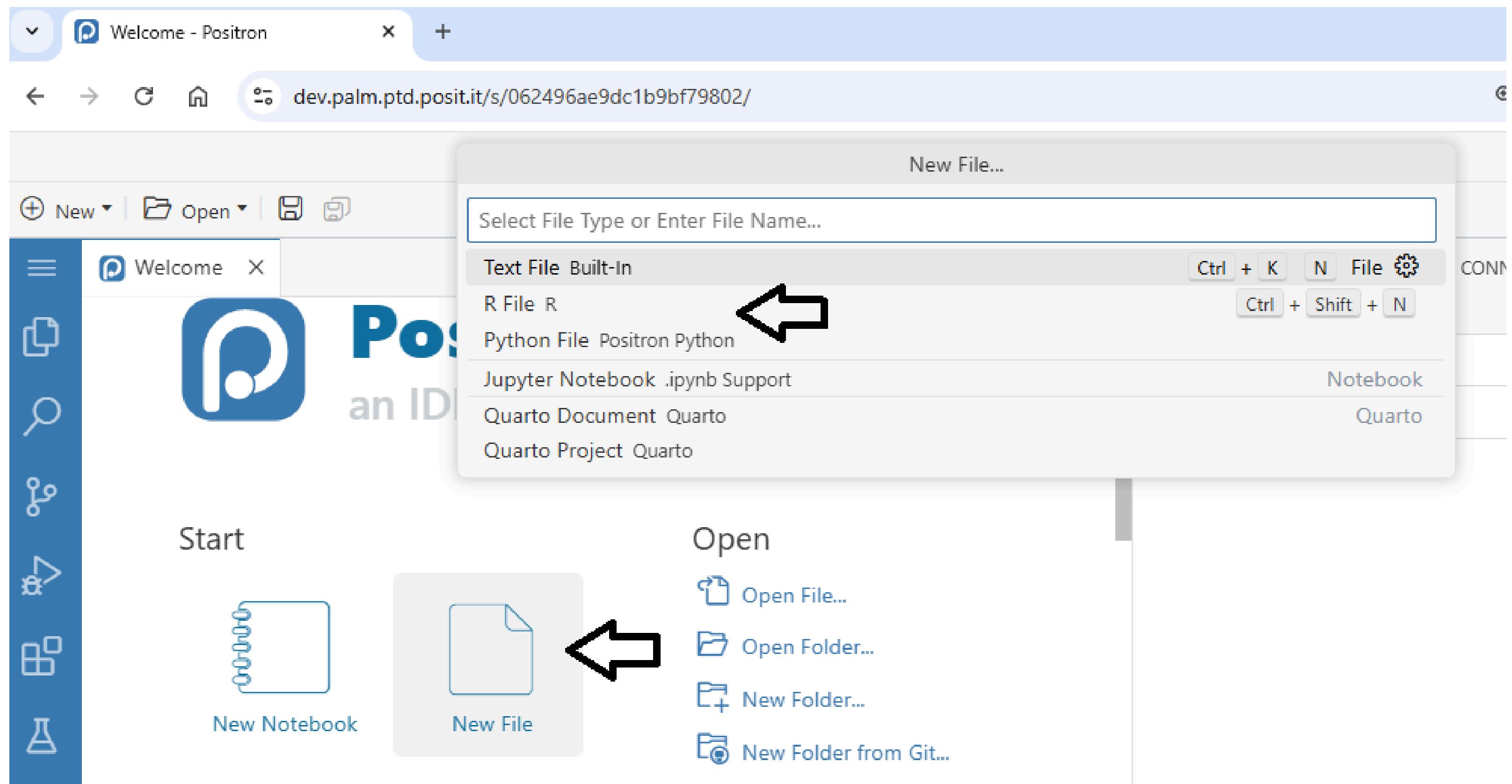
| | year int | month int | day int |
|-------|-------------|--------------|------------|
| 27005 | 2013 | 10 | |
| 27006 | 2013 | 10 | |
| 27007 | 2013 | 10 | |
| 27008 | 2013 | 10 | |
| 27009 | 2013 | 10 | |
| 27010 | 2013 | 10 | |
| 27011 | 2013 | 10 | |
| 27012 | 2013 | 10 | |

>

 **First-class, built-in support for R and/or Python** 

<

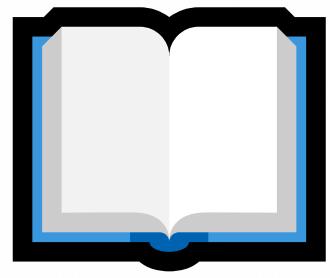




>



Shiny for Python



<

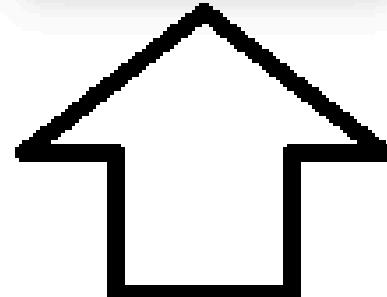
polyglot example

-  clicking the “Run” button = out of the box for R & Python
-  “Publish” Button = Built in with no additional extensions required

Welcome app-core.py X

app-core.py > [o] app_ui

```
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",
18     ),
19     ui.layout_column_wrap(
20         ui.value_box(
```



Run Shiny App

Welcome app-core.py

app-core.py > [app_ui]

```
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     ),
```

SESSION HELP VIEWER CONNECTIONS

Deploy with Posit Publisher https://dev.palm.ptd.posit.it/s/062496ae

Penguins dashboard

Filter controls

Mass

2,000 6,000

Species

✓ Adelie
✓ Gentoo
✓ Chinstrap

Nun
33

TERMINAL

```
phil@session-062496ae9dc1b9bf79802-phil---phils-positron-k4
4xm-5vlxn:~/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
```

GenAI Options in Positron

- 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)
```

```

The screenshot shows a code editor interface with two tabs: "chatlas_python.py" and "app.R".

chatlas_python.py:

```
chatlas_python.py
home > phil > chatlas_python.py
1 import os
2 from chatlas import ChatOpenAI
3 from dotenv import load_dotenv
4
5 load_dotenv()
6
7 chat = ChatOpenAI(
8     model = "gpt-4o",
9     system_prompt = "You are a friendly but terse assistant.",
10)
11
12 chat = ChatOpenAI(api_key=os.getenv("API_KEY"))
13
14 chat.console()
15
16 chat.chat("Create a R Shiny application that uses ggplot2, plotly and the diamonds data")
```

Terminal:

```
CONSOLE TERMINAL PROBLEMS OUTPUT PORTS DEBUG CONSOLE
step-by-step guide to building this application:
```

1. Set Up Your Shiny Application

Create a directory for your Shiny app with the following files:

- **app.R**

2. Write the Shiny Application Code

Open **app.R** and add the following code:

```
# app.R
library(shiny)
library(ggplot2)
library(plotly)

# Define UI for application
ui <- fluidPage(
    # Application title
    titlePanel("Diamonds Data Visualization"),
    # Sidebar with a slider input for price and a select input for cut
    sidebarLayout(
```

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



KEYNOTE SUMMER IS COMING: AI FOR R, SHINY, AND PHARMA



Joe Cheng
Posit

**TUE, OCT 29, 2024
10:10AM EDT**

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

Thank you!



@philbowsher

▶ youtube.com/rinpharma

🔗 rinpharma.com

