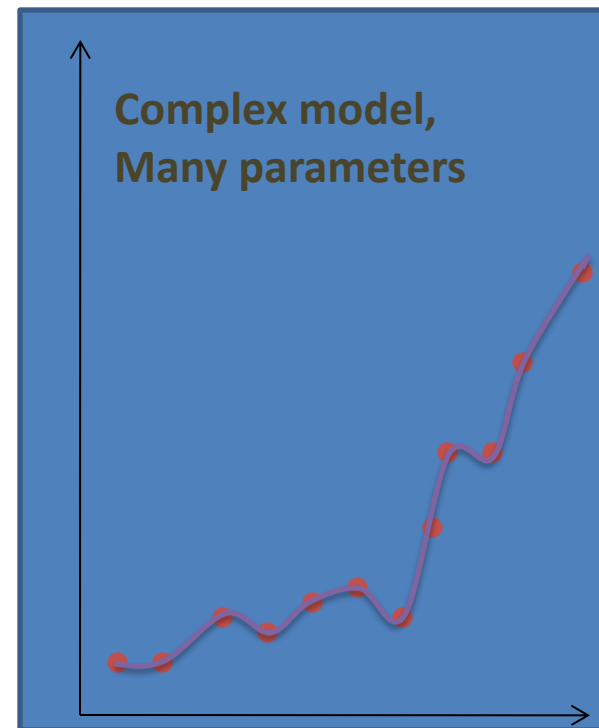
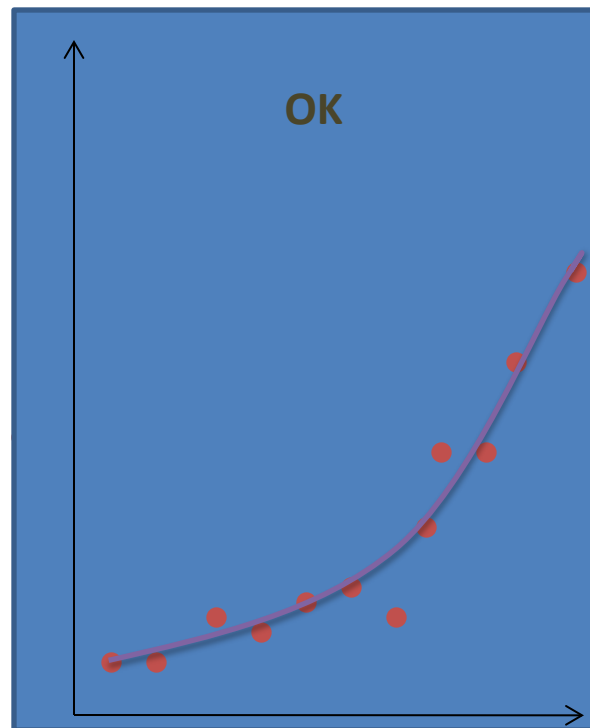
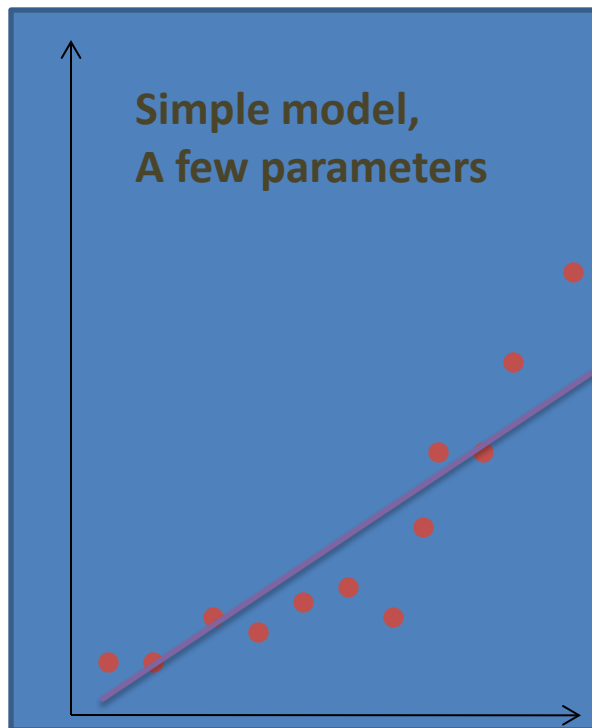
The background is a solid blue color with a subtle, abstract pattern. On the right side, there are several curved lines of binary code (0s and 1s) that appear to be receding into the distance, creating a sense of depth. On the left side, there is a dark, semi-transparent sphere that also seems to be part of the same receding perspective.

