Simulation

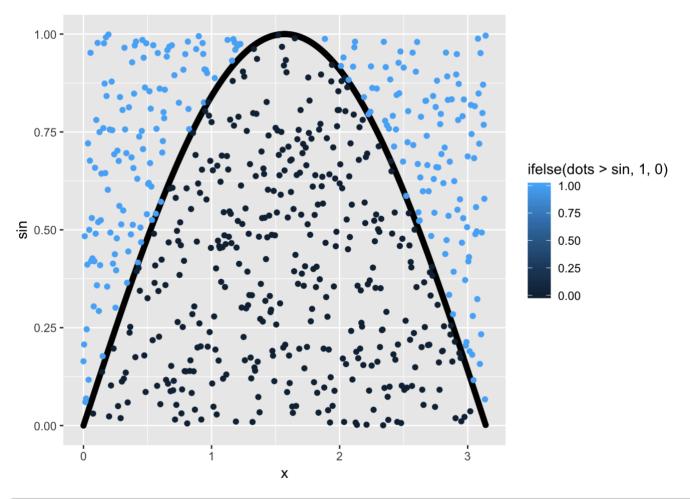
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1 Estimation

Area under the function (integral): 0.6289809 (x = 0..PI)

```
df <- data.frame(x=seq(0,pi, 0.005))
df$sin = sin(df$x)
N <- nrow(df)
dots <- runif(N, 0, 1)

ggplot(data=df, aes(x=x)) +
  geom_point(aes(y=sin)) +
  geom_point(aes(y=dots, color = ifelse(dots > sin, 1, 0)))
```



```
ratio <- sum(dots < df$sin) / N
ratio</pre>
```

```
## [1] 0.6168521
```

2 Dices

Probability of having the same mumbers: 0.6289809

```
set.seed(9313)
dices <- function(x) {
  return (round(runif(1,1,6)) == round(runif(1,1,6)))
}

N <- 1000
p <- N / sum(sapply(seq(N), dices))
p ## probability</pre>
```

```
## [1] 6.060606
```

3 Weight mean confidence level bootstrap

```
myMean <- function(d, i) {
   return( mean(d[i]))
}

s <- c(119,120,131,209,210,337,332,287,146,129,232,169,208,253,142,105,419,179,324,28
7)
b <- boot(data=s, R=200, statistic = myMean)
boot.ci(b, conf=0.9)</pre>
```

```
## Warning in boot.ci(b, conf = 0.9): bootstrap variances needed for
## studentized intervals
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 200 bootstrap replicates
## CALL :
## boot.ci(boot.out = b, conf = 0.9)
##
## Intervals :
                                Basic
## Level Normal
       (183.3, 252.4) (177.5, 254.2)
##
## Level
           Percentile
                                  BCa
## 90%
        (179.6, 256.3)
                          (185.7, 258.0)
## Calculations and Intervals on Original Scale
## Some BCa intervals may be unstable
```

4 Regression – coefficient bootstrap

```
bootMod <- function(df, i) {
   m <- lm(y ~ x, df[i,])
   return (m$coefficients)
}

df <- data.frame(x = c(1,2,3,5,4), y = c(13,14,15,18,22))
b <- boot(df, bootMod, 10)
b</pre>
```

```
##
## ORDINARY NONPARAMETRIC BOOTSTRAP
##
##
## Call:
## boot(data = df, statistic = bootMod, R = 10)
##
##
## Bootstrap Statistics :
##
       original
                   bias
                          std. error
         11.0 -2.5301053
## t1*
                            5.783164
## t2*
          1.8 0.8056662
                             1.880736
```

```
boot.ci(b, conf=0.9)
```

```
## Warning in norm.inter(t, (1 + c(conf, -conf))/2): extreme order statistics
## used as endpoints
```

```
## Warning in norm.inter(z, (1 + c(conf, -conf))/2): extreme order statistics ## used as endpoints
```

Warning in norm.inter(t, alpha): extreme order statistics used as endpoints

```
## Warning in norm.inter(t, adj.alpha): extreme order statistics used as
## endpoints
```

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = b, conf = 0.9)
##
## Intervals :
                                                   Studentized
## Level
            Normal
                                 Basic
## 90%
       (4.02, 23.04) (8.53, 28.00) (8.13, 19.62)
##
## Level
            Percentile
                                  BCa
## 90%
        (-6.00, 13.47) (-1.41, 13.47)
## Calculations and Intervals on Original Scale
## Warning : Basic Intervals used Extreme Quantiles
## Some basic intervals may be unstable
## Warning : Studentized Intervals used Extreme Quantiles
## Some studentized intervals may be unstable
## Warning : Percentile Intervals used Extreme Quantiles
## Some percentile intervals may be unstable
## Warning : BCa Intervals used Extreme Quantiles
## Some BCa intervals may be unstable
```

5 Placebo test

From this we can conclude that the average blind effect is somewhere without -1.5 - +1.5, while the effect from the data is 3.36. So the effect is significant.

```
set.seed(10)
df <- data.frame(bottle = c(0,1,1,0,0,0,1,0,0,0,1,1,0,1,1,1,1,0,1), age = c(9,14,15,1
0,12,6,19,10,8,6,12,13,20,13,16,14,9,12,12))

caries_bottle1 = mean(subset(df, bottle == 1)$age)
caries_bottle1</pre>
```

```
## [1] 13.7
```

```
caries_bottle0 = mean(subset(df, bottle == 0)$age)
caries_bottle0
```

```
## [1] 10.33333
```

```
bottle_effect = caries_bottle1 - caries_bottle0
bottle_effect
```

```
## [1] 3.366667
```

```
placebo <- function(x) {
    si = sample(2, 19, replace=T, prob=c(0.5, 0.5))
    group1 <- df[si==1,]
    group2 <- df[si==2,]

    random_effect = mean(group1$age) - mean(group2$age)
    return (random_effect)
}

qplot(sapply(seq(1000), placebo))</pre>
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

