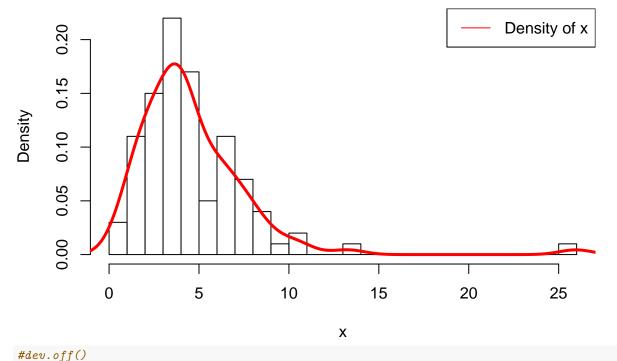
code Yaqiong Yao 12/15/2018

Univariate Case

Generate dataset

```
n <- 100
set.seed(123)
u <- runif(100, 0, 1)
x <- as.numeric(u < 0.3) * rgamma(100, shape = 1, scale = 5) +
    as.numeric(u > 0.3) * rgamma(100, shape = 5, scale = 1)
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/plot1.pdf")
hist(x, breaks = 20, probability = TRUE, main = "")
lines(density(x), lty = 1, lwd = 3, col = "red")
legend("topright", lty = 1, col = "red", "Density of x")
```



Generate sample by estimated CDF by using KDE

Uniform Kernel

```
sample.kernel <- function(x, u, adj){
  y <- sort(x)
  bw <- adj*density(x)$bw</pre>
```

```
interval <- cbind(y-bw/2, y+bw/2)</pre>
  int.point <- NULL</pre>
  for (i in 1:dim(interval)[1]) {
    num.s <- sum((interval[1:i, 1] <= interval[i, 1]) &</pre>
                    (interval[1:i, 2] >= interval[i, 1]))
    num.e <- sum((interval[(i):dim(interval)[1], 1] <= interval[i, 2]) &</pre>
                    (interval[(i):dim(interval)[1], 2] >= interval[i, 2])) - 1
    num.m <- matrix(c(interval[i, 1], interval[i, 2], num.s, num.e), nrow = 2)</pre>
    int.point <- rbind(int.point, num.m)</pre>
  int.point <- int.point[order(int.point[,1]),]</pre>
  int.point <- cbind(int.point, c((int.point[2:dim(int.point)[1], 1] - int.point[1:(dim(int.point)[1]-1</pre>
                                      int.point[1:(dim(int.point)[1]-1), 2]*(1/bw)*(1/length(x)), 0))
  int.point <- cbind(int.point, c(0,cumsum(int.point[,3])[-dim(int.point)[1]]))</pre>
  num.int <- sapply(1:length(u), function(i) sum(int.point[,4] < u[i]))</pre>
  sample <- int.point[num.int, 1] + (u - int.point[num.int, 4])/(int.point[num.int, 2]*(1/bw))</pre>
  return(sample)
}
N <- 1000
set.seed(123)
u <- runif(N, 0, 1)
sample <- sample.kernel(x, u, adj = 1)</pre>
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample1.pdf")
hist(sample, breaks = 20, probability = TRUE, main = "")
lines(density(sample), col = "blue", lty = 1, lwd = 3)
lines(density(x), col = "red", lty = 1, lwd = 3)
legend("topright", lty = c(1,1), col = c("red", "blue"), c("Density of x", "Density of samples"), cex =
                                                               Density of x
     0.20
                                                               Density of samples
      0.15
Density
     0.10
     0.05
     0.00
                           5
                                                      15
             0
                                        10
                                                                    20
                                                                                  25
                                              sample
```