Lecture 5: Numerical model selection and hypothesis testing

Model selection

Overfitting



The background of the slide features a blue gradient with a pattern of binary code (0s and 1s) and a magnifying glass icon positioned over the text.

Model selection

- Necessary tools for selection:
 - Comparison between models
 - Cross-validation
 - Hypothesis testing
 - Uncertainty estimation
 - Confidence intervals

Hypothesis testing

- Given data X
- Null-hypothesis and alternative hypothesis
- Test statistics
 - Some function of a sample
 - Various test statistics have various efficiency (power)
- Distribution of test statistics under H_0
- Decision making: unusual values of test statistics $\rightarrow H_0$ is rejected.
 - Two-sided and one-sided tests

Hypothesis testing

- Data

```
> x
[1] 6.204793 5.868617 5.021237 3.179392 3.577037 4.862277 5.642055 4.007396
[9] 5.540461 5.596270
```

- Hypotheses:

- $H_0: \mu = 4, X \sim N(\mu, \sigma^2)$

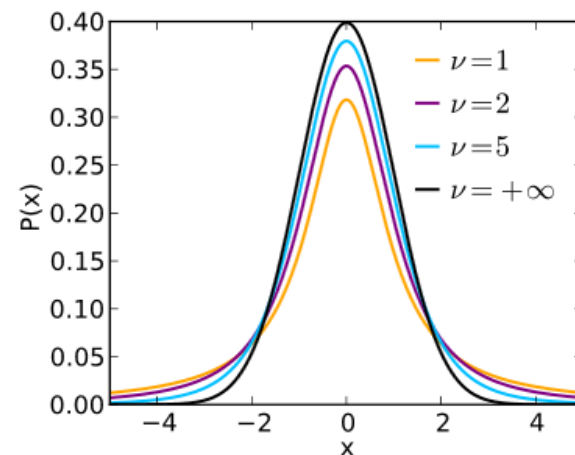
- $H_A: \mu \neq 4, X \sim N(\mu, \sigma^2)$

- Test statistics

- $t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{n}}} \in t(n - 1)$

- Evaluate t for our sample $\rightarrow t_0$

- Check if t_0 is in the critical area \rightarrow reject H_0



Hypothesis testing

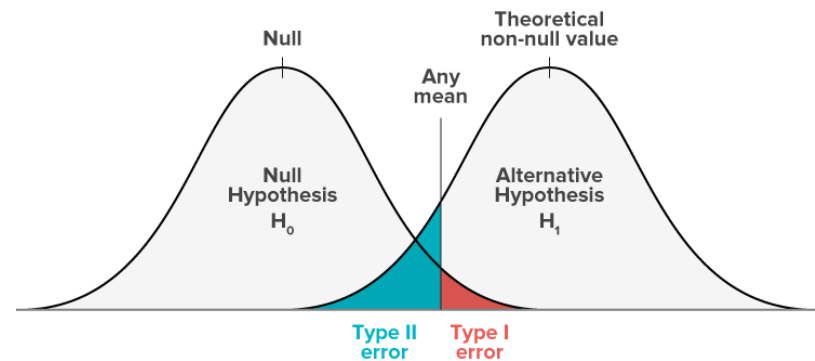
- Monte Carlo Hypothesis testing
 - Use any test statistics
 - We do not need to know how it is distributed
- Hypotheses:
 - $H_0: \mu = 4, X \sim N(\mu, \sigma^2)$
 - $H_A: \mu \neq 4, X \sim N(\mu, \sigma^2)$
- Assume $t = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{n}}}$
 1. For $i = 1$ to B
 1. Generate from $Y \sim N(\mu, \sigma^2) \rightarrow$ get Y_1, \dots, Y_n
 2. Compute t_i from Y
 2. Use $t_1, \dots, t_B \rightarrow$ build a histogram.
 3. Use the histogram as the distribution of t under H_0

Hypothesis testing

- How good is the test statistics? Power!
- $Power = 1 - Type\ II\ error$

- How to compute Power?

