# Lecture 8: Robust Inference II

POL-GA 1251
Quantitative Political Analysis II
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NYU Politics

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- Number of sample units ($n$) goes to infinity.
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Particularly a problem if the data are "ill-behaved" (high maximal leverage – cf. Young, 2015a,b).

Then, asymptotically valid standard errors may be too small and asymptotic test distributions may be highly inaccurate.

When this happens, we could be duped into thinking our estimates are more precise than they actually are given the size of our sample.

More formally,

- Our 95% confidence intervals would cover the true $\beta$ less than 95% of the time (error in coverage probability).
- Our null hypothesis tests would reject the null more often than $100\alpha\%$ of the time (error in rejection probability).

```
. reg income program presesirt, cluster(clu)

Linear regression                               Number of obs =       177
                                                F(  2,     3) =     12.83
                                                Prob > F      =    0.0339
                                                R-squared     =    0.0450
                                                Root MSE      =     38720

                                    (Std. Err. adjusted for 4 clusters in clus)
------------------------------------------------------------------------------
             |               Robust
      income |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     program |   12462.21   2495.431     4.99   0.015     4520.631    20403.78
   presesirt |   1104.258   427.3683     2.58   0.082    -255.8186    2464.334
       _cons |   11279.24   3933.729     2.87   0.064    -1239.641    23798.12
------------------------------------------------------------------------------

. di tprob(3,2.58)
.08177981

. di tprob(174, 2.58)
.01070555

. di 2*(1-normprob(2.58))
.00988003
```

Analytical finite sample adjustments — e.g., Stata's cluster robust command uses (i) a degrees of freedom correction factor in computing the s.e. and (ii) tests against a $t$ distribution with $H-1$ rather than $n-k$ *df* — but these are based on approximations (for normal, iid data). See Young (2015b) for more on such corrections.

Estimators we consider are usually simple linear statistics (means, OLS coefficients, etc.) that have "asymptotically pivotal" test statistics with rather *simple* asymptotic distributions.[1]

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Estimators we consider are usually simple linear statistics (means, OLS coefficients, etc.) that have "asymptotically pivotal" test statistics with rather *simple* asymptotic distributions.[1]

Sometimes we might work with statistics with asymptotic distributions that are simply harder to characterize or with large first-order approximation error (e.g., ratio estimators, predicted values from non-linear models, complicated test statistics).

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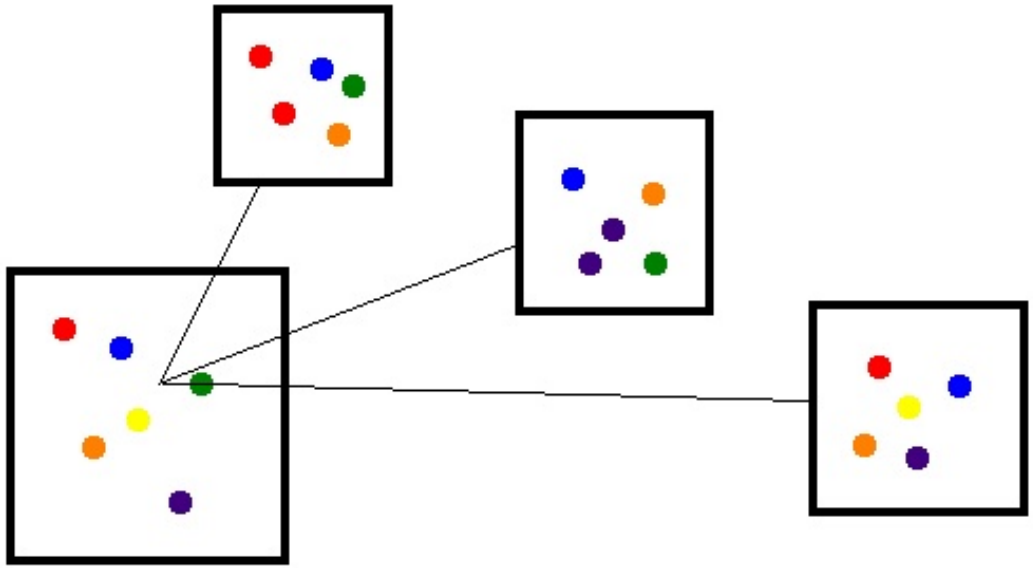
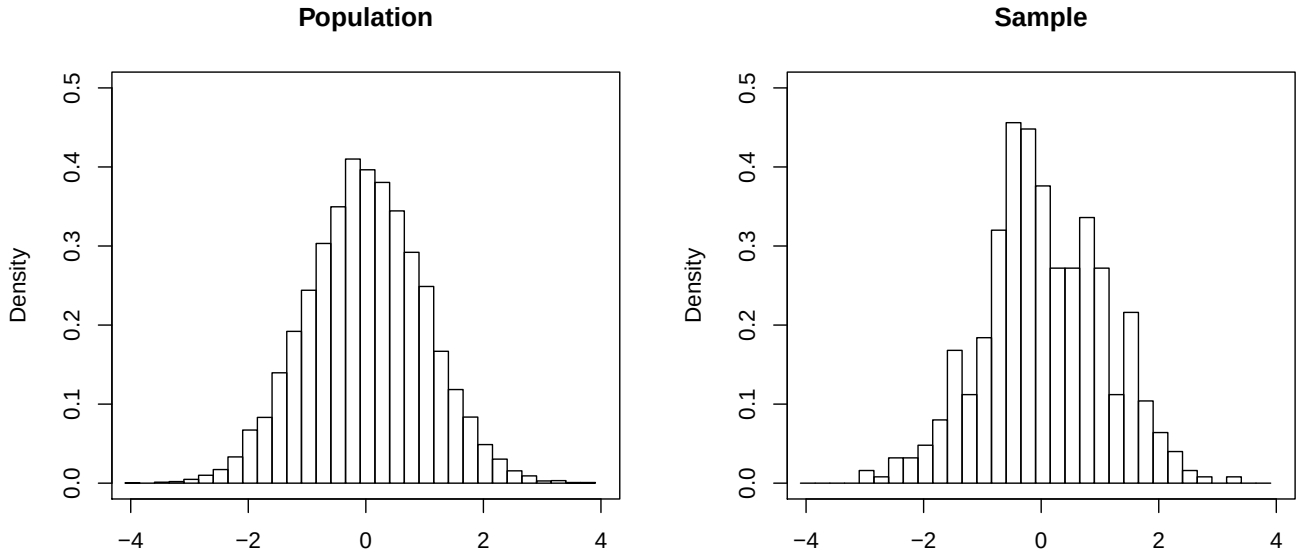
# Bootstrapping Overview



