

Bootstrapping

FW8051 Statistics for Ecologists

Department of Fisheries, Wildlife and Conservation Biology



Objectives

- To understand how a bootstrap can be used to quantify uncertainty, particularly when assumptions of linear regression may not be met.
- To further your coding skills by implementing a cluster-level bootstrap appropriate for certain types of data sets containing repeated observations.

RIKZ [Dutch governmental institute] data

Abundances from ~ 75 invertebrate species measured on various beaches along Dutch Coast.



Selected from: Zuur, A. F., E. N. Ieno, and G. M. Smith. 2009. Analyzing Ecological Data. Springer, New York.

RIKZ data

Sampling Effort:

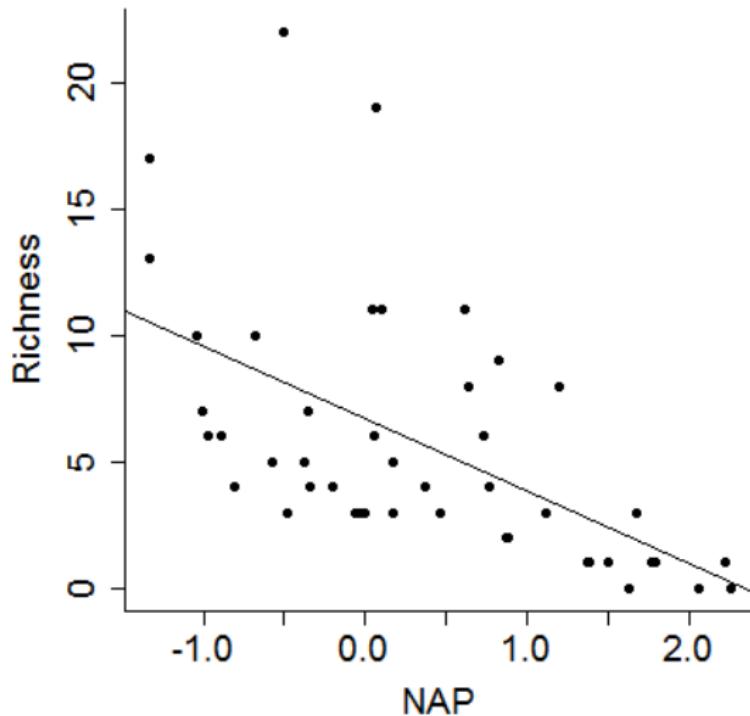
- 9 beaches (high, medium, low exposure)
- 5 stations at each beach.

Variables:

- Richness = species richness (number of species counted).
- NAP = height of the sample site (relative to sea level).
 - Lower values imply more time spent under water.
 - Higher values typically found further up the beach.



Gerard Janssen, RIKZ



$$\hat{Y}_i = 6.886 - 2.867X_i + E_i$$

Regression Output

```
lmfit.R<-lm(Richness~NAP, data=RIKZdat)
summary(lmfit.R)
```

Call:

```
lm(formula = Richness ~ NAP, data = RIKZdat)
```

Residuals:

Min	1Q	Median	3Q	Max
-5.0675	-2.7607	-0.8029	1.3534	13.8723

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	6.6857	0.6578	10.164	5.25e-13	***
NAP	-2.8669	0.6307	-4.545	4.42e-05	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.16 on 43 degrees of freedom

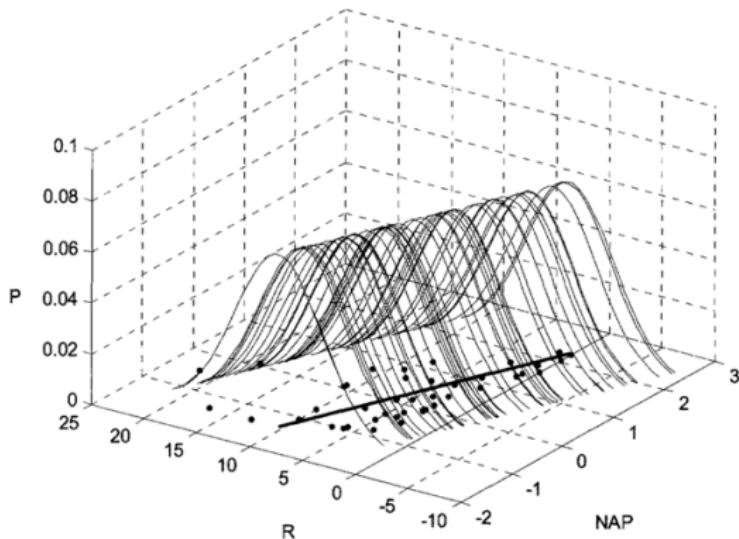
Multiple R-squared: 0.3245, Adjusted R-squared: 0.3088

F-statistic: 20.66 on 1 and 43 DF, p-value: 4.418e-05

Model for the Data

$$Y_i = \beta_0 + \beta_1 X_i + \epsilon_i$$

$$\epsilon_i \sim N(0, \sigma^2)$$



\end{center}

Linear Regression

Assumptions (HILE Gauss):

Linear Regression

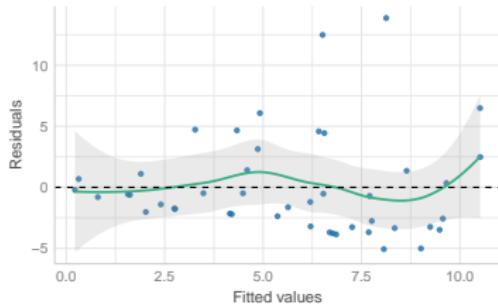
Assumptions (HILE Gauss):

- Homogeneity of variance (constant scatter about the line);
 $var(\epsilon_i) = \sigma^2$
- Independence: Correlation(ϵ_i, ϵ_j) = 0
- Linearity: $E[Y_i | X_i] = \beta_0 + X_i\beta_1$
- Existence (we observe random variables that have finite variance)
- **Gauss:** ϵ_i come from a Normal (Gaussian) distribution

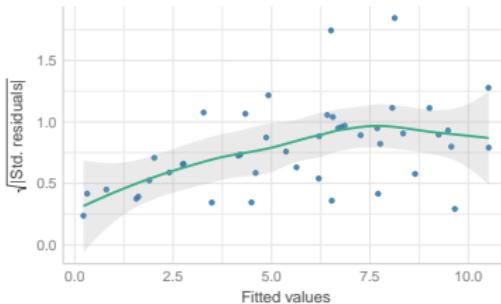
Assumptions

```
performance::check_model(lmfit.R,  
    check = c("linearity", "homogeneity", "qq", "normality"))
```

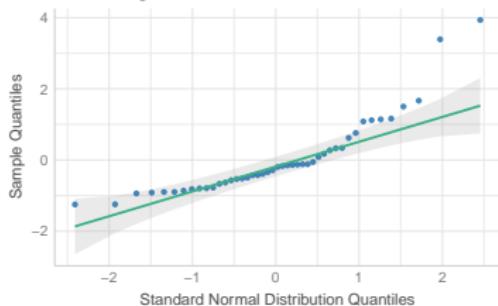
Linearity
Reference line should be flat and horizontal



