#1-a

> standardized<-function(numbers){

+ numbers<-(numbers- mean(numbers))/sd(numbers)

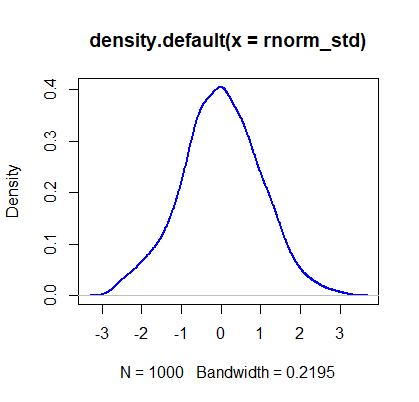
+ return (numbers)

+ }

> rnorm<-rnorm(n=1000,mean=940,sd=190)

> rnorm\_std<-standardized(rnorm)

> plot(density(rnorm\_std),col="blue",lwd=2)



> #1-b

> minday\_std<-standardized(minday)

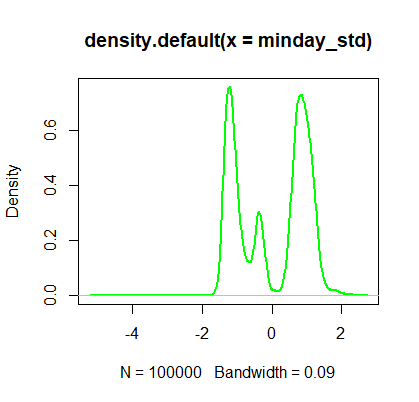
> plot(density(minday\_std), col="green", lwd=2)

> mean(minday\_std)

[1] -4.25589e-17

> sd(minday\_std)

[1] 1



> visualize\_sample\_ci <- function(num\_samples, sample\_size, pop\_size,mean,sd) {

+ # Simulate a large population

+ population\_data <- rnorm(n=pop\_size, mean=mean,sd=sd)

+ pop\_mean <- mean(population\_data)

+ pop\_sd <- sd(population\_data)

+

+ # Simulate samples

+ samples <- replicate(num\_samples,

+ sample(population\_data, sample\_size, replace=FALSE))

+

+ # Calculate descriptives of samples

+ sample\_means = apply(samples, 2, FUN=mean)

+ sample\_stdevs = apply(samples, 2, FUN=sd)

+ sample\_stderrs <- sample\_stdevs/sqrt(sample\_size)

+ ci95\_low <- sample\_means - sample\_stderrs\*1.96

+ ci95\_high <- sample\_means + sample\_stderrs\*1.96

+ ci99\_low <- sample\_means - sample\_stderrs\*2.58

+ ci99\_high <- sample\_means + sample\_stderrs\*2.58

+

+ # Visualize confidence intervals of all samples

+ plot(NULL, xlim=c(pop\_mean-(pop\_sd/2), pop\_mean+(pop\_sd/2)),

+ ylim=c(1,num\_samples), ylab="Samples", xlab="Confidence Intervals")

+ add\_ci\_segment(ci95\_low, ci95\_high, ci99\_low, ci99\_high,

+ sample\_means, 1:num\_samples, good=TRUE)

+

+ # Visualize samples with CIs that don't include population mean

+ bad = which(((ci95\_low > pop\_mean) | (ci95\_high < pop\_mean)) |

+ ((ci99\_low > pop\_mean) | (ci99\_high < pop\_mean)))

+ add\_ci\_segment(ci95\_low[bad], ci95\_high[bad], ci99\_low[bad], ci99\_high[bad],

+ sample\_means[bad], bad, good=FALSE)

+

+ # Draw true population mean

+ abline(v=mean(population\_data))

+ }

> add\_ci\_segment <- function(ci95\_low, ci95\_high, ci99\_low, ci99\_high,

+ sample\_means, indices, good=TRUE) {

+ segment\_colors <- list(c("lightcoral", "coral3", "coral4"),

+ c("lightskyblue", "skyblue3", "skyblue4"))

+ color <- segment\_colors[[as.integer(good)+1]]

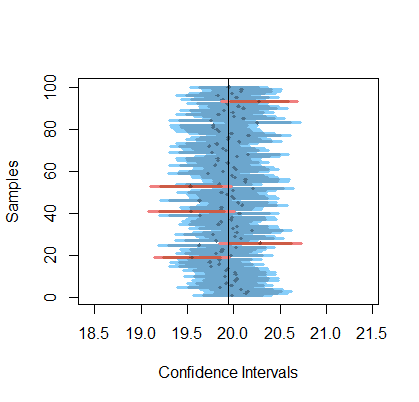
+

+ segments(ci99\_low, indices, ci99\_high, indices, lwd=3, col=color[1])

+ segments(ci95\_low, indices, ci95\_high, indices, lwd=3, col=color[2])

