Multiple random variables

Multiple random variables

We essentially always consider multiple random variables at once.

— The key concepts: Joint, conditional and marginal distributions, and independence of RVs.

Let *X* and *Y* be discrete random variables.

 \longrightarrow Joint distribution:

 $p_{XY}(x,y) = Pr(X = x \text{ and } Y = y)$

→ Marginal distributions:

 $\begin{array}{l} \mathsf{p}_{\mathsf{X}}(\mathsf{x}) = \mathsf{Pr}(X = \mathsf{x}) = \sum_{\mathsf{y}} \mathsf{p}_{\mathsf{X}\mathsf{Y}}(\mathsf{x},\mathsf{y}) \\ \mathsf{p}_{\mathsf{Y}}(\mathsf{y}) = \mathsf{Pr}(Y = \mathsf{y}) = \sum_{\mathsf{x}} \mathsf{p}_{\mathsf{X}\mathsf{Y}}(\mathsf{x},\mathsf{y}) \end{array}$

→ Conditional distributions:

 $p_{X|Y=y}(x) = Pr(X = x | Y = y) = p_{XY}(x,y) / p_Y(y)$

Sample a couple who are both carriers of some disease gene.

X = number of children they have

Y = number of affected children they have

	Х							
p _{>}	_{(Y} (x,y)	0	1	2	3	4	5	p _Y (y)
	0	0.160	0.248	0.124	0.063	0.025	0.014	0.634
	1	0	0.082	0.082	0.063	0.034	0.024	0.285
у	2	0	0	0.014	0.021	0.017	0.016	0.068
	3	0	0	0	0.003	0.004	0.005	0.012
	4	0	0	0	0	0.000	0.001	0.001
	5	0	0	0	0	0	0.000	0.000
	p _X (x)	0.160	0.330	0.220	0.150	0.080	0.060	

Pr(Y = y | X = 2)

	х							
p _{>}	_{(Y} (x,y)	0	1	2	3	4	5	p _Y (y)
	0	0.160	0.248	0.124	0.063	0.025	0.014	0.634
	1	0	0.082	0.082	0.063	0.034	0.024	0.285
у	2	0	0	0.014	0.021	0.017	0.016	0.068
	3	0	0	0	0.003	0.004	0.005	0.012
	4	0	0	0	0	0.000	0.001	0.001
	5	0	0	0	0	0	0.000	0.000
	p _X (x)	0.160	0.330	0.220	0.150	0.080	0.060	
		У	0	1	2	3	4	5
Pr	r(Y=y ∣	X=2)	0.564	0.373	0.064	0.000	0.000	0.000

Pr(X = x | Y = 1)



Independence

Random variables X and Y are independent if

 $\longrightarrow p_{XY}(x,y) = p_X(x) p_Y(y)$

for every pair x,y.

In other words/symbols:

$$\longrightarrow$$
 Pr(X = x and Y = y) = Pr(X = x) Pr(Y = y)

for every pair x,y.

Equivalently,

$$\longrightarrow$$
 Pr(X = x | Y = y) = Pr(X = x)

for all x,y.

Sample a subject from some high-risk population.

X = 1 if the subject is infected with virus A, and = 0 otherwise Y = 1 if the subject is infected with virus B, and = 0 otherwise

	Х					
p ₂	_{XY} (x,y)	0	1	p _Y (y)		
y	0	0.72	0.18	0.90		
	1	0.08	0.02	0.10		
	p _X (x)	0.80	0.20			

Continuous random variables

Continuous random variables have joint densities, $f_{XY}(x,y)$.

 \longrightarrow The marginal densities are obtained by integration:

$$f_X(x) = \int f_{XY}(x,y) \, dy \quad \text{and} \quad f_Y(y) = \int f_{XY}(x,y) \, dx$$

 \longrightarrow Conditional density:

$$\mathbf{f}_{\mathbf{X}|\mathbf{Y}=\mathbf{y}}(\mathbf{x}) = \mathbf{f}_{\mathbf{X}\mathbf{Y}}(\mathbf{x},\mathbf{y}) / \mathbf{f}_{\mathbf{Y}}(\mathbf{y})$$

 \longrightarrow X and Y are independent if:

$$f_{XY}(x,y) = f_X(x) f_Y(y)$$
 for all x,y.

