post2-Zhanyuan-Zhang

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Inverse Sampling and Its Visualization on R

1. Introduction

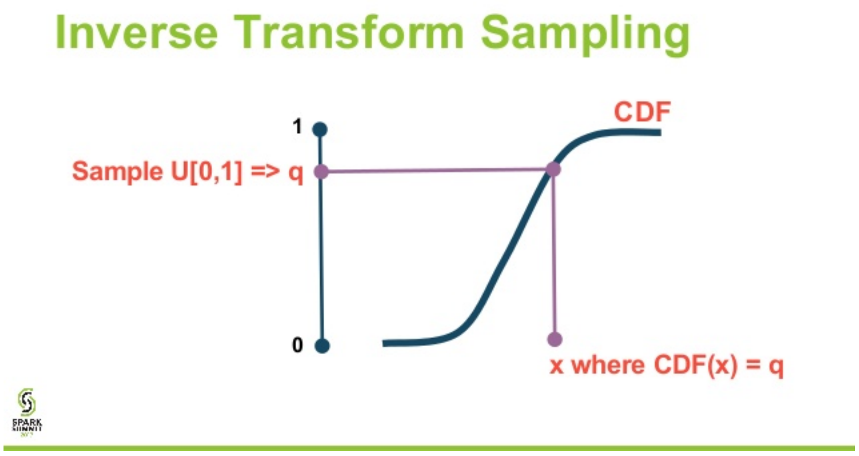
One awesome thing that people can do with computer is to generate random samples from arbitrary distribution. This technique called **Inverse Sampling** (see Wikipedia). This post will focus on how the computer generates some common continous distributions by simply sampling numbers randomly and uniformly from interval \([0, 1]\). **This has important application because it allows people to simulate many distributions from one of the simplest distribution – standard uniform distribution.** Finally, I will try to find a way to visualize this sampling process via `Shiny` app.

2. Theoratical Basis and Packages Preparation

The following theorem supports the idea of inverse sampling: Source.

> Let \(U \sim Uniform(0, 1)\), and F be a CDF which is strictly increasing. Also, consider a random variable X defined as \[X = F^{-1}(U)\] Then, \[X \sim F\] In other words, the CDF of X is F

The following picture illustrates the transformation described in the theorem:



This picture shows how the transformation performs

To facilitate the illustration, we need to import some packages.
Note: we did not mention the package `GoFKernel` . It is a package, by Jose Pavia, for testing goodness-of-fit based on a kernel smoothing of the data. You can run the following code to install this package. We need its `inverse()` function to find the inverse CDF handily.
For more information, see source

```r
install.packages("GoFKernel")
```

```r
library(ggplot2)
library(GoFKernel)
library(dplyr)
```

3. Simple Demonstrations

In this section, I am going to use three examples to demonstrate how this simulation sampling works. First, I am going to get a big enough amount of sample numbers uniformly from 0 to 1. Then, I will generate random samples from \(Exponential(\lambda = 3)\), \(Normal (\mu = 0, \sigma^{2} = 1)\), and \(Beta(r = 2, s = 3)\) respectively from the uniform samples. By plotting their histograms, the upper edge of the histograms can illustrate the resulting density curve nicely, as you are going to see.