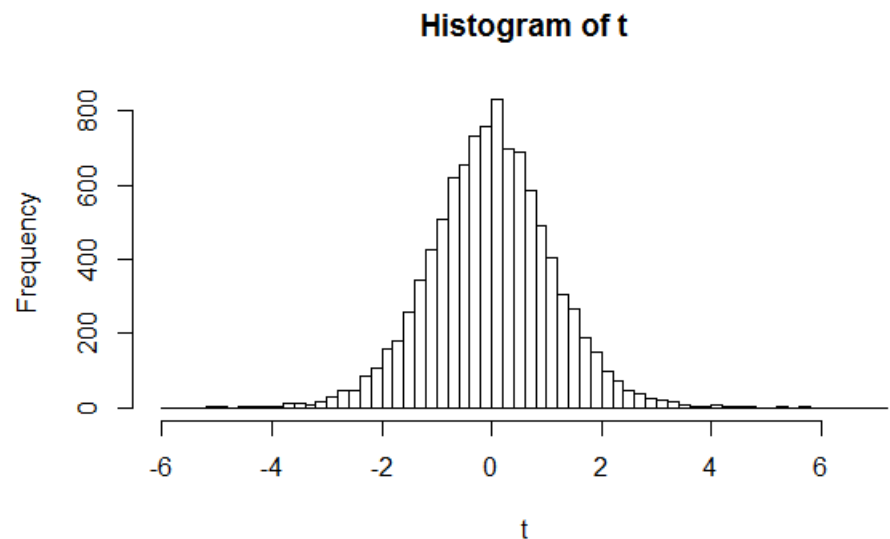
- Generate data samples that satisfy H_a
- Compute percent of correct rejections



Source: grasshopper.com

Hypothesis testing

```
s=var(X)
B=10000
n=10
t=numeric(B)
for (i in 1:B) {
  Y=rnorm(10,4,s)
  t[i]=(mean(Y)-4)/(sd(Y)/sqrt(10))
}
hist(t,50)
```



What to do if we don't know the distribution of the data? →
permutation tests or bootstrap tests!

Permutation tests

- Introduced by Fisher 1930's → not used in practice because computationally expensive
- Applicable to certain types of hypothesis testing
 - Equality of models, populations,...
- No assumptions on distributions
- **Two-sample problem:**
 - Two samples coming from distributions F and G
 - $H_0: F = G$
 - $H_a: F \neq G$

Permutation tests

- Example: mouse data

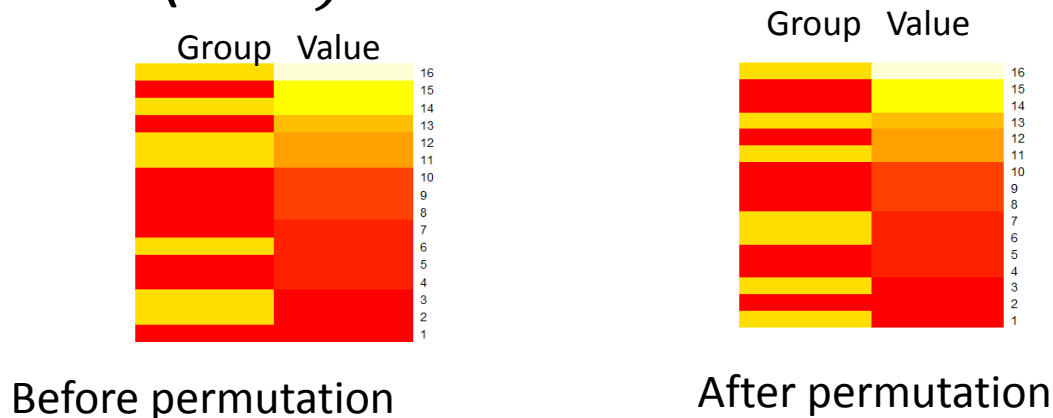
- Control group
- Treatment group
 - Group variable g
 - Values variable v

```
> t(mouse)
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13]
Group "y"  "z"  "z"  "y"  "y"  "z"  "y"  "y"  "y"  "y"  "x"  "x"  "y"
Value " 10" " 16" " 23" " 27" " 31" " 38" " 40" " 46" " 50" " 52" " 94" " 99" "104"
      [,14] [,15] [,16]
Group "z"  "y"  "z"
Value "141" "146" "197"
```

- Does the value differ in control and treatment groups?

