

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 $1 - \beta(\theta_1)$.

— Ceffect size. Why is power important?

- 1. If we have multiple statistical testing methods for the same hypothesis, choose lest that has highest power.
- 2. If you are going to spend time / money to do on experiment, reed to check beforehard that your study will be powerful enough to do test an effect.

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

All others: use Monte calo methods to estimate power.

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

Ho: M=Mo Us. Ha: M > Mo.

Using statistic Z* = \frac{\pi}{5/\sigma} crit. valve

We reject to if Z*> Z1-0

If No = 5 (hypothesized value) but true mean M, = 6.

What is probability of correctly rejecting to: M=5? This is Power!

Effect size: pl, -plo = 6-5=1. If effect size is 10, our test would have

easile to detect the fruth!

For Z-test we can analytically derive power (Chihara & blestoberg p. 229-230).

$$|-\beta = \beta(\text{reject Ho } | \text{Ho is fulse})$$

$$= \beta(Z^* > Z_{1-d} - \frac{(\mu_1 - \mu_0)}{6/5n})$$

So power is a function of

smallest Z-value when you will reject the

- 1. Significance level: as 29, power 1 (trade-off box/ Type I and Type II error)
- 2. Effect size: MI-NO as effect size P, pover 9
- 3. Sample size: as NT pover T
- 4. Variance: as variance 1, power / (no control over this impractice).

Notes: (1) as power=1-pT, $P(tyre\ Ierrar) = \alpha 9$. For fixed 1,6, $\frac{1}{2}\mu_1 - \mu_0$ the only way to inexast power is to 1d.

(2) Only way to s. multaneously I power & La is 9 n.

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 $(1-\beta)$

- 1) Select model, setup hypothesis test.
- (2) Select value of alterative O,
- 3) Set n, oper paran values (e.g. 62), and of
- (4) For each j=1,..., M
 - a) Sample X(i), --, Xn from model under alternative hypothesis $\theta = \theta_1$
 - b) Compute Tx(i) based on data from Ca)
 - c) compute y; = I { reject to based on T*(j)}.
- (5) Compute $1-\hat{\beta} = \frac{1}{M} \sum_{j=1}^{M} y_j$ (i.e. count # of correct answers).

Your Turn

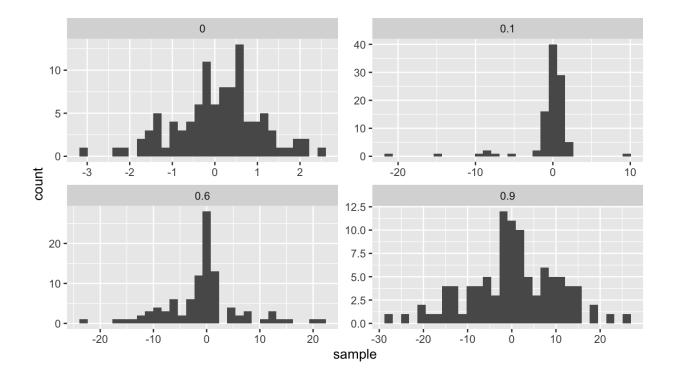
Consider data generated from the following mixture distribution:

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

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, 0.9))) %>%
  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,

The consider the following hypothesis test,
$$H_0: F_x \in N \qquad \text{vs.} \qquad H_a: F_x \notin N,$$

$$H_a: F_x$$

where N denotes the family of univariate Normal distributions.

 $0 \le \epsilon \le 1$). We will use $\alpha = 0.1$, n = 100, and m = 100.

Recall Pearson's moment coefficient of skewness (See Example 2.2). Ho: $\sqrt{\rho_1} = 0$ Ha: $\sqrt{\beta_1} \neq 0$. We will compare Monte Carlo estimates of power for different levels of contamination (

```
# 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
}
                                          3E(p)= [p(1-p) | m
## 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
```

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 that power depends on 3 things:

(1) level of the test &

(2) sample size n

(3) effect size

for N=100 tre can detect contemination levels between .015 and o15 at pone = 0.8 (E x effect size).

For n=10, power < 0.8 for all values of E.