

# Chapter 3: Methods for Simulating Data

Statisticians (and other users of data) need to simulate data for many reasons.

For example, I simulate as a way to check whether a model is appropriate. If the observed data are similar to the data I generated, then this is one way to show my model may be a good one.

It is also sometimes useful to simulate data from a distribution when I need to estimate an expected value (approximate an integral). — Ch. 5

R can already generate data from many (named) distributions:

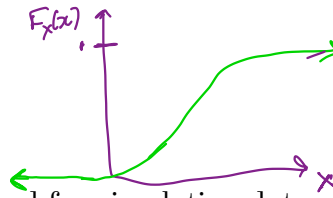
```
set.seed(400) #reproducibility set the seed so that we can reproduce our results later...  
rnorm(10) # 10 observations of a  $N(0,1)$  r.v.  
  
## [1] -1.0365488  0.6152833  1.4729326 -0.6826873 -0.6018386 -1.3526097  
## [7]  0.8607387  0.7203705  0.1078532 -0.5745512  
  
rnorm(10, 0, 5) # 10 observations of a  $N(0,5^2)$  r.v.  
  
## [1] -4.5092359  0.4464354 -7.9689786 -0.4342956 -5.8546081  2.7596877  
## [7] -3.2762745 -2.1184014  2.8218477 -5.0927654  
  
rexp(10) # 10 observations from an  $Exp(1)$  r.v.  
  
## [1] 0.67720831 0.04377997 5.38745038 0.48773005 1.18690322 0.92734297  
## [7] 0.33936255 0.99803323 0.27831305 0.94257810
```

But what about when we don't have a function to do it?

↳ we need to write our own functions to simulate data from other distributions.

# 1 Inverse Transform Method

**Theorem 1.1 (Probability Integral Transform)** If  $X$  is a continuous r.v. with cdf  $F_X$ , then  $U = F_X(X) \sim \text{Uniform}[0, 1]$ .



This leads to the following method for simulating data.

## Inverse Transform Method:

First, generate  $u$  from  $\text{Uniform}[0, 1]$ . Then,  $x = F_X^{-1}(u)$  is a realization from  $F_X$ .

**Note:**

$F^{-1}$  may not be available in closed form! If that's the case, use something else...

## 1.1 Algorithm

- on paper* 1. Derive the inverse function  $F_X^{-1}$ . To do this, let  $F(x) = u$ , solve for  $x$  to find  $x = F^{-1}(u)$ .
- in R* 2. Write a function to compute  $x = F_X^{-1}(u)$ .
3. For each realization, *simulated value*
  - a. generate a random value  $u$  from  $\text{Unif}(0,1)$
  - b. compute  $x = F^{-1}(u)$ .

**Example 1.1** Simulate a random sample of size 1000 from the pdf  $f_X(x) = 3x^2, 0 \leq x \leq 1$ .

1. Find the cdf  $F$

$$F(x) = \int_0^x 3y^2 dy = y^3 \Big|_0^x = \begin{cases} 0 & \text{for } x < 0 \\ x^3 & \text{for } x \in [0, 1] \\ 1 & \text{for } x > 1 \end{cases}$$

2. Find  $F^{-1}$

for  $x \in [0, 1]$   $u = F(x) = x^3 \Rightarrow u^{1/3} = x = F^{-1}(u)$ .

$$\text{so } F^{-1}(u) = u^{1/3} \quad 0 \leq u \leq 1$$

3. # write code for inverse transform example

#  $f_X(x) = 3x^2, 0 \leq x \leq 1$

① Write function for  $F^{-1}$

② Sample  $u$  from  $\text{Unif}(0, 1)$

③ evaluate  $x = F^{-1}(u)$ .

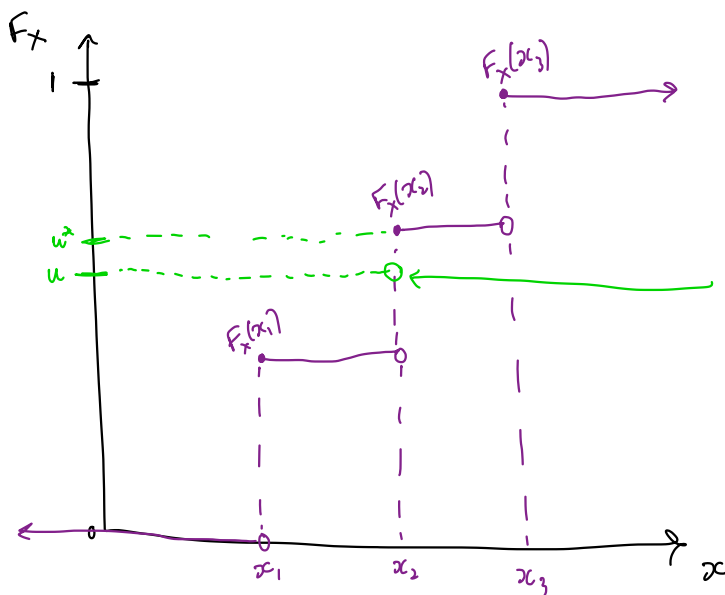
## 1.2 Discrete RVs $\rightarrow$ inverse function won't be so straightforward.

jumps in cdf  $\Leftrightarrow$  support of  $X$

If  $X$  is a discrete random variable and  $\dots < x_{i-1} < x_i < \dots$  are the points of discontinuity of  $F_X(x)$ , then the inverse transform is  $F_X^{-1}(u) = x_i$  where  $F_X(x_{i-1}) < u \leq F_X(x_i)$ . This leads to the following algorithm:

1. Generate a r.v.  $U$  from  $\text{Unif}(0, 1)$ .

2. Select  $x_i$  where  $F_X(x_{i-1}) < U \leq F_X(x_i)$ .



$F(x_1) < u \leq F(x_2)$   
 $\Rightarrow$  pick  $x_2$  still!