Permutation tests

- **Main idea:** if $F = G \rightarrow$ group label does not matter \rightarrow we can permute those and still get a valid sample from F (or G)



- Suggest test statistics $T = S(g, v)$
 - For example $T = \text{mean}(v_i | g_i = z) - \text{mean}(v_i | g_i = y)$

Permutation tests

Algorithm

1. Create permutations g_1^*, \dots, g_B of group variable
2. Evaluate test statistics on each permutation
 - All permutations are too many? \rightarrow Sample n elements **without replacement** from g
3. Evaluate p-value $\hat{p} = \#\{T(b) \geq T\}/B$
 - In two-sided test, $\hat{p} = \#\{|T(b)| \geq |T|\}/B$

Permutation tests

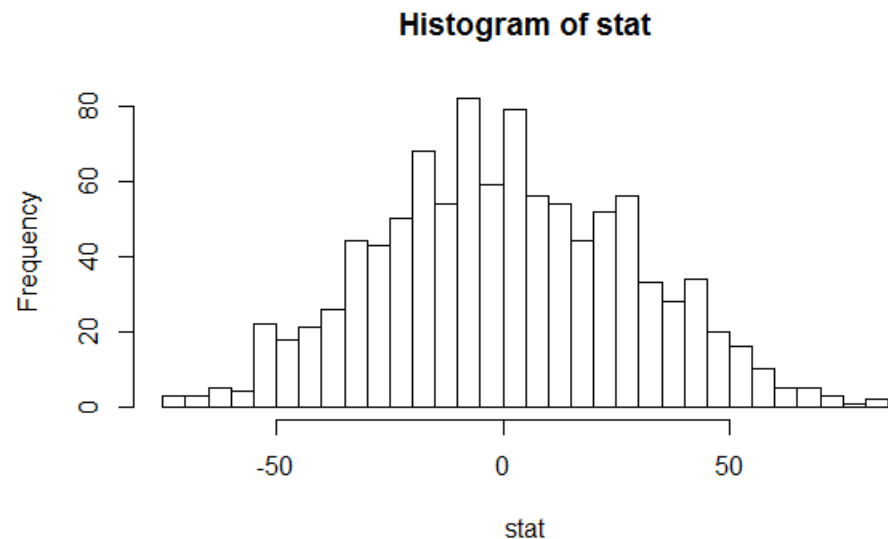
- Code

```
B=1000
stat=numeric(B)
n=dim(mouse)[1]
for(b in 1:B){
  Gb=sample(mouse$Group, n)
  stat[b]=mean(mouse$Value[Gb=='z'])-mean(
(mouse$Value[Gb=='y']))
}
hist(stat,50)

stat0=mean(mouse$Value[mouse$Group=='z'])-
mean(mean(mouse$Value[mouse$Group=='y']))

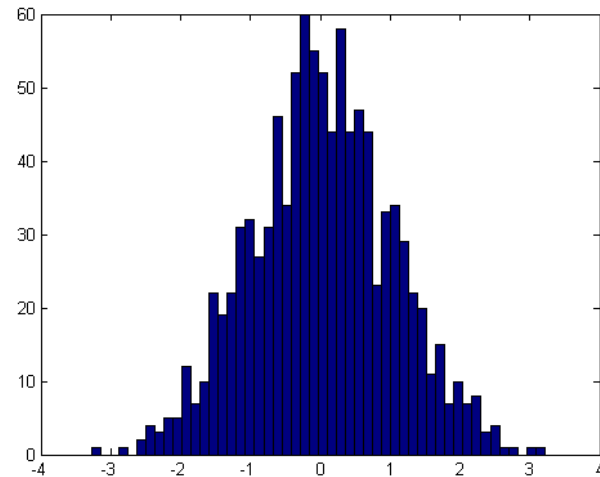
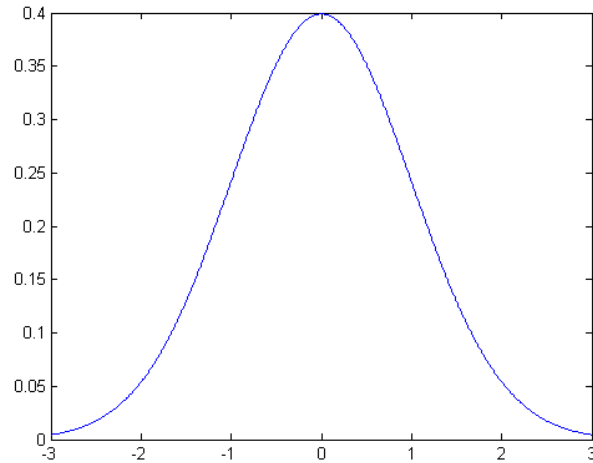
mean(stat>stat0)
```

