Example Acceptance-rejection is difficult to apply

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Acceptance/rejection methods: Example

Truncated to positive half–axis $\mathcal{N}(0,1)$

$$f(x) = \sqrt{\frac{2}{\pi}} \exp\left(-x^2/2\right) \mathbf{1}_{[0,\infty)}(x).$$

$$\mathbf{1}_A(x) = \left\{ \begin{array}{ll} 1 & x \in A \\ 0 & x \notin A. \end{array} \right.$$

or equivalently as a mixture density

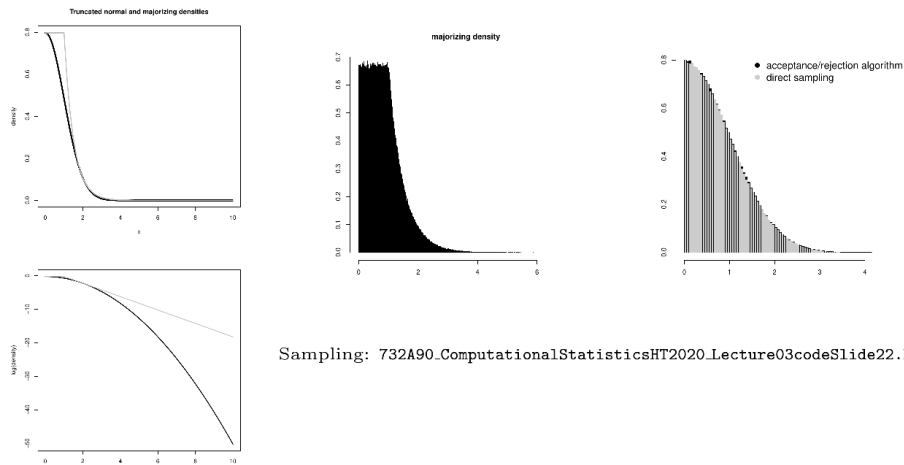$$f(x) = \alpha_1 f_1(x) g_1(x) + \alpha_2 f_1(x) g_1(x),$$

where

$\alpha_1 = \sqrt{\frac{2}{\pi}}$
$f_1(x) = \mathbf{1}_{[0,1]}(x)$
$g_1(x) = \exp\left(-x^2/2\right)$

$\alpha_2 = \frac{1}{\sqrt{2\pi}}$
$f_2(x) = 2\exp\left(-2(x-1)\right)\mathbf{1}_{(1,\infty)}(x)$
$g_2(x) = \exp\left(-(x-2)^2/2\right)$

1.png

Direct sampling: `x<-rnorm(N);x<-x[x>=0]`

Majorizing density ($c = 1$), mixture of uniform and normal:

$$g(x) = \sqrt{\frac{2}{\pi}} \cdot \mathbf{1}_{[0,1]}(x) + \frac{1}{\sqrt{2\pi}} \cdot 2\exp\left(-2(x-1)\right)\mathbf{1}_{(1,\infty)}(x)$$

Sampling: `732A90_ComputationalStatisticsHT2020_Lecture03codeSlide22.R`

2.png

```
[5]: par(family  = "Arial")
     #install.packages("showtext")
     library(showtext)
     showtext_auto()
     options(repr.plot.width=5, repr.plot.height=5)
```

```
[1]: ptruncnormal<-function(x){
         res<-0
         res<-exp((-1)*x*x/2)*sqrt(2/pi)
         res[x<0]<-0
         res
     }
```

```
[2]: pmajorizing<-function(x){
         sapply(x,function(y){
             res<-NA
             if (y<0){res<-0}
             if ((y>=0)&&(y<=1)){
                 res<-sqrt(2/pi) ## uniform
             }
             if (y>1){
                 res<-2*exp(-2*(y-1))/(sqrt(2*pi)) ## exponential with rate 2␣
     ↪shifted by 1
             }
             res
         },simplify=TRUE)
```
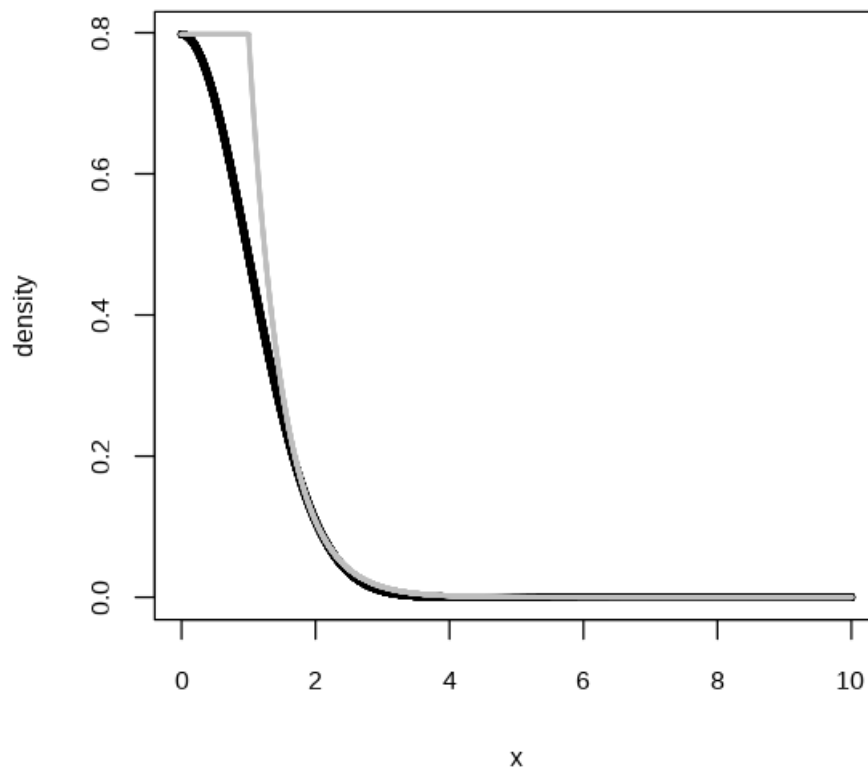
2

```
}
```