An approach to inference in such settings is bootstrapping:

- Generate a large number of pseudo-samples (e.g., 1,000 of them) drawn from the original sample.
- Use these pseudo-samples to approximate the true sampling distribution.

# Bootstrapping Overview

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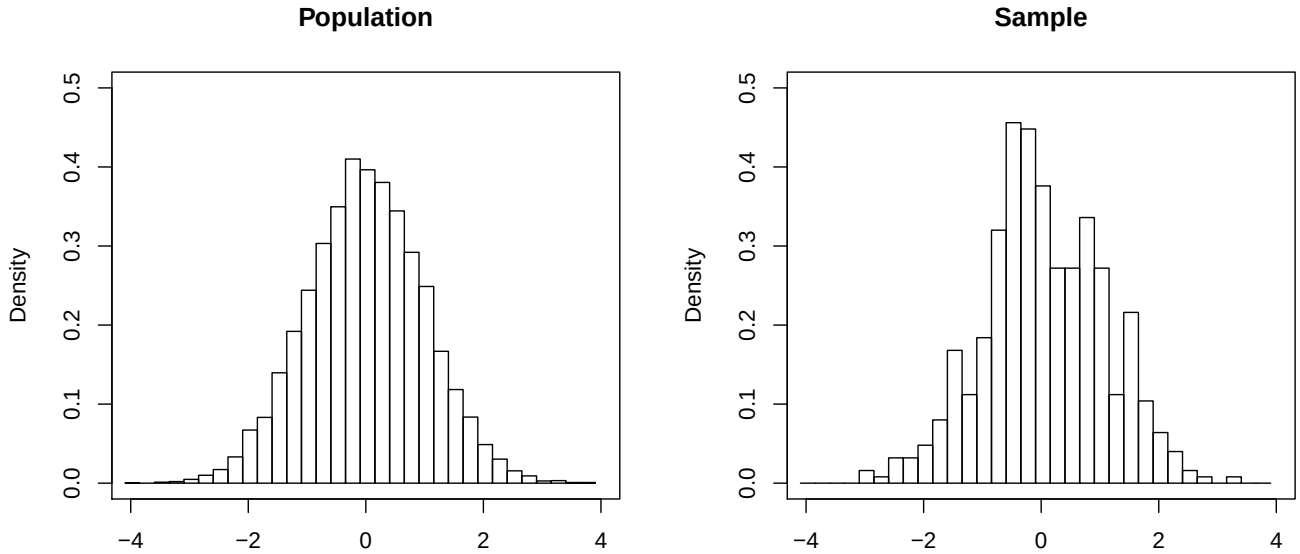


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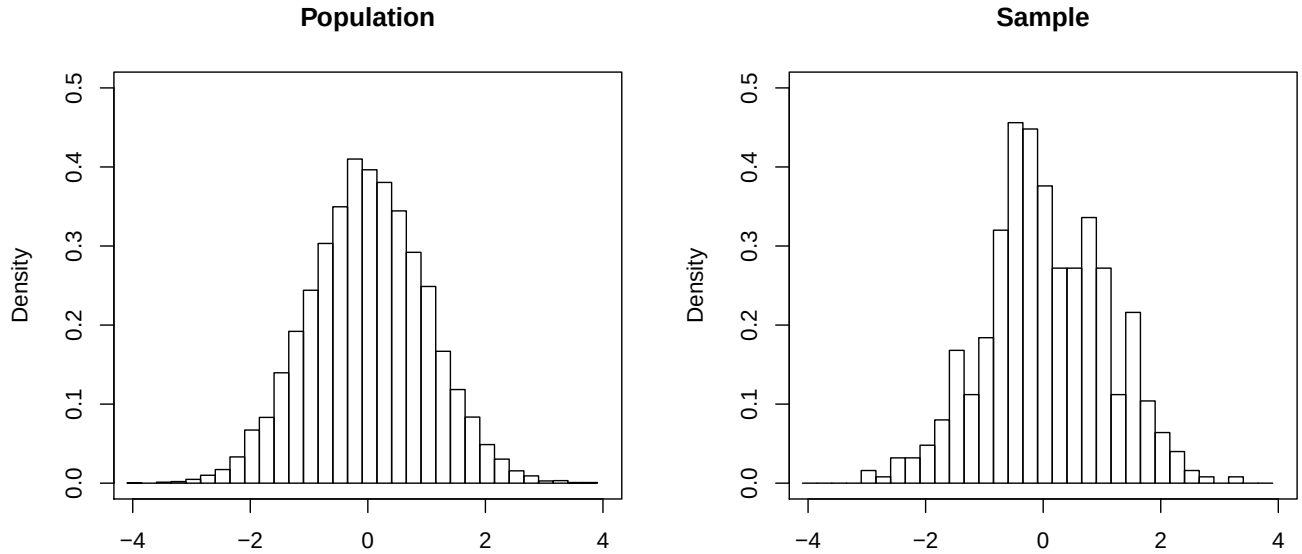