Do we reject null hypothesis?



```
> stat0
[1] 30.63492
> mean(stat>stat0)
[1] 0.154
> |
```


The bootstrap: general principle



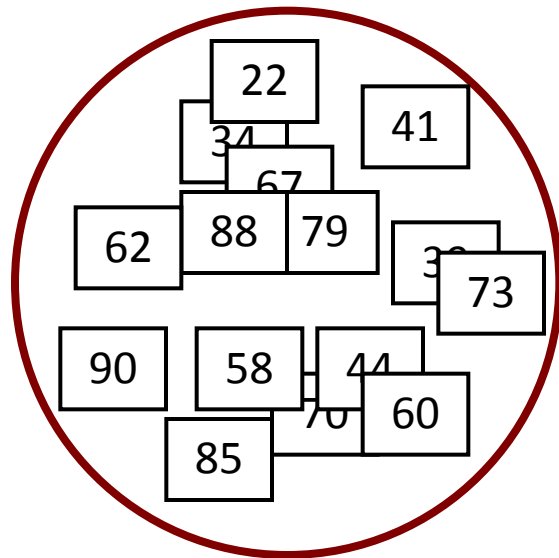
We want to determine uncertainty of $T(D)$

1. Generate many different D_i from their distribution
2. Use histogram of $T(D_i)$ to determine confidence limits → unfortunately can not be done (distr of D is *often unknown*)

Instead: Generate many different D_i^* from the empirical distribution (histogram)

Nonparametric bootstrap

Observed data

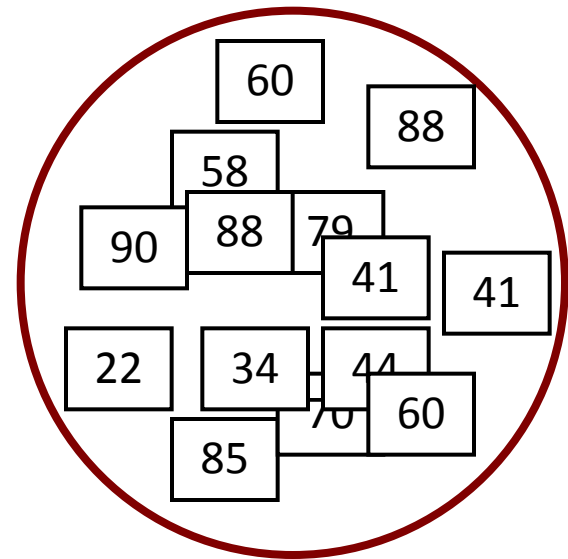


\bar{x}

Sampling with
replacement



Resampled data



$\bar{x}_1^*, \bar{x}_2^*, \dots, \bar{x}_N^*$

Nonparametric bootstrap

Given estimator $\hat{w} = T(D)$

Assume $X \sim F(X, w)$, F and w are unknown

1. Estimate \hat{w} from data $\mathbf{D}=(X_1, \dots, X_n)$
2. Generate $\mathbf{D}_1=(X_1^*, \dots, X_n^*)$ by sampling with replacement
3. Repeat step 2 B times
4. The distribution of w is given by $T(D_1), \dots, T(D_B)$

Nonparametric bootstrap can be applied to any deterministic estimator, distribution-free

Parametric bootstrap

Given estimator $\hat{w} = T(D)$

Assume $X \sim F(X, w)$, F is known and w is unknown

1. Estimate \hat{w} from data $\mathbf{D}=(X_1, \dots, X_n)$
2. Generate $\mathbf{D}_1=(X_1^*, \dots, X_n^*)$ by generating from $F(X, \hat{w})$
3. Repeat step 2 B times
4. The distribution of θ is given by $T(D_1), \dots, T(D_B)$