The bivariate normal distribution



The bivariate normal distribution



IID

More jargon:

Random variables $X_1, X_2, X_3, \ldots, X_n$ are said to be independent and identically distributed (iid) if

- \longrightarrow they are independent,
- \longrightarrow they all have the same distribution.

Usually such RVs are generated by

- \longrightarrow repeated independent measurements, or
- \longrightarrow random sampling from a large population.

Means and SDs



Sampling distributions

Populations and samples

 We are interested in the distribution of measurements in an underlying (possibly hypothetical) population.

- Examples: Infinite number of mice from strain A; cytokine response to treatment.
 - All T cells in a person; respond or not to an antigen.
 - All possible samples from the Baltimore water supply; concentration of cryptospiridium.
 - All possible samples of a particular type of cancer tissue; expression of a certain gene.
 - → We can't see the entire population (whether it is real or hypothetical), but we can see a random sample of the population (perhaps a set of independent, replicated measurements).

Parameters

We are interested in the population distribution or, in particular, certain numerical attributes of the population distribution, called parameters.



Parameters are usually assigned greek letters (like θ , μ , and σ).

We make *n* independent measurements (or draw a random sample of size *n*). This gives X_1, X_2, \ldots, X_n independent and identically distributed (iid), following the population distribution.

\rightarrow Statistic:

A numerical summary (function) of the X's. For example, the sample mean, sample SD, etc.

→ Estimator:

A statistic, viewed as estimating some population parameter.

We write:

 $\overline{X} = \hat{\mu}$ as an estimator of μ , $S = \hat{\sigma}$ as an estimator of σ , \hat{p} as an estimator of p, $\hat{\theta}$ as an estimator of θ , ...

Parameters, estimators, estimates

- The population mean
 - A parameter
 - A fixed quantity
 - Unknown, but what we want to know
- \overline{X} The sample mean
 - An estimator of μ
 - A function of the data (the X's)
 - A random quantity
- \overline{x} The observed sample mean
 - An estimate of μ
 - A particular realization of the estimator, \overline{X}
 - A fixed quantity, but the result of a random process.

Estimators have distributions, means, SDs, etc.



3.8	8.0	9.9	13.1	15.5	16.6	22.3	25.4	31.0	40.0	\longrightarrow	18.6
6.0	10.6	13.8	17.1	20.2	22.5	22.9	28.6	33.1	36.7	\longrightarrow	21.2
8.1	9.0	9.5	12.2	13.3	20.5	20.8	30.3	31.6	34.6	\longrightarrow	19.0
4.2	10.3	11.0	13.9	16.5	18.2	18.9	20.4	28.4	34.4	\longrightarrow	17.6
8.4	15.2	17.1	17.2	21.2	23.0	26.7	28.2	32.8	38.0	\longrightarrow	22.8

Sampling distribution



The sampling distribution depends on:

- The type of statistic
- The population distribution
- The sample size





Consider $\hat{\theta}$, an estimator of the parameter θ .

The sample mean



Assume X_1, X_2, \ldots, X_n are iid with mean μ and SD σ .

- \longrightarrow Mean of $\overline{X} = E(\overline{X}) = \mu$.
- \longrightarrow Bias = E(\overline{X}) μ = 0.
- \longrightarrow SE of $\overline{X} = SD(\overline{X}) = \sigma/\sqrt{n}$.
- $\longrightarrow \text{ RMS error of } \overline{X}: \\ \sqrt{(\text{bias})^2 + (\text{SE})^2} = \sigma/\sqrt{n}.$

If the population is normally distributed



Example

Suppose $X_1, X_2, ..., X_{10}$ are iid Normal(mean=10,SD=4) Then $\overline{X} \sim$ Normal(mean=10, SD \approx 1.26). Let $Z = (\overline{X} - 10)/1.26$.



Central limit theorm

 \rightarrow If X_1, X_2, \ldots, X_n are iid with mean μ and SD σ , and the sample size (n) is large, then

 \overline{X} is approximately Normal(μ , σ/\sqrt{n}).

 \longrightarrow How large is large?

It depends on the population distribution. (But, generally, not too large.)