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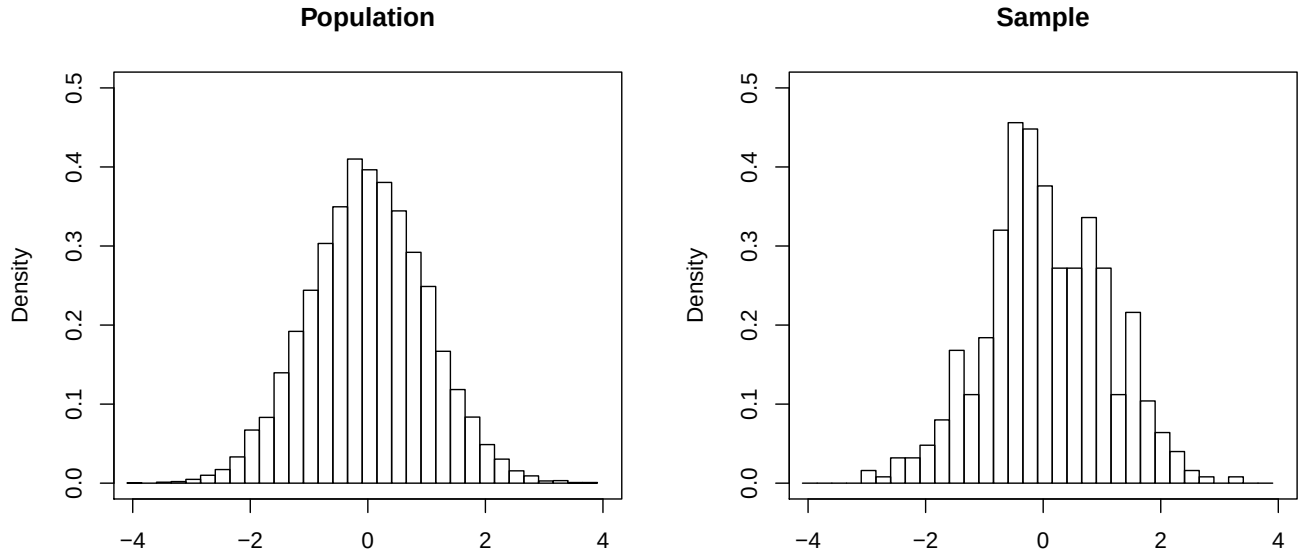


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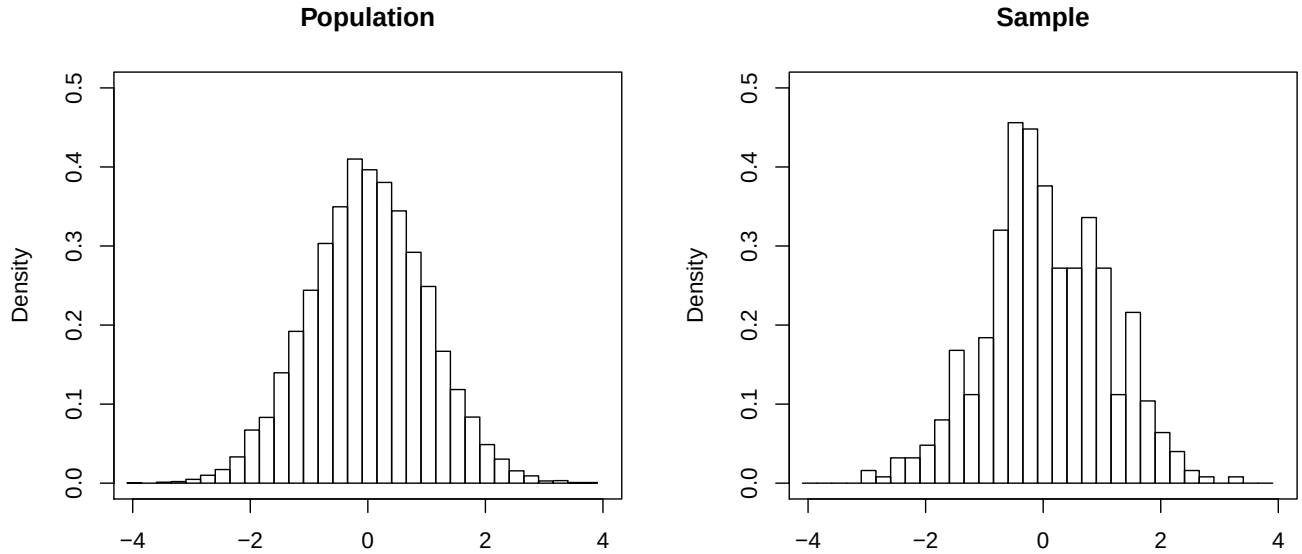


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- $\Rightarrow$ bootstrap validity is asymptotic.
- Convergence of bootstrap variance estimators is often faster than those based on analytical (first order) approximations $\Rightarrow$ "asymptotic refinement".

