Resampled inference

Statistical Inference

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The jackknife

- The jackknife is a tool for estimating standard errors and the bias of estimators
- As its name suggests, the jackknife is a small, handy tool; in contrast to the bootstrap, which is then the moral equivalent of a giant workshop full of tools
- Both the jackknife and the bootstrap involve resampling data; that is, repeatedly creating new data sets from the original data

The jackknife

- The jackknife deletes each observation and calculates an estimate based on the remaining $n-1$ of them
- It uses this collection of estimates to do things like estimate the bias and the standard error
- Note that estimating the bias and having a standard error are not needed for things like sample means, which we know are unbiased estimates of population means and what their standard errors are

The jackknife

- We'll consider the jackknife for univariate data
- Let $X_1, \ldots, X_n$ be a collection of data used to estimate a parameter θ
- Let $\hat{\theta}$ be the estimate based on the full data set
- Let $\hat{\theta}_i$ be the estimate of θ obtained by deleting observation i
- Let $\bar{\theta} = \frac{1}{n}\sum_{i=1}^{n} \hat{\theta}_i$

Avg der neu-gesampelten theta^s.

e.g. the mean [but why, when on the last slide he just said that we don't need this for unbiased things like the mean?]

Continued

- Then, the jackknife estimate of the bias is

$$(n-1)\left(\bar{\theta} - \hat{\theta}\right)$$

(how far the average delete-one estimate is from the actual estimate)

- The jackknife estimate of the standard error is

$$\left[\frac{n-1}{n}\sum_{i=1}^{n}(\hat{\theta}_i - \bar{\theta})^2\right]^{1/2}$$

(the deviance of the delete-one estimates from the average delete-one estimate)

Example

We want to estimate the bias and standard error of the median

```
library(UsingR)
data(father.son)
x <- father.son$sheight
n <- length(x)
theta <- median(x)
jk <- sapply(1 : n,
             function(i) median(x[-i])
             )
thetaBar <- mean(jk)
biasEst <- (n - 1) * (thetaBar - theta)
seEst <- sqrt((n - 1) * mean((jk - thetaBar)^2))
```

-> Umsetzung der obigen Formeln in R

Example

```
c(biasEst, seEst)
```

```
[1] 0.0000 0.1014
```

Dasselbe mit der bootstrap library:

```
library(bootstrap)
temp <- jackknife(x, median)
c(temp$jack.bias, temp$jack.se)
```

```
[1] 0.0000 0.1014
```

Example

- Both methods (of course) yield an estimated bias of 0 and a se of 0.1014
- Odd little fact: the jackknife estimate of the bias for the median is always 0 when the number of observations is even
- It has been shown that the jackknife is a linear approximation to the bootstrap
- Generally do not use the jackknife for sample quantiles like the median; as it has been shown to have some poor properties

Pseudo observations

- Another interesting way to think about the jackknife uses pseudo observations
- Let

$$\text{Pseudo Obs} = n\hat{\theta} - (n-1)\hat{\theta}_i$$

- Think of these as ``whatever observation i contributes to the estimate of θ"
- Note when $\hat{\theta}$ is the sample mean, the pseudo observations are the data themselves
- Then the sample standard error of these observations is the previous jackknife estimated standard error.
- The mean of these observations is a bias-corrected estimate of θ

The bootstrap

- The bootstrap is a tremendously useful tool for constructing confidence intervals and calculating standard errors for difficult statistics
- For example, how would one derive a confidence interval for the median?
- The bootstrap procedure follows from the so called bootstrap principle

The bootstrap principle

- Suppose that I have a statistic that estimates some population parameter, but I don't know its sampling distribution
- The bootstrap principle suggests using the distribution defined by the data to approximate its sampling distribution

```
Fuer den Mittelwert wissen wir, dass gilt: m ~ N(mu, sigma^2/sqrt(n)) fuer genuegend grosse n.

Fuer andere Statistiken wissen wir jedoch nicht, wie sie verteilt sind -> Bootstrap.
```