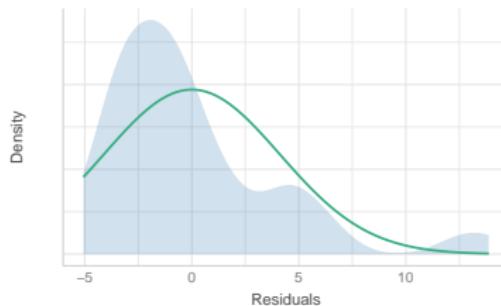
Homogeneity of Variance
Reference line should be flat and horizontal



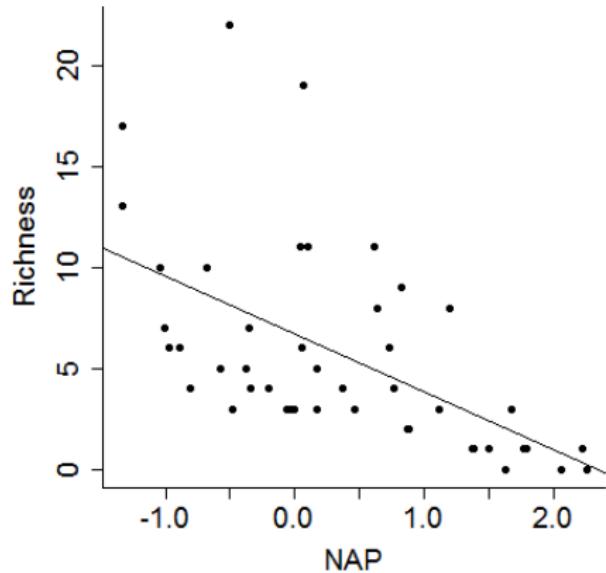
Normality of Residuals
Dots should fall along the line



Normality of Residuals
Distribution should be close to the normal curve

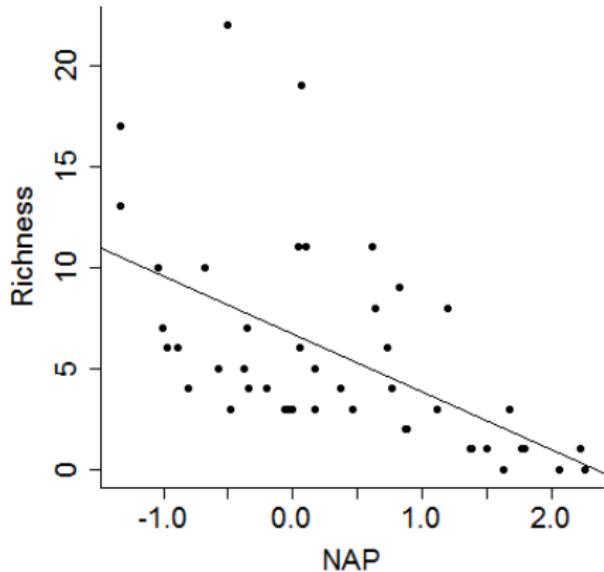


Linearity?



$$\widehat{Richness}_i = 6.886 - 2.867 * NAP_i + E_i$$

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What if $NAP > 2.3$?

Independence

Are 2 observations from the same beach more alike than 2 observations from 2 different beaches (after accounting for NAP)?

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Consequence? SE's for $\hat{\beta}$ too small?

Solutions?

- Transformations (constant variance, normality, linearity)

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- Can model mean and variance using “Generalized least squares” (gls) (Ch 4 of Zuur et al.)

$$Y_i = \beta_0 + X_i\beta + \epsilon_i, \text{ with}$$

$$\epsilon_i \sim N(0, \sigma^2 f(X_i; \theta))$$

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- Use generalized linear models for count data (naturally allows the variance to increase with the mean)
- Bootstrap (to deal with non-constant variance, clustering)

Assumptions

Linear regression relies on least-squares:

$$\hat{\beta} \text{ minimizes: } \sum_{i=1}^n (Y_i - [\beta_0 + X_i\beta_1])^2.$$

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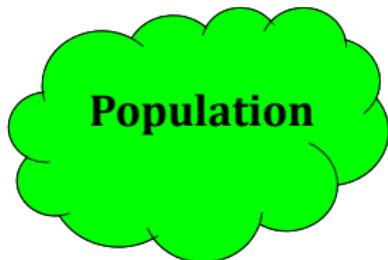
To relax these assumptions, we will consider using a bootstrap for inference.

Confidence Intervals

Confidence Interval

$$statistic \pm ME$$

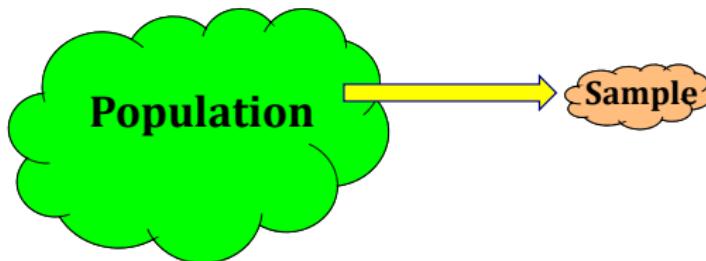
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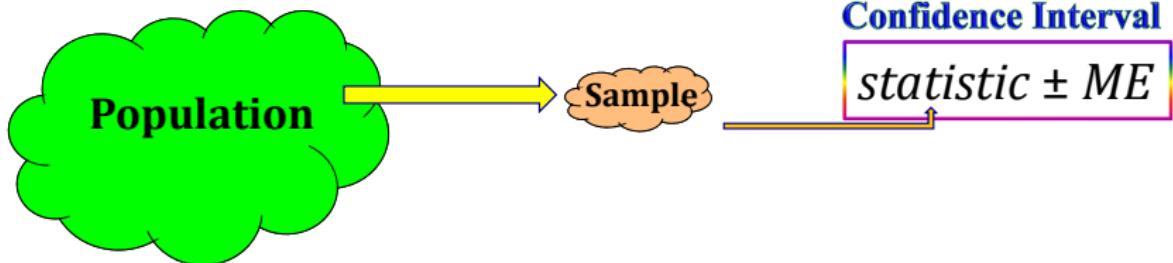
Confidence Intervals



