Lecture 01b – The fundamentals

ENVX2001 Applied Statistical Methods

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A refresher (for most)

You should be familiar with the following concepts:

1. Populations, samples and statistical inference
2. Probability distributions
3. Parameter estimation: central tendency, spread and variability
4. Sampling distribution of the mean: standard error, confidence intervals
5. Central Limit Theorem

That's it!

Why review these concepts?

- These are concepts taught in first year statistics courses which we consider to be fundamental
- Even if you come from a unit/course that does not do R, **you should at least be familiar with the basic building blocks of statistical thinking**

Let's go through these concepts together!

Samples, populations

Populations

- **All** the possible units and their associated observations of interest
- Scientists are often interested in making *inferences* about populations, but measuring every unit is impractical

Samples

- A collection of observations from any population is a sample, and the number of observations in it is the **sample size**
- We assume samples that we collect can be used to make inferences about the population
- **NEW**: Samples need to be *representative* of the population

Statistics vs parameters

- Characteristics of the **population** are called *parameters* (e.g. the true average height of all trees in a forest)
- Characteristics of the **sample** are called *statistics* (e.g. the average height of 30 trees that we measured)
- In practice, we usually don't know the true population parameters, so we use sample statistics as our best estimates
- Drawing conclusions about a population from sample data is called **statistical inference**

Not all statistical techniques are inferential – some are purely descriptive (e.g. summarising data with graphs or tables) – but inference is the main focus of this course.

Sample data

Sample data are usually collected as **variables** – the characteristics we measure or record from each unit in our sample.

Variables can be:

Categorical Variables

- **Nominal**: categories without a natural order (e.g. soil type, land use)
- **Ordinal**: categories with a natural order (e.g. soil quality: poor, fair, good)

Numerical Variables

- **Continuous**: can take any value within a range (e.g. height, temperature)
- **Discrete**: can take only specific values (e.g. number of species, presence/absence)

Variable types can overlap

The categories on the previous slide are useful guidelines, but in practice, variables can cross between types depending on how you use them.

Examples

- **height (in cm)** – a numerical, **continuous** variable, but can be treated as categorical if you group it into categories (short, medium, tall)
- **age (in years)** – a numerical, **discrete** variable, but often treated as continuous because the gaps between values are small relative to the range
- **treatment (A, B, C)** – a categorical variable, but can be treated as numerical if we assign numbers to the treatments (1, 2, 3) and assume they are **ordered** e.g. effect of $1 < 2 < 3$

Be careful when converting variables

Converting a numerical variable to a categorical one means **losing information** – once you group heights into "short", "medium" and "tall", the exact measurements are gone.

- A tree that is 5.1 m and a tree that is 9.9 m might both be called "tall", but they are very different
- Only categorise when there is good reason to do so, as this reduces your analysis power
- Going the other way (categorical $\rightarrow$ numerical) doesn't lose data, but it does **add assumptions** – e.g. that your categories have a meaningful order

Distribution of data

Types of probability distributions

Populations can be described by probability distributions. You may have encountered these common ones in first-year statistics:

- **Normal Distribution**: Bell-shaped curve, symmetric around the mean. **Data is continuous** (e.g. heights, weights)
- **Binomial Distribution**: Models success/failure outcomes in a fixed number of trials. **Data is discrete** (e.g. how many seeds germinate out of 10 planted)
- **Poisson Distribution**: Models count data over a fixed area or time period. **Data is discrete** (e.g. number of weeds found in a 1 m² quadrat)

Knowing the distribution of your data helps you choose the right statistical model. We will return to this throughout the course.

```r
library(tidyverse)

set.seed(908)
normal_data <- data.frame(x = rnorm(10000, mean = 0, sd = 1))
binomial_data <- data.frame(x = rbinom(10000, size = 10, prob = 0.5))
poisson_data <- data.frame(x = rpois(500, lambda = 3))

# normal
p1 <- ggplot(normal_data, aes(x = x)) +
  geom_histogram(aes(y = after_stat(density)), bins = 30, fill = "lightblue", color = "black") +
  geom_density(color = "red") +
  ggtitle("Normal Distribution")

# binomial
p2 <- ggplot(binomial_data, aes(x = x)) +
  geom_bar(fill = "lightgreen", color = "black") +
  ggtitle("Binomial Distribution")

# poisson
p3 <- ggplot(poisson_data, aes(x = x)) +
```
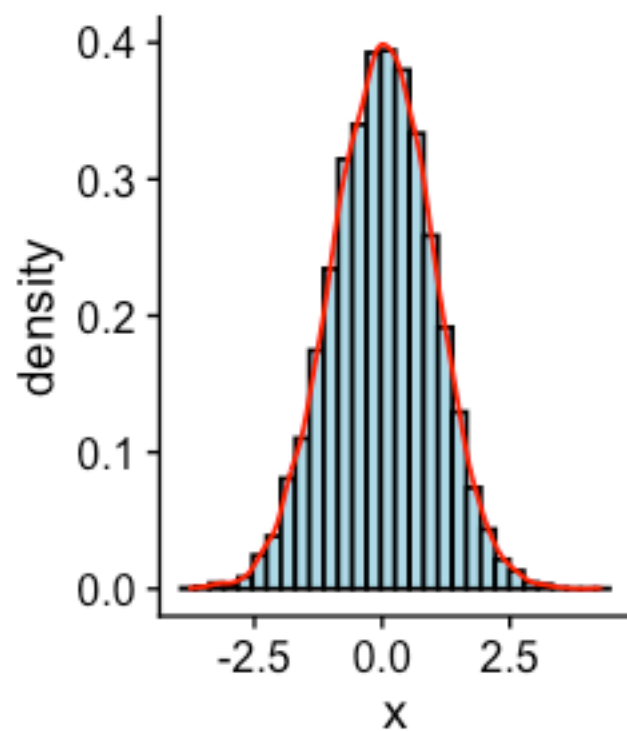
```r
  geom_bar(fill = "lightpink", color = "black") +
  ggtitle("Poisson Distribution")

# Arrange plots
library(patchwork)
p1 | p2 / p3
```
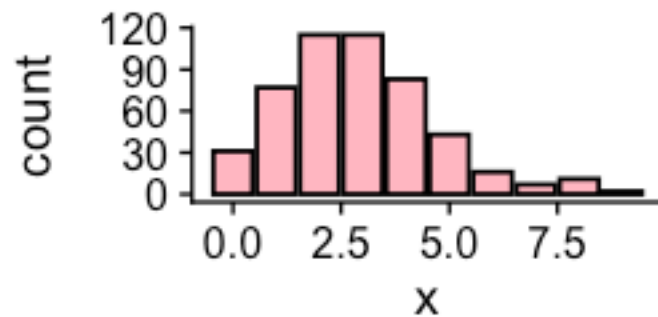
Parameter estimation

Measures of central tendency

Central tendency tells you where the "middle" or "typical" value of your data falls. There are several ways to measure it, each with trade-offs.

