E1 (a) Testing a coin is fair corresponds to hypotheses

$$H_0: \pi = 0.5 \qquad \text{vs.} \qquad H_a: \pi \neq 0.5$$

The count X of heads, assuming H_0 holds has the Binom(200, 0.5) distribution. We use qbinom( ) to search for the 0.025-quantile

qbinom(0.025, 200, 0.5) $\longrightarrow$ answer: 86

But, in fact, with a test statisic $X = 86$ we would get P-value

2 * pbinom(86, 200, 0.5) $\longrightarrow$ answer: 0.056

which is not below 0.05. But

2 * pbinom(85, 200, 0.5) $\longrightarrow$ answer: 0.0400

Thus $X \leq 85$ is the lower part of the rejection region and, by symmetry, $X \geq 115$ is the upper part.

Now if, in actual fact, $\pi = 0.55$, the dbinom($\cdot$, 200, 0.55) is the correct pmf to consult for the value of $Pr(X \leq 85 \text{ or } X \geq 115)$. Either of these commands yield the answer:

sum(dbinom(c(0:85, 115:200), 200, 0.55)) $\longrightarrow$ answer: 0.262

pbinom(85, 200, 0.55) + 1 - pbinom(114, 200, 0.55) $\nearrow$

(b) The suggestion is to replace Binom(200, 0.55) by Norm($110, \sqrt{200(0.5)^2}$).
Doing so, we have

$$Pr(X \leq 85 \text{ or } X \geq 115) \doteq \text{pnorm}(85, 110, \sqrt{50}) + 1 - \text{pnorm}(115, 110, \sqrt{50}) \doteq 0.240.$$

(c) Now

$$Pr(X \leq 85.5 \text{ or } X \geq 114.5) \doteq \text{pnorm}(85.5, 110, \sqrt{50}) + 1 - \text{pnorm}(114.5, 110, \sqrt{50})$$
$$\doteq 0.2625$$

noticeably closer (using continuity correction) to the answer in (a) than (b) is.

4.21   We have

$$\pi^2 > \pi^2(1-\pi) = \frac{n\pi}{n}\pi(1-\pi) \geq \frac{10}{n}\pi(1-\pi) > \frac{9}{n}\pi(1-\pi).$$

Taking square roots gives $\qquad \pi > 3\sqrt{\dfrac{\pi(1-\pi)}{n}}$.

4.27 (a) There are several ways to attack this one. Under the null hypothesis

$$H_0: \pi = 0.95,$$

the count X of successes in 10000 runs has a Binom(10000, 0.95) distribution. The command to get 0.025- and 0.975-quantiles is

$$\text{qbinom}(\ c(0.025, 0.975),\ 10000,\ 0.95\ )$$

yielding 9457 and 9542, but

$$\text{pbinom}(\ c(9456, 9542),\ 10000,\ 0.95)$$

vs.

$$\text{pbinom}(\ c(9457, 9541),\ 10000,\ 0.95)$$

shows the former to be at the edges of the rejection region. That is, he should reject H_0 if his coverage rate is

0.9456   or lower,   or

0.9542   or higher.

This approach, however, does not take advantage of the Central Limit Theorem, which we may do since

$$np = (10000)(0.95) > 10 \quad \text{and}$$
$$n(1-p) = (10000)(0.05) > 10.$$

Under H_0, $\hat{\pi} \sim \text{Norm}(0.95, \sqrt{(0.95)(0.05)/10000})$, approximately. Solving

$$\frac{\hat{\pi} - 0.95}{\sqrt{(0.95)(0.05)/10000}} \geq 1.96 \quad \Longrightarrow \quad \hat{\pi} \geq 0.9543$$

$$\frac{\hat{\pi} - 0.95}{\sqrt{(0.95)(0.05)/10000}} \leq -1.96 \quad \Longrightarrow \quad \hat{\pi} \leq 0.9457$$

approximately the same values as above.

4.28 (a) The sample mean is in the center of the confidence interval:

$$\bar{x} = \frac{1}{2}(11.2 + 54.7) = 32.95$$

(b) The hypothesized value for "no weight gain", 0, is outside the 95% confidence interval. That means that, under $H_0: \mu = 0$, with $\alpha = 0.05$, $\bar{x} = 32.95$ is in the rejection region — so the P-value is < 0.05.

4.29 This is completely wrong. The 95% CI changes with the sample, and shrinks in width as the sample size n grows. If 10 different studies offered 10 different 95% CIs, your biologist friend would be contradicting himself making such a statement about each of the CIs.

4.32. Given that $E(\hat\theta^2) = \theta^2$, we have

$$Var(\hat\theta) = E(\hat\theta^2) - E(\hat\theta)^2$$

$$\Rightarrow E(\hat\theta) = \sqrt{E(\hat\theta^2) - Var(\hat\theta)} = \sqrt{\hat\theta^2 - Var(\hat\theta)},$$

and this latter expression is $\hat\theta$ only when $Var(\hat\theta) = 0$ (an uninteresting case).

4.34 Assuming the second sample is independent from the first, we have

$$Var(\bar{X} - \bar{Y}) = Var(\bar{X}) + Var(\bar{Y}) = \frac{\sigma^2}{n} + \frac{\sigma^2}{n} = \frac{2}{n}\sigma^2, \text{ and}$$

$\bar{X} - \bar{Y} \sim Norm(0, \sigma\sqrt{\frac{2}{n}})$. The lower and upper bounds of the 95% CI are positions in $Norm(0, \sigma\sqrt{2}/\sqrt{n})$ which correspond to standardized Z-scores

$$Z = \pm \frac{1.96\, \sigma/\sqrt{n}}{\sigma\sqrt{2}/\sqrt{n}} = \pm \frac{1.96}{\sqrt{2}}.$$

The probability, then, that $\bar{Y}$ is inside the 95% CI is

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> pnorm(1.96/√2) - pnorm(-1.96/√2),
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which is 0.8342.

4.44 The command

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> favstats(~ Sepal.Width | Species, data = iris)
> qt(0.975, df = 49)
```

tell us that the critical value $t^* = 2.0096$, and

Species	$\bar{x}$	s	n	95% CI
setosa	3.428	0.3791	50	(3.320, 3.536)
versicolor	2.770	0.3138	50	(2.681, 2.859)
virginica	2.974	0.3225	50	(2.882, 3.066)

The final column of confidence intervals are computed as

$$\bar{x} \pm t^* \frac{s}{\sqrt{50}}.$$

Since there is no overlap between CIs, it seems reasonable to expect the (population) mean sepal width is different across each of the 3 species.