[6]:
```
vx<-seq(0,10,by=0.01)
plot(vx,log(ptruncnormal(vx)),pch=19,cex=0.
 ↪2,xlab="x",ylab="log(density)",main="")
points(vx,log(pmajorizing(vx)),pch=19,cex=0.1,col="gray")
```
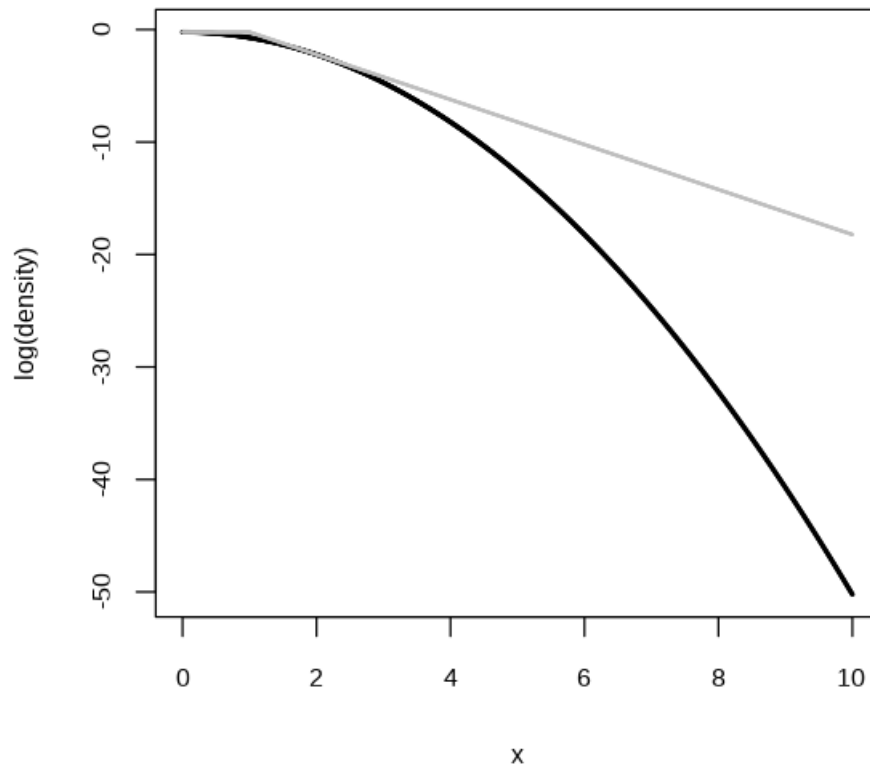