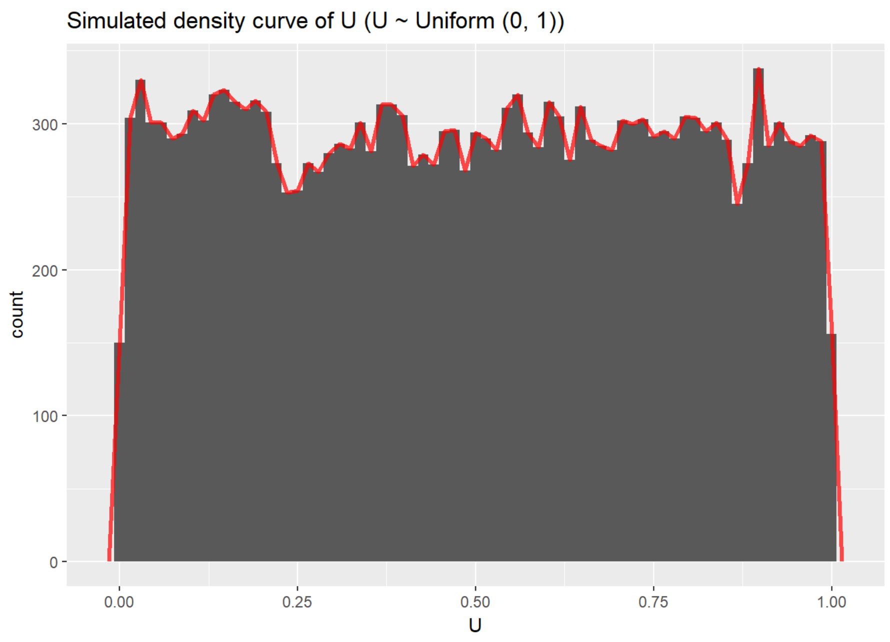
1). Uniform Sampling

I first sample 20000 numbers uniformly \([0, 1]\) (I guess this is big enough). To get the same sampling result, you can code `set.seed(42` before sampling. To facilitate our plotting, I generate a data frame saving the uniform samples, and later it will also store all the transformation samples.

```r
set.seed(42)
U <- runif(20000, min = 0, max = 1)
dat <- as.data.frame(U)
```

Try to plot the histogram of the uniform samples:

```r
ggdat <- ggplot(data = dat)
ggdat +
  geom_histogram(aes(x = U), bins = 69) +
  geom_freqpoly(aes(x = U), bins = 69, color = "red", size = 1.2, alpha = 0.7) +
  ggtitle("Simulated density curve of U (U ~ Uniform (0, 1))")
```



Regardless of the line at the two endes, the red line shows that each number has roughly same amount.

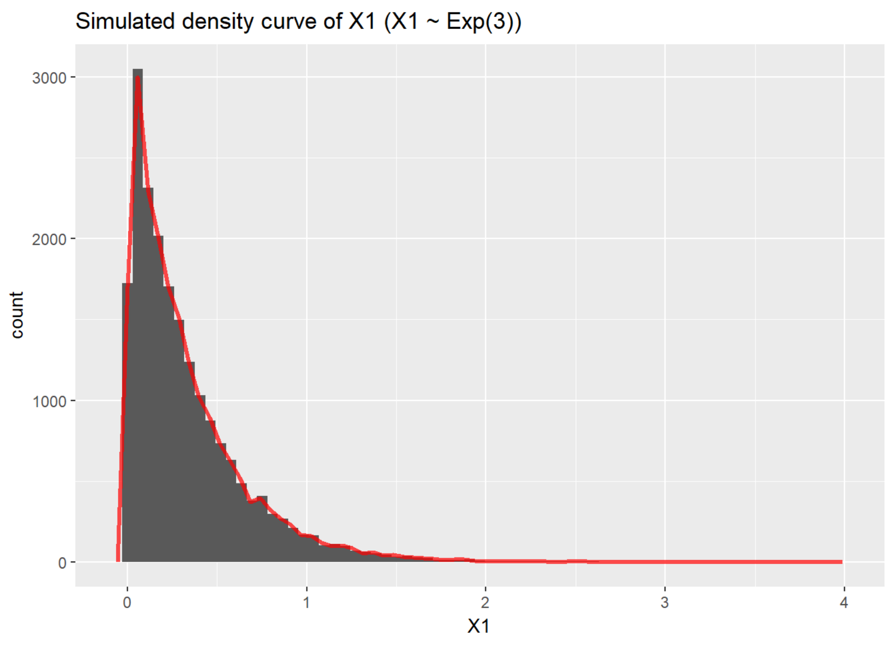
2). Simulated Exponential Distribution

Now let's find out the inverse CDF of an \(Exponential(\lambda = 3)\) by the `inverse()` from the package `GoFKernel`. After doing this, we can add a column of transformed samples called *X1* in the data frame.

```r
expon <- function(x) pexp(x, rate = 3)
invexpon <- inverse(expon, lower = 0, upper = Inf)
X1 <- c()
for (i in 1:length(U)) {
  X1[i] <- invexpon(U[i])
}
dat <- mutate(dat, X1 = X1)
```

Now, we can plot the histogram of the samples transformed by the inverse exponential CDF

```r
ggdat +
  geom_histogram(aes(x = X1), bins = 69) +
  geom_freqpoly(aes(x = X1), bins = 70, color = "red", size = 1.2, alpha = 0.7) +
  ggtitle("Simulated density curve of X1 (X1 ~ Exp(3))")
```



With the help of graphic calculator, you can find that it looks pretty closed to the graph of function \(f_{X}(x) = 3e^{-3x}\), which is the density function of \(X \sim Exponential(\lambda = 3)\).