Mean $\bar{x}$

- The sum of all values divided by the number of observations – what `mean()` does in R
- Sensitive to extreme values (outliers)

> ⚠️ **Formula**
>
> $$\bar{x} = \frac{1}{n} \sum_{i=1}^{n} x_i$$
>
> - where n is the number of observations
> - x_i represents each individual value
> - $\sum$ means we add up all values from $i = 1$ to n
> - Example: for data {2,4,6,8}, $n = 4$ and $\bar{x} = \frac{2+4+6+8}{4} = 5$
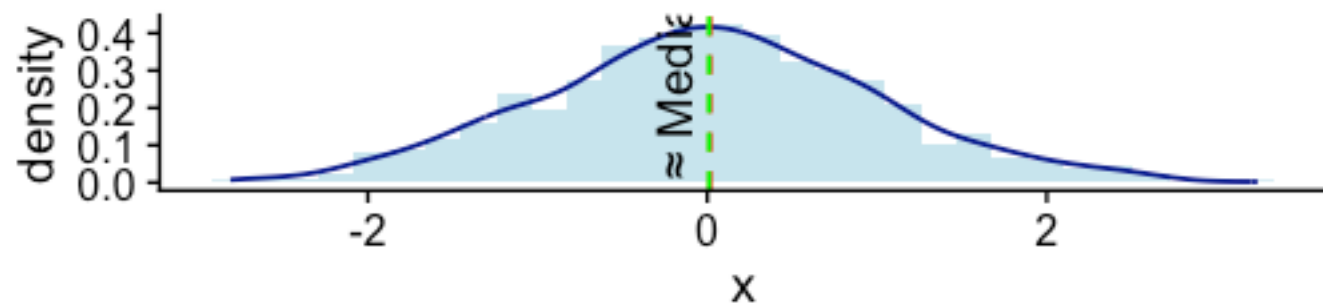
Median and mode

Median

- Sort your data from smallest to largest and take the middle value
- The median is resistant to extreme values, making it a better representation of typical observations when data is skewed
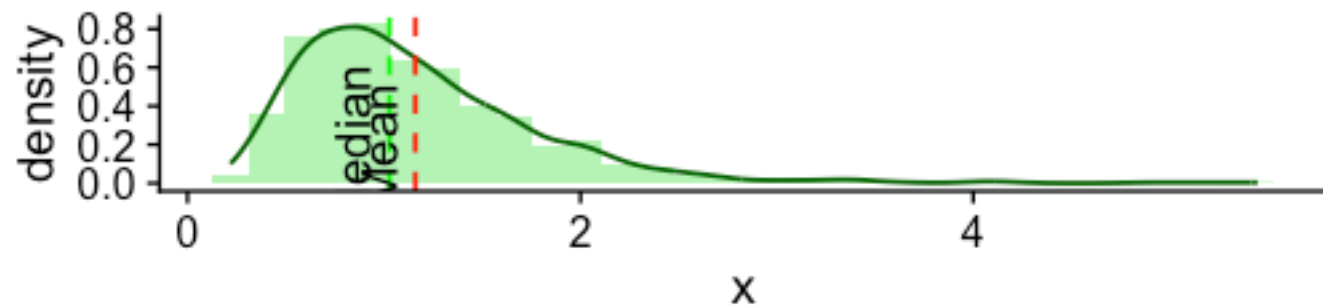
Mode

- The most frequently occurring value in a dataset
- Can have multiple modes (e.g. a bimodal distribution has two peaks)
- The only measure of central tendency that works for categorical data

How they compare

Symmetric Distribution

density | 0.4 0.3 0.2 0.1 0.0

≈ Media

x: -2, 0, 2

Skewed Distribution

density | 0.8 0.6 0.4 0.2 0.0

Median
Mean

x: 0, 2, 4

When the mean and median are close, your data is roughly symmetric. When they differ substantially, the data is skewed – the mean shifts toward extreme values.

Measures of dispersion

Dispersion measures how spread out your data is. Two datasets can have identical means but very different spreads.

Variance s^2

- The average squared distance of each value from the mean
- Since the result is in squared units (e.g. m²), it's hard to interpret directly – we usually take the square root to get standard deviation

Measures of dispersion

> ⚠️ **Formula**
>
> $$s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2$$
>
> - where n is the number of observations
> - x_i represents each individual value
> - $\bar{x}$ is the sample mean
> - For data {2,4,6,8}:
>   - mean = 5
>   - differences = (-3,-1,1,3), squares = (9,1,1,9), sum = 20
>   - Therefore, $s^2 = \frac{20}{3} \approx 6.67$

Measures of dispersion

Standard Deviation s

- The square root of variance – expressed in your data's original units (e.g. metres, not metres²)
- Shows how far a typical observation is from the mean

> ⚠️ Formula
>
> $$s = \sqrt{s^2}$$
>
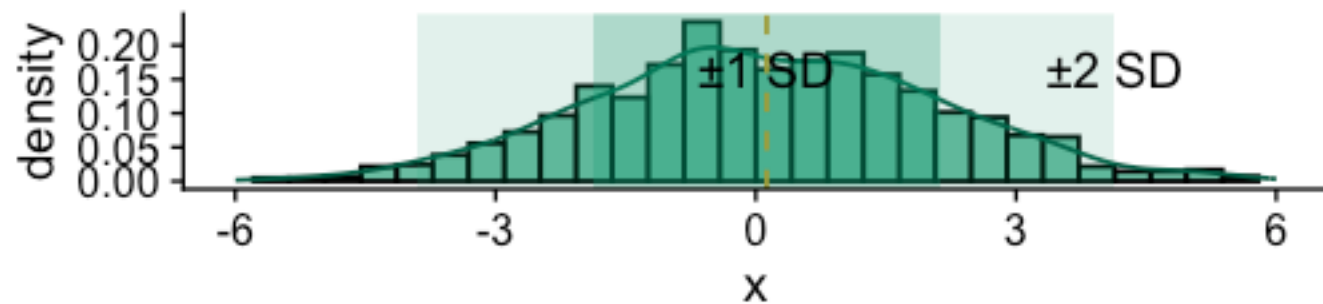> - For our example data {2,4,6,8}: $s = \sqrt{6.67} \approx 2.58$

Visualising standard deviation

For normally distributed data, standard deviation tells you what proportion of values fall within each range of the mean:

- about **68%** of values fall within ±1 SD
- about **95%** within ±2 SD
- about **99.7%** within ±3 SD

Smaller dispersion (SD = 1)

±1 SD ±2 SD

Larger dispersion (SD = 2)

±1 SD ±2 SD

Population parameters vs sample statistics

Throughout the course you'll see Greek letters (μ, σ) for population parameters and Roman letters ($\bar{x}$, s) for sample statistics:

Mean

Population Parameter	Sample Statistic
$\mu = \frac{1}{N} \sum_{i=1}^{N} x_i$	$\bar{x} = \frac{1}{n} \sum_{i=1}^{n} x_i$

Variance

Population Parameter	Sample Statistic
$\sigma^2 = \frac{1}{N} \sum_{i=1}^{N} (x_i - \mu)^2$	$s^2 = \frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2$

Standard Deviation

Population Parameter	Sample Statistic
$\sigma = \sqrt{\sigma^2}$	$s = \sqrt{s^2}$

> **i Note**
>
> Notice the use of $n-1$ in sample variance and standard deviation

Why n-1?

- Sample variance uses $n - 1$ instead of n in the denominator
- This correction (Bessel's correction) accounts for bias when estimating the mean from the sample itself

