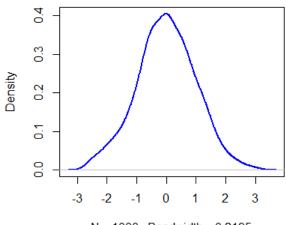
#1-a

- > 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)

density.default(x = rnorm_std)

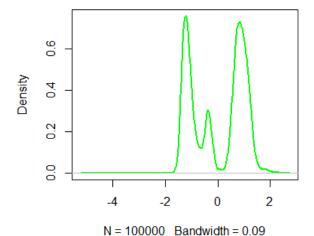


N = 1000 Bandwidth = 0.2195

> #1-b

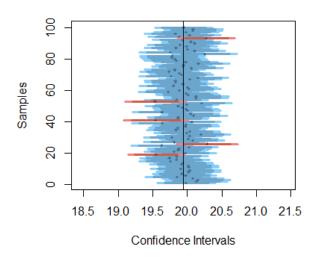
- > minday_std<-standardized(minday)
- > plot(density(minday_std), col="green", lwd=2)
- > mean(minday_std)
- [1] -4.25589e-17
- > sd(minday_std)
- [1] 1

density.default(x = minday_std)

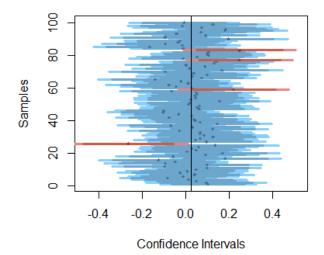


```
> visualize sample ci <- function(num samples, sample size, pop size, mean, sd) {
    # Simulate a large population
    population_data <- rnorm(n=pop_size, mean=mean,sd=sd)</pre>
+
+
    pop mean <- mean(population data)
    pop sd <- sd(population data)
+
+
    # Simulate samples
+
+
    samples <- 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)</pre>
+
    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])
+ }</pre>
```



> #2-a
> visualize_sample_ci(num_samples = 100, sample_size = 100, pop_size=10000,
distr_func = rnorm)



> #2-a-i

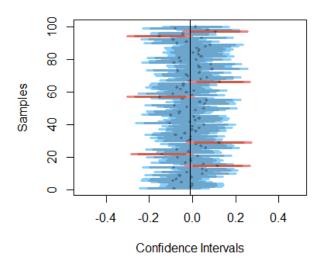
We expect 5% of sample not include in the population mean in its 95% CI, that is 5 of 100 will not be included in 95% CI.

> #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.

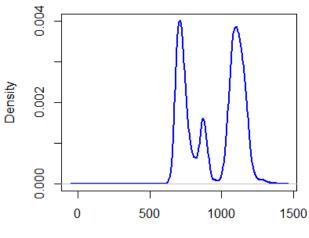
> #2-b-ii

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

Minute (of the day) of first ever booking



N = 100000 Bandwidth = 17.07

- > 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

[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22]

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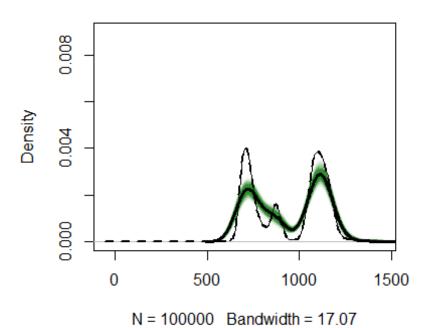
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[reached getOption("max.print") -- omitted 300 rows]

population vs. bootstrapped samples



```
> #3-a-ii
> 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)
```