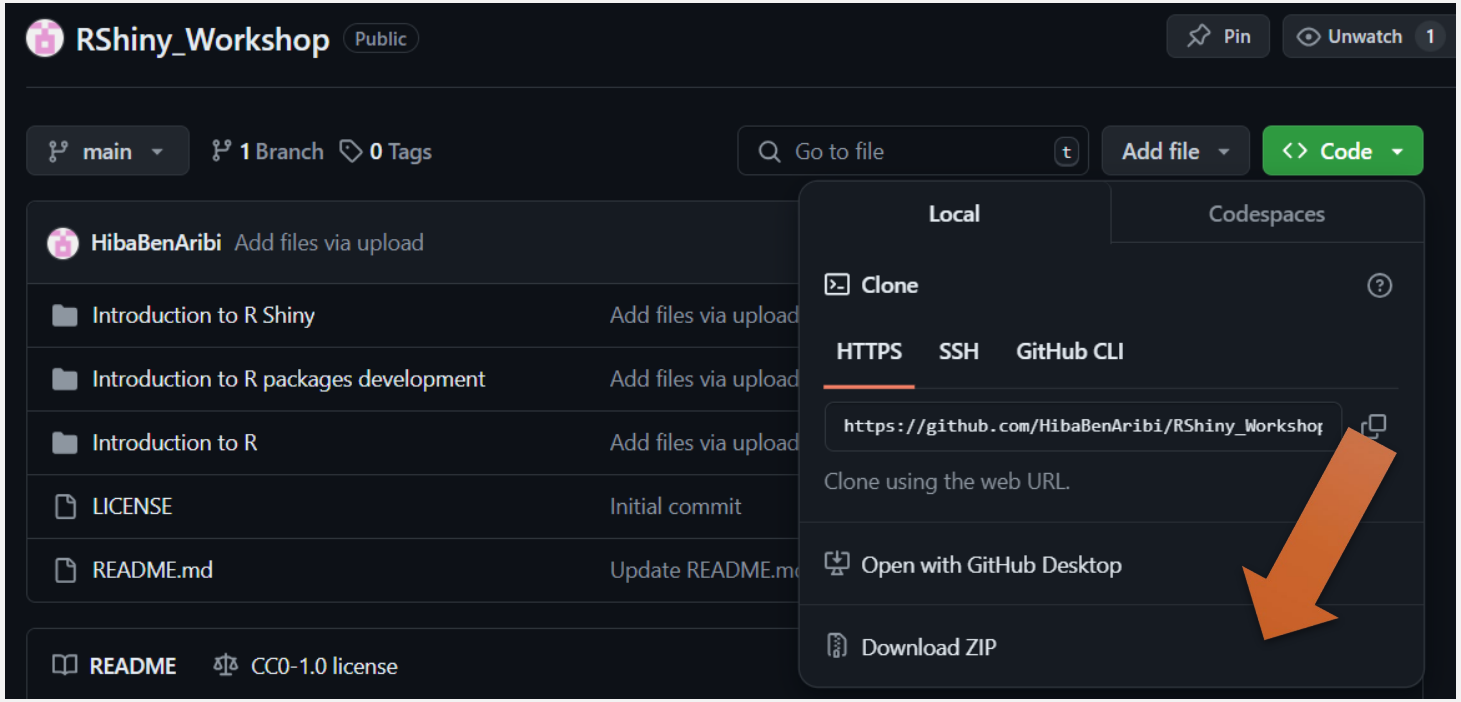
WORKSHOP : R SHINY

By: Hiba Ben Aribi

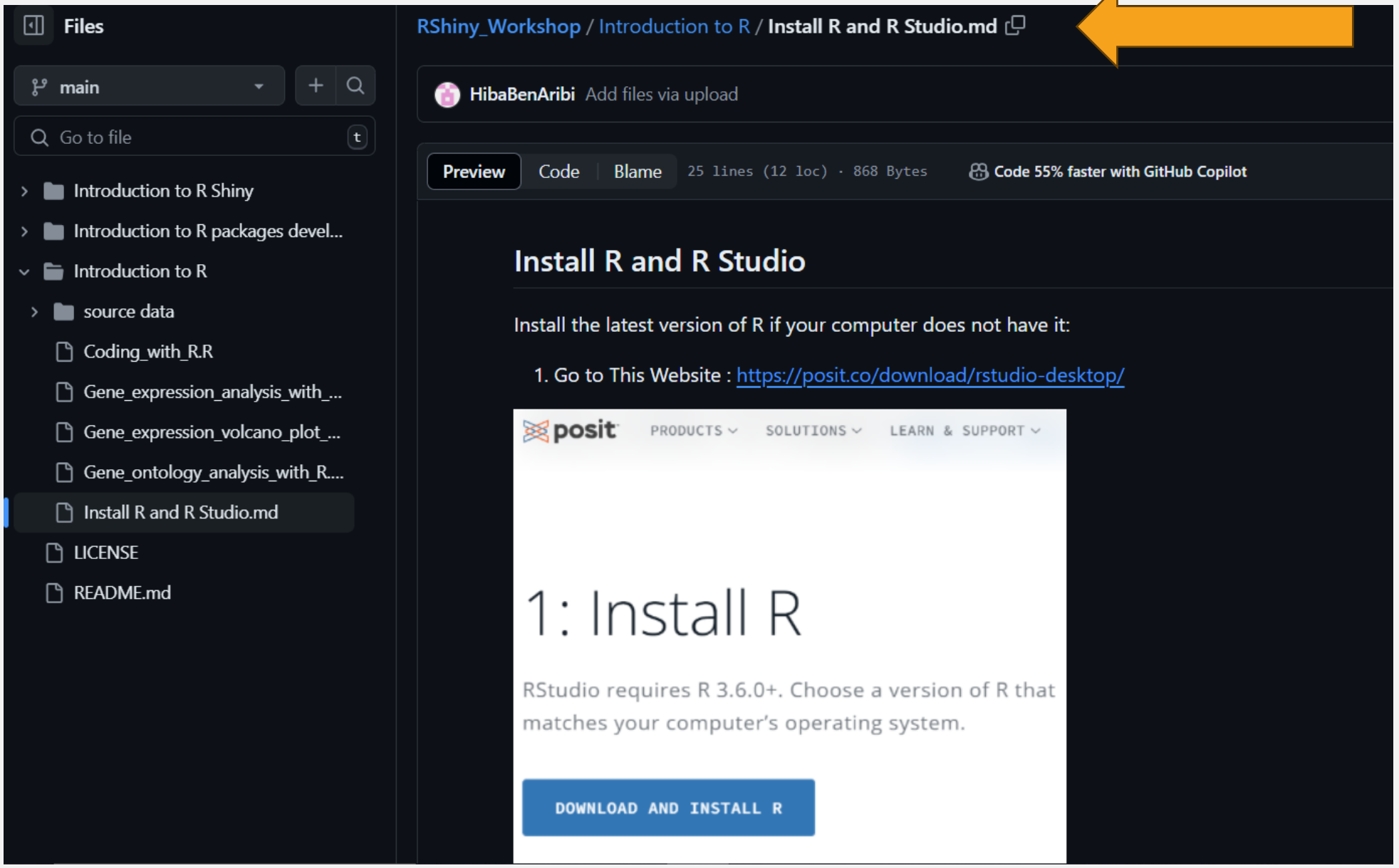
WORKSHOP

GitHub Repository :

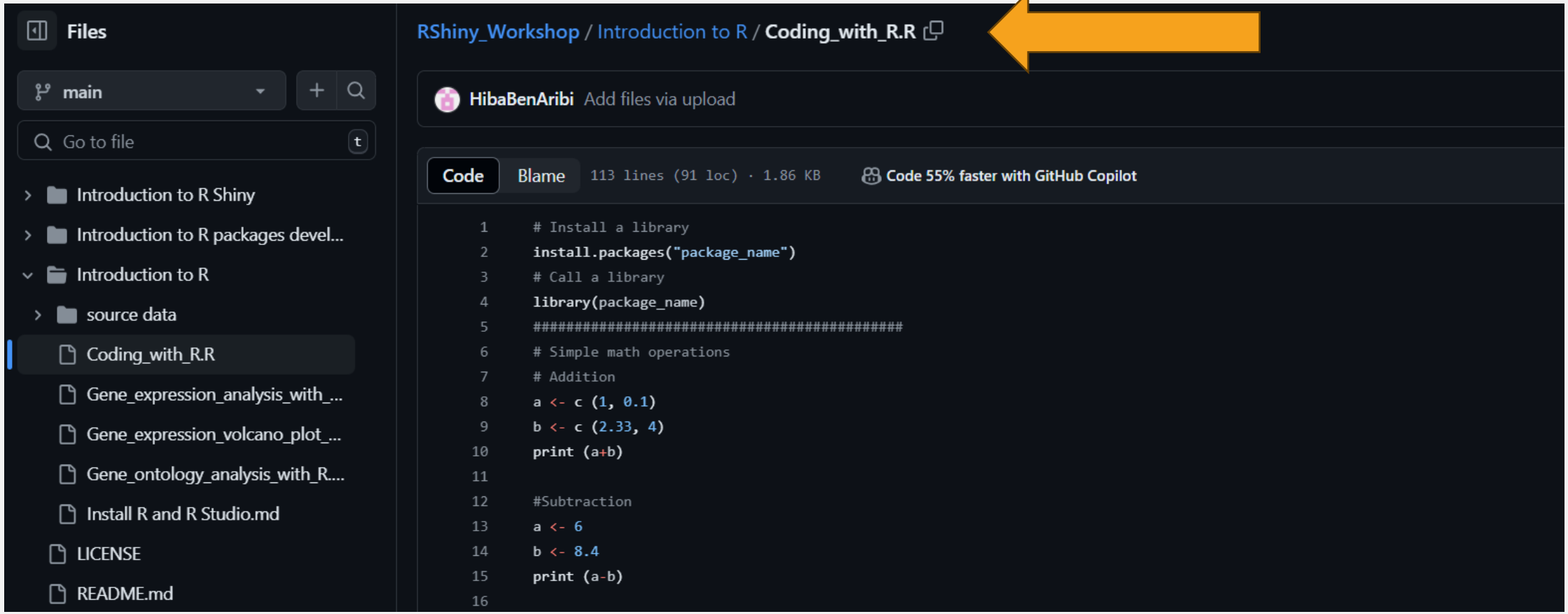
- https://github.com/omicscodeathon/rshinyworkshop



