9.4b Appendix: Investigating Power with R

by EV Nordheim, MK Clayton & BS Yandell, October 30, 2003

We can use R to investigate power. We already have several tools for this. These commands for questions about the population mean when the variance is known (`pnorm` and `qnorm` from Appendix 4.4) or unknown (`pt` and `qt` from Appendix 6.9). In addition, we have briefly studied p-values in Chapter 6. Below we redo some examples from this chapter, and then show a property of p-values under a null and alternative.

9.4b.1 Power curve

A power curve helps is evaluate our chances of rejecting the null hypothesis when it is false. Reconsider the foresters' problem, where the null hypothesis is $H_0 : \mu = 75$, or $\bar{X} \sim N(75, 21^2/15)$ based on random samples of 15 seedlings. The foresters posed the question: what is the probability of rejecting H_0 if the true terminal shoot mean length is something other than 75? Under the null hypothesis, the 5% rejection region is defined by

```
> n = 15
> pop.sd = 21
> SD = pop.sd/sqrt(n)
> SD

[1] 5.422177

> mu = 75
> region = qnorm(c(0.025, 0.975), mu, SD)
> region

[1] 64.37273 85.62727
```

That is, we reject H_0 if $\bar{X}$ is below 64.37 or above 85.63.

The power for alternative $H_A : \mu = 80$ can be found by determining the tail probabilities for each rejection region

```
> mu = 80
> pnorm(region[1], mu, SD)

[1] 0.001975154

> pnorm(region[2], mu, SD, lower.tail = FALSE)

[1] 0.1496757
```

and adding them together to get 0.1517.

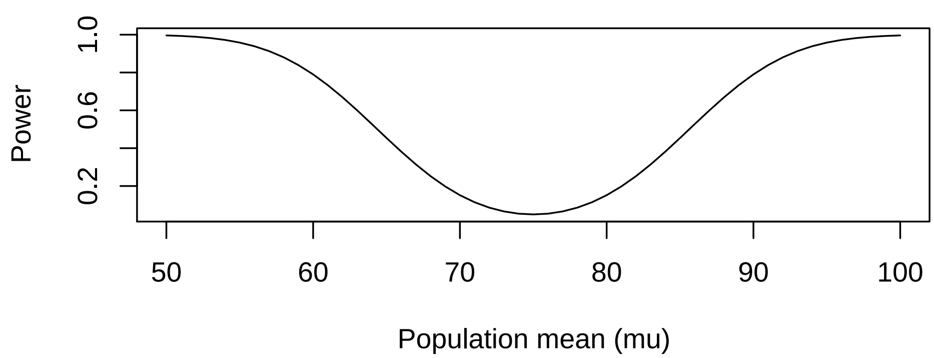
We can reproduce the power curve table in Section 9.2.1, up to roundoff error, with the following commands. Here `mus` is a sequence (using the `seq` command) of 55, 60, $\cdots$, 95. The `power` is calculated as above using the `pnorm` command. The `cbind` command just binds these together as two columns in a table.

```
> mus = seq(55, 95, by = 5)
> cbind(mu = mus, power = pnorm(region[1], mus, SD) + pnorm(region[2],
+     mus, SD, lower.tail = FALSE))
```

```
      mu     power
 [1,] 55 0.9580589
 [2,] 60 0.7900102
 [3,] 65 0.4540217
 [4,] 70 0.1516509
 [5,] 75 0.0500000
 [6,] 80 0.1516509
 [7,] 85 0.4540217
 [8,] 90 0.7900102
 [9,] 95 0.9580589
```

In addition, we can reproduce the power curve plot by filling in a bit more (now `mus` steps through every 1 percent). The `plot` command plots the `mus` against the `power` (again calculated using two calls to `pnorm`). The other options to `plot` make the curve into a line (`type="l"`) and provide axis labels (`xlab` and `ylab`).