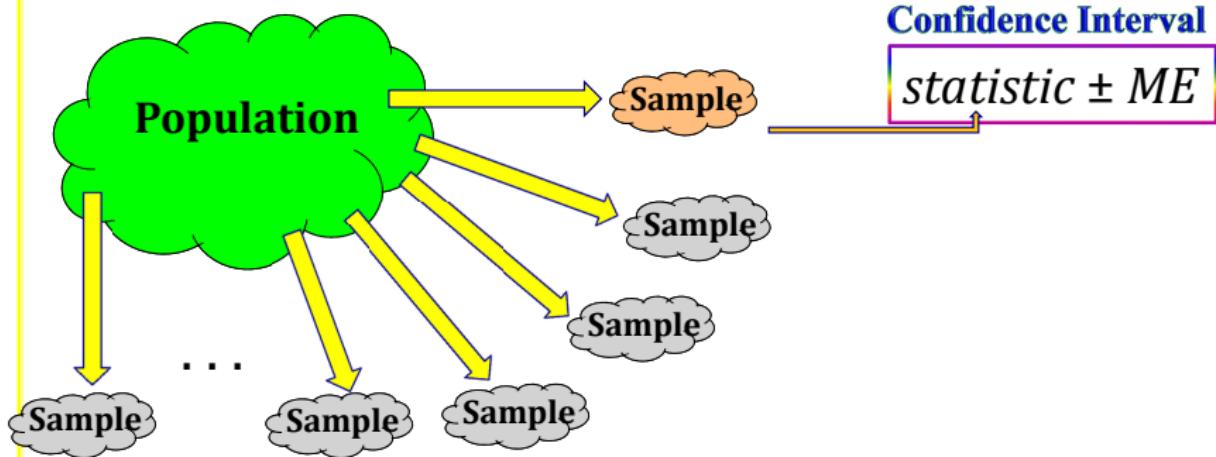
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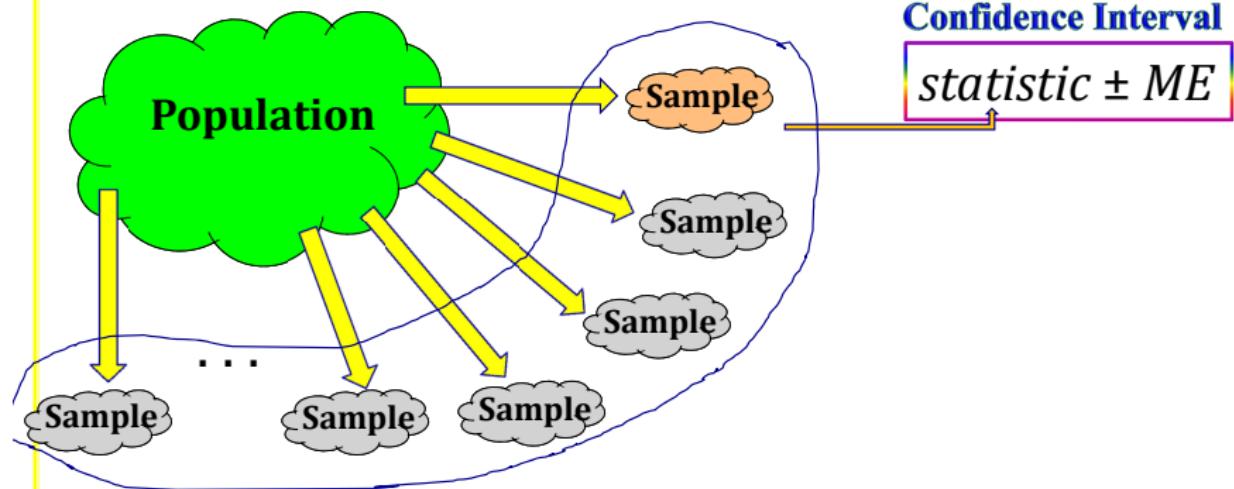
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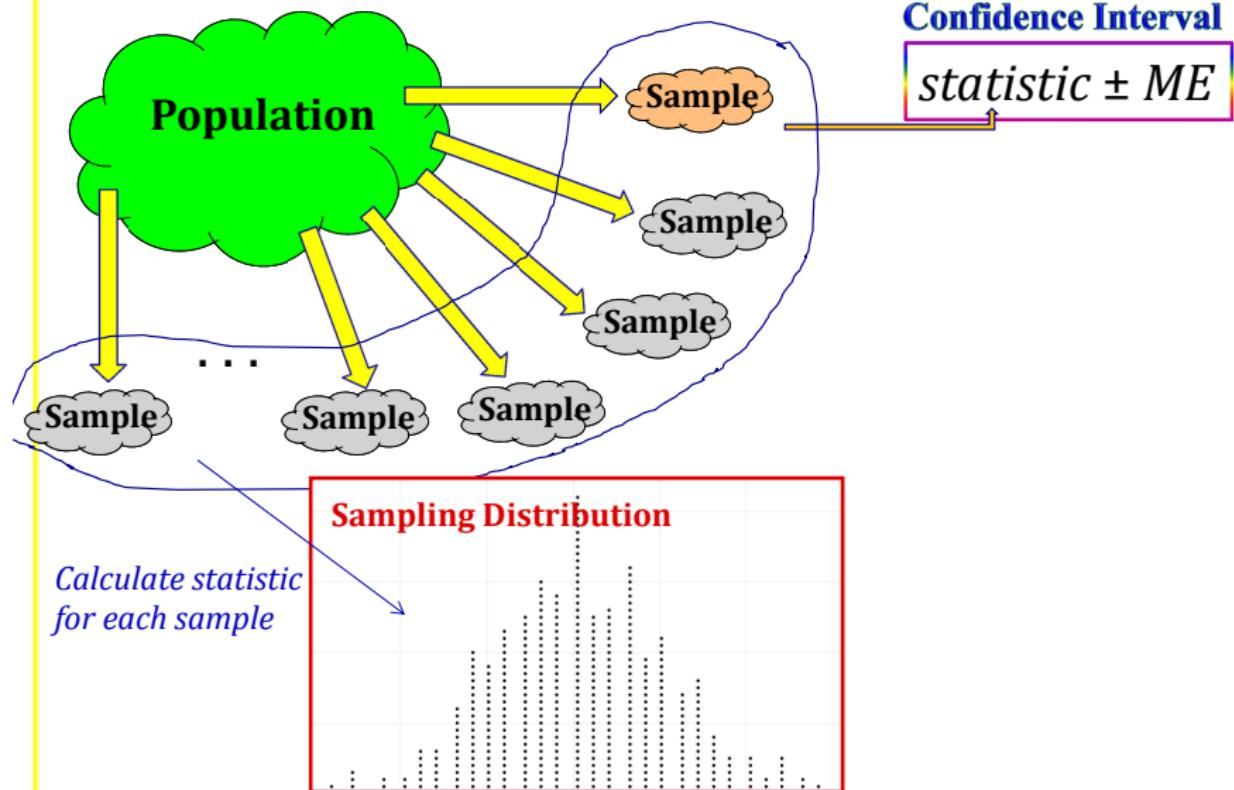