REQUIREMENTS



REQUIREMENTS

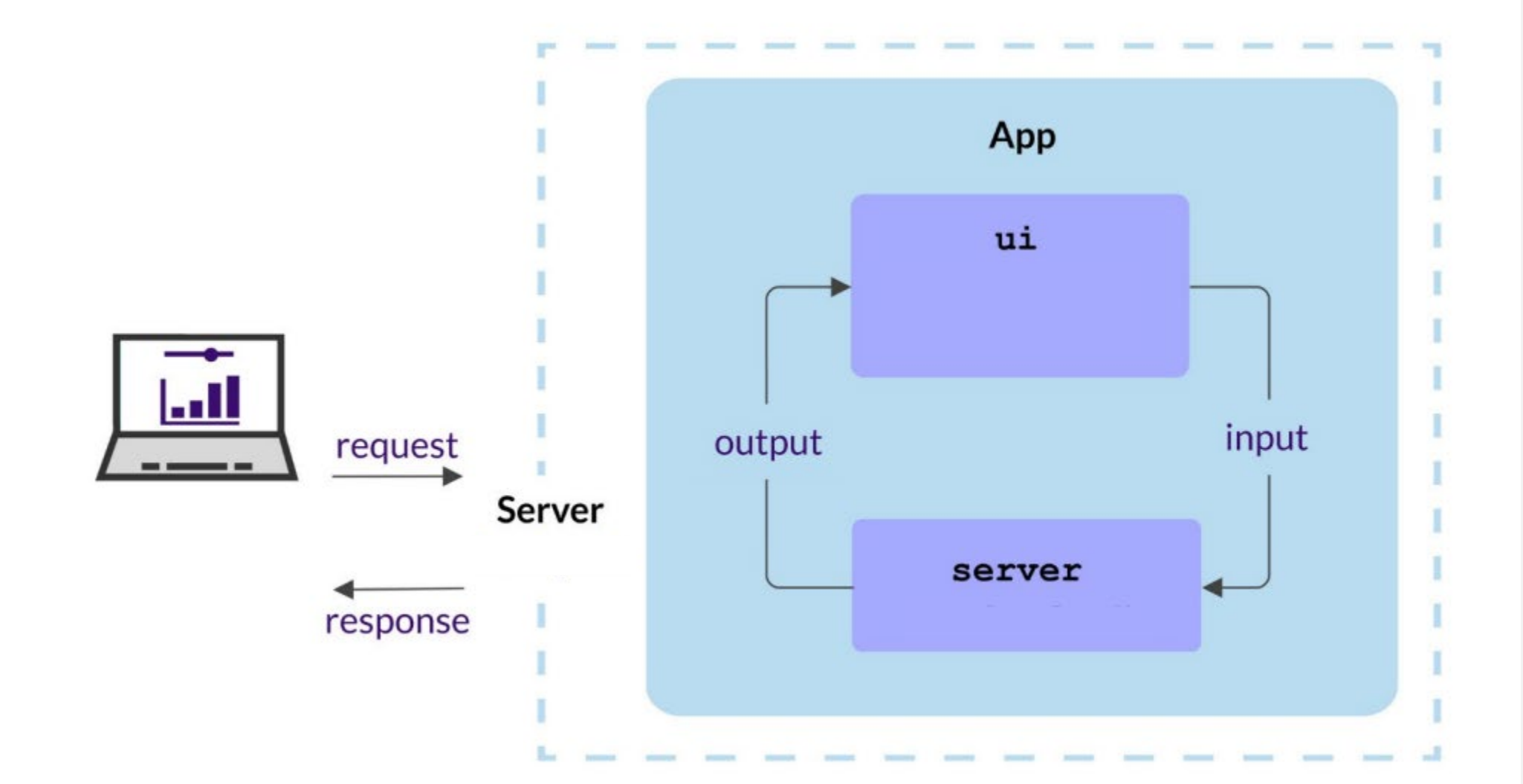


SHINY

Shiny is :

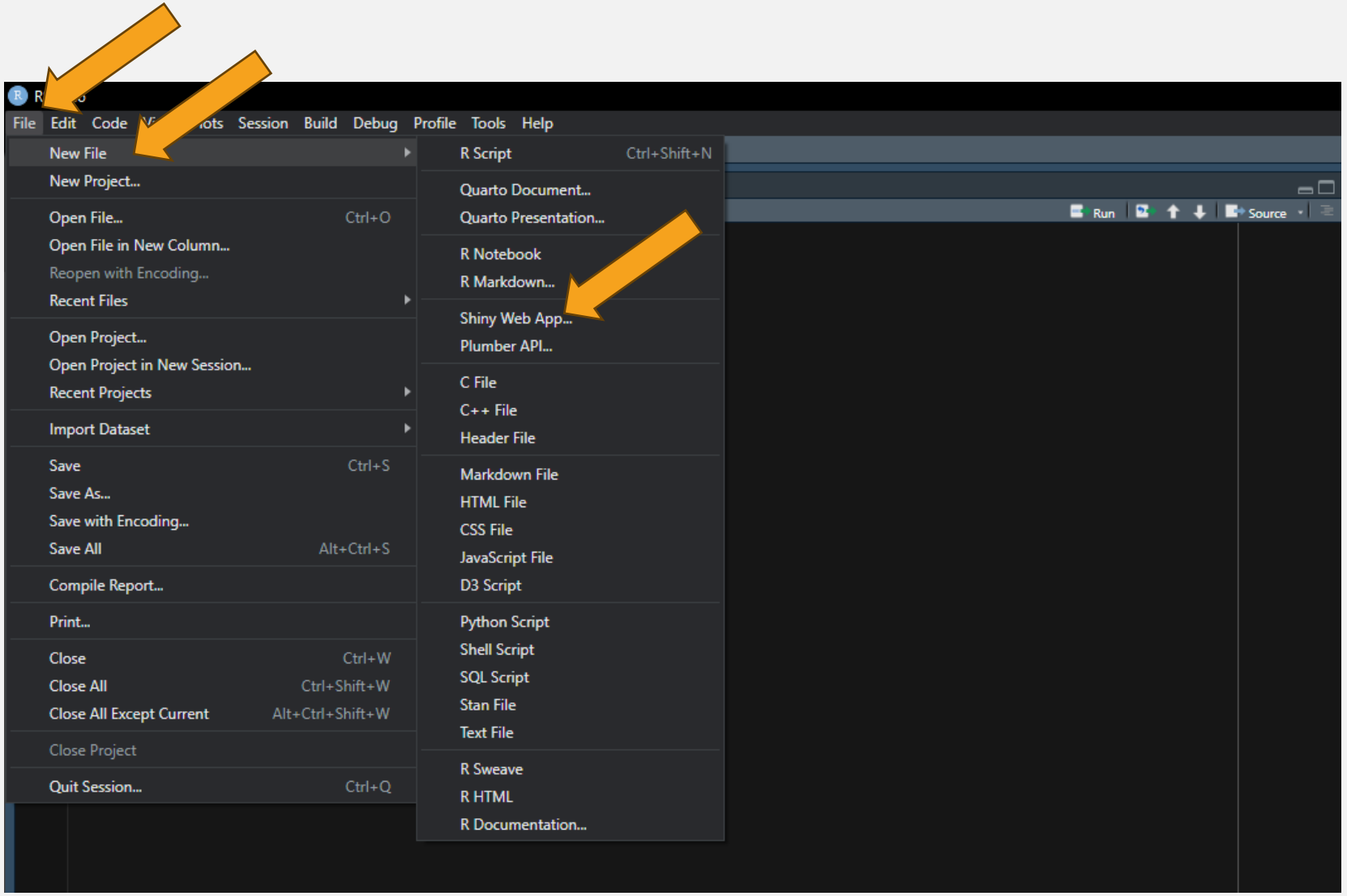
- ✓An R package
- ✓Allows the creation of web applications
- ✓With interactive graphical user interfaces
- ✓Using R instead of JS

