Midterm Review

Key Concepts from Lessons 1–9

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Today's Agenda

- Quick overview of exam structure
- Key concepts review
  - Study design
  - Probability and Bayes' Theorem
  - Distributions (focus on R functions!)
  - Sampling distributions and CLT
  - Confidence intervals
  - Hypothesis testing
- Your questions

The midterm opens TODAY at 3:00 PM and closes Monday at 11:00 PM

Exam Logistics

Exam Details

Format:

- 8 parts, 120 points total
- Designed for 3-5 hours completion
- Mix of conceptual questions, R code, and interpretation

Resources allowed:

- ✅ Course materials (slides, homework, textbook)
- ✅ R documentation
- ✅ Your notes
- ❌ Other students
- ❌ AI assistants
- ❌ Online help forums

Submit both `.qmd` and `.html` files!

What’s Covered

Part 1: Study design (10 pts)

Part 2: Descriptive stats & viz (15 pts)

Part 3: Probability (15 pts)

Part 4: Distributions (20 pts)

Part 5: Sampling distributions & CLT (15 pts)

Part 6: Confidence intervals (15 pts)

Part 7: Hypothesis testing (20 pts)

Part 8: Integration (10 pts)

Key datasets: `nhanes.samp` (you’ve used this in HW!)

General Tips

Before you start:

- Read all instructions carefully
- Set up your workspace (load packages, data)
- Check that code chunks run

While working:

- Show your work and reasoning
- Provide interpretations in complete sentences
- Use comments in your R code
- Check that your document renders frequently
- **Save regularly**

Before submitting:

- Render one final time
- Check that all answers are complete
- Verify both files are being submitted

Quick Concepts Review

Study Design: The Basics

Experiments vs. Observational Studies

Experiment:

- Researchers assign treatments
- Random assignment
- Can establish causation
- Example: Drug trial with treatment vs. placebo

Observational Study:

- Researchers observe without interfering
- No random assignment
- Can only show association
- Example: Reviewing medical records

Why does this matter?

Only randomized experiments can establish causal relationships!

Sampling Concepts

Key terms:

- **Population** vs. **Sample**
- **Simple random sample** (each individual has equal chance)
- **Convenience sample** (easily accessible - often biased)

Confounding variables:

- Associated with both explanatory and response variables
- Can make it look like there's a causal relationship when there isn't
- Example: Exercise and cardiovascular health might both be related to socioeconomic status

R Skills Review: Data Wrangling & Visualization

dplyr: The grammar of data manipulation

`dplyr` provides a consistent set of **verbs** for data manipulation:

Function	What it does
`filter()`	Keep rows that meet conditions
`select()`	Keep or drop columns
`mutate()`	Create or modify columns
`arrange()`	Sort rows
`group_by()`	Group data for summaries
`summarize()`	Calculate summary statistics

These verbs can be chained together with `%>%` for powerful data transformations.

ggplot2: The Basic Template

The ggplot2 pattern

```r
library(ggplot2)

ggplot(data = dataset,
       aes(x = variable, y = variable)) +
  geom_*() +                    # Choose your geometry
  labs(title = "...",           # Add labels
       x = "...",
       y = "...")
```

Key geoms you need to know:

```r
# Histogram (one continuous variable)
geom_histogram(bins = 20)

# Boxplot (continuous by categorical)
geom_boxplot()

# Scatterplot (two continuous variables)
geom_point()
```

ggplot2: Example

```r
library(ggplot2)
library(oibiostat)
data("nhanes.samp")

# Histogram
ggplot(nhanes.samp, aes(x = Height)) +
  geom_histogram(bins = 20) +
  labs(title = "Distribution of Height",
       x = "Height (cm)",
       y = "Count")

# Boxplot by group
ggplot(nhanes.samp,
       aes(x = Gender, y = Weight, fill = Gender)) +
  geom_boxplot() +
  labs(title = "Weight by Gender",
       x = "Weight (kg)",
       y = "Age (years)")
```

Remember: Start with `ggplot()`, then add layers with `+`

dplyr + rstatix: Summary Statistics

The pattern: group_by() then summarize

```r
library(dplyr)
library(rstatix)

dataset %>%
  group_by(grouping_variable) %>%
  get_summary_stats(numeric_variable, type = "mean_sd")
```

Example:

```r
# Summary stats by one group
nhanes.samp %>%
  group_by(Gender) %>%
  get_summary_stats(Height, type = "mean_sd")

# Summary stats by multiple groups
nhanes.samp %>%
  group_by(Gender, SmokeNow) %>%
  get_summary_stats(Weight, type = "mean_sd")
```

dplyr only: Summary Statistics

The pattern: group_by() then summarize

```r
library(dplyr)

dataset %>%
  group_by(grouping_variable) %>%
  summarise(...)
```

Example:

```r
# Summary stats by one group
nhanes.samp %>%
  group_by(Gender) %>%
  summarise(n = sum(!is.na(Height)),
            mean = mean(Height, na.rm = TRUE),
            sd = sd(Height, na.rm = TRUE))

# Summary stats by multiple groups
nhanes.samp %>%
  group_by(Gender, SmokeNow) %>%
  summarise(n = sum(!is.na(Weight)),
            mean = mean(Weight, na.rm = TRUE),
            sd = sd(Weight, na.rm = TRUE))
```

Categorical Data: janitor::tabyl()

The pattern for frequency tables

```r
library(janitor)

# One-way table
dataset %>%
  tabyl(variable)

# Two-way table with row percentages
dataset %>%
  tabyl(row_variable, column_variable) %>%
  adorn_totals(where = "row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting(digits = 1)
```

Example:

```r
# Two-way table
nhanes.samp %>%
  tabyl(Gender, SmokeNow) %>%
  adorn_totals(where = "row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting(digits = 1) %>%
  adorn_ns()
```

Probability

Probability Notation Quick Reference

Basic probabilities:

- **Marginal:** $P(A)$ - probability of A alone
- **Joint:** $P(A \text{ and } B)$ - probability of both
- **Conditional:** $P(A \mid B)$ - probability of A given B

Key formula:

$$P(A \mid B) = \frac{P(A \text{ and } B)}{P(B)}$$

Independence:

Events A and B are independent if: $P(A \text{ and } B) = P(A) \times P(B)$

Probability Rules to Remember

General Addition Rule:

If A and B are any two events:

$$P(A \text{ or } B) = P(A) + P(B) - P(A \text{ and } B)$$

We subtract $P(A \text{ and } B)$ because those outcomes were counted twice.

General Multiplication Rule:

$$P(A \text{ and } B) = P(A \mid B) \times P(B)$$

This connects **joint** and **conditional** probabilities, and leads directly to Bayes' Theorem!

Special case: Independent events

If A and B are independent: $P(A \text{ and } B) = P(A) \times P(B)$

Bayes' Theorem: The Pattern

You'll almost always use it in this form:

$$P(A \mid B) = \frac{P(B \mid A) \times P(A)}{P(B)}$$

$$= \frac{P(B \mid A) \times P(A)}{P(B \mid A) \times P(A) + P(B \mid A^c) \times P(A^c)}$$

In medical testing context:

$$P(\text{Disease} \mid \text{Test+}) = \frac{\text{sensitivity} \times \text{prevalence}}{\text{sensitivity} \times \text{prevalence} + (1 - \text{specificity}) \times (1 - \text{prevalence})}$$

Pro tip: Calculate numerator and denominator separately, then divide!

Bayes’ Theorem: Step-by-Step

Given: Sensitivity = 0.90, Specificity = 0.85, Prevalence = 0.02

```r
# Step 1: Set up
sensitivity <- 0.90     # P(Test + | Disease)
specificity <- 0.85     # P(Test - | No Disease)
prevalence <- 0.02      # P(Disease)

# Step 2: Calculate P(Test + | No Disease)
p_pos_given_healthy <- 1 - specificity
p_pos_given_healthy
```

```
[1] 0.15
```

```r
# Step 3: Numerator (true positives)
numerator <- sensitivity * prevalence
numerator
```

```
[1] 0.018
```

```r
# Step 4: Denominator (all positives)
denominator <- sensitivity * prevalence + p_pos_given_healthy * (1 - prevalence)
denominator
```

```
[1] 0.165
```

```r
# Step 5: PPV
ppv <- numerator / denominator
ppv
```

```
[1] 0.1090909
```

Distributions: The R Functions

The Four Functions Pattern

Every distribution in R has 4 functions:

d-functions: `dbinom()`, `dnorm()`, `dpois()`

- "density" or "probability mass"
- **Exactly** x
- Returns: P(X = x)

p-functions: `pbinom()`, `pnorm()`, `ppois()`

- "cumulative probability"
- **At most** x (or **at least** with `lower.tail = FALSE`)
- Returns: P(X ≤ x) or P(X > x)

q-functions: `qbinom()`, `qnorm()`, `qpois()`

- "quantile"
- What value gives this probability?
- Returns: value of x

r-functions: `rbinom()`, `rnorm()`, `rpois()`

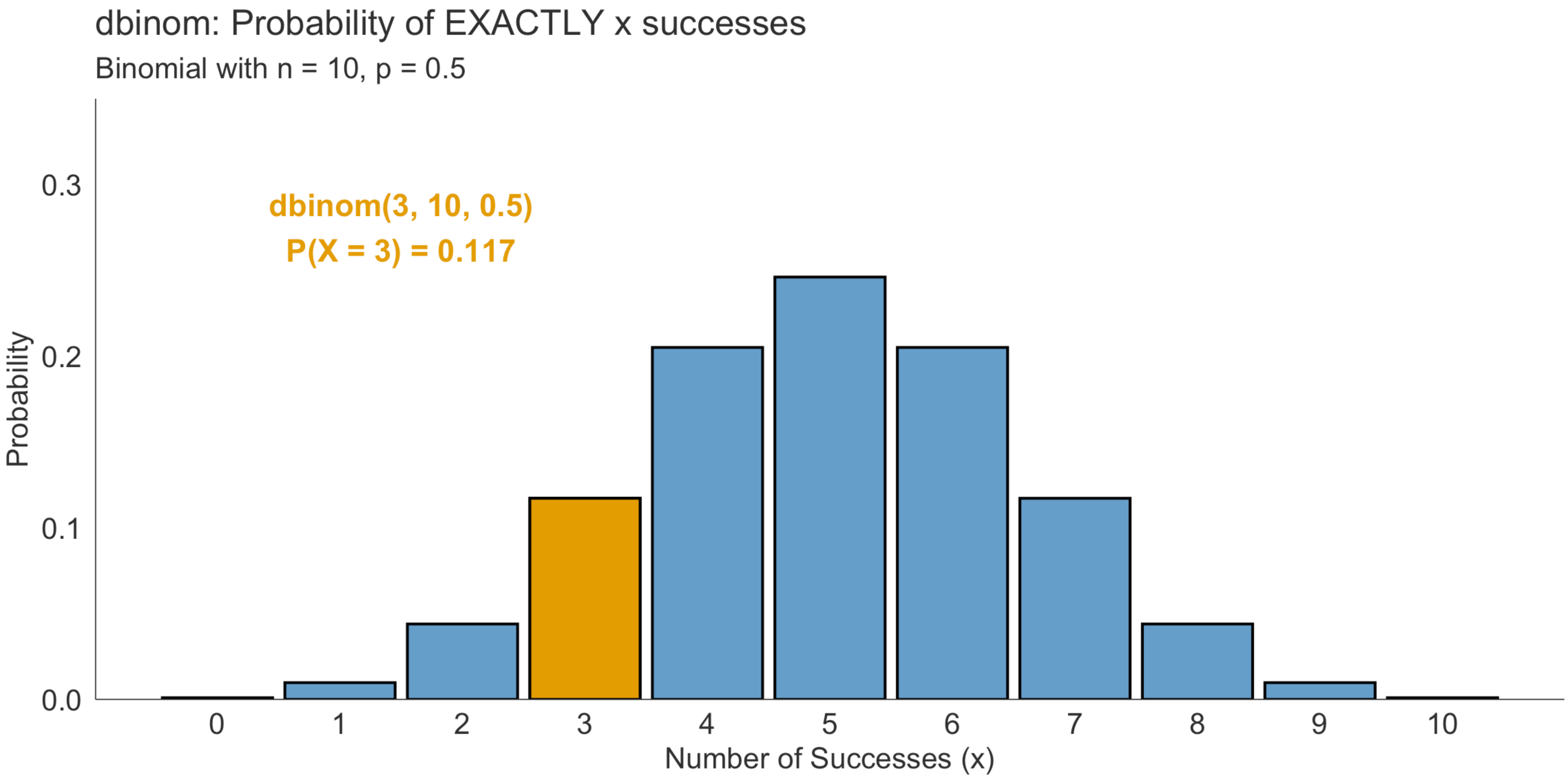
- "random"
- Generate random samples
- Returns: random values

Binomial Functions in R

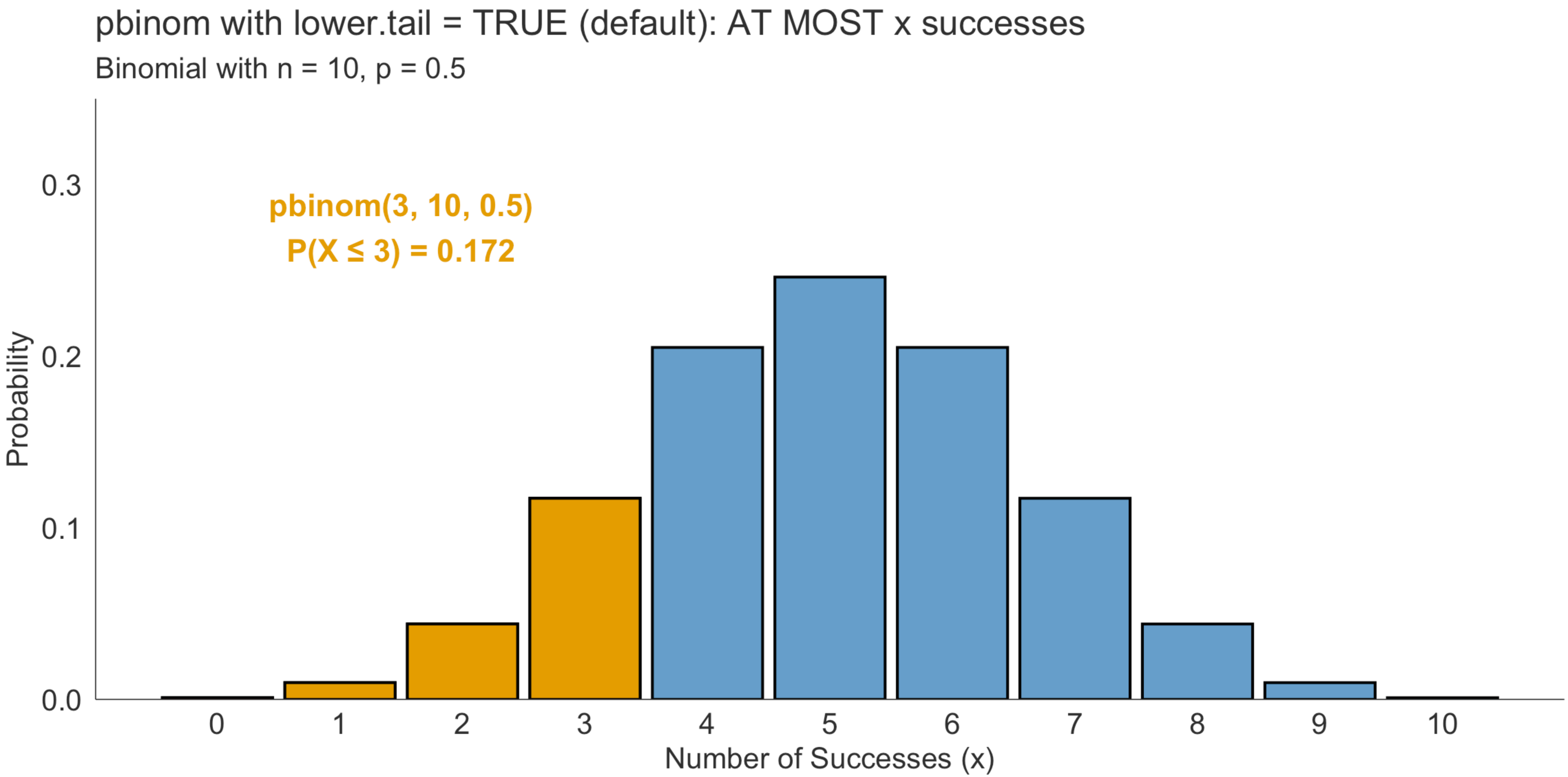
The four binomial functions:

```r
# d = probability of EXACTLY x successes
dbinom(x = 3, size = 10, prob = 0.5)
# "What's P(X = 3)?"

# p = cumulative probability (at most x OR at least x)
pbinom(q = 3, size = 10, prob = 0.5)
# "What's P(X ≤ 3)?" (default)

pbinom(q = 3, size = 10, prob = 0.5, lower.tail = FALSE)
# "What's P(X > 3)?"

# q = quantile (what value gives this probability?)
qbinom(p = 0.25, size = 10, prob = 0.5)
# "What value has 25% of the distribution below it?"

# r = random samples
rbinom(n = 100, size = 10, prob = 0.5)
# "Give me 100 random draws"
```

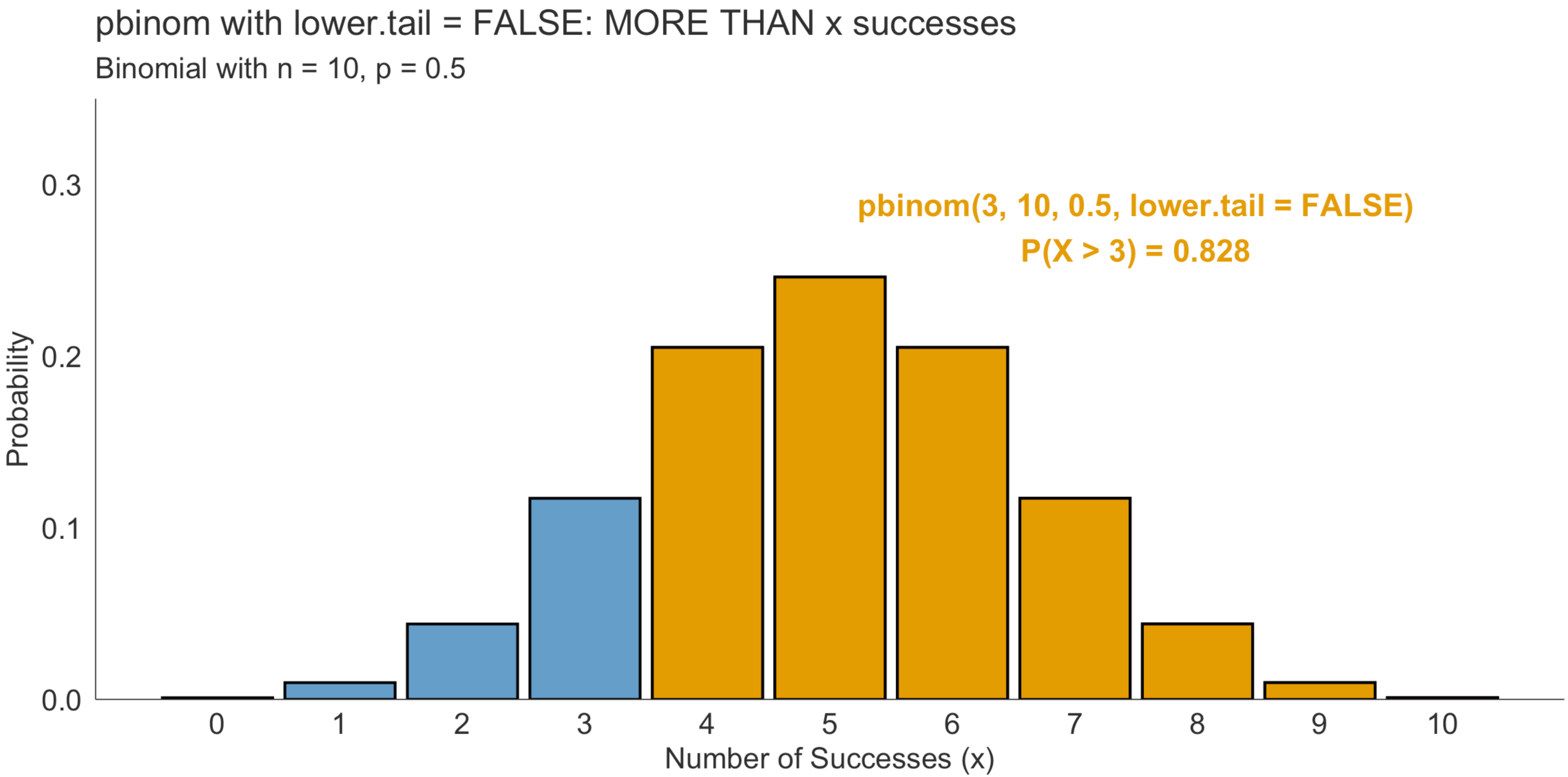
Visual: dbinom() - EXACTLY



Visual: pbinom() - AT MOST (default)



Visual: pbinom(..., lower.tail = FALSE) - MORE THAN



The lower.tail = TRUE/FALSE Concept

Visual Guide

```
|--------------●-------------|
lower tail     x    upper tail
(left)                 (right)
```

lower.tail = TRUE → gives you $P(X \leq x)$ — everything to the **LEFT** of (and including) x

lower.tail = FALSE → gives you $P(X > x)$ — everything to the **RIGHT** of x

Quick decision rule:

- Question has “**less than**” or “**at most**” → `lower.tail = TRUE` (default)
- Question has “**greater than**” or “**at least**” → `lower.tail = FALSE`

Common Confusion: "At least 5" (Discrete Distributions)

Question: What is $P(X \geq 5)$ for a binomial distribution?

Step 1: Translate to something the computer understands

- "At least 5" = "5 or more" = "greater than 4"
- So: $P(X \geq 5)$ = $P(X > 4)$

Step 2: Code it

```r
# Correct!
pbinom(q = 4, size = 10, prob = 0.5, lower.tail = FALSE)

# Also correct (but slightly more work)
1 - pbinom(q = 4, size = 10, prob = 0.5)
```

Key Point

For discrete distributions: "$X \geq 5$" is the same as "$X > 4$" because we can't have 4.5 successes!

This slide applies to **binomial and Poisson** (discrete). For Normal (continuous), $P(X \geq 5) = P(X > 5)$ - no adjustment needed!

Common Confusion: "At least 5" (Discrete Distributions)

DISCRETE distributions only!

This applies to **binomial and Poisson** (discrete). For Normal (continuous), $P(X \geq 5) = P(X > 5)$.

Question: What is $P(X \geq 5)$ for a binomial distribution?

Translate to computer language: "At least 5" = "5 or more" = "greater than 4"

$$P(X \geq 5) = P(X > 4)$$

Code it:

```r
pbinom(q = 4, size = 10, prob = 0.5, lower.tail = FALSE)  # Correct!
1 - pbinom(q = 4, size = 10, prob = 0.5)                  # Also works
```

Key point: For discrete distributions, "$X \geq 5$" equals "$X > 4$" because we can't have 4.5 successes!

Practice: Binomial Questions

A vaccine is 75% effective. You vaccinate 20 people.

Which R function do you use?

Question 1: What's the probability that *exactly* 15 are protected?

```
# Your answer:
```

Question 2: What's the probability that *at most* 12 are protected?

```
# Your answer:
```

Question 3: What's the probability that *at least* 18 are protected?

```
# Your answer:
```

Question 4: What's the expected number protected?

```
# Your answer:
```

Practice: Binomial Answers (1/2)

A vaccine is 75% effective. You vaccinate 20 people.

Question 1: What's the probability that *exactly* 15 are protected?

```r
# Question 1: Exactly 15
dbinom(x = 15, size = 20, prob = 0.75)
```

```
[1] 0.2023312
```

Question 2: What's the probability that *at most* 12 are protected?

```r
# Question 2: At most 12
pbinom(q = 12, size = 20, prob = 0.75)
```

```
[1] 0.1018119
```

```r
# OR: pbinom(q = 12, size = 20, prob = 0.75, lower.tail = TRUE)
```

Practice: Binomial Answers (2/2)

Question 3: What's the probability that *at least* 18 are protected?

```r
# Question 3: At least 18 (same as > 17)
pbinom(q = 17, size = 20, prob = 0.75, lower.tail = FALSE)
```

```
[1] 0.09126043
```

```r
# OR: 1 - pbinom(q = 17, size = 20, prob = 0.75)
```

Question 4: What's the expected number protected?

```r
# Question 4: Expected value
n <- 20
p <- 0.75
expected <- n * p
expected
```

```
[1] 15
```

```r
# Bonus: standard deviation
variance <- n * p * (1 - p)
st_dev <- sqrt(variance)
st_dev
```

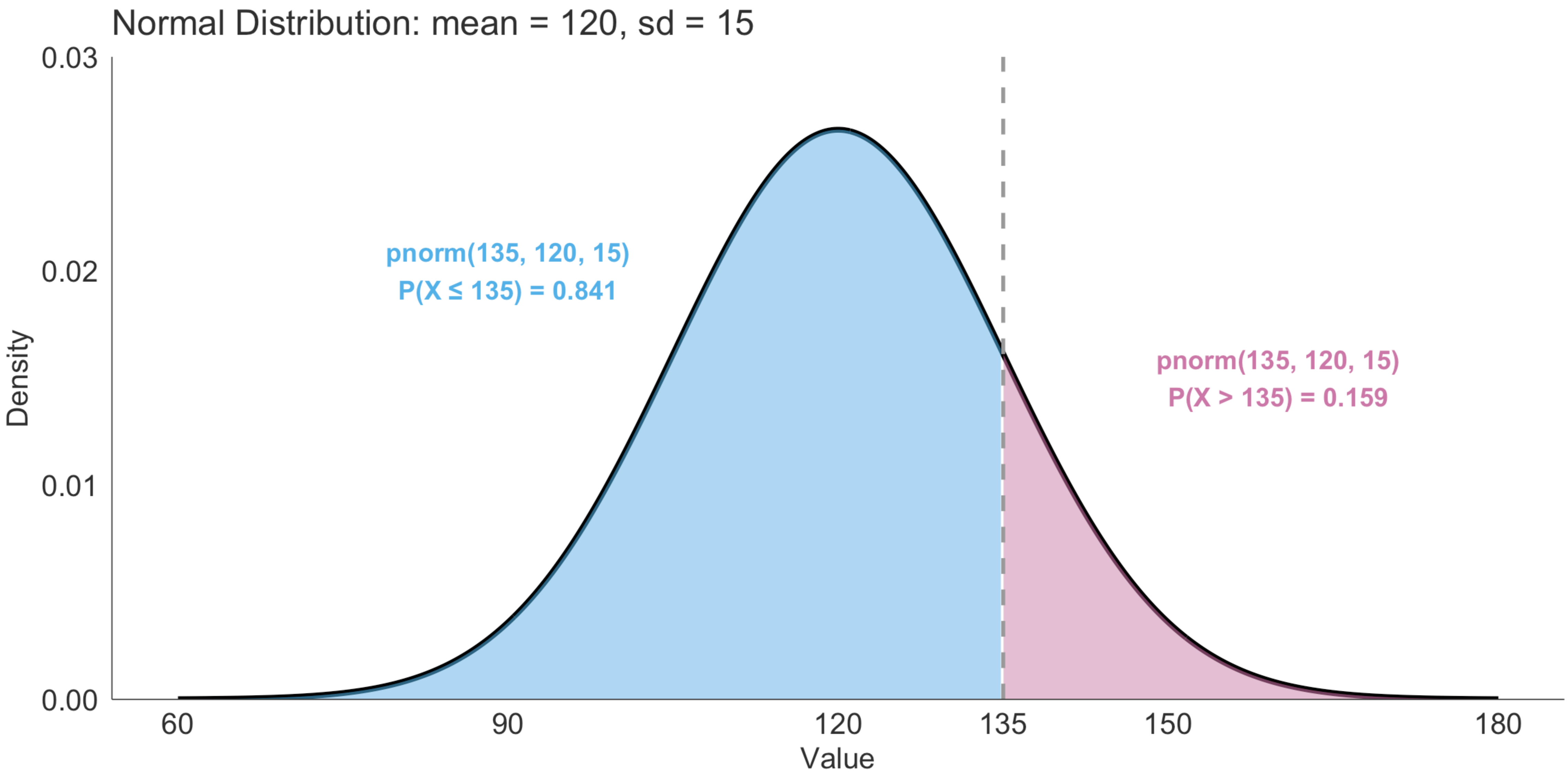
```
[1] 1.936492
```

Normal Distribution Functions

The same pattern applies!

```r
# d = density (height of curve at x)
dnorm(x = 120, mean = 100, sd = 15)
# Rarely used in practice

# p = cumulative probability
pnorm(q = 120, mean = 100, sd = 15)
# "What proportion have values ≤ 120?"

pnorm(q = 120, mean = 100, sd = 15, lower.tail = FALSE)
# "What proportion have values > 120?"

# q = quantile (most common!)
qnorm(p = 0.95, mean = 100, sd = 15)
# "What value has 95% below it?" (95th percentile)

# r = random samples
rnorm(n = 100, mean = 100, sd = 15)
# "Give me 100 random values from this distribution"
```

Visual: Normal Distribution



Practice: Normal Distribution

Blood pressure is Normal with mean = 120 mmHg, sd = 15 mmHg.

Which R function?

Question 1: What proportion have BP above 135?

```
# Your answer:
```

Question 2: What proportion have BP between 110 and 130?

```
# Your answer:
```

Question 3: What BP value is the 90th percentile?

```
# Your answer:
```

Question 4: If we want the middle 95%, what are the cutoffs?

```
# Your answer:
```

Practice: Normal Answers (1/2)

```r
mu <- 120
sigma <- 15

# Question 1: Above 135
pnorm(135, mean = mu, sd = sigma, lower.tail = FALSE)
```

```
[1] 0.1586553
```

```r
# OR
1 - pnorm(135, mean = mu, sd = sigma, lower.tail = TRUE)
```

```
[1] 0.1586553
```

```r
# Question 2: Between 110 and 130
pnorm(130, mean = mu, sd = sigma) - pnorm(110, mean = mu, sd = sigma)
```

```
[1] 0.4950149
```

Practice: Normal Answers (2/2)

```r
# Question 3: 90th percentile
qnorm(0.90, mean = mu, sd = sigma)
```

```
[1] 139.2233
```

```r
# Question 4: Middle 95% (2.5th to 97.5th percentiles)
qnorm(0.025, mean = mu, sd = sigma)  # Lower
```

```
[1] 90.60054
```

```r
qnorm(0.975, mean = mu, sd = sigma)  # Upper
```

```
[1] 149.3995
```

Sampling Distributions & CLT

Central Limit Theorem: What You Need to Know

The CLT in plain language

For a random sample of size n from ANY population with mean μ and SD σ:

The sampling distribution of $\bar{X}$ is approximately normal when n is large (≥ 30)

With:

- Mean = μ
- Standard Error = $\sigma/\sqrt{n}$

Why this matters:

1. We can use normal distribution tools even if data aren't normal
2. Larger samples → smaller standard error → more precise estimates
3. This is the foundation for confidence intervals and hypothesis tests!

Standard Error vs. Standard Deviation

Don't confuse these!

Standard Deviation (s or σ):

- Measures spread of *individual observations*
- Describes variability in the data
- Formula: $s = \sqrt{\frac{\sum(x_i - \bar{x})^2}{n-1}}$

Standard Error (SE):

- Measures uncertainty of the *sample mean*
- Describes variability of $\bar{x}$ across (theoretical) samples
- Formula: $SE = \frac{s}{\sqrt{n}}$

Key insight: SE gets smaller as n increases, but s stays roughly the same!

Example: CLT in Action

Population: Mean = 5.1 hours, SD = 1.9 hours, right-skewed

Sample: n = 40

What's the sampling distribution of $\bar{X}$?

```r
# Parameters
mu <- 5.1
sigma <- 1.9
n <- 40

# Sampling distribution
mean_xbar <- mu
se_xbar <- sigma / sqrt(n)

mean_xbar
```

```
[1] 5.1
```

```r
se_xbar
```

```
[1] 0.3004164
```

```r
# Example probability about the sample mean, P(Xbar > 5.6)
pnorm(5.6, mean = mean_xbar, sd = se_xbar, lower.tail = FALSE)
```

```
[1] 0.04802059
```

Sampling distribution: approximately Normal(mean = mu, sd = $\frac{s}{\sqrt{n}}$). Even though the original data are right-skewed!

Confidence Intervals

Confidence Interval Formula

General form

$$\text{point estimate} \pm \text{critical value} \times SE$$

For a mean:

$$\bar{x} \pm t^* \times \frac{s}{\sqrt{n}}$$

Where:

- $\bar{x}$ = sample mean
- t^* = critical value from t-distribution with $df = n - 1$
- s = sample standard deviation
- n = sample size

Calculating a 95% CI in R (1/2)

```r
# Sample data
n <- 25
xbar <- 14.2
s <- 1.8
confidence_level <- 0.95

# Step 1: Find critical value
t_star <- qt((1 + confidence_level) / 2, df = n - 1)
# OR: qt(0.975, df = 24)
t_star
```

```
[1] 2.063899
```

```r
# Step 2: Calculate standard error
SE <- s / sqrt(n)
SE
```

```
[1] 0.36
```

Calculating a 95% CI in R (2/2)

```r
# Step 3: Calculate margin of error
margin_error <- t_star * SE
margin_error
```

```
[1] 0.7430035
```

```r
# Step 4: Build the interval
lower <- xbar - margin_error
upper <- xbar + margin_error

c(lower, upper)
```

```
[1] 13.457 14.943
```

Interpreting Confidence Intervals

Correct interpretation

"We are 95% confident that the population mean is between 13.5 and 14.9."

What this means:

- If we repeated this process many times (new samples, new CIs)
- About 95% of those intervals would contain the true μ
- We don't know if *this specific interval* contains μ, but we're using a reliable method

Common mistakes - DON'T SAY:

- ❌ "There's a 95% probability that μ is in this interval"
- ❌ "95% of the data are in this interval"
- ❌ "We're 95% sure the sample mean is in this interval"

What Affects CI Width?