Confidence Intervals

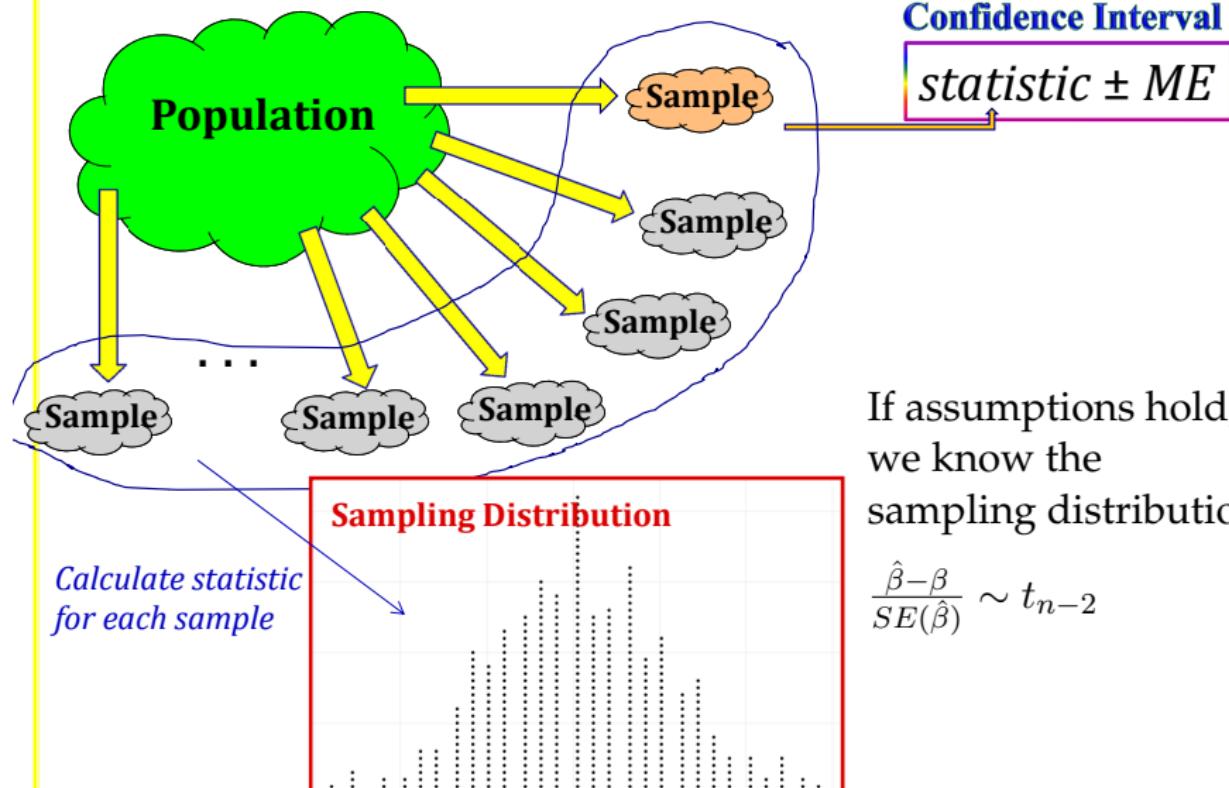


*Calculate statistic
for each sample*

Confidence Intervals



Confidence Intervals



Reality

We only have 1 sample, what do we do?

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What do you have to assume?

Reality

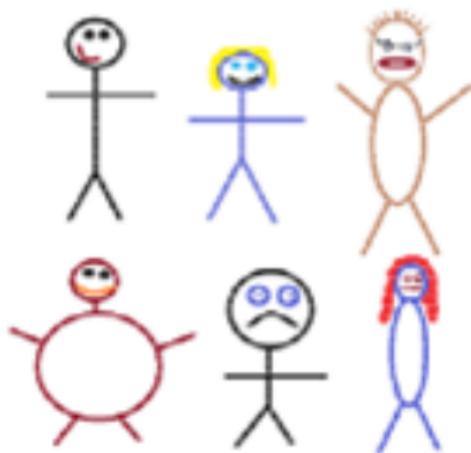
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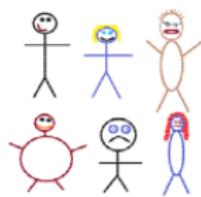
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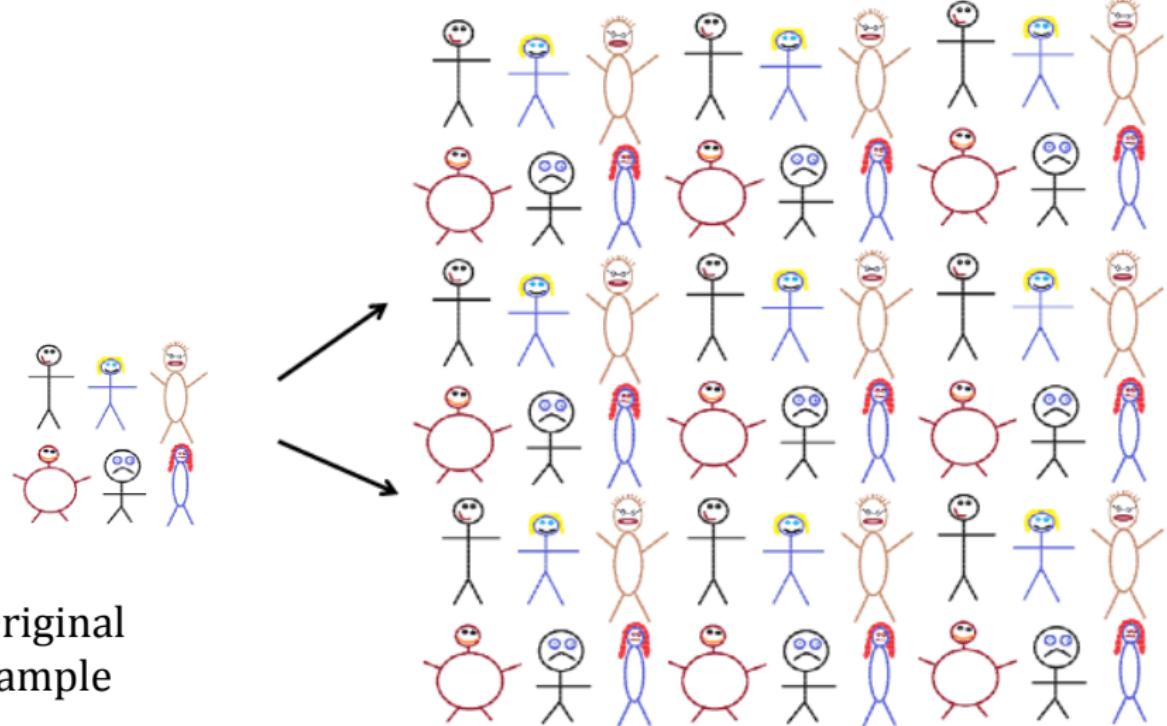
- The sample is representative of the population (otherwise, it's pointless to try to generalize from sample to population)

Suppose we have a random sample of 6 people:





Original
Sample



A simulated “population” to sample from

Sampling with Replacement

- To simulate a sampling distribution, we can just take repeated random samples from this “population” made up of many copies of the sample

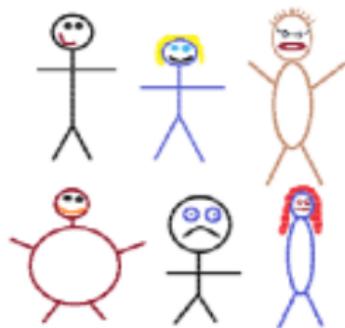
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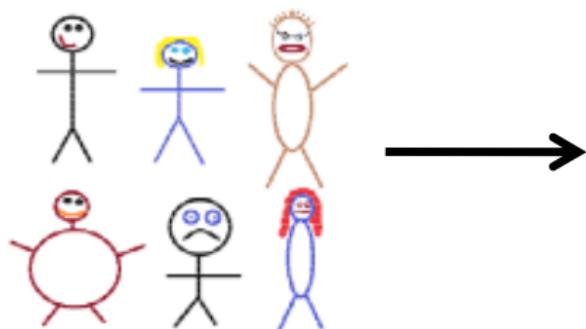
- To simulate a sampling distribution, we can just take repeated random samples from this “population” made up of many copies of the sample
- In practice, we can’t actually make infinite copies of the sample...
- ...but we can do this by sampling with replacement from the sample we have (each unit can be selected more than once)

Bootstrap Sample: Sample with replacement from the original sample, using the same sample size.