SHINY

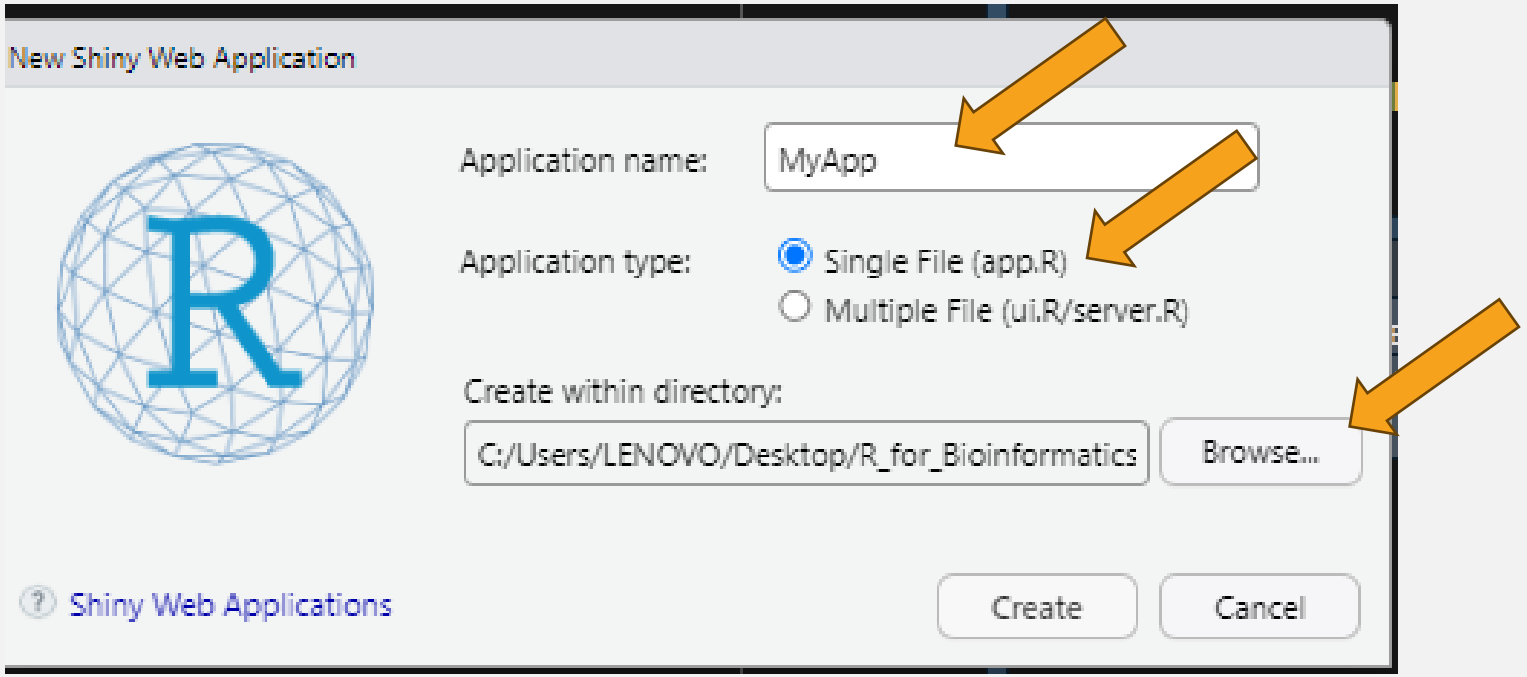


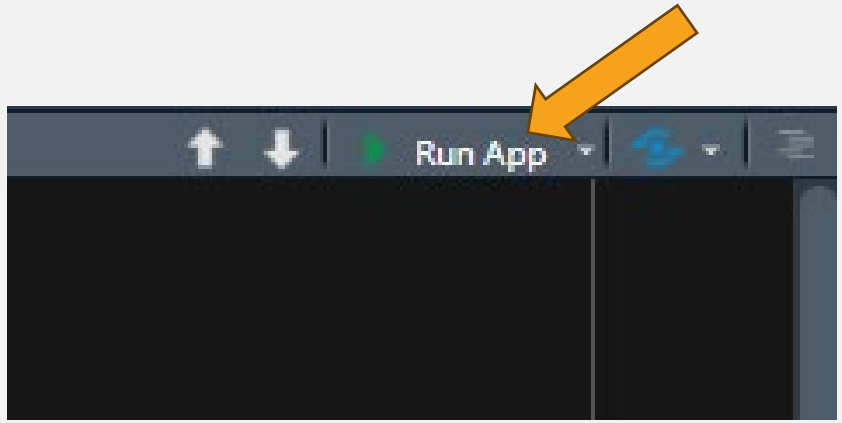
LET'S CREATE A SHINY APP

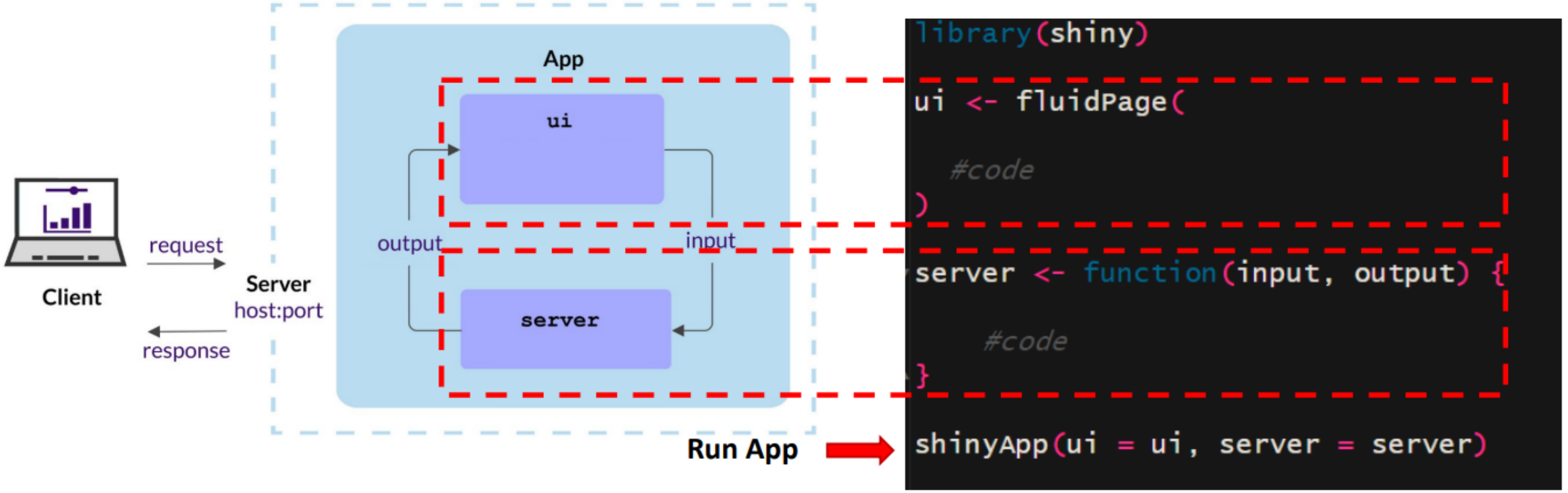
1. Open R Studio
2. New File
3. Shiny web app



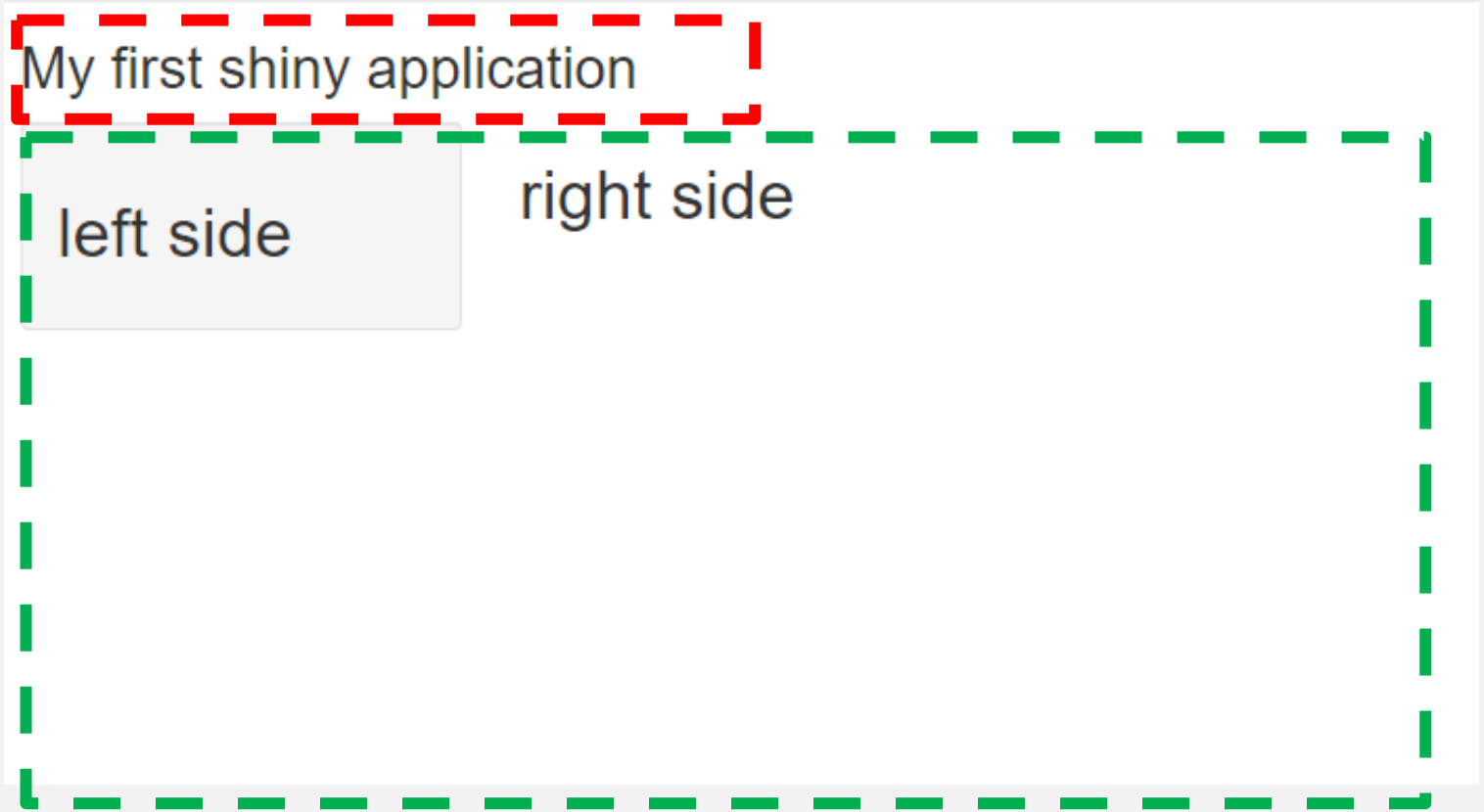
1. Name it
2. Choose single file
3. Define directory
4. Run App