$F(x_1) < u \leq F(x_2)$   
 $\Rightarrow x_2$

**Example 1.2** Generate 1000 samples from the following discrete distribution.

```
x <- 1:3  
p <- c(0.1, 0.2, 0.7)
```

x	1.0	2.0	3.0
f	0.1	0.2	0.7

pmf

```
# write code to sample from discrete dsn  
n <- 1000
```

There is a simpler way to do this using the `sample()` function  
\* remember to allow replacement and specify the probability vector \*

something we can try  
 if we can't find  $F^{-1}$  analytically

## 2 Acceptance-Reject Method

The goal is to generate realizations from a target density,  $f$ .

density we want to sample from.

Most cdfs cannot be inverted in closed form.  $x = F^{-1}(u)$

The Acceptance-Reject (or "Accept-Reject") samples from a distribution that is similar to  $f$  and then adjusts by only accepting a certain proportion of those samples.

target

and rejecting the rest.

The method is outlined below:

Let  $g$  denote another density from which we **know how to sample** and we can **easily calculate**  $g(x)$ .

Let  $e(\cdot)$  denote an *envelope*, having the property  $e(x) = cg(x) \geq f(x)$  for all  $x \in \mathcal{X} = \{x : f(x) > 0\}$  for a given constant  $c \geq 1$ .

envelope covers all of  $f$ .

support of  $g$  must include the support of  $f$ !

The Accept-Reject method then follows by sampling  $Y \sim g$  and  $U \sim \text{Unif}(0, 1)$ .

If  $U < f(Y)/e(Y)$ , accept  $Y$ . Set  $X = Y$  and consider  $X$  to be an element of the target random sample.

Question:

What might be hard/slow about accept-reject?

\* **Note:**  $1/c$  is the expected proportion of candidates that are accepted.

We can use this to evaluate the efficiency of our algorithm.

- If  $c$  is big  $\Rightarrow$  low efficiency  $\Rightarrow$  rejecting a lot  
 Sample a lot more from  $g$ .

- Need to pick  $g$  and find  $c$ .

### 2.1 Algorithm

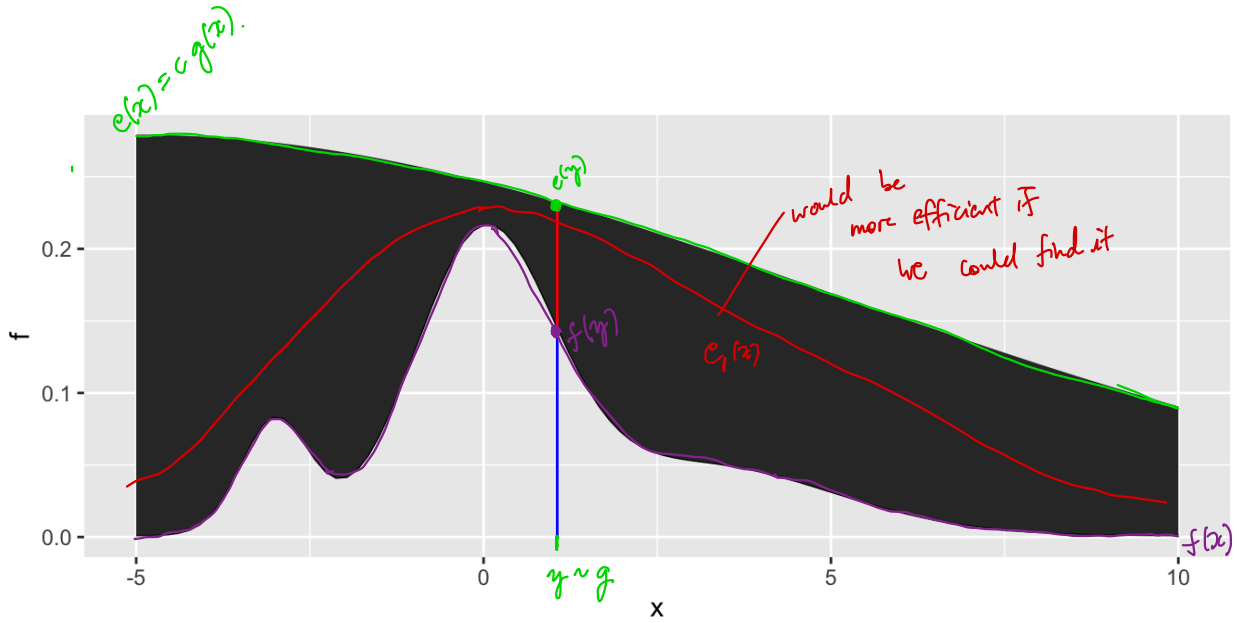
1. Find a suitable density  $g$  and envelope  $e$ .
2. Sample  $Y \sim g$ .
3. Sample  $U \sim \text{Unif}(0, 1)$ .
4. If  $U < f(Y)/e(Y)$ , accept  $Y$ .
5. Repeat from Step 2 until you have generated your desired sample size.

find constant  $c$  s.t.  $cg(x) \geq f(x) \forall x \in \mathcal{X}$ .