Parametric bootstrap is **more** precise if the distribution form is correct

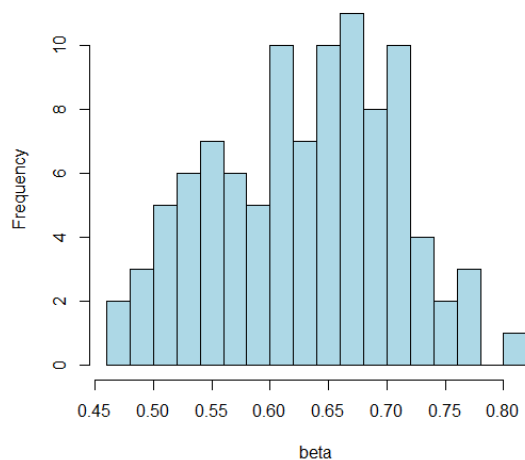
Example

- Distribution of regression coefficient

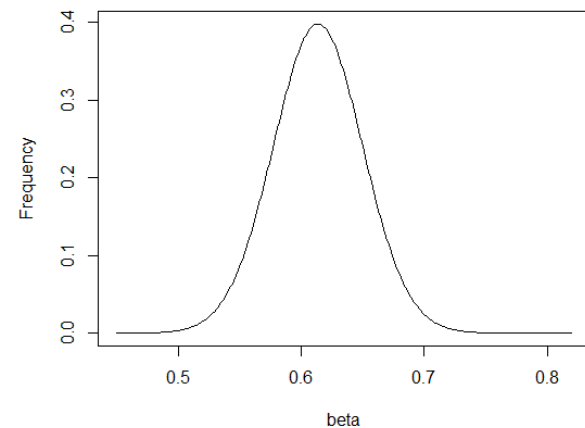
$$\hat{\beta} = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^n (x_i - \bar{x})^2}$$

```
stat1<-function(data,n){  
  data1=data[n,];  
  res<-lm(Price~Area, data1)  
  ret=res$coefficients[2]  
  return(ret)  
}  
res=boot(data,stat1,R=100)  
hist(res$t,20)
```

Distribution of beta by bootstrap



Distribution of beta, theoretical (normal error)



Bootstrap confidence intervals

- obtained from the distribution given by the bootstrap
 - **R**: `boot.ci()` for one variable, `envelope()` for many variables

```
boot.ci(res)
```

```
> boot.ci(res)
BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
Based on 1000 bootstrap replicates

CALL :
boot.ci(boot.out = res)

Intervals :
Level      Normal              Basic
95%   ( 0.4569,  0.7595 )   ( 0.4665,  0.7631 )

Level      Percentile          BCa
95%   ( 0.4642,  0.7609 )   ( 0.4289,  0.7346 )
Calculations and Intervals on Original Scale
```

Uncertainty estimation

1. Get D_1, \dots, D_B by bootstrap
 2. Use $T(D_1), \dots, T(D_B)$ to estimate the uncertainty
 - Bootstrap percentile
 - Bootstrap-t
 - Bootstrap Bca
 - ...
- Bootstrap works for all distribution types but approximate
 - Can be bad accuracy for small data sets $n < 40$ (empirical is far from true)
 - Parametric bootstrap works even for small samples

Bootstrap confidence intervals

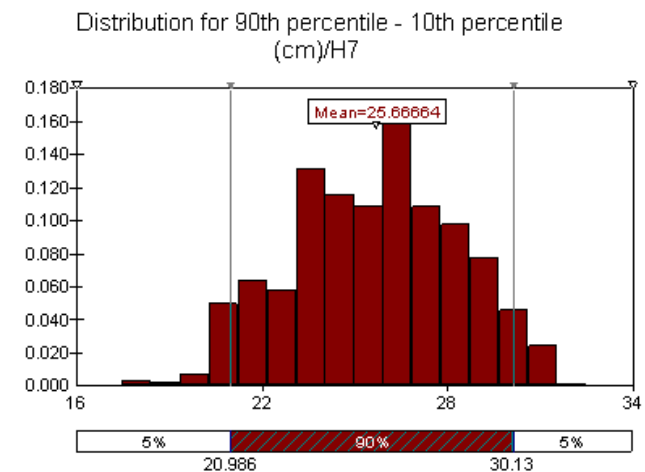
- To estimate $100(1-\alpha)$ confidence interval for w

Bootstrap percentile method

- Using bootstrap, compute $T(D_1), \dots, T(D_B)$, sort in ascending order, get $w_1 \dots w_B$
- Define $A_1 = \text{ceil}(B \alpha/2)$, $A_2 = \text{floor}(B - B \alpha/2)$
- Confidence interval is given by

$$(w_{A_1}, w_{A_2})$$

Look at the plot...



