

Monte Carlo Methods in Inference

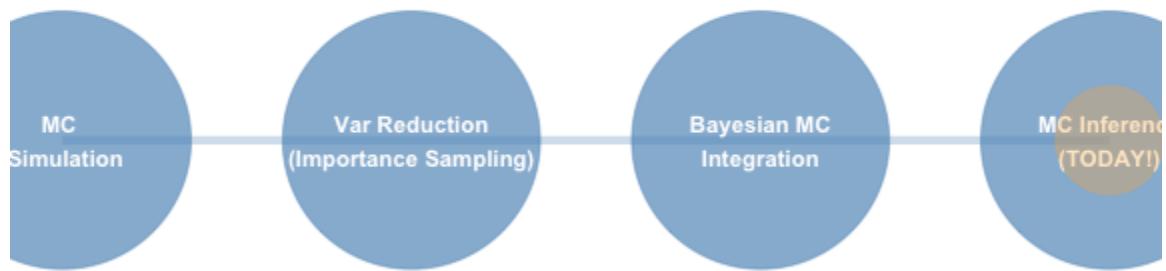
PSTAT 194CS

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Where We've Been & Where We

Course Journey: MC Methods To...

Monte Carlo Methods: Building Your Toolkit



Previously:

- Generating random samples
- Estimating integrals
- Making simulations efficient
- Bayesian posterior estimation

Today:

- Using simulation for inference
- Understanding estimation
- Real-world applications
- Hands-on experiments



Today's Big Question

When we estimate something from data,
how do we know if our method is any good?

MC Inference: The Core Idea

Traditional Statistics

- Derive formulas analytically
- Make distributional assumptions
- Hope assumptions hold!
- Limited to simple cases

Example: "Assume normality, then the sample mean has variance σ^2/n "

Monte Carlo Ap

- Simulate the data-
- Compute estimato
- Observe actual be
- Works for complex

Example: "Let's generate and see what actually h



Key Insight

MC lets us study estimator properties empirically **when theoretical properties are unknown**

Part 1: Estimating Expected Value

Motivating Example: Difference Normals

Setup: $X_1, X_2 \sim N(0, 1)$ independently

Question: What is $E[|X_1 - X_2|]$?

🤔 Think-Pair-Share (2 minutes)

1. **Think:** Can you compute this analytically? What distribution does $|X_1 - X_2|$ follow?
2. **Pair:** Discuss with your neighbor
3. **Share:** Let's hear some thoughts!

The MC Answer: Just Simulate It!

```
m ← 10000
x1 ← rnorm(m)
x2 ← rnorm(m)
theta_hat ← mean(abs(x1 - x2))
theta_hat # Our estimate
```

