

CSSS/POLS 510 MLE Lab

Lab 4. Prediction and Quantities of Interest

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Agenda

1. Review HW1
2. Last lab review
3. Quantities of Interest

1. Review HW1: simulation precision

```
dbinom(x=16, size=30, prob=0.49)
```

```
## [1] 0.1293457
```

```
set.seed(12345)
```

```
sims <- 100      # 100 simulations
```

```
nmen <- rep(NA,sims)
```

```
for (i in 1:sims) {
```

```
  nmen[i] <- sum(sample(c(0,1),  
                       30,  
                       replace = TRUE,  
                       prob = c(0.51, 0.49) ))
```

```
}
```

```
sum(nmen==16)/length(nmen) # sum of trials with 16 males
```

```
## [1] 0.16
```

1. Review HW1: simulation precision

```
dbinom(x=16, size=30, prob=0.49)
```

```
## [1] 0.1293457
```

```
set.seed(12345)
```

```
sims <- 1000      # 1000 simulations
```

```
nmen <- rep(NA,sims)
```

```
for (i in 1:sims) {
```

```
  nmen[i] <- sum(sample(c(0,1),  
                       30,  
                       replace = TRUE,  
                       prob = c(0.51, 0.49) ))
```

```
}
```

```
sum(nmen==16)/length(nmen) # sum of trials with 16 males
```

```
## [1] 0.131
```

1. Review HW1: simulation precision

```
dbinom(x=16, size=30, prob=0.49)
```

```
## [1] 0.1293457
```

```
set.seed(12345)
```

```
sims <- 10000      # 10000 simulations
```

```
nmen <- rep(NA,sims)
```

```
for (i in 1:sims) {
```

```
  nmen[i] <- sum(sample(c(0,1),  
                       30,  
                       replace = TRUE,  
                       prob = c(0.51, 0.49) ))
```

```
}
```

```
sum(nmen==16)/length(nmen) # sum of trials with 16 males
```

```
## [1] 0.1285
```

1. Review HW1: simulation precision

```
dbinom(x=16, size=30, prob=0.49)
```

```
## [1] 0.1293457
```

```
set.seed(12345)
```

```
sims <- 100000      # 100000 simulations
```

```
nmen <- rep(NA,sims)
```

```
for (i in 1:sims) {
```

```
  nmen[i] <- sum(sample(c(0,1),  
                       30,  
                       replace = TRUE,  
                       prob = c(0.51, 0.49) ))
```

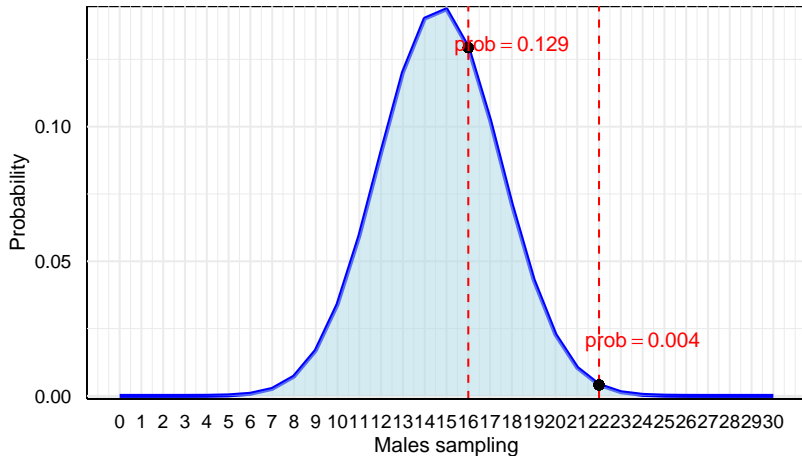
```
}
```

```
sum(nmen==16)/length(nmen) # sum of trials with 16 males
```

```
## [1] 0.1294
```

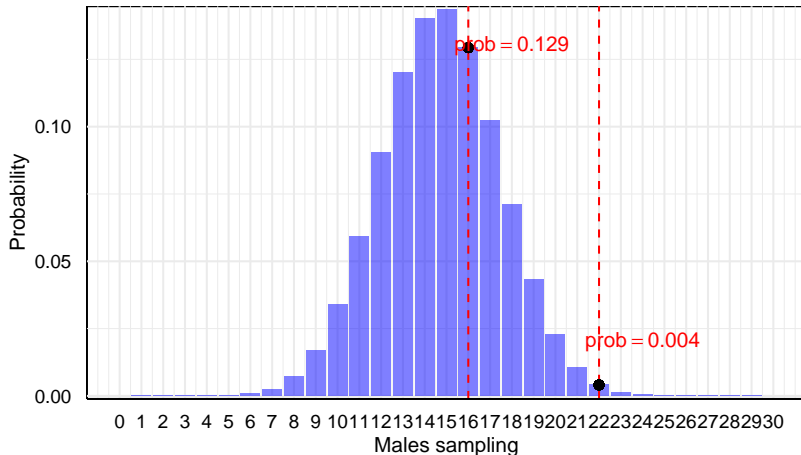
1. Review HW1: Probability Mass Functions

Q1 – Binomial distribution



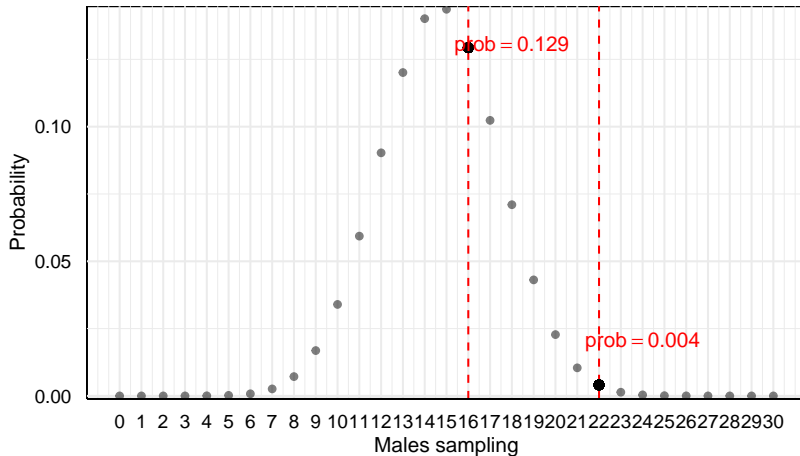
1. Review HW1: Probability Mass Functions