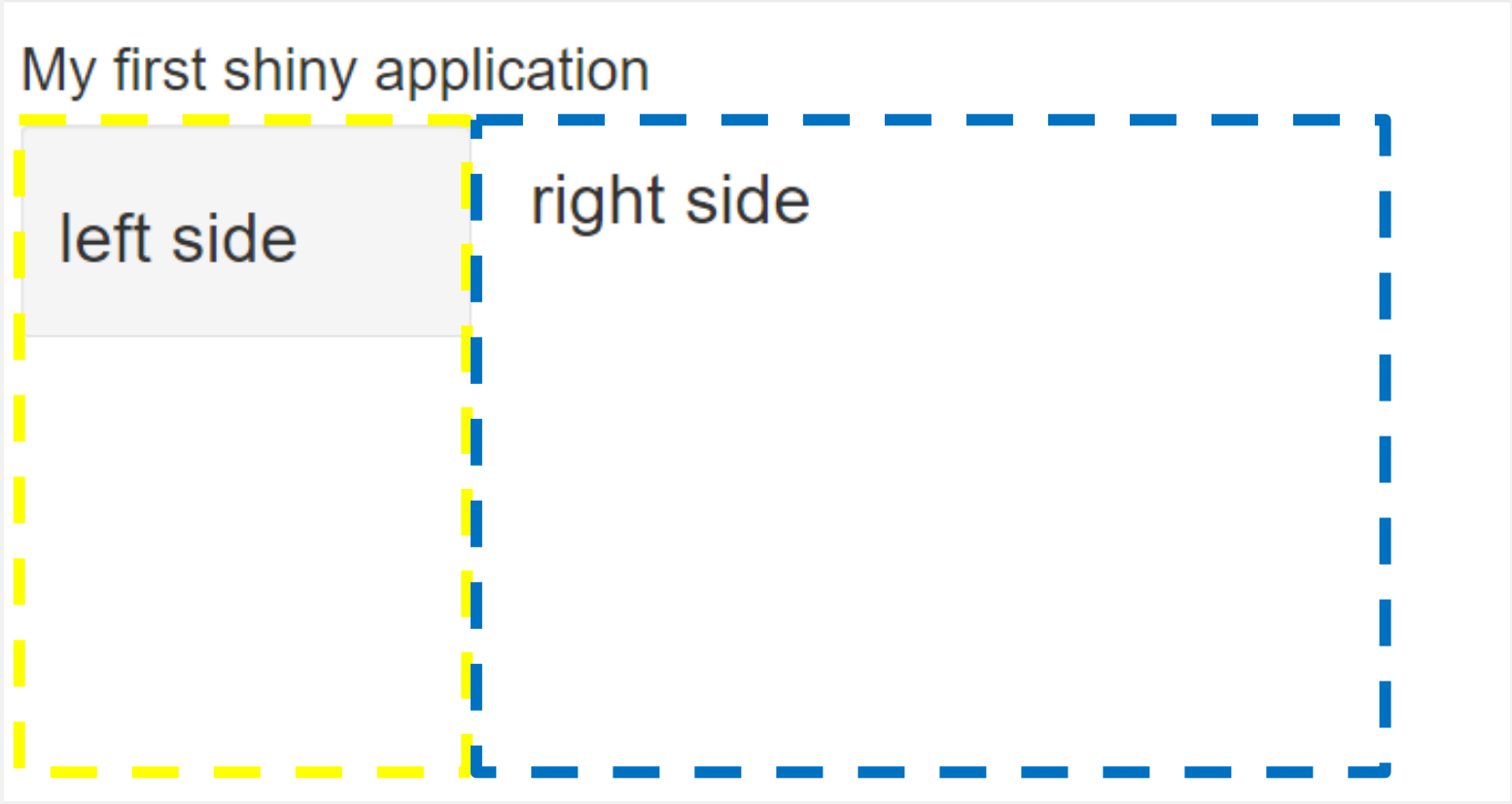



App
ui
server
output
input
Client
request
response
Server
host:port
Run App
library(shiny)
ui <- fluidPage(
#code
)
server <- function(input, output) {
#code
}
shinyApp(ui = ui, server = server)

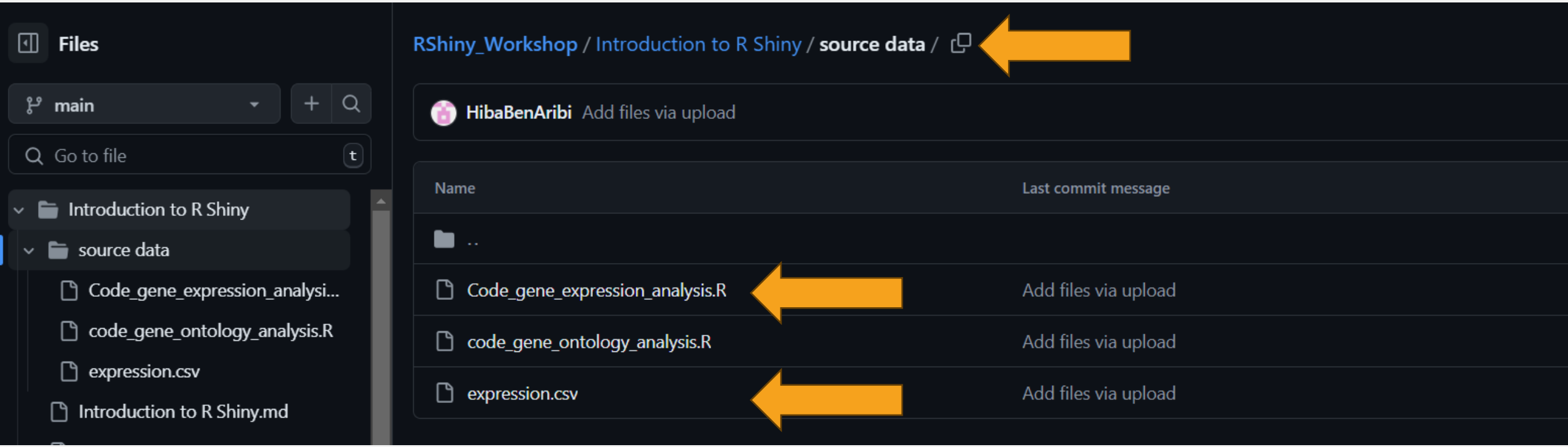
```r
library(shiny)

# Define UI
ui <- fluidPage(
  # Application title
  titlePanel("My first shiny application"),
  # Layout
  sidebarLayout(
    #left side
    sidebarPanel(
      h1("left side")
    ),

    #right side
    mainPanel(
      h1("right side")
    )

  )
)
```

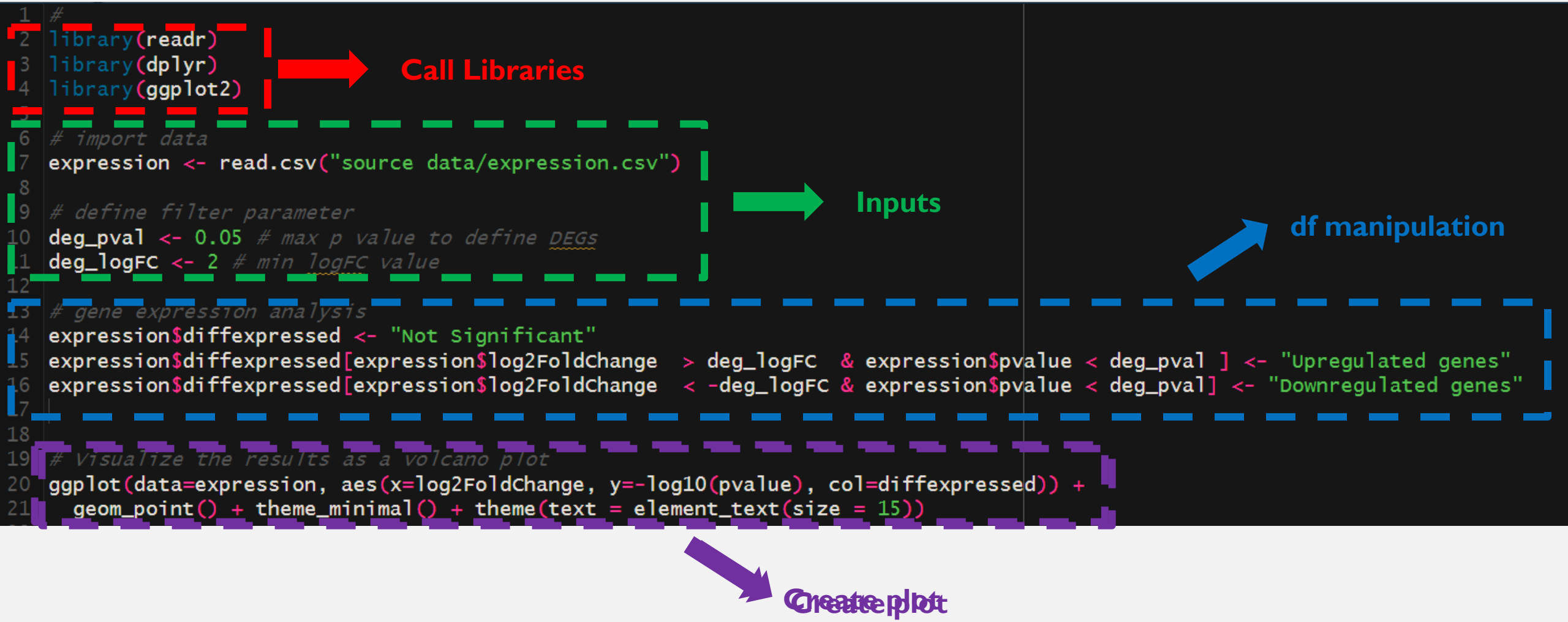


```r
library(shiny)

# Define UI
ui <- fluidPage(
  # Application title
  titlePanel("My first shiny application"),
  # Layout
  sidebarLayout(
    #left side
    sidebarPanel(
      h1("left side")
    ),
    #right side
    mainPanel(
      h1("right side")
    )
  )
)
```