Code:

```
set.seed(123)
m ← 10000

# Generate samples
X1 ← rnorm(m)
X2 ← rnorm(m)

# Compute estimator
theta_hat ← mean(abs(X1 - X2))

# Standard error
se_theta ← sd(abs(X1 - X2)) / sqrt(m)

# Results
cat("Estimate:", round(theta_hat, 4), "\n")

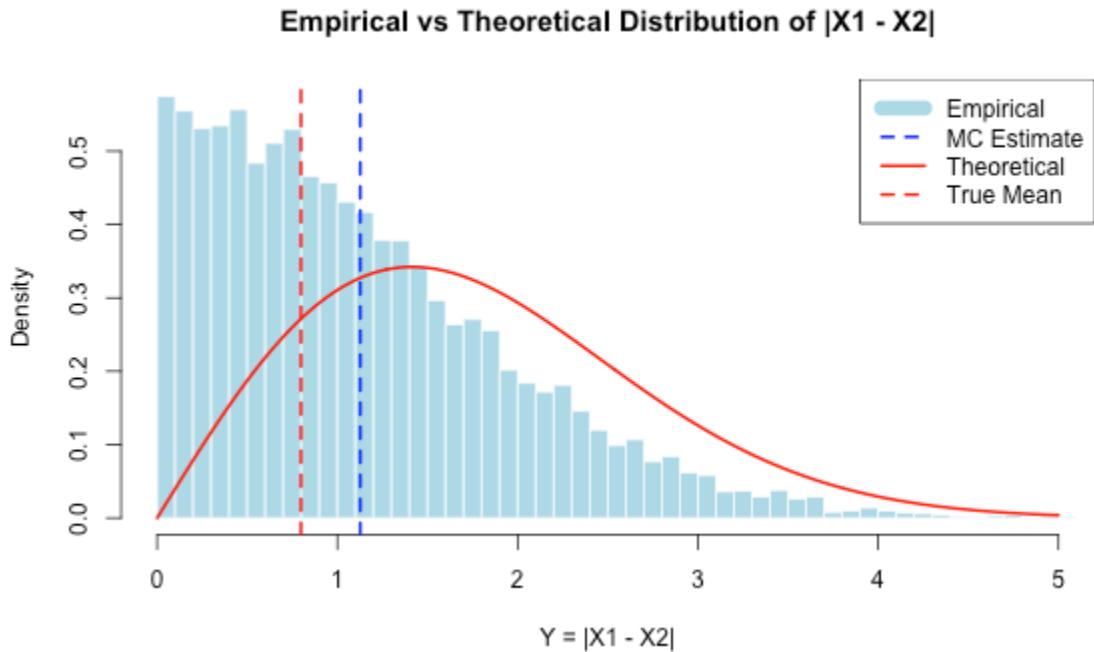
## Estimate: 1.1268

cat("SE:", round(se_theta, 5), "\n")

## SE: 0.00848

cat("95% CI: [", round(theta_hat - 1.96*se_theta, 4), ",",
    round(theta_hat + 1.96*se_theta, 4), "]")
```

Visualizing the Distribution



Estimating Probabilities

Question: What is $P[|X_1 - X_2| > 1]$?

Key Insight: Any probability is an expected value!

$$P[Y > 1] = E[1_{Y>1}]$$

where $1_{Y>1}$ is the indicator function.

MC Algorithm

```
m ← 100000
Y ← abs(rnorm(m) - rnorm(m))

# Estimate probability
p_hat ← mean(Y > 1)
se_p ← sqrt(p_hat * (1 - p_hat) / m)

cat("P[Y > 1] ≈", round(p_hat, 4), "±", round(se_p, 4))

## P[Y > 1] ≈ 0.4818 ± 0.0016
```



Quick Poll

Part 2: Comparing Estimators w

The Contaminated Data Problem

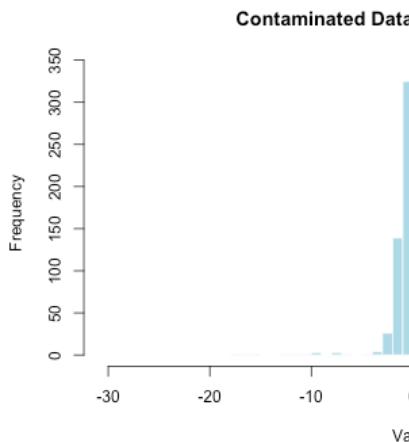
Scenario:

- Most data from $N(0, 1)$
- Some contaminated from $N(0, 100)$
- Want to estimate the mean (should be 0)

Contamination model:

$$pN(0, 1) + (1 - p)N(0, 100)$$

Question: Should we use \bar{X} or something more robust?



Trimmed Mean to the Rescue

Idea: Remove extreme values before computing mean

$$\bar{X}_{[-k]} = \frac{1}{n - 2k} \sum_{i=k+1}^{n-k} X_{(i)}$$

where $X_{(1)} \leq X_{(2)} \leq \dots \leq X_{(n)}$ are ordered observations.

🎯 Your Turn! (Think)

Before we simulate, make a prediction:

1. When there's **no contamination** ($p=1$), which is better: \bar{X} or $\bar{X}_{[-k]}$?
2. When there's **5% contamination** ($p=0.95$), which is better?
3. What happens as we increase the trim level k ?

Now let's find out with simulation!