Q1 – Binomial distribution



1. Review HW1: Probability Mass Functions

Q1 – Binomial distribution



1. Review HW1: summary

- ▶ When displaying PMFs, provide visuals with a discrete sample space.
- ▶ **Sanity checks:**
 - ▶ Use R built-in or packages programs/functions to **double-check**.
 - ▶ Increase simulations/sample **size**.
 - ▶ Convergence in probability ($N \rightarrow \infty$)

2. Last lab review: MLE

- ▶ How do we estimate the MLE?
 1. Define a probability model (PDF): $Y_i \sim N(\mu_i, \sigma^2)$.
 2. Derive the log-likelihood function.
 3. Reduce to sufficient statistics and substitute systematic component.
 4. Use `optim()` or any other function to find the maxima.

2. Normal homoskedastic

Two **different** notations for the **same** model.

LS notation:

$$\varepsilon \sim N(0, \sigma^2) \quad (\textit{stochastic})$$

$$Y_i = x_i\beta \quad (\textit{systematic})$$

$$Y_i = x_i\beta + \varepsilon \quad (\textit{stochastic} + \textit{systematic})$$

MLE notation:

$$Y_i \sim N(\mu_i, \sigma^2) \quad (\textit{stochastic})$$

$$\mu_i = x_i\beta \quad (\textit{systematic})$$

$$Y_i \sim N(x_i\beta, \sigma^2) \quad (\textit{stochastic} + \textit{systematic})$$

2. MLE general notation

$$Y_i \sim f(\theta_i, \alpha) \quad (\text{stochastic})$$

$$\theta_i = g(\mathbf{x}_i\boldsymbol{\beta}) \quad (\text{systematic})$$

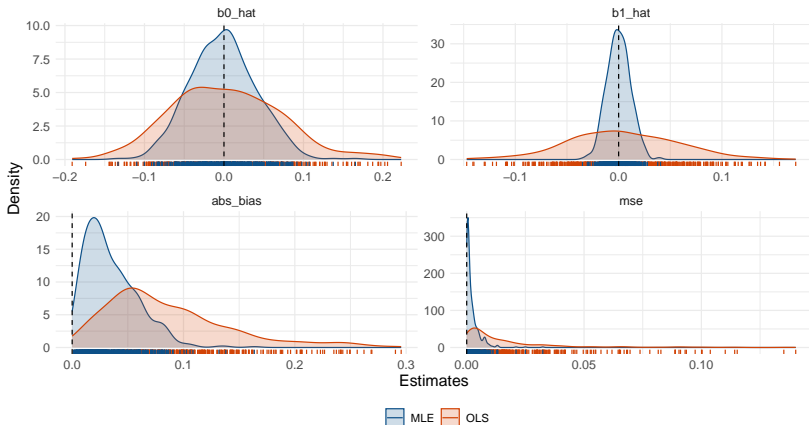
where

- ▶ Y_i is a random outcome variable.
- ▶ $f(\cdot)$ is a probability density function.
- ▶ θ_i is a systematic feature of the PDF that varies over i .
- ▶ α is an ancillary parameter (feature of f that we treat as constant).
- ▶ $g(\cdot)$ functional form for reparametrization of the data model.
- ▶ \mathbf{x}_i explanatory variables vector.
- ▶ $\boldsymbol{\beta}$ vector of effect parameters.

2. Last lab review: MLE - Heteroskedastic normal

Heteroskedasticity: OLS vs MLE-Heteroskedastic Normal

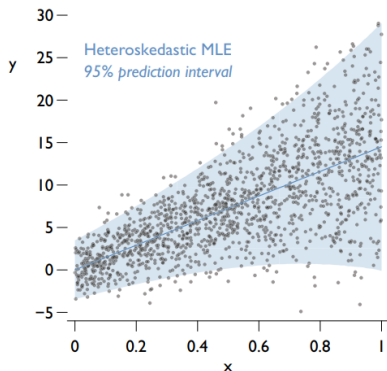
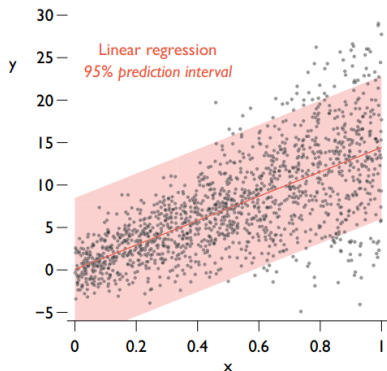
Simulation: 500 regression estimate samples (n=600)



Note: Estimates distributions are mean-centered on the true parameters. Each facet's axes are free to vary.

3. Quantities of Interest: prediction

Once we have estimated the model, we can compare the predictive performance of each model. Refer to [Chris's MLE lecture \(slide 80\)](#) for more details.



3. Quantities of Interest

Motivation: We want to study how the change in a particular explanatory variable affects the outcome variable, *all else being equal*.

We will focus on how to simulate predictions from *estimands* or **quantities of interest**.

Let's open RStudio and [Lab4.html](#) file jointly with the [Lab4.Rmd](#) file with the code and contents of today's lab!

FIN