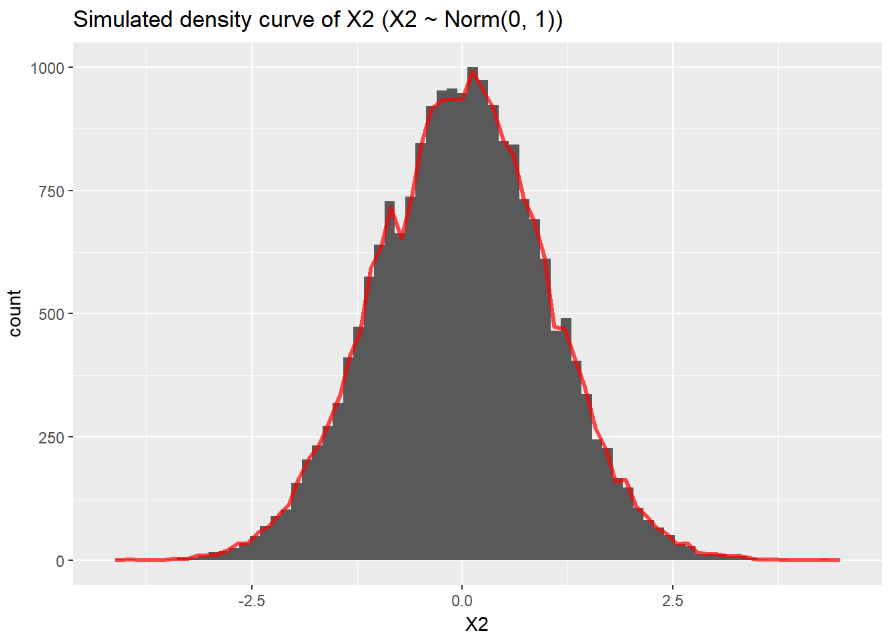
3). Simulated Normal Distribution

Next, add another column called *X2* containing transformed samples by inverse standard normal CDF:

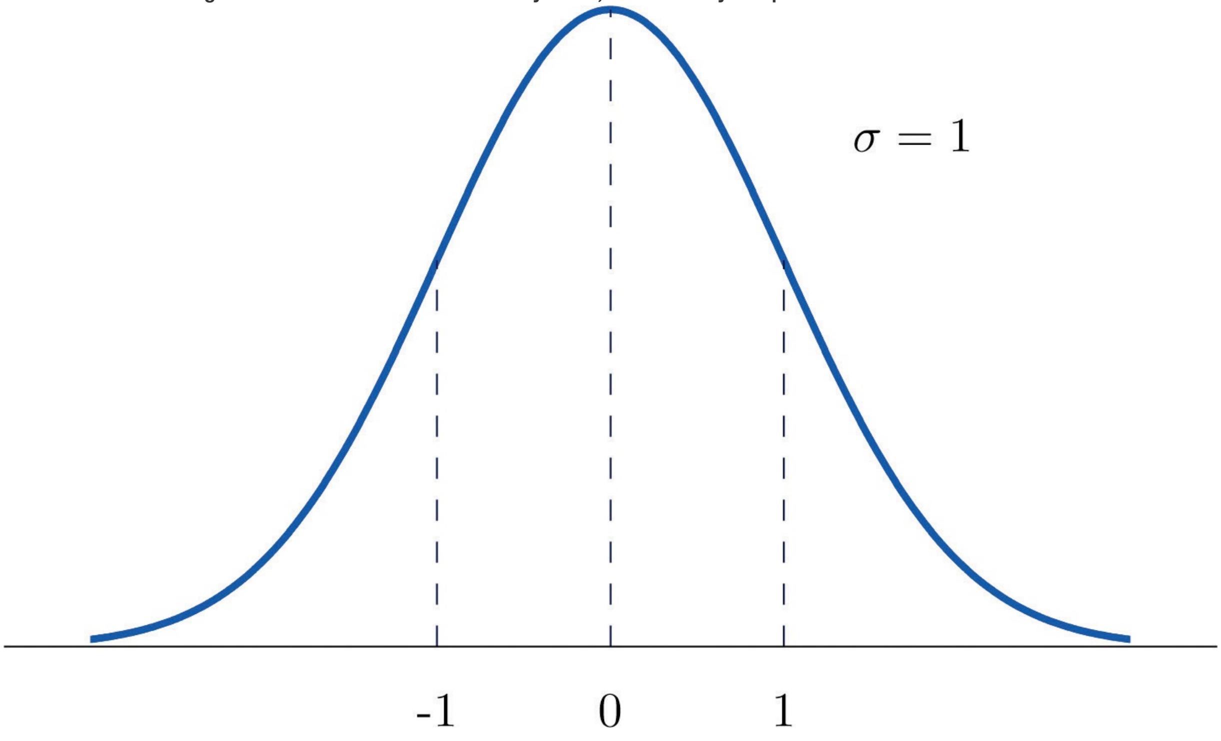
```
stnorm <- function(x) pnorm(x, mean = 0, sd = 1)
invnorm <- inverse(stnorm)
X2 <- c()
for (i in 1:length(U)) {
  X2[i] <- invnorm(U[i])
}
dat <- mutate(dat, X2 = X2)
```

