Bootstrapping in R – A Tutorial

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Bootstrapping

- Resampling technique with replacement
  - “The population is to the sample as the sample is to the bootstrap samples”
- Allows estimation of the sampling distribution of a statistic
  - Confidence intervals, bias, variance, etc.

Procedure

- Resample a dataset a given number of times
- Calculate a statistic from each sample
- Accumulate the results and calculate sample distribution of the statistic

Objective

- Calculate a series of linear regressions to determine which variable or combination of variables best explains the volume of black cherry trees
  - Comparisons made using coefficient of determination (R-squared)
- Bootstrap the linear regressions (for each bootstrap sample) to determine 95% confidence intervals of their respective R-squared values

Data

- “trees” dataset (included in R)
- Volume (cubic feet), girth (diameter in inches, measured at breast height), and height (feet) measurements of 31 felled black cherry trees

```
help(trees)
```

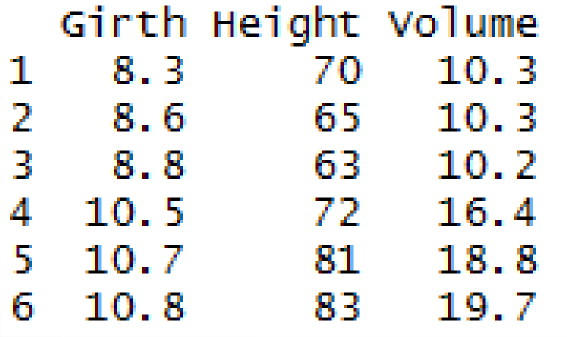
Code Walkthrough

- Load the boot library
  - Contains functions to conduct bootstrapping

```
library(boot)
```

- Investigate the “trees” dataset

```
head(trees)
```

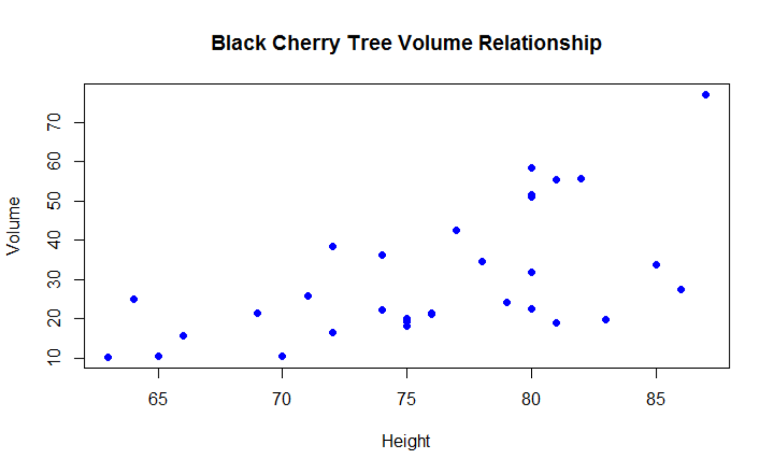


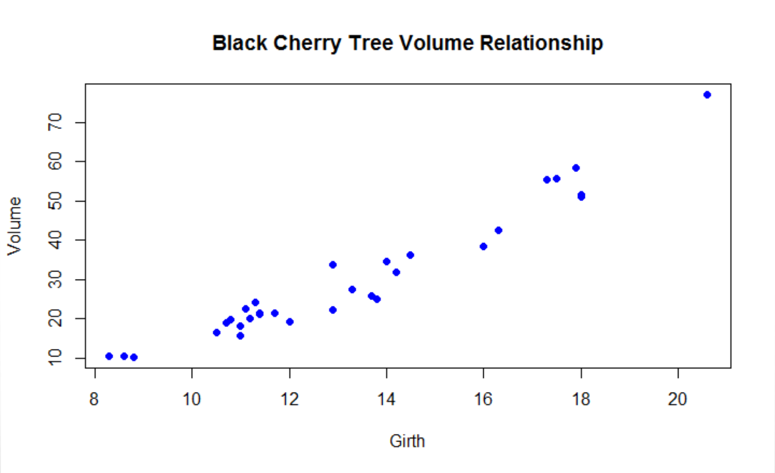
```
  Girth Height Volume
1   8.3     70   10.3
2   8.6     65   10.3
3   8.8     63   10.2
4  10.5     72   16.4
5  10.7     81   18.8
6  10.8     83   19.7
```

- Explore relationships between volume, girth, and height

```
plot(trees$Volume~trees$Height, main = 'Black Cherry Tree Volume Relationship', xlab = 'Height', ylab = 'Volume', pch = 16, col = 'blue')
```

```
plot(trees$Volume~trees$Girth, main = 'Black Cherry Tree Volume Relationship', xlab = 'Girth', ylab = 'Volume', pch = 16, col = 'blue')
```





- Create a function that will calculate a statistic (or multiple statistics) on each bootstrap sample
- Function syntax in R

```
foo = function(parameter_1, parameter_2,… parameter_n){
  bar = *do something to data passed as parameters*
  return(bar)
}
```

- Statistic-calculation function for the boot package takes two specific parameters (simple example) and will be applied to each bootstrap sample

```
sample_mean = function(data, indices){
  sample = data[indices, ]
  bar = mean(sample)
  return(bar)
}
```

Calculate the mean of the bootstrap sample

Creates the bootstrap sample (i.e., subset the provided data by the “indices” parameter). “indices” is automatically provided by the “boot” function; this is the sampling with replacement portion of bootstrapping

Or, more concisely:

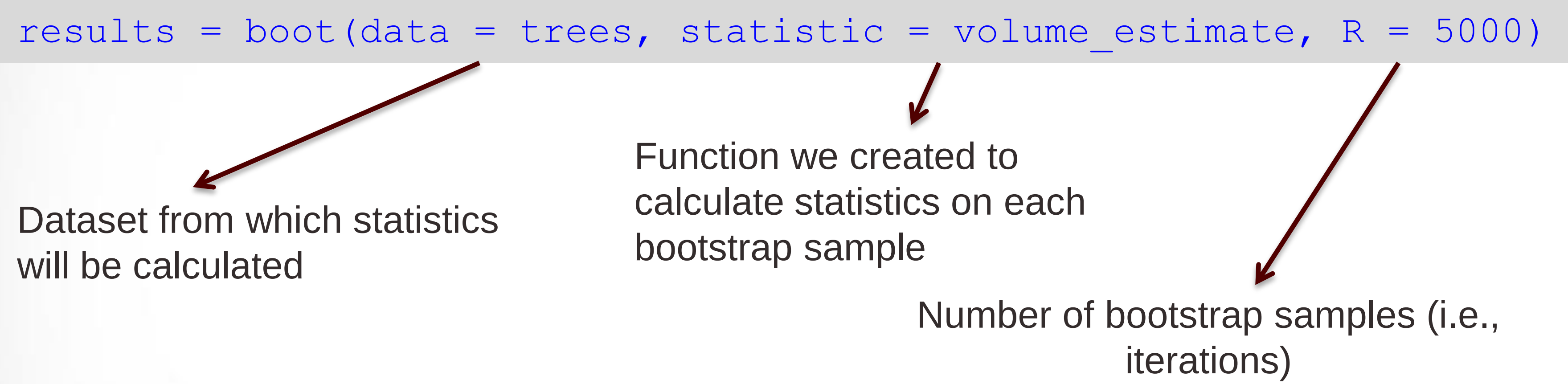
```
sample_mean = function(data, indices){
  return(mean(data[indices]))
}
```

- Create a function to calculate linear regressions of several variable combinations and return their respective R-squared values
  - Height only,
  - Girth only
  - Girth / height ratio
  - Girth and height
  - Girth, height, and girth / height ratio
- Note that we are calculating (and returning) multiple statistics simultaneously
  - These statistics will be calculated for each bootstrap sample

```
volume_estimate = function(data, indices){
  d = data[indices, ]
  H_relationship = lm(d$Volume~d$Height, data = d)
  H_r_sq = summary(H_relationship)$r.square
  G_relationship = lm(d$Volume~d$Girth, data = d)
  G_r_sq = summary(G_relationship)$r.square
  G_H_ratio = d$Girth / d$Height
  G_H_relationship = lm(d$Volume~G_H_ratio, data = d)
  G_H_r_sq = summary(G_H_relationship)$r.square
  combined_relationship = lm(d$Volume~d$Height + d$Girth, data = d)
  combined_r_sq = summary(combined_relationship)$r.square
  combined_2_relationship = lm(d$Volume~d$Height +d$Girth + G_H_ratio, data = d)
  combined_2_r_sq = summary(combined_2_relationship)$r.square
  relationships = c(H_r_sq, G_r_sq, G_H_r_sq, combined_r_sq, combined_2_r_sq)
  return(relationships)
}
```

Statistics are added to a vector, which is then returned to the “boot” function

- Conduct the bootstrapping
  - Use “boot” function



```
results = boot(data = trees, statistic = volume_estimate, R = 5000)
```

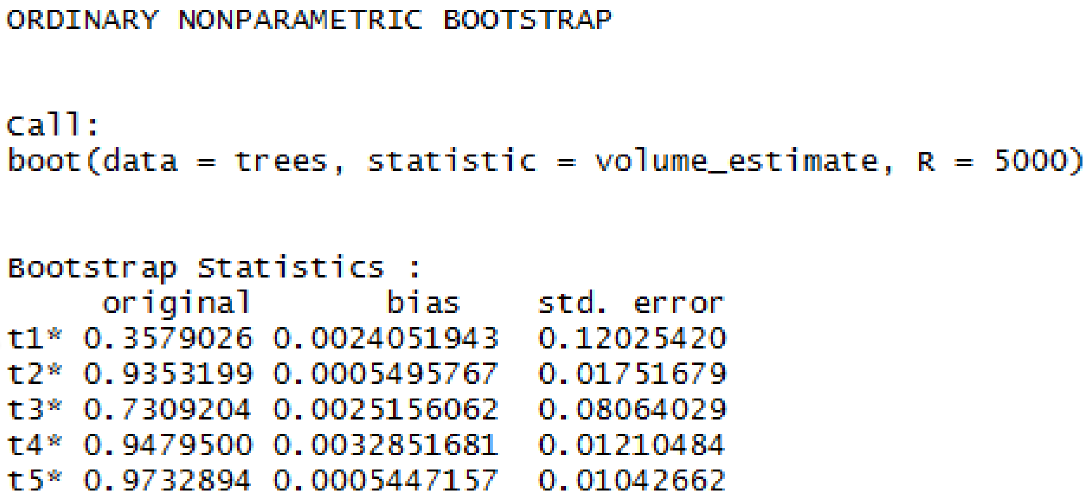
Dataset from which statistics will be calculated

Function we created to calculate statistics on each bootstrap sample

Number of bootstrap samples (i.e., iterations)

- View some calculated statistics of boot object

```
print(results)
```



```
ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
boot(data = trees, statistic = volume_estimate, R = 5000)


Bootstrap Statistics :
     original        bias    std. error
t1* 0.3579026 0.0024051943  0.12025420
t2* 0.9353199 0.0005495767  0.01751679
t3* 0.7309204 0.0025156062  0.08064029
t4* 0.9479500 0.0032851681  0.01210484
t5* 0.9732894 0.0005447157  0.01042662
```

t* corresponds to index of “relationships” vector (e.g., t1* refers to height only R-squared value

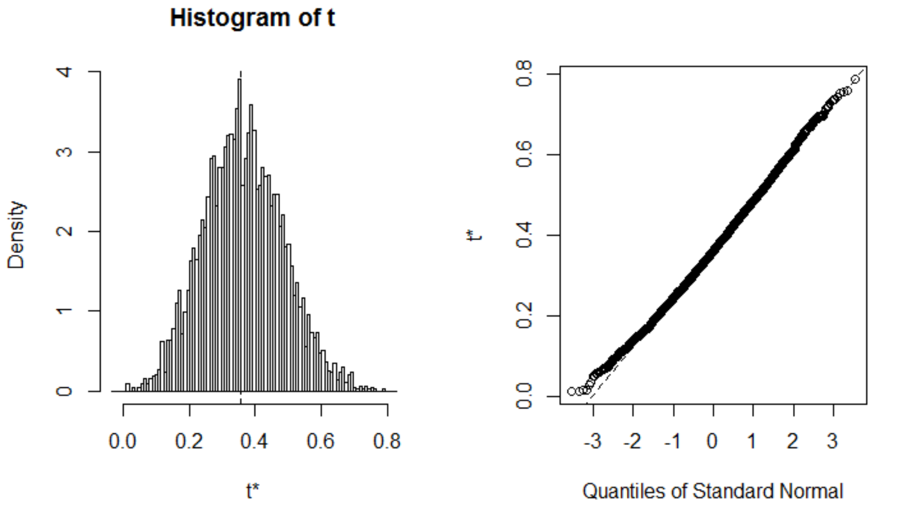
- Plot the boot objects
  - – Provides histogram and Q-Q plot

```
plot(results, index = 1)
```

The index parameter corresponds to the indices of the vector (“relationships”) returned by the “volume_estimation” function (e.g., index 1 is the first item in the vector, which is the height only R-squared value)

```
relationships = c(H_r_sq, G_r_sq, G_H_r_sq, combined_r_sq, combined_2_r_sq)
```

Height only R-squared distribution:

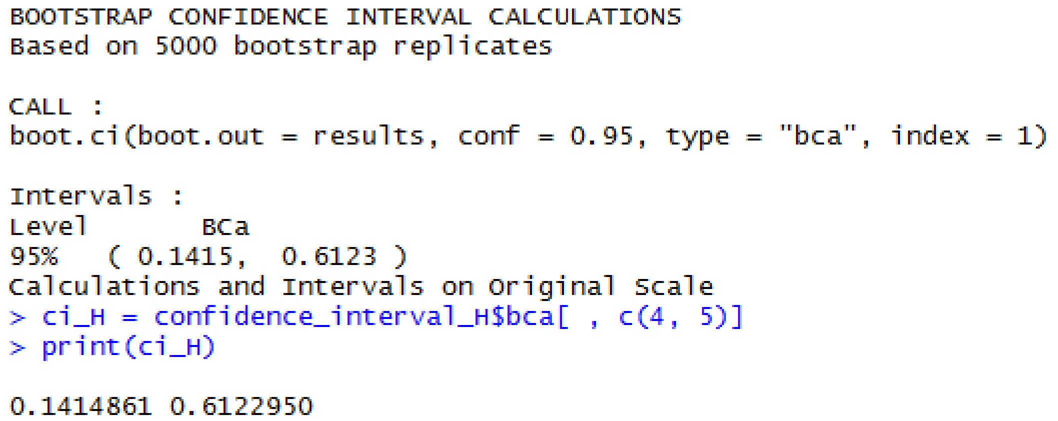


- Calculate 95% confidence intervals for each of the bootstrapped R-squared values
  - Using “Bias Corrected and Accelerated” (BCa) method

Specify index corresponding to position in vector for each statistic

```
confidence_interval_H = boot.ci(results, index = 1, conf = 0.95, type = 'bca')
print(confidence_interval_H)
ci_H = confidence_interval_H$bca[ , c(4, 5)]
print(ci_H)
```

Store confidence intervals in a variable in order to plot later

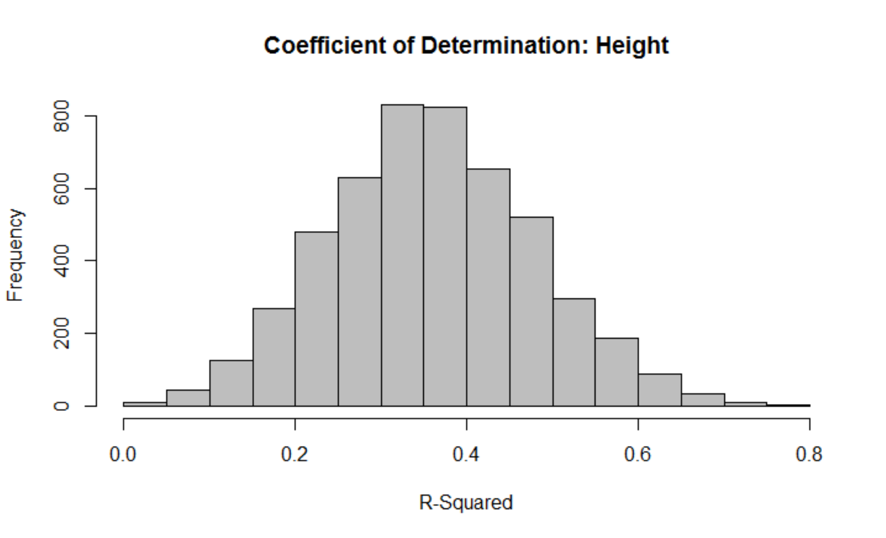


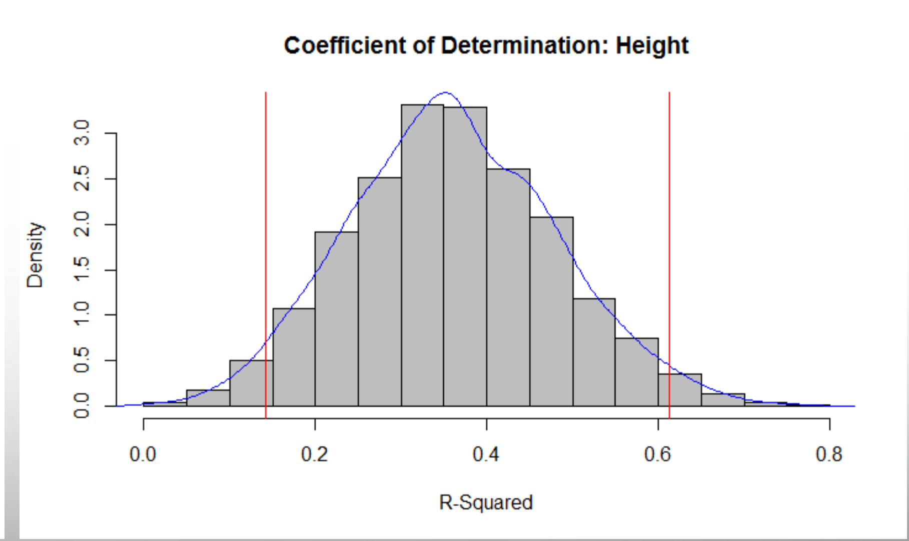
```
BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
Based on 5000 bootstrap replicates

CALL :
boot.ci(boot.out = results, conf = 0.95, type = "bca", index = 1)

Intervals :
Level       BCa
95%   ( 0.1415,  0.6123 )
Calculations and Intervals on Original Scale
> ci_H = confidence_interval_H$bca[ , c(4, 5)]
> print(ci_H)

0.1414861 0.6122950
```

- View histograms (frequency and density)
- Add kernel density line (blue)
- Add 95% confidence intervals (red)

```
hist(results$t[,1], main = 'Coefficient of Determination: Height', xlab = 'R-
    Squared', col = 'grey')
hist(results$t[,1], main = 'Coefficient of Determination: Height', xlab = 'R-
    Squared', col = 'grey', prob = T)
lines(density(results$t[,1]), col = 'blue')
abline(v = ci_H, col = 'red')
```

Note syntax to call desired sample distribution





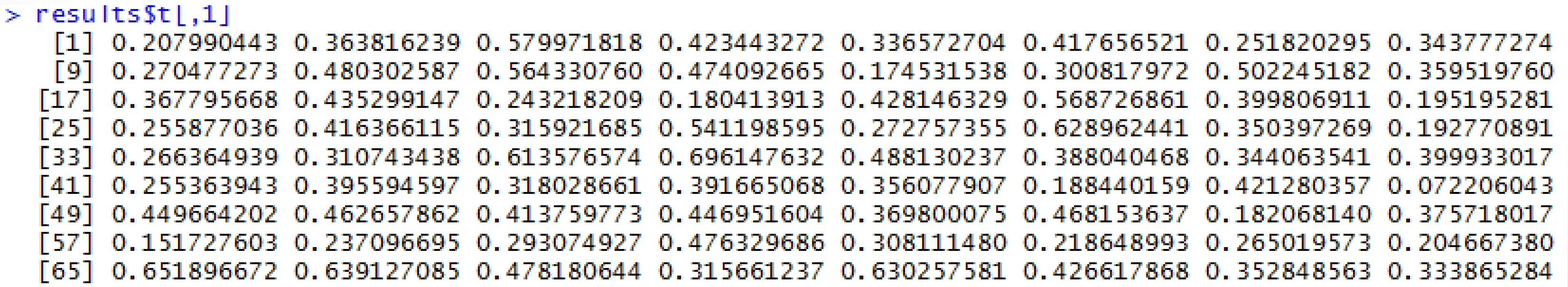
- Can also call the entire sample distribution to further manipulate, save, etc.

```
results$t[ , 1]
```

Access the sample statistics of each bootstrap sample

Subset to particular statistic; first column of the boot object “t” corresponds to the first item in the vector returned by the “volume_esitmate” function