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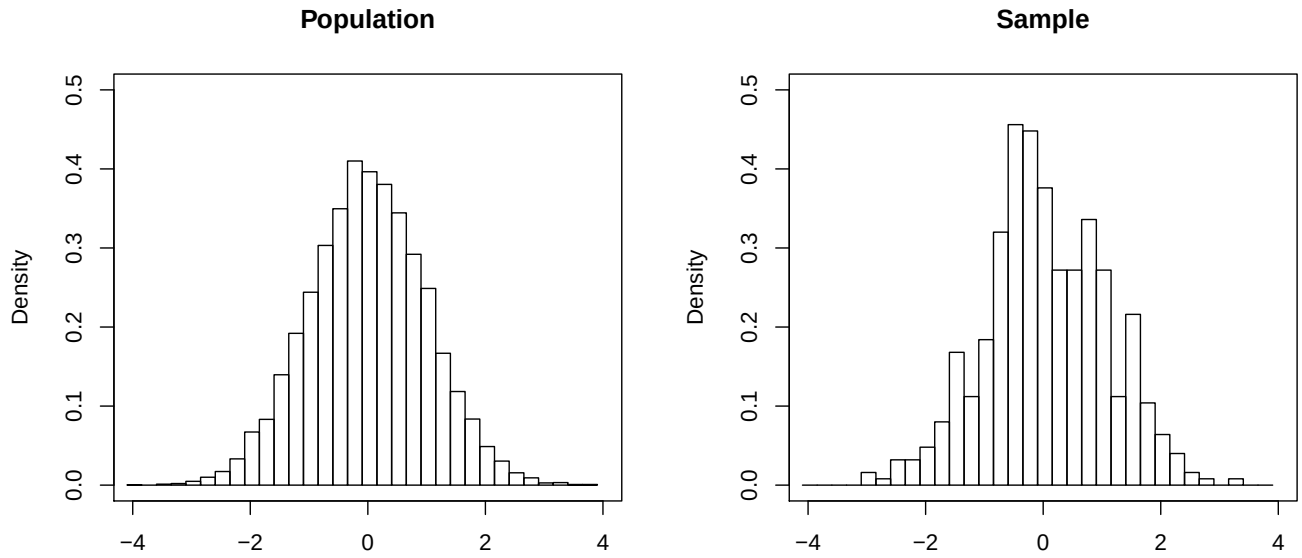
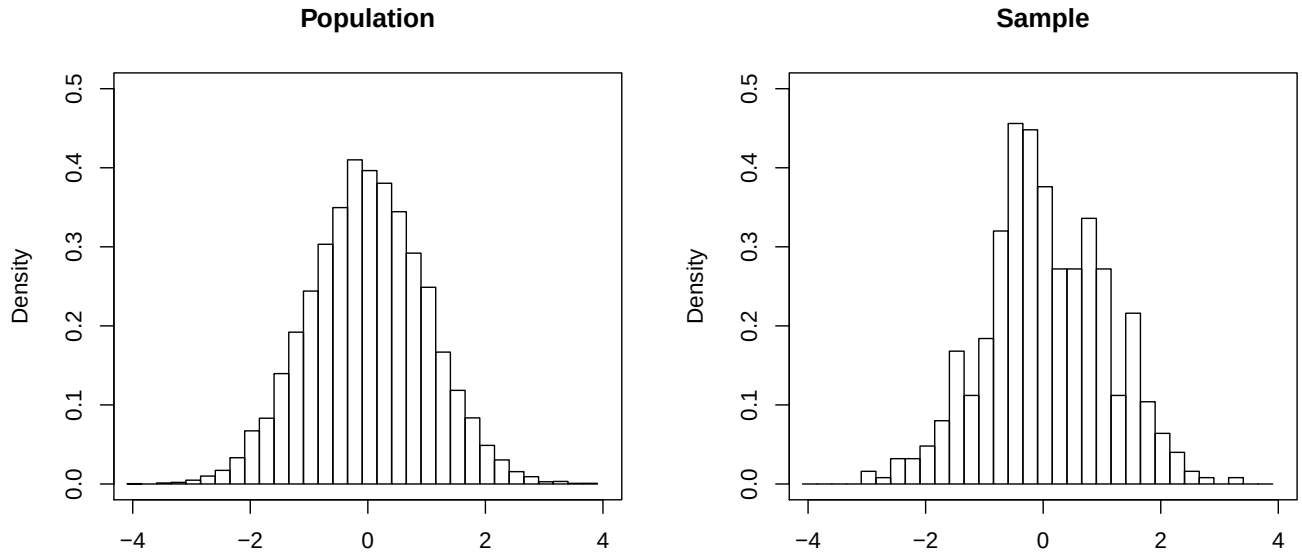



- Sampling $n$ values *with replacement* from $S_n = \{1, \ldots, n\}$ approximates sampling $n$ values of $X$ from $P$.
- The distribution of statistics computed on the bootstrap samples drawn from $S_n$ approximates the distribution of statistics computed on samples from $P$.

