The Bootstrap[1]

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Overview

Sampling distributions

- Let $\mathbf{x} = (X_1, \ldots, X_n)$ be a random sample from some distribution F.
- $t = t(\mathbf{x})$ is a statistic (could be a vector of statistics).
- Need to know about the distribution of t.
- Sometimes it's not easy, even asymptotically.

Sampling distribution of t: The elementary version

For example $t = \overline{X}$

- Sample repeatedly from this population (pretend).
- For each sample, calculate t.
- Make a relative frequency histogram of the t values you observe.
- As the number of samples becomes very large, the histogram approximates the distribution of t.

Bootstrap?

Pull yourself up by your bootstraps

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The (statistical) Bootstrap

Bradley Efron, 1979

- Select a random sample from the population.
- If the sample size is large, the sample is similar to the population.
- Sample repeatedly *from the sample.* This is called *resampling*.
- Sample from the sample? Think of putting the sample data values in a jar . . .
- Calculate the statistic for every bootstrap sample.
- A histogram of the resulting values approximates the shape of the sampling distribution of the statistic.

Notation

- Let $\mathbf{x} = (X_1, \ldots, X_n)$ be a random sample from some distribution F.
- $t = t(\mathbf{x})$ is a statistic (could be a vector of statistics).
- Form a "bootstrap sample" $\mathbf{x}^*$ by sampling n values from $\mathbf{x}$ *with replacement*.
- Repeat this process B times, obtaining $\mathbf{x}_1^*, \ldots, \mathbf{x}_B^*$.
- Calculate the statistic for each bootstrap sample, obtaining $t_1^*, \ldots, t_B^*$.
- Relative frequencies of $t_1^*, \ldots, t_B^*$ approximate the sampling distribution of t.

Why does it work?

Empirical distribution function

$$\widehat{F}(x) = \frac{1}{n}\sum_{i=1}^{n} I\{X_i \leq x\} \xrightarrow{p} E(I\{X_i \leq x\}) = F(x)$$

- Resampling from $\mathbf{x}$ with replacement is the same as simulating a random variable whose distribution is the empirical distribution function $\widehat{F}(x)$.
- Suppose the distribution function of t is a nice smooth function of F.
- Then as $n \to \infty$ and $B \to \infty$, bootstrap sample moments and quantiles of $t_1^*, \ldots, t_B^*$ converge to the corresponding moments and quantiles of the unknown distribution of t.
- If the distribution of $\mathbf{x}$ is discrete and supported on a finite number of points, the technical issues are minor.

Main Application for This Course

Skipping quantile bootstrap confidence intervals and many other interesting things

- $t = \widehat{\boldsymbol{\theta}}_n$.
- Even when the data are non-normal and the model is wrong, $\widehat{\boldsymbol{\theta}}_n$ is asymptotically normal and converges to a definite target, provided the MLE is unique.
- For the models that appear in this class,
- If the model is correct (except for the distribution) and the parameters are identifiable, $\widehat{\boldsymbol{\theta}}_n$ is consistent as well as asymptotically normal.
- The only problem is that the variances and covariances in $\mathbf{V}_n = \frac{1}{n}\mathcal{I}(\boldsymbol{\theta})$ may be wrong.
- Need a different asymptotic covariance matrix (sometimes).

Bootstrap the covariance matrix of $\widehat{\boldsymbol{\theta}}_n$

- Asymptotic distribution is multivariate normal
- Centered on the right thing.
- The only other thing we need to know about the distribution of $\widehat{\boldsymbol{\theta}}_n$ is its covariance matrix.

Procedure

- The data ‘jar” contains not balls with single numbers, but strings of beads with a vector of observed values $\mathbf{d}_i$ written on them. Data values for a case stay together.
- Select n strings of beads with replacement, obtaining $\mathbf{x}_1^*$. .
- Do this B times. Now you have $\mathbf{x}_1^*, \ldots, \mathbf{x}_B^*$.
- Calculate $\widehat{\boldsymbol{\theta}}_1^*, \ldots \widehat{\boldsymbol{\theta}}_B^*$.
- You have a lot of information about the multivariate distribution of $\widehat{\boldsymbol{\theta}}_n$, but all you care about is the covariance matrix.
- If there are m parameters, you have a $B \times m$ matrix of numbers, with one column for each parameter in the model.
- Calculate the sample covariance matrix for the data (using `var`).
- This is the new $\widehat{\mathbf{V}}_n$.
- Use it for Wald tests and z-tests.
- All this applies to MOM as well as MLE.