Example 1







Example 2 (rescaled)







The sample SD

 \longrightarrow Why use (n – 1) in the sample SD?

$$S=\sqrt{\frac{\sum(X_i-\overline{X})^2}{n-1}}$$

 \longrightarrow In other words:

∘ Bias(S²) = 0 ∘ Bias ($\frac{n-1}{n}$ S²) = $\frac{n-1}{n}\sigma^2 - \sigma^2 = -\frac{1}{n}\sigma^2$

The distribution of the sample SD

 \longrightarrow If X_1, X_2, \ldots, X_n are iid Normal(μ, σ), then the sample SD S satisfies

(n – 1)
$$S^2/\sigma^2 \sim \chi^2_{n-1}$$

(When the X_i are not normally distributed, this is not true.)





Example



A non-normal example





Inference about one group

Review

 \longrightarrow If X_1, \ldots, X_n are iid with mean μ and SD σ and the sample size n is large, then

 $\overline{X} \sim \text{Normal}(\text{mean} = \mu, \text{SD} = \sigma/\sqrt{n}).$

Confidence intervals

Suppose we measure some response in 100 male subjects, and find that the sample average (\bar{x}) is 3.52 and sample SD (s) is 1.61.

Our estimate of the SE of the sample mean is $1.61/\sqrt{100} = 0.161$.

A 95% confidence interval for the population mean (μ) is roughly

 $3.52 \pm (2 \times 0.16) = 3.52 \pm 0.32 = (3.20, 3.84).$

What does this mean?

Confidence intervals

Suppose that X_1, \ldots, X_n are iid Normal(mean= μ , SD= σ). Suppose that we actually know σ .

Then $\overline{X} \sim \text{Normal}(\text{mean}=\mu, \text{SD}=\sigma/\sqrt{n})$ σ is known but μ is not! \longrightarrow How close is \overline{X} to μ ? $\Pr\left(\frac{|\overline{X}-\mu|}{\sigma/\sqrt{n}} \le 1.96\right) = 95\%$ $\Pr\left(\frac{-1.96\sigma}{\sqrt{n}} \le \overline{X} - \mu \le \frac{1.96\sigma}{\sqrt{n}}\right) = 95\%$ $\Pr\left(\overline{X} - \frac{1.96\sigma}{\sqrt{n}} \le \mu \le \overline{X} + \frac{1.96\sigma}{\sqrt{n}}\right) = 95\%$

What is a confidence interval?

A 95% confidence interval is an interval calculated from the data that in advance has a 95% chance of covering the population parameter.

In advance, $\overline{X} \pm 1.96\sigma/\sqrt{n}$ has a 95% chance of covering μ .

Thus, it is called a 95% confidence interval for μ .

Note that, after the data is gathered (for instance, n=100, $\bar{x} = 3.52$, $\sigma = 1.61$), the interval becomes fixed:

$$\bar{x} \pm 1.96\sigma/\sqrt{n} = 3.52 \pm 0.32.$$

We can't say that there's a 95% chance that μ is in the interval 3.52 \pm 0.32. It either is or it isn't; we just don't know.

What is a confidence interval?



500 confidence intervals for μ (σ known)

Longer and shorter intervals

→ If we use 1.64 in place of 1.96, we get shorter intervals with lower confidence.

Since
$$\Pr\left(\frac{|\overline{X} - \mu|}{\sigma/\sqrt{n}} \le 1.64\right) = 90\%$$
,

 $\overline{X} \pm 1.64\sigma/\sqrt{n}$ is a 90% confidence interval for μ .

 \rightarrow If we use 2.58 in place of 1.96, we get longer intervals with higher confidence.

Since
$$\Pr\left(\frac{|\overline{X} - \mu|}{\sigma/\sqrt{\mathsf{n}}} \le 2.58\right) = 99\%$$
,

 $\overline{X} \pm 2.58\sigma/\sqrt{n}$ is a 99% confidence interval for μ .

What is a confidence interval? (cont)

A 95% confidence interval is obtained from a procedure for producing an interval, based on data, that 95% of the time will produce an interval covering the population parameter.

In advance, there's a 95% chance that the interval will cover the population parameter.

After the data has been collected, the confidence interval either contains the parameter or it doesn't.

Thus we talk about confidence rather than probability.

But we don't know the SD

Use of $\overline{X} \pm 1.96 \sigma / \sqrt{n}$ as a 95% confidence interval for μ requires knowledge of σ .

That the above is a 95% confidence interval for μ is a result of the following:

$$\frac{\overline{X} - \mu}{\sigma / \sqrt{n}} \sim \text{Normal(0,1)}$$

What if we don't know σ ?

 \longrightarrow We plug in the sample SD *S*, but then we need to widen the intervals to account for the uncertainty in *S*.