- Here's the logic: once you know the mean and all but one value, the last value is determined – it must satisfy the mean. Only $n - 1$ values are truly free to vary
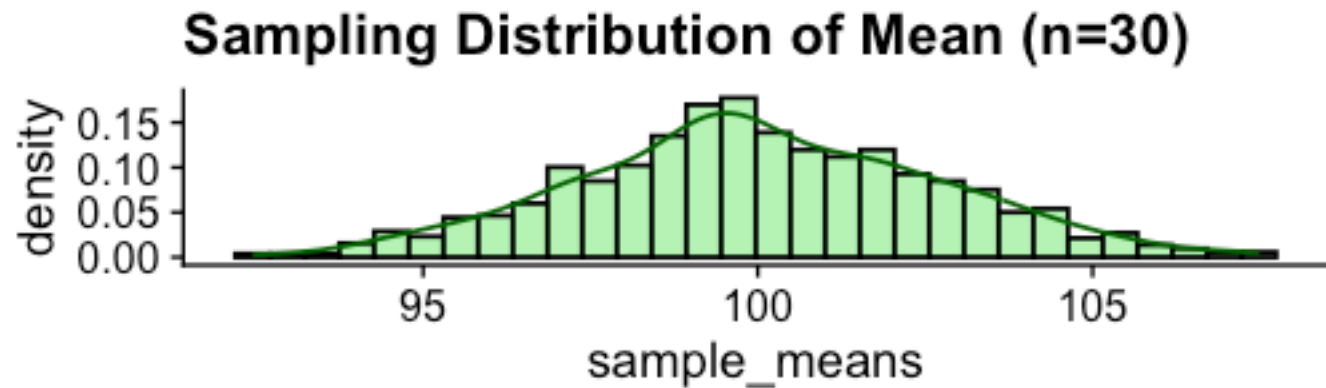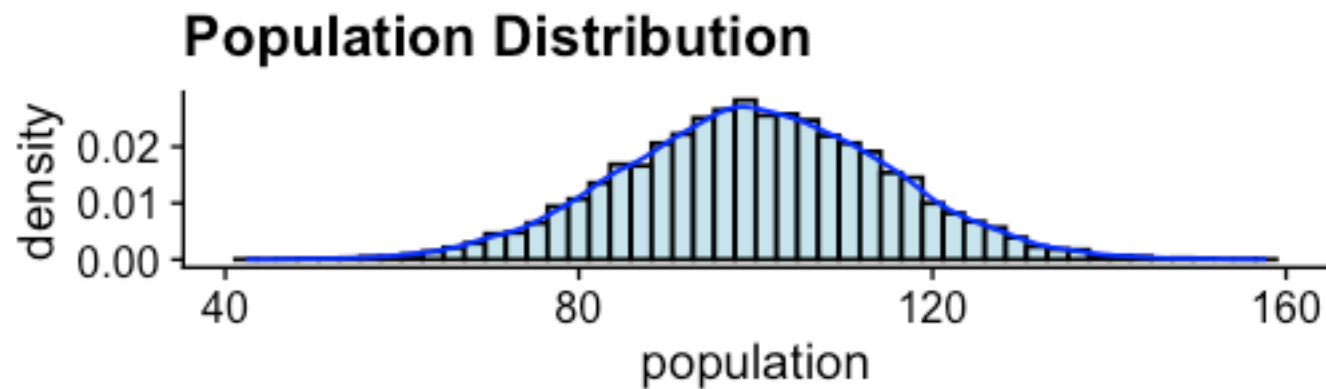- These independent values are your **degrees of freedom**

Sampling distributions and CLT

What is a sampling distribution?

Imagine you collected your sample of 30 trees, calculated the mean height, then did it again – 1000 times. Each time, you'd get a slightly different mean.

- The distribution of all those means is a **sampling distribution**
- It shows how much your estimate (the sample mean) varies due to sampling randomness
- This foundation of statistical inference lets you quantify confidence in your estimates

Sampling distribution of the mean

Central Limit Theorem

> I know of scarcely anything so apt to impress the imagination as the wonderful form of **cosmic order** expressed by the Central Limit Theorem. The law would have been personified by the Greeks and deified, if they had known of it."

– Sir Francis Galton, 1889, Natural Inheritance

The Central Limit Theorem (CLT) states that for sufficiently large samples:

1. The distribution of sample means becomes **approximately normal**, regardless of the population's shape
2. The average of those sample means equals the **true population mean**
3. The spread of the sampling distribution decreases as sample size increases: $SE = \frac{\sigma}{\sqrt{n}}$

In short: with larger samples, their means form a predictable, bell-shaped pattern – even if the original data is skewed.

CLT in action

```r
# Create a skewed population
set.seed(456)
skewed_pop ← exp(rnorm(10000, mean = 0, sd = 0.5))

# Sample means for different sample sizes (ordered small to large)
sample_sizes ← c(5, 30, 100)
sample_labels ← factor(paste("n =", sample_sizes),
  levels = paste("n =", sample_sizes)
) # preserve order
sample_dist_data ← lapply(sample_sizes, function(n) {
  means ← replicate(1000, mean(sample(skewed_pop, size = n)))
  data.frame(means = means, size = factor(paste("n =", n), levels = levels(sample_labels)))
})
sample_dist_df ← do.call(rbind, sample_dist_data)

# Plot
ggplot() +
  geom_histogram(aes(x = means, y = after_stat(density)),
    data = sample_dist_df,
```

```
  bins = 30, fill = "lightblue", color = "black", alpha = 0.7
) +
geom_density(aes(x = means), data = sample_dist_df, color = "blue") +
facet_wrap(~size, scales = "free_x") +
ggtitle("Sampling distributions for different sample sizes")
```
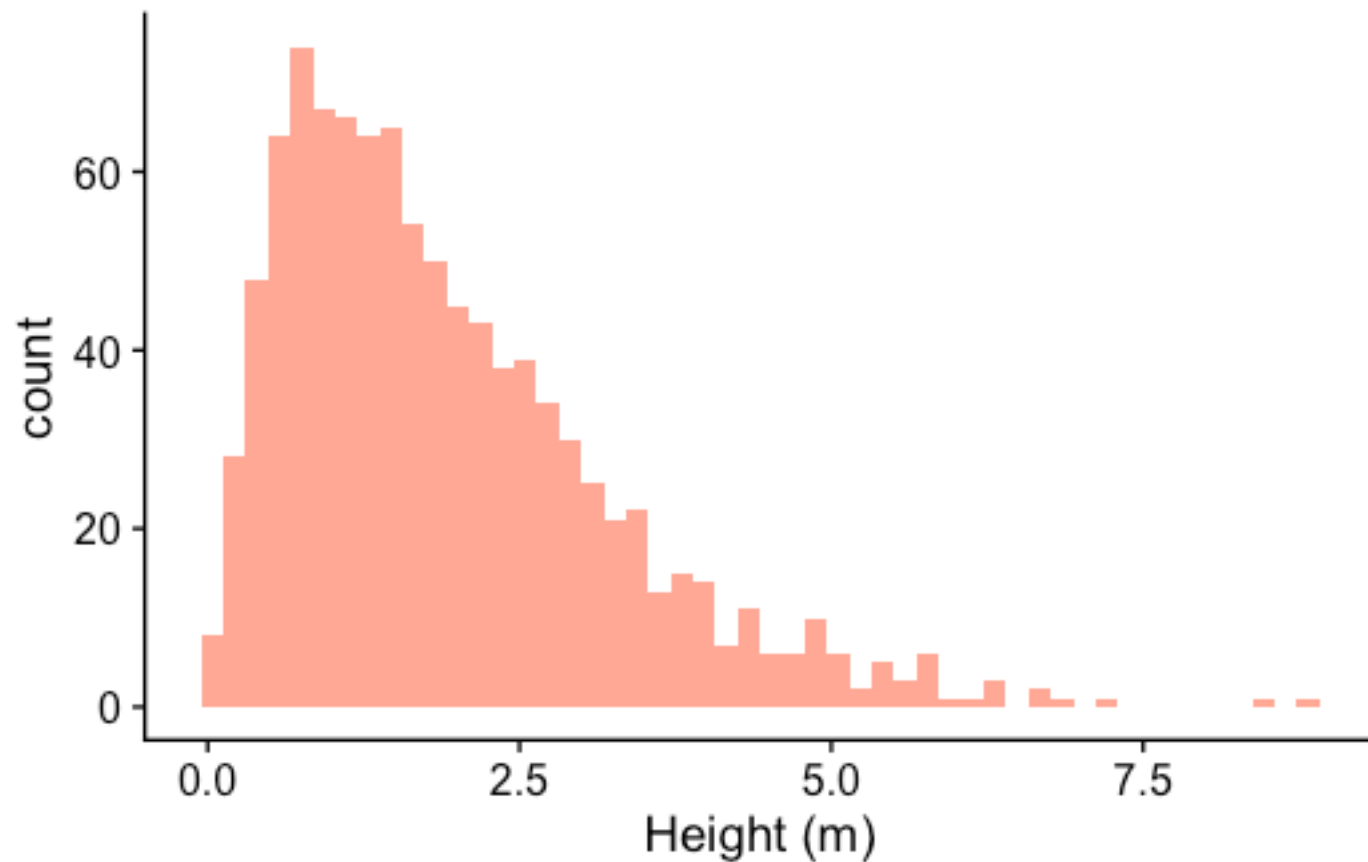
Sampling distributions for different sample size