\* Requirement: the support of  $g$  must include the support of  $f$ \*

(BAD) Example: If  $f \equiv N(0, 2)$  and  $g \equiv \text{Unif}(-10, 10)$ .

This is NOT an appropriate choice of  $g$  because support of  $f$  is  $\mathbb{R}$ .



## 2.2 Envelopes

Good envelopes have the following properties:

- requirement ① Envelope must exceed target everywhere ← support of  $g$  MUST include support of  $f$ .
- nice ② Easy to sample from  $g$ .
- nicer ③ Generate few rejected draws (sure time).

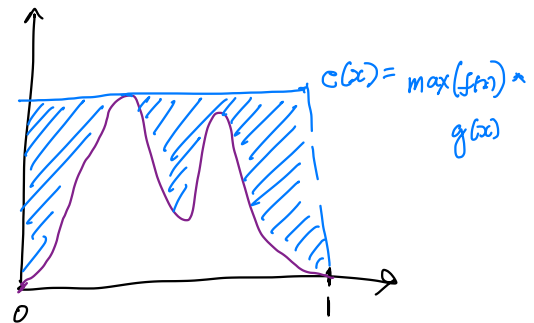
A simple approach to finding the envelope: ↙ in some cases

Say support of  $f$  is  $0 \leq x \leq 1$

Find  $\max_{x \in [0,1]} f(x)$  and  $c = \max_{x \in [0,1]} f(x)$

Let  $g(x) \equiv \text{Unif}(0,1) = \begin{cases} 1 & \text{if } x \in [0,1] \\ 0 & \text{o.w.} \end{cases}$

support matches support of  $f$ !



This is often not efficient if we know more about shape of  $f$  we can maybe select a better envelope

Plotting is our friend here.

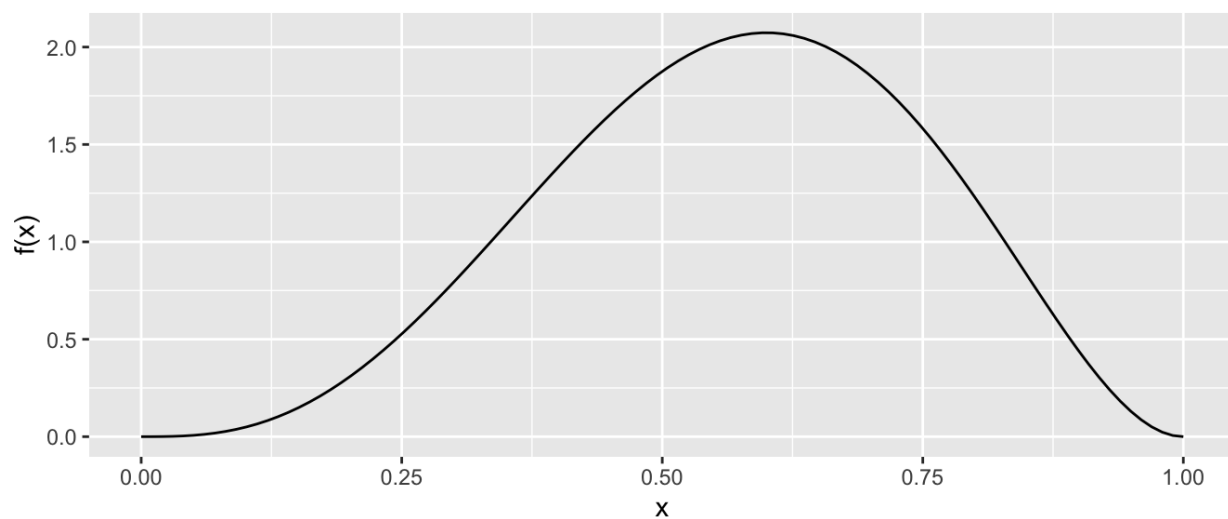
★ This is only relevant if  $\mathcal{X} = [0,1]$ .

**Example 2.1** We want to generate a random variable with pdf  $f(x) = 60x^3(1-x)^2$ ,  $0 \leq x \leq 1$ . This is a Beta(4, 3) distribution.

Can we invert  $F(x)$  analytically?

