P8160 Simulation Project - Hierarchical Logistic Model for Mulit-Center Clinical Trial

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Introduction and Background

Statistical Methods

1. Initialization and Function Definitions

We specified the clinic random effect (b) as b ~ t_5 and the patient-level covariates (X) as X ~ Gamma(2, 1).

```
# logistic function
logistic <- function(z) {
  1 / (1 + exp(-z))
}

# Set model parameters
alpha <- 0        # Intercept
beta  <- 1        # Covariate coefficient

# Define random generators for non-normal distributions
#                   of random effect b and covariate x
# Example: b ~ t_5 (heavy-tailed distribution)
r_b <- function(n) {
  rt(n, df = 5)
}

# Example: x ~ Gamma(shape=2, rate=1)
r_x <- function(n) {
  rgamma(n, shape = 2, rate = 1)
}
```

2. Sampling from Simple Monte Carlo

```
simpleMC <- function(N) {
  # Sample b from f(b)
  b_samp <- r_b(N)
  # Sample x from f(x)
  x_samp <- r_x(N)

  # Compute p_i = logistic(alpha + b_i + beta*x_i)
  p_values <- logistic(alpha + b_samp + beta * x_samp)

  # Simple MC estimate is the average of p_values
  est <- mean(p_values)
```

```r
  # Approximate standard error using sample SD / sqrt(N)
  #se  <- sd(p_values) / sqrt(N)

  #return(list(est = est, se = se))
  return(list(est = est))
}
```

3. Designing Control Variate (CV)

4. Importance Sampling (IS)

Results

5. Comparing Bias, Variance, and CPU Time for Simple MC, Control variates, and Importance Sampling

6. (Extra credit) Use cumulative convergence plots

Discussion and Practical Implications

Conclusion