What is a confidence interval? (cont)



500 BAD confidence intervals for μ (σ unknown)

What is a confidence interval? (cont)



The Student t distribution

If X_1, X_2, \ldots, X_n are iid Normal(mean= μ , SD= σ), then

$$\frac{\overline{X} - \mu}{S/\sqrt{n}} \sim t(df = n - 1)$$

Discovered by William Gossett ("Student") who worked for Guinness.



- → qt(0.975,9) returns 2.26 (compare to 1.96)
- → pt(1.96,9)-pt(-1.96,9) returns 0.918 (compare to 0.95)

The t interval

If X_1, \ldots, X_n are iid Normal(mean= μ , SD= σ), then

$$\overline{X} \pm t(\alpha/2, n-1) S/\sqrt{n}$$

- is a 1α confidence interval for μ .
- \longrightarrow t($\alpha/2, n-1$) is the 1 $\alpha/2$ quantile of the t distribution with n 1 "degrees of freedom."



Suppose we have measured some response in 10 male subjects, and obtained the following numbers:

Data		
0.2 1.3 1.4 2.3 4.2	$\bar{x} = 3.68$	n = 10
4.7 4.7 5.1 5.9 7.0	s = 2.24	qt(0.975,9) = 2.26

 \longrightarrow 95% confidence interval for μ (the population mean):

 $3.68 \pm 2.26 \times 2.24$ / $\sqrt{10} \approx 3.68 \pm 1.60$ = (2.1, 5.3)



Example 2

Suppose we have measured (by RT-PCR) the log_{10} expression of a gene in 3 tissue samples, and obtained the following numbers:

Data 1.17 6.35 7.76 $\bar{x} = 5.09$ n = 3s = 3.47 qt(0.975, 2) = 4.30

 \longrightarrow 95% confidence interval for μ (the population mean):

5.09 \pm 4.30 imes 3.47 / $\sqrt{3}$ pprox 5.09 \pm 8.62 = (–3.5, 13.7)



Suppose we have weighed the mass of tumor in 20 mice, and obtained the following numbers

Data34.928.534.338.429.6 $\bar{x} = 30.7$ n = 2028.225.3...32.1s = 6.06qt(0.975, 19) = 2.09

 \longrightarrow 95% confidence interval for μ (the population mean):

 $30.7 \pm 2.09 \times 6.06$ / $\sqrt{20} \approx 30.7 \pm 2.84$ = (27.9, 33.5)



Confidence interval for the mean



 X_1, X_2, \ldots, X_n independent Normal(μ, σ).

95% confidence interval for μ :

 $\overline{X} \pm t S/\sqrt{n}$ where t = 97.5 percentile of t distribution with (n – 1) d.f.

Confidence interval for the population SD

Suppose we observe X_1, X_2, \ldots, X_n iid Normal(μ, σ).

Suppose we wish to create a 95% CI for the population SD, σ .

Our estimate of σ is the sample SD, *S*.

The sampling distribution of S is such that



Confidence interval for the population SD



Population A: n = 10; sample SD: $s_A = 7.64$ L = qchisq(0.025,9) = 2.70 U = qchisq(0.975,9) = 19.0

 $\longrightarrow 95\% \text{ CI for } \sigma_{\mathsf{A}}:$ $(7.64 \times \sqrt{\frac{9}{19.0}}, 7.64 \times \sqrt{\frac{9}{2.70}}) = (7.64 \times 0.69, 7.64 \times 1.83) = (5.3, 14.0)$

Population B: n = 16; sample SD: $s_B = 18.1$ L = qchisq(0.025,15) = 6.25 U = qchisq(0.975,15) = 27.5

 \longrightarrow 95% Cl for $\sigma_{\rm B}$:

$$(18.1 \times \sqrt{\frac{15}{27.5}}, 18.1 \times \sqrt{\frac{15}{6.25}}) = (18.1 \times 0.74, 18.1 \times 1.55) = (13.4, 28.1)$$

Tests of hypotheses

Confidence interval:	Form an interval (on the basis of data) of plausible values for a population pa- rameter.
Test of hypothesis:	Answer a yes or no question regarding

a population parameter.

Examples:

- \longrightarrow Do the two strains have the same average response?
- \longrightarrow Is the concentration of substance X in the water supply above the safe limit?
- → Does the treatment have an effect?