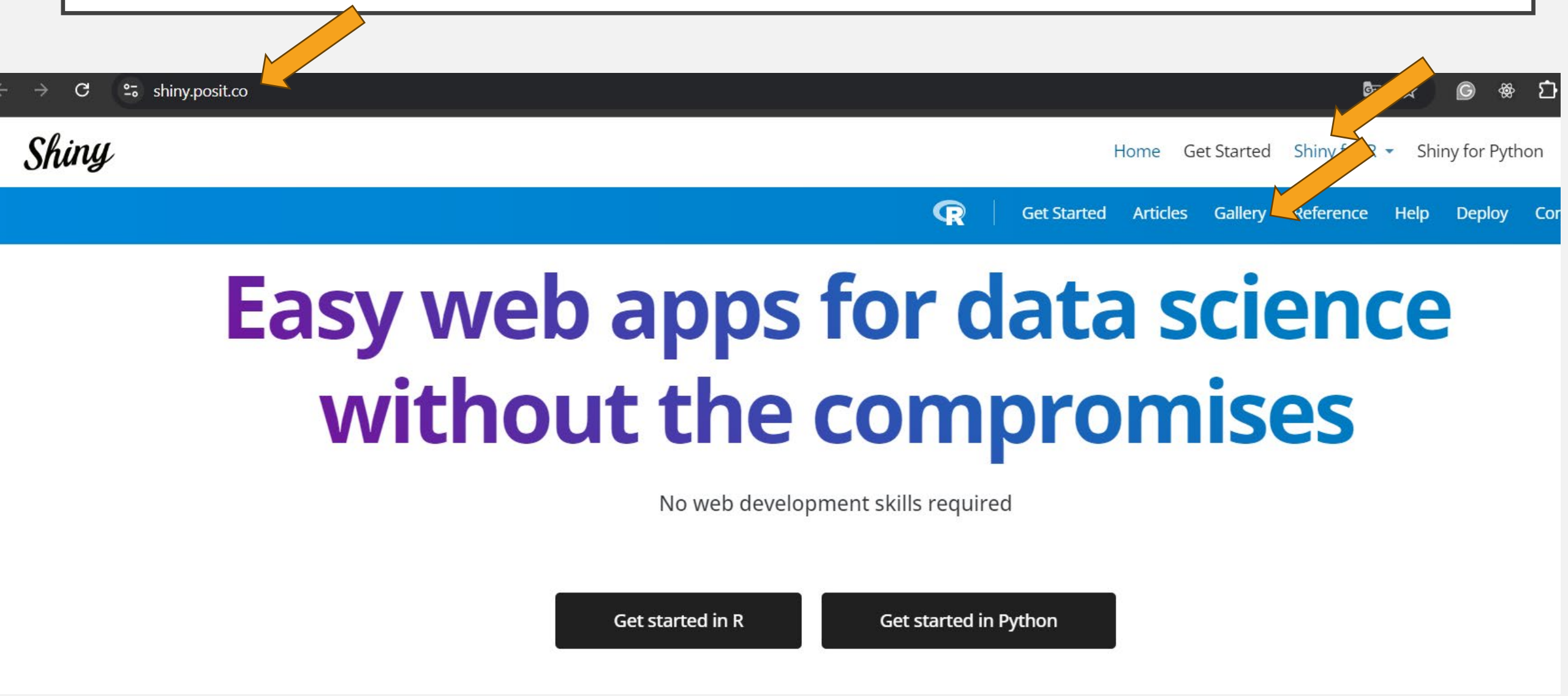


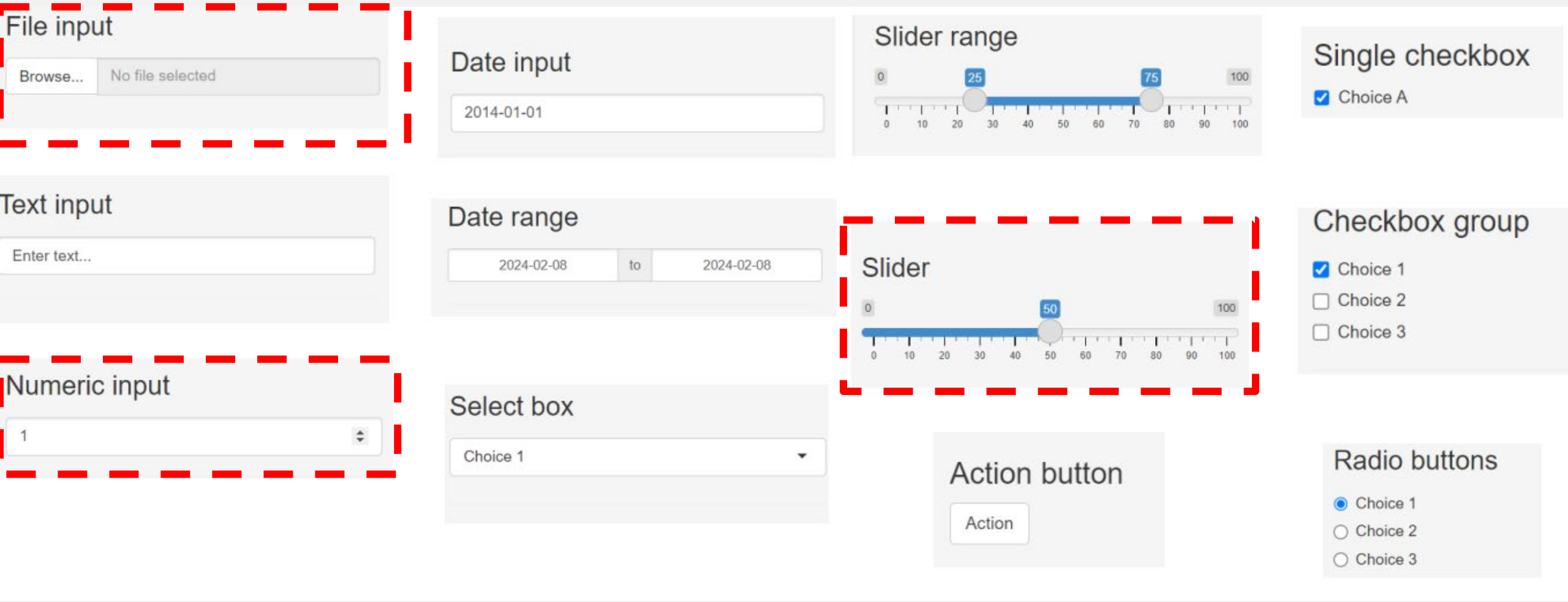
INTEGRATE OUR CODE


Files
main
Go to file
t
Introduction to R Shiny
source data
Code_gene_expression_analysi...
code_gene_ontology_analysis.R
expression.csv
Introduction to R Shiny.md
RShiny_Workshop / Introduction to R Shiny / source data /
HibaBenAribi Add files via upload
Name
Last commit message
..
Code_gene_expression_analysis.R
Add files via upload
code_gene_ontology_analysis.R
Add files via upload
expression.csv
Add files via upload


#
library(readr)
library(dplyr)
library(ggplot2)
# import data
expression <- read.csv("source data/expression.csv")
# define filter parameter
deg_pval <- 0.05 # max p value to define DEGs
deg_logFC <- 2 # min logFC value
# gene expression analysis
expression$diffexpressed <- "Not Significant"
expression$diffexpressed[expression$log2FoldChange > deg_logFC & expression$pvalue < deg_pval] <- "Upregulated genes"
expression$diffexpressed[expression$log2FoldChange < -deg_logFC & expression$pvalue < deg_pval] <- "Downregulated genes"
visualize the results as a volcano plot
ggplot(data=expression, aes(x=log2FoldChange, y=-log10(pvalue), col=diffexpressed)) +
geom_point() + theme_minimal() + theme(text = element_text(size = 15))
Call Libraries
Inputs
df manipulation
Create plot

INPUTS


shiny.posit.co
Shiny
Home
Get Started
Shiny for Python
Get Started
Articles
Gallery
Reference
Help
Deploy
Easy web apps for data science without the compromises
No web development skills required
Get started in R
Get started in Python


File input
Browse...
No file selected
Date input
2014-01-01
Slider range
0
25
75
100
0 10 20 30 40 50 60 70 80 90 100
Single checkbox
Choice A
Text input
Enter text...
Date range
2024-02-08
to
2024-02-08
Slider
0
50
100
0 10 20 30 40 50 60 70 80 90 100
Checkbox group
Choice 1
Choice 2
Choice 3
Numeric input
1
Select box
Choice 1
Action button
Action
Radio buttons
Choice 1
Choice 2
Choice 3

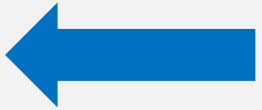
FILE INPUT

```
library(DT) # package for table management
```

```
    sidebarPanel(
      fileInput('ID', 'Text...'),
    ),
```

Request File Path in UI

```
server <- function(input, output) {
  #import file
  data<- reactive({
    inFile <- input$data_file
    df <- read.csv(inFile$datapath, header = TRUE)
    return(df)
  })
```

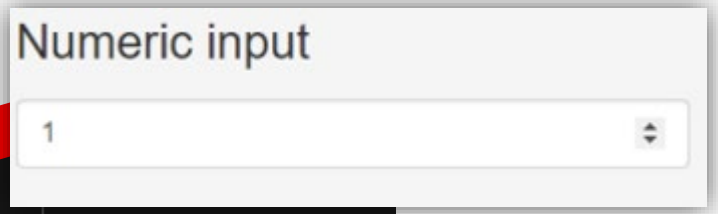


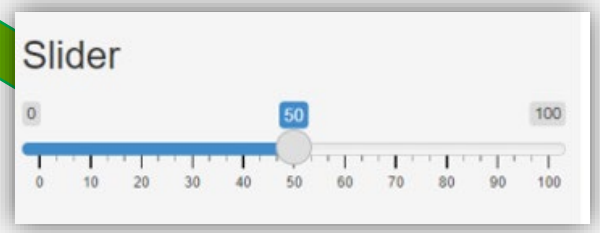
Read the file in server

NUMERIC INPUTS

Request File Path in UI

```
sidebarPanel(
  # Numeric input
  numericInput("ID", label = h3("Text"), value = Default_Value),
  # Slider input
  sliderInput("ID", label = h3("Text"), min = number, max = number, value = Default_Value)
),
```






```
value <- input$ID
```

Call value in server

TABLES / PLOTS

In UI

```
DTOutput('table_name')
```

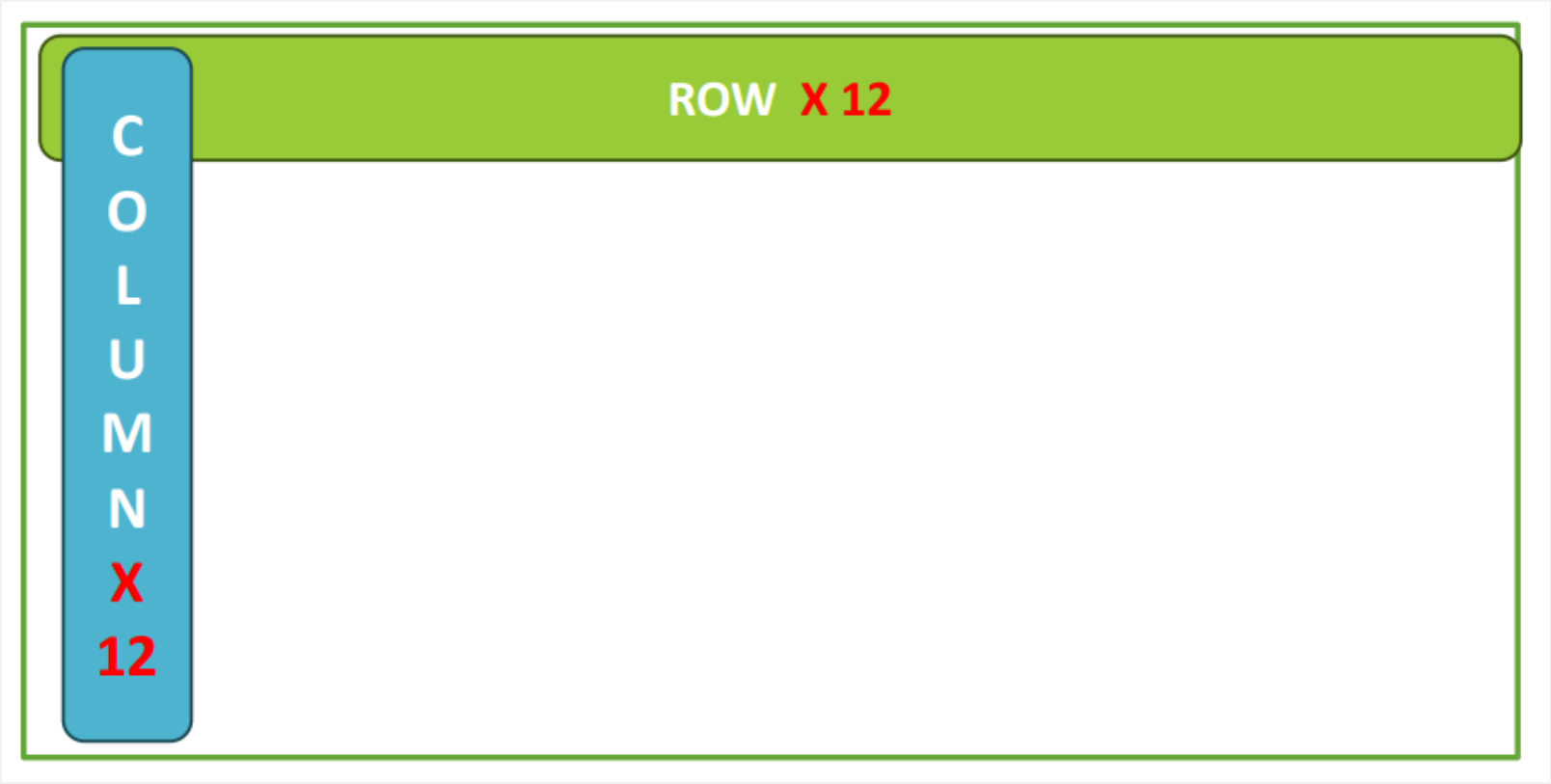
```
plotOutput("plot_name")
```

In Server

```
output$table_name <- renderDT({

  #code

})
```

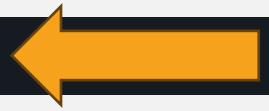
```
output$plot_name <- renderPlot({

  #code

})
```