# Bootstrapping Overview




In this case, $n = 500$ and $\sigma = 1$, and so the variance of the sample mean, $\bar{X}$ is $1/500 = 0.002$.

```
> ## Population ##
> n <- 10000
> set.seed(123)
> x <- rnorm(n)
> ## Sample ##
> n.s <- 500
> sampled.indices <- sample(1:n, n.s)
> x.s <- x[sample(sampled.indices, n.s)]
> ## X.bar for this sample ##
> mean(x.s)
[1] 0.04966862
> ## Bootstrap the mean ##
> n.boot <- 1000
> x.bar.b <- rep(NA,n.boot)
> for(i in 1:n.boot){
+  x.bar.b[i] <- mean(x[sample(sampled.indices,n.s, replace=T)])
+ }
> ## True mean and variance of X.bar ##
> 0;1/500
[1] 0
[1] 0.002
> ## Bootstrap mean and variance estimates ##
> mean(x.bar.b);var(x.bar.b)
[1] 0.04865665
[1] 0.00192289
```

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- We don't know $H_n$, so use bootstrap to approximate:
  - Draw $B$ bootstrap samples. Estimate $\hat{\theta}_1^*, ..., \hat{\theta}_B^*$.
  - Then $\hat{H}_n(t) = \frac{1}{B}\sum_{b=1}^{B} \mathbb{I}\left(\sqrt{n}(\hat{\theta}_b^* - \hat{\theta}) \leq t\right)$.
  - Get $(\alpha/2, 1-\alpha/2)$ quantiles of $\hat{H}_n(t)$, call them $(\hat{t}_{\alpha/2}, \hat{t}_{1-\alpha/2})$.
  - Bootstrap CI: $C_n = \left[\hat{\theta} - \frac{\hat{t}_{1-\alpha/2}}{\sqrt{n}}, \hat{\theta} - \frac{\hat{t}_{\alpha/2}}{\sqrt{n}}\right]$.
  - (Not a typo– $t_{\alpha/2}$ often negative. See Wasserman blog post.)

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- More refined version uses "studentized" quantities.
- Consistency of these bootstrap CIs depends on whether the limit for $H_n$ is continuous.

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  - Suppose we have $Y \sim P$, and want to test $H_0 : \mathrm{E}[Y] = 0$.
  - Test statistic: $\hat{t} = \frac{\bar{Y}}{\hat{\sigma}_{\tilde{Y}}/\sqrt{n}}$
  - Compute $\tilde{Y}_i = Y_i - \bar{Y}$ (this imposes $H_0$ on $P_n$).
  - Draw $B$ bootstrap and compute $\hat{t}_b^* = \frac{\bar{\tilde{Y}}_b^*}{\hat{\sigma}_{b,\tilde{Y}}^*/\sqrt{n}}$ for each.
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  - Estimated $p$ value: $\frac{1}{B}\sum_{b=1}^{B} \mathbb{I}(|\hat{t}_b^*| \geq |\hat{t}|)$.
- Bias correction:
  - If $P_n \approx P$, then $\mathrm{E}[\hat{\theta}^*] - \hat{\theta} \approx \mathrm{E}[\hat{\theta}_n] - \theta$.
  - Can use the LHS to correct bias in $\hat{\theta}$.

# Bootstrapping Overview

Bootstrapping has many flavors, based on:

- Observational units sampled–individual units, clusters.
- Objects sampled—$(Y, X)$ values, residuals.
- Statistic calculated with sample objects–parameter estimate, test statistic.
- Uses of the bootstrap distribution: variance estimation, estimate CI, hypothesis test, etc.

# Ratio estimators

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- Last week we discussed inverse-propensity score weighting (IPSW) as an alternative to matching as a way to make use of the CIA assumption.
- The simple (unstabilized) IPSW estimator for the ATE takes the form,

$$\hat{\rho}_{IPSW} = \frac{1}{n}\sum_i \frac{D_i Y_i}{\hat{e}(X_i)} - \frac{1}{n}\sum_i \frac{(1-D_i)Y_i}{1-\hat{e}(X_i)}.$$

  where $\hat{e}(X_i)$ is the estimated propensity score.
  (See Busso et al. for expressions for ATT, etc.)
- What is $\mathrm{Var}[\hat{\rho}_{IPSW}]$? What would be a good estimator for it?

# Ratio estimators

- When $\hat{e}(X_i)$ is estimated using a relatively simple model (viz., $M$-estimator with smooth estimating equations), first order asymptotic approximation of the variance is easy with Taylor expansion (aka "linearization" or "delta method").

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- E.g., with logistic regression ($\hat{e}(X_i) = \Lambda(X_i\hat{\gamma})$):

$$\hat{\theta} = \begin{pmatrix} \hat{\gamma} \\ \hat{\rho}_{IPSW} \end{pmatrix} \text{ solves } \sum_i \psi(Y_i, X_i; \hat{\theta}) = \begin{pmatrix} \sum_i X_i \left[D_i - \Lambda(X_i\hat{\gamma})\right] \\ \sum_i \left[\frac{D_i Y_i}{\Lambda(X_i\hat{\gamma})} - \frac{(1-D_i)Y_i}{1-\Lambda(X_i\hat{\gamma})} - \hat{\rho}_{IPSW}\right] \end{pmatrix} = \mathbf{0}$$

and

$$\sqrt{n}(\hat{\theta} - \theta_0) \xrightarrow{d} \text{MVN}\left(0, V_{\hat{\theta}}\right), \text{ with } V_{\hat{\theta}} = A^{-1}B\left(A^{-1}\right)'$$

and

$$A = \text{E}\left[-\frac{\partial}{\partial \theta'}\psi(Y_i, X_i, \theta_0)\right], B = \text{E}\left[\psi(Y_i, X_i, \theta_0)\psi(Y_i, X_i, \theta_0)'\right].$$

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- A consistent sandwich estimator applies sample analogues (cf. Wooldridge $M$ estimation chapter).