We have a quantitative assay for the concentration of antibodies against a certain virus in blood from a mouse.

We apply our assay to a set of ten mice before and after the injection of a vaccine. (This is called a "paired" experiment.)

Let X_i denote the differences between the measurements ("after" minus "before") for mouse i.

We imagine that the X_i are independent and identically distributed Normal(μ , σ).

 \rightarrow Does the vaccine have an effect? In other words: Is $\mu \neq 0$?



The data

Hypothesis testing

We consider two hypotheses:

Null hypothesis, H₀: $\mu = 0$ Alternative hypothesis, H_a: $\mu \neq 0$

Type I	error:	Reject H ₀ when it is true	(false positive)
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Type II error: Fail to reject H₀ when it is false (false negative)

We set things up so that a Type I error is a worse error (and so that we are seeking to prove the alternative hypothesis). We want to control the rate (the significance level, α) of such errors.

 \longrightarrow Test statistic: $T = (\overline{X} - 0)/(S/\sqrt{10})$

 $\begin{array}{ll} \longrightarrow & \text{We reject } H_0 \text{ if } |\mathsf{T}| > \mathsf{t}^\star, \text{ where } \mathsf{t}^\star \text{ is chosen so that} \\ & \mathsf{Pr}(\mathsf{Reject } H_0 \mid \mathsf{H}_0 \text{ is true}) = \mathsf{Pr}(|\mathsf{T}| > \mathsf{t}^\star \mid \mu = \mathsf{0}) = \alpha. \\ & \text{(generally } \alpha = 5\%) \end{array}$

Example (continued)



As a result, if H_0 is true, there's a 5% chance that you'll reject it!

For the observed data:

 $\bar{x} = 1.93$, s = 2.24, n = 10 T = (1.93 - 0) / (2.24/ $\sqrt{10}$) = 2.72

 \longrightarrow Thus we reject H₀.

The goal

- \longrightarrow We seek to prove the alternative hypothesis.
- \longrightarrow We are happy if we reject H₀.
- \longrightarrow In the case that we reject H₀, we might say: Either H₀ is false, or a rare event occurred.

Another example

Question: is the concentration of substance X in the water supply above the safe level?

 $X_1, X_2, \ldots, X_4 \sim \text{iid Normal}(\mu, \sigma).$

 \longrightarrow We want to test H₀: $\mu \ge 6$ (unsafe) versus H_a: $\mu < 6$ (safe).

Test statistic:
$$T = \frac{\overline{X} - 6}{S/\sqrt{4}}$$

If we wish to have the significance level α = 5%, the rejection region is T < t^{*} = -2.35.



One-tailed vs two-tailed tests

If you are trying to prove that a treatment improves things, you want a one-tailed (or one-sided) test.

You'll reject H_0 only if $T < t^*$.

If you are just looking for a difference, use a two-tailed (or two-sided) test.

You'll reject H_0 if $T < t^*$ or $T > t^*$.



P-values

- P-value: \longrightarrow the smallest significance level (α) for which you would fail to reject H₀ with the observed data.
 - \longrightarrow the probability, if H₀ was true, of receiving data as extreme as what was observed.

$$X_1,\ldots,X_{10}$$
 ~ iid Normal(μ,σ),

 $H_0: \mu = 0; H_a: \mu \neq 0.$

x = 1.93; s = 2.24

$$T_{\rm obs} = \frac{1.93 - 0}{2.24/\sqrt{10}} = 2.72$$

P-value = $Pr(|T| > T_{obs}) = 2.4\%$.



Another example

 $X_1, \ldots, X_4 \sim \text{Normal}(\mu, \sigma)$ $H_0: \mu \ge 6; H_a: \mu < 6.$

 $\bar{x} = 5.51$; s = 0.43 t(df=3) distribution $T_{obs} = \frac{5.51-6}{0.43/\sqrt{4}} = -2.28$ P-value = Pr(T < T_{obs} | $\mu = 6$) = 5.4%.

Recall: We want to prove the alternative hypothesis (i.e., reject H_0 , receive a small P-value)

T_{obs}

Hypothesis tests and confidence intervals

The 95% confidence interval for μ is the set of values, μ_0 , such that the null hypothesis $H_0 : \mu = \mu_0$ would not be rejected by a two-sided test with $\alpha = 5\%$.

The 95% CI for μ is the set of plausible values of μ . If a value of μ is plausible, then as a null hypothesis, it would not be rejected.