CUSTOMIZE UI



CUSTOMIZE UI

RShiny_Workshop / Introduction to R Shiny / **Introduction to R Shiny.md**



Resources to Customize the UI

https://shiny.posit.co/r/getstarted/build-an-app/customizing-ui/theming.html

https://shiny.posit.co/r/articles/build/dashboards/

https://rstudio.github.io/shinydashboard/get_started.html

https://daattali.com/shiny/shinycssloaders-demo/

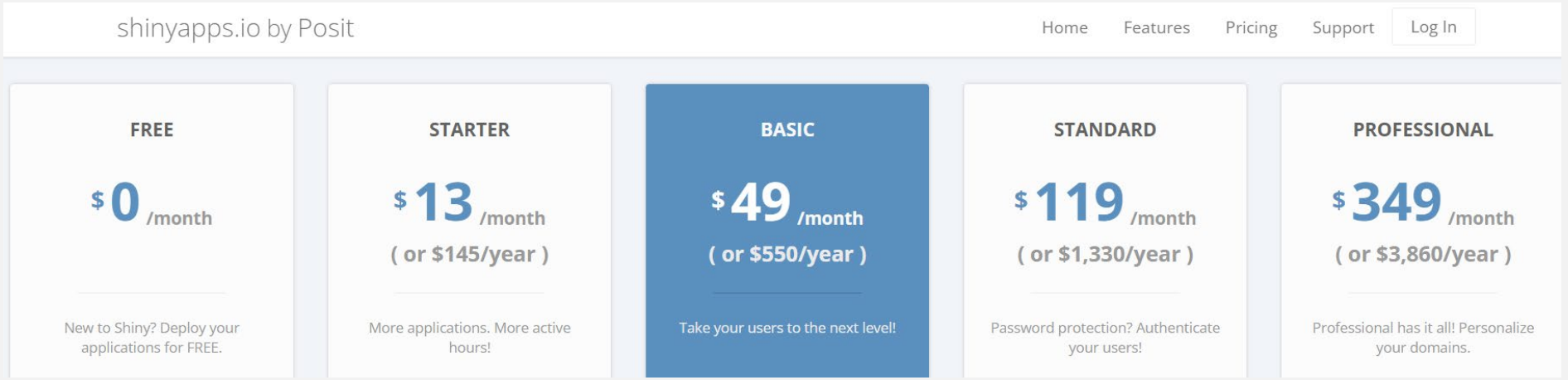
https://github.com/daattali/shinycssloaders

DEPLOYMENT

SHINY APP DEPLOYMENT

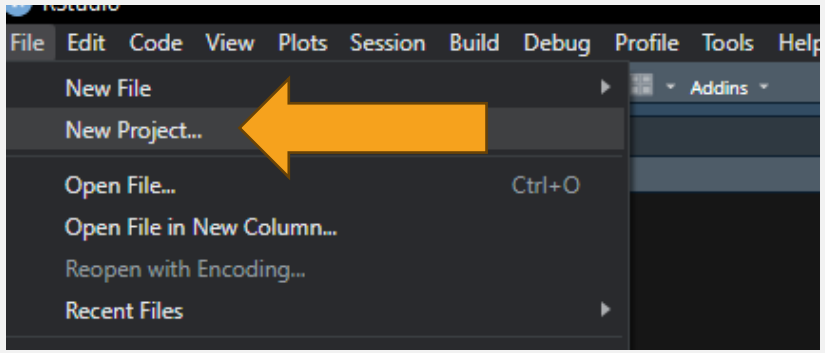
Shiny could be shared as:

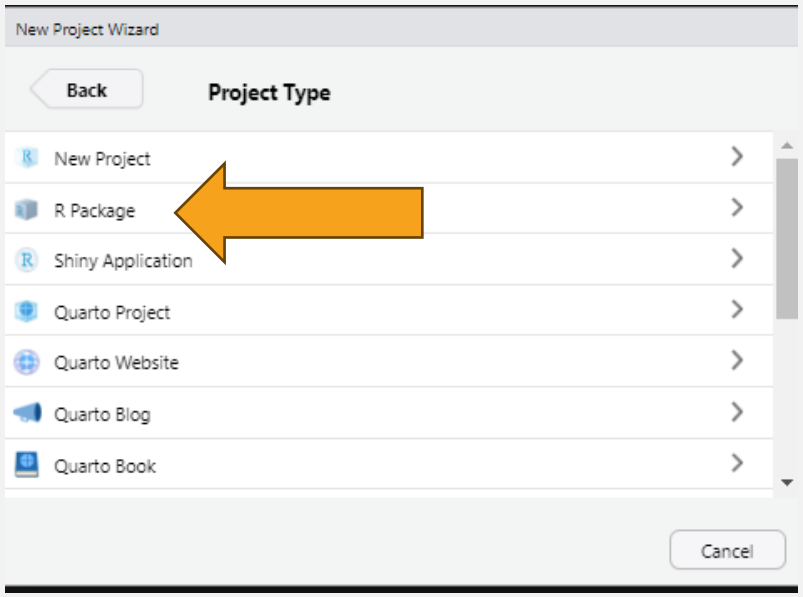
- ✓R code
- ✓Host it on https://www.shinyapps.io/

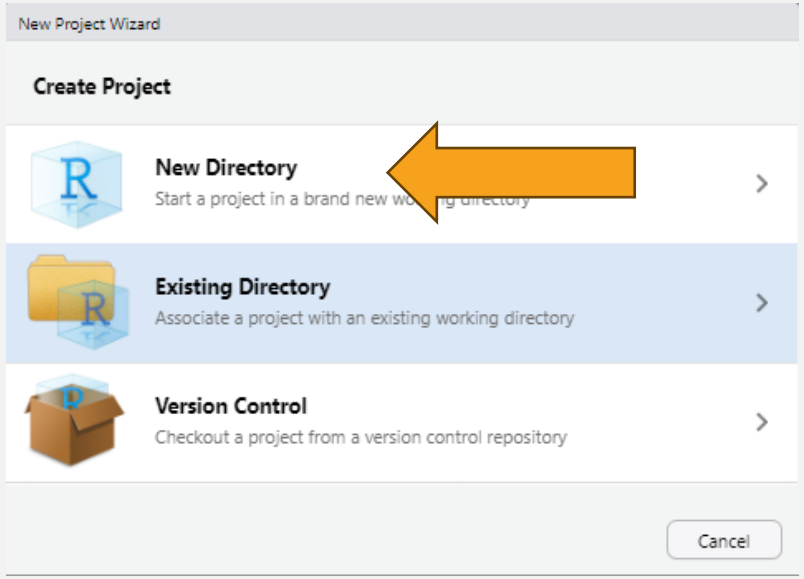


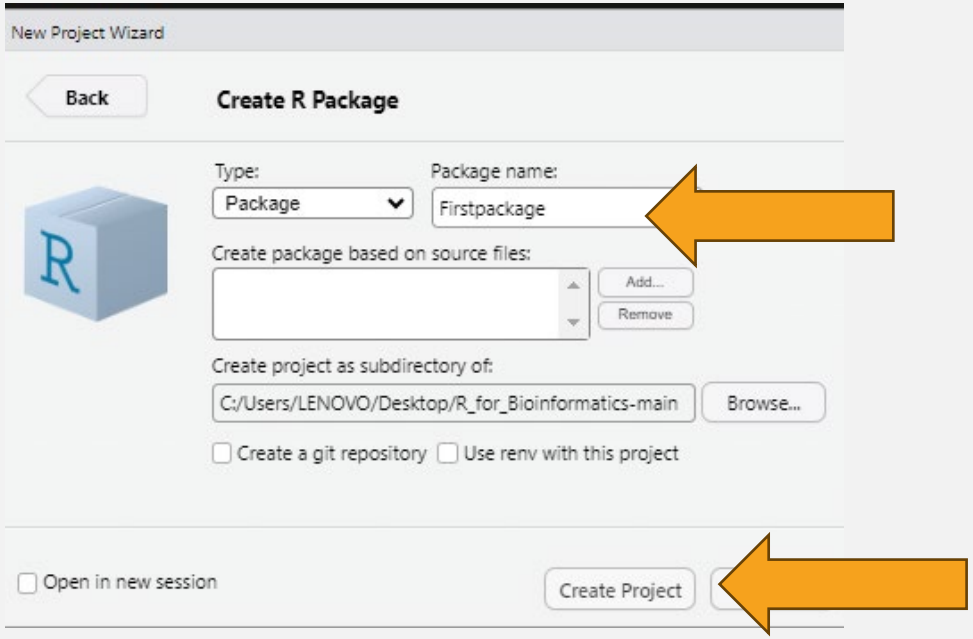
- ✓Host on private server
- ✓Implement as a function in an R package