Margin of error = $t^* \times \frac{s}{\sqrt{n}}$

To get a narrower CI:

1. **Increase sample size** ($n \uparrow$ → SE ↓ → narrower CI)
2. **Decrease confidence level** (95% → 90% → smaller t^* → narrower CI)
   - But this means less confidence!
3. **Reduce variability** ($s \downarrow$ → SE ↓ → narrower CI)
   - Often not under our control

Trade-off: Precision vs. Confidence

Hypothesis Testing

The Hypothesis Testing Framework

Six steps:

1. **State hypotheses:** H_0 and H_A
2. **Set significance level:** Usually $\alpha = 0.05$
3. **Check assumptions:** Independence, normality/large sample
4. **Calculate test statistic:** $t = \frac{\bar{x}-\mu_0}{s/\sqrt{n}}$
5. **Find p-value:** Probability of seeing data this extreme if H_0 true
6. **Make conclusion:** Reject H_0 if p-value < α

Writing Hypotheses

Template

$H_0 : \mu = \mu_0$ (null value)

$H_A : \mu \neq \mu_0$ (two-sided) OR $\mu > \mu_0$ OR $\mu < \mu_0$ (one-sided)

Example: Is mean body temperature different from 98.6°F?

- $H_0 : \mu = 98.6$
- $H_A : \mu \neq 98.6$

In words:

- H_0: The population mean body temperature is 98.6°F
- H_A: The population mean body temperature is not 98.6°F

P-values: What They Mean

Definition

The p-value is the probability of observing data as extreme as (or more extreme than) what we observed, **assuming** H_0 is true.

Interpretation guide:

- p-value < 0.05 → Strong evidence against H_0 → Reject H_0
- p-value ≥ 0.05 → Insufficient evidence → Fail to reject H_0

What p-values are NOT

- ❌ NOT the probability that H_0 is true
- ❌ NOT the probability of making an error
- ❌ NOT a measure of effect size or importance

One-Sample t-test in R

```r
# Using raw data
t.test(data$variable,
       mu = null_value,
       alternative = "two.sided")  # or "less" or "greater"
```

Example:

```r
# Test if mean pulse rate is different from 72 bpm
data("nhanes.samp")

t.test(nhanes.samp$Pulse,
       mu = 72,
       alternative = "two.sided")
```

Understanding t.test() Output

```
	One Sample t-test

data:  nhanes.samp$Pulse
t = 2.1383, df = 170, p-value = 0.03392
alternative hypothesis: true mean is not equal to 72
95 percent confidence interval:
 72.15999 76.00376
sample estimates:
mean of x 
 74.08187 
```

What to report:

- **t-statistic:** How many SEs away from null value
- **p-value:** Evidence against H_0
- **95% CI:** Range of plausible values for μ
- **Sample mean:** Our point estimate

Connection: CIs and Hypothesis Tests

Key relationship

For a two-sided test at $\alpha = 0.05$:

If the 95% CI does NOT contain μ_0, then we reject $H_0 : \mu = \mu_0$

If the 95% CI DOES contain μ_0, then we fail to reject H_0

Both methods use the same math - just different framing!

- CI: "What values are plausible for μ?"
- Hypothesis test: "Is this specific value plausible?"

Final Reminders

Statistical Significance vs. Practical Significance

Don’t confuse these!

Statistical significance ($p < 0.05$):

- Evidence that there’s a real effect
- Doesn’t tell you if the effect matters

Practical/Clinical significance:

- Effect is large enough to matter in real-world terms
- You must judge this based on context

Example: A drug lowers blood pressure by 0.5 mmHg ($p = 0.001$)

- Statistically significant? ✅ Yes
- Clinically meaningful? ❌ No (too small to affect patient outcomes)

Common Mistakes to Avoid

1. **Forgetting to check assumptions** before running tests
2. **Confusing standard deviation and standard error**
3. **Using `lower.tail = TRUE` when you need `FALSE`** (or vice versa)
4. **Misinterpreting p-values and confidence intervals**
5. **Forgetting to include** `na.rm = TRUE` when there are missing values
6. **Not rendering your document before submitting**

Pro tip: When using `pbinom()` or `ppois()`, sketch a quick picture to check if you want the left or right tail!

Exam Strategy

Time management:

- Don’t get stuck on one question
- Move on and come back if needed
- Leave buffer time for rendering and checking

Interpretation questions:

- Write in complete sentences
- Reference numbers from your calculations
- Connect to context (not just abstract statistics)

Coding questions:

- Show your work (don’t just give answers)
- Use comments to explain your logic
- Check that your code actually runs!

Resources

During the exam:

- Lecture slides (especially the summary slides)
- Homework solutions (you've seen similar questions!)
- R help: `?t.test`, `?pnorm`, etc.

After you submit:

- The exam will close Monday at 11 PM
- Solutions will be available after
- We'll get feedback to you within a week
- Remember: This is a learning experience!

Questions?

Your Turn!

What questions do you have?

- Concepts that are still unclear?
- R functions you're unsure about?
- Specific exam questions you want to discuss?

Remember:

- Exam opens today at 3 PM
- You have until Monday at 11 PM
- You've got this! 💪

Good luck!

You’re well prepared:

- ✅ You’ve done the homework
- ✅ You’ve come to class
- ✅ You’ve practiced with R
- ✅ You know where to find help

Trust your preparation and think carefully about each question.