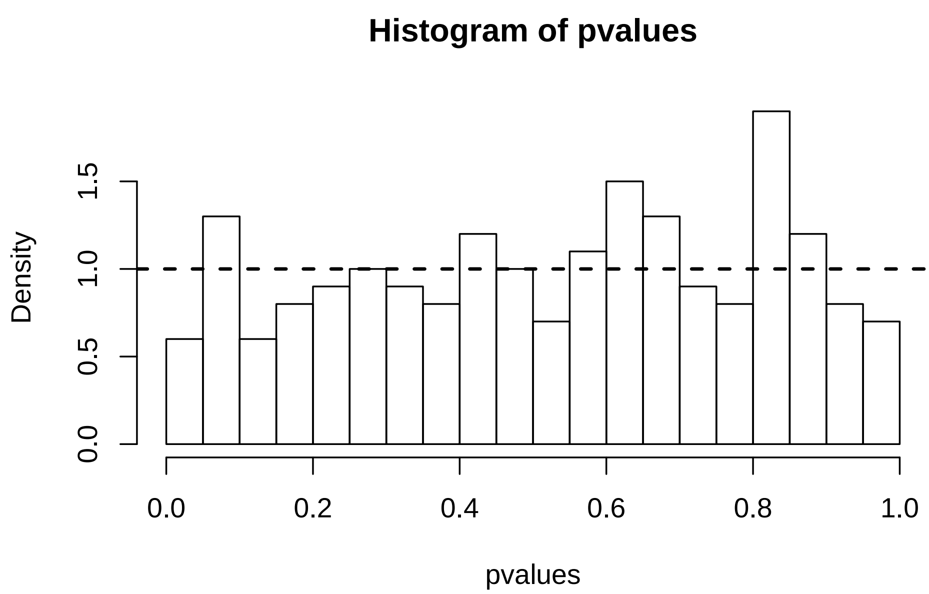
```
> mus = seq(50, 100, by = 1)
> plot(mus, pnorm(region[1], mus, SD) + pnorm(region[2], mus, SD,
+     lower.tail = FALSE), type = "l", xlab = "Population mean (mu)",
+     ylab = "Power")
```



9.4b.2 Histograms of p-values (optional)

What shape is a histogram of p-values? First draw samples of size 18 of simulated white pine seedlings from $N(40, 100)$ and use a T-test to find evidence whether $\mu = 40$ or not as in Appendix 6.9.2. Here is a density-scaled histogram of the p-values for the test of $\mu = 40$, with a horizontal dashed line corresponding to an exact uniform distribution.

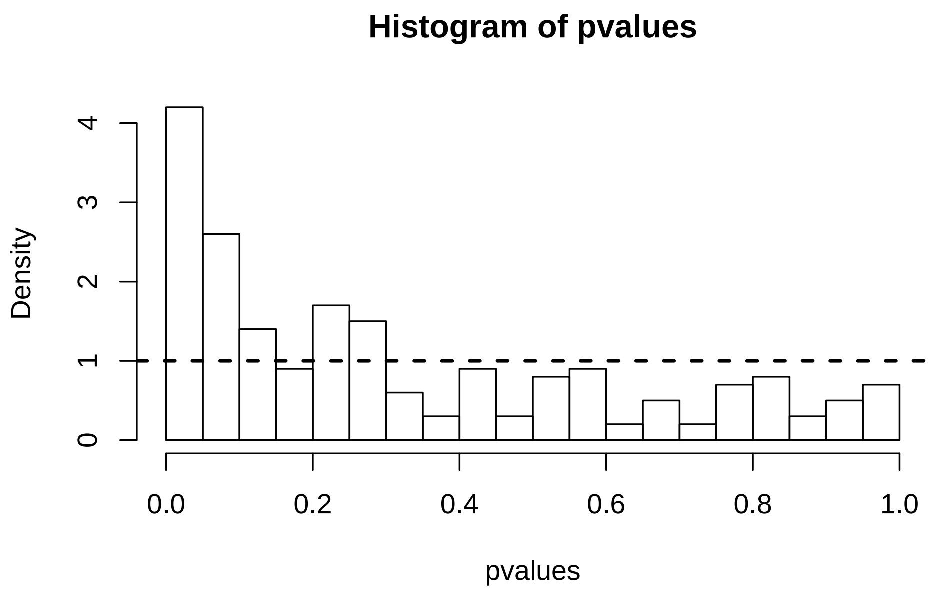
```
> n.draws = 200
> mu = 40
> pop.sd = 10
> n = 18
> draws = matrix(rnorm(n.draws * n, mu, pop.sd), 18)
> get.p.value = function(x) t.test(x, mu = 40)$p.value
> pvalues = apply(draws, 2, get.p.value)
> hist(pvalues, breaks = 20, prob = TRUE)
> abline(h = 1, lwd = 2, lty = 2)
```



In this sample from the null $H_0 : \mu = 40$, there are 33 of 200 p-values less than or equal to 0.20.

Suppose the random draws have mean $\mu = 37$ instead of 40? Below is a histogram of p-values for the test of $H_0 : \mu = 40$ when the mean is actually from the alternative $H_A : \mu = 37$. The horizontal dashed line is added to indicate roughly what a histogram would look like if the null hypothesis were true. But in this case, the null is false. Notice how the distribution skews toward small p-values. That is, we are more likely to get very small p-values than we would expect by chance under H_0. This would lead us to reject the null hypothesis

```
> mu = 37
> draws = matrix(rnorm(n.draws * n, mu, pop.sd), 18)
> pvalues = apply(draws, 2, get.p.value)
> hist(pvalues, breaks = 20, prob = TRUE)
> abline(h = 1, lwd = 2, lty = 2)
```



In this sample from the alternative $H_A : \mu = 37$ there are 91 of 200 p-values less than or equal to 0.20.