The bootstrap in practice

- In practice, the bootstrap principle is always carried out using simulation
- We will cover only a few aspects of bootstrap resampling
- The general procedure follows by first simulating complete data sets from the observed data with replacement
  - This is approximately drawing from the sampling distribution of that statistic, at least as far as the data is able to approximate the true population distribution
- Calculate the statistic for each simulated data set
- Use the simulated statistics to either define a confidence interval or take the standard deviation to calculate a standard error

Nonparametric bootstrap algorithm example

- Bootstrap procedure for calculating confidence interval for the median from a data set of n observations

  i. Sample n observations with replacement from the observed data resulting in one simulated complete data set

  ii. Take the median of the simulated data set

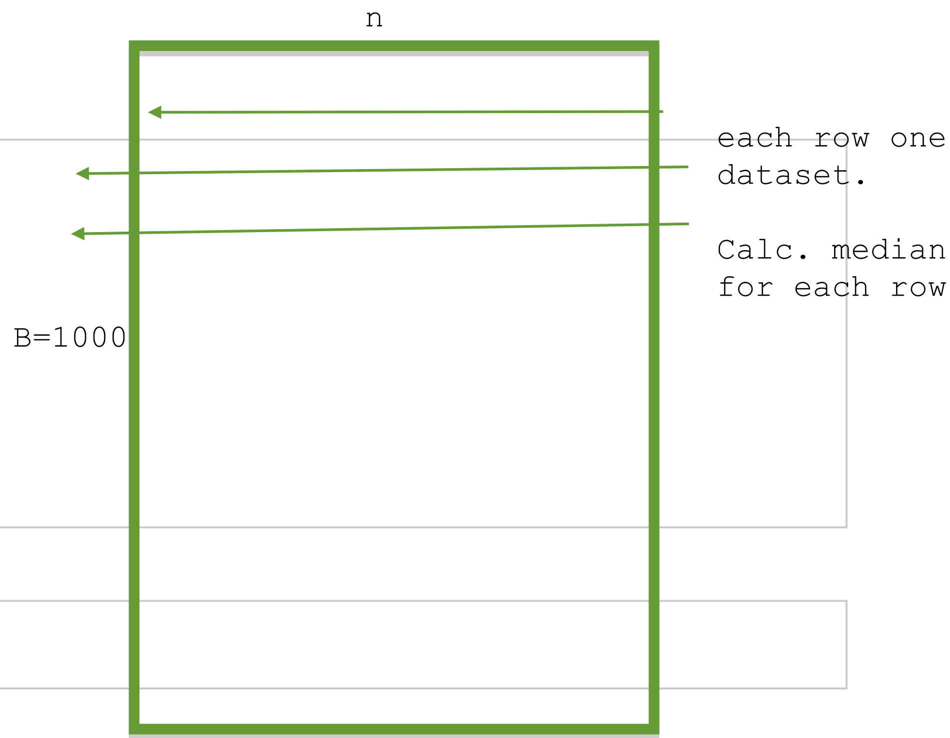
  iii. Repeat these two steps B times, resulting in B simulated medians

  iv. These medians are approximately drawn from the sampling distribution of the median of n observations; therefore we can

    - Draw a histogram of them
    - Calculate their standard deviation to estimate the standard error of the median
    - Take the 2.5^{th} and 97.5^{th} percentiles as a confidence interval for the median

Example code

```
B <- 1000
resamples <- matrix(sample(x,
                           n * B,
                           replace = TRUE),
                    B, n)
medians <- apply(resamples, 1, median)
sd(medians)
```




```
[1] 0.08546
```

```
quantile(medians, c(.025, .975))
```