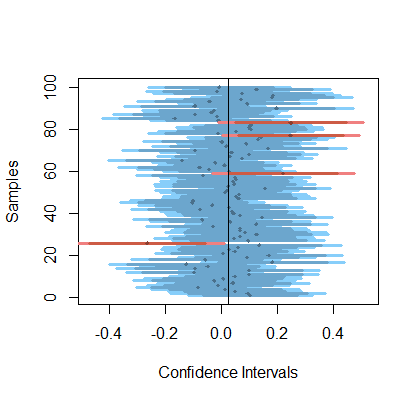
+ points(sample\_means, indices, pch=18, cex=0.6, col=color[3])

+ }



> #2-a

> visualize\_sample\_ci(num\_samples = 100, sample\_size = 100, pop\_size=10000, distr\_func = rnorm)



> #2-a-i

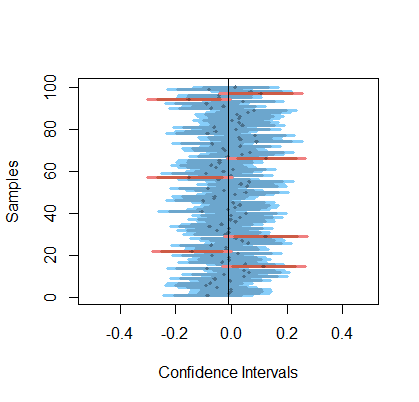
We expect 5% of sample not include in the population mean in its 95% CI, that is 5 of 100 will not be included in 95% CI.

> #2-a-ii

We expect 1% of sample not include in the population mean in its 99% CI, that is 1 of 100 will not be included in 95% CI.

> #2-b

> visualize\_sample\_ci(num\_samples = 100, sample\_size = 300, pop\_size=10000,distr\_func = rnorm)



> #2-b-i

Since 95% (99%) CI equal to (sample mean-1.96(2.58) \* sample deviation / sqrt(sample size) , sample mean+1.96(2.58) \* sample deviation / sqrt(sample size)) .From above, we can see that the width of CI is inversely proportional to sample size.

> #2-b-ii

We expect 5% of sample not include in the population mean in its 95% CI, that is 5 of 100 will not be included in 95% CI.

>#3-a-i

> bookings <- read.table("first\_bookings\_datetime\_sample.txt", header=TRUE)

> bookings$datetime[1:9]

[1] "4/16/2014 17:30" "1/11/2014 20:00" "3/24/2013 12:00"

[4] "8/8/2013 12:00" "2/16/2013 18:00" "5/25/2014 15:00"

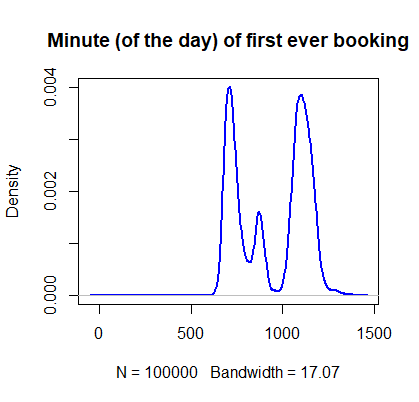
[7] "12/18/2013 19:00" "12/23/2012 12:00" "10/18/2013 20:00"

> hours <- as.POSIXlt(bookings$datetime, format="%m/%d/%Y %H:%M")$hour

> mins <- as.POSIXlt(bookings$datetime, format="%m/%d/%Y %H:%M")$min

> minday <- hours\*60 + mins

> plot(density(minday), main="Minute (of the day) of first ever booking", col="blue", lwd=2)



> mean(minday)

[1] 942.4964

> sd(minday)

[1] 189.6631

> interval<-mean(minday)+c(-1.96,1.96)\*sd(minday)/sqrt(length(minday))

> interval

[1] 941.3208 943.6719

> #3-a-ii

> minday\_size=300

> minday2=sample(minday,minday\_size)

> minday\_mean=mean(minday)

> resamples<-replicate(2000,sample(minday2 ,length(minday2), replace=TRUE))

> resamples

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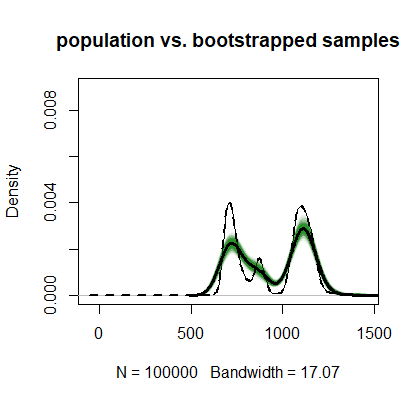
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> #3-a-iii

> plot(density(minday),lwd=0,ylim=c(0, 0.009), main="population vs. bootstrapped samples")

> plot\_resample\_density<-function(sample\_i) {

+ lines(density(sample\_i), col=rgb(0.0, 0.4, 0.0, 0.01))

+ return(mean(sample\_i))

+ }

> sample\_means<-apply(resamples, 2, FUN=plot\_resample\_density)

> lines(density(minday2),lwd=3)

> lines(density(minday),lwd=2,lty="dashed")

> #3-a-iv

> interval<-function(data){

+ return (c(mean(data)-1.96\*sd(data),mean(data)+1.96\*sd(data)))

+ }

> bootstrap\_interval<-sapply(resamples,interval)