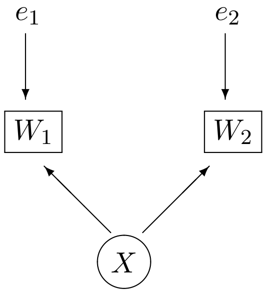
Sometimes it's Unnecessary

- Linear structural equation models have a lot of robustness to the multivariate normal assumption.
- When it fails, it's usually for data with "excess kurtosis" (heavy tails).
- And even then, not necessarily for all parameters.
- Trouble arises when the variance of the sample variance is involved.

$$Var\left(\frac{1}{n}\sum_{i=1}^{n}(x_i-\overline{x}_n)^2\right)$$

  Fourth moments of the normal distribution will be too small, leading to an under-estimate.
- For the double measurement design, standard errors of the regression coefficients are robust to normality.

Example: Double measurement


$$\begin{tikzcd} e_1 \arrow[d] & & e_2 \arrow[d] \\ \boxed{W_1} & & \boxed{W_2} \\ & X \arrow[ul] \arrow[ur] & \end{tikzcd}$$

$$\begin{aligned} W_1 &= X + e_1 \\ W_2 &= X + e_2, \end{aligned}$$

where $E(X) = \mu$, $Var(X) = \phi$, $E(e_1) = E(e_2) = 0$, $Var(e_1) = \omega_1$, $Var(e_2) = \omega_2$, and X, e_1 and e_2 are all independent.

Equivalent measurements?

$$\begin{tikzcd}
e_1 \arrow[d] & & e_2 \arrow[d] \\
\boxed{W_1} & & \boxed{W_2} \\
& X \arrow[ul] \arrow[ur] &
\end{tikzcd}$$

If $\omega_1 = Var(e_1)$ and $\omega_2 = Var(e_2)$ are equal, W_1 and W_2 are *equivalent measurements*, and $Corr(W_1, W_2) = \frac{\phi}{\phi+\omega}$, the reliability.

Simulate from the t Distribution: Heavy-tailed

$Var(t) = \nu/(\nu-2)$, so with $\nu = 3$, $Var(t) = 3$

```
> rm(list=ls())
> # Parameter values and sample size
> phi = 7; omega1 = 3; omega2 = 3
> rel1 = round(phi/(phi+omega1),3); rel2 = round(phi/(phi+omega2),3)
> c(rel1,rel2) # Reliabilities
[1] 0.7 0.7
> n = 1500
> # Simulate from t distribution -- heavy tails
> # Var(t) = nu/(nu-2)
> set.seed(9999)
> x = sqrt(phi) * rt(n,3)/sqrt(3)
> e1 = sqrt(omega1) * rt(n,3)/sqrt(3); e2 = sqrt(omega2) * rt(n,3)/sqrt(3)
> w1 = x + e1; w2 = x + e2
> ww = cbind(w1,w2)
> vcovW = var(ww) * (n-1)/n; vcovW # Divide by n to get MLEs
          w1       w2
w1 10.120663 6.727376
w2  6.727376 9.347715
```

Normal Theory Fit with `lavaan`

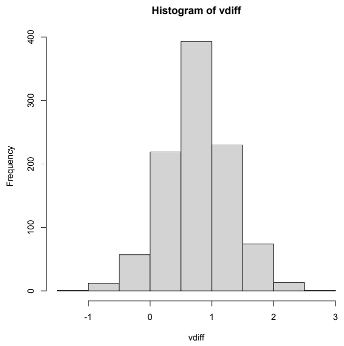
```
> # install.packages("lavaan", dependencies = TRUE) # Only need to do this once
> library(lavaan)
This is lavaan 0.6-11
lavaan is FREE software! Please report any bugs.
> # Normal theory with lavaan
> mod =   "x =~ 1.0*w1 + 1.0*w2
+          x ~~ phi*x; w1 ~~ omega1*w1; w2 ~~ omega2*w2
+          vardiff := omega1-omega2
+          "
> fit = lavaan(mod, data=ww)
> # summary(fit)
> parameterEstimates(fit)
      lhs op           rhs   label   est    se      z pvalue ci.lower ci.upper
1       x =~            w1         1.000 0.000     NA     NA    1.000    1.000
2       x =~            w2         1.000 0.000     NA     NA    1.000    1.000
3       x ~~             x     phi 6.727 0.305 22.031  0.000    6.129    7.326
4      w1 ~~            w1  omega1 3.393 0.220 15.448  0.000    2.963    3.824
5      w2 ~~            w2  omega2 2.620 0.205 12.778  0.000    2.218    3.022
6 vardiff := omega1-omega2 vardiff 0.773 0.364  2.124  0.034    0.060    1.486
> thetahat = coef(fit); thetahat
   phi omega1 omega2
 6.727  3.393  2.620
```