For example:

9.98 9.87 10.05 10.08 9.99 9.90 assumed to be iid Normal(μ,σ)

 $\bar{x} = 9.98$; s = 0.082; n = 6; qt(0.975, 5) = 2.57

The 95% CI for μ is

 $9.98 \pm 2.57 \times 0.082$ / $\sqrt{6}$ = 9.98 ± 0.086 = (9.89,10.06)

The power of a test = $Pr(reject H_0 | H_0 is false)$.



- The power depends on: The null hypothesis and test statistic
 - The sample size
 - The true value of μ
 - The true value of σ

Why "fail to reject"?

If the data are insufficient to reject H_0 , we say,

The data are insufficient to reject H_0 .

We shouldn't say, We have proven H_0 .

- We may only have low power to detect anything but extreme differences.
- We control the rate of type I errors ("false positives") at 5% (or whatever), but we may have little or no control over the rate of type II errors.

The effect of sample size

Let X_1, \ldots, X_n be iid Normal(μ, σ). We wish to test $H_0 : \mu = \mu_0$ vs $H_a : \mu \neq \mu_0$.

Imagine $\mu = \mu_a$.



Test for a proportion

Suppose $X \sim \text{Binomial}(n, p)$.

Test $H_0: p = \frac{1}{2}$ vs $H_a: p \neq \frac{1}{2}$.

Reject H_0 if $X \ge H$ or $X \le L$.

Choose H and L such that

 $\Pr(X \ge H \mid p = \frac{1}{2}) \le \alpha/2$ and $\Pr(X \le L \mid p = \frac{1}{2}) \le \alpha/2$.

Thus $Pr(Reject H_0 | H_0 \text{ is true}) \leq \alpha$.

 \rightarrow The difficulty: The Binomial distribution is hard to work with. Because of its discrete nature, you can't get exactly your desired significance level (α).

Rejection region

Consider X \sim Binomial(n=29, p).

Test of $H_0: p = \frac{1}{2}$ vs $H_a: p \neq \frac{1}{2}$ at significance level $\alpha = 0.05$.

Lower critical value:

 $\begin{aligned} &\mathsf{Pr}(\mathsf{X} \leq \mathsf{8}) = 0.012 \\ &\mathsf{Pr}(\mathsf{X} \leq \mathsf{9}) = 0.031 \ \rightarrow \ \mathsf{L} = \mathsf{8} \end{aligned}$

Upper critical value:

 $\label{eq:prior} \begin{array}{l} \mbox{Pr}(X \geq 21) = 0.012 \\ \\ \mbox{Pr}(X \geq 20) = 0.031 \ \rightarrow \ H = 21 \end{array}$

 $\label{eq:rescaled} \mbox{Reject H_0 if $X \leq 8$ or $X \geq 21$.} \qquad \mbox{(For testing $H_0: p = \frac{1}{2}$, $H = n-L$)}$

Binomial(n=29, p=1/2)



Consider X \sim Binomial(n=29, p).

Test of $H_0: p = \frac{1}{2}$ vs $H_a: p \neq \frac{1}{2}$ at significance level $\alpha = 0.05$.

Reject H_0 if $X \le 8$ or $X \ge 21$.

Actual significance level:

$$\alpha = \Pr(X \le 8 \text{ or } X \ge 21 \mid p = \frac{1}{2})$$

= $\Pr(X \le 8 \mid p = \frac{1}{2}) + [1 - \Pr(X \le 20 \mid p = \frac{1}{2})]$
= 0.024

If we used instead "Reject H_0 if $X \le 9$ or $X \ge 20$ ", the significance level would be 0.061!

Confidence interval for a proportion

Suppose X \sim Binomial(n=29, p) and we observe X = 24.

Consider the test of $H_0: p = p_0$ vs $H_a: p \neq p_0$.

We reject H₀ if

 $\Pr(X \le 24 \mid p = p_0) \le \alpha/2$ or $\Pr(X \ge 24 \mid p = p_0) \le \alpha/2$

95% confidence interval for p:

- \longrightarrow The set of p₀ for which a two-tailed test of H₀ : p = p₀ would not be rejected, for the observed data, with α = 0.05.
- \longrightarrow The "plausible" values of p.

 $X \sim Binomial(n=29, p)$; observe X = 24.