Triangular Kernel

```
sample.kernel.t <- function(x, u){</pre>
  y <- sort(x)
  bw <- density(x)$bw</pre>
  interval <- cbind(y-bw/2, y+bw/2)</pre>
  int.point <- NULL</pre>
  for (i in 1:dim(interval)[1]) {
    num.s <- sum((interval[1:i, 1] \leftarrow interval[i, 1]) &
                     (interval[1:i, 2] >= interval[i, 1]))
    m.num.s <- cbind(interval[i, 1], y[(i-num.s+1):i])</pre>
    num.y \leftarrow sum(abs(y-y[i]) \leftarrow bw/2)
    m.num.y \leftarrow cbind(y[i], y[which(abs(y-y[i]) \leftarrow bw/2)])
    num.e <- sum((interval[(i):dim(interval)[1], 1] <= interval[i, 2]) &</pre>
                     (interval[(i):dim(interval)[1], 2] >= interval[i, 2])) - 1
    m.num.e <- if(num.e != 0){
      cbind(interval[i, 2], y[(i+1): (i+num.e)])
    } else {
      cbind(interval[i, 2], NA)
    }
    int.point <- rbind(int.point, m.num.s, m.num.y, m.num.e)</pre>
  int.point <- int.point[order(int.point[,1]),]</pre>
  int.point <- cbind(int.point, 0)</pre>
  int.point[int.point[,2]-int.point[,1] > 0,3] <- 1L</pre>
  int.point[int.point[,2]-int.point[,1] \leftarrow 0,3] \leftarrow -1L
  int.point <- cbind(int.point, (2*bw - 4*abs(int.point[,2] - int.point[,1]))/(bw^2))</pre>
  int.point.s <- as.data.frame(table(int.point[,1]))</pre>
  int.point.s[,1] <- as.numeric(levels(int.point.s[,1]))[int.point.s[,1]]</pre>
  j <- 0
  a <- NULL
  for (i in seq_along(int.point.s[,1])) {
    m.tmp <- matrix(int.point[(j + 1):(j + int.point.s[i,2]),], nrow = int.point.s[i,2])</pre>
    if(!is.na(m.tmp[1,4])){
      a \leftarrow c(a, sum((2/bw^2)*(int.point.s[(i+1),1] - int.point.s[i,1]) *
                        (bw - (2*m.tmp[,2] - int.point.s[(i+1),1] - int.point.s[i,1])*m.tmp[,3])))
    } else {
      a < -c(a, 0)
    j \leftarrow j + int.point.s[i,2]
  int.point.s <- cbind(int.point.s, a/length(x))</pre>
  int.point.s <- cbind(int.point.s, c(0,cumsum(int.point.s[,3])[-dim(int.point.s)[1]]))</pre>
  colnames(int.point.s) <- NULL</pre>
  num.int <- sapply(1:length(u), function(i) sum(int.point.s[,4] < u[i]))</pre>
  u1 <- u - int.point.s[[4]][num.int]
  sample <- NULL
  for (i in 1:length(u)) {
    m.tmp <- matrix(int.point[(sum(int.point.s[[2]][1:(num.int[i]-1)])+1):sum(int.point.s[[2]][1:num.in</pre>
                      ncol = 4)
    sum <- sum(m.tmp[,4])
```

```
n.s <- sum(m.tmp[,3])</pre>
    if(n.s >0){
      sample[i] \leftarrow -sum/(4*n.s/bw^2) + sqrt(sum^2 + 8*n.s*u1[i]/bw^2)/(4*n.s/bw^2) + m.tmp[1,1]
    } else if(n.s < 0){</pre>
      sample[i] <- sum/(4*n.s/bw^2) - sqrt(sum^2 - 8*n.s*u1[i]/bw^2)/(4*n.s/bw^2) + m.tmp[1,1]
      sample[i] <- u1[i]/sum + m.tmp[1,1]</pre>
    }
  }
  return(sample)
}
N <- 1000
set.seed(123)
u <- runif(N, 0, 1)
sample <- sample.kernel.t(x, u)</pre>
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample2.pdf")
hist(sample, breaks = 20, probability = TRUE, main = "")
lines(density(sample), col = "blue", lty = 1, lwd = 3)
lines(density(x), col = "red", lty = 1, lwd = 3)
legend("topright", lty = c(1,1), col = c("red", "blue"), c("Density of x", "Density of samples"), cex =
                                                              Density of x
     0.20
                                                               Density of samples
     0.15
Density
     0.10
     0.05
             0
                           5
                                        10
                                                      15
                                                                    20
                                                                                 25
                                              sample
```

Multivariate Case

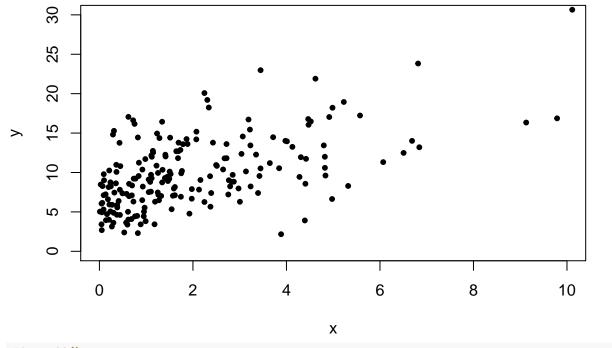
#dev.off()