Bootstrap

```
> # Bootstrap the "hard" way
> # n = dim(ww)[1] is not needed
> jar = 1:n; B = 1000
> tstar = matrix(NA,B,3) # Rows will hold theta-hat values
> colnames(tstar) = names(coef(fit))
> for(j in 1:B)
+     {
+     rowz = sample(jar,size=n,replace=TRUE)
+     xstar = ww[rowz,]
+     fitstar = lavaan(mod, data=xstar)
+     tstar[j,] = coef(fitstar)
+     } # Next bootstrap sample
> head(tstar)
          phi   omega1   omega2
[1,] 6.969279 4.360700 2.182922
[2,] 6.324895 4.075226 2.259924
[3,] 6.607809 3.034017 2.047602
[4,] 6.931564 3.314822 3.254835
[5,] 6.157233 3.992400 2.434781
[6,] 8.465813 3.019230 2.719412
```

Sampling Distribution of $\widehat{\omega}_1 - \widehat{\omega}_2$

```
> vdiff = tstar[,2] - tstar[,3] # Vector of omega1hat - omega2hat values
> hist(vdiff)
```



```
> shapiro.test(vdiff) # Test of normality
Shapiro-Wilk normality test

data:  vdiff
W = 0.99873, p-value = 0.7097
```

Standard error of $\widehat{\omega}_1 - \widehat{\omega}_2$

```
> var(vdiff)
[1] 0.2889961
> bootse = sqrt(var(vdiff))
> bootse # Compare normal theory estimate of 0.364
[1] 0.5375836
> z = (thetahat[2]-thetahat[3])/bootse; z # Compare z = 2.124
  omega1
1.437819
> # Now bootstrap with lavaan: The easy way
> fitB = lavaan(mod, data=ww, se = "bootstrap")
> parameterEstimates(fitB)
      lhs op           rhs   label   est    se     z pvalue ci.lower ci.upper
1       x =~            w1           1.000 0.000    NA     NA    1.000    1.000
2       x =~            w2           1.000 0.000    NA     NA    1.000    1.000
3       x ~~             x     phi 6.727 0.922 7.295  0.000    5.255    8.734
4      w1 ~~            w1  omega1 3.393 0.386 8.781  0.000    2.685    4.213
5      w2 ~~            w2  omega2 2.620 0.353 7.419  0.000    1.996    3.390
6 vardiff := omega1-omega2 vardiff 0.773 0.525 1.473  0.141   -0.192    1.833
```

Advantages and Disadvantages

Of bootstrapping the normal MLEs

Advantages

- No assumptions about the distribution of the data.
- Works for *any* linear structural equation model provided the observed data have finite fourth moments.
- It's easy.

Disadvantages

- It might take a minute or two.
- The answer is slightly different every time.
- You need the raw data.

$$L(\boldsymbol{\mu},\boldsymbol{\Sigma}) = |\boldsymbol{\Sigma}|^{-n/2}(2\pi)^{-np/2}\exp -\frac{n}{2}\left\{tr(\widehat{\boldsymbol{\Sigma}}\boldsymbol{\Sigma}^{-1}) + (\overline{\mathbf{d}}-\boldsymbol{\mu})^\top\boldsymbol{\Sigma}^{-1}(\overline{\mathbf{d}}-\boldsymbol{\mu})\right\}$$

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http://www.utstat.toronto.edu/brunner/oldclass/431s23