Original
Sample

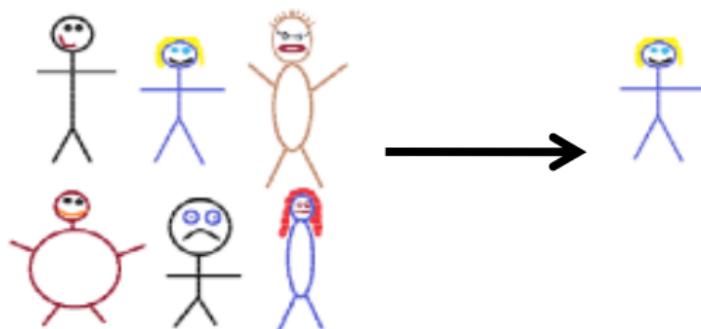
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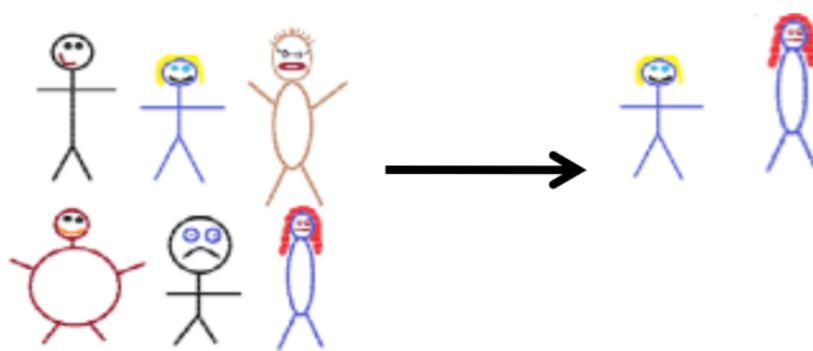
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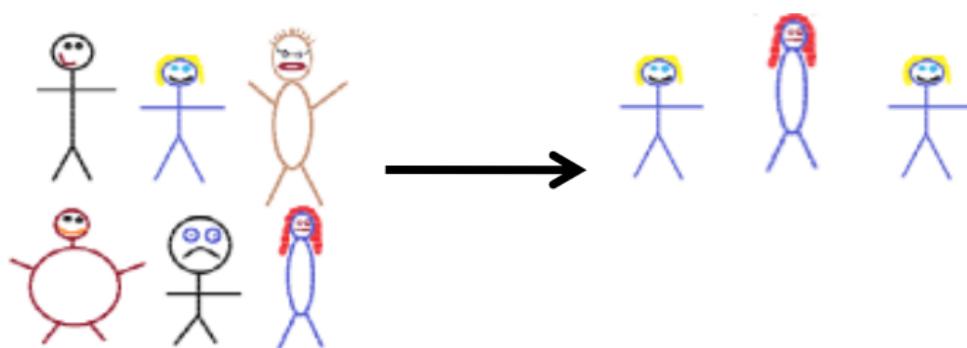
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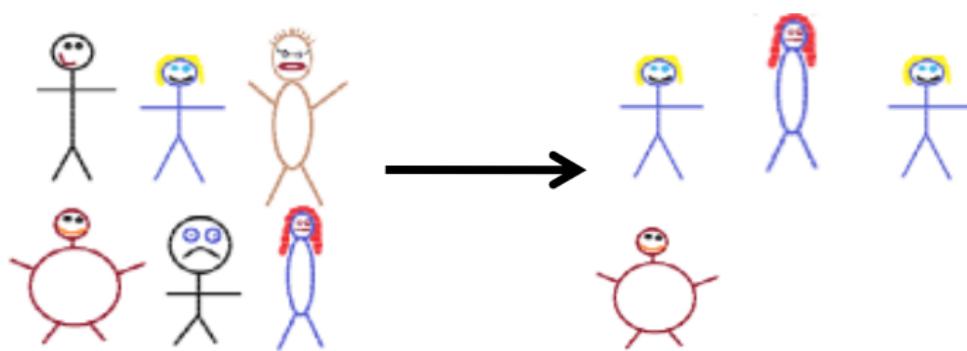
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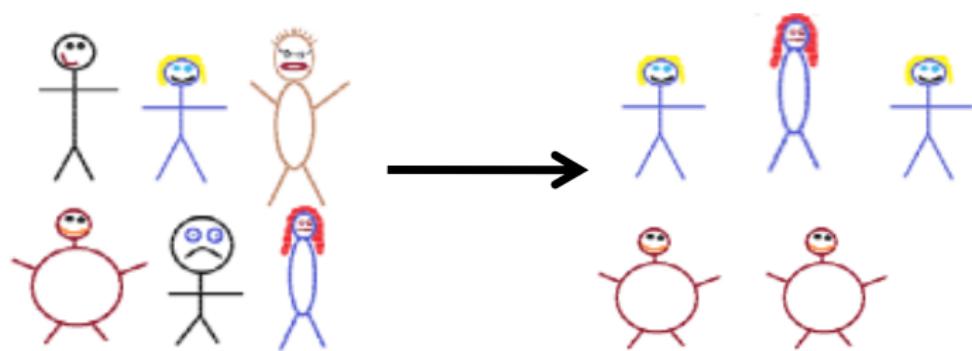
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Original
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Bootstrap Sample

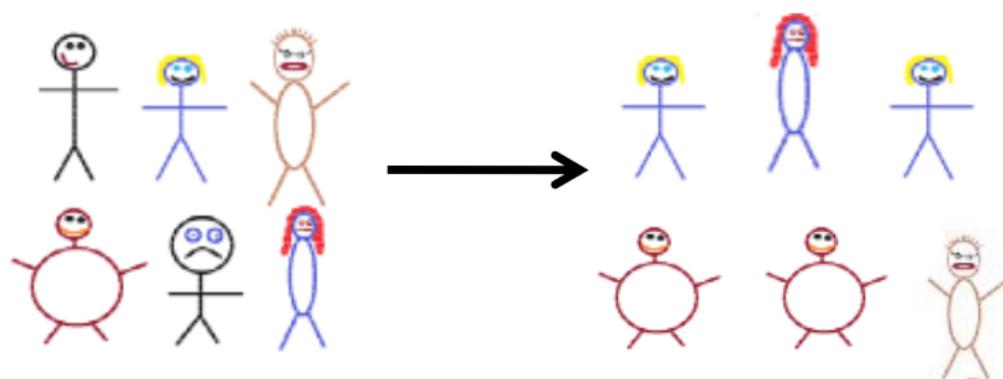
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Bootstrap Sample

Your original sample has data values

18, 19, 19, 20, 21

Is the following a possible bootstrap sample: 18, 19, 20, 21, 22

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No, 22 is not a value from the original sample

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Is the following a possible bootstrap sample: 18, 18, 19, 20, 21
YES. Same size, could be gotten by sampling with replacement

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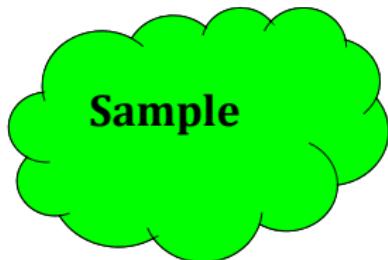
- A **bootstrap sample** is a random sample taken with replacement from the original sample, of the same size as the original sample
- A **bootstrap statistic** is the statistic computed on a bootstrap sample
- A **bootstrap distribution** is the distribution of many bootstrap statistics

Confidence Intervals

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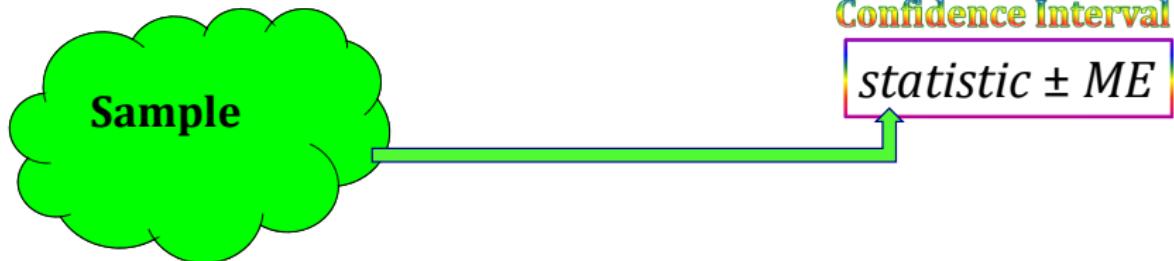
Confidence Intervals



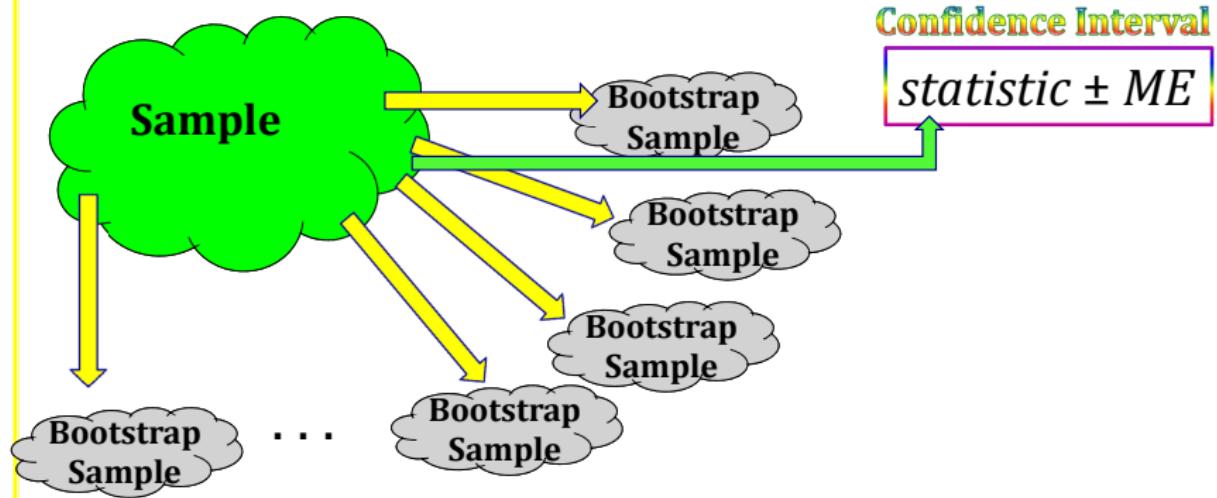
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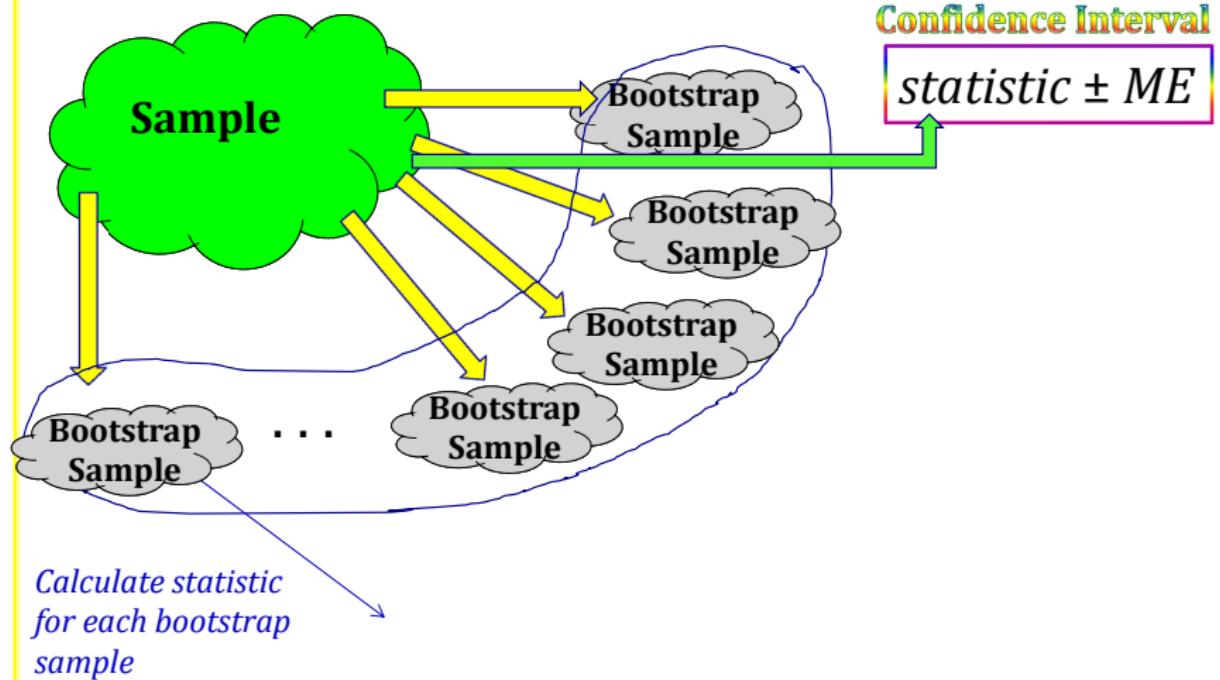
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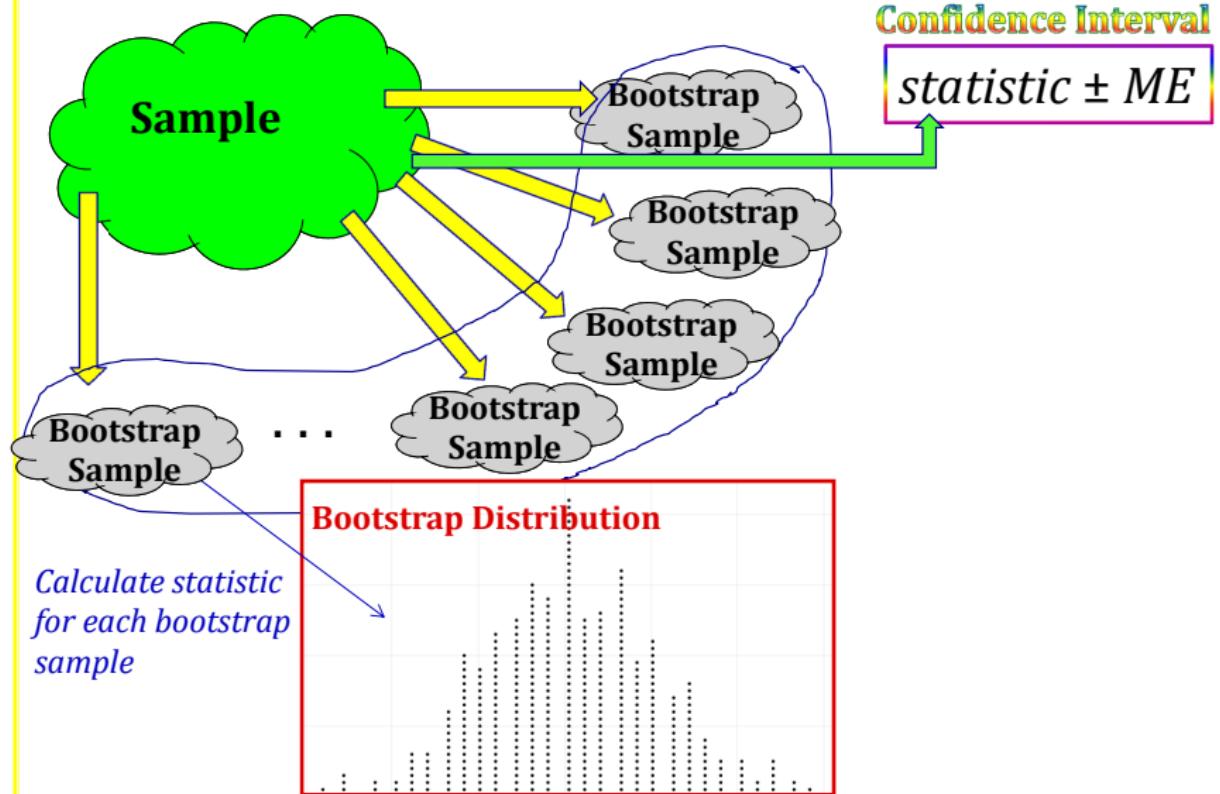
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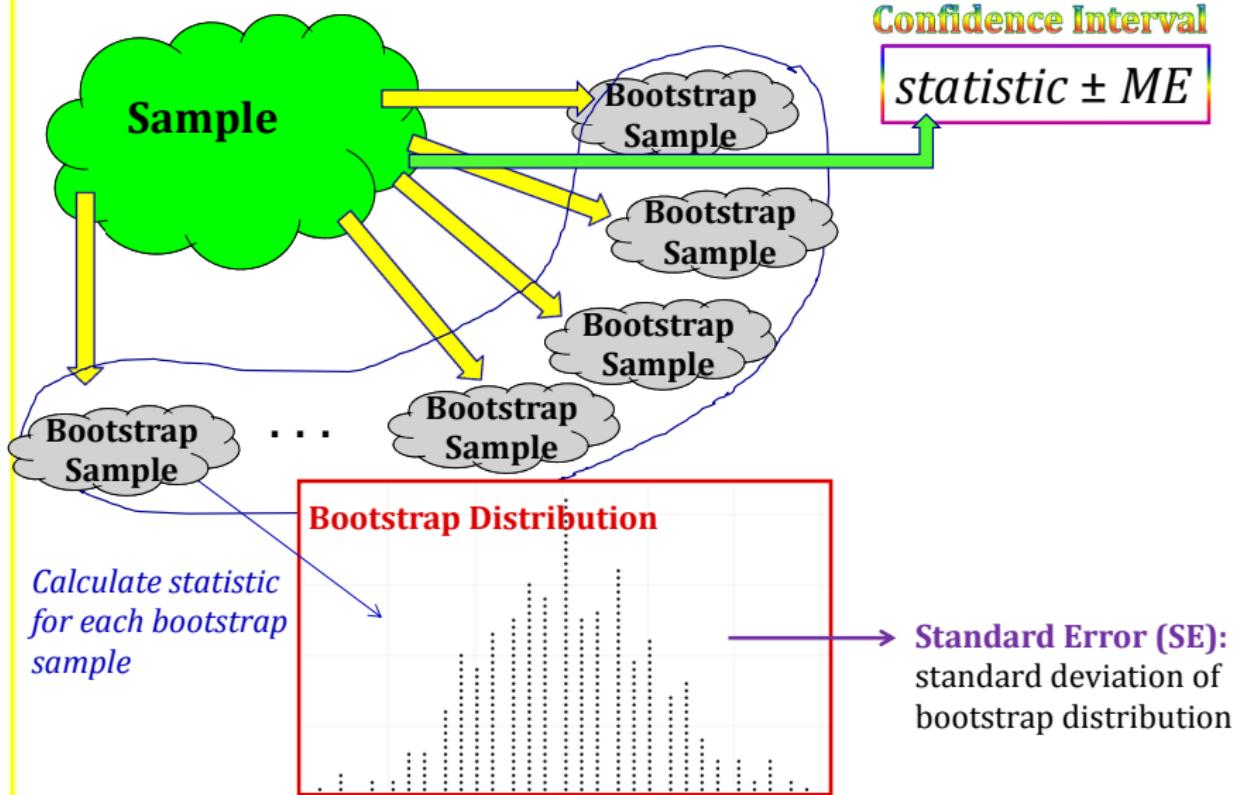
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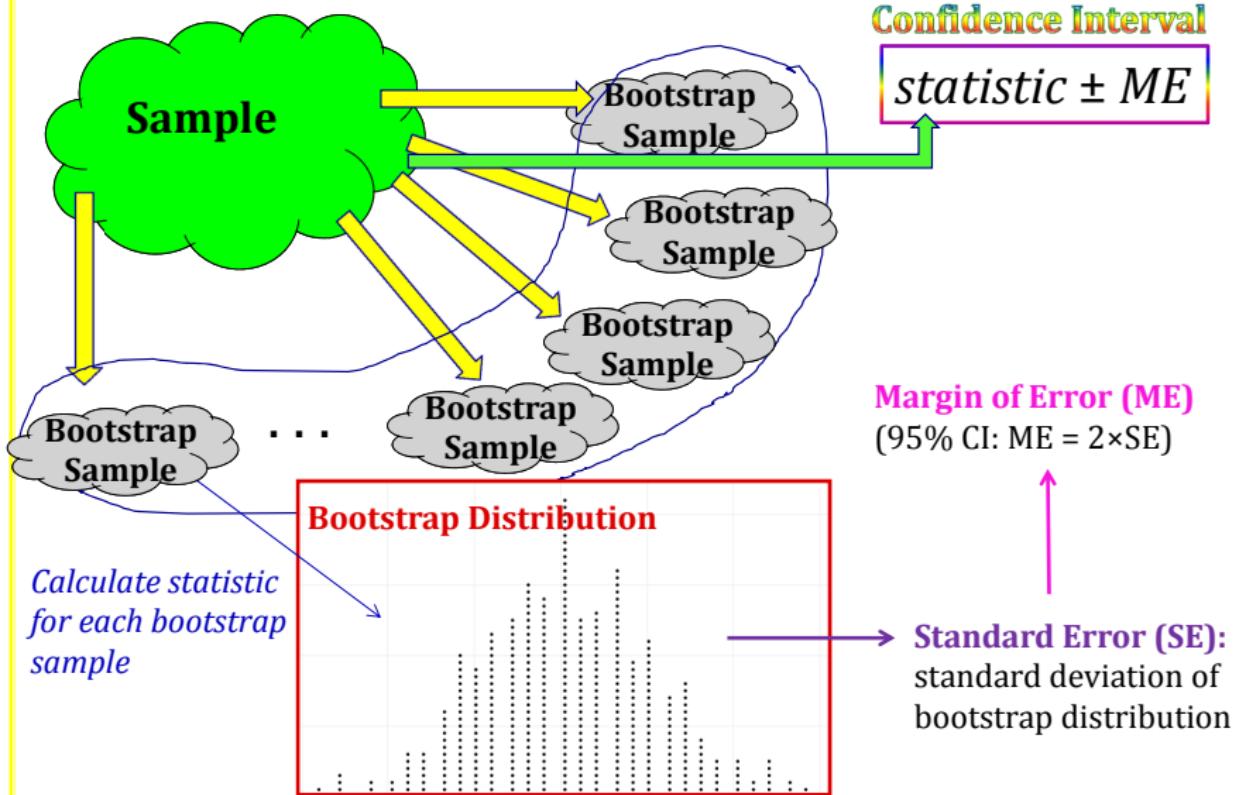
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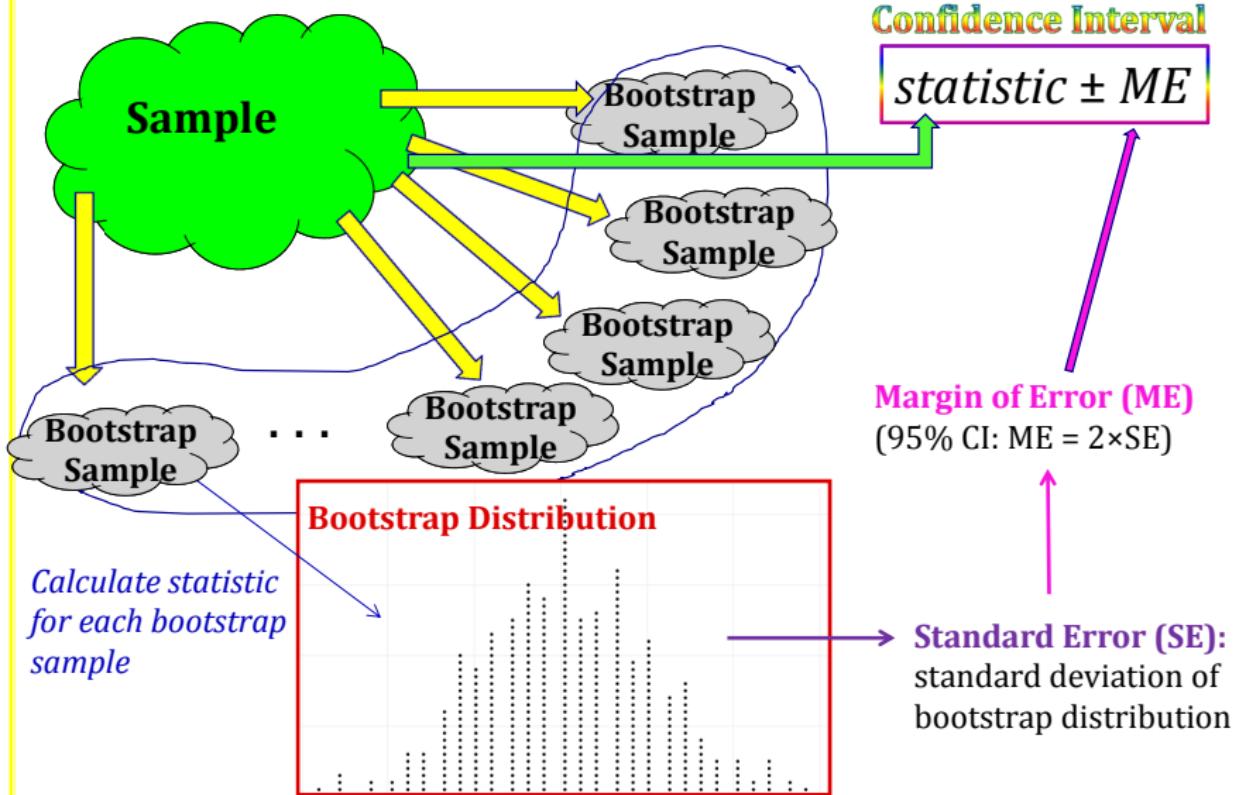
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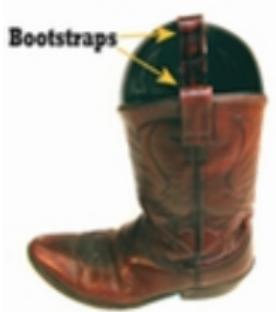
Confidence Intervals