If not, find the maximum of  $f(x)$ .

```
# pdf function, could use dbeta() instead  
f <- function(x) {  
  60*x^3*(1-x)^2  
}  
  
# plot pdf  
x <- seq(0, 1, length.out = 100)  
ggplot() +  
  geom_line(aes(x, f(x)))
```



```

envelope <- function(x) {
  ## create the envelope function
}

# Accept reject algorithm
n <- 1000 # number of samples wanted
accepted <- 0 # number of accepted samples
samples <- rep(NA, n) # store the samples here

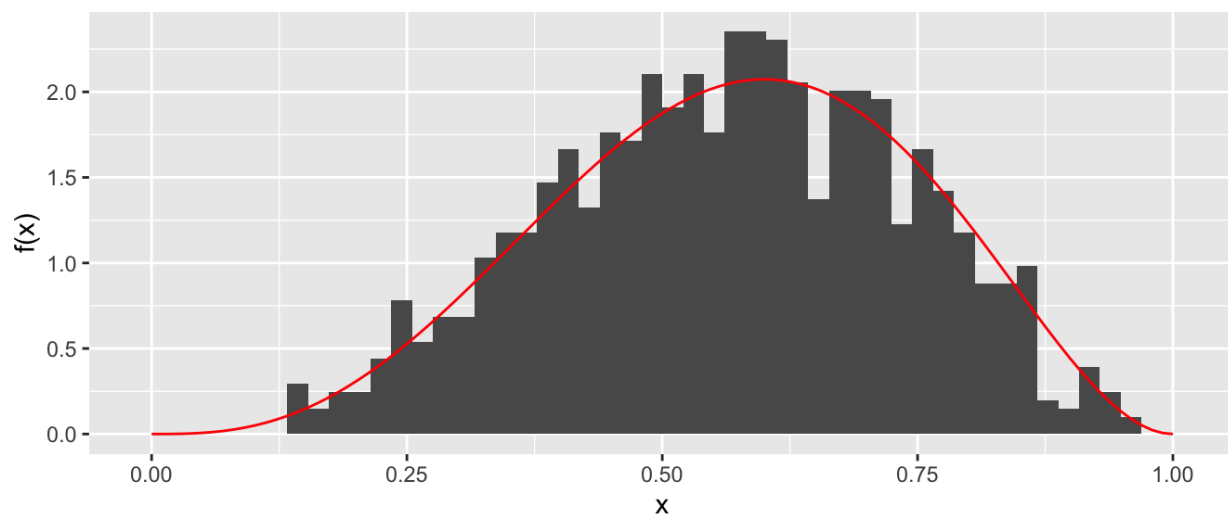
while(accepted < n) {
  # sample y from g

  # sample u from uniform(0,1)
  u <- runif(1)

  if(u < f(y)/envelope(y)) {
    # accept
    accepted <- accepted + 1
    samples[accepted] <- y
  }
}

ggplot() +
  geom_histogram(aes(sample, y = ..density..), bins = 50, ) +
  geom_line(aes(x, f(x)), colour = "red") +
  xlab("x") + ylab("f(x)")

```





## 2.3 Why does this work?

Recall that we require

$$cg(y) \geq f(y) \quad \forall y \in \{y : f(y) > 0\}.$$

Thus,

The larger the ratio  $\frac{f(y)}{cg(y)}$ , the more the random variable  $Y$  looks like a random variable distributed with pdf  $f$  and the more likely  $Y$  is to be accepted.

## 2.4 Additional Resources

See p.g. 69-70 of Rizzo for a proof of the validity of the method.

## 3 Transformation Methods

We have already used one transformation method – **Inverse transform method** – but there are many other transformations we can apply to random variables.

1. If  $Z \sim N(0, 1)$ , then  $V = Z^2 \sim$
2. If  $U \sim \chi_m^2$  and  $V \sim \chi_n^2$  are independent, then  $F = \frac{U/m}{V/n} \sim$
3. If  $Z \sim N(0, 1)$  and  $V \sim \chi_n^2$  are independent, then  $T = \frac{Z}{\sqrt{V/n}} \sim$
4. If  $U \sim \text{Gamma}(r, \lambda)$  and  $V \sim \text{Gamma}(s, \lambda)$  are independent, then  $X = \frac{U}{U+V} \sim$

**Definition 3.1** A *transformation* is any function of one or more random variables.

Sometimes we want to transform random variables if observed data don't fit a model that might otherwise be appropriate. Sometimes we want to perform inference about a new statistic.

**Example 3.1** If  $X_1, \dots, X_n \stackrel{iid}{\sim} \text{Bernoulli}(p)$ . What is the distribution of  $\sum_{i=1}^n X_i$ ?

**Example 3.2** If  $X \sim N(0, 1)$ , what is the distribution of  $X + 5$ ?

**Example 3.3** For  $X_1, \dots, X_n$  iid random variables, what is the distribution of the median of  $X_1, \dots, X_n$ ? What is the distribution of the order statistics?  $X_{[i]}$ ?

There are many approaches to deriving the pdf of a transformed variable.

But the theory isn't always available. What can we do?

## 3.1 Algorithm

Let  $X_1, \dots, X_p$  be a set of independent random variables with pdfs  $f_{X_1}, \dots, f_{X_p}$ , respectively, and let  $g(X_1, \dots, X_p)$  be some transformation we are interested in simulating from.

1. Simulate  $X_1 \sim f_{X_1}, \dots, X_p \sim f_{X_p}$ .
2. Compute  $G = g(X_1, \dots, X_p)$ . This is one draw from  $g(X_1, \dots, X_p)$ .
3. Repeat Steps 1-2 many times to simulate from the target distribution.