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- Moreover, first-order approximation error may be large.
- An approach is to use the bootstrap to estimate $\text{Var}\left[\hat{\rho}_{IPSW}\right]$:
  R example...
- Works when estimating equations (including for estimating the pscores) are asymptotically linear.
- Many possible refinements—e.g., working with bootstrap distributions of pivotal statistics (e.g., $t$ statistics), and then rescaling to obtain standard errors on the scale of the outcome variable.

  (cf. Efron & Tibshirani, 1993; Horowitz, 2001, 2003)

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- Horowitz (2001) reviews formal conditions for the bootstrap to be consistent in characterizing the sampling distribution.
- Essentially *smoothness* conditions (Beran & Ducharme 1991):
  - Estimator of interest must be smooth in perturbations of the sample values
  - Limiting distribution of the estimator must be smooth in perturbations of the estimator value.
- With linear-functional estimators (i.e., estimators that we can write as scaled sums of transformed variables, like means, regression coefficients, etc.), asymptotic normality necessary and sufficient for bootstrap consistency (Mammen 1992).

# Application: Bootstrap Inference with Clustered Data

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Another application relevant to our discussion last week is presented in Cameron et al. (2008), who review bootstrap methods for clustered data when number of clusters ($H$) is small.

They compare asymptotically valid cluster robust variance estimators to a variety of bootstrap estimators for clustered data.

# Application: Inference with Clustered Data

Pairs cluster bootstrap-s.e. (a.k.a. "block bootstrap"): sample $H$ clusters of $(Y,X)$ values with replacement, compute $\hat{\beta}_b^*$. Use $s.d.(\hat{\beta}_b^*)$ as s.e. estimate. Use usual tests, although perhaps against a modified distribution (e.g., use $t$ with $H-1$ $df$, like Stata with cluster-robust).

# Application: Inference with Clustered Data

Pairs cluster bootstrap-$t$: sample $H$ clusters of $(Y,X)$ values with replacement, compute $w_b^*(\theta) = (\hat{\beta}_b^* - \theta)/\widehat{s.e.}_{CR}(\hat{\beta}_b^*)$. For confidence intervals, use,

$$\hat{\beta} \pm t^*_{1-\alpha/2}\widehat{s.e.}_{CR}(\hat{\beta}),$$

where $t^*_{1-\alpha/2}$ is the appropriate quantile of the distribution of $w_b^*(\hat{\beta})$. For a two-sided $p$-value, use proportion of $w_b^*(0)$ values that are at least $|\hat{\beta}/\widehat{s.e.}_{CR}(\hat{\beta})|$ from zero.

# Application: Inference with Clustered Data

Some issues arise for these pair clusters bootstrap methods:

- For pair clusters bootstrap-s.e., using "usual tests" means no asymptotic refinement—does not account for irregularity of small sample distributions.
- Pair clusters bootstrap-$t$ provides asymptotic refinement to account for this.
- When treatment is binary and $H$ is small, bootstrap samples may yield all 0's or all 1's, making $\hat{\beta}_b^*$ inestimable. Would be better if we could avoid this.

# Application: Inference with Clustered Data

Residual cluster bootstrap (s.e. or $t$): sample $H$ clusters of residuals with replacement to form $\{\hat{e}_1^*, ..., \hat{e}_H^*\}$, then apply these to the $H$ clusters of $X\hat{\beta}$ values to construct $\{(\hat{y}_1^*, X_1)..., (\hat{y}_H^*, X_H)\}$. Compute $\hat{\beta}_b^*$, and perform either bootstrap or bootstrap-$t$ inference with each bootstrap sample.

For testing the null hypothesis, use residuals from the regression that imposes the null, and construct the $y_h^*$ values with the null imposed. Then proceed as above.

Problem: based on assumption that $e_h$ vectors are iid from cluster to cluster, and presumes that clusters are all equal size, which are not things that cluster-robust standard errors assume.

# Application: Inference with Clustered Data

Wild cluster bootstrap (s.e. or $t$): form $\{\hat{e}_1^*, ..., \hat{e}_H^*\}$ by letting $\hat{e}_h^* = \hat{e}_h$ with probability 0.5 and $\hat{e}_h^* = -\hat{e}_h$ with probability 0.5 (justified for symmetric error distributions). Then apply these to the $H$ clusters of $X\hat{\beta}$ values to construct $\{(\hat{y}_1^*, X_1)..., (\hat{y}_H^*, X_H)\}$. Compute $\hat{\beta}_b^*$, and perform either bootstrap or bootstrap-$t$ inference with each bootstrap sample.

Again, for testing the null hypothesis, use residuals from the regression that imposes the null, and construct the $y_h^*$ values with the null imposed. Then proceed as above.

(See MacKinnon & Webb 2014 and MacKinnon 2015 for a current discussion.)

# Application: Inference with Clustered Data

TABLE 4.—1,000 SIMULATIONS FROM DIFFERENT DGPS (SEE TEXT) AND $G = 10$ Groups
(Rejection rates for tests of nominal size 0.05 with simulation standard errors in parentheses)