Code: Comparing Estimators

```
# Function to compute MSE of trimmed mean
trimmed_mse <- function(n, m, k, p) {
  tmean <- numeric(m)

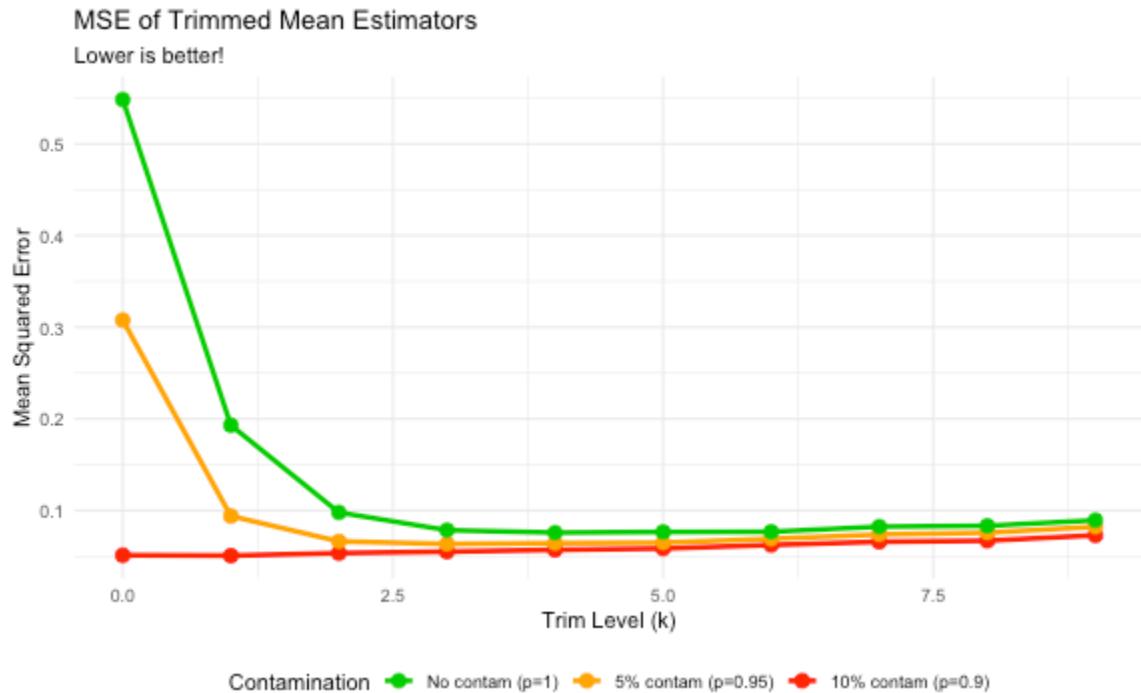
  for(i in 1:m) {
    # Generate contaminated sample
    sigma <- sample(c(1, 10), size = n, replace = TRUE,
                    prob = c(p, 1-p))
    x <- rnorm(n, 0, sigma)
    x_sorted <- sort(x)

    # Compute trimmed mean
    if(k == 0) {
      tmean[i] <- mean(x_sorted)
    } else {
      tmean[i] <- mean(x_sorted[(k+1):(n-k)])
    }
  }

  # MSE (true mean is 0)
  mse <- mean(tmean^2)
  se_mse <- sd(tmean^2) / sqrt(m)

  return(c(mse = mse, se = se_mse))
}
```

Results: MSE for Different Scenarios



What Did We Learn?



Table: MSE by Trim Level and Contamination Rate

k	0%	5%	10%
0	0.0512	0.3077	0.5484
1	0.0508	0.0939	0.1931
2	0.0535	0.0663	0.0978
3	0.0551	0.0635	0.0785
4	0.0570	0.0644	0.0758
5	0.0585	0.0649	0.0765
6	0.0624	0.0691	0.0768
7	0.0658	0.0738	0.0824
8	0.0670	0.0758	0.0833
9	0.0729	0.0822	0.0894

Key Insights:

Part 3: Power Analysis for Experiments

The Deliveroo Problem

Business Context:

- Testing new app feature
- Measure: order completion rate
- Question: **How many users do we need to detect a 3% improvement?**

MC Approach:

- Use actual historical data
- Simulate experiments
- Account for real distribution
- More accurate sample size