Bootstrap confidence intervals

Bootstrap-t method

- Done by analogy with t test
 1. Using bootstrap, compute $T^{*1}=T(\mathbf{D}_1)\dots T^{*B}=T(\mathbf{D}_B)$
 2. Compute
$$t_j = \frac{T^{*j} - T(\mathbf{D})}{se(T^{*j})}, j = 1\dots B$$
 3. Define $A_1=\text{ceil}(B \alpha/2)$, $A_2=\text{floor}(B-B \alpha/2)$
 4. Confidence interval is $(T(D) - se(T) \cdot t_{A_2}, T(D) - se(T) \cdot t_{A_1})$

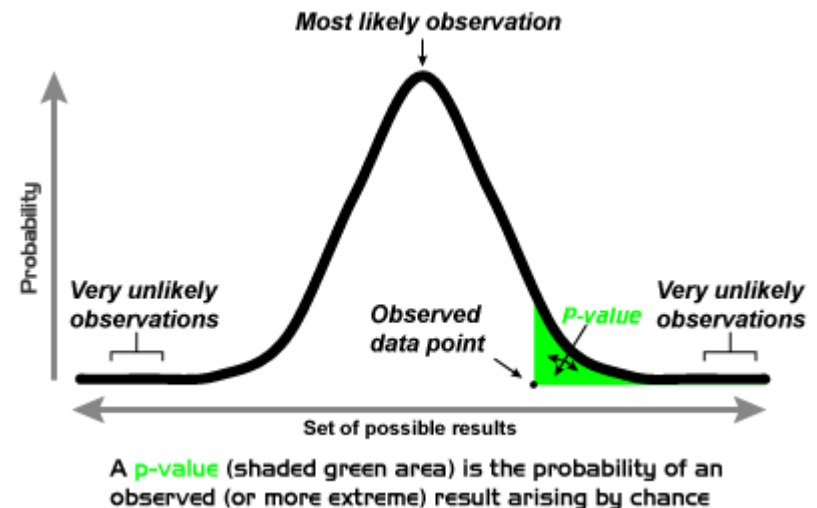
Bootstrap confidence intervals

Comments

- se is square root of estimated variance
- Estimation $se(T^{*j})$ typically requires second-level bootstrap -> bootstrap-t is computationally intensive
- Bootstrap-t is more accurate than percentile (coverage error)
- Bootstrap BC_a is a more advanced bootstrap CI method

Bootstrap hypothesis testing

- Bootstrap distribution
 $T^{*1}=T(\mathbf{D}_1) \dots T^{*B}=T(\mathbf{D}_B)$
- Assume $H_0: T = T_0$
 - For ex $\beta = 0$ in regression
- Compute P-value by checking the tail corresponding T_0
- Much more complicated bootstrap hypothesis testing methods exist



Source: Wikipedia

Bootstrap tests vs permutation tests

- Permutation tests do sampling **without** replacement, bootstrap does sampling **with** replacement
- Permutation p-value is exact if all permutations considered, bootstrap is always approximate (becomes more exact as $n \rightarrow \infty$)
- Bootstrap histograms centered around T , permutation histograms around 0
- Bootstrap tests cover larger class of problems
- $sample_variance(T^{*b})$ has no meaning for permutation tests, but for bootstrap it is an estimate of variance of T .
- Both methods require no distributional assumptions
- For permutation test, the accuracy of p-value depends on B
 - 10% accuracy achieved for $p=0.05$ if $B \approx 2000$

Permutation tests for model selection

- Given $X_0 = (X_a, X_b, Y)$, model M
- Test
 - H_0 : variables X_b should not be in M
 - H_a : all variables are significant
- Given test statistics $T(M)$
- Algorithm
 1. Get \hat{X} by permuting columns X_a and fit model $Y = M(\hat{X}, X_b)$
 2. Compute test statistics for this model
 3. Repeat steps 1-2 B times and get a distribution of T
 4. Use it and $T(M(X_0))$ to compute p-value