Confidence Intervals



Why “Bootstrap”?



“Pull yourself up by your bootstraps”

- Lift yourself in the air simply by pulling up on the laces of your boots

Why “Bootstrap”?



“Pull yourself up by your bootstraps”

- Lift yourself in the air simply by pulling up on the laces of your boots
- Metaphor for accomplishing an “impossible” task without any outside help

Center

- The sampling distribution is centered on the population parameter

Center

- The sampling distribution is centered on the population parameter
- The bootstrap distribution is centered on the sample statistic

Center

- The sampling distribution is centered on the population parameter
- The bootstrap distribution is centered on the sample statistic
- Luckily, we don't care about the center... we care about the **variability!**

Standard Error

- The variability of the bootstrap statistics should be similar to the variability of the sample statistics

Standard Error

- The variability of the bootstrap statistics should be similar to the variability of the sample statistics
- The standard error of a statistic can be estimated using the standard deviation of the bootstrap distribution!

Bootstrap Sampling Must Mimic Original Sampling Design

What do we do if we have clustered data (multiple obs. on same sampling unit)?

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Bootstrap Sampling Must Mimic Original Sampling Design

What do we do if we have clustered data (multiple obs. on same sampling unit)?

- Sample clusters with replacement (keeping all observations associated with the cluster)
- Number of clusters in the bootstrap sample is the same as in the original sample
- Treats "clusters" as independent

RIKZ Data - Bootstrapping

Cluster-level bootstrapping

Field Plot Layout

A	B	C
D	E	F



Original Sample

Plot A (4, 2, 1, 6, 2)

Plot B (7, 3, 2, 1, 1)

Plot C (4, 2, 3, 2, 4)

Plot D (6, 4, 3, 3, 1)

Plot E (5, 4, 2, 3, 1)

Plot F (2, 4, 3, 5, 6)

Cluster-Level Bootstrapping Example

Bootstrap Sample

Plot B (7, 3, 2, 1, 1)

Plot D (6, 4, 3, 3, 1)

Plot A (4, 2, 1, 6, 2)

Plot C (4, 2, 3, 2, 4)

Plot E (5, 4, 2, 3, 1)

Plot A (4, 2, 1, 6, 2)



Cluster-level bootstrap

This approach is most appropriate when:

- clusters have equal numbers of observations (all have 5 in this case)
- our interest lies in predictors that do not vary within a cluster

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Cluster-level Bootstrap: Sample Beaches with replacement

The code below shows how you can get 1 bootstrap data set using cluster resampling:

```
# let's use the bootstrap to deal with non-constant variance and clustering
uid<-unique(RIKZdat$Beach)
nBeach<-length(uid)

# Single bootstrap sample & fit
(bootids<-data.frame(Beach=sample(uid, nBeach, replace=T)))
```

	Beach
1	3
2	5
3	7
4	8
5	8
6	1
7	9
8	3
9	5

```
bootdat<-merge(bootids, RIKZdat)
table(bootdat$Beach)
```

1	3	5	7	8	9
5	10	10	5	10	5