Example

```r
set.seed(239)
# Generate a skewed distribution
skewed ← tibble(
  x = rgamma(1000, shape = 2, scale = 1)
)

# plot in ggplot2
ggplot(data = skewed, aes(x = x)) +
  geom_histogram(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlab("Height (m)")
```
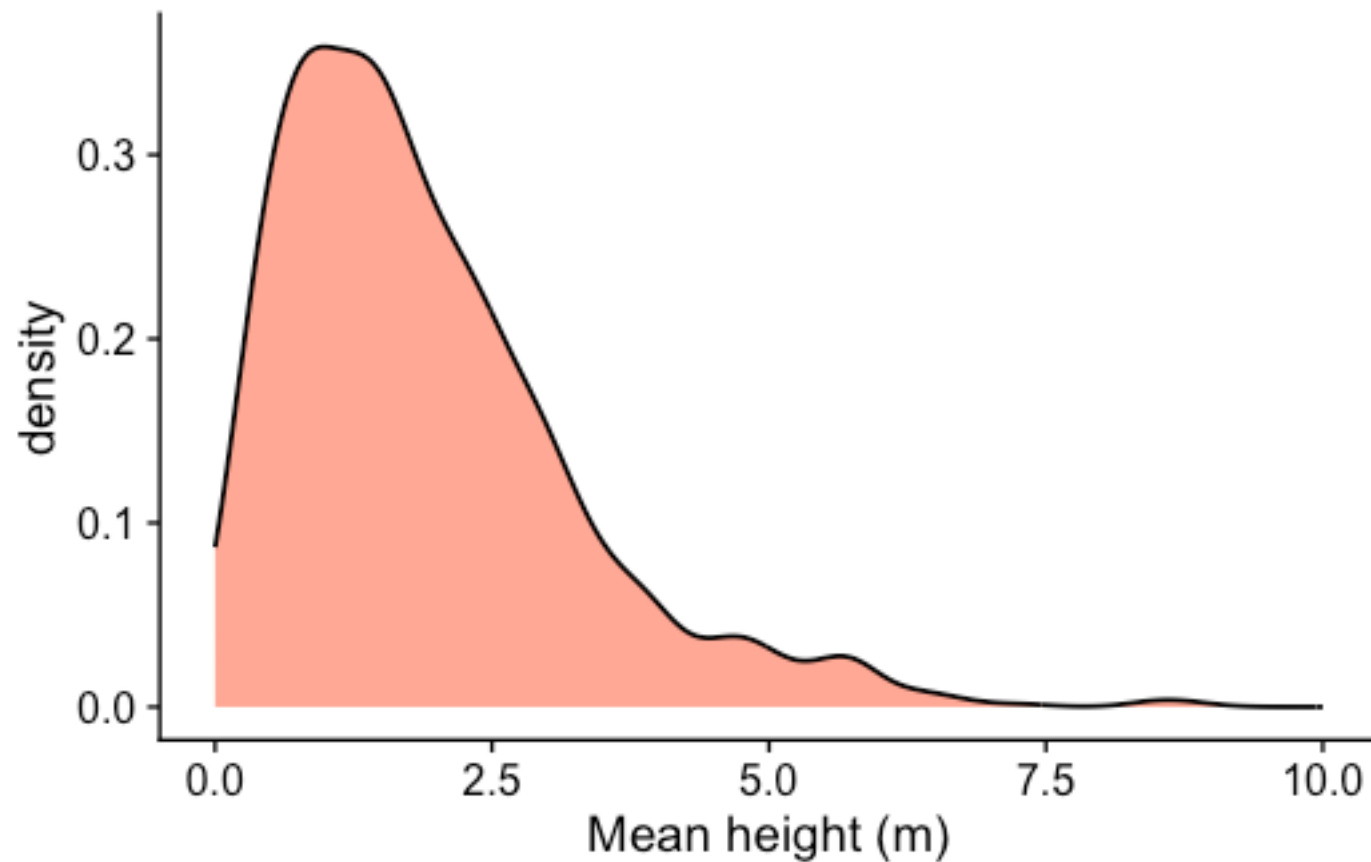
- Skewed population distribution for tree heights.
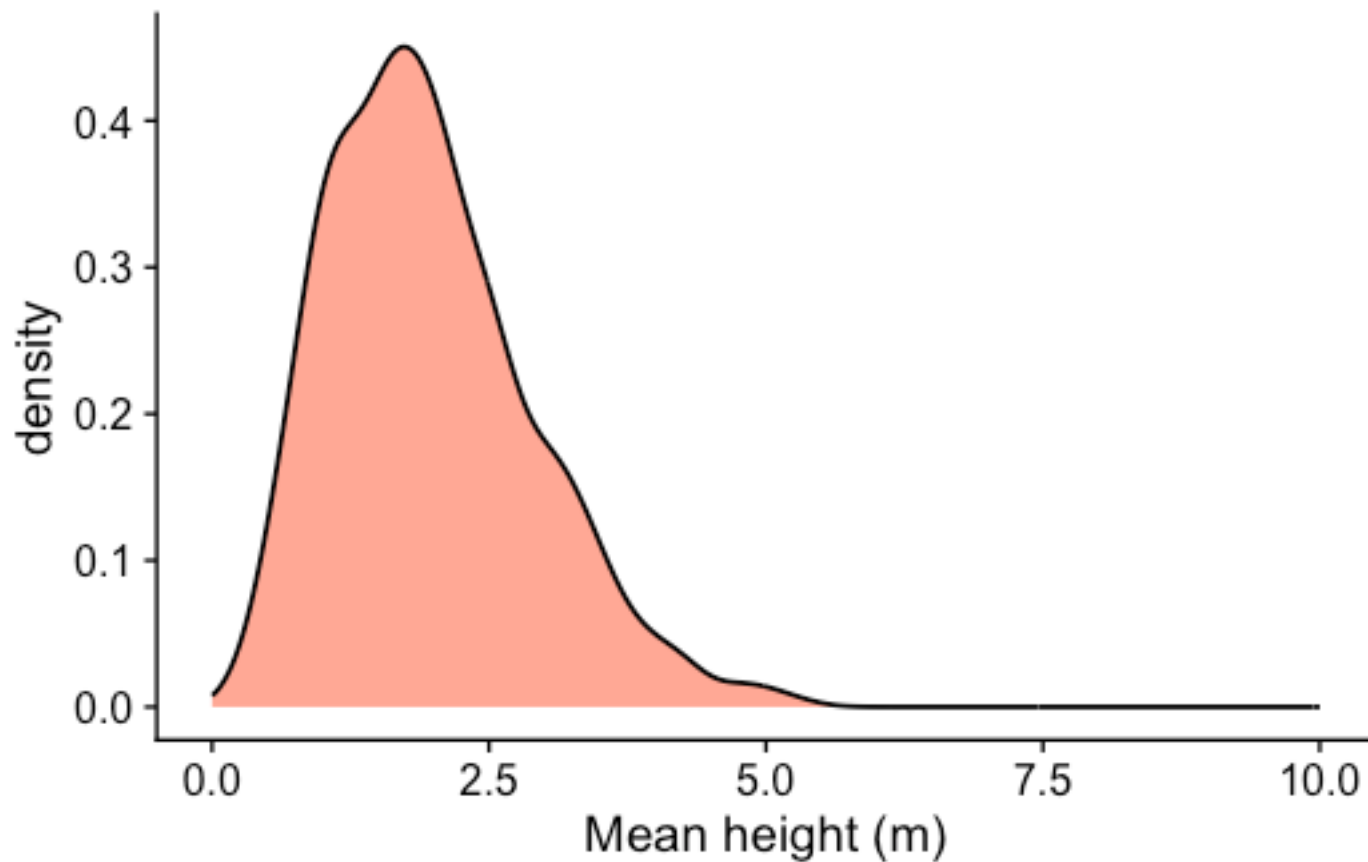- We want to estimate the mean height of the trees in the forest.
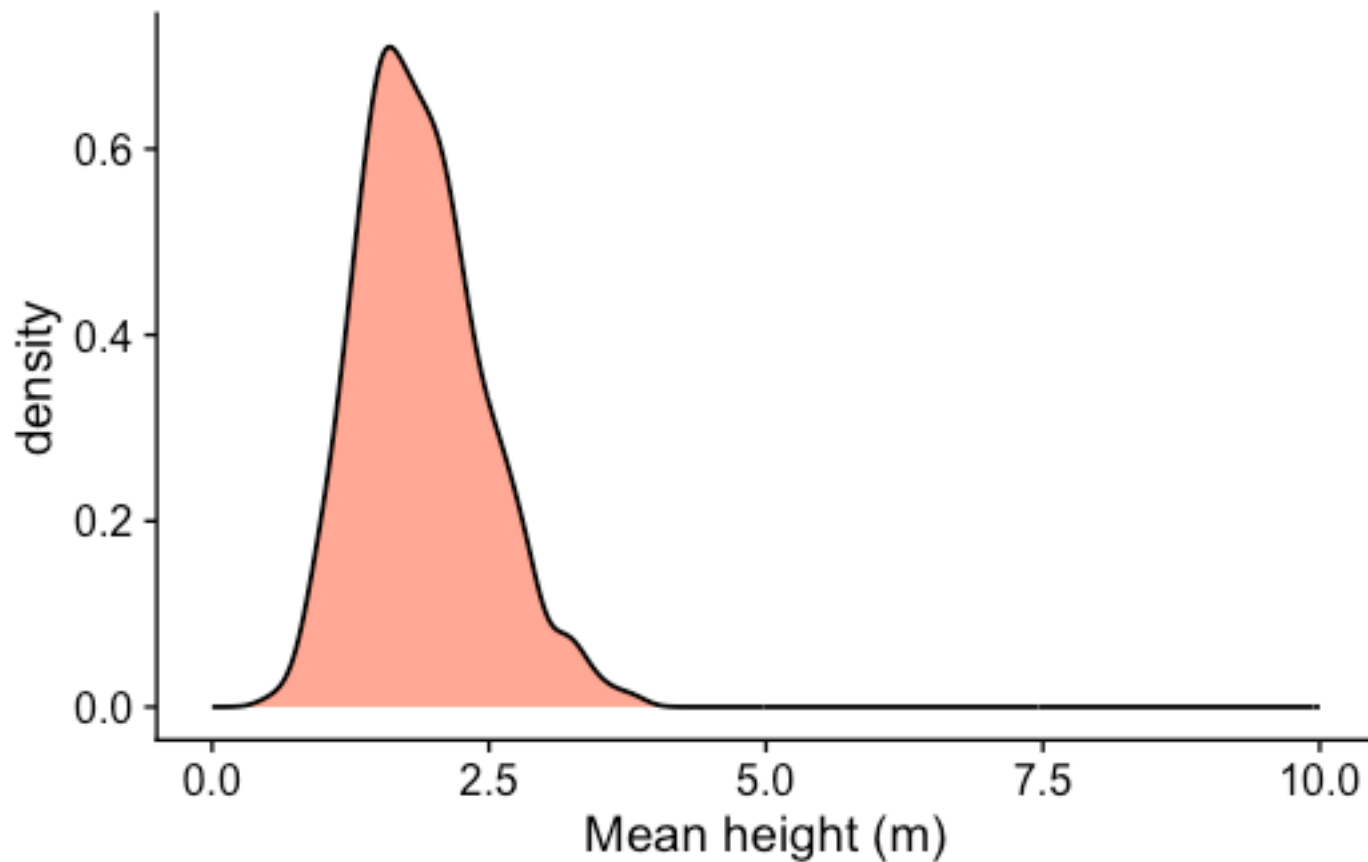
Sample size: n = 1

```r
skewed |>
  infer::rep_sample_n(
    size = 1,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlim(0, 10) +
  xlab("Mean height (m)")
```

With a sample size of one, the sampling distribution mirrors the population – larger samples are needed to see convergence to normality.

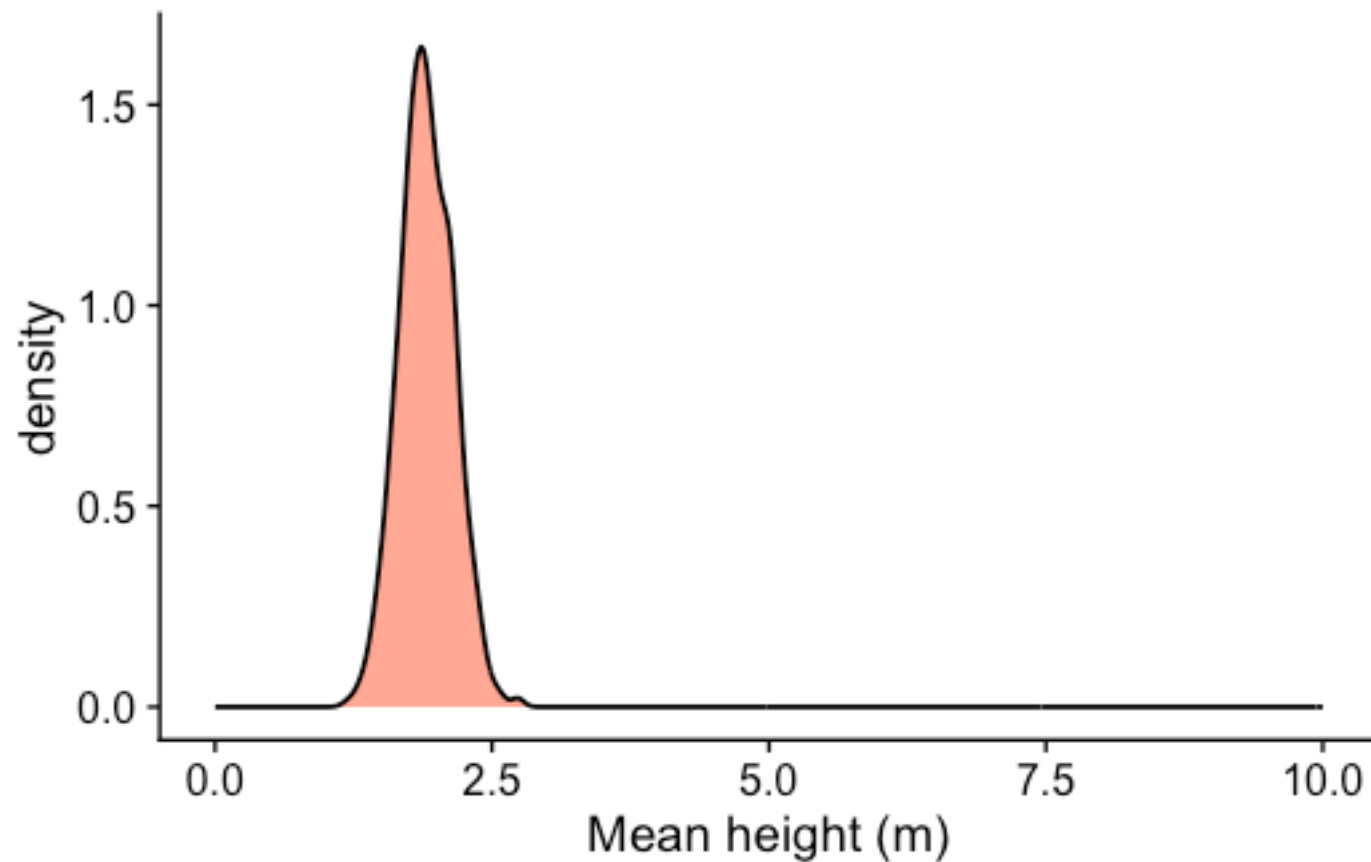## Sample size: n = 2

```r
skewed |>
  infer::rep_sample_n(
    size = 2,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlim(0, 10) +
  xlab("Mean height (m)")
```