Generate Dataset

```
require(mvtnorm)
```

Loading required package: mvtnorm

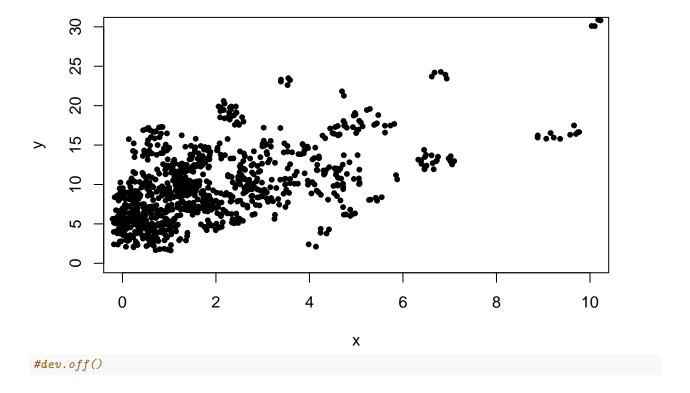
```
n <- 200
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
set.seed(098)
dat <- rmvnorm(n, sigma = sigma)
dat <- pnorm(dat)
x <- qgamma(dat[,1], shape = 1, scale = 2)
y <- qchisq(dat[,2], df = 10)
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/plot2.pdf")
plot(x, y, pch = 20, xlim = c(0, 10), ylim = c(0, 30))</pre>
```



#dev.off()

Using method proposed by whuber (2018)

```
sample.kernel.w <- function(n, x, y, adj){
    bw_x <- adj * density(x)$bw/2
    bw_y <- adj * density(y)$bw/2
    ind <- sample(1:length(x), n, replace = TRUE)
    x_kde <- x[ind] + runif(n, -bw_x, bw_x)
    y_kde <- y[ind] + runif(n, -bw_y, bw_y)
    cbind(x_kde, y_kde)
}
adj = 1
N <- 1000
set.seed(23)
xy_kde <- sample.kernel.w(N, x, y, adj = 1)
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample_w.pdf")
plot(xy_kde[,1], xy_kde[,2], xlim = c(0, 10), ylim = c(0, 30), pch = 20, xlab = "x", ylab = "y")</pre>
```

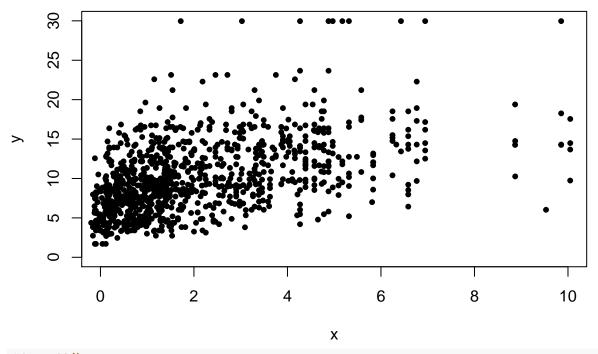


Generate Samples by estimated CDF

Uniform Kernel

```
n <- 1000
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
set.seed(456)
dat <- rmvnorm(n, sigma = sigma)
dat <- pnorm(dat)

x_ecdf <- sample.kernel(x, dat[,1], adj = 1)
y_ecdf <- sample.kernel(y, dat[,2], adj = 1)
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample_u.pdf")
plot(x_ecdf, y_ecdf, xlim = c(0, 10), ylim = c(0, 30), pch = 20, xlab = "x", ylab = "y")</pre>
```

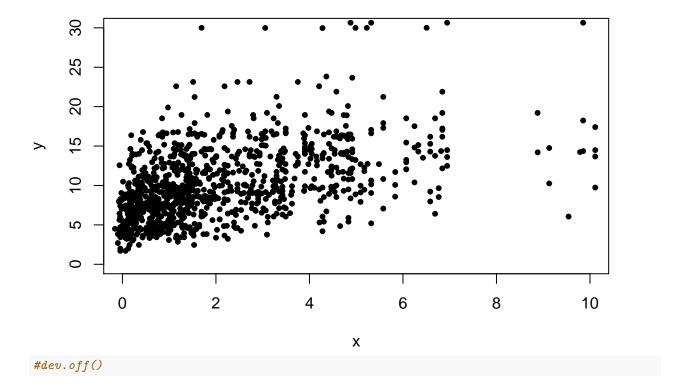


#dev.off()

Triangular Kernel

```
n <- 1000
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
set.seed(456)
dat <- rmvnorm(n, sigma = sigma)
dat <- pnorm(dat)

x_ecdf <- sample.kernel.t(x, dat[,1])
y_ecdf <- sample.kernel.t(y, dat[,2])
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample_t.pdf")
plot(x_ecdf, y_ecdf, xlim = c(0, 10), ylim = c(0, 30), pch = 20, xlab = "x", ylab = "y")</pre>
```



Generate samples from true density

```
require(mvtnorm)
n <- 1000
sigma <- matrix(c(1, 0.5, 0.5, 1), nrow = 2)
set.seed(098)
dat <- rmvnorm(n, sigma = sigma)
dat <- pnorm(dat)
x <- qgamma(dat[,1], shape = 1, scale = 2)
y <- qchisq(dat[,2], df = 10)
#pdf("/Users/YaqiongYao/Dropbox/5361proj/Figure/sample_true.pdf")
plot(x, y, pch = 20, xlim = c(0, 10), ylim = c(0, 30))</pre>
```