Similarly as above, do the plotting:

```
ggdat +
  geom_histogram(aes(x = X2), bins = 69) +
  geom_freqpoly(aes(x = X2), bins = 70, color = "red", size = 1.2, alpha = 0.7) +
  ggtitle("Simulated density curve of X2 (X2 ~ Norm(0, 1))")
```



Since we are simulating the *famous* standard normal density curve, we can easily compare it to the *correct* one:



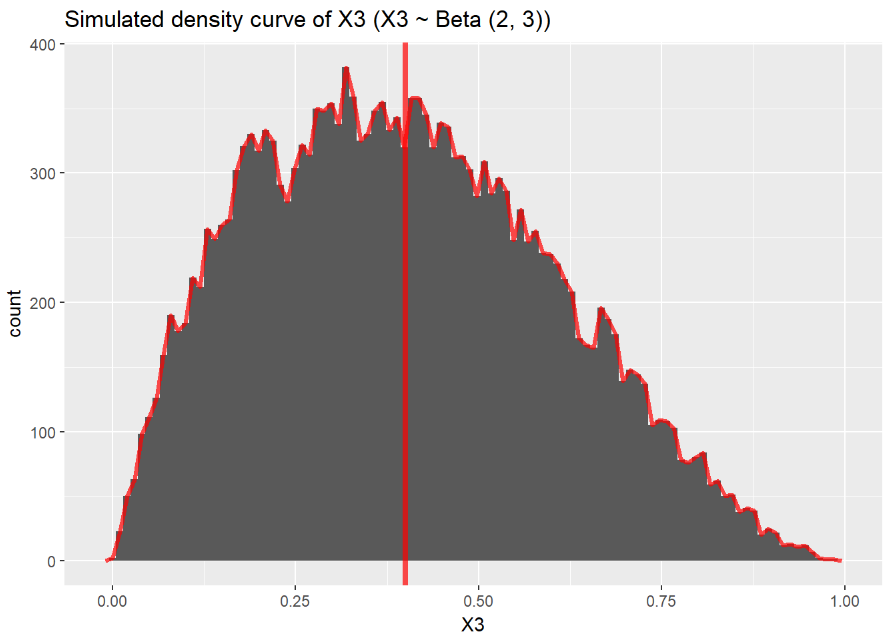
4). Simulated Beta Distribution

Now, let's find out the inverse CDF of the \(Beta(r = 2, s = 3)\), and then add another column called *X3* containing the transformed samples:

```r
beta23 <- function(x) pbeta(x, shape1 = 2, shape2 = 3)
invbeta23 <- inverse(beta23, lower = 0, upper = 1)
X3 <- c()
for (i in 1:length(U)) {
  X3[i] <- invbeta23(U[i])
}
dat <- mutate(dat, X3 = X3)
```

Let's see the plotting:

```r
ggdat +
  geom_histogram(aes(x = X3), bins = 100) +
  geom_vline(xintercept = 2/5, color = "red", size = 1.5, alpha = 0.7) +
  geom_freqpoly(aes(x = X3), bins = 100, color = "red", size = 1.2, alpha = 0.7) +
  ggtitle("Simulated density curve of X3 (X3 ~ Beta (2, 3))")
```



We know that the expectation value of \(X \sim Beta(r = 2, s = 3)\) is \(E(X) = \frac{r}{r+s} = \frac{2}{5}\), which is shown by the vertical red line. The peak of the simulated curve is closed to the actual expectation, which tells us that the transformed samples give a decent simulation.