- We sample 2 trees, calculate the sample mean, and repeat 1000 times.
- The distribution of sample means is starting to look more like a normal distribution.
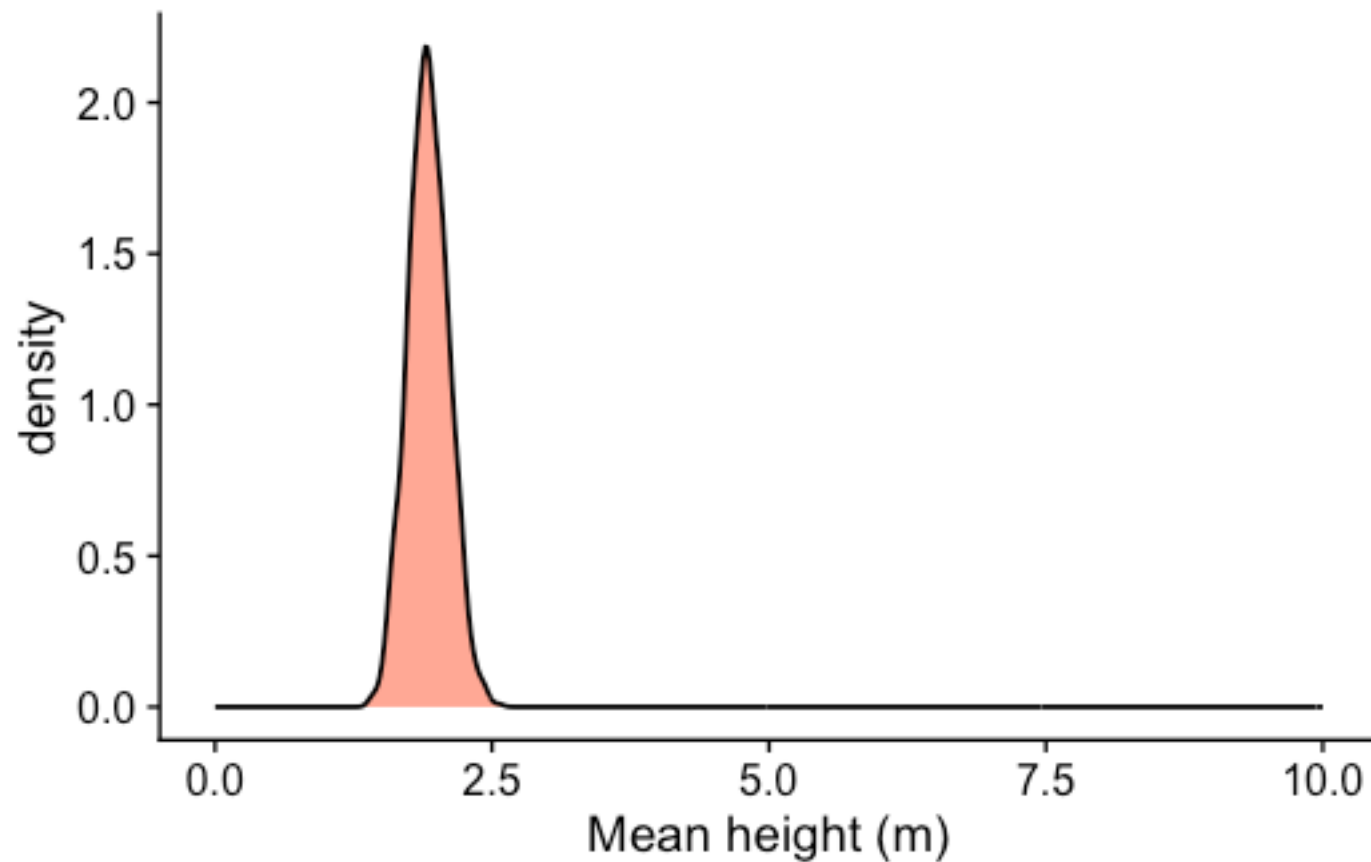
Sample size: n = 5

```r
skewed |>
  infer::rep_sample_n(
    size = 5,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlim(0, 10) +
  xlab("Mean height (m)")
```

- Each sample mean is based on 5 observations, repeated 1000 times.
- The distribution is becoming more normal, and the spread is decreasing: estimate is getting more **precise**.

Sample size: n = 30

```r
skewed |>
  infer::rep_sample_n(
    size = 30,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlim(0, 10) +
  xlab("Mean height (m)")
```
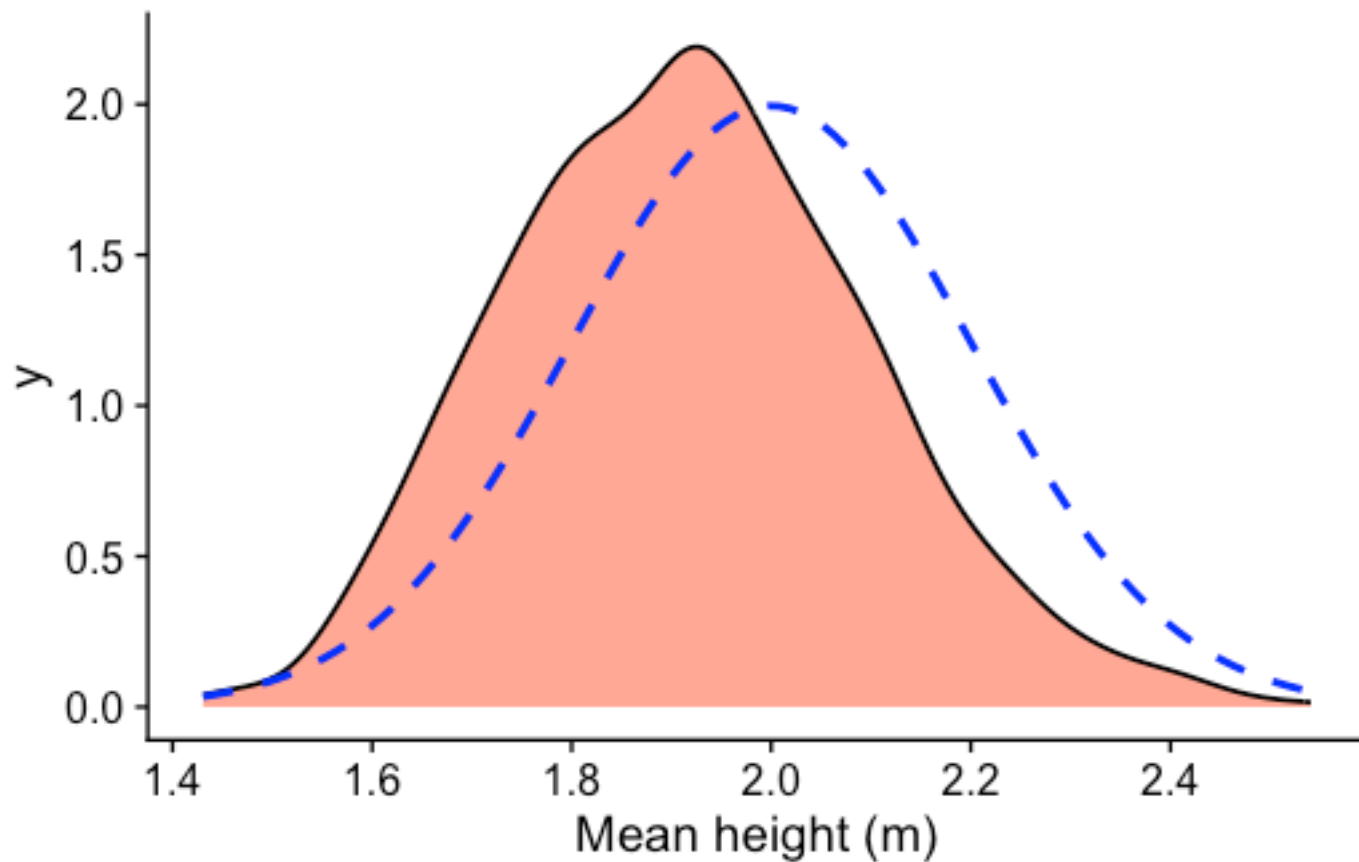
- Each sample mean is based on 30 observations, repeated 1000 times.
- The distribution of sample means is very close to a normal distribution.

