

We let $\beta = P(\text{fail to reject } H_0|H_0 \text{ is false}) = P(\text{Type II error})$, then Power = $P(\text{reject } H_0|H_0 \text{ is false}) = 1 - \beta$.

Power depends on the distance between the hypothesized value of the parameter θ_0 and the actual value θ_1 , so we can write $1 - \beta(\theta_1)$.

Why is power important?

- 1. If you have multiple statistical testing methods for the same hypothesis, choose test that is the most powerful.
- 2. If you are going to spend time/morey to do an experiment, need to check beforehand that your study will be ponerful emough to detect an effect.

2.3 Power 13

For a few simple cases, you can derive a closed form expression of power.

All others: use Monte Carlo methods to estimate power.

Example 2.4 Consider a one-sample z-test. Sample $X_1, \ldots, X_n \stackrel{iid}{\sim} N(\mu, \sigma^2)$.

Ho: $\mu = \mu_b$ vs. $H_a! \quad \mu > \mu_b$.

Using statific $Z^* = \frac{\pi - \mu_b}{\epsilon / \epsilon_n}$, we right H_b if $Z^* > Z_{loc}$

If Mo=5 (hypothesized value) but the true mean is M = 6, What is the probability of correctly ejectly to : m=5? This is fower!

Effect size: $\mu_1 - \mu_0 = 6 - 5 = 1$. If the effect size is 10, our test will have more power (earlier to detect the touth).

For the Z-test, he can derin power (Chihara & Hesterberg p. 229-230).

So power is a function of

- 1. Significance level: as at , power of [trade off btv/ Type I ad Type II error]
- 2. Effect size = Mi-Mo. as effect size), power ?
- Sample size: as no pour T
- variance: as voriance I, power I (no control over this in practice).

Notes (1) as power = 1-B 1, P(type I error) = a 1. for fixed n, 6, i M,-no, the only way to power is to Td.

(2) Only way to simultaneously I power & I a, must

direction depends

2.4 MC Estimator of $1 - \beta$

Assume $X_1, \ldots, X_n \sim F(\theta_0)$ (i.e., assume H_0 is true).

Then, we have the following hypothesis test -

$$H_0: heta = heta_0 \ H_a: heta > heta_0$$

and the statistics T^* , which is a test statistic computed from data. Then we **reject** H_0 if $T^* >$ the critical value from the distribution of the test statistic.

This leads to the following algorithm to estimate the power of the test $(1 - \beta)$

Sample
$$X_1^{(j)}$$
, ..., $X_n^{(j)}$ from model under the alternative hypothesis $\theta = \theta_1$.

e.g. $1\{T_j > crit value\}$

(5) Compute
$$1-\beta = \frac{1}{m} \sum_{i=1}^{m} y_i$$
 (i.e. count # of correct answers)

Your Turn

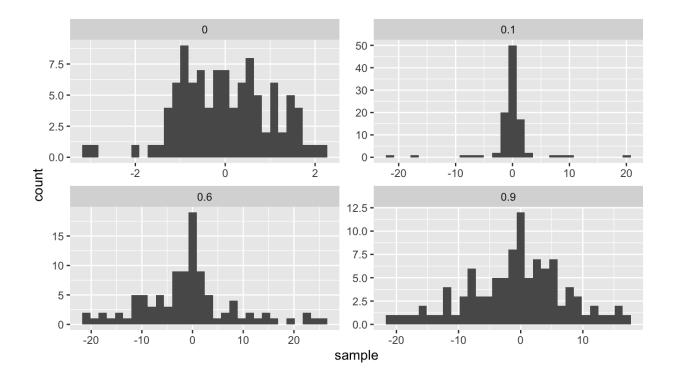
Consider data generated from the following mixture distribution:

$$f(x) = (1-\epsilon)f_1(x) + \epsilon f_2(x), \quad x \in \mathbb{R}$$

where f_1 is the pdf of a N(0,1) distribution, f_2 is the pdf of a N(0,100) distribution, and $\epsilon \in [0,1]$.

```
r_noisy_normal <- function(n, epsilon) {
  z <- rbinom(n, 1, 1 - epsilon)
  z*rnorm(n, 0, 1) + (1 - z)*rnorm(n, 0, 10)
}

n <- 100
data.frame(e = 0, sample = r_noisy_normal(n, 0)) %>%
  rbind(data.frame(e = 0.1, sample = r_noisy_normal(n, 0.1))) %>%
  rbind(data.frame(e = 0.6, sample = r_noisy_normal(n, 0.6))) %>%
  rbind(data.frame(e = 0.9, sample = r_noisy_normal(n, 0.6))) %>%
  rbind(data.frame(e = 0.9, sample = r_noisy_normal(n, 0.9))) %>%
  ggplot() +
  geom_histogram(aes(sample)) +
  facet wrap(.~e, scales = "free")
```



We will compare the power of various tests of normality. Let F_X be the distribution of a random variable X. We will consider the following hypothesis test,

 $H_0: F_x \in N \qquad ext{vs.} \qquad H_a: F_x
otin N,$

i.e. the says X is normly distributed and the says it isnut.

where N denotes the family of univariate Normal distributions.

Recall Pearson's moment coefficient of skewness (See Example 2.2). and cordsponding

We will compare Monte Carlo estimates of power for different levels of contamination ($0 \le \epsilon \le 1$). We will use $\alpha = 0.1$, n = 100, and m = 100.

```
# skewness statistic function
skew <- function(x) {</pre>
  xbar <- mean(x)
  num \leftarrow mean((x - xbar)^3)
  denom \leftarrow mean((x - xbar)^2)
  num/denom<sup>1.5</sup>
}
# setup for MC
alpha <- .1
n < -100
m < -100
epsilon \leftarrow seq(0, 1, length.out = 200)
var sqrt b1 \leftarrow 6*(n - 2)/((n + 1)*(n + 3)) # adjusted variance for
 skewness test
crit val <- qnorm(1 - alpha/2, 0, sqrt(var sqrt b1)) #crit value for</pre>
 the test
empirical pwr <- rep(NA, length(epsilon)) #storage</pre>
# estimate power for each value of epsilon
for(j in 1:length(epsilon)) {
  # perform MC to estimate empirical power
  ## Your turn
}
## store empirical se
empirical_se <- "Your Turn: fill this in"</pre>
## plot results --
## x axis = epsilon values
## y axis = empirical power
## use lines + add band of estimate +/- se
```

we can detect contamination levels between .015 and .15 at power z 0.8 when n=100. -> & is like the effect size (distance from 0).

Compare the power with n=100 to the power with n=10. Make a plot to compare the two for many values of ϵ .

Recall pat power depends on 3 things:

- 2) sample size n
- (3) effect size,

When n=10, power is < 0.8 for all lends of E.