**Example 3.4** It is possible to show for  $X_1, \dots, X_p \stackrel{iid}{\sim} N(0, 1)$ ,  $Z = \sum_{i=1}^p X_i^2 \sim \chi_p^2$ . Imagine that we cannot use the `rchisq` function. How would you simulate  $Z$ ?

```
library(tidyverse)

# function for squared r.v.s
squares <- function(x) x^2

sample_z <- function(n, p) {
  # store the samples
  samples <- data.frame(matrix(rnorm(n*p), nrow = n))

  samples %>%
    mutate_all("squares") %>% # square the rvs
    rowSums() # sum over rows
}

# get samples
n <- 1000 # number of samples

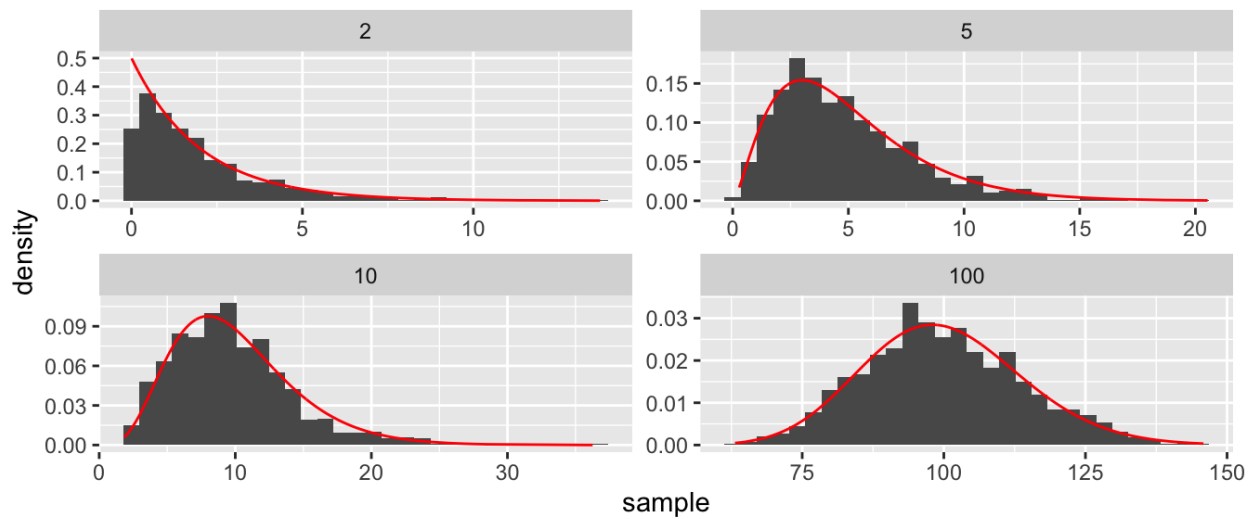
# apply our function over different degrees of freedom
samples <- data.frame(chisq_2 = sample_z(n, 2),
                     chisq_5 = sample_z(n, 5),
                     chisq_10 = sample_z(n, 10),
```

```

chisq_100 = sample_z(n, 100))

# plot results
samples %>%
  gather(distribution, sample, everything()) %>% # make easier to
  plot w/ facets
  separate(distribution, into = c("dsn_name", "df")) %>% # get the df
  mutate(df = as.numeric(df)) %>% # make numeric
  mutate(pdf = dchisq(sample, df)) %>% # add density function values
  ggplot() + # plot
  geom_histogram(aes(sample, y = ..density..)) + # samples
  geom_line(aes(sample, pdf), colour = "red") + # true pdf
  facet_wrap(~df, scales = "free")

```



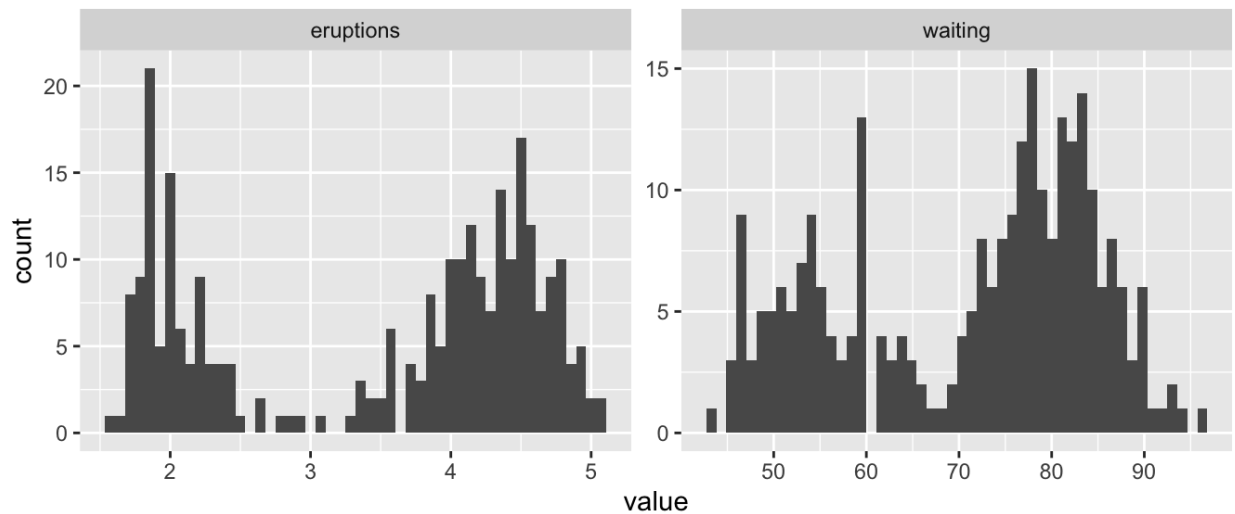
## 4 Mixture Distributions

The `faithful` dataset in R contains data on eruptions of Old Faithful (Geyser in Yellowstone National Park).

```
head(faithful)
```

```
##   eruptions waiting  
## 1     3.600      79  
## 2     1.800      54  
## 3     3.333      74  
## 4     2.283      62  
## 5     4.533      85  
## 6     2.883      55
```

```
faithful %>%  
  gather(variable, value) %>%  
  ggplot() +  
  geom_histogram(aes(value), bins = 50) +  
  facet_wrap(~variable, scales = "free")
```



What is the shape of these distributions?