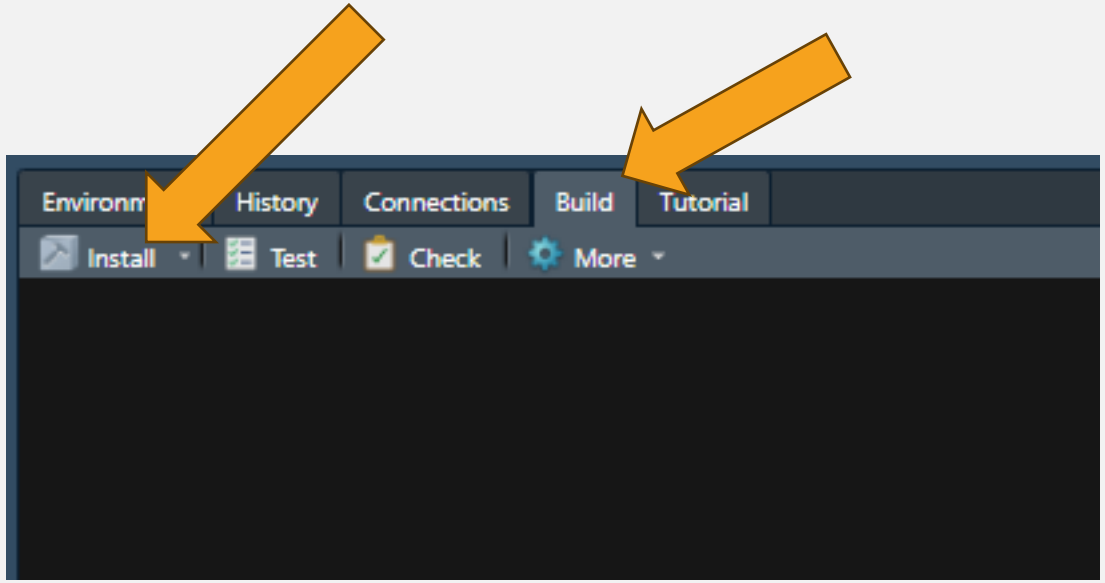
R PACKAGE DEVELOPMENT


File Edit Code View Plots Session Build Debug Profile Tools Help
New File
New Project...
Open File... Ctrl+O
Open File in New Column...
Reopen with Encoding...
Recent Files
Addins


New Project Wizard
Back
Project Type
New Project
R Package
Shiny Application
Quarto Project
Quarto Website
Quarto Blog
Quarto Book
Cancel


New Project Wizard
Create Project
New Directory
Start a project in a brand new working directory
Existing Directory
Associate a project with an existing working directory
Version Control
Checkout a project from a version control repository
Cancel


New Project Wizard
Back
Create R Package
Type:
Package
Package name:
Firstpackage
Create package based on source files:
Add...
Remove
Create project as subdirectory of:
C:/Users/LENOVO/Desktop/R_for_Bioinformatics-main
Browse...
Create a git repository
Use renv with this project
Open in new session
Create Project




```
> library(Firstpackage)
> hello()
[1] "Hello, world!"
```

BUILD A FUNCTION

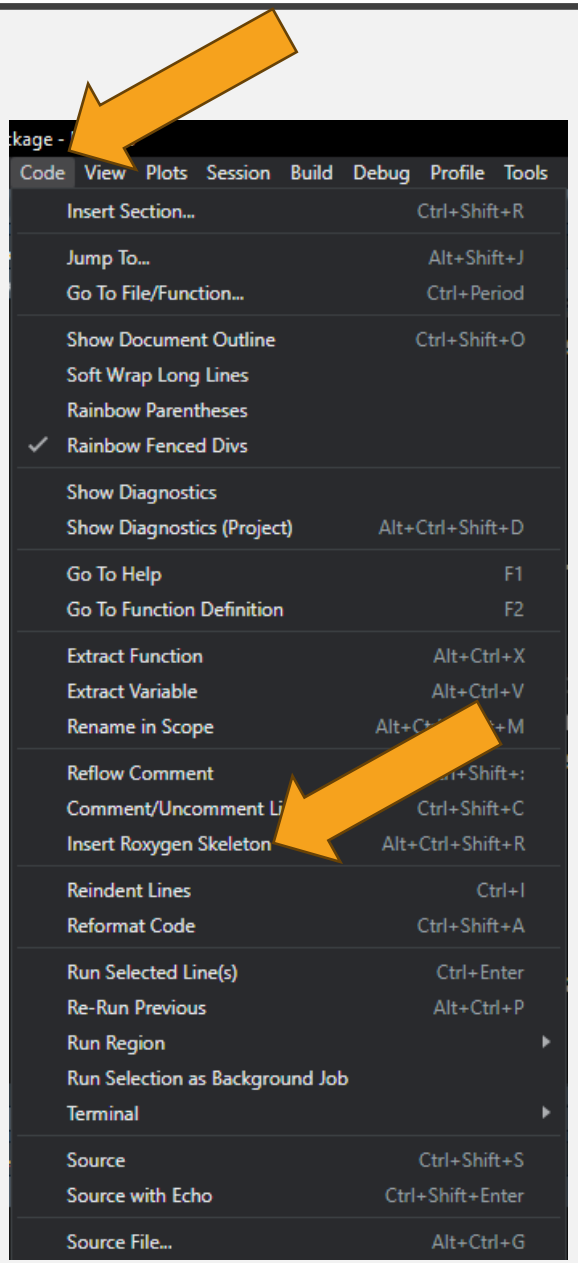
To build a function

- ✓Crate a R file
- ✓Name it with the function name
- ✓Write code inside function

```
function_name <- function() {
  #code
}
```

