

Consider a hypothesis test about the parameter θ :

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

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 $1 - \beta(\theta_1)$.

the effect size.

Why is power important?

- 1. If we have multiple statistical festing methods for the same hypothesis (similar size) choose test that is the most powerful.
- 2. If we are goly to spend time/money to run an experiment, need to check beforehand that the study is powerful enough to detect an effect.

2.3 Power

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

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

Ho: $\mu = \mu_0$ Ho: $\mu = \mu_0$ Using statistic $Z^* = \frac{\bar{x} - \mu_0}{6/\tau_0}$, where reject the if $Z^* > Z_{1-\alpha}$ control where $\chi_1 = \chi_2 = \chi_3 = \chi_4 = \chi_4 = \chi_5 =$

$$|-\beta| = P(reject Ho | Ho is false)$$

$$= P(Z^* > Z_{1-q} - \frac{(\mu_1 - \mu_0)}{6/6})$$

So power is a function of

Smillest Z where you will right Ho.

- (1.) Significance level: as &1, power 1 (trade-off between type I and type I error).
- 2. Effect size: M.-M. as effect size 1, power 1.
- 3.) Sample size: as no, power T
- 4. Variance: as variance to power? (no control over this in practice).

Notes: (Das porce = 1-BT, P(type I error) = al. For fixed n, o, & Mi-Mo,
the only way to increase power is to 9 a

2) Only way to simultaneously 1 pour + dod, must 1 n. (fixed effect size).

new

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 $(1 - \beta)$

$$(x, \alpha)$$
 Sample (x, α) , (x, α) from model under the alternative hypothesis (x, α) (x, α)

Your Turn

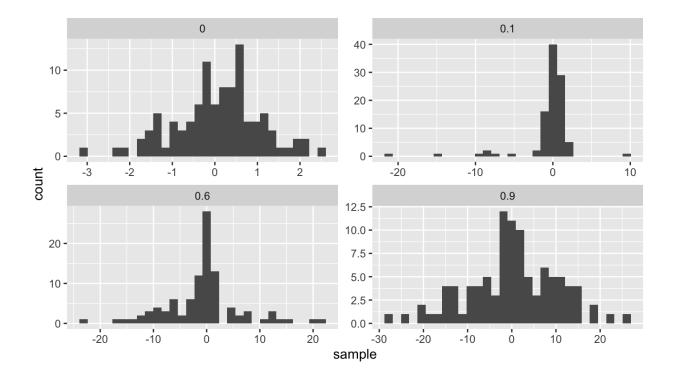
Consider data generated from the following mixture distribution:

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

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, 0.9))) %>%
  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, i.e. Ho says x is Normlly distributed and Ha says it isn't.

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

where N denotes the family of univariate Normal distributions.

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

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.

```
H_0: \sqrt{\beta_1} = 0
   # skewness statistic function
                                                                Ha: JB, 70.
   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 < 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
   }
                                                     \int \hat{\rho} (1-\hat{\rho})/m
   ## store empirical se
   empirical se <- "Your Turn: fill this in"
   ## plot results --
   ## x axis = epsilon values
   ## y axis = empirical power
   ## use lines + add band of estimate +/- se
     can detect contamination levels between 003 to .14 at pover 2.8 when n=100
We
```

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

for what levels of contamination (E) will be have power = 0,8

Recall pour dyeds on.

(1) led of test
(2) scriple size
(3) effect size
(4) variance.

When N=10, power < 0.8 for all leads of Σ .