Sample size: n = 50

```r
skewed |>
  infer::rep_sample_n(
    size = 50,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  xlim(0, 10) +
  xlab("Mean height (m)")
```

- Each sample mean is based on 50 observations, repeated 1000 times.
- **How many samples is enough?**

Is n = 50 "normal" enough?

```r
skewed |>
  infer::rep_sample_n(
    size = 50,
    reps = 1000
  ) |>
  group_by(replicate) |>
  summarise(xbar = mean(x)) |>
  ggplot(aes(x = xbar)) +
  geom_density(
    fill = "orangered",
    alpha = 0.5, bins = 50
  ) +
  stat_function(
    fun = dnorm,
    args = list(
      mean = 2, # population mean for gamma(2,1)
      sd = sqrt(2) / sqrt(50) # theoretical SE for gamma(2,1)
    ),
    linewidth = 1,
```

```
    color = "blue",
    linetype = "dashed"
) +
xlab("Mean height (m)")
```

- Each sample mean is based on 50 observations, repeated 1000 times.
- **How many samples is enough?**

Effect of sample size

```r
library(tidymodels)
library(patchwork)
set.seed(642)

heights <- tibble(heights = rnorm(1000, 1.99, 1))
popmean <- mean(heights$heights)
sample_sizes <- c(2, 5, 25, 100)
n <- length(sample_sizes)

heights <- tibble(heights = rgamma(1000, shape = 2, scale = 1))
sample_sizes <- c(2, 5, 25, 100)
n <- length(sample_sizes)

plots <- lapply(sample_sizes, function(size) {
  df <- heights |>
    rep_sample_n(size = size, reps = 2000) |>
    group_by(replicate) |>
    summarise(xbar = mean(heights))
```
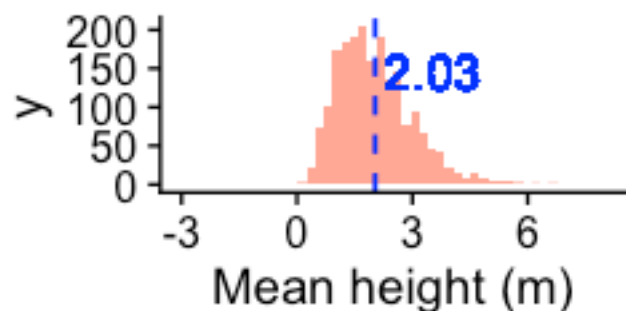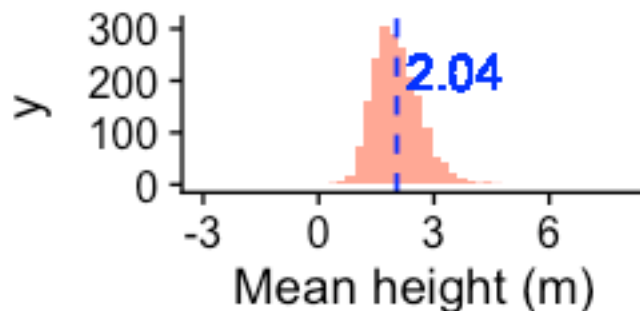
```r
  mean_xbar ← mean(df$xbar)

  ggplot(df, aes(x = xbar)) +
    geom_histogram(fill = "orangered", alpha = 0.5, bins = 50) +
    geom_vline(aes(xintercept = mean_xbar), color = "blue", linetype = "dashed") +
    geom_text(aes(x = mean_xbar, label = sprintf("%.2f", mean_xbar), y = Inf), hjust = -0.1, vjust
= 2, color = "blue") +
    ggtitle(paste0("Sample Size: ", size)) +
    xlab("Mean height (m)") +
    xlim(-3, 8)
})
wrap_plots(plots)
```
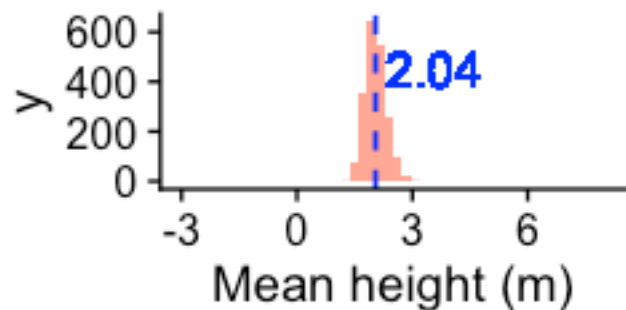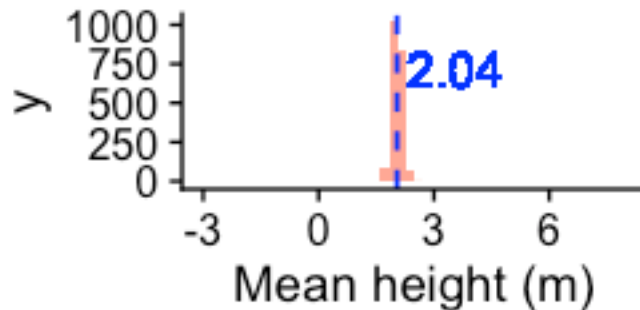
Larger samples give more precise estimates of the population mean. The **narrower distribution** of sample means reflects this precision, measured by the **standard error**.
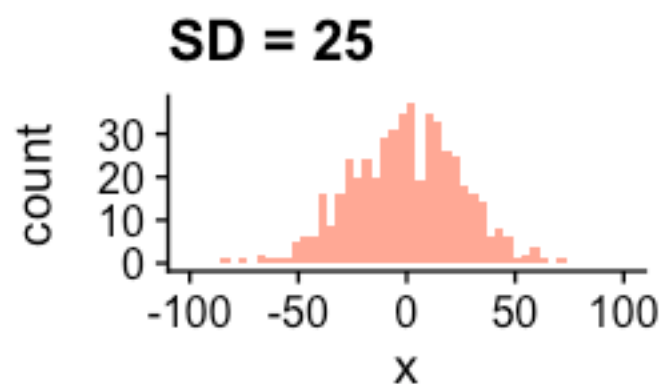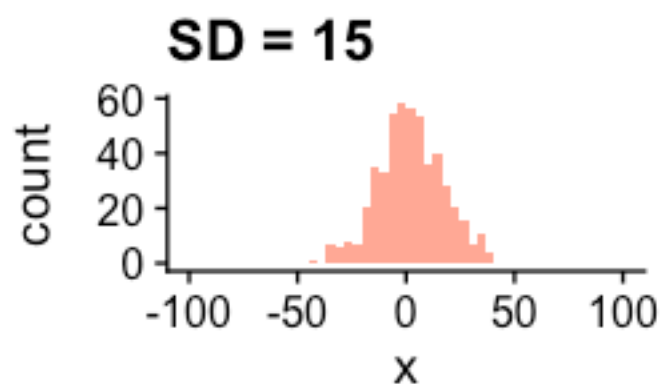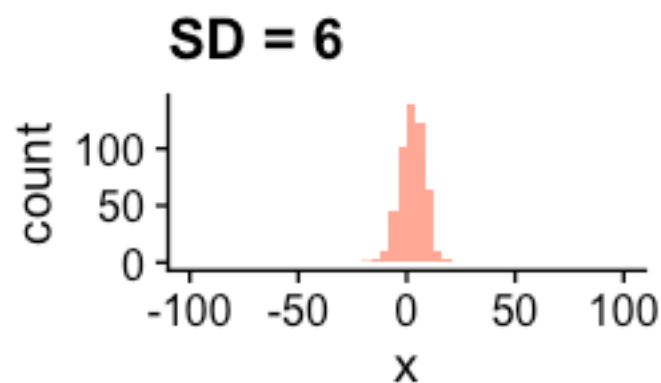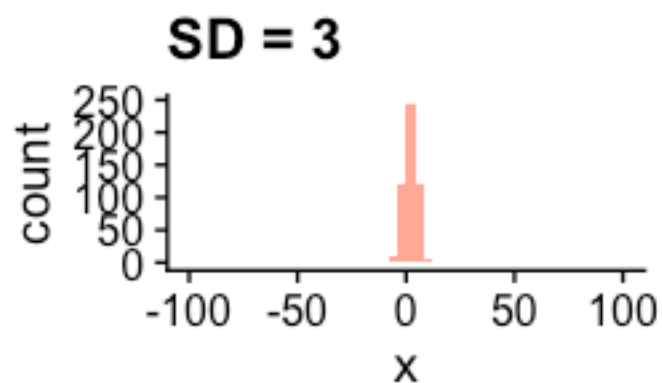
Effect of variability

```r
set.seed(1221)

# Define a function to generate ggplot objects
generate_plot ← function(sd) {
  data ← rnorm(500, 1.99, sd)
  p ← ggplot(data = tibble(x = data), aes(x = x)) +
    geom_histogram(fill = "orangered", alpha = 0.5, bins = 50) +
    ggtitle(paste("SD =", sd)) +
    xlim(-100, 100)
  return(p)
}

# Apply the function to a list of standard deviations
sds ← c(3, 6, 15, 25)
plots ← lapply(sds, generate_plot)

# Wrap the plots
wrap_plots(plots)
```