**Definition 4.1** A random variable  $Y$  is a discrete mixture if the distribution of  $Y$  is a weighted sum  $F_Y(y) = \sum \theta_i F_{X_i}(y)$  for some sequence of random variables  $X_1, X_2, \dots$  and  $\theta_i > 0$  such that  $\sum \theta_i = 1$ .

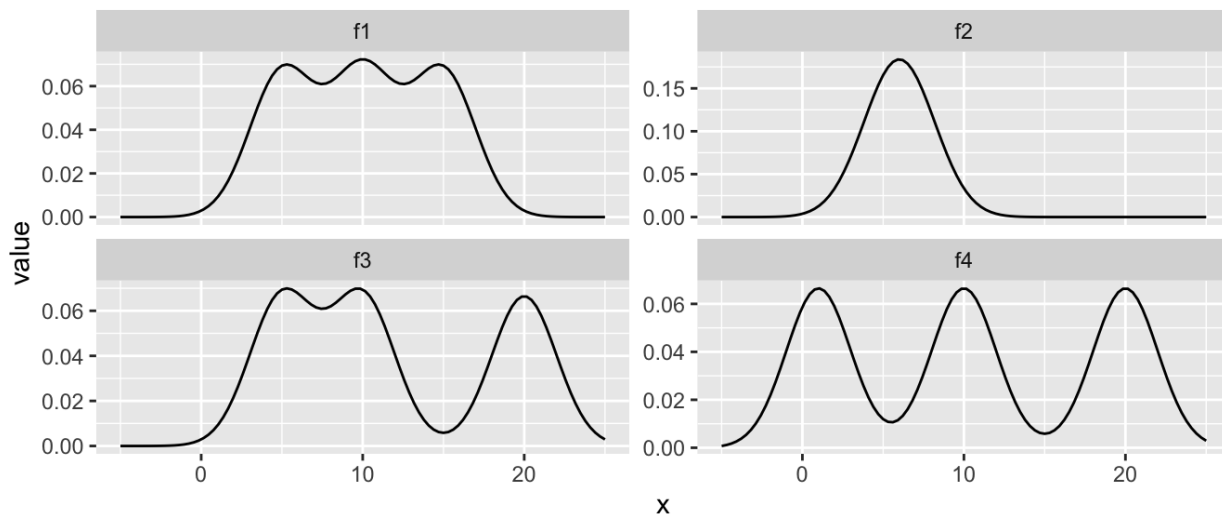
For 2 r.v.s,

**Example 4.1**

```
x <- seq(-5, 25, length.out = 100)

mixture <- function(x, means, sd) {
  # x is the vector of points to evaluate the function at
  # means is a vector, sd is a single number
  f <- rep(0, length(x))
  for(mean in means) {
    f <- f + dnorm(x, mean, sd)/length(means) # why do I divide?
  }
  f
}

# look at mixtures of N(mu, 4) for different values of mu
data.frame(x,
  f1 = mixture(x, c(5, 10, 15), 2),
  f2 = mixture(x, c(5, 6, 7), 2),
  f3 = mixture(x, c(5, 10, 20), 2),
  f4 = mixture(x, c(1, 10, 20), 2)) %>%
gather(mixture, value, -x) %>%
ggplot() +
geom_line(aes(x, value)) +
facet_wrap(~mixture, scales = "free_y")
```

**4.1 Mixtures vs. Sums**

Note that mixture distributions are *not* the same as the distribution of a sum of r.v.s.