[7]:
```
vx<-seq(0,10,by=0.001)
plot(vx,(ptruncnormal(vx)),pch=19,cex=0.
 ↪4,xlab="x",ylab="density",main="Truncated normal and majorizing densities")
points(vx,(pmajorizing(vx)),pch=19,cex=0.2,col="gray")
```
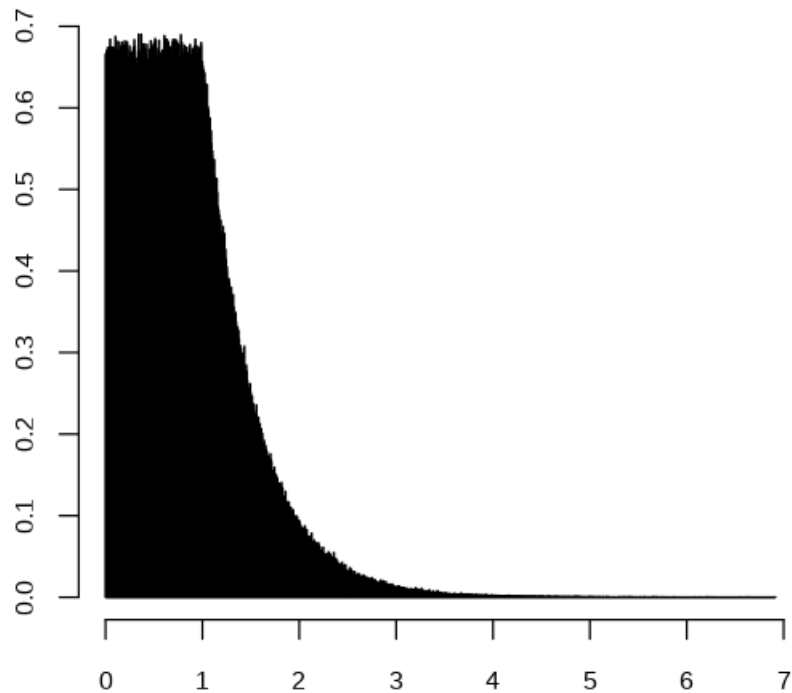
Truncated normal and majorizing densities


```
[8]: rmajorizing<-function(n){
         sapply(1:n,function(i){
             res<-NA
             component<-sample(1:2,1,prob=c(2/3,1/3))
             if(component==1){res<-runif(1)}
             if(component==2){res<-rexp(1,rate=2)+1}
             res
         })
     }
```

```
[9]: Nsample<-1000000
     num_histbreaks<-1000
     hist(rmajorizing(Nsample),breaks=1000,col="black",xlab="",ylab="",main="majorizing␣
      ↪density",freq=FALSE)
```

majorizing density
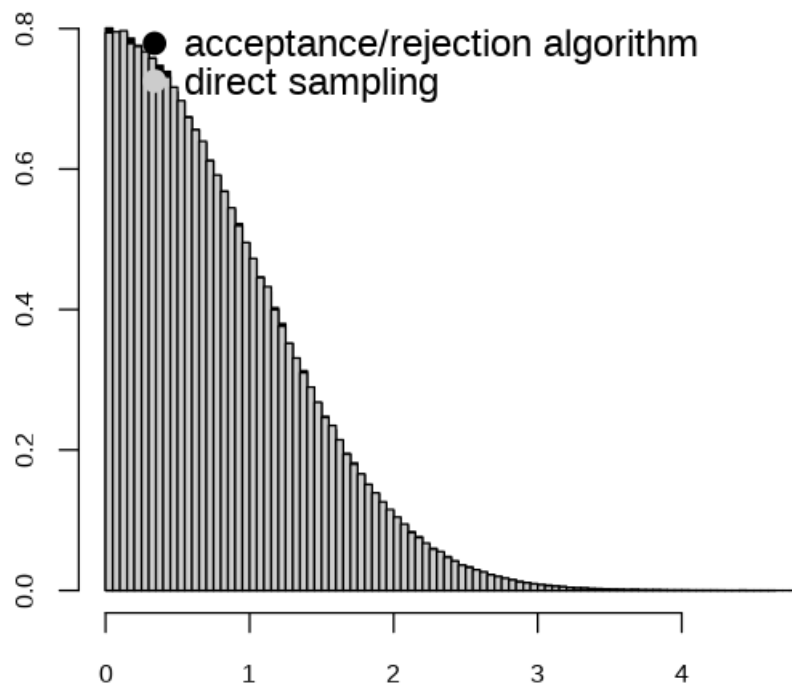
```
[10]: fgentruncnormal<-function(c){
          x<-NA
          num_reject<-0
          while (is.na(x)){
              y<-rmajorizing(1)
              u<-runif(1)
              if (u<=ptruncnormal(y)/(c*pmajorizing(y))){x<-y}
              else{num_reject<-num_reject+1}
          }
          c(x,num_reject)
      }
```

```
[11]: c<- 1
      vtruncnormal_acceptreject<-sapply(rep(c,Nsample),fgentruncnormal)[1,]
      vtruncnormal_direct<-rnorm(2*Nsample) ;␣
       ↪vtruncnormal_direct<-vtruncnormal_direct[vtruncnormal_direct>=0]
```

```
[12]: hist(vtruncnormal_acceptreject,col="black",breaks=100,xlab="",ylab="",freq=FALSE,main="")
```

```
hist(vtruncnormal_direct,col=gray(0.
  →8),breaks=100,xlab="",ylab="",freq=FALSE,main="",add=TRUE)
legend("topright",pch=19,cex=1.5,legend=c("acceptance/rejection␣
  →algorithm","direct sampling"),
        col=c("black",gray(0.8)),bty="n")
```


[ ]: