

## Fundamentals and applications of resampling methods for the analysis of speech production and perception data.

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## Talk outline

- 1 Asymptotic vs. Resampling frameworks
  - Example: simulated Normal data
  - Example: simulated non-Gaussian (log-normal) data
- 2 The resampling framework
  - The standard bootstrap
  - Drawing a random sample from an existing sample
  - Performing the standard bootstrap
- 3 Advanced bootstrap: the `boot` library
- 4 Application to "real life" data

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## Aims of statistical analyses

- ▶ Estimating properties of a population or evaluating hypotheses on a population. . .
- ▶ . . . from the observation of a random sample;

## Specific applications

- ▶ Estimating a statistical parameter (central tendency, dispersion, correlation...) and computing associated confidence intervals...
- ▶ Hypothesis testing (comparing means...);

## Approaches

- ▶ Asymptotic results (traditional inference approach);
- ▶ Resampling methods
  - Bootstrap — Parameter estimation;
  - Permutation tests — Hypothesis testing;
  - Outlier detection Data cleanup (though one should consider the implications “definitely removing” observations from the data, computing confidence intervals may often be sufficient);
- ▶ Bayesian framework (not included in this presentation);



## Asymptotic results

- ▶ Assumptions about the underlying distribution;
- ▶ A mathematical model of the underlying distribution is referred to;
- ▶ The sample is viewed as a random exemplar that is drawn from the underlying population;
- ▶ Computing a Confidence Interval requires a specific mathematical formula for each parameter (mean, median...);

## Resampling approaches

- ▶ No assumptions about the underlying distribution;
- ▶ The mathematical model of the underlying distribution is replaced with a computational simulated estimation of the "population" by generating "bootstrap samples";
- ▶ The (original) sample is the source of this computing simulation;
- ▶ Computing a Confidence Interval is possible for any parameter without requiring specific formulas;

## A Gaussian distributed variable

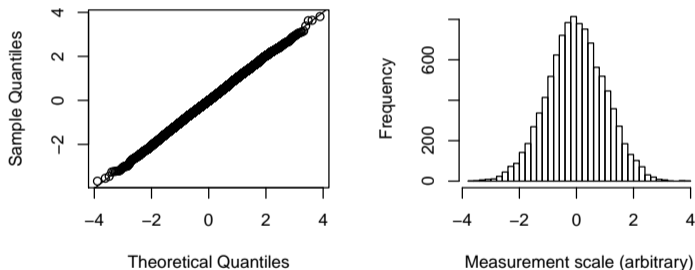


Figure 1: An illustration of a Gaussian distribution from which data may be randomly sampled. The QQ-plot on the left shows compatibility with the Gaussian assumption.

## Confidence Intervals

### Recalls

- ▶ We talk about 95%, 99%... Confidence Intervals (CIs);
- ▶ These mean that, in the long run, 95% (resp. 99%) of the computed CIs would contain the true value for the measured parameter;

## Asymptotic framework

Estimating 95% CI for the mean

Estimating a 95% CI for a parameter's mean is done with the following formula:

$$\delta = \frac{1.96 * SD}{\sqrt{n}} \quad (1)$$

$$CI = \text{mean} \pm \delta \quad (2)$$

- ▶ Gaussian assumption: the formula is valid for a normally distributed variable;
- ▶ 95% of the area under a normal curve lies within the mean  $\pm 1.96 \times \text{sd}$ ;
- ▶ 99% of the area under a normal curve lies within the mean  $\pm 2.58 \times \text{sd}$ .

## Conventional CI for the mean

Function definition in R

```
CI <- function(vector, targetprob = 0.95) {  
  # CI for the mean  
  
  # Compute the required percentile point from the target probability  
  param <- qnorm(1 - ((1 - targetprob) / 2))  
  
  # Estimate the delta  
  delta <- ((param * sd(vector)) / (sqrt(length(vector))))  
  
  # Generate the CI values  
  ci <- c(mean(vector) - delta, mean(vector) + delta)  
  
  # Give a name to the resulting vector values  
  names(ci) <- as.character(  
    c(  
      paste0((1-targetprob)/2*100,"%"),  
      paste0((1-(1-targetprob)/2)*100,"%")  
    )  
  )  
  
  return(ci)  
}
```

## Conventional CI for the mean

### Function application

```
samplesize <- 10
set.seed(1)
vecn <- rnorm(samplesize, mean = 0);
vecn

[1] -0.626  0.184 -0.836  1.595  0.330 -0.820  0.487  0.738  0.576 -0.305

CI(vecn)

  2.5%  97.5%
-0.352  0.616

CI(vecn, targetprob = .99)

  0.5%  99.5%
-0.504  0.768
```

```
par(mfrow=c(1,1), cex=0.85)  
hist(vecn, breaks=40, main = "", xlab = "Measurement scale (arbitrary)")  
abline(v = CI(vecn), col = "red")
```

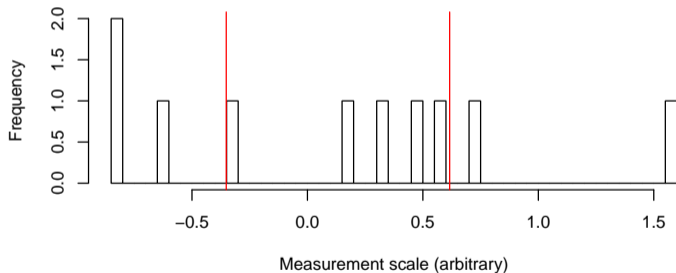


Figure 2: Conventional Confidence Interval for the mean.



## Conventional CI for the mean

### Function application

```
samplesize <- 50
set.seed(1)
vecn <- rnorm(samplesize, mean = 0);
vecn

 [1] -0.6265  0.1836 -0.8356  1.5953  0.3295 -0.8205  0.4874  0.7383
 [9]  0.5758 -0.3054  1.5118  0.3898 -0.6212 -2.2147  1.1249 -0.0449
[17] -0.0162  0.9438  0.8212  0.5939  0.9190  0.7821  0.0746 -1.9894
[25]  0.6198 -0.0561 -0.1558 -1.4708 -0.4782  0.4179  1.3587 -0.1028
[33]  0.3877 -0.0538 -1.3771 -0.4150 -0.3943 -0.0593  1.1000  0.7632
[41] -0.1645 -0.2534  0.6970  0.5567 -0.6888 -0.7075  0.3646  0.7685
[49] -0.1123  0.8811

CI(vecn)

 2.5% 97.5%
-0.130 0.331
```

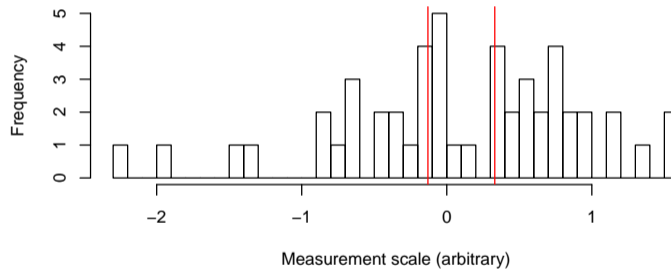


Figure 3: Conventional Confidence Interval for the mean.

## Conventional CI for the mean

### Function application

```
samplesize <- 1000
set.seed(1)
vecn <- rnorm(samplesize, mean = 0);
CI(vecn)

      2.5%   97.5%
-0.0758  0.0525
```

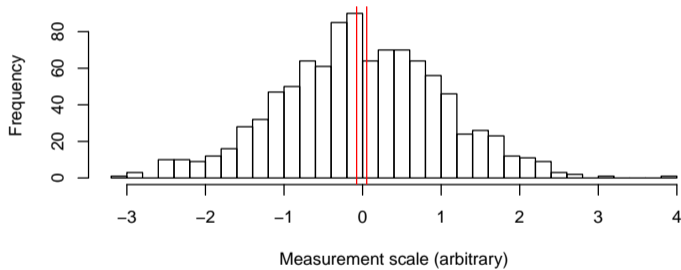


Figure 4: Conventional Confidence Interval for the mean.

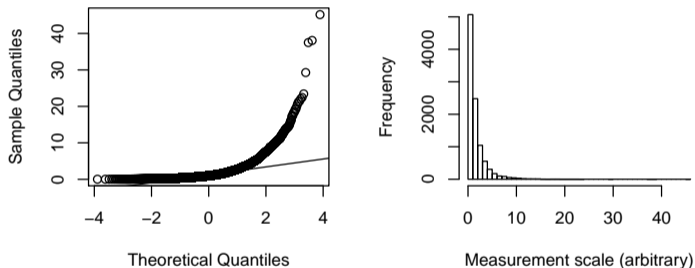


Figure 5: An illustration of a (strongly) non-Gaussian distribution from which data may be randomly sampled. The QQ-plot on the left shows strong departure from the Gaussian assumption. This distribution will be used as an example for the computation of Confidence Intervals in both the asymptotic and the resampling framework.

## Conventional CI for the mean

### Function application

```
samplesize <- 1000
set.seed(1)
vec <- rlnorm(samplesize, meanlog = 0);
CI(vec)
```

```
2.5% 97.5%
1.54  1.83
```

```
par(mfrow=c(1,1), cex=0.85)  
hist(vec, breaks=40, main = "", xlab = "Measurement scale (arbitrary)")  
abline(v = CI(vec), col = "red")
```

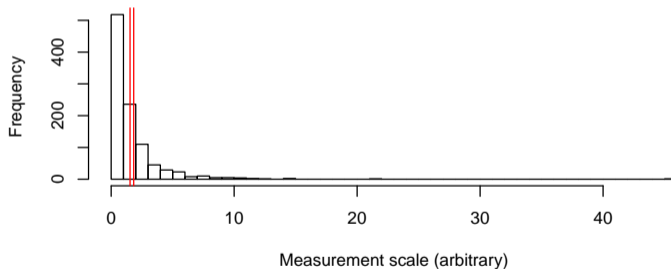


Figure 6: Conventional Confidence Interval for the mean.

## Conventional CI for the mean

### Function application

```
samplesize <- 50
set.seed(1)
vec <- rlnorm(samplesize, meanlog = 0);
CI(vec)
```

```
2.5% 97.5%
1.17  1.77
```



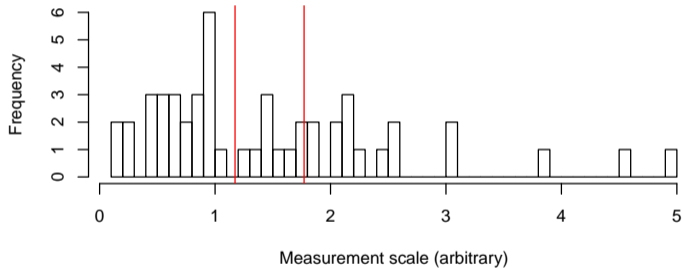


Figure 7: Conventional Confidence Interval for the mean.

## Conventional CI for the mean

### Function application

```
samplesize <- 10  
set.seed(1)  
vec <- rlnorm(samplesize, meanlog = 0);  
CI(vec)
```

```
 2.5% 97.5%  
0.688 2.345
```

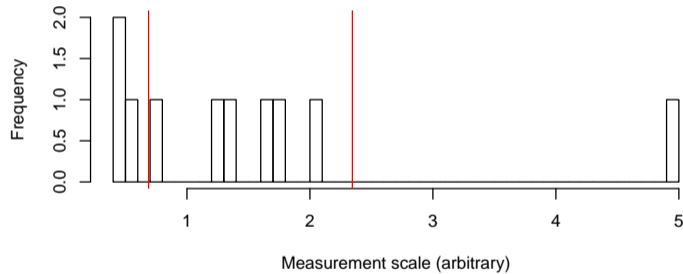


Figure 8: Conventional Confidence Interval for the mean.

## Issues with conventional CIs

- ▶ They rely on distributional assumptions;
- ▶ These distributional assumptions imply that estimating different parameters involves different formulas;

## Resampling or “bootstrap” framework

### The “bootstrap principle”

- ▶ “The sample is to the population. . .
- ▶ what the bootstrap sample is to the sample”;

## Resampling or “bootstrap” framework

### The “bootstrap principle”

- ▶ We can then use this principle to “build” a population of bootstrap samples;
- ▶ Principle: Draw random samples from the original sample (with replacement) *a very high number of times*;
- ▶ This can be done for *any* parameter (mean, median, linear regression parameter. . . );

## Resampling or “bootstrap” framework

Drawing a single bootstrap sample

```
vec  
  
[1] 0.534 1.202 0.434 4.930 1.390 0.440 1.628 2.092 1.779 0.737  
  
median(vec)  
  
[1] 1.3
```

## Resampling or “bootstrap” framework

Drawing a single bootstrap sample ( $n^\circ 1$ )

Note that the call to `set.seed(n)` is used only to enforce reproducibility in a pedagogical setting. It should not be used in real settings as we really need to get random samples.

```
set.seed(10)
n <- length(vec) # Bootstrap sample size
samB <- sample(vec, n, replace = TRUE)

samB

[1] 0.440 4.930 1.390 1.628 0.534 0.434 0.434 0.434 1.628 1.390

median(samB)

[1] 0.962

vec

[1] 0.534 1.202 0.434 4.930 1.390 0.440 1.628 2.092 1.779 0.737
```



## Comparing the sample and a given bootstrap sample

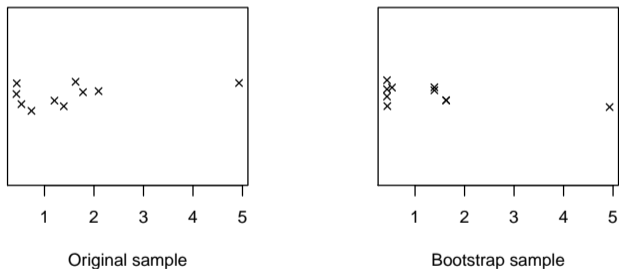


Figure 9: Comparing the original and a bootstrap sample.

## Resampling or "bootstrap" framework

Drawing a single bootstrap sample ( $n^{\circ} 2$ )

```
set.seed(20)
n <- length(vec) # Bootstrap sample size
samB <- sample(vec, n, replace = TRUE)

samB

[1] 1.779 2.092 0.434 0.440 0.737 0.737 0.534 0.534 4.930 4.930

median(samB)

[1] 0.737

vec

[1] 0.534 1.202 0.434 4.930 1.390 0.440 1.628 2.092 1.779 0.737
```

## Comparing the sample and a given bootstrap sample

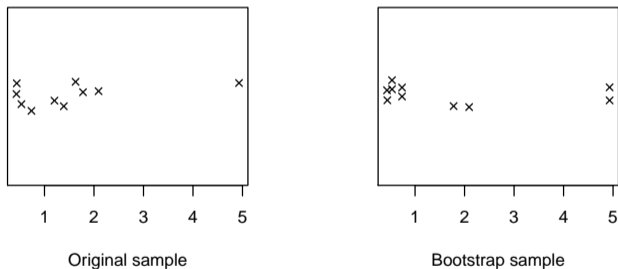


Figure 10: Comparing the original and a bootstrap sample.

## Resampling or "bootstrap" framework

Drawing a single bootstrap sample ( $n^\circ 3$ )

```
set.seed(30)
n <- length(vec) # Bootstrap sample size
samB <- sample(vec, n, replace = TRUE)

samB

[1] 0.534 1.390 4.930 1.390 4.930 1.202 1.779 0.434 0.737 1.202

median(samB)

[1] 1.3

vec

[1] 0.534 1.202 0.434 4.930 1.390 0.440 1.628 2.092 1.779 0.737
```

## Comparing the sample and a given bootstrap sample

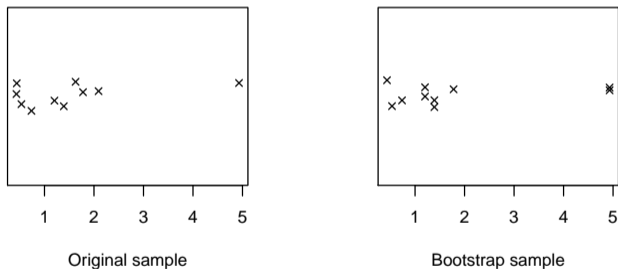


Figure 11: Comparing the original and a bootstrap sample.

## Performing a bootstrap estimation

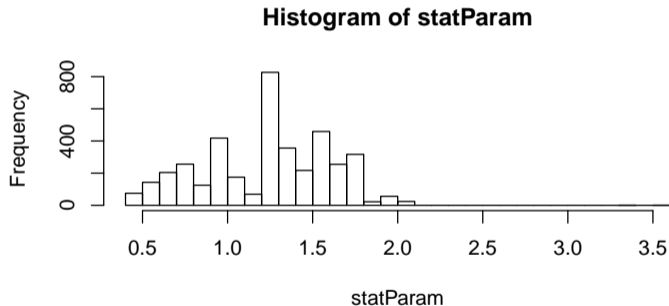
- ▶ Define the number of replications;
- ▶ Generate a loop and repeat the following for each replication / iteration:
  1. Generate a bootstrap sample;
  2. Compute the required statistical parameter on this bootstrap sample;
  3. Store the result in a vector;
- ▶ Then compute the distribution of these results (the parameter distribution);
- ▶ Estimate the relevant quantiles in order to compute the CI;

## Performing a bootstrap estimation

```
n <- length(vec) # Bootstrap sample size
nreps <- 4000 # Number of replications
statParam <- rep(NA, nreps) # Storage vector for the estimate

for (i in 1:nreps) {
  samB <- sample(vec, n, replace = TRUE)
  statParam[i] <- median(samB)
}
```

## Performing a bootstrap estimation





## Performing a bootstrap estimation

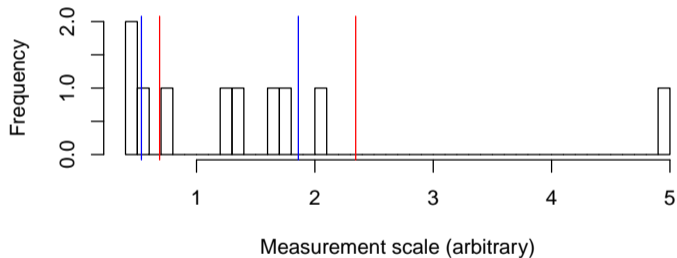
```
bCI <- quantile(statParam, prob = c(2.5, 97.5)/100)
bCI

 2.5% 97.5%
0.534 1.860
```

Compare with the original CI (for the mean):

```
CI(vec)

 2.5% 97.5%
0.688 2.345
```



## Issues with the standard bootstrap

- ▶ The number of replication samples is chosen in order to reach relative stability of the estimate. Some time must be spent on evaluating the adequate number of replications;
- ▶ Standard bootstrap interval estimates are *inaccurate*: they will include the true value less often than the predicted probability;
- ▶ They are *imprecise*: they will include more erroneous values than is desirable (Good, 2005a);
- ▶ Using the R boot library provides CI computation functions with methods to deal with these errors;

## Issues with sample size

- ▶ Issues may arise concerning the applicability of bootstrap methods to small initial sample sizes;
- ▶ As mentioned *supra*, it has been shown that the standard bootstrap generates *inaccurate* and *imprecise* CI end-points;
- ▶ There are several solutions that are available in order to solve this issue;
- ▶ Efron (1987) describes the "non-parametric  $BC_\alpha$ " (*Bias Corrected accelerated*) Confidence Interval (see also DiCiccio & Efron, 1996);
- ▶ See also Ho & Lee (2005) for evaluations of various solutions (among which *parametric* bootstraps);

## The boot library

The boot library is made available by Canty & Ripley (2016). If it is not already installed:

```
install.packages("boot")
```

Then load the library:

```
library(boot)
```

## Bootstrapping with the boot library

- ▶ The bootstrap parameter estimation must be defined in a home-made function;
- ▶ Then the `boot()` function calls this home-made function;

## Bootstrapping with the boot library

### Defining the parameter estimation function

The parameter estimation function takes 2 arguments:

1. The data object;
2. The indexing vector in the data object;

```
SPar <- function(data, index) {  
  res <- median(data[index])  
  return(res)  
}
```

## Bootstrapping with the boot library

It is useful to verify the function application

```
SPar(vec, 1:length(vec))
```

```
[1] 1.3
```

Confirm that it is equal to:

```
median(vec)
```

```
[1] 1.3
```



## Bootstrapping with the boot library

### Performing the bootstrap

```
nreps = 2000
```

```
#bootRes <- boot(vec, statistic = SPar, R = nreps, sim = "ordinary", stype = "i")
```

```
bootRes <- boot(vec, statistic = SPar, R = nreps)
```

```
str(bootRes)
```

```
List of 11
```

```
$ t0      : num 1.3
```

```
$ t       : num [1:2000, 1] 1.628 1.202 1.703 0.534 1.415 ...
```

```
$ R       : num 2000
```

```
$ data    : num [1:10] 0.534 1.202 0.434 4.93 1.39 ...
```

```
$ seed    : int [1:626] 403 84 356515316 1424289583 -339859737 -1122151017 963274428 -22198097 -430865073 -146139
```

```
$ statistic: function (data, index)
```

```
..- attr(*, "srcref")=Class 'srcref' atomic [1:8] 1 9 4 1 9 1 1 4
```

```
.. .. ..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0x7da0930>
```

```
$ sim     : chr "ordinary"
```

```
$ call    : language boot(data = vec, statistic = SPar, R = nreps)
```

```
$ stype   : chr "i"
```

```
$ strata  : num [1:10] 1 1 1 1 1 1 1 1 1 1
```

```
$ weights : num [1:10] 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
```

```
- attr(*, "class")= chr "boot"
```

## Bootstrapping with the boot library

Accessing the information

The `boot()` function returns a list object which contains the following information (among others):

- `t0` Contains the original sample's value for the statistical parameter;
- `t` Contains the bootstrapped values (as many as there are replications);
- `R` The number of replications;
- `data` The original sample's data;

## Bootstrapping with the boot library

- ▶ It is then possible to use the library to compute various (uncorrected and corrected) estimates of a Confidence Interval;

## Bootstrapping with the boot library

### Computing a Confidence Interval

For example,

```
CIIs <- boot.ci(bootRes, conf = 0.95, type = c("norm", "basic", "bca"))  
str(CIIs)
```

List of 6

```
$ R      : int 2000  
$ t0     : num 1.3  
$ call   : language boot.ci(boot.out = bootRes, conf = 0.95, type = c("norm", "basic", "bca"))  
$ normal: num [1, 1:3] 0.95 0.61 2.11  
.. attr(*, "dimnames")=List of 2  
.. ..$ : NULL  
.. ..$ : chr [1:3] "conf" "" ""  
$ basic : num [1, 1:5] 0.95 1950.97 50.03 0.732 2.057  
.. attr(*, "dimnames")=List of 2  
.. ..$ : NULL  
.. ..$ : chr [1:5] "conf" "" "" "" ...  
$ bca   : num [1, 1:5] 0.95 29.15 1919.61 0.487 1.779  
.. attr(*, "dimnames")=List of 2  
.. ..$ : NULL  
.. ..$ : chr [1:5] "conf" "" "" "" ...  
- attr(*, "class")= chr "bootci"
```

## Bootstrapping with the boot library

### Computing a Confidence Interval

For example, Efron (1987)'s "non-parametric  $BC_a$ " Confidence Interval is available:

```
CI$bca[4:5]
```

```
[1] 0.487 1.779
```

Compare with what we found:

```
bCI
```

```
 2.5% 97.5%
```

```
0.534 1.860
```

```
CI(vec)
```

```
 2.5% 97.5%
```

```
0.688 2.345
```

## Bootstrapping a linear regression from real data

- ▶ We will use a subset of a dataset that was generated from a speech production study in which locus equations in Jordanian Arabic were investigated (Abuoudeh & Crouzet, 2014);
- ▶ In order to replicate these analyses, you will need to download the corresponding dataset extract from:
  - ▶ <https://osf.io/j8pys/download>
- ▶ and then load the corresponding file in R:

```
load("locusdata.Rdata")
```

## Bootstrapping a linear regression from real data

Data are usually stored in 2D datasets (dataframes in R);

```
  C V position num locuteur atburst F2ons F2mid F3mid duration length
2422 d a  attaque 623      Mo    1593 1619 1464 2480      81.2 courte
2443 d i  attaque 644      Mo    1759 1922 1964 2791      68.8 courte
2463 d u  attaque 664      Mo    1705 1580 1326 2192      87.5 courte
2489 d u  attaque 691      Mo      NA 1450   NA 2368      75.0 courte
2506 d i  attaque 708      Mo    1724 1754 1852 2721      93.8 courte
2518 d a  attaque 720      Mo    1595 1588 1596 2524      87.5 courte
  intervalsize sex
2422          101  m
2443           93  m
2463          101  m
2489           96  m
2506          114  m
2518           101  m
```

## Bootstrapping a linear regression from real data

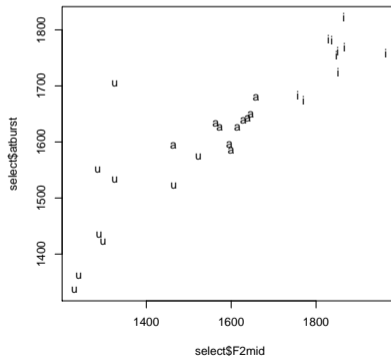
- ▶ These data originate from speech recordings aimed at investigating "locus equations";
- ▶ "locus equations" are linear regressions expressing the relation between the frequencies of  $F_2$  at the burst of a consonant and at the middle of a coarticulated vowel (e.g. in a CV sequence);
- ▶ A linear function of the form  $y = ax + b$  (with  $a$  the slope and  $b$  the intercept) is usually described as an indicator of the degree of coarticulation between the consonant and the vowel;

```
'data.frame': 30 obs. of 13 variables:
 $ C      : Factor w/ 5 levels "b","d","g","k",...: 2 2 2 2 2 2 2 2 2 2 ...
 $ V      : Factor w/ 6 levels "a","a:","i","i:",...: 1 3 5 5 3 1 1 3 5 5 ...
 $ position : Factor w/ 2 levels "attaque","finale": 1 1 1 1 1 1 1 1 1 1 ...
 $ num    : int  623 644 664 691 708 720 761 765 791 802 ...
 $ locuteur : Factor w/ 7 levels "Ah","Al","As",...: 5 5 5 5 5 5 5 5 5 5 ...
 $ atburst : int  1593 1759 1705 NA 1724 1595 1639 1755 1434 1550 ...
 $ F2ons   : int  1619 1922 1580 1450 1754 1588 1609 1879 1550 1660 ...
 $ F2mid   : int  1464 1964 1326 NA 1852 1596 1629 1848 1289 1286 ...
 $ F3mid   : int  2480 2791 2192 2368 2721 2524 2528 2552 2332 2282 ...
 $ duration : num  81.2 68.8 87.5 75 93.8 ...
 $ length  : Factor w/ 2 levels "courte","longue": 1 1 1 1 1 1 1 1 1 1 ...
 $ intervalsize: int  101 93 101 96 114 101 100 108 100 98 ...
 $ sex     : Factor w/ 1 level "m": 1 1 1 1 1 1 1 1 1 1 ...
```



## Bootstrapping a linear regression from real data

Let's take a LE for the voiced alveolar stop /d/ in various vocalic contexts (Jordanian Arabic, short vowels only):

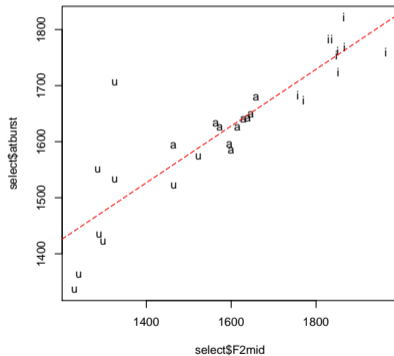


## Bootstrapping a linear regression from real data

### Computing Locus Equations

```
## Compute LE = (simple) linear regression  
model <- lm(select$atburst ~ select$F2mid)
```