Bootstrap bias corrections

- Theory shows

$$T_1 = 2T(P_n) - E\left(T(P_n^{(1)}) \mid P_n\right)$$

- The last term is computed by
 1. Using observation set $\mathbf{D}=(X_1,...X_n)$, sample with replacement and get bootstrap sample $\mathbf{D}_1=(X^*_1,...X^*_n)$,
 2. Repeat step 1 B times
 3. Take the mean of $T(\mathbf{D}_1)...\ T(\mathbf{D}_B)$
- The first term is the $2T(\mathbf{D})$

Bootstrap variance estimation

- Using bootstrap, compute $T^{*1}=T(\mathbf{D}_1)\dots T^{*m}=T(\mathbf{D}_B)$

$$\hat{V}(T) = \frac{1}{m-1} \sum (T^{*j} - \bar{T}^*)^2$$

Jackknife methods

- **Idea:** similar to CV, but used in statistical inference
 - Bias estimation
 - Variance estimation

“Jackknife methods make use of systematic partitions of a dataset to estimate properties of an estimator computed from the full sample”

- Suppose, we are given a random sample $\mathbf{Y}=(Y_1,\dots,Y_n)$ and some estimator $T(\mathbf{Y})$

Jackknife methods

First-order jackknife

1. Obtain $\mathbf{Y}_{(-j)}$ by dropping group of observations j from \mathbf{Y}
2. For each j , compute $T_{(-j)} = T(\mathbf{Y}_{(-j)})$
3. Compute pseudovalues and $J(T)$, called *jackknifed* T :

$$\bar{T}_{(\bullet)} = \frac{1}{r} \sum_{j=1}^r T_{(-j)}$$

$$T_j^* = rT - (r-1)T_{(-j)}$$

$$J(T) = \frac{1}{r} \sum_{j=1}^r T_j^* = \bar{T}^*$$

- Equivalently, $J(T) = rT - (r-1)\bar{T}_{(\bullet)}$

Jackknife variance estimate

- We can use $T_{(-j)}$ or pseudovalues as estimates of T for different samples (both give equivalent expression).
- Variance becomes

$$\widehat{V(T)}_J = \frac{\sum_{j=1}^r (T_j^* - J(T))^2}{r(r-1)}$$

Sometimes, one takes $\frac{\sum_{j=1}^r (T_j^* - T)^2}{r(r-1)}$

!The variance is often overestimated

Jackknife bias correction

First-order jackknife

- The bias reduced to order n^{-1} (we take $r=n$)

$$\text{Bias}(T) = E(T) - \theta = \sum_{q=1}^{\infty} \frac{a_q}{n^q}$$

$$\text{Bias}(J(T)) = E(J(T)) - \theta$$

$$\begin{aligned} &= n(E(T) - \theta) - \frac{n-1}{n} \sum_{j=1}^n E(T_{(-j)} - \theta) \\ &= n \sum_{q=1}^{\infty} \frac{a_q}{n^q} - (n-1) \left(\sum_{q=1}^{\infty} \frac{a_q}{(n-1)^q} \right) \\ &= a_2 \left(\frac{1}{n} - \frac{1}{n-1} \right) + a_3 \left(\frac{1}{n^2} - \frac{1}{(n-1)^2} \right) + \dots \\ &= -a_2 \left(\frac{1}{n(n-1)} \right) + a_3 \left(\frac{1}{n^2} - \frac{1}{(n-1)^2} \right) + \dots \end{aligned}$$

Jackknife estimation of bias

- We see that

$$E(J(T)) - \theta = E(T) - \theta + (n - 1) \left(E(T) - \frac{1}{n} \sum_{j=1}^n E(T_{(-j)}) \right)$$

- Hence, bias is $B_J = (n - 1) (\bar{T}_{(\bullet)} - T)$

Higher-order jackknife

The order of the bias can be further reduced

- Second-order jackknife

$$J^2(T) = \frac{n^2 J(T) - (n-1)^2 \sum_{j=1}^n J(T)_{(-j)} / n}{n^2 - (n-1)^2}$$

- Higher order jackknives –combining jackknives of lower orders:

$$T_w = \frac{T_1 - wT_2}{1 - w}$$

Higher-order jackknife

Comments

- High order jackknives reduce the bias but they increase the variance
- Delete-1 jackknife is not always appropriate (median). Use delete-k