| Estimator # | Method | Column Number | Main—from Table 2 | Reject based on T (8 dof) | Cluster Size = 2 | Cluster Size = 10 | Cluster Size = 100 | 4 RHS Variables | Xs are Constant Within Group | Xs Are i.i.d. | Unbalanced Group Sizes (10, 50) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
| 1 | Assume i.i.d. | | 0.491 (0.016) | | 0.106 (0.010) | 0.268 (0.014) | 0.679 (0.015) | 0.687 (0.015) | 0.770 (0.013) | 0.054 (0.007) | 0.524 (0.016) |
| 2 | Moulton-type estimator | | 0.092 (0.009) | 0.044 (0.006) | 0.095 (0.009) | 0.098 (0.009) | 0.088 (0.009) | 0.089 (0.009) | 0.125 (0.010) | 0.061 (0.008) | 0.129 (0.011) |
| 3 | Cluster-robust | | 0.129 (0.010) | 0.082 (0.009) | 0.137 (0.010) | 0.126 (0.010) | 0.115 (0.010) | 0.129 (0.010) | 0.183 (0.013) | 0.103 (0.010) | 0.183 (0.012) |
| 4 | CR3 residual correction | | 0.090 (0.009) | 0.054 (0.007) | 0.094 (0.009) | 0.086 (0.009) | 0.077 (0.008) | 0.080 (0.009) | 0.090 (0.009) | 0.086 (0.009) | 0.091 (0.009) |
| 5 | Pairs cluster bootstrap-se | | 0.120 (0.010) | 0.071 (0.008) | 0.100 (0.009) | 0.114 (0.010) | 0.120 (0.010) | 0.128 (0.010) | 0.063 (0.008) | 0.122 (0.010) | 0.138 (0.011) |
| 6 | Residual cluster bootstrap-se | | 0.058 (0.007) | 0.013 (0.004) | 0.069 (0.008) | 0.068 (0.008) | 0.060 (0.008) | 0.057 (0.007) | 0.054 (0.007) | 0.080 (0.009) | |
| 7 | Wild cluster bootstrap-se | | 0.028 (0.005) | 0.006 (0.002) | 0.048 (0.007) | 0.044 (0.006) | 0.032 (0.006) | 0.030 (0.005) | 0.036 (0.006) | 0.053 (0.007) | 0.019 (0.004) |
| 8 | Pairs cluster bootstrap-BCA | | 0.111 (0.010) | | 0.125 (0.010) | 0.112 (0.010) | 0.109 (0.010) | 0.112 (0.010) | 0.100 (0.009) | 0.134 (0.011) | 0.140 (0.011) |
| 9 | BDM bootstrap-t | | 0.119 (0.010) | | 0.086 (0.009) | 0.115 (0.010) | 0.112 (0.010) | 0.119 (0.010) | 0.121 (0.010) | 0.097 (0.009) | 0.128 (0.011) |
| 10 | Pairs cluster bootstrap-t | | 0.096 (0.009) | | 0.085 (0.009) | 0.083 (0.009) | 0.086 (0.009) | 0.090 (0.009) | 0.066 (0.008) | 0.079 (0.009) | 0.120 (0.010) |
| 11 | Pairs CR3 bootstrap-t | | 0.090 (0.009) | | 0.075 (0.008) | 0.077 (0.008) | 0.081 (0.009) | 0.084 (0.009) | 0.050 (0.007) | 0.082 (0.009) | 0.110 (0.010) |
| 12 | Residual cluster bootstrap-t | | 0.055 (0.007) | | 0.052 (0.007) | 0.056 (0.007) | 0.050 (0.007) | 0.043 (0.006) | 0.043 (0.006) | 0.065 (0.008) | |
| 13 | Wild cluster bootstrap-t | | 0.055 (0.007) | | 0.064 (0.008) | 0.056 (0.007) | 0.048 (0.007) | 0.052 (0.007) | 0.045 (0.007) | 0.064 (0.008) | 0.061 (0.008) |
| | T_distribution(8) | | 0.086 | | | | | | | | |

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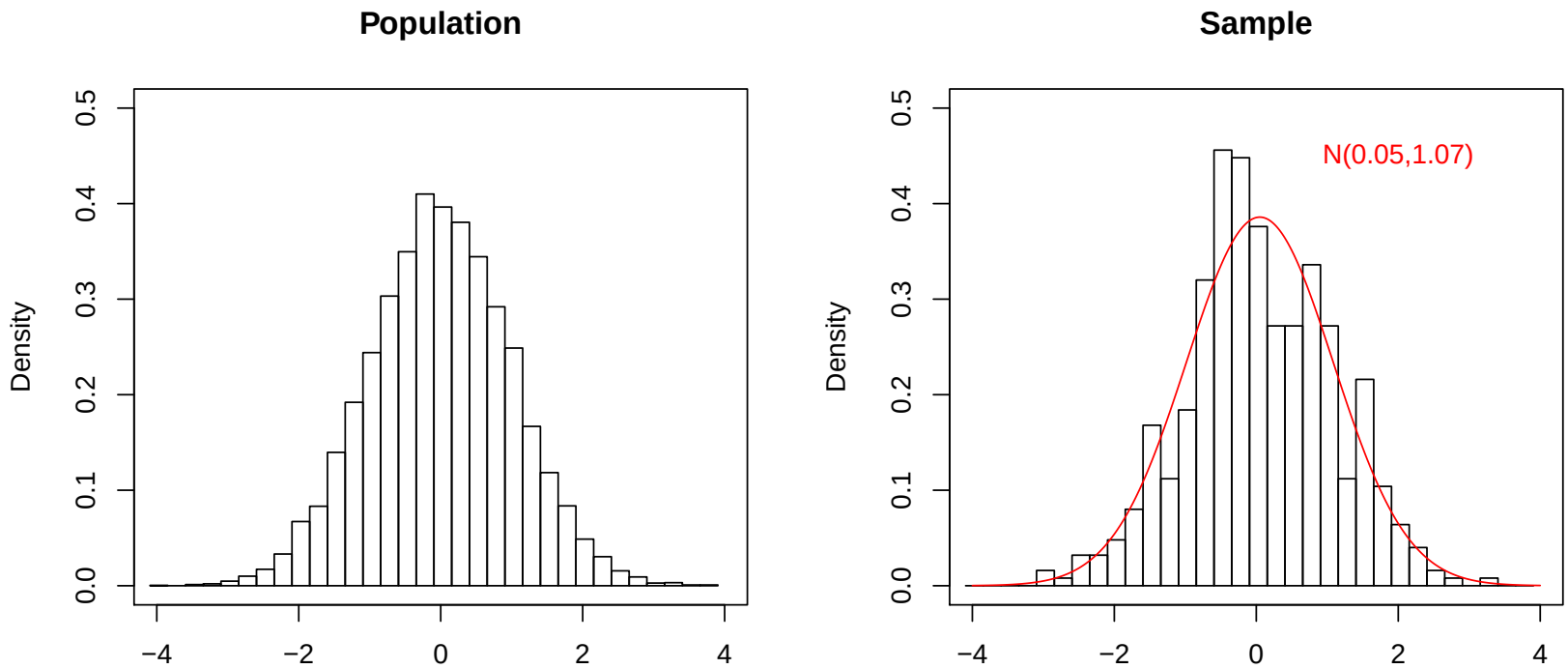
  - Abadie and Imbens (2008) review bootstrapping for unconditional variance estimation for matching estimators:
    - Ordinary bootstrapping fails for nearest-neighbor matching due to such non-smoothness problems. They derive a consistent analytic variance estimator instead.
    - They conjecture that other types of bootstrapping may be okay (e.g., subsampling from exact-match stratification cells or bootstrapped kernel-weighting matching).
    - See Bodory et al. (2016) for an update.