## Bootstrapping a linear regression from real data



## Bootstrapping a linear regression from real data

```
## Extract LE parameters
slope <- model$coefficients[2]
intercept <- model$coefficients[1]

slope

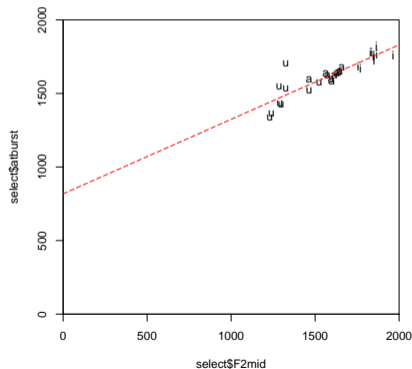
select$F2mid
  0.506

intercept

(Intercept)
  818
```

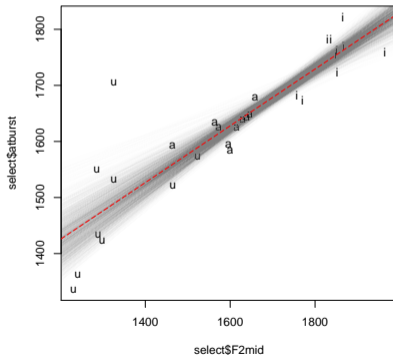
## Bootstrapping a linear regression from real data

$$y = 0.506 \times x + 817.709 \quad (3)$$



## Bootstrapping a linear regression from real data

Only for illustrating the process, one may plot the results of linear regressions over all bootstrap samples:



## Bootstrapping a linear regression from real data

Using the `boot` library

Define the parameter estimation function:

```
bslope <- function(data, index) {  
  slope <- lm(data[index, ]$atburst ~ data[index, ]$F2mid)$coefficients[2]  
  return(slope)  
}  
  
bintercept <- function(data, index) {  
  intercept <- lm(data[index, ]$atburst ~ data[index, ]$F2mid)$coefficients[1]  
  return(intercept)  
}
```

## Bootstrapping a linear regression from real data

Test the function

```
bslope(select, 1:length(select))  
  
data[index, ]$F2mid  
0.353  
  
bintercept(select, 1:length(select))  
  
(Intercept)  
1087
```



## Bootstrapping a linear regression from real data

Perform the bootstrap (separately on the slope / intercept)

```
nreps = 2000  
bootS1 <- boot(select, statistic = bslope, R = nreps)  
bootS1
```

ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = select, statistic = bslope, R = nreps)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	0.506	9.45e-05	0.068

## Bootstrapping a linear regression from real data

Perform the bootstrap (separately on the slope / intercept)

```
bootInt <- boot(select, statistic = bintercept, R = nreps)
bootInt
```

ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = select, statistic = bintercept, R = nreps)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	818	-2.98	113

## Bootstrapping a linear regression from real data

Compute the bootstrapped CIs

```
CISl <- boot.ci(bootSl, conf = 0.95, type = "bca")
CIS$bca[4:5]

[1] 0.487 1.779

CIIInt <- boot.ci(bootInt, conf = 0.95, type = "bca")
CIIInt$bca[4:5]

[1] 642 1118
```

## Bootstrap procedures: There’s more to discover

- ▶ We’ve only adressed parameter estimation (partially);
- ▶ It may also be used for hypothesis testing (comparing means for continuous variables, comparing frequencies for categorical variables) in so-called “permutation tests”;
- ▶ Though it is then still part of the NHST (*Null-Hypothesis Significance Testing*) framework, it may also help (me) understanding “parts of” Bayesian approaches to statistics;

## (incomplete) Suggested readings

- ▶ Good, P. I. (2005c). *Resampling Methods: A Practical Guide to Data Analysis*. Birkhäuser, 3rd ed.
- ▶ Good, P. (2005b). *Permutation, Parametric and Bootstrap Tests of Hypotheses*. Springer Series in Statistics, New-York, USA: Springer-Verlag Inc., 3rd ed.
- ▶ Robert, C., & Casella, G. (2010). *Introducing Monte Carlo Methods with R*. UseR!, New-York, USA: Springer-Verlag.
- ▶ Carpenter, J., & Bithell, J. (2000). Bootstrap confidence intervals: when, which, what? A practical guide for medical statisticians.
- ▶ ...

Concerning the specific issues associated with the computation of Confidence Intervals, several interesting sources are available (DiCiccio & Efron, 1996; Efron, 1987; Ho & Lee, 2005).

## Bibliographie I

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