SD = 3

SD = 6

SD = 15

SD = 25

More variable populations (e.g. tree heights ranging from 1 m to 50 m) produce more spread in sample means. The **standard error** captures this reduced precision.

CLT drives statistical inference

The CLT enables inference about the population mean without knowing the population distribution.

- With sufficient observations, the sampling distribution of the mean is approximately normal
- The centre of that distribution is the true population mean
- The standard error measures the spread – how precise your estimate is

Standard error and confidence intervals

Standard Error of the Mean

- The standard deviation of the sampling distribution – how much sample means vary across samples
- Decreases as sample size increases, so larger samples yield more precise estimates

> ⚠️ Formula
>
> $$SE_{\bar{x}} = \frac{s}{\sqrt{n}}$$
>
> - where s is the sample standard deviation
> - n is the sample size

When to report SD or SE

Standard Deviation (SD)

- Describes variability in your **data**
- Does not change with sample size

Standard Error (SE)

- Describes precision of your **mean estimate**
- Shrinks as sample size increases ($SE = \frac{SD}{\sqrt{n}}$)

When reporting:

- **mean ± SE** shows how precisely you've estimated the mean — but SE can be misleadingly small with large samples, so always report n
- **mean ± SD** shows the spread of your raw data

Confidence intervals

What is a confidence interval?

- A range of values that likely contains the true population parameter, computed from your sample
- 95% is the standard choice
- Wider intervals indicate less precision

> ⚠️ **Formula for 95% CI**
>
> $$\bar{x} \pm (t_{n-1} \times SE_{\bar{x}})$$
>
> - where t_{n-1} comes from the t-distribution (covered next lecture)
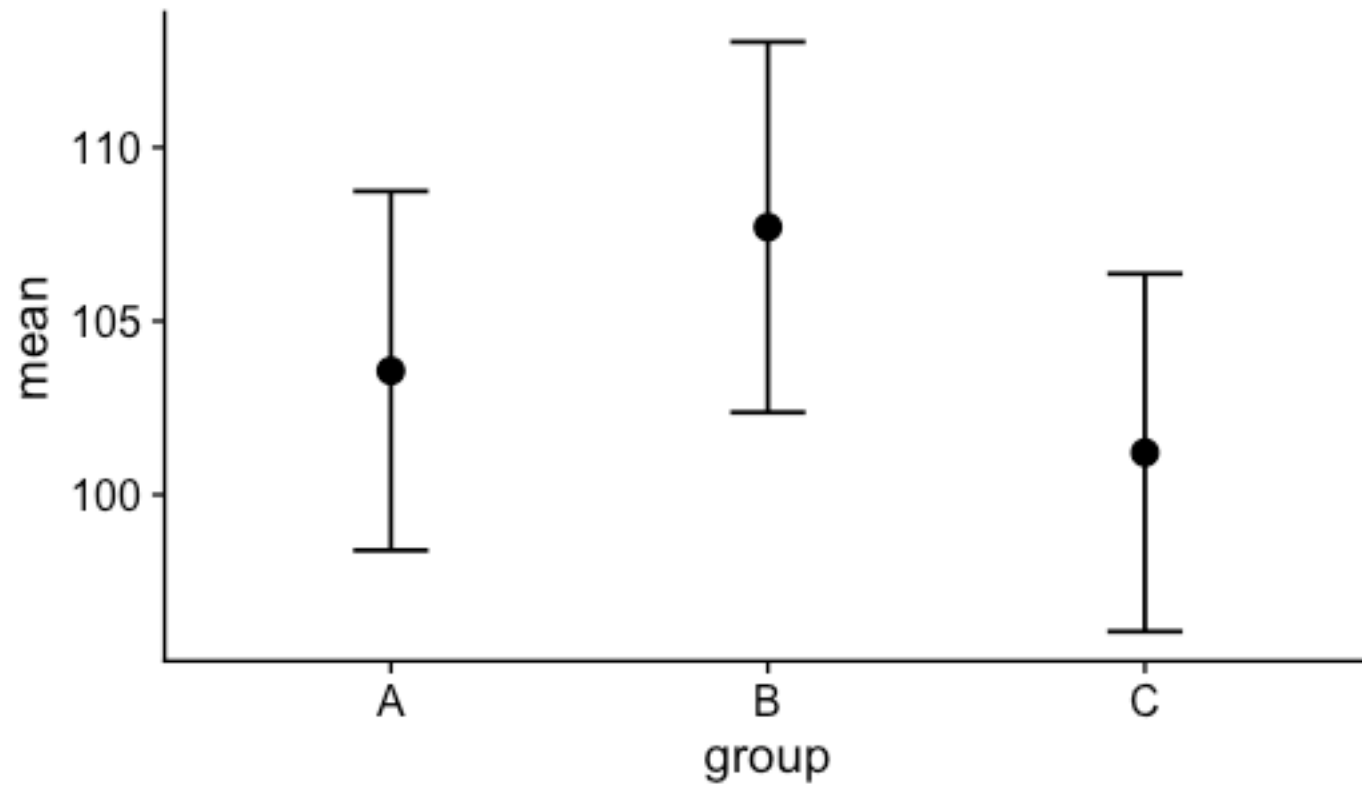
Visualising confidence intervals

```
#| warning: false

# Generate sample data
set.seed(253)
sample_data ← data.frame(
  group = rep(c("A", "B", "C"), each = 30),
  value = c(
    rnorm(30, 100, 15),
    rnorm(30, 110, 15),
    rnorm(30, 105, 15)
  )
)

# Calculate means and CIs
ci_data ← sample_data %>%
  group_by(group) %>%
  summarise(
    mean = mean(value),
    se = sd(value) / sqrt(n()),
```

```
    ci_lower = mean - qt(0.975, n() - 1) * se,
    ci_upper = mean + qt(0.975, n() - 1) * se
  )

# Plot
ggplot(ci_data, aes(x = group, y = mean)) +
  geom_point(size = 3) +
  geom_errorbar(aes(ymin = ci_lower, ymax = ci_upper), width = 0.2) +
  ggtitle("Means with 95% Confidence Intervals")
```

Means with 95% Confidence Intervals

We will learn more about confidence intervals in the next lecture.

Thanks for listening! Questions?

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