4. Turn into a `Shiny` App

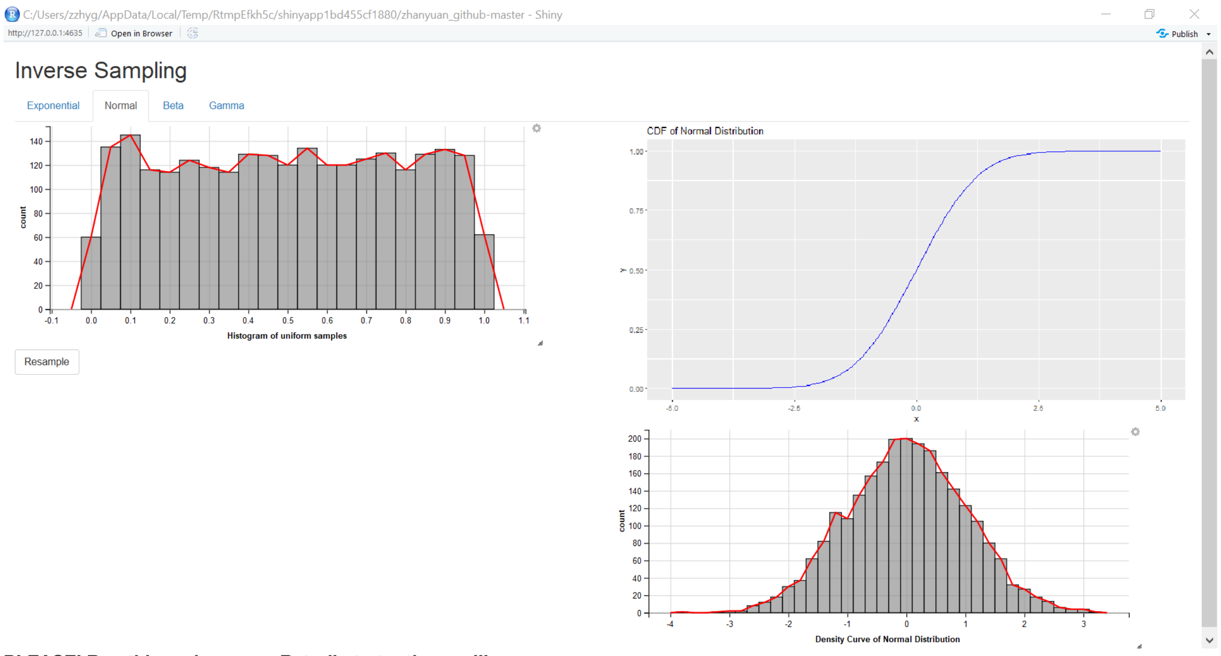
Now we know how to utilize the `inverse()` function in `GoFKernel` to find inverse function of a CDF, and the demonstrations above shows graphically how to conduct inverse sampling via those inverse functions.
Since we have already had the general ideas in mind, why not turn all these into a `Shiny` app?

In this section, I will show you how to build up an app that allows people to:

1). sample certain amount of numbers uniformly from \([0, 1]\);
2). transform the uniform samples into samples from other distributions;
3). Show the cdf curve of the given distribution;
4). visualize the simulated density curves of both the uniform samples and the transformed samples.
Note: Since this app intends to visualize *inverse sampling,* we don't have to consider the parameters of the distributions.

For guidance purpose, I will code the app step-by-step with full explanations. To reproduce this app, you can either copy-paste my code, **OR** you can run the code right after the preview picture of the app on your **Rstudio** to run the app.

Here is how the app looks like: (Note that the larger the slope of CDF, the more likely that the corresponding samples to be turned into, since the slope of CDF represents the probability density, by definition.)