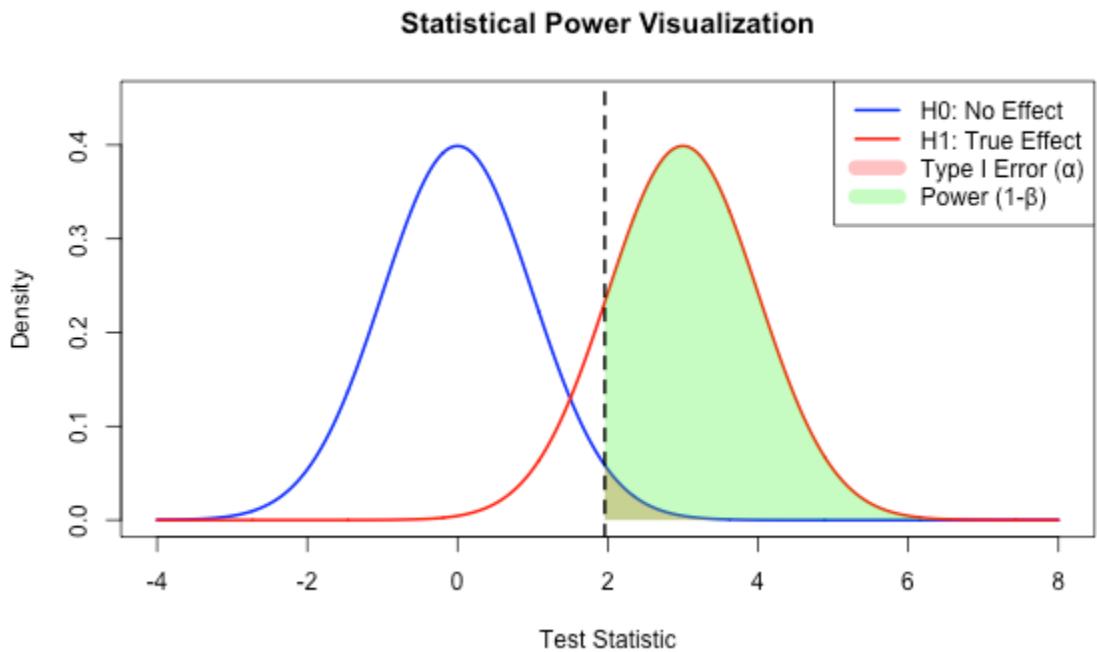
Classical Approach:

- Use formula for proportion test
- Assumes normality (CLT)
- Ignores real data quirks

 This is REAL

Companies like Deliveroo use this daily.

What is Statistical Power?



Power = Probability of detecting a true effect

MC Power Analysis: The Algorithm

Steps:

1. Collect historical data on your metric
2. Choose your experiment parameters:
 - Sample size to test (N)
 - Effect size you want to detect (δ)
 - Significance level ($\alpha = 0.05$)
3. For each sample size (repeat many times):
 - Generate control group from historical data
 - Generate treatment group with effect applied
 - Run statistical test
 - Record if test was significant
4. Power = fraction of significant results