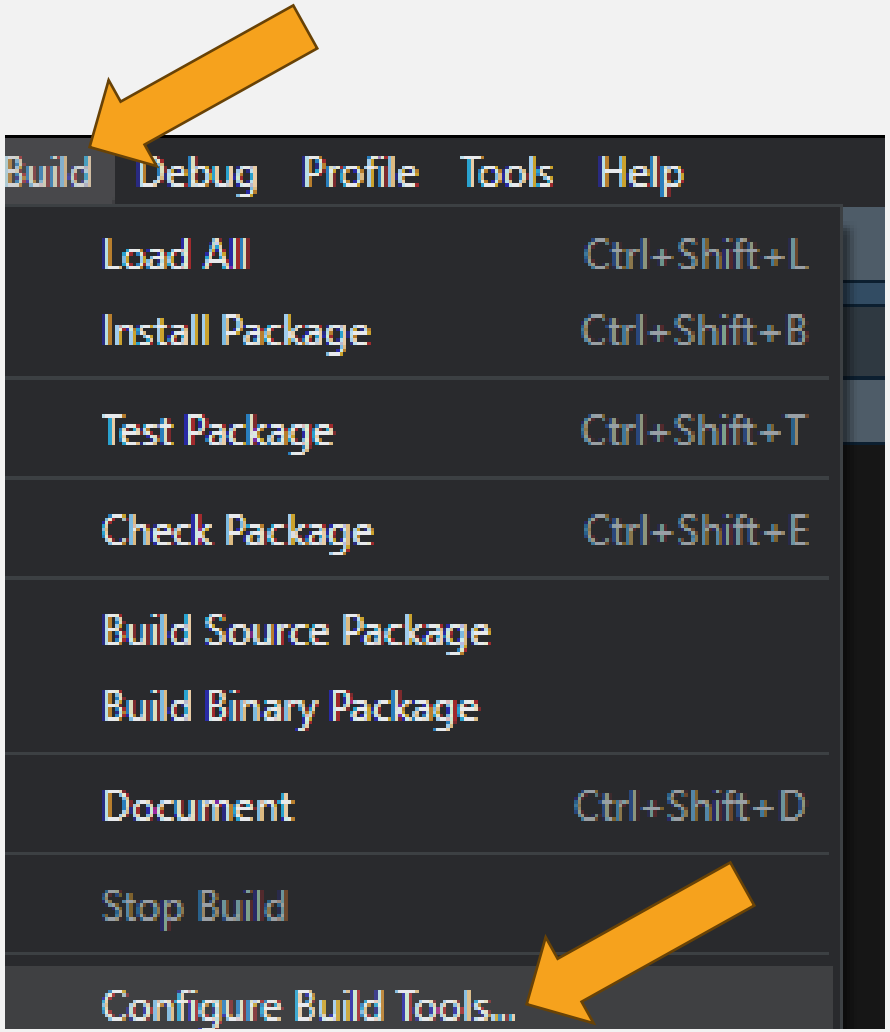
- ✓Build package again

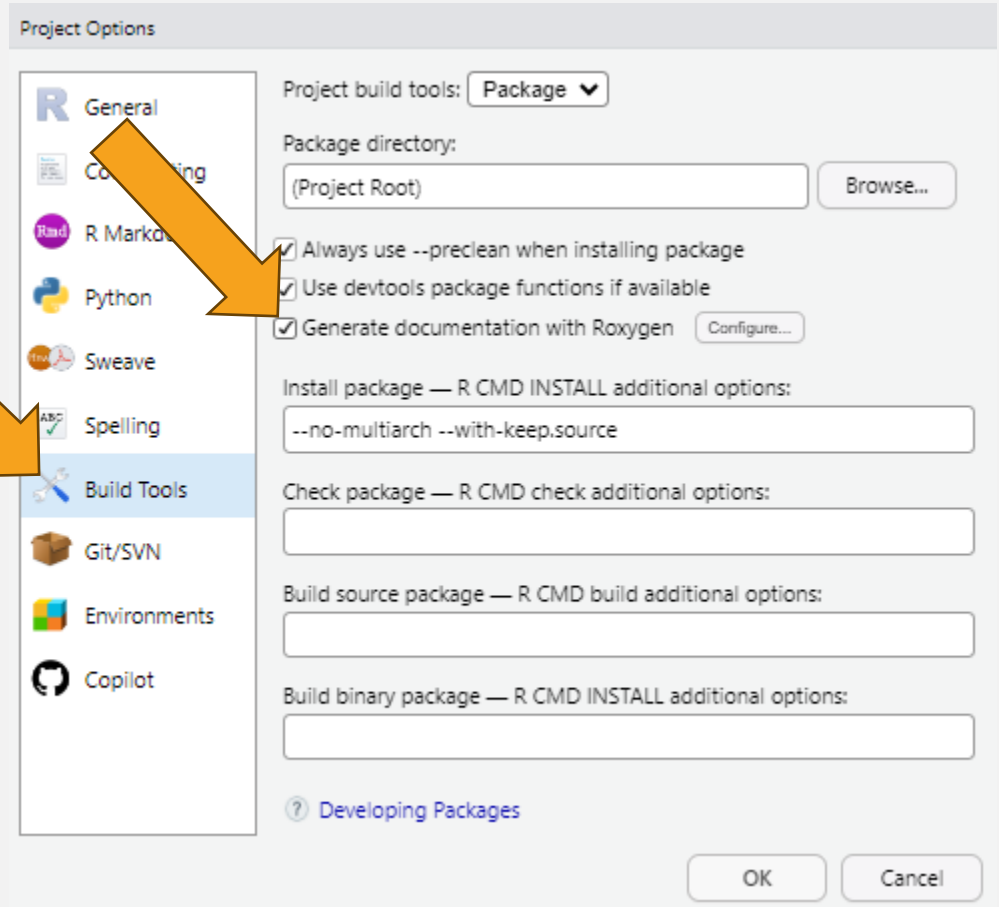
DOCUMENT FUNCTION

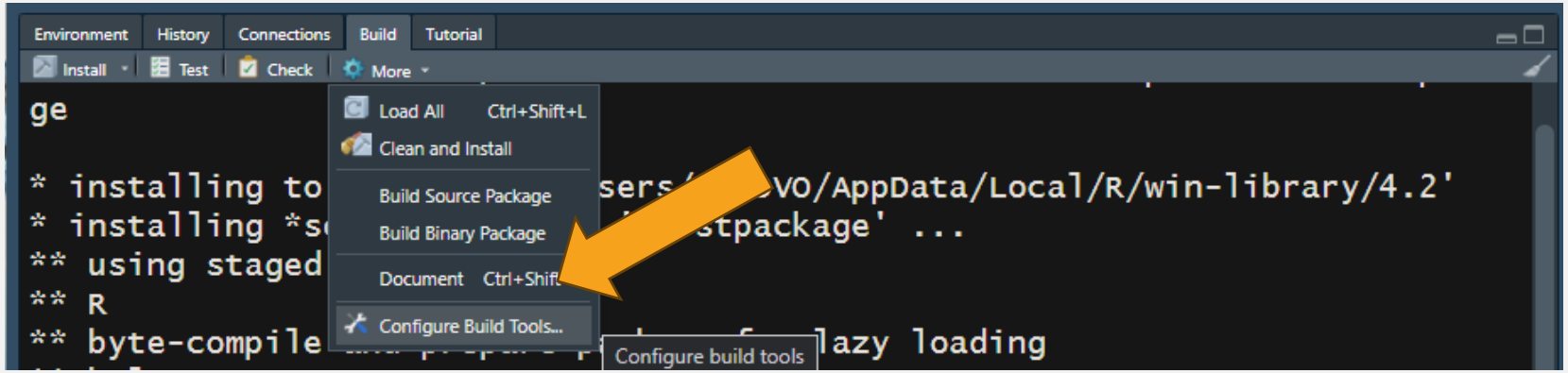


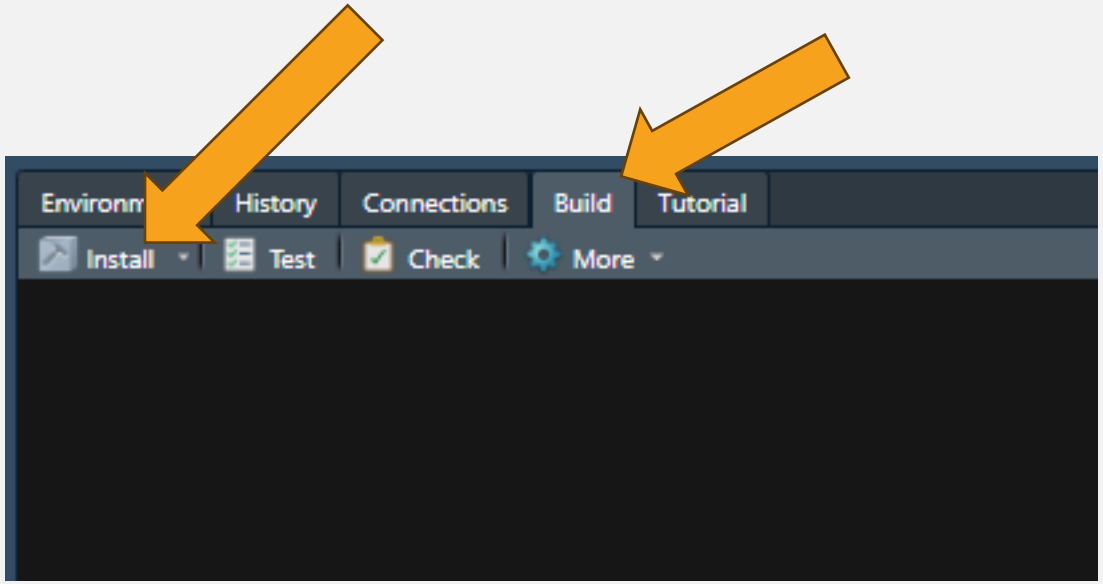
Insert Roxygen Skeleton

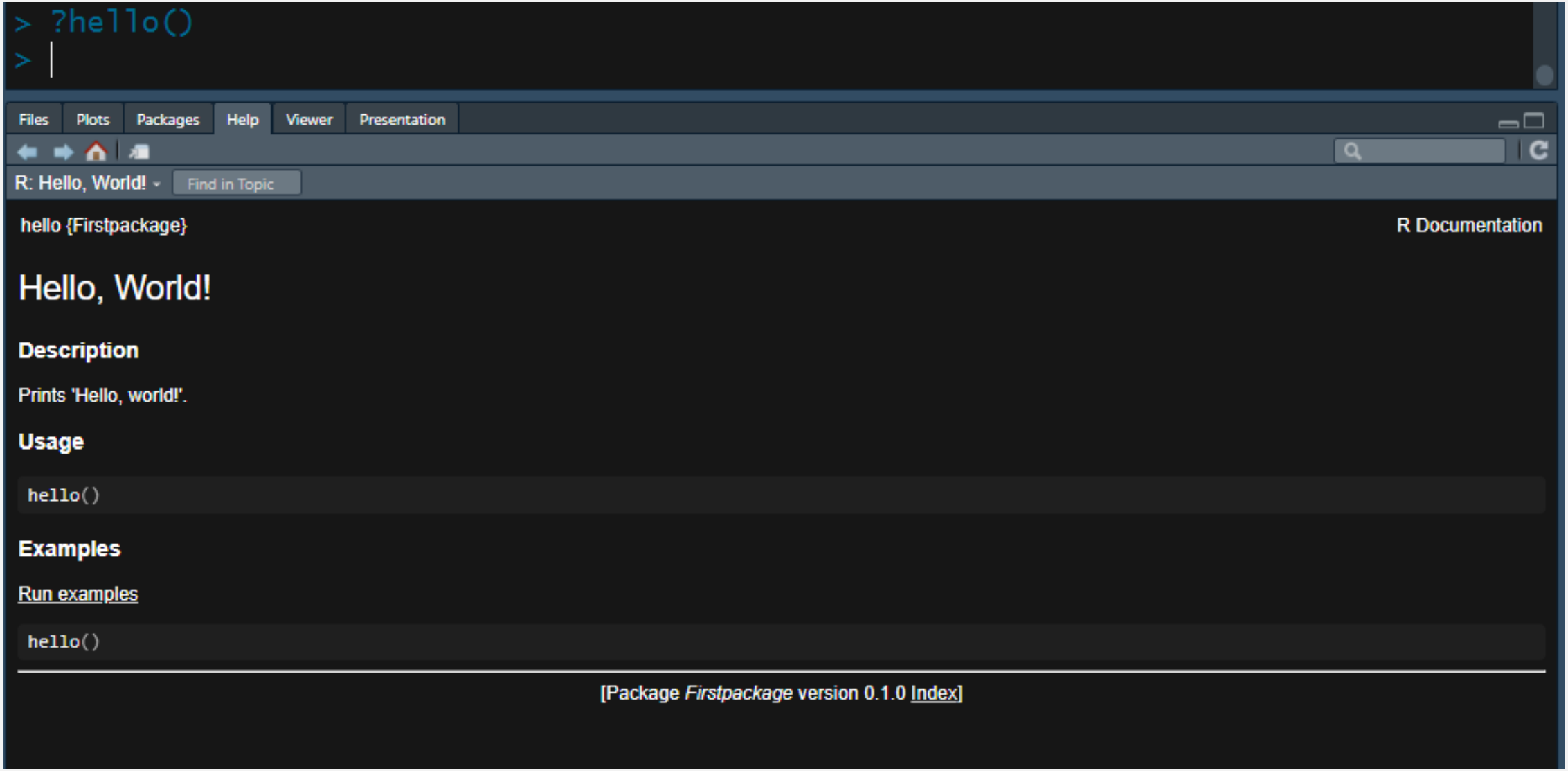
```
#' Title
#'
#' @param path
#'
#' @return
#' @export
#'
#' @examples
```


Build
Debug
Profile
Tools
Help
Load All Ctrl+Shift+L
Install Package Ctrl+Shift+B
Test Package Ctrl+Shift+T
Check Package Ctrl+Shift+E
Build Source Package
Build Binary Package
Document Ctrl+Shift+D
Stop Build
Configure Build Tools...


Project Options
General
Python
Sweave
Spelling
Build Tools
Git/SVN
Environments
Copilot
Project build tools: Package
Package directory:
(Project Root)
Browse...
Always use --preclean when installing package
Use devtools package functions if available
Generate documentation with Roxygen
Configure...
Install package — R CMD INSTALL additional options:
--no-multiarch --with-keep.source
Check package — R CMD check additional options:
Build source package — R CMD build additional options:
Build binary package — R CMD INSTALL additional options:
Developing Packages
OK
Cancel


Environment
History
Connections
Build
Tutorial
Install
Test
Check
More
Load All Ctrl+Shift+L
Clean and Install
Build Source Package
Build Binary Package
Document Ctrl+Shift
Configure Build Tools...
Configure build tools
ge
* installing to
* installing *s
** using staged
** R
** byte-compile
VO/AppData/Local/R/win-library/4.2'
tpackage' ...
lazy loading


Environm
History
Connections
Build
Tutorial
Install
Test
Check
More


> ?hello()
>
Files
Plots
Packages
Help
Viewer
Presentation
R: Hello, World!
Find in Topic
hello {Firstpackage}
R Documentation
Hello, World!
Description
Prints 'Hello, world!'.
Usage
hello()
Examples
Run examples
hello()
[Package Firstpackage version 0.1.0 Index]

INSTALLATION

- ✓ Import the package folder to GitHub
- ✓ You should be able to install it using a similar command

```
install.packages("devtools")

library(devtools)

devtools::install_github("omicscodeathon/repository/path")

library(package_name)
```

THANK YOU FOR YOU ATTENTION !

Contact me via :

Email : benaribi.hiba@gmail.com

Linkedin :

https://www.linkedin.com/in/hiba-ben-aribi-b29634239/