# Remarks: Parametric bootstrap

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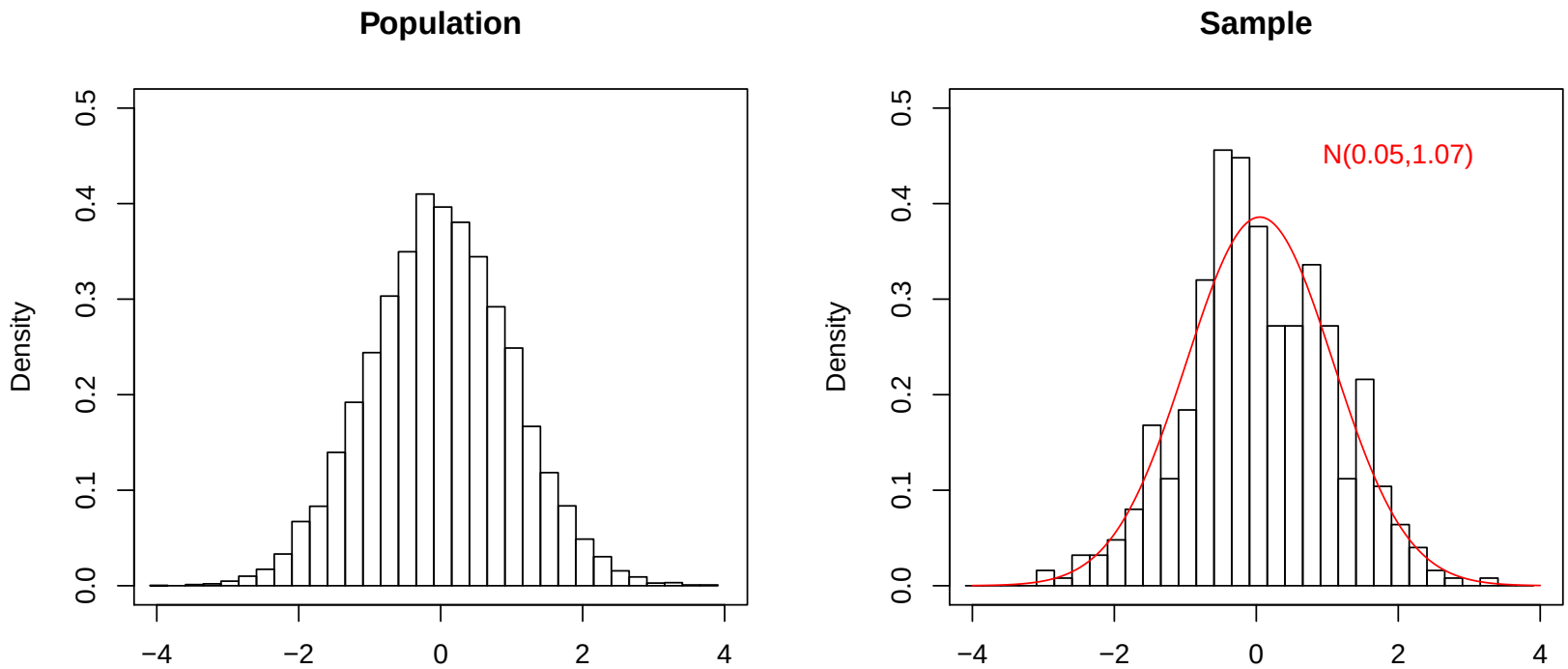


Examples we have considered here are all non-parametric, which involves approximating the population distribution with the *empirical* distribution of the sample. Parametric bootstrap draws from a parametric distribution fit to the observed data (e.g., `Clarify` in Stata or `zelig` in R).

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- See Morgan (2017) for a discussion of how bootstrap and permutation tests compare for inference with experiments.

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- Such procedures can be applied in observational studies under an assumption of conditional random assignment (Rosenbaum, 2002).