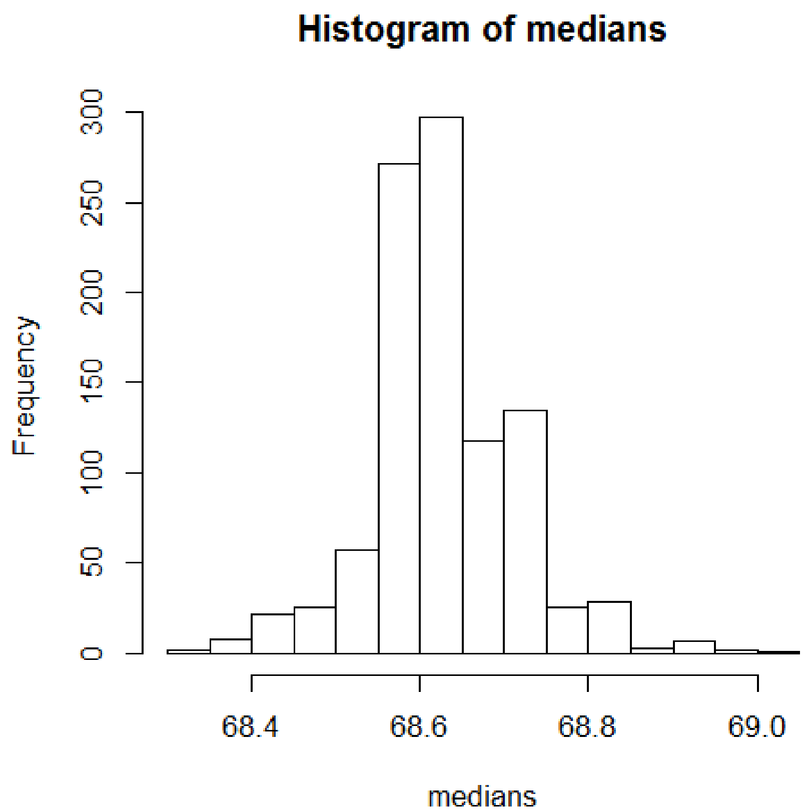
```
 2.5% 97.5%
68.43 68.82
```

Conf.intervall for the (simulated) median

compare with histogram on next slide

Histogram of bootstrap resamples

```
hist(medians)
```



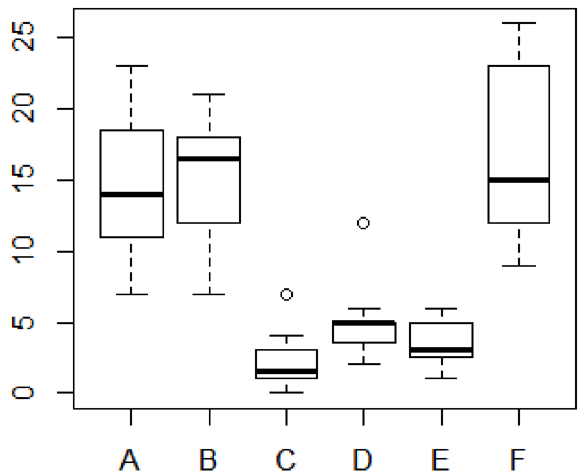
Notes on the bootstrap

- The bootstrap is non-parametric
- Better percentile bootstrap confidence intervals correct for bias
- There are lots of variations on bootstrap procedures; the book "An Introduction to the Bootstrap"" by Efron and Tibshirani is a great place to start for both bootstrap and jackknife information

Group comparisons

- Consider comparing two independent groups.
- Example, comparing sprays B and C

```
data(InsectSprays)
boxplot(count ~ spray, data = InsectSprays)
```



Permutation tests

- Consider the null hypothesis that the distribution of the observations from each group is the same
- Then, the group labels are irrelevant `-> die Sprays wirken alle gleich, heissen nur anders`
- We then discard the group levels and permute the combined data `-> alle gleich, also koennen wir alle zusammenwerfen (combine), dann kombinieren.`
- Split the permuted data into two groups with n_A and n_B observations (say by always treating the first n_A observations as the first group)
- Evaluate the probability of getting a statistic as large or large than the one observed
- An example statistic would be the difference in the averages between the two groups; one could also use a t-statistic