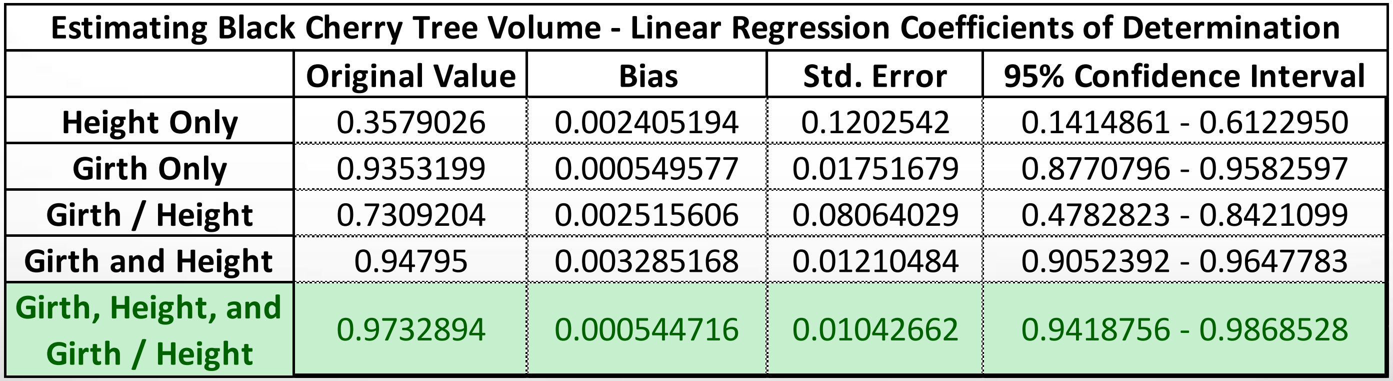
R-squared values of height only linear regression:



```
> results$t[,1]
   [1] 0.207990443 0.363816239 0.579971818 0.423443272 0.336572704 0.417656521 0.251820295 0.343777274
   [9] 0.270477273 0.480302587 0.564330760 0.474092665 0.174531538 0.300817972 0.502245182 0.359519760
  [17] 0.367795668 0.435299147 0.243218209 0.180413913 0.428146329 0.568726861 0.399806911 0.195195281
  [25] 0.255877036 0.416366115 0.315921685 0.541198595 0.272757355 0.628962441 0.350397269 0.192770891
  [33] 0.266364939 0.310743438 0.613576574 0.696147632 0.488130237 0.388040468 0.344063541 0.399933017
  [41] 0.255363943 0.395594597 0.318028661 0.391665068 0.356077907 0.188440159 0.421280357 0.072206043
  [49] 0.449664202 0.462657862 0.413759773 0.446951604 0.369800075 0.468153637 0.182068140 0.375718017
  [57] 0.151727603 0.237096695 0.293074927 0.476329686 0.308111480 0.218648993 0.265019573 0.204667380
  [65] 0.651896672 0.639127085 0.478180644 0.315661237 0.630257581 0.426617868 0.352848563 0.333865284
```

Results

- Linear regression with explanatory variables of girth, height, and girth / height ratio provided best coefficients of determination to model the volume of black cherry trees
- 5,000 sample bootstrap allowed estimation of R-squared sampling distribution
  - Could have also bootstrapped values of coefficients, additional models, etc.



Estimating Black Cherry Tree Volume - Linear Regression Coefficients of Determination

	Original Value	Bias	Std. Error	95% Confidence Interval
Height Only	0.3579026	0.002405194	0.1202542	0.1414861 - 0.6122950
Girth Only	0.9353199	0.000549577	0.01751679	0.8770796 - 0.9582597
Girth / Height	0.7309204	0.002515606	0.08064029	0.4782823 - 0.8421099
Girth and Height	0.94795	0.003285168	0.01210484	0.9052392 - 0.9647783
Girth, Height, and Girth / Height	0.9732894	0.000544716	0.01042662	0.9418756 - 0.9868528

References

http://www.statmethods.net/advstats/bootstrapping.html

http://www.mayin.org/ajayshah/KB/R/documents/boot.html

http://www.r-bloggers.com/bootstrap-example/

http://cran.r-project.org/web/packages/boot/boot.pdf

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