

Power Analysis with R Examples

Problem 1

It is believed that about 10% of the population is left-handed. However, China has claimed that less than one percent of its students are left-handed. Suppose we are interested in evaluating whether there is something special about Chinese people, or whether the Chinese government is lying. Suppose further that we have devised a scientifically perfect test to measure a person's dominant hand. Would a random sample of 50 Chinese students be large enough to detect a population difference of 10% vs. 1%?

Step 1

Identify the parameter of interest and its value under the null and alternative hypothesis.

The parameter of interest is p = the proportion of all Chinese students who are left-handed. We have two possible values of p that we are considering. If the Chinese population looks like the rest of the world, we would expect $p = 0.1$. If the Chinese population is different from the rest of the world, we would expect $p = 0.01$.

Remember that the null hypothesis is that nothing unexpected is happening. Generally, this will mean “no effect” or “no difference.” In this case, “no difference” would suggest that the Chinese population is not different from the rest of the world, and $p = 0.1$. The alternative hypothesis is that something unexpected (which we would like to detect) is happening. In this case, “something different is happening” would suggest that the Chinese population is different, and $p = 0.01$.

Step 2

Construct the distribution of a test statistic under the null hypothesis.

Here we use the test statistic X = number of people in our sample who are left-handed. X has a binomial distribution. Since we have a sample size of 50, $n = 50$, and by H_0 , $p = 0.1$. Thus, under H_0 , $X \sim B(50, 0.1)$.

Step 3

Using a standard α value ($\alpha = 0.05$ or $\alpha = 0.01$) and your distribution, obtain the critical region.

Let's use $\alpha = 0.05$. First, we set up all of the known information in the problem.

```
alpha <- 0.05
n <- 50
p0 <- 0.1
p1 <- 0.01
```

Next, we use the `qbinom` command to find the critical region:

```
qbinom(alpha, n, p0)
```

```
## [1] 2
```

Note that since our alternative value of $p = 0.01$ is less than our null value of $p = 0.1$, we use the default argument `lower.tail = TRUE`.

According to R, our critical value is 2. Since `lower.tail = TRUE`, this corresponds to a region of $X \leq 2$. We check to see if $P(X \leq 2) \leq 0.05$:

```
pbinom(2, n, p0)
```

```
## [1] 0.1117288
```

$P(X \leq 2) = 0.112$, which is too big. Therefore, our critical region is $X < 2$, or equivalently, $X \leq 1$. We check to make sure:

```
pbinom(1, n, p0)
```

```
## [1] 0.03378586
```

$P(X \leq 1) = 0.034$, so we do indeed have the correct critical region now.

Step 4

Find the probability of the test statistic being in the critical region under the *alternative* hypothesis.

Since we know the critical region, all we need to do is change the probability p from p_0 to p_1 :

```
pbinom(1, n, p1)
```

```
## [1] 0.9105647
```

According to Rguroo, the probability of getting 1 or fewer left-handed students in our sample, if the Chinese government is telling the truth, is 0.91. Since this value is above 0.8, we say that 50 students is a large enough sample size for us to detect the difference we want to observe.

Problem 2

In a clinical trial for a cancer drug (Creelan *et al.*, 2019), researchers hypothesized that if the drug were ineffective, 26% of patients would be progression-free after 6 months. A clinically relevant increase in progression-free survival would be doubling that rate to 52%. The study was able to enroll 14 patients. Is this a large enough sample to detect that clinically relevant increase?

Step 1

Identify the parameter of interest and its value under the null and alternative hypothesis.

The parameter of interest is p = the proportion of all cancer patients on this drug who would be progression-free after 6 months. We have two possible values of p that we are considering. If the drug is ineffective, we would expect $p = 0.26$. If the drug has a “clinically relevant” effect, we would expect $p = 0.52$.

Remember that the null hypothesis is that nothing unexpected is happening. Generally, this will mean “no effect” or “no difference.” In this case, “no difference” would suggest that the drug is ineffective, and $p = 0.26$. The alternative hypothesis is that something unexpected (which we would like to detect) is happening. In this case, “something different is happening” would suggest that the drug is effective, and $p = 0.52$.

Step 2

Construct the distribution of a test statistic under the null hypothesis.

Here we use the test statistic X = number of patients in our sample who are progression-free after 6 months. X has a binomial distribution. Since we have a sample size of 14, $n = 14$, and by H_0 , $p = 0.26$. Thus, under H_0 , $X \sim B(14, 0.26)$.

Step 3

Using a standard α value ($\alpha = 0.05$ or $\alpha = 0.01$) and your distribution, obtain the critical region.

Let's use $\alpha = 0.05$. First, we set up all of the known information in the problem.

```
alpha <- 0.05
n <- 14
p0 <- 0.26
p1 <- 0.52
```

Next, we use the `qbinom` command to find the critical region:

```
qbinom(alpha, n, p0, lower.tail = FALSE)
```

```
## [1] 6
```

Note that since our alternative value of $p = 0.52$ is greater than our null value of $p = 0.26$, we use the argument `lower.tail = FALSE`.

According to R, our critical value is 6. Since `lower.tail = FALSE`, this corresponds to a region of $X > 6$, or equivalently, $X \geq 7$. We check to see if $P(X > 6) \leq 0.05$:

```
pbinom(6, n, p0, lower.tail = FALSE)
```

```
## [1] 0.04668765
```

$P(X > 6) = 0.047$, which is just smaller than our *alpha* value. Therefore, our critical region is $X > 6$, or equivalently, $X \geq 7$. We check to make sure that we do not want $X \geq 6$:

```
pbinom(5, n, p0, lower.tail = FALSE)
```

```
## [1] 0.1301036
```

$P(X > 5) = 0.130$, which is too large, so $X > 6$ is indeed the correct critical region now.

Step 4

Find the probability of the test statistic being in the critical region under the *alternative* hypothesis.

Since we know the critical region, all we need to do is change the probability p from p_0 to p_1 :

```
pbinom(6, n, p1, lower.tail = FALSE)
```

```
## [1] 0.662034
```

According to R, the probability of getting 7 or more progression-free patients in our sample, if the drug is effective, is 0.66. Since this value is less than 0.8, we say that 14 patients is not a large enough sample size for us to detect the clinically relevant difference.