Live Example: Testing Conversion

```
# Historical data: 31.5% conversion rate
base_rate ← 0.315
target_effect ← 1.03 # Want to detect 3% lift
alpha ← 0.05
sims ← 1000

# Function to estimate power for given sample size
estimate_power ← function(n_per_group, base_rate, effect, sims) {
  significant ← numeric(sims)

  for(i in 1:sims) {
    # Generate data
    control ← rbinom(n_per_group, 1, base_rate)
    treatment ← rbinom(n_per_group, 1, base_rate * effect)

    # Run test
    test ← prop.test(c(sum(control), sum(treatment)),
                     c(n_per_group, n_per_group))

    significant[i] ← test$p.value < alpha
  }

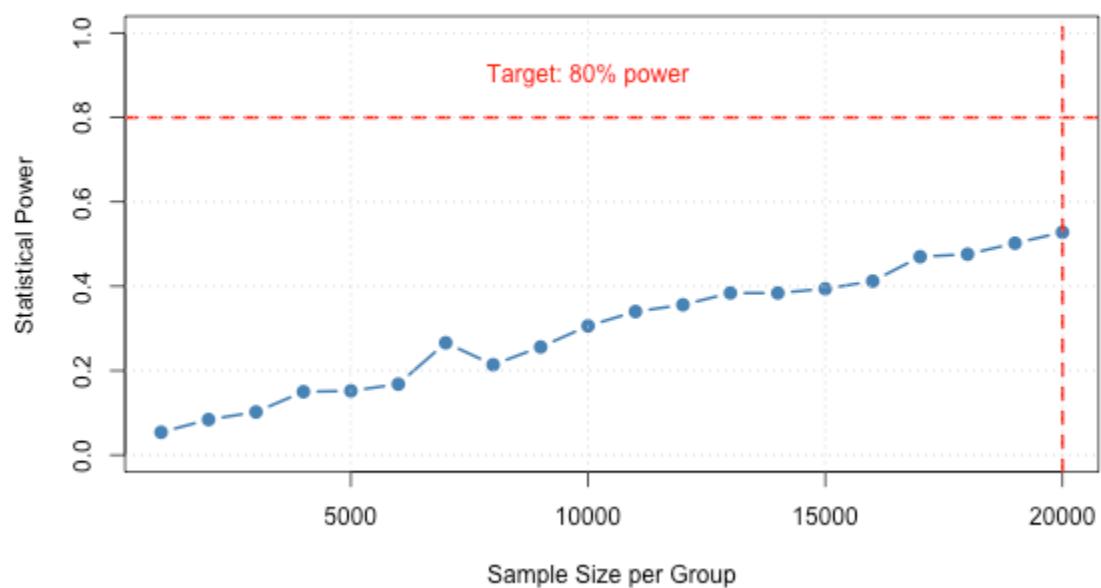
  return(mean(significant))
}
```

Building the Power Curve

```
# Test different sample sizes
sample_sizes ← seq(1000, 20000, 1000)
power_estimates ← numeric(length(sample_sizes))

set.seed(42)
for(i in seq_along(sample_sizes)) {
  power_estimates[i] ← estimate_power(sample_sizes[i],
                                         base_rate, target_effect,
                                         5)
}
```

Power Analysis: Sample Size vs. Power



Result: Need $\sim 2 \times 10^4$ users per group!



Time to Get Your Hands On It

Activity: Trimmed Mean Analysis

Break into groups of 2-3

Activity Overview

You'll investigate three questions:

1 Median vs Trimmed Mean

How does the sample median perform compared to different trim levels?

2 Increased Contamination

What happens when contamination rate increases to 40%?

3 Your Own Question!

Design and run your own MC study:

- Different distributions?
- Different estimators?
- Different contamination patterns?

Time: 30 minutes

Deliverable: Brief presentation (3 minutes) of findings

Activity Tips & Resources



Worksheet provided with:

- Starter code
- Guiding questions
- Space for your discoveries



Remember to:

1. Start with intuition (what do you expect?)
2. Design your MC study carefully
3. Interpret results, don't just report numbers
4. Compare to theory when possible



Need help?

- Check the code examples from slides
- Consult with neighboring groups
- Ask instructor!

Wrap-Up & Takeaways

What You Can Do with MC Inference

Things we covered:

1. Estimate properties of estimators (bias, variance, MSE)
2. Compare different estimation methods
3. Compute probabilities for complex distributions
4. Design proper experiments (power analysis)

Beyond this class:

- Bootstrap and resampling methods
- Bayesian credible intervals
- Sequential testing
- Adaptive designs

Real-world impact:

This is literally how companies make million-dollar decisions!

Key Insights

Why MC Inference Matters

1. **Flexibility:** Works when formulas don't exist
2. **Realism:** Use actual data distributions
3. **Transparency:** See what's happening
4. **Scalability:** Same approach for simple & complex problems

Best Practices

1. ✓ Always check a few points of intuition
2. ✓ Report standard errors
3. ✓ Visualize results
4. ✓ Compare to theoretical values
5. ✓ Document your parameters

For Next Time



Recommended Reading:

- Deliveroo article (linked in worksheet)

Questions?

Extra: Keep exploring!



```
# Example: Build your own MC study
my_mc_study <- function(estimator, data_generator,
                         true_value, n_sims = 10000) {
  estimates <- replicate(n_sims, {
    data <- data_generator()
    estimator(data)
  })
  list(
    bias = mean(estimates) - true_value,
    variance = var(estimates),
    mse = mean((estimates - true_value)^2)
  )
}
```