C:/Users/zzhyg/AppData/Local/Temp/RtmpEfkh5c/shinyapp1bd455cf1880/zhanyuan_github-master - Shiny
http://127.0.0.1:4635
Open in Browser
Publish
Inverse Sampling
Exponential
Normal
Beta
Gamma
count
Histogram of uniform samples
Resample
CDF of Normal Distribution
y
x
count
Density Curve of Normal Distribution

PLEASE! Run this code on you Rstudio to try the app!!!

```
shiny::runGitHub('zhanyuan_github', 'ucbzhanyuan')
```

Ok! Let see how I make this app:

Here is the entire Shiny app code for this app. Take a glance to find the functions that you are not familiar with and then scroll down to see their explanations.

```
# required packages
library(shiny)
library(ggplot2)
library(ggvis)
library(dplyr)
library(GoFKernel)

# import cdf
source("../functions.R")

# Define UI for application that draws a histogram
ui <- fluidPage(

   # Application title
   titlePanel("Inverse Sampling"),

   tabsetPanel(
     tabPanel(title = "Exponential",
              fluidRow(
                column(6, ggvisOutput("unif"),
                       actionButton("resample", "Resample")),
                column(6, plotOutput("expdens"))
              ),
              fluidRow(
                column(6),
                column(6, ggvisOutput("exp"))
              )
              ),
     tabPanel(title = "Normal",
              fluidRow(
                column(6, ggvisOutput("unif2"),
                       actionButton("resample2", "Resample")),
                column(6, plotOutput("nordens"))
              ),
              fluidRow(
                column(6),
                column(6, ggvisOutput("nor"))
              )
              ),
     tabPanel(title = "Beta",
              fluidRow(
                column(6, ggvisOutput("unif3"),
                       actionButton("resample3", "Resample")),
                column(6, plotOutput("betdens"))
              ),
              fluidRow(
                column(6),
                column(6, ggvisOutput("bet"))
              )
```

```r
               ),
      tabPanel(title = "Gamma",
               fluidRow(
                 column(6, ggvisOutput("unif4"),
                        actionButton("resample4", "Resample")),
                 column(6, plotOutput("gamdens"))
               ),
               fluidRow(
                 column(6),
                 column(6, ggvisOutput("gam"))
               )
               )
    )
)

# Define server logic required to draw a histogram
server <- function(input, output) {
  # Uniform sampling
  rv <- reactiveValues(
    U1 = runif(2500),
    U2 = runif(2500),
    U3 = runif(2500),
    U4 = runif(2500))
  # resample button
  observeEvent(input$resample, { rv$U1 <- runif(2500) })
  observeEvent(input$resample2, { rv$U2 <- runif(2500) })
  observeEvent(input$resample3, { rv$U3 <- runif(2500) })
  observeEvent(input$resample4, { rv$U4 <- runif(2500) })

  vis_unif <- reactive({
    dat <- data.frame(u = rv$U1)
    dat %>% ggvis(~u) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Histogram of uniform samples") %>%
      set_options(width = 700, height = 300)
  })
  vis_unif %>% bind_shiny("unif")

  vis_unif <- reactive({
    dat <- data.frame(u = rv$U2)
    dat %>% ggvis(~u) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Histogram of uniform samples") %>%
      set_options(width = 700, height = 300)
  })
  vis_unif %>% bind_shiny("unif2")

  vis_unif <- reactive({
    dat <- data.frame(u = rv$U3)
    dat %>% ggvis(~u) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Histogram of uniform samples") %>%
      set_options(width = 700, height = 300)
  })
  vis_unif %>% bind_shiny("unif3")

  vis_unif <- reactive({
    dat <- data.frame(u = rv$U4)
    dat %>% ggvis(~u) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Histogram of uniform samples") %>%
      set_options(width = 700, height = 300)
  })
  vis_unif %>% bind_shiny("unif4")

  # exponential cdf
  output$expdens <- renderPlot({
    ggplot(data = data.frame(x = c(0, 10)), aes(x = x)) +
      stat_function(fun = function(x) 1 - exp(-3 * x), color = "blue") +
      ggtitle("CDF of Exponential Distribution")
  })

  # normal cdf
  output$nordens <- renderPlot({
    ggplot(data = data.frame(x = c(-5, 5)), aes(x = x)) +
      stat_function(fun = pnorm, args = list(mean = 0, sd = 1), color = "blue") +
      ggtitle("CDF of Normal Distribution")

  })

  # beta cdf
  output$betdens <- renderPlot({
    ggplot(data = data.frame(x = c(0, 1)), aes(x = x)) +
      stat_function(fun = pbeta, args = list(shape1 = 2, shape2 = 3), color = "blue") +
      ggtitle("CDF of Beta Distribution")
  })

  # gamma cdf
  output$gamdens <- renderPlot({
    ggplot(data = data.frame(x = c(0, 0.6)), aes(x = x)) +
      stat_function(fun = pgamma, args = list(shape = 3, scale = 0.05), color = "blue") +
      ggtitle("CDF of Gamma Distribution")
  })


  # exponential
  vis_exp <- reactive({
    dat <- data.frame(u = rv$U1)
    X1 <- c()
    for (i in 1:length(rv$U1)) {
      X1[i] <- invexpon(rv$U1[i])
    }
    dat <- mutate(dat, X1 = X1)
    dat %>% ggvis(~X1) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Density Curve of Exponential Distribution") %>%
      set_options(width = 700, height = 300)
  })
  vis_exp %>% bind_shiny("exp")

  # normal
  vis_nor <- reactive({
    dat2 <- data.frame(u = rv$U2)
    X2 <- c()
    for (i in 1:length(rv$U2)) {
      X2[i] <- invnorm(rv$U2[i])
    }
    dat2 <- mutate(dat2, X2 = X2)
    dat2 %>% ggvis(~X2) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Density Curve of Normal Distribution") %>%
      set_options(width = 700, height = 300)
  })
  vis_nor %>% bind_shiny("nor")

  # beta
  vis_bet <- reactive({
    dat3 <- data.frame(u = rv$U3)
    X3 <- c()
    for (i in 1:length(rv$U3)) {
      X3[i] <- invbeta23(rv$U3[i])
    }
    dat3 <- mutate(dat3, X3 = X3)
    dat3 %>% ggvis(~X3) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Density Curve of Beta Distribution") %>%
      set_options(width = 700, height = 300)
  })
  vis_bet %>% bind_shiny("bet")

  # Gamma
  vis_gam <- reactive({
    dat4 <- data.frame(u = rv$U4)
    X4 <- c()
    for (i in 1:length(rv$U4)) {
      X4[i] <- invgamma6(rv$U4[i])
    }
    dat3 <- mutate(dat4, X4 = X4)
    dat3 %>% ggvis(~X4) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Density Curve of Gamma Distribution") %>%
      set_options(width = 700, height = 300)
  })
  vis_gam %>% bind_shiny("gam")

}

# Run the application
shinyApp(ui = ui, server = server)
```

Here are the step-by-step explanations of how to build this app:

1). **Preparations:** I want this app shows the simulated sampling from the following distributions:
a. Exponential b. Normal c. Beta d. Gamma Therefore, we can **create a R script file** to save the cdf's and inverse cdf's we need. Here is the code for the functions.

```
# inverse exp cdf
expon <- function(x) pexp(x, rate = 3)
invexpon <- inverse(expon, lower = 0, upper = Inf)

# inverse normal cdf
stnorm <- function(x) pnorm(x, mean = 0, sd = 1)
invnorm <- inverse(stnorm)

# inverse beta cdf
beta23 <- function(x) pbeta(x, shape1 = 2, shape2 = 3)
invbeta23 <- inverse(beta23, lower = 0, upper = 1)

# inverse gamma cdf
gamma6 <- function(x) pgamma(x, rate = 0.5, shape = 6)
invgamma6 <- inverse(gamma6, lower = 0, upper = Inf)

unif <- function(x) x = x
```

2). **Ui section:** To build the layout in the Shiny app, we need to utilize `fluidRow()` and `column()` functions. In addition, we need an **action button** for the resample purpose. Since the layouts of the four tabs are almost identical, in the *ui* section, we basically copy-paste this code for three more times. For more information about building layouts, see source
In the example of the first tab *ui* (for exponential distribution):

```
     tabPanel(title = "Exponential",
              fluidRow(
                column(6, ggvisOutput("unif"),
                       actionButton("resample", "Resample")),
                column(6, plotOutput("expdens"))
              ),
              fluidRow(
                column(6),
                column(6, ggvisOutput("exp"))
              )
              )
```

3). **Server section:** Server is the place that makes thing difficult.
a). First I need to activate the **Resample** button. In order to ask the app to do the resampling once we click, we need functions called `reactiveValues()` and `observeEvent()`. For more information about the practical use of these functions, see source.

```
  rv <- reactiveValues(
    U1 = runif(2500),
    U2 = runif(2500),
    U3 = runif(2500),
    U4 = runif(2500))
  # resample button
  observeEvent(input$resample, { rv$U1 <- runif(2500) })
  observeEvent(input$resample2, { rv$U2 <- runif(2500) })
  observeEvent(input$resample3, { rv$U3 <- runif(2500) })
  observeEvent(input$resample4, { rv$U4 <- runif(2500) })
```

b). Next, we should plot the histogram of the uniform sampling. Here, we use `ggvis` to do the plotting. As they need to show up in all four tabs, we need to write the following code four times with different variables (U1, U2…):

```
  vis_unif <- reactive({
    dat <- data.frame(u = rv$U1)
    dat %>% ggvis(~u) %>%
      layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
      layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
      add_axis("x", title = "Histogram of uniform samples") %>%
      set_options(width = 700, height = 300)
  })
  vis_unif %>% bind_shiny("unif")
```

c). Analogously, we can plot the histogram for all the transformed samples. Take the **Normal Distribution** as an example:

```r
# normal
vis_nor <- reactive({
  dat2 <- data.frame(u = rv$U2)
  X2 <- c()
  for (i in 1:length(rv$U2)) {
    X2[i] <- invnorm(rv$U2[i])
  }
  dat2 <- mutate(dat2, X2 = X2)
  dat2 %>% ggvis(~X2) %>%
    layer_histograms(fill := "grey", fillOpacity := 0.6, fillOpacity.hover := 0.8) %>%
    layer_freqpolys(stroke := "red", strokeWidth := 2) %>%
    add_axis("x", title = "Density Curve of Normal Distribution") %>%
    set_options(width = 700, height = 300)
})
vis_nor %>% bind_shiny("nor")
```

d). Finally, we want to plot the cdf curve of distribution as a reference. I found that `ggplot2` can easily do so with the assistance of the *cdf* functions in the built-in package `stats`, as following. To know about *Probability Plots,* see source

```r
# normal cdf
output$nordens <- renderPlot({
  ggplot(data = data.frame(x = c(-5, 5)), aes(x = x)) +
    stat_function(fun = pnorm, args = list(mean = 0, sd = 1), color = "blue") +
    ggtitle("CDF of Normal Distribution")
})
```

That's all about it!!! For your convenience, here is the code for running the app:

```r
shiny::runGitHub('zhanyuan_github', 'ucbzhanyuan')
```

5. Take Home Message

1). This post visualizes the technique of inverse sampling through `Shiny` app.
2). In `Shiny` app, we can use `fluidRow()` and `cloumn()` functions to constimize the layouts of the apps.
3). Regarding interactive plot, `ggvis` is better than `ggplot2`.
4). Designing an app is fun!

6. Conclusion

Thanks for reading this post!

One thing that this post taught me was that building a *shiny* app was definitely not as simple as I thought when I hadn't stated. During the coding process, I designed the layout of the app, I learned how to fully control the layout through `fluidRow()` and `column()`, I realized that the **Resample** button was not as easy as I thought… I made a lot of mistakes and came across many difficulties, and yet I learned from errors and overcame the difficulties.
In this post, I try to utilize some packages I've learned about R and combine them with the *inverse sampling*. As you can see, this app is based on `shiny`, `ggvis`, `ggplot`, `dplyr`,and `GoFKernel`. Building a app without guidance is hard, for the workloads of debugging and designing are way more heavier. However, this *is* an effective way to check whether I understand R well enough.

7. Suggestions? Let me know!

Are there any way to improve this app? I'll say "definitely YES!" For instance, I may be able to use `for` loop to simplify my code, or I may be able to find a way to avoid creating so many variables, or maybe the app can allow users to download the data, or I might be able to find some ways to animate the sampling process… Anyway, if you have any suggestions for me, feel free to let me know!
Here is my email: zhang_zhanyuan AT berkeley DOT edu

8. References:

1). https://image.slidesharecdn.com/203erikerlandson-170615194512/95/smart-scalable-feature-reduction-with-random-forests-with-erik-erlandson-20-638.jpg?cb=1497555953
2). https://saylordotorg.github.io/text_introductory-statistics/section_09/e7a042db29b39bb94416c06789301faa.jpg
3). https://www.probabilitycourse.com/chapter13/Chapter_13.pdf
4). https://www.rdocumentation.org/packages/GoFKernel/versions/2.1-0
5). https://vimeo.com/rstudioinc/review/131218530/212d8a5a7a/#t=1h59m4s
6). https://www.statmethods.net/advgraphs/probability.html
7). https://shiny.rstudio.com/gallery/widgets.html
8). https://en.wikipedia.org/wiki/Inverse_transform_sampling