Lower bound of 95% confidence interval:

Largest p_0 such that $Pr(X \ge 24 \mid p = p_0) \le 0.025$

Upper bound of 95% confidence interval:

Smallest p_0 such that $\text{Pr}(X \leq 24 \mid p = p_0) \leq 0.025$

→ 95% CI for p: (0.642, 0.942)

Note: $\hat{p} = 24/29 = 0.83$ is not the midpoint of the CI.

Example 1



 $X \sim Binomial(n=25, p)$; observe X = 17.

Lower bound of 95% confidence interval:

 p_L such that 17 is the 97.5 percentile of Binomial(n=25, p_L)

Upper bound of 95% confidence interval:

 p_H such that 17 is the 2.5 percentile of Binomial(n=25, p_H)

→ 95% CI for p: (0.465, 0.851)

Again, $\hat{p} = 17/25 = 0.68$ is not the midpoint of the CI

Example 2



The case X = 0

Suppose $X \sim \text{Binomial}(n, p)$ and we observe X = 0.

Lower limit of 95% confidence interval for $p \colon \to 0$

Upper limit of 95% confidence interval for p:

 p_H such that

$$\begin{split} & \mathsf{Pr}(\mathsf{X} \leq \mathbf{0} \mid \mathsf{p} = \mathsf{p}_{\mathsf{H}}) = 0.025 \\ \Longrightarrow & \mathsf{Pr}(\mathsf{X} = \mathbf{0} \mid \mathsf{p} = \mathsf{p}_{\mathsf{H}}) = 0.025 \\ \Longrightarrow & (1 - \mathsf{p}_{\mathsf{H}})^n = 0.025 \\ \Longrightarrow & 1 - \mathsf{p}_{\mathsf{H}} = \sqrt[n]{0.025} \\ \Longrightarrow & \mathsf{p}_{\mathsf{H}} = 1 - \sqrt[n]{0.025} \end{split}$$

In the case n = 10 and X = 0, the 95% CI for p is (0, 0.31).

A mad cow example

New York Times, Feb 3, 2004:

The department [of Agriculture] has not changed last year's plans to test 40,000 cows nationwide this year, out of 30 million slaughtered. Janet Riley, a spokeswoman for the American Meat Institute, which represents slaughterhouses, called that "plenty sufficient from a statistical standpoint."

Suppose that the 40,000 cows tested are chosen at random from the population of 30 million cows, and suppose that 0 (or 1, or 2) are found to be infected.

- How many of the 30 million total cows would we estimate to be infected?
- What is the 95% confidence interval for the total number of infected cows?

No. ir	nfected	
Obs'd	Est'd	95% CI
0	0	0 – 2767
1	750	19 – 4178
2	1500	182 – 5418

The case X = n

Suppose $X \sim \text{Binomial}(n, p)$ and we observe X = n.

Upper limit of 95% confidence interval for $p : \rightarrow 1$

Lower limit of 95% confidence interval for p:

 p_L such that

$$\begin{aligned} & \mathsf{Pr}(\mathsf{X} \geq \mathsf{n} \mid \mathsf{p} = \mathsf{p}_{\mathsf{L}}) = 0.025 \\ & \Longrightarrow \ & \mathsf{Pr}(\mathsf{X} = \mathsf{n} \mid \mathsf{p} = \mathsf{p}_{\mathsf{L}}) = 0.025 \\ & \Longrightarrow \ & (\mathsf{p}_{\mathsf{L}})^{\mathsf{n}} = 0.025 \\ & \Longrightarrow \ & \mathsf{p}_{\mathsf{L}} = \sqrt[n]{0.025} \end{aligned}$$

In the case n = 25 and X = 25, the 95% CI for p is (0.86, 1.00).

Large n and medium p

Suppose $X \sim \text{Binomial}(n, p)$.

$$E(X) = n p \qquad SD(X) = \sqrt{n p(1-p)}$$

$$\hat{p} = X/n \qquad E(\hat{p}) = p \qquad SD(\hat{p}) = \sqrt{\frac{p(1-p)}{n}}$$
For large n and medium p, $\longrightarrow \hat{p} \sim Normal\left(p, \sqrt{\frac{p(1-p)}{n}}\right)$
Use 95% confidence interval $\hat{p} \pm 1.96 \sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$

 \longrightarrow Unfortunately, this can behave poorly.

 \longrightarrow Fortunately, you can just calculate exact confidence intervals.