**Example 4.2** Let  $X_1 \sim N(0, 1)$  and  $X_2 \sim N(4, 1)$ , independent.

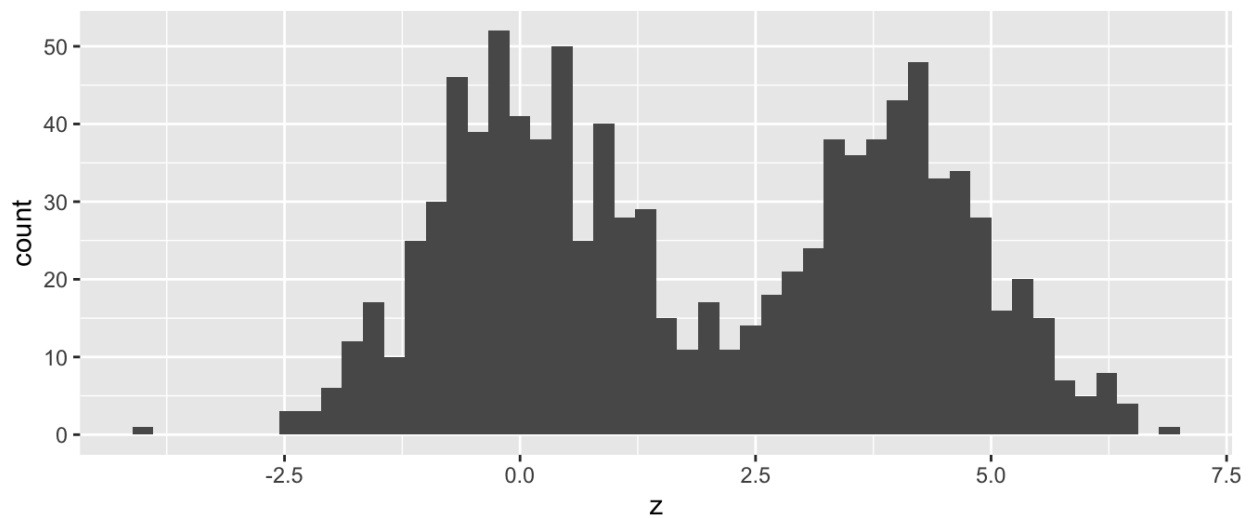
$$S = \frac{1}{2}(X_1 + X_2)$$

$Z$  such that  $f_Z(z) = 0.5f_{X_1}(z) + 0.5f_{X_2}(z)$ .

```
n <- 1000
u <- rbinom(n, 1, 0.5)

z <- u*rnorm(n) + (1 - u)*rnorm(n, 4, 1)

ggplot() +
  geom_histogram(aes(z), bins = 50)
```



What about  $f_Z(z) = 0.7f_{X_1}(z) + 0.3f_{X_2}(z)$ ?



## 4.2 Models for Count Data (refresher)

Recall that the Poisson( $\lambda$ ) distribution is useful for modeling count data.

$$f(x) = \frac{\lambda^x \exp\{-\lambda\}}{x!}, \quad x = 0, 1, 2, \dots$$

Where  $X$  = number of events occurring in a fixed period of time or space.

When the mean  $\lambda$  is low, then the data consists of mostly low values (i.e. 0, 1, 2, etc.) and less frequently higher values.

As the mean count increases, the skewness goes away and the distribution becomes approximately normal.

With the Poisson distribution,

$$E[X] = VarX = \lambda.$$

### Example 4.3

**Example 4.4** The Colorado division of Parks and Wildlife has hired you to analyze their data on the number of fish caught in Horsetooth resevoir by visitors. Each visitor was asked - How long did you stay? - How many fish did you catch? - Other questions: How many people in your group, were children in your group, etc.

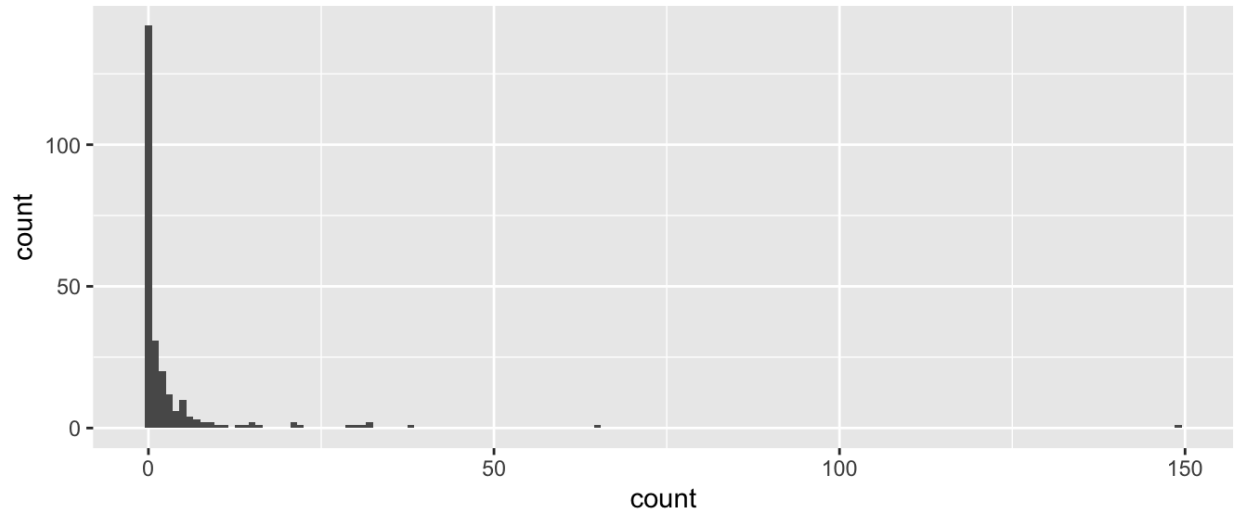
Some visiteres do not fish, but there is not data on if a visitor fished or not. Some visitors who did fish did not catch any fish.

Note, this is modified from <https://stats.idre.ucla.edu/r/dae/zip/>.

```
fish <- read_csv("https://stats.idre.ucla.edu/stat/data/fish.csv")
```

```
# with zeroes
```

```
ggplot(fish) + geom_histogram(aes(count), binwidth = 1)
```



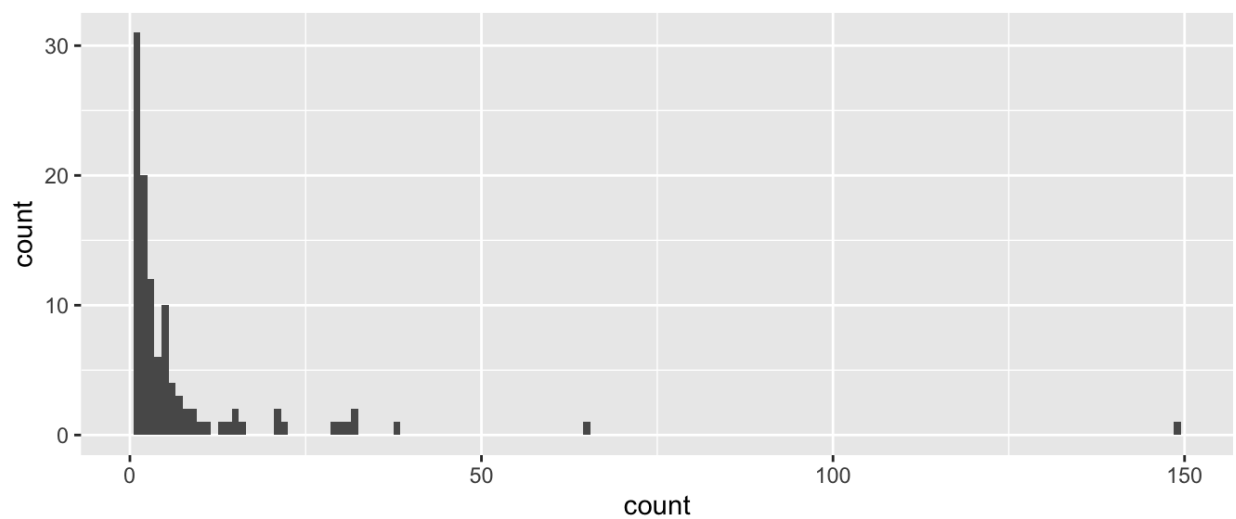
```
# without zeroes
```

```
fish %>%
```

```
  filter(count > 0) %>%
```

```
  ggplot() +
```

```
  geom_histogram(aes(count), binwidth = 1)
```



A *zero-inflated* model assumes that the zero observations have two different origins – structural and sampling zeroes.

### Example 4.5

A zero-inflated model is a **mixture model** because the distribution is a weighted average of the sampling model (i.e. Poisson) and a point-mass at 0.

For  $Y \sim ZIP(\lambda)$ ,

$$Y \sim \begin{cases} 0 & \text{with probability } \pi \\ \text{Poisson}(\lambda) & \text{with probability } 1 - \pi \end{cases}$$

So that,

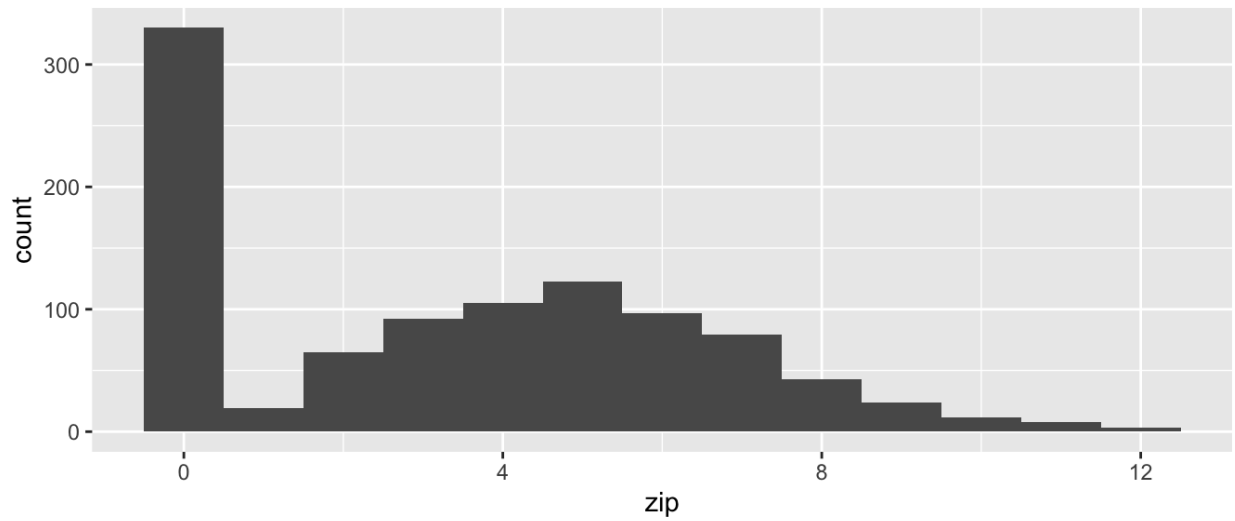
$$Y =$$

To simulate from this distribution,

```
n <- 1000
lambda <- 5
pi <- 0.3

u <- rbinom(n, 1, pi)
zip <- u*0 + (1-u)*rpois(n, lambda)
```

```
# zero inflated model  
ggplot() + geom_histogram(aes(zip), binwidth = 1)
```



```
# Poisson(5)  
ggplot() + geom_histogram(aes(rpois(n, lambda)), binwidth = 1)
```