Variations on permutation testing

DATA TYPE	STATISTIC	TEST NAME
Ranks	rank sum	rank sum test
Binary	hypergeometric prob	Fisher's exact test
Raw data		ordinary permutation test

- Also, so-called randomization tests are exactly permutation tests, with a different motivation.
- For matched data, one can randomize the signs
  - For ranks, this results in the signed rank test
- Permutation strategies work for regression as well
  - Permuting a regressor of interest
- Permutation tests work very well in multivariate settings

```
H0: group labels are irrelevant
-> wir koennen permutieren und das macht
keinen Unterschied.
```

```
Matched data:

Group a        Group b     a-b
------------------------------
obs1           obs1        -
obs2           obs2        +
…
obsn           obsn        +
```

Permutation test for pesticide data

```
subdata <- InsectSprays[InsectSprays$spray %in% c("B", "C"),]   -> to test whether spray B and C
                                                                  are different.
y <- subdata$count  Num dead insects
group <- as.character(subdata$spray)
testStat <- function(w, g) mean(w[g == "B"]) - mean(w[g == "C"])   Diff zwischen mean B-group and
                                                                   C-group in der outcome var (count)
observedStat <- testStat(y, group)
permutations <- sapply(1 : 10000, function(i) testStat(y, sample(group)))
observedStat                                                   Group-Variable permutieren
```

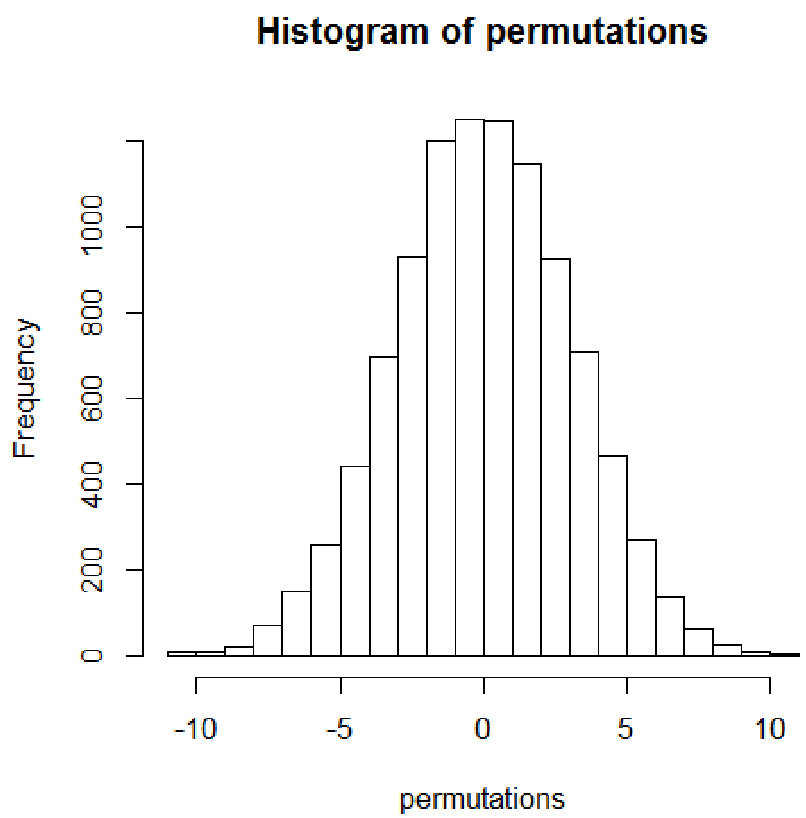
```
[1] 13.25        Tatsaechlicher Unterschied in unseren Daten (observed).
```

```
mean(permutations > observedStat)
```

```
[1] 0            In den permutierten Daten kommt so ein grosser Unterschied gar nie Zustande!
```

Histogram of permutations

Immer das Histogram zeichnen
bei